

METHODS OF TREATING GLAUCOMA

RELATED APPLICATION DATA

5 The present application claims priority from Australian Patent Application No. 2022900727 filed on 23 March 2022 entitled “Methods of Treating Glaucoma”, the entire contents of which is hereby incorporated by reference.

SEQUENCE LISTING

10 The present application is filed together with a Sequence Listing in electronic form. The entire contents of the Sequence Listing are hereby incorporated by reference.

TECHNICAL FIELD

15 The present disclosure generally relates to methods of treating, preventing and/or delaying progression of glaucoma in a subject, the method comprising administering an antisense oligonucleotide that modulates mRNA translation, stability, and productive transcript of *OPA1* gene transcript or part thereof.

BACKGROUND

20 Glaucoma, a progressive optic neuropathy and the leading cause of blindness, is characterized by impairment or degeneration of retinal ganglion cells (RGCs), which transmit visual information to the brain. Currently, about 80 million people are affected by glaucoma worldwide, and this number is expected to increase to over 120 million by 2040. The prevalence of glaucoma increases with aging, and this increase is strongly affected by the African and Asian populations.

25 Glaucoma can be triggered when the aqueous humour builds up in the front part of the eye. Excess production or reduced draining of the aqueous humour increases the intraocular pressure (IOP), which irreversibly damages the optic nerve and RGCs. Glaucoma can be classified as either primary or secondary, with secondary glaucoma attributable to another disorder or problem within the eye, such as injury, surgery, drugs, or other ocular diseases. 30 Primary glaucoma is classified as open-angle glaucoma (POAG), normal-tension glaucoma (NTG), angle-closure glaucoma and congenital glaucoma. Secondary glaucoma is classified into neovascular glaucoma, pigmentary glaucoma, exfoliation glaucoma and uveitic glaucoma. In all subtypes of glaucoma, the gradual loss of RGCs is the hallmark. RGC dysfunction and death lead to vision impairment and ultimately blindness.

35 There is no approved treatment for glaucoma that directly targets RGCs. Of the drugs that have been clinically studied for neuroprotective activity and to reduce vision loss in POAG patients, e.g. brimonidine and memantine, none have conclusively proven effective thus far. Instead, the only available treatments to reduce IOP levels are indirectly protective for RGCs.

Further, it has been reported that in about one-third of cases of glaucoma the characteristic optic nerve changes and visual field loss can develop in an eye with normal IOP levels. Therefore, there is an urgent need to identify therapeutic strategies for RGC neuroprotection to limit the projected burden of vision impairment and blindness from glaucoma. The use of neurotrophic factors such as brain derived-, ciliary derived-, glial cell derived, and nerve growth factor has been a focus of recent research for it is known to prevent uncontrolled RGCs loss and aid to the cell viability. However, their effectiveness is limited by a relatively short half-life, insufficient permeability, and poor concentrations in target RGCs.

Therefore, there remains a need for new interventions for treating, preventing and/or delaying progression of glaucoma.

SUMMARY

In producing the present invention, the inventors identified optic atrophy gene 1 (OPA1) as a potential target for pharmacological intervention for treating or preventing glaucoma. The inventors have identified antisense oligonucleotides (ASOs) that increase expression of OPA1 expression that are useful for the treatment or prevention of glaucoma. The inventors have identified ASOs that rely on any of a variety of mechanisms of action to upregulate OPA1 expression. For example, an ASO identified by the inventors increase OPA1 expression by:

- Binding to an *OPA1* gene pre-mRNA in a cell to promote exclusion of a nonsense-mediated RNA decay-inducing (NMD) exon during splicing of the *OPA1* pre-mRNA to increase the level of *OPA1* mRNA transcripts encoding full length, functional OPA1
- Binding to the 5' untranslated region (UTR) of an *OPA1* gene transcript in a cell to increase translation efficiency and /or transcript stability of an OPA1 mRNA
- Binding to the 3' UTR of an *OPA1* gene transcript in a cell to increase transcript stability of an *OPA1* mRNA

These findings additionally provide the basis for methods of treating, preventing and/or delaying progression of glaucoma.

Accordingly, the present disclosure provides a method of treating, preventing and/or delaying progression of glaucoma in a subject, the method comprising administering an antisense oligonucleotide that increases functional OPA1 protein levels in the subject. For example, the level of OPA1 protein is increased in the subject compared to the level in the subject prior to administration of the OPA1.

In one example, the ASO increases the level of *OPA1* mRNA and the amount of functional OPA1 protein in a cell and/or a tissue of the subject. For example, the ASO increases the level of *OPA1* mRNA in a cell and/or a tissue of the subject. In another example, the ASO increases the amount of functional OPA1 protein in a cell and/or a tissue of the subject.

In one example, the amount of functional OPA1 protein in the cell and/or the tissue is increased by about 1.1 to about 10-fold. For example, the amount of functional OPA1 protein

in the cell and/or the tissue is increased by about 1.5 to about 10-fold, about 2 to about 10-fold, about 3 to about 10-fold, about 4 to about 10-fold, about 1.1 to about 5-fold, about 1.1 to about 6-fold, about 1.1 to about 7-fold, about 1.1 to about 8-fold, about 1.1 to about 9-fold, about 2 to about 5-fold, about 2 to about 6-fold, about 2 to about 7-fold, about 2 to about 8-fold, about 2 to about 9-fold, about 3 to about 6-fold, about 3 to about 7-fold, about 3 to about 8-fold, about 3 to about 9-fold, about 4 to about 7-fold, about 4 to about 8-fold, about 4 to about 9-fold, at least about 1.1-fold. For example, the amount of functional *OPA1* protein in the cell and/or the tissue is increased by at least about 1.5-fold, at least about 2-fold, at least about 2.5-fold, at least about 3-fold, at least about 3.5-fold, at least about 4-fold, at least about 5-fold, or at least about 10-fold. For example, the amount of functional *OPA1* protein in the cell and/or the tissue is increased compared to the level in the tissue prior to the administration or contact. In one example, administration to a subject or contact with cells with any of the ASOs or pharmaceutical compositions disclosed herein increases the level of *OPA1* protein about 1.1 to about 2.5-fold compared to the level in the tissue prior to the administration or contact.

In one example, the cell and/or tissue is selected from the group consisting of an ocular tissue, retinal pigment epithelium (RPE) cells, Müller glial cells, endothelial cells, glial cells, astrocytes, photoreceptors. For example, the cell and/or tissue is selected from the group consisting of the retina, RPE cells and combinations thereof.

In one example, the ASOs bind to a targeted portion of:

- (i) an *OPA1* gene pre-mRNA in a cell to promote exclusion of a nonsense-mediated RNA decay-inducing (NMD) exon during splicing of the *OPA1* pre-mRNA to increase the level of *OPA1* mRNA transcripts encoding full length, functional *OPA1*;
- (ii) the 5' untranslated region (UTR) of an *OPA1* gene transcript in a cell to increase translation efficiency of an *OPA1* mRNA;
- (iii) the 5' UTR of an *OPA1* gene transcript in a cell to increase transcript stability, e.g., by inhibiting the activity of a decapping enzyme; and/or
- (iv) the 3' UTR of an *OPA1* gene transcript in a cell to increase transcript stability, e.g., by preventing binding of a miRNA to the 3' UTR.

In one example, the ASOs binds to a targeted portion of an *OPA1* pre-mRNA in a cell to promote exclusion of a NMD exon during splicing of the *OPA1* pre-mRNA to increase the level of *OPA1* mRNA transcripts encoding full length, functional *OPA1*.

In one example, the ASO binds to a targeted portion of intron 7 *OPA1* pre-mRNA. Exemplary ASOs bind within a targeted portion of *OPA1* pre-mRNA nucleotide sequence corresponding to one or more of **SEQ ID NO:1**.

In one example, the ASO binds to intron 7 of an *OPA1* gene pre-mRNA in a cell and increases the level of *OPA1* gene transcripts encoding full length, functional *OPA1* by exclusion of NMD exon 7x. For example, the ASO is within sufficient proximity to an acceptor site of exon 7x to promote exclusion of exon 7x in splicing of *OPA1* mRNA.

In one example, the ASO that binds to a targeted portion of intron 7 *OPAI* pre-mRNA comprises or consists of any one of **SEQ ID NOs: 2-54**.

In one example, the ASO that binds to a targeted portion of intron 7 *OPAI* pre-mRNA comprises or consists of any one of **SEQ ID NOs: 2-54** or **SEQ ID NOs: 2491-2503**.

5 In one example, the ASO that binds to a targeted portion of intron 7 *OPAI* pre-mRNA comprises or consists of any one of **SEQ ID NOs: 2491-2503**

In one example, the ASO binds to a targeted portion of the 5' UTR of an *OPAI* gene transcript in a cell to increase translation efficiency or transcript stability of an *OPAI* mRNA. For example, the ASO increases expression of OPA1 protein. Without being bound by theory or mode of action, such ASOs may sterically inhibit translation from upstream Open Reading Frames (uORF) start site and/or sterically inhibit secondary structure in the 5' UTR and/or inhibiting the activity of a decapping enzyme.

In one example, the ASO binds within a targeted portion of the 5' UTR of *OPAI* mRNA, wherein the targeted portion is within the nucleotide sequence corresponding to **SEQ ID NO:**
15 **55**.

In one example, the ASO that binds to a targeted portion of the 5' UTR of *OPAI* mRNA comprises or consists of any one of **SEQ ID NOs: 56-138**.

In one example, the ASO that binds to a targeted portion of the 5' UTR of *OPAI* mRNA comprises or consists of **SEQ ID NO: 112**.

20 In one example, the ASO binds to a targeted portion of the 3' UTR of an *OPAI* gene transcript in a cell to increase transcript stability of an *OPAI* mRNA. For example, the ASO increases expression of OPA1 protein. Without being bound by theory or mode of action, such ASOs may sterically inhibit binding of a miRNA to the 3' UTR.

In one example, the ASO binds within a targeted portion of the 3' UTR of *OPAI* mRNA, wherein the targeted portion is within the nucleotide sequence corresponding to **SEQ ID NO:**
25 **139**.

In one example, the ASO that binds to a targeted portion of the 3' UTR of *OPAI* mRNA comprises or consists of any one of **SEQ ID NOs: 140-2488**.

30 In one example, the nucleotide sequence of the ASO is at least 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% complementary to the nucleotide sequence of the targeted portion over the length of the ASO.

In one example, the ASO comprises a backbone modification. For example, the backbone modification comprises a phosphorothioate linkage or a phosphorodiamidate linkage. In one example, the ASO comprises a phosphorothioate linkage. In another example,
35 the ASO comprises a phosphorodiamidate linkage.

In one example, the ASO comprises a phosphorodiamidate morpholino, a locked nucleic acid, a peptide nucleic acid, a 2'-*O*-methyl, a 2'-Fluoro, or a 2'-*O*-methoxyethyl moiety. For example, the ASO comprises a phosphorodiamidate morpholino moiety. In another

example, the ASO comprises a locked nucleic acid. In a further example, the ASO comprises a 2'-*O*-methyl moiety. In one example, the ASO comprises a 2'-Fluoro moiety. In another example, the ASO comprises a 2'-*O*-methoxyethyl moiety.

5 In one example, the ASO comprises at least one modified sugar moiety. For example, each sugar moiety in the antisense oligonucleotide is a modified sugar moiety.

In one example, the ASO comprises a 2'-*O*-methoxyethyl moiety. For example, each nucleotide of the ASO comprises a 2'-*O*-methoxyethyl moiety.

10 In one example, the nucleotide sequence of the ASO consists of 10 to 50 nucleotides, 15 to 40 nucleotides, 18 to 40 nucleotides, 17 to 25 nucleotides, 20 to 35 nucleotides, 20 to 30 nucleotides, 22 to 30 nucleotides, 22 to 28 nucleotides, 24 to 30 nucleotides, 25 to 30 nucleotides, or 26 to 30 nucleotides. In one example, the nucleotide sequence of the ASO consists of 20 to 30 nucleotides. For example, the nucleotide sequence of the ASO consists of 17 nucleotides. In one example, the nucleotide sequence of the ASO consists of 19 nucleotides. In another example, the nucleotide sequence of the ASO consists of 21 nucleotides. In a further
15 example, the nucleotide sequence of the ASO consists of 22 nucleotides. In one example, the nucleotide sequence of the ASO consists of 23 nucleotides. In another example, the nucleotide sequence of the ASO consists of 24 nucleotides. In another example, the nucleotide sequence of the ASO consists of 25 nucleotides. In another example, the nucleotide sequence of the ASO consists of 26 nucleotides. In another example, the nucleotide sequence of the ASO consists of
20 27 nucleotides. In another example, the nucleotide sequence of the ASO consists of 28 nucleotides. In another example, the nucleotide sequence of the ASO consists of 29 nucleotides. In another example, the nucleotide sequence of the ASO consists of 30 nucleotides.

25 In one example, the ASO comprises one or more phosphorodiamidate morpholino moieties.

In one example of any method described herein, the ASO is linked to a functional moiety. The functional moiety can be covalently linked or non-covalently linked to the ASO. The functional moiety can be at the 5' end and/or 3' end of the ASO.

30 In some examples, the functional moiety comprises a delivery moiety. For example, the delivery moiety is selected from the group consisting of lipids, peptides, carbohydrates, and antibodies. An exemplary delivery moiety comprises a cell-penetrating peptide (CPP). The present disclosure additionally contemplates delivery moieties such as a N-acetylgalactosamine (GalNAc) moiety, a fatty acid moiety, or a lipid moiety.

In some examples, the functional moiety comprises a stabilising moiety.

35 The present disclosure additionally provides a pharmaceutical composition comprising an ASO of the disclosure, and a pharmaceutically acceptable excipient, for use in any method of the disclosure.

In one example, the ASO is complexed with a delivery nanocarrier. For example, the delivery nanocarrier is selected from the group consisting of: lipoplexes, liposomes, exosomes, inorganic nanoparticles, and DNA nanostructures. In one example, the delivery nanocarrier comprises a lipid nanoparticle (LNP) encapsulating the antisense oligonucleotide.

5 In one example of any method described herein, the ASO is formulated for a route of administration selected from the group consisting of intravitreal, suprachoroidal, subretinal, ciliary intramuscular, intravenous, intra-arterial, subcutaneous, and topical routes.

The present disclosure also provides use of an ASO in the manufacture of a medicament for treating, preventing and/or delaying progression of glaucoma in a subject, wherein the ASO
10 modulates mRNA translation of the *OPA1* gene transcript or part thereof.

The disclosure also provides a modified cell comprising an ASO of the disclosure for use in any method described herein. For example, the modified cell is a mammalian cell, such as a human cell.

The disclosure additionally provides an ASO that binds to a targeted portion of the
15 intron 7x of an *OPA1* gene transcript in a cell and increases the level of *OPA1* gene transcripts encoding full length, functional *OPA1* by exclusion of NMD exon 7x. For example, the ASO comprises or consists of any one of **SEQ ID NOs: 2-54**. In one example, the ASO comprises or consists of any one of **SEQ ID NOs: 2-54** or **SEQ ID NOs: 2491-2503**. In another example, the ASO comprises or consists of any one of **SEQ ID NOs: 2491-2503**.

20 The disclosure additionally provides an ASO that binds to a targeted portion of the 5' UTR of an *OPA1* gene transcript in a cell and increases transcript stability of an *OPA1* mRNA, e.g., by inhibiting the activity of a decapping enzyme.

In one example, the ASO comprises or consists of any one of **SEQ ID NOs: 56-138**.

The disclosure additionally provides an ASO that binds to a targeted portion of the 3'
25 UTR of an *OPA1* gene transcript in a cell and increases transcript stability of an *OPA1* mRNA, e.g., sterically inhibiting binding of a miRNA to the 3' UTR.

In one example, the ASO binds within a targeted portion of the 3' UTR of *OPA1* mRNA, wherein the targeted portion is within the nucleotide sequence corresponding to **SEQ ID NO: 139**.

30 In one example, the ASO that binds to a targeted portion of the 3' UTR of *OPA1* mRNA comprises or consists of any one of **SEQ ID NOs: 140-2488**.

The present disclosure additionally provides a method of treating a condition, the method comprising administering an ASO of the disclosure. In one example, the condition is associated with *OPA1* expression, e.g., reduced *OPA1* expression. In one example, the
35 condition is glaucoma. In another example, the condition is autosomal dominant optic atrophy.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 includes a series of graphical representations showing the binding sites for ASOs that increase OPA1 protein levels. (A) Schematic illustration of exon structure of OPA1 (Transcript ID: ENST00000361510), indicating start and stop codons and the regions of 5' UTR, NMD exon 7x (in case of unspliced) and 3' UTR. (B) Prediction for secondary structure of the 5' UTR of *OPA1* transcript (corresponding to **SEQ ID NO: 55**) using RNAfold web tool (<http://rna.tbi.univie.ac.at/cgi-bin/RNAWebSuite/RNAfold.cgi>). The free energy of the thermodynamic ensemble is -137.26 kcal/mol. ASOs 56-138 were designed, which target start codons of upstream open reading frames (uORFs), regulatory binding sites, inhibitory 5' UTR secondary structures and/or G-quadruplexes. (C) Exon 7x (black box) containing the premature termination codon (PTC), is located between exons 7 and 8 (not drawn to scale). ASOs (**SEQ ID NOs: 2-54**) were designed to target splicing regulatory elements within intron 7 (dash line, corresponding to **SEQ ID NO: 1**) to mediate exclusion of exon 7x during pre-mRNA splicing to increase productive *OPA1* transcript. (D) Schematic illustration of the 3' UTR (not drawn to scale) located in exon 31. ASOs were designed to hybridize with the transcript and mask/inhibit binding of miRNA(s) to prevent mRNA degradation and increase in OPA1 protein levels.

Figure 2 shows screening of PMOs (25 and 50 μ M) in ADOA patient fibroblasts. Patient fibroblasts were transfected for 48 hr with PMOs targeting removal of the OPA1 exon 7x as indicated. OPA1 transcript expression was assessed by digital droplet PCR (ddPCR) and normalised to *GAPDH*, *RPL27* and *SCL25A3* transcript levels. The OPA1 expression in untreated cells was set to 1.

Figure 3 shows screening of PMOs (50 and 100 μ M) in ADOA patient fibroblasts. (A) The western blot gel image shows expression of long and short OPA1 isoforms in patient fibroblasts transfected with PMOs targeting intron 7 of the OPA1 transcript at 48 hr. (B) The band intensity of OPA1 expression was normalised to beta-actin (assessed by ImageJ™). The OPA1 expression in untreated cells was set to 1.

Figure 4 is a schematic of the refinement of antisense oligonucleotides to improve OPA1 upregulation. (A) Illustration of OPA1 exons and the location of exon7x exists in the transcript. (B) Binding region of parental PMOs on OPA1 transcript upstream of exon7x. Exon 7x is not drawn to scale. (C) Binding region of daughter sequences with microwalk, nucleotide base substitution and lengthening to improve the efficacy of PMOs.

Figure 5 shows screening of cell penetrating peptide-conjugated PMOs (PPMOs) (5, 10 and 20 μ M) in ADOA patient fibroblasts. ADOA patient fibroblasts were transfected for 5 days with PPMOs targeting intron 7 of the OPA1 transcript as indicated. OPA1 transcript expression was assessed by ddPCR and normalised to *HPRT1*. The OPA1 expression in untreated cells was set to 1.

Figure 6 shows screening of PMOs targeting exon 7x exclusion (25 and 50 μ M) in ADOA patient fibroblasts. Patient fibroblasts were transfected in triplicates for 48 hr with

PMOs targeting removal of the *OPA1* exon 7x as indicated. Experiments were performed in 1-4 biological replicates as indicated with the number of data points within a bar graph. *OPA1* transcript expression was assessed by ddPCR and normalised to the *HPRT1* transcript level. The *OPA1* expression in untreated cells was set to 1.

5 **Figure 7** shows screening of 5' UTR PMOs (25 and 50 μ M) in ADOA patient fibroblasts. PMOs with **SEQ ID NOs: 78, 112 and 2500-2503** were transfected into ADOA patient fibroblasts in triplicates for 72 hr with PMOs targeting the 5' UTR of an *OPA1* mRNA. Western blot analysis was used to determine the upregulation of OPA1 protein in PMO-treated cells. The band intensity of OPA1 expression was normalised to HPRT1 (assessed by
10 ImageJ™). The OPA1 expression in untreated cells was set to 1. PMOs **SEQ ID NOs: 78, 112 and 2502** significantly increased OPA1 protein upregulation (greater than 1.3 fold) in patient fibroblasts. Student's *t* test was used for statistical analysis.

Figure 8 shows the PMO OPA1 H1A(+10+32)Imm10C>T (**SEQ ID NO: 112**) was conjugated with CPP for enhanced cell penetrating ability. The CPP-PMO (or PPMO) was
15 incubated for 7 days to dermal skin fibroblasts derived from ADOA patients containing OPA1 mutations c. 2708_2711delTTAG (patient 1) and c.985-1G>A (patient 2). The efficacy of PPMO-induced OPA1 upregulation was assessed using western blot assay. The results showed significant OPA1 protein upregulation in a dose dependent manner in 2 patients with distinct OPA1 mutations. Student's *t* test was used for statistical analysis.

20 **Figure 9** shows the mitochondrial functional improvement following PPMO treatment in ADOA patient-derived fibroblasts. A PMO OPA1 H1A(+10+32)Imm10C>T (**SEQ ID NO: 112**) was incubated to fibroblasts for 7 days in a 6-well plate format. Upon day 7, cells were trypsinised and reseeded into a 96-well plate at 8,000 cells/well and incubated in glucose-depleted DMEM cell culture media supplemented with 2.5 mM 2-deoxy-D-glucose and 5mM
25 pyruvate for 18 hrs. A CellTiter-Glo® assay was used to assess mitochondrial ATP and calculate the concentration of ATP according to a standard curve using (14.7-10,000 nM of ATP standard dilutions (ThermoFisher). Student's *t* test was used for statistical analysis.

Figure 10 shows the PMO OPA1 H1A(+10+32)Imm10C>T (**SEQ ID NO: 112**) enhance OPA1 protein upregulation in enriched iPSC-derived RGCs obtained from an ADOA
30 patient harbouring OPA1 c.985-1G>A mutation. iPSC-RGCs were incubated with PPMO for 5 days prior to protein harvest. The efficacy of PPMO-induced OPA1 upregulation was assessed using western blot assay and normalised to beta-actin expression. The results showed significant OPA1 protein upregulation at 10 μ M. Student's *t* test was used for statistical analysis.

35

DETAILED DESCRIPTION

General

Throughout this specification, unless specifically stated otherwise or the context requires otherwise, reference to a single step, composition of matter, group of steps or group of compositions of matter shall be taken to encompass one and a plurality (i.e. one or more) of those steps, compositions of matter, groups of steps or groups of compositions of matter. Thus, as used herein, the singular forms “a”, “an” and “the” include plural aspects unless the context clearly dictates otherwise. For example, reference to “a” includes a single as well as two or more; reference to “an” includes a single as well as two or more; reference to “the” includes a single as well as two or more and so forth.

Those skilled in the art will appreciate that the present disclosure is susceptible to variations and modifications other than those specifically described. It is to be understood that the disclosure includes all such variations and modifications. The disclosure also includes all of the steps, features, compositions and compounds referred to or indicated in this specification, individually or collectively, and any and all combinations or any two or more of said steps or features.

The present disclosure is not to be limited in scope by the specific examples described herein, which are intended for the purpose of exemplification only. Functionally-equivalent products, compositions and methods are clearly within the scope of the present disclosure.

Any example of the present disclosure herein shall be taken to apply *mutatis mutandis* to any other example of the disclosure unless specifically stated otherwise. Stated another way, any specific example of the present disclosure may be combined with any other specific example of the disclosure (except where mutually exclusive).

Any example of the present disclosure disclosing a specific feature or group of features or method or method steps will be taken to provide explicit support for disclaiming the specific feature or group of features or method or method steps.

Unless specifically defined otherwise, all technical and scientific terms used herein shall be taken to have the same meaning as commonly understood by one of ordinary skill in the art (for example, molecular biology, microbiology, virology, recombinant DNA technology, peptide synthesis in solution, solid phase peptide synthesis, and immunology).

Unless otherwise indicated, the conventional techniques of molecular biology, microbiology, virology, recombinant DNA technology, peptide synthesis in solution, solid phase peptide synthesis, and immunology utilized in the present disclosure are standard procedures, well known to those skilled in the art. Such techniques are described and explained throughout the literature in sources such as, J. Perbal, A Practical Guide to Molecular Cloning, John Wiley and Sons (1984), J. Sambrook *et al.* Molecular Cloning: A Laboratory Manual, Cold Spring Harbour Laboratory Press (1989), T.A. Brown (editor), Essential Molecular Biology: A Practical Approach, Volumes 1 and 2, IRL Press (1991), D.M. Glover and B.D.

Hames (editors), *DNA Cloning: A Practical Approach*, Volumes 1-4, IRL Press (1995 and 1996), and F.M. Ausubel *et al.* (editors), *Current Protocols in Molecular Biology*, Greene Pub. Associates and Wiley-Interscience (1988, including all updates until present), Ed Harlow and David Lane (editors) *Antibodies: A Laboratory Manual*, Cold Spring Harbour Laboratory, 5 (1988), and J.E. Coligan *et al.* (editors) *Current Protocols in Immunology*, John Wiley & Sons (including all updates until present).

The term “and/or”, e.g., “X and/or Y” shall be understood to mean either “X and Y” or “X or Y” and shall be taken to provide explicit support for both meanings or for either meaning.

10 The term “about”, unless stated to the contrary, refers to +/- 20%, more preferably +/- 10%, of the designated value. For the avoidance of doubt, the term “about” followed by a designated value is to be interpreted as also encompassing the exact designated value itself (for example, “about 10” also encompasses 10 exactly).

15 Throughout this specification the word “comprise”, or variations such as “comprises” or “comprising”, will be understood to imply the inclusion of a stated element, integer or step, or group of elements, integers or steps, but not the exclusion of any other element, integer or step, or group of elements, integers or steps.

Selected Definitions

20 The term “antisense oligonucleotide” “antisense oligomer” or “ASO,” as used herein, encompasses oligonucleotides and any other oligomeric molecule that comprises nucleobases capable of hybridizing to a complementary sequence on a target RNA transcript, but does not comprise a sugar moiety, such as in the case of a peptide nucleic acid (PNA). Preferably, the ASO is an ASO that is resistant to nuclease cleavage or degradation.

25 The phrase “binds to a targeted portion” or “binds within a targeted portion,” in reference to an ASO, as used herein, refers to specific hybridization between the ASO nucleotide sequence and a target nucleotide sequence that is complementary within the ranges set forth herein. In some examples, specific hybridization occurs where, under *ex vivo* conditions, the hybridization occurs under high stringency conditions. By “high stringency conditions” is meant that the ASO, under such *ex vivo* conditions, hybridize to a target sequence 30 in an amount that is detectably stronger than non-specific hybridization. High stringency conditions, then, are conditions that distinguish a polynucleotide with an exact complementary sequence, or one containing only a few scattered mismatches from a random sequence that happened to have a few small regions (e.g., 1-5 bases) that matched the probe. Such small regions of complementarity are more easily melted than a full-length complement of 12-17 or 35 more bases, and moderate stringency hybridization makes them easily distinguishable. In one example, high stringency conditions include, for example, low salt and/or high temperature conditions, such as provided by about 0.02-0.1 M NaCl or the equivalent, at temperatures of about 50-70 °C. The skilled person will appreciate that under *in vivo* conditions, the specificity

of hybridization between an ASO and its target sequence is defined in terms of the level of complementarity between the ASO and the target sequence to which it hybridizes within a cell.

The term “nonsense-mediated RNA decay-inducing (NMD) exon” or “NMD exon” refers to an exon or a pseudo-exon that is a region within an intron and can activate the NMD pathway if included in a mature RNA transcript. In the constitutive splicing events, the intron containing an NMD exon is usually spliced out, but the intron or a portion of it can be retained during alternative or aberrant splicing events. Mature mRNA transcripts containing such an NMD exon can be non-productive due to a frame shift which induces the NMD pathway. Inclusion of an NMD exon in mature *OPA1* RNA transcripts can downregulate overall *OPA1* mRNA and OPA1 protein expression.

The term “precursor mRNA” or “pre-mRNA” refers to the primary transcript is the single-stranded RNA product synthesized by transcription of the genomic DNA sequence of the transcription unit for a particular gene, which generally encompasses the nucleotide sequence between a transcription start site and a termination signal.

The term “peptide” is intended to include compounds composed of amino acid residues linked by amide bonds. A peptide may be natural or unnatural, ribosome encoded or synthetically derived. Typically, a peptide will consist of between 2 and 200 amino acids. For example, the peptide may have a length in the range of 10 to 20 amino acids or 10 to 30 amino acids or 10 to 40 amino acids or 10 to 50 amino acids or 10 to 60 amino acids or 10 to 70 amino acids or 10 to 80 amino acids or 10 to 90 amino acids or 10 to 100 amino acids, including any length within said range(s). The peptide may comprise or consist of fewer than about 150 amino acids or fewer than about 125 amino acids or fewer than about 100 amino acids or fewer than about 90 amino acids or fewer than about 80 amino acids or fewer than about 70 amino acids or fewer than about 60 amino acids or fewer than about 50 amino acids.

Peptides, as referred to herein, include “inverso” peptides in which all L-amino acids are substituted with the corresponding D-amino acids, “retro-inverso” peptides in which the sequence of amino acids is reversed and all L-amino acids are replaced with D-amino acids.

Peptides may comprise amino acids in both L- and/or D-form. For example, both L- and D-forms may be used for different amino acids within the same peptide sequence. In some examples the amino acids within the peptide sequence are in L-form, such as natural amino acids. In some examples the amino acids within the peptide sequence are a combination of L- and D-form. Further, peptides may comprise unusual, but naturally occurring, amino acids including, but not limited to, hydroxyproline (Hyp), beta-alanine, citrulline (Cit), ornithine (Orn), norleucine (Nle), 3-nitrotyrosine, nitroarginine, pyroglutamic acid (Pyr). Peptides may also incorporate unnatural amino acids including, but not limited to, homo amino acids, N-methyl amino acids, alpha-methyl amino acids, beta (homo) amino acids, gamma amino acids, and N-substituted glycines. Peptides may be linear peptides or cyclic peptides.

The term “protein” shall be taken to include a single polypeptide chain, i.e., a series of contiguous amino acids linked by peptide bonds or a series of polypeptide chains covalently or non-covalently linked to one another (i.e., a polypeptide complex). For example, the series of polypeptide chains can be covalently linked using a suitable chemical bond or a disulfide bond.

5 Examples of non-covalent bonds include hydrogen bonds, ionic bonds, Van der Waals forces, and hydrophobic interactions.

Percentage amino acid sequence identity with respect to a given amino acid sequence is defined as the percentage of amino acid residues in a candidate sequence that are identical to the amino acid residues in the reference sequence, after aligning the sequences and introducing

10 gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Amino acid sequence identity may be determined using the EMBOSS Pairwise Alignment Algorithms tool available from The European Bioinformatics Institute (EMBL-EBI), which is part of the European Molecular Biology Laboratory. This tool is accessible at the website located at

15 www.ebi.ac.uk/Tools/emboss/align/. This tool utilizes the Needleman-Wunsch global alignment algorithm (Needleman and Wunsch, 1970). Default settings are utilized which include Gap Open: 10.0 and Gap Extend 0.5. The default matrix “Blosom62” is utilized for amino acid sequences and the default matrix.

The term “cell penetrating peptide” (CPP) refers to a peptide that is capable of crossing

20 a cellular membrane. In one example, a CPP is capable of translocating across a mammalian cell membrane and entering into a cell. In another example, a CPP may direct a conjugate to a desired subcellular compartment. Thus, a CPP may direct or facilitate penetration of a molecule of interest across a phospholipid, mitochondrial, endosomal, lysosomal, vesicular, or nuclear membrane. A CPP may be translocated across the membrane with its amino acid sequence

25 complete and intact, or alternatively partially degraded.

A CPP may direct a molecule of interest, such as an antisense oligonucleotide disclosed herein, from outside a cell through the plasma membrane, and into the cytoplasm or a desired subcellular compartment. Alternatively, or in addition, a CPP may direct a molecule of interest across the blood-brain, trans-mucosal, hematoretinal, skin, gastrointestinal and/or pulmonary

30 barriers.

The term “peptide ligand” or “receptor binding domain” refers to a peptide that is capable of binding to a membrane surface receptor to enable translocation of the peptide across a cellular membrane. In one example a peptide ligand may enable translocation across the cellular membrane via the natural endocytosis of the targeted receptor. In another example the

35 peptide ligand may utilise a complementary mechanism of translocation across the cellular membrane including utilising a conjugated CPP. In one example, a peptide ligand is capable of translocating across a mammalian cell membrane and to enter a cell. In another example, a peptide ligand may direct a conjugate to a desired subcellular compartment. Thus, a peptide

ligand may direct or facilitate cellular uptake of a molecule of interest across a phospholipid, mitochondrial, endosomal, lysosomal, vesicular, or nuclear membrane. A peptide ligand may be translocated across the membrane with its amino acid sequence complete and intact, or alternatively partially degraded.

- 5 A peptide ligand via its binding to a target receptor may direct a molecule of interest, such as an ASO disclosed herein, from outside a cell through the plasma membrane, and into the cytoplasm or a desired subcellular compartment. Alternatively, or in addition, a peptide ligand via its binding to a target receptor may direct a molecule of interest across a relevant biological barrier, e.g., the blood-brain, trans-mucosal, hematoretinal, skin, gastrointestinal, and/or pulmonary barriers.
- 10

Methods of Treating or Preventing Glaucoma

- The present disclosure provides, for example, a method of treating, preventing and/or delaying progression of glaucoma in a subject. The methods described herein include a method for treating, preventing and/or delaying progression of glaucoma in a subject in need thereof by administering to the subject a therapeutically effective amount of a pharmaceutical composition comprising any of the ASOs disclosed herein. Likewise, in some examples, any of the ASOs herein are used in the manufacture of a medicament for treating, preventing and/or delaying progression of glaucoma.
- 15

- 20 Glaucoma is a group of eye diseases that result in vision loss. It is typically caused by an increase in intraocular pressure (IOP) which can result in damage to the optic nerve. Glaucoma can be classified as either primary or secondary, with secondary glaucoma attributable to another disorder or problem within the eye, such as injury, surgery, drugs, or other ocular diseases. Primary glaucoma is classified as open-angle glaucoma (POAG), normal-tension glaucoma (NTG), angle-closure glaucoma and congenital glaucoma. Secondary glaucoma is classified into neovascular glaucoma, pigmentary glaucoma, exfoliation glaucoma and uveitic glaucoma.
- 25

- In one example of the methods of the present disclosure, the glaucoma is primary glaucoma. For example, the primary glaucoma is open-angle glaucoma (POAG), normal-tension glaucoma (NTG), angle-closure glaucoma or congenital glaucoma.
- 30

In one example, the primary glaucoma is open-angle glaucoma (POAG).

In one example, the primary glaucoma is normal-tension glaucoma (NTG).

In one example, the primary glaucoma is angle-closure glaucoma.

In one example, the primary glaucoma is congenital glaucoma.

- 35 In one example of the methods of the present disclosure, the glaucoma is secondary glaucoma. For example, the secondary glaucoma is neovascular glaucoma, pigmentary glaucoma, exfoliation glaucoma or uveitic glaucoma.

In one example, the secondary glaucoma is neovascular glaucoma.

In one example, the secondary glaucoma is pigmentary glaucoma.

In one example, the secondary glaucoma is exfoliation glaucoma.

In one example, the secondary glaucoma is uveitic glaucoma.

5 In one example, the subject to be treated is suffering from glaucoma. For example, the subject has been diagnosed as having or suffering from glaucoma. In one example, the subject suffers from glaucoma. For example, the subject is in need of treatment. Such subjects can be administered the ASOs as described here to treat or prevent the progression of glaucoma.

In one example, administration of an ASO as described herein slows progression of glaucoma.

10 In one example, the subject is at risk of developing glaucoma. Such subjects can be administered the ASOs as described here to prevent onset of glaucoma.

As used herein, the term “at risk” means that the subject has an increased chance of developing glaucoma compared to a normal individual. Subjects can be identified as at risk of developing glaucoma using any method known in the art and/or those described herein. For
15 example, the subject may be identified at risk of developing glaucoma if that subject has one or more common risk factors including family history, high eye pressure, diabetes, high or low blood pressure and prolonged use of steroidal medication.

Also provided herein is a method for increasing the OPA1 protein in a cell, the method comprising contacting the cell with a composition or pharmaceutical composition, as disclosed
20 herein, whereby the amount of OPA1 protein in the cell is increased. Also provided herein is a method for increasing the level of OPA1 protein in a cell, *ex vivo* or in a tissue *in vivo*, the method comprising contacting the cell with an ASO or pharmaceutical composition, as disclosed herein, whereby the amount of OPA1 protein in the cell is increased. In some examples, the cell is a retinal cell. In some examples, the tissue is a retinal tissue, e.g., retina
25 and/or retinal pigment epithelium.

In some examples, administration to a subject or contact with cells with any of the ASOs or pharmaceutical compositions disclosed herein increases the level of OPA1 protein about 1.1 to about 10-fold, e.g., 1.5 to about 10-fold, about 2 to about 10-fold, about 3 to about 10-fold, about 4 to about 10-fold, about 1.1 to about 5-fold, about 1.1 to about 6-fold, about 1.1 to about
30 7-fold, about 1.1 to about 8-fold, about 1.1 to about 9-fold, about 2 to about 5-fold, about 2 to about 6-fold, about 2 to about 7-fold, about 2 to about 8-fold, about 2 to about 9-fold, about 3 to about 6-fold, about 3 to about 7-fold, about 3 to about 8-fold, about 3 to about 9-fold, about 4 to about 7-fold, about 4 to about 8-fold, about 4 to about 9-fold, at least about 1.1-fold, at least about 1.5-fold, at least about 2-fold, at least about 2.5-fold, at least about 3-fold, at least
35 about 3.5-fold, at least about 4-fold, at least about 5-fold, or at least about 10-fold compared to the level in the tissue prior to the administration or contact.

Suitable routes of administration for treatment with the compositions, pharmaceutical compositions, or medicaments disclosed herein include, but are not limited to, intravitreal,

suprachoroidal, subretinal, ciliary intramuscular, intravenous, intra-arterial, subcutaneous, and topical.

In some examples administration is into the eye by an intravitreal, suprachoroidal, or sub-retinal route. For example, administration to the eye is by intravitreal administration. In another example, administration to the eye is by suprachoroidal administration. In a further example, administration to the eye is by sub-retinal administration. In one example, administration to the eye is by a topical administration.

As the skilled person will understand, the treatment methods disclosed herein include administration of the compositions and pharmaceutical compositions disclosed herein in a therapeutically effective amount to a subject (e.g., a human subject). The terms "effective amount" or "therapeutically effective amount," as used herein, refer to a sufficient amount of a disclosed ASO being administered to relieve to some extent one or more of the symptoms and/or clinical indicia associated with pathological inflammation in a particular disease or health condition. In some examples, an "effective amount" for therapeutic uses is the amount of one of the foregoing agents required to provide a clinically significant decrease in disease symptoms and/or inflammatory markers or to prevent disease symptoms without undue adverse side effects. An appropriate "effective amount" in any individual case may be determined using techniques, such as a dose escalation study. The term "therapeutically effective amount" includes, for example, a prophylactically effective amount. It is understood that "an effective amount" or "a therapeutically effective amount" can vary from subject to subject, due to variation in metabolism of the compound of any age, weight, general condition of the subject, the condition being treated, the severity of the condition being treated, and the judgment of the prescribing physician. By way of example only, therapeutically effective amounts may be determined by routine experimentation, including but not limited to a dose escalation clinical trial. Where more than one therapeutic agent is used in combination, a "therapeutically effective amount" of each therapeutic agent can refer to an amount of the therapeutic agent that would be therapeutically effective when used on its own, or may refer to a reduced amount that is therapeutically effective by virtue of its combination with one or more additional therapeutic agents.

Compositions for Increasing OPA1 Protein Levels

OPA1 mitochondrial dynamin like GTPase gene (also known as OPA1, FLJ12460, KIAA0567, MGM1, NPG and NTG; referred to herein as OPA1) is composed of 30 coding exons distributed across more than 90 kb of genomic DNA. It is located on chromosome 3q29 and encodes for a ubiquitously expressed dynamic-related GTPase, which is imported into mitochondria by an N-terminal import sequence and localizes to the inner membrane facing the intermembrane space. OPA1 contains a highly conserved functional GTPase domain shared by members of the dynamin superfamily of mechanoenzymes and regulates several important

cellular processes including the stability of the mitochondrial network. In humans, OPA1 generates at least eight isoforms via differential splicing of exons 4, 4b and 5b. For the purposes of nomenclature only and not limitation the sequence of the entire human OPA1 gene sequence and known transcript maps and sequences are publicly available through the online
 5 ensembl database under record ENSG00000198836. An exemplary gene sequence of human OPA1 is set out in NCBI Reference Sequence NM_130837, or **SEQ ID NO: 2489**, and UniProt ID O60313, or **SEQ ID NO: 2490**.

The *OPA1* gene contains an intron with a premature termination codon (PTC) in intron 7 (located between exons 7 and 8). In some subjects, a proportion of the *OPA1* RNA transcripts from wild-type *OPA1* genes retain a section of intron 7 containing this PTC; this retained intron section is called exon 7x in the transcribed RNA. The RNA transcripts that contain exon 7x (the retained intron segment containing the PTC) are subject to nonsense-mediated RNA decay. Therefore, a proportion of *OPA1* RNA that is translated to mature wild-type protein, and a portion of *OPA1* RNA that is degraded by RNase almost immediately due to the presence of
 15 the PTC.

As described herein, the ASOs according to any example bind to a targeted portion of human OPA1 pre-mRNA and which increase expression of OPA1 protein by promoting the exclusion of exon 7x in splicing of OPA1 in mammalian cells.

Without being bound by theory or mode of action, the ASOs that bind to targeted
 20 portions of human *OPA1* pre-mRNA in mammalian cells and which result in the exclusion of NMD exon 7x, are thought to increase expression of OPA1 protein by preventing the translation of NMD exon 7x.

Also described herein, the ASOs according to any example bind to the 5' UTR or 3' UTR of *OPA1* mRNA and increase expression of OPA1 protein.

Without being bound by theory or mode of action, the ASOs that bind to the 5' UTR are thought to increase expression of OPA1 protein through steric inhibition of translation from upstream Open Reading Frames (uORF) start site and/or steric inhibition of secondary structure in the UTR and/or inhibiting the binding and/or activity of a decapping enzyme.

Also described herein, the ASOs according to any example bind to the 3' UTR or 3' UTR of *OPA1* mRNA and increase expression of OPA1 protein. Without being bound by
 30 theory or mode of action, such ASOs may sterically inhibit binding of a miRNA to the 3' UTR.

Antisense Oligonucleotides (ASOs)

In some examples of the compositions and methods described herein, ASOs have a
 35 sequence that is completely complementary across its length to the target sequence or a sequence near complementarity (e.g., sufficient complementarity to bind the target sequence to promote exon splicing). ASOs are designed so that they bind (hybridize) to a target RNA sequence (e.g., a targeted portion of a pre-mRNA transcript) and remain hybridized under

physiological conditions. Selection of suitable sequences for ASOs generally avoids, where possible, similar nucleic acid sequences in other (i.e., off-target) locations in the genome or in cellular mRNAs or miRNAs, such that the likelihood the ASO will hybridize at such sites is limited.

5 In some examples, ASOs “specifically hybridize” to or are “specific” to a target nucleic acid or a targeted portion of the *OPAI* mRNA 5' UTR. In some examples, ASOs “specifically hybridize” to or are “specific” to a target nucleic acid or a targeted portion of the *OPAI* pre-mRNA. At a given ionic strength and pH, the T_m is the temperature at which 50% of a target sequence hybridizes to a complementary oligonucleotide.

