AGENTS FOR TREATMENT OF CONDITIONS ASSOCIATED WITH OPTIC ATROPHY 1

RELATED APPLICATION DATA

This application claims priority from Australian Patent Application No. 2024901550 filed 24 May 2024 and entitled "Agents for Treatment of Conditions Associated with Optic Atrophy 1", the entire contents of which is hereby incorporated by reference.

SEQUENCE LISTING

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

The present invention relates to a cell-penetrating peptide (CPP) comprising a sequence set forth in SEQ ID NO: 2504 and conjugates thereof. The present invention also relates to antisense oligonucleotides that modulates mRNA productive transcript, stability and/or translation of *OPA1* gene transcript or part thereof linked to a cell-penetrating peptide (CPP) comprising a sequence set forth in SEQ ID NO: 2504.

BACKGROUND

OPA1 consists of 30 coding exons spanning 100 kb of genomic DNA on the long arm of chromosome 3 (3q28–q29), and the protein product is a 1,015 amino acid polypeptide that co-localizes to the inner mitochondrial membrane. 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. Over 400 different OPA1 mutations have been reported to be responsible for optic nerve degeneration and visual loss, ranging from isolated 'Dominant Optic Atrophy' (DOA; OMIM #165500) to more severe multi-systemic syndromes named 'ADOAplus' (OMIM #125250), including some bi-allelic cases with Behr Syndrome (OMIM #210000).

OPA1 is a ubiquitously expressed mitochondrial GTPase that is indispensable for mitochondrial function. In humans, OPA1 generates at least eight isoforms via differential splicing of exons 4, 4b and 5b or equivalent to exon 4, 5 and 7 according to Figure 1A. OPA1 precursor proteins are targeted and mobilised to the mitochondria by their mitochondrial targeting sequence (MTS). In the mitochondria, the OPA1 precursor

proteins are cleaved into either long forms (l forms) that are anchored to the inner mitochondrial membrane, or into short, soluble forms (s forms).

The coding sequence of the full *OPA1* gene is beyond the packaging capacity of AAV vectors, which have a limit of less than 5 kb. Furthermore, certain forms of CRISPR/Cas9 gene correction will require a different product for each unique OPA1 mutation, and splicing switching strategies using antisense oligomers targeted to the *OPA1* pre-mRNA may only target regions of mutations (e.g., within an exon, as with antisense oligomer drugs like Eteplirsen) and may not provide a functional protein product. In addition, both the gene replacement and gene editing approaches require, for ocular conditions, subretinal injection of viral vectors to achieve adequate transfection. The procedure carries risks of retinal trauma.

There is a need to provide new treatments or preventative measures for conditions associated with mutations in the *OPA1* gene. The present invention seeks to provide an improved or alternative method for treating, preventing or ameliorating the effects of conditions associated with mutations in the *OPA1* gene.

The previous discussion of the background art is intended to facilitate an understanding of the present invention only. The discussion is not an acknowledgement or admission that any of the material referred to is or was part of the common general knowledge as at the priority date of the application.

SUMMARY

In producing the present invention, the inventors identified a sequence defined cell penetrating peptide (CPP) useful for intracellular delivery of a CPP-linked cargo, e.g., a polynucleotide such as an oligonucleotide. The inventors further identified that conjugates comprising antisense oligonucleotides (ASOs) that increase expression of *OPA1* expression linked to the sequence defined CPP are useful for pharmacological intervention for treating or preventing conditions associated with the *OPA1* gene, e.g., ocular conditions, such as autosomal dominant optic atrophy (ADOA), glaucoma, geographic atrophy, acute ischemic optic neuritis and acute ischemic optic neuropathy. The present inventors identified that ASOs linked to the sequence defined CPP (i.e., as set forth in SEQ ID NO: 2504) were capable of upregulating OPA1 protein expression. Thus, the findings by the inventors provide the basis for a sequence defined CPP, as well as conjugates comprising ASOs that increase expression of OPA1 expression linked to the sequence defined CPP.

These findings additionally provide the basis for methods of treating, preventing and/or delaying progression of an ocular condition. For example, ADOA, glaucoma, geographic atrophy, acute ischemic optic neuritis and acute ischemic optic neuropathy.

Accordingly, the present disclosure provides a CPP comprising a sequence set forth in SEQ ID NO: 2504. The present disclosure also provides a CPP, wherein the sequence of the CPP consists of a sequence set forth in SEQ ID NO: 2504.

The present disclosure also provides a CPP comprising a sequence set forth in SEQ ID NO: 2504 for targeting retinal cells in a subject in need thereof. For example, retinal ganglion cells. The present disclosure further provides a CPP, wherein the sequence of the CPP consists of a sequence set forth in SEQ ID NO: 2504, for targeting retinal cells in a subject in need thereof.

Accordingly, the present disclosure provides an antisense oligonucleotide that modulates mRNA productive transcript, stability and/or translation of *OPA1* gene transcript or part thereof, wherein the antisense oligonucleotide is linked to a CPP comprising a sequence set forth in SEQ ID NO: 2504.

The present disclosure further provides an antisense oligonucleotide that modulates mRNA productive transcript, stability and/or translation of *OPA1* gene transcript or part thereof, wherein the antisense oligonucleotide is linked to a CPP, wherein the CPP consists of a sequence set forth in SEQ ID NO: 2504.

The present disclosure provides an antisense oligonucleotide that increases functional OPA1 protein levels in the subject, wherein the antisense oligonucleotide is linked to a CPP comprising a sequence set forth in SEQ ID NO: 2504. For example, the level of OPA1 protein is increased in the subject compared to the level in the subject prior to administration of the ASO.

The present disclosure also provides an antisense oligonucleotide that increases functional OPA1 protein levels in the subject, wherein the antisense oligonucleotide is linked to a CPP comprising a sequence set forth in SEQ ID NO: 2504. The present disclosure further provides an antisense oligonucleotide that increases functional OPA1 protein levels in the subject, wherein the antisense oligonucleotide is linked to a CPP, wherein the CPP consists of a sequence set forth in SEQ ID NO: 2504.

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 the ASO 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, retinal ganglion 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:

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;

i. the 5' untranslated region (UTR) of an *OPA1* gene transcript in a cell to increase translation efficiency of an *OPA1* mRNA;
ii. 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
iii. 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 ASO 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 binds to intron 7 of an *OPA1* transcript and reduces expression of *OPA1* gene transcript lacking exon 7x but does not substantially affect the relative expression levels of *OPA1* gene transcripts comprising exon 7 or lacking exon 7.

In one example, the ASO binds within a targeted portion of the OPA1 pre-mRNA nucleotide sequence corresponding to SEQ ID NOs: 1, 55, 139.

In one example, the ASO comprises one or more mismatches relative to the sequence set forth in SEQ ID NO: 1.

In one example, the antisense oligonucleotide significantly increases the level of a transcript comprising exons 3, 4, 6, 7 and 8 in a cell to which the antisense oligonucleotide is contacted relative to the level of the transcript in a cell to which the antisense oligonucleotide has not been contacted. In one example, the level of expression is determined using quantitative RT-PCR, digital droplet PCR or RNA sequencing.

In one example, the antisense oligonucleotide comprises two mismatches relative to the sequence set forth in SEQ ID NO: 1.

In one example, the ASO comprises one or more G residue mismatches corresponding to an A residue in SEQ ID NO: 1.

In one example, the mismatch is not at a terminus of the antisense oligonucleotide.

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.

The present disclosure provides an antisense oligonucleotide comprising a sequence set forth in any one of SEQ ID NOs: 2505-2517 or a sequence having at least about 50% or 60% or 70% or 80% or 95% identity thereto, wherein the antisense oligonucleotide is linked to a cell-penetrating peptide (CPP) comprising a sequence set forth in SEQ ID NO: 2504.

The present disclosure provides an antisense oligonucleotide comprising a sequence set forth in any one of SEQ ID NOs: 2505-2517 or a sequence having at least about 50% or 60% or 70% or 80% or 95% identity thereto, wherein the antisense

oligonucleotide is linked to a cell-penetrating peptide (CPP), wherein the CPP consists of a sequence set forth in SEQ ID NO: 2504.

The present disclosure provides an antisense oligonucleotide comprising or consisting of a sequence set forth in any one of SEQ ID NOs: 2505-2517 or a sequence having at least about 80% identity thereto, wherein the antisense oligonucleotide is linked to a cell-penetrating peptide (CPP) comprising a sequence set forth in SEQ ID NO: 2504.

The present disclosure provides an antisense oligonucleotide comprising or consisting of a sequence set forth in any one of SEQ ID NOs: 2505-2517 or a sequence having at least about 80% identity thereto, wherein the antisense oligonucleotide is linked to a cell-penetrating peptide (CPP), wherein the CPP consists of a sequence set forth in SEQ ID NO: 2504.

In one example, the ASO comprises or consists of a sequence set forth in SEQ ID NO: 2505.

In one example, the ASO comprises or consists of a sequence set forth in SEQ ID NO: 2506.

In one example, the ASO comprises or consists of a sequence set forth in SEQ ID NO: 2507.

In one example, the ASO comprises or consists of a sequence set forth in SEQ ID NO: 2508.

In one example, the ASO comprises or consists of a sequence set forth in SEQ ID NO: 2509.

In one example, the ASO comprises or consists of a sequence set forth in SEQ ID NO: 2510.

In one example, the ASO comprises or consists of a sequence set forth in SEQ ID NO: 2511.

In one example, the ASO comprises or consists of a sequence set forth in SEQ ID NO: 2512.

In one example, the ASO comprises or consists of a sequence set forth in SEQ ID NO: 2513.

In one example, the ASO comprises or consists of a sequence set forth in SEQ ID NO: 2514.

In one example, the ASO comprises or consists of a sequence set forth in SEQ ID NO: 2515.

In one example, the ASO comprises or consists of a sequence set forth in SEQ ID NO: 2516.

In one example, the ASO comprises or consists of a sequence set forth in SEQ ID NO: 2517.

The present disclosure provides an antisense oligonucleotide comprising or consisting of a sequence set forth in SEQ ID NO: 2512 linked to a cell-penetrating peptide (CPP), wherein the CPP consists of a sequence set forth in SEQ ID NO: 2504.

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.

The present disclosure further provides an antisense oligonucleotide that binds to a targeted portion of the 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, wherein the antisense oligonucleotide is linked to a cell-penetrating peptide (CPP) comprising a sequence set forth in SEQ ID NO: 2504.

The present disclosure further provides an antisense oligonucleotide that binds to a targeted portion of the 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, wherein the antisense oligonucleotide is linked to a cell-penetrating peptide (CPP), wherein the CPP consists of a sequence set forth in SEQ ID NO: 2504.

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 *OPA1* pre-mRNA comprises or consists of any one of SEQ ID NOs: 2-54. For example, the ASO 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 *OPA1* pre-mRNA comprises or consists of any one of SEQ ID NOs: 2-54 or SEQ ID NOs: 2491-2499 or SEQ ID NOs: 2505-2517. In one example, the ASO comprises or consists of any one of SEQ ID NOs: 2-54 or SEQ ID NOs: 2491-2499 or SEQ ID NOs: 2505-2517.

In one example, the ASO that binds to a targeted portion of intron 7 *OPA1* pre-mRNA comprises or consists of any one of SEQ ID NOs: 2491-2499. In another example, the ASO comprises or consists of any one of SEQ ID NOs: 2491-2499.

In one example, the ASO that binds to a targeted portion of intron 7 *OPA1* pre-mRNA comprises or consists of any one of SEQ ID NOs: 2505-2517. In another example, the ASO comprises or consists of any one of SEQ ID NOs: 2505-2517.

In one example, the ASO binds to a targeted portion of the 5' UTR of an *OPA1* gene transcript in a cell to increase translation efficiency or transcript stability of an *OPA1* 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 *OPA1* mRNA, wherein the targeted portion is within the nucleotide sequence corresponding to SEQ ID NO: 55.

The present disclosure also provides an antisense oligonucleotide 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, wherein the targeted portion is within the nucleotide sequence corresponding to SEQ ID NO: 55, wherein the antisense oligonucleotide is linked to a cell-penetrating peptide (CPP) comprising a sequence set forth in SEQ ID NO: 2504.

The present disclosure also provides an antisense oligonucleotide 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, wherein the targeted portion is within the nucleotide sequence corresponding to SEQ ID NO: 55, wherein the antisense oligonucleotide is linked to a cell-penetrating peptide (CPP), wherein the CPP consists of a sequence set forth in SEQ ID NO: 2504.

In one example, the ASO that binds to a targeted portion of the 5' UTR of *OPA1* mRNA comprises or consists of any one of SEQ ID NOs: 56-138 or SEQ ID NOs: 2500-2503. For example, the ASO comprises or consists of any one of SEQ ID NOs: 56-138. In another example, the ASO comprises or consists of any one of SEQ ID NOs: 2500-2503. In a further example, the ASO comprises or consists of any one of SEQ ID NOs: 56-138 or 2500-2503.

In one example, the ASO that binds to a targeted portion of the 5' UTR of *OPA1* mRNA comprises or consists of SEQ ID NO: 112. For example, the ASO comprises or consists of SEQ ID NO: 112.

The present disclosure provides an antisense oligonucleotide comprising or consisting of a sequence set forth in SEQ ID NO: 112, wherein the antisense oligonucleotide is linked to a cell-penetrating peptide (CPP) comprising a sequence set forth in SEQ ID NO: 2504.

The present disclosure also provides an antisense oligonucleotide comprising or consisting of a sequence set forth in SEQ ID NO: 112, wherein the antisense oligonucleotide is linked to a cell-penetrating peptide (CPP), wherein the CPP consists of a sequence set forth in SEQ ID NO: 2504.

The present disclosure provides a pharmaceutical composition comprising an antisense oligonucleotide comprising or consisting of a sequence set forth in SEQ ID NO: 112, wherein the antisense oligonucleotide is linked to a cell-penetrating peptide (CPP) comprising a sequence set forth in SEQ ID NO: 2504.

The present disclosure further provides a pharmaceutical composition comprising an antisense oligonucleotide comprising or consisting of a sequence set forth in SEQ ID NO: 112, wherein the antisense oligonucleotide is linked to a cell-penetrating peptide (CPP), wherein the CPP consists of a sequence set forth in SEQ ID NO: 2504.

In one example, the ASO binds to a targeted portion of the 3' UTR of an *OPA1* gene transcript in a cell to increase transcript stability of an *OPA1* 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.

The present disclosure provides an antisense oligonucleotide that binds to a targeted portion of the 3' UTR of an *OPA1* gene transcript in a cell and increases transcript stability of an *OPA1* mRNA, wherein the antisense oligonucleotide is linked to a cell-penetrating peptide (CPP) comprising a sequence set forth in SEQ ID NO: 2504.

The present disclosure provides an antisense oligonucleotide that binds to a targeted portion of the 3' UTR of an *OPA1* gene transcript in a cell and increases transcript stability of an *OPA1* mRNA, wherein the antisense oligonucleotide is linked to a cell-penetrating peptide (CPP), wherein the CPP consists of a sequence set forth in SEQ ID NO: 2504.

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.

The present disclosure provides an antisense oligonucleotide that binds to a targeted portion of the 3' UTR of an *OPA1* gene transcript in a cell and increases transcript stability of an *OPA1* mRNA, wherein the targeted portion is within the nucleotide sequence corresponding to SEQ ID NO: 139, wherein the antisense oligonucleotide is linked to a cell-penetrating peptide (CPP) comprising a sequence set forth in SEQ ID NO: 2504.

The present disclosure also provides an antisense oligonucleotide that binds to a targeted portion of the 3' UTR of an *OPA1* gene transcript in a cell and increases transcript stability of an *OPA1* mRNA, wherein the targeted portion is within the nucleotide sequence corresponding to SEQ ID NO: 139, wherein the antisense oligonucleotide is linked to a cell-penetrating peptide (CPP), wherein the CPP consists of a sequence set forth in SEQ ID NO: 2504.

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.

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 disclosure provides an oligonucleotide comprising 12 or 13 or 14 or 15 or 16 or 17 or 18 or 19 or 20 consecutive nucleotides of any one of the foregoing nucleotides.

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 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 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.

In other examples the ASO comprises at least 10 contiguous nucleotides of an ASO sequence described herein. In some examples ASO comprises at least 10 contiguous nucleotides (subsequence) from each of two or more ASO sequences described herein or one sequence described herein and another sequence known in the art, where the two or more subsequences are not contiguous in a OPA1 mRNA sequence.

In some examples for each occurrence of “G” in an ASO sequence disclosed herein, the “G” is guanosine or inosine. In some examples for each occurrence of “T” in an ASO sequence disclosed herein, the “T” is any one of: thymidine, inosine, uracil, or an isomeric or modified form of uracil (*e.g.*, pseudouridine or N1-methyl-pseudouridine). In some examples for each occurrence of “C” in an ASO sequence disclosed herein, the C is cytosine or a modified form of cytosine (*e.g.*, 5-methylcytosine).

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, the ASO comprises a phosphorodiamidate linkage.

In one example, the ASO comprises a phosphorodiamidate morpholino, a locked nucleic acid, a peptide nucleic acid, a bridged 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. In a further example, the ASO comprises a bridged nucleic acid.

In one example, the ASO comprises at least one modified sugar moiety. In one example, one or more sugar moieties in the antisense oligonucleotide is a 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. In one example, one or more nucleotides of the ASO comprises a 2'-*O*-methoxyethyl moiety. For example, each nucleotide of the ASO comprises a 2'-*O*-methoxyethyl moiety.

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

In one example of any composition described herein, the CPP can be covalently linked or non-covalently linked to the ASO. The CPP can be at the 5' end and/or 3' end of the ASO. In one example, the CPP is at the 3' end of the ASO. For example, the C terminus of the CPP is at the 3' end of the ASO. In one example, the carboxylic acid C terminus of the CPP is linked to the 3' end of the ASO.

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.

In one example, 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 further provides a pharmaceutical composition comprising the antisense oligonucleotide of the present disclosure and a pharmaceutically acceptable excipient.

The present disclosure additionally provides a method of treating a condition, the method comprising administering an antisense oligonucleotide or pharmaceutical composition of the disclosure. In one example, the condition is associated with OPA1 expression, e.g., reduced OPA1 expression. In one example, the condition is an ocular condition. For example, the ocular condition is ADOA, glaucoma, geographic atrophy, acute ischemic optic neuritis or acute ischemic optic neuropathy. In one example, the condition is glaucoma. In another example, the condition is autosomal dominant optic atrophy. In a further example, the condition is geographic atrophy. In one example, the condition is acute ischemic optic neuritis. In another example, the condition is acute ischemic optic neuropathy.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a series of graphical representations showing the binding sites for oligonucleotides to mediate increasing 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. Oligonucleotides **SEQ ID NOs: 56-138**, **2500-2503** 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). PMOs (**SEQ ID NOs: 2-54, 2491-2499, 2505-2512**) 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. Oligonucleotides (**SEQ ID NOs: 140-2488)** 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 the effect of a PMO **(SEQ ID NO: 2512)** targeting exon 7x exclusion in ADOA derived iPSC-RGCs harboring an OPA1 c.2708_2711delTTAG mutation, conjugated to a CPP (**SEQ ID NO: 2504**). Patient iPSC-RGCs were transfected in triplicates for 5 days with the CPP-PMO targeting removal of the *OPA1* exon 7x as indicated. *OPA1* transcript expression was assessed by ddPCR and normalised

to the *HPRT1* transcript level. The *OPA1* expression in untreated cells was set to 1. A non-targeting control PMO, conjugated with the same CPP, was employed as a negative control. Statistical analysis was conducted using Two-Way ANOVA. The CPP-PMO targeting exon 7x showed a significant upregulation of *OPA1* mRNA in iPSC-RGCs derived from an ADOA patient in a dose dependent manner.

Figure 3 shows the effect of a PMO **(SEQ ID NO: 2512)** targeting exon 7x exclusion in ADOA derived iPSC-RGCs to increase OPA1 protein, conjugated to a CPP (**SEQ ID NO: 2504**). Patient iPSC-RGCs were incubated at indicated concentrations in triplicates for 5-7 days with CPP-PMO targeting removal of the OPA1 exon 7x as indicated. OPA1 transcript expression was assessed by ddPCR and normalised to the *HPRT1* transcript level. The OPA1 expression in untreated cells was set to 1. A non-targeting control PMO, conjugated with the same CPP, was employed as a negative control. Statistical analysis was conducted using Student's *t*-test. The CPP-PMO targeting exon 7x showed a significant upregulation of OPA1 protein in multiple ADOA patient iPSC-RGCs. Patient#1 harboring OPA1 c.985-1G>C mutation, Patient #2 harboring OPA1 c.2608delA mutation and Patient#4 harboring OPA1 c.2708_2711delTTAG mutation.

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, (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.

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).

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

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 may or may 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.

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 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 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 ºC. 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 and 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. 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 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 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 "Blosum62" is utilized for amino acid sequences and the default matrix.

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 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.

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.

Cell Penetrating Peptides (CPP)

The present disclosure provides a CPP comprising a sequence set forth in SEQ ID NO: 2504. The present disclosure further provides a CPP, wherein the CPP consists of a sequence set forth in SEQ ID NO: 2504.

The present disclosure provides a CPP comprising a sequence RASARRASARRANARRANARRSGGR (SEQ ID NO: 2504).

The present disclosure also provides a CPP, wherein the CPP consists of a sequence RASARRASARRANARRANARRSGGR (SEQ ID NO: 2504).

The term "cell penetrating peptide" (CPP) refers to a peptide that is capable of crossing 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 complete and intact, or alternatively partially degraded.

In some examples the amino acid sequence of a CPP provided herein includes at least one D-amino acid. In some examples the amino acid sequence of a CPP includes only D-amino acids. For example, the amino acid sequence of the CPP is D-arginyl-D-alanyl-D-seryl-D-alanyl-D-arginyl-D-arginyl-D-alanyl-D-seryl-D-alanyl-D-arginyl-D-arginyl-D-alanyl-D-asparagyl-D-alanyl-D-arginyl-D-arginyl-D-alanyl-D-asparagyl-D-alanyl-D-arginyl-D-arginyl-D-seryl-glycyl-glycyl-D-arginyl. In other examples, a CPP includes at least one L-amino acid. In some examples, the CPP includes only L-amino acids. In some examples the amino acid sequence of a CPP provided herein is the retro-inverso sequence of any of the CPP amino acid sequence enumerated herein.

In one example, the CPP consists of a sequence D-arginyl-D-alanyl-D-seryl-D-alanyl-D-arginyl-D-arginyl-D-alanyl-D-seryl-D-alanyl-D-arginyl-D-arginyl-D-alanyl-D-asparagyl-D-alanyl-D-arginyl-D-arginyl-D-alanyl-D-asparagyl-D-alanyl-D-arginyl-D-arginyl-D-seryl-glycyl-glycyl-D-arginyl.

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 barriers.

Modified CPPs

In some examples, the CPP is a modified CPP. In some examples, a CPP provided herein is a modified CPP by virtue of comprising a moiety other than a canonical amino acid. Such modifications include, but are not limited to, non-peptide linkers, and detectable labels, as described in further detail herein. In some examples a CPP is a modified CPP comprising a moiety other than a canonical amino acid. Such modified CPPs may confer additional functionalities to a CPP, such as facilitating detection of CPP entry, localisation within cells, enhanced cell entry, and/or reduced CPP degradation *in vitro* or *in vivo*. Suitable moieties for a modified CPP include, but are not limited to, any moiety selected from the group consisting of: a detectable label, a non-canonical amino acid, a reactive group, a fatty acid, cholesterol, a bioactive carbohydrate, a lipid, a nanoparticle, a small molecule drug, and a polynucleotide. In some examples the moiety in a modified CPP is a detectable label.

The term "detectable label" refers to any type of molecule which can be detected by optical, fluorescent, isotopic imaging or by mass spectroscopic techniques, or by performing simple enzymatic assays. Any detectable label known in the art may be used. In some examples the detectable label is selected from among a fluorophore, a fluorogenic substrate, a luminogenic substrate, and a biotin.

A fluorescent tag may be a fluorophore. For example, a fluorophore may be fluorescein isothiocyanate, fluorescein thiosemicarbazide, rhodamine, Texas Red, a CyDye such as Cy3, Cy5 and Cy5.5, a Alexa Fluor such as Alexa488, Alexa555, Alexa594 and Alexa647) or a near infrared fluorescent dye. A fluorophore may be a pH-sensitive fluorescent probe. For example, a pH-sensitive fluorescent probe may be naphthofluorescein, A fluorescent tag may be a fluorescent protein. For example, a fluorescent protein may be green fluorescent protein (GFP), enhanced green fluorescent protein (EGFP), AcGFP or TurboGFP, Emerald, Azami Green, ZsGreen, EBFP, Sapphire, T-Sapphire, ECFP, mCFP, Cerulean, CyPet, AmCyanl, Midori-Ishi Cyan, mTFPl (Teal), enhanced yellow fluorescent protein (EYFP), Topaz, Venus, mCitrine, YPet, PhiYFP, ZsYellowl, mBanana, Kusabira,ange, mOrange, dTomato, dTomato-Tandem, AsRed2, mRFPl, Jred, mCherry, HcRedl, mRaspberry, HcRedl, HcRed-Tandem, mPlum, AQ 143. A fluorescent tag may be a quantum dot. In some examples, where the detectable label is a fluorophore, the fluorophore is a pH-sensitive fluorescent probe. Suitable pH-sensitive fluorescent probes include, but are not limited to,

naphthofluorescein, pHrodo® Green (ThermoFisher), and pHrodo® Red (ThermoFisher). Fluorescent tags may be detected using fluorescent microscopes such as epifluorescence or confocal microscopes, fluorescence scanners such as microarray readers, spectrofluorometers, microplate readers and/or flow cytometers.

In some examples the detectable label is a fluorogenic substrate. Suitable fluorogenic substrates include fluorogenic substrates of β lactamase (e.g, CCF-2-AM, CCF4-AM, and any of those described in U.S. Patent No. 7,427,680) and β-gal (e.g, HMRef-βGal described in Asanuma et al 2015, Nature Comm., 6:6463).

In some examples the detectable label is a luminogenic substrate. Suitable luminogenic substrates include, but are not limited to, D-Luciferin, L-Luciferin, Coelenterazine,

An epitope tag may be a poly-histidine tag such as a hexahistidine tag or a dodecahistidine, a FLAG tag, a Myc tag, a HA tag, a GST tag or a V5 tag. Epitope tags are routinely detected with commercially available antibodies. A person skilled in the art will be aware that an epitope tag may facilitate purification and/or detection. For example, a conjugate containing a hexahistidine tag may be purified using methods known in the art, such as, by contacting a sample comprising the protein with nickel-nitrilotriacetic acid (Ni-NTA) that specifically binds a hexahistidine tag immobilized on a solid or semi-solid support, washing the sample to remove unbound protein, and subsequently eluting the bound protein. Alternatively, or in addition a ligand or antibody that binds to an epitope tag may be used in an affinity purification method.

An isobaric tag may be a mass tag or an isobaric tag for relative absolute quantification (iTRAQ). A mass tag is a chemical label used for mass spectrometry based quantification of proteins and peptides. In such methods mass spectrometers recognise the mass difference between the labeled and unlabeled forms of a protein or peptide, and quantification is achieved by comparing their respective signal intensities as described, for example, in Bantscheff et al. 2007. Examples of mass tags include TMTzero, TMTduplex, TMTsixplex and TMT 10-plex. An isobaric tag for relative absolute quantification (iTRAQ) is a chemical tag used in quantitative proteomics by tandem mass spectrometry to determine the amount of proteins from different sources in a single experiment as described, for example, in Wiese et al. 2007.

In some examples the moiety is a non-canonical amino acid. Suitable non-canonical amino acids include, but are not limited to, ornithine, citrulline (Cit), diaminobutyric acid (Dab), diaminopropionic acid (Dap), 2-Aminoisobutyric acid α Amino-n-butyric acid, Norvaline, Norleucine, Alloisoleucine, t-leucine, Ornithine,

Allothreonine, β-Alanine, β -Amino-n-butyric acid, N-isopropyl glycine, Isoserine, and Sarcosine.

In other examples a moiety in a modified CPP is a reactive group. Suitable reactive groups include, but are not limited to, azide groups, amine-reactive groups, thiol-reactive groups, and carbonyl-reactive groups. In some examples the reactive groups are part of a chemical tag. Suitable chemical tags include, but are not limited to, a SNAP tag, a CLIP tag, a HaloTag or a TMP-tag. In one example, the chemical tag is a SNAP-tag or a CLIP-tag. SNAP and CLIP fusion proteins enable the specific, covalent attachment of virtually any molecule to a protein or peptide of interest as described, for example, in Corrêa 2015 (Methods Mol Biol, 1266:55-79). In another example, the chemical tag is a HaloTag. HaloTag involves a modular protein tagging system that allows different molecules to be covalently linked, either in solution, in living cells, or in chemically fixed cells. In another example, the chemical tag is a TMP-tag. TMP-tags are able to label intracellular, as opposed to cell-surface, proteins with high selectivity.

In some examples the moiety in a modified CPP is a fatty acid. Suitable fatty acids for modified peptides include, but are not limited to, palmitic acid, myristic acid, caprylic acid, lauric acid, n-octanoic acid, and n-decanoic acid.

In other examples the moiety in a modified CPP is cholesterol.

CPP Conjugates

The term "CPP conjugate," as used herein, refers to a CPP that is linked (covalently or non-covalently) to a polynucleotide as described herein.

In some examples, a CPP conjugate protein comprises a flexible linker linking the CPP and a heterologous amino acid sequence such a peptide or protein. Examples of flexible linkers include, but are not limited to, GGGGS (SEQ ID NO: 2518), GGGGSGGGGS (SEQ ID NO: 2519), GAS, GGG, GSG, GTG, GGTAGSTGG (SEQ ID NO: 2520), GASGGASG (SEQ ID NO: 2521) and GASG (SEQ ID NO: 2522). Other examples of such flexible linkers are known in the art as described in, e.g., Chen et al (2013), Adv Drug Deliv Rev., 65(10):1357-1369. In one example, the amino acid sequence of the linker only includes D-amino acids.

In one example, the carboxylic acid C-terminus of the CPP is linked to the 3' end of the antisense oligonucleotide via a linker.

The present disclosure provides a CPP conjugate comprising a sequence set forth in SEQ ID NO: 2504 linked to an antisense oligonucleotide that modulates mRNA productive transcript, stability and/or translation of *OPA1* gene transcript or part thereof,

The present disclosure also provides a CPP conjugate comprising a sequence set forth in SEQ ID NO: 2504, linked to an antisense oligonucleotide comprising or consisting of a sequence set forth in SEQ ID NO: 2512.

The present disclosure further provides a CPP conjugate comprising a sequence set forth in SEQ ID NO: 2504, linked to an antisense oligonucleotide that binds to a targeted portion of the 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.

The present disclosure provides a CPP conjugate comprising a sequence set forth in SEQ ID NO: 2504, linked to an antisense oligonucleotide 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, wherein the targeted portion is within the nucleotide sequence corresponding to SEQ ID NO: 55.

The present disclosure also provides a CPP conjugate comprising a sequence set forth in SEQ ID NO: 2504, linked to an antisense oligonucleotide comprising or consisting of a sequence set forth in SEQ ID NO: 112.

The present disclosure provides a CPP conjugate comprising or consisting of a CPP consisting of a sequence RASARRASARRANARRANARRSGGR (SEQ ID NO: 2504), a GASGGASG (SEQ ID NO: 2521) linker and an antisense oligonucleotide comprising or consisting of a sequence set forth in SEQ ID NO: 112.

The present disclosure provides a CPP conjugate consisting of:

(i) a CPP consisting of a sequence set forth in SEQ ID NO: 2504

(ii) a linker consisting of a sequence set forth in SEQ ID NO: 2521; and

(iii) an antisense oligonucleotide consisting of a sequence set forth in SEQ ID NO: 112,

wherein the C-terminus of the CPP is linked to the 3' end of the antisense oligonucleotide via the linker.

The present disclosure provides a CPP conjugate comprising a CPP consisting of a sequence set forth in SEQ ID NO: 2504, and an antisense oligonucleotide comprising or consisting of a sequence set forth in SEQ ID NO: 112, wherein the C-terminus of the CPP is linked to the 3' end of the antisense oligonucleotide via a linker. For example, the linker comprises or consists of a sequence set forth in SEQ ID NO: 2521. In one example, the amino acid sequence of the linker only includes D-amino acids. For example, the linker comprises or consists of the sequence glycyl-D-alanyl-D-seryl-glycyl-glycyl-D-alanyl-D-seryl-glycyl (SEQ ID NO: 2521).

In one example, the C-terminus of the CPP is linked to the secondary amino at the 3' end of the antisense oligonucleotide via a linker. For example, the carboxylic acid C-terminus of the CPP is linked to the secondary amino at the 3' end of the antisense oligonucleotide via a linker.

The present disclosure further provides a CPP conjugate consisting of:

(i) a CPP consisting of a sequence set forth in SEQ ID NO: 2504, wherein the amino acid sequence of the CPP includes only D-amino acids;

(ii) a linker consisting of a sequence set forth in SEQ ID NO: 2521; and

(iii) an antisense oligonucleotide consisting of a sequence set forth in SEQ ID NO: 112,

wherein the C-terminus of the CPP is linked to the 3' end of the antisense oligonucleotide via the linker.

The present disclosure further provides a CPP conjugate comprising a sequence set forth in SEQ ID NO: 2504, linked to an antisense oligonucleotide that binds to a targeted portion of the 3' UTR of an *OPA1* gene transcript in a cell and increases transcript stability of an *OPA1* mRNA.

Agents 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 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 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 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 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 ASOs, compositions and methods described herein, ASOs have a 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.

In some examples, ASOs "specifically hybridize" to or are "specific" to a target nucleic acid or a targeted portion of the *OPA1* mRNA 5' UTR. In some examples, ASOs

"specifically hybridize" to or are "specific" to a target nucleic acid or a targeted portion of the *OPA1* 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.

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% 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 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" 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).

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 *OPA1* 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).

In some examples the nucleotide sequences of ASOs described herein are complementary to a targeted portion of *OPA1* mRNA 5' UTR. For example, the ASOs are complementary to a targeted portion of the 5' UTR of an *OPA1* mRNA corresponding to SEQ ID NO:55. In some examples, the ASOs are complementary to a targeted portion of an *OPA1* 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 *OPA1* 5' UTR over the length of the ASO.

In some examples, the nucleotide sequences of ASOs that bind to targeted portions of the 5' UTR of *OPA1* 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 *OPA1* 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 *OPA1* 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 *OPA1* mRNA e.g. the antisense oligonucleotide comprises any one of SEQ ID NOs: 2-54 or SEQ ID NOs: 2491-2499 or SEQ ID NOs: 2505-2517 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 *OPA1* mRNA e.g. the antisense oligonucleotide comprises any one of SEQ ID NOs: 2491-2499 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 *OPA1* mRNA e.g. the antisense oligonucleotide comprises any one of SEQ ID NOs: 2505-2517. 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 *OPA1* 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 *OPA1* mRNA 3' UTR. For example, the ASOs are complementary to a targeted portion of the 3' UTR of an *OPA1* mRNA corresponding to SEQ ID NO: 139. In some examples, the ASOs are complementary to a targeted portion of an *OPA1* 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 *OPA1* 3' UTR over the length of the ASO.

In some examples the nucleotide sequences of ASOs described herein are complementary to a targeted portion of intron 7 of the *OPA1* 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 *OPA1* mRNA e.g. the antisense oligonucleotide comprises any one of SEQ ID NOs: 2505-2517.

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 *OPA1* mRNA e.g. the antisense oligonucleotide comprises any one of SEQ ID NOs: 2505-517.

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 an intron 7 of the *OPA1* 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).

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.

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.

ASO Chemistry and Modifications

The ASOs 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'dimethylaminooxyethoxy, 2'dimethylaminoethoxyethoxy, 2'-guanidinidium, 2'-*O*-guanidinium 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 2'4'-constrained 2'-*O*-methyloxyethyl (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-methylcarbamoylethyl) (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 *OPA1* mRNA 5' UTR. In other examples, two or more ASOs that are complementary to different targeted portions of the *OPA1* 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 *OPA1* pre-mRNA. In other examples, two or more ASOs that are complementary to different targeted portions of intron 7 of the *OPA1* 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 *OPA1* mRNA 3' UTR. In other examples, two or more ASOs that are complementary to different targeted portions of the *OPA1* mRNA 3' UTR.

The present disclosure provides an ASO described herein linked to a cell-penetrating peptide (CPP) comprising a sequence set forth in SEQ ID NO: 2504.

The present disclosure provides an ASO described herein linked to a CPP comprising the sequence RASARRASARRANARRANARRSGGR (SEQ ID NO: 2504).

The present disclosure also provides an ASO described herein linked to a CPP, wherein the CPP consists of the sequence RASARRASARRANARRANARRSGGR (SEQ ID NO: 2504).

In some examples, the CPP is covalently linked to the ASO. In other examples, the CPP is non-covalently linked to the ASO.

The CPP of the present disclosure 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 CPP is linked to the 5' end of the ASO. In other examples, the CPP is linked to the 3' end of the ASO. For example, the C terminus of the CPP is linked to the 3' end of the ASO. In further examples, the CPP 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 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.*

In one example, the ASO is 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 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 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, 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, 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, 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 an ocular condition.

Methods of Treating or Preventing Ocular Conditions

The present disclosure provides, for example, a method of treating, preventing and/or delaying progression of an ocular condition, e.g., ADOA or glaucoma in a subject. The methods described herein include a method for treating, preventing and/or delaying progression of an ocular condition in a subject in need thereof by administering to the subject a therapeutically effective amount of an ASO of the present disclosure or 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 an ocular condition.

In one example, the subject to be treated is suffering from an ocular condition, such as ADOA, glaucoma, geographic atrophy, acute ischemic optic neuritis or acute ischemic optic neuropathy. For example, the subject has been diagnosed as having or suffering from an ocular condition, such as ADOA, glaucoma, geographic atrophy, acute ischemic optic neuritis or acute ischemic optic neuropathy. In one example, the subject suffers from an ocular condition, such as ADOA, glaucoma, geographic atrophy, acute ischemic optic neuritis or acute ischemic optic neuropathy. 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 an ocular condition, such as ADOA, glaucoma, geographic atrophy, acute ischemic optic neuritis or acute ischemic optic neuropathy.

In one example, administration of an ASO or pharmaceutical composition as described herein slows progression of an ocular condition, such as ADOA, glaucoma, geographic atrophy, acute ischemic optic neuritis or acute ischemic optic neuropathy.

In one example, the subject is at risk of developing an ocular condition, such as ADOA, glaucoma, geographic atrophy, acute ischemic optic neuritis or acute ischemic optic neuropathy. Such subjects can be administered the ASOs or pharmaceutical composition as described here to prevent onset of an ocular condition, such as ADOA, glaucoma, geographic atrophy, acute ischemic optic neuritis or acute ischemic optic neuropathy.

As used herein, the term "at risk" means that the subject has an increased chance of developing an ocular condition, compared to a normal individual. Subjects can be identified as at risk of developing an ocular condition using any method known in the art and/or those described herein. For example, the subject may be identified at risk of developing an ocular condition 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 transcript or OPA1 protein in a cell, the method comprising contacting the cell with an ASO or pharmaceutical composition, as disclosed herein, whereby the amount of OPA1 transcript or OPA1 protein in the cell is increased. Also provided herein is a method for increasing the level of OPA1 transcript or 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 transcript or 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 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 transcript or 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 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 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 ASO or 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.

Combination Therapies

The ASOs described herein or 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 an ocular condition, such as ADOA, glaucoma, geographic atrophy, acute ischemic optic neuritis or acute ischemic optic neuropathy. 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.

ASOs 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 ocular condition 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 ocular condition 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.

EXAMPLES

Example 1: ASO design to target exclusion of an *OPA1* NMD exon 7x

ASOs with 24-25 nucleotides in length **(Table 1, SEQ ID NOs: 2-9)** were 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 OPA1 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 *OPA1* 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 *OPA1* transcript is assessed by digital droplet PCR (Qiagen; probe catalogue number: dHsaCPE5043545). OPA1 transcript expression is normalized to *GAPDH, RPL27* and *SCL25A3* transcript levels (Qiagen; probe catalogue number: dHsaCPE5031596, dHsaCPE5036407, dHsaCPE5032926 respectively). PMOs that show induced *OPA1* mRNA levels were further validated for the ability to increase OPA1 protein upregulation using a western blot assay. Further refinement of ASO sequences (**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.

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 μM and 50 μM 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 was subsequently re-validated using a western blot assay.

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 was 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: PMOs targeting intron 7 of *OPA1*

Antisense oligonucleotides with 26-30 nucleotides in length (**SEQ ID NO: 2505-2517**) were designed to target the intronic splice enhancer motifs in intron 7 to mediate exclusion of exon 7x and generate productive *OPA1* transcripts. A single base pair microwalk and engineered mismatch oligos were applied to PMO sequences to identify the most efficacious PMO sequences capable of inducing exclusion of exon 7x. To maximise the coverage of ESE, PMO length was designed and optimised. The efficacy of PMOs in inducing exon 7x exclusion and improving total *OPA1* transcript was assessed using ddPCR and protein assays.

Example 5: Synthesis of peptide-oligonucleotide conjugate

The peptide with **SEQ ID NO: 2504** was synthesised using standard Fmoc solid phase peptide synthesis techniques. Upon cleavage from the supporting resin, the peptide was purified using reverse phase HPLC chromatography, and lyophilized to yield a fluffy white solid.

