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(71) Applicant: THE TEXAS A&M UNIVERSITY SYSTEM [US/US]; 3369 TAMU, College Station, Texas 77843-3369 (US).

(72) Inventor: DINDOT, Scott Victor; 2608 Warkworth Lane, College Station, Texas 77845 (US).

(74) Agent: GILES, P. Brian; THOMAS | HORSTEMEYER LLP, 3200 Windy Hill Rd SE, Suite 1600E, Atlanta, Georgia 30339 (US).

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(54) Title: ANGELMAN SYNDROME ANTISENSE TREATMENT

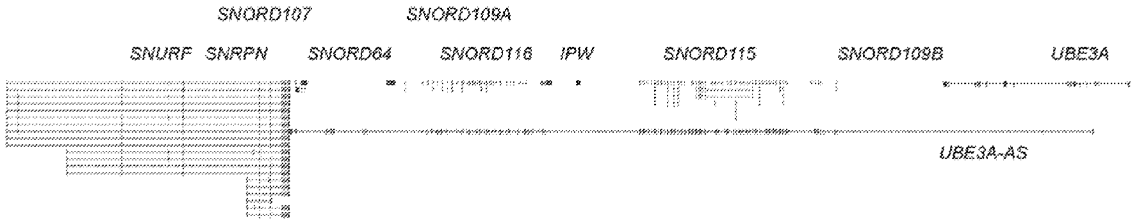

FIG. 1A

(57) Abstract: Disclosed herein are antisense oligonucleotides that are capable of inducing expression of ubiquitin-protein ligase E3A (*UBE3A*) from the paternal allele in animal or human neurons. The oligonucleotides target the suppressor of the *UBE3A* paternal allele by hybridization to *SNHG14* long non-coding RNA at the 5'-end of *UBE3A-AS*, which is downstream of *SNORD115-45* snoRNA. Also disclosed are pharmaceutical compositions and methods for treatment of Angelman syndrome.

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ANGELMAN SYNDROME ANTISENSE TREATMENT

CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims benefit of U.S. Provisional Application No. 62/593,431, filed December 1, 2017, and Application Serial No. 62/676,034, filed May 24, 2018, which are hereby incorporated herein by reference in their entirety.

SEQUENCE LISTING

This application contains a sequence listing filed in electronic form as an ASCII.txt file entitled "922001-2020 Sequence Listing_ST25" created on November 30, 2018. The content of the sequence listing is incorporated herein in its entirety.

BACKGROUND

Angelman syndrome (AS) is a neurodevelopmental disorder that is associated with severe cognitive and motor deficits, epilepsy, sleep-disorder, and an atypical 'happy' disposition. Individuals with AS are often diagnosed at 2-3 years of age and have a normal life-span. They require assisted living and medical care throughout their lives. There are currently few treatment options for individuals with AS, most of which involve anti-epileptic medications to treat seizures.

Angelman syndrome is caused by mutations that affect the expression or function of the maternally inherited ubiquitin-protein ligase E3A (*UBE3A*) gene. Unlike most genes, *UBE3A* is subject to genomic imprinting, which is a rare, naturally occurring phenomenon that turns-off one allele of a gene while leaving the other allele on. In neurons of the central nervous system (CNS), the paternal *UBE3A* allele is off, whereas in all other cell types of the body, both alleles of *UBE3A* are on. Because of this, AS is always caused by mutations that affect the maternally inherited *UBE3A* allele.

The paternal *UBE3A* allele is turned-off by the *UBE3A* antisense transcript (*UBE3A-AS*), which is a component of a long RNA transcript that expresses several protein coding and noncoding transcripts. *UBE3A-AS* is expressed from the paternal allele and only in neurons of the CNS and is both sufficient and necessary to turn-off expression of the paternal *UBE3A* allele. It's unclear why *UBE3A* is imprinted in neurons, but it creates a unique opportunity to treat individuals with AS, because there is a functional, albeit inactive, copy of *UBE3A* on the paternal chromosome. Studies to date indicate that turning on the paternal *UBE3A* allele is a viable therapy to treat AS.

SUMMARY

Disclosed herein is a region in the 5′-end of *UBE3A-AS* transcript that is important for its stability. Based on these findings, antisense oligonucleotides (ASOs) were designed to target this region in order to terminate transcription of *UBE3A-AS* and reactivate expression of the paternal *UBE3A* allele. These ASOs targeting the 5′-end of *UBE3A-AS* are capable of stopping transcription of *UBE3A-AS* and turning on the paternal *UBE3A* allele. *SNHG14* is a polycistronic transcript that encodes several different RNAs, including *UBE3A-AS*.

Accordingly, disclosed herein are ASOs containing a contiguous nucleotide sequence of 10 to 30 nucleotides (i.e., 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) in length with at least 98% (i.e. 98%, 99%, or 100%) complementarity to target exons between the 3′-end of the *SNORD115* and the 5′-end of *SNORD109B*, which is thought to represent the 5′-end of the *UBE3A* antisense transcript (*UBE3A-AS*). In particular the target exons can be in the 5′-end of *UBE3A-AS*, corresponding to position 25,511,577 to 25,516,681 on human chromosome 15 human genome assembly hg19. In some embodiments, the target nucleic acid is one of five exons located in the 5′-end of *UBE3A-AS*, which can correspond to positions 25,511,577 to 25,511,761 (exon 1), 25,512,059 to 25,512,191 (exon 2), 25,513,476 to 25,513,600 (exon 3), 25,514,752 to 25,514,880 (exon 4), and 25,516,565 to 25,516,681 (exon 5). Therefore, the target nucleic acid can be a contiguous nucleic acid sequence of 10 to 30 nucleotides within SEQ ID NO:1, 2, 3, 4, or 5.