10 ASO sequences are “complementary” to their target sequences when hybridization occurs in an antiparallel configuration between two single-stranded polynucleotides. Complementarity is quantifiable in terms of the proportion (e.g., the percentage) of bases in opposing strands that are expected to form hydrogen bonds with each other, according to generally accepted base-pairing rules. The nucleotide sequence of an ASO need not be 100%
15 complementary to that of its target nucleic acid to hybridize. In certain examples, the nucleotide sequences of ASOs in the compositions disclosed herein can be at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or 100% complementary to the nucleotide sequence of the targeted portion of an RNA transcript over the length of the ASO nucleotide sequence. For example, an ASO in which 18 of 20
20 nucleotides of ASO sequence are complementary to a target region, and would therefore specifically hybridize, would represent 90 percent complementarity. In such an example, the remaining non-complementary nucleotides of the ASO could be clustered together or interspersed with complementary nucleotides and need not be contiguous. Complementarity of an ASO sequence to a target nucleotide sequence (expressed as “percent complementarity”
25 to its target sequence; or “percent identity” to its reverse complement sequence) can be determined routinely using algorithms known in the art, as exemplified in the BLAST programs (basic local alignment search tools) and PowerBLAST programs (Altschul, *et al.*, 1990, *J. Mol. Biol.*, 215:403-410; Zhang *et al.*, 1997, *Genome Res.*, 7:649-656).

30 In some examples, an ASO does not hybridize to all nucleotides in a target sequence and the nucleotide positions at which it does hybridize may be contiguous or noncontiguous. ASOs may hybridize over one or more segments of a 5' UTR region of a mRNA or over one or more segments of intron 7 of the *OPAI* pre-mRNA, such that intervening or adjacent segments are not involved in the hybridization event (e.g., a loop structure or hairpin structure may be formed).

35 In some examples the nucleotide sequences of ASOs described herein are complementary to a targeted portion of *OPAI* mRNA 5' UTR. For example, the ASOs are complementary to a targeted portion of the 5' UTR of an *OPAI* mRNA corresponding to **SEQ ID NO:55**. In some examples, the ASOs are complementary to a targeted portion of an *OPAI*

mRNA corresponding to **SEQ ID NO:55**, which encompasses the 5' UTR. In some examples the nucleotide sequence of the ASO is at least 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% complementary to the nucleotide sequence of the targeted portion of the *OPAI* 5' UTR over the length of the ASO.

5 In some examples, the nucleotide sequences of ASOs that bind to targeted portions of the 5' UTR of *OPAI* mRNA comprise or consist of any one of **SEQ ID NOs: 56-138**.

In some examples the nucleotide sequences of ASOs described herein are complementary to a targeted portion of intron 7 of the *OPAI* pre-mRNA. In some examples, the ASOs are complementary to a targeted portion within sufficient proximity to an acceptor site of exon 7x to promote exclusion of exon 7x in splicing of *OPAI* mRNA e.g. the antisense oligonucleotide comprises any one of **SEQ ID NOs: 2-54**. In some examples, the ASOs are complementary to a targeted portion within sufficient proximity to an acceptor site of exon 7x to promote exclusion of exon 7x in splicing of *OPAI* mRNA e.g. the antisense oligonucleotide comprises any one of **SEQ ID NOs: 2-54** or **SEQ ID NOs: 2491-2503**. In some examples, the ASOs are complementary to a targeted portion within sufficient proximity to an acceptor site of exon 7x to promote exclusion of exon 7x in splicing of *OPAI* mRNA e.g. the antisense oligonucleotide comprises any one of **SEQ ID NOs: 2491-2503**. In some examples the nucleotide sequence of the ASO is at least 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% complementary to the nucleotide sequence of the targeted portion of intron 7 of the *OPAI* pre-mRNA over the length of the ASO.

In some examples the nucleotide sequences of ASOs described herein are complementary to a targeted portion of *OPAI* mRNA 3' UTR. For example, the ASOs are complementary to a targeted portion of the 3' UTR of an *OPAI* mRNA corresponding to **SEQ ID NO: 139**. In some examples, the ASOs are complementary to a targeted portion of an *OPAI* mRNA corresponding to **SEQ ID NO: 139**, which encompasses the 3' UTR. In some examples the nucleotide sequence of the ASO is at least 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% complementary to the nucleotide sequence of the targeted portion of the *OPAI* 3' UTR over the length of the ASO.

The ASOs described herein may be of any length suitable for specific hybridization to a target sequence. In some examples, the nucleotide sequence of the ASOs consist of 8 to 50 nucleotides. For example, the ASO sequence can be 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, 40, 45, or 50 nucleotides in length. In some examples, the ASOs consist of more than 50 nucleotides, but no more than 100 nucleotides in length.

35 In some examples, the ASO nucleotide sequence is from 8 to 50 nucleotides, 8 to 40 nucleotides, 8 to 35 nucleotides, 8 to 30 nucleotides, 8 to 25 nucleotides, 8 to 20 nucleotides, 8 to 15 nucleotides, 9 to 50 nucleotides, 9 to 40 nucleotides, 9 to 35 nucleotides, 9 to 30 nucleotides, 9 to 25 nucleotides, 9 to 20 nucleotides, 9 to 15 nucleotides, 10 to 50 nucleotides,

10 to 40 nucleotides, 10 to 35 nucleotides, 10 to 30 nucleotides, 10 to 25 nucleotides, 10 to 20 nucleotides, 10 to 15 nucleotides, 11 to 50 nucleotides, 11 to 40 nucleotides, 11 to 35 nucleotides, 11 to 30 nucleotides, 11 to 25 nucleotides, 11 to 20 nucleotides, 11 to 15 nucleotides, 12 to 50 nucleotides, 12 to 40 nucleotides, 12 to 35 nucleotides, 12 to 30 nucleotides, 12 to 25 nucleotides, 12 to 20 nucleotides, 12 to 15 nucleotides, 13 to 50 nucleotides, 13 to 40 nucleotides, 13 to 35 nucleotides, 13 to 30 nucleotides, 13 to 25 nucleotides, 13 to 20 nucleotides, 14 to 50 nucleotides, 14 to 40 nucleotides, 14 to 35 nucleotides, 14 to 30 nucleotides, 14 to 25 nucleotides, 14 to 20 nucleotides, 15 to 50 nucleotides, 15 to 40 nucleotides, 15 to 35 nucleotides, 15 to 30 nucleotides, 15 to 25 nucleotides, 15 to 20 nucleotides, 20 to 50 nucleotides, 20 to 40 nucleotides, 20 to 35 nucleotides, 20 to 30 nucleotides, 20 to 25 nucleotides, 25 to 50 nucleotides, 25 to 40 nucleotides, 25 to 35 nucleotides, or 25 to 30 nucleotides in length. In some examples, the ASOs are 17 nucleotides in length. In some preferred examples, the nucleotide sequence of the ASO nucleotide is 25 nucleotides in length.

15

ASO Chemistry and Modifications

The ASOs used in the compositions described herein may comprise naturally-occurring nucleotides, nucleotide analogues, modified nucleotides, or any combination thereof. The term “naturally occurring nucleotides” includes deoxyribonucleotides and ribonucleotides. The term “modified nucleotides” includes nucleotides with modified or substituted sugar groups and/or having a modified backbone. In some examples, all the nucleotides of an ASO are modified nucleotides. Chemical modifications of ASOs or components of ASOs that are compatible with the compositions and methods described herein are known in the art as disclosed in, e.g., in U.S. Patent No. 8,258,109, U.S. Patent No. 5,656,612, U.S. Patent Publication No. 2012/0190728, and Roberts *et al.*, 2020, *Nature Rev. Drug Disc.*, 19:673-694.

One or more nucleotides of an ASO may be any naturally occurring, unmodified nucleobase such as adenine, guanine, cytosine, thymine, uracil and inosine, or any synthetic or modified nucleobase that is sufficiently similar to an unmodified nucleobase such that it is capable of hydrogen bonding with a nucleobase present on a target RNA transcript. Examples of suitable modified nucleobases include, but are not limited to, hypoxanthine, xanthine, 7-methylguanine, 5, 6-dihydrouracil, 5-methylcytosine, and 5 hydroxymethoylcytosine.

ASOs include a “backbone” structure that refers to the connection between nucleotides/monomers of the ASO. In naturally occurring oligonucleotides, the backbone comprises a 3'-5' phosphodiester linkage connecting sugar moieties of adjacent nucleotides. Suitable types of backbone linkages for the ASOs described herein include, but are not limited to, phosphodiester, phosphorothioate, phosphorodithioate, phosphorodiamidate, phosphoroselenoate, phosphorodiselenoate, phosphoroanilothioate, phosphoraniladate, phosphoramidate, and the like. In some examples, the backbone modification is a

phosphorothioate linkage. In other examples, the backbone modification is a phosphorodiamidate linkage. See, e.g., Roberts *et al.* supra; and Agrawal (2021), *Biomedicines*, 9:503. In some examples, the backbone structure of the ASO does not contain phosphorous-based linkages, but rather contains peptide bonds, for example in a peptide nucleic acid (PNA), or linking groups including carbamate, amides, and linear and cyclic hydrocarbon groups.

In some examples, the stereochemistry at each of the phosphorus internucleotide linkages of the ASO backbone is random. In other examples, the stereochemistry at each of the phosphorus internucleotide linkages of the ASO backbone is controlled and is not random. For example, U.S. Pat. No. 9,605,019 describes methods for independently selecting the handedness of chirality at each phosphorous atom in an oligonucleotide. In some examples, a composition or composition used in the methods disclosed herein comprises a pure diastereomeric ASO. In other examples, the composition comprises an ASO that has diastereomeric purity of at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, about 100%, about 90% to about 100%, about 91% to about 100%, about 92% to about 100%, about 93% to about 100%, about 94% to about 100%, about 95% to about 100%, about 96% to about 100%, about 97% to about 100%, about 98% to about 100%, or about 99% to about 100%.

In some examples, the ASO has a non-random mixture of Rp and Sp configurations at its phosphorus internucleotide linkages. In some examples, an ASO used in the compositions and methods disclosed herein, comprises about 5-100% Rp, at least about 5% Rp, at least about 10% Rp, at least about 15% Rp, at least about 20% Rp, at least about 25% Rp, at least about 30% Rp, at least about 35% Rp, at least about 40% Rp, at least about 45% Rp, at least about 50% Rp, at least about 55% Rp, at least about 60% Rp, at least about 65% Rp, at least about 70% Rp, at least about 75% Rp, at least about 80% Rp, at least about 85% Rp, at least about 90% Rp, or at least about 95% Rp, with the remainder Sp, or about 100% Rp.

In some examples, the ASOs described herein contain a sugar moiety that comprises ribose or deoxyribose, or a modified sugar moiety or sugar analog, including a morpholine ring. Suitable examples of modified sugar moieties include, but are not limited to, 2' substitutions such as 2'-O-modifications, 2'-O-methyl (2'-O-Me), 2'-O-methoxyethyl (2'MOE), 2'-O-aminoethyl, 2'F, N3'->P5' phosphoramidate, 2'dimethylaminoethoxyethoxy, 2'dimethylaminoethoxyethoxy, 2'-guanidinidinium, 2'-O-guanidinidinium ethyl, carbamate modified sugars, and bicyclic modified sugars. In some examples, the sugar moiety modification is selected from among 2'-O-Me, 2'F, and 2'MOE. In other examples, the sugar moiety modification is an extra bridge bond, such as in a locked nucleic acid (LNA). In some examples the sugar analogue contains a morpholine ring, such as phosphorodiamidate morpholino (PMO). In some examples, the sugar moiety comprises a ribofuransyl or 2'deoxyribofuransyl

modification. In some examples, the sugar moiety comprises 2'-O-methoxyethyl (cMOE) modifications. In some examples, the sugar moiety comprises cEt 2', 4' constrained 2'-O ethyl BNA modifications. In other examples, the sugar moiety comprises tricycloDNA (tcDNA) modifications. In some examples, the sugar moiety comprises ethylene nucleic acid (ENA) modifications. In some examples, the sugar moiety comprises 2'-O-(2-N-methylcarbamoyl) (MCE). Modifications are known in the art as exemplified in Jarver, *et al.*, 2014, *Nucleic Acid Therapeutics*, 24(1): 37-47.

In some examples, each constituent nucleotide of the ASO is modified in the same way, e.g., every linkage of the backbone of the ASO comprises a phosphorothioate linkage, or each ribose sugar moiety comprises a 2'-O-methyl modification. In other examples, a combination of different modifications is used, e.g., an ASO comprising a combination of phosphorodiamidate linkages and sugar moieties comprising morpholine rings (morpholinos).

In some examples, the ASO comprises one or more backbone modifications. In some examples, the ASO comprises one or more sugar moiety modification. In some examples, the ASO comprises one or more backbone modifications and one or more sugar moiety modifications. In some examples, the ASO comprises a 2'MOE modification and a phosphorothioate backbone. In some examples, the ASO comprises a peptide nucleic acid (PNA).

In some examples, the ASO comprises a phosphorodiamidate morpholino (PMO). The skilled person in the art will appreciate that ASOs may be modified in order to achieve desired properties or activities of the ASO or reduce undesired properties or activities of the ASO. In some examples, an ASO is modified to alter one or more properties. For example, such modifications can: enhance binding affinity to a target sequence on a pre-mRNA transcript; reduce binding to any non-target sequence; reduce degradation by cellular nucleases (e.g., RNase H); improve uptake of an ASO into a cell and/or particular subcellular compartments; alter the pharmacokinetics or pharmacodynamics of the ASO; and/or modulate the half-life of the ASO *in vivo*.

In some examples, the ASOs comprise one or more 2'-O-(2-methoxyethyl) (MOE) phosphorothioate-modified nucleotides, which have been shown to confer significantly enhanced resistance of ASOs to nuclease degradation and increased bioavailability.

Methods for synthesis and chemical modification of ASOs, as well as synthesis of ASO conjugates is well known in the art, and such ASOs are available commercially.

In some examples, a composition (e.g., a pharmaceutical composition) provided here includes two or more ASOs with different chemistries but complementary to the same targeted portion of the *OPAI* mRNA 5' UTR. In other examples, two or more ASOs that are complementary to different targeted portions of the *OPAI* mRNA 5' UTR.

In some examples, a composition (e.g., a pharmaceutical composition) provided here includes two or more ASOs with different chemistries but complementary to the same targeted

portion of intron 7 of the *OPAI* pre-mRNA. In other examples, two or more ASOs that are complementary to different targeted portions of intron 7 of the *OPAI* pre-mRNA.

In some examples, a composition (e.g., a pharmaceutical composition) provided here includes two or more ASOs with different chemistries but complementary to the same targeted portion of the *OPAI* mRNA 3' UTR. In other examples, two or more ASOs that are complementary to different targeted portions of the *OPAI* mRNA 3' UTR.

In some examples, the compositions disclosed herein include ASOs that are linked to a functional moiety. In some examples, the functional moiety is a delivery moiety, a targeting moiety, a detection moiety, a stabilizing moiety, or a therapeutic moiety. In some examples the functional moiety includes a delivery moiety or a targeting moiety. In some examples the functional moiety includes a stabilizing moiety. In some examples the functional moiety is a delivery moiety.

Suitable delivery moieties include, but are not limited to, lipids, peptides, carbohydrates, and antibodies.

In some examples, the delivery moiety includes a cell-penetrating peptide (CPP). Suitable examples of CPPs are described in, e.g., PCT/AU2020/051397. In some examples the amino acid sequence of the CPP comprises or consists of: RRSRTARAGRPGRNSSRPSAPRGASGGASG (SEQ ID NO: 2504). In one example, the CPP comprises the sequence RRSRTARAGRPGRNSSRPSAPRGASGGASG (SEQ ID NO: 2504), optionally wherein any amino acid other than glycine is a D amino acid. In other examples, the delivery moiety includes a receptor binding domain. In other examples, the delivery moiety includes a carbohydrate. In some examples, a carbohydrate delivery moiety is selected from among N acetylgalactosamine (GalNAc), N-Ac-Glucosamine (GluNAc), and a mannose. In one example, the carbohydrate delivery moiety is GalNAc.

In other examples, the delivery moiety includes a lipid. Examples of suitable lipids as delivery moieties include, but are not limited to, cholesterol moiety, a cholesteryl moiety, and aliphatic lipids. In some examples the delivery moiety includes a fatty acid or lipid moiety. In some embodiments the fatty acid chain length is about C8 to C20. Examples of suitable fatty acid moieties and their conjugation to oligonucleotides are found in, e.g., International Patent Publication WO 2019232255 and in Prakash *et al.*, (2019).

In further examples, the delivery moiety includes an antibody, as described in, e.g., Dugal-Tessier *et al.*, (2021), *J Clin Med.*, 10(4):838.

Suitable examples of stabilizing moieties include, but are not limited to, polyethylene glycol (PEG), poly(oligo(ethylene glycol) methyl ether methacrylate) (POEGMA), and Poly(2-oxazoline)s (POx).

In some examples, where an ASO is linked to a functional moiety, the functional moiety is covalently linked to the ASO. In other examples, the functional moiety is non-covalently linked to the ASO.

- Functional moieties can be linked to one or more of any nucleotides in an ASO at any of several positions on the sugar, base or phosphate group, as understood in the art and described in the literature, e.g., using a linker. Linkers can include a bivalent or trivalent branched linker. In some examples, the functional moiety is linked to the 5' end of the ASO.
- 5 In other examples, the functional moiety is linked to the 3' end of the ASO. In further examples, the functional moiety is linked to the 5' end and the 3' of the ASO.

- In some examples compositions comprising any of the ASOs disclosed herein also include a delivery nanocarrier complexed with ASO. In some examples, a delivery nanocarrier is selected from among lipoplexes, liposomes, exosomes, inorganic nanoparticles, and DNA
- 10 nanostructures. In other examples the delivery nanocarrier includes a lipid nanoparticle encapsulating the ASO. Various delivery ASO-nanocarrier complex formats are known in the art, as reviewed in, e.g., Roberts *et al.*, *supra*.

Pharmaceutical Compositions

- 15 Also provided herein are pharmaceutical compositions comprising any of the foregoing ASOs, and modified messenger RNAs (mmRNAs) disclosed herein, and formulated with at least a pharmaceutically acceptable excipient, including a carrier, filler, preservative, adjuvant, solubilizer and/or diluent.

- Pharmaceutical compositions containing any of the ASOs compositions described
- 20 herein, for use in the methods disclosed herein, can be prepared according to conventional techniques well known in the pharmaceutical industry and described in the published literature. In some examples, a pharmaceutical composition for treating a subject comprises a therapeutically effective amount of any ASO disclosed herein.

- Pharmaceutically acceptable salts are suitable for use in contact with the tissues of
- 25 humans and lower animals without undue toxicity, irritation, allergic response, etc., and are commensurate with a reasonable benefit/risk ratio. Examples of pharmaceutically acceptable, nontoxic acid addition salts are salts of an amino group formed with inorganic acids such as hydrochloric acid, hydrobromic acid, phosphoric acid, sulfuric acid and perchloric acid or with organic acids such as acetic acid, oxalic acid, maleic acid, tartaric acid, citric acid, succinic acid or malonic acid. Other pharmaceutically acceptable salts include adipate, alginate,
- 30 ascorbate, aspartate, benzenesulfonate, benzoate, bisulfate, borate, butyrate, camphorate, camphorsulfonate, citrate, cyclopentanepropionate, digluconate, dodecylsulfate, ethanesulfonate, formate, fumarate, glucoheptonate, glycerophosphate, gluconate, hemisulfate, heptanoate, hexanoate, hydroiodide, 2-hydroxy-ethanesulfonate, lactobionate, lactate, laurate, lauryl sulfate, malate, maleate, malonate, methanesulfonate, 2-naphthalenesulfonate,
- 35 nicotinate, nitrate, oleate, oxalate, palmitate, pamoate, pectinate, persulfate, 3-phenylpropionate, phosphate, picrate, pivalate, propionate, stearate, succinate, sulfate, tartrate, thiocyanate, p-toluenesulfonate, undecanoate, valerate salts, and the like. Representative alkali

or alkaline earth metal salts include sodium, lithium, potassium, calcium, magnesium, and the like. Further pharmaceutically acceptable salts include, when appropriate, nontoxic ammonium, quaternary ammonium, and amine cations formed using counterions such as halide, hydroxide, carboxylate, sulfate, phosphate, nitrate, lower alkyl sulfonate and aryl sulfonate.

Exemplary salts useful in a composition of the present disclosure include calcium chloride, magnesium chloride or sodium chloride.

In one example, a composition comprises a buffer. Exemplary buffers useful in a composition of the present disclosure include sodium phosphate.

In some examples, pharmaceutical compositions are formulated into any of a number of possible dosage forms including, but not limited to, ocular emulsions, topical ointments, solutions for intravitreal injection, intravenous administration, intrathecal administration, intracisterna magna administration, tablets, capsules, gel capsules, liquid syrups, and soft gels. In some examples, the compositions are formulated as suspensions in aqueous, non-aqueous or mixed media. Aqueous suspensions may further contain substances that increase the viscosity of the suspension including, for example, sodium carboxymethylcellulose, sorbitol and/or dextran. The suspension may also contain stabilizers. In some examples, a pharmaceutical formulation disclosed herein is provided in a form including, but not limited to, a solution, emulsion, microemulsion, foam or liposome-containing formulation (e.g., cationic or noncationic liposomes).

In some examples, pharmaceutical formulations comprising any of the ASOs described herein may comprise one or more penetration enhancers, carriers, excipients or other active or inactive ingredients as appropriate and known to the skilled person. In some examples, where a pharmaceutical composition includes liposomes, such liposomes can also include sterically stabilized liposomes, e.g., liposomes comprising one or more specialized lipids. These specialized lipids result in liposomes with enhanced circulation lifetimes. In some examples, a sterically stabilized liposome comprises one or more glycolipids or is derivatized with one or more hydrophilic polymers, such as PEG moiety. In some examples, a surfactant is included in the pharmaceutical formulation.

In some examples, a pharmaceutical composition also includes a penetration enhancer to enhance the delivery of ASOs, e.g., to aid diffusion across cell membranes and /or enhance the permeability of a lipophilic drug. In some examples, the penetration enhancers include a surfactant, a fatty acid, a bile salt, or a chelating agent.

In some examples, a pharmaceutical composition comprises a dose of ASOs ranging from about 0.01 mg/kg to 20 mg/kg, e.g., 0.05 mg/kg, 0.1 mg/kg, 0.2 mg/kg, 0.5 mg/kg, 1 mg/kg, 3 mg/kg, 5 mg/kg, 8 mg/kg, 10 mg/kg, 15 mg/kg, or another dose ranging from about 0.01 mg/kg to 20 mg/kg.

In some examples, a pharmaceutical composition comprises multiple ASOs. In some examples, a pharmaceutical composition comprises, in addition to ASOs, another drug or therapeutic agent suitable for treatment of a subject suffering from glaucoma.

5 Combination Therapies

The pharmaceutical compositions comprising any of the ASOs disclosed herein, can also be used in combination with other agents of therapeutic value in the treatment of glaucoma. In general, other agents do not necessarily have to be administered in the same pharmaceutical composition, and may, because of different physical and chemical characteristics, be administered by different routes. The determination of the mode of administration and the advisability of administration, where possible, in the same pharmaceutical composition, is well within the knowledge of the skilled clinician. The initial administration can be made according to established protocols known in the art, and then, based upon the observed effects, the dosage, modes of administration and times of administration can be modified by the skilled clinician.

15 Compositions and pharmaceutical compositions comprising ASOs and an additional therapeutic agent may be administered concurrently (e.g., simultaneously, essentially simultaneously or within the same treatment protocol) or sequentially, depending upon the stage and progression of the glaucoma to be treated, the condition of the patient, and the choice of specific therapeutic agents used. The determination of the order of administration, and the number of repetitions of administration of each therapeutic agent during a treatment protocol, is well within the knowledge of the skilled physician after evaluation of the glaucoma being treated and the condition of the patient.

It is known to those of skill in the art that therapeutically-effective dosages can vary when the drugs are used in treatment combinations. Methods for experimentally determining therapeutically-effective dosages of drugs and other agents for use in combination treatment regimens are described in the literature. For example, the use of metronomic dosing, i.e., providing more frequent, lower doses in order to minimize toxic side effects, has been described extensively in the literature. Combination treatment further includes periodic treatments that start and stop at various times to assist with the clinical management of the patient.

For combination therapies, dosages of co-administered therapeutic agents will of course vary depending on the type of co-agents employed, ASO, and the disease stage of the patient to be treated.

Pharmaceutical compositions comprising ASOs and an additional therapeutic agent which make up a combination therapy disclosed herein may be a combined dosage form or in separate dosage forms intended for substantially simultaneous administration. The pharmaceutical compositions that make up the combination therapy may also be administered sequentially, with either therapeutic agent being administered by a regimen calling for two-

step administration. The two-step administration regimen may call for sequential administration of the active agents or spaced-apart administration of the separate active agents. The time period between the multiple administration steps may range from, a few minutes to several hours, depending upon the properties of each pharmaceutical agent, such as potency, solubility, bioavailability, plasma half-life and kinetic profile of the pharmaceutical agent. Circadian variation of various physiological parameters may also be evaluated to determine the optimal dose interval.

Examples of suitable therapeutic agents for co-administration with a composition or a pharmaceutical composition disclosed herein include, but are not limited to, prostaglandins (e.g., latanoprost (Xalatan®), travoprost (Travatan Z®), tafluprost (Zioptan®), bimatoprost (Lumigan®) and latanoprostene bunod (Vyzulta®)), beta blockers (e.g., timolol (Betimol®), Istalol®, Timoptic®) and betaxolol (Betoptic®)), alpha-adrenergic agonists (e.g., apraclonidine (Iopidine®) and brimonidine (Alphagan P, Qoliana®)), carbonic anhydrase inhibitors (e.g., dorzolamide (Trusopt®) and brinzolamide (Azopt®)), a rho kinase inhibitor (e.g., netarsudil (Rhopressa®)) and miotic or cholinergic agents (e.g., pilocarpine (Isopto Carpine®)).

The present disclosure is not to be limited by the following non-limiting examples.

20 EXAMPLES

Example 1: ASO design to target exclusion of an *OPAI* NMD exon 7x

The ASO target region of *OPAI* intron 7 and exon 7x is shown in Figure 1A and C. ASOs with 24-25 nucleotides in length (Table 1, SEQ ID NOs: 2-9) are designed to target the intronic splice enhancer motifs (prediction using SpliceAid online tool) in intron 7 to mediate exclusion of exon 7x and generate productive *OPAI* transcripts. The identified ASO sequences are synthesized as PMOs and/or 2'MOE chemistry) and nucleofected into HEK293 cells or ADOA patient fibroblasts carrying the *OPAI* mutation (c.2708_2711delTTAG) using the NEON® electroporation system (ThermoFisher) at 25 µM and 50 µM and the nucleofected cells are cultured for 48 hr. Total RNA was extracted using the MagMAX™- 96 Total RNA Isolation kit and the level of *OPAI* transcript is assessed by digital droplet PCR (Qiagen; probe catalogue number: dHsaCPE5043545). *OPAI* transcript expression is normalized to *GAPDH*, *RPL27* and *SCL25A3* transcript levels (Qiagen; probe catalogue number: dHsaCPE5031596, dHsaCPE5036407, dHsaCPE5032926 respectively). The result of ASO screening is shown in Figure 2. PMOs that show induced *OPAI* mRNA levels were further validated for the ability to increase *OPAI* protein upregulation using a western blot assay as shown in Figure 3. Further refinement of ASO sequences (Figures 4, Table 1; SEQ ID NOs: 10-31 and Table 2; SEQ ID NOs: 32-54) is performed to reduce or extend ASO length and micro-walk or engineered

mismatch oligos and re-validated by ddPCR and protein assays. The efficacy of refined ASOs in inducing *OPA1* upregulation is shown in Figures 5 and 6.

Example 2 ASO design to target the 5' UTR of an *OPA1* transcript

- ASOs with 18-25 nucleotides in length (**Table 3, SEQ ID NOs: 56-116**) are designed to sterically inhibit a uORF or reduce the complexity of RNA secondary structure in the 5' UTR. The secondary structure of RNA is predicted using RNAfold online tool. The identified ASO sequences are synthesized as PMO and/or 2'MOE chemistry and nucleofected into HEK293 cells or ADOA patient fibroblasts carrying *OPA1* mutation (c.2708_2711delTTAG) using the NEON® electroporation system (ThermoFisher) at 25 μ M and 50 μ M and the nucleofected cells were cultured for 48 hr. Total protein is harvested from the transfected cells using the CytoBuster protein extraction reagent (Merck Millipore) following the manufacturer's instruction and assessed by Western blot assay using rabbit anti-*OPA1* monoclonal antibody (Cell Signaling, catalogue number 67589) at a dilution of 1:250 in 5% BSA in TBST buffer followed by goat anti-rabbit IgG H&L antibody (Abcam, catalogue number ab216773, IRDye® 800CW). Beta-actin serves as loading control and is detected using monoclonal mouse anti-beta actin antibody (Sigma-Aldrich, catalogue number A5441) followed by goat anti-mouse IgG H&L antibody (Abcam, catalogue number ab216776, IRDye® 680RD). ASO sequences are further refined by micro-walk or engineered mismatch oligos and/or extended up to 30 nucleotides (**Table 3; SEQ ID NOs: 117-138**). ASOs were subsequently re-validated using a western blot assay and the results are shown in Figure 7.

Example 3 ASO design to target the 3' UTR to increase *OPA1* expression levels

- An ASO sequence "micro-walk" of 25-mers (**Table 4; SEQ ID NOs: 140-1312**) or 17-mers (**Table 5; SEQ ID NOs: 1313-2488**) in 3 bp increments of distance is performed over the sequences of the 3' UTR of the ENST00000361510 transcript to mediate improvement in RNA stability. ASOs are screened to guide the ASO selection for *OPA1* expression upregulation using ddPCR and western blot assays described in Examples 1 and 2.

Example 4 PPMO-mediated *OPA1* upregulation to improve mitochondrial ATP production

- PMO *OPA1* H1A(+10+32)1mm10C>T (**SEQ ID NO: 112**) was conjugated with CPP for enhanced delivery into cells. The CPP-PMO (or PPMO) was tested for the ability to improve *OPA1* protein upregulation in fibroblasts derived from ADOA patients with distinct *OPA1* mutations. PPMO was incubated to patient fibroblasts and the efficacy of PPMO-induced *OPA1* upregulation was assessed using a western blot assay. Total protein was harvested from the transfected cells using RIPA buffer (ThermoFisher) following the manufacturer's instruction and assessed by western blot assay using rabbit anti-*OPA1*

monoclonal antibody (Cell Signaling Technology, catalogue number 67589) at a dilution of 1:250 in 5% BSA in TBST buffer followed by goat anti-rabbit IgG H&L antibody (Abcam, catalogue number ab216773, IRDye® 800CW). HPRT1 served as the loading control and was detected using HPRT1 Polyclonal antibody (ProteinTech, catalogue number 15059-1-AP).

5 Expression levels of OPA1 protein were compared between no PPMO-transfected cells (UT) and OPA1 PPMO-incubated cells. Figure 8 shows the PPMO exhibited upregulation of OPA1 protein expression compared to untreated patient fibroblasts (n=3 biological replicates). In addition, PPMO-treated cells were evaluated for the improvement of mitochondrial function using a CellTiter-Glo® assay to assess ATP levels. PPMO-treated cells were culture in a

10 glucose starvation condition supplemented with 5 mM pyruvate (cat#11360070, ThermoFisher) to continuously supply a substrate for mitochondrial respiratory chain reaction while glycolysis was inhibited using 2.5 mM D-deoxy glucose (catalogue number D8375, Sigma-Aldrich). An ATP standard curve was analysed using 14.7-10,000 nM ATP (catalogue number R0441, ThermoFisher). Results in Figure 9 show improvement in mitochondrial ATP

15 production in patient fibroblasts treated with the PPMO (SEQ ID NO: 112) targeting the 5' UTR of *OPA1* transcript.

Example 5 PPMO treatment induces total OPA1 protein in RGC enriched culture derived from an ADOA patient

20 PPMO OPA1 H1A(+10+32)1mm10C>T (SEQ ID NO: 112) was incubated to iPSC-RGCs derived from an ADOA patient carrying the *OPA1* mutation (c.985-1G>A) for 120 hr in triplicates. Total protein was harvested from the transfected cells using the CytoBuster protein extraction reagent (Merck Millipore) following the manufacturer's instruction and assessed by western blot assay using rabbit anti-OPA1 monoclonal antibody (Cell Signaling

25 Technology, catalogue number 67589) at a dilution of 1:250 in 5% BSA in TBST buffer followed by goat anti-rabbit IgG H&L antibody (Abcam, catalogue number ab216773, IRDye® 800CW). Beta-actin served as loading control and was detected using monoclonal mouse anti-beta actin antibody (Sigma-Aldrich, catalogue number A5441) followed by goat anti-mouse IgG H&L antibody (Abcam, catalogue number ab216776, IRDye® 680RD). Figure

30 10 shows the PPMO mediated upregulation of total OPA1 protein by up to 1.3-fold at 10 µM as compared to untreated patient fibroblasts. Student's *t* test was used for statistical analysis.

SEQUENCES

SEQ ID NO: 1: *OPAI* intron 7 (lowercase) and exon7X (uppercase) cDNA sequence (GRCh38/hg38: chr3 193626203-193628616)

```
5  gtgatggatgggttaagggggtaccgatacattcacactaatcagccatttctccaagatcatgtcacctcaatctgttcattggactcca
   aatacaagaaattaatttgacaaagtgaaaatataaaagatgcatcatataaatgttaacttttctggagtgaggtagtataggtaaagcca
   aaagaaacaaattcaagcagaggaaatttggttctgaaaattagggttctgttagggccctgtatttatactagaacaaaattaggaatt
   tctgtttatgtgtccagttattgagtcaccctaagttttaggcattctacctacacttctctcccaagttttatttctaaatgaaaagca
   ttgctgtagatgaccagtttacactaaagaataacatttatttattgttttagctaaagtatatggacagggaaacattcatattctgtagaag
10  aaaattattttgacttttggcacaagcatgtagttcttatacactttgacaaactattgctgacattttcacattaatcaaagtcagcacia
   ataaattttcaccttgaccacggagggttgaaactggaaattgatataattctggttgctaaagaacaagtctataaaaagcttaagt
   gtataccaatatgtggctgttgctgaatcagcaggtccgtaaaaatatgttttaagggttaggtaatccacaacggagatcccaaagt
   tcatgtttggaagagacttttgggtcaaagtgaaatcagtgtaatgaattaaaattatactctgagatcttgaaatcagctaattatgttacat
   ctattagctcagaaaagtttgaagttatatacaaatgctagtcaggaaaaaagattcagtcattgttaattctgtacattctactatttaaac
15  aaccaatattatagattatgatttagtcagtaattctgctggctaaccttatctcatttgggtgggttagtacttcagagtactcaccatagt
   ttcaattatgttttcagcatcacttctggtttttctcaattccatggctgtggaatcaattcatatgtataattagcttcggtgagcaaaaacata
   gctagaaaaagaaaagaagtgagtttccactctggtaaaattaaagtcgatgtgtaagccaaggaggactctttgaatggtactttaac
   aatccctgttctgtatactgtgaatatacatttaaatagcctaataaattggatgcttaggctgagccacctatacttttagttttgtagaaa
   gaagggagaggagcaagatgttcttatatgttacttagaataaagaatgtagctgtagttacacattgttcttaagtttttctgaagacaa
20  ctgaaatgagtccttaggctgtatttaacattctaagatatgacttaagggttaatgatgagctttgaaatctgacaattcaagagatatc
   cataatgaatactgattcattttctacattgctgaaagctaatttcattttaagcctacttttagtagcctttatttgggcttagagatgttattcct
   cttctgatatttattgggttatctgtttaacccttttatatctccctttccgatttgaattagagactggcaagacttttaccctgagtagag
   caccacaatggtgtttctgcccacactgtagttacctgagggggaagtaaattgggactttaaaagcaatttatgctcttttatagtgaag
   ttatccctcttactatcccgaagactgttaccttacaataatctccactctttccctctgtagttactatagagatgacttttgggttcttcac
25  tgccataatgatcaaaatcctaattcatgagattttatcattccaggcatgtgagggttactgtatgcataaaaccgcaagtacttttggttgt
   ttttaattgtttttctctcttattcttctgaaagtctaagtagatcatcattttgatgtcttattagtagcaactaataaatttccctgtatcttctca
   gcaaaagaactcaagcagagacagaagattagaactaccattggtagttttgcttctatggatatgttcacatacatagaatttttaca
   tgaccttttatatatgtatttcagaatttcagaatggcctcaatgccttaataggaagaatactgaaatttttaattagggttgggtttgtg
   aggagctagtaaagggttttctcttcagCTTTAGCTTGTTCCTGCGGAGGATTCCGCTCTTCTCCA
30  TCAGTTTCATAGCCCTGGAATTGTAGAAAAGCTCTGGTTTCAAGACCATTGATAT
   CCATTTCTGTCAGG
```

Table 1: List of antisense oligonucleotide sequences targeting removal of NMD exon 7X of an *OPAI* transcript

SEQ ID	ASO Coordinates	Sequence 5'>3'	SE Q ID	ASO Coordinates	Sequence 5'>3'
2	hOPAI_Ex7xA(-99-76)	CTGAAAATACATATATAAAAAAGGTC	17	hOPAI_Ex7xA(-108-79)	GGCATTGAGGCCATTCTGAAAATTCTGAAAT
3	hOPAI_Ex7xA(-99-76)1mm	CTGAAAATACATATATAAAGAGGTC	18	hOPAI_Ex7xA(-107-78)	AGGCATTGAGGCCATTCTGAAAATTC TGAAA
4	hOPAI_Ex7xA(-100-76)1mmA-G	CTGAAAATACATATATAAAGAGGTC A	19	hOPAI_Ex7xA(-106-77)	AAGGCATTGAGGCCATTCTGAAAAT CTGAA
5	hOPAI_Ex7xA(-106-82)1mmA-G	TACATATATAAAGAGGTCATTGTA A	20	hOPAI_Ex7xA(-105-76)	TAAAGGCATTGAGGCCATTCTGAAAAT TCTGA
6	hOPAI_Ex7xA(-117-93)1mmA-G	AAAGGTCATTGTAAAGAAATTTCTATG	21	hOPAI_Ex7xA(-104-76)	TAAAGGCATTGAGGCCATTCTGAAAAT TCTG
7	hOPAI_Ex7xA(-127-103)	GTAAAAAATTTCTATGTATGTGAACA	22	hOPAI_Ex7xA(-103-76)	TAAAGGCATTGAGGCCATTCTGAAAAT TCT
8	hOPAI_Ex7xA(-139-115)	TCTATGTATGTGAACATATCCATAG	23	hOPAI_Ex7xA(-102-76)	TAAAGGCATTGAGGCCATTCTGAAAAT TC
9	hOPAI_Ex7xA(-187-163)	AATCTTCTGTCTCTGCTTGAGTTCT	24	hOPAI_Ex7xA(-101-76)	TAAAGGCATTGAGGCCATTCTGAAAAT T
10	hOPAI_Ex7xA(-113-84)	TGAGGCCATTCTGAAAATTTCTGAAAT ACATA	25	hOPAI_Ex7xA(-100-76)22mmA>G	TAAAGGCATTGAGGCCATTCTGAAA T
11	hOPAI_Ex7xA(-113-84)14mmA>G	TGAGGCCATTCTGGAATTTCTGAAAT ACATA	26	hOPAI_Ex7xA(-104-75)	TAAAGGCATTGAGGCCATTCTGAAA TTCTG
12	hOPAI_Ex7xA(-112-83)	TTGAGGCCATTCTGAAAATTTCTGAAA TACAT	27	hOPAI_Ex7xA(-103-74)	ATTAAGGCATTGAGGCCATTCTGAA ATTCT
13	hOPAI_Ex7xA(-111-82)	ATTGAGGCCATTCTGAAAATTTCTGAA ATACA	28	hOPAI_Ex7xA(-102-73)	TATTAAGGCATTGAGGCCATTCTGA AATTC
14	hOPAI_Ex7xA(-110-81)	CATTGAGGCCATTCTGAAAATTTCTGA AATAC	29	hOPAI_Ex7xA(-101-72)	CTATTAAGGCATTGAGGCCATTCTG AAATT
15	hOPAI_Ex7xA(-110-81)25mmA>G	CATTGAGGCCATTCTGAAAATTTCTGG AATAC	30	hOPAI_Ex7xA(-100-71)	CCTATTAAGGCATTGAGGCCATTCT GAAAT
16	hOPAI_Ex7xA(-109-80)	GCATTGAGGCCATTCTGAAAATTTCTG AAATA	31	hOPAI_Ex7xA(-99-70)	TCCTATTAAGGCATTGAGGCCATTCT TGAAA

Table 2: List of antisense oligonucleotide micro-walked sequences with 17 nucleotides targeting intron 7 of an *OPA1* transcript.

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
32	OPA1 H7XA(-215-199)	CTCTGCTTGAGTTCTTT	44	OPA1 H7XA(-143-127)	TTGTAAAAATTTCATG
33	OPA1 H7XA(-212-196)	TGTCCTCTGCTTGAGTTC	45	OPA1 H7XA(-140-124)	TCATTGTAAAAATTCT
34	OPA1 H7XA(-209-193)	TTCTGTCTCTGCTTGAG	46	OPA1 H7XA(-137-121)	AGGTCATTGTAAAAATT
35	OPA1 H7XA(-206-190)	ATCTTCTGTCTCTGCTT	47	OPA1 H7XA(-134-118)	AAAAGGTCATTGTAAAA
36	OPA1 H7XA(-203-187)	CTAACTTCTGTCTCTG	48	OPA1 H7XA(-131-115)	ATAAAAAGGTCATTGTA
37	OPA1 H7XA(-164-148)	TGAACATATCCATAGGA	49	OPA1 H7XA(-128-112)	TATATAAAAAGGTCATT
38	OPA1 H7XA(-161-145)	ATGTGAACATATCCATA	50	OPA1 H7XA(-125-109)	ACATATATAAAAAGGTC
39	OPA1 H7XA(-158-142)	TGTATGTGAACATATCC	51	OPA1 H7XA(-122-106)	AATACATATATAAAAAG
40	OPA1 H7XA(-155-139)	CTATGTATGTGAACATA	52	OPA1 H7XA(-119-103)	TGAAATACATATATAAA
41	OPA1 H7XA(-152-136)	TTTCTATGTATGTGAAC	53	OPA1 H7XA(-116-100)	TTCTGAAATACATATAT
42	OPA1 H7XA(-149-133)	AAATTTCTATGTATGTG	54	OPA1 H7XA(-113-97)	AAATTCTGAAATACATA
43	OPA1 H7XA(-146-130)	TAAAAATTTCTATGTAT			

SEQ ID:55: cDNA sequence of the 5' UTR of an *OPA1* transcript (GRCh38/hg38: chr3: 193593064-193593380).

GTCCGTTCCCGACGACTGTGCGCATGGCTGGTCTCCGGGACCGTTCGTGCTGCCCGCCTAGAAAGGGTGAAGTGGTTGTTCCGTGACGGACTGAGTA
CGGGTGCCCTGTCAGGCTCTTGGGGAAATCCATGCGCCAATGGGAGGGCCCTCGGCCGCGGGCTCTGTGCCCTTGTGCTGAGGGCCACTTCCTGGGGTCAITTCCTG
GACCGGAGCCGGCTGGGGCTCACACGGGGGCTCCCGCGTGGCCGCTCTCGGGCCCTGCGTGACCTCCCCCGCGCGGG

Table 3: List of antisense oligonucleotide sequences targeting the 5' UTR of an *OPAI* transcript.