Conjugation to the phosphorodiamidate morpholino oligomer (PMO) cargo (OPA1 H1A(+10+32)1mm10C>T (**SEQ ID NO: 112**)) was achieved through standard amide conjugation conditions using HATU and DIEA. The carboxylic acid C-terminus of the peptide was conjugated to the secondary amine located at the PMO 3' end. The PPMO conjugate was then purified through strong cation exchange chromatography and desalting to yield the PPMO conjugates used for subsequent *in vitro* and *in vivo* experiments.

Example 6: Evaluation of a peptide-PMO conjugate to target the 5' UTR of OPA1 in iPSC-RGCs derived from ADOA patients

A phosphorodiamidate morpholino oligomer was designed for steric inhibition of the 5' UTR of *OPA1* mRNA (**SEQ ID NO: 112**) and conjugated with the CPP (**SEQ ID NO: 2504)** and utilized to assess OPA1 upregulation. iPSC-RGCs derived from three non-familial ADOA patients, each harbor distinct OPA1 mutation were used in the study. The cell culture conditions involved the systematic differentiation of induced pluripotent stem cells (iPSCs) sourced from ADOA patients into retinal ganglion cells (RGCs) over a minimum period of 35 days. On day 35 of RGC differentiation, iPSC-RGCs were seeded at $7x10^4$ cells/well in a 24-well tissue culture plate with 3 technical replicates for protein assessment. iPSC-RGCs were allowed to continue to mature for at least 10 days prior to PPMO treatment. The CPP-PMO conjugate was incubated with ADOA patient iPSC-RGCs carrying the OPA1 mutations (c.2708_2711delTTAG, c.985-1G>A and c.2608delA) for 5 days. At day 3 post-treatment media top up to 1 mL with 0.5 mL/well N2B27 media (DMEM/F12, Neurobasal media, GlutaMAX, Antibiotic/Antimycotic, N2 supplement and B27 supplement).

To assess of OPA1 protein, cells were harvested on day 5 post-treatment and equal amounts (10 µg) of each protein samples were denatured with 4X laemlli and TCEP for 5 minutes at 95°C. Denatured protein was loaded onto 4-15% Criterion™ TGX™ Precast Midi Protein Gel (18 wells) in 1 x Tris/Glycine/SDS running buffer and run at 150 V for 60 min. Protein was transferred from the gel to nitrocellulose membrane by wet transfer in 25 mM Tris, 192 mM Glycine, 10% methanol at 25 V overnight (18 hours) at 4 °C. Following an overnight transfer, the membrane was stained for total protein using the REVERT® 700 total protein stain. Then, the membrane was blocked with 5%

BSA/TBST for 1 hour. After blocking, the membrane was trimmed between 55 kDa to 200 kDa prior to incubation with rabbit anti-OPA1 antibody (Cell Signaling, 67589S) primary antibody, clone D7C1A, diluted 1:250 in 5% BSA/TBST for 16 hours at 4°C. Then, the membrane was washed 3 times in 1X TBST for 5-10 mins and subsequently incubated with goat anti-rabbit (IRDye® 800CW preadsorbed) secondary antibody diluted 1 in 10,000 in 5% BSA in 1X TBST for 1 hour at room temperature on a rocker. Finally, the membrane was washed 3 times in 1X TBST for 5-10 mins. Protein bands were visualized using an Odyssey Imager and densitometry was performed using Image Studio Lite version 5.2 software (LI-COR Biosciences).

Western blot analysis was used to determine the upregulation of OPA1 protein in CPP-PMO-treated cells. The band intensity of OPA1 expression was normalised to total protein staining (assessed by ImageJ™). The untreated cells served as the baseline with a normalized value of 1. A non-targeting control (NTC) PMO [5'-GTCACGATCGAACAAGGTATCACGA-3'], conjugated with the same CPP, was employed as a negative control. Statistical analysis was conducted using Student's *t*-test. The CPP-PMO targeting the 5' UTR showed a significant upregulation of OPA1 protein in multiple ADOA patient iPSC-RGCs. Patient#1 harboring OPA1 c.985-1G>C mutation (1.3-fold upregulation), Patient #2 harboring OPA1 c.2608delA mutation (1.4-fold upregulation) and Patient#3 harboring OPA1 c.2708_2711delTTAG mutation (1.3-fold upregulation).

Example 7: Evaluation of a peptide-PMO conjugate to target the NMD exon 7x of OPA1 to increase OAP1 levels in iPSC-RGCs derived from ADOA patients

A phosphorodiamidate morpholino oligomer was designed for steric inhibition of the intron 7 of the *OPA1* mRNA **(SEQ ID NO: 2512)** and conjugated with the CPP **(SEQ ID NO: 2504)** to evaluate its potential for enhancing *OPA1* mRNA levels. iPSC-RGCs derived from an ADOA patient carrying OPA1 c.2708_2711delTTAG mutation was studied. The cells were systematically differentiated from iPSCs obtained from the patient into retinal ganglion cells (RGCs) over a minimum period of 35 days. Upon reaching day 35 of RGC differentiation, iPSC-RGCs were seeded at a density of $7x10^4$ cells/well in a 24-well tissue culture plate, with three technical replicates for protein assessment. Following seeding, iPSC-RGCs were allowed to mature for a minimum of 10 days before PPMO treatment. The CPP-PMO conjugate was then incubated with the ADOA patient iPSC-RGCs for 5 days. At day 3 post-treatment media top up to 1 mL with 0.5 mL/well N2B27 media (DMEM/F12, Neurobasal media, GlutaMAX, Antibiotic/Antimycotic, N2 supplement and B27 supplement).

For the assessment of *OPA1* mRNA, total RNA was extracted using the MagMAX™- 96 Total RNA Isolation kit and the level of *OPA1* transcript is assessed by digital droplet PCR (Qiagen; probe catalogue number: dHsaCPE5043545). OPA1 transcript expression is normalized to *GAPDH, RPL27* and *SCL25A3* transcript levels (Qiagen; probe catalogue number: dHsaCPE5031596, dHsaCPE5036407, dHsaCPE5032926 respectively). The results presented in Figure 2 illustrate that the CPP-PMO conjugate induced up to 1.44-fold increase in *OPA1* mRNA levels.

The ability of the CPP-PMO to enhance OPA1 protein levels was further validated in multiple patient lines. Patient iPSC-RGCs were incubated with the CPP-PMO for 5 days, and subsequently, OPA1 protein upregulation was assessed using a western blot assay. For the evaluation of OPA1 protein, cells were harvested on day 5 post-treatment and equal amounts (10 µg) of each protein samples were denatured with 4X laemlli and TCEP for 5 minutes at 95°C. Denatured protein was loaded onto 4-15% Criterion™ TGX™ Precast Midi Protein Gel (18 wells) in 1 x Tris/Glycine/SDS running buffer and run at 150 V for 60 min. Protein was transferred from the gel to nitrocellulose membrane by wet transfer in 25 mM Tris, 192 mM Glycine, 10% methanol at 25 V overnight (18 hours) at 4 °C. Following an overnight transfer, the membrane was stained for total protein using the REVERT® 700 total protein stain. Then, the membrane was blocked with 5% BSA/TBST for 1 hour. After blocking, the membrane was trimmed between 55 kDa to 200 kDa prior to incubation with rabbit anti-OPA1 antibody (Cell Signaling, 67589S) primary antibody, clone D7C1A, diluted 1:250 in 5% BSA/TBST for 16 hours at 4°C. Then, the membrane was washed 3 times in 1X TBST for 5-10 mins and subsequently incubated with goat anti-rabbit (IRDye® 800CW preadsorbed) secondary antibody diluted 1 in 10,000 in 5% BSA in 1X TBST for 1 hour at room temperature on a rocker. Finally, the membrane was washed 3 times in 1X TBST for 5-10 mins. Protein bands were visualized using an Odyssey Imager and densitometry was performed using Image Studio Lite version 5.2 software (LI-COR Biosciences). The findings depicted in Figure 3 indicate a significant increase in OPA1 protein expression induced by the CPP-PMO, irrespective of the mutation.

SEQUENCES

SEQ ID NO: 1: *OPA1* intron 7 (lowercase) and exon7x (uppercase) cDNA sequence (GRCh38/hg38: chr3 193626203-193628616)

gtgatggatggtttaaggggggctaccgatacattcacactaatcagccatttctgccaagatcatgtcacctcaatctgttcatgg
actccaaatacaagaaattaatttgacaaagtgaaaatataaaagatgcatcatataaatatgtaacttttctggagtgggtagtat
aggtaaagccaaaagaaacaaattcaagcagaggaattttggtttctgaaaattaggttgtctgtagggtccctgtatttatactta
gaacaaaattaggaatttctgtttatgtggtccagttattgagtcaccctaagtttgtaggcatcttacctacctacttgctccccaa
gtttttatttctaaaatgaaaagcattgctgtagatgaccagtttacactaaagaataacatttatttatttgttttagctaaagtatatg
gacagggaacattcatattcttgtagaagaaaattattttgacttttgggcaaaagcatgtagttcttatacactttgacaaactcatt
gcgtacatttttcacattaatcaaagtcagcacaaataaattttcaccttggaccacggagggtttgaacactggaaatttgatata
attctggttgctaaagaacaagttctaataaaagcttaagtgtataccaatatgtggctgttggtgcaatcagcaggtccgtaaaa
atatgattttaatggttaggtaatcccacaacggagatcccaaagttcatgtttggaagagacttttgggtcaaagtgaaatcagt
gtaatgaatttaaaattatactctgagatcttgaaatcagctaattatgttacatcttattagctcagaaaagttttgaagttatataca
aatgctagtcaggaaaaaagattcagtcatgtaattcttgtacattctactatttaaatcaaccaatattatagattatgatttagtgc
agtaattctgctggctaaccttatctcatttggtggtggttagtacttcagagtactcaccatagtttcatttatgttttcagcatcactt
cctggtttttctcaattccatggctgtggaatcaattcatatgtatatttagcttcggtgagcaaaaacatagctagaaaaagaaaa
gaagtgagtttcctacctggttaaattaaagtcgatgtgttaagccaaggaggacttcttttgaatggtactttaacaatccctgttc
tgtatactgtgaatatatcatttaaatagcctaataaattggatgcttaggctgagccacctatactttagttttgttatggaaagaag
ggagaggagcaagtatgttcttatatgttacttagaaataagaatgtagctgtagttacacattgttcttaagttttttcgtaagaca
acttgaaatgagtcccataggcctgctatttaacattctaagatatgacttaaggttaatgatgagcttttgaatctgacaattcaag
agatatccataatgaatactgattcattttctacattgctgaaagctaatgttcattttaagcctactttagtagcctttatttgggctta
gagatgttattcctctttctgatatttattgggttatctgtttaaccctttatatctccctttcccgatttgtaaattagagactggcaag
acttttttaccctgagtagagcaccaaacatggcttgtttctgcccacactgtagttaccttgaggggaagtaaatgggactttaaa
agcaatttatgctcttttatagtgaaattatccctcttactatcccgaaagactgttaccttacaatatcctccactcctttcccccctgt
agttactatagagatgacttttcggttcttcactgccataatgatcaaaatcctaattcatgagatttttatcattccaggcatgtgag
gtttacttgatgcataaaaccgcaagtacttttttgttgtttttttaattgtttttctctcttatcttcttgaaagtctaagtagatcatcatttt
tgatgtcttattagtagcaactaataaattttccctgtatcttctcagcaaaagaactcaagcagagacagaagattagaactacc
attggtagttttgcttcctatggatatgttcacatacatagaaatttttacaatgacctttttatatatgtatttcagaatttcagaatggc
ctcaatgccttaataggaagaaatacttgaaatttttaaattagggcttggttttgtgaggagctagtaaaggtttttctctttcagC
TTTAGCTTGTTTCTGCGGAGGATTCCGCTCTTTCTCCATCAGTTTCATAGCCC
TGGAATTGTAGAAAAGCTCTGGTTTCAAGACCATTGATATCCATTTCTGTCA
GG

Table 1: List of antisense oligonucleotide sequences targeting removal of NMD exon 7*x* of an *OPA1* transcript

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
2	hOPA1_Ex7xA(-99-76)	CTGAAATACATATATAAAAAGGTC	17	hOPA1_Ex7xA(-108-79)	GGCATTGAGGCCATTCTGAAATTCTGAAAT
3	hOPA1_Ex7xA(-99-76)1mm	CTGAAATACATATATAAGAAGGTC	18	hOPA1_Ex7xA(-107-78)	AGGCATTGAGGCCATTCTGAAATTCTGAAA
4	hOPA1_Ex7xA(-100-76)1mmA-G	CTGAAATACATATATAAGAAGGTCA	19	hOPA1_Ex7xA(-106-77)	AAGGCATTGAGGCCATTCTGAAATTCTGAA
5	hOPA1_Ex7xA(-106-82)1mmA-G	TACATATATAAGAAGGTCATTGTAA	20	hOPA1_Ex7xA(-105-76)	TAAGGCATTGAGGCCATTCTGAAATTCTGA
6	hOPA1_Ex7xA(-117-93)1mmA-G	AAAGGTCATTGTAAGAATTTCTATG	21	hOPA1_Ex7xA(-104-76)	TAAGGCATTGAGGCCATTCTGAAATTCTG
7	hOPA1_Ex7xA(-127-103)	GTAAAAATTTCTATGTATGTGAACA	22	hOPA1_Ex7xA(-103-76)	TAAGGCATTGAGGCCATTCTGAAATTCT
8	hOPA1_Ex7xA(-139-115)	TCTATGTATGTGAACATATCCATAG	23	hOPA1_Ex7xA(-102-76)	TAAGGCATTGAGGCCATTCTGAAATTC
9	hOPA1_Ex7xA(-187-163)	AATCTTCTGTCTCTGCTTGAGTTCT	24	hOPA1_Ex7xA(-101-76)	TAAGGCATTGAGGCCATTCTGAAATT
10	hOPA1_Ex7xA(-113-84)	TGAGGCCATTCTGAAATTCTGAAATACATA	25	hOPA1_Ex7xA(-100-76)22mmA>G	TAAGGCATTGAGGCCATTCTGGAAT
11	hOPA1_Ex7xA(-113-84)14mmA>G	TGAGGCCATTCTGGAATTCTGAAATACATA	26	hOPA1_Ex7xA(-104-75)	TTAAGGCATTGAGGCCATTCTGAAATTCTG
12	hOPA1_Ex7xA(-112-83)	TTGAGGCCATTCTGAAATTCTGAAATACAT	27	hOPA1_Ex7xA(-103-74)	ATTAAGGCATTGAGGCCATTCTGAAATTCT
13	hOPA1_Ex7xA(-111-82)	ATTGAGGCCATTCTGAAATTCTGAAATACA	28	hOPA1_Ex7xA(-102-73)	TATTAAGGCATTGAGGCCATTCTGAAATTC
14	hOPA1_Ex7xA(-110-81)	CATTGAGGCCATTCTGAAATTCTGAAATAC	29	hOPA1_Ex7xA(-101-72)	CTATTAAGGCATTGAGGCCATTCTGAAATT
15	hOPA1_Ex7xA(-110-81)25mmA>G	CATTGAGGCCATTCTGAAATTCTGGAATAC	30	hOPA1_Ex7xA(-100-71)	CCTATTAAGGCATTGAGGCCATTCTGAAAT
16	hOPA1_Ex7xA(-109-80)	GCATTGAGGCCATTCTGAAATTCTGAAATA	31	hOPA1_Ex7xA(-99-70)	TCCTATTAAGGCATTGAGGCCATTCTGAAA

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)	TTGTAAAAATTTCTATG
33	OPA1 H7XA(-212-196)	TGTCTCTGCTTGAGTTC	45	OPA1 H7XA(-140-124)	TCATTGTAAAAATTTCT
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)	CTAATCTTCTGTCTCTG	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).

GTCCGTTCCCGACGCACTGTGCGCATGCGCTGGTCCTCCGCGGACCGTTCGTGCTGCCCGCCTAGAAAGGGTGAAGTGGTTGTTTCCGTGACGGAC
TGAGTACGGGTGCCTGTCAGGCTCTTGCGGAAGTCCATGCGCCATTGGGAGGGCCTCGGCCGCGGCTCTGTGCCCTTGCTGCTGAGGGCCACTTCC
TGGGTCATTCCTGGACCGGGAGCCGGGCTGGGGCTCACACGGGGGCTCCCGCGTGGCCGTCTCGGCGCCTGCGTGACCTCCCCGCCGGCGGG

Table 3: List of antisense oligonucleotide sequences targeting the 5' UTR of an *OPA1* transcript

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
56	OPA1_H1A(-39-17)	ACCAGGGCATGCGCACAGTGCGT	75	hOPA1_H1A(-10+12)2mmT(C>T)	GGTGGCACGCACGAATGGTCCG
57	OPA1_H1A(-35-14)	AGGACCAGCGCATGCGCACAGT	76	hOPA1_H1A(-6+16)	TCTAGGCGGGCAGCACGAACGG
58	OPA1_H1A(-26-6)1mm	GTCCGCTGAGGACCAGCGCAT	77	hOPA1_H1A(-2+21)	CCTTCTAGGCGGGCAGCACGA
59	OPA1_H1A(-3+18)	TTTCTAGCCGGGCAGCACGAA	78	hOPA1_H1A(+2+25)	TCACCCTTTCTAGGCGGGCAGC
60	OPA1_H1A(+10+32)	CAACCACTTCACCCTTTCTAGGC	79	hOPA1_H1A(+7+31)	AACCACTTCACCCTTTCTAGGCGGG
61	OPA1_H1A(+13+31)	AACCACTTCACCCTTTCTA	80	hOPA1_H1A(+12+36)	GAAACAACCACTTCACCCTTTCTAG
62	OPA1_H1A(+33+57)	ACCCGTACTCAGTCCGTCACGGAA A	81	hOPA1_H1A(+17+41)	TCACGGAAACAACCACTTCACCCTT
63	OPA1_H1A(+33+54)	CGTACTCAGTCCGTCACGGAAA	82	hOPA1_H1A(+22+46)	GTCCGTCACGGAAACAACCACTTC
64	OPA1_H1A(+36+80)	ACTTCCGCAAGAGCCTGACAGGCA C	83	hOPA1_H1A(+27+51)	ACTCAGTCCGTCACGGAAACAACC A
65	hOPA1_H1A(+63+82)	GGACTTCCGCAAGAGCCTGA	84	hOPA1_H1A(+38+62)	CAGGCACCCGTACTCAGTCCGTCAC
66	OPA1_H1A(+68+92)	CAATGGCGCATGGACTTCCGCAAG A	85	hOPA1_H1A(+44+67)	CCTGACAGGCACCCGTACTCAGTCC
67	OPA1_H1A(+78+98)	CTCCCAATGGCGCATGGACT	86	hOPA1_H1A(+50+71)	GAGCCTGACAGGCACCCGTACTC
68	OPA1_H1A(+128+146)1mm	CCCAGGAAGTGGTCCTCAG	87	hOPA1_H1A(+56+75)	GCAAGAGCCTGACAGGCACCCG
69	OPA1_H1A(+148+166)	GGCTCCCGGTCCAGGAATG	88	hOPA1_H1A(+120+141)	AAGTGGCCCTCAGCAGCAAGGG
70	OPA1_H1A(+200+218)2mm	TCACGCAGGTGCTGAGACG	89	hOPA1_H1A(+125+148)2mmT(C>T)	ACCTAGGAAGTGGTCCTCAGCAGC
71	hOPA1_H1A(-30-9)2mmT(C>T)	CGTGGAGGACCAGTGCATGCGC	90	hOPA1_H1A(+129+154)	GGAATGACCCAGGAAGTGGCCCTC A
72	hOPA1_H1A(-22-2)	AACGGTCCGCGGAGGACCAGC	91	hOPA1_H1A(+134+159)	GTCCAGGAATGACCCAGGAAGTGG C
73	hOPA1_H1A(-18+4)	GCACGAACGGTCCGCGGAGGAC	92	hOPA1_H1A(+42+66)	CTGACAGGCACCCGTACTCAGTCC G
74	hOPA1_H1A(-14+8)2mmT(C>T)	GGCAGTACGAACGGTCTGCGGA	93	hOPA1_H1A(+44+68)	GCCTGACAGGCACCCGTACTCAGT C
94	hOPA1_H1A(+45+69)	AGCCTGACAGGCACCCGTACTCAG T	112	OPA1 H1A(+10+32)1mm10C>T	CAACCACTTTACCCTTTCTAGGC

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
95	hOPA1_H1A(+46+70)	GAGCCTGACAGGCACCCGTACTCA G	113	OPA1 H1A(+10+32)1mm12C>T	CAACCACTTCATCCTTTCTAGGC
96	hOPA1_H1A(+47+71)	AGAGCCTGACAGGCACCCGTACTC A	114	hOPA1_H1A(+63+80)	ACTTCCGCAAGAGCCTGA
97	hOPA1_H1A(+48+72)	AAGAGCCTGACAGGCACCCGTACT C	115	hOPA1_H1A(+79+96)	TCCCAATGGCGCATGGAC
98	hOPA1_H1A(+49+73)	CAAGAGCCTGACAGGCACCCGTAC T	116	hOPA1_H1A(-50-21)	GCGCATGCGCACAGTGCGTCGGGA ACCGAC
99	hOPA1_H1A(+50+74)	GCAAGAGCCTGACAGGCACCCGTA C	117	hOPA1_H1A(-49-20)	AGCGCATGCGCACAGTGCGTCGGG AACGGA
100	hOPA1_H1A(+42+66)2mmC>T	CTGACAGGCATTCGTACTCAGTCC G	118	hOPA1_H1A(-48-19)	CAGCGCATGCGCACAGTGCGTCGG GAACGG
101	hOPA1_H1A(+44+68)2mmC>T	GCCTGACAGGCACTTGTACTCAGT C	119	hOPA1_H1A(-47-18)	CCAGCGCATGCGCACAGTGCGTCG GGAACG
102	hOPA1_H1A(+43+69)2mmC>T	AGCCTGACAGGCATTCGTACTCAG T	120	hOPA1_H1A(-46-17)	ACCAGCGCATGCGCACAGTGCGTC GGGAAC
103	hOPA1_H1A(+46+70)2mmC>T	GAGCCTGACAGGCACCTGTACTCA G	121	hOPA1_H1A(-45-16)	GACCAGCGCATGCGCACAGTGCGT CGGGAA
104	hOPA1_H1A(+47+71)2mmC>T	AGAGCCTGACAGGCACTCGTACTC A	122	hOPA1_H1A(-44-15)	GGACCAGCGCATGCGCACAGTGCG TCGGGA
105	hOPA1_H1A(+48+72)2mmC>T	AAGAGCCTGACAGGCACTCGTACT C	123	hOPA1_H1A(-43-14)	AGGACCAGCGCATGCGCACAGTGC GTCGGG
106	hOPA1_H1A(+49+73)2mmC>T	CAAGAGCCTGACAGGCATCCGTAC T	124	hOPA1_H1A(-42-13)	GAGGACCAGCGCATGCGCACAGTG CGTCGG
107	hOPA1_H1A(+50+74)2mmC>T	GCAAGAGCCTGACAGGCATCCGTA C	125	hOPA1_H1A(-41-12)	GGAGGACCAGCGCATGCGCACAGT GCGTCG
108	OPA1 H1A(+10+34)	AACAACCACTTCACCCTTTCTAGG C	126	hOPA1_H1A(-40-11)	CGGAGGACCAGCGCATGCGCACAG TGCGTC
109	OPA1 H1A(+10+33)	ACAACCACTTCACCCTTTCTAGGC	127	hOPA1_H1A(-2+28)mm	CACTTTACCCTTTCTAGGCGGGCAG CACGA
110	OPA1 H1A(+9+33)	ACAACCACTTCACCCTTTCTAGGC G	128	hOPA1_H1A(-1+29)mm	CCACTTTACCCTTTCTAGGCGGGCA GCACG
111	OPA1 H1A(+11+35)	AAACAACCACTTCACCCTTTCTAG G	129	hOPA1_H1A(+1+30)mm	ACCACTTTACCCTTTCTAGGCGGGC AGCAC
130	hOPA1_H1A(+2+31)mm	AACCACTTTACCCTTTCTAGGCGG GCAGCA	134	hOPA1_H1A(+6+32)mm	CAACCACTTTACCCTTTCTAGGCGG GC
131	hOPA1_H1A(+3+32)mm	CAACCACTTTACCCTTTCTAGGCG GGCAGC	135	hOPA1_H1A(+7+32)mm	CAACCACTTTACCCTTTCTAGGCGG G

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
132	hOPA1_H1A(+4+32)mm	CAACCACTTTACCCTTTCTAGGCG GGCAG	136	hOPA1_H1A(+8+32)mm	CAACCACTTTACCCTTTCTAGGCGG
133	hOPA1_H1A(+5+32)mm	CAACCACTTTACCCTTTCTAGGCG GGCA	137	hOPA1_H1A(+9+32)mm	CAACCACTTTACCCTTTCTAGGCG
			138	hOPA1_H1A(+10+34)mm	AACAACCACTTTACCCTTTCTAGGC

SEQ ID:139: cDNA sequence of the 3' UTR located within exon 30 of an *OPA1* transcript (GRCh38/hg38: chr3: 193694606-193697811)

GTCCGTTCCCCGACGCACTGTGCGCATGCGCTGGTCCTCCGCGGACCGTTCGTGCTGCCCCGCCTAGAAAGGGTGAAGAATCGTACTCATAATCAGCT

CTGCATACATCTGAAGAACAAAAACATCAACGTCTTTTTCTTCTGCTGTTCCACCTTTCTAAACATACAATAAAGTCATGGGA

TAAAAATAATCGATGTATGTTACCGGGCGCTTTAACCATCAGCTGCCTCTCGAATGGAAGAACAGTGGTAATGGATTAACATCCTATTTGTTGTAC

TAAAGTGACAAATCGGAATAATATAATTGGTATGGCCATTAGGTTCAGTCCTTGAAGATAAGAAACTTGTTCTCTGTTTGTTCTTATTTGTGGTG

GCACTCGTTTAATGGATTAACTGAGGTTGCTCAATGTTCAGTTTCTTTTCCAGAAATACAATGCTAGGTGTTTGAAATAAAACTTATATAGCAATT

GTTTAAAGTTATCAATTGTATATAAAATCACAGTAGCCTGCTAAATCATTGTATGTCTGTAGTATTCTATTCCCAGAAACTATTTGACCATGATA

ATTCAGTTTATATTCACCACATGAAAGAAAAATGGGGTAACAGAAGAACCCTTAAAACAGGTTAATTTGGATTGTAACGTTCAGTGAAAGAAATTT

CAACCCTTCATAGCCAGCGAAGAAATTTGCCTTGGAAGCCAAGTCAGTACCAGCTTACCTATTTGATTCAGTTGCTGTTTTCTCACTCTCTATATCC

ATTTGAAATTGATTTATTTTAGATGTTGTATACTTACGTTAATAGTGGTTTTTCTCCTGTTGACAGAGCCACCGGATTATGACACA

GGATGAGGAAGATTAAGGATAATCAATTTCATTTAGAATATTATCAAACATTTCAACTAGGTATCAGAAAAAGGCTTTCTTTCATAAG

ACTATTTTAAATAGAAATTATTTCAACAATTAAGTTGTGACCATCCCCCTCTCAGCTGAATAAAGAAAAATTTAGTTCAATTTATTGCAATTT

AATTACAATACTACCTTCACAACATTTTCATGTGTTTTAAATATTTTTTAATTGGCTAAAGGACATTCAAGCAAAGAAATGCTTTCTTTACTT

AAAATGTCTATCTCATTTGCTGCCTTTTTCACTAAGCCTTTACTTTGTTAATAAAAGTGTCCATTGTGTGATGTTTTTTGATTTTACAGTTTGCTAAATC

TTATTTTCTTGGAGTTGCTTTTTTGGTAACAGCCCCATTGCTACTCCCCATTTTATTGTTTTACATCAATGCATGCTTCGTTGTGATCCCTCAAGATGT

AACACTTGGTATGCTCCGGTTGAGGATATGAAAAAATACTTCCGAAACCAGGAATTCAATGTATGTTTGTTTTATACTGTTTGATAAGAAAAGTAGG

TCCAGCCTTAAGCAGCACAGATGCGCTGGTAGATGCATAGTCAGGAACTTTTTTTATTTCTTTTAGGTCTAGGGACAGGAGTGAATAGAAAGGGA

GGAGAGCTCTATTATGTTCTATACACAGATTAGGAGATGACCTTACTGGGTACACCCCTCTAACCAGTGCTTACAGGTTAATGCATGTTAATGAAT

ATTTTTGCAGTTGTAAAGCATAACAACTACACACATCTATTTCTAAAGAATAAAACAGGACCATATTTATTTACTTCTGTCAACTATAGAAA

GAAAGACCTTCAGCTGTATTTCCACAGATTTCTCCCAAGGAAAAGGCTAATATTAGTCACTACTGTTATCACATCCCTTTGTATAAGTTTTAAAAA

GAGATGGAGGGAGATCTTCATTCTTTGAGGAGATCAGTATTTGTAACGTATGTGAATAGATGATAACAATTAATATTACTAAAAGTCCCACATGA

GAGTCCTGACGCCCTCTCCATGCCCCACAGTAATGTGGCTTCTTTCATGGGTTTTTTTTTCTTCTTTTTAGCTGATCTCATCCTAAGCATGCTTTATTT

TTCCTTGAAAGCTAGGTATTTATCAACTGCAGATGTTATTGAAAGAAAATAAAAATTCAGTCTCAAGAGTAAACCCTGTGTCTTGTGGTCTGTAGTTC

AAAAGTCAGAAATGATTCTAATTTAAACAAAAAAGATACTAAATATACAGAAGTTAAATTCGAACTAGCCACAGAATCATTTGTTTTTATGTCAGA

ATTTGCAAAGAGTGGAGTGGACAAAGCTCTGTATGGAAGACTGAACAACTGTAAATAGATGATATCCAAACTTAATTTGGCTAGGACTTCAATTT

TAAAAATCAGTGTACCTAGGCAGTGCACAGCACGAAATAAGTGGCCCTTGCAGCTTCCCCGTTTAACCCACTGTGCTATAGTTGCGGGTGGAACA

GTCAACCTTTTCTAGTAGTTTATGATATTGCCCTCTTTGTATTCCCATTTTCTACAGTTTTTTTCCGCAGACTTCTTTCTGCAAATTATTCAGCCTCCAAA

TGCAAATTGAATGATATAAAAATAAGTAGGGAACATGGCAGAGAGTGGTGCTTCCCAGCCTCACAATGTGGGAATTTGACATAGGATGAGAGTCA

GAGTATAGGTTTAAAAGATAAAATCTTTAGTTAATAATTTGTATTTATTTCTAGATGTATGTATCTGAGGAAAGAAATCTGGTATTTTTGCTT

TCCAATAAAGGGGATCAAAGTAATGGTTTTTCTCTCAGTTCTCTAAGCTGGTCTATGTTATAGCTCTAGCAGTATGGAAATGTGCTTTTAAAATATGC

TTACCTTTTGAATGATCATGGCTATATGTTGTTGAGATATTTGAAACTTACCTTGTTTTCACTTGTGCACTGTGAATGAACTTTGTATTATTTTTTTA

AAACCTTCACATTACGTGTAGATATTATTTTGCCTGAGCTTGATCAAAGGTCATTTGTGTAGATGAGTAATTAAAAAAATATTTAA

ATCACATTATAATTCTATTATTGGAGAGCATCTTTTAAATTTTTTTTCTGTTTTTAACGAGGGAAAGAGAAACCTGTATACCTAGGGTCATTATTTGAC

CCCATAGTATAACCAGATTCATGGTCTAACAAGCTCTCAGTGTGGCTTTTCTCTGAATGCTTGAATTTCACATGCCTTGCATTTCACAGTTGTACTC

CATGGTCAACCGGTGCTTTTTTTCACATCGTGGTACTTGTCAAAACATTTTGTTATTTTCCTTGGTAAAATATATAAAAAAGGTTTTCTAATTTCA

Table 4. List of antisense oligonucleotide sequences with 25 nucleotides in length that target the 3' UTR of an *OPA1* transcript.

SEQ	ASO Coordinates	Sequence 5'>3'	SEQ	ASO Coordinates	Sequence 5'>3'
140	OPA1 H30:31 3UTR(+1+25)	AGCTGATTATGAGTACGATTTTAAT	156	OPA1 H31 3UTR(+49+73)	GAGGCTGGACAAAAGACGTTGATGT
141	OPA1 H30:31 3UTR(+4+28)	CAGAGCTGATTATGAGTACGATTTT	157	OPA1 H31 3UTR(+52+76)	AAAGAGGCTGGACAAAAGACGTTGA
142	OPA1 H31 3UTR(+7+31)	ATGCAGAGCTGATTATGAGTACGAT	158	OPA1 H31 3UTR(+55+79)	GAAAAAGAGGCTGGACAAAAGACGT
143	OPA1 H31 3UTR(+10+34)	TGTATGCAGAGCTGATTATGAGTAC	159	OPA1 H31 3UTR(+58+82)	GAAGAAAAAGAGGCTGGACAAAAGA
144	OPA1 H31 3UTR(+13+37)	AGATGTATGCAGAGCTGATTATGAG	160	OPA1 H31 3UTR(+61+85)	GCAGAAGAAAAAGAGGCTGGACAAA
145	OPA1 H31 3UTR(+16+40)	TTCAGATGTATGCAGAGCTGATTAT	161	OPA1 H31 3UTR(+64+88)	ACAGCAGAAGAAAAAGAGGCTGGAC
146	OPA1 H31 3UTR(+19+43)	TTCTTCAGATGTATGCAGAGCTGAT	162	OPA1 H31 3UTR(+67+91)	GGAACAGCAGAAGAAAAAGAGGCTG
147	OPA1 H31 3UTR(+22+46)	TTGTTCTTCAGATGTATGCAGAGCT	163	OPA1 H31 3UTR(+70+94)	GGTGGAACAGCAGAAGAAAAAGAGG
148	OPA1 H31 3UTR(+25+49)	TTTTTGTTCTTCAGATGTATGCAGA	164	OPA1 H31 3UTR(+73+97)	AAAGGTGGAACAGCAGAAGAAAAAG
149	OPA1 H31 3UTR(+28+52)	ATGTTTTTGTTCTTCAGATGTATGC	165	OPA1 H31 3UTR(+76+100)	TAGAAAGGTGGAACAGCAGAAGAAA
150	OPA1 H31 3UTR(+31+55)	TTGATGTTTTTGTTCTTCAGATGTA	166	OPA1 H31 3UTR(+79+103)	GTTTAGAAAGGTGGAACAGCAGAAG
151	OPA1 H31 3UTR(+34+58)	ACGTTGATGTTTTTGTTCTTCAGAT	167	OPA1 H31 3UTR(+82+106)	TATGTTTAGAAAGGTGGAACAGCAG
152	OPA1 H31 3UTR(+37+61)	AAGACGTTGATGTTTTTGTTCTTCA	168	OPA1 H31 3UTR(+85+109)	TTGTATGTTTAGAAAGGTGGAACAG
153	OPA1 H31 3UTR(+40+64)	CAAAAGACGTTGATGTTTTTGTTCT	169	OPA1 H31 3UTR(+88+112)	TTATTGTATGTTTAGAAAGGTGGAA
154	OPA1 H31 3UTR(+43+67)	GGACAAAAGACGTTGATGTTTTTGT	170	OPA1 H31 3UTR(+91+115)	ACTTTATTGTATGTTTAGAAAGGTG
155	OPA1 H31 3UTR(+46+70)	GCTGGACAAAAGACGTTGATGTTTT			
171	OPA1 H31 3UTR(+94+118)	ATGACTTTATTGTATGTTTAGAAAG	189	OPA1 H31 3UTR(+148+172)	GAGAGGCAGCTGATGGTTAAAGCGC

SEQ	ASO Coordinates	Sequence 5'>3'	SEQ	ASO Coordinates	Sequence 5'>3'
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)	CCATTCGAGAGGCAGCTGATGGTTA
174	OPA1 H31 3UTR(+103+127)	TTTTATCCCATGACTTTATTGTATG	192	OPA1 H31 3UTR(+157+181)	CTTCCATTCGAGAGGCAGCTGATGG
175	OPA1 H31 3UTR(+106+130)	TATTTTTATCCCATGACTTTATTGT	193	OPA1 H31 3UTR(+160+184)	GTTCTTCCATTCGAGAGGCAGCTGA
176	OPA1 H31 3UTR(+109+133)	GATTATTTTTATCCCATGACTTTAT	194	OPA1 H31 3UTR(+163+187)	ACTGTTCTTCCATTCGAGAGGCAGC
177	OPA1 H31 3UTR(+112+136)	ATCGATTATTTTTATCCCATGACTT	195	OPA1 H31 3UTR(+166+190)	ACCACTGTTCTTCCATTCGAGAGGC
178	OPA1 H31 3UTR(+115+139)	TACATCGATTATTTTTATCCCATGA	196	OPA1 H31 3UTR(+169+193)	ATTACCACTGTTCTTCCATTCGAGA
179	OPA1 H31 3UTR(+118+142)	ACATACATCGATTATTTTTATCCCA	197	OPA1 H31 3UTR(+172+196)	TCCATTACCACTGTTCTTCCATTCG
180	OPA1 H31 3UTR(+121+145)	GTAACATACATCGATTATTTTTATC	198	OPA1 H31 3UTR(+175+199)	TAATCCATTACCACTGTTCTTCCAT
181	OPA1 H31 3UTR(+124+148)	CCCGTAACATACATCGATTATTTTT	199	OPA1 H31 3UTR(+178+202)	TGTTAATCCATTACCACTGTTCTTC
182	OPA1 H31 3UTR(+127+151)	GCGCCCGTAACATACATCGATTATT	200	OPA1 H31 3UTR(+181+205)	GGATGTTAATCCATTACCACTGTTC
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)	AAAATAGGATGTTAATCCATTACCA
185	OPA1 H31 3UTR(+136+160)	ATGGTTAAAGCGCCCGTAACATACA	203	OPA1 H31 3UTR(+190+214)	AACAAAATAGGATGTTAATCCATTA
186	OPA1 H31 3UTR(+139+163)	CTGATGGTTAAAGCGCCCGTAACAT	204	OPA1 H31 3UTR(+193+217)	TACAACAAAATAGGATGTTAATCCA
187	OPA1 H31 3UTR(+142+166)	CAGCTGATGGTTAAAGCGCCCGTAA	205	OPA1 H31 3UTR(+196+220)	TAGTACAACAAAATAGGATGTTAAT
188	OPA1 H31 3UTR(+145+169)	AGGCAGCTGATGGTTAAAGCGCCCG	206	OPA1 H31 3UTR(+199+223)	CTTTAGTACAACAAAATAGGATGTT
207	OPA1 H31 3UTR(+202+226)	TCACTTTAGTACAACAAAATAGGAT	225	OPA1 H31 3UTR(+256+280)	CTTATCTTCAAGGACTGAACCTAAT

SEQ	ASO Coordinates	Sequence 5'>3'	SEQ	ASO Coordinates	Sequence 5'>3'
208	OPA1 H31 3UTR(+205+229)	TTGTCACTTTAGTACAACAAAATAG	226	OPA1 H31 3UTR(+259+283)	TTTCTTATCTTCAAGGACTGAACCT
209	OPA1 H31 3UTR(+208+232)	GATTTGTCACTTTAGTACAACAAAA	227	OPA1 H31 3UTR(+262+286)	AAGTTTCTTATCTTCAAGGACTGAA
210	OPA1 H31 3UTR(+211+235)	TCCGATTTGTCACTTTAGTACAACA	228	OPA1 H31 3UTR(+265+289)	AACAAGTTTCTTATCTTCAAGGACT
211	OPA1 H31 3UTR(+214+238)	TATTCCGATTTGTCACTTTAGTACA	229	OPA1 H31 3UTR(+268+292)	GAGAACAAGTTTCTTATCTTCAAGG
212	OPA1 H31 3UTR(+217+241)	TATTATTCCGATTTGTCACTTTAGT	230	OPA1 H31 3UTR(+271+295)	ACAGAGAACAAGTTTCTTATCTTCA
213	OPA1 H31 3UTR(+220+244)	TTATATTATTCCGATTTGTCACTTT	231	OPA1 H31 3UTR(+274+298)	CAAACAGAGAACAAGTTTCTTATCT
214	OPA1 H31 3UTR(+223+247)	CAATTATATTATTCCGATTTGTCAC	232	OPA1 H31 3UTR(+277+301)	CAACAAACAGAGAACAAGTTTCTTA
215	OPA1 H31 3UTR(+226+250)	TACCAATTATATTATTATTCCGATTTGT	233	OPA1 H31 3UTR(+280+304)	AGACAACAAACAGAGAACAAGTTTC
216	OPA1 H31 3UTR(+229+253)	CCATACCAATTATATTATTATTCCGATT	234	OPA1 H31 3UTR(+283+307)	ATAAGACAACAAACAGAGAACAAGT
217	OPA1 H31 3UTR(+232+256)	TGGCCATACCAATTATATTATTATTCCG	235	OPA1 H31 3UTR(+286+310)	CAAATAAGACAACAAACAGAGAACA
218	OPA1 H31 3UTR(+235+259)	TAATGGCCATACCAATTATATTATTATT	236	OPA1 H31 3UTR(+289+313)	CCACAAATAAGACAACAAACAGAGA
219	OPA1 H31 3UTR(+238+262)	ACCTAATGGCCATACCAATTATATTATT	237	OPA1 H31 3UTR(+292+316)	CCACCACAAATAAGACAACAAACAG
220	OPA1 H31 3UTR(+241+265)	TGAACCTAATGGCCATACCAATTATT	238	OPA1 H31 3UTR(+295+319)	GTGCCACCACAAATAAGACAACAAA
221	OPA1 H31 3UTR(+244+268)	GACTGAACCTAATGGCCATACCAATT	239	OPA1 H31 3UTR(+298+322)	CGAGTGCCACCACAAATAAGACAAC
222	OPA1 H31 3UTR(+247+271)	AAGGACTGAACCTAATGGCCATACC	240	OPA1 H31 3UTR(+301+325)	AAACGAGTGCCACCACAAATAAGAC
223	OPA1 H31 3UTR(+250+274)	TTCAAGGACTGAACCTAATGGCCAT	241	OPA1 H31 3UTR(+304+328)	ATTAAACGAGTGCCACCACAAATAA
224	OPA1 H31 3UTR(+253+277)	ATCTTCAAGGACTGAACCTAATGGC	242	OPA1 H31 3UTR(+307+331)	TCCATTAAACGAGTGCCACCACAAA
243	OPA1 H31 3UTR(+310+334)	TAATCCATTAAACGAGTGCCACCAC	261	OPA1 H31 3UTR(+364+388)	AAACACCTAGCATTGTATTTCTGGA