In some embodiments, the target sequence is an exonic boundary involving *UBE3A-AS* exons 1-5, *UBE3A-AS* exon 5 and *SNORD109B* exon 1, and/or *SNORD109B* exons 1-2.

Methods and strategies for designing ASOs are known in the art. In some embodiments, the ASO is designed to target sequences that are conserved among human subjects. In some embodiments, the ASO is designed to target sequences that are conserved among primate subjects.

The oligonucleotide can be an antisense oligonucleotide (i.e., as will be understood by those of ordinary skill in the art – antisense to its target nucleic acid), e.g., with a gapmer design. The disclosed oligonucleotide is capable of inducing paternal *UBE3A* expression in a neuron by degradation, reduction, or removal of the *UBE3A-AS* transcript. It does this by targeting the 5′-end of *UBE3A-AS* at a site upstream of *SNORD109B* snoRNA. Examples of ASO designed to target exons 1-5

are provided in Tables 1, 2, 3, 4, or 5. For example, in some embodiments, the ASO comprises the nucleic acid sequence SEQ ID NO: 6, 7, 8, 9, 10, or 11.

The disclosed ASOs can also have one or more modifications to improve stability, solubility, activity, cellular distribution, and/or cellular uptake. For example, the disclosed ASO can contain one or more sugar-modified nucleosides and/or modified internucleoside linkages. For example, in some embodiments, the oligonucleotide comprises one or more internucleoside linkages modified from the natural phosphodiester to a linkage that is for example more resistant to nuclease attack. In some embodiments, the ASO contains one or more modified nucleobases that differ from naturally occurring nucleobases, but are functional during nucleic acid hybridization.

In some embodiments, the ASO is a DNA oligonucleotide. In some embodiments, the ASO is an RNA oligonucleotide. In still other embodiments, the ASO contains both deoxynucleotides and ribonucleotides. For example, the ASO can be a gapmer, headmer, or tailmer oligonucleotide. In some embodiments, the central block of a gapmer is flanked by blocks of modified ribonucleotides that protect the internal block from nuclease degradation. For example, the ASO can contain a stretch of 7, 8, 9, 10, or more natural DNA monomers to activate RNase H cleavage of the target RNA, along with 3, 4, or 5 modified ribonucleotide monomers at the 3′- and 5′-ends for protection against exonucleases. In some cases, the modified ribonucleotides are 2′-O-Methyl (OMe) RNA nucleotides, 2′-O-methoxyethyl (MOE)-modified nucleotides, or 2′-Locked Nucleic Acids (LNAs). Examples of gapmer ASOs are provided Tables 7, 11, and 17. Therefore, in some embodiments, the disclosed ASO has a nucleic acid sequence selected from SEQ ID NOs:362 to 392.

Also disclosed are pharmaceutical compositions comprising one or more of the ASOs disclosed herein and pharmaceutically acceptable diluents, carriers, salts and/or adjuvants.

Also disclosed are methods for *in vivo* or *in vitro* induction of *UBE3A* expression in a target cell where expression of paternal *UBE3A* is suppressed, by administering one or more of the disclosed ASOs or composition disclosed herein in an effective amount to said cell.

Also disclosed are methods for treating or preventing a disease, disorder or dysfunction associated with *in vivo* activity of UBE3A comprising administering a therapeutically or prophylactically effective amount of one or more of the disclosed ASOs to a subject suffering from or susceptible to the disease, disorder or dysfunction, such as Angelman syndrome.

The details of one or more embodiments of the invention are set forth in the accompanying drawings and the description below. Other features, objects, and advantages of the invention will be apparent from the description and drawings, and from the claims. For example, those skilled in the art, reading the specification will appreciate that the present disclosure demonstrates usefulness of certain sequences as described herein to impact expression of *UBE3A*, and furthermore teaches usefulness of oligonucleotide formats that are, or target (e.g., are complementary to), such sequences. Those skilled in the art will appreciate that the present disclosure is not limited to any particular mechanism of action – provided oligonucleotides may be useful regardless of whether they act via an antisense mechanism, for example, involving RNase H activity, and other therapeutic formats (e.g., siRNA, shRNA, nuclease gRNA, etc.) of oligonucleotides that are or target such sequences are also provided. Analogously, those skilled in the art will appreciate that the present disclosure, by defining useful sequences as described herein, also describes a variety of formats for such sequences (e.g., as part of a nucleic acid vector such as a vector from which they may be expressed (e.g., *in vivo*, *in vitro*, or both, etc.). Thus, those skilled in the art, reading the present disclosure, will appreciate that reference to “ASOs” herein is exemplary, and appropriate nucleic acids (e.g., oligonucleotides) may be utilized regardless of mechanism of action; those skilled in the art are aware of extensive literature regarding appropriate format and structure of nucleic acids (e.g., oligonucleotides) that operate via any of a variety of mechanisms (e.g., siRNA, shRNA, nuclease gRNA, etc.). In some embodiments, provided nucleic acids incorporate format and/or structural features known in the art to be useful in one or more mechanistic contexts (e.g., involving RNase H, RISC, a nucleic-acid-directed nuclease such as a Cas, etc.).