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
56	OPAI_H1A(-39-17)	ACCAGCGCATGCGCACAGTGGT	75	hOPAI_H1A(-10+12)2mmT(C>T)	GGTGGCAGCACGAATGGTCCG
57	OPAI_H1A(-35-14)	AGGACCAAGCGCATGCGCACAGT	76	hOPAI_H1A(-6+16)	TC TAGGCGGGCAGCACGAACGG
58	OPAI_H1A(-26-6)1mm	GTCCGCTGAGGACCAAGGCAT	77	hOPAI_H1A(-2+21)	CC TTTCTAGGCGGGCAGCACGA
59	OPAI_H1A(-3+18)	TTTCTAGGCGGGCAGCACGA	78	hOPAI_H1A(+2+25)	TCACCCCTTTCTAGGCGGGCAGC
60	OPAI_H1A(+10+32)	CAACCACTTCACCCCTTTCTAGGC	79	hOPAI_H1A(+7+31)	AACCACTTCACCCCTTTCTAGGCGGG
61	OPAI_H1A(+13+31)	AACCACTTCACCCCTTTCTA	80	hOPAI_H1A(+12+36)	GAAACAAACCACTTCACCCCTTTCTAG
62	OPAI_H1A(+33+57)	ACCCGTACTCAGTCCGTACGGAA A	81	hOPAI_H1A(+17+41)	TCACGGAAACAAACCACTTCACCCCT T
63	OPAI_H1A(+33+54)	CGTACTCAGTCCGTACGGAA	82	hOPAI_H1A(+22+46)	GTCCGTACGGAAACCAACCACTTC A
64	OPAI_H1A(+56+80)	ACTTCCGCAAGACCTGACAGGCA C	83	hOPAI_H1A(+27+51)	ACTCAGTCCGTACGGAAACCAAC A
65	hOPAI_H1A(+63+82)	GGACTTCCGCAAGACCTGA	84	hOPAI_H1A(+38+62)	CAGGCACCCGTACTCAGTCCGTCA C
66	OPAI_H1A(+68+92)	CAATGGCGCATGGACTTCCGCAAG A	85	hOPAI_H1A(+44+67)	CCTGACAGGCACCCCGTACTCAGTC C
67	OPAI_H1A(+78+98)	CTCCCAATGGCGCATGGACT	86	hOPAI_H1A(+50+71)	GAGCCTGACAGGCACCCCGTACTC C
68	OPAI_H1A(+128+146)1mm	CCCAGGAAGTGGTCTCTCAG	87	hOPAI_H1A(+56+75)	GCAAGAGCCTGACAGGCACCCG C
69	OPAI_H1A(+148+166)	GGCTCCCGGTCCAGGAATG	88	hOPAI_H1A(+120+141)	AAGTGGCCCTCAGCAGCAAGGG C
70	OPAI_H1A(+230+218)2mm	TCACGCAGGTGCTGAGACG	89	hOPAI_H1A(+125+148)2mm T(C>T)	ACCTAGGAAGTGGTCTCTCAGCAGC T
71	hOPAI_H1A(-30-9)2mmT(C>T)	CGTGGAGGACCAAGTGCATGCGC	90	hOPAI_H1A(+129+154)	GGAATGACCCAGGAAGTGGCCCTC A
72	hOPAI_H1A(-22-2)	AA CGGTCCGCGGAGGACCAGC	91	hOPAI_H1A(+134+159)	GTCCAGGAATGACCCAGGAAGTGG C
73	hOPAI_H1A(-18+4)	GCACGAACGGTCCGCGGAGGAC	92	hOPAI_H1A(+42+66)	CTGACAGGCACCCCGTACTCAGTCC G
74	hOPAI_H1A(-14+8)2mmT(C>T)	GGCAGTACGAACGGTCTGCGGA	93	hOPAI_H1A(+44+68)	GCCTGACAGGCACCCCGTACTCAGT C

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
94	hOPAI_H1A(+45+69)	AGCCTGACAGGCCACCCGTACTCAG T	112	OPAI_H1A(+10+32)1mm10C>T	CAACCACTTTACCTTTCTAGGC
95	hOPAI_H1A(+46+70)	GAGCCTGACAGGCCACCCGTACTCA G	113	OPAI_H1A(+10+32)1mm12C>T	CAACCACTTTCATCCTTTCTAGGC
96	hOPAI_H1A(+47+71)	AGAGCCTGACAGGCCACCCGTACTC A	114	hOPAI_H1A(+63+80)	ACTTCCGCAAGAGCCTGA
97	hOPAI_H1A(+48+72)	AAGAGCCTGACAGGCCACCCGTACTC C	115	hOPAI_H1A(+79+96)	TCCCAATGGCGCATGGAC
98	hOPAI_H1A(+49+73)	CAAGAGCCTGACAGGCCACCCGTACTC T	116	hOPAI_H1A(-50-21)	GCGCATGCGCACACAGTGCCTCGGGA ACGGAC
99	hOPAI_H1A(+50+74)	GCAAGAGCCTGACAGGCCACCCCGT AC	117	hOPAI_H1A(-49-20)	AGCGCATGCGCACACAGTGCCTCGGG AACGGA
100	hOPAI_H1A(+42+66)2mmC >T	CTGACAGGCATTCTGTACTCAGTCC G	118	hOPAI_H1A(-48-19)	CAGCGCATGCGCACACAGTGCCTCGG GAACGG
101	hOPAI_H1A(+44+68)2mmC >T	GCCTGACAGGCATTGTACTCAGT C	119	hOPAI_H1A(-47-18)	CCAGCGCATGCGCACACAGTGCCTCG GGAACG
102	hOPAI_H1A(+45+69)2mmC >T	AGCCTGACAGGCATTCTGTACTCAG T	120	hOPAI_H1A(-46-17)	ACCAGCGCATGCGCACACAGTGCCTC GGGAAC
103	hOPAI_H1A(+46+70)2mmC >T	GAGCTTGACAGGCACCTGTACTCA G	121	hOPAI_H1A(-45-16)	GACCAAGCATGCGCACACAGTGCCT CGGGAA
104	hOPAI_H1A(+47+71)2mmC >T	AGAGCTTGACAGGCACCTCGTACTC A	122	hOPAI_H1A(-44-15)	GGACCAGCATGCGCACACAGTGCCTC TCGGGA
105	hOPAI_H1A(+48+72)2mmC >T	AAGAGCTTGACAGGCACCTCGTACTC C	123	hOPAI_H1A(-43-14)	AGGACCAGCATGCGCACACAGTGC GTCGGG
106	hOPAI_H1A(+49+73)2mmC >T	CAAGAGCTTGACAGGCATCCGTAC T	124	hOPAI_H1A(-42-13)	GAGGACCAGCATGCGCACACAGTGC CGTCGG
107	hOPAI_H1A(+50+74)2mmC >T	GCAAGAGCTTGACAGGCATCCGTA C	125	hOPAI_H1A(-41-12)	GGAGGACCAGCATGCGCACACAGT GCGTCG
108	OPAI_H1A(+10+34)	AACAACCACTTCACCCCTTTCTAGG C	126	hOPAI_H1A(-40-11)	CGGAGGACCAGGCATGCGCACACAG TGCCTC
109	OPAI_H1A(+10+33)	ACAACCACTTCACCCCTTTCTAGGC	127	hOPAI_H1A(-2+28)mm	CACCTTACCCCTTTCTAGGCGGGCAG CACGA
110	OPAI_H1A(+9+33)	ACAACCACTTCACCCCTTTCTAGGC G	128	hOPAI_H1A(-1+29)mm	CCACTTTACCCCTTTCTAGGCGGGCA GCACG
111	OPAI_H1A(+11+35)	AAACAACCACTTCACCCCTTTCTAG G	129	hOPAI_H1A(+1+30)mm	ACCACTTTACCCCTTTCTAGGCGGGC AGCAC

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
130	hOPAI_H1A(+2+31)mm	AACCACTTTACCCCTTTCTAGGCGG GCAGCA	134	hOPAI_H1A(+6+32)mm	CAACCACTTTACCCCTTTCTAGGCGG GC
131	hOPAI_H1A(+3+32)mm	CAACCACTTTACCCCTTTCTAGGCGG GGCAGC	135	hOPAI_H1A(+7+32)mm	CAACCACTTTACCCCTTTCTAGGCGG G
132	hOPAI_H1A(+4+32)mm	CAACCACTTTACCCCTTTCTAGGCGG GGCAG	136	hOPAI_H1A(+8+32)mm	CAACCACTTTACCCCTTTCTAGGCGG
133	hOPAI_H1A(+5+32)mm	CAACCACTTTACCCCTTTCTAGGCGG GGCA	137	hOPAI_H1A(+9+32)mm	CAACCACTTTACCCCTTTCTAGGCGG
			138	hOPAI_H1A(+10+34)mm	AACAACCACTTTACCCCTTTCTAGGCG

SEQ ID:139: cDNA sequence of the 3' UTR located within exon 30 of an *OP4* transcript (GRCh38/hg38: chr3 193694606-193697811)

GTCCGTTCCCGACGCACTGTGCGCATGCGTGGTCCCGCGGACCGCTGTGCTGCGCCCTAGAGAAAGGGTGAAGAAATCGTACTCATAATCAAGCTCTGCAT
ACATCTGAAGAACAAAAACATCAACAGTCTTTTGTCCAGCTCTTTTCTCTGCTGTTCCACCTTTCTAAACATACAATAAAGTCATGGGATAAAAAATAATCG
ATGTATGTTACGGGCGCTTTAACCATCAGTCGCTCGAATGGAACACAGTGGTAATGGAATTAACATCTATTTTGTGTAATAAGTGACAAATCGGAA
TAATATAATTGGTATGGCCATTAGGTTGAGTCTGAGGATAAGAACTTGTCTCTGTTGTGCTTATTTGTGGTGCGCACTCGTTTAAATGGAATTAATGAG
GTTGCTCAATGTTGAGTCTTTTCCAGAAATACATGCTAGGTGTTTGAATAAACTTATATAGCAATTTGTTAAAGTTATCAATGTATATATAAAATCAC
AGTAGCTGCTAAATCAATTGATGTGCTGTAGTATTTCTCCAGAAACTATTTGACCATGATTAATTCAGTTTATATTTCAACCATCAATGAAAGAAAAATGGGT
AACAGAAACCCCTTAAACACAGTTAATTGGATTGTAACTGTAGTAAAGAAATTTCAACCTTCATAGCCAGCGAAGAAATTTGCCTTGGAAAGCCCAAG
TCAGTACCAGCTTACCTATTGATTCAGTTGCTGTTTCTCACTCTATATCCATTTGAAATGATTAATTTAGATGTTGATATCTACGTTAGGCTTTCTGT
TAATAGTGGTTTCTCTGTTGACAGAGCCCGGATTATGACACAGGATGAGGAAGATTAAAGGATAATCAATGACTAATTTCAATTTAGAATATATCAAA
ACATTTCAACTAGGTATCAGAAAGGGCTTCTTTTCAAGACTATTTAAATAGAAATTAATTTCAACAAATTAAGAGTAATTTGACCATCCCTCTCAGCTG
AATAAGAAATAATTTAGTTCAATTTATGCAATTTTAAATACAATACCTCTCACAACATTTTCATGTGTTTAAATAAATATTTTAAATGGCTAAAGGAC
ATTCAAGCAAGAAATGCTTTCTTCTTACTTAAATGTCTATCTCATTTGCTGCTTTTCACTAAGCCTTTACTTTGTTAAATAAAGGTCCATTGTGTGATGTTT
TTGATTTTACAGTTTGTCTAAATCTTATTTTCTTGGAGTTGCTTTTGGTAAACAGCCCAATGCTACCTCCCAATTTATTTGTTTACATCAATGCATGCTCTGTTG
TGATCCCTCAAGATGAACACTGGTATGCTCGGTTGAGGATATGAAAAATACCTCCGAAACCAAGGAATTCATGATGTTGTTTATCTGTTGATGATAAG
AAAAGTAGTCCAGCCTTAAAGCAGCACAGATGCGCTGGTAGATGATGATGAGGAACCTTTTATTTTCTTTTAGGCTAGGGACAGGAGTGAATAGAAAGG
GAGGAGAGCTCTATTATGTTCTATACACAGATTAGGAGATGACCTTACTGGGTACACCCCTCAACCCAGTCTACAGGTTAATGCATGTTAATGAATATTTT
TGCAAGTTGTAAAGCATAAACAAATACAACTACATCTATTTCTAAAGAAATAAACAGGACCATATTATTTACTTCTGTCACACTATAGAAAGAAAGACCTTC
AGCTGATTTCCACAGATTTCTCCAAAGGAAAGGCTAATATTAGTCACTACTGTTATCAGATCCCTTGTATAAGTTTAAAGAGATGGAGGGAGATCTT
CATTTCTTTGAGGAGATCAGTATTTGTAACGATGTGGAATAGATGAACAAATTAATATTACTAAAGTCCACATGAGAGTCTGACGCTCTCCATGCCCC
ACAGTAATGTGGCTTTTCATGGGTTTTTTTCTCTTTTCTAGCTGATCCTCAAGCATTTTCTTCTGTTGTTTCTTGAAGAGTAGGTTATTTCAACTGCAG
ATGTTATTGAAAGAAATAAAATTCAGTCTCAAGAGTAAACCTGCTGCTGCTGTTGTTGTTTCAAAAGTCAAGAAATGATTTAAATTAACAAAGATAC
TAAATATACAGAAAGTTAAATTCGAACCTAGCCACAGAAATCAATTGTTTATATGTCAGAAATTTGCAAGAGTGGAGTGGACAAGCTCTGTATGGAAAGACTGAA
CAACTGTAAATAGATGATATCCAACTTAATTGGCTAGGACTCAATTTTAAATCAAGTGTACCTAGGAGTGCACAGACGAAATAGTGGCCCTTGCA
GCTTCCCGGTTTAAACCACTGTGCTATAGTTGCGGGTGGAAACAGTCAACCTTTCTAGTAGTTTATGATAATTGCCCTCTTTTGTATTCCTATTTCTACAGTTTTT

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CCGAGACCTCTTTCTGCAAAATTATTACAGCCTCCAAATGCAATGAATGATATATAAATAAGTAGGGAACATGGCAGAGAGTGGTCTTCCAGCCTCACAA
TGTGGGAATTTGACATAGGATGAGAGTCAGAGTATAGTTTAAAGATAAATCTTTAGTTAATAATTTTGTATTTATTATCTAGATGTATGTATCTGAGG
AAAGAAATCTGGTATTTTGTCTTCCAAATAAAGGGATCAAGTAATGGTTTCTCTCAGITCTCTAAGCTGTATGTATAGCTCTAGCAGTATGGA
TGTGCTTTAAATATGCTTACCTTTGAATGATCATGGCTATATGTTGTGAGATATTTGAAACCTTACCTTGTCTTCTACTTGTGCACTGTGAATGAACCTTGT
TTATTTTAAACCTTCAATACGTTGATGATATTTGCAACTTATATTTGCTGAGCTGATCAAAAGGTCATTTGTGTAGATGAGTAATTAATAAATAT
TTAAATCACATTATAATCTATTATTGGAGAGCATCTTTTAAATTTTCTGTTTAAACGAGGGGAAAGAAACCTGTATACAGGTCATTTATTGACCCC
ATAGTATAACCAAGATTCATGGTCTAAACAGCTCTAGTGGCTTCTCTGAATTCACATGCCTTGCATTCACAGTTGTACTTCCATGGTCAAC
CGGTGCTTTTTCACATCGTGGTACTTGTCAAAACATTITGTTATTTCTTGGTAAATATATAAAAAGGTTTCTTAATTCA

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10 **Table 4.** List of antisense oligonucleotide sequences with 25 nucleotides in length that target the 3' UTR of an *OPAI* transcript.

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
140	OPAI H30:31 3UTR(+1+25)	AGCTGATTATGAGTACGATTTTAAT	156	OPAI H31 3UTR(+49+73)	GAGGCTGGACAAAAGACGTTGATGT
141	OPAI H30:31 3UTR(+4+28)	CAGAGCTGATTATGAGTACGATTTT	157	OPAI H31 3UTR(+52+76)	AAAGAGGCTGGACAAAAGACGTTGA
142	OPAI H31 3UTR(+7+31)	ATGCAGAGCTGATTATGAGTACGAT	158	OPAI H31 3UTR(+55+79)	GAAAAAGAGGCTGGACAAAAGACGT
143	OPAI H31 3UTR(+10+34)	TGTATGCAGAGCTGATTATGAGTAC	159	OPAI H31 3UTR(+58+82)	GAAAGAAAAAGAGGCTGGACAAAAGA
144	OPAI H31 3UTR(+13+37)	AGATGATGCAGAGCTGATTATGAG	160	OPAI H31 3UTR(+61+85)	GCAGAAAGAAAAAGAGGCTGGACAAA
145	OPAI H31 3UTR(+16+40)	TTCAGATGTATGCAGAGCTGATTAT	161	OPAI H31 3UTR(+64+88)	ACAGCAGAAAGAAAAAGAGGCTGGAC
146	OPAI H31 3UTR(+19+43)	TTCCTCAGATGTATGCAGAGCTGAT	162	OPAI H31 3UTR(+67+91)	GGAAACAGCAGAAAGAAAAAGAGGCTG
147	OPAI H31 3UTR(+22+46)	TTGTTCTCAGATGTATGCAGAGCT	163	OPAI H31 3UTR(+70+94)	GGTGGAACAGCAGAAAGAAAAAGAGG
148	OPAI H31 3UTR(+25+49)	TTTTTGTCTCAGATGTATGCAGA	164	OPAI H31 3UTR(+73+97)	AAAGGTGGAAACAGCAGAAAGAAAAAG
149	OPAI H31 3UTR(+28+52)	ATGTTTTTGTCTTCAGATGTATGC	165	OPAI H31 3UTR(+76+100)	TAGAAAGGTGGAAACAGCAGAAAGAAA
150	OPAI H31 3UTR(+31+55)	TTGATGTTTTTGTCTTCAGATGTAT	166	OPAI H31 3UTR(+79+103)	GTTTAGAAAGGTGGAAACAGCAGAAAG
151	OPAI H31 3UTR(+34+58)	ACGTTGATGTTTTTGTCTTCAGAT	167	OPAI H31 3UTR(+82+106)	TATGTTTAGAAAGGTGGAAACAGCAG
152	OPAI H31 3UTR(+37+61)	AAGACGTTGATGTTTTTGTCTTCA	168	OPAI H31 3UTR(+85+109)	TTGTAATGTTTAGAAAGGTGGAAACAG
153	OPAI H31 3UTR(+40+64)	CAAAAAGACGTTGATGTTTTTGTCT	169	OPAI H31 3UTR(+88+112)	TTATTGTATGTTTAGAAAGGTGGAA
154	OPAI H31 3UTR(+43+67)	GGACAAAAGACGTTGATGTTTTTGT	170	OPAI H31 3UTR(+91+115)	ACTTTATTGTATGTTTAGAAAGGTG
155	OPAI H31 3UTR(+46+70)	GCTGGACAAAAGACGTTGATGTTT			

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
171	OPA1 H31 3UTR(+94+118)	ATGACTTTATTGTATGTTTAGAAAG	189	OPA1 H31 3UTR(+148+172)	GAGAGGCAGCTGATGGTTAAAGCGC
172	OPA1 H31 3UTR(+97+121)	CCCATGACTTTATTGTATGTTTAGA	190	OPA1 H31 3UTR(+151+175)	TTCGAGAGGCAGCTGATGGTTAAAG
173	OPA1 H31 3UTR(+100+124)	TATCCCATGACTTTATTGTATGTTT	191	OPA1 H31 3UTR(+154+178)	CCATTTCGAGAGGCAGCTGATGGTTA
174	OPA1 H31 3UTR(+103+127)	TTTTATCCCATGACTTTATTGTATG	192	OPA1 H31 3UTR(+157+181)	CTTCCATTTCGAGAGGCAGCTGATGG
175	OPA1 H31 3UTR(+106+130)	TATTTTATCCCATGACTTTATTGT	193	OPA1 H31 3UTR(+160+184)	GTTCTTCCATTTCGAGAGGCAGCTGA
176	OPA1 H31 3UTR(+109+133)	GATTATTTTATCCCATGACTTTAT	194	OPA1 H31 3UTR(+163+187)	ACTGTTCTTCCATTTCGAGAGGCAGC
177	OPA1 H31 3UTR(+112+136)	ATCGATTATTTTATCCCATGACTT	195	OPA1 H31 3UTR(+166+190)	ACCACTGTTCTTCCATTTCGAGAGGC
178	OPA1 H31 3UTR(+115+139)	TACATCGATTATTTTATCCCATGA	196	OPA1 H31 3UTR(+169+193)	ATTACCACTGTTCTTCCATTTCGAGA
179	OPA1 H31 3UTR(+118+142)	ACATACATCGATTATTTTATCCCA	197	OPA1 H31 3UTR(+172+196)	TCCATTACCACTGTTCTTCCATTTCG
180	OPA1 H31 3UTR(+121+145)	GTAACATACATCGATTATTTTATC	198	OPA1 H31 3UTR(+175+199)	TAATCCATTACCACTGTTCTTCCAT
181	OPA1 H31 3UTR(+124+148)	CCCGTAACATACATCGATTATTTT	199	OPA1 H31 3UTR(+178+202)	TGTTAATCCATTACCACTGTTCTTC
182	OPA1 H31 3UTR(+127+151)	GCGCCCGTAACATACATCGATTAT	200	OPA1 H31 3UTR(+181+205)	GGATGTTAATCCATTACCACTGTTTC
183	OPA1 H31 3UTR(+130+154)	AAAGCGCCCGTAACATACATCGATT	201	OPA1 H31 3UTR(+184+208)	ATAGGATGTTAATCCATTACCACTG
184	OPA1 H31 3UTR(+133+157)	GTTAAAGCGCCCGTAACATACATCG	202	OPA1 H31 3UTR(+187+211)	AAATAGGATGTTAATCCATTACCA
185	OPA1 H31 3UTR(+136+160)	ATGGTTAAAGCGCCCGTAACATACA	203	OPA1 H31 3UTR(+190+214)	AACAAAAATAGGATGTTAATCCATTA
186	OPA1 H31 3UTR(+139+163)	CTGATGGTTAAAGCGCCCGTAACAT	204	OPA1 H31 3UTR(+193+217)	TACAACAAAAATAGGATGTTAATCCA
187	OPA1 H31 3UTR(+142+166)	CAGCTGATGGTTAAAGCGCCCGTAA	205	OPA1 H31 3UTR(+196+220)	TAGTACAACAAAAATAGGATGTTAAT
188	OPA1 H31 3UTR(+145+169)	AGGCAGCTGATGGTTAAAGCGCCCG	206	OPA1 H31 3UTR(+199+223)	CTTTAGTACAACAAAAATAGGATGTT

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
207	OPAI H31 3UTR(+202+226)	TCACCTTTAGTACAACAAAATAGGAT	225	OPAI H31 3UTR(+256+280)	CTTATCTTCAAGGACTGAACCTAAT
208	OPAI H31 3UTR(+205+229)	TTGTCACCTTTAGTACAACAAAATAG	226	OPAI H31 3UTR(+259+283)	TTTCTTATCTTCAAGGACTGAACCT
209	OPAI H31 3UTR(+208+232)	GATTTGTCACCTTTAGTACAACAAA	227	OPAI H31 3UTR(+262+286)	AAGTTCTTATCTTCAAGGACTGAA
210	OPAI H31 3UTR(+211+235)	TCCGATTTGTCACCTTTAGTACAACA	228	OPAI H31 3UTR(+265+289)	AACAAGTTTCTTATCTTCAAGGACT
211	OPAI H31 3UTR(+214+238)	TATTCGATTTGTCACCTTTAGTACA	229	OPAI H31 3UTR(+268+292)	GAGAAACAAGTTTCTTATCTTCAAGG
212	OPAI H31 3UTR(+217+241)	TATTATCCGATTTGTCACCTTTAGT	230	OPAI H31 3UTR(+271+295)	ACAGAGAACAAAGTTTCTTATCTTCA
213	OPAI H31 3UTR(+220+244)	TTATATTTATCCGATTTGTCACCTTT	231	OPAI H31 3UTR(+274+298)	CAAAACAGAGAACAAAGTTTCTTATCT
214	OPAI H31 3UTR(+223+247)	CAATTATATTATCCGATTTGTCAC	232	OPAI H31 3UTR(+277+301)	CAACAAAACAGAGAACAAAGTTTCTTA
215	OPAI H31 3UTR(+226+250)	TACCAATTATATTATTCGATTTGT	233	OPAI H31 3UTR(+280+304)	AGACAAACAAACAGAGAACAAAGTTTC
216	OPAI H31 3UTR(+229+253)	CCATACCAATTATATTATTCGATT	234	OPAI H31 3UTR(+283+307)	ATAAGACAACAAACAGAGAACAAAGT
217	OPAI H31 3UTR(+232+256)	TGGCCATACCAATTATATTATTCG	235	OPAI H31 3UTR(+286+310)	CAATAAGACAACAAACAGAGAACAA
218	OPAI H31 3UTR(+235+259)	TAATGGCCATACCAATTATATTAT	236	OPAI H31 3UTR(+289+313)	CCACAAAATAAGACAACAAACAGAGA
219	OPAI H31 3UTR(+238+262)	ACCTAATGGCCATACCAATTATATT	237	OPAI H31 3UTR(+292+316)	CCACCACAAATAAGACAACAAACACAG
220	OPAI H31 3UTR(+241+265)	TGAACCTAATGGCCATACCAATTAT	238	OPAI H31 3UTR(+295+319)	GTGCCACCACAAATAAGACAACAA
221	OPAI H31 3UTR(+244+268)	GACTGAACCTAATGGCCATACCAAT	239	OPAI H31 3UTR(+298+322)	CGAGTGCCACCACAAATAAGACAAAC
222	OPAI H31 3UTR(+247+271)	AAGGACTGAACCTAATGGCCATACC	240	OPAI H31 3UTR(+301+325)	AAACGAGTGCCACCACAAATAAGAC
223	OPAI H31 3UTR(+250+274)	TTCAAGGACTGAACCTAATGGCCAT	241	OPAI H31 3UTR(+304+328)	ATTAAACGAGTGCCACCACCAATAA
224	OPAI H31 3UTR(+253+277)	ATCTTCAAGGACTGAACCTAATGGC	242	OPAI H31 3UTR(+307+331)	TCCATTAAACGAGTGCCACCACCA

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
243	OPAI H31 3UTR(+310+334)	TAAATCCATTAAACGAGTGCCACCCAC	261	OPAI H31 3UTR(+364+388)	AAACACCTAGCATTTGTATTTCTGGA
244	OPAI H31 3UTR(+313+337)	AGTTAATCCATTAAACGAGTGCCAC	262	OPAI H31 3UTR(+367+391)	TCAAAACACCTAGCATTTGTATTTCT
245	OPAI H31 3UTR(+316+340)	CTCAGTTAATCCATTAAACGAGTGC	263	OPAI H31 3UTR(+370+394)	ATTTCAAAACACCTAGCATTTGTATT
246	OPAI H31 3UTR(+319+343)	AACCTCAGTTAATCCATTAAACGAG	264	OPAI H31 3UTR(+373+397)	TTTATTTCAAAACACCTAGCATTTGT
247	OPAI H31 3UTR(+322+346)	AGCAACCTCAGTTAATCCATTAAAC	265	OPAI H31 3UTR(+376+400)	AGTTTATTTCAAAACACCTAGCAT
248	OPAI H31 3UTR(+325+349)	TTGAGCAACCTCAGTTAATCCATTA	266	OPAI H31 3UTR(+379+403)	ATAAGTTTTATTTCAAAACACCTAG
249	OPAI H31 3UTR(+328+352)	ACATTGAGCAACCTCAGTTAATCCA	267	OPAI H31 3UTR(+382+406)	TATATAAGTTTTATTTCAAAACACC
250	OPAI H31 3UTR(+331+355)	TGAACATTGAGCAACCTCAGTTAAT	268	OPAI H31 3UTR(+385+409)	TGCTATATAAGTTTTATTTCAAAAC
251	OPAI H31 3UTR(+334+358)	AACTGAACATTGAGCAACCTCAGTT	269	OPAI H31 3UTR(+388+412)	AAATGCTATATAAGTTTTATTTCAA
252	OPAI H31 3UTR(+337+361)	AGAAACTGAACATTGAGCAACCTCA	270	OPAI H31 3UTR(+391+415)	AACAAATTGCTATATAAGTTTTATTT
253	OPAI H31 3UTR(+340+364)	AAAAGAAACTGAACATTGAGCAACC	271	OPAI H31 3UTR(+394+418)	TTAAACAAATTGCTATATAAGTTTTA
254	OPAI H31 3UTR(+343+367)	TGGAAAAAGAAACTGAACATTGAGCA	272	OPAI H31 3UTR(+397+421)	ACTTTAAACAAATTGCTATATAAGTT
255	OPAI H31 3UTR(+346+370)	TTCTGGAAAAGAAACTGAACATTGA	273	OPAI H31 3UTR(+400+424)	ATAACTTTTAAACAAATTGCTATATA
256	OPAI H31 3UTR(+349+373)	TATTTCTGGAAAAGAAACTGAACAT	274	OPAI H31 3UTR(+403+427)	TTGATAAACTTTTAAACAAATTGCTATA
257	OPAI H31 3UTR(+352+376)	TTGTATTTCTGGAAAAGAAACTGAA	275	OPAI H31 3UTR(+406+430)	CAATTGATAAACTTTTAAACAAATTGCT
258	OPAI H31 3UTR(+355+379)	GCATTGTATTTCTGGAAAAGAAACT	276	OPAI H31 3UTR(+409+433)	ATACAAATTGATAAACTTTTAAACAAATT
259	OPAI H31 3UTR(+358+382)	CTAGCATTGTATTTCTGGAAAAGAA	277	OPAI H31 3UTR(+412+436)	TATATACAAATTGATAAACTTTTAAACA
260	OPAI H31 3UTR(+361+385)	CACCTAGCATTGTATTTCTGGAAAA	278	OPAI H31 3UTR(+415+439)	TTTTATATACAAATTGATAAACTTTTAA

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
279	OPAI H31 3UTR(+418+442)	TGATTTTATATACAAATTGATAACTT	297	OPAI H31 3UTR(+472+496)	TAGTTTCTGGGAATAGAACTACTACA
280	OPAI H31 3UTR(+421+445)	CTGTGATTTTATATACAAATTGATAA	298	OPAI H31 3UTR(+475+499)	AAATAGTTTCTGGGAATAGAACTACT
281	OPAI H31 3UTR(+424+448)	CTACTGTGATTTTATATACAAATTGA	299	OPAI H31 3UTR(+478+502)	GTCAAAATAGTTTCTGGGAATAGAAAT
282	OPAI H31 3UTR(+427+451)	AGGCTACTGTGATTTTATATACAAT	300	OPAI H31 3UTR(+481+505)	ATGGTCAAAATAGTTTCTGGGAATAG
283	OPAI H31 3UTR(+430+454)	AGCAGGCTACTGTGATTTTATATAC	301	OPAI H31 3UTR(+484+508)	ATCATGGTCAAAATAGTTTCTGGGAA
284	OPAI H31 3UTR(+433+457)	TTTAGCAGGCTACTGTGATTTTATA	302	OPAI H31 3UTR(+487+511)	ATTATCATGGTCAAAATAGTTTCTGG
285	OPAI H31 3UTR(+436+460)	TGATTTAGCAGGCTACTGTGATTTT	303	OPAI H31 3UTR(+490+514)	TGAATTATCATGGTCAAAATAGTTTC
286	OPAI H31 3UTR(+439+463)	CAATGATTTAGCAGGCTACTGTGAT	304	OPAI H31 3UTR(+493+517)	AACTGAAATTATCATGGTCAAAATAGT
287	OPAI H31 3UTR(+442+466)	ATACAATGATTTAGCAGGCTACTGT	305	OPAI H31 3UTR(+496+520)	ATAAACTGAAATTATCATGGTCAAAAT
288	OPAI H31 3UTR(+445+469)	CACATACAATGATTTAGCAGGCTAC	306	OPAI H31 3UTR(+499+523)	AATATAAACTGAAATTATCATGGTCA
289	OPAI H31 3UTR(+448+472)	AGACACATACAATGATTTAGCAGGC	307	OPAI H31 3UTR(+502+526)	GTGAATATAAACTGAAATTATCATGG
290	OPAI H31 3UTR(+451+475)	TACAGACACATACAATGATTTAGCA	308	OPAI H31 3UTR(+505+529)	GTGGTGAATATAAACTGAAATTATCA
291	OPAI H31 3UTR(+454+478)	TACTACAGACACATACAATGATTTA	309	OPAI H31 3UTR(+508+532)	CATGTGGTGAATATAAACTGAAATTA
292	OPAI H31 3UTR(+457+481)	GAATACTACAGACACATACAATGAT	310	OPAI H31 3UTR(+511+535)	TTTCATGTGGTGAATATAAACTGAA
293	OPAI H31 3UTR(+460+484)	ATAGAATACTACAGACACATACAAT	311	OPAI H31 3UTR(+514+538)	TTCTTTTCATGTGGTGAATATAAACT
294	OPAI H31 3UTR(+463+487)	GGAATAGAATACTACAGACACATAC	312	OPAI H31 3UTR(+517+541)	TTTTTCTTTTCATGTGGTGAATATAA
295	OPAI H31 3UTR(+466+490)	CTGGGAATAGAATACTACAGACACA	313	OPAI H31 3UTR(+520+544)	CCATTTTCTTTTCATGTGGTGAATA
296	OPAI H31 3UTR(+469+493)	TTTCTGGGAATAGAATACTACAGAC	314	OPAI H31 3UTR(+523+547)	TACCCATTTTCTTTTCATGTGGTGA

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
315	OPAI H31 3UTR(+526+550)	TGTTACCCATTTTCTTTCATGTGG	333	OPAI H31 3UTR(+580+604)	AAATTTCTTTCACTGAACGTTACAA
316	OPAI H31 3UTR(+529+553)	TTCTGTTACCCATTTTCTTTCATG	334	OPAI H31 3UTR(+583+607)	TTGAAATTTTCTTTCACTGAACGTTA
317	OPAI H31 3UTR(+532+556)	TTCTTCTGTTACCCATTTTCTTTTC	335	OPAI H31 3UTR(+586+610)	GGGTTGAAATTTTCTTTCACTGAACG
318	OPAI H31 3UTR(+535+559)	GGGTTCTTCTGTTACCCATTTTCT	336	OPAI H31 3UTR(+589+613)	GAAAGGTTGAAATTTTCTTTCACTGA
319	OPAI H31 3UTR(+538+562)	TAAAGGTTCTTCTGTTACCCATTTT	337	OPAI H31 3UTR(+592+616)	TATGAAGGTTGAAATTTTCTTTTCAC
320	OPAI H31 3UTR(+541+565)	TTTTAAGGTTCTTCTGTTACCCAT	338	OPAI H31 3UTR(+595+619)	GGCTATGAAGGTTGAAATTTCTTTT
321	OPAI H31 3UTR(+544+568)	CTGTTTAAAGGTTCTTCTGTTACC	339	OPAI H31 3UTR(+598+622)	GCTGGCTATGAAGGTTGAAATTTTC
322	OPAI H31 3UTR(+547+571)	AACCTGTTTAAAGGTTCTTCTGTT	340	OPAI H31 3UTR(+601+625)	TTCGCTGGCTATGAAGGTTGAAAT
323	OPAI H31 3UTR(+550+574)	ATTAACCTGTTTAAAGGTTCTTCT	341	OPAI H31 3UTR(+604+628)	TTCTTCGCTGGCTATGAAGGTTGA
324	OPAI H31 3UTR(+553+577)	CAAAATTAACCTGTTTAAAGGTTCT	342	OPAI H31 3UTR(+607+631)	AATTTCTTCGCTGGCTATGAAGGCT
325	OPAI H31 3UTR(+556+580)	ATCCAAATTAACCTGTTTAAAGGCT	343	OPAI H31 3UTR(+610+634)	GCAAAATTTCTTCGCTGGCTATGAAG
326	OPAI H31 3UTR(+559+583)	ACAATCCAAATTAACCTGTTTAAAG	344	OPAI H31 3UTR(+613+637)	AAGGCAAAATTTCTTCGCTGGCTATG
327	OPAI H31 3UTR(+562+586)	GTTACAATCCAAATTAACCTGTTT	345	OPAI H31 3UTR(+616+640)	TCCAAGGCAAAATTTCTTCGCTGGCT
328	OPAI H31 3UTR(+565+589)	AACGTTACAATCCAAATTAACCTGT	346	OPAI H31 3UTR(+619+643)	GCTTCCAAGGCAAAATTTCTTCGCTG
329	OPAI H31 3UTR(+568+592)	CTGAACGTTACAATCCAAATTAAC	347	OPAI H31 3UTR(+622+646)	TTGGCTTCCAAGGCAAAATTTCTTCG
330	OPAI H31 3UTR(+571+595)	TCACTGAACGTTACAATCCAAATTA	348	OPAI H31 3UTR(+625+649)	GACTTGGCTTCCAAGGCAAAATTTCT
331	OPAI H31 3UTR(+574+598)	CTTTCACGAAACGTTACAATCCAAA	349	OPAI H31 3UTR(+628+652)	ACTGACTTGGCTTCCAAGGCAAAAT
332	OPAI H31 3UTR(+577+601)	TTTCTTTCACGAAACGTTACAATCC	350	OPAI H31 3UTR(+631+655)	GGTACTGACTTGGCTTCCAAGGCAAA

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
351	OPAI H31 3UTR(+634+658)	GCTGGTACTGACTTGGCTTCCAAGG	369	OPAI H31 3UTR(+688+712)	CAATTTCAAATGGATATAGAGGTG
352	OPAI H31 3UTR(+637+661)	TAAAGCTGGTACTGACTTGGCTTCCA	370	OPAI H31 3UTR(+691+715)	AATCAATTTTCAAATGGATATAGAGA
353	OPAI H31 3UTR(+640+664)	AGGTAAGCTGGTACTGACTTGGCTT	371	OPAI H31 3UTR(+694+718)	ATAAATCAAATTTCAAATGGATATAG
354	OPAI H31 3UTR(+643+667)	AATAGGTAAGCTGGTACTGACTTGG	372	OPAI H31 3UTR(+697+721)	AAAAATAAATCAAATTTCAAATGGATA
355	OPAI H31 3UTR(+646+670)	TCAAATAGGTAAGCTGGTACTGACT	373	OPAI H31 3UTR(+700+724)	TCTAAAAATAAATCAAATTTCAAATGG
356	OPAI H31 3UTR(+649+673)	GAATCAAATAGGTAAGCTGGTACTG	374	OPAI H31 3UTR(+703+727)	ACATCTAAAAATAAATCAAATTTCAAA
357	OPAI H31 3UTR(+652+676)	ACTGAATCAAATAGGTAAGCTGGTA	375	OPAI H31 3UTR(+706+730)	ACAACATCTAAAAATAAATCAAATTC
358	OPAI H31 3UTR(+655+679)	GCAACTGAATCAAATAGGTAAGCTG	376	OPAI H31 3UTR(+709+733)	TATACAACATCTAAAAATAAATCAAT
359	OPAI H31 3UTR(+658+682)	ACAGCAACTGAATCAAATAGGTAAG	377	OPAI H31 3UTR(+712+736)	AAGTATACAACATCTAAAAATAAATC
360	OPAI H31 3UTR(+661+685)	AAAACAGCAACTGAATCAAATAGGT	378	OPAI H31 3UTR(+715+739)	CGTAAAGTATACAACATCTAAAAATAA
361	OPAI H31 3UTR(+664+688)	GAGAAAACAGCAACTGAATCAAATA	379	OPAI H31 3UTR(+718+742)	TAAACGTAAGTATACAACATCTAAAA
362	OPAI H31 3UTR(+667+691)	AGTGAGAAAAACAGCAACTGAATCAA	380	OPAI H31 3UTR(+721+745)	GCCTAACGTAAGTATACAACATCTA
363	OPAI H31 3UTR(+670+694)	GAGAGTGAGAAAAACAGCAACTGAAT	381	OPAI H31 3UTR(+724+748)	AAAGCCTAACGTAAGTATACAACAT
364	OPAI H31 3UTR(+673+697)	ATAGAGAGTGAGAAAAACAGCAACTG	382	OPAI H31 3UTR(+727+751)	CAGAAAAGCCTAACGTAAGTATACAA
365	OPAI H31 3UTR(+676+700)	GATATAGAGAGTGAGAAAAACAGCAA	383	OPAI H31 3UTR(+730+754)	TAAACAGAAAAGCCTAACGTAAGTATA
366	OPAI H31 3UTR(+679+703)	ATGGATATAGAGAGTGAGAAAAACAG	384	OPAI H31 3UTR(+733+757)	TATTAACAGAAAAGCCTAACGTAAGT
367	OPAI H31 3UTR(+682+706)	CAAAATGGATATAGAGAGTGAGAAAA	385	OPAI H31 3UTR(+736+760)	CACTATTAAACAGAAAAGCCTAACGTA
368	OPAI H31 3UTR(+685+709)	TTTCAAATGGATATAGAGAGTGAGA	386	OPAI H31 3UTR(+739+763)	AACCACTATTAAACAGAAAAGCCTAAC

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
387	OPAI H31 3UTR(+742+766)	AAAAACCACTATTAAACAGAAAGCCT	405	OPAI H31 3UTR(+796+820)	TATCCTTAATCTTCCTCATCCTGTG
388	OPAI H31 3UTR(+745+769)	GAGAAAAACCACTATTAAACAGAAAG	406	OPAI H31 3UTR(+799+823)	GATTATCCTTAATCTTCCTCATCCT
389	OPAI H31 3UTR(+748+772)	CAGGAGAAAAACCACTATTAAACAGA	407	OPAI H31 3UTR(+802+826)	ATTGATTATCCTTAATCTTCCTCAT
390	OPAI H31 3UTR(+751+775)	CAACAGGAGAAAAACCACTATTAAAC	408	OPAI H31 3UTR(+805+829)	TCAATTGATTATCCTTAATCTTCCT
391	OPAI H31 3UTR(+754+778)	TGTCAACAGGAGAAAAACCACTATT	409	OPAI H31 3UTR(+808+832)	TAGTCAATTGATTATCCTTAATCTT
392	OPAI H31 3UTR(+757+781)	CTCTGTCAACAGGAGAAAAACCACT	410	OPAI H31 3UTR(+811+835)	AATTAGTCAATTGATTATCCTTAAT
393	OPAI H31 3UTR(+760+784)	TGGCTCTGTCAACAGGAGAAAAACC	411	OPAI H31 3UTR(+814+838)	TGAAATTAGTCAATTGATTATCCTT
394	OPAI H31 3UTR(+763+787)	CGGTGGCTCTGTCAACAGGAGAAAA	412	OPAI H31 3UTR(+817+841)	AAATGAAATTAGTCAATTGATTATC
395	OPAI H31 3UTR(+766+790)	ATCCGGTGGCTCTGTCAACAGGAGA	413	OPAI H31 3UTR(+820+844)	TCTAAATGAAATTAGTCAATTGATT
396	OPAI H31 3UTR(+769+793)	ATAATCCGGTGGCTCTGTCAACAGG	414	OPAI H31 3UTR(+823+847)	TATTCTAAATGAAATTAGTCAATTG
397	OPAI H31 3UTR(+772+796)	GTCATAATCCGGTGGCTCTGTCAAC	415	OPAI H31 3UTR(+826+850)	TAATATTCTAAATGAAATTAGTCAA
398	OPAI H31 3UTR(+775+799)	TGTGTCATAATCCGGTGGCTCTGTGTC	416	OPAI H31 3UTR(+829+853)	TGATAATATTCTAAATGAAATTAGT
399	OPAI H31 3UTR(+778+802)	TCCTGTGTCATAATCCGGTGGCTCT	417	OPAI H31 3UTR(+832+856)	GTTTGATAATATTCTAAATGAAATT
400	OPAI H31 3UTR(+781+805)	TCATCCTGTGTCATAATCCGGTGGC	418	OPAI H31 3UTR(+835+859)	AATGTTTGATAATATTCTAAATGAA
401	OPAI H31 3UTR(+784+808)	TCCTCATCCTGTGTCATAATCCGGT	419	OPAI H31 3UTR(+838+862)	TGAAATGTTTGATAATATTCTAAAT
402	OPAI H31 3UTR(+787+811)	TCTTCCTCATCCTGTGTCATAATCC	420	OPAI H31 3UTR(+841+865)	AGTTGAAATGTTTGATAATATTCTA
403	OPAI H31 3UTR(+790+814)	TAATCTCCTCATCCTGTGTCATAA	421	OPAI H31 3UTR(+844+868)	CCTAGTTGAAATGTTTGATAATATT
404	OPAI H31 3UTR(+793+817)	CCTTAATCTTCCTCATCCTGTGTCA	422	OPAI H31 3UTR(+847+871)	ATACCTAGTTGAAATGTTTGATAAT