SEQ	ASO Coordinates	Sequence 5'>3'	SEQ	ASO Coordinates	Sequence 5'>3'
244	OPA1 H31 3UTR(+313+337)	AGTTAATCCATTAAACGAGTGCCAC	262	OPA1 H31 3UTR(+367+391)	TCAAAACACCTAGCATTGTATTTCT
245	OPA1 H31 3UTR(+316+340)	CTCAGTTAATCCATTAAACGAGTGC	263	OPA1 H31 3UTR(+370+394)	ATTTCAAAACACCTAGCATTGTATT
246	OPA1 H31 3UTR(+319+343)	AACCTCAGTTAATCCATTAAACGAG	264	OPA1 H31 3UTR(+373+397)	TTTATTTCAAAACACCTAGCATTGT
247	OPA1 H31 3UTR(+322+346)	AGCAACCTCAGTTAATCCATTAAAC	265	OPA1 H31 3UTR(+376+400)	AGTTTTATTTCAAAACACCTAGCAT
248	OPA1 H31 3UTR(+325+349)	TTGAGCAACCTCAGTTAATCCATTA	266	OPA1 H31 3UTR(+379+403)	ATAAGTTTTATTTCAAAACACCTAG
249	OPA1 H31 3UTR(+328+352)	ACATTGAGCAACCTCAGTTAATCCA	267	OPA1 H31 3UTR(+382+406)	TATATAAGTTTTATTTCAAAACACC
250	OPA1 H31 3UTR(+331+355)	TGAACATTGAGCAACCTCAGTTAAT	268	OPA1 H31 3UTR(+385+409)	TGCTATATAAGTTTTATTTCAAAAC
251	OPA1 H31 3UTR(+334+358)	AACTGAACATTGAGCAACCTCAGTT	269	OPA1 H31 3UTR(+388+412)	AATTGCTATATAAGTTTTATTTCAA
252	OPA1 H31 3UTR(+337+361)	AGAAACTGAACATTGAGCAACCTCA	270	OPA1 H31 3UTR(+391+415)	AACAATTGCTATATAAGTTTTATTT
253	OPA1 H31 3UTR(+340+364)	AAAAGAAACTGAACATTGAGCAACC	271	OPA1 H31 3UTR(+394+418)	TTAAACAATTGCTATATAAGTTTTA
254	OPA1 H31 3UTR(+343+367)	TGGAAAAGAAACTGAACATTGAGCA	272	OPA1 H31 3UTR(+397+421)	ACTTTAAACAATTGCTATATAAGTT
255	OPA1 H31 3UTR(+346+370)	TTCTGGAAAAGAAACTGAACATTGA	273	OPA1 H31 3UTR(+400+424)	ATAACTTTAAACAATTGCTATATAA
256	OPA1 H31 3UTR(+349+373)	TATTTCTGGAAAAGAAACTGAACAT	274	OPA1 H31 3UTR(+403+427)	TTGATAACTTTAAACAATTGCTATA
257	OPA1 H31 3UTR(+352+376)	TTGTATTTCTGGAAAAGAAACTGAA	275	OPA1 H31 3UTR(+406+430)	CAATTGATAACTTTAAACAATTGCT
258	OPA1 H31 3UTR(+355+379)	GCATTGTATTTCTGGAAAAGAAACT	276	OPA1 H31 3UTR(+409+433)	ATACAATTGATAACTTTAAACAATT
259	OPA1 H31 3UTR(+358+382)	CTAGCATTGTATTTCTGGAAAAGAA	277	OPA1 H31 3UTR(+412+436)	TATATACAATTGATAACTTTAAACA
260	OPA1 H31 3UTR(+361+385)	CACCTAGCATTGTATTTCTGGAAAA	278	OPA1 H31 3UTR(+415+439)	TTTTATATACAATTGATAACTTTAA
279	OPA1 H31 3UTR(+418+442)	TGATTTTATATACAATTGATAACTT	297	OPA1 H31 3UTR(+472+496)	TAGTTTCTGGGAATAGAATACTACA

SEQ	ASO Coordinates	Sequence 5'>3'	SEQ	ASO Coordinates	Sequence 5'>3'
280	OPA1 H31 3UTR(+421+445)	CTGTGATTTTTATATACAATTGATAA	298	OPA1 H31 3UTR(+475+499)	AAATAGTTTCTGGGAATAGAATACT
281	OPA1 H31 3UTR(+424+448)	CTACTGTGATTTTTATATACAATTGA	299	OPA1 H31 3UTR(+478+502)	GTCAAATAGTTTCTGGGAATAGAAT
282	OPA1 H31 3UTR(+427+451)	AGGCTACTGTGATTTTTATATACAAT	300	OPA1 H31 3UTR(+481+505)	ATGGTCAAATAGTTTCTGGGAATAG
283	OPA1 H31 3UTR(+430+454)	AGCAGGCTACTGTGATTTTTATATAC	301	OPA1 H31 3UTR(+484+508)	ATCATGGTCAAATAGTTTCTGGGAA
284	OPA1 H31 3UTR(+433+457)	TTTAGCAGGCTACTGTGATTTTTATA	302	OPA1 H31 3UTR(+487+511)	ATTATCATGGTCAAATAGTTTCTGG
285	OPA1 H31 3UTR(+436+460)	TGATTTAGCAGGCTACTGTGATTTT	303	OPA1 H31 3UTR(+490+514)	TGAATTATCATGGTCAAATAGTTTC
286	OPA1 H31 3UTR(+439+463)	CAATGATTTAGCAGGCTACTGTGAT	304	OPA1 H31 3UTR(+493+517)	AACTGAATTATCATGGTCAAATAGT
287	OPA1 H31 3UTR(+442+466)	ATACAATGATTTAGCAGGCTACTGT	305	OPA1 H31 3UTR(+496+520)	ATAAACTGAATTATCATGGTCAAAT
288	OPA1 H31 3UTR(+445+469)	CACATACAATGATTTAGCAGGCTAC	306	OPA1 H31 3UTR(+499+523)	AATATAAACTGAATTATCATGGTCA
289	OPA1 H31 3UTR(+448+472)	AGACACATACAATGATTTAGCAGGC	307	OPA1 H31 3UTR(+502+526)	GTGAATATAAACTGAATTATCATGG
290	OPA1 H31 3UTR(+451+475)	TACAGACACATACAATGATTTAGCA	308	OPA1 H31 3UTR(+505+529)	GTGGTGAATATAAACTGAATTATCA
291	OPA1 H31 3UTR(+454+478)	TACTACAGACACATACAATGATTTA	309	OPA1 H31 3UTR(+508+532)	CATGTGGTGAATATAAACTGAATTA
292	OPA1 H31 3UTR(+457+481)	GAATACTACAGACACATACAATGAT	310	OPA1 H31 3UTR(+511+535)	TTTCATGTGGTGAATATAAACTGAA
293	OPA1 H31 3UTR(+460+484)	ATAGAATACTACAGACACATACAAT	311	OPA1 H31 3UTR(+514+538)	TTCTTTCATGTGGTGAATATAAACT
294	OPA1 H31 3UTR(+463+487)	GGAATAGAATACTACAGACACATAC	312	OPA1 H31 3UTR(+517+541)	TTTTTCTTTCATGTGGTGAATATAA
295	OPA1 H31 3UTR(+466+490)	CTGGGAATAGAATACTACAGACACA	313	OPA1 H31 3UTR(+520+544)	CCATTTTTCTTTCATGTGGTGAATA
296	OPA1 H31 3UTR(+469+493)	TTTCTGGGAATAGAATACTACAGAC	314	OPA1 H31 3UTR(+523+547)	TACCCATTTTTCTTTCATGTGGTGA
315	OPA1 H31 3UTR(+526+550)	TGTTACCCATTTTTCTTTCATGTGG	333	OPA1 H31 3UTR(+580+604)	AAATTTCTTTCACTGAACGTTACAA

SEQ	ASO Coordinates	Sequence 5'>3'	SEQ	ASO Coordinates	Sequence 5'>3'
316	OPA1 H31 3UTR(+529+553)	TTCTGTTACCCATTTTTCTTTCATG	334	OPA1 H31 3UTR(+583+607)	TTGAAATTTCTTTCACTGAACGTTA
317	OPA1 H31 3UTR(+532+556)	TTCTTCTGTTACCCATTTTTCTTTC	335	OPA1 H31 3UTR(+586+610)	GGGTTGAAATTTCTTTCACTGAACG
318	OPA1 H31 3UTR(+535+559)	GGGTTCTTCTGTTACCCATTTTTCT	336	OPA1 H31 3UTR(+589+613)	GAAGGGTTGAAATTTCTTTCACTGA
319	OPA1 H31 3UTR(+538+562)	TAAGGGTTCTTCTGTTACCCATTTT	337	OPA1 H31 3UTR(+592+616)	TATGAAGGGTTGAAATTTCTTTCAC
320	OPA1 H31 3UTR(+541+565)	TTTTAAGGGTTCTTCTGTTACCCAT	338	OPA1 H31 3UTR(+595+619)	GGCTATGAAGGGTTGAAATTTCTTT
321	OPA1 H31 3UTR(+544+568)	CTGTTTTAAGGGTTCTTCTGTTACC	339	OPA1 H31 3UTR(+598+622)	GCTGGCTATGAAGGGTTGAAATTTC
322	OPA1 H31 3UTR(+547+571)	AACCTGTTTTAAGGGTTCTTCTGTT	340	OPA1 H31 3UTR(+601+625)	TTCGCTGGCTATGAAGGGTTGAAAT
323	OPA1 H31 3UTR(+550+574)	ATTAACCTGTTTTAAGGGTTCTTCT	341	OPA1 H31 3UTR(+604+628)	TTCTTCGCTGGCTATGAAGGGTTGA
324	OPA1 H31 3UTR(+553+577)	CAAATTAACCTGTTTTAAGGGTTCT	342	OPA1 H31 3UTR(+607+631)	AATTTCTTCGCTGGCTATGAAGGGT
325	OPA1 H31 3UTR(+556+580)	ATCCAAATTAACCTGTTTTAAGGGT	343	OPA1 H31 3UTR(+610+634)	GCAAATTTCTTCGCTGGCTATGAAG
326	OPA1 H31 3UTR(+559+583)	ACAATCCAAATTAACCTGTTTTAAG	344	OPA1 H31 3UTR(+613+637)	AAGGCAAATTTCTTCGCTGGCTATG
327	OPA1 H31 3UTR(+562+586)	GTTACAATCCAAATTAACCTGTTTT	345	OPA1 H31 3UTR(+616+640)	TCCAAGGCAAATTTCTTCGCTGGCT
328	OPA1 H31 3UTR(+565+589)	AACGTTACAATCCAAATTAACCTGT	346	OPA1 H31 3UTR(+619+643)	GCTTCCAAGGCAAATTTCTTCGCTG
329	OPA1 H31 3UTR(+568+592)	CTGAACGTTACAATCCAAATTAACC	347	OPA1 H31 3UTR(+622+646)	TTGGCTTCCAAGGCAAATTTCTTCG
330	OPA1 H31 3UTR(+571+595)	TCACTGAACGTTACAATCCAAATTA	348	OPA1 H31 3UTR(+625+649)	GACTTGGCTTCCAAGGCAAATTTCT
331	OPA1 H31 3UTR(+574+598)	CTTTCACTGAACGTTACAATCCAAA	349	OPA1 H31 3UTR(+628+652)	ACTGACTTGGCTTCCAAGGCAAATT
332	OPA1 H31 3UTR(+577+601)	TTTCTTTCACTGAACGTTACAATCC	350	OPA1 H31 3UTR(+631+655)	GGTACTGACTTGGCTTCCAAGGCAA
351	OPA1 H31 3UTR(+634+658)	GCTGGTACTGACTTGGCTTCCAAGG	369	OPA1 H31 3UTR(+688+712)	CAATTTCAAATGGATATAGAGAGTG

SEQ	ASO Coordinates	Sequence 5'>3'	SEQ	ASO Coordinates	Sequence 5'>3'
352	OPA1 H31 3UTR(+637+661)	TAAGCTGGTACTGACTTGGCTTCCA	370	OPA1 H31 3UTR(+691+715)	AATCAATTTCAAATGGATATAGAGA
353	OPA1 H31 3UTR(+640+664)	AGGTAAGCTGGTACTGACTTGGCTT	371	OPA1 H31 3UTR(+694+718)	ATAAATCAATTTCAAATGGATATAG
354	OPA1 H31 3UTR(+643+667)	AATAGGTAAGCTGGTACTGACTTGG	372	OPA1 H31 3UTR(+697+721)	AAAATAAATCAATTTCAAATGGATA
355	OPA1 H31 3UTR(+646+670)	TCAAATAGGTAAGCTGGTACTGACT	373	OPA1 H31 3UTR(+700+724)	TCTAAAATAAATCAATTTCAAATGG
356	OPA1 H31 3UTR(+649+673)	GAATCAAATAGGTAAGCTGGTACTG	374	OPA1 H31 3UTR(+703+727)	ACATCTAAAATAAATCAATTTCAAA
357	OPA1 H31 3UTR(+652+676)	ACTGAATCAAATAGGTAAGCTGGTA	375	OPA1 H31 3UTR(+706+730)	ACAACATCTAAAATAAATCAATTTC
358	OPA1 H31 3UTR(+655+679)	GCAACTGAATCAAATAGGTAAGCTG	376	OPA1 H31 3UTR(+709+733)	TATACAACATCTAAAATAAATCAAT
359	OPA1 H31 3UTR(+658+682)	ACAGCAACTGAATCAAATAGGTAAG	377	OPA1 H31 3UTR(+712+736)	AAGTATACAACATCTAAAATAAATC
360	OPA1 H31 3UTR(+661+685)	AAAACAGCAACTGAATCAAATAGGT	378	OPA1 H31 3UTR(+715+739)	CGTAAGTATACAACATCTAAAATAA
361	OPA1 H31 3UTR(+664+688)	GAGAAAACAGCAACTGAATCAAATA	379	OPA1 H31 3UTR(+718+742)	TAACGTAAGTATACAACATCTAAAA
362	OPA1 H31 3UTR(+667+691)	AGTGAGAAAACAGCAACTGAATCAA	380	OPA1 H31 3UTR(+721+745)	GCCTAACGTAAGTATACAACATCTA
363	OPA1 H31 3UTR(+670+694)	GAGAGTGAGAAAACAGCAACTGAAT	381	OPA1 H31 3UTR(+724+748)	AAAGCCTAACGTAAGTATACAACAT
364	OPA1 H31 3UTR(+673+697)	ATAGAGAGTGAGAAAACAGCAACTG	382	OPA1 H31 3UTR(+727+751)	CAGAAAGCCTAACGTAAGTATACAA
365	OPA1 H31 3UTR(+676+700)	GATATAGAGAGTGAGAAAACAGCAA	383	OPA1 H31 3UTR(+730+754)	TAACAGAAAGCCTAACGTAAGTATA
366	OPA1 H31 3UTR(+679+703)	ATGGATATAGAGAGTGAGAAAACAG	384	OPA1 H31 3UTR(+733+757)	TATTAACAGAAAGCCTAACGTAAGT
367	OPA1 H31 3UTR(+682+706)	CAAATGGATATAGAGAGTGAGAAAA	385	OPA1 H31 3UTR(+736+760)	CACTATTAACAGAAAGCCTAACGTA
368	OPA1 H31 3UTR(+685+709)	TTTCAAATGGATATAGAGAGTGAGA	386	OPA1 H31 3UTR(+739+763)	AACCACTATTAACAGAAAGCCTAAC
387	OPA1 H31 3UTR(+742+766)	AAAAACCACTATTAACAGAAAGCCT	405	OPA1 H31 3UTR(+796+820)	TATCCTTAATCTTCCTCATCCTGTG

SEQ	ASO Coordinates	Sequence 5'>3'	SEQ	ASO Coordinates	Sequence 5'>3'
388	OPA1 H31 3UTR(+745+769)	GAGAAAAACCACTATTAACAGAAAG	406	OPA1 H31 3UTR(+799+823)	GATTATCCTTAATCTTCCTCATCCT
389	OPA1 H31 3UTR(+748+772)	CAGGAGAAAAACCACTATTAACAGA	407	OPA1 H31 3UTR(+802+826)	ATTGATTATCCTTAATCTTCCTCAT
390	OPA1 H31 3UTR(+751+775)	CAACAGGAGAAAAACCACTATTAAC	408	OPA1 H31 3UTR(+805+829)	TCAATTGATTATCCTTAATCTTCCT
391	OPA1 H31 3UTR(+754+778)	TGTCAACAGGAGAAAAACCACTATT	409	OPA1 H31 3UTR(+808+832)	TAGTCAATTGATTATCCTTAATCTT
392	OPA1 H31 3UTR(+757+781)	CTCTGTCAACAGGAGAAAAACCACT	410	OPA1 H31 3UTR(+811+835)	AATTAGTCAATTGATTATCCTTAAT
393	OPA1 H31 3UTR(+760+784)	TGGCTCTGTCAACAGGAGAAAAACC	411	OPA1 H31 3UTR(+814+838)	TGAAATTAGTCAATTGATTATCCTT
394	OPA1 H31 3UTR(+763+787)	CGGTGGCTCTGTCAACAGGAGAAAA	412	OPA1 H31 3UTR(+817+841)	AAATGAAATTAGTCAATTGATTATC
395	OPA1 H31 3UTR(+766+790)	ATCCGGTGGCTCTGTCAACAGGAGA	413	OPA1 H31 3UTR(+820+844)	TCTAAATGAAATTAGTCAATTGATT
396	OPA1 H31 3UTR(+769+793)	ATAATCCGGTGGCTCTGTCAACAGG	414	OPA1 H31 3UTR(+823+847)	TATTCTAAATGAAATTAGTCAATTG
397	OPA1 H31 3UTR(+772+796)	GTCATAATCCGGTGGCTCTGTCAAC	415	OPA1 H31 3UTR(+826+850)	TAATATTCTAAATGAAATTAGTCAA
398	OPA1 H31 3UTR(+775+799)	TGTGTCATAATCCGGTGGCTCTGTC	416	OPA1 H31 3UTR(+829+853)	TGATAATATTCTAAATGAAATTAGT
399	OPA1 H31 3UTR(+778+802)	TCCTGTGTCATAATCCGGTGGCTCT	417	OPA1 H31 3UTR(+832+856)	GTTTGATAATATTCTAAATGAAATT
400	OPA1 H31 3UTR(+781+805)	TCATCCTGTGTCATAATCCGGTGGC	418	OPA1 H31 3UTR(+835+859)	AATGTTTGATAATATTCTAAATGAA
401	OPA1 H31 3UTR(+784+808)	TCCTCATCCTGTGTCATAATCCGGT	419	OPA1 H31 3UTR(+838+862)	TGAAATGTTTGATAATATTCTAAAT
402	OPA1 H31 3UTR(+787+811)	TCTTCCTCATCCTGTGTCATAATCC	420	OPA1 H31 3UTR(+841+865)	AGTTGAAATGTTTGATAATATTCTA
403	OPA1 H31 3UTR(+790+814)	TAATCTTCCTCATCCTGTGTCATAA	421	OPA1 H31 3UTR(+844+868)	CCTAGTTGAAATGTTTGATAATATT
404	OPA1 H31 3UTR(+793+817)	CCTTAATCTTCCTCATCCTGTGTCA	422	OPA1 H31 3UTR(+847+871)	ATACCTAGTTGAAATGTTTGATAAT
423	OPA1 H31 3UTR(+850+874)	CTGATACCTAGTTGAAATGTTTGAT	441	OPA1 H31 3UTR(+904+928)	TTAATTGTTGAAATAATTTCTATTT

SEQ	ASO Coordinates	Sequence 5'>3'	SEQ	ASO Coordinates	Sequence 5'>3'
424	OPA1 H31 3UTR(+853+877)	TTTCTGATACCTAGTTGAAATGTTT	442	OPA1 H31 3UTR(+907+931)	ACTTTAATTGTTGAAATAATTTCTA
425	OPA1 H31 3UTR(+856+880)	CTTTTTCTGATACCTAGTTGAAATG	443	OPA1 H31 3UTR(+910+934)	ATTACTTTTAATTGTTTGAAATAATTT
426	OPA1 H31 3UTR(+859+883)	AGCCTTTTTTCTGATACCTAGTTGAA	444	OPA1 H31 3UTR(+913+937)	AACATTACTTTAATTGTTTGAAATAA
427	OPA1 H31 3UTR(+862+886)	GAAAGCCTTTTTTCTGATACCTAGTT	445	OPA1 H31 3UTR(+916+940)	GTCAACATTACTTTAATTGTTTGAAA
428	OPA1 H31 3UTR(+865+889)	AAAGAAAGCCTTTTTCTGATACCTA	446	OPA1 H31 3UTR(+919+943)	ATGGTCAACATTACTTTAATTGTTTG
429	OPA1 H31 3UTR(+868+892)	ATGAAAGAAAGCCTTTTTTCTGATAC	447	OPA1 H31 3UTR(+922+946)	GGGATGGTCAACATTACTTTAATTG
430	OPA1 H31 3UTR(+871+895)	CTTATGAAAGAAAGCCTTTTTTCTGA	448	OPA1 H31 3UTR(+925+949)	AGGGGGATGGTCAACATTACTTTAA
431	OPA1 H31 3UTR(+874+898)	AGTCTTATGAAAGAAAGCCTTTTTTC	449	OPA1 H31 3UTR(+928+952)	GAGAGGGGGATGGTCAACATTACTT
432	OPA1 H31 3UTR(+877+901)	AATAGTCTTATGAAAGAAAGCCTTTT	450	OPA1 H31 3UTR(+931+955)	GCTGAGAGGGGGATGGTCAACATTA
433	OPA1 H31 3UTR(+880+904)	TAAAATAGTCTTATGAAAGAAAGCC	451	OPA1 H31 3UTR(+934+958)	TCAGCTGAGAGGGGGATGGTCAACA
434	OPA1 H31 3UTR(+883+907)	ATTTAAAATAGTCTTATGAAAGAAA	452	OPA1 H31 3UTR(+937+961)	TATTCAGCTGAGAGGGGGATGGTCA
435	OPA1 H31 3UTR(+886+910)	TCTATTTAAAATAGTCTTATGAAAG	453	OPA1 H31 3UTR(+940+964)	CTTTATTCAGCTGAGAGGGGGATGG
436	OPA1 H31 3UTR(+889+913)	ATTTCTATTTAAAATAGTCTTATGA	454	OPA1 H31 3UTR(+943+967)	TTTCTTTATTCAGCTGAGAGGGGGA
437	OPA1 H31 3UTR(+892+916)	ATAATTTCTATTTAAAATAGTCTTA	455	OPA1 H31 3UTR(+946+970)	ATTTTTCTTTATTCAGCTGAGAGGG
438	OPA1 H31 3UTR(+895+919)	GAAATAATTTCTATTTAAAATAGTC	456	OPA1 H31 3UTR(+949+973)	TAAATTTTTCTTTATTCAGCTGAGA
439	OPA1 H31 3UTR(+898+922)	GTTGAAATAATTTCTATTTAAAATA	457	OPA1 H31 3UTR(+952+976)	AACTAAATTTTTCTTTATTCAGCTG
440	OPA1 H31 3UTR(+901+925)	ATTGTTGAAATAATTTCTATTTAAA	458	OPA1 H31 3UTR(+955+979)	TTGAACTAAATTTTTCTTTATTCAG
459	OPA1 H31 3UTR(+958+982)	AAATTGAACTAAATTTTTCTTTATT	477	OPA1 H31 3UTR(+1012+1036)	TTATTTAAAACACATGAAAAATGTTG

SEQ	ASO Coordinates	Sequence 5'>3'	SEQ	ASO Coordinates	Sequence 5'>3'
460	OPA1 H31 3UTR(+961:+985)	AATAAAATTGAACTAAATTTTTTCTTT	478	OPA1 H31 3UTR(+1015:+1039)	TATTTATTTAAAACACATGAAAATG
461	OPA1 H31 3UTR(+964:+988)	TGCAATAAATTGAACTAAATTTTTTC	479	OPA1 H31 3UTR(+1018:+1042)	AAATATTTATTTAAAACACATGAAA
462	OPA1 H31 3UTR(+967:+991)	AATTGCAATAAATTGAACTAAATTT	480	OPA1 H31 3UTR(+1021:+1045)	AAAAAATATTTATTTAAAACACATG
463	OPA1 H31 3UTR(+970:+994)	TTAAATTGCAATAAATTGAACTAAA	481	OPA1 H31 3UTR(+1024:+1048)	ATTAAAAAATATTTATTTAAAACAC
464	OPA1 H31 3UTR(+973:+997)	TAATTAAATTGCAATAAATTGAACT	482	OPA1 H31 3UTR(+1027:+1051)	CCAATTAAAAAAATATTTATTTAAAA
465	OPA1 H31 3UTR(+976:+1000)	TTGTAATTAAATTGCAATAAATTGA	483	OPA1 H31 3UTR(+1030:+1054)	TAGCCAATTAAAAAAATATTTATTTA
466	OPA1 H31 3UTR(+979:+1003)	GTATTGTAATTAAATTGCAATAAAT	484	OPA1 H31 3UTR(+1033:+1057)	CTTTAGCCAATTAAAAAAATATTTAT
467	OPA1 H31 3UTR(+982:+1006)	GTAGTATTGTAATTAAATTGCAATA	485	OPA1 H31 3UTR(+1036:+1060)	GTCCTTTAGCCAATTAAAAAAATATT
468	OPA1 H31 3UTR(+985:+1009)	AAGGTAGTATTGTAATTAAATTGCA	486	OPA1 H31 3UTR(+1039:+1063)	AATGTCCTTTAGCCAATTAAAAAAT
469	OPA1 H31 3UTR(+988:+1012)	GTGAAGGTAGTATTGTAATTAAATT	487	OPA1 H31 3UTR(+1042:+1066)	TTGAATGTCCTTTAGCCAATTAAAA
470	OPA1 H31 3UTR(+991:+1015)	GTTGTGAAGGTAGTATTGTAATTAA	488	OPA1 H31 3UTR(+1045:+1069)	TGCTTGAATGTCCTTTAGCCAATTA
471	OPA1 H31 3UTR(+994:+1018)	AATGTTGTGAAGGTAGTATTGTAAT	489	OPA1 H31 3UTR(+1048:+1072)	CTTTGCTTGAATGTCCTTTAGCCAA
472	OPA1 H31 3UTR(+997:+1021)	GAAAATGTTGTGAAGGTAGTATTGT	490	OPA1 H31 3UTR(+1051:+1075)	TTTCTTTGCTTGAATGTCCTTTAGC
473	OPA1 H31 3UTR(+1000:+1024)	CATGAAAATGTTGTGAAGGTAGTAT	491	OPA1 H31 3UTR(+1054:+1078)	GCATTTCTTTGCTTGAATGTCCTTT
474	OPA1 H31 3UTR(+1003:+1027)	ACACATGAAAATGTTGTGAAGGTAG	492	OPA1 H31 3UTR(+1057:+1081)	AAAGCATTTCTTTGCTTGAATGTCC
475	OPA1 H31 3UTR(+1006:+1030)	AAAACACATGAAAATGTTGTGAAGG	493	OPA1 H31 3UTR(+1060:+1084)	AAGAAAGCATTTCTTTGCTTGAATG
476	OPA1 H31 3UTR(+1009:+1033)	TTTAAAACACATGAAAATGTTGTGA	494	OPA1 H31 3UTR(+1063:+1087)	GTAAAGAAAGCATTTCTTTGCTTGA
495	OPA1 H31 3UTR(+1066:+1090)	TAAGTAAAGAAAGCATTTCTTTGCT	513	OPA1 H31 3UTR(+1120:+1144)	TTTTATTAACAAAGTAAAGGCTTAG

SEQ	ASO Coordinates	Sequence 5'>3'	SEQ	ASO Coordinates	Sequence 5'>3'
496	OPA1 H31 3UTR(+1069+1093)	TTTTAAGTAAAGAAAGCATTTCTTT	514	OPA1 H31 3UTR(+1123+1147)	CACTTTTATTAACAAAGTAAAGGCT
497	OPA1 H31 3UTR(+1072+1096)	ACATTTTAAGTAAAGAAAGCATTTC	515	OPA1 H31 3UTR(+1126+1150)	GGACACTTTTATTAACAAAGTAAAG
498	OPA1 H31 3UTR(+1075+1099)	TAGACATTTTAAGTAAAGAAAGCAT	516	OPA1 H31 3UTR(+1129+1153)	AATGGACACTTTTATTAACAAAGTA
499	OPA1 H31 3UTR(+1078+1102)	AGATAGACATTTTAAGTAAAGAAAG	517	OPA1 H31 3UTR(+1132+1156)	CACAATGGACACTTTTATTAACAAA
500	OPA1 H31 3UTR(+1081+1105)	ATGAGATAGACATTTTAAGTAAAGA	518	OPA1 H31 3UTR(+1135+1159)	TCACACAATGGACACTTTTATTAAC
501	OPA1 H31 3UTR(+1084+1108)	CAAATGAGATAGACATTTTAAGTAA	519	OPA1 H31 3UTR(+1138+1162)	ACATCACACAATGGACACTTTTATT
502	OPA1 H31 3UTR(+1087+1111)	CAGCAAATGAGATAGACATTTTAAG	520	OPA1 H31 3UTR(+1141+1165)	AAAACATCACACAATGGACACTTTT
503	OPA1 H31 3UTR(+1090+1114)	AGGCAGCAAATGAGATAGACATTTT	521	OPA1 H31 3UTR(+1144+1168)	TCAAAAACATCACACAATGGACACT
504	OPA1 H31 3UTR(+1093+1117)	AAAAGGCAGCAAATGAGATAGACAT	522	OPA1 H31 3UTR(+1147+1171)	AAATCAAAAAACATCACACAATGGAC
505	OPA1 H31 3UTR(+1096+1120)	GTGAAAAGGCAGCAAATGAGATAGA	523	OPA1 H31 3UTR(+1150+1174)	GTAAAATCAAAAACATCACACAATG
506	OPA1 H31 3UTR(+1099+1123)	TTAGTGAAAAGGCAGCAAATGAGAT	524	OPA1 H31 3UTR(+1153+1177)	ACTGTAAAATCAAAAACATCACACA
507	OPA1 H31 3UTR(+1102+1126)	GGCTTAGTGAAAAGGCAGCAAATGA	525	OPA1 H31 3UTR(+1156+1180)	CAAACTGTAAAATCAAAAACATCAC
508	OPA1 H31 3UTR(+1105+1129)	AAAGGCTTAGTGAAAAGGCAGCAAA	526	OPA1 H31 3UTR(+1159+1183)	TAGCAAACTGTAAAATCAAAAACAT
509	OPA1 H31 3UTR(+1108+1132)	AGTAAAGGCTTAGTGAAAAGGCAGC	527	OPA1 H31 3UTR(+1162+1186)	ATTTAGCAAACTGTAAAATCAAAAA
510	OPA1 H31 3UTR(+1111+1135)	CAAAGTAAAGGCTTAGTGAAAAGGC	528	OPA1 H31 3UTR(+1165+1189)	AAGATTTAGCAAACTGTAAAATCAA
511	OPA1 H31 3UTR(+1114+1138)	TAACAAAGTAAAGGCTTAGTGAAAA	529	OPA1 H31 3UTR(+1168+1192)	AATAAGATTTAGCAAACTGTAAAAT
512	OPA1 H31 3UTR(+1117+1141)	TATTAACAAAGTAAAGGCTTAGTGA	530	OPA1 H31 3UTR(+1171+1195)	GAAAATAAGATTTAGCAAACTGTAA
531	OPA1 H31 3UTR(+1174+1198)	CAAGAAAATAAGATTTAGCAAACTG	549	OPA1 H31 3UTR(+1228+1252)	ATGTAAAACAATAAAATGGGGAGTA

SEQ	ASO Coordinates	Sequence 5'>3'	SEQ	ASO Coordinates	Sequence 5'>3'
532	OPA1 H31 3UTR(+1177+1201)	CTCCAAGAAAATAAGATTTAGCAAA	550	OPA1 H31 3UTR(+1231+1255)	TTGATGTAAAACAATAAAATGGGGA
533	OPA1 H31 3UTR(+1180+1204)	CAACTCCAAGAAAATAAGATTTAGC	551	OPA1 H31 3UTR(+1234+1258)	GCATTGATGTAAAACAATAAAATGG
534	OPA1 H31 3UTR(+1183+1207)	AAGCAACTCCAAGAAAATAAGATTT	552	OPA1 H31 3UTR(+1237+1261)	CATGCATTGATGTAAAACAATAAAA
535	OPA1 H31 3UTR(+1186+1210)	AAAAAGCAACTCCAAGAAAATAAGA	553	OPA1 H31 3UTR(+1240+1264)	AAGCATGCATTGATGTAAAACAATA
536	OPA1 H31 3UTR(+1189+1213)	ACCAAAAAGCAACTCCAAGAAAATA	554	OPA1 H31 3UTR(+1243+1267)	ACGAAGCATGCATTGATGTAAAACA
537	OPA1 H31 3UTR(+1192+1216)	GTTACCAAAAAGCAACTCCAAGAAA	555	OPA1 H31 3UTR(+1246+1270)	ACAACGAAGCATGCATTGATGTAAA
538	OPA1 H31 3UTR(+1195+1219)	GCTGTTACCAAAAAGCAACTCCAAG	556	OPA1 H31 3UTR(+1249+1273)	ATCACAACGAAGCATGCATTGATGT
539	OPA1 H31 3UTR(+1198+1222)	GGGGCTGTTACCAAAAAGCAACTCC	557	OPA1 H31 3UTR(+1252+1276)	GGGATCACAACGAAGCATGCATTGA
540	OPA1 H31 3UTR(+1201+1225)	AATGGGGCTGTTACCAAAAAGCAAC	558	OPA1 H31 3UTR(+1255+1279)	TGAGGGATCACAACGAAGCATGCAT
541	OPA1 H31 3UTR(+1204+1228)	AGCAATGGGGCTGTTACCAAAAAGC	559	OPA1 H31 3UTR(+1258+1282)	TCTTGAGGGATCACAACGAAGCATG
542	OPA1 H31 3UTR(+1207+1231)	AGTAGCAATGGGGCTGTTACCAAAA	560	OPA1 H31 3UTR(+1261+1285)	ACATCTTGAGGGATCACAACGAAGC
543	OPA1 H31 3UTR(+1210+1234)	GGGAGTAGCAATGGGGCTGTTACCA	561	OPA1 H31 3UTR(+1264+1288)	GTTACATCTTGAGGGATCACAACGA
544	OPA1 H31 3UTR(+1213+1237)	ATGGGGAGTAGCAATGGGGCTGTTA	562	OPA1 H31 3UTR(+1267+1291)	AGTGTTACATCTTGAGGGATCACAA
545	OPA1 H31 3UTR(+1216+1240)	AAAATGGGGAGTAGCAATGGGGCTG	563	OPA1 H31 3UTR(+1270+1294)	CCAAGTGTTACATCTTGAGGGATCA
546	OPA1 H31 3UTR(+1219+1243)	AATAAAATGGGGAGTAGCAATGGGG	564	OPA1 H31 3UTR(+1273+1297)	ATACCAAGTGTTACATCTTGAGGGA
547	OPA1 H31 3UTR(+1222+1246)	AACAATAAAATGGGGAGTAGCAATG	565	OPA1 H31 3UTR(+1276+1300)	AGCATACCAAGTGTTACATCTTGAG
548	OPA1 H31 3UTR(+1225+1249)	TAAAACAATAAAATGGGGAGTAGCA	566	OPA1 H31 3UTR(+1279+1303)	CCGAGCATACCAAGTGTTACATCTT
567	OPA1 H31 3UTR(+1282+1306)	CAACCGAGCATACCAAGTGTTACAT	585	OPA1 H31 3UTR(+1336+1360)	TATAAAACAAACATACATTGAATTC

SEQ	ASO Coordinates	Sequence 5'>3'	SEQ	ASO Coordinates	Sequence 5'>3'
568	OPA1 H31 3UTR(+1285:+1309)	CCTCAACCGAGCATACCAAGTGTTA	586	OPA1 H31 3UTR(+1339+1363)	CAGTATAAAACAAACATACATTGAA
569	OPA1 H31 3UTR(+1288:+1312)	TATCCTCAACCGAGCATACCAAGTG	587	OPA1 H31 3UTR(+1342+1366)	AAACAGTATAAAACAAACATACATT
570	OPA1 H31 3UTR(+1291:+1315)	TCATATCCTCAACCGAGCATACCAA	588	OPA1 H31 3UTR(+1345+1369)	ATCAAACAGTATAAAACAAACATAC
571	OPA1 H31 3UTR(+1294:+1318)	TTTTCATATCCTCAACCGAGCATAC	589	OPA1 H31 3UTR(+1348+1372)	CTTATCAAACAGTATAAAACAAACA
572	OPA1 H31 3UTR(+1297:+1321)	ATTTTTTCATATCCTCAACCGAGCA	590	OPA1 H31 3UTR(+1351+1375)	TTTCTTATCAAACAGTATAAAACAA
573	OPA1 H31 3UTR(+1300:+1324)	AGTATTTTTTTCATATCCTCAACCGA	591	OPA1 H31 3UTR(+1354+1378)	ACTTTTCTTATCAAACAGTATAAAA
574	OPA1 H31 3UTR(+1303:+1327)	GGAAGTATTTTTTTCATATCCTCAAC	592	OPA1 H31 3UTR(+1357+1381)	CCTACTTTTCTTATCAAACAGTATA
575	OPA1 H31 3UTR(+1306:+1330)	TTCGGAAGTATTTTTTTCATATCCTC	593	OPA1 H31 3UTR(+1360+1384)	GGACCTACTTTTCTTATCAAACAGT
576	OPA1 H31 3UTR(+1309:+1333)	GGTTTCGGAAGTATTTTTTTCATATC	594	OPA1 H31 3UTR(+1363+1387)	GCTGGACCTACTTTTCTTATCAAAC
577	OPA1 H31 3UTR(+1312:+1336)	CCTGGTTTCGGAAGTATTTTTTTCAT	595	OPA1 H31 3UTR(+1366+1390)	AAGGCTGGACCTACTTTTCTTATCA
578	OPA1 H31 3UTR(+1315:+1339)	ATTCCTGGTTTCGGAAGTATTTTTT	596	OPA1 H31 3UTR(+1369+1393)	CTTAAGGCTGGACCTACTTTTCTTA
579	OPA1 H31 3UTR(+1318:+1342)	TGAATTCCTGGTTTCGGAAGTATTT	597	OPA1 H31 3UTR(+1372+1396)	CTGCTTAAGGCTGGACCTACTTTTC
580	OPA1 H31 3UTR(+1321:+1345)	CATTGAATTCCTGGTTTCGGAAGTA	598	OPA1 H31 3UTR(+1375+1399)	GTGCTGCTTAAGGCTGGACCTACTT
581	OPA1 H31 3UTR(+1324:+1348)	ATACATTGAATTCCTGGTTTCGGAA	599	OPA1 H31 3UTR(+1378+1402)	TCTGTGCTGCTTAAGGCTGGACCTA
582	OPA1 H31 3UTR(+1327:+1351)	AACATACATTGAATTCCTGGTTTCG	600	OPA1 H31 3UTR(+1381:+1405)	GCATCTGTGCTGCTTAAGGCTGGAC
583	OPA1 H31 3UTR(+1330:+1354)	ACAAACATACATTGAATTCCTGGTT	601	OPA1 H31 3UTR(+1384+1408)	AGCGCATCTGTGCTGCTTAAGGCTG
584	OPA1 H31 3UTR(+1333:+1357)	AAAACAAACATACATTGAATTCCTG	602	OPA1 H31 3UTR(+1387+1411)	ACCAGCGCATCTGTGCTGCTTAAGG
603	OPA1 H31 3UTR(+1390:+1414)	TCTACCAGCGCATCTGTGCTGCTTA	621	OPA1 H31 3UTR(+1444+1468)	TATTCACTCCTGTCCCTAGACCTAA