DESCRIPTION OF DRAWINGS

FIGs. 1A to 1D illustrate the Prader-Willi /Angelman syndrome (PWS/AS) imprinted region in human and mouse. FIG. 1A shows RefSeq annotation of human PWS/AS imprinted region. FIG. 1B shows RefSeq annotation of PWS/AS imprinted orthologous region in mouse. FIG. 1C shows *UBE3A-AS* and 3'-end of *UBE3A*. FIG. 1D shows chain alignment showing orthologous regions between human, macaque (Cynomolgus macaque), pig, elephant, mouse, and rat. The target region is conserved among non-human primates but not rodents. FIG. 1D also shows genomic evolutionary rate profiling (GERP) plot of region. Positive values represent evolutionary constraint at specific DNA bases.

FIGs. 2A to 2E show an analysis of ASOs targeting mouse *Ube3a-AS*. FIG. 2A is a schematic of mouse *Ube3a-AS* transcript and approximate location of mouse-specific ASOs. Boxes and lines represent exons and introns, respectively. Arrow represents direction of transcription. FIG. 2B is a schematic of *Ube3aYFP* reporter allele used to measure paternal Ube3a protein levels. The Ube3aYFP mouse model was generated by targeting the yellow fluorescent protein (YFP) to the 3'-end of the endogenous *Ube3a* locus. Expression of *Ube3a-AS* inhibits transcription of the paternal Ube3aYFP allele, and loss of *Ube3a-AS* reactivates paternal Ube3aYFP expression, which can be detected by immunofluorescence imaging using an anti-YFP antibody. FIG. 2C is a schematic of experimental timeline to examine ASOs in mouse primary hippocampal neurons. Mouse primary hippocampal neurons were generated from newborn mice with a paternally inherited Ube3aYFP allele (0 DIV) and treated after 7 days *in vitro* (7 DIV). Three days post-treatment (10 DIV), Ube3aYFP protein levels were measured in individual cells. FIG. 2D contains immunofluorescent images showing paternal Ube3aYFP protein in primary neurons treated with vehicle (veh), a negative control ASO (ASO-C), Topotecan (Topo), ASO-B, and ASO 1.1. FIG. 2E shows mean paternal Ube3aYFP intensity levels in individual neuronal cells treated with vehicle (veh, 1% DMSO; n = 3), control ASO (ASO-C, 15 μM; n = 3), Topotecan (Topo, 0.3 μM; n = 3), ASO-B (1, 5, 15 μM; n = 3), ASO-1.1 (1, 5, 15 μM), ASO-1.2 (1, 5, 15 μM), and ASO 3.1 (1, 5, 15 μM). Abbreviations: YFP, yellow fluorescent protein; Tx, treatment; DIV, days *in vitro*; n.s., not significant. Error bars represent standard error of mean.

FIGs. 3A to 3D show analysis of ASOs targeting human *UBE3A-AS*. FIG. 3A is a schematic showing of human *UBE3A-AS* and approximate location of human-specific ASOs (ASOs 1-6). ASO-7 is located in an intron of *UBE3A-AS*. Boxes and lines represent exons and introns, respectively. FIG. 3B is a schematic of experimental timeline to examine ASOs in human GABAergic induced pluripotent stem cell (iPSC) derived neurons from a karyotypically normal individual. Human iPSC-derived neurons were treated after 14 DIV and then processed for RNA isolation at 20 DIV. FIGs. 3C and 3D show relative steady state RNA levels (normalized to ASO-C) of *UBE3A-AS* (FIG. 3C) and *UBE3A* (FIG. 3D) in iPSC-derived neurons treated with control ASO (ASO-C, 10 μM), and ASOs 1-7 (10 μM), and Topotecan (Topo, 1 μM). Abbreviations: Tx, treatment; DIV, days *in vitro*. Error bars represent standard error of mean.

FIGs. 4A to 4I show analysis of human ASO-4 and Topotecan in GABAergic iPSC-derived neurons. FIGs. 4A to 4F show relative expression (normalized to 1 nM) of *UBE3A-AS* (FIG. 4A), *SNORD116* (FIG. 4B), *IPW* (FIG. 4C), *SNORD115* (FIG. 4D), *SNORD109A/B* (FIG. 4E), and *UBE3A* (FIG. 4F) steady state RNA levels in iPSC-derived neurons treated with a 10-point ½ log dose curve of ASO-4 and Topotecan (1 nM, 3 nM, 10 nM, 30 nM, 100 nM, 300 nM, 1 µM, 3 µM, 10 µM, and 30 µM). FIG. 4G is a schematic of experimental timeline to examine ASO-4 in GABAergic iPSC-derived neurons treated at 59 DIV. FIG. 4H to 4I shows relative expression (normalized to ASO-C) of *UBE3A-AS* (Fig. 4H) and *UBE3A* (Fig. 4I) steady state RNA levels in iPSC-derived neurons treated with ASO-C (10 µM) and ASO-4 (1, 5, and 10 µM). Abbreviations: Tx, treatment. Error bars represent standard error of mean.