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
423	OPAI H31 3UTR(+850+874)	CTGATACCTAGTTGAAATGTTGAT	441	OPAI H31 3UTR(+904+928)	TTAATTGTTGAAATAAATTTCTATTT
424	OPAI H31 3UTR(+853+877)	TTTCTGATACCTAGTTGAAATGTTT	442	OPAI H31 3UTR(+907+931)	ACTTTAAATTTGTTGAAATAAATTTCTA
425	OPAI H31 3UTR(+856+880)	CTTTTCTGATACCTAGTTGAAATG	443	OPAI H31 3UTR(+910+934)	ATTACTTTAAATTTGTTGAAATAAATTT
426	OPAI H31 3UTR(+859+883)	AGCCTTTTCTGATACCTAGTTGAA	444	OPAI H31 3UTR(+913+937)	AACATTACTTTAAATTTGTTGAAATAA
427	OPAI H31 3UTR(+862+886)	GAAAGCCTTTTCTGATACCTAGTT	445	OPAI H31 3UTR(+916+940)	GTCAACATTACTTTAAATTTGTGAAA
428	OPAI H31 3UTR(+865+889)	AAAGAAAGCCTTTTCTGATACCTA	446	OPAI H31 3UTR(+919+943)	ATGGTCAACATTACTTTAAATTTGTTG
429	OPAI H31 3UTR(+868+892)	ATGAAAGAAAGCCTTTTCTGATAC	447	OPAI H31 3UTR(+922+946)	GGGATGGTCAACATTACTTTAAATTTG
430	OPAI H31 3UTR(+871+895)	CTTATGAAAGAAAGCCTTTTCTGA	448	OPAI H31 3UTR(+925+949)	AGGGGGATGGTCAACATTACTTTAA
431	OPAI H31 3UTR(+874+898)	AGTCTTATGAAAGAAAGCCTTTTTC	449	OPAI H31 3UTR(+928+952)	GAGAGGGGGATGGTCAACATTACTTT
432	OPAI H31 3UTR(+877+901)	AATAGTCTTATGAAAGAAAGCCTTT	450	OPAI H31 3UTR(+931+955)	GCTGAGAGGGGGATGGTCAACATTAA
433	OPAI H31 3UTR(+880+904)	TAAATAGTCTTATGAAAGAAAGGCC	451	OPAI H31 3UTR(+934+958)	TCAGCTGAGAGGGGGATGGTCAACA
434	OPAI H31 3UTR(+883+907)	ATTTAAATAGTCTTATGAAAGAAA	452	OPAI H31 3UTR(+937+961)	TATTCAGCTGAGAGGGGGATGGTCA
435	OPAI H31 3UTR(+886+910)	TCTATTTAAATAGTCTTATGAAAG	453	OPAI H31 3UTR(+940+964)	CTTTATTCAGCTGAGAGGGGGATGG
436	OPAI H31 3UTR(+889+913)	ATTCTATTTAAATAGTCTTATGA	454	OPAI H31 3UTR(+943+967)	TTTCTTTTATTCAGCTGAGAGGGGGA
437	OPAI H31 3UTR(+892+916)	ATAATTTCTATTTAAATAGTCTTA	455	OPAI H31 3UTR(+946+970)	ATTTTCTTTTATTCAGCTGAGAGGG
438	OPAI H31 3UTR(+895+919)	GAAATAATTTCTATTTAAATAGTC	456	OPAI H31 3UTR(+949+973)	TAAATTTTCTTTTATTCAGCTGAGA
439	OPAI H31 3UTR(+898+922)	GTTGAAATAATTTCTATTTAAATA	457	OPAI H31 3UTR(+952+976)	AACTAAATTTTCTTTTATTCAGCTG
440	OPAI H31 3UTR(+901+925)	ATTGTTGAAATAATTTCTATTTAAA	458	OPAI H31 3UTR(+955+979)	TTGAACTAAATTTTCTTTTATTCAG

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
459	OPAI H31 3UTR(+958+982)	AAATTGAACATAAATTTTCTTTATT	477	OPAI H31 3UTR(+1012+1036)	TTATTTAAACACATGAAAAATGTTG
460	OPAI H31 3UTR(+961+985)	AATAAATTGAACATAAATTTTCTTT	478	OPAI H31 3UTR(+1015+1039)	TATTTATTTAAACACATGAAATG
461	OPAI H31 3UTR(+964+988)	TGCAATAAATTGAACATAAATTTTTC	479	OPAI H31 3UTR(+1018+1042)	AAATATTTATTTAAACACACATGAAA
462	OPAI H31 3UTR(+967+991)	AATTGCAATAAATTGAACATAAATTT	480	OPAI H31 3UTR(+1021+1045)	AAAAAATATTTATTTAAACACATG
463	OPAI H31 3UTR(+970+994)	TTAAATTGCAATAAATTGAACATAA	481	OPAI H31 3UTR(+1024+1048)	ATTAATAAATATTTATTTAAACAC
464	OPAI H31 3UTR(+973+997)	TAATTAATTTGCAATAAATTGAACT	482	OPAI H31 3UTR(+1027+1051)	CCAAATTAATAAATATTTATTTAAAA
465	OPAI H31 3UTR(+976+1000)	TTGTAATTAATTTGCAATAAATTGA	483	OPAI H31 3UTR(+1030+1054)	TAGCCAAATTAATAAATATTTATTTA
466	OPAI H31 3UTR(+979+1003)	GTATTGTAATTAATTTGCAATAAAT	484	OPAI H31 3UTR(+1033+1057)	CTTTAGCCAAATTAATAAATATTTAT
467	OPAI H31 3UTR(+982+1006)	GTAGTATTGTAATTAATTTGCAATA	485	OPAI H31 3UTR(+1036+1060)	GTCTTTTAGCCAAATTAATAAATATTT
468	OPAI H31 3UTR(+985+1009)	AAGGTAGTATTGTAATTAATTTGCA	486	OPAI H31 3UTR(+1039+1063)	AATGTCTTTTAGCCAAATTAATAAAT
469	OPAI H31 3UTR(+988+1012)	GTGAAGGTAGTATTGTAATTTAAAT	487	OPAI H31 3UTR(+1042+1066)	TTGAATGTCTTTTAGCCAAATTAATA
470	OPAI H31 3UTR(+991+1015)	GTTGTGAAGGTAGTATTGTAATTA	488	OPAI H31 3UTR(+1045+1069)	TGCTTGAATGTCTTTTAGCCAAATTA
471	OPAI H31 3UTR(+994+1018)	AATGTTGTGAAGGTAGTATTGTAAT	489	OPAI H31 3UTR(+1048+1072)	CTTTGCTTGAATGTCTTTTAGCCAA
472	OPAI H31 3UTR(+997+1021)	GAAAAATGTTGTGAAGGTAGTATTGT	490	OPAI H31 3UTR(+1051+1075)	TTTCTTTGCTTGAATGTCTTTTAGC
473	OPAI H31 3UTR(+1000+1024)	CATGAAAAATGTTGTGAAGGTAGTAT	491	OPAI H31 3UTR(+1054+1078)	GCATTTCTTTGCTTGAATGTCTTTT
474	OPAI H31 3UTR(+1003+1027)	ACACATGAAAAATGTTGTGAAGGTAG	492	OPAI H31 3UTR(+1057+1081)	AAAGCATTTCTTTGCTTGAATGTCTC
475	OPAI H31 3UTR(+1006+1030)	AAAACACATGAAAAATGTTGTGAAGG	493	OPAI H31 3UTR(+1060+1084)	AAGAAAGCATTTCTTTGCTTGAATG
476	OPAI H31 3UTR(+1009+1033)	TTTAAAAACACATGAAAAATGTTGTGA	494	OPAI H31 3UTR(+1063+1087)	GTAAAGAAAGCATTTCTTTGCTTGA

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
495	OPAI H31 3UTR(+1066+1090)	TAAGTAAAGAAAGCATTTCTTGCT	513	OPAI H31 3UTR(+1120+1144)	TTTTATTAAACAAAGTAAAGGCTTAG
496	OPAI H31 3UTR(+1069+1093)	TTTTAAGTAAAGAAAGCATTTCTTT	514	OPAI H31 3UTR(+1123+1147)	CACTTTTATTAAACAAAGTAAAGGCT
497	OPAI H31 3UTR(+1072+1096)	ACATTTTAAAGTAAAGAAAGCATTTTC	515	OPAI H31 3UTR(+1126+1150)	GGACACTTTTATTAAACAAAGTAAAG
498	OPAI H31 3UTR(+1075+1099)	TAGACATTTTAAAGTAAAGAAAGCAT	516	OPAI H31 3UTR(+1129+1153)	AATGGACACTTTTATTAAACAAAGTA
499	OPAI H31 3UTR(+1078+1102)	AGATAGACATTTTAAAGTAAAGAAAG	517	OPAI H31 3UTR(+1132+1156)	CACAAATGGACACTTTTATTAAACAAA
500	OPAI H31 3UTR(+1081+1105)	ATGAGATAGACATTTTAAAGTAAAGA	518	OPAI H31 3UTR(+1135+1159)	TCACACAATGGACACTTTTATTAAAC
501	OPAI H31 3UTR(+1084+1108)	CAAAATGAGATAGACATTTTAAAGTAA	519	OPAI H31 3UTR(+1138+1162)	ACATCACACAATGGACACTTTTATT
502	OPAI H31 3UTR(+1087+1111)	CAGCAAAATGAGATAGACATTTTAAAG	520	OPAI H31 3UTR(+1141+1165)	AAAACATCACACAATGGACACTTTT
503	OPAI H31 3UTR(+1090+1114)	AGGCAGCAAAATGAGATAGACATTTT	521	OPAI H31 3UTR(+1144+1168)	TCAAAAACATCACACAATGGACACT
504	OPAI H31 3UTR(+1093+1117)	AAAAAGCAGCAAAATGAGATAGACAT	522	OPAI H31 3UTR(+1147+1171)	AAATCAAAAAACATCACACAATGGAC
505	OPAI H31 3UTR(+1096+1120)	GTGAAAAAGGCAGCAAAATGAGATAGA	523	OPAI H31 3UTR(+1150+1174)	GTAAAAATCAAAAAACATCACACAATG
506	OPAI H31 3UTR(+1099+1123)	TTAGTAAAAAGGCAGCAAAATGAGAT	524	OPAI H31 3UTR(+1153+1177)	ACTGTAAAAATCAAAAAACATCACACA
507	OPAI H31 3UTR(+1102+1126)	GGCTTAGTAAAAAGGCAGCAAAATGA	525	OPAI H31 3UTR(+1156+1180)	CAAACTGTAAAAATCAAAAAACATCAC
508	OPAI H31 3UTR(+1105+1129)	AAAGGCTTAGTAAAAAGGCAGCAAA	526	OPAI H31 3UTR(+1159+1183)	TAGCAAACTGTAAAAATCAAAAAACAT
509	OPAI H31 3UTR(+1108+1132)	AGTAAAGGCTTAGTAAAAAGGCAGC	527	OPAI H31 3UTR(+1162+1186)	ATTAGCAAACTGTAAAAATCAAAAA
510	OPAI H31 3UTR(+1111+1135)	CAAAGTAAAGGCTTAGTAAAAAGGC	528	OPAI H31 3UTR(+1165+1189)	AAGATTTAGCAAACTGTAAAAATCAA
511	OPAI H31 3UTR(+1114+1138)	TAAACAAAGTAAAGGCTTAGTAAAAA	529	OPAI H31 3UTR(+1168+1192)	AATAAGATTTAGCAAACTGTAAAAAT
512	OPAI H31 3UTR(+1117+1141)	TATTAACAAAGTAAAGGCTTAGTGA	530	OPAI H31 3UTR(+1171+1195)	GAAAAATAAGATTTAGCAAACTGTAA

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
531	OPAI H31 3UTR(+1174+1198)	CAAGAAAAATAAGATTTAGCAAACTG	549	OPAI H31 3UTR(+1228+1252)	ATGTAAAAACAATAAAATGGGGAGTA
532	OPAI H31 3UTR(+1177+1201)	CTCCAAGAAAAATAAGATTTAGCAAA	550	OPAI H31 3UTR(+1231+1255)	TTGATGTAAAAACAATAAAATGGGGA
533	OPAI H31 3UTR(+1180+1204)	CAACTCCAAGAAAAATAAGATTTAGC	551	OPAI H31 3UTR(+1234+1258)	GCATTGATGTAAAAACAATAAAATGG
534	OPAI H31 3UTR(+1183+1207)	AAGCAACTCCAAGAAAAATAAGATTT	552	OPAI H31 3UTR(+1237+1261)	CATGCATTGATGTAAAAACAATAAAAA
535	OPAI H31 3UTR(+1186+1210)	AAAAAGCAACTCCAAGAAAAATAAGA	553	OPAI H31 3UTR(+1240+1264)	AAGCATGCATTGATGTAAAAACAATA
536	OPAI H31 3UTR(+1189+1213)	ACCAAAAAAGCAACTCCAAGAAAAATA	554	OPAI H31 3UTR(+1243+1267)	ACGAAAGCATGCATTGATGTAAAAACA
537	OPAI H31 3UTR(+1192+1216)	GTTACCAAAAAAGCAACTCCAAGAAA	555	OPAI H31 3UTR(+1246+1270)	ACAAACGAAGCATGCATTGATGTAAAA
538	OPAI H31 3UTR(+1195+1219)	GCTGTTACCAAAAAAGCAACTCCAAG	556	OPAI H31 3UTR(+1249+1273)	ATCAACAACGAAGCATGCATTGATGT
539	OPAI H31 3UTR(+1198+1222)	GGGGCTGTTACCAAAAAAGCAACTCC	557	OPAI H31 3UTR(+1252+1276)	GGGATCACAACGAAGCATGCATTGA
540	OPAI H31 3UTR(+1201+1225)	AATGGGGCTGTTACCAAAAAAGCAAC	558	OPAI H31 3UTR(+1255+1279)	TGAGGGATCACAACGAAGCATGCAT
541	OPAI H31 3UTR(+1204+1228)	AGCAATGGGGCTGTTACCAAAAAAGC	559	OPAI H31 3UTR(+1258+1282)	TCTTGAGGGATCACAACGAAGCATG
542	OPAI H31 3UTR(+1207+1231)	AGTAGCAATGGGGCTGTTACCAAAAA	560	OPAI H31 3UTR(+1261+1285)	ACATCTTGAGGGATCACAACGAAGC
543	OPAI H31 3UTR(+1210+1234)	GGGAGTAGCAATGGGGCTGTTACCA	561	OPAI H31 3UTR(+1264+1288)	GTTACATCTTGAGGGATCACAACGA
544	OPAI H31 3UTR(+1213+1237)	ATGGGGAGTAGCAATGGGGCTGTTA	562	OPAI H31 3UTR(+1267+1291)	AGTGTTACATCTTGAGGGATCACA
545	OPAI H31 3UTR(+1216+1240)	AAAAATGGGGAGTAGCAATGGGGCTG	563	OPAI H31 3UTR(+1270+1294)	CCAAAGTGTACATCTTGAGGGATCA
546	OPAI H31 3UTR(+1219+1243)	AATAAAAAATGGGGAGTAGCAATGGGG	564	OPAI H31 3UTR(+1273+1297)	ATACCAAAGTGTACATCTTGAGGGA
547	OPAI H31 3UTR(+1222+1246)	AACAATAAAAAATGGGGAGTAGCAATG	565	OPAI H31 3UTR(+1276+1300)	AGCATACCAAGTGTACATCTTGAG
548	OPAI H31 3UTR(+1225+1249)	TAAAAACAATAAAAAATGGGGAGTAGCA	566	OPAI H31 3UTR(+1279+1303)	CCGAGCATACCAAGTGTACATCTT

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
567	OPAI H31 3UTR(+1282+1306)	CAACCGAGCATACCAAGTTACAT	585	OPAI H31 3UTR(+1336+1360)	TATAAACAAACATACATTGAATTC
568	OPAI H31 3UTR(+1285+1309)	CCTCAACCGAGCATACCAAGTGTTA	586	OPAI H31 3UTR(+1339+1363)	CAGTATAAAACAAACATACATTGAA
569	OPAI H31 3UTR(+1288+1312)	TATCCTCAACCGAGCATACCAAGTG	587	OPAI H31 3UTR(+1342+1366)	AAACAGTATAAAACAAACATACATT
570	OPAI H31 3UTR(+1291+1315)	TCATATCCTCAACCGAGCATACCAA	588	OPAI H31 3UTR(+1345+1369)	ATCAACAGTATAAAACAAACATAC
571	OPAI H31 3UTR(+1294+1318)	TTTTCATATCCTCAACCGAGCATAC	589	OPAI H31 3UTR(+1348+1372)	CTTATCAAAACAGTATAAAACAAACA
572	OPAI H31 3UTR(+1297+1321)	ATTTTTCATATCCTCAACCGAGCA	590	OPAI H31 3UTR(+1351+1375)	TTTCTTATCAAAACAGTATAAAACAA
573	OPAI H31 3UTR(+1300+1324)	AGTATTTTTCATATCCTCAACCGA	591	OPAI H31 3UTR(+1354+1378)	ACTTTTCTTATCAAAACAGTATAAAA
574	OPAI H31 3UTR(+1303+1327)	GGAAGTATTTTTCATATCCTCAAC	592	OPAI H31 3UTR(+1357+1381)	CCTACTTTTCTTATCAAAACAGTATA
575	OPAI H31 3UTR(+1306+1330)	TTTCGGAAGTATTTTTCATATCCTC	593	OPAI H31 3UTR(+1360+1384)	GGACCTACTTTTCTTATCAAAACAGT
576	OPAI H31 3UTR(+1309+1333)	GGTTTCGGAAGTATTTTTCATATC	594	OPAI H31 3UTR(+1363+1387)	GCTGGACCTACTTTTCTTATCAAAAC
577	OPAI H31 3UTR(+1312+1336)	CCTGGTTTCGGAAGTATTTTTCAT	595	OPAI H31 3UTR(+1366+1390)	AAGGCTGGACCTACTTTTCTTATCA
578	OPAI H31 3UTR(+1315+1339)	ATTCCTGGTTTCGGAAGTATTTTTC	596	OPAI H31 3UTR(+1369+1393)	CTTAAGGCTGGACCTACTTTTCTTA
579	OPAI H31 3UTR(+1318+1342)	TGAATTCCTGGTTTCGGAAGTATTT	597	OPAI H31 3UTR(+1372+1396)	CTGCTTAAGGCTGGACCTACTTTTC
580	OPAI H31 3UTR(+1321+1345)	CATTGAATTCCTGGTTTCGGAAGTA	598	OPAI H31 3UTR(+1375+1399)	GTGCTGCTTAAGGCTGGACCTACTT
581	OPAI H31 3UTR(+1324+1348)	ATACATTGAATTCCTGGTTTCGGAA	599	OPAI H31 3UTR(+1378+1402)	TCTGTGCTGCTTAAGGCTGGACCTA
582	OPAI H31 3UTR(+1327+1351)	AACATACATTGAATTCCTGGTTTCG	600	OPAI H31 3UTR(+1381+1405)	GCATCTGTGCTGCTTAAGGCTGGAC
583	OPAI H31 3UTR(+1330+1354)	ACAAACATACATTGAATTCCTGGTT	601	OPAI H31 3UTR(+1384+1408)	AGCGCATCTGTGCTGCTTAAGGCTG
584	OPAI H31 3UTR(+1333+1357)	AAAAACATACATTGAATTCCTG	602	OPAI H31 3UTR(+1387+1411)	ACCAGCGCATCTGTGCTGCTTAAGG

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603	OPAI H31 3UTR(+1390+1414)	TCTACCAGCGCATCTGTGCTTA	621	OPAI H31 3UTR(+1444+1468)	TATTCACCTCCTGTCCCTAGACCTAA
604	OPAI H31 3UTR(+1393+1417)	GCATCTACCAGCGCATCTGTGCTGC	622	OPAI H31 3UTR(+1447+1471)	TTCTATTACACTCCTGTGCCCTAGACC
605	OPAI H31 3UTR(+1396+1420)	TATGCATCTACCAGCGCATCTGTGTC	623	OPAI H31 3UTR(+1450+1474)	CCTTTCTATTCACTCCTGTGCCCTAG
606	OPAI H31 3UTR(+1399+1423)	GACTATGCATCTACCAGCGCATCTG	624	OPAI H31 3UTR(+1453+1477)	CTCCCTTTCTATTCACTCCTGTGCC
607	OPAI H31 3UTR(+1402+1426)	CCTGACTATGCATCTACCAGCGCAT	625	OPAI H31 3UTR(+1456+1480)	CTCCTCCCTTTCTATTCACTCCTGT
608	OPAI H31 3UTR(+1405+1429)	GTTCCCTGACTATGCATCTACCAGCG	626	OPAI H31 3UTR(+1459+1483)	GCCTCTCCCTTTCTATTCACTCC
609	OPAI H31 3UTR(+1408+1432)	AAAGTTCTGACTATGCATCTACCA	627	OPAI H31 3UTR(+1462+1486)	AGAGCTCTCCTCCCTTTCTATTCAAC
610	OPAI H31 3UTR(+1411+1435)	AAAAAAGTTCTGACTATGCATCTA	628	OPAI H31 3UTR(+1465+1489)	AATAGAGCTCTCCTCCCTTTCTATT
611	OPAI H31 3UTR(+1414+1438)	ATAAAAAAAGTTCTGACTATGCAT	629	OPAI H31 3UTR(+1468+1492)	CATAATAGAGCTCTCCTCCCTTTCT
612	OPAI H31 3UTR(+1417+1441)	GAAATAAAAAAGTTCTGACTATG	630	OPAI H31 3UTR(+1471+1495)	GAACATAATAGAGCTCTCCTCCCTT
613	OPAI H31 3UTR(+1420+1444)	AAAGAAATAAAAAAGTTCTGACT	631	OPAI H31 3UTR(+1474+1498)	ATAGAACATAATAGAGCTCTCCTCC
614	OPAI H31 3UTR(+1423+1447)	CTAAAAAGAAATAAAAAAGTTCTCTG	632	OPAI H31 3UTR(+1477+1501)	TGTATAGAACATAATAGAGCTCTCC
615	OPAI H31 3UTR(+1426+1450)	GACCTAAAGAAATAAAAAAGTTCT	633	OPAI H31 3UTR(+1480+1504)	CTGTGTATAGAACATAATAGAGCTC
616	OPAI H31 3UTR(+1429+1453)	CTAGACCTAAAGAAATAAAAAAG	634	OPAI H31 3UTR(+1483+1507)	AATCTGTGTATAGAACATAATAGAG
617	OPAI H31 3UTR(+1432+1456)	TCCCTAGACCTAAAGAAATAAAAA	635	OPAI H31 3UTR(+1486+1510)	CCTAATCTGTGTATAGAACATAATA
618	OPAI H31 3UTR(+1435+1459)	CTGTCCCTAGACCTAAAGAAATAA	636	OPAI H31 3UTR(+1489+1513)	TCTCCTAATCTGTGTATAGAACATA
619	OPAI H31 3UTR(+1438+1462)	CTCCTGTCCCTAGACCTAAAGAAA	637	OPAI H31 3UTR(+1492+1516)	TCATCTCCTAATCTGTGTATAGAAC
620	OPAI H31 3UTR(+1441+1465)	TCACTCCTGTCCCTAGACCTAAAG	638	OPAI H31 3UTR(+1495+1519)	AGGTCATCTCCTAATCTGTGTATAG

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639	OPAI H31 3UTR(+1498+1522)	GTAAGGTCATCTCTCCTAATCTGTGTA	657	OPAI H31 3UTR(+1552+1576)	AAATATTCAATTAACATGCATTAAACC
640	OPAI H31 3UTR(+1501+1525)	CCAGTAAGGTCATCTCCTAATCTGT	658	OPAI H31 3UTR(+1555+1579)	CAAAAATATTTCATTAAACATGCATTA
641	OPAI H31 3UTR(+1504+1528)	TACCCAGTAAAGGTCATCTCCTAATC	659	OPAI H31 3UTR(+1558+1582)	CTGCAAAAAATATTTCATTAAACATGCA
642	OPAI H31 3UTR(+1507+1531)	GTGTACCCAGTAAGGTCATCTCCTA	660	OPAI H31 3UTR(+1561+1585)	CAACTGCAAAAAATATTTCATTAAACAT
643	OPAI H31 3UTR(+1510+1534)	GGGGTGTACCCAGTAAGGTCATCTC	661	OPAI H31 3UTR(+1564+1588)	TTACAACTGCAAAAAATATTTCATTAA
644	OPAI H31 3UTR(+1513+1537)	AGAGGGGTGTACCCAGTAAGGTCAT	662	OPAI H31 3UTR(+1567+1591)	GCCTTACAACTGCAAAAAATATTTCAT
645	OPAI H31 3UTR(+1516+1540)	GTTAGAGGGGTGTACCCAGTAAGGT	663	OPAI H31 3UTR(+1570+1594)	TATGCTTTACAACTGCAAAAAATATT
646	OPAI H31 3UTR(+1519+1543)	CTGGTTAGAGGGGTGTACCCAGTAA	664	OPAI H31 3UTR(+1573+1597)	TGTTATGCTTTACAACTGCAAAAAAT
647	OPAI H31 3UTR(+1522+1546)	GCACTGGTTAGAGGGGTGTACCCAG	665	OPAI H31 3UTR(+1576+1600)	AATGTATTGCTTTACAACTGCAAAA
648	OPAI H31 3UTR(+1525+1549)	TAAGCACTGGTTAGAGGGGTGTACC	666	OPAI H31 3UTR(+1579+1603)	TGTAATTGTTATGCTTTACAACTGC
649	OPAI H31 3UTR(+1528+1552)	CTGTAAGCACTGGTTAGAGGGGTGT	667	OPAI H31 3UTR(+1582+1606)	AGTTGTAATTGTTATGCTTTACAAC
650	OPAI H31 3UTR(+1531+1555)	AACCTGTAAGCACTGGTTAGAGGGG	668	OPAI H31 3UTR(+1585+1609)	TGTAGTTGTAATTGTTATGCTTTAC
651	OPAI H31 3UTR(+1534+1558)	ATTAACTGTAAGCACTGGTTAGAG	669	OPAI H31 3UTR(+1588+1612)	ATGTGTAATTGTTATGTTATGCTT
652	OPAI H31 3UTR(+1537+1561)	TGCATTAACTGTAAGCACTGGTTA	670	OPAI H31 3UTR(+1591+1615)	TAGATGTGTAGTTGTAATTGTTATG
653	OPAI H31 3UTR(+1540+1564)	ACATGCATTAACTGTAAGCACTGG	671	OPAI H31 3UTR(+1594+1618)	AAATAGATGTGTAGTTGTAATTGTT
654	OPAI H31 3UTR(+1543+1567)	TTAACATGCATTAACTGTAAGCAC	672	OPAI H31 3UTR(+1597+1621)	TAGAAAATAGATGTGTAGTTGTAATT
655	OPAI H31 3UTR(+1546+1570)	TCATTAACTGCATTAACTGTAAG	673	OPAI H31 3UTR(+1600+1624)	CTTTAGAAAATAGATGTGTAGTTGTA
656	OPAI H31 3UTR(+1549+1573)	TATTCATTAACTGCATTAACTGT	674	OPAI H31 3UTR(+1603+1627)	ATTCTTTAGAAAATAGATGTGTAGTT

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675	OPAI H31 3UTR(+1606+1630)	TTTATTCTTTTAGAAATAGATGTGA	693	OPAI H31 3UTR(+1660+1684)	CAGCTGAAGGCTCTTTCTTTCTATAG
676	OPAI H31 3UTR(+1609+1633)	TGTTTTATTCTTTAGAAATAGATGT	694	OPAI H31 3UTR(+1663+1687)	ATACAGCTGAAGGCTCTTTCTTTCTA
677	OPAI H31 3UTR(+1612+1636)	TCCTGTTTTATTCTTTAGAAATAGA	695	OPAI H31 3UTR(+1666+1690)	GAAATACAGCTGAAGGCTCTTTCTTT
678	OPAI H31 3UTR(+1615+1639)	TGGTCCTGTTTTATTCTTTAGAAAT	696	OPAI H31 3UTR(+1669+1693)	GTGGAAATACAGCTGAAGGCTTTTC
679	OPAI H31 3UTR(+1618+1642)	ATATGGTCCTGTTTTATTCTTTAGA	697	OPAI H31 3UTR(+1672+1696)	TCTGTGAAATACAGCTGAAGGCTCT
680	OPAI H31 3UTR(+1621+1645)	TAAATATGGTCCTGTTTTATTCTTTT	698	OPAI H31 3UTR(+1675+1699)	AAATCTGTGGAATACAGCTGAAGG
681	OPAI H31 3UTR(+1624+1648)	AAATAAATATGGTCCTGTTTTATTCT	699	OPAI H31 3UTR(+1678+1702)	GAGAAATCTGTGGGAAATACAGCTGA
682	OPAI H31 3UTR(+1627+1651)	AGTAAATAAATATGGTCCTGTTTTTA	700	OPAI H31 3UTR(+1681+1705)	TGGGAGAAATCTGTGGGAAATACAGC
683	OPAI H31 3UTR(+1630+1654)	AGAAATAAATAAATATGGTCCTGTT	701	OPAI H31 3UTR(+1684+1708)	CCTTGGGAGAAATCTGTGGGAAATAC
684	OPAI H31 3UTR(+1633+1657)	GACAGAAATAAATAAATATGGTCCT	702	OPAI H31 3UTR(+1687+1711)	TTTCCTTGGGAGAAATCTGTGGAAA
685	OPAI H31 3UTR(+1636+1660)	GTTGACAGAAATAAATAAATATGGT	703	OPAI H31 3UTR(+1690+1714)	CCTTTTCTTGGGAGAAATCTGTGG
686	OPAI H31 3UTR(+1639+1663)	ATAGTTGACAGAAATAAATAAATAT	704	OPAI H31 3UTR(+1693+1717)	TAGCCTTTTCTTGGGAGAAATCTG
687	OPAI H31 3UTR(+1642+1666)	TCTATAGTTGACAGAAATAAATAA	705	OPAI H31 3UTR(+1696+1720)	TATTAGCCTTTTCTTGGGAGAAAT
688	OPAI H31 3UTR(+1645+1669)	CTTCTATAGTTGACAGAAATAAAT	706	OPAI H31 3UTR(+1699+1723)	TAATATTAGCCTTTTCTTGGGAGA
689	OPAI H31 3UTR(+1648+1672)	TTTCTTTCTATAGTTGACAGAAATA	707	OPAI H31 3UTR(+1702+1726)	GACTAATAATTAGCCTTTTCTTGGG
690	OPAI H31 3UTR(+1651+1675)	GTCTTTCTTTCTATAGTTGACAGAA	708	OPAI H31 3UTR(+1705+1729)	AGTGACTAATAATTAGCCTTTTCTCT
691	OPAI H31 3UTR(+1654+1678)	AAGGCTTTCTTTCTATAGTTGACA	709	OPAI H31 3UTR(+1708+1732)	AGTAGTGACTAATAATTAGCCTTTTC
692	OPAI H31 3UTR(+1657+1681)	CTGAAGGCTTTTCTTTCTATAGTTG	710	OPAI H31 3UTR(+1711+1735)	AACAGTAGTGACTAATAATTAGCCTT

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711	OPAI H31 3UTR(+1714+1738)	GATAACAGTAGTGACTAATATTAGC	729	OPAI H31 3UTR(+1768+1792)	CAAAAGAAATGAAGATCTCCCTCCAT
712	OPAI H31 3UTR(+1717+1741)	TGTGATAACAGTAGTGACTAATATT	730	OPAI H31 3UTR(+1771+1795)	CCTCAAAAGAAATGAAGATCTCCCTC
713	OPAI H31 3UTR(+1720+1744)	GGATGTGATAACAGTAGTGACTAAT	731	OPAI H31 3UTR(+1774+1798)	TCTCCTCAAAAGAAATGAAGATCTCC
714	OPAI H31 3UTR(+1723+1747)	AAGGGATGTGATAACAGTAGTGACT	732	OPAI H31 3UTR(+1777+1801)	TGATCTCCTCAAAAGAAATGAAGATC
715	OPAI H31 3UTR(+1726+1750)	ACAAAAGGGATGTGATAACAGTAGTG	733	OPAI H31 3UTR(+1780+1804)	TACTGATCTCCTCAAAAGAAATGAAG
716	OPAI H31 3UTR(+1729+1753)	TATACAAAAGGGATGTGATAACAGTA	734	OPAI H31 3UTR(+1783+1807)	CAATACTGATCTCCTCAAAAGAAATG
717	OPAI H31 3UTR(+1732+1756)	ACTTATACAAAAGGGATGTGATAACA	735	OPAI H31 3UTR(+1786+1810)	TTACAATACTGATCTCCTCAAAAGAA
718	OPAI H31 3UTR(+1735+1759)	AAAACTTATACAAAAGGGATGTGATA	736	OPAI H31 3UTR(+1789+1813)	ACGTTACAATACTGATCTCCTCAAAA
719	OPAI H31 3UTR(+1738+1762)	TTTAAAACTTATACAAAAGGGATGTG	737	OPAI H31 3UTR(+1792+1816)	CATACGTTACAATACTGATCTCCTC
720	OPAI H31 3UTR(+1741+1765)	CTTTTAAAACTTATACAAAAGGGAT	738	OPAI H31 3UTR(+1795+1819)	TCACATACGTTACAATACTGATCTC
721	OPAI H31 3UTR(+1744+1768)	TCTCTTTTAAAACTTATACAAAAGG	739	OPAI H31 3UTR(+1798+1822)	TATTCACATACGTTACAATACTGAT
722	OPAI H31 3UTR(+1747+1771)	CCATCTCTTTTAAAACTTATACAAA	740	OPAI H31 3UTR(+1801+1825)	ATCTATTACATACGTTACAATACT
723	OPAI H31 3UTR(+1750+1774)	CCTCCATCTCTTTTAAAACTTATA	741	OPAI H31 3UTR(+1804+1828)	ATCATCTATTACATACGTTACAAT
724	OPAI H31 3UTR(+1753+1777)	CTCCCTCCATCTCTTTTAAAACTT	742	OPAI H31 3UTR(+1807+1831)	GTTATCATCTATTACATACGTTAC
725	OPAI H31 3UTR(+1756+1780)	GATCTCCCTCCATCTCTTTTAAAA	743	OPAI H31 3UTR(+1810+1834)	ATTGTTATCATCTATTACATACGTT
726	OPAI H31 3UTR(+1759+1783)	GAAAGATCTCCCTCCATCTCTTTTA	744	OPAI H31 3UTR(+1813+1837)	TTAATTGTTATCATCTATTACATA
727	OPAI H31 3UTR(+1762+1786)	AATGAAGATCTCCCTCCATCTCTTT	745	OPAI H31 3UTR(+1816+1840)	ATATTAATTGTTATCATCTATTAC
728	OPAI H31 3UTR(+1765+1789)	AGAAATGAAGATCTCCCTCCATCTC	746	OPAI H31 3UTR(+1819+1843)	GTAATATTAATTGTTATCATCTATT

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747	OPAI H31 3UTR(+1822+1846)	TTAGTAATATTAATTGTTATCATCT	765	OPAI H31 3UTR(+1876+1900)	AAGCCACATTACTGTGGGGCATGGA
748	OPAI H31 3UTR(+1825+1849)	CTTTTAGTAATAATTAAATTGTTATCA	766	OPAI H31 3UTR(+1879+1903)	AAGAAAGCCACATTACTGTGTGGGCAT
749	OPAI H31 3UTR(+1828+1852)	GGACTTTTAGTAATAATTAAATTGTTA	767	OPAI H31 3UTR(+1882+1906)	TGAAAAGAAAGCCACATTACTGTGTGGG
750	OPAI H31 3UTR(+1831+1855)	GTGGGACTTTTAGTAATAATTAAATTG	768	OPAI H31 3UTR(+1885+1909)	CCATGAAAGAAAGCCACATTACTGTG
751	OPAI H31 3UTR(+1834+1858)	CATGTGGGACTTTTAGTAATAATTAA	769	OPAI H31 3UTR(+1888+1912)	AACCCATGAAAGAAAGCCACATTACT
752	OPAI H31 3UTR(+1837+1861)	TCTCATGTGGGACTTTTAGTAATAT	770	OPAI H31 3UTR(+1891+1915)	AAAAACCCATGAAAGAAAGCCACATT
753	OPAI H31 3UTR(+1840+1864)	GACTCTCATGTGGGACTTTTAGTA	771	OPAI H31 3UTR(+1894+1918)	AAAAAAACCCATGAAAGAAAGCCAC
754	OPAI H31 3UTR(+1843+1867)	CAGGACTCTCATGTGGGACTTTTAG	772	OPAI H31 3UTR(+1897+1921)	AGAAAAAAACCCATGAAAGAAAGC
755	OPAI H31 3UTR(+1846+1870)	CGTCAGGACTCTCATGTGGGACTTT	773	OPAI H31 3UTR(+1900+1924)	AGAAAGAAAAAAACCCATGAAAGA
756	OPAI H31 3UTR(+1849+1873)	GGGCGTCAGGACTCTCATGTGGGAC	774	OPAI H31 3UTR(+1903+1927)	AAAAAGAAAGAAAAAAACCCATGAA
757	OPAI H31 3UTR(+1852+1876)	AGAGGGCGTCAGGACTCTCATGTGG	775	OPAI H31 3UTR(+1906+1930)	CTAAAAAGAAAGAAAAAAACCCAT
758	OPAI H31 3UTR(+1855+1879)	TGGAGAGGGCGTCAGGACTCTCATG	776	OPAI H31 3UTR(+1909+1933)	CAGCTAAAAAGAAAGAAAAAAACCC
759	OPAI H31 3UTR(+1858+1882)	GCATGGAGAGGGCGTCAGGACTCTC	777	OPAI H31 3UTR(+1912+1936)	GATCAGCTAAAAAGAAAGAAAAAAA
760	OPAI H31 3UTR(+1861+1885)	GGGGCATGGAGAGGGCGTCAGGACT	778	OPAI H31 3UTR(+1915+1939)	TGAGATCAGCTAAAAAGAAAGAAAAA
761	OPAI H31 3UTR(+1864+1888)	TGTGGGCGCATGGAGAGGGCGTCAGG	779	OPAI H31 3UTR(+1918+1942)	GGATGAGATCAGCTAAAAAGAAAGAA
762	OPAI H31 3UTR(+1867+1891)	TACTGTGGGCGCATGGAGAGGGCGTC	780	OPAI H31 3UTR(+1921+1945)	TTAGGATGAGATCAGCTAAAAAGAA
763	OPAI H31 3UTR(+1870+1894)	CATTACTGTGGGCGCATGGAGAGGGC	781	OPAI H31 3UTR(+1924+1948)	TGCTTAGGATGAGATCAGCTAAAAA
764	OPAI H31 3UTR(+1873+1897)	CCACATTACTGTGGGCGCATGGAGAG	782	OPAI H31 3UTR(+1927+1951)	GCATGCTTAGGATGAGATCAGCTAA

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783	OPAI H31 3UTR(+1930+1954)	AAAGCATGCTTAGGATGAGATCAGC	801	OPAI H31 3UTR(+1984+2008)	ATTTTCTTTCAATAACATCTGCAGT
784	OPAI H31 3UTR(+1933+1957)	AATAAAGCATGCTTAGGATGAGATC	802	OPAI H31 3UTR(+1987+2011)	TTTATTTTCTTTTCAATAACATCTGC
785	OPAI H31 3UTR(+1936+1960)	AAAAATAAAGCATGCTTAGGATGAG	803	OPAI H31 3UTR(+1990+2014)	AATTTTAATTTCTTTTCAATAACATC
786	OPAI H31 3UTR(+1939+1963)	AGGAAAAATAAAGCATGCTTAGGAT	804	OPAI H31 3UTR(+1993+2017)	CTGAAATTTTATTTTCTTTCAATAAC
787	OPAI H31 3UTR(+1942+1966)	TCAAGGAAAAATAAAGCATGCTTAG	805	OPAI H31 3UTR(+1996+2020)	AGACTGAAATTTTATTTTCTTTCAAT
788	OPAI H31 3UTR(+1945+1969)	CTTTCAGGAAAAATAAAGCATGCT	806	OPAI H31 3UTR(+1999+2023)	TTGAGACTGAAATTTTATTTTCTTTC
789	OPAI H31 3UTR(+1948+1972)	TAGCTTTCAAGGAAAAATAAAGCAT	807	OPAI H31 3UTR(+2002+2026)	CTCTTGAGACTGAAATTTTATTTTCT
790	OPAI H31 3UTR(+1951+1975)	ACCTAGCTTTCAAGGAAAAATAAAG	808	OPAI H31 3UTR(+2005+2029)	TTACTCTTGAGACTGAAATTTTATTT
791	OPAI H31 3UTR(+1954+1978)	AATACCTAGCTTTCAAGGAAAAATA	809	OPAI H31 3UTR(+2008+2032)	GGTTTACTCTTGAGACTGAAATTTTA
792	OPAI H31 3UTR(+1957+1981)	ATAAATACCTAGCTTTCAAGGAAAA	810	OPAI H31 3UTR(+2011+2035)	CAGGGTTTACTCTTGAGACTGAAAT
793	OPAI H31 3UTR(+1960+1984)	TTGATAAATACCTAGCTTTCAAGGA	811	OPAI H31 3UTR(+2014+2038)	ACACAGGGTTTACTCTTGAGACTGA
794	OPAI H31 3UTR(+1963+1987)	CAGTTGATAAATACCTAGCTTTCAA	812	OPAI H31 3UTR(+2017+2041)	AAGACACAGGGTTTACTCTTGAGAC
795	OPAI H31 3UTR(+1966+1990)	CTGCAGTTGATAAATACCTAGCTTT	813	OPAI H31 3UTR(+2020+2044)	CACAAAGACACAGGGTTTACTCTTGA
796	OPAI H31 3UTR(+1969+1993)	CATCTGCAGTTGATAAATACCTAGC	814	OPAI H31 3UTR(+2023+2047)	AGACACAAGACACAGGGTTTACTCT
797	OPAI H31 3UTR(+1972+1996)	TAACATCTGCAGTTGATAAATACCT	815	OPAI H31 3UTR(+2026+2050)	TACAGACACAAGACACAGGGTTTAC
798	OPAI H31 3UTR(+1975+1999)	CAATAACATCTGCAGTTGATAAATA	816	OPAI H31 3UTR(+2029+2053)	AACTACAGACACAAGACACAGGGTT
799	OPAI H31 3UTR(+1978+2002)	TTTCAATAACATCTGCAGTTGATAA	817	OPAI H31 3UTR(+2032+2056)	TTGAACTACAGACACAAGACACAGG
800	OPAI H31 3UTR(+1981+2005)	TTCTTTCAATAACATCTGCAGTTGA	818	OPAI H31 3UTR(+2035+2059)	CTTTTGAACCTACAGACACAAGACAC

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819	OPAI H31 3UTR(+2038+2062)	TGACTTTTGAACACTACAGACACAAGA	837	OPAI H31 3UTR(+2092+2116)	TCGAATTTAACTTCTGTATATTTAG
820	OPAI H31 3UTR(+2041+2065)	TTCTGACTTTTGAACACTACAGACACA	838	OPAI H31 3UTR(+2095+2119)	AGTTCGAATTTAACTTCTGTATATT
821	OPAI H31 3UTR(+2044+2068)	CATTTCTGACTTTTGAACACTACAGAC	839	OPAI H31 3UTR(+2098+2122)	GCTAGTTCGAATTTAACTTCTGTAT
822	OPAI H31 3UTR(+2047+2071)	AATCAATTTCTGACTTTTGAACACTACA	840	OPAI H31 3UTR(+2101+2125)	GTGGCTAGTTCGAATTTAACTTCTG
823	OPAI H31 3UTR(+2050+2074)	TAGAAATCAATTTCTGACTTTTGAACACT	841	OPAI H31 3UTR(+2104+2128)	TCTGTGGCTAGTTCGAATTTAACTT
824	OPAI H31 3UTR(+2053+2077)	AATTAGAATCAATTTCTGACTTTTGA	842	OPAI H31 3UTR(+2107+2131)	GATTCTGTGGCTAGTTCGAATTTAA
825	OPAI H31 3UTR(+2056+2080)	TTAAATTTAGAATCAATTTCTGACTTT	843	OPAI H31 3UTR(+2110+2134)	AATGATTTCTGTGGCTAGTTCGAATT
826	OPAI H31 3UTR(+2059+2083)	TGTTTAAATTAGAATCAATTTCTGAC	844	OPAI H31 3UTR(+2113+2137)	ACAAATGATTTCTGTGGCTAGTTCGA
827	OPAI H31 3UTR(+2062+2086)	TTTGTGTTAAATTTAGAATCAATTTCT	845	OPAI H31 3UTR(+2116+2140)	AAAACAAAATGATTTCTGTGGCTAGTT
828	OPAI H31 3UTR(+2065+2089)	TCCTTTTGTGTTAAATTTAGAATCAATT	846	OPAI H31 3UTR(+2119+2143)	ATAAAAAACAAATGATTTCTGTGGCTA
829	OPAI H31 3UTR(+2068+2092)	GTATCTTTTGTGTTAAATTTAGAAATC	847	OPAI H31 3UTR(+2122+2146)	GACATAAAAAACAAATGATTTCTGTGG
830	OPAI H31 3UTR(+2071+2095)	TTAGTATCTTTTGTGTTAAATTTAGA	848	OPAI H31 3UTR(+2125+2149)	TCTGACATAAAAAACAAATGATTTCTG
831	OPAI H31 3UTR(+2074+2098)	TATTTAGTATCTTTTGTGTTAAATTT	849	OPAI H31 3UTR(+2128+2152)	AATTCTGACATAAAAAACAAATGATT
832	OPAI H31 3UTR(+2077+2101)	GTATAATTTAGTATCTTTTGTGTTAA	850	OPAI H31 3UTR(+2131+2155)	GCAAAATTTCTGACATAAAAAACAAATG
833	OPAI H31 3UTR(+2080+2104)	TCTGTATATTTAGTATCTTTTGTGTT	851	OPAI H31 3UTR(+2134+2158)	TTTGCAAAATTTCTGACATAAAAAACAA
834	OPAI H31 3UTR(+2083+2107)	ACTTCTGTATATTTAGTATCTTTT	852	OPAI H31 3UTR(+2137+2161)	CTCTTTGCAAAATTTCTGACATAAAAA
835	OPAI H31 3UTR(+2086+2110)	TTAACTTCTGTATATTTAGTATCTT	853	OPAI H31 3UTR(+2140+2164)	CCACTCTTTTGCAAAATTTCTGACATAA
836	OPAI H31 3UTR(+2089+2113)	AATTTAACTTCTGTATATTTAGTAT	854	OPAI H31 3UTR(+2143+2167)	ACTCCACTCTTTTGCAAAATTTCTGACA