SEQ	ASO Coordinates	Sequence 5'>3'	SEQ	ASO Coordinates	Sequence 5'>3'
604	OPA1 H31 3UTR(+1393:+1417)	GCATCTACCAGCGCATCTGTGCTGC	622	OPA1 H31 3UTR(+1447:+1471)	TTCTATTCACTCCTGTCCCTAGACC
605	OPA1 H31 3UTR(+1396:+1420)	TATGCATCTACCAGCGCATCTGTGC	623	OPA1 H31 3UTR(+1450:+1474)	CCTTTCTATTCACTCCTGTCCCTAG
606	OPA1 H31 3UTR(+1399:+1423)	GACTATGCATCTACCAGCGCATCTG	624	OPA1 H31 3UTR(+1453:+1477)	CTCCCTTTCTATTCACTCCTGTCCC
607	OPA1 H31 3UTR(+1402:+1426)	CCTGACTATGCATCTACCAGCGCAT	625	OPA1 H31 3UTR(+1456:+1480)	CTCCTCCCTTTCTATTCACTCCTGT
608	OPA1 H31 3UTR(+1405:+1429)	GTTCCTGACTATGCATCTACCAGCG	626	OPA1 H31 3UTR(+1459:+1483)	GCTCTCCTCCCTTTCTATTCACTCC
609	OPA1 H31 3UTR(+1408:+1432)	AAAGTTCCTGACTATGCATCTACCA	627	OPA1 H31 3UTR(+1462:+1486)	AGAGCTCTCCTCCCTTTCTATTCAC
610	OPA1 H31 3UTR(+1411:+1435)	AAAAAAGTTCCTGACTATGCATCTA	628	OPA1 H31 3UTR(+1465:+1489)	AATAGAGCTCTCCTCCCTTTCTATT
611	OPA1 H31 3UTR(+1414:+1438)	ATAAAAAAAGTTCCTGACTATGCAT	629	OPA1 H31 3UTR(+1468:+1492)	CATAATAGAGCTCTCCTCCCTTTCT
612	OPA1 H31 3UTR(+1417:+1441)	GAAATAAAAAAAAGTTCCTGACTATG	630	OPA1 H31 3UTR(+1471:+1495)	GAACATAATAGAGCTCTCCTCCCTT
613	OPA1 H31 3UTR(+1420:+1444)	AAAGAAATAAAAAAAAGTTCCTGACT	631	OPA1 H31 3UTR(+1474:+1498)	ATAGAACATAATAGAGCTCTCCTCC
614	OPA1 H31 3UTR(+1423:+1447)	CTAAAAGAAATAAAAAAAAGTTCCTG	632	OPA1 H31 3UTR(+1477:+1501)	TGTATAGAACATAATAGAGCTCTCC
615	OPA1 H31 3UTR(+1426:+1450)	GACCTAAAAGAAATAAAAAAAAGTTC	633	OPA1 H31 3UTR(+1480:+1504)	CTGTGTATAGAACATAATAGAGCTC
616	OPA1 H31 3UTR(+1429:+1453)	CTAGACCTAAAAGAAATAAAAAAAAG	634	OPA1 H31 3UTR(+1483:+1507)	AATCTGTGTATAGAACATAATAGAG
617	OPA1 H31 3UTR(+1432:+1456)	TCCCTAGACCTAAAAGAAATAAAAA	635	OPA1 H31 3UTR(+1486:+1510)	CCTAATCTGTGTATAGAACATAATA
618	OPA1 H31 3UTR(+1435:+1459)	CTGTCCCTAGACCTAAAAGAAATAA	636	OPA1 H31 3UTR(+1489:+1513)	TCTCCTAATCTGTGTATAGAACATA
619	OPA1 H31 3UTR(+1438:+1462)	CTCCTGTCCCTAGACCTAAAAGAAA	637	OPA1 H31 3UTR(+1492:+1516)	TCATCTCCTAATCTGTGTATAGAAC
620	OPA1 H31 3UTR(+1441:+1465)	TCACTCCTGTCCCTAGACCTAAAAG	638	OPA1 H31 3UTR(+1495:+1519)	AGGTCATCTCCTAATCTGTGTATAG
639	OPA1 H31 3UTR(+1498:+1522)	GTAAGGTCATCTCCTAATCTGTGTA	657	OPA1 H31 3UTR(+1552:+1576)	AAATATTCATTAACATGCATTAACC

SEQ	ASO Coordinates	Sequence 5'>3'	SEQ	ASO Coordinates	Sequence 5'>3'
640	OPA1 H31 3UTR(+1501+1525)	CCAGTAAGGTCATCTCCTAATCTGT	658	OPA1 H31 3UTR(+1555+1579)	CAAAAATATTCATTAACATGCATTA
641	OPA1 H31 3UTR(+1504+1528)	TACCCAGTAAGGTCATCTCCTAATC	659	OPA1 H31 3UTR(+1558+1582)	CTGCAAAAATATTCATTAACATGCA
642	OPA1 H31 3UTR(+1507+1531)	GTGTACCCAGTAAGGTCATCTCCTA	660	OPA1 H31 3UTR(+1561+1585)	CAACTGCAAAAATATTCATTAACAT
643	OPA1 H31 3UTR(+1510+1534)	GGGGTGTACCCAGTAAGGTCATCTC	661	OPA1 H31 3UTR(+1564+1588)	TTACAACTGCAAAAATATTCATTAA
644	OPA1 H31 3UTR(+1513+1537)	AGAGGGGTGTACCCAGTAAGGTCAT	662	OPA1 H31 3UTR(+1567+1591)	GCTTTACAACTGCAAAAATATTCAT
645	OPA1 H31 3UTR(+1516+1540)	GTTAGAGGGGTGTACCCAGTAAGGT	663	OPA1 H31 3UTR(+1570+1594)	TATGCTTTACAACTGCAAAAATATT
646	OPA1 H31 3UTR(+1519+1543)	CTGGTTAGAGGGGTGTACCCAGTAA	664	OPA1 H31 3UTR(+1573+1597)	TGTTATGCTTTACAACTGCAAAAAT
647	OPA1 H31 3UTR(+1522+1546)	GCACTGGTTAGAGGGGTGTACCCAG	665	OPA1 H31 3UTR(+1576+1600)	AATTGTTATGCTTTACAACTGCAAA
648	OPA1 H31 3UTR(+1525+1549)	TAAGCACTGGTTAGAGGGGTGTACC	666	OPA1 H31 3UTR(+1579+1603)	TGTAATTGTTATGCTTTACAACTGC
649	OPA1 H31 3UTR(+1528+1552)	CTGTAAGCACTGGTTAGAGGGGTGT	667	OPA1 H31 3UTR(+1582+1606)	AGTTGTAATTGTTATGCTTTACAAC
650	OPA1 H31 3UTR(+1531+1555)	AACCTGTAAGCACTGGTTAGAGGGG	668	OPA1 H31 3UTR(+1585+1609)	TGTAGTTGTAATTGTTATGCTTTAC
651	OPA1 H31 3UTR(+1534+1558)	ATTAACCTGTAAGCACTGGTTAGAG	669	OPA1 H31 3UTR(+1588+1612)	ATGTGTAGTTGTAATTGTTATGCTT
652	OPA1 H31 3UTR(+1537+1561)	TGCATTAACCTGTAAGCACTGGTTA	670	OPA1 H31 3UTR(+1591+1615)	TAGATGTGTAGTTGTAATTGTTATG
653	OPA1 H31 3UTR(+1540+1564)	ACATGCATTAACCTGTAAGCACTGG	671	OPA1 H31 3UTR(+1594+1618)	AAATAGATGTGTAGTTGTAATTGTT
654	OPA1 H31 3UTR(+1543+1567)	TTAACATGCATTAACCTGTAAGCAC	672	OPA1 H31 3UTR(+1597+1621)	TAGAAATAGATGTGTAGTTGTAATT
655	OPA1 H31 3UTR(+1546+1570)	TCATTAACATGCATTAACCTGTAAG	673	OPA1 H31 3UTR(+1600+1624)	CTTTAGAAATAGATGTGTAGTTGTA
656	OPA1 H31 3UTR(+1549+1573)	TATTCATTAACATGCATTAACCTGT	674	OPA1 H31 3UTR(+1603+1627)	ATTCTTTAGAAATAGATGTGTAGTT
675	OPA1 H31 3UTR(+1606+1630)	TTTATTCTTTAGAAATAGATGTGTA	693	OPA1 H31 3UTR(+1660+1684)	CAGCTGAAGGTCTTTCTTTCTATAG

SEQ	ASO Coordinates	Sequence 5'>3'	SEQ	ASO Coordinates	Sequence 5'>3'
676	OPA1 H31 3UTR(+1609+1633)	TGTTTTATTCTTTAGAAATAGATGT	694	OPA1 H31 3UTR(+1663+1687)	ATACAGCTGAAGGTCTTTCTTTTCTA
677	OPA1 H31 3UTR(+1612+1636)	TCCTGTTTTATTCTTTAGAAATAGA	695	OPA1 H31 3UTR(+1666+1690)	GAAATACAGCTGAAGGTCTTTCTTT
678	OPA1 H31 3UTR(+1615+1639)	TGGTCCTGTTTTATTCTTTAGAAAT	696	OPA1 H31 3UTR(+1669+1693)	GTGGAAATACAGCTGAAGGTCTTTC
679	OPA1 H31 3UTR(+1618+1642)	ATATGGTCCTGTTTTATTCTTTAGA	697	OPA1 H31 3UTR(+1672+1696)	TCTGTGGAAATACAGCTGAAGGTCT
680	OPA1 H31 3UTR(+1621+1645)	TAAATATGGTCCTGTTTTATTCTTT	698	OPA1 H31 3UTR(+1675+1699)	AAATCTGTGGAAATACAGCTGAAGG
681	OPA1 H31 3UTR(+1624+1648)	AAATAAATATGGTCCTGTTTTATTC	699	OPA1 H31 3UTR(+1678+1702)	GAGAAATCTGTGGAAATACAGCTGA
682	OPA1 H31 3UTR(+1627+1651)	AGTAAATAAATATGGTCCTGTTTTA	700	OPA1 H31 3UTR(+1681+1705)	TGGGAGAAATCTGTGGAAATACAGC
683	OPA1 H31 3UTR(+1630+1654)	AGAAGTAAATAAATATGGTCCTGTT	701	OPA1 H31 3UTR(+1684+1708)	CCTTGGGAGAAATCTGTGGAAATAC
684	OPA1 H31 3UTR(+1633+1657)	GACAGAAGTAAATAAATATGGTCCT	702	OPA1 H31 3UTR(+1687+1711)	TTTCCTTGGGAGAAATCTGTGGAAA
685	OPA1 H31 3UTR(+1636+1660)	GTTGACAGAAGTAAATAAATATGGT	703	OPA1 H31 3UTR(+1690+1714)	CCTTTTCCTTGGGAGAAATCTGTGG
686	OPA1 H31 3UTR(+1639+1663)	ATAGTTGACAGAAGTAAATAAATAT	704	OPA1 H31 3UTR(+1693+1717)	TAGCCTTTTCCTTGGGAGAAATCTG
687	OPA1 H31 3UTR(+1642+1666)	TCTATAGTTGACAGAAGTAAATAAA	705	OPA1 H31 3UTR(+1696+1720)	TATTAGCCTTTTCCTTGGGAGAAAT
688	OPA1 H31 3UTR(+1645+1669)	CTTTCTATAGTTGACAGAAGTAAAT	706	OPA1 H31 3UTR(+1699+1723)	TAATATTAGCCTTTTCCTTGGGAGA
689	OPA1 H31 3UTR(+1648+1672)	TTTCTTTCTATAGTTGACAGAAGTA	707	OPA1 H31 3UTR(+1702+1726)	GACTAATATTAGCCTTTTCCTTGGG
690	OPA1 H31 3UTR(+1651+1675)	GTCTTTCTTTCTATAGTTGACAGAA	708	OPA1 H31 3UTR(+1705+1729)	AGTGACTAATATTAGCCTTTTCCTT
691	OPA1 H31 3UTR(+1654+1678)	AAGGTCTTTCTTTCTATAGTTGACA	709	OPA1 H31 3UTR(+1708+1732)	AGTAGTGACTAATATTAGCCTTTTC
692	OPA1 H31 3UTR(+1657+1681)	CTGAAGGTCTTTCTTTCTATAGTTG	710	OPA1 H31 3UTR(+1711+1735)	AACAGTAGTGACTAATATTAGCCTT
711	OPA1 H31 3UTR(+1714+1738)	GATAACAGTAGTGACTAATATTAGC	729	OPA1 H31 3UTR(+1768+1792)	CAAAGAAATGAAGATCTCCCTCCAT

SEQ	ASO Coordinates	Sequence 5'>3'	SEQ	ASO Coordinates	Sequence 5'>3'
712	OPA1 H31 3UTR(+1717+1741)	TGTGATAACAGTAGTGACTAATATT	730	OPA1 H31 3UTR(+1771+1795)	CCTCAAAGAAATGAAGATCTCCCTC
713	OPA1 H31 3UTR(+1720+1744)	GGATGTGATAACAGTAGTGACTAAT	731	OPA1 H31 3UTR(+1774+1798)	TCTCCTCAAAGAAATGAAGATCTCC
714	OPA1 H31 3UTR(+1723+1747)	AAGGGATGTGATAACAGTAGTGACT	732	OPA1 H31 3UTR(+1777+1801)	TGATCTCCTCAAAGAAATGAAGATC
715	OPA1 H31 3UTR(+1726+1750)	ACAAAGGGATGTGATAACAGTAGTG	733	OPA1 H31 3UTR(+1780+1804)	TACTGATCTCCTCAAAGAAATGAAG
716	OPA1 H31 3UTR(+1729+1753)	TATACAAAGGGATGTGATAACAGTA	734	OPA1 H31 3UTR(+1783+1807)	CAATACTGATCTCCTCAAAGAAATG
717	OPA1 H31 3UTR(+1732+1756)	ACTTATACAAAGGGATGTGATAACA	735	OPA1 H31 3UTR(+1786+1810)	TTACAATACTGATCTCCTCAAAGAA
718	OPA1 H31 3UTR(+1735+1759)	AAAACTTATACAAAGGGATGTGATA	736	OPA1 H31 3UTR(+1789+1813)	ACGTTACAATACTGATCTCCTCAAA
719	OPA1 H31 3UTR(+1738+1762)	TTTAAAACTTATACAAAGGGATGTG	737	OPA1 H31 3UTR(+1792+1816)	CATACGTTACAATACTGATCTCCTC
720	OPA1 H31 3UTR(+1741+1765)	CTTTTTAAAACTTATACAAAGGGAT	738	OPA1 H31 3UTR(+1795+1819)	TCACATACGTTACAATACTGATCTC
721	OPA1 H31 3UTR(+1744+1768)	TCTCTTTTTAAAACTTATACAAAGG	739	OPA1 H31 3UTR(+1798+1822)	TATTCACATACGTTACAATACTGAT
722	OPA1 H31 3UTR(+1747+1771)	CCATCTCTTTTTAAAACTTATACAA	740	OPA1 H31 3UTR(+1801+1825)	ATCTATTCACATACGTTACAATACT
723	OPA1 H31 3UTR(+1750+1774)	CCTCCATCTCTTTTTAAAACTTATA	741	OPA1 H31 3UTR(+1804+1828)	ATCATCTATTCACATACGTTACAAT
724	OPA1 H31 3UTR(+1753+1777)	CTCCCTCCATCTCTTTTTAAAACTT	742	OPA1 H31 3UTR(+1807+1831)	GTTATCATCTATTCACATACGTTAC
725	OPA1 H31 3UTR(+1756+1780)	GATCTCCCTCCATCTCTTTTTAAAA	743	OPA1 H31 3UTR(+1810+1834)	ATTGTTATCATCTATTCACATACGT
726	OPA1 H31 3UTR(+1759+1783)	GAAGATCTCCCTCCATCTCTTTTTA	744	OPA1 H31 3UTR(+1813+1837)	TTAATTGTTATCATCTATTCACATA
727	OPA1 H31 3UTR(+1762+1786)	AATGAAGATCTCCCTCCATCTCTTT	745	OPA1 H31 3UTR(+1816+1840)	ATATTAATTGTTATCATCTATTCAC
728	OPA1 H31 3UTR(+1765+1789)	AGAAATGAAGATCTCCCTCCATCTC	746	OPA1 H31 3UTR(+1819+1843)	GTAATATTAATTGTTATCATCTATT
747	OPA1 H31 3UTR(+1822+1846)	TTAGTAATATTAATTGTTATCATCT	765	OPA1 H31 3UTR(+1876+1900)	AAGCCACATTACTGTGGGGCATGGA

SEQ	ASO Coordinates	Sequence 5'>3'	SEQ	ASO Coordinates	Sequence 5'>3'
748	OPA1 H31 3UTR(+1825+1849)	CTTTTAGTAATATTAATTGTTATCA	766	OPA1 H31 3UTR(+1879+1903)	AAGAAGCCACATTACTGTGGGGCAT
749	OPA1 H31 3UTR(+1828+1852)	GGACTTTTAGTAATATTAATTGTTA	767	OPA1 H31 3UTR(+1882+1906)	TGAAAGAAGCCACATTACTGTGGGG
750	OPA1 H31 3UTR(+1831+1855)	GTGGGACTTTTAGTAATATTAATTG	768	OPA1 H31 3UTR(+1885+1909)	CCATGAAAGAAGCCACATTACTGTG
751	OPA1 H31 3UTR(+1834+1858)	CATGTGGGACTTTTAGTAATATTAA	769	OPA1 H31 3UTR(+1888+1912)	AACCCATGAAAGAAGCCACATTACT
752	OPA1 H31 3UTR(+1837+1861)	TCTCATGTGGGACTTTTAGTAATAT	770	OPA1 H31 3UTR(+1891+1915)	AAAAACCCATGAAAGAAGCCACATT
753	OPA1 H31 3UTR(+1840+1864)	GACTCTCATGTGGGACTTTTAGTAA	771	OPA1 H31 3UTR(+1894+1918)	AAAAAAAACCCATGAAAGAAGCCAC
754	OPA1 H31 3UTR(+1843+1867)	CAGGACTCTCATGTGGGACTTTTAG	772	OPA1 H31 3UTR(+1897+1921)	AGAAAAAAAAACCCATGAAAGAAGC
755	OPA1 H31 3UTR(+1846+1870)	CGTCAGGACTCTCATGTGGGACTTT	773	OPA1 H31 3UTR(+1900+1924)	AGAAGAAAAAAAAAACCCATGAAAGA
756	OPA1 H31 3UTR(+1849+1873)	GGGCGTCAGGACTCTCATGTGGGAC	774	OPA1 H31 3UTR(+1903+1927)	AAAAGAAGAAAAAAAAAACCCATGAA
757	OPA1 H31 3UTR(+1852+1876)	AGAGGGCGTCAGGACTCTCATGTGG	775	OPA1 H31 3UTR(+1906+1930)	CTAAAAAGAAGAAAAAAAAAACCCAT
758	OPA1 H31 3UTR(+1855+1879)	TGGAGAGGGCGTCAGGACTCTCATG	776	OPA1 H31 3UTR(+1909+1933)	CAGCTAAAAAAGAAGAAAAAAAAACC
759	OPA1 H31 3UTR(+1858+1882)	GCATGGAGAGGGCGTCAGGACTCTC	777	OPA1 H31 3UTR(+1912+1936)	GATCAGCTAAAAAGAAGAAAAAAAA
760	OPA1 H31 3UTR(+1861+1885)	GGGGCATGGAGAGGGCGTCAGGACT	778	OPA1 H31 3UTR(+1915+1939)	TGAGATCAGCTAAAAAAGAAGAAAAA
761	OPA1 H31 3UTR(+1864+1888)	TGTGGGGCATGGAGAGGGCGTCAGG	779	OPA1 H31 3UTR(+1918+1942)	GGATGAGATCAGCTAAAAAGAAGAA
762	OPA1 H31 3UTR(+1867+1891)	TACTGTGGGGCATGGAGAGGGCGTC	780	OPA1 H31 3UTR(+1921+1945)	TTAGGATGAGATCAGCTAAAAAGAA
763	OPA1 H31 3UTR(+1870+1894)	CATTACTGTGGGGCATGGAGAGGGC	781	OPA1 H31 3UTR(+1924+1948)	TGCTTAGGATGAGATCAGCTAAAAA
764	OPA1 H31 3UTR(+1873+1897)	CCACATTACTGTGGGGCATGGAGAG	782	OPA1 H31 3UTR(+1927+1951)	GCATGCTTAGGATGAGATCAGCTAA
783	OPA1 H31 3UTR(+1930+1954)	AAAGCATGCTTAGGATGAGATCAGC	801	OPA1 H31 3UTR(+1984+2008)	ATTTTCTTTCAATAACATCTGCAGT

SEQ	ASO Coordinates	Sequence 5'>3'	SEQ	ASO Coordinates	Sequence 5'>3'
784	OPA1 H31 3UTR(+1933+1957)	AATAAAGCATGCTTAGGATGAGATC	802	OPA1 H31 3UTR(+1987+2011)	TTTATTTCTTTCAATAACATCTGC
785	OPA1 H31 3UTR(+1936+1960)	AAAAATAAAGCATGCTTAGGATGAG	803	OPA1 H31 3UTR(+1990+2014)	AATTTTATTTTCTTTCAATAACATC
786	OPA1 H31 3UTR(+1939+1963)	AGGAAAAATAAAGCATGCTTAGGAT	804	OPA1 H31 3UTR(+1993+2017)	CTGAATTTTATTTTCTTTCAATAAC
787	OPA1 H31 3UTR(+1942+1966)	TCAAGGAAAAATAAAGCATGCTTAG	805	OPA1 H31 3UTR(+1996+2020)	AGACTGAATTTTATTTTCTTTCAAT
788	OPA1 H31 3UTR(+1945+1969)	CTTTCAAGGAAAAATAAAGCATGCT	806	OPA1 H31 3UTR(+1999+2023)	TTGAGACTGAATTTTATTTTCTTTC
789	OPA1 H31 3UTR(+1948+1972)	TAGCTTTCAAGGAAAAATAAAGCAT	807	OPA1 H31 3UTR(+2002+2026)	CTCTTGAGACTGAATTTTATTTTCT
790	OPA1 H31 3UTR(+1951+1975)	ACCTAGCTTTCAAGGAAAAATAAAG	808	OPA1 H31 3UTR(+2005+2029)	TTACTCTTGAGACTGAATTTTATTT
791	OPA1 H31 3UTR(+1954+1978)	AATACCTAGCTTTCAAGGAAAAATA	809	OPA1 H31 3UTR(+2008+2032)	GGTTTACTCTTGAGACTGAATTTTA
792	OPA1 H31 3UTR(+1957+1981)	ATAAATACCTAGCTTTCAAGGAAAA	810	OPA1 H31 3UTR(+2011+2035)	CAGGGTTTACTCTTGAGACTGAATT
793	OPA1 H31 3UTR(+1960+1984)	TTGATAAATACCTAGCTTTCAAGGA	811	OPA1 H31 3UTR(+2014+2038)	ACACAGGGTTTACTCTTGAGACTGA
794	OPA1 H31 3UTR(+1963+1987)	CAGTTGATAAATACCTAGCTTTCAA	812	OPA1 H31 3UTR(+2017+2041)	AAGACACAGGGTTTACTCTTGAGAC
795	OPA1 H31 3UTR(+1966+1990)	CTGCAGTTGATAAATACCTAGCTTT	813	OPA1 H31 3UTR(+2020+2044)	CACAAGACACAGGGTTTACTCTTGA
796	OPA1 H31 3UTR(+1969+1993)	CATCTGCAGTTGATAAATACCTAGC	814	OPA1 H31 3UTR(+2023+2047)	AGACACAAGACACAGGGTTTACTCT
797	OPA1 H31 3UTR(+1972+1996)	TAACATCTGCAGTTGATAAATACCT	815	OPA1 H31 3UTR(+2026+2050)	TACAGACACAAGACACAGGGTTTAC
798	OPA1 H31 3UTR(+1975+1999)	CAATAACATCTGCAGTTGATAAATA	816	OPA1 H31 3UTR(+2029+2053)	AACTACAGACACAAGACACAGGGTT
799	OPA1 H31 3UTR(+1978+2002)	TTTCAATAACATCTGCAGTTGATAA	817	OPA1 H31 3UTR(+2032+2056)	TTGAACTACAGACACAAGACACAGG
800	OPA1 H31 3UTR(+1981+2005)	TTCTTTCAATAACATCTGCAGTTGA	818	OPA1 H31 3UTR(+2035+2059)	CTTTTGAACTACAGACACAAGACAC
819	OPA1 H31 3UTR(+2038+2062)	TGACTTTTGAACTACAGACACAAGA	837	OPA1 H31 3UTR(+2092+2116)	TCGAATTTAACTTCTGTATATTTAG

SEQ	ASO Coordinates	Sequence 5'>3'	SEQ	ASO Coordinates	Sequence 5'>3'
820	OPA1 H31 3UTR(+2041+2065)	TTCTGACTTTTTGAACTACAGACACA	838	OPA1 H31 3UTR(+2095+2119)	AGTTCGAATTTAACTTCTGTATATT
821	OPA1 H31 3UTR(+2044+2068)	CATTTCTGACTTTTTGAACTACAGAC	839	OPA1 H31 3UTR(+2098+2122)	GCTAGTTCGAATTTAACTTCTGTAT
822	OPA1 H31 3UTR(+2047+2071)	AATCATTTCTGACTTTTTGAACTACA	840	OPA1 H31 3UTR(+2101+2125)	GTGGCTAGTTCGAATTTAACTTCTG
823	OPA1 H31 3UTR(+2050+2074)	TAGAATCATTTCTGACTTTTTGAACT	841	OPA1 H31 3UTR(+2104+2128)	TCTGTGGCTAGTTCGAATTTAACTT
824	OPA1 H31 3UTR(+2053+2077)	AATTAGAATCATTTCTGACTTTTTGA	842	OPA1 H31 3UTR(+2107+2131)	GATTCTGTGGCTAGTTCGAATTTAA
825	OPA1 H31 3UTR(+2056+2080)	TTAAATTAGAATCATTTCTGACTTT	843	OPA1 H31 3UTR(+2110+2134)	AATGATTCTGTGGCTAGTTCGAATT
826	OPA1 H31 3UTR(+2059+2083)	TGTTTAAATTAGAATCATTTCTGAC	844	OPA1 H31 3UTR(+2113+2137)	ACAAATGATTCTGTGGCTAGTTCGA
827	OPA1 H31 3UTR(+2062+2086)	TTTTGTTTAAATTAGAATCATTTCT	845	OPA1 H31 3UTR(+2116+2140)	AAAACAAATGATTCTGTGGCTAGTT
828	OPA1 H31 3UTR(+2065+2089)	TCTTTTGTTTAAATTAGAATCATT	846	OPA1 H31 3UTR(+2119+2143)	ATAAAAACAAATGATTCTGTGGCTA
829	OPA1 H31 3UTR(+2068+2092)	GTATCTTTTTGTTTAAATTAGAATC	847	OPA1 H31 3UTR(+2122+2146)	GACATAAAAACAAATGATTCTGTGG
830	OPA1 H31 3UTR(+2071+2095)	TTAGTATCTTTTTGTTTAAATTAGA	848	OPA1 H31 3UTR(+2125+2149)	TCTGACATAAAAACAAATGATTCTG
831	OPA1 H31 3UTR(+2074+2098)	TATTTAGTATCTTTTTGTTTAAATT	849	OPA1 H31 3UTR(+2128+2152)	AATTCTGACATAAAAACAAATGATT
832	OPA1 H31 3UTR(+2077+2101)	GTATATTTAGTATCTTTTTGTTTAA	850	OPA1 H31 3UTR(+2131+2155)	GCAAATTCTGACATAAAAACAAATG
833	OPA1 H31 3UTR(+2080+2104)	TCTGTATATTTAGTATCTTTTTGTT	851	OPA1 H31 3UTR(+2134+2158)	TTTGCAAATTCTGACATAAAAACAA
834	OPA1 H31 3UTR(+2083+2107)	ACTTCTGTATATTTAGTATCTTTTT	852	OPA1 H31 3UTR(+2137+2161)	CTCTTTGCAAATTCTGACATAAAAA
835	OPA1 H31 3UTR(+2086+2110)	TTAACTTCTGTATATTTAGTATCTT	853	OPA1 H31 3UTR(+2140+2164)	CCACTCTTTGCAAATTCTGACATAA
836	OPA1 H31 3UTR(+2089+2113)	AATTTAACTTCTGTATATTTAGTAT	854	OPA1 H31 3UTR(+2143+2167)	ACTCCACTCTTTGCAAATTCTGACA
855	OPA1 H31 3UTR(+2146+2170)	TCCACTCCACTCTTTGCAAATTCTG	873	OPA1 H31 3UTR(+2200+2224)	TTAAGTTTGGATATCATCTATTTAC

SEQ	ASO Coordinates	Sequence 5'>3'	SEQ	ASO Coordinates	Sequence 5'>3'
856	OPA1 H31 3UTR(+2149+2173)	TTGTCCACTCCACTCTTTGCAAATT	874	OPA1 H31 3UTR(+2203+2227)	AAATTAAGTTTGGATATCATCTATT
857	OPA1 H31 3UTR(+2152+2176)	GCTTTGTCCACTCCACTCTTTGCAA	875	OPA1 H31 3UTR(+2206+2230)	GCCAAATTAAGTTTGGATATCATCT
858	OPA1 H31 3UTR(+2155+2179)	AGAGCTTTGTCCACTCCACTCTTTG	876	OPA1 H31 3UTR(+2209+2233)	CTAGCCAAATTAAGTTTGGATATCA
859	OPA1 H31 3UTR(+2158+2182)	TACAGAGCTTTGTCCACTCCACTCT	877	OPA1 H31 3UTR(+2212+2236)	GTCCTAGCCAAATTAAGTTTGGATA
860	OPA1 H31 3UTR(+2161+2185)	CCATACAGAGCTTTGTCCACTCCAC	878	OPA1 H31 3UTR(+2215+2239)	GAAGTCCTAGCCAAATTAAGTTTGG
861	OPA1 H31 3UTR(+2164+2188)	CTTCCATACAGAGCTTTGTCCACTC	879	OPA1 H31 3UTR(+2218+2242)	ATTGAAGTCCTAGCCAAATTAAGTT
862	OPA1 H31 3UTR(+2167+2191)	AGTCTTCCATACAGAGCTTTGTCCA	880	OPA1 H31 3UTR(+2221+2245)	AAAATTGAAGTCCTAGCCAAATTAA
863	OPA1 H31 3UTR(+2170+2194)	TTCAGTCTTCCATACAGAGCTTTGT	881	OPA1 H31 3UTR(+2224+2248)	TTTAAAATTGAAGTCCTAGCCAAAT
864	OPA1 H31 3UTR(+2173+2197)	TTGTTCAGTCTTCCATACAGAGCTT	882	OPA1 H31 3UTR(+2227+2251)	ATTTTTAAAATTGAAGTCCTAGCCA
865	OPA1 H31 3UTR(+2176+2200)	CAGTTGTTCAGTCTTCCATACAGAG	883	OPA1 H31 3UTR(+2230+2254)	CTGATTTTTAAAATTGAAGTCCTAG
866	OPA1 H31 3UTR(+2179+2203)	TTACAGTTGTTCAGTCTTCCATACA	884	OPA1 H31 3UTR(+2233+2257)	ACACTGATTTTTAAAATTGAAGTCC
867	OPA1 H31 3UTR(+2182+2206)	TATTTACAGTTGTTCAGTCTTCCAT	885	OPA1 H31 3UTR(+2236+2260)	GGTACACTGATTTTTAAAATTGAAG
868	OPA1 H31 3UTR(+2185+2209)	ATCTATTTACAGTTGTTCAGTCTTC	886	OPA1 H31 3UTR(+2239+2263)	CTAGGTACACTGATTTTTAAAATTG
869	OPA1 H31 3UTR(+2188+2212)	ATCATCTATTTACAGTTGTTCAGTC	887	OPA1 H31 3UTR(+2242+2266)	TGCCTAGGTACACTGATTTTTAAAA
870	OPA1 H31 3UTR(+2191+2215)	GATATCATCTATTTACAGTTGTTCA	888	OPA1 H31 3UTR(+2245+2269)	CACTGCCTAGGTACACTGATTTTTA
871	OPA1 H31 3UTR(+2194+2218)	TTGGATATCATCTATTTACAGTTGT	889	OPA1 H31 3UTR(+2248+2272)	GTGCACTGCCTAGGTACACTGATTT
872	OPA1 H31 3UTR(+2197+2221)	AGTTTGGATATCATCTATTTACAGT	890	OPA1 H31 3UTR(+2251+2275)	GCTGTGCACTGCCTAGGTACACTGA
891	OPA1 H31 3UTR(+2254+2278)	CGTGCTGTGCACTGCCTAGGTACAC	909	OPA1 H31 3UTR(+2308+2332)	CCCGCAACTATAGCACAGTGGGTTA

SEQ	ASO Coordinates	Sequence 5'>3'	SEQ	ASO Coordinates	Sequence 5'>3'
892	OPA1 H31 3UTR(+2257+2281)	TTTCGTGCTGTGCACTGCCTAGGTA	910	OPA1 H31 3UTR(+2311+2335)	CCACCCGCAACTATAGCACAGTGGG
893	OPA1 H31 3UTR(+2260+2284)	TTATTTCGTGCTGTGCACTGCCTAG	911	OPA1 H31 3UTR(+2314+2338)	GTTCCACCCGCAACTATAGCACAGT
894	OPA1 H31 3UTR(+2263+2287)	CACTTATTTCGTGCTGTGCACTGCC	912	OPA1 H31 3UTR(+2317+2341)	ACTGTTCCACCCGCAACTATAGCAC
895	OPA1 H31 3UTR(+2266+2290)	GGCCACTTATTTCGTGCTGTGCACT	913	OPA1 H31 3UTR(+2320+2344)	TTGACTGTTCCACCCGCAACTATAG
896	OPA1 H31 3UTR(+2269+2293)	AAGGGCCACTTATTTCGTGCTGTGC	914	OPA1 H31 3UTR(+2323+2347)	AGGTTGACTGTTCCACCCGCAACTA
897	OPA1 H31 3UTR(+2272+2296)	TGCAAGGGCCACTTATTTCGTGCTG	915	OPA1 H31 3UTR(+2326+2350)	GAAAGGTTGACTGTTCCACCCGCAA
898	OPA1 H31 3UTR(+2275+2299)	AGCTGCAAGGGCCACTTATTTCGTG	916	OPA1 H31 3UTR(+2329+2353)	CTAGAAAGGTTGACTGTTCCACCCG
899	OPA1 H31 3UTR(+2278+2302)	GGAAGCTGCAAGGGCCACTTATTTC	917	OPA1 H31 3UTR(+2332+2356)	CTACTAGAAAGGTTGACTGTTCCAC
900	OPA1 H31 3UTR(+2281+2305)	CGGGGAAGCTGCAAGGGCCACTTAT	918	OPA1 H31 3UTR(+2335+2359)	AAACTACTAGAAAGGTTGACTGTTC
901	OPA1 H31 3UTR(+2284+2308)	AAACGGGGAAGCTGCAAGGGCCACT	919	OPA1 H31 3UTR(+2338+2362)	CATAAACTACTAGAAAGGTTGACTG
902	OPA1 H31 3UTR(+2287+2311)	GTTAAACGGGGAAGCTGCAAGGGCC	920	OPA1 H31 3UTR(+2341+2365)	TATCATAAACTACTAGAAAGGTTGA
903	OPA1 H31 3UTR(+2290+2314)	TGGGTTAAACGGGGAAGCTGCAAGG	921	OPA1 H31 3UTR(+2344+2368)	CAATATCATAAACTACTAGAAAGGT
904	OPA1 H31 3UTR(+2293+2317)	CAGTGGGTTAAACGGGGAAGCTGCA	922	OPA1 H31 3UTR(+2347+2371)	GGGCAATATCATAAACTACTAGAAA
905	OPA1 H31 3UTR(+2296+2320)	GCACAGTGGGTTAAACGGGGAAGCT	923	OPA1 H31 3UTR(+2350+2374)	AGAGGGCAATATCATAAACTACTAG
906	OPA1 H31 3UTR(+2299+2323)	ATAGCACAGTGGGTTAAACGGGGAA	924	OPA1 H31 3UTR(+2353+2377)	CAAAGAGGGCAATATCATAAACTAC
907	OPA1 H31 3UTR(+2302+2326)	ACTATAGCACAGTGGGTTAAACGGG	925	OPA1 H31 3UTR(+2356+2380)	ATACAAAGAGGGCAATATCATAAAC
908	OPA1 H31 3UTR(+2305+2329)	GCAACTATAGCACAGTGGGTTAAAC	926	OPA1 H31 3UTR(+2359+2383)	GGAATACAAAGAGGGCAATATCATA
927	OPA1 H31 3UTR(+2362+2386)	ATGGGAATACAAAGAGGGCAATATC	945	OPA1 H31 3UTR(+2416+2440)	CATTTGGAGGCTGAATAATTTGCAG

SEQ	ASO Coordinates	Sequence 5'>3'	SEQ	ASO Coordinates	Sequence 5'>3'
928	OPA1 H31 3UTR(+2365+2389)	AAAATGGGAATACAAAGAGGGCAAT	946	OPA1 H31 3UTR(+2419+2443)	TTGCATTTGGAGGCTGAATAATTTG
929	OPA1 H31 3UTR(+2368+2392)	TAGAAAATGGGAATACAAAGAGGGC	947	OPA1 H31 3UTR(+2422+2446)	CATTTGCATTTGGAGGCTGAATAAT
930	OPA1 H31 3UTR(+2371+2395)	CTGTAGAAAATGGGAATACAAAGAG	948	OPA1 H31 3UTR(+2425+2449)	ATTCATTTGCATTTGGAGGCTGAAT
931	OPA1 H31 3UTR(+2374+2398)	AAACTGTAGAAAATGGGAATACAAA	949	OPA1 H31 3UTR(+2428+2452)	ATCATTCATTTGCATTTGGAGGCTG
932	OPA1 H31 3UTR(+2377+2401)	AAAAAACTGTAGAAAATGGGAATAC	950	OPA1 H31 3UTR(+2431+2455)	TATATCATTCATTTGCATTTGGAGG
933	OPA1 H31 3UTR(+2380+2404)	CGGAAAAAACTGTAGAAAATGGGAA	951	OPA1 H31 3UTR(+2434+2458)	TTTTATATCATTCATTTGCATTTGG
934	OPA1 H31 3UTR(+2383+2407)	CTGCGGAAAAAACTGTAGAAAATGG	952	OPA1 H31 3UTR(+2437+2461)	TATTTTTATATCATTCATTTGCATT
935	OPA1 H31 3UTR(+2386+2410)	AGTCTGCGGAAAAAACTGTAGAAAA	953	OPA1 H31 3UTR(+2440+2464)	ACTTATTTTTATATCATTCATTTGC
936	OPA1 H31 3UTR(+2389+2413)	AGAAGTCTGCGGAAAAAACTGTAGA	954	OPA1 H31 3UTR(+2443+2467)	CCTACTTATTTTTATATCATTCATT
937	OPA1 H31 3UTR(+2392+2416)	GAAAGAAGTCTGCGGAAAAAACTGT	955	OPA1 H31 3UTR(+2446+2470)	TTCCCTACTTATTTTTATATCATTC
938	OPA1 H31 3UTR(+2395+2419)	GCAGAAAGAAGTCTGCGGAAAAAAC	956	OPA1 H31 3UTR(+2449+2473)	ATGTTCCCTACTTATTTTTATATCA
939	OPA1 H31 3UTR(+2398+2422)	TTTGCAGAAAGAAGTCTGCGGAAAA	957	OPA1 H31 3UTR(+2452+2476)	GCCATGTTCCCTACTTATTTTTATA
940	OPA1 H31 3UTR(+2401+2425)	TAATTTGCAGAAAGAAGTCTGCGGA	958	OPA1 H31 3UTR(+2455+2479)	TCTGCCATGTTCCCTACTTATTTTT
941	OPA1 H31 3UTR(+2404+2428)	GAATAATTTGCAGAAAGAAGTCTGC	959	OPA1 H31 3UTR(+2458+2482)	CTCTCTGCCATGTTCCCTACTTATT
942	OPA1 H31 3UTR(+2407+2431)	GCTGAATAATTTGCAGAAAGAAGTC	960	OPA1 H31 3UTR(+2461+2485)	CCACTCTCTGCCATGTTCCCTACTT
943	OPA1 H31 3UTR(+2410+2434)	GAGGCTGAATAATTTGCAGAAAGAA	961	OPA1 H31 3UTR(+2464+2488)	GCACCACTCTCTGCCATGTTCCCTA
944	OPA1 H31 3UTR(+2413+2437)	TTGGAGGCTGAATAATTTGCAGAAA	962	OPA1 H31 3UTR(+2467+2491)	GAAGCACCACTCTCTGCCATGTTCC
963	OPA1 H31 3UTR(+2470+2494)	TGGGAAGCACCACTCTCTGCCATGT	981	OPA1 H31 3UTR(+2524+2548)	TTTTAAACCTATACTCTGACTCTCA