FIGs. 5A to 5F shows analysis of optimized ASOs in human GABAergic and glutamatergic iPSC-derived neurons. FIG. 5A is a schematic of experimental timeline to examine optimized ASOs in GABAergic iPSC-derived neurons. FIG. 5B shows relative expression of (normalized to water control) of *UBE3A-AS* steady state RNA levels in iPSC-derived neurons treated with a 5-point ½ log dose curve (30 nM, 100 nM, 300 nM, 1 µM, 3 µM; n = 6) of ASO-3.1, ASO-3.2, ASO-4.1, ASO-4.2, ASO-4.3, ASO-4.4, ASO-6.1, ASO-4.I, and ASO-4.S. ASO-4.I and ASO-4.S represent ASO-4 manufactured by two companies (ASO-4.I, Integrated DNA Technologies; ASO-4.S, Sigma-Aldrich). FIG. 5C is a schematic of experimental timeline to examine ASO-4 and ASO-6.1 in GABAergic iPSC-derived neurons. FIG. 5D shows relative expression of (normalized to 1 nM) of *UBE3A-AS* and *UBE3A* steady state RNA levels in iPSC-derived neurons treated with a 10-point ½ log dose curve (1 nM, 3 nM, 10 nM, 30 nM, 100 nM, 300 nM, 1 µM, 3 µM, 10 µM, and 30 µM; n = 3) of ASO-4 (ASO-4.I and ASO-4.S) and ASO-6.1. FIG. 5E is a schematic of experimental timeline to examine ASO-4 and ASO-6.1 in glutamatergic iPSC-derived neurons. FIG. 5F shows relative expression of (normalized to water control) of *UBE3A-AS* and *UBE3A* steady state RNA levels in iPSC-derived neurons treated with a 10-point ½ log dose curve (1 nM, 3 nM, 10 nM, 30 nM, 100 nM, 300 nM, 1 µM, 3 µM, 10 µM, and 30 uM; n = 3) of ASO-4 (ASO-4.I and ASO-4.S) and ASO-6.1. Error bars represent standard error of mean.

FIG. 6A to 6D show identification of ASO target region in mouse PWS/AS imprinted region. FIG. 6A shows RefSeq annotation of the orthologous PWS/AS imprinted region on mouse chromosome 7C. FIG. 6B illustrates a transcript assembly generated from RNA-sequencing (RNA-seq) data from mouse brain. FIG. 6C shows ASO target region showing *Snord115* snoRNAs retained in exons of the *Snord115* host-gene transcript/5′-end of *Ube3a-AS*. Aligned RNA-seq reads are depicted below assembled transcripts. Exons and introns are depicted by boxes and lines, respectively. FIG. 6D is a sequence alignment of snoRNAs in retained exons Snord115_ENSMUST00000101836 (SEQ ID NO:490), Snord115_ENSMUST00000101936 (SEQ ID NO:491), Snord115_ENSMUST00000104493 (SEQ ID NO:492), Snord115_ENSMUST00000082443 (SEQ ID NO:493), andSnord115_ENSMUST00000104427 (SEQ ID NO:494), showing retained snoRNAs have a degenerate C Box, which is required for functional snoRNA formation.

FIGs. 7A to 7G show identification of ASO target region in human PWS/AS imprinted region. FIG. 7A shows RefSeq annotation of Prader-Willi/Angelman syndrome (PWS/AS) imprinted region. FIG. 7B shows RNA-seq assembly of the human PWS polycistronic transcript. FIG. 7C shows *SNORD115-45* is retained in an exon at the 3′-end of the *SNORD115* host-gene transcript/5′-end of *UBE3A-AS*. Aligned RNA-seq reads generated from adult human brain showing L1 LINE is transcribed. FIG. 7D shows RefSeq annotation of 3′-end of *SNORD115* cluster (*SNORD115*-39-48 and *SNORD109B*). FIG. 7E shows location of L1 LINE element between *SNORD115*-44 and *SNORD115*-45. FIG. 7F shows chain alignment of placental mammals representing major clades showing conservation at *SNORD115*-45-48 region, albeit reduced in rodents. FIG. 7G shows sequence alignment of snoRNAs in target region to SNORD115-44 (functional snoRNA) (SEQ ID NO:495), SNORD115-48 (SEQ ID NO:496), SNORD115-45 (SEQ ID NO:497), SNORD115-46 (SEQ ID NO:498), and SNORD115-47 (SEQ ID NO:499), showing SNORD115-45 (retained), SNORD115-46 (partially retained), and SNORD116-47 have degenerate C Box, which is required for functional snoRNA formation.

FIGs. 8A to 8C show pharmacodynamic analysis of candidate ASOs. FIG. 8A shows fitted dose response curves of normalized *UBE3A-AS* steady state RNA levels in GABAergic iPSC-derived neurons treated with a 10-point ½ log dose curve (1 nM, 3 nM, 10 nM, 30 nM, 100 nM, 300 nM, 1 µM, 3 µM, 10 µM, and 30 µM; n = 2) of ASO-4 and ASO-6.1 with different backbone and RNA modification designs. Dose response curves fitted using a 4-parameter logistic regression model (Hill). Graphs represent fitted models and standard error. The Y axis represents relative *UBE3A-AS* RNA levels and X axis represents log molar (M) concentrations of ASO. FIGs. 8B and 8C are hierarchical clustering dendrogram and constellation plots of fitted dose response curves showing relationship between candidate ASOs and grouping into 3 clusters.

FIG. 9 shows pharmacodynamic analysis of ASO-6.1.PO-1.O and ASO-4.4.PS.L in Angelman syndrome iPSC-derived neurons. 4-Parameter logistic regression model (Hill) of normalized *UBE3A-AS* steady state RNA levels in Angelman syndrome iPSC-derived neurons treated with a 10-point ½ log dose curve (1 nM, 3 nM, 10 nM, 30 nM, 100 nM, 300 nM, 1 μM, 3 μM, 10 μM, and 30 μM; n = 3) of ASO-6.1.PO-1.O and ASO-4.4.PS.L.