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
855	OPAI H31 3UTR(+2146+2170)	TCCACTCCACTCTTTGCAAAATTCGTG	873	OPAI H31 3UTR(+2200+2224)	TTAAGTTTGGATATCATCTATTTAC
856	OPAI H31 3UTR(+2149+2173)	TTGTCCACTCCACTCTTTTGCAAAATT	874	OPAI H31 3UTR(+2203+2227)	AAATTAAGTTTGGATATCATCTATT
857	OPAI H31 3UTR(+2152+2176)	GCTTTGTCCACTCCACTCTTTTGCAA	875	OPAI H31 3UTR(+2206+2230)	GCCAAAATTAAGTTTGGATATCATCT
858	OPAI H31 3UTR(+2155+2179)	AGAGCTTTGTCCACTCCACTCTTTTG	876	OPAI H31 3UTR(+2209+2233)	CTAGCCAAAATTAAGTTTGGATATCA
859	OPAI H31 3UTR(+2158+2182)	TACAGAGCTTTGTCCACTCCACTCT	877	OPAI H31 3UTR(+2212+2236)	GTCTAGCCAAAATTAAGTTTGGATA
860	OPAI H31 3UTR(+2161+2185)	CCATACAGAGCTTTGTCCACTCCAC	878	OPAI H31 3UTR(+2215+2239)	GAAAGTCCTAGCCAAAATTAAGTTTGG
861	OPAI H31 3UTR(+2164+2188)	CTTCCATACAGAGCTTTGTCCACTC	879	OPAI H31 3UTR(+2218+2242)	ATTGAAATCTAGCCAAAATTAAGTT
862	OPAI H31 3UTR(+2167+2191)	AGTCTTCCATACAGAGCTTTGTCCA	880	OPAI H31 3UTR(+2221+2245)	AAAATTGAAGTCCTAGCCAAAATTAA
863	OPAI H31 3UTR(+2170+2194)	TTCAGTCTTCCATACAGAGCTTTGT	881	OPAI H31 3UTR(+2224+2248)	TTTAAAATTAAGTCCTAGCCAAAAT
864	OPAI H31 3UTR(+2173+2197)	TTGTTCAAGTCTTCCATACAGAGCTT	882	OPAI H31 3UTR(+2227+2251)	ATTTTAAAATTAAGTCCTAGCCA
865	OPAI H31 3UTR(+2176+2200)	CAGTTGTTCAAGTCTTCCATACAGAG	883	OPAI H31 3UTR(+2230+2254)	CTGATTTTAAAATTAAGAGTCCTAG
866	OPAI H31 3UTR(+2179+2203)	TTACAGTTGTTCAAGTCTTCCATACA	884	OPAI H31 3UTR(+2233+2257)	ACACTGATTTTAAAATTAAGAGTCC
867	OPAI H31 3UTR(+2182+2206)	TATTTACAGTTGTTCAAGTCTTCCAT	885	OPAI H31 3UTR(+2236+2260)	GGTACACTGATTTTAAAATTAAGAG
868	OPAI H31 3UTR(+2185+2209)	ATCTATTTACAGTTGTTCAAGTCTTC	886	OPAI H31 3UTR(+2239+2263)	CTAGGTACACTGATTTTAAAATTAAG
869	OPAI H31 3UTR(+2188+2212)	ATCATCTATTTACAGTTGTTCAAGTC	887	OPAI H31 3UTR(+2242+2266)	TGCCTAGGTACACTGATTTTAAAAA
870	OPAI H31 3UTR(+2191+2215)	GATATCATCTATTTACAGTTGTTCA	888	OPAI H31 3UTR(+2245+2269)	CACTGCCTAGGTACACTGATTTTA
871	OPAI H31 3UTR(+2194+2218)	TTGGATATCATCTATTTACAGTTGT	889	OPAI H31 3UTR(+2248+2272)	GTGCACTGCCTAGGTACACTGATTT
872	OPAI H31 3UTR(+2197+2221)	AGTTTGGATATCATCTATTTACAGT	890	OPAI H31 3UTR(+2251+2275)	GCTGTGCACTGCCTAGGTACACTGA

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
891	OPAI H31 3UTR(+2254+2278)	CGTGTCTGTCACACTGCCTAGGTACAC	909	OPAI H31 3UTR(+2308+2332)	CCCGCAACTATAGCACAGTGGGTTA
892	OPAI H31 3UTR(+2257+2281)	TTTCGTGCTGTGCACACTGCCTAGGTA	910	OPAI H31 3UTR(+2311+2335)	CCACCCGCAACTATAGCACAGTGGG
893	OPAI H31 3UTR(+2260+2284)	TTATTTCTGCTGTGCACACTGCCTAG	911	OPAI H31 3UTR(+2314+2338)	GTTCCACCCCGCAACTATAGCACAGT
894	OPAI H31 3UTR(+2263+2287)	CACCTATTTCGTGCTGTGCACACTGCC	912	OPAI H31 3UTR(+2317+2341)	ACTGTTCCACCCGCAACTATAGCAC
895	OPAI H31 3UTR(+2266+2290)	GGCCACTTATTTCGTGCTGTGCACCT	913	OPAI H31 3UTR(+2320+2344)	TTGACTGTTCCACCCGCAACTATAG
896	OPAI H31 3UTR(+2269+2293)	AAGGGCCACTTATTTCGTGCTGTGC	914	OPAI H31 3UTR(+2323+2347)	AGGTTGACTGTTCCACCCCGCAACTA
897	OPAI H31 3UTR(+2272+2296)	TGCAAGGGCCACTTATTTCGTGCTG	915	OPAI H31 3UTR(+2326+2350)	GAAAGGTTGACTGTTCCACCCGCAAA
898	OPAI H31 3UTR(+2275+2299)	AGCTGCAAGGGCCACTTATTTCGTG	916	OPAI H31 3UTR(+2329+2353)	CTAGAAAAGGTTGACTGTTCCACCCG
899	OPAI H31 3UTR(+2278+2302)	GGAAAGCTGCAAGGGCCACTTATTTC	917	OPAI H31 3UTR(+2332+2356)	CTACTAGAAAAGGTTGACTGTTCCAC
900	OPAI H31 3UTR(+2281+2305)	CGGGGAAGCTGCAAGGGCCACTTAT	918	OPAI H31 3UTR(+2335+2359)	AAACTACTAGAAAAGGTTGACTGTTT
901	OPAI H31 3UTR(+2284+2308)	AAACGGGGAAGCTGCAAGGGCCACT	919	OPAI H31 3UTR(+2338+2362)	CATAAACTACTAGAAAAGGTTGACTG
902	OPAI H31 3UTR(+2287+2311)	GTTAAACGGGGAAAGCTGCAAGGGCC	920	OPAI H31 3UTR(+2341+2365)	TATCATAAACTACTAGAAAAGGTTGA
903	OPAI H31 3UTR(+2290+2314)	TGGGTTAAACGGGGAAAGCTGCAAGG	921	OPAI H31 3UTR(+2344+2368)	CAATATCATAAACTACTAGAAAAGGT
904	OPAI H31 3UTR(+2293+2317)	CAGTGGGTTAAACGGGGAAAGCTGCA	922	OPAI H31 3UTR(+2347+2371)	GGGCAATATCATAAACTACTAGAAA
905	OPAI H31 3UTR(+2296+2320)	GCACAGTGGGTTAAACGGGGAAAGCT	923	OPAI H31 3UTR(+2350+2374)	AGAGGGCAATATCATAAACTACTAG
906	OPAI H31 3UTR(+2299+2323)	ATAGCACAGTGGGTTAAACGGGGAA	924	OPAI H31 3UTR(+2353+2377)	CAAAAGAGGGCAATATCATAAACTAC
907	OPAI H31 3UTR(+2302+2326)	ACTATAGCACAGTGGGTTAAACGGG	925	OPAI H31 3UTR(+2356+2380)	ATACAAAAGAGGGCAATATCATAAAC
908	OPAI H31 3UTR(+2305+2329)	GCAACTATAGCACAGTGGGTTAAAC	926	OPAI H31 3UTR(+2359+2383)	GGAAATACAAAAGAGGGCAATATCATA

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
927	OPAI H31 3UTR(+2362+2386)	ATGGGAATACAAAGAGGGCAATATC	945	OPAI H31 3UTR(+2416+2440)	CATTTGGAGGCTGAATAATTTGCAG
928	OPAI H31 3UTR(+2365+2389)	AAATGGGAATACAAAGAGGGCAAT	946	OPAI H31 3UTR(+2419+2443)	TTGCATTTGGAGGCTGAATAATTTG
929	OPAI H31 3UTR(+2368+2392)	TAGAAAATGGGAATACAAAGAGGGC	947	OPAI H31 3UTR(+2422+2446)	CATTTGCATTTGGAGGCTGAATAAT
930	OPAI H31 3UTR(+2371+2395)	CTGTAGAAAATGGGAATACAAAGAG	948	OPAI H31 3UTR(+2425+2449)	ATTCATTTGCATTTGGAGGCTGAAT
931	OPAI H31 3UTR(+2374+2398)	AAACTGTAGAAAATGGGAATACAAA	949	OPAI H31 3UTR(+2428+2452)	ATCATTCATTTGCATTTGGAGGCTG
932	OPAI H31 3UTR(+2377+2401)	AAAAAACTGTAGAAAATGGGAATAC	950	OPAI H31 3UTR(+2431+2455)	TATATCATTCATTTGCATTTGGAGG
933	OPAI H31 3UTR(+2380+2404)	CGGAAAAAACTGTAGAAAATGGGAA	951	OPAI H31 3UTR(+2434+2458)	TTTTATATCATTCATTTGCATTTGG
934	OPAI H31 3UTR(+2383+2407)	CTGCGGAAAAAACTGTAGAAAATGG	952	OPAI H31 3UTR(+2437+2461)	TATTTTATATCATTCATTTGCATTT
935	OPAI H31 3UTR(+2386+2410)	AGTCTGCGGAAAAAACTGTAGAAAA	953	OPAI H31 3UTR(+2440+2464)	ACTTATTTTATATATCATTCATTTGC
936	OPAI H31 3UTR(+2389+2413)	AGAAAGTCTGCGGAAAAAACTGTAGA	954	OPAI H31 3UTR(+2443+2467)	CCTACTTATTTTATATATCATTCATTT
937	OPAI H31 3UTR(+2392+2416)	GAAAGAAAGTCTGCGGAAAAAACTGT	955	OPAI H31 3UTR(+2446+2470)	TTCCCTACTTATTTTATATATCATTC
938	OPAI H31 3UTR(+2395+2419)	GCAGAAAGAAAGTCTGCGGAAAAAAAC	956	OPAI H31 3UTR(+2449+2473)	ATGTTCCCTACTTATTTTATATATCA
939	OPAI H31 3UTR(+2398+2422)	TTTGCAGAAAGAAAGTCTGCGGAAAA	957	OPAI H31 3UTR(+2452+2476)	GCCATGTTCCCTACTTATTTTATATA
940	OPAI H31 3UTR(+2401+2425)	TAAATTTGCAGAAAGAAAGTCTGCGGA	958	OPAI H31 3UTR(+2455+2479)	TCTGCCATGTTCCCTACTTATTTT
941	OPAI H31 3UTR(+2404+2428)	GAATAATTTGCAGAAAGAAAGTCTGC	959	OPAI H31 3UTR(+2458+2482)	CTCTCTGCCATGTTCCCTACTTATTT
942	OPAI H31 3UTR(+2407+2431)	GCTGAATAATTTGCAGAAAGAAAGTC	960	OPAI H31 3UTR(+2461+2485)	CCACTCTCTGCCATGTTCCCTACTT
943	OPAI H31 3UTR(+2410+2434)	GAGGCTGAATAATTTGCAGAAAGAA	961	OPAI H31 3UTR(+2464+2488)	GCACCACTCTCTGCCATGTTCCCTA
944	OPAI H31 3UTR(+2413+2437)	TTGGAGGCTGAATAATTTGCAGAAA	962	OPAI H31 3UTR(+2467+2491)	GAAACCACTCTCTGCCATGTTCC

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963	OPAI H31 3UTR(+2470+2494)	TGGGAAGCACCACACTCTCTGCCATGT	981	OPAI H31 3UTR(+2524+2548)	TTTTAAACCTATACTCTGACTCTCA
964	OPAI H31 3UTR(+2473+2497)	GGCTGGGAAGCACCACACTCTCTGCCA	982	OPAI H31 3UTR(+2527+2551)	ATCTTTTAAACCTATACTCTGACTC
965	OPAI H31 3UTR(+2476+2500)	TGAGGCTGGGAAGCACCACACTCTCTG	983	OPAI H31 3UTR(+2530+2554)	TTTATCTTTTAAACCTATACTCTGA
966	OPAI H31 3UTR(+2479+2503)	TTGTGAGGCTGGGAAGCACCACACTCT	984	OPAI H31 3UTR(+2533+2557)	GATTTTATCTTTTAAACCTATACTC
967	OPAI H31 3UTR(+2482+2506)	ACATTGTGAGGCTGGGAAGCACCAC	985	OPAI H31 3UTR(+2536+2560)	AAAGATTTTATCTTTTAAACCTATA
968	OPAI H31 3UTR(+2485+2509)	CCCACATTGTGAGGCTGGGAAGCAC	986	OPAI H31 3UTR(+2539+2563)	ACTAAAGATTTTATCTTTTAAACCT
969	OPAI H31 3UTR(+2488+2512)	ATTCCCACATTGTGAGGCTGGGAAG	987	OPAI H31 3UTR(+2542+2566)	TTAACTAAAGATTTTATCTTTTAAA
970	OPAI H31 3UTR(+2491+2515)	CAAAATCCCACATTGTGAGGCTGGG	988	OPAI H31 3UTR(+2545+2569)	TTATTAACTAAAGATTTTATCTTTT
971	OPAI H31 3UTR(+2494+2518)	TGTCAAAATCCCACATTGTGAGGCT	989	OPAI H31 3UTR(+2548+2572)	AAATTATTAACTAAAGATTTTATCT
972	OPAI H31 3UTR(+2497+2521)	CTATGTCAAAATCCCACATTGTGAG	990	OPAI H31 3UTR(+2551+2575)	ACAAAAATTATTAACTAAAGATTTTA
973	OPAI H31 3UTR(+2500+2524)	ATCCTATGTCAAAATCCCACATTGT	991	OPAI H31 3UTR(+2554+2578)	AATACAAAAATTATTAACTAAAGATT
974	OPAI H31 3UTR(+2503+2527)	CTCATCCTATGTCAAAATCCCACAT	992	OPAI H31 3UTR(+2557+2581)	ATAAATACAAAAATTATTAACTAAAG
975	OPAI H31 3UTR(+2506+2530)	ACTCTCATCCTATGTCAAAATCCCA	993	OPAI H31 3UTR(+2560+2584)	TAAATAAATACAAAAATTATTAACTA
976	OPAI H31 3UTR(+2509+2533)	CTGACTCTCATCCTATGTCAAAATTC	994	OPAI H31 3UTR(+2563+2587)	GAATAAATAAATAACAAAAATTATTAA
977	OPAI H31 3UTR(+2512+2536)	ACTCTGACTCTCATCCTATGTCAAA	995	OPAI H31 3UTR(+2566+2590)	CTAGAATAAATAAATAACAAAAATTAT
978	OPAI H31 3UTR(+2515+2539)	TATACTCTGACTCTCATCCTATGTC	996	OPAI H31 3UTR(+2569+2593)	CATCTAGAATAAATAAATAACAAAAAT
979	OPAI H31 3UTR(+2518+2542)	ACCTATACTCTGACTCTCATCCTAT	997	OPAI H31 3UTR(+2572+2596)	ATACATCTAGAATAAATAAATAACAA
980	OPAI H31 3UTR(+2521+2545)	TAAACCTATACTCTGACTCTCATCC	998	OPAI H31 3UTR(+2575+2599)	TACATACATCTAGAATAAATAAATAA

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
999	OPAI H31 3UTR(+2578+2602)	AGATACATACATCTAGAAATAATAA	1017	OPAI H31 3UTR(+2632+2656)	ACCATTACTTTGATCCCCCTTTATTG
1000	OPAI H31 3UTR(+2581+2605)	CTCAGATACATACATCTAGAAATAAA	1018	OPAI H31 3UTR(+2635+2659)	AAAAACCATTACTTTTGATCCCCCTTTA
1001	OPAI H31 3UTR(+2584+2608)	TTCTCTCAGATACATACATCTAGAAT	1019	OPAI H31 3UTR(+2638+2662)	AGAAAAACCATTACTTTTGATCCCTCT
1002	OPAI H31 3UTR(+2587+2611)	TCCTTCTCAGATACATACATCTAG	1020	OPAI H31 3UTR(+2641+2665)	GAGAGAAAAAACCAATTACTTTTGATCC
1003	OPAI H31 3UTR(+2590+2614)	ATTCTTTCTCAGATACATACATC	1021	OPAI H31 3UTR(+2644+2668)	ACTGAGAGAAAAAACCAATTACTTTGA
1004	OPAI H31 3UTR(+2593+2617)	CAGATTCTTTCTCAGATACATAC	1022	OPAI H31 3UTR(+2647+2671)	AGAACTGAGAGAAAAAACCAATTACTT
1005	OPAI H31 3UTR(+2596+2620)	TACCAGATTCTTTCTCAGATACA	1023	OPAI H31 3UTR(+2650+2674)	TAGAGAACTGAGAGAAAAAACCAATTA
1006	OPAI H31 3UTR(+2599+2623)	AAATACCAGATTCTTTCTCCTCAGAT	1024	OPAI H31 3UTR(+2653+2677)	GCCTTAGAGAACTGAGAGAAAAACCA
1007	OPAI H31 3UTR(+2602+2626)	CAAAAAATACCAGATTCTTTCTCTCA	1025	OPAI H31 3UTR(+2656+2680)	CCAGCTTAGAGAACTGAGAGAAAAA
1008	OPAI H31 3UTR(+2605+2629)	AAGCAAAAAATACCAGATTCTTTCTC	1026	OPAI H31 3UTR(+2659+2683)	AGACCAGCTTAGAGAACTGAGAGAA
1009	OPAI H31 3UTR(+2608+2632)	GGAAAGCAAAAAATACCAGATTCTT	1027	OPAI H31 3UTR(+2662+2686)	CATAGACCAGCTTAGAGAACTGAGA
1010	OPAI H31 3UTR(+2611+2635)	ATTGGAAAGCAAAAAATACCAGATT	1028	OPAI H31 3UTR(+2665+2689)	TAAACATAGACCAGCTTAGAGAACTG
1011	OPAI H31 3UTR(+2614+2638)	TTTATTGGAAAGCAAAAAATACCAGA	1029	OPAI H31 3UTR(+2668+2692)	CTATAACATAGACCAGCTTAGAGAA
1012	OPAI H31 3UTR(+2617+2641)	CCCTTTATTGGAAAGCAAAAAATACC	1030	OPAI H31 3UTR(+2671+2695)	GAGCTATAACATAGACCAGCTTAGA
1013	OPAI H31 3UTR(+2620+2644)	ATCCCCTTTATTGGAAAGCAAAAAAT	1031	OPAI H31 3UTR(+2674+2698)	CTAGAGCTATAACATAGACCAGCTT
1014	OPAI H31 3UTR(+2623+2647)	TTGATCCCCTTTATTGGAAAGCAAAA	1032	OPAI H31 3UTR(+2677+2701)	CTGCTAGAGCTATAACATAGACCAG
1015	OPAI H31 3UTR(+2626+2650)	ACTTTGATCCCCTTTATTGGAAAGC	1033	OPAI H31 3UTR(+2680+2704)	ATACTGCTAGAGCTATAACATAGAC
1016	OPAI H31 3UTR(+2629+2653)	ATTACTTTGATCCCCTTTATTGGAA	1034	OPAI H31 3UTR(+2683+2707)	TCCATACTGCTAGAGCTATAACATA

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1035	OPAI H31 3UTR(+2686+2710)	ATTTCCATACTGCTAGAGCTATAAC	1053	OPAI H31 3UTR(+2740+2764)	ATCTCAACAACATATAGCCATGATC
1036	OPAI H31 3UTR(+2689+2713)	CACATTTCCATACTGCTAGAGCTAT	1054	OPAI H31 3UTR(+2743+2767)	AATATCTCAACAACATATAGCCATG
1037	OPAI H31 3UTR(+2692+2716)	AAGCACATTTCCATACTGCTAGAGC	1055	OPAI H31 3UTR(+2746+2770)	TCAAAATATCTCAACAACATATAGCC
1038	OPAI H31 3UTR(+2695+2719)	TTAAAGCACATTTCCATACTGCTAG	1056	OPAI H31 3UTR(+2749+2773)	GTTTCAAAATATCTCAACAACATATA
1039	OPAI H31 3UTR(+2698+2722)	ATTTTAAAGCACATTTCCATACTGC	1057	OPAI H31 3UTR(+2752+2776)	TAAAGTTTCAAAATATCTCAACAACAT
1040	OPAI H31 3UTR(+2701+2725)	CATATTTTAAAGCACATTTCCATAC	1058	OPAI H31 3UTR(+2755+2779)	AGGTAAGTTTCAAAATATCTCAACAA
1041	OPAI H31 3UTR(+2704+2728)	AAGCATATTTTAAAGCACATTTCCA	1059	OPAI H31 3UTR(+2758+2782)	ACAAAGGTAAGTTTCAAAATATCTCAA
1042	OPAI H31 3UTR(+2707+2731)	GGTAAGCATATTTTAAAGCACATTT	1060	OPAI H31 3UTR(+2761+2785)	AAAACAAGGTAAGTTTCAAAATATCT
1043	OPAI H31 3UTR(+2710+2734)	AAAGGTAAGCATATTTTAAAGCACACA	1061	OPAI H31 3UTR(+2764+2788)	GTGAAAAACAAGGTAAGTTTCAAAATA
1044	OPAI H31 3UTR(+2713+2737)	TCAAAAAGGTAAGCATATTTTAAAGC	1062	OPAI H31 3UTR(+2767+2791)	CAAGTGAAAAACAAGGTAAGTTTCAA
1045	OPAI H31 3UTR(+2716+2740)	CATTCAAAAAGGTAAGCATATTTTAA	1063	OPAI H31 3UTR(+2770+2794)	GCACAAAGTGAAAAACAAGGTAAGTTT
1046	OPAI H31 3UTR(+2719+2743)	GATCATTTCAAAAAGGTAAGCATATTT	1064	OPAI H31 3UTR(+2773+2797)	AGTGCACAAAGTGAAAAACAAGGTAAG
1047	OPAI H31 3UTR(+2722+2746)	CATGATCATTTCAAAAAGGTAAGCATA	1065	OPAI H31 3UTR(+2776+2800)	CACAGTGCACAAAGTGAAAAACAAGGT
1048	OPAI H31 3UTR(+2725+2749)	AGCCATGATCATTTCAAAAAGGTAAGC	1066	OPAI H31 3UTR(+2779+2803)	ATTCACAGTGCACAAAGTGAAAAACA
1049	OPAI H31 3UTR(+2728+2752)	TATAGCCATGATCATTTCAAAAAGGTA	1067	OPAI H31 3UTR(+2782+2806)	TTCATTACAGTGCACAAAGTGAAAA
1050	OPAI H31 3UTR(+2731+2755)	ACATATAGCCATGATCATTTCAAAAAG	1068	OPAI H31 3UTR(+2785+2809)	AAGTTTCAATTCACAGTGCACAAAGTGA
1051	OPAI H31 3UTR(+2734+2758)	ACAACATATAGCCATGATCATTTCAA	1069	OPAI H31 3UTR(+2788+2812)	ACAAAAGTTTCAATTCACAGTGCACAAAG
1052	OPAI H31 3UTR(+2737+2761)	TCAACAAACATATAGCCATGATCATTT	1070	OPAI H31 3UTR(+2791+2815)	AATACAAAAGTTTCAATTCACAGTGAC

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
1071	OPAI H31 3UTR(+2794+2818)	AATAATACAAAGTTCAATTCACAGTG	1089	OPAI H31 3UTR(+2848+2872)	CAGGCAAAATATAAGTTGCAATAAT
1072	OPAI H31 3UTR(+2797+2821)	AAAAATAATACAAAGTTCAATTCACA	1090	OPAI H31 3UTR(+2851+2875)	GCTCAGGCAAAATATAAGTTGCAAT
1073	OPAI H31 3UTR(+2800+2824)	TAAAAAAATAATACAAAGTTTCATTC	1091	OPAI H31 3UTR(+2854+2878)	CAAGCTCAGGCAAAATATAAGTTGTC
1074	OPAI H31 3UTR(+2803+2827)	TTTTAAAAAAATAATACAAAGTTCA	1092	OPAI H31 3UTR(+2857+2881)	GATCAAGCTCAGGCAAAATATAAGT
1075	OPAI H31 3UTR(+2806+2830)	AGGTTTTAAAAAAATAATACAAAGT	1093	OPAI H31 3UTR(+2860+2884)	TTTGATCAAGCTCAGGCAAAATATA
1076	OPAI H31 3UTR(+2809+2833)	TGAAGGTTTTAAAAAAATAATACAA	1094	OPAI H31 3UTR(+2863+2887)	ACCTTTGATCAAGCTCAGGCAAAAT
1077	OPAI H31 3UTR(+2812+2836)	ATGTGAAGTTTTAAAAAAATAATA	1095	OPAI H31 3UTR(+2866+2890)	ATGACCTTTGATCAAGCTCAGGCAA
1078	OPAI H31 3UTR(+2815+2839)	GTAATGTGAAGGTTTTAAAAAAATA	1096	OPAI H31 3UTR(+2869+2893)	CAAAATGACCTTTGATCAAGCTCAGG
1079	OPAI H31 3UTR(+2818+2842)	CACGTAATGTGAAGGTTTTAAAAAA	1097	OPAI H31 3UTR(+2872+2896)	ACACAAATGACCTTTGATCAAGCTC
1080	OPAI H31 3UTR(+2821+2845)	CTACACGTAATGTGAAGGTTTAA	1098	OPAI H31 3UTR(+2875+2899)	TCTACACAAATGACCTTTGATCAAG
1081	OPAI H31 3UTR(+2824+2848)	TATCTACACGTAATGTGAAGGTTTT	1099	OPAI H31 3UTR(+2878+2902)	TCATCTACACAAATGACCTTTGATC
1082	OPAI H31 3UTR(+2827+2851)	TAATATCTACACGTAATGTGAAGGT	1100	OPAI H31 3UTR(+2881+2905)	TACTCATCTACACAAATGACCTTTG
1083	OPAI H31 3UTR(+2830+2854)	CAATAATATCTACACGTAATGTGAA	1101	OPAI H31 3UTR(+2884+2908)	AATTACTCATCTACACAAATGACCT
1084	OPAI H31 3UTR(+2833+2857)	TTGCAATAATATCTACACGTAATGT	1102	OPAI H31 3UTR(+2887+2911)	TTTAAATTACTCATCTACACAAATGA
1085	OPAI H31 3UTR(+2836+2860)	AAGTTGCAATAATATCTACACGTAA	1103	OPAI H31 3UTR(+2890+2914)	TTTTTAAATTACTCATCTACACAAA
1086	OPAI H31 3UTR(+2839+2863)	TATAAGTTGCAATAATATCTACACG	1104	OPAI H31 3UTR(+2893+2917)	ATATTTTAAATTACTCATCTACAC
1087	OPAI H31 3UTR(+2842+2866)	AAATATAAGTTGCAATAATATCTAC	1105	OPAI H31 3UTR(+2896+2920)	TAAATATTTTAAATTACTCATCTA
1088	OPAI H31 3UTR(+2845+2869)	GCAAAATATAAGTTGCAATAATATC	1106	OPAI H31 3UTR(+2899+2923)	ATTTAAATATTTTAAATTACTCAT

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
1107	OPAI H31 3UTR(+2902+2926)	GTGATTTAAATATTTTTTAAATTAAT	1125	OPAI H31 3UTR(+2956+2980)	CTCGTTAAAAACAGAAAAAATTTAA
1108	OPAI H31 3UTR(+2905+2929)	AATGTGATTTAAATATTTTTTAAAT	1126	OPAI H31 3UTR(+2959+2983)	TCCCTCGTTAAAAACAGAAAAAATTT
1109	OPAI H31 3UTR(+2908+2932)	TATAATGTGATTTAAATATTTTTTA	1127	OPAI H31 3UTR(+2962+2986)	CTTCCCTCGTTAAAAACAGAAAAA
1110	OPAI H31 3UTR(+2911+2935)	AATTATAATGTGATTTAAATATTTT	1128	OPAI H31 3UTR(+2965+2989)	TCTCTTTCCCTCGTTAAAAACAGAAA
1111	OPAI H31 3UTR(+2914+2938)	TAGAAATTAATGTGATTTAAATAT	1129	OPAI H31 3UTR(+2968+2992)	GTTTCTCTTTCCCTCGTTAAAAACAG
1112	OPAI H31 3UTR(+2917+2941)	TAATAGAAATTAATGTGATTTAAA	1130	OPAI H31 3UTR(+2971+2995)	CAGGTTTCTCTTTCCCTCGTTAAAA
1113	OPAI H31 3UTR(+2920+2944)	CAATAATAGAAATTAATGTGATTT	1131	OPAI H31 3UTR(+2974+2998)	ATACAGGTTTCTCTTTCCCTCGTTA
1114	OPAI H31 3UTR(+2923+2947)	CTCCAATAATAGAAATTAATGTGA	1132	OPAI H31 3UTR(+2977+3001)	GGTATACAGGTTTCTCTTTCCCTCG
1115	OPAI H31 3UTR(+2926+2950)	GCTCTCCAATAATAGAAATTAATG	1133	OPAI H31 3UTR(+2980+3004)	CTAGGTATACAGGTTTCTCTTTCC
1116	OPAI H31 3UTR(+2929+2953)	GATGCTCTCCAATAATAGAAATTA	1134	OPAI H31 3UTR(+2983+3007)	ACCCCTAGGTATACAGGTTTCTCTTT
1117	OPAI H31 3UTR(+2932+2956)	AAAGATGCTCTCCAATAATAGAAAT	1135	OPAI H31 3UTR(+2986+3010)	ATGACCCCTAGGTATACAGGTTTCTC
1118	OPAI H31 3UTR(+2935+2959)	TTAAAAAGATGCTCTCCAATAATAGA	1136	OPAI H31 3UTR(+2989+3013)	ATAATGACCCCTAGGTATACAGGTTT
1119	OPAI H31 3UTR(+2938+2962)	AATTTAAAAAGATGCTCTCCAATAAT	1137	OPAI H31 3UTR(+2992+3016)	CAAAATAATGACCCCTAGGTATACAGG
1120	OPAI H31 3UTR(+2941+2965)	AAAAATTTAAAAAGATGCTCTCCAAT	1138	OPAI H31 3UTR(+2995+3019)	GGTCAAAATAATGACCCCTAGGTATAC
1121	OPAI H31 3UTR(+2944+2968)	GAAAAAAATTTAAAAAGATGCTCTCC	1139	OPAI H31 3UTR(+2998+3022)	TGGGGTCAAAATAATGACCCCTAGGTA
1122	OPAI H31 3UTR(+2947+2971)	ACAGAAAAAAATTTAAAAAGATGCTC	1140	OPAI H31 3UTR(+3001+3025)	CTATGGGGTCAAAATAATGACCCCTAG
1123	OPAI H31 3UTR(+2950+2974)	AAAACAGAAAAAAATTTAAAAAGATG	1141	OPAI H31 3UTR(+3004+3028)	ATACTATGGGGTCAAAATAATGACCC
1124	OPAI H31 3UTR(+2953+2977)	GTAAAAACAGAAAAAAATTTAAAAAG	1142	OPAI H31 3UTR(+3007+3031)	GTTATACTATGGGGTCAAAATAATGA

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
1143	OPAI H31 3UTR(+3010+3034)	CTGGTTATACTATGGGGTCAAATAA	1161	OPAI H31 3UTR(+3064+3088)	TGAAATTCAAGCATTGAGAGAAAAG
1144	OPAI H31 3UTR(+3013+3037)	AATCTGGTTATACTATGGGGTCAAAA	1162	OPAI H31 3UTR(+3067+3091)	ATGTGAAATTCAAGCATTGAGAGAA
1145	OPAI H31 3UTR(+3016+3040)	ATGAATCTGGTTATACTATGGGGTGC	1163	OPAI H31 3UTR(+3070+3094)	GGCATGTGAAATTCAAGCATTGAGAA
1146	OPAI H31 3UTR(+3019+3043)	ACCATGAATCTGGTTATACTATGGG	1164	OPAI H31 3UTR(+3073+3097)	CAAGGCATGTGAAATTCAAGCATTTC
1147	OPAI H31 3UTR(+3022+3046)	TAGACCATGAATCTGGTTATACTAT	1165	OPAI H31 3UTR(+3076+3100)	ATGCAAGGCATGTGAAATTCAAGCA
1148	OPAI H31 3UTR(+3025+3049)	TGTTAGACCATGAATCTGGTTATAC	1166	OPAI H31 3UTR(+3079+3103)	GAAATGCAAGGCATGTGAAATTCAA
1149	OPAI H31 3UTR(+3028+3052)	GCTTGTAGACCATGAATCTGGTTA	1167	OPAI H31 3UTR(+3082+3106)	TGTGAAATGCAAGGCATGTGAAATT
1150	OPAI H31 3UTR(+3031+3055)	AGAGCTTGTAGACCATGAATCTGG	1168	OPAI H31 3UTR(+3085+3109)	AACTGTGAAATGCAAGGCATGTGAA
1151	OPAI H31 3UTR(+3034+3058)	CTGAGAGCTTGTAGACCATGAATC	1169	OPAI H31 3UTR(+3088+3112)	TACAACTGTGAAATGCAAGGCATGT
1152	OPAI H31 3UTR(+3037+3061)	ACACTGAGAGCTTGTAGACCATGA	1170	OPAI H31 3UTR(+3091+3115)	GAGTACAACTGTGAAATGCAAGGCA
1153	OPAI H31 3UTR(+3040+3064)	GCCACACTGAGAGCTTGTAGACCA	1171	OPAI H31 3UTR(+3094+3118)	ATGGAGTACAACTGTGAAATGCAAG
1154	OPAI H31 3UTR(+3043+3067)	AAAGCCACACTGAGAGCTTGTAGA	1172	OPAI H31 3UTR(+3097+3121)	ACCATGGAGTACAACTGTGAAATGC
1155	OPAI H31 3UTR(+3046+3070)	AGAAAAGCCACACTGAGAGCTTGT	1173	OPAI H31 3UTR(+3100+3124)	TTGACCATGGAGTACAACTGTGAAA
1156	OPAI H31 3UTR(+3049+3073)	CAGAGAAAAGCCACACTGAGAGCTT	1174	OPAI H31 3UTR(+3103+3127)	CGGTTGACCATGGAGTACAACTGTG
1157	OPAI H31 3UTR(+3052+3076)	ATTCAGAGAAAAGCCACACTGAGAG	1175	OPAI H31 3UTR(+3106+3130)	CACCGGTTGACCATGGAGTACAAC
1158	OPAI H31 3UTR(+3055+3079)	AGCATTCAGAGAAAAGCCACACTGA	1176	OPAI H31 3UTR(+3109+3133)	AAGCACCGGTTGACCATGGAGTACA
1159	OPAI H31 3UTR(+3058+3082)	TCAAGCATTCAGAGAAAAGCCACAC	1177	OPAI H31 3UTR(+3112+3136)	AAAAAGCACCGGTTGACCATGGAGT
1160	OPAI H31 3UTR(+3061+3085)	AATTCAGCATTCAGAGAAAAGCCA	1178	OPAI H31 3UTR(+3115+3139)	GAAAAAAGCACCGGTTGACCATGG

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
1179	OPAI H31 3UTR(+3118+3142)	TGTGAAAAAAGCACCAGGTTGACCA	1197	OPAI H31 3UTR(+3172+3196)	TTTTTATATATTTTACCAAGGAAA
1180	OPAI H31 3UTR(+3121+3145)	CGATGTGAAAAAAGCACCAGGTTGA	1198	OPAI H31 3UTR(+3175+3199)	ACCTTTTTTATATATTTTACCAAGG
1181	OPAI H31 3UTR(+3124+3148)	CCACGATGTGAAAAAAGCACCAGGT	1199	OPAI H31 3UTR(+3178+3202)	AAAACTTTTTTATATATTTTACCA
1182	OPAI H31 3UTR(+3127+3151)	GTACCACGATGTGAAAAAAGCACC	1200	OPAI H31 3UTR(+3181+3205)	TAGAAAAACCTTTTTTATATATTTA
1183	OPAI H31 3UTR(+3130+3154)	CAAGTACCACGATGTGAAAAAAGC	1201	OPAI H31 3UTR(+3184+3208)	AATTAGAAAAACCTTTTTTATATATT
1184	OPAI H31 3UTR(+3133+3157)	TGACAAAGTACCACGATGTGAAAAA	1202	OPAI H31 3UTR(+3187+3211)	TGAAATTAGAAAAACCTTTTTTATAT
1185	OPAI H31 3UTR(+3136+3160)	TTTGTGACAAAGTACCACGATGTGAAA	1203	OPAI H31 3UTR(+3190+3214)	AAGTGAAATTAGAAAAACCTTTTTTA
1186	OPAI H31 3UTR(+3139+3163)	ATGTTTTTGACAAAGTACCACGATGTG	1204	OPAI H31 3UTR(+3193+3217)	GC AAAAGTGAAATTAGAAAAACCTTTT
1187	OPAI H31 3UTR(+3142+3166)	AAAAATGTTTTTGACAAAGTACCACGAT	1205	OPAI H31 3UTR(+3196+3220)	GCAGCAAAAGTGAAATTAGAAAAACCT
1188	OPAI H31 3UTR(+3145+3169)	AACAAAAATGTTTTTGACAAAGTACCAC	1206	OPAI H31 3UTR(+3199+3223)	TTGGCAGCAAAAGTGAAATTAGAAAA
1189	OPAI H31 3UTR(+3148+3172)	AATAACAAAAATGTTTTTGACAAAGTAC	1207	OPAI H31 3UTR(+3202+3226)	GCCTTGGCAGCAAAAGTGAAATTAGA
1190	OPAI H31 3UTR(+3151+3175)	GAAAAATAACAAAAATGTTTTTGACAAAG	1208	OPAI H31 3UTR(+3205+3229)	ACAGCCTTGGCAGCAAAAGTGAAATT
1191	OPAI H31 3UTR(+3154+3178)	AAGGAAAAATAACAAAAATGTTTTTGAC	1209	OPAI H31 3UTR(+3208+3232)	ATGACAGCCTTGGCAGCAAAAGTGAA
1192	OPAI H31 3UTR(+3157+3181)	ACCAAGGAAAAATAACAAAAATGTTTTT	1210	OPAI H31 3UTR(+3211-24)	AAAAATGACAGCCTTGGCAGCAAAAGT
1193	OPAI H31 3UTR(+3160+3184)	TTTACCAAGGAAAAATAACAAAAATGT	1211	OPAI H31 3UTR(+3-27)	ATGAAAAATGACAGCCTTGGCAGCAA
1194	OPAI H31 3UTR(+3163+3187)	TATTTTACCAAGGAAAAATAACAAAA	1212	OPAI H31 3UTR(+6-30)	TAAATGAAAAATGACAGCCTTGGCAG
1195	OPAI H31 3UTR(+3166+3190)	ATATATTTTACCAAGGAAAAATAACA	1213	OPAI H31 3UTR(+9-33)	GCATTAATGAAAAATGACAGCCTTGG
1196	OPAI H31 3UTR(+3169+3193)	TTTATATATTTTACCAAGGAAAAATA	1214	OPAI H31 3UTR(+12-36)	GCAGCATTAATGAAAAATGACAGCCT

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
1215	OPAI H31 3UTR(-15-39)	TTGGCAGCATTAATGAAAAATGACAG	-		
1216	OPAI H31 3UTR(-18-42)	ATGTTGGCAGCATTAATGAAAAATGA	1237	OPAI H31 3UTR(-81-105)	GAAATTAAAGTCTCTTCCAGTTCTA
1217	OPAI H31 3UTR(-21-45)	AACATGTTGGCAGCATTAATGAAAA	1238	OPAI H31 3UTR(-84-108)	GATGAAATTAAAGTCTCTTCCAGTT
1218	OPAI H31 3UTR(-24-48)	ATGAACATGTTGGCAGCATTAATGA	1239	OPAI H31 3UTR(-87-111)	GTAGATGAAATTAAAGTCTCTTCCA
1219	OPAI H31 3UTR(-27-51)	CATATGAACATGTTGGCAGCATTA	1240	OPAI H31 3UTR(-90-114)	ATGGTAGATGAAATTAAAGTCTCTT
1220	OPAI H31 3UTR(-30-54)	CCTCATATGAACATGTTGGCAGCAT	1241	OPAI H31 3UTR(-93-117)	CAGATGGTAGATGAAATTAAAGTCT
1221	OPAI H31 3UTR(-33-57)	AAGCCTCATATGAACATGTTGGCAG	1242	OPAI H31 3UTR(-96-120)	AATCAGATGGTAGATGAAATTAAAG
1222	OPAI H31 3UTR(-36-60)	AGTAAGCCTCATATGAACATGTTGG	1243	OPAI H31 3UTR(-99-123)	TATAATCAGATGGTAGATGAAATTA
1223	OPAI H31 3UTR(-39-63)	CTTAGTAAGCCTCATATGAACATGT		OPAI H31 3UTR(-102-126)	GTTTATAATCAGATGGTAGATGAAA
1224	OPAI H31 3UTR(-42-66)	CTTCTTAGTAAGCCTCATATGAACA	1245	OPAI H31 3UTR(-105-129)	GGAGTTTATAATCAGATGGTAGATG
1225	OPAI H31 3UTR(-45-69)	TAACTTCTTAGTAAGCCTCATATGA	1246	OPAI H31 3UTR(-108-132)	ACAGGAGTTTATAATCAGATGGTAG
1226	OPAI H31 3UTR(-48-72)	TTATAAAGCCTTAGTAAGCCTCATATA	1247	OPAI H31 3UTR(-111-135)	GTTAAACAGGAGTTTATAATCAGATGG
1227	OPAI H31 3UTR(-51-75)	TAGTTATAAAGCCTTAGTAAGCCTC	1248	OPAI H31 3UTR(-114-138)	TGAGTAACAGGAGTTTATAATCAGA
1228	OPAI H31 3UTR(-54-78)	GCTTAGTTATAAAGCCTTAGTAAGC	1249	OPAI H31 3UTR(-117-141)	AAGTGAGTAACAGGAGTTTATAATC
1229	OPAI H31 3UTR(-57-81)	AAAGCCTTAGTTATAAAGCCTTAGTA	1250	OPAI H31 3UTR(-120-144)	ACAAAAGTGAGTAACAGGAGTTTATA
1230	OPAI H31 3UTR(-60-84)	TCTAAAGCCTTAGTTATAAAGCCTTCTTA	1251	OPAI H31 3UTR(-123-147)	ATAACAAAAGTGAGTAACAGGAGTTT
1231	OPAI H31 3UTR(-63-87)	AGTTCTAAAGCCTTAGTTATAAAGCCTTC	1252	OPAI H31 3UTR(-126-150)	GGAAATAACAAAAGTGAGTAACAGGAG
1232	OPAI H31 3UTR(-66-90)	TCCAGTTCTAAAGCCTTAGTTATAAC	1253	OPAI H31 3UTR(-129-153)	GGAGGAATAACAAAAGTGAGTAACAG
1233	OPAI H31 3UTR(-69-93)	TCTTCCAGTTCTAAAGCCTTAGTTAT	1254	OPAI H31 3UTR(-132-156)	TCTGGAGGAATAACAAAAGTGAGTAA
1234	OPAI H31 3UTR(-72-96)	GTCTCTTCCAGTTCTAAAGCCTTAGT	1255	OPAI H31 3UTR(-135-159)	AGTTCTGGAGGAATAACAAAAGTGAG
1235	OPAI H31 3UTR(-75-99)	AAAGTCTCTTCCAGTTCTAAAGCCTT	1256	OPAI H31 3UTR(-138-162)	CAAGGTTCTGGAGGAATAACAAAAGT
1236	OPAI H31 3UTR(-78-102)	ATTAAAGTCTCTTCCAGTTCTTAAAG	1257	OPAI H31 3UTR(-141-165)	GAGCAAAAGTTCTGGAGGAATAACAA