SEQ	ASO Coordinates	Sequence 5'>3'	SEQ	ASO Coordinates	Sequence 5'>3'
964	OPA1 H31 3UTR(+2473:+2497)	GGCTGGGAAGCACCACTCTCTGCCA	982	OPA1 H31 3UTR(+2527:+2551)	ATCTTTTAAACCTATACTCTGACTC
965	OPA1 H31 3UTR(+2476:+2500)	TGAGGCTGGGAAGCACCACTCTCTG	983	OPA1 H31 3UTR(+2530:+2554)	TTTATCTTTTAAACCTATACTCTGA
966	OPA1 H31 3UTR(+2479:+2503)	TTGTGAGGCTGGGAAGCACCACTCT	984	OPA1 H31 3UTR(+2533:+2557)	GATTTTATCTTTTAAACCTATACTC
967	OPA1 H31 3UTR(+2482:+2506)	ACATTGTGAGGCTGGGAAGCACCAC	985	OPA1 H31 3UTR(+2536:+2560)	AAAGATTTTATCTTTTAAACCTATA
968	OPA1 H31 3UTR(+2485:+2509)	CCCACATTGTGAGGCTGGGAAGCAC	986	OPA1 H31 3UTR(+2539:+2563)	ACTAAAGATTTTATCTTTTAAACCT
969	OPA1 H31 3UTR(+2488:+2512)	ATTCCCACATTGTGAGGCTGGGAAG	987	OPA1 H31 3UTR(+2542:+2566)	TTAACTAAAGATTTTATCTTTTAAA
970	OPA1 H31 3UTR(+2491:+2515)	CAAATTCCCACATTGTGAGGCTGGG	988	OPA1 H31 3UTR(+2545:+2569)	TTATTAACTAAAGATTTTATCTTTT
971	OPA1 H31 3UTR(+2494:+2518)	TGTCAAATTCCCACATTGTGAGGCT	989	OPA1 H31 3UTR(+2548:+2572)	AAATTATTAACTAAAGATTTTATCT
972	OPA1 H31 3UTR(+2497:+2521)	CTATGTCAAATTCCCACATTGTGAG	990	OPA1 H31 3UTR(+2551:+2575)	ACAAAATTATTAACTAAAGATTTTA
973	OPA1 H31 3UTR(+2500:+2524)	ATCCTATGTCAAATTCCCACATTGT	991	OPA1 H31 3UTR(+2554:+2578)	AATACAAAATTATTAACTAAAGATT
974	OPA1 H31 3UTR(+2503:+2527)	CTCATCCTATGTCAAATTCCCACAT	992	OPA1 H31 3UTR(+2557:+2581)	ATAAATACAAAATTATTAACTAAAG
975	OPA1 H31 3UTR(+2506:+2530)	ACTCTCATCCTATGTCAAATTCCCA	993	OPA1 H31 3UTR(+2560:+2584)	TAAATAAATACAAAATTATTAACTA
976	OPA1 H31 3UTR(+2509:+2533)	CTGACTCTCATCCTATGTCAAATTC	994	OPA1 H31 3UTR(+2563:+2587)	GAATAAATAAATACAAAATTATTAA
977	OPA1 H31 3UTR(+2512:+2536)	ACTCTGACTCTCATCCTATGTCAAA	995	OPA1 H31 3UTR(+2566:+2590)	CTAGAATAAATAAATACAAAATTAT
978	OPA1 H31 3UTR(+2515:+2539)	TATACTCTGACTCTCATCCTATGTC	996	OPA1 H31 3UTR(+2569:+2593)	CATCTAGAATAAATAAATACAAAAT
979	OPA1 H31 3UTR(+2518:+2542)	ACCTATACTCTGACTCTCATCCTAT	997	OPA1 H31 3UTR(+2572:+2596)	ATACATCTAGAATAAATAAATACAA
980	OPA1 H31 3UTR(+2521:+2545)	TAAACCTATACTCTGACTCTCATCC	998	OPA1 H31 3UTR(+2575:+2599)	TACATACATCTAGAATAAATAAATA
999	OPA1 H31 3UTR(+2578:+2602)	AGATACATACATCTAGAATAAATAA	1017	OPA1 H31 3UTR(+2632:+2656)	ACCATTACTTTGATCCCCTTTATTG

SEQ	ASO Coordinates	Sequence 5'>3'	SEQ	ASO Coordinates	Sequence 5'>3'
1000	OPA1 H31 3UTR(+2581+2605)	CTCAGATACATACATCTAGAATAAA	1018	OPA1 H31 3UTR(+2635+2659)	AAAACCATTACTTTGATCCCCTTTA
1001	OPA1 H31 3UTR(+2584+2608)	TTCCTCAGATACATACATCTAGAAT	1019	OPA1 H31 3UTR(+2638+2662)	AGAAAAACCATTACTTTGATCCCCT
1002	OPA1 H31 3UTR(+2587+2611)	TCTTTCCTCAGATACATACATCTAG	1020	OPA1 H31 3UTR(+2641+2665)	GAGAGAAAAACCATTACTTTGATCC
1003	OPA1 H31 3UTR(+2590+2614)	ATTTCTTTCCTCAGATACATACATC	1021	OPA1 H31 3UTR(+2644+2668)	ACTGAGAGAAAAACCATTACTTTGA
1004	OPA1 H31 3UTR(+2593+2617)	CAGATTTCTTTCCTCAGATACATAC	1022	OPA1 H31 3UTR(+2647+2671)	AGAACTGAGAGAAAAACCATTACTT
1005	OPA1 H31 3UTR(+2596+2620)	TACCAGATTTCTTTCCTCAGATACA	1023	OPA1 H31 3UTR(+2650+2674)	TAGAGAACTGAGAGAAAAACCATTA
1006	OPA1 H31 3UTR(+2599+2623)	AAATACCAGATTTCTTTCCTCAGAT	1024	OPA1 H31 3UTR(+2653+2677)	GCTTAGAGAACTGAGAGAAAAACCA
1007	OPA1 H31 3UTR(+2602+2626)	CAAAAATACCAGATTTCTTTCCTCA	1025	OPA1 H31 3UTR(+2656+2680)	CCAGCTTAGAGAACTGAGAGAAAAA
1008	OPA1 H31 3UTR(+2605+2629)	AAGCAAAAATACCAGATTTCTTTCC	1026	OPA1 H31 3UTR(+2659+2683)	AGACCAGCTTAGAGAACTGAGAGAA
1009	OPA1 H31 3UTR(+2608+2632)	GGAAAGCAAAAATACCAGATTTCTT	1027	OPA1 H31 3UTR(+2662+2686)	CATAGACCAGCTTAGAGAACTGAGA
1010	OPA1 H31 3UTR(+2611+2635)	ATTGGAAAGCAAAAATACCAGATTT	1028	OPA1 H31 3UTR(+2665+2689)	TAACATAGACCAGCTTAGAGAACTG
1011	OPA1 H31 3UTR(+2614+2638)	TTTATTGGAAAGCAAAAATACCAGA	1029	OPA1 H31 3UTR(+2668+2692)	CTATAACATAGACCAGCTTAGAGAA
1012	OPA1 H31 3UTR(+2617+2641)	CCCTTTATTGGAAAGCAAAAATACC	1030	OPA1 H31 3UTR(+2671+2695)	GAGCTATAACATAGACCAGCTTAGA
1013	OPA1 H31 3UTR(+2620+2644)	ATCCCCTTTATTGGAAAGCAAAAAT	1031	OPA1 H31 3UTR(+2674+2698)	CTAGAGCTATAACATAGACCAGCTT
1014	OPA1 H31 3UTR(+2623+2647)	TTGATCCCCTTTATTGGAAAGCAAA	1032	OPA1 H31 3UTR(+2677+2701)	CTGCTAGAGCTATAACATAGACCAG
1015	OPA1 H31 3UTR(+2626+2650)	ACTTTGATCCCCTTTATTGGAAAGC	1033	OPA1 H31 3UTR(+2680+2704)	ATACTGCTAGAGCTATAACATAGAC
1016	OPA1 H31 3UTR(+2629+2653)	ATTACTTTGATCCCCTTTATTGGAA	1034	OPA1 H31 3UTR(+2683+2707)	TCCATACTGCTAGAGCTATAACATA
1035	OPA1 H31 3UTR(+2686+2710)	ATTTCCATACTGCTAGAGCTATAAC	1053	OPA1 H31 3UTR(+2740+2764)	ATCTCAACAACATATAGCCATGATC

SEQ	ASO Coordinates	Sequence 5'>3'	SEQ	ASO Coordinates	Sequence 5'>3'
1036	OPA1 H31 3UTR(+2689+2713)	CACATTTCCATACTGCTAGAGCTAT	1054	OPA1 H31 3UTR(+2743+2767)	AATATCTCAACACATATAGCCATG
1037	OPA1 H31 3UTR(+2692+2716)	AAGCACATTTCCATACTGCTAGAGC	1055	OPA1 H31 3UTR(+2746+2770)	TCAAATATCTCAACACATATAGCC
1038	OPA1 H31 3UTR(+2695+2719)	TTAAAGCACATTTCCATACTGCTAG	1056	OPA1 H31 3UTR(+2749+2773)	GTTTCAAATATCTCAACACATATA
1039	OPA1 H31 3UTR(+2698+2722)	ATTTTAAAGCACATTTCCATACTGC	1057	OPA1 H31 3UTR(+2752+2776)	TAAGTTTCAAATATCTCAACACAT
1040	OPA1 H31 3UTR(+2701+2725)	CATATTTTAAAGCACATTTCCATAC	1058	OPA1 H31 3UTR(+2755+2779)	AGGTAAGTTTCAAATATCTCAACAA
1041	OPA1 H31 3UTR(+2704+2728)	AAGCATATTTTAAAGCACATTTCCA	1059	OPA1 H31 3UTR(+2758+2782)	ACAAGGTAAGTTTCAAATATCTCAA
1042	OPA1 H31 3UTR(+2707+2731)	GGTAAGCATATTTTAAAGCACATTT	1060	OPA1 H31 3UTR(+2761+2785)	AAAACAAGGTAAGTTTCAAATATCT
1043	OPA1 H31 3UTR(+2710+2734)	AAAGGTAAGCATATTTTAAAGCACA	1061	OPA1 H31 3UTR(+2764+2788)	GTGAAAACAAGGTAAGTTTCAAATA
1044	OPA1 H31 3UTR(+2713+2737)	TCAAAAGGTAAGCATATTTTAAAGC	1062	OPA1 H31 3UTR(+2767+2791)	CAAGTGAAAAACAAGGTAAGTTTCAA
1045	OPA1 H31 3UTR(+2716+2740)	CATTCAAAAGGTAAGCATATTTTAA	1063	OPA1 H31 3UTR(+2770+2794)	GCACAAGTGAAAAACAAGGTAAGTTT
1046	OPA1 H31 3UTR(+2719+2743)	GATCATTCAAAAGGTAAGCATATTT	1064	OPA1 H31 3UTR(+2773+2797)	AGTGCACAAGTGAAAAACAAGGTAAG
1047	OPA1 H31 3UTR(+2722+2746)	CATGATCATTCAAAAGGTAAGCATA	1065	OPA1 H31 3UTR(+2776+2800)	CACAGTGCACAAGTGAAAAACAAGGT
1048	OPA1 H31 3UTR(+2725+2749)	AGCCATGATCATTCAAAAGGTAAGC	1066	OPA1 H31 3UTR(+2779+2803)	ATTCACAGTGCACAAGTGAAAAACAA
1049	OPA1 H31 3UTR(+2728+2752)	TATAGCCATGATCATTCAAAAGGTA	1067	OPA1 H31 3UTR(+2782+2806)	TTCATTCACAGTGCACAAGTGAAAA
1050	OPA1 H31 3UTR(+2731+2755)	ACATATAGCCATGATCATTCAAAAG	1068	OPA1 H31 3UTR(+2785+2809)	AAGTTCATTCACAGTGCACAAGTGA
1051	OPA1 H31 3UTR(+2734+2758)	ACAACATATAGCCATGATCATTCAA	1069	OPA1 H31 3UTR(+2788+2812)	ACAAAGTTCATTCACAGTGCACAAG
1052	OPA1 H31 3UTR(+2737+2761)	TCAACAACATATAGCCATGATCATT	1070	OPA1 H31 3UTR(+2791+2815)	AATACAAAGTTCATTCACAGTGCAC
1071	OPA1 H31 3UTR(+2794+2818)	AATAATACAAAGTTCATTCACAGTG	1089	OPA1 H31 3UTR(+2848+2872)	CAGGCAAAATATAAGTTGCAATAAT

SEQ	ASO Coordinates	Sequence 5'>3'	SEQ	ASO Coordinates	Sequence 5'>3'
1072	OPA1 H31 3UTR(+2797+2821)	AAAAATAATACAAAGTTCATTCACA	1090	OPA1 H31 3UTR(+2851+2875)	GCTCAGGCAAAATATAAGTTGCAAT
1073	OPA1 H31 3UTR(+2800+2824)	TAAAAAAATAATACAAAGTTCATTC	1091	OPA1 H31 3UTR(+2854+2878)	CAAGCTCAGGCAAAATATAAGTTGC
1074	OPA1 H31 3UTR(+2803+2827)	TTTTAAAAAAATAATACAAAGTTCA	1092	OPA1 H31 3UTR(+2857+2881)	GATCAAGCTCAGGCAAAATATAAGT
1075	OPA1 H31 3UTR(+2806+2830)	AGGTTTTTAAAAAAATAATACAAAGT	1093	OPA1 H31 3UTR(+2860+2884)	TTTGATCAAGCTCAGGCAAAATATA
1076	OPA1 H31 3UTR(+2809+2833)	TGAAGGTTTTTAAAAAAATAATACAA	1094	OPA1 H31 3UTR(+2863+2887)	ACCTTTGATCAAGCTCAGGCAAAAT
1077	OPA1 H31 3UTR(+2812+2836)	ATGTGAAGGTTTTTAAAAAAATAATA	1095	OPA1 H31 3UTR(+2866+2890)	ATGACCTTTGATCAAGCTCAGGCAA
1078	OPA1 H31 3UTR(+2815+2839)	GTAATGTGAAGGTTTTTAAAAAAATA	1096	OPA1 H31 3UTR(+2869+2893)	CAAATGACCTTTGATCAAGCTCAGG
1079	OPA1 H31 3UTR(+2818+2842)	CACGTAATGTGAAGGTTTTTAAAAAA	1097	OPA1 H31 3UTR(+2872+2896)	ACACAAATGACCTTTGATCAAGCTC
1080	OPA1 H31 3UTR(+2821+2845)	CTACACGTAATGTGAAGGTTTTTAAA	1098	OPA1 H31 3UTR(+2875+2899)	TCTACACAAATGACCTTTGATCAAG
1081	OPA1 H31 3UTR(+2824+2848)	TATCTACACGTAATGTGAAGGTTTTT	1099	OPA1 H31 3UTR(+2878+2902)	TCATCTACACAAATGACCTTTGATC
1082	OPA1 H31 3UTR(+2827+2851)	TAATATCTACACGTAATGTGAAGGT	1100	OPA1 H31 3UTR(+2881+2905)	TACTCATCTACACAAATGACCTTTG
1083	OPA1 H31 3UTR(+2830+2854)	CAATAATATCTACACGTAATGTGAA	1101	OPA1 H31 3UTR(+2884+2908)	AATTACTCATCTACACAAATGACCT
1084	OPA1 H31 3UTR(+2833+2857)	TTGCAATAATATCTACACGTAATGT	1102	OPA1 H31 3UTR(+2887+2911)	TTTAATTACTCATCTACACAAATGA
1085	OPA1 H31 3UTR(+2836+2860)	AAGTTGCAATAATATCTACACGTAA	1103	OPA1 H31 3UTR(+2890+2914)	TTTTTTAATTACTCATCTACACAAA
1086	OPA1 H31 3UTR(+2839+2863)	TATAAGTTGCAATAATATCTACACG	1104	OPA1 H31 3UTR(+2893+2917)	ATATTTTTTAATTACTCATCTACAC
1087	OPA1 H31 3UTR(+2842+2866)	AAATATAAGTTGCAATAATATCTAC	1105	OPA1 H31 3UTR(+2896+2920)	TAAATATTTTTTAATTACTCATCTA
1088	OPA1 H31 3UTR(+2845+2869)	GCAAAAATATAAGTTGCAATAATATC	1106	OPA1 H31 3UTR(+2899+2923)	ATTTAAATATTTTTTAATTACTCAT
1107	OPA1 H31 3UTR(+2902+2926)	GTGATTTAAATATTTTTTAATTACT	1125	OPA1 H31 3UTR(+2956+2980)	CTCGTTAAAACAGAAAAAAAATTTAA

SEQ	ASO Coordinates	Sequence 5'>3'	SEQ	ASO Coordinates	Sequence 5'>3'
1108	OPA1 H31 3UTR(+2905:+2929)	AATGTGATTTAAATATTTTTTAATT	1126	OPA1 H31 3UTR(+2959:+2983)	TCCCTCGTTAAAACAGAAAAAATT
1109	OPA1 H31 3UTR(+2908:+2932)	TATAATGTGATTTAAATATTTTTTA	1127	OPA1 H31 3UTR(+2962:+2986)	CTTTCCCTCGTTAAAACAGAAAAAA
1110	OPA1 H31 3UTR(+2911:+2935)	AATTATAATGTGATTTAAATATTTT	1128	OPA1 H31 3UTR(+2965:+2989)	TCTCTTTCCCTCGTTAAAACAGAAA
1111	OPA1 H31 3UTR(+2914:+2938)	TAGAATTATAATGTGATTTAAATAT	1129	OPA1 H31 3UTR(+2968:+2992)	GTTTCTCTTTCCCTCGTTAAAACAG
1112	OPA1 H31 3UTR(+2917:+2941)	TAATAGAATTATAATGTGATTTAAA	1130	OPA1 H31 3UTR(+2971:+2995)	CAGGTTTCTCTTTCCCTCGTTAAAA
1113	OPA1 H31 3UTR(+2920:+2944)	CAATAATAGAATTATAATGTGATTT	1131	OPA1 H31 3UTR(+2974:+2998)	ATACAGGTTTCTCTTTCCCTCGTTA
1114	OPA1 H31 3UTR(+2923:+2947)	CTCCAATAATAGAATTATAATGTGA	1132	OPA1 H31 3UTR(+2977:+3001)	GGTATACAGGTTTCTCTTTCCCTCG
1115	OPA1 H31 3UTR(+2926:+2950)	GCTCTCCAATAATAGAATTATAATG	1133	OPA1 H31 3UTR(+2980:+3004)	CTAGGTATACAGGTTTCTCTTTCCC
1116	OPA1 H31 3UTR(+2929:+2953)	GATGCTCTCCAATAATAGAATTATA	1134	OPA1 H31 3UTR(+2983:+3007)	ACCCTAGGTATACAGGTTTCTCTTT
1117	OPA1 H31 3UTR(+2932:+2956)	AAAGATGCTCTCCAATAATAGAATT	1135	OPA1 H31 3UTR(+2986:+3010)	ATGACCCTAGGTATACAGGTTTCTC
1118	OPA1 H31 3UTR(+2935:+2959)	TTAAAAGATGCTCTCCAATAATAGA	1136	OPA1 H31 3UTR(+2989:+3013)	ATAATGACCCTAGGTATACAGGTTT
1119	OPA1 H31 3UTR(+2938:+2962)	AATTTAAAAGATGCTCTCCAATAAT	1137	OPA1 H31 3UTR(+2992:+3016)	CAAATAATGACCCTAGGTATACAGG
1120	OPA1 H31 3UTR(+2941:+2965)	AAAAATTTAAAAGATGCTCTCCAAT	1138	OPA1 H31 3UTR(+2995:+3019)	GGTCAAATAATGACCCTAGGTATAC
1121	OPA1 H31 3UTR(+2944:+2968)	GAAAAAAATTTAAAAGATGCTCTCC	1139	OPA1 H31 3UTR(+2998:+3022)	TGGGGTCAAATAATGACCCTAGGTA
1122	OPA1 H31 3UTR(+2947:+2971)	ACAGAAAAAAAATTTAAAAGATGCTC	1140	OPA1 H31 3UTR(+3001:+3025)	CTATGGGGTCAAATAATGACCCTAG
1123	OPA1 H31 3UTR(+2950:+2974)	AAAACAGAAAAAAAATTTAAAAGATG	1141	OPA1 H31 3UTR(+3004:+3028)	ATACTATGGGGTCAAATAATGACCC
1124	OPA1 H31 3UTR(+2953:+2977)	GTTAAAACAGAAAAAAAATTTAAAAG	1142	OPA1 H31 3UTR(+3007:+3031)	GTTATACTATGGGGTCAAATAATGA
1143	OPA1 H31 3UTR(+3010:+3034)	CTGGTTATACTATGGGGTCAAATAA	1161	OPA1 H31 3UTR(+3064:+3088)	TGAAATTCAAGCATTCAGAGAAAAG

SEQ	ASO Coordinates	Sequence 5'>3'	SEQ	ASO Coordinates	Sequence 5'>3'
1144	OPA1 H31 3UTR(+3013+3037)	AATCTGGTTATACTATGGGGTCAAA	1162	OPA1 H31 3UTR(+3067+3091)	ATGTGAAATTCAAGCATTCAGAGAA
1145	OPA1 H31 3UTR(+3016+3040)	ATGAATCTGGTTATACTATGGGGTC	1163	OPA1 H31 3UTR(+3070+3094)	GGCATGTGAAATTCAAGCATTCAGA
1146	OPA1 H31 3UTR(+3019+3043)	ACCATGAATCTGGTTATACTATGGG	1164	OPA1 H31 3UTR(+3073+3097)	CAAGGCATGTGAAATTCAAGCATTC
1147	OPA1 H31 3UTR(+3022+3046)	TAGACCATGAATCTGGTTATACTAT	1165	OPA1 H31 3UTR(+3076+3100)	ATGCAAGGCATGTGAAATTCAAGCA
1148	OPA1 H31 3UTR(+3025+3049)	TGTTAGACCATGAATCTGGTTATAC	1166	OPA1 H31 3UTR(+3079+3103)	GAAATGCAAGGCATGTGAAATTCAA
1149	OPA1 H31 3UTR(+3028+3052)	GCTTGTTAGACCATGAATCTGGTTA	1167	OPA1 H31 3UTR(+3082+3106)	TGTGAAATGCAAGGCATGTGAAATT
1150	OPA1 H31 3UTR(+3031+3055)	AGAGCTTGTTAGACCATGAATCTGG	1168	OPA1 H31 3UTR(+3085+3109)	AACTGTGAAATGCAAGGCATGTGAA
1151	OPA1 H31 3UTR(+3034+3058)	CTGAGAGCTTGTTAGACCATGAATC	1169	OPA1 H31 3UTR(+3088+3112)	TACAACTGTGAAATGCAAGGCATGT
1152	OPA1 H31 3UTR(+3037+3061)	ACACTGAGAGCTTGTTAGACCATGA	1170	OPA1 H31 3UTR(+3091+3115)	GAGTACAACTGTGAAATGCAAGGCA
1153	OPA1 H31 3UTR(+3040+3064)	GCCACACTGAGAGCTTGTTAGACCA	1171	OPA1 H31 3UTR(+3094+3118)	ATGGAGTACAACTGTGAAATGCAAG
1154	OPA1 H31 3UTR(+3043+3067)	AAAGCCACACTGAGAGCTTGTTAGA	1172	OPA1 H31 3UTR(+3097+3121)	ACCATGGAGTACAACTGTGAAATGC
1155	OPA1 H31 3UTR(+3046+3070)	AGAAAAGCCACACTGAGAGCTTGTT	1173	OPA1 H31 3UTR(+3100+3124)	TTGACCATGGAGTACAACTGTGAAA
1156	OPA1 H31 3UTR(+3049+3073)	CAGAGAAAAGCCACACTGAGAGCTT	1174	OPA1 H31 3UTR(+3103+3127)	CGGTTGACCATGGAGTACAACTGTG
1157	OPA1 H31 3UTR(+3052+3076)	ATTCAGAGAAAAGCCACACTGAGAG	1175	OPA1 H31 3UTR(+3106+3130)	CACCGGTTGACCATGGAGTACAACT
1158	OPA1 H31 3UTR(+3055+3079)	AGCATTCAGAGAAAAGCCACACTGA	1176	OPA1 H31 3UTR(+3109+3133)	AAGCACCGGTTGACCATGGAGTACA
1159	OPA1 H31 3UTR(+3058+3082)	TCAAGCATTCAGAGAAAAGCCACAC	1177	OPA1 H31 3UTR(+3112+3136)	AAAAAGCACCGGTTGACCATGGAGT
1160	OPA1 H31 3UTR(+3061+3085)	AATTCAAGCATTCAGAGAAAAGCCA	1178	OPA1 H31 3UTR(+3115+3139)	GAAAAAAAGCACCGGTTGACCATGG
1179	OPA1 H31 3UTR(+3118+3142)	TGTGAAAAAAAGCACCGGTTGACCA	1197	OPA1 H31 3UTR(+3172+3196)	TTTTTATATATTTTACCAAGGAAA

SEQ	ASO Coordinates	Sequence 5'>3'	SEQ	ASO Coordinates	Sequence 5'>3'
1180	OPA1 H31 3UTR(+3121+3145)	CGATGTGAAAAAAAGCACCGGTTGA	1198	OPA1 H31 3UTR(+3175+3199)	ACCTTTTTTATATATTTTACCAAGG
1181	OPA1 H31 3UTR(+3124+3148)	CCACGATGTGAAAAAAAGCACCGGT	1199	OPA1 H31 3UTR(+3178+3202)	AAAACCTTTTTTATATATTTTACCA
1182	OPA1 H31 3UTR(+3127+3151)	GTACCACGATGTGAAAAAAAGCACC	1200	OPA1 H31 3UTR(+3181+3205)	TAGAAAACCTTTTTTTATATATTTTA
1183	OPA1 H31 3UTR(+3130+3154)	CAAGTACCACGATGTGAAAAAAAGC	1201	OPA1 H31 3UTR(+3184+3208)	AATTAGAAAACCTTTTTTTATATATT
1184	OPA1 H31 3UTR(+3133+3157)	TGACAAGTACCACGATGTGAAAAAA	1202	OPA1 H31 3UTR(+3187+3211)	TGAAATTAGAAAACCTTTTTTTATAT
1185	OPA1 H31 3UTR(+3136+3160)	TTTTGACAAGTACCACGATGTGAAA	1203	OPA1 H31 3UTR(+3190+3214)	AAGTGAAATTAGAAAACCTTTTTTA
1186	OPA1 H31 3UTR(+3139+3163)	ATGTTTTGACAAGTACCACGATGTG	1204	OPA1 H31 3UTR(+3193+3217)	GCAAAGTGAAATTAGAAAACCTTTT
1187	OPA1 H31 3UTR(+3142+3166)	AAAATGTTTTGACAAGTACCACGAT	1205	OPA1 H31 3UTR(+3196+3220)	GCAGCAAAGTGAAATTAGAAAACCT
1188	OPA1 H31 3UTR(+3145+3169)	AACAAAATGTTTTGACAAGTACCAC	1206	OPA1 H31 3UTR(+3199+3223)	TTGGCAGCAAAGTGAAATTAGAAAA
1189	OPA1 H31 3UTR(+3148+3172)	AATAACAAAATGTTTTGACAAGTAC	1207	OPA1 H31 3UTR(+3202+3226)	GCCTTGGCAGCAAAGTGAAATTAGA
1190	OPA1 H31 3UTR(+3151+3175)	GAAAATAACAAAATGTTTTGACAAG	1208	OPA1 H31 3UTR(+3205+3229)	ACAGCCTTGGCAGCAAAGTGAAATT
1191	OPA1 H31 3UTR(+3154+3178)	AAGGAAAATAACAAAATGTTTTGAC	1209	OPA1 H31 3UTR(+3208+3232)	ATGACAGCCTTGGCAGCAAAGTGAA
1192	OPA1 H31 3UTR(+3157+3181)	ACCAAGGAAAATAACAAAATGTTTT	1210	OPA1 H31 3UTR(+3211-24)	AAAATGACAGCCTTGGCAGCAAAGT
1193	OPA1 H31 3UTR(+3160+3184)	TTTACCAAGGAAAATAACAAAATGT	1211	OPA1 H31 3UTR(-3-27)	ATGAAAATGACAGCCTTGGCAGCAA
1194	OPA1 H31 3UTR(+3163+3187)	TATTTTACCAAGGAAAATAACAAAA	1212	OPA1 H31 3UTR(-6-30)	TTAATGAAAATGACAGCCTTGGCAG
1195	OPA1 H31 3UTR(+3166+3190)	ATATATTTTACCAAGGAAAATAACA	1213	OPA1 H31 3UTR(-9-33)	GCATTAATGAAAATGACAGCCTTGG
1196	OPA1 H31 3UTR(+3169+3193)	TTTATATATTTTACCAAGGAAAATA	1214	OPA1 H31 3UTR(-12-36)	GCAGCATTAATGAAAATGACAGCCT
1215	OPA1 H31 3UTR(-15-39)	TTGGCAGCATTAATGAAAATGACAG	1233	OPA1 H31 3UTR(-69-93)	TCTTCCAGTTCTAAAGCTTAGTTAT

SEQ	ASO Coordinates	Sequence 5'>3'	SEQ	ASO Coordinates	Sequence 5'>3'
1216	OPA1 H31 3UTR(-18-42)	ATGTTGGCAGCATTAATGAAAATGA	1234	OPA1 H31 3UTR(-72-96)	GTCTCTTCCAGTTCTAAAGCTTAGT
1217	OPA1 H31 3UTR(-21-45)	AACATGTTGGCAGCATTAATGAAAA	1235	OPA1 H31 3UTR(-75-99)	AAAGTCTCTTCCAGTTCTAAAGCTT
1218	OPA1 H31 3UTR(-24-48)	ATGAACATGTTGGCAGCATTAATGA	1236	OPA1 H31 3UTR(-78-102)	ATTAAAGTCTCTTCCAGTTCTAAAG
1219	OPA1 H31 3UTR(-27-51)	CATATGAACATGTTGGCAGCATTAA	1237	OPA1 H31 3UTR(-81-105)	GAAATTAAAGTCTCTTCCAGTTCTA
1220	OPA1 H31 3UTR(-30-54)	CCTCATATGAACATGTTGGCAGCAT	1238	OPA1 H31 3UTR(-84-108)	GATGAAATTAAAGTCTCTTCCAGTT
1221	OPA1 H31 3UTR(-33-57)	AAGCCTCATATGAACATGTTGGCAG	1239	OPA1 H31 3UTR(-87-111)	GTAGATGAAATTAAAGTCTCTTCCA
1222	OPA1 H31 3UTR(-36-60)	AGTAAGCCTCATATGAACATGTTGG	1240	OPA1 H31 3UTR(-90-114)	ATGGTAGATGAAATTAAAGTCTCTT
1223	OPA1 H31 3UTR(-39-63)	CTTAGTAAGCCTCATATGAACATGT	1241	OPA1 H31 3UTR(-93-117)	CAGATGGTAGATGAAATTAAAGTCT
1224	OPA1 H31 3UTR(-42-66)	CTTCTTAGTAAGCCTCATATGAACA	1242	OPA1 H31 3UTR(-96-120)	AATCAGATGGTAGATGAAATTAAAG
1225	OPA1 H31 3UTR(-45-69)	TAACTTCTTAGTAAGCCTCATATGA	1243	OPA1 H31 3UTR(-99-123)	TATAATCAGATGGTAGATGAAATTA
1226	OPA1 H31 3UTR(-48-72)	TTATAACTTCTTAGTAAGCCTCATA	1244	OPA1 H31 3UTR(-102-126)	GTTTATAATCAGATGGTAGATGAAA
1227	OPA1 H31 3UTR(-51-75)	TAGTTATAACTTCTTAGTAAGCCTC	1245	OPA1 H31 3UTR(-105-129)	GGAGTTTATAATCAGATGGTAGATG
1228	OPA1 H31 3UTR(-54-78)	GCTTAGTTATAACTTCTTAGTAAGC	1246	OPA1 H31 3UTR(-108-132)	ACAGGAGTTTATAATCAGATGGTAG
1229	OPA1 H31 3UTR(-57-81)	AAAGCTTAGTTATAACTTCTTAGTA	1247	OPA1 H31 3UTR(-111-135)	GTAACAGGAGTTTATAATCAGATGG
1230	OPA1 H31 3UTR(-60-84)	TCTAAAGCTTAGTTATAACTTCTTA	1248	OPA1 H31 3UTR(-114-138)	TGAGTAACAGGAGTTTATAATCAGA
1231	OPA1 H31 3UTR(-63-87)	AGTTCTAAAGCTTAGTTATAACTTC	1249	OPA1 H31 3UTR(-117-141)	AAGTGAGTAACAGGAGTTTATAATC
1232	OPA1 H31 3UTR(-66-90)	TCCAGTTCTAAAGCTTAGTTATAAC	1250	OPA1 H31 3UTR(-120-144)	ACAAAGTGAGTAACAGGAGTTTATA
1251	OPA1 H31 3UTR(-123-147)	ATAACAAAGTGAGTAACAGGAGTTT	1269	OPA1 H31 3UTR(-177-201)	ATATCCAATGATCGACAATTAGTAG

SEQ	ASO Coordinates	Sequence 5'>3'	SEQ	ASO Coordinates	Sequence 5'>3'
1252	OPA1 H31 3UTR(-126-150)	GGAATAACAAAGTGAGTAACAGGAG	1270	OPA1 H31 3UTR(-180-204)	GACATATCCAATGATCGACAATTAG
1253	OPA1 H31 3UTR(-129-153)	GGAGGAATAACAAAGTGAGTAACAG	1271	OPA1 H31 3UTR(-183-207)	CTTGACATATCCAATGATCGACAATT
1254	OPA1 H31 3UTR(-132-156)	TCTGGAGGAATAACAAAGTGAGTAA	1272	OPA1 H31 3UTR(-186-210)	TAACTTGACATATCCAATGATCGAC
1255	OPA1 H31 3UTR(-135-159)	AGTTCTGGAGGAATAACAAAGTGAG	1273	OPA1 H31 3UTR(-189-213)	ACCTAACTTGACATATCCAATGATC
1256	OPA1 H31 3UTR(-138-162)	CAAAGTTCTGGAGGAATAACAAAGT	1274	OPA1 H31 3UTR(-192-216)	GCTACCTAACTTGACATATCCAATG
1257	OPA1 H31 3UTR(-141-165)	GAGCAAAGTTCTGGAGGAATAACAA	1275	OPA1 H31 3UTR(-195-219)	TACGCTACCTAACTTGACATATCCA
1258	OPA1 H31 3UTR(-144-168)	TATGAGCAAAGTTCTGGAGGAATAA	1276	OPA1 H31 3UTR(-198-222)	CTATACGCTACCTAACTTGACATAT
1259	OPA1 H31 3UTR(-147-171)	ATTTATGAGCAAAGTTCTGGAGGAA	1277	OPA1 H31 3UTR(-201-225)	CACCTATACGCTACCTAACTTGACA
1260	OPA1 H31 3UTR(-150-174)	ATCATTTATGAGCAAAGTTCTGGAG	1278	OPA1 H31 3UTR(-204-228)	GCACACCTATACGCTACCTAACTTG
1261	OPA1 H31 3UTR(-153-177)	GGTATCATTTATGAGCAAAGTTCTG	1279	OPA1 H31 3UTR(-207-231)	AAGGCACACCTATACGCTACCTAAC
1262	OPA1 H31 3UTR(-156-180)	GTAGGTATCATTTATGAGCAAAGTT	1280	OPA1 H31 3UTR(-210-234)	AAGAAGGCACACCTATACGCTACCT
1263	OPA1 H31 3UTR(-159-183)	TTAGTAGGTATCATTTATGAGCAAA	1281	OPA1 H31 3UTR(-213-237)	ATTAAGAAGGCACACCTATACGCTA
1264	OPA1 H31 3UTR(-162-186)	CAATTAGTAGGTATCATTTATGAGC	1282	OPA1 H31 3UTR(-216-240)	GGAATTAAGAAGGCACACCTATACG
1265	OPA1 H31 3UTR(-165-189)	CGACAATTAGTAGGTATCATTTATG	1283	OPA1 H31 3UTR(-219-243)	GAAGGAATTAAGAAGGCACACCTAT
1266	OPA1 H31 3UTR(-168-192)	GATCGACAATTAGTAGGTATCATTT	1284	OPA1 H31 3UTR(-222-246)	TCTGAAGGAATTAAGAAGGCACACC
1267	OPA1 H31 3UTR(-171-195)	AATGATCGACAATTAGTAGGTATCA	1285	OPA1 H31 3UTR(-225-249)	TCTTCTGAAGGAATTAAGAAGGCAC
1268	OPA1 H31 3UTR(-174-198)	TCCAATGATCGACAATTAGTAGGTA	1286	OPA1 H31 3UTR(-228-252)	GCATCTTCTGAAGGAATTAAGAAGG
1287	OPA1 H31 3UTR(-231-255)	TCTGCATCTTCTGAAGGAATTAAGA	1300	OPA1 H31 3UTR(-270-294)	AGAAAACCAATGCTAACACGATTGA

SEQ	ASO Coordinates	Sequence 5'>3'	SEQ	ASO Coordinates	Sequence 5'>3'
1288	OPA1 H31 3UTR(-234-258)	GCCTCTGCATCTTCTGAAGGAATTA	1301	OPA1 H31 3UTR(-273-297)	TAAAGAAAACCAATGCTAACACGAT
1289	OPA1 H31 3UTR(-237-261)	CTTGCCTCTGCATCTTCTGAAGGAA	1302	OPA1 H31 3UTR(-276-300)	TGATAAAGAAAACCAATGCTAACAC
1290	OPA1 H31 3UTR(-240-264)	GTTCTTGCCTCTGCATCTTCTGAAG	1303	OPA1 H31 3UTR(-279-303)	CACTGATAAAGAAAACCAATGCTAA
1291	OPA1 H31 3UTR(-243-267)	CATGTTCTTGCCTCTGCATCTTCTG	1304	OPA1 H31 3UTR(-282-306)	TAGCACTGATAAAGAAAACCAATGC
1292	OPA1 H31 3UTR(-246-270)	AAACATGTTCTTGCCTCTGCATCTT	1305	OPA1 H31 3UTR(-285-309)	TGTTAGCACTGATAAAGAAAACCAA
1293	OPA1 H31 3UTR(-249-273)	TTGAAACATGTTCTTGCCTCTGCAT	1306	OPA1 H31 3UTR(-288-312)	GTCTGTTAGCACTGATAAAGAAAAC
1294	OPA1 H31 3UTR(-252-276)	CGATTGAAACATGTTCTTGCCTCTG	1307	OPA1 H31 3UTR(-291-315)	TGAGTCTGTTAGCACTGATAAAGAA
1295	OPA1 H31 3UTR(-255-279)	ACACGATTGAAACATGTTCTTGCCT	1308	OPA1 H31 3UTR(-294-318)	CACTGAGTCTGTTAGCACTGATAAA
1296	OPA1 H31 3UTR(-258-282)	CTAACACGATTGAAACATGTTCTTG	1309	OPA1 H31 3UTR(-297-321)	TCACACTGAGTCTGTTAGCACTGAT
1297	OPA1 H31 3UTR(-261-285)	ATGCTAACACGATTGAAACATGTTC	1310	OPA1 H31 3UTR(-300-324)	GCCTCACACTGAGTCTGTTAGCACT
1298	OPA1 H31 3UTR(-264-288)	CCAATGCTAACACGATTGAAACATG	1311	OPA1 H31 3UTR(-303-327)	GGGGCCTCACACTGAGTCTGTTAGC
1299	OPA1 H31 3UTR(-267-291)	AAACCAATGCTAACACGATTGAAAC	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	1332	OPA1 H31 3UTR(+58+74)	AGAGGCTGGACAAAAGA
1314	OPA1 H30:31 3UTR(+4+20)	ATTATGAGTACGATTTT	1333	OPA1 H31 3UTR(+61+77)	AAAAGAGGCTGGACAAA
1315	OPA1 H31 3UTR(+7+23)	CTGATTATGAGTACGAT	1334	OPA1 H31 3UTR(+64+80)	AGAAAAAGAGGCTGGAC
1316	OPA1 H31 3UTR(+10+26)	GAGCTGATTATGAGTAC	1335	OPA1 H31 3UTR(+67+83)	AGAAGAAAAAGAGGCTG
1317	OPA1 H31 3UTR(+13+29)	GCAGAGCTGATTATGAG	1336	OPA1 H31 3UTR(+70+86)	AGCAGAAGAAAAAGAGG
1318	OPA1 H31 3UTR(+16+32)	TATGCAGAGCTGATTAT	1337	OPA1 H31 3UTR(+73+89)	AACAGCAGAAGAAAAAG
1319	OPA1 H31 3UTR(+19+35)	ATGTATGCAGAGCTGAT	1338	OPA1 H31 3UTR(+76+92)	TGGAACAGCAGAAGAAA
1320	OPA1 H31 3UTR(+22+38)	CAGATGTATGCAGAGCT	1339	OPA1 H31 3UTR(+79+95)	AGGTGGAACAGCAGAAG
1321	OPA1 H31 3UTR(+25+41)	CTTCAGATGTATGCAGA	1340	OPA1 H31 3UTR(+82+98)	GAAAGGTGGAACAGCAG
1322	OPA1 H31 3UTR(+28+44)	GTTCTTCAGATGTATGC	1341	OPA1 H31 3UTR(+85+101)	TTAGAAAGGTGGAACAG
1323	OPA1 H31 3UTR(+31+47)	TTGTTCTTCAGATGTA	1342	OPA1 H31 3UTR(+88+104)	TGTTTAGAAAGGTGGAA
1324	OPA1 H31 3UTR(+34+50)	GTTTTTGTTCTTCAGAT	1343	OPA1 H31 3UTR(+91+107)	GTATGTTTAGAAAGGTG
1325	OPA1 H31 3UTR(+37+53)	GATGTTTTTGTTCTTCA	1344	OPA1 H31 3UTR(+94+110)	ATTGTATGTTTAGAAAG
1326	OPA1 H31 3UTR(+40+56)	GTTGATGTTTTTGTTCT	1345	OPA1 H31 3UTR(+97+113)	TTTATTGTATGTTTAGA
1327	OPA1 H31 3UTR(+43+59)	GACGTTGATGTTTTTGT	1346	OPA1 H31 3UTR(+100+116)	GACTTTATTGTATGTTT
1328	OPA1 H31 3UTR(+46+62)	AAAGACGTTGATGTTTT	1347	OPA1 H31 3UTR(+103+119)	CATGACTTTATTGTATG
1329	OPA1 H31 3UTR(+49+65)	ACAAAAGACGTTGATGT	1348	OPA1 H31 3UTR(+106+122)	TCCCATGACTTTATTGT
1330	OPA1 H31 3UTR(+52+68)	TGGACAAAAGACGTTGA	1349	OPA1 H31 3UTR(+109+125)	TTATCCCATGACTTTAT
1331	OPA1 H31 3UTR(+55+71)	GGCTGGACAAAAGACGT	1350	OPA1 H31 3UTR(+112+128)	TTTTTATCCCATGACTT
1351	OPA1 H31 3UTR(+115+131)	TTATTTTTATCCCATGA	1372	OPA1 H31 3UTR(+178+194)	CATTACCACTGTTCTTC