FIG. 10 shows expression analysis of RNAs encoded by the PWS polycistronic transcript in Angelman syndrome iPSC neurons treated with ASO-6.1-PO-1.O and ASO-4.4.PS.L. Shown are normalized steady state RNA levels of *SNURF*, *SNRPN*, *SNHG116*, *SNORD116* snoRNAs, *IPW*, *SNHG115*, *SNORD115* snoRNAs, *UBE3A-AS*, and *UBE3A* in AS iPSC-derived neurons treated with vehicle (1% H_2O; n = 3), ASO-6.1.PO-1.O (30 μM; n = 3), and ASO-4.4.PS.L (30 μM; n =3). Data represents mean percentage of RNA relative to vehicle. Error bars represent standard error of mean. Asterisk (*) denotes statistically significant differences ($p < 0.05$) using one-way ANOVA with Dunnett's multiple comparison test relative to vehicle.

FIG. 11 shows pharmacodynamic analysis of ASO-6.1.PO-1.O and ASO-4.4.PS.L in Cynomolgus macaque. Shown are steady state RNA levels of *UBE3A-AS* in macaque CNS regions treated with vehicle (0.9% saline; n = 5), ASO-6.1.PO-1.O (10 mg; n = 3), and ASO-4.4.PS.L (10 mg; n = 3). Data represents means percentage of *UBE3A-AS* RNA relative to vehicle. Error bars represent standard error of mean. Asterisk (*) denotes statistically significant differences ($p < 0.05$) using one-way ANOVA with Dunnett's multiple comparison test relative to vehicle.

DETAILED DESCRIPTION

The *UBE3A-AS/Ube3a-AS* transcript, otherwise known as ubiquitin-protein ligase *E3A* antisense transcript and *UBE3A-AS/Ube3a-AS*, is the name for the transcript generated by transcription of the *UBE3A-AS* transcript, which is on the antisense DNA strand relative to the *UBE3A* gene. Note that gene names with all caps indicate human genes (e.g. *UBE3A*) and gene names with only the first letter capped indicate mouse genes (e.g. *Ube3a*). The *UBE3A-AS* transcript is transcribed as part of a large polycistronic transcription unit that encodes *SNURF-SNRPN,* a cluster of orphan C/D box small nucleolar RNAs (SNORDs), and several uncharacterized long noncoding RNAs. In both mouse and human, the *UBE3A/Ube3a* gene is imprinted in neurons of the central nervous system, where it is expressed only from the maternal allele. The *UBE3A-AS/Ube3a-AS* transcript is both necessary and sufficient to silence transcription of the paternal *UBE3A/Ube3a* allele, and inhibition of *UBE3A-AS/Ube3a-AS* reactivates transcription of the paternal *UBE3A/Ube3a* allele. Mutations affecting the function or expression of the maternally inherited *UBE3A* allele cause Angelman syndrome (AS). In AS, the paternal allele is functional but epigenetically silenced. If unsilenced in AS patients, the paternal *UBE3A* allele could be a source of functional *UBE3A* in neurons.

The polycistronic transcription unit (hereafter referred to as the PTU) encoding *UBE3A-AS* is about 450,000 base-pairs long. Transcription of the PTU starts at upstream exons (U-exons) in the *SNURF-SNRPN* locus and stops towards the 5′-end of *UBE3A*. The PTU is organized (5′-3′) as follows: *SNURF-SNRPN*, *SNORD107*, *SNORD64*, *SNORD109A*, *SNORD116* (29 copies), *IPW*, *SNORD115* (48 copies), *SNORD109B*, and *UBE3A*, which is orientated in the opposite direction of the upstream transcripts. The polycistronic transcript is alternatively spliced and subject to alternative 3′-processing. *SNURF-SNRPN* encodes two polypeptides. The SNORDs are in the introns of a host-gene transcript (*SNHG14*) and are generated by exonucleolytic debranching of the spliced introns. *UBE3A-AS* represents the 3′-end of the transcript that overlaps the *UBE3A* gene. Most C/D box snoRNAs play a role in ribosome biogenesis where they direct 2′-O-methylation of ribosomal RNAs (rRNA); however, the snoRNAs located in the PWS/AS region lack any sequence complementarity to known rRNAs; however, the *SNORD115* snoRNA has been found to change the alternative splicing of the serotonin receptor 2C pre-mRNA.

Disclosed herein is evidence that the 5′-end of *UBE3A-AS* transcript is important for its stability. As disclosed herein, ASOs targeting the 5′-end of *UBE3A-AS* are capable of reducing *UBE3A-AS* levels, presumably by stopping transcription of *UBE3A-AS*, and turning-on the paternal *UBE3A* allele.

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

The term “antisense oligonucleotide” as used herein is defined as oligonucleotides capable of modulating expression of a target gene by hybridizing to a target nucleic acid, in particular to a contiguous sequence on a target nucleic acid. In some embodiments, the antisense oligonucleotides disclosed herein are single stranded.

The term “contiguous nucleotide sequence” refers to the region of the oligonucleotide which is complementary to the target nucleic acid. The term is used interchangeably herein with the term “contiguous nucleobase sequence” and the term “oligonucleotide motif sequence”. In some embodiments all the nucleotides of the oligonucleotide are present in the contiguous nucleotide sequence. In some embodiments the oligonucleotide comprises the contiguous nucleotide sequence and may, optionally comprise further nucleotide(s), for example a nucleotide linker region which may be used to attach a functional group to the contiguous nucleotide sequence. The nucleotide linker region may or may not be complementary to the target nucleic acid.