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
1258	OPA1 H31 3UTR(-144-168)	TATGAGCAAGTTCTGGAGGAATAA	1276	OPA1 H31 3UTR(-198-222)	CTATACGCTACCTAACTTGACATAT
1259	OPA1 H31 3UTR(-147-171)	ATTTATGAGCAAAAGTTCTGGAGGAA	1277	OPA1 H31 3UTR(-201-225)	CACCTATACGCTACCTAACTTGACA
1260	OPA1 H31 3UTR(-150-174)	ATCAATTTATGAGCAAAAGTTCTGGAG	1278	OPA1 H31 3UTR(-204-228)	GCACACCTATACGCTACCTAACTTG
1261	OPA1 H31 3UTR(-153-177)	GGTATCATTTATGAGCAAAAGTTCTG	1279	OPA1 H31 3UTR(-207-231)	AAGGCACACCTATACGCTACCTAAC
1262	OPA1 H31 3UTR(-156-180)	GTAGGTATCATTTATGAGCAAAAGTT	1280	OPA1 H31 3UTR(-210-234)	AAGAAAGGCACACCTATACGCTACCT
1263	OPA1 H31 3UTR(-159-183)	TTAGTAGGTATCATTTATGAGCAAAA	1281	OPA1 H31 3UTR(-213-237)	ATTAAGAAAGGCACACCTATACGCTA
1264	OPA1 H31 3UTR(-162-186)	CAATTAGGTATCATTTATGAGC	1282	OPA1 H31 3UTR(-216-240)	GGAAATTAAGAAAGGCACACCTATACG
1265	OPA1 H31 3UTR(-165-189)	CGACAAATTAGTAGGTATCATTTATG	1283	OPA1 H31 3UTR(-219-243)	GAAGGAATTAAGAAAGGCACACCTAT
1266	OPA1 H31 3UTR(-168-192)	GATCGACAAATTAGTAGGTATCATTT	1284	OPA1 H31 3UTR(-222-246)	TCTGAAGGAATTAAGAAAGGCACACCC
1267	OPA1 H31 3UTR(-171-195)	AATGATCGACAAATTAGTAGGTATCA	1285	OPA1 H31 3UTR(-225-249)	TCTTCTGAAGGAATTAAGAAAGGCAC
1268	OPA1 H31 3UTR(-174-198)	TCCAATGATCGACAAATTAGTAGGTA	1286	OPA1 H31 3UTR(-228-252)	GCATCTTCTGAAGGAATTAAGAAAGG
1269	OPA1 H31 3UTR(-177-201)	ATATCCAATGATCGACAAATTAGTAG	1287	OPA1 H31 3UTR(-231-255)	TCTGCATCTTCTGAAGGAATTAAGA
1270	OPA1 H31 3UTR(-180-204)	GACATATCCAATGATCGACAAATTAG	1288	OPA1 H31 3UTR(-234-258)	GCCTCTGCATCTTCTGAAGGAATTA
1271	OPA1 H31 3UTR(-183-207)	CTTGACATATCCAATGATCGACAAT	1289	OPA1 H31 3UTR(-237-261)	CTTGCCCTCTGCATCTTCTGAAGGAA
1272	OPA1 H31 3UTR(-186-210)	TAACTTGACATATCCAATGATCGAC	1290	OPA1 H31 3UTR(-240-264)	GTCTTGGCCCTCTGCATCTTCTGAAG
1273	OPA1 H31 3UTR(-189-213)	ACCTAACTTGACATATCCAATGATC	1291	OPA1 H31 3UTR(-243-267)	CATGTTCTTGGCCCTCTGCATCTTCTG
1274	OPA1 H31 3UTR(-192-216)	GCTACCTAACTTGACATATCCAATG	1292	OPA1 H31 3UTR(-246-270)	AAACATGTTCTTGGCCCTCTGCATCTT
1275	OPA1 H31 3UTR(-195-219)	TACGCTACCTAACTTGACATATCCA	1293	OPA1 H31 3UTR(-249-273)	TTGAAACATGTTCTTGGCCCTCTGCAT

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
1294	OPA1 H31 3UTR(-252-276)	CGATTGAAACATGTTCTTGCCTCTG	-		
1295	OPA1 H31 3UTR(-255-279)	ACACGATTGAAACATGTTCTTGCCT	1304	OPA1 H31 3UTR(-282-306)	TAGCACTGATAAAGAAAAACCAATGC
1296	OPA1 H31 3UTR(-258-282)	CTAACACGATTGAAACATGTTCTTG	1305	OPA1 H31 3UTR(-285-309)	TGTTAGCACTGATAAAGAAAAACCAA
1297	OPA1 H31 3UTR(-261-285)	ATGCTAACACGATTGAAACATGTTTC	1306	OPA1 H31 3UTR(-288-312)	GTCTGTTAGCACTGATAAAGAAAAAC
1298	OPA1 H31 3UTR(-264-288)	CCAATGCTAACACGATTGAAACATG	1307	OPA1 H31 3UTR(-291-315)	TGAGTCTGTTAGCACTGATAAAGAA
1299	OPA1 H31 3UTR(-267-291)	AAACCAATGCTAACACGATTGAAAC	1308	OPA1 H31 3UTR(-294-318)	CACTGAGTCTGTTAGCACTGATAAA
1300	OPA1 H31 3UTR(-270-294)	AGAAAAACCAATGCTAACACGATTGA	1309	OPA1 H31 3UTR(-297-321)	TCACACTGAGTCTGTTAGCACTGAT
1301	OPA1 H31 3UTR(-273-297)	TAAAGAAAAACCAATGCTAACACGAT	1310	OPA1 H31 3UTR(-300-324)	GCCTCACACTGAGTCTGTTAGCACT
1302	OPA1 H31 3UTR(-276-300)	TGATAAAGAAAAACCAATGCTAACAC	1311	OPA1 H31 3UTR(-303-327)	GGGGCCTCACACTGAGTCTGTTAGC
1303	OPA1 H31 3UTR(-279-303)	CACTGATAAAGAAAAACCAATGCTAA	1312	OPA1 H31 3UTR(-306-330)	TATGGGGCCTCACACTGAGTCTGTT

Table 5. List of antisense oligonucleotide micro-walked sequences with 17 nucleotides in that target the 3' UTR of an *OPA1* transcript.

SEQ ID	ASO coordinates	Sequence 5'>3'	SEQ ID	ASO coordinates	Sequence 5'>3'
1313	OPA1 H30:31 3UTR(+1+17)	ATGAGTACGATTTTAAT	1319	OPA1 H31 3UTR(+19+35)	ATGTATGCAGAGCTGAT
1314	OPA1 H30:31 3UTR(+4+20)	ATTATGAGTACGATTTT	1320	OPA1 H31 3UTR(+22+38)	CAGATGTATGCAGAGCT
1315	OPA1 H31 3UTR(+7+23)	CTGATTATGAGTACGAT	1321	OPA1 H31 3UTR(+25+41)	CTTCAGATGTATGCAGA
1316	OPA1 H31 3UTR(+10+26)	GAGCTGATTATGAGTAC	1322	OPA1 H31 3UTR(+28+44)	GTTCCTCAGATGTATGC
1317	OPA1 H31 3UTR(+13+29)	GCAGAGCTGATTATGAG	1323	OPA1 H31 3UTR(+31+47)	TTTGTCTTCAGATGTA
1318	OPA1 H31 3UTR(+16+32)	TATGCAGAGCTGATTAT	1324	OPA1 H31 3UTR(+34+50)	GTTTTGTCTTCAGAT

SEQ ID	ASO oordinates	Sequence 5'>3'	SEQ ID	ASO oordinates	Sequence 5'>3'
1325	OPA1 H31 3UTR(+37+53)	GATGTTTTTTTGTTCTTCA	1343	OPA1 H31 3UTR(+91+107)	GTATGTTTAGAAAGGTG
1326	OPA1 H31 3UTR(+40+56)	GTTGATGTTTTTGTCT	1344	OPA1 H31 3UTR(+94+110)	ATTGTATGTTAGAAAG
1327	OPA1 H31 3UTR(+43+59)	GACGTTGATGTTTTTGT	1345	OPA1 H31 3UTR(+97+113)	TTTATTGTATGTTTAGA
1328	OPA1 H31 3UTR(+46+62)	AAAGACGTTGATGTTTT	1346	OPA1 H31 3UTR(+100+116)	GACTTTATTGTATGTTT
1329	OPA1 H31 3UTR(+49+65)	ACAAAAGACGTTGATGT	1347	OPA1 H31 3UTR(+103+119)	CATGACTTTATTGTATG
1330	OPA1 H31 3UTR(+52+68)	TGGACAAAAGACGTTGA	1348	OPA1 H31 3UTR(+106+122)	TCCCATGACTTTATTGT
1331	OPA1 H31 3UTR(+55+71)	GGCTGGACAAAAGACGT	1349	OPA1 H31 3UTR(+109+125)	TTATCCCATGACTTTAT
1332	OPA1 H31 3UTR(+58+74)	AGAGGCTGGACAAAAGA	1350	OPA1 H31 3UTR(+112+128)	TTTTATCCCATGACTT
1333	OPA1 H31 3UTR(+61+77)	AAAAGAGGCTGGACAAA	1351	OPA1 H31 3UTR(+115+131)	TTATTTTATCCCATGA
1334	OPA1 H31 3UTR(+64+80)	AGAAAAAGAGGCTGGAC	1352	OPA1 H31 3UTR(+118+134)	CGATTATTTTATATCCCA
1335	OPA1 H31 3UTR(+67+83)	AGAAAGAAAAGAGGCTG	1353	OPA1 H31 3UTR(+121+137)	CATCGATTATTTTATC
1336	OPA1 H31 3UTR(+70+86)	AGCAGAAAGAAAAGAGG	1354	OPA1 H31 3UTR(+124+140)	ATACATCGATTATTTT
1337	OPA1 H31 3UTR(+73+89)	AACAGCAGAAAGAAAAG	1355	OPA1 H31 3UTR(+127+143)	AACATACATCGATTATT
1338	OPA1 H31 3UTR(+76+92)	TGGAACAGCAGAAAGAA	1356	OPA1 H31 3UTR(+130+146)	CGTAAACATACATCGATT
1339	OPA1 H31 3UTR(+79+95)	AGGTGGAACAGCAGAAAG	1357	OPA1 H31 3UTR(+133+149)	GCCCCGTAACATACATCG
1340	OPA1 H31 3UTR(+82+98)	GAAAGGTGGAACAGCAG	1358	OPA1 H31 3UTR(+136+152)	AGCGCCCGTAACATACA
1341	OPA1 H31 3UTR(+85+101)	TTAGAAAAGGTGGAAACAG	1359	OPA1 H31 3UTR(+139+155)	TAAAGCGCCCGTAACAT
1342	OPA1 H31 3UTR(+88+104)	TGTTTAGAAAGGTGGAA	1360	OPA1 H31 3UTR(+142+158)	GGTTAAAGCGCCCGTAA

SEQ ID	ASO coordinates	Sequence 5'>3'	SEQ ID	ASO coordinates	Sequence 5'>3'
1361	OPAI H31 3UTR(+145+161)	GATGGTTAAAGCGCCCG	1379	OPAI H31 3UTR(+199+215)	CAACAAAATAGGATGTT
1362	OPAI H31 3UTR(+148+164)	GCTGATGGTTAAAGCGC	1380	OPAI H31 3UTR(+202+218)	GTACAACAAAAATAGGAT
1363	OPAI H31 3UTR(+151+167)	GCAGCTGATGGTTAAAG	1381	OPAI H31 3UTR(+205+221)	TTAGTACAACAAAAATAG
1364	OPAI H31 3UTR(+154+170)	GAGGCAGCTGATGGTTA	1382	OPAI H31 3UTR(+208+224)	ACTTTAGTACAACAAAA
1365	OPAI H31 3UTR(+157+173)	CGAGAGGCAGCTGATGG	1383	OPAI H31 3UTR(+211+227)	GTCACCTTTAGTACAACA
1366	OPAI H31 3UTR(+160+176)	ATTCGAGAGGCAGCTGA	1384	OPAI H31 3UTR(+214+230)	TTTGTCACTTTAGTACA
1367	OPAI H31 3UTR(+163+179)	TCCATTTCGAGAGGCAGC	1385	OPAI H31 3UTR(+217+233)	CGATTTGTCACTTTAGT
1368	OPAI H31 3UTR(+166+182)	TCTTCCATTTCGAGAGGC	1386	OPAI H31 3UTR(+220+236)	TTCCGATTTGTCACTTT
1369	OPAI H31 3UTR(+169+185)	TGTTCTTCCATTTCGAGA	1387	OPAI H31 3UTR(+223+239)	TTATTCCGATTTGTCAAC
1370	OPAI H31 3UTR(+172+188)	CACTGTTCTTCCATTTCG	1388	OPAI H31 3UTR(+226+242)	ATATTATTCCGATTTGT
1371	OPAI H31 3UTR(+175+191)	TACCACTGTTCTTCCCAT	1389	OPAI H31 3UTR(+229+245)	ATTATATTATTCCGATT
1372	OPAI H31 3UTR(+178+194)	CATTACCACTGTTCTTTC	1390	OPAI H31 3UTR(+232+248)	CCAAATTATATTATTCCG
1373	OPAI H31 3UTR(+181+197)	ATCCAATTACCACTGTTTC	1391	OPAI H31 3UTR(+235+251)	ATACCAATTATATTATT
1374	OPAI H31 3UTR(+184+200)	TTAATCCATTACCACTG	1392	OPAI H31 3UTR(+238+254)	GCCATACCAATTATATT
1375	OPAI H31 3UTR(+187+203)	ATGTTAATCCATTACCA	1393	OPAI H31 3UTR(+241+257)	ATGGCCATACCAATTAT
1376	OPAI H31 3UTR(+190+206)	AGGATGTTAATCCATTA	1394	OPAI H31 3UTR(+244+260)	CTAATGGCCATACCAAT
1377	OPAI H31 3UTR(+193+209)	AATAGGATGTTAATCCA	1395	OPAI H31 3UTR(+247+263)	AACCTAATGGCCATACC
1378	OPAI H31 3UTR(+196+212)	CAAAAATAGGATGTTAAT	1396	OPAI H31 3UTR(+250+266)	CTGAACCTAATGGCCAT

SEQ ID	ASO oordinates	Sequence 5'>3'	SEQ ID	ASO oordinates	Sequence 5'>3'
1397	OPAI H31 3UTR(+253+269)	GGACTGAACCTAATGGC	1415	OPAI H31 3UTR(+307+323)	ACGAGTGCCACCACAAA
1398	OPAI H31 3UTR(+256+272)	CAAGGACTGAACCTAAT	1416	OPAI H31 3UTR(+310+326)	TAAACGAGTGCCACCAC
1399	OPAI H31 3UTR(+259+275)	CTTCAAGGACTGAACCT	1417	OPAI H31 3UTR(+313+329)	CATTAAACGAGTGCCAC
1400	OPAI H31 3UTR(+262+278)	TATCTTCAAGGACTGAA	1418	OPAI H31 3UTR(+316+332)	ATCCATTAAACGAGTGC
1401	OPAI H31 3UTR(+265+281)	TCCTATCTTCAAGGACT	1419	OPAI H31 3UTR(+319+335)	TTAATCCATTAAACGAG
1402	OPAI H31 3UTR(+268+284)	GTTTCTTATCTTCAAGG	1420	OPAI H31 3UTR(+322+338)	CAGTTAAATCCATTAAAC
1403	OPAI H31 3UTR(+271+287)	CAAGTTTCTTATCTTCA	1421	OPAI H31 3UTR(+325+341)	CCTCAGTTAATCCATTA
1404	OPAI H31 3UTR(+274+290)	GAACAAAGTTTCTTATCT	1422	OPAI H31 3UTR(+328+344)	CAACCTCAGTTAATCCA
1405	OPAI H31 3UTR(+277+293)	AGAGAACAAAGTTTCTTA	1423	OPAI H31 3UTR(+331+347)	GAGCAACCTCAGTTAAT
1406	OPAI H31 3UTR(+280+296)	AACAGAGAACAAAGTTTC	1424	OPAI H31 3UTR(+334+350)	ATTGAGCAACCTCAGTT
1407	OPAI H31 3UTR(+283+299)	ACAAACAGAGAACAAAGT	1425	OPAI H31 3UTR(+337+353)	AACATTGAGCAACCTCA
1408	OPAI H31 3UTR(+286+302)	ACAACAAACAGAGAACAA	1426	OPAI H31 3UTR(+340+356)	CTGAAACATTGAGCAACC
1409	OPAI H31 3UTR(+289+305)	AAGACAAACAAACAGAGA	1427	OPAI H31 3UTR(+343+359)	AAACTGAAACATTGAGCA
1410	OPAI H31 3UTR(+292+308)	AATAAGACAAACAAACAG	1428	OPAI H31 3UTR(+346+362)	AAGAAACTGAACACATTGA
1411	OPAI H31 3UTR(+295+311)	ACAAATAAGACAAACAAA	1429	OPAI H31 3UTR(+349+365)	GAAAAGAAACTGAACAT
1412	OPAI H31 3UTR(+298+314)	ACCACAAATAAGACAAAC	1430	OPAI H31 3UTR(+352+368)	CTGGAAAAAGAAACTGAA
1413	OPAI H31 3UTR(+301+317)	GCCACCACAAATAAGAC	1431	OPAI H31 3UTR(+355+371)	TTTCTGGAAAAAGAAACT
1414	OPAI H31 3UTR(+304+320)	AGTGCCACCACAAATAAA	1432	OPAI H31 3UTR(+358+374)	GTATTTCTGGAAAAAGAA

SEQ ID	ASO coordinates	Sequence 5'>3'	SEQ ID	ASO coordinates	Sequence 5'>3'
1433	OPAI H31 3UTR(+361+377)	ATTGTAATTTCTGGAAA	1451	OPAI H31 3UTR(+415+431)	ACAAATTGATAACTTTAA
1434	OPAI H31 3UTR(+364+380)	AGCAATGTATTTCTGGA	1452	OPAI H31 3UTR(+418+434)	TATACAAATTGATAACTT
1435	OPAI H31 3UTR(+367+383)	CCTAGCAATGTATTCT	1453	OPAI H31 3UTR(+421+437)	TTATATACAATTGATAA
1436	OPAI H31 3UTR(+370+386)	ACACCTAGCATTTGTAAT	1454	OPAI H31 3UTR(+424+440)	ATTTATATACAATTGA
1437	OPAI H31 3UTR(+373+389)	AAAACACCTAGCATTTGT	1455	OPAI H31 3UTR(+427+443)	GTGATTTTATATACAAT
1438	OPAI H31 3UTR(+376+392)	TTCAAAAACACCTAGCAT	1456	OPAI H31 3UTR(+430+446)	ACTGTGATTTTATATAC
1439	OPAI H31 3UTR(+379+395)	TATTTCAAAAACACCTAG	1457	OPAI H31 3UTR(+433+449)	GCTACTGTGATTTTATA
1440	OPAI H31 3UTR(+382+398)	TTTTATTTCAAAAACACC	1458	OPAI H31 3UTR(+436+452)	CAGGCTACTGTGATTTT
1441	OPAI H31 3UTR(+385+401)	AAGTTTTATTTCAAAAC	1459	OPAI H31 3UTR(+439+455)	TAGCAGGCTACTGTGAT
1442	OPAI H31 3UTR(+388+404)	TATAAGTTTTTATTTCAA	1460	OPAI H31 3UTR(+442+458)	ATTAGCAGGCTACTGT
1443	OPAI H31 3UTR(+391+407)	CTATATAAGTTTTTATTT	1461	OPAI H31 3UTR(+445+461)	ATGATTTAGCAGGCTAC
1444	OPAI H31 3UTR(+394+410)	TTGCTATATAAGTTTTTA	1462	OPAI H31 3UTR(+448+464)	ACAATGATTTAGCAGGC
1445	OPAI H31 3UTR(+397+413)	CAATTGCTATATAAGTT	1463	OPAI H31 3UTR(+451+467)	CATACAAATGATTTAGCA
1446	OPAI H31 3UTR(+400+416)	AAACAAATTGCTATATAA	1464	OPAI H31 3UTR(+454+470)	ACACATACAATGATTTA
1447	OPAI H31 3UTR(+403+419)	TTTAAACAATTGCTATA	1465	OPAI H31 3UTR(+457+473)	CAGACACATACAATGAT
1448	OPAI H31 3UTR(+406+422)	AACTTTAAACAATTGCT	1466	OPAI H31 3UTR(+460+476)	CTACAGACACATACAAT
1449	OPAI H31 3UTR(+409+425)	GATAACTTTAAACAATT	1467	OPAI H31 3UTR(+463+479)	ATACTACAGACACATAC
1450	OPAI H31 3UTR(+412+428)	ATTGATAACTTTAAACA	1468	OPAI H31 3UTR(+466+482)	AGAATACTACAGACACA

SEQ ID	ASO coordinates	Sequence 5'>3'	SEQ ID	ASO coordinates	Sequence 5'>3'
1469	OPAI H31 3UTR(+469+485)	AATAGAAATACTACAGAC	1487	OPAI H31 3UTR(+523+539)	TTTCTTTTCATGTGGTGA
1470	OPAI H31 3UTR(+472+488)	GGGAATAGAAATACTACA	1488	OPAI H31 3UTR(+526+542)	ATTTTCTTTTCATGTGG
1471	OPAI H31 3UTR(+475+491)	TCTGGGAATAGAATACT	1489	OPAI H31 3UTR(+529+545)	CCCAATTTTCTTTTCATG
1472	OPAI H31 3UTR(+478+494)	GTTTCTGGGAATAGAAT	1490	OPAI H31 3UTR(+532+548)	TTACCCATTTTCTTTCT
1473	OPAI H31 3UTR(+481+497)	ATAGTTTCTGGGAATAG	1491	OPAI H31 3UTR(+535+551)	CTGTACCCCATTTTCT
1474	OPAI H31 3UTR(+484+500)	CAAAATAGTTTCTGGGAA	1492	OPAI H31 3UTR(+538+554)	CTTCTGTTACCCATTTT
1475	OPAI H31 3UTR(+487+503)	GGTCAAAATAGTTTCTGG	1493	OPAI H31 3UTR(+541+557)	GTTCTTCTGTTACCCAT
1476	OPAI H31 3UTR(+490+506)	CATGGTCAAAATAGTTTC	1494	OPAI H31 3UTR(+544+560)	AGGGTCTTCTGTTACC
1477	OPAI H31 3UTR(+493+509)	TATCATGGTCAAAATAGT	1495	OPAI H31 3UTR(+547+563)	TTAAAGGGTCTTCTGTT
1478	OPAI H31 3UTR(+496+512)	AATTATCATGGTCAAAAT	1496	OPAI H31 3UTR(+550+566)	GTTTAAAGGGTCTTCT
1479	OPAI H31 3UTR(+499+515)	CTGAAATTATCATGGTCA	1497	OPAI H31 3UTR(+553+569)	CCTGTTTTAAAGGGTCT
1480	OPAI H31 3UTR(+502+518)	AAACTGAAATTATCATGG	1498	OPAI H31 3UTR(+556+572)	TAACTGTTTTTAAAGGGT
1481	OPAI H31 3UTR(+505+521)	TATAAACTGAATTATCA	1499	OPAI H31 3UTR(+559+575)	AATTAACTGTTTTAAG
1482	OPAI H31 3UTR(+508+524)	GAATATAAACTGAATTA	1500	OPAI H31 3UTR(+562+578)	CCAAATTAACCTGTTTT
1483	OPAI H31 3UTR(+511+527)	GGTGAATATAAACTGAA	1501	OPAI H31 3UTR(+565+581)	AATCCAAATTAACCTGT
1484	OPAI H31 3UTR(+514+530)	TGTGGTGAATATAAACT	1502	OPAI H31 3UTR(+568+584)	TACAATCCAAATTAACC
1485	OPAI H31 3UTR(+517+533)	TCATGTGGTGAATATAA	1503	OPAI H31 3UTR(+571+587)	CGTTACAATCCAAATTA
1486	OPAI H31 3UTR(+520+536)	CTTTCATGTGGTGAATA	1504	OPAI H31 3UTR(+574+590)	GAACGTTACAATCCAAA

SEQ ID	ASO coordinates	Sequence 5'>3'	SEQ ID	ASO coordinates	Sequence 5'>3'
1505	OPAI H31 3UTR(+577+593)	ACTGAACGTTTCAATCC	1523	OPAI H31 3UTR(+631+647)	CTTGGCTTCCAAAGGCAA
1506	OPAI H31 3UTR(+580+596)	TTCACCTGAACGTTACAA	1524	OPAI H31 3UTR(+634+650)	TGACTTGGCTTCCAAAGG
1507	OPAI H31 3UTR(+583+599)	TCCTTCACTGAACGTTA	1525	OPAI H31 3UTR(+637+653)	TACTGACTTGGCTTCCA
1508	OPAI H31 3UTR(+586+602)	ATTTCTTCACTGAACG	1526	OPAI H31 3UTR(+640+656)	TGGTACTGACTTGGCTT
1509	OPAI H31 3UTR(+589+605)	GAAATTTCTTCACTGA	1527	OPAI H31 3UTR(+643+659)	AGCTGGTACTGACTTGG
1510	OPAI H31 3UTR(+592+608)	GTTGAAATTTCTTTCAC	1528	OPAI H31 3UTR(+646+662)	GTAAAGCTGGTACTGACT
1511	OPAI H31 3UTR(+595+611)	AGGGTTGAAATTTCTTT	1529	OPAI H31 3UTR(+649+665)	TAGGTAAAGCTGGTACTG
1512	OPAI H31 3UTR(+598+614)	TGAAGGGTTGAAATTTTC	1530	OPAI H31 3UTR(+652+668)	AAATAGGTAAAGCTGGTA
1513	OPAI H31 3UTR(+601+617)	CTATGAAGGGTTGAAAT	1531	OPAI H31 3UTR(+655+671)	ATCAAAATAGGTAAAGCTG
1514	OPAI H31 3UTR(+604+620)	TGGCTATGAAGGGTTGA	1532	OPAI H31 3UTR(+658+674)	TGAATCAAAATAGGTAAG
1515	OPAI H31 3UTR(+607+623)	CGCTGGCTATGAAGGGT	1533	OPAI H31 3UTR(+661+677)	AACTGAATCAAAATAGGT
1516	OPAI H31 3UTR(+610+626)	CTTCGCTGGCTATGAAG	1534	OPAI H31 3UTR(+664+680)	AGCAACTGAATCAAAATA
1517	OPAI H31 3UTR(+613+629)	TTTCTTCGCTGGCTATG	1535	OPAI H31 3UTR(+667+683)	AACAGCAACTGAATCAA
1518	OPAI H31 3UTR(+616+632)	AAATTTCTTCGCTGGCT	1536	OPAI H31 3UTR(+670+686)	GAAAACAGCAACTGAAT
1519	OPAI H31 3UTR(+619+635)	GGCAAAATTTCTTCGCTG	1537	OPAI H31 3UTR(+673+689)	TGAGAAAAACAGCAACTG
1520	OPAI H31 3UTR(+622+638)	CAAGGCAAAATTTCTTCG	1538	OPAI H31 3UTR(+676+692)	GAGTGAGAAAAACAGCAA
1521	OPAI H31 3UTR(+625+641)	TTCCAAGGCAAAATTTCT	1539	OPAI H31 3UTR(+679+695)	AGAGAGTGAGAAAAACAG
1522	OPAI H31 3UTR(+628+644)	GGCTTCCAAGGCAAAAT	1540	OPAI H31 3UTR(+682+698)	TATAGAGAGTGAGAAAA

SEQ ID	ASO coordinates	Sequence 5'>3'	SEQ ID	ASO coordinates	Sequence 5'>3'
1541	OPAI H31 3UTR(+685+701)	GGATATAGAGAGTGAGA	1559	OPAI H31 3UTR(+739+755)	TTAACAGAAAGCCTAAC
1542	OPAI H31 3UTR(+688+704)	AATGGATATAGAGAGTG	1560	OPAI H31 3UTR(+742+758)	CTATTAAACAGAAAGCCT
1543	OPAI H31 3UTR(+691+707)	TCAAATGGATATAGAGA	1561	OPAI H31 3UTR(+745+761)	CCACTATTAAACAGAAAG
1544	OPAI H31 3UTR(+694+710)	ATTCAAATGGATATAG	1562	OPAI H31 3UTR(+748+764)	AAACCACTATTAAACAGA
1545	OPAI H31 3UTR(+697+713)	TCAATTTCAAATGGATA	1563	OPAI H31 3UTR(+751+767)	GAAAAACCACTATTAAAC
1546	OPAI H31 3UTR(+700+716)	AAATCAAATTTCAAATGG	1564	OPAI H31 3UTR(+754+770)	GGAGAAAAACCACTAATT
1547	OPAI H31 3UTR(+703+719)	AATAAAATCAAATTTCAAAA	1565	OPAI H31 3UTR(+757+773)	ACAGGAGAAAAACCACT
1548	OPAI H31 3UTR(+706+722)	TAAAAATAAATCAATTTTC	1566	OPAI H31 3UTR(+760+776)	TCAACAGGAGAAAAAACCC
1549	OPAI H31 3UTR(+709+725)	ATCTAAAAATAAATCAAT	1567	OPAI H31 3UTR(+763+779)	CTGTCAACAGGAGAAAA
1550	OPAI H31 3UTR(+712+728)	AACATCTAAAAATAAATC	1568	OPAI H31 3UTR(+766+782)	GCCTCTGTCAACAGGAGA
1551	OPAI H31 3UTR(+715+731)	TACAACATCTAAAAATAA	1569	OPAI H31 3UTR(+769+785)	GTGGCTCTGTCAACAGG
1552	OPAI H31 3UTR(+718+734)	GTATACAACATCTAAAA	1570	OPAI H31 3UTR(+772+788)	CCGGTGGCTCTGTCAAC
1553	OPAI H31 3UTR(+721+737)	TAAGTATACAACATCTA	1571	OPAI H31 3UTR(+775+791)	AATCCGGTGGCTCTGTCTC
1554	OPAI H31 3UTR(+724+740)	ACGTAAGTATACAACAT	1572	OPAI H31 3UTR(+778+794)	CATAATCCGGTGGCTCT
1555	OPAI H31 3UTR(+727+743)	CTAACGTAAGTATACAA	1573	OPAI H31 3UTR(+781+797)	TGTCATAATCCGGTGGC
1556	OPAI H31 3UTR(+730+746)	AGCCTAACGTAAGTATA	1574	OPAI H31 3UTR(+784+800)	CTGTGTCATAAATCCGGT
1557	OPAI H31 3UTR(+733+749)	GAAAGCCTAACGTAAGT	1575	OPAI H31 3UTR(+787+803)	ATCCTGTGTCAATAATCC
1558	OPAI H31 3UTR(+736+752)	ACA GAAAGCCTAACGTA	1576	OPAI H31 3UTR(+790+806)	CTCATCTCTGTGTCAATAA

SEQ ID	ASO oordinates	Sequence 5'>3'	SEQ ID	ASO oordinates	Sequence 5'>3'
1577	OPAI H31 3UTR(+793+809)	TTCTTCATCCTGTGTCA	1595	OPAI H31 3UTR(+847+863)	TTGAAATGTTTGTAAAT
1578	OPAI H31 3UTR(+796+812)	ATCTTCCTCATCCTGTG	1596	OPAI H31 3UTR(+850+866)	TAGTTGAAATGTTTGAT
1579	OPAI H31 3UTR(+799+815)	TTAAATCTTCCTCATCCT	1597	OPAI H31 3UTR(+853+869)	ACCTAGTTGAAATGTTT
1580	OPAI H31 3UTR(+802+818)	TCCTTAATCTTCCTCAT	1598	OPAI H31 3UTR(+856+872)	GATACCTAGTTGAAATG
1581	OPAI H31 3UTR(+805+821)	TTATCCTTAATCTTCCT	1599	OPAI H31 3UTR(+859+875)	TCTGATACCTAGTTGAA
1582	OPAI H31 3UTR(+808+824)	TGATTATCCTTAATCTT	1600	OPAI H31 3UTR(+862+878)	TTTTCTGATACCTAGTT
1583	OPAI H31 3UTR(+811+827)	AATTGATTATCCTTAAT	1601	OPAI H31 3UTR(+865+881)	CCTTTTCTGATACCTA
1584	OPAI H31 3UTR(+814+830)	GTCAAATTGATTATCCTT	1602	OPAI H31 3UTR(+868+884)	AAGCCTTTTCTGATAC
1585	OPAI H31 3UTR(+817+833)	TTAGTCAATTGATTATC	1603	OPAI H31 3UTR(+871+887)	AGAAAGCCTTTTCTGA
1586	OPAI H31 3UTR(+820+836)	AAATTAGTCAATTGATT	1604	OPAI H31 3UTR(+874+890)	GAAAGAAAGCCTTTTTC
1587	OPAI H31 3UTR(+823+839)	ATGAAATTAGTCAATTG	1605	OPAI H31 3UTR(+877+893)	TATGAAAGAAAGCCTTT
1588	OPAI H31 3UTR(+826+842)	TAAATGAAATTAGTCAA	1606	OPAI H31 3UTR(+880+896)	TCTTATGAAAGAAAGCC
1589	OPAI H31 3UTR(+829+845)	TTCTAAATGAAATTAGT	1607	OPAI H31 3UTR(+883+899)	TAGTCTTATGAAAGAAA
1590	OPAI H31 3UTR(+832+848)	ATATTCTAAATGAAATT	1608	OPAI H31 3UTR(+886+902)	AAATAGTCTTATGAAAG
1591	OPAI H31 3UTR(+835+851)	ATAATATTCTAAATGAA	1609	OPAI H31 3UTR(+889+905)	TTAAAAATAGTCTTATGA
1592	OPAI H31 3UTR(+838+854)	TTGATAAATTCTAAAT	1610	OPAI H31 3UTR(+892+908)	TATTTAAAAATAGTCTTA
1593	OPAI H31 3UTR(+841+857)	TGTTTGATAAATATTCTA	1611	OPAI H31 3UTR(+895+911)	TTCTATTTAAAAATAGTC
1594	OPAI H31 3UTR(+844+860)	AAATGTTTGATAAATT	1612	OPAI H31 3UTR(+898+914)	AAITTTCTATTTAAAAATA

SEQ ID	ASO coordinates	Sequence 5'>3'	SEQ ID	ASO coordinates	Sequence 5'>3'
1613	OPAI H31 3UTR(+901+917)	AATAAATTTCTATTTAAA	1631	OPAI H31 3UTR(+955+971)	AAATTTTCTTTATTCAG
1614	OPAI H31 3UTR(+904+920)	TGAAATAAATTTCTAATTT	1632	OPAI H31 3UTR(+958+974)	CTAAATTTTCTTTAAT
1615	OPAI H31 3UTR(+907+923)	TGTTGAAATAAATTTCTA	1633	OPAI H31 3UTR(+961+977)	GAACATAAATTTTCTTT
1616	OPAI H31 3UTR(+910+926)	AATTGTTGAAATAATTT	1634	OPAI H31 3UTR(+964+980)	ATTGAACATAAATTTTTC
1617	OPAI H31 3UTR(+913+929)	TTTAAATTTGTTGAAATAA	1635	OPAI H31 3UTR(+967+983)	TAAATTTGAACTAAATTT
1618	OPAI H31 3UTR(+916+932)	TACTTTAAATTTGTTGAAA	1636	OPAI H31 3UTR(+970+986)	CAATAAATTTGAACTAAA
1619	OPAI H31 3UTR(+919+935)	CATTACTTTAAATTTGTTG	1637	OPAI H31 3UTR(+973+989)	TTGCAATAAATTTGAACT
1620	OPAI H31 3UTR(+922+938)	CAACATTACTTTAAATTTG	1638	OPAI H31 3UTR(+976+992)	AAATTTGCAATAAATTTGA
1621	OPAI H31 3UTR(+925+941)	GGTCAACATTACTTTTAA	1639	OPAI H31 3UTR(+979+995)	ATTAAATTTGCAATAAAT
1622	OPAI H31 3UTR(+928+944)	GATGGTCAACATTACTTT	1640	OPAI H31 3UTR(+982+998)	GTAATTTAAATTTGCAATA
1623	OPAI H31 3UTR(+931+947)	GGGGATGGTCAACATTA	1641	OPAI H31 3UTR(+985+1001)	ATTGTAATTTAAATTTGCA
1624	OPAI H31 3UTR(+934+950)	GAGGGGGATGGTCAACA	1642	OPAI H31 3UTR(+988+1004)	AGTATTGTAAATTTAAAT
1625	OPAI H31 3UTR(+937+953)	TGAGAGGGGGATGGTCA	1643	OPAI H31 3UTR(+991+1007)	GGTAGTATTGTAAATTA
1626	OPAI H31 3UTR(+940+956)	AGCTGAGAGGGGGATGG	1644	OPAI H31 3UTR(+994+1010)	GAAGGTAGTATTGTAAAT
1627	OPAI H31 3UTR(+943+959)	TTCAGCTGAGAGGGGGA	1645	OPAI H31 3UTR(+997+1013)	TGTGAAAGGTAGTATTGT
1628	OPAI H31 3UTR(+946+962)	TTATTCAGCTGAGAGGG	1646	OPAI H31 3UTR(+1000+1016)	TGTTGTGAAAGGTAGTAT
1629	OPAI H31 3UTR(+949+965)	TCTTTATTCAGCTGAGA	1647	OPAI H31 3UTR(+1003+1019)	AAATGTTGTGAAGGTAG
1630	OPAI H31 3UTR(+952+968)	TTTCTTTTATTCAGCTG	1648	OPAI H31 3UTR(+1006+1022)	TGAAAAATGTTGTGAAGG

SEQ ID	ASO coordinates	Sequence 5'>3'	SEQ ID	ASO coordinates	Sequence 5'>3'
1649	OPA1 H31 3UTR(+1009+1025)	ACATGAAAAATGTTGTGA	1667	OPA1 H31 3UTR(+1063+1079)	AGCATTCTTTTGCTTGA
1650	OPA1 H31 3UTR(+1012+1028)	AACACATGAAAAATGTTG	1668	OPA1 H31 3UTR(+1066+1082)	GAAAGCATTTCTTTTGCT
1651	OPA1 H31 3UTR(+1015+1031)	TAAAAACACATGAAAAATG	1669	OPA1 H31 3UTR(+1069+1085)	AAAGAAAGCATTTCTTT
1652	OPA1 H31 3UTR(+1018+1034)	ATTTAAACACATGAAA	1670	OPA1 H31 3UTR(+1072+1088)	AGTAAAGAAAGCATTTTC
1653	OPA1 H31 3UTR(+1021+1037)	TTTATTTAAACACATG	1671	OPA1 H31 3UTR(+1075+1091)	TTAAGTAAAGAAAGCAT
1654	OPA1 H31 3UTR(+1024+1040)	ATATTTATTTAAACAC	1672	OPA1 H31 3UTR(+1078+1094)	ATTTTAAAGTAAAGAAAG
1655	OPA1 H31 3UTR(+1027+1043)	AAAAATATTTATTTAAAA	1673	OPA1 H31 3UTR(+1081+1097)	GACATTTTAAAGTAAAGA
1656	OPA1 H31 3UTR(+1030+1046)	TAAAAAATATTTATTTA	1674	OPA1 H31 3UTR(+1084+1100)	ATAGACATTTTAAAGTAA
1657	OPA1 H31 3UTR(+1033+1049)	AATTAATAATAATTTAT	1675	OPA1 H31 3UTR(+1087+1103)	GAGATAGACATTTTAAAG
1658	OPA1 H31 3UTR(+1036+1052)	GCCAAATTAATAATAAT	1676	OPA1 H31 3UTR(+1090+1106)	AATGAGATAGACATTTT
1659	OPA1 H31 3UTR(+1039+1055)	TTAGCCCAATTAAAAAAT	1677	OPA1 H31 3UTR(+1093+1109)	GCAAAATGAGATAGACAT
1660	OPA1 H31 3UTR(+1042+1058)	CCTTTAGCCCAATTAAAA	1678	OPA1 H31 3UTR(+1096+1112)	GCAGCAAAATGAGATAGA
1661	OPA1 H31 3UTR(+1045+1061)	TGTCTTTTAGCCCAATTA	1679	OPA1 H31 3UTR(+1099+1115)	AAGGCAGCAAAATGAGAT
1662	OPA1 H31 3UTR(+1048+1064)	GAATGTCTCTTAGCCAA	1680	OPA1 H31 3UTR(+1102+1118)	GAAAAGGCAGCAAAATGA
1663	OPA1 H31 3UTR(+1051+1067)	CTTGAATGTCCTTTAGC	1681	OPA1 H31 3UTR(+1105+1121)	AGTGAAAAAGGCAGCAAA
1664	OPA1 H31 3UTR(+1054+1070)	TTGCTTGAATGTCCTTT	1682	OPA1 H31 3UTR(+1108+1124)	CTTAGTAAAAAGGCAGC
1665	OPA1 H31 3UTR(+1057+1073)	TCTTTGCTTGAATGTCC	1683	OPA1 H31 3UTR(+1111+1127)	AGGCTTAGTAAAAAGGC
1666	OPA1 H31 3UTR(+1060+1076)	ATTTCTTTGCTTGAATG	1684	OPA1 H31 3UTR(+1114+1130)	TAAAGGCTTAGTGAAAA