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
1352	OPA1 H31 3UTR(+118+134)	CGATTATTTTTATCCCA	1373	OPA1 H31 3UTR(+181+197)	ATCCATTACCACTGTTC
1353	OPA1 H31 3UTR(+121+137)	CATCGATTATTTTTATC	1374	OPA1 H31 3UTR(+184+200)	TTAATCCATTACCACTG
1354	OPA1 H31 3UTR(+124+140)	ATACATCGATTATTTTT	1375	OPA1 H31 3UTR(+187+203)	ATGTTAATCCATTACCA
1355	OPA1 H31 3UTR(+127+143)	AACATACATCGATTATT	1376	OPA1 H31 3UTR(+190+206)	AGGATGTTAATCCATTA
1356	OPA1 H31 3UTR(+130+146)	CGTAACATACATCGATT	1377	OPA1 H31 3UTR(+193+209)	AATAGGATGTTAATCCA
1357	OPA1 H31 3UTR(+133+149)	GCCCGTAACATACATCG	1378	OPA1 H31 3UTR(+196+212)	CAAAATAGGATGTTAAT
1358	OPA1 H31 3UTR(+136+152)	AGCGCCCGTAACATACA	1379	OPA1 H31 3UTR(+199+215)	CAACAAAATAGGATGTT
1359	OPA1 H31 3UTR(+139+155)	TAAAGCGCCCGTAACAT	1380	OPA1 H31 3UTR(+202+218)	GTACAACAAAATAGGAT
1360	OPA1 H31 3UTR(+142+158)	GGTTAAAGCGCCCGTAA	1381	OPA1 H31 3UTR(+205+221)	TTAGTACAACAAAATAG
1361	OPA1 H31 3UTR(+145+161)	GATGGTTAAAGCGCCCG	1382	OPA1 H31 3UTR(+208+224)	ACTTTAGTACAACAAAA
1362	OPA1 H31 3UTR(+148+164)	GCTGATGGTTAAAGCGC	1383	OPA1 H31 3UTR(+211+227)	GTCACTTTAGTACAACA
1363	OPA1 H31 3UTR(+151+167)	GCAGCTGATGGTTAAAG	1384	OPA1 H31 3UTR(+214+230)	TTTGTCACTTTAGTACA
1364	OPA1 H31 3UTR(+154+170)	GAGGCAGCTGATGGTTA	1385	OPA1 H31 3UTR(+217+233)	CGATTTGTCACTTTAGT
1365	OPA1 H31 3UTR(+157+173)	CGAGAGGCAGCTGATGG	1386	OPA1 H31 3UTR(+220+236)	TTCCGATTTGTCACTTT
1366	OPA1 H31 3UTR(+160+176)	ATTCGAGAGGCAGCTGA	1387	OPA1 H31 3UTR(+223+239)	TTATTCCGATTTGTCAC
1367	OPA1 H31 3UTR(+163+179)	TCCATTCGAGAGGCAGC	1388	OPA1 H31 3UTR(+226+242)	ATATTATTCCGATTTGT
1368	OPA1 H31 3UTR(+166+182)	TCTTCCATTCGAGAGGC	1389	OPA1 H31 3UTR(+229+245)	ATTATATTATTCCGATT
1369	OPA1 H31 3UTR(+169+185)	TGTTCTTCCATTCGAGA	1390	OPA1 H31 3UTR(+232+248)	CCAATTATATTATTCCG
1370	OPA1 H31 3UTR(+172+188)	CACTGTTCTTCCATTCG	1391	OPA1 H31 3UTR(+235+251)	ATACCAATTATATTATT
1371	OPA1 H31 3UTR(+175+191)	TACCACTGTTCTTCCAT	1392	OPA1 H31 3UTR(+238+254)	GCCATACCAATTATATT
1393	OPA1 H31 3UTR(+241+257)	ATGGCCATACCAATTAT	1414	OPA1 H31 3UTR(+304+320)	AGTGCCACCACAAATAA
1394	OPA1 H31 3UTR(+244+260)	CTAATGGCCATACCAAT	1415	OPA1 H31 3UTR(+307+323)	ACGAGTGCCACCACAAA

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
1395	OPA1 H31 3UTR(+247+263)	AACCTAATGGCCATACC	1416	OPA1 H31 3UTR(+310+326)	TAAACGAGTGCCACCAC
1396	OPA1 H31 3UTR(+250+266)	CTGAACCTAATGGCCAT	1417	OPA1 H31 3UTR(+313+329)	CATTAAACGAGTGCCAC
1397	OPA1 H31 3UTR(+253+269)	GGACTGAACCTAATGGC	1418	OPA1 H31 3UTR(+316+332)	ATCCATTAAACGAGTGC
1398	OPA1 H31 3UTR(+256+272)	CAAGGACTGAACCTAAT	1419	OPA1 H31 3UTR(+319+335)	TTAATCCATTAAACGAG
1399	OPA1 H31 3UTR(+259+275)	CTTCAAGGACTGAACCT	1420	OPA1 H31 3UTR(+322+338)	CAGTTAATCCATTAAAC
1400	OPA1 H31 3UTR(+262+278)	TATCTTCAAGGACTGAA	1421	OPA1 H31 3UTR(+325+341)	CCTCAGTTAATCCATTA
1401	OPA1 H31 3UTR(+265+281)	TCTTATCTTCAAGGACT	1422	OPA1 H31 3UTR(+328+344)	CAACCTCAGTTAATCCA
1402	OPA1 H31 3UTR(+268+284)	GTTTCTTATCTTCAAGG	1423	OPA1 H31 3UTR(+331+347)	GAGCAACCTCAGTTAAT
1403	OPA1 H31 3UTR(+271+287)	CAAGTTTCTTATCTTCA	1424	OPA1 H31 3UTR(+334+350)	ATTGAGCAACCTCAGTT
1404	OPA1 H31 3UTR(+274+290)	GAACAAGTTTCTTATCT	1425	OPA1 H31 3UTR(+337+353)	AACATTGAGCAACCTCA
1405	OPA1 H31 3UTR(+277+293)	AGAGAACAAGTTTCTTA	1426	OPA1 H31 3UTR(+340+356)	CTGAACATTGAGCAACC
1406	OPA1 H31 3UTR(+280+296)	AACAGAGAACAAGTTTC	1427	OPA1 H31 3UTR(+343+359)	AAACTGAACATTGAGCA
1407	OPA1 H31 3UTR(+283+299)	ACAAACAGAGAACAAGT	1428	OPA1 H31 3UTR(+346+362)	AAGAAACTGAACATTGA
1408	OPA1 H31 3UTR(+286+302)	ACAACAAACAGAGAACA	1429	OPA1 H31 3UTR(+349+365)	GAAAAGAAACTGAACAT
1409	OPA1 H31 3UTR(+289+305)	AAGACAACAAACAGAGA	1430	OPA1 H31 3UTR(+352+368)	CTGGAAAAGAAACTGAA
1410	OPA1 H31 3UTR(+292+308)	AATAAGACAACAAACAG	1431	OPA1 H31 3UTR(+355+371)	TTTCTGGAAAAGAAACT
1411	OPA1 H31 3UTR(+295+311)	ACAAATAAGACAACAAA	1432	OPA1 H31 3UTR(+358+374)	GTATTTCTGGAAAAGAA
1412	OPA1 H31 3UTR(+298+314)	ACCACAAATAAGACAAC	1433	OPA1 H31 3UTR(+361+377)	ATTGTATTTCTGGAAAA
1413	OPA1 H31 3UTR(+301+317)	GCCACCACAAATAAGAC	1434	OPA1 H31 3UTR(+364+380)	AGCATTGTATTTCTGGA
1435	OPA1 H31 3UTR(+367+383)	CCTAGCATTGTATTTCT	1456	OPA1 H31 3UTR(+430+446)	ACTGTGATTTTATATAC
1436	OPA1 H31 3UTR(+370+386)	ACACCTAGCATTGTATT	1457	OPA1 H31 3UTR(+433+449)	GCTACTGTGATTTTATA
1437	OPA1 H31 3UTR(+373+389)	AAAACACCTAGCATTGT	1458	OPA1 H31 3UTR(+436+452)	CAGGCTACTGTGATTTT

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
1438	OPA1 H31 3UTR(+376+392)	TTCAAAAACACCTAGCAT	1459	OPA1 H31 3UTR(+439+455)	TAGCAGGCTACTGTGAT
1439	OPA1 H31 3UTR(+379+395)	TATTTCAAAACACCTAG	1460	OPA1 H31 3UTR(+442+458)	ATTTAGCAGGCTACTGT
1440	OPA1 H31 3UTR(+382+398)	TTTTATTTCAAAACACC	1461	OPA1 H31 3UTR(+445+461)	ATGATTTAGCAGGCTAC
1441	OPA1 H31 3UTR(+385+401)	AAGTTTTATTTCAAAAC	1462	OPA1 H31 3UTR(+448+464)	ACAATGATTTAGCAGGC
1442	OPA1 H31 3UTR(+388+404)	TATAAGTTTTATTTCAA	1463	OPA1 H31 3UTR(+451+467)	CATACAATGATTTAGCA
1443	OPA1 H31 3UTR(+391+407)	CTATATAAGTTTTATTT	1464	OPA1 H31 3UTR(+454+470)	ACACATACAATGATTTA
1444	OPA1 H31 3UTR(+394+410)	TTGCTATATAAGTTTTA	1465	OPA1 H31 3UTR(+457+473)	CAGACACATACAATGAT
1445	OPA1 H31 3UTR(+397+413)	CAATTGCTATATAAGTT	1466	OPA1 H31 3UTR(+460+476)	CTACAGACACATACAAT
1446	OPA1 H31 3UTR(+400+416)	AAACAATTGCTATATAA	1467	OPA1 H31 3UTR(+463+479)	ATACTACAGACACATAC
1447	OPA1 H31 3UTR(+403+419)	TTTAAACAATTGCTATA	1468	OPA1 H31 3UTR(+466+482)	AGAATACTACAGACACA
1448	OPA1 H31 3UTR(+406+422)	AACTTTAAACAATTGCT	1469	OPA1 H31 3UTR(+469+485)	AATAGAATACTACAGAC
1449	OPA1 H31 3UTR(+409+425)	GATAACTTTAAACAATT	1470	OPA1 H31 3UTR(+472+488)	GGGAATAGAATACTACA
1450	OPA1 H31 3UTR(+412+428)	ATTGATAACTTTAAACA	1471	OPA1 H31 3UTR(+475+491)	TCTGGGAATAGAATACT
1451	OPA1 H31 3UTR(+415+431)	ACAATTGATAACTTTAA	1472	OPA1 H31 3UTR(+478+494)	GTTTCTGGGAATAGAAT
1452	OPA1 H31 3UTR(+418+434)	TATACAATTGATAACTT	1473	OPA1 H31 3UTR(+481+497)	ATAGTTTCTGGGAATAG
1453	OPA1 H31 3UTR(+421+437)	TTATATACAATTGATAA	1474	OPA1 H31 3UTR(+484+500)	CAAATAGTTTCTGGGAA
1454	OPA1 H31 3UTR(+424+440)	ATTTTATATACAATTGA	1475	OPA1 H31 3UTR(+487+503)	GGTCAAATAGTTTCTGG
1455	OPA1 H31 3UTR(+427+443)	GTGATTTTATATACAAT	1476	OPA1 H31 3UTR(+490+506)	CATGGTCAAATAGTTTC
1477	OPA1 H31 3UTR(+493+509)	TATCATGGTCAAATAGT	1498	OPA1 H31 3UTR(+556+572)	TAACCTGTTTTAAGGGT
1478	OPA1 H31 3UTR(+496+512)	AATTATCATGGTCAAAT	1499	OPA1 H31 3UTR(+559+575)	AATTAACCTGTTTTAAG
1479	OPA1 H31 3UTR(+499+515)	CTGAATTATCATGGTCA	1500	OPA1 H31 3UTR(+562+578)	CCAAATTAACCTGTTTT
1480	OPA1 H31 3UTR(+502+518)	AAACTGAATTATCATGG	1501	OPA1 H31 3UTR(+565+581)	AATCCAAATTAACCTGT

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
1481	OPA1 H31 3UTR(+505+521)	TATAAACTGAATTATCA	1502	OPA1 H31 3UTR(+568+584)	TACAATCCAAATTAACC
1482	OPA1 H31 3UTR(+508+524)	GAATATAAACTGAATTA	1503	OPA1 H31 3UTR(+571+587)	CGTTACAATCCAAATTA
1483	OPA1 H31 3UTR(+511+527)	GGTGAATATAAACTGAA	1504	OPA1 H31 3UTR(+574+590)	GAACGTTACAATCCAAA
1484	OPA1 H31 3UTR(+514+530)	TGTGGTGAATATAAACT	1505	OPA1 H31 3UTR(+577+593)	ACTGAACGTTACAATCC
1485	OPA1 H31 3UTR(+517+533)	TCATGTGGTGAATATAA	1506	OPA1 H31 3UTR(+580+596)	TTCACTGAACGTTACAA
1486	OPA1 H31 3UTR(+520+536)	CTTTCATGTGGTGAATA	1507	OPA1 H31 3UTR(+583+599)	TCTTTCACTGAACGTTA
1487	OPA1 H31 3UTR(+523+539)	TTTCTTTCATGTGGTGA	1508	OPA1 H31 3UTR(+586+602)	ATTTCTTTCACTGAACG
1488	OPA1 H31 3UTR(+526+542)	ATTTTTCTTTCATGTGG	1509	OPA1 H31 3UTR(+589+605)	GAAATTTCTTTCACTGA
1489	OPA1 H31 3UTR(+529+545)	CCCATTTTTCTTTCATG	1510	OPA1 H31 3UTR(+592+608)	GTTGAAATTTCTTTCAC
1490	OPA1 H31 3UTR(+532+548)	TTACCCATTTTTCTTTC	1511	OPA1 H31 3UTR(+595+611)	AGGGTTGAAATTTCTTT
1491	OPA1 H31 3UTR(+535+551)	CTGTTACCCATTTTTCT	1512	OPA1 H31 3UTR(+598+614)	TGAAGGGTTGAAATTTC
1492	OPA1 H31 3UTR(+538+554)	CTTCTGTTACCCATTTT	1513	OPA1 H31 3UTR(+601+617)	CTATGAAGGGTTGAAAT
1493	OPA1 H31 3UTR(+541+557)	GTTCTTCTGTTACCCAT	1514	OPA1 H31 3UTR(+604+620)	TGGCTATGAAGGGTTGA
1494	OPA1 H31 3UTR(+544+560)	AGGGTTCTTCTGTTACC	1515	OPA1 H31 3UTR(+607+623)	CGCTGGCTATGAAGGGT
1495	OPA1 H31 3UTR(+547+563)	TTAAGGGTTCTTCTGTT	1516	OPA1 H31 3UTR(+610+626)	CTTCGCTGGCTATGAAG
1496	OPA1 H31 3UTR(+550+566)	GTTTTAAGGGTTCTTCT	1517	OPA1 H31 3UTR(+613+629)	TTTCTTCGCTGGCTATG
1497	OPA1 H31 3UTR(+553+569)	CCTGTTTTAAGGGTTCT	1518	OPA1 H31 3UTR(+616+632)	AAATTTCTTCGCTGGCT
1519	OPA1 H31 3UTR(+619+635)	GGCAAATTTCTTCGCTG	1544	OPA1 H31 3UTR(+694+710)	ATTTCAAATGGATATAG
1520	OPA1 H31 3UTR(+622+638)	CAAGGCAAATTTCTTCG	1545	OPA1 H31 3UTR(+697+713)	TCAATTTCAAATGGATA
1521	OPA1 H31 3UTR(+625+641)	TTCCAAGGCAAATTTCT	1546	OPA1 H31 3UTR(+700+716)	AAATCAATTTCAAATGG
1522	OPA1 H31 3UTR(+628+644)	GGCTTCCAAGGCAAATT	1547	OPA1 H31 3UTR(+703+719)	AATAAATCAATTTCAAA
1527	OPA1 H31 3UTR(+643+659)	AGCTGGTACTGACTTGG	1548	OPA1 H31 3UTR(+706+722)	TAAAATAAATCAATTTC

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
1528	OPA1 H31 3UTR(+646+662)	GTAAGCTGGTACTGACT	1549	OPA1 H31 3UTR(+709+725)	ATCTAAAATAAATCAAT
1529	OPA1 H31 3UTR(+649+665)	TAGGTAAGCTGGTACTG	1550	OPA1 H31 3UTR(+712+728)	AACATCTAAAATAAATC
1530	OPA1 H31 3UTR(+652+668)	AAATAGGTAAGCTGGTA	1551	OPA1 H31 3UTR(+715+731)	TACAACATCTAAAATAA
1531	OPA1 H31 3UTR(+655+671)	ATCAAATAGGTAAGCTG	1552	OPA1 H31 3UTR(+718+734)	GTATACAACATCTAAAA
1532	OPA1 H31 3UTR(+658+674)	TGAATCAAATAGGTAAG	1553	OPA1 H31 3UTR(+721+737)	TAAGTATACAACATCTA
1533	OPA1 H31 3UTR(+661+677)	AACTGAATCAAATAGGT	1554	OPA1 H31 3UTR(+724+740)	ACGTAAGTATACAACAT
1534	OPA1 H31 3UTR(+664+680)	AGCAACTGAATCAAATA	1555	OPA1 H31 3UTR(+727+743)	CTAACGTAAGTATACAA
1535	OPA1 H31 3UTR(+667+683)	AACAGCAACTGAATCAA	1556	OPA1 H31 3UTR(+730+746)	AGCCTAACGTAAGTATA
1536	OPA1 H31 3UTR(+670+686)	GAAAACAGCAACTGAAT	1557	OPA1 H31 3UTR(+733+749)	GAAAGCCTAACGTAAGT
1537	OPA1 H31 3UTR(+673+689)	TGAGAAAACAGCAACTG	1558	OPA1 H31 3UTR(+736+752)	ACAGAAAGCCTAACGTA
1538	OPA1 H31 3UTR(+676+692)	GAGTGAGAAAACAGCAA	1559	OPA1 H31 3UTR(+739+755)	TTAACAGAAAGCCTAAC
1539	OPA1 H31 3UTR(+679+695)	AGAGAGTGAGAAAACAG	1560	OPA1 H31 3UTR(+742+758)	CTATTAACAGAAAGCCT
1540	OPA1 H31 3UTR(+682+698)	TATAGAGAGTGAGAAAA	1561	OPA1 H31 3UTR(+745+761)	CCACTATTAACAGAAAG
1541	OPA1 H31 3UTR(+685+701)	GGATATAGAGAGTGAGA	1562	OPA1 H31 3UTR(+748+764)	AAACCACTATTAACAGA
1542	OPA1 H31 3UTR(+688+704)	AATGGATATAGAGAGTG	1563	OPA1 H31 3UTR(+751+767)	GAAAAACCACTATTAAC
1543	OPA1 H31 3UTR(+691+707)	TCAAATGGATATAGAGA	1564	OPA1 H31 3UTR(+754+770)	GGAGAAAAACCACTATT
1565	OPA1 H31 3UTR(+757+773)	ACAGGAGAAAAACCACT	1586	OPA1 H31 3UTR(+820+836)	AAATTAGTCAATTGATT
1566	OPA1 H31 3UTR(+760+776)	TCAACAGGAGAAAAACC	1587	OPA1 H31 3UTR(+823+839)	ATGAAATTAGTCAATTG
1567	OPA1 H31 3UTR(+763+779)	CTGTCAACAGGAGAAAA	1588	OPA1 H31 3UTR(+826+842)	TAAATGAAATTAGTCAA
1568	OPA1 H31 3UTR(+766+782)	GCTCTGTCAACAGGAGA	1589	OPA1 H31 3UTR(+829+845)	TTCTAAATGAAATTAGT
1569	OPA1 H31 3UTR(+769+785)	GTGGCTCTGTCAACAGG	1590	OPA1 H31 3UTR(+832+848)	ATATTCTAAATGAAATT
1570	OPA1 H31 3UTR(+772+788)	CCGGTGGCTCTGTCAAC	1591	OPA1 H31 3UTR(+835+851)	ATAATATTCTAAATGAA

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
1571	OPA1 H31 3UTR(+775+791)	AATCCGGTGGCTCTGTC	1592	OPA1 H31 3UTR(+838+854)	TTGATAATATTCTAAAT
1572	OPA1 H31 3UTR(+778+794)	CATAATCCGGTGGCTCT	1593	OPA1 H31 3UTR(+841+857)	TGTTTGATAATATTCTA
1573	OPA1 H31 3UTR(+781+797)	TGTCATAATCCGGTGGC	1594	OPA1 H31 3UTR(+844+860)	AAATGTTTGATAATATT
1574	OPA1 H31 3UTR(+784+800)	CTGTGTCATAATCCGGT	1595	OPA1 H31 3UTR(+847+863)	TTGAAATGTTTGATAAT
1575	OPA1 H31 3UTR(+787+803)	ATCCTGTGTCATAATCC	1596	OPA1 H31 3UTR(+850+866)	TAGTTGAAATGTTTGAT
1576	OPA1 H31 3UTR(+790+806)	CTCATCCTGTGTCATAA	1597	OPA1 H31 3UTR(+853+869)	ACCTAGTTGAAATGTTT
1577	OPA1 H31 3UTR(+793+809)	TTCCTCATCCTGTGTCA	1598	OPA1 H31 3UTR(+856+872)	GATACCTAGTTGAAATG
1578	OPA1 H31 3UTR(+796+812)	ATCTTCCTCATCCTGTG	1599	OPA1 H31 3UTR(+859+875)	TCTGATACCTAGTTGAA
1579	OPA1 H31 3UTR(+799+815)	TTAATCTTCCTCATCCT	1600	OPA1 H31 3UTR(+862+878)	TTTTCTGATACCTAGTT
1580	OPA1 H31 3UTR(+802+818)	TCCTTAATCTTCCTCAT	1601	OPA1 H31 3UTR(+865+881)	CCTTTTTCTGATACCTA
1581	OPA1 H31 3UTR(+805+821)	TTATCCTTAATCTTCCT	1602	OPA1 H31 3UTR(+868+884)	AAGCCTTTTTCTGATAC
1582	OPA1 H31 3UTR(+808+824)	TGATTATCCTTAATCTT	1603	OPA1 H31 3UTR(+871+887)	AGAAAGCCTTTTTCTGA
1583	OPA1 H31 3UTR(+811+827)	AATTGATTATCCTTAAT	1604	OPA1 H31 3UTR(+874+890)	GAAAGAAAGCCTTTTTC
1584	OPA1 H31 3UTR(+814+830)	GTCAATTGATTATCCTT	1605	OPA1 H31 3UTR(+877+893)	TATGAAAGAAAGCCTTT
1585	OPA1 H31 3UTR(+817+833)	TTAGTCAATTGATTATC	1606	OPA1 H31 3UTR(+880+896)	TCTTATGAAAGAAAGCC
1607	OPA1 H31 3UTR(+883+899)	TAGTCTTATGAAAGAAA	1628	OPA1 H31 3UTR(+946+962)	TTATTCAGCTGAGAGGG
1608	OPA1 H31 3UTR(+886+902)	AAATAGTCTTATGAAAG	1629	OPA1 H31 3UTR(+949+965)	TCTTTATTCAGCTGAGA
1609	OPA1 H31 3UTR(+889+905)	TTAAAATAGTCTTATGA	1630	OPA1 H31 3UTR(+952+968)	TTTTCTTTATTCAGCTG
1610	OPA1 H31 3UTR(+892+908)	TATTTAAAATAGTCTTA	1631	OPA1 H31 3UTR(+955+971)	AATTTTTCTTTATTCAG
1611	OPA1 H31 3UTR(+895+911)	TTCTATTTAAAATAGTC	1632	OPA1 H31 3UTR(+958+974)	CTAAATTTTTCTTTATT
1612	OPA1 H31 3UTR(+898+914)	AATTTCTATTTAAAATA	1633	OPA1 H31 3UTR(+961+977)	GAACTAAATTTTTCTTT
1613	OPA1 H31 3UTR(+901+917)	AATAATTTCTATTTAAA	1634	OPA1 H31 3UTR(+964+980)	ATTGAACTAAATTTTTC

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
1614	OPA1 H31 3UTR(+904+920)	TGAAATAATTTCTATTT	1635	OPA1 H31 3UTR(+967+983)	TAAATTGAACTAAATTT
1615	OPA1 H31 3UTR(+907+923)	TGTTGAAATAATTTCTA	1636	OPA1 H31 3UTR(+970+986)	CAATAAATTGAACTAAA
1616	OPA1 H31 3UTR(+910+926)	AATTGTTGAAATAATTT	1637	OPA1 H31 3UTR(+973+989)	TTGCAATAAATTGAACT
1617	OPA1 H31 3UTR(+913+929)	TTTAATTGTTGAAATAA	1638	OPA1 H31 3UTR(+976+992)	AAATTGCAATAAATTGA
1618	OPA1 H31 3UTR(+916+932)	TACTTTAATTGTTGAAA	1639	OPA1 H31 3UTR(+979+995)	ATTAAATTGCAATAAAT
1619	OPA1 H31 3UTR(+919+935)	CATTACTTTAATTGTTG	1640	OPA1 H31 3UTR(+982+998)	GTAATTAAATTGCAATA
1620	OPA1 H31 3UTR(+922+938)	CAACATTACTTTAATTG	1641	OPA1 H31 3UTR(+985+1001)	ATTGTAATTAAATTGCA
1621	OPA1 H31 3UTR(+925+941)	GGTCAACATTACTTTAA	1642	OPA1 H31 3UTR(+988+1004)	AGTATTGTAATTAAATT
1622	OPA1 H31 3UTR(+928+944)	GATGGTCAACATTACTT	1643	OPA1 H31 3UTR(+991+1007)	GGTAGTATTGTAATTAA
1623	OPA1 H31 3UTR(+931+947)	GGGGATGGTCAACATTA	1644	OPA1 H31 3UTR(+994+1010)	GAAGGTAGTATTGTAAT
1624	OPA1 H31 3UTR(+934+950)	GAGGGGGATGGTCAACA	1645	OPA1 H31 3UTR(+997+1013)	TGTGAAGGTAGTATTGT
1625	OPA1 H31 3UTR(+937+953)	TGAGAGGGGGATGGTCA	1646	OPA1 H31 3UTR(+1000+1016)	TGTTGTGAAGGTAGTAT
1626	OPA1 H31 3UTR(+940+956)	AGCTGAGAGGGGGATGG	1647	OPA1 H31 3UTR(+1003+1019)	AAATGTTGTGAAGGTAG
1627	OPA1 H31 3UTR(+943+959)	TTCAGCTGAGAGGGGGA	1648	OPA1 H31 3UTR(+1006+1022)	TGAAAATGTTGTGAAGG
1649	OPA1 H31 3UTR(+1009+1025)	ACATGAAAATGTTGTGA	1669	OPA1 H31 3UTR(+1069+1085)	AAAGAAAGCATTTCTTT
1650	OPA1 H31 3UTR(+1012+1028)	AACACATGAAAATGTTG	1670	OPA1 H31 3UTR(+1072+1088)	AGTAAAGAAAGCATTTC
1651	OPA1 H31 3UTR(+1015+1031)	TAAAACACATGAAAATG	1671	OPA1 H31 3UTR(+1075+1091)	TTAAGTAAAGAAAGCAT
1652	OPA1 H31 3UTR(+1018+1034)	ATTTAAAACACATGAAA	1672	OPA1 H31 3UTR(+1078+1094)	ATTTTAAGTAAAGAAAG
1653	OPA1 H31 3UTR(+1021+1037)	TTTATTTAAAACACATG	1673	OPA1 H31 3UTR(+1081+1097)	GACATTTTAAGTAAAGA
1654	OPA1 H31 3UTR(+1024+1040)	ATATTTATTTAAAACAC	1674	OPA1 H31 3UTR(+1084+1100)	ATAGACATTTTAAGTAA
1655	OPA1 H31 3UTR(+1027+1043)	AAAATATTTATTTAAAA	1675	OPA1 H31 3UTR(+1087+1103)	GAGATAGACATTTTAAG
1656	OPA1 H31 3UTR(+1030+1046)	TAAAAAATATTTATTTA	1676	OPA1 H31 3UTR(+1090+1106)	AATGAGATAGACATTTT

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
1657	OPA1 H31 3UTR(+1033+1049)	AATTAAAAAAATATTTAT	1677	OPA1 H31 3UTR(+1093+1109)	GCAAATGAGATAGACAT
1658	OPA1 H31 3UTR(+1036+1052)	GCCAATTAAAAAATATT	1678	OPA1 H31 3UTR(+1096+1112)	GCAGCAAATGAGATAGA
1659	OPA1 H31 3UTR(+1039+1055)	TTAGCCAATTAAAAAAT	1679	OPA1 H31 3UTR(+1099+1115)	AAGGCAGCAAATGAGAT
1660	OPA1 H31 3UTR(+1042+1058)	CCTTTAGCCAATTAAAA	1680	OPA1 H31 3UTR(+1102+1118)	GAAAAGGCAGCAAATGA
1661	OPA1 H31 3UTR(+1045+1061)	TGTCCTTTAGCCAATTA	1681	OPA1 H31 3UTR(+1105+1121)	AGTGAAAAGGCAGCAAA
1662	OPA1 H31 3UTR(+1048+1064)	GAATGTCCTTTAGCCAA	1682	OPA1 H31 3UTR(+1108+1124)	CTTAGTGAAAAGGCAGC
1663	OPA1 H31 3UTR(+1051+1067)	CTTGAATGTCCTTTAGC	1683	OPA1 H31 3UTR(+1111+1127)	AGGCTTAGTGAAAAGGC
1664	OPA1 H31 3UTR(+1054+1070)	TTGCTTGAATGTCCTTT	1684	OPA1 H31 3UTR(+1114+1130)	TAAAGGCTTAGTGAAAA
1665	OPA1 H31 3UTR(+1057+1073)	TCTTTGCTTGAATGTCC	1685	OPA1 H31 3UTR(+1117+1133)	AAGTAAAGGCTTAGTGA
1666	OPA1 H31 3UTR(+1060+1076)	ATTTCTTTGCTTGAATG	1686	OPA1 H31 3UTR(+1120+1136)	ACAAAGTAAAGGCTTAG
1667	OPA1 H31 3UTR(+1063+1079)	AGCATTTCTTTGCTTGA	1687	OPA1 H31 3UTR(+1123+1139)	TTAACAAAGTAAAGGCT
1668	OPA1 H31 3UTR(+1066+1082)	GAAAGCATTTCTTTGCT	1688	OPA1 H31 3UTR(+1126+1142)	TTATTAACAAAGTAAAG
1689	OPA1 H31 3UTR(+1129+1145)	CTTTTATTAACAAAGTA			
1690	OPA1 H31 3UTR(+1132+1148)	ACACTTTTATTAACAAA	1711	OPA1 H31 3UTR(+1195+1211)	CAAAAAGCAACTCCAAG
1691	OPA1 H31 3UTR(+1135+1151)	TGGACACTTTTATTAAC	1712	OPA1 H31 3UTR(+1198+1214)	TACCAAAAAGCAACTCC
1692	OPA1 H31 3UTR(+1138+1154)	CAATGGACACTTTTATT	1713	OPA1 H31 3UTR(+1201+1217)	TGTTACCAAAAAGCAAC
1693	OPA1 H31 3UTR(+1141+1157)	ACACAATGGACACTTTT	1714	OPA1 H31 3UTR(+1204+1220)	GGCTGTTACCAAAAAGC
1694	OPA1 H31 3UTR(+1144+1160)	ATCACACAATGGACACT	1715	OPA1 H31 3UTR(+1207+1223)	TGGGGCTGTTACCAAAA
1695	OPA1 H31 3UTR(+1147+1163)	AACATCACACAATGGAC	1716	OPA1 H31 3UTR(+1210+1226)	CAATGGGGCTGTTACCA
1696	OPA1 H31 3UTR(+1150+1166)	AAAAACATCACACAATG	1717	OPA1 H31 3UTR(+1213+1229)	TAGCAATGGGGCTGTTA
1697	OPA1 H31 3UTR(+1153+1169)	ATCAAAAACATCACACA	1718	OPA1 H31 3UTR(+1216+1232)	GAGTAGCAATGGGGCTG
1698	OPA1 H31 3UTR(+1156+1172)	AAAATCAAAAACATCAC	1719	OPA1 H31 3UTR(+1219+1235)	GGGGAGTAGCAATGGGG

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
1699	OPA1 H31 3UTR(+1159+1175)	TGTAAAATCAAAAACAT	1720	OPA1 H31 3UTR(+1222+1238)	AATGGGAGTAGCAATG
1700	OPA1 H31 3UTR(+1162+1178)	AACTGTAAAATCAAAAA	1721	OPA1 H31 3UTR(+1225+1241)	TAAAATGGGGAGTAGCA
1701	OPA1 H31 3UTR(+1165+1181)	GCAAACTGTAAAATCAA	1722	OPA1 H31 3UTR(+1228+1244)	CAATAAAATGGGGAGTA
1702	OPA1 H31 3UTR(+1168+1184)	TTAGCAAACTGTAAAAT	1723	OPA1 H31 3UTR(+1231+1247)	AAACAATAAAATGGGGA
1703	OPA1 H31 3UTR(+1171+1187)	GATTTAGCAAACTGTAA	1724	OPA1 H31 3UTR(+1234+1250)	GTAAAACAATAAAATGG
1704	OPA1 H31 3UTR(+1174+1190)	TAAGATTTAGCAAACTG	1725	OPA1 H31 3UTR(+1237+1253)	GATGTAAAACAATAAAA
1705	OPA1 H31 3UTR(+1177+1193)	AAATAAGATTTAGCAAA	1726	OPA1 H31 3UTR(+1240+1256)	ATTGATGTAAAACAATA
1706	OPA1 H31 3UTR(+1180+1196)	AGAAAATAAGATTTAGC	1727	OPA1 H31 3UTR(+1243+1259)	TGCATTGATGTAAAACA
1707	OPA1 H31 3UTR(+1183+1199)	CCAAGAAAATAAGATTT	1728	OPA1 H31 3UTR(+1246+1262)	GCATGCATTGATGTAAA
1708	OPA1 H31 3UTR(+1186+1202)	ACTCCAAGAAAATAAGA	1729	OPA1 H31 3UTR(+1249+1265)	GAAGCATGCATTGATGT
1709	OPA1 H31 3UTR(+1189+1205)	GCAACTCCAAGAAAATA	1730	OPA1 H31 3UTR(+1252+1268)	AACGAAGCATGCATTGA
1710	OPA1 H31 3UTR(+1192+1208)	AAAGCAACTCCAAGAAA	1731	OPA1 H31 3UTR(+1255+1271)	CACAACGAAGCATGCAT
1732	OPA1 H31 3UTR(+1258+1274)	GATCACAACGAAGCATG	1753	OPA1 H31 3UTR(+1321+1337)	TCCTGGTTTCGGAAGTA
1733	OPA1 H31 3UTR(+1261+1277)	AGGGATCACAACGAAGC	1754	OPA1 H31 3UTR(+1324+1340)	AATTCCTGGTTTCGGAA
1734	OPA1 H31 3UTR(+1264+1280)	TTGAGGGATCACAACGA	1755	OPA1 H31 3UTR(+1327+1343)	TTGAATTCCTGGTTTCG
1735	OPA1 H31 3UTR(+1267+1283)	ATCTTGAGGGATCACAA	1756	OPA1 H31 3UTR(+1330+1346)	ACATTGAATTCCTGGTT
1736	OPA1 H31 3UTR(+1270+1286)	TACATCTTGAGGGATCA	1757	OPA1 H31 3UTR(+1333+1349)	CATACATTGAATTCCTG
1737	OPA1 H31 3UTR(+1273+1289)	TGTTACATCTTGAGGGA	1758	OPA1 H31 3UTR(+1336+1352)	AAACATACATTGAATTC
1738	OPA1 H31 3UTR(+1276+1292)	AAGTGTTACATCTTGAG	1759	OPA1 H31 3UTR(+1339+1355)	AACAAACATACATTGAA
1739	OPA1 H31 3UTR(+1279+1295)	ACCAAGTGTTACATCTT	1760	OPA1 H31 3UTR(+1342+1358)	TAAAACAAACATACATT
1740	OPA1 H31 3UTR(+1282+1298)	CATACCAAGTGTTACAT	1761	OPA1 H31 3UTR(+1345+1361)	GTATAAAACAAACATAC
1741	OPA1 H31 3UTR(+1285+1301)	GAGCATACCAAGTGTTA	1762	OPA1 H31 3UTR(+1348+1364)	ACAGTATAAAACAAACA

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
1742	OPA1 H31 3UTR(+1288+1304)	ACCGAGCATACCAAGTG	1763	OPA1 H31 3UTR(+1351+1367)	CAAACAGTATAAAACAA
1743	OPA1 H31 3UTR(+1291+1307)	TCAACCGAGCATACCAA	1764	OPA1 H31 3UTR(+1354+1370)	TATCAAACAGTATAAAA
1744	OPA1 H31 3UTR(+1294+1310)	TCCTCAACCGAGCATAC	1765	OPA1 H31 3UTR(+1357+1373)	TCTTATCAAACAGTATA
1745	OPA1 H31 3UTR(+1297+1313)	ATATCCTCAACCGAGCA	1766	OPA1 H31 3UTR(+1360+1376)	TTTTCTTATCAAACAGT
1746	OPA1 H31 3UTR(+1300+1316)	TTCATATCCTCAACCGA	1767	OPA1 H31 3UTR(+1363+1379)	TACTTTTCTTATCAAAC
1747	OPA1 H31 3UTR(+1303+1319)	TTTTTCATATCCTCAAC	1768	OPA1 H31 3UTR(+1366+1382)	ACCTACTTTTCTTATCA
1748	OPA1 H31 3UTR(+1306+1322)	TATTTTTTCATATCCTC	1769	OPA1 H31 3UTR(+1369+1385)	TGGACCTACTTTTCTTA
1749	OPA1 H31 3UTR(+1309+1325)	AAGTATTTTTTCATATC	1770	OPA1 H31 3UTR(+1372+1388)	GGCTGGACCTACTTTTC
1750	OPA1 H31 3UTR(+1312+1328)	CGGAAGTATTTTTTCAT	1771	OPA1 H31 3UTR(+1375+1391)	TAAGGCTGGACCTACTT
1751	OPA1 H31 3UTR(+1315+1331)	TTTCGGAAGTATTTTTT	1772	OPA1 H31 3UTR(+1378+1394)	GCTTAAGGCTGGACCTA
1752	OPA1 H31 3UTR(+1318+1334)	TGGTTTCGGAAGTATTT	1773	OPA1 H31 3UTR(+1381+1397)	GCTGCTTAAGGCTGGAC
1774	OPA1 H31 3UTR(+1384+1400)	TGTGCTGCTTAAGGCTG	1796	OPA1 H31 3UTR(+1450+1466)	TTCACTCCTGTCCCTAG
1776	OPA1 H31 3UTR(+1390+1406)	CGCATCTGTGCTGCTTA	1797	OPA1 H31 3UTR(+1453+1469)	CTATTCACTCCTGTCCC
1777	OPA1 H31 3UTR(+1393+1409)	CAGCGCATCTGTGCTGC	1798	OPA1 H31 3UTR(+1456+1472)	TTTCTATTCACTCCTGT
1778	OPA1 H31 3UTR(+1396+1412)	TACCAGCGCATCTGTGC	1799	OPA1 H31 3UTR(+1459+1475)	CCCTTTCTATTCACTCC
1779	OPA1 H31 3UTR(+1399+1415)	ATCTACCAGCGCATCTG	1800	OPA1 H31 3UTR(+1462+1478)	CCTCCCTTTCTATTCAC
1780	OPA1 H31 3UTR(+1402+1418)	TGCATCTACCAGCGCAT	1801	OPA1 H31 3UTR(+1465+1481)	TCTCCTCCCTTTCTATT
1781	OPA1 H31 3UTR(+1405+1421)	CTATGCATCTACCAGCG	1802	OPA1 H31 3UTR(+1468+1484)	AGCTCTCCTCCCTTTCT
1782	OPA1 H31 3UTR(+1408+1424)	TGACTATGCATCTACCA	1803	OPA1 H31 3UTR(+1471+1487)	TAGAGCTCTCCTCCCTT
1783	OPA1 H31 3UTR(+1411+1427)	TCCTGACTATGCATCTA	1804	OPA1 H31 3UTR(+1474+1490)	TAATAGAGCTCTCCTCC
1784	OPA1 H31 3UTR(+1414+1430)	AGTTCCTGACTATGCAT	1805	OPA1 H31 3UTR(+1477+1493)	ACATAATAGAGCTCTCC
1785	OPA1 H31 3UTR(+1417+1433)	AAAAGTTCCTGACTATG	1806	OPA1 H31 3UTR(+1480+1496)	AGAACATAATAGAGCTC