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

The term “modified nucleoside” or “nucleoside modification” as used herein refers to nucleosides modified as compared to the equivalent DNA or RNA nucleoside by the introduction of one or more modifications of the sugar moiety or the (nucleo)base moiety. In some embodiments, the modified nucleoside comprises a modified sugar moiety. The term modified nucleoside may also be used herein interchangeably with the term “nucleoside analogue” or modified “units” or modified “monomers”.

The term “modified internucleoside linkage” is defined as generally understood by the skilled person as linkages other than phosphodiester (PO) linkages or natural phosphate linkages that covalently couples two nucleosides together. Nucleotides with modified internucleoside linkage are also termed “modified nucleotides”. In some embodiments, the modified internucleoside linkage increases the nuclease resistance of the oligonucleotide compared to a phosphodiester linkage. For naturally occurring oligonucleotides, the internucleoside linkage includes phosphate groups creating a phosphodiester bond between adjacent nucleosides.

Modified internucleoside linkages are particularly useful in stabilizing oligonucleotides for *in vivo* use, and may serve to protect against nuclease cleavage at regions of DNA or RNA nucleosides in the oligonucleotide disclosed herein, for example, within the gap region of a gapmer oligonucleotide, as well as in regions of modified nucleosides.

In some embodiments, the oligonucleotide comprises one or more internucleoside linkages modified from the natural phosphodiester to a linkage that is, for example, more resistant to nuclease attack. Nuclease resistance may be determined by incubating the oligonucleotide in blood serum or by using a nuclease resistance assay [e.g., snake venom phosphodiesterase (SVPD)], both are well known in the art. Internucleoside linkages which are capable of enhancing the nuclease resistance of an oligonucleotide are referred to as nuclease resistant internucleoside linkages.

In some embodiments at least 50% of the internucleoside linkages in the oligonucleotide, or contiguous nucleotide sequence thereof, are modified, such as at least 60%, such as at least 70%, such as at least 80% or such as at least 90% of the internucleoside linkages in the oligonucleotide, or contiguous nucleotide sequence thereof, are modified. In some embodiments all of the internucleoside linkages of the oligonucleotide, or contiguous nucleotide sequence thereof, are modified.

It will be recognized that, in some embodiments, the internucleoside linkages which link the oligonucleotide to a non-nucleotide functional group, such as a conjugate, may be phosphodiester. In some embodiments, the internucleoside linkages which link the oligonucleotide to a non-nucleotide functional group are modified.

In some embodiments all of the internucleoside linkages of the oligonucleotide, or contiguous nucleotide sequence thereof, are nuclease resistant internucleoside linkages.

Modified internucleoside linkages may, for example, be selected from the group comprising phosphorothioate, diphosphorothioate, and boranophosphate. In some embodiments, the modified internucleoside linkages are compatible with the RNase H recruitment of the oligonucleotide disclosed herein, for example, phosphorothioate, diphosphorothioate, or boranophosphate.

In some embodiments the internucleoside linkage comprises sulphur (S), such as a phosphorothioate internucleoside linkage.

A phosphorothioate internucleoside linkage is particularly useful due to nuclease resistance, beneficial pharmacokinetics and ease of manufacture. In preferred embodiments at least 50% of the internucleoside linkages in the oligonucleotide, or contiguous nucleotide sequence thereof, are phosphorothioate, such as at least 60%, such as at least 70%, such as at least 80%, or such as at least 90% of the internucleoside linkages in the oligonucleotide, or contiguous nucleotide sequence thereof, are phosphorothioate. In some embodiments all of the internucleoside linkages of the oligonucleotide, or contiguous nucleotide sequence thereof, are phosphorothioate.

In some embodiments, the oligonucleotide comprises one or more neutral internucleoside linkage, particularly a internucleoside linkage selected from phosphotriester, methylphosphonate, MMI, amide-3, formacetal or thioformacetal. Further internucleoside linkages are disclosed in WO2009/124238 (incorporated herein by reference). In an embodiment the internucleoside linkage is selected from linkers disclosed in WO2007/031091 (incorporated herein by reference).

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

Each of the design regions may however comprise internucleoside linkages other than phosphorothioate, such as phosphodiester linkages, in particularly in regions where modified nucleosides, such as LNA, protect the linkage against nuclease degradation. Inclusion of phosphodiester linkages, such as one or two linkages, particularly between or adjacent to modified nucleoside units (typically in the non-nuclease recruiting regions) can modify the bioavailability and/or bio-distribution of an oligonucleotide. WO2008/113832 is incorporated herein by reference for the teaching of oligonucleotides having phosphodiester linkages.

In some embodiments, all the internucleoside linkages in the oligonucleotide are phosphorothioate and/or boranophosphate linkages. In some embodiments, all the internucleoside linkages in the oligonucleotide are phosphorothioate linkages.

The term nucleobase includes the purine (e.g., adenine and guanine) and pyrimidine (e.g., uracil, thymine, and cytosine) moiety present in nucleosides and nucleotides which form hydrogen bonds in nucleic acid hybridization. The term nucleobase also encompasses modified nucleobases which may differ from naturally occurring nucleobases but are functional during nucleic acid hybridization. In this context "nucleobase" refers to both naturally occurring nucleobases, such as adenine, guanine, cytosine, thymidine, uracil, xanthine, and hypoxanthine, as well as non-naturally occurring variants.