SEQ ID	ASO coordinates	Sequence 5'>3'	SEQ ID	ASO coordinates	Sequence 5'>3'
1685	OPAI H31 3UTR(+1117+1133)	AAGTAAAGGCTTAGTGA	1703	OPAI H31 3UTR(+1171+1187)	GATTTAGCAAACTGTAA
1686	OPAI H31 3UTR(+1120+1136)	ACAAAAGTAAAGGCTTAG	1704	OPAI H31 3UTR(+1174+1190)	TAAAGATTTAGCAAACTG
1687	OPAI H31 3UTR(+1123+1139)	TTAACAAAAGTAAAGGCT	1705	OPAI H31 3UTR(+1177+1193)	AAATAAGATTTAGCAAA
1688	OPAI H31 3UTR(+1126+1142)	TTATTAAACAAAGTAAAG	1706	OPAI H31 3UTR(+1180+1196)	AGAAAAATAAGATTTAGC
1689	OPAI H31 3UTR(+1129+1145)	CTTTTATTAAACAAAGTA	1707	OPAI H31 3UTR(+1183+1199)	CCAAAGAAAAATAAGATTT
1690	OPAI H31 3UTR(+1132+1148)	ACACTTTTATTAAACAAA	1708	OPAI H31 3UTR(+1186+1202)	ACTCCAAAGAAAAATAAGA
1691	OPAI H31 3UTR(+1135+1151)	TGGACACTTTTATTAAAC	1709	OPAI H31 3UTR(+1189+1205)	GCAACTCCAAAGAAAAATA
1692	OPAI H31 3UTR(+1138+1154)	CAATGGACACTTTTATT	1710	OPAI H31 3UTR(+1192+1208)	AAAGCAACTCCAAAGAAA
1693	OPAI H31 3UTR(+1141+1157)	ACACAATGGACACTTTT	1711	OPAI H31 3UTR(+1195+1211)	CAAAAAAGCAACTCCAAG
1694	OPAI H31 3UTR(+1144+1160)	ATCACACAATGGACACT	1712	OPAI H31 3UTR(+1198+1214)	TACCAAAAAAGCAACTCC
1695	OPAI H31 3UTR(+1147+1163)	AACATCACACAATGGAC	1713	OPAI H31 3UTR(+1201+1217)	TGTTACCAAAAAAGCAAC
1696	OPAI H31 3UTR(+1150+1166)	AAAAACATCACACAATG	1714	OPAI H31 3UTR(+1204+1220)	GGCTGTTACCAAAAAAGC
1697	OPAI H31 3UTR(+1153+1169)	ATCAAAAAACATCACACA	1715	OPAI H31 3UTR(+1207+1223)	TGGGGCTGTTACCAAAA
1698	OPAI H31 3UTR(+1156+1172)	AAAAATCAAAAAACATCAC	1716	OPAI H31 3UTR(+1210+1226)	CAATGGGGCTGTTACCA
1699	OPAI H31 3UTR(+1159+1175)	TGTAAAAATCAAAAAACAT	1717	OPAI H31 3UTR(+1213+1229)	TAGCAATGGGGCTGTTA
1700	OPAI H31 3UTR(+1162+1178)	AACGTGAAAAATCAAAAA	1718	OPAI H31 3UTR(+1216+1232)	GAGTAGCAATGGGGCTG
1701	OPAI H31 3UTR(+1165+1181)	GCAAACTGTAAAAATCAA	1719	OPAI H31 3UTR(+1219+1235)	GGGGAGTAGCAATGGGG
1702	OPAI H31 3UTR(+1168+1184)	TTAGCAAACTGTAAAAAT	1720	OPAI H31 3UTR(+1222+1238)	AATGGGAGTAGCAATG

SEQ ID	ASO coordinates	Sequence 5'>3'	SEQ ID	ASO coordinates	Sequence 5'>3'
1721	OPAI H31 3UTR(+1225+1241)	TAAAAATGGGAGTAGCA	1739	OPAI H31 3UTR(+1279+1295)	ACCAAGTGTACATCTT
1722	OPAI H31 3UTR(+1228+1244)	CAATAAAATGGGAGTA	1740	OPAI H31 3UTR(+1282+1298)	CATACCAAGTGTTACAT
1723	OPAI H31 3UTR(+1231+1247)	AAACAATAAAATGGGA	1741	OPAI H31 3UTR(+1285+1301)	GAGCATACCAAGTGTTA
1724	OPAI H31 3UTR(+1234+1250)	GTAAAAACAATAAATGG	1742	OPAI H31 3UTR(+1288+1304)	ACCGAGCATACCAAGTG
1725	OPAI H31 3UTR(+1237+1253)	GATGTAAAAACAATAAAA	1743	OPAI H31 3UTR(+1291+1307)	TCAACCGAGCATACCAA
1726	OPAI H31 3UTR(+1240+1256)	ATTGATGTAAAAACAATA	1744	OPAI H31 3UTR(+1294+1310)	TCCTCAACCGAGCATAC
1727	OPAI H31 3UTR(+1243+1259)	TGCAATTGATGTAAAAACA	1745	OPAI H31 3UTR(+1297+1313)	ATATCTCAACCGAGCA
1728	OPAI H31 3UTR(+1246+1262)	GCATGCATTGATGTAAA	1746	OPAI H31 3UTR(+1300+1316)	TTCATATCTCAACCGA
1729	OPAI H31 3UTR(+1249+1265)	GAAGCATGCATTGATGT	1747	OPAI H31 3UTR(+1303+1319)	TTTTTCATATCCTCAAC
1730	OPAI H31 3UTR(+1252+1268)	AACGAAAGCATGCATTGA	1748	OPAI H31 3UTR(+1306+1322)	TATTTTTTCATATCCTC
1731	OPAI H31 3UTR(+1255+1271)	CACAAACGAAAGCATGCAT	1749	OPAI H31 3UTR(+1309+1325)	AAGTATTTTTTCATATC
1732	OPAI H31 3UTR(+1258+1274)	GATCACAAACGAAAGCATG	1750	OPAI H31 3UTR(+1312+1328)	CGGAAAGTATTTTTTCAT
1733	OPAI H31 3UTR(+1261+1277)	AGGGATCACAAACGAAAGC	1751	OPAI H31 3UTR(+1315+1331)	TTTCGGAAAGTATTTTTT
1734	OPAI H31 3UTR(+1264+1280)	TTGAGGGATCACAAACGA	1752	OPAI H31 3UTR(+1318+1334)	TGGTTTCGGAAAGTATTT
1735	OPAI H31 3UTR(+1267+1283)	ATCTTGAGGGATCACAA	1753	OPAI H31 3UTR(+1321+1337)	TCCTGGTTTCGGAAAGTA
1736	OPAI H31 3UTR(+1270+1286)	TACATCTTGAGGGATCA	1754	OPAI H31 3UTR(+1324+1340)	AATTCCTGGTTTCGGAA
1737	OPAI H31 3UTR(+1273+1289)	TGTTACATCTTGAGGGA	1755	OPAI H31 3UTR(+1327+1343)	TTGAAATTCCTGGTTTCG
1738	OPAI H31 3UTR(+1276+1292)	AAGTGTTACATCTTGAG	1756	OPAI H31 3UTR(+1330+1346)	ACATTGAATTCCTGGTT

SEQ ID	ASO coordinates	Sequence 5'>3'	SEQ ID	ASO coordinates	Sequence 5'>3'
1757	OPA1 H31 3UTR(+1333+1349)	CATACATTGGAATTCCTG	1775	OPA1 H31 3UTR(+1387+1403)	ATCTGTGCTGCTTAAAGG
1758	OPA1 H31 3UTR(+1336+1352)	AAACATACATTGAATTC	1776	OPA1 H31 3UTR(+1390+1406)	CGCATCTGTGCTGCTTA
1759	OPA1 H31 3UTR(+1339+1355)	AACAAACATACATTGAA	1777	OPA1 H31 3UTR(+1393+1409)	CAGCGCATCTGTGCTGC
1760	OPA1 H31 3UTR(+1342+1358)	TAAACAAACATACATT	1778	OPA1 H31 3UTR(+1396+1412)	TACCAGCGCATCTGTGC
1761	OPA1 H31 3UTR(+1345+1361)	GTATAAAACAAACATAC	1779	OPA1 H31 3UTR(+1399+1415)	ATCTACCAGCGCATCTG
1762	OPA1 H31 3UTR(+1348+1364)	ACAGTATAAAACAAACA	1780	OPA1 H31 3UTR(+1402+1418)	TGCATCTACCAAGCGCAT
1763	OPA1 H31 3UTR(+1351+1367)	CAAACAGTATAAAACAA	1781	OPA1 H31 3UTR(+1405+1421)	CTATGCATCTACCAGCG
1764	OPA1 H31 3UTR(+1354+1370)	TATCAAACAGTATAAAA	1782	OPA1 H31 3UTR(+1408+1424)	TGACTATGCATCTACCA
1765	OPA1 H31 3UTR(+1357+1373)	TCTTATCAAACAGTATA	1783	OPA1 H31 3UTR(+1411+1427)	TCCTGACTATGCATCTA
1766	OPA1 H31 3UTR(+1360+1376)	TTTTCTTATCAAACAGT	1784	OPA1 H31 3UTR(+1414+1430)	AGTTCCTGACTATGCAT
1767	OPA1 H31 3UTR(+1363+1379)	TACTTTTCTTATCAAAC	1785	OPA1 H31 3UTR(+1417+1433)	AAAAAGTTCCTGACTATG
1768	OPA1 H31 3UTR(+1366+1382)	ACCTACTTTTCTTATCA	1786	OPA1 H31 3UTR(+1420+1436)	AAAAAAAGTTCCTGACT
1769	OPA1 H31 3UTR(+1369+1385)	TGGACCTACTTTTCTTA	1787	OPA1 H31 3UTR(+1423+1439)	AATAAAAAAGTTCCTG
1770	OPA1 H31 3UTR(+1372+1388)	GGCTGGACCTACTTTTC	1788	OPA1 H31 3UTR(+1426+1442)	AGAAATAAAAAAAGTTC
1771	OPA1 H31 3UTR(+1375+1391)	TAAAGGCTGGACCTACTT	1789	OPA1 H31 3UTR(+1429+1445)	AAAAGAAATAAAAAAAG
1772	OPA1 H31 3UTR(+1378+1394)	GCTTAAGGCTGGACCTA	1790	OPA1 H31 3UTR(+1432+1448)	CCTAAAAAGAAATAAAAA
1773	OPA1 H31 3UTR(+1381+1397)	GCTGCTTAAAGGCTGGAC	1791	OPA1 H31 3UTR(+1435+1451)	AGACCTAAAAAGAAATAA
1774	OPA1 H31 3UTR(+1384+1400)	TGTGCTGCTTAAAGGCTG	1792	OPA1 H31 3UTR(+1438+1454)	CCTAGACCTAAAAAGAAA

SEQ ID	ASO oordinates	Sequence 5'>3'	SEQ ID	ASO oordinates	Sequence 5'>3'
1793	OPAI H31 3UTR(+1441+1457)	GTCCCTAGACCTAAAAG	1811	OPAI H31 3UTR(+1495+1511)	TCCTAATCTGTGTATAG
1794	OPAI H31 3UTR(+1444+1460)	CCTGTCCCTAGACCTAA	1812	OPAI H31 3UTR(+1498+1514)	ATCTCTAAATCTGTGTA
1795	OPAI H31 3UTR(+1447+1463)	ACTCCTGTCCCTAGACC	1813	OPAI H31 3UTR(+1501+1517)	GTCAATCTCCTAATCTGT
1796	OPAI H31 3UTR(+1450+1466)	TTCACCTCCTGTCCCTAG	1814	OPAI H31 3UTR(+1504+1520)	AAGGTCATCTCCTAATC
1797	OPAI H31 3UTR(+1453+1469)	CTATTCACTCCTGTCCC	1815	OPAI H31 3UTR(+1507+1523)	AGTAAGGTCATCTCCTA
1798	OPAI H31 3UTR(+1456+1472)	TTTCTATTCACTCCTGT	1816	OPAI H31 3UTR(+1510+1526)	CCCAGTAAGGTCATCTC
1799	OPAI H31 3UTR(+1459+1475)	CCCTTTCTATTCACTCC	1817	OPAI H31 3UTR(+1513+1529)	GTACCCAGTAAGGTCAT
1800	OPAI H31 3UTR(+1462+1478)	CCTCCCTTTCTATTAC	1818	OPAI H31 3UTR(+1516+1532)	GGTGTAACCCAGTAAGGT
1801	OPAI H31 3UTR(+1465+1481)	TCTCCTCCCTTTCTATT	1819	OPAI H31 3UTR(+1519+1535)	AGGGGTGTACCCAGTAA
1802	OPAI H31 3UTR(+1468+1484)	AGCTCTCCTCCCTTTCT	1820	OPAI H31 3UTR(+1522+1538)	TAGAGGGGTGTACCCAG
1803	OPAI H31 3UTR(+1471+1487)	TAGAGCTCTCCTCCCTT	1821	OPAI H31 3UTR(+1525+1541)	GGTTAGAGGGGTGTACC
1804	OPAI H31 3UTR(+1474+1490)	TAATAGAGCTCTCCTCC	1822	OPAI H31 3UTR(+1528+1544)	ACTGGTTAGAGGGGTGT
1805	OPAI H31 3UTR(+1477+1493)	ACATAATAGAGCTCTCC	1823	OPAI H31 3UTR(+1531+1547)	AGCACTGGTTAGAGGGG
1806	OPAI H31 3UTR(+1480+1496)	AGAACATAATAGAGCTC	1824	OPAI H31 3UTR(+1534+1550)	GTAAGCACTGGTTAGAG
1807	OPAI H31 3UTR(+1483+1499)	TATAGAACATAATAGAG	1825	OPAI H31 3UTR(+1537+1553)	CCTGTAAGCACTGGTTA
1808	OPAI H31 3UTR(+1486+1502)	GTGTATAGAACATAATA	1826	OPAI H31 3UTR(+1540+1556)	TAACCTGTAAGCACTGG
1809	OPAI H31 3UTR(+1489+1505)	TCTGTGTATAGAACATA	1827	OPAI H31 3UTR(+1543+1559)	CATTAACTGTAAAGCAC
1810	OPAI H31 3UTR(+1492+1508)	TAACTCTGTATAGAAC	1828	OPAI H31 3UTR(+1546+1562)	ATGCATTAAACCTGTAAG

SEQ ID	ASO coordinates	Sequence 5'>3'	SEQ ID	ASO coordinates	Sequence 5'>3'
1829	OPAI H31 3UTR(+1549+1565)	AACATGCATTAACTGT	1847	OPAI H31 3UTR(+1603+1619)	GAAATAGATGTGTAGTT
1830	OPAI H31 3UTR(+1552+1568)	ATTAACATGCATTAAACC	1848	OPAI H31 3UTR(+1606+1622)	TTAGAAAATAGATGTGTA
1831	OPAI H31 3UTR(+1555+1571)	TTCATTAAACATGCATTA	1849	OPAI H31 3UTR(+1609+1625)	TCCTTAGAAAATAGATGT
1832	OPAI H31 3UTR(+1558+1574)	ATATTCAATTAACATGCA	1850	OPAI H31 3UTR(+1612+1628)	TATCTTTAGAAAATAGA
1833	OPAI H31 3UTR(+1561+1577)	AAAAATATTCATTAAACAT	1851	OPAI H31 3UTR(+1615+1631)	TTTTATTCTTTAGAAAAT
1834	OPAI H31 3UTR(+1564+1580)	GCAAAAATATTCATTAA	1852	OPAI H31 3UTR(+1618+1634)	CTGTTTTATTCTTTTAGA
1835	OPAI H31 3UTR(+1567+1583)	ACTGCAAAAATATTCAT	1853	OPAI H31 3UTR(+1621+1637)	GTCCTGTTTTATTCTTT
1836	OPAI H31 3UTR(+1570+1586)	ACAACTGCAAAAATATT	1854	OPAI H31 3UTR(+1624+1640)	ATGGTCCTGTTTTATTTC
1837	OPAI H31 3UTR(+1573+1589)	TTTACAACCTGCAAAAAT	1855	OPAI H31 3UTR(+1627+1643)	AATATGGTCCTGTTTTA
1838	OPAI H31 3UTR(+1576+1592)	TGCTTTACAACCTGCAAA	1856	OPAI H31 3UTR(+1630+1646)	ATAAATATGGTCCTGTT
1839	OPAI H31 3UTR(+1579+1595)	TTATGCTTTACAACCTGC	1857	OPAI H31 3UTR(+1633+1649)	TAAATAAATATGGTCCT
1840	OPAI H31 3UTR(+1582+1598)	TTGTTATGCTTTACAAAC	1858	OPAI H31 3UTR(+1636+1652)	AAGTAAATAAATATGGT
1841	OPAI H31 3UTR(+1585+1601)	TAATTGTTATGCTTTAC	1859	OPAI H31 3UTR(+1639+1655)	CAGAAGTAAATAAATAT
1842	OPAI H31 3UTR(+1588+1604)	TTGTAATTGTTATGCTT	1860	OPAI H31 3UTR(+1642+1658)	TGACAGAAAGTAAATAAA
1843	OPAI H31 3UTR(+1591+1607)	TAGTTGTAATTGTTATG	1861	OPAI H31 3UTR(+1645+1661)	AGTTGACAGAAAGTAAAT
1844	OPAI H31 3UTR(+1594+1610)	GTGTAGTTGTAATTGTT	1862	OPAI H31 3UTR(+1648+1664)	TATAGTTGACAGAAAGTA
1845	OPAI H31 3UTR(+1597+1613)	GATGTGTAGTTGTAATT	1863	OPAI H31 3UTR(+1651+1667)	TTCTATAGTTGACAGAA
1846	OPAI H31 3UTR(+1600+1616)	ATAGATGTGTAGTTGTA	1864	OPAI H31 3UTR(+1654+1670)	TCCTTCTATAGTTGACA

SEQ ID	ASO coordinates	Sequence 5'>3'	SEQ ID	ASO coordinates	Sequence 5'>3'
1865	OPA1 H31 3UTR(+1657+1673)	CTTCTTTTCTATAGTTG	1883	OPA1 H31 3UTR(+1711+1727)	TGACTAAATATTAGCCTT
1866	OPA1 H31 3UTR(+1660+1676)	GGTCTTTTCTTCTATAG	1884	OPA1 H31 3UTR(+1714+1730)	TAGTGACTAATATTAGC
1867	OPA1 H31 3UTR(+1663+1679)	GAAAGGTCTTCTTCTA	1885	OPA1 H31 3UTR(+1717+1733)	CAGTAGTGACTAATAAT
1868	OPA1 H31 3UTR(+1666+1682)	GCTGAAGGTCTTCTTT	1886	OPA1 H31 3UTR(+1720+1736)	TAAACAGTAGTGACTAAT
1869	OPA1 H31 3UTR(+1669+1685)	ACAGCTGAAGGTCTTTC	1887	OPA1 H31 3UTR(+1723+1739)	TGATAACAGTAGTGACT
1870	OPA1 H31 3UTR(+1672+1688)	AATACAGCTGAAGGTCT	1888	OPA1 H31 3UTR(+1726+1742)	ATGTGATAACAGTAGTG
1871	OPA1 H31 3UTR(+1675+1691)	GGAAAATACAGCTGAAGG	1889	OPA1 H31 3UTR(+1729+1745)	GGGATGTGATAACAGTA
1872	OPA1 H31 3UTR(+1678+1694)	TGTGGAAAATACAGCTGA	1890	OPA1 H31 3UTR(+1732+1748)	AAAGGGATGTGATAACA
1873	OPA1 H31 3UTR(+1681+1697)	ATCTGTGGAAAATACAGC	1891	OPA1 H31 3UTR(+1735+1751)	TACAAAAGGGATGTGATA
1874	OPA1 H31 3UTR(+1684+1700)	GAAATCTGTGGAAAATAC	1892	OPA1 H31 3UTR(+1738+1754)	TTATACAAAAGGGATGTG
1875	OPA1 H31 3UTR(+1687+1703)	GGAGAAAATCTGTGGAAA	1893	OPA1 H31 3UTR(+1741+1757)	AAC TTATACAAAAGGGAT
1876	OPA1 H31 3UTR(+1690+1706)	TTGGGAGAAAATCTGTGG	1894	OPA1 H31 3UTR(+1744+1760)	TAAAACTTATACAAAAGG
1877	OPA1 H31 3UTR(+1693+1709)	TCCTTGGGAGAAAATCTG	1895	OPA1 H31 3UTR(+1747+1763)	TTTTAAAACTTATACAA
1878	OPA1 H31 3UTR(+1696+1712)	TTTTCTTGGGAGAAAAT	1896	OPA1 H31 3UTR(+1750+1766)	TC TTTTAAAACTTATA
1879	OPA1 H31 3UTR(+1699+1715)	GCCTTTTCTTGGGAGA	1897	OPA1 H31 3UTR(+1753+1769)	ATCTCTTTTAAAACTT
1880	OPA1 H31 3UTR(+1702+1718)	TTAGCC TTTTCTTGGG	1898	OPA1 H31 3UTR(+1756+1772)	TCCATCTCTTTTAAAA
1881	OPA1 H31 3UTR(+1705+1721)	ATATTAGCC TTTTCTT	1899	OPA1 H31 3UTR(+1759+1775)	CCCTCCATCTCTTTTAA
1882	OPA1 H31 3UTR(+1708+1724)	CTAATATTAGCC TTTTC	1900	OPA1 H31 3UTR(+1762+1778)	TCCTCCCTCCATCTCTTT

SEQ ID	ASO coordinates	Sequence 5'>3'	SEQ ID	ASO coordinates	Sequence 5'>3'
1901	OPAI H31 3UTR(+1765+1781)	AGATCTCCCTCCATCTC	1919	OPAI H31 3UTR(+1819+1835)	AAITGTTATCATCTATT
1902	OPAI H31 3UTR(+1768+1784)	TGAAGATCTCCCTCCAT	1920	OPAI H31 3UTR(+1822+1838)	ATTAAATTGTTATCATCT
1903	OPAI H31 3UTR(+1771+1787)	AAATGAAAGATCTCCCTC	1921	OPAI H31 3UTR(+1825+1841)	AATATTAAATTGTTATCA
1904	OPAI H31 3UTR(+1774+1790)	AAGAAATGAAGATCTCC	1922	OPAI H31 3UTR(+1828+1844)	AGTAATATTAAATTGTTA
1905	OPAI H31 3UTR(+1777+1793)	TCAAAGAAAATGAAGATC	1923	OPAI H31 3UTR(+1831+1847)	TTTAGTAATATTAAATTG
1906	OPAI H31 3UTR(+1780+1796)	TCCTCAAAGAAAATGAAG	1924	OPAI H31 3UTR(+1834+1850)	ACTTTTAGTAATATTAA
1907	OPAI H31 3UTR(+1783+1799)	ATCTCTCAAAGAAAATG	1925	OPAI H31 3UTR(+1837+1853)	GGGACTTTTAGTAATAT
1908	OPAI H31 3UTR(+1786+1802)	CTGATCTCTCAAAGAA	1926	OPAI H31 3UTR(+1840+1856)	TGTGGGACTTTTAGTAA
1909	OPAI H31 3UTR(+1789+1805)	ATACTGATCTCTCTCAA	1927	OPAI H31 3UTR(+1843+1859)	TCATGTGGGACTTTTAG
1910	OPAI H31 3UTR(+1792+1808)	ACAATACTGATCTCTCTC	1928	OPAI H31 3UTR(+1846+1862)	CTCTCATGTGGGACTTT
1911	OPAI H31 3UTR(+1795+1811)	GTTACAATACTGATCTC	1929	OPAI H31 3UTR(+1849+1865)	GGACTCTCATGTGGGAC
1912	OPAI H31 3UTR(+1798+1814)	TACGTTACAATACTGAT	1930	OPAI H31 3UTR(+1852+1868)	TCAGGACTCTCATGTGG
1913	OPAI H31 3UTR(+1801+1817)	ACATACGTTACAATACT	1931	OPAI H31 3UTR(+1855+1871)	GCGTCAGGACTCTCATG
1914	OPAI H31 3UTR(+1804+1820)	TTCACATACGTTACAAT	1932	OPAI H31 3UTR(+1858+1874)	AGGGCGTCAGGACTCTC
1915	OPAI H31 3UTR(+1807+1823)	CTATTACATACGTTAC	1933	OPAI H31 3UTR(+1861+1877)	GAGAGGGCGTCAGGACT
1916	OPAI H31 3UTR(+1810+1826)	CATCTATTACATACGT	1934	OPAI H31 3UTR(+1864+1880)	ATGGAGAGGGCGTCAGG
1917	OPAI H31 3UTR(+1813+1829)	TATCATCTATTACATA	1935	OPAI H31 3UTR(+1867+1883)	GGCATGGAGAGGGCGTC
1918	OPAI H31 3UTR(+1816+1832)	TGTTATCATCTATTAC	1936	OPAI H31 3UTR(+1870+1886)	TGGGGCATGGAGAGGGC

SEQ ID	ASO coordinates	Sequence 5'>3'	SEQ ID	ASO coordinates	Sequence 5'>3'
1937	OPAI H31 3UTR(+1873+1889)	CTGTGGGGCATGGAGAG	1955	OPAI H31 3UTR(+1927+1943)	AGGATGAGATCAGCTAA
1938	OPAI H31 3UTR(+1876+1892)	TTACTGTGGGGCATGGA	1956	OPAI H31 3UTR(+1930+1946)	CTTAGGATGAGATCAGC
1939	OPAI H31 3UTR(+1879+1895)	ACATTACTGTGGGGCAT	1957	OPAI H31 3UTR(+1933+1949)	ATGCTTAGGATGAGATC
1940	OPAI H31 3UTR(+1882+1898)	GCCACATTACTGTGGGG	1958	OPAI H31 3UTR(+1936+1952)	AGCATGCTTAGGATGAG
1941	OPAI H31 3UTR(+1885+1901)	GAAAGCCACATTACTGTG	1959	OPAI H31 3UTR(+1939+1955)	TAAAGCATGCTTAGGAT
1942	OPAI H31 3UTR(+1888+1904)	AAAGAAAGCCACATTACT	1960	OPAI H31 3UTR(+1942+1958)	AAATAAAGCATGCTTAG
1943	OPAI H31 3UTR(+1891+1907)	ATGAAAGAAAGCCACATT	1961	OPAI H31 3UTR(+1945+1961)	GAAAAATAAAGCATGCT
1944	OPAI H31 3UTR(+1894+1910)	CCCATGAAAGAAAGCCAC	1962	OPAI H31 3UTR(+1948+1964)	AAGGAAAAATAAAGCAT
1945	OPAI H31 3UTR(+1897+1913)	AAACCCATGAAAGAAAGC	1963	OPAI H31 3UTR(+1951+1967)	TTCAAGGAAAAATAAAG
1946	OPAI H31 3UTR(+1900+1916)	AAAAAACCCATGAAAGA	1964	OPAI H31 3UTR(+1954+1970)	GCTTTCAAGGAAAAATA
1947	OPAI H31 3UTR(+1903+1919)	AAAAAAAACCCATGAA	1965	OPAI H31 3UTR(+1957+1973)	CTAGCTTTCAAGGAAAA
1948	OPAI H31 3UTR(+1906+1922)	AAGAAAAAAAACCCCAT	1966	OPAI H31 3UTR(+1960+1976)	TACCTAGCTTTCAAGGA
1949	OPAI H31 3UTR(+1909+1925)	AAGAAAGAAAAAAAACC	1967	OPAI H31 3UTR(+1963+1979)	AAATACCTAGCTTTCAA
1950	OPAI H31 3UTR(+1912+1928)	AAAAAGAAAGAAAAAAA	1968	OPAI H31 3UTR(+1966+1982)	GATAAATACCTAGCTTT
1951	OPAI H31 3UTR(+1915+1931)	GCTAAAAAGAAAGAAAA	1969	OPAI H31 3UTR(+1969+1985)	GTTGATAAATACCTAGC
1952	OPAI H31 3UTR(+1918+1934)	TCAGCTAAAAAGAAAGAA	1970	OPAI H31 3UTR(+1972+1988)	GCAGTTGATAAATACCT
1953	OPAI H31 3UTR(+1921+1937)	AGATCAGCTAAAAAGAA	1971	OPAI H31 3UTR(+1975+1991)	TCTGCAGTTGATAAATA
1954	OPAI H31 3UTR(+1924+1940)	ATGAGATCAGCTAAAAA	1972	OPAI H31 3UTR(+1978+1994)	ACATCTGCAGTTGATAA

SEQ ID	ASO oordinates	Sequence 5'>3'	SEQ ID	ASO oordinates	Sequence 5'>3'
1973	OPAI H31 3UTR(+1981+1997)	ATAACATCTGCAGTTGA	1991	OPAI H31 3UTR(+2035+2051)	CTACAGACACAAGACAC
1974	OPAI H31 3UTR(+1984+2000)	TCAATAACATCTGCAGT	1992	OPAI H31 3UTR(+2038+2054)	GAACACAGACACAAGA
1975	OPAI H31 3UTR(+1987+2003)	CTTCAATAACATCTGC	1993	OPAI H31 3UTR(+2041+2057)	TTTGAACACAGACACA
1976	OPAI H31 3UTR(+1990+2006)	TTTCTTTCAATAACATC	1994	OPAI H31 3UTR(+2044+2060)	ACTTTGAACTACAGAC
1977	OPAI H31 3UTR(+1993+2009)	TATTTCTTTCAATAAC	1995	OPAI H31 3UTR(+2047+2063)	CTGACTTTTGAACAC
1978	OPAI H31 3UTR(+1996+2012)	TTTTATTTCTTTCAAT	1996	OPAI H31 3UTR(+2050+2066)	TTTCTGACTTTTGAAC
1979	OPAI H31 3UTR(+1999+2015)	GAAATTTATTTCTTTC	1997	OPAI H31 3UTR(+2053+2069)	TCATTTCTGACTTTTGA
1980	OPAI H31 3UTR(+2002+2018)	ACTGAAATTTATTTTCT	1998	OPAI H31 3UTR(+2056+2072)	GAATCAATTTCTGACTTT
1981	OPAI H31 3UTR(+2005+2021)	GAGACTGAAATTTATTT	1999	OPAI H31 3UTR(+2059+2075)	TTAGAAATCAATTTCTGAC
1982	OPAI H31 3UTR(+2008+2024)	CTTGAGACTGAAATTTA	2000	OPAI H31 3UTR(+2062+2078)	AAATTAGAAATCAATTTCT
1983	OPAI H31 3UTR(+2011+2027)	ACTCTTGAGACTGAAAT	2001	OPAI H31 3UTR(+2065+2081)	TTTAAATTAGAAATCAAT
1984	OPAI H31 3UTR(+2014+2030)	TTTACTCTTGAGACTGA	2002	OPAI H31 3UTR(+2068+2084)	TTGTTTAAATTAGAAATC
1985	OPAI H31 3UTR(+2017+2033)	GGGTTTACTCTTGAGAC	2003	OPAI H31 3UTR(+2071+2087)	TTTTTGTTTAAATTAGA
1986	OPAI H31 3UTR(+2020+2036)	ACAGGGTTTACTCTTGA	2004	OPAI H31 3UTR(+2074+2090)	ATCTTTTGTGTTTAAAT
1987	OPAI H31 3UTR(+2023+2039)	GACACAGGGTTTACTCT	2005	OPAI H31 3UTR(+2077+2093)	AGTATCTTTTGTGTTAA
1988	OPAI H31 3UTR(+2026+2042)	CAAGACACAGGGTTTAC	2006	OPAI H31 3UTR(+2080+2096)	TTTAGTATCTTTTGTGTT
1989	OPAI H31 3UTR(+2029+2045)	ACACAAGACACAGGGTT	2007	OPAI H31 3UTR(+2083+2099)	ATATTAGTATCTTTT
1990	OPAI H31 3UTR(+2032+2048)	CAGACACAAGACACAGG	2008	OPAI H31 3UTR(+2086+2102)	TGTATATTTAGTATCTTT

SEQ ID	ASO coordinates	Sequence 5'>3'	SEQ ID	ASO coordinates	Sequence 5'>3'
2009	OPAI H31 3UTR(+2089+2105)	TTCTGTATATTTAGTAT	2027	OPAI H31 3UTR(+2143+2159)	CTTTGCAAAITTCAGACA
2010	OPAI H31 3UTR(+2092+2108)	AACTTCTGTATATTTAG	2028	OPAI H31 3UTR(+2146+2162)	ACTCTTTTGCAAAITTCG
2011	OPAI H31 3UTR(+2095+2111)	TTTAACTTCTGTATATT	2029	OPAI H31 3UTR(+2149+2165)	TCCACTCTTTTGCAAAATT
2012	OPAI H31 3UTR(+2098+2114)	GAAATTTAACTTCTGTAT	2030	OPAI H31 3UTR(+2152+2168)	CACTCCACTCTTTTGCAA
2013	OPAI H31 3UTR(+2101+2117)	TTCGAAATTTAACTTCTG	2031	OPAI H31 3UTR(+2155+2171)	GTCCACTCCACTCTTTG
2014	OPAI H31 3UTR(+2104+2120)	TAGTTCGAAATTTAACTT	2032	OPAI H31 3UTR(+2158+2174)	TTTGTCCTCCACTCTCT
2015	OPAI H31 3UTR(+2107+2123)	GGCTAGTTCGAAATTTAA	2033	OPAI H31 3UTR(+2161+2177)	AGCTTTGTCCACTCCAC
2016	OPAI H31 3UTR(+2110+2126)	TGTGGCTAGTTCGAAATT	2034	OPAI H31 3UTR(+2164+2180)	CAGAGCTTTGTCCACTC
2017	OPAI H31 3UTR(+2113+2129)	TTCTGTGGCTAGTTCGA	2035	OPAI H31 3UTR(+2167+2183)	ATACAGAGCTTTGTCCA
2018	OPAI H31 3UTR(+2116+2132)	TGATTCTGTGGCTAGTT	2036	OPAI H31 3UTR(+2170+2186)	TCCATACAGAGCTTTGT
2019	OPAI H31 3UTR(+2119+2135)	AAATGATTCTGTGGCTA	2037	OPAI H31 3UTR(+2173+2189)	TCCTCCATACAGAGCTT
2020	OPAI H31 3UTR(+2122+2138)	AACAAATGATTCTGTGG	2038	OPAI H31 3UTR(+2176+2192)	CAGTCTTCCATACAGAG
2021	OPAI H31 3UTR(+2125+2141)	AAAAACAAATGATTCTG	2039	OPAI H31 3UTR(+2179+2195)	GTTCAGTCTTCCATACA
2022	OPAI H31 3UTR(+2128+2144)	CATAAAAAACAAATGATT	2040	OPAI H31 3UTR(+2182+2198)	GTTGTTTCAGTCTTCCAT
2023	OPAI H31 3UTR(+2131+2147)	TGACATAAAAAACAAATG	2041	OPAI H31 3UTR(+2185+2201)	ACAGTTGTTTCAGTCTTC
2024	OPAI H31 3UTR(+2134+2150)	TTCTGACATAAAAAACAA	2042	OPAI H31 3UTR(+2188+2204)	TTTACAGTTGTTTCAGTC
2025	OPAI H31 3UTR(+2137+2153)	AAATCTGACATAAAAA	2043	OPAI H31 3UTR(+2191+2207)	CTATTACAGTTGTTTCA
2026	OPAI H31 3UTR(+2140+2156)	TGCAAAATTCAGACATAA	2044	OPAI H31 3UTR(+2194+2210)	CATCTATTTACAGTTGT

SEQ ID	ASO coordinates	Sequence 5'>3'	SEQ ID	ASO coordinates	Sequence 5'>3'
2045	OPAI H31 3UTR(+2197+2213)	TATCATCTATTTACAGT	2063	OPAI H31 3UTR(+2251+2267)	CTGCCTAGGTACACTGA
2046	OPAI H31 3UTR(+2200+2216)	GGATATCATCTATTTAC	2064	OPAI H31 3UTR(+2254+2270)	GCACCTGCCTAGGTACAC
2047	OPAI H31 3UTR(+2203+2219)	TTTGGATATCATCTATT	2065	OPAI H31 3UTR(+2257+2273)	TGTGCACCTGCCTAGGTA
2048	OPAI H31 3UTR(+2206+2222)	AAGTTTGGATATCATCT	2066	OPAI H31 3UTR(+2260+2276)	TGCTGTGCACCTGCCTAG
2049	OPAI H31 3UTR(+2209+2225)	ATTAAGTTTGGATATCA	2067	OPAI H31 3UTR(+2263+2279)	TCGTGCTGTGCACCTGCC
2050	OPAI H31 3UTR(+2212+2228)	CAAAATTAAGTTTGGATA	2068	OPAI H31 3UTR(+2266+2282)	ATTTCTGTGCTGTGCACCT
2051	OPAI H31 3UTR(+2215+2231)	AGCCAAAATTAAGTTTGG	2069	OPAI H31 3UTR(+2269+2285)	CTTATTTCTGTGCTGTGC
2052	OPAI H31 3UTR(+2218+2234)	CCTAGCCAAAATTAAGTT	2070	OPAI H31 3UTR(+2272+2288)	CCACTTATTTCTGTGCTG
2053	OPAI H31 3UTR(+2221+2237)	AGTCCTAGCCAAAATTA	2071	OPAI H31 3UTR(+2275+2291)	GGGCCACTTATTTCTGTG
2054	OPAI H31 3UTR(+2224+2240)	TGAAAGTCCTAGCCAAAT	2072	OPAI H31 3UTR(+2278+2294)	CAAGGGCCACTTATTTTC
2055	OPAI H31 3UTR(+2227+2243)	AATTGAAAGTCCTAGCCA	2073	OPAI H31 3UTR(+2281+2297)	CTGCAAGGGCCACTTAT
2056	OPAI H31 3UTR(+2230+2246)	TAAAAATTGAAAGTCCTAG	2074	OPAI H31 3UTR(+2284+2300)	AAGCTGCAAGGGCCACT
2057	OPAI H31 3UTR(+2233+2249)	TTTTAAAAATTGAAAGTCC	2075	OPAI H31 3UTR(+2287+2303)	GGGAAGCTGCAAGGGGCC
2058	OPAI H31 3UTR(+2236+2252)	GATTTTAAAAAATTGAAG	2076	OPAI H31 3UTR(+2290+2306)	ACGGGGAAAGCTGCAAGG
2059	OPAI H31 3UTR(+2239+2255)	ACTGATTTTAAAAATTG	2077	OPAI H31 3UTR(+2293+2309)	TAAACGGGGAAAGCTGCA
2060	OPAI H31 3UTR(+2242+2258)	TACACTGATTTTAAAAA	2078	OPAI H31 3UTR(+2296+2312)	GGTTAAACGGGGAAGCT
2061	OPAI H31 3UTR(+2245+2261)	AGGTACACTGATTTTAA	2079	OPAI H31 3UTR(+2299+2315)	GTGGGTTAAACGGGGAA
2062	OPAI H31 3UTR(+2248+2264)	CCTAGGTACACTGATTT	2080	OPAI H31 3UTR(+2302+2318)	ACAGTGGGTTAAACGGGG

SEQ ID	ASO coordinates	Sequence 5'>3'	SEQ ID	ASO coordinates	Sequence 5'>3'
2081	OPAI H31 3UTR(+2305+2321)	AGCACAGTGGGTAAAC	2099	OPAI H31 3UTR(+2359+2375)	AAGAGGGCAATATCATA
2082	OPAI H31 3UTR(+2308+2324)	TATAGCACAGTGGGTTA	2100	OPAI H31 3UTR(+2362+2378)	ACAAAGAGGGCAATATC
2083	OPAI H31 3UTR(+2311+2327)	AACATATAGCACAGTGGG	2101	OPAI H31 3UTR(+2365+2381)	AATACAAAGAGGGCAAT
2084	OPAI H31 3UTR(+2314+2330)	CGCAACTATAGCACAGT	2102	OPAI H31 3UTR(+2368+2384)	GGGAATACAAAGAGGGC
2085	OPAI H31 3UTR(+2317+2333)	ACCGCAACTATAGCAC	2103	OPAI H31 3UTR(+2371+2387)	AATGGGAATACAAAGAG
2086	OPAI H31 3UTR(+2320+2336)	TCCACCCGCAACTATAG	2104	OPAI H31 3UTR(+2374+2390)	GAAAATGGGAATACAAA
2087	OPAI H31 3UTR(+2323+2339)	TGTTCCACCCGCAACTA	2105	OPAI H31 3UTR(+2377+2393)	GTAGAAAATGGGAATAC
2088	OPAI H31 3UTR(+2326+2342)	GACTGTTCCACCCGCAA	2106	OPAI H31 3UTR(+2380+2396)	ACTGTAGAAAATGGGAA
2089	OPAI H31 3UTR(+2329+2345)	GTTGACTGTTCCACCCG	2107	OPAI H31 3UTR(+2383+2399)	AAAACTGTAGAAAATGG
2090	OPAI H31 3UTR(+2332+2348)	AAGGTTGACTGTTCCAC	2108	OPAI H31 3UTR(+2386+2402)	GAAAAAACTGTAGAAAA
2091	OPAI H31 3UTR(+2335+2351)	AGAAAGGTTGACTGTTT	2109	OPAI H31 3UTR(+2389+2405)	GCGGAAAAAACTGTAGA
2092	OPAI H31 3UTR(+2338+2354)	ACTAGAAAGGTTGACTG	2110	OPAI H31 3UTR(+2392+2408)	TCTGCGGAAAAAACTGT
2093	OPAI H31 3UTR(+2341+2357)	ACTACTAGAAAGGTTGA	2111	OPAI H31 3UTR(+2395+2411)	AAGTCTGCGGAAAAAAAC
2094	OPAI H31 3UTR(+2344+2360)	TAAACTACTAGAAAGGT	2112	OPAI H31 3UTR(+2398+2414)	AAGAAGTCTGCGGAAAA
2095	OPAI H31 3UTR(+2347+2363)	TCATAAACTACTAGAAA	2113	OPAI H31 3UTR(+2401+2417)	AGAAAGAAAGTCTGCGGA
2096	OPAI H31 3UTR(+2350+2366)	ATATCATAACTACTAG	2114	OPAI H31 3UTR(+2404+2420)	TGCAGAAAAGAAAGTCTGC
2097	OPAI H31 3UTR(+2353+2369)	GCAATATCATAACTAC	2115	OPAI H31 3UTR(+2407+2423)	ATTTGCAGAAAAGAAAGTC
2098	OPAI H31 3UTR(+2356+2372)	AGGGCAATATCATAAAC	2116	OPAI H31 3UTR(+2410+2426)	ATAATTTGCAGAAAAGAA

SEQ ID	ASO coordinates	Sequence 5'>3'	SEQ ID	ASO coordinates	Sequence 5'>3'
2117	OPAI H31 3UTR(+2413+2429)	TGAATAAATTTGCAGAAA	2135	OPAI H31 3UTR(+2467+2483)	ACTCTCTGCCCATGTTC
2118	OPAI H31 3UTR(+2416+2432)	GGCTGAATAAATTTGCAG	2136	OPAI H31 3UTR(+2470+2486)	ACCACTCTCTGCCATGT
2119	OPAI H31 3UTR(+2419+2435)	GGAGGCTGAATAAATTTG	2137	OPAI H31 3UTR(+2473+2489)	AGCACCACTCTCTGCCA
2120	OPAI H31 3UTR(+2422+2438)	TTTGGAGGCTGAATAAT	2138	OPAI H31 3UTR(+2476+2492)	GGAAGCACCACTCTCTG
2121	OPAI H31 3UTR(+2425+2441)	GCATTTGGAGGCTGAAT	2139	OPAI H31 3UTR(+2479+2495)	CTGGGAAAGCACCACTCT
2122	OPAI H31 3UTR(+2428+2444)	TTTGCAATTTGGAGGCTG	2140	OPAI H31 3UTR(+2482+2498)	AGGCTGGGAAAGCACCCAC
2123	OPAI H31 3UTR(+2431+2447)	TCATTTGCATTTGGAGG	2141	OPAI H31 3UTR(+2485+2501)	GTGAGGCTGGGAAAGCAC
2124	OPAI H31 3UTR(+2434+2450)	CATTCAATTTGCATTTGG	2142	OPAI H31 3UTR(+2488+2504)	ATTGTGAGGCTGGGAAG
2125	OPAI H31 3UTR(+2437+2453)	TATCATTTCAATTTGCATT	2143	OPAI H31 3UTR(+2491+2507)	CACATTTGTGAGGCTGGG
2126	OPAI H31 3UTR(+2440+2456)	TTATATCATTCATTTGCG	2144	OPAI H31 3UTR(+2494+2510)	TCCCACATTTGTGAGGCT
2127	OPAI H31 3UTR(+2443+2459)	TTTTTATATCATTCATT	2145	OPAI H31 3UTR(+2497+2513)	AATTCACACATTTGTGAG
2128	OPAI H31 3UTR(+2446+2462)	TTATTTTATATCATTC	2146	OPAI H31 3UTR(+2500+2516)	TCAAATTTCCCACATTGT
2129	OPAI H31 3UTR(+2449+2465)	TACTTATTTTATATCA	2147	OPAI H31 3UTR(+2503+2519)	ATGTCAAATTTCCCACAT
2130	OPAI H31 3UTR(+2452+2468)	CCCTACTTATTTTATA	2148	OPAI H31 3UTR(+2506+2522)	CCTATGTCAAATTTCCCA
2131	OPAI H31 3UTR(+2455+2471)	GTTCCCTACTTATTTT	2149	OPAI H31 3UTR(+2509+2525)	CATCCTATGTCAAATTC
2132	OPAI H31 3UTR(+2458+2474)	CATGTTCCCTACTTATT	2150	OPAI H31 3UTR(+2512+2528)	TCATCATCCTATGTCAAA
2133	OPAI H31 3UTR(+2461+2477)	TGCCATGTTCCCTACTT	2151	OPAI H31 3UTR(+2515+2531)	GACTCTCATCCTATGTC
2134	OPAI H31 3UTR(+2464+2480)	CTCTGCCATGTTCCCTA	2152	OPAI H31 3UTR(+2518+2534)	TCTGACTCTCATCCTAT