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
1786	OPA1 H31 3UTR(+1420+1436)	AAAAAAAGTTCCTGACT	1807	OPA1 H31 3UTR(+1483+1499)	TATAGAACATAATAGAG
1787	OPA1 H31 3UTR(+1423+1439)	AATAAAAAAAGTTCCTG	1808	OPA1 H31 3UTR(+1486+1502)	GTGTATAGAACATAATA
1788	OPA1 H31 3UTR(+1426+1442)	AGAAATAAAAAAAGTTC	1809	OPA1 H31 3UTR(+1489+1505)	TCTGTGTATAGAACATA
1789	OPA1 H31 3UTR(+1429+1445)	AAAAGAAATAAAAAAAG	1810	OPA1 H31 3UTR(+1492+1508)	TAATCTGTGTATAGAAC
1790	OPA1 H31 3UTR(+1432+1448)	CCTAAAAGAAATAAAAA	1811	OPA1 H31 3UTR(+1495+1511)	TCCTAATCTGTGTATAG
1791	OPA1 H31 3UTR(+1435+1451)	AGACCTAAAAGAAATAA	1812	OPA1 H31 3UTR(+1498+1514)	ATCTCCTAATCTGTGTA
1792	OPA1 H31 3UTR(+1438+1454)	CCTAGACCTAAAAGAAA	1813	OPA1 H31 3UTR(+1501+1517)	GTCATCTCCTAATCTGT
1793	OPA1 H31 3UTR(+1441+1457)	GTCCCTAGACCTAAAAG	1814	OPA1 H31 3UTR(+1504+1520)	AAGGTCATCTCCTAATC
1794	OPA1 H31 3UTR(+1444+1460)	CCTGTCCCTAGACCTAA	1815	OPA1 H31 3UTR(+1507+1523)	AGTAAGGTCATCTCCTA
1795	OPA1 H31 3UTR(+1447+1463)	ACTCCTGTCCCTAGACC	1816	OPA1 H31 3UTR(+1510+1526)	CCCAGTAAGGTCATCTC
1817	OPA1 H31 3UTR(+1513+1529)	GTACCCAGTAAGGTCAT	1838	OPA1 H31 3UTR(+1576+1592)	TGCTTTACAACTGCAAA
1818	OPA1 H31 3UTR(+1516+1532)	GGTGTACCCAGTAAGGT	1839	OPA1 H31 3UTR(+1579+1595)	TTATGCTTTACAACTGC
1819	OPA1 H31 3UTR(+1519+1535)	AGGGGTGTACCCAGTAA	1840	OPA1 H31 3UTR(+1582+1598)	TTGTTATGCTTTACAAC
1820	OPA1 H31 3UTR(+1522+1538)	TAGAGGGGTGTACCCAG	1841	OPA1 H31 3UTR(+1585+1601)	TAATTGTTATGCTTTAC
1821	OPA1 H31 3UTR(+1525+1541)	GGTTAGAGGGGTGTACC	1842	OPA1 H31 3UTR(+1588+1604)	TTGTAATTGTTATGCTT
1822	OPA1 H31 3UTR(+1528+1544)	ACTGGTTAGAGGGGTGT	1843	OPA1 H31 3UTR(+1591+1607)	TAGTTGTAATTGTTATG
1823	OPA1 H31 3UTR(+1531+1547)	AGCACTGGTTAGAGGGG	1844	OPA1 H31 3UTR(+1594+1610)	GTGTAGTTGTAATTGTT
1824	OPA1 H31 3UTR(+1534+1550)	GTAAGCACTGGTTAGAG	1845	OPA1 H31 3UTR(+1597+1613)	GATGTGTAGTTGTAATT
1825	OPA1 H31 3UTR(+1537+1553)	CCTGTAAGCACTGGTTA	1846	OPA1 H31 3UTR(+1600+1616)	ATAGATGTGTAGTTGTA
1826	OPA1 H31 3UTR(+1540+1556)	TAACCTGTAAGCACTGG	1847	OPA1 H31 3UTR(+1603+1619)	GAAATAGATGTGTAGTT
1827	OPA1 H31 3UTR(+1543+1559)	CATTAACCTGTAAGCAC	1848	OPA1 H31 3UTR(+1606+1622)	TTAGAAATAGATGTGTA
1828	OPA1 H31 3UTR(+1546+1562)	ATGCATTAACCTGTAAG	1849	OPA1 H31 3UTR(+1609+1625)	TCTTTAGAAATAGATGT

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
1829	OPA1 H31 3UTR(+1549+1565)	AACATGCATTAACCTGT	1850	OPA1 H31 3UTR(+1612+1628)	TATTCTTTAGAAATAGA
1830	OPA1 H31 3UTR(+1552+1568)	ATTAACATGCATTAACC	1851	OPA1 H31 3UTR(+1615+1631)	TTTTATTCTTTAGAAAT
1831	OPA1 H31 3UTR(+1555+1571)	TTCATTAACATGCATTA	1852	OPA1 H31 3UTR(+1618+1634)	CTGTTTTATTCTTTAGA
1832	OPA1 H31 3UTR(+1558+1574)	ATATTCATTAACATGCA	1853	OPA1 H31 3UTR(+1621+1637)	GTCCTGTTTTATTCTTT
1833	OPA1 H31 3UTR(+1561+1577)	AAAATATTCATTAACAT	1854	OPA1 H31 3UTR(+1624+1640)	ATGGTCCTGTTTTATTC
1834	OPA1 H31 3UTR(+1564+1580)	GCAAAAATATTCATTAA	1855	OPA1 H31 3UTR(+1627+1643)	AATATGGTCCTGTTTTA
1835	OPA1 H31 3UTR(+1567+1583)	ACTGCAAAAATATTCAT	1856	OPA1 H31 3UTR(+1630+1646)	ATAAATATGGTCCTGTT
1836	OPA1 H31 3UTR(+1570+1586)	ACAACTGCAAAAATATT	1857	OPA1 H31 3UTR(+1633+1649)	TAAATAAATATGGTCCT
1837	OPA1 H31 3UTR(+1573+1589)	TTTACAACTGCAAAAAT	1858	OPA1 H31 3UTR(+1636+1652)	AAGTAAATAAATATGGT
1859	OPA1 H31 3UTR(+1639+1655)	CAGAAGTAAATAAATAT	1880	OPA1 H31 3UTR(+1702+1718)	TTAGCCTTTTCCTTGGG
1860	OPA1 H31 3UTR(+1642+1658)	TGACAGAAGTAAATAAA	1881	OPA1 H31 3UTR(+1705+1721)	ATATTAGCCTTTTCCTT
1861	OPA1 H31 3UTR(+1645+1661)	AGTTGACAGAAGTAAAT	1882	OPA1 H31 3UTR(+1708+1724)	CTAATATTAGCCTTTTC
1862	OPA1 H31 3UTR(+1648+1664)	TATAGTTGACAGAAGTA	1883	OPA1 H31 3UTR(+1711+1727)	TGACTAATATTAGCCTT
1863	OPA1 H31 3UTR(+1651+1667)	TTCTATAGTTGACAGAA	1884	OPA1 H31 3UTR(+1714+1730)	TAGTGACTAATATTAGC
1864	OPA1 H31 3UTR(+1654+1670)	TCTTTCTATAGTTGACA	1885	OPA1 H31 3UTR(+1717+1733)	CAGTAGTGACTAATATT
1865	OPA1 H31 3UTR(+1657+1673)	CTTTCTTTCTATAGTTG	1886	OPA1 H31 3UTR(+1720+1736)	TAACAGTAGTGACTAAT
1866	OPA1 H31 3UTR(+1660+1676)	GGTCTTTCTTTCTATAG	1887	OPA1 H31 3UTR(+1723+1739)	TGATAACAGTAGTGACT
1867	OPA1 H31 3UTR(+1663+1679)	GAAGGTCTTTCTTTCTA	1888	OPA1 H31 3UTR(+1726+1742)	ATGTGATAACAGTAGTG
1868	OPA1 H31 3UTR(+1666+1682)	GCTGAAGGTCTTTCTTT	1889	OPA1 H31 3UTR(+1729+1745)	GGGATGTGATAACAGTA
1869	OPA1 H31 3UTR(+1669+1685)	ACAGCTGAAGGTCTTTC	1890	OPA1 H31 3UTR(+1732+1748)	AAAGGGATGTGATAACA
1870	OPA1 H31 3UTR(+1672+1688)	AATACAGCTGAAGGTCT	1891	OPA1 H31 3UTR(+1735+1751)	TACAAAGGGATGTGATA
1871	OPA1 H31 3UTR(+1675+1691)	GGAAATACAGCTGAAGG	1892	OPA1 H31 3UTR(+1738+1754)	TTATACAAAGGGATGTG

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
1872	OPA1 H31 3UTR(+1678+1694)	TGTGGAAATACAGCTGA	1893	OPA1 H31 3UTR(+1741+1757)	AACTTATACAAAGGGAT
1873	OPA1 H31 3UTR(+1681+1697)	ATCTGTGGAAATACAGC	1894	OPA1 H31 3UTR(+1744+1760)	TAAAACTTATACAAAGG
1874	OPA1 H31 3UTR(+1684+1700)	GAAATCTGTGGAAATAC	1895	OPA1 H31 3UTR(+1747+1763)	TTTTAAAACTTATACAA
1875	OPA1 H31 3UTR(+1687+1703)	GGAGAAATCTGTGGAAA	1896	OPA1 H31 3UTR(+1750+1766)	TCTTTTTAAAACTTATA
1876	OPA1 H31 3UTR(+1690+1706)	TTGGGAGAAATCTGTGG	1897	OPA1 H31 3UTR(+1753+1769)	ATCTCTTTTTAAAACTT
1877	OPA1 H31 3UTR(+1693+1709)	TCCTTGGGAGAAATCTG	1898	OPA1 H31 3UTR(+1756+1772)	TCCATCTCTTTTTAAAA
1878	OPA1 H31 3UTR(+1696+1712)	TTTTCCTTGGGAGAAAT	1899	OPA1 H31 3UTR(+1759+1775)	CCCTCCATCTCTTTTTA
1879	OPA1 H31 3UTR(+1699+1715)	GCCTTTTCCTTGGGAGA	1900	OPA1 H31 3UTR(+1762+1778)	TCTCCCTCCATCTCTTT
1901	OPA1 H31 3UTR(+1765+1781)	AGATCTCCCTCCATCTC	1922	OPA1 H31 3UTR(+1828+1844)	AGTAATATTAATTGTTA
1902	OPA1 H31 3UTR(+1768+1784)	TGAAGATCTCCCTCCAT	1923	OPA1 H31 3UTR(+1831+1847)	TTTAGTAATATTAATTG
1903	OPA1 H31 3UTR(+1771+1787)	AAATGAAGATCTCCCTC	1924	OPA1 H31 3UTR(+1834+1850)	ACTTTTAGTAATATTAA
1904	OPA1 H31 3UTR(+1774+1790)	AAGAAATGAAGATCTCC	1925	OPA1 H31 3UTR(+1837+1853)	GGGACTTTTAGTAATAT
1905	OPA1 H31 3UTR(+1777+1793)	TCAAAGAAATGAAGATC	1926	OPA1 H31 3UTR(+1840+1856)	TGTGGGACTTTTAGTAA
1906	OPA1 H31 3UTR(+1780+1796)	TCCTCAAAGAAATGAAG	1927	OPA1 H31 3UTR(+1843+1859)	TCATGTGGGACTTTTAG
1907	OPA1 H31 3UTR(+1783+1799)	ATCTCCTCAAAGAAATG	1928	OPA1 H31 3UTR(+1846+1862)	CTCTCATGTGGGACTTT
1908	OPA1 H31 3UTR(+1786+1802)	CTGATCTCCTCAAAGAA	1929	OPA1 H31 3UTR(+1849+1865)	GGACTCTCATGTGGGAC
1909	OPA1 H31 3UTR(+1789+1805)	ATACTGATCTCCTCAAA	1930	OPA1 H31 3UTR(+1852+1868)	TCAGGACTCTCATGTGG
1910	OPA1 H31 3UTR(+1792+1808)	ACAATACTGATCTCCTC	1931	OPA1 H31 3UTR(+1855+1871)	GCGTCAGGACTCTCATG
1911	OPA1 H31 3UTR(+1795+1811)	GTTACAATACTGATCTC	1932	OPA1 H31 3UTR(+1858+1874)	AGGGCGTCAGGACTCTC
1912	OPA1 H31 3UTR(+1798+1814)	TACGTTACAATACTGAT	1933	OPA1 H31 3UTR(+1861+1877)	GAGAGGGCGTCAGGACT
1913	OPA1 H31 3UTR(+1801+1817)	ACATACGTTACAATACT	1934	OPA1 H31 3UTR(+1864+1880)	ATGGAGAGGGCGTCAGG
1914	OPA1 H31 3UTR(+1804+1820)	TTCACATACGTTACAAT	1935	OPA1 H31 3UTR(+1867+1883)	GGCATGGAGAGGGCGTC

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1915	OPA1 H31 3UTR(+1807+1823)	CTATTCACATACGTTAC	1936	OPA1 H31 3UTR(+1870+1886)	TGGGGCATGGAGAGGGC
1916	OPA1 H31 3UTR(+1810+1826)	CATCTATTCACATACGT	1937	OPA1 H31 3UTR(+1873+1889)	CTGTGGGGCATGGAGAG
1917	OPA1 H31 3UTR(+1813+1829)	TATCATCTATTCACATA	1938	OPA1 H31 3UTR(+1876+1892)	TTACTGTGGGGCATGGA
1918	OPA1 H31 3UTR(+1816+1832)	TGTTATCATCTATTCAC	1939	OPA1 H31 3UTR(+1879+1895)	ACATTACTGTGGGGCAT
1919	OPA1 H31 3UTR(+1819+1835)	AATTGTTATCATCTATT	1940	OPA1 H31 3UTR(+1882+1898)	GCCACATTACTGTGGGG
1920	OPA1 H31 3UTR(+1822+1838)	ATTAATTGTTATCATCT	1941	OPA1 H31 3UTR(+1885+1901)	GAAGCCACATTACTGTG
1921	OPA1 H31 3UTR(+1825+1841)	AATATTAATTGTTATCA	1942	OPA1 H31 3UTR(+1888+1904)	AAAGAAGCCACATTACT
1943	OPA1 H31 3UTR(+1891+1907)	ATGAAAGAAGCCACATT	1964	OPA1 H31 3UTR(+1954+1970)	GCTTTCAAGGAAAAAATA
1944	OPA1 H31 3UTR(+1894+1910)	CCCATGAAAGAAGCCAC	1965	OPA1 H31 3UTR(+1957+1973)	CTAGCTTTCAAGGAAAA
1945	OPA1 H31 3UTR(+1897+1913)	AAACCCATGAAAGAAGC	1966	OPA1 H31 3UTR(+1960+1976)	TACCTAGCTTTCAAGGA
1946	OPA1 H31 3UTR(+1900+1916)	AAAAAACCCATGAAAGA	1967	OPA1 H31 3UTR(+1963+1979)	AAATACCTAGCTTTCAA
1947	OPA1 H31 3UTR(+1903+1919)	AAAAAAAAACCCATGAA	1968	OPA1 H31 3UTR(+1966+1982)	GATAAATACCTAGCTTT
1948	OPA1 H31 3UTR(+1906+1922)	AAGAAAAAAAAACCCAT	1969	OPA1 H31 3UTR(+1969+1985)	GTTGATAAATACCTAGC
1949	OPA1 H31 3UTR(+1909+1925)	AAGAAGAAAAAAAAACC	1970	OPA1 H31 3UTR(+1972+1988)	GCAGTTGATAAATACCT
1950	OPA1 H31 3UTR(+1912+1928)	AAAAAGAAGAAAAAAAA	1971	OPA1 H31 3UTR(+1975+1991)	TCTGCAGTTGATAAATA
1951	OPA1 H31 3UTR(+1915+1931)	GCTAAAAAGAAGAAAAA	1972	OPA1 H31 3UTR(+1978+1994)	ACATCTGCAGTTGATAA
1952	OPA1 H31 3UTR(+1918+1934)	TCAGCTAAAAAGAAGAA	1973	OPA1 H31 3UTR(+1981+1997)	ATAACATCTGCAGTTGA
1953	OPA1 H31 3UTR(+1921+1937)	AGATCAGCTAAAAAGAA	1974	OPA1 H31 3UTR(+1984+2000)	TCAATAACATCTGCAGT
1954	OPA1 H31 3UTR(+1924+1940)	ATGAGATCAGCTAAAAA	1975	OPA1 H31 3UTR(+1987+2003)	CTTTCAATAACATCTGC
1955	OPA1 H31 3UTR(+1927+1943)	AGGATGAGATCAGCTAA	1976	OPA1 H31 3UTR(+1990+2006)	TTTCTTTCAATAACATC
1956	OPA1 H31 3UTR(+1930+1946)	CTTAGGATGAGATCAGC	1977	OPA1 H31 3UTR(+1993+2009)	TATTTTCTTTCAATAAC
1957	OPA1 H31 3UTR(+1933+1949)	ATGCTTAGGATGAGATC	1978	OPA1 H31 3UTR(+1996+2012)	TTTTATTTTCTTTCAAT

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1958	OPA1 H31 3UTR(+1936+1952)	AGCATGCTTAGGATGAG	1979	OPA1 H31 3UTR(+1999+2015)	GAATTTTATTTTCTTTC
1959	OPA1 H31 3UTR(+1939+1955)	TAAAGCATGCTTAGGAT	1980	OPA1 H31 3UTR(+2002+2018)	ACTGAATTTTATTTTCT
1960	OPA1 H31 3UTR(+1942+1958)	AAATAAAGCATGCTTAG	1981	OPA1 H31 3UTR(+2005+2021)	GAGACTGAATTTTATTT
1961	OPA1 H31 3UTR(+1945+1961)	GAAAAATAAAGCATGCT	1982	OPA1 H31 3UTR(+2008+2024)	CTTGAGACTGAATTTTA
1962	OPA1 H31 3UTR(+1948+1964)	AAGGAAAAATAAAGCAT	1983	OPA1 H31 3UTR(+2011+2027)	ACTCTTGAGACTGAATT
1963	OPA1 H31 3UTR(+1951+1967)	TTCAAGGAAAAATAAAG	1984	OPA1 H31 3UTR(+2014+2030)	TTTACTCTTGAGACTGA
1985	OPA1 H31 3UTR(+2017+2033)	GGGTTTACTCTTGAGAC	2006	OPA1 H31 3UTR(+2080+2096)	TTTAGTATCTTTTTTGTT
1986	OPA1 H31 3UTR(+2020+2036)	ACAGGGTTTACTCTTGA	2007	OPA1 H31 3UTR(+2083+2099)	ATATTTAGTATCTTTTT
1987	OPA1 H31 3UTR(+2023+2039)	GACACAGGGTTTACTCT	2008	OPA1 H31 3UTR(+2086+2102)	TGTATATTTAGTATCTT
1988	OPA1 H31 3UTR(+2026+2042)	CAAGACACAGGGTTTAC	2009	OPA1 H31 3UTR(+2089+2105)	TTCTGTATATTTAGTAT
1989	OPA1 H31 3UTR(+2029+2045)	ACACAAGACACAGGGTT	2010	OPA1 H31 3UTR(+2092+2108)	AACTTCTGTATATTTAG
1990	OPA1 H31 3UTR(+2032+2048)	CAGACACAAGACACAGG	2011	OPA1 H31 3UTR(+2095+2111)	TTTAACTTCTGTATATT
1991	OPA1 H31 3UTR(+2035+2051)	CTACAGACACAAGACAC	2012	OPA1 H31 3UTR(+2098+2114)	GAATTTAACTTCTGTAT
1992	OPA1 H31 3UTR(+2038+2054)	GAACTACAGACACAAGA	2013	OPA1 H31 3UTR(+2101+2117)	TTCGAATTTAACTTCTG
1993	OPA1 H31 3UTR(+2041+2057)	TTTGAACTACAGACACA	2014	OPA1 H31 3UTR(+2104+2120)	TAGTTCGAATTTAACTT
1994	OPA1 H31 3UTR(+2044+2060)	ACTTTTGAACTACAGAC	2015	OPA1 H31 3UTR(+2107+2123)	GGCTAGTTCGAATTTAA
1995	OPA1 H31 3UTR(+2047+2063)	CTGACTTTTGAACTACA	2016	OPA1 H31 3UTR(+2110+2126)	TGTGGCTAGTTCGAATT
1996	OPA1 H31 3UTR(+2050+2066)	TTTCTGACTTTTGAACT	2017	OPA1 H31 3UTR(+2113+2129)	TTCTGTGGCTAGTTCGA
1997	OPA1 H31 3UTR(+2053+2069)	TCATTTCTGACTTTTGA	2018	OPA1 H31 3UTR(+2116+2132)	TGATTCTGTGGCTAGTT
1998	OPA1 H31 3UTR(+2056+2072)	GAATCATTTCTGACTTT	2019	OPA1 H31 3UTR(+2119+2135)	AAATGATTCTGTGGCTA
1999	OPA1 H31 3UTR(+2059+2075)	TTAGAATCATTTCTGAC	2020	OPA1 H31 3UTR(+2122+2138)	AACAAATGATTCTGTGG
2000	OPA1 H31 3UTR(+2062+2078)	AAATTAGAATCATTTCT	2021	OPA1 H31 3UTR(+2125+2141)	AAAAACAAATGATTCTG

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
2001	OPA1 H31 3UTR(+2065+2081)	TTTAAATTAGAATCATT	2022	OPA1 H31 3UTR(+2128+2144)	CATAAAAACAAATGATT
2002	OPA1 H31 3UTR(+2068+2084)	TTGTTTAAATTAGAATC	2023	OPA1 H31 3UTR(+2131+2147)	TGACATAAAAACAAATG
2003	OPA1 H31 3UTR(+2071+2087)	TTTTTGTTTAAATTAGA	2024	OPA1 H31 3UTR(+2134+2150)	TTCTGACATAAAAACAA
2004	OPA1 H31 3UTR(+2074+2090)	ATCTTTTTGTTTAAATT	2025	OPA1 H31 3UTR(+2137+2153)	AAATTCTGACATAAAAA
2005	OPA1 H31 3UTR(+2077+2093)	AGTATCTTTTTGTTTAA	2026	OPA1 H31 3UTR(+2140+2156)	TGCAAATTCTGACATAA
2027	OPA1 H31 3UTR(+2143+2159)	CTTTGCAAATTCTGACA	2048	OPA1 H31 3UTR(+2206+2222)	AAGTTTGGATATCATCT
2028	OPA1 H31 3UTR(+2146+2162)	ACTCTTTGCAAATTCTG	2049	OPA1 H31 3UTR(+2209+2225)	ATTAAGTTTGGATATCA
2029	OPA1 H31 3UTR(+2149+2165)	TCCACTCTTTGCAAATT	2050	OPA1 H31 3UTR(+2212+2228)	CAAATTAAGTTTGGATA
2030	OPA1 H31 3UTR(+2152+2168)	CACTCCACTCTTTGCAA	2051	OPA1 H31 3UTR(+2215+2231)	AGCCAAATTAAGTTTGG
2031	OPA1 H31 3UTR(+2155+2171)	GTCCACTCCACTCTTTG	2052	OPA1 H31 3UTR(+2218+2234)	CCTAGCCAAATTAAGTT
2032	OPA1 H31 3UTR(+2158+2174)	TTTGTCCACTCCACTCT	2053	OPA1 H31 3UTR(+2221+2237)	AGTCCTAGCCAAATTAA
2033	OPA1 H31 3UTR(+2161+2177)	AGCTTTGTCCACTCCAC	2054	OPA1 H31 3UTR(+2224+2240)	TGAAGTCCTAGCCAAAT
2034	OPA1 H31 3UTR(+2164+2180)	CAGAGCTTTGTCCACTC	2055	OPA1 H31 3UTR(+2227+2243)	AATTGAAGTCCTAGCCA
2035	OPA1 H31 3UTR(+2167+2183)	ATACAGAGCTTTGTCCA	2056	OPA1 H31 3UTR(+2230+2246)	TAAAATTGAAGTCCTAG
2036	OPA1 H31 3UTR(+2170+2186)	TCCATACAGAGCTTTGT	2057	OPA1 H31 3UTR(+2233+2249)	TTTTAAAATTGAAGTCC
2037	OPA1 H31 3UTR(+2173+2189)	TCTTCCATACAGAGCTT	2058	OPA1 H31 3UTR(+2236+2252)	GATTTTTAAAATTGAAG
2038	OPA1 H31 3UTR(+2176+2192)	CAGTCTTCCATACAGAG	2059	OPA1 H31 3UTR(+2239+2255)	ACTGATTTTTTAAAATTG
2039	OPA1 H31 3UTR(+2179+2195)	GTTCAGTCTTCCATACA	2060	OPA1 H31 3UTR(+2242+2258)	TACACTGATTTTTTAAAA
2040	OPA1 H31 3UTR(+2182+2198)	GTTGTTCAGTCTTCCAT	2061	OPA1 H31 3UTR(+2245+2261)	AGGTACACTGATTTTTA
2041	OPA1 H31 3UTR(+2185+2201)	ACAGTTGTTCAGTCTTC	2062	OPA1 H31 3UTR(+2248+2264)	CCTAGGTACACTGATTT
2042	OPA1 H31 3UTR(+2188+2204)	TTTACAGTTGTTCAGTC	2063	OPA1 H31 3UTR(+2251+2267)	CTGCCTAGGTACACTGA
2043	OPA1 H31 3UTR(+2191+2207)	CTATTTACAGTTGTTCA	2064	OPA1 H31 3UTR(+2254+2270)	GCACTGCCTAGGTACAC

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
2044	OPA1 H31 3UTR(+2194+2210)	CATCTATTTACAGTTGT	2065	OPA1 H31 3UTR(+2257+2273)	TGTGCACTGCCTAGGTA
2045	OPA1 H31 3UTR(+2197+2213)	TATCATCTATTTACAGT	2066	OPA1 H31 3UTR(+2260+2276)	TGCTGTGCACTGCCTAG
2046	OPA1 H31 3UTR(+2200+2216)	GGATATCATCTATTTAC	2067	OPA1 H31 3UTR(+2263+2279)	TCGTGCTGTGCACTGCC
2047	OPA1 H31 3UTR(+2203+2219)	TTTGGATATCATCTATT	2068	OPA1 H31 3UTR(+2266+2282)	ATTTCGTGCTGTGCACT
2069	OPA1 H31 3UTR(+2269+2285)	CTTATTTCGTGCTGTGC	2090	OPA1 H31 3UTR(+2332+2348)	AAGGTTGACTGTTCCAC
2070	OPA1 H31 3UTR(+2272+2288)	CCACTTATTTCGTGCTG	2091	OPA1 H31 3UTR(+2335+2351)	AGAAAGGTTGACTGTTC
2071	OPA1 H31 3UTR(+2275+2291)	GGGCCACTTATTTCGTG	2092	OPA1 H31 3UTR(+2338+2354)	ACTAGAAAGGTTGACTG
2072	OPA1 H31 3UTR(+2278+2294)	CAAGGGCCACTTATTTC	2093	OPA1 H31 3UTR(+2341+2357)	ACTACTAGAAAGGTTGA
2073	OPA1 H31 3UTR(+2281+2297)	CTGCAAGGGCCACTTAT	2094	OPA1 H31 3UTR(+2344+2360)	TAAACTACTAGAAAGGT
2074	OPA1 H31 3UTR(+2284+2300)	AAGCTGCAAGGGCCACT	2095	OPA1 H31 3UTR(+2347+2363)	TCATAAACTACTAGAAA
2075	OPA1 H31 3UTR(+2287+2303)	GGGAAGCTGCAAGGGCC	2096	OPA1 H31 3UTR(+2350+2366)	ATATCATAAACTACTAG
2076	OPA1 H31 3UTR(+2290+2306)	ACGGGGAAGCTGCAAGG	2097	OPA1 H31 3UTR(+2353+2369)	GCAATATCATAAACTAC
2077	OPA1 H31 3UTR(+2293+2309)	TAAACGGGGAAGCTGCA	2098	OPA1 H31 3UTR(+2356+2372)	AGGGCAATATCATAAAC
2078	OPA1 H31 3UTR(+2296+2312)	GGTTAAACGGGGAAGCT	2099	OPA1 H31 3UTR(+2359+2375)	AAGAGGGCAATATCATA
2079	OPA1 H31 3UTR(+2299+2315)	GTGGGTTAAACGGGGAA	2100	OPA1 H31 3UTR(+2362+2378)	ACAAAGAGGGCAATATC
2080	OPA1 H31 3UTR(+2302+2318)	ACAGTGGGTTAAACGGG	2101	OPA1 H31 3UTR(+2365+2381)	AATACAAAGAGGGCAAT
2081	OPA1 H31 3UTR(+2305+2321)	AGCACAGTGGGTTAAAC	2102	OPA1 H31 3UTR(+2368+2384)	GGGAATACAAAGAGGGC
2082	OPA1 H31 3UTR(+2308+2324)	TATAGCACAGTGGGTTA	2103	OPA1 H31 3UTR(+2371+2387)	AATGGGAATACAAAGAG
2083	OPA1 H31 3UTR(+2311+2327)	AACTATAGCACAGTGGG	2104	OPA1 H31 3UTR(+2374+2390)	GAAAATGGGAATACAAA
2084	OPA1 H31 3UTR(+2314+2330)	CGCAACTATAGCACAGT	2105	OPA1 H31 3UTR(+2377+2393)	GTAGAAAATGGGAATAC
2085	OPA1 H31 3UTR(+2317+2333)	ACCCGCAACTATAGCAC	2106	OPA1 H31 3UTR(+2380+2396)	ACTGTAGAAAATGGGAA
2086	OPA1 H31 3UTR(+2320+2336)	TCCACCCGCAACTATAG	2107	OPA1 H31 3UTR(+2383+2399)	AAAACTGTAGAAAATGG

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
2087	OPA1 H31 3UTR(+2323+2339)	TGTTCCACCCGCAACTA	2108	OPA1 H31 3UTR(+2386+2402)	GAAAAAACTGTAGAAAA
2088	OPA1 H31 3UTR(+2326+2342)	GACTGTTCCACCCGCAA	2109	OPA1 H31 3UTR(+2389+2405)	GCGGAAAAAACTGTAGA
2089	OPA1 H31 3UTR(+2329+2345)	GTTGACTGTTCCACCCG	2110	OPA1 H31 3UTR(+2392+2408)	TCTGCGGAAAAAACTGT
2111	OPA1 H31 3UTR(+2395+2411)	AAGTCTGCGGAAAAAAC	2132	OPA1 H31 3UTR(+2458+2474)	CATGTTCCCTACTTATT
2112	OPA1 H31 3UTR(+2398+2414)	AAGAAGTCTGCGGAAAA	2133	OPA1 H31 3UTR(+2461+2477)	TGCCATGTTCCCTACTT
2113	OPA1 H31 3UTR(+2401+2417)	AGAAAGAAGTCTGCGGA	2134	OPA1 H31 3UTR(+2464+2480)	CTCTGCCATGTTCCCTA
2114	OPA1 H31 3UTR(+2404+2420)	TGCAGAAAGAAGTCTGC	2135	OPA1 H31 3UTR(+2467+2483)	ACTCTCTGCCATGTTCC
2115	OPA1 H31 3UTR(+2407+2423)	ATTTGCAGAAAGAAGTC	2136	OPA1 H31 3UTR(+2470+2486)	ACCACTCTCTGCCATGT
2116	OPA1 H31 3UTR(+2410+2426)	ATAATTTGCAGAAAGAA	2137	OPA1 H31 3UTR(+2473+2489)	AGCACCACTCTCTGCCA
2117	OPA1 H31 3UTR(+2413+2429)	TGAATAATTTGCAGAAA	2138	OPA1 H31 3UTR(+2476+2492)	GGAAGCACCACTCTCTG
2118	OPA1 H31 3UTR(+2416+2432)	GGCTGAATAATTTGCAG	2139	OPA1 H31 3UTR(+2479+2495)	CTGGGAAGCACCACTCT
2119	OPA1 H31 3UTR(+2419+2435)	GGAGGCTGAATAATTTG	2140	OPA1 H31 3UTR(+2482+2498)	AGGCTGGGAAGCACCAC
2120	OPA1 H31 3UTR(+2422+2438)	TTTGGAGGCTGAATAAT	2141	OPA1 H31 3UTR(+2485+2501)	GTGAGGCTGGGAAGCAC
2121	OPA1 H31 3UTR(+2425+2441)	GCATTTGGAGGCTGAAT	2142	OPA1 H31 3UTR(+2488+2504)	ATTGTGAGGCTGGGAAG
2122	OPA1 H31 3UTR(+2428+2444)	TTTGCATTTGGAGGCTG	2143	OPA1 H31 3UTR(+2491+2507)	CACATTGTGAGGCTGGG
2123	OPA1 H31 3UTR(+2431+2447)	TCATTTGCATTTGGAGG	2144	OPA1 H31 3UTR(+2494+2510)	TCCCACATTGTGAGGCT
2124	OPA1 H31 3UTR(+2434+2450)	CATTCATTTGCATTTGG	2145	OPA1 H31 3UTR(+2497+2513)	AATTCCCACATTGTGAG
2125	OPA1 H31 3UTR(+2437+2453)	TATCATTCATTTGCATT	2146	OPA1 H31 3UTR(+2500+2516)	TCAAATTCCCACATTGT
2126	OPA1 H31 3UTR(+2440+2456)	TTATATCATTCATTTGC	2147	OPA1 H31 3UTR(+2503+2519)	ATGTCAAATTCCCACAT
2127	OPA1 H31 3UTR(+2443+2459)	TTTTTATATCATTCATT	2148	OPA1 H31 3UTR(+2506+2522)	CCTATGTCAAATTCCCA
2128	OPA1 H31 3UTR(+2446+2462)	TTATTTTTATATCATTC	2149	OPA1 H31 3UTR(+2509+2525)	CATCCTATGTCAAATTC
2129	OPA1 H31 3UTR(+2449+2465)	TACTTATTTTTATATCA	2150	OPA1 H31 3UTR(+2512+2528)	TCTCATCCTATGTCAAA

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
2130	OPA1 H31 3UTR(+2452+2468)	CCCTACTTATTTTTATA	2151	OPA1 H31 3UTR(+2515+2531)	GACTCTCATCCTATGTC
2131	OPA1 H31 3UTR(+2455+2471)	GTTCCCTACTTATTTTT	2152	OPA1 H31 3UTR(+2518+2534)	TCTGACTCTCATCCTAT
2153	OPA1 H31 3UTR(+2521+2537)	TACTCTGACTCTCATCC	2174	OPA1 H31 3UTR(+2584+2600)	ATACATACATCTAGAAT
2154	OPA1 H31 3UTR(+2524+2540)	CTATACTCTGACTCTCA	2175	OPA1 H31 3UTR(+2587+2603)	CAGATACATACATCTAG
2155	OPA1 H31 3UTR(+2527+2543)	AACCTATACTCTGACTC	2176	OPA1 H31 3UTR(+2590+2606)	CCTCAGATACATACATC
2156	OPA1 H31 3UTR(+2530+2546)	TTAAACCTATACTCTGA	2177	OPA1 H31 3UTR(+2593+2609)	TTTCCTCAGATACATAC
2157	OPA1 H31 3UTR(+2533+2549)	CTTTTAAACCTATACTC	2178	OPA1 H31 3UTR(+2596+2612)	TTCTTTCCTCAGATACA
2158	OPA1 H31 3UTR(+2536+2552)	TATCTTTTAAACCTATA	2179	OPA1 H31 3UTR(+2599+2615)	GATTTCTTTCCTCAGAT
2159	OPA1 H31 3UTR(+2539+2555)	TTTTATCTTTTAAACCT	2180	OPA1 H31 3UTR(+2602+2618)	CCAGATTTCTTTCCTCA
2160	OPA1 H31 3UTR(+2542+2558)	AGATTTTATCTTTTAAA	2181	OPA1 H31 3UTR(+2605+2621)	ATACCAGATTTCTTTCC
2161	OPA1 H31 3UTR(+2545+2561)	TAAAGATTTTATCTTTT	2182	OPA1 H31 3UTR(+2608+2624)	AAAATACCAGATTTCTT
2162	OPA1 H31 3UTR(+2548+2564)	AACTAAAGATTTTATCT	2183	OPA1 H31 3UTR(+2611+2627)	GCAAAAATACCAGATTT
2163	OPA1 H31 3UTR(+2551+2567)	ATTAACTAAAGATTTTA	2184	OPA1 H31 3UTR(+2614+2630)	AAAGCAAAAATACCAGA
2164	OPA1 H31 3UTR(+2554+2570)	ATTATTAACTAAAGATT	2185	OPA1 H31 3UTR(+2617+2633)	TGGAAAGCAAAAATACC
2165	OPA1 H31 3UTR(+2557+2573)	AAAATTATTAACTAAAG	2186	OPA1 H31 3UTR(+2620+2636)	TATTGGAAAGCAAAAAT
2166	OPA1 H31 3UTR(+2560+2576)	TACAAAATTATTAACTA	2187	OPA1 H31 3UTR(+2623+2639)	CTTTATTGGAAAGCAAA
2167	OPA1 H31 3UTR(+2563+2579)	AAATACAAAATTATTAA	2188	OPA1 H31 3UTR(+2626+2642)	CCCCTTTATTGGAAAGC
2168	OPA1 H31 3UTR(+2566+2582)	AATAAATACAAAATTAT	2189	OPA1 H31 3UTR(+2629+2645)	GATCCCCTTTATTGGAA
2169	OPA1 H31 3UTR(+2569+2585)	ATAAATAAATACAAAAT	2190	OPA1 H31 3UTR(+2632+2648)	TTTGATCCCCTTTATTG
2170	OPA1 H31 3UTR(+2572+2588)	AGAATAAATAAATACAA	2191	OPA1 H31 3UTR(+2635+2651)	TACTTTGATCCCCTTTA
2171	OPA1 H31 3UTR(+2575+2591)	TCTAGAATAAATAAATA	2192	OPA1 H31 3UTR(+2638+2654)	CATTACTTTGATCCCCT
2172	OPA1 H31 3UTR(+2578+2594)	ACATCTAGAATAAATAA	2193	OPA1 H31 3UTR(+2641+2657)	AACCATTACTTTGATCC

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
2173	OPA1 H31 3UTR(+2581+2597)	CATACATCTAGAATAAA	2194	OPA1 H31 3UTR(+2644+2660)	AAAAACCATTACTTTGA
2195	OPA1 H31 3UTR(+2647+2663)	GAGAAAAACCATTACTT	2216	OPA1 H31 3UTR(+2710+2726)	GCATATTTTAAAGCACA
2196	OPA1 H31 3UTR(+2650+2666)	TGAGAGAAAAAACCATTA	2217	OPA1 H31 3UTR(+2713+2729)	TAAGCATATTTTAAAGC
2197	OPA1 H31 3UTR(+2653+2669)	AACTGAGAGAAAAACCA	2218	OPA1 H31 3UTR(+2716+2732)	AGGTAAGCATATTTTAA
2198	OPA1 H31 3UTR(+2656+2672)	GAGAACTGAGAGAAAAA	2219	OPA1 H31 3UTR(+2719+2735)	AAAAGGTAAGCATATTT
2199	OPA1 H31 3UTR(+2659+2675)	TTAGAGAACTGAGAGAA	2220	OPA1 H31 3UTR(+2722+2738)	TTCAAAAGGTAAGCATA
2200	OPA1 H31 3UTR(+2662+2678)	AGCTTAGAGAACTGAGA	2221	OPA1 H31 3UTR(+2725+2741)	TCATTCAAAAGGTAAGC
2201	OPA1 H31 3UTR(+2665+2681)	ACCAGCTTAGAGAACTG	2222	OPA1 H31 3UTR(+2728+2744)	TGATCATTCAAAAGGTA
2202	OPA1 H31 3UTR(+2668+2684)	TAGACCAGCTTAGAGAA	2223	OPA1 H31 3UTR(+2731+2747)	CCATGATCATTCAAAAG
2203	OPA1 H31 3UTR(+2671+2687)	ACATAGACCAGCTTAGA	2224	OPA1 H31 3UTR(+2734+2750)	TAGCCATGATCATTCAA
2204	OPA1 H31 3UTR(+2674+2690)	ATAACATAGACCAGCTT	2225	OPA1 H31 3UTR(+2737+2753)	ATATAGCCATGATCATT
2205	OPA1 H31 3UTR(+2677+2693)	GCTATAACATAGACCAG	2226	OPA1 H31 3UTR(+2740+2756)	AACATATAGCCATGATC
2206	OPA1 H31 3UTR(+2680+2696)	AGAGCTATAACATAGAC	2227	OPA1 H31 3UTR(+2743+2759)	AACAACATATAGCCATG
2207	OPA1 H31 3UTR(+2683+2699)	GCTAGAGCTATAACATA	2228	OPA1 H31 3UTR(+2746+2762)	CTCAACAACATATAGCC
2208	OPA1 H31 3UTR(+2686+2702)	ACTGCTAGAGCTATAAC	2229	OPA1 H31 3UTR(+2749+2765)	TATCTCAACAACATATA
2209	OPA1 H31 3UTR(+2689+2705)	CATACTGCTAGAGCTAT	2230	OPA1 H31 3UTR(+2752+2768)	AAATATCTCAACAACAT
2210	OPA1 H31 3UTR(+2692+2708)	TTCCATACTGCTAGAGC	2231	OPA1 H31 3UTR(+2755+2771)	TTCAAATATCTCAACAA
2211	OPA1 H31 3UTR(+2695+2711)	CATTTCCATACTGCTAG	2232	OPA1 H31 3UTR(+2758+2774)	AGTTTCAAATATCTCAA
2212	OPA1 H31 3UTR(+2698+2714)	GCACATTTCCATACTGC	2233	OPA1 H31 3UTR(+2761+2777)	GTAAGTTTCAAATATCT
2213	OPA1 H31 3UTR(+2701+2717)	AAAGCACATTTCCATAC	2234	OPA1 H31 3UTR(+2764+2780)	AAGGTAAGTTTCAAATA
2214	OPA1 H31 3UTR(+2704+2720)	TTTAAAGCACATTTCCA	2235	OPA1 H31 3UTR(+2767+2783)	AACAAGGTAAGTTTCAA
2215	OPA1 H31 3UTR(+2707+2723)	TATTTTAAAGCACATTT	2236	OPA1 H31 3UTR(+2770+2786)	GAAAACAAGGTAAGTTT