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

The nucleobase moieties may be indicated by the letter code for each corresponding nucleobase, e.g., A, T, G, C, or U, wherein each letter may optionally include modified nucleobases of equivalent function. For example, in the exemplified oligonucleotides, the nucleobase moieties are selected from A, T, G, C, and 5-methyl cytosine (5mC). Combinations of these modifications may also be used. For example, 5mC LNA nucleosides may be used. Likewise, 2´-hydroxymethyl (2´-OMe) 5mC may be used.

The term "complementarity" describes the capacity for Watson-Crick base-pairing of nucleosides/nucleotides. Watson-Crick base pairs are guanine (G)-cytosine (C) and adenine (A)-thymine (T)/uracil (U). It will be understood that oligonucleotides may comprise nucleosides with modified nucleobases, for example, 5-methyl cytosine is often used in place of cytosine, and as such the term complementarity encompasses Watson Crick base-paring between non-modified and modified nucleobases.

The term "% complementary" as used herein, refers to the number of nucleotides in percent of a contiguous nucleotide sequence in a nucleic acid molecule (e.g., oligonucleotide) which, at a given position, are complementary to (i.e., form Watson Crick base pairs with) a contiguous nucleotide sequence, at a given position of a separate nucleic acid molecule (e.g., the target nucleic acid). The percentage is calculated by counting the number of aligned bases that form pairs between the two sequences, dividing by the total number of nucleotides in the oligonucleotide and multiplying by 100. In such a comparison a nucleobase/ nucleotide which does not align (form a base pair) is termed a mismatch.

The term "hybridizing" or "hybridizes" as used herein is to be understood as two nucleic acid strands (e.g., an oligonucleotide and a target nucleic acid) forming hydrogen bonds between base pairs on opposite strands thereby forming a duplex.

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

In some embodiments, the disclosed oligonucleotide comprises a contiguous nucleotide sequence of at least 8 nucleotides which is complementary to or hybridizes to a target sequence present in the target nucleic acid molecule. The contiguous nucleotide sequence (and therefore the target sequence) comprises of at least 8 contiguous nucleotides, such as 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29 or 30 contiguous nucleotides, such as from 12-25, such as from 14-18 contiguous nucleotides.

In some embodiments, the disclosed oligonucleotide is a functional nucleic acid, such as a siRNA, shRNA, or nuclease gRNA, that inhibits, mutates, or deletes the target nucleic acid sequence.

The term "modulation of expression" as used herein is to be understood as an overall term for an oligonucleotide's ability to alter the amount of UBE3A RNA/protein when compared to the amount of UBE3A before administration of the oligonucleotide. Alternatively modulation of expression may be determined by reference to a control experiment where the disclosed oligonucleotide is not administered. The modulation effected by the oligonucleotide is related to its ability to reduce, remove, prevent, lessen, lower or terminate the suppression of the paternal *UBE3A-AS* transcript, i.e., by targeting the 5′-end of *UBE3A-AS*, which is downstream of *SNORD115-45* snoRNA. The modulation can also be viewed as the oligonucleotide's ability to restore, increase or enhance expression of paternal *UBE3A*, e.g., by removal or blockage of inhibitory mechanisms affected by *UBE3A-AS*.

The disclosed oligonucleotide may comprise one or more nucleosides which have a modified sugar moiety, i.e., a modification of the sugar moiety when compared to the ribose sugar moiety found in DNA and RNA. Numerous nucleosides with modification of the ribose sugar moiety have been made, primarily with the aim of improving certain properties of oligonucleotides, such as affinity and/or nuclease resistance. Such modifications include those where the ribose ring structure is modified, e.g., by replacement with a hexose ring (HNA), or a bicyclic ring, which typically have a biradicle bridge between the C2 and C4 carbons on the ribose ring (LNA), or an unlinked ribose ring which typically lacks a bond between the C2 and C3 carbons (e.g., UNA). Other sugar modified nucleosides include, for example, bicyclohexose nucleosides (WO2011/017521) or tricyclic nucleosides (WO2013/154798). Modified nucleosides also include nucleosides where the sugar moiety is replaced with a non-sugar moiety, for example, in the case of peptide nucleic acids (PNA) or morpholino nucleic acids.

Sugar modifications also include modifications made via altering the substituent groups on the ribose ring to groups other than hydrogen, or the 2′-OH group naturally found in DNA and RNA nucleosides. Substituents may, for example, be introduced at the 2′, 3′, 4′ or 5′ positions. Nucleosides with modified sugar moieties also include 2′ modified nucleosides, such as 2′ substituted nucleosides. Indeed, much focus has been spent on developing 2′ substituted nucleosides, and numerous 2′ substituted nucleosides have been found to have beneficial properties when incorporated into oligonucleotides, such as enhanced nucleoside resistance and enhanced affinity.

A 2′ sugar modified nucleoside is a nucleoside which has a substituent other than H or —OH at the 2′ position (2′ substituted nucleoside) or comprises a 2′ linked biradical, and includes 2′ substituted nucleosides and LNA (2′-4′ biradical bridged) nucleosides. For example, the 2′ modified sugar may provide enhanced binding affinity and/or increased nuclease resistance to the oligonucleotide. Examples of 2′ substituted modified nucleosides are 2′-O-alkyl-RNA, 2′-O-methyl-RNA (O-Me), 2′-alkoxy-RNA, 2′-O-methoxyethyl-RNA (MOE), 2′-amino-DNA, 2′-Fluoro-RNA, and 2′-fluoro-ANA (F-ANA). For further examples, please see Freier & Altmann; Nucl. Acid Res., 1997, 25, 4429-4443 and Uhlmann; Curr. Opinion in Drug Development, 2000, 3(2), 293-213; and Deleavey and Damha, Chemistry and Biology 2012, 19, 937.