SEQ ID	ASO coordinates	Sequence 5'>3'	SEQ ID	ASO coordinates	Sequence 5'>3'
2153	OPAI H31 3UTR(+2521+2537)	TACTCTGACTCTCATCC	2171	OPAI H31 3UTR(+2575+2591)	TCTAGAAATAAATAAATA
2154	OPAI H31 3UTR(+2524+2540)	CTATACTCTGACTCTCA	2172	OPAI H31 3UTR(+2578+2594)	ACATCTAGAATAAATAA
2155	OPAI H31 3UTR(+2527+2543)	AACCTATACTCTGACTC	2173	OPAI H31 3UTR(+2581+2597)	CATACATCTAGAATAAAA
2156	OPAI H31 3UTR(+2530+2546)	TTAAACCTATACTCTGA	2174	OPAI H31 3UTR(+2584+2600)	ATACATACATCTAGAAT
2157	OPAI H31 3UTR(+2533+2549)	CTTTTAAACCTATACTC	2175	OPAI H31 3UTR(+2587+2603)	CAGATACATACATCTAG
2158	OPAI H31 3UTR(+2536+2552)	TATCTTTTAAACCTATA	2176	OPAI H31 3UTR(+2590+2606)	CCTCAGATACATACATC
2159	OPAI H31 3UTR(+2539+2555)	TTTTATCTTTTAAACCT	2177	OPAI H31 3UTR(+2593+2609)	TTTCTCTCAGATACATAC
2160	OPAI H31 3UTR(+2542+2558)	AGATTTTATCTTTTAAA	2178	OPAI H31 3UTR(+2596+2612)	TTCTTTCTCAGATACA
2161	OPAI H31 3UTR(+2545+2561)	TAAAGATTTTATCTTTT	2179	OPAI H31 3UTR(+2599+2615)	GATTTCTTTCTCTCAGAT
2162	OPAI H31 3UTR(+2548+2564)	AACTAAAGATTTTATCT	2180	OPAI H31 3UTR(+2602+2618)	CCAGATTTCTTTCTCTCA
2163	OPAI H31 3UTR(+2551+2567)	ATTAACCTAAAGATTTTA	2181	OPAI H31 3UTR(+2605+2621)	ATACCAGATTTCTTTCC
2164	OPAI H31 3UTR(+2554+2570)	ATTATTAACTAAAGATT	2182	OPAI H31 3UTR(+2608+2624)	AAAATACCAGATTTCTTT
2165	OPAI H31 3UTR(+2557+2573)	AAAAATTATTAACCTAAAG	2183	OPAI H31 3UTR(+2611+2627)	GCAAAAAATACCAGATTT
2166	OPAI H31 3UTR(+2560+2576)	TACAAAAATTATTAACCTA	2184	OPAI H31 3UTR(+2614+2630)	AAAGCAAAAAATACCAGA
2167	OPAI H31 3UTR(+2563+2579)	AAATACAAAAATTATTAA	2185	OPAI H31 3UTR(+2617+2633)	TGGAAAGCAAAAAATACC
2168	OPAI H31 3UTR(+2566+2582)	AATAAATACAAAAATTAT	2186	OPAI H31 3UTR(+2620+2636)	TATTGGAAAGCAAAAAAT
2169	OPAI H31 3UTR(+2569+2585)	ATAAATAAATACAAAAAT	2187	OPAI H31 3UTR(+2623+2639)	CTTTATTGGAAAGCAAA
2170	OPAI H31 3UTR(+2572+2588)	AGAAATAAATAAATACAA	2188	OPAI H31 3UTR(+2626+2642)	CCCCTTTATTGGAAAGC

SEQ ID	ASO oordinates	Sequence 5'>3'	SEQ ID	ASO oordinates	Sequence 5'>3'
2189	OPAI H31 3UTR(+2629+2645)	GATCCCCCTTTATTGGAA	2207	OPAI H31 3UTR(+2683+2699)	GCTAGAGCTATAACATA
2190	OPAI H31 3UTR(+2632+2648)	TTTGATCCCCCTTTATTG	2208	OPAI H31 3UTR(+2686+2702)	ACTGCTAGAGCTATAAC
2191	OPAI H31 3UTR(+2635+2651)	TACTTTGATCCCCCTTTA	2209	OPAI H31 3UTR(+2689+2705)	CATACTGCTAGAGCTAT
2192	OPAI H31 3UTR(+2638+2654)	CATTACTTTGATCCCCCT	2210	OPAI H31 3UTR(+2692+2708)	TTCCATACTGCTAGAGC
2193	OPAI H31 3UTR(+2641+2657)	AACCACTTACTTTGATCC	2211	OPAI H31 3UTR(+2695+2711)	CATTTCCATACTGCTAG
2194	OPAI H31 3UTR(+2644+2660)	AAAAACCACTTACTTTGA	2212	OPAI H31 3UTR(+2698+2714)	GCACATTTCCATACTGC
2195	OPAI H31 3UTR(+2647+2663)	GAGAAAAACCACTTACTT	2213	OPAI H31 3UTR(+2701+2717)	AAAGCACATTTCCATAC
2196	OPAI H31 3UTR(+2650+2666)	TGAGAGAAAAACCACTTA	2214	OPAI H31 3UTR(+2704+2720)	TTTAAAGCACATTTCCA
2197	OPAI H31 3UTR(+2653+2669)	AACTGAGAGAAAAACCA	2215	OPAI H31 3UTR(+2707+2723)	TATTTTAAAGCACATTT
2198	OPAI H31 3UTR(+2656+2672)	GAGAACTGAGAGAAAAA	2216	OPAI H31 3UTR(+2710+2726)	GCATATTTTAAAGCAC
2199	OPAI H31 3UTR(+2659+2675)	TTAGAGAACTGAGAGAA	2217	OPAI H31 3UTR(+2713+2729)	TAAGCATATTTTAAAGC
2200	OPAI H31 3UTR(+2662+2678)	AGCTTAGAGAACTGAGA	2218	OPAI H31 3UTR(+2716+2732)	AGGTAAAGCATATTTTAA
2201	OPAI H31 3UTR(+2665+2681)	ACCAGCTTAGAGAACTG	2219	OPAI H31 3UTR(+2719+2735)	AAAAGGTAAAGCATATTT
2202	OPAI H31 3UTR(+2668+2684)	TAGACCAGCTTAGAGAA	2220	OPAI H31 3UTR(+2722+2738)	TTCAAAAAGGTAAAGCATA
2203	OPAI H31 3UTR(+2671+2687)	ACATAGACCAGCTTAGA	2221	OPAI H31 3UTR(+2725+2741)	TCATTTCAAAAAGGTAAAGC
2204	OPAI H31 3UTR(+2674+2690)	ATAACATAGACCAGCTT	2222	OPAI H31 3UTR(+2728+2744)	TGATCATTTCAAAAAGGTA
2205	OPAI H31 3UTR(+2677+2693)	GCTATAACATAGACCAG	2223	OPAI H31 3UTR(+2731+2747)	CCATGATCATTTCAAAAAG
2206	OPAI H31 3UTR(+2680+2696)	AGAGCTATAACATAGAC	2224	OPAI H31 3UTR(+2734+2750)	TAGCCATGATCATTTCAA

SEQ ID	ASO coordinates	Sequence 5'>3'	SEQ ID	ASO coordinates	Sequence 5'>3'
2225	OPAI H31 3UTR(+2737+2753)	ATATAGCCATGATCATT	2243	OPAI H31 3UTR(+2791+2807)	GTTTCATTCCACAGTGAC
2226	OPAI H31 3UTR(+2740+2756)	AACATATAGCCATGATC	2244	OPAI H31 3UTR(+2794+2810)	AAAGTTCATTCCACAGTG
2227	OPAI H31 3UTR(+2743+2759)	AACAACATATAGCCATG	2245	OPAI H31 3UTR(+2797+2813)	TACAAAAGTTCATTCCACA
2228	OPAI H31 3UTR(+2746+2762)	CTCAACAACATATAGCC	2246	OPAI H31 3UTR(+2800+2816)	TAATACAAAAGTTCATTTC
2229	OPAI H31 3UTR(+2749+2765)	TATCTCAACAACATATA	2247	OPAI H31 3UTR(+2803+2819)	AAATAATACAAAAGTTCA
2230	OPAI H31 3UTR(+2752+2768)	AAATATCTCAACAACAT	2248	OPAI H31 3UTR(+2806+2822)	AAAAAATAATACAAAAGT
2231	OPAI H31 3UTR(+2755+2771)	TTCAAAATATCTCAACAA	2249	OPAI H31 3UTR(+2809+2825)	TTAAAAAATAATACAAA
2232	OPAI H31 3UTR(+2758+2774)	AGTTTCAAAATATCTCAA	2250	OPAI H31 3UTR(+2812+2828)	GTTTAAAAAATAATA
2233	OPAI H31 3UTR(+2761+2777)	GTAAGTTTCAAAATATCT	2251	OPAI H31 3UTR(+2815+2831)	AAGGTTTTAAAAAATA
2234	OPAI H31 3UTR(+2764+2780)	AAGGTAAGTTTCAAAATA	2252	OPAI H31 3UTR(+2818+2834)	GTGAAGGTTTTAAAAAA
2235	OPAI H31 3UTR(+2767+2783)	AACAAGGTAAGTTTCAA	2253	OPAI H31 3UTR(+2821+2837)	AATGTGAAGGTTTTTAAA
2236	OPAI H31 3UTR(+2770+2786)	GAAAAACAAGGTAAGTTT	2254	OPAI H31 3UTR(+2824+2840)	CGTAATGTGAAGGTTTT
2237	OPAI H31 3UTR(+2773+2789)	AGTGAAAAACAAGGTAAG	2255	OPAI H31 3UTR(+2827+2843)	ACACGTAATGTGAAGGT
2238	OPAI H31 3UTR(+2776+2792)	ACAAAGTGAAAAACAAGGT	2256	OPAI H31 3UTR(+2830+2846)	TCTACACGTAATGTGAA
2239	OPAI H31 3UTR(+2779+2795)	TGCACAAAGTGAAAAACA	2257	OPAI H31 3UTR(+2833+2849)	ATATCTACACGTAATGT
2240	OPAI H31 3UTR(+2782+2798)	CAGTGCACAAGTGAAAA	2258	OPAI H31 3UTR(+2836+2852)	ATAATATCTACACGTAA
2241	OPAI H31 3UTR(+2785+2801)	TCACAGTGCACAAGTGA	2259	OPAI H31 3UTR(+2839+2855)	GCAATAATATCTACACG
2242	OPAI H31 3UTR(+2788+2804)	CATTACACAGTGACAAG	2260	OPAI H31 3UTR(+2842+2858)	GTTGCAATAATATCTAC

SEQ ID	ASO coordinates	Sequence 5'>3'	SEQ ID	ASO coordinates	Sequence 5'>3'
2261	OPAI H31 3UTR(+2845+2861)	TAAAGTTGCAATAATATC	2279	OPAI H31 3UTR(+2899+2915)	ATTTTTTAATTACTCAT
2262	OPAI H31 3UTR(+2848+2864)	ATATAAGTTGCAATAAT	2280	OPAI H31 3UTR(+2902+2918)	AATAATTTTTTAATTACT
2263	OPAI H31 3UTR(+2851+2867)	AAAAATATAAGTTGCAAT	2281	OPAI H31 3UTR(+2905+2921)	TTAAATATTTTTTAATT
2264	OPAI H31 3UTR(+2854+2870)	GGCAAAATATAAGTTGC	2282	OPAI H31 3UTR(+2908+2924)	GATTTAAATATTTTTTA
2265	OPAI H31 3UTR(+2857+2873)	TCAGGCAAAATATAAGT	2283	OPAI H31 3UTR(+2911+2927)	TGTGATTTTAAATATTTT
2266	OPAI H31 3UTR(+2860+2876)	AGCTCAGGCAAAATATA	2284	OPAI H31 3UTR(+2914+2930)	TAATGTGATTTTAAATAT
2267	OPAI H31 3UTR(+2863+2879)	TCAAGCTCAGGCAAAAT	2285	OPAI H31 3UTR(+2917+2933)	TTATAATGTGATTTTAAA
2268	OPAI H31 3UTR(+2866+2882)	TGATCAAGCTCAGGCAA	2286	OPAI H31 3UTR(+2920+2936)	GAATTATAATGTGATTT
2269	OPAI H31 3UTR(+2869+2885)	CTTTGATCAAGCTCAGG	2287	OPAI H31 3UTR(+2923+2939)	ATAGAAATTATAATGTGA
2270	OPAI H31 3UTR(+2872+2888)	GACCTTTTGATCAAGCTC	2288	OPAI H31 3UTR(+2926+2942)	ATAATAGAAATTATAATG
2271	OPAI H31 3UTR(+2875+2891)	AATGACCTTTTGATCAAG	2289	OPAI H31 3UTR(+2929+2945)	CCAATAATAGAAATTATA
2272	OPAI H31 3UTR(+2878+2894)	ACAAATGACCTTTTGATC	2290	OPAI H31 3UTR(+2932+2948)	TCTCCAATAATAGAAATT
2273	OPAI H31 3UTR(+2881+2897)	TACACAAATGACCTTTTG	2291	OPAI H31 3UTR(+2935+2951)	TGCTCTCCAATAATAGAGA
2274	OPAI H31 3UTR(+2884+2900)	ATCTACACAAATGACCT	2292	OPAI H31 3UTR(+2938+2954)	AGATGCTCTCCAATAAT
2275	OPAI H31 3UTR(+2887+2903)	CTCATCTACACAAATGA	2293	OPAI H31 3UTR(+2941+2957)	AAAAGATGCTCTCCAAT
2276	OPAI H31 3UTR(+2890+2906)	TTACTCATCTACACAAA	2294	OPAI H31 3UTR(+2944+2960)	TTTTAAAAGATGCTCTCC
2277	OPAI H31 3UTR(+2893+2909)	TAATTACTCATCTACAC	2295	OPAI H31 3UTR(+2947+2963)	AAATTTAAAAGATGCTC
2278	OPAI H31 3UTR(+2896+2912)	TTTTAATTACTCATCTA	2296	OPAI H31 3UTR(+2950+2966)	AAAAAATTTTAAAAGATG

SEQ ID	ASO coordinates	Sequence 5'>3'	SEQ ID	ASO coordinates	Sequence 5'>3'
2297	OPAI H31 3UTR(+2953+2969)	AGAAAAAATTTAAAAAG	2315	OPAI H31 3UTR(+3007+3023)	ATGGGGTCAAAATAATGA
2298	OPAI H31 3UTR(+2956+2972)	AACAGAAAAAAATTTAA	2316	OPAI H31 3UTR(+3010+3026)	ACTATGGGGTCAAAATAA
2299	OPAI H31 3UTR(+2959+2975)	TAAAAACAGAAAAAAATT	2317	OPAI H31 3UTR(+3013+3029)	TATACTATGGGGTCAAAA
2300	OPAI H31 3UTR(+2962+2978)	CGTTAAACACAGAAAAAA	2318	OPAI H31 3UTR(+3016+3032)	GGTTATACTATGGGGTTC
2301	OPAI H31 3UTR(+2965+2981)	CCTCGTTAAACACAGAAA	2319	OPAI H31 3UTR(+3019+3035)	TCTGGTTATACTATGGG
2302	OPAI H31 3UTR(+2968+2984)	TTCCCTCTGTTAAACACAG	2320	OPAI H31 3UTR(+3022+3038)	GAATCTGGTTATACTAT
2303	OPAI H31 3UTR(+2971+2987)	TCTTTCCCTCGTTAAAAA	2321	OPAI H31 3UTR(+3025+3041)	CATGAATCTGGTTATAC
2304	OPAI H31 3UTR(+2974+2990)	TTCCTCTTTCCCTCGTTA	2322	OPAI H31 3UTR(+3028+3044)	GACCATGAATCTGGTTA
2305	OPAI H31 3UTR(+2977+2993)	GGTTTCTCTTTCCCTCG	2323	OPAI H31 3UTR(+3031+3047)	TTAGACCATGAATCTGG
2306	OPAI H31 3UTR(+2980+2996)	ACAGGTTTCTCTTTCC	2324	OPAI H31 3UTR(+3034+3050)	TTGTTAGACCATGAATC
2307	OPAI H31 3UTR(+2983+2999)	TATACAGGTTTCTCTTT	2325	OPAI H31 3UTR(+3037+3053)	AGCTTGTAGACCATGA
2308	OPAI H31 3UTR(+2986+3002)	AGGTATACAGGTTTCTC	2326	OPAI H31 3UTR(+3040+3056)	GAGAGCTTGTAGACCA
2309	OPAI H31 3UTR(+2989+3005)	CCTAGGTATACAGGTTT	2327	OPAI H31 3UTR(+3043+3059)	ACTGAGAGCTTGTAGAG
2310	OPAI H31 3UTR(+2992+3008)	GACCCTAGGTATACAGG	2328	OPAI H31 3UTR(+3046+3062)	CACACTGAGAGCTTGT
2311	OPAI H31 3UTR(+2995+3011)	AATGACCCTAGGTATAC	2329	OPAI H31 3UTR(+3049+3065)	AGCCACACTGAGAGCTT
2312	OPAI H31 3UTR(+2998+3014)	AATAATGACCCTAGGTA	2330	OPAI H31 3UTR(+3052+3068)	AAAAGCCACACTGAGAG
2313	OPAI H31 3UTR(+3001+3017)	TCAAATAATGACCCTAG	2331	OPAI H31 3UTR(+3055+3071)	GAGAAAAAGCCACACTGA
2314	OPAI H31 3UTR(+3004+3020)	GGGTCAAATAATGACCC	2332	OPAI H31 3UTR(+3058+3074)	TCAGAGAAAAAGCCACAC

SEQ ID	ASO coordinates	Sequence 5'>3'	SEQ ID	ASO coordinates	Sequence 5'>3'
2333	OPAI H31 3UTR(+3061+3077)	CATTGAGAGAAAAGCCA	2351	OPAI H31 3UTR(+3115+3131)	GCACCGTTGACCATGG
2334	OPAI H31 3UTR(+3064+3080)	AAGCATTGAGAAAAAG	2352	OPAI H31 3UTR(+3118+3134)	AAAGCACCGTTGACCA
2335	OPAI H31 3UTR(+3067+3083)	TTCAAGCATTGAGAGAA	2353	OPAI H31 3UTR(+3121+3137)	AAAAAAGCACCGTTGA
2336	OPAI H31 3UTR(+3070+3086)	AAATTCAAGCATTGAGA	2354	OPAI H31 3UTR(+3124+3140)	TGAAAAAAGCACCGGT
2337	OPAI H31 3UTR(+3073+3089)	GTGAAATTCAAGCATTC	2355	OPAI H31 3UTR(+3127+3143)	ATGTGAAAAAAGCACCC
2338	OPAI H31 3UTR(+3076+3092)	CATGTGAAATTCAAGCA	2356	OPAI H31 3UTR(+3130+3146)	ACGATGTGAAAAAAGC
2339	OPAI H31 3UTR(+3079+3095)	AGGCATGTGAAATTCAA	2357	OPAI H31 3UTR(+3133+3149)	ACCACGATGTGAAAAAA
2340	OPAI H31 3UTR(+3082+3098)	GCAAGGCATGTGAAATT	2358	OPAI H31 3UTR(+3136+3152)	AGTACCACGATGTGAAA
2341	OPAI H31 3UTR(+3085+3101)	AATGCAAGGCATGTGAA	2359	OPAI H31 3UTR(+3139+3155)	ACAAAGTACCACGATGTG
2342	OPAI H31 3UTR(+3088+3104)	TGAAATGCAAGGCATGT	2360	OPAI H31 3UTR(+3142+3158)	TTGACAAAGTACCACGAT
2343	OPAI H31 3UTR(+3091+3107)	CTGTGAAATGCAAGGCA	2361	OPAI H31 3UTR(+3145+3161)	GTTTTGACAAAGTACCAC
2344	OPAI H31 3UTR(+3094+3110)	CAACTGTGAAATGCAAG	2362	OPAI H31 3UTR(+3148+3164)	AATGTTTTGACAAAGTAC
2345	OPAI H31 3UTR(+3097+3113)	GTACAACTGTGAAATGC	2363	OPAI H31 3UTR(+3151+3167)	CAAAATGTTTTTGACAAAG
2346	OPAI H31 3UTR(+3100+3116)	GGAGTACAACTGTGAAA	2364	OPAI H31 3UTR(+3154+3170)	TAACAAAATGTTTTTGAC
2347	OPAI H31 3UTR(+3103+3119)	CATGGAGTACAACTGTG	2365	OPAI H31 3UTR(+3157+3173)	AAATAACAAAATGTTTT
2348	OPAI H31 3UTR(+3106+3122)	GACCATGGAGTACAACT	2366	OPAI H31 3UTR(+3160+3176)	GGAAAAATAACAAAATGT
2349	OPAI H31 3UTR(+3109+3125)	GTTGACCATGGAGTACA	2367	OPAI H31 3UTR(+3163+3179)	CAAGGAAAAATAACAAAA
2350	OPAI H31 3UTR(+3112+3128)	CCGGTTGACCATGGAGT	2368	OPAI H31 3UTR(+3166+3182)	TACCAAGGAAAAATAACA

SEQ ID	ASO coordinates	Sequence 5'>3'	SEQ ID	ASO coordinates	Sequence 5'>3'
2369	OPA1 H31 3UTR(+3169+3185)	TTTACCAGGAAAAATA	2388	OPA1 H31 3UTR(-15-31)	ATTAATGAAAAATGACAG
2370	OPA1 H31 3UTR(+3172+3188)	ATATTTTACCAAGGAAA	2389	OPA1 H31 3UTR(-18-34)	AGCATTAATGAAAAATGA
2371	OPA1 H31 3UTR(+3175+3191)	TATATAATTTACCAAGG	2390	OPA1 H31 3UTR(-21-37)	GGCAGCATTAAATGAAAA
2372	OPA1 H31 3UTR(+3178+3194)	TTTATATATTTTACCA	2391	OPA1 H31 3UTR(-24-40)	GTTGGCAGCATTAAATGA
2373	OPA1 H31 3UTR(+3181+3197)	CTTTTATATATATTTTA	2392	OPA1 H31 3UTR(-27-43)	CATGTTGGCAGCATTA
2374	OPA1 H31 3UTR(+3184+3200)	AACCTTTTATATATATT	2393	OPA1 H31 3UTR(-30-46)	GAACATGTTGGCAGCAT
2375	OPA1 H31 3UTR(+3187+3203)	GAAAAACCTTTTATATAT	2394	OPA1 H31 3UTR(-33-49)	TATGAACATGTTGGCAG
2376	OPA1 H31 3UTR(+3190+3206)	TTAGAAAAACCTTTTATA	2395	OPA1 H31 3UTR(-36-52)	TCATATGAACATGTTGG
2377	OPA1 H31 3UTR(+3193+3209)	AAATTAGAAAAACCTTTT	2396	OPA1 H31 3UTR(-39-55)	GCCTCATATGAACATGT
2378	OPA1 H31 3UTR(+3196+3212)	GTGAAATTAGAAAAACCT	2397	OPA1 H31 3UTR(-42-58)	TAAAGCCTCATATGAACA
2379	OPA1 H31 3UTR(+3199+3215)	AAAGTGAAATTAGAAAA	2398	OPA1 H31 3UTR(-45-61)	TAGTAAGCCTCATATGA
2380	OPA1 H31 3UTR(+3202+3218)	AGCAAAAGTGAAATTAGA	2399	OPA1 H31 3UTR(-48-64)	TCTTAGTAAGCCTCATATA
2381	OPA1 H31 3UTR(+3205+3221)	GGCAGCAAAAGTGAAATT	2400	OPA1 H31 3UTR(-51-67)	ACTTCTTAGTAAGCCTC
2382	OPA1 H31 3UTR(+3208+3224)	CTTGGCAGCAAAAGTGAA	2401	OPA1 H31 3UTR(-54-70)	ATAACTTCTTAGTAAGC
2383	OPA1 H31 3UTR(+3211-16)	AGCCTTGGCAGCAAAAGT	2402	OPA1 H31 3UTR(-57-73)	GTTATAAAGCTTCTTAGTA
2384	OPA1 H31 3UTR(-3-19)	GACAGCCTTGGCAGCAA	2403	OPA1 H31 3UTR(-60-76)	TTAGTTATAAAGCTTCTTA
2385	OPA1 H31 3UTR(-6-22)	AATGACAGCCTTGGCAG	2404	OPA1 H31 3UTR(-63-79)	AGCTTAGTTATAAAGCTTC
2386	OPA1 H31 3UTR(-9-25)	GAAAAATGACAGCCTTGG	2405	OPA1 H31 3UTR(-66-82)	TAAAGCTTAGTTATAAC
2387	OPA1 H31 3UTR(-12-28)	AATGAAAAATGACAGCCT	2406	OPA1 H31 3UTR(-69-85)	TTCTAAAGCTTAGTTAT

SEQ ID	ASO oordinates	Sequence 5'>3'	SEQ ID	ASO oordinates	Sequence 5'>3'
2407	OPA1 H31 3UTR(-72-88)	CAGTTCTAAAGCTTAGT	2425	OPA1 H31 3UTR(-126-142)	AAAGTGAGTAACAGGAG
2408	OPA1 H31 3UTR(-75-91)	TTCCAGTTCTAAAGCTT	2426	OPA1 H31 3UTR(-129-145)	AACAAAAGTGAGTAACAG
2409	OPA1 H31 3UTR(-78-94)	CTCTTCCAGTTCTAAAG	2427	OPA1 H31 3UTR(-132-148)	AATAACAAAAGTGAGTAA
2410	OPA1 H31 3UTR(-81-97)	AGTCTCTTCCAGTTCTA	2428	OPA1 H31 3UTR(-135-151)	AGGAATAACAAAAGTGAG
2411	OPA1 H31 3UTR(-84-100)	TAAAGTCTCTTCCAGTT	2429	OPA1 H31 3UTR(-138-154)	TGGAGGAATAACAAAAGT
2412	OPA1 H31 3UTR(-87-103)	AATTAAAGTCTCTTCCA	2430	OPA1 H31 3UTR(-141-157)	TTCTGGAGGAATAACAA
2413	OPA1 H31 3UTR(-90-106)	TGAAATTTAAAGTCTCTT	2431	OPA1 H31 3UTR(-144-160)	AAGTTCTGGAGGAATAA
2414	OPA1 H31 3UTR(-93-109)	AGATGAAATTTAAAGTCT	2432	OPA1 H31 3UTR(-147-163)	GCAAAAGTTCTGGAGGAA
2415	OPA1 H31 3UTR(-96-112)	GGTAGATGAAATTTAAAG	2433	OPA1 H31 3UTR(-150-166)	TGAGCAAAAGTTCTGGAG
2416	OPA1 H31 3UTR(-99-115)	GATGGTAGATGAAATTA	2434	OPA1 H31 3UTR(-153-169)	TTATGAGCAAAAGTTCTG
2417	OPA1 H31 3UTR(-102-118)	TCAGATGGTAGATGAAA	2435	OPA1 H31 3UTR(-156-172)	CATTATGAGCAAAAGTT
2418	OPA1 H31 3UTR(-105-121)	TAATCAGATGGTAGATG	2436	OPA1 H31 3UTR(-159-175)	TATCATTTTATGAGCAAA
2419	OPA1 H31 3UTR(-108-124)	TTATAATCAGATGGTAG	2437	OPA1 H31 3UTR(-162-178)	AGGTATCATTTTATGAGC
2420	OPA1 H31 3UTR(-111-127)	AGTTTATAATCAGATGG	2438	OPA1 H31 3UTR(-165-181)	AGTAGGTATCAITTTATG
2421	OPA1 H31 3UTR(-114-130)	AGGAGTTTATAATCAGA	2439	OPA1 H31 3UTR(-168-184)	ATTAGTAGGTATCATTT
2422	OPA1 H31 3UTR(-117-133)	AACAGGAGTTTATAATC	2440	OPA1 H31 3UTR(-171-187)	ACAATTAGTAGGTATCA
2423	OPA1 H31 3UTR(-120-136)	AGTAACAGGAGTTTATA	2441	OPA1 H31 3UTR(-174-190)	TCGACAAATTAGTAGGTA
2424	OPA1 H31 3UTR(-123-139)	GTGAGTAACAGGAGTTT	2442	OPA1 H31 3UTR(-177-193)	TGATCGACAATTAGTAG

SEQ ID	ASO oordinates	Sequence 5'>3'	SEQ ID	ASO oordinates	Sequence 5'>3'
2443	OPA1 H31 3UTR(-180-196)	CAATGATCGACAATTAG	2461	OPA1 H31 3UTR(-234-250)	ATCTTCTGAAGGAATTA
2444	OPA1 H31 3UTR(-183-199)	ATCCAATGATCGACAAT	2462	OPA1 H31 3UTR(-237-253)	TGCATCTTCTGAAGGAA
2445	OPA1 H31 3UTR(-186-202)	CATATCCAATGATCGAC	2463	OPA1 H31 3UTR(-240-256)	CTCTGCATCTTCTGAAG
2446	OPA1 H31 3UTR(-189-205)	TGACATATCCAATGATC	2464	OPA1 H31 3UTR(-243-259)	TGCCCTCTGCATCTTCTG
2447	OPA1 H31 3UTR(-192-208)	ACTTGACATATCCAATG	2465	OPA1 H31 3UTR(-246-262)	TCCTTGCCTCTGCATCTT
2448	OPA1 H31 3UTR(-195-211)	CTAACTTGACATATCCA	2466	OPA1 H31 3UTR(-249-265)	TGTTCTTGCCTCTGCAT
2449	OPA1 H31 3UTR(-198-214)	TACCTAACTTGACATAT	2467	OPA1 H31 3UTR(-252-268)	ACATGTTCTTGCCTCTG
2450	OPA1 H31 3UTR(-201-217)	CGCTACCTAACTTGACA	2468	OPA1 H31 3UTR(-255-271)	GAAACATGTTCTTGCCT
2451	OPA1 H31 3UTR(-204-220)	ATACGCTACCTAACTTG	2469	OPA1 H31 3UTR(-258-274)	ATTGAAACATGTTCTTG
2452	OPA1 H31 3UTR(-207-223)	CCTATACGCTACCTAAC	2470	OPA1 H31 3UTR(-261-277)	ACGATTGAAACATGTTT
2453	OPA1 H31 3UTR(-210-226)	ACACCTATACGCTACCT	2471	OPA1 H31 3UTR(-264-280)	AACACGATTGAAACATG
2454	OPA1 H31 3UTR(-213-229)	GGCACACCTATACGCTA	2472	OPA1 H31 3UTR(-267-283)	GCTAACACGATTGAAAC
2455	OPA1 H31 3UTR(-216-232)	GAAAGGCACACCTATACG	2473	OPA1 H31 3UTR(-270-286)	AATGCTAACACGATTGA
2456	OPA1 H31 3UTR(-219-235)	TAAGAAAGGCACACCTAT	2474	OPA1 H31 3UTR(-273-289)	ACCAATGCTAACACGAT
2457	OPA1 H31 3UTR(-222-238)	AATTAAGAAAGGCACACC	2475	OPA1 H31 3UTR(-276-292)	AAAAACCAATGCTAACAC
2458	OPA1 H31 3UTR(-225-241)	AGGAATTAAGAAGGCAC	2476	OPA1 H31 3UTR(-279-295)	AAGAAAAACCAATGCTAA
2459	OPA1 H31 3UTR(-228-244)	TGAAGGAATTGAAGAGG	2477	OPA1 H31 3UTR(-282-298)	ATAAAGAAAAACCAATGC
2460	OPA1 H31 3UTR(-231-247)	TTCTGAAGGAATTAAGA	2478	OPA1 H31 3UTR(-285-301)	CTGATAAAAGAAAAACCAA

SEQ ID	ASO oordinates	Sequence 5'>3'	SEQ ID	ASO oordinates	Sequence 5'>3'
2479	OPA1 H31 3UTR(-288-304)	GCACTGATAAAGAAAC	2484	OPA1 H31 3UTR(-303-319)	ACACTGAGTCTGTTAGC
2480	OPA1 H31 3UTR(-291-307)	TTAGCACTGATAAAGAA	2485	OPA1 H31 3UTR(-306-322)	CTCACACTGAGTCTGTT
2481	OPA1 H31 3UTR(-294-310)	CTGTTAGCACTGATAAA	2486	OPA1 H31 3UTR(-309-325)	GGCCTCACACTGAGTCT
2482	OPA1 H31 3UTR(-297-313)	AGTCTGTTAGCACTGAT	2487	OPA1 H31 3UTR(-312-328)	TGGGGCCTCACACTGAG
2483	OPA1 H31 3UTR(-300-316)	CTGAGTCTGTTAGCACT	2488	OPA1 H31 3UTR(-315-331)	GTATGGGGCCTCACACT

SEQ ID:2489: *OPA1* transcript cDNA sequence (NM_130837)

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5

10

15

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SEQ ID:2490: OPA1 protein sequence (UniProt ID O60313)

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SEYKWIVPDIVWEIDEYIDFEKIRKALPSSDLVKLAPDFDKIVESLSLLKDFFTSGPSPEETAFRAT
5 DRGSESDKHFRKVSDKEKIDQLQEELLHTQLKYQRILERLEKENKELRKLVLQKDDKGIHHRKL
KKSLIDMYSEVLDVLSDYDASYNTQDHLPRVVVVGDSAGKTSVLEMIAQARIFPRGSGEMMT
RSPVKVTLSEGGPHVAFKDSREFDLTKEEDLAALRHEIELMRKNVKEGCTVSPETISLVNKG
PGLQRMVLDLPGVINTVTSGLMAPDTKETIFSISKAYMQNPNAIILCIQDGSVDAERSIVTDLVSQ
MDPHGRRITIFVLTKVDLAEKNVASPSRIQIIEGKLFPMKALGYFAVVTGKGNSSIESIAIREYEE
10 EFFQNSKLLKTSMLKAHQVTTRNLSLAVSDCFWKMVRESVEQQADSFKATRFNLETWKNKY
PRLRELDNRNLFKAKNEILDEVISLSQVTPKHWEELQQSLWERVSTHVIENIYLPAAQTMNSG
TFNTTVDIKLKQWTDKQLPNKAVEVAWETLQEEFSRFMTPEPKGEHDDIFDKLKEAVKEESIKR
HKWNDFAEDSLRVIQHNALEDRSISDKQQWDAAIYFMEEALQARLKDTENAIENMVGPDWKK
RWLYWKNRTQEQCVHNETKNELEKMLKCNEEHPAYLASDEITTVRKNLESRGVEVDPSLIKDT
15 WHQVYRRHFLKTALNHCNLCRRGFYYYQRHFVDSELCNDVVLFWRIQRMALAITANLRQQL
TNTEVRRLEKNVKEVLEDFAEDEGKKIKLLTGKRVQLAEDLKKVREIQEKLDAFIEALHQEK

Table 6 : PMO refinement to target intron 7 of an OPA1 transcript

SEQ ID	ASO Coordinates	Sequence 5'>3'
2491	OPA1_H7xA(-134-105)	AAATACATATATAAAAAGGTCATTGTAAAA
2492	OPA1_H7xA(-133-104)	GAAATACATATATAAAAAGGTCATTGTAAA
2493	OPA1_H7xA(-132-108)	TACATATATATAAAAAGGTCATTGTAA
2494	OPA1_H7xA(-132-103)	TGAAATACATATATAAAAAGGTCATTGTAA
2495	OPA1_H7xA(-131-102)	CTGAAATACATATATAAAAAGGTCATTGTA
2496	OPA1_H7xA(-127-98)	AATTCTGAAATACATATATAAAAAGGTCAT
2497	OPA1_H7xA(-126-97)	AAATTCTGAAATACATATATAAAAAGGTCA
2498	OPA1_H7xA(-126-102)	CTGAAATACATATATAAAAAGGTCAT
2499	OPA1_H7xA(-125-96)	GAAATTCTGAAATACATATATAAAAAGGTC

20 **Table 7 :** PMO refinement to target the 5'UTR of an OPA1 transcript

SEQ ID	ASO Coordinates	Sequence 5'>3'
2500	hOPA1_H1A(-45-24)2MM	CATGCGCACAGTGCCTCGGAAT
2501	hOPA1_H1A(-2+21)2MM	CCTTTCTAGGCGTGCAGCACTA
2502	hOPA1_H1A(+64+85)2MM	CATGGACTTCTGCAAGAGCCTA
2503	hOPA1_H1A(+66+87)2MM	CGCATGGACTTCCGCAAGAGAT

SEQ ID NO: 2504: CPP Sequence

RRSRTARAGRPGRNSSRPSAPRGASGGASG

CLAIMS

1. A method of treating, preventing and/or delaying progression of glaucoma in a subject, the method comprising administering an antisense oligonucleotide that modulates mRNA productive transcript, stability and/or translation of *OPA1* gene transcript or part thereof.
2. The method of claim 1, wherein the antisense oligonucleotide increases the level of *OPA1* mRNA or the amount of functional OPA1 protein in a cell and/or a tissue of the subject.
3. The method of claim 2, wherein the amount of functional OPA1 protein in the cell and/or the tissue is increased by about 1.1 to about 10-fold.
4. The method of claims 2 or 3, wherein the tissue is selected from the group consisting of the retina, retinal pigment epithelium and combinations thereof.
5. The method of any one of claims 1 to 4, wherein the antisense oligonucleotide binds to a targeted portion of:
 - (i) an *OPA1* gene pre-mRNA in a cell to promote exclusion of a nonsense-mediated RNA decay-inducing (NMD) exon during splicing of the *OPA1* pre-mRNA to increase the level of *OPA1* mRNA transcripts encoding full length, functional OPA1;
 - (ii) the 5' untranslated region (UTR) of an *OPA1* gene transcript in a cell to increase translation efficiency of an *OPA1* mRNA;
 - (iii) the 5' UTR of an *OPA1* gene transcript in a cell to increase transcript stability; and/or
 - (iv) the 3' UTR of an *OPA1* gene transcript in a cell to increase transcript stability.
6. The method of claim 5, wherein the antisense oligonucleotide binds to intron 7 of an *OPA1* gene pre-mRNA in a cell and increases the level of *OPA1* gene transcripts encoding full length, functional OPA1 by exclusion of NMD exon 7x.
7. The method of any one of claims 1 to 6, wherein the antisense oligonucleotide binds within a targeted portion of the *OPA1* pre-mRNA nucleotide sequence corresponding to **SEQ ID NOs: 1, 55, 139**.

8. The method of any one of claims 1 to 5, wherein the antisense oligonucleotide binds within a targeted portion of the 5' UTR of *OPAI* mRNA, wherein the targeted portion is within the nucleotide sequence corresponding to **SEQ ID NO: 55**.
9. The method of any one of claims 1 to 5, wherein the antisense oligonucleotide binds within a targeted portion of the 3' UTR of *OPAI* mRNA, wherein the targeted portion is within the nucleotide sequence corresponding to **SEQ ID NO: 139**.
10. The method of any one of claims 1 to 9, wherein the antisense oligonucleotide comprises a backbone modification.
11. The method of claim 10, wherein the antisense oligonucleotide comprises a backbone modification comprising a phosphorothioate linkage or a phosphorodiamidate linkage.
12. The method of any one of claims 1 to 11, wherein the antisense oligonucleotide comprises a phosphorodiamidate morpholino, a locked nucleic acid, a peptide nucleic acid, a 2'-*O*-methyl, a 2' -Fluoro, or a 2'-*O*-methoxyethyl moiety.
13. The method of any one of claims 1 to 12, wherein the antisense oligonucleotide comprises at least one modified sugar moiety.
14. The method of any one of claims 1 to 13, wherein each sugar moiety in the antisense oligonucleotide is a modified sugar moiety.
15. The method of any one of claims 1 to 14, wherein the antisense oligonucleotide comprises a 2'-*O*-methoxyethyl moiety.
16. The method of claim 15, wherein each nucleotide of the antisense oligonucleotide comprises a 2'-*O*-methoxyethyl moiety.
17. The method of any one of claims 1 to 16, wherein the nucleotide sequence of the antisense oligonucleotide consists of 10 to 50 nucleotides, 15 to 40 nucleotides, 18 to 40 nucleotides, 17 to 25 nucleotides, 20 to 35 nucleotides, 20 to 30 nucleotides, 22 to 30

nucleotides, 22 to 28 nucleotides, 24 to 30 nucleotides, 25 to 30 nucleotides, or 26 to 30 nucleotides.

18. The method of claim 17, wherein the nucleotide sequence of the antisense oligonucleotide consists of 20 to 30 nucleotides.

19. The method of claim 18, wherein the antisense oligonucleotide comprises one or more phosphorodiamidate morpholino moieties.

20. The method of any one of claims 1 to 19, wherein the antisense oligonucleotide is linked to a functional moiety.

21. The method of claim 20, wherein the functional moiety comprises or consists of a delivery moiety or a stabilising moiety.

22. The method of claim 21, wherein the delivery moiety is selected from the group consisting of lipids, peptides, carbohydrates, and antibodies.

23. The method of claims 21 or 22, wherein the delivery moiety comprises a cell-penetrating peptide (CPP) or a N-acetylgalactosamine (GalNAc) moiety.

24. The method of any one of claims 20 to 23, wherein the functional moiety is covalently or non-covalently linked to the antisense oligonucleotide.

25. The method of any one of claims 20 to 24, wherein the functional moiety is linked to the 5' end of the antisense oligonucleotide or is linked to the 3' end of the antisense oligonucleotide.

26. The method of any one of claims 1 to 25, wherein the nucleotide sequence of the antisense oligonucleotide is at least 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% complementary to the nucleotide sequence of the targeted portion over the length of the antisense oligonucleotide.

27. The method of any one of claims 1 to 26, wherein the nucleotide sequence of the antisense oligonucleotide corresponds to any one of **SEQ ID NOs: 2-54, 56-138, 140-2488 or 2491-2503**

28. The method of any one of claims 1 to 27, wherein the antisense oligonucleotide is complexed with a delivery nanocarrier.

29. The method of claim 28, wherein the delivery nanocarrier is selected from the group consisting of: lipoplexes, liposomes, exosomes, inorganic nanoparticles, and DNA nanostructures.

30. The method of claim 29, wherein the delivery nanocarrier comprises a lipid nanoparticle (LNP) encapsulating the antisense oligonucleotide.

31. The method of any one of claims 1 to 30, wherein the antisense oligonucleotide is formulated for a route of administration selected from the group consisting of intravitreal, suprachoroidal, subretinal, ciliary intramuscular, intravenous, intra-arterial, subcutaneous, and topical routes.

32. Use of an antisense oligonucleotide in the manufacture of a medicament for treating, preventing and/or delaying progression of glaucoma in a subject, wherein the antisense oligonucleotide modulates mRNA translation of the *OPAI* gene transcript or part thereof.

33. An antisense oligonucleotide that binds to a targeted portion of the intron 7x of an *OPAI* gene transcript in a cell and increases the level of *OPAI* gene transcripts encoding full length, functional *OPAI* by exclusion of NMD exon 7x.

34. The antisense oligonucleotide of claim 33 comprising or consisting of any one of **SEQ ID NOs: 2-54** or **SEQ ID NOs: 2491-2503**.

35. An antisense oligonucleotide that binds to a targeted portion of the 5' UTR of an *OPAI* gene transcript in a cell and increases transcript stability of an *OPAI* mRNA, wherein the targeted portion is within the nucleotide sequence corresponding to **SEQ ID NO: 55**.

36. The antisense oligonucleotide of claim 35 comprising or consisting of any one of **SEQ ID NOs: 56-138**.

37. An antisense oligonucleotide that binds to a targeted portion of the 3' UTR of an *OPAI* gene transcript in a cell and increases transcript stability of an *OPAI* mRNA.
38. The antisense oligonucleotide of claim 37, wherein the antisense oligonucleotide binds within a targeted portion of the 3' UTR of *OPAI* mRNA, wherein the targeted portion is within the nucleotide sequence corresponding to **SEQ ID NO: 139**.
39. The antisense oligonucleotide of claim 37 or 38 comprising or consisting of any one of **SEQ ID NOs: 140-2488**.