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
2237	OPA1 H31 3UTR(+2773:+2789)	AGTGAAAACAAGGTAAG	2258	OPA1 H31 3UTR(+2836+2852)	ATAATATCTACACGTAA
2238	OPA1 H31 3UTR(+2776+2792)	ACAAGTGAAAACAAGGT	2259	OPA1 H31 3UTR(+2839+2855)	GCAATAATATCTACACG
2239	OPA1 H31 3UTR(+2779+2795)	TGCACAAGTGAAAACAA	2260	OPA1 H31 3UTR(+2842+2858)	GTTGCAATAATATCTAC
2240	OPA1 H31 3UTR(+2782+2798)	CAGTGCACAAGTGAAAA	2261	OPA1 H31 3UTR(+2845+2861)	TAAGTTGCAATAATATC
2241	OPA1 H31 3UTR(+2785+2801)	TCACAGTGCACAAGTGA	2262	OPA1 H31 3UTR(+2848+2864)	ATATAAGTTGCAATAAT
2242	OPA1 H31 3UTR(+2788+2804)	CATTCACAGTGCACAAG	2263	OPA1 H31 3UTR(+2851+2867)	AAAATATAAGTTGCAAT
2243	OPA1 H31 3UTR(+2791+2807)	GTTCATTCACAGTGCAC	2264	OPA1 H31 3UTR(+2854+2870)	GGCAAAATATAAGTTGC
2244	OPA1 H31 3UTR(+2794+2810)	AAAGTTCATTCACAGTG	2265	OPA1 H31 3UTR(+2857+2873)	TCAGGCAAAATATAAGT
2245	OPA1 H31 3UTR(+2797+2813)	TACAAAGTTCATTCACA	2266	OPA1 H31 3UTR(+2860+2876)	AGCTCAGGCAAAATATA
2246	OPA1 H31 3UTR(+2800+2816)	TAATACAAAGTTCATTC	2267	OPA1 H31 3UTR(+2863+2879)	TCAAGCTCAGGCAAAAT
2247	OPA1 H31 3UTR(+2803+2819)	AAATAATACAAAGTTCA	2268	OPA1 H31 3UTR(+2866+2882)	TGATCAAGCTCAGGCAA
2248	OPA1 H31 3UTR(+2806+2822)	AAAAAATAATACAAAGT	2269	OPA1 H31 3UTR(+2869+2885)	CTTTGATCAAGCTCAGG
2249	OPA1 H31 3UTR(+2809:+2825)	TTAAAAAAATAATACAA	2270	OPA1 H31 3UTR(+2872+2888)	GACCTTTGATCAAGCTC
2250	OPA1 H31 3UTR(+2812+2828)	GTTTTAAAAAAATAATA	2271	OPA1 H31 3UTR(+2875+2891)	AATGACCTTTGATCAAG
2251	OPA1 H31 3UTR(+2815+2831)	AAGGTTTTAAAAAAATA	2272	OPA1 H31 3UTR(+2878+2894)	ACAAATGACCTTTGATC
2252	OPA1 H31 3UTR(+2818+2834)	GTGAAGGTTTTAAAAAA	2273	OPA1 H31 3UTR(+2881+2897)	TACACAAATGACCTTTG
2253	OPA1 H31 3UTR(+2821+2837)	AATGTGAAGGTTTTAAA	2274	OPA1 H31 3UTR(+2884+2900)	ATCTACACAAATGACCT
2254	OPA1 H31 3UTR(+2824+2840)	CGTAATGTGAAGGTTTT	2275	OPA1 H31 3UTR(+2887+2903)	CTCATCTACACAAATGA
2255	OPA1 H31 3UTR(+2827+2843)	ACACGTAATGTGAAGGT	2276	OPA1 H31 3UTR(+2890+2906)	TTACTCATCTACACAAA
2256	OPA1 H31 3UTR(+2830+2846)	TCTACACGTAATGTGAA	2277	OPA1 H31 3UTR(+2893+2909)	TAATTACTCATCTACAC
2257	OPA1 H31 3UTR(+2833+2849)	ATATCTACACGTAATGT	2278	OPA1 H31 3UTR(+2896+2912)	TTTTAATTACTCATCTA
2279	OPA1 H31 3UTR(+2899+2915)	ATTTTTTTAATTACTCAT	2300	OPA1 H31 3UTR(+2962+2978)	CGTTAAAACAGAAAAAA

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
2280	OPA1 H31 3UTR(+2902+2918)	AATATTTTTTAATTACT	2301	OPA1 H31 3UTR(+2965+2981)	CCTCGTTAAAACAGAAA
2281	OPA1 H31 3UTR(+2905+2921)	TTAAATATTTTTTAATT	2302	OPA1 H31 3UTR(+2968+2984)	TTCCCTCGTTAAAACAG
2282	OPA1 H31 3UTR(+2908+2924)	GATTTAAATATTTTTTA	2303	OPA1 H31 3UTR(+2971+2987)	TCTTTCCCTCGTTAAAA
2283	OPA1 H31 3UTR(+2911+2927)	TGTGATTTAAATATTTT	2304	OPA1 H31 3UTR(+2974+2990)	TTCTCTTTCCCTCGTTA
2284	OPA1 H31 3UTR(+2914+2930)	TAATGTGATTTAAATAT	2305	OPA1 H31 3UTR(+2977+2993)	GGTTTCTCTTTCCCTCG
2285	OPA1 H31 3UTR(+2917+2933)	TTATAATGTGATTTAAA	2306	OPA1 H31 3UTR(+2980+2996)	ACAGGTTTCTCTTTCCC
2286	OPA1 H31 3UTR(+2920+2936)	GAATTATAATGTGATTT	2307	OPA1 H31 3UTR(+2983+2999)	TATACAGGTTTCTCTTT
2287	OPA1 H31 3UTR(+2923+2939)	ATAGAATTATAATGTGA	2308	OPA1 H31 3UTR(+2986+3002)	AGGTATACAGGTTTCTC
2288	OPA1 H31 3UTR(+2926+2942)	ATAATAGAATTATAATG	2309	OPA1 H31 3UTR(+2989+3005)	CCTAGGTATACAGGTTT
2289	OPA1 H31 3UTR(+2929+2945)	CCAATAATAGAATTATA	2310	OPA1 H31 3UTR(+2992+3008)	GACCCTAGGTATACAGG
2290	OPA1 H31 3UTR(+2932+2948)	TCTCCAATAATAGAATT	2311	OPA1 H31 3UTR(+2995+3011)	AATGACCCTAGGTATAC
2291	OPA1 H31 3UTR(+2935+2951)	TGCTCTCCAATAATAGA	2312	OPA1 H31 3UTR(+2998+3014)	AATAATGACCCTAGGTA
2292	OPA1 H31 3UTR(+2938+2954)	AGATGCTCTCCAATAAT	2313	OPA1 H31 3UTR(+3001+3017)	TCAAATAATGACCCTAG
2293	OPA1 H31 3UTR(+2941+2957)	AAAAGATGCTCTCCAAT	2314	OPA1 H31 3UTR(+3004+3020)	GGGTCAAATAATGACCC
2294	OPA1 H31 3UTR(+2944+2960)	TTTAAAAGATGCTCTCC	2315	OPA1 H31 3UTR(+3007+3023)	ATGGGGTCAAATAATGA
2295	OPA1 H31 3UTR(+2947+2963)	AAATTTAAAAGATGCTC	2316	OPA1 H31 3UTR(+3010+3026)	ACTATGGGGTCAAATAA
2296	OPA1 H31 3UTR(+2950+2966)	AAAAAATTTAAAAGATG	2317	OPA1 H31 3UTR(+3013+3029)	TATACTATGGGGTCAAA
2297	OPA1 H31 3UTR(+2953+2969)	AGAAAAAAATTTAAAAG	2318	OPA1 H31 3UTR(+3016+3032)	GGTTATACTATGGGGTC
2298	OPA1 H31 3UTR(+2956+2972)	AACAGAAAAAAAATTTAA	2319	OPA1 H31 3UTR(+3019+3035)	TCTGGTTATACTATGGG
2299	OPA1 H31 3UTR(+2959+2975)	TAAAACAGAAAAAAAAT	2320	OPA1 H31 3UTR(+3022+3038)	GAATCTGGTTATACTAT
2321	OPA1 H31 3UTR(+3025+3041)	CATGAATCTGGTTATAC	2342	OPA1 H31 3UTR(+3088+3104)	TGAAATGCAAGGCATGT
2322	OPA1 H31 3UTR(+3028+3044)	GACCATGAATCTGGTTA	2343	OPA1 H31 3UTR(+3091+3107)	CTGTGAAATGCAAGGCA

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
2323	OPA1 H31 3UTR(+3031+3047)	TTAGACCATGAATCTGG	2344	OPA1 H31 3UTR(+3094+3110)	CAACTGTGAAATGCAAG
2324	OPA1 H31 3UTR(+3034+3050)	TTGTTAGACCATGAATC	2345	OPA1 H31 3UTR(+3097+3113)	GTACAACTGTGAAATGC
2325	OPA1 H31 3UTR(+3037+3053)	AGCTTGTTAGACCATGA	2346	OPA1 H31 3UTR(+3100+3116)	GGAGTACAACTGTGAAA
2326	OPA1 H31 3UTR(+3040+3056)	GAGAGCTTGTTAGACCA	2347	OPA1 H31 3UTR(+3103+3119)	CATGGAGTACAACTGTG
2327	OPA1 H31 3UTR(+3043+3059)	ACTGAGAGCTTGTTAGA	2348	OPA1 H31 3UTR(+3106+3122)	GACCATGGAGTACAACT
2328	OPA1 H31 3UTR(+3046+3062)	CACACTGAGAGCTTGTT	2349	OPA1 H31 3UTR(+3109+3125)	GTTGACCATGGAGTACA
2329	OPA1 H31 3UTR(+3049+3065)	AGCCACACTGAGAGCTT	2350	OPA1 H31 3UTR(+3112+3128)	CCGGTTGACCATGGAGT
2330	OPA1 H31 3UTR(+3052+3068)	AAAAGCCACACTGAGAG	2351	OPA1 H31 3UTR(+3115+3131)	GCACCGGTTGACCATGG
2331	OPA1 H31 3UTR(+3055+3071)	GAGAAAAGCCACACTGA	2352	OPA1 H31 3UTR(+3118+3134)	AAAGCACCGGTTGACCA
2332	OPA1 H31 3UTR(+3058+3074)	TCAGAGAAAAGCCACAC	2353	OPA1 H31 3UTR(+3121+3137)	AAAAAAGCACCGGTTGA
2333	OPA1 H31 3UTR(+3061+3077)	CATTCAGAGAAAAGCCA	2354	OPA1 H31 3UTR(+3124+3140)	TGAAAAAAAGCACCGGT
2334	OPA1 H31 3UTR(+3064+3080)	AAGCATTCAGAGAAAAG	2355	OPA1 H31 3UTR(+3127+3143)	ATGTGAAAAAAAGCACC
2335	OPA1 H31 3UTR(+3067+3083)	TTCAAGCATTCAGAGAA	2356	OPA1 H31 3UTR(+3130+3146)	ACGATGTGAAAAAAAGC
2336	OPA1 H31 3UTR(+3070+3086)	AAATTCAAGCATTCAGA	2357	OPA1 H31 3UTR(+3133+3149)	ACCACGATGTGAAAAAA
2337	OPA1 H31 3UTR(+3073+3089)	GTGAAATTCAAGCATTC	2358	OPA1 H31 3UTR(+3136+3152)	AGTACCACGATGTGAAA
2338	OPA1 H31 3UTR(+3076+3092)	CATGTGAAATTCAAGCA	2359	OPA1 H31 3UTR(+3139+3155)	ACAAGTACCACGATGTG
2339	OPA1 H31 3UTR(+3079+3095)	AGGCATGTGAAATTCAA	2360	OPA1 H31 3UTR(+3142+3158)	TTGACAAGTACCACGAT
2340	OPA1 H31 3UTR(+3082+3098)	GCAAGGCATGTGAAATT	2361	OPA1 H31 3UTR(+3145+3161)	GTTTTGACAAGTACCAC
2341	OPA1 H31 3UTR(+3085+3101)	AATGCAAGGCATGTGAA	2362	OPA1 H31 3UTR(+3148+3164)	AATGTTTTGACAAGTAC
2363	OPA1 H31 3UTR(+3151+3167)	CAAAATGTTTTGACAAG	2384	OPA1 H31 3UTR(-3-19)	GACAGCCTTGGCAGCAA
2364	OPA1 H31 3UTR(+3154+3170)	TAACAAAATGTTTTGAC	2385	OPA1 H31 3UTR(-6-22)	AATGACAGCCTTGGCAG
2365	OPA1 H31 3UTR(+3157+3173)	AAATAACAAAATGTTTT	2386	OPA1 H31 3UTR(-9-25)	GAAAATGACAGCCTTGG

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
2366	OPA1 H31 3UTR(+3160+3176)	GGAAAATAACAAAATGT	2387	OPA1 H31 3UTR(-12-28)	AATGAAAATGACAGCCT
2367	OPA1 H31 3UTR(+3163+3179)	CAAGGAAAATAACAAAA	2388	OPA1 H31 3UTR(-15-31)	ATTAATGAAAATGACAG
2368	OPA1 H31 3UTR(+3166+3182)	TACCAAGGAAAATAACA	2389	OPA1 H31 3UTR(-18-34)	AGCATTAATGAAAATGA
2369	OPA1 H31 3UTR(+3169+3185)	TTTTACCAAGGAAAATA	2390	OPA1 H31 3UTR(-21-37)	GGCAGCATTAATGAAAA
2370	OPA1 H31 3UTR(+3172+3188)	ATATTTTACCAAGGAAA	2391	OPA1 H31 3UTR(-24-40)	GTTGGCAGCATTAATGA
2371	OPA1 H31 3UTR(+3175+3191)	TATATATTTTACCAAGG	2392	OPA1 H31 3UTR(-27-43)	CATGTTGGCAGCATTAA
2372	OPA1 H31 3UTR(+3178+3194)	TTTTATATATTTTACCA	2393	OPA1 H31 3UTR(-30-46)	GAACATGTTGGCAGCAT
2373	OPA1 H31 3UTR(+3181+3197)	CTTTTTTATATATTTTA	2394	OPA1 H31 3UTR(-33-49)	TATGAACATGTTGGCAG
2374	OPA1 H31 3UTR(+3184+3200)	AACCTTTTTTATATATT	2395	OPA1 H31 3UTR(-36-52)	TCATATGAACATGTTGG
2375	OPA1 H31 3UTR(+3187+3203)	GAAAAACCTTTTTTATAT	2396	OPA1 H31 3UTR(-39-55)	GCCTCATATGAACATGT
2376	OPA1 H31 3UTR(+3190+3206)	TTAGAAAACCTTTTTTA	2397	OPA1 H31 3UTR(-42-58)	TAAGCCTCATATGAACA
2377	OPA1 H31 3UTR(+3193+3209)	AAATTAGAAAACCTTTT	2398	OPA1 H31 3UTR(-45-61)	TAGTAAGCCTCATATGA
2378	OPA1 H31 3UTR(+3196+3212)	GTGAAATTAGAAAACCT	2399	OPA1 H31 3UTR(-48-64)	TCTTAGTAAGCCTCATA
2379	OPA1 H31 3UTR(+3199+3215)	AAAGTGAAATTAGAAAA	2400	OPA1 H31 3UTR(-51-67)	ACTTCTTAGTAAGCCTC
2380	OPA1 H31 3UTR(+3202+3218)	AGCAAAGTGAAATTAGA	2401	OPA1 H31 3UTR(-54-70)	ATAACTTCTTAGTAAGC
2381	OPA1 H31 3UTR(+3205+3221)	GGCAGCAAAGTGAAATT	2402	OPA1 H31 3UTR(-57-73)	GTTATAACTTCTTAGTA
2382	OPA1 H31 3UTR(+3208+3224)	CTTGGCAGCAAAGTGAA	2403	OPA1 H31 3UTR(-60-76)	TTAGTTATAACTTCTTA
2383	OPA1 H31 3UTR(+3211-16)	AGCCTTGGCAGCAAAGT	2404	OPA1 H31 3UTR(-63-79)	AGCTTAGTTATAACTTC
2405	OPA1 H31 3UTR(-66-82)	TAAAGCTTAGTTATAAC	2426	OPA1 H31 3UTR(-129-145)	AACAAAGTGAGTAACAG
2406	OPA1 H31 3UTR(-69-85)	TTCTAAAGCTTAGTTAT	2427	OPA1 H31 3UTR(-132-148)	AATAACAAAGTGAGTAA
2407	OPA1 H31 3UTR(-72-88)	CAGTTCTAAAGCTTAGT	2428	OPA1 H31 3UTR(-135-151)	AGGAATAACAAAGTGAG
2408	OPA1 H31 3UTR(-75-91)	TTCCAGTTCTAAAGCTT	2429	OPA1 H31 3UTR(-138-154)	TGGAGGAATAACAAAGT

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
2409	OPA1 H31 3UTR(-78-94)	CTCTTCCAGTTCTAAAG	2430	OPA1 H31 3UTR(-141-157)	TTCTGGAGGAATAACAA
2410	OPA1 H31 3UTR(-81-97)	AGTCTCTTCCAGTTCTA	2431	OPA1 H31 3UTR(-144-160)	AAGTTCTGGAGGAATAA
2411	OPA1 H31 3UTR(-84-100)	TAAAGTCTCTTCCAGTT	2432	OPA1 H31 3UTR(-147-163)	GCAAAGTTCTGGAGGAA
2412	OPA1 H31 3UTR(-87-103)	AATTAAAGTCTCTTCCA	2433	OPA1 H31 3UTR(-150-166)	TGAGCAAAGTTCTGGAG
2413	OPA1 H31 3UTR(-90-106)	TGAAATTAAAGTCTCTT	2434	OPA1 H31 3UTR(-153-169)	TTATGAGCAAAGTTCTG
2414	OPA1 H31 3UTR(-93-109)	AGATGAAATTAAAGTCT	2435	OPA1 H31 3UTR(-156-172)	CATTTATGAGCAAAGTT
2415	OPA1 H31 3UTR(-96-112)	GGTAGATGAAATTAAAG	2436	OPA1 H31 3UTR(-159-175)	TATCATTTATGAGCAAA
2416	OPA1 H31 3UTR(-99-115)	GATGGTAGATGAAATTA	2437	OPA1 H31 3UTR(-162-178)	AGGTATCATTTATGAGC
2417	OPA1 H31 3UTR(-102-118)	TCAGATGGTAGATGAAA	2438	OPA1 H31 3UTR(-165-181)	AGTAGGTATCATTTATG
2418	OPA1 H31 3UTR(-105-121)	TAATCAGATGGTAGATG	2439	OPA1 H31 3UTR(-168-184)	ATTAGTAGGTATCATTT
2419	OPA1 H31 3UTR(-108-124)	TTATAATCAGATGGTAG	2440	OPA1 H31 3UTR(-171-187)	ACAATTAGTAGGTATCA
2420	OPA1 H31 3UTR(-111-127)	AGTTTATAATCAGATGG	2441	OPA1 H31 3UTR(-174-190)	TCGACAATTAGTAGGTA
2421	OPA1 H31 3UTR(-114-130)	AGGAGTTTATAATCAGA	2442	OPA1 H31 3UTR(-177-193)	TGATCGACAATTAGTAG
2422	OPA1 H31 3UTR(-117-133)	AACAGGAGTTTATAATC	2443	OPA1 H31 3UTR(-180-196)	CAATGATCGACAATTAG
2423	OPA1 H31 3UTR(-120-136)	AGTAACAGGAGTTTATA	2444	OPA1 H31 3UTR(-183-199)	ATCCAATGATCGACAAT
2424	OPA1 H31 3UTR(-123-139)	GTGAGTAACAGGAGTTT	2445	OPA1 H31 3UTR(-186-202)	CATATCCAATGATCGAC
2425	OPA1 H31 3UTR(-126-142)	AAAGTGAGTAACAGGAG	2446	OPA1 H31 3UTR(-189-205)	TGACATATCCAATGATC
2447	OPA1 H31 3UTR(-192-208)	ACTTGACATATCCAATG	2468	OPA1 H31 3UTR(-255-271)	GAAACATGTTCTTGCCT
2448	OPA1 H31 3UTR(-195-211)	CTAACTTGACATATCCA	2469	OPA1 H31 3UTR(-258-274)	ATTGAAACATGTTCTTG
2449	OPA1 H31 3UTR(-198-214)	TACCTAACTTGACATAT	2470	OPA1 H31 3UTR(-261-277)	ACGATTGAAACATGTTC
2450	OPA1 H31 3UTR(-201-217)	CGCTACCTAACTTGACA	2471	OPA1 H31 3UTR(-264-280)	AACACGATTGAAACATG
2451	OPA1 H31 3UTR(-204-220)	ATACGCTACCTAACTTG	2472	OPA1 H31 3UTR(-267-283)	GCTAACACGATTGAAAC

SEQ ID	ASO Coordinates	Sequence 5'>3'	SEQ ID	ASO Coordinates	Sequence 5'>3'
2452	OPA1 H31 3UTR(-207-223)	CCTATACGCTACCTAAC	2473	OPA1 H31 3UTR(-270-286)	AATGCTAACACGATTGA
2453	OPA1 H31 3UTR(-210-226)	ACACCTATACGCTACCT	2474	OPA1 H31 3UTR(-273-289)	ACCAATGCTAACACGAT
2454	OPA1 H31 3UTR(-213-229)	GGCACACCTATACGCTA	2475	OPA1 H31 3UTR(-276-292)	AAAACCAATGCTAACAC
2455	OPA1 H31 3UTR(-216-232)	GAAGGCACACCTATACG	2476	OPA1 H31 3UTR(-279-295)	AAGAAAACCAATGCTAA
2456	OPA1 H31 3UTR(-219-235)	TAAGAAGGCACACCTAT	2477	OPA1 H31 3UTR(-282-298)	ATAAAGAAAACCAATGC
2457	OPA1 H31 3UTR(-222-238)	AATTAAGAAGGCACACC	2478	OPA1 H31 3UTR(-285-301)	CTGATAAAGAAAACCAA
2458	OPA1 H31 3UTR(-225-241)	AGGAATTAAGAAGGCAC	2479	OPA1 H31 3UTR(-288-304)	GCACTGATAAAGAAAAC
2459	OPA1 H31 3UTR(-228-244)	TGAAGGAATTAAGAAGG	2480	OPA1 H31 3UTR(-291-307)	TTAGCACTGATAAAGAA
2460	OPA1 H31 3UTR(-231-247)	TTCTGAAGGAATTAAGA	2481	OPA1 H31 3UTR(-294-310)	CTGTTAGCACTGATAAA
2461	OPA1 H31 3UTR(-234-250)	ATCTTCTGAAGGAATTA	2482	OPA1 H31 3UTR(-297-313)	AGTCTGTTAGCACTGAT
2462	OPA1 H31 3UTR(-237-253)	TGCATCTTCTGAAGGAA	2483	OPA1 H31 3UTR(-300-316)	CTGAGTCTGTTAGCACT
2463	OPA1 H31 3UTR(-240-256)	CTCTGCATCTTCTGAAG	2484	OPA1 H31 3UTR(-303-319)	ACACTGAGTCTGTTAGC
2464	OPA1 H31 3UTR(-243-259)	TGCCTCTGCATCTTCTG	2485	OPA1 H31 3UTR(-306-322)	CTCACACTGAGTCTGTT
2465	OPA1 H31 3UTR(-246-262)	TCTTGCCTCTGCATCTT	2486	OPA1 H31 3UTR(-309-325)	GGCCTCACACTGAGTCT
2466	OPA1 H31 3UTR(-249-265)	TGTTCTTGCCTCTGCAT	2487	OPA1 H31 3UTR(-312-328)	TGGGGCCTCACACTGAG
2467	OPA1 H31 3UTR(-252-268)	ACATGTTCTTGCCTCTG	2488	OPA1 H31 3UTR(-315-331)	GTATGGGGCCTCACACT

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

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

MWRLRRAAVACEVCQSLVKHSSGIKGSLPLQKLHLVSRSIYHSHHPTLKLQRPQLRTSFQQFSSLTNLPLRKLKFSPIKYGYQPRRNFWPARLATRLLKL
RYLILGSAVGGGYTAKKTFDQWKDMIPDLSEYKWIVPDIVWEIDEYIDFEKIRKALPSSEDLVKLAPDFDKIVESLSLLKDFFTSGSPEETAFRATDRGSES
DKHFRKVSDKEKIDQLQEELLHTQLKYQRILERLEKENKELRKLVLQKDDKGHHRKLKKSLIDMYSEVLDVLSDYDASYNTQDHLPRVVVVGDQSAG
5 KTSVLEMIAQARIFPRGSGEMMTRSPVKVTLSEGPHHVALFKDSSREFDLTKEEDLAALRHEIELRMRKNVKEGCTVSPETISLNVKGPGLQRMVLVDLP
GVINTVTSGMAPDTKETIFSISKAYMQNPNAIILCIQDGSVDAERSIVTDLVSQMDPHGRRTIFVLTKVDLAEKNVASPSRIQQIIEGKLFPMKALGYFAVV
TGKGNSSESIEAIREYEEEFFQNSKLLKTSMLKAHQVTTRNLSLAVSDCFWKMVRESVEQQADSFKATRFNLETEWKNNYPRLRELDRNELFEKAKNEIL
DEVISLSQVTPKHWEEILQQSLWERVSTHVIENIYLPAAQTMNSGTFNTTVDIKLKQWTDKQLPNKAVEVAWETLQEEFSRFMTEPKGKEHDDIFDKLKE
AVKEESIKRHKWNDFAEDSLRVFQHNALEDRSISDKQQWDAATYFMEEALQARLKDTENAIENMVGPDWKKRWLYWKNRTQEQCVHNETKNELEKM
10 LKCNEEHPAYLASDEITTVRKNLESRGVEVDPSLIKDTWHQVYRRHFLKTALNHCNLCRRGFYYYQRHFVDSELECNDVVLFWRIQRMLAITANTLRQQ
LTNTEVRRLEKNVKEVLEDFAEDGEKKIKLLTGKRVQLAEDLKKVREIQEKLDAFIEALHQEK

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)	TACATATATAAAAAGGTCATTGTAA
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)	CTGAAATACATATATAAAAAGGTCA
2499	OPA1_H7xA(-125-96)	GAAATTCTGAAATACATATATAAAAAGGTC

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	CATGCGCACAGTGCGTCGGAAT
2501	hOPA1_H1A(-3+21)2MM	CCTTTCTAGGCGTGCAGCACTA
2502	hOPA1_H1A(+64+85)2MM	CATGGACTTCTGCAAGAGCCTA
2503	hOPA1_H1A(+66+87)2MM	CGCATGGACTTCCGCAAGAGAT

SEQ ID NO: 2504: CPP Sequence (N to C terminus)
RASARRASARRANARRANARRSGGR

Table 8: List of antisense oligonucleotide sequences targeting intron 7 of *OPA1* transcript

SEQ ID	PMO coordinate	Sequence 5'->3'	Length
2505	OPA1_H7xA(-127-102)1mmA>G_V2	CTGAAATACATATATAAGAAGGTCAT	26
2506	OPA1_H7xA(-128-102)1mmA>G_V2	CTGAAATACATATATAAGAAGGTCATT	27
2507	OPA1_H7xA(-129-102)1mmA>G_V2	CTGAAATACATATATAAGAAGGTCATTG	28
2508	OPA1_H7xA(-130-102)1mmA>G_V2	CTGAAATACATATATAAGAAGGTCATTGT	29
2509	OPA1_H7xA(-131-102)1mmA>G_V2	CTGAAATACATATATAAGAAGGTCATTGTA	30
2510	OPA1_H7xA(-132-103)1mmA>G_V2	TGAAATACATATATAAGAAGGTCATTGTAA	30
2511	OPA1_H7xA(-133-104)1mmA>G_V2	GAAATACATATATAAGAAGGTCATTGTAAA	30
2512	OPA1_H7xA(-134-105)2mmA>G_V2	AAATACATATATAAGAAGGTCATTGTAAGA	30
2513	OPA1_H7xA(-135-106)2mmA>G_V2	AATACATATATAAGAAGGTCATTGTAAGAA	30
2514	OPA1_H7xA(-136-107)2mmA>G_V2	ATACATATATAAGAAGGTCATTGTAAGAAT	30
2515	OPA1_H7xA(-137-108)2mmA>G_V2	TACATATATAAGAAGGTCATTGTAAGAATT	30
2516	OPA1_H7xA(-138-109)2mmA>G_V2	ACATATATAAGAAGGTCATTGTAAGAATTT	30
2517	OPA1_H7xA(-139-110)2mmA>G_V2	CATATATAAGAAGGTCATTGTAAGAATTTC	30

SEQ ID	Description	Sequence	SEQ ID	Description	Sequence
2518	Linker	GGGGS	2521	Linker	GASGGASG
2519	Linker	GGGGSGGGGS	2522	Linker	GASG
2520	Linker	GGTAGSTGG			

CLAIMS

1. A cell-penetrating peptide (CPP) comprising a sequence set forth in SEQ ID NO: 2504.

2. A cell-penetrating peptide (CPP), wherein the CPP consists of a sequence set forth in SEQ ID NO: 2504.

3. The CPP of claim 1 or 2, wherein the CPP is linked to an antisense oligonucleotide that modulates mRNA productive transcript, stability and/or translation of *OPA1* gene transcript or part thereof.

4. A cell-penetrating peptide (CPP) conjugate comprising a sequence set forth in SEQ ID NO: 2504 linked to an antisense oligonucleotide that modulates mRNA productive transcript, stability and/or translation of *OPA1* gene transcript or part thereof.

5. An antisense oligonucleotide that modulates mRNA productive transcript, stability and/or translation of *OPA1* gene transcript or part thereof, wherein the antisense oligonucleotide is linked to a cell-penetrating peptide (CPP) comprising a sequence set forth in SEQ ID NO: 2504.

6. The CPP of claim 3, or the CPP conjugate of claim 4, or the antisense oligonucleotide of claim 5, 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.

7. The CPP of claims 3 or 6, or the CPP conjugate of claims 4 or 6, or the antisense oligonucleotide of claims 5 or 6, wherein the amount of functional OPA1 protein in the cell and/or the tissue is increased by about 1.1 to about 10-fold.

8. The CPP of any one of claims 3, 6 or 7, or the CPP conjugate of any one of claims 4, 6 or 7, or the antisense oligonucleotide of any one of claims 5 to 7, wherein the tissue is selected from the group consisting of the retina, retinal pigment epithelium and combinations thereof.

9. The CPP of any one of claims 3 or 6 to 8, or the CPP conjugate of any one of claims 4 or 6 to 8, or the antisense oligonucleotide of any one of claims 5 to 8, 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.

10. The CPP, the CPP conjugate or antisense oligonucleotide of claim 9, wherein:

i. 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; or

ii. the antisense oligonucleotide binds to intron 7 of an *OPA1* transcript and reduces expression of *OPA1* gene transcript lacking exon 7x but does not substantially affect the relative expression levels of *OPA1* gene transcripts comprising exon 7 or lacking exon 7.

11. The CPP of any one of claims 3 or 6 to 10, or the CPP conjugate of any one of claims 4 to 6 to 10, or the antisense oligonucleotide of any one of claims 5 to 10, wherein the antisense oligonucleotide binds within a targeted portion of the *OPA1* pre-mRNA nucleotide sequence corresponding to SEQ ID NOs: 1, 55, 139.

12. The CPP of any one of claims 3 or 6 to 11, or the CPP conjugate of any one of claims 4 to 6 to 11, or the antisense oligonucleotide of any one of claims 5 to 11, wherein the antisense oligonucleotide comprises one or more mismatches relative to the sequence set forth in SEQ ID NO: 1.

13. The CPP, the CPP conjugate or the antisense oligonucleotide of claim 12, which comprises two mismatches relative to the sequence set forth in SEQ ID NO: 1.

14. The CPP, the CPP conjugate or the antisense oligonucleotide of claims 12 or 13, wherein the antisense oligonucleotide significantly increases the level of a transcript comprising exons 3, 4, 6, 7 and 8 in a cell to which the antisense oligonucleotide is contacted relative to the level of the transcript in a cell to which the antisense oligonucleotide has not been contacted.

15. The CPP of any one of claims 3 or 6 to 14, or the CPP conjugate of any one of claims 4 to 6 to 14, or the antisense oligonucleotide of any one of claims 5 to 14, 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.

16. An antisense oligonucleotide comprising or consisting of a sequence set forth in any one of SEQ ID NOs: 2-54 or SEQ ID NOs: 2491-2677 or SEQ ID NOs: 2505-2517 or a sequence having at least about 50% identity thereto, wherein the antisense oligonucleotide is linked to a cell-penetrating peptide (CPP) comprising a sequence set forth in SEQ ID NO: 2504.

17. An antisense oligonucleotide comprising or consisting of a sequence set forth in SEQ ID NO: 2512, wherein the antisense oligonucleotide is linked to a cell-penetrating peptide (CPP) comprising a sequence set forth in SEQ ID NO: 2504.

18. An antisense oligonucleotide that binds to a targeted portion of the 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, wherein the antisense oligonucleotide is linked to a cell-penetrating peptide (CPP) comprising a sequence set forth in SEQ ID NO: 2504.

19. The CPP of any one of claims 3 or 6 to 11, or the CPP conjugate of any one of claims 4 to 6 to 11, or the antisense oligonucleotide of any one of claims 5 to 11 or 18, wherein the antisense oligonucleotide comprises or consists of any one of SEQ ID NOs: 2-54 or SEQ ID NOs: 2491-2499 or SEQ ID NOs: 2505-2517.

20. An antisense oligonucleotide 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, wherein the antisense oligonucleotide is linked to a cell-penetrating peptide (CPP)

comprising a sequence set forth in SEQ ID NO: 2504 and wherein the targeted portion is within the nucleotide sequence corresponding to SEQ ID NO: 55.

21. The CPP of any one of claims 3 or 6 to 9, or the CPP conjugate of any one of claims 4 to 6 to 9, or the antisense oligonucleotide of any one of claims 5 to 9 or 20, wherein the antisense oligonucleotide comprises or consists of any one of SEQ ID NOs: 56-138 or SEQ ID NOs: 2500-2503.

22. An antisense oligonucleotide comprising or consisting of a sequence set forth in SEQ ID NO: 112, wherein the antisense oligonucleotide is linked to a cell-penetrating peptide (CPP) comprising a sequence set forth in SEQ ID NO: 2504.

23. An antisense oligonucleotide that binds to a targeted portion of the 3' UTR of an *OPA1* gene transcript in a cell and increases transcript stability of an *OPA1* mRNA, wherein the antisense oligonucleotide is linked to a cell-penetrating peptide (CPP) comprising a sequence set forth in SEQ ID NO: 2504.

24. The CPP of any one of claims 3 or 6 to 9, or the CPP conjugate of any one of claims 4 to 6 to 9, or the antisense oligonucleotide of any one of claims 5 to 9 or 23, wherein the antisense oligonucleotide 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.

25. The CPP, or the CPP conjugate or the antisense oligonucleotide of claim 24, wherein the antisense oligonucleotide comprises or consists of any one of SEQ ID NOs: 140-2488.

26. The CPP of any one of claims 3 or 6 to 15, or 19, or 21 or 24, or 25, or the CPP conjugate of any one of claims 4 to 6 to 15, or 19, or 21 or 24, or 25, or the antisense oligonucleotide of any one of claims 5 to 25, wherein the antisense oligonucleotide comprises a backbone modification.

27. The CPP, the CPP conjugate or the antisense oligonucleotide of claim 26, wherein the antisense oligonucleotide comprises a backbone modification comprising a phosphorothioate linkage or a phosphorodiamidate linkage.

28. The CPP of any one of claims 3 or 6 to 15, or 19, or 21 or 24, or 25 to 27, or the CPP conjugate of any one of claims 4 to 6 to 15, or 19, or 21 or 24, or 25 to 27, or the antisense oligonucleotide of any one of claims 5 to 27, 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.

29. The CPP of any one of claims 3 or 6 to 15, or 19, or 21 or 24, or 25 to 28, or the CPP conjugate of any one of claims 4 to 6 to 15, or 19, or 21 or 24, or 25 to 28, or the antisense oligonucleotide of any one of claims 5 to 28, wherein the antisense oligonucleotide comprises at least one modified sugar moiety.

30. The CPP of any one of claims 3 or 6 to 15, or 19, or 21 or 24, or 25 to 29, or the CPP conjugate of any one of claims 4 to 6 to 15, or 19, or 21 or 24, or 25 to 29, or the antisense oligonucleotide of any one of claims 5 to 29, wherein each sugar moiety in the antisense oligonucleotide is a modified sugar moiety.

31. The CPP of any one of claims 3 or 6 to 15, or 19, or 21 or 24, or 25 to 30, or the CPP conjugate of any one of claims 4 to 6 to 15, or 19, or 21 or 24, or 25 to 30, or the antisense oligonucleotide of any one of claims 5 to 30, wherein the antisense oligonucleotide comprises a 2'-*O*-methoxyethyl moiety.

32. The CPP, or the CPP conjugate, or the antisense oligonucleotide of claim 31, wherein each nucleotide of the antisense oligonucleotide comprises a 2'-*O*-methoxyethyl moiety.

33. The CPP of any one of claims 3 or 6 to 15, or 19, or 21 or 24, or 25 to 32, or the CPP conjugate of any one of claims 4 to 6 to 15, or 19, or 21 or 24, or 25 to 32, or the antisense oligonucleotide of any one of claims 5 to 32, 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.

34. The CPP, or the CPP conjugate, or the antisense oligonucleotide of claim 33, wherein the nucleotide sequence of the antisense oligonucleotide consists of 20 to 30 nucleotides.

35. The CPP, or the CPP conjugate or the antisense oligonucleotide of claim 34, wherein the antisense oligonucleotide comprises one or more phosphorodiamidate morpholino moieties.

36. The CPP of any one of claims 3 or 6 to 15, or 19, or 21 or 24, or 25 to 35, or the CPP conjugate of any one of claims 4 to 6 to 15, or 19, or 21 or 24, or 25 to 35, or the antisense oligonucleotide of any one of claims 5 to 35, wherein the antisense oligonucleotide is covalently or non-covalently linked to the CPP.

37. The CPP, or the CPP conjugate, or the antisense oligonucleotide of claim 36, wherein the CPP is linked to the 5' end of the antisense oligonucleotide or is linked to the 3' end of the antisense oligonucleotide.

38. The CPP of any one of claims 3 or 6 to 15, or 19, or 21 or 24, or 25 to 37, or the CPP conjugate of any one of claims 4 to 6 to 15, or 19, or 21 or 24, or 25 to 37, or the antisense oligonucleotide of any one of claims 5 to 37, wherein the antisense oligonucleotide is complexed with a delivery nanocarrier.

39. The CPP, or the CPP conjugate, or the antisense oligonucleotide of claim 38, wherein the delivery nanocarrier is selected from the group consisting of: lipoplexes, liposomes, exosomes, inorganic nanoparticles, and DNA nanostructures.

40. The CPP, or the CPP conjugate, or the antisense oligonucleotide of claim 39, wherein the delivery nanocarrier comprises a lipid nanoparticle (LNP) encapsulating the antisense oligonucleotide.

41. The CPP of any one of claims 3 or 6 to 15, or 19, or 21 or 24, or 25 to 40, or the CPP conjugate of any one of claims 4 to 6 to 15, or 19, or 21 or 24, or 25 to 40, or the antisense oligonucleotide of any one of claims 5 to 40, 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.

42. A pharmaceutical composition comprising the CPP of any one of claims 3 or 6 to 15, or 19, or 21 or 24, or 25 to 41, or the CPP conjugate of any one of claims 4 to 6 to

15, or 19, or 21 or 24, or 25 to 41, or the antisense oligonucleotide of any one of claims 5 to 41 and a pharmaceutically acceptable excipient.

43. A method of treating , preventing and/or delaying progression of a condition associated with OPA1 expression in a subject, the method comprising administering the CPP of any one of claims 3 or 6 to 15, or 19, or 21 or 24, or 25 to 41, or the CPP conjugate of any one of claims 4 to 6 to 15, or 19, or 21 or 24, or 25 to 41, or the antisense oligonucleotide of any one of claims 5 to 41 or the pharmaceutical composition of claim 38 to the subject.

44. The method of claim 43, wherein the condition is glaucoma, autosomal dominant optic atrophy (ADOA), geographic atrophy, acute ischemic optic neuritis or acute ischemic optic neuropathy.