Locked Nucleic Acid (LNA) nucleosides are modified nucleosides which comprise a linker group (referred to as a biradical or a bridge) between C2′ and C4′ of the ribose sugar ring of a nucleotide. These nucleosides are also termed bridged nucleic acid or bicyclic nucleic acid (BNA) in the literature.

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

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

The term “gapmer” as used herein refers to an antisense oligonucleotide which comprises a region of RNase H recruiting oligonucleotides (gap) which is flanked 5′ and 3′ by one or more affinity enhancing modified nucleosides (flanks). Various gapmer designs are described herein. Headmers and tailmers are oligonucleotides capable of recruiting RNase H where one of the flanks is missing, i.e., only one of the ends of the oligonucleotide comprises affinity enhancing modified nucleosides. For headmers the 3′ flank is missing (i.e. the 5′ flank comprise affinity enhancing modified nucleosides) and for tailmers the 5′ flank is missing (i.e. the 3′ flank comprises affinity enhancing modified nucleosides).

Conjugation of the disclosed oligonucleotide to one or more non-nucleotide moieties may improve the pharmacology of the oligonucleotide, e.g., by affecting the activity, cellular distribution, cellular uptake, or stability of the oligonucleotide. In some embodiments the conjugate moiety modify or enhance the pharmacokinetic properties of the oligonucleotide by improving cellular distribution, bioavailability, metabolism, excretion, permeability, and/or cellular uptake of the oligonucleotide. In particular the conjugate may target the oligonucleotide to a specific organ, tissue, or cell type and thereby enhance the effectiveness of the oligonucleotide in that organ, tissue, or cell type. At the same time the conjugate may serve to reduce activity of the oligonucleotide in non-target cell types, tissues or organs, e.g., off target activity or activity in non-target cell types, tissues or organs. WO 93/07883 and WO 2013/033230 provides suitable conjugate moieties, which are hereby incorporated by reference. WO 2012/143379 provides a method of delivering a drug across the blood-brain-barrier by conjugation to an antibody fragment with affinity to the transferrin receptor, which are hereby incorporated by reference.

In some embodiments, the non-nucleotide moiety (conjugate moiety) is selected from the group consisting of carbohydrates, cell surface receptor ligands, drug substances, hormones, lipophilic substances, polymers, proteins, peptides, toxins (e.g., bacterial toxins), vitamins, viral proteins (e.g., capsids) or combinations thereof. In some embodiments the non-nucleotide moiety an antibody or antibody fragment, such as an antibody or antibody fragment that facilitates delivery across the blood-brain-barrier, in particular an antibody or antibody fragment targeting the transferrin receptor.

The term “subject” refers to any individual who is the target of administration or treatment. The subject can be a vertebrate, for example, a mammal. Thus, the subject can be a human or veterinary patient. The term “patient” refers to a subject under the treatment of a clinician, e.g., physician.

The term “therapeutically effective” refers to the amount of the composition used is of sufficient quantity to ameliorate one or more causes or symptoms of a disease or disorder. Such amelioration only requires a reduction or alteration, not necessarily elimination.

The term “pharmaceutically acceptable” refers to those compounds, materials, compositions, and/or dosage forms, which are within the scope of sound medical judgment, suitable for use in contact with the tissues of human beings and animals without excessive toxicity, irritation, allergic response, or other problems or complications commensurate with a reasonable benefit/risk ratio.

The term "treatment" refers to the medical management of a patient with the intent to cure, ameliorate, stabilize, or prevent a disease, pathological condition, or disorder. This term includes active treatment, that is, treatment directed specifically toward the improvement of a disease, pathological condition, or disorder, and also includes causal treatment, that is, treatment directed toward removal of the cause of the associated disease, pathological condition, or disorder. In addition, this term includes palliative treatment, that is, treatment designed for the relief of symptoms rather than the curing of the disease, pathological condition, or disorder; preventative treatment, that is, treatment directed to minimizing or partially or completely inhibiting the development of the associated disease, pathological condition, or disorder; and supportive treatment, that is, treatment employed to supplement another specific therapy directed toward the improvement of the associated disease, pathological condition, or disorder.

The term "inhibit" refers to a decrease in an activity, response, condition, disease, or other biological parameter, which those skilled in the art will appreciate may be assessed at a particular point in time, such that in some embodiments, inhibition may be or comprise a delay in onset or reduction in frequency. In some embodiments, inhibition can include, but is not limited to, the complete ablation of the activity, response, condition, or disease. This may also include, for example, a 10% reduction in the activity, response, condition, or disease as compared to the native or control level. Thus, the reduction can be a 10, 20, 30, 40, 50, 60, 70, 80, 90, 100%, or any amount of reduction in between as compared to native or control levels.

Antisense oligonucleotides (ASOs) were designed to target exons at the 5′-end of the *SNORD115* host-gene transcript (AF400500), which encompasses *SNORD115-46*, *SNORD115-47*, *SNORD115-48*, and *SNORD109B* snoRNAs and is thought to represent the 5′-end of the *UBE3A* antisense transcript (*UBE3A-AS*). In particular the target nucleic acid can be the 5′-end of *UBE3A-AS*, corresponding to position 25,511,577 to 25,516,681 on human chromosome 15 human genome assembly hg19. In some embodiments, the target nucleic acid is one of five exons located in the 5′-end of *UBE3A-AS*, which can correspond to positions 25,511,577 to 25,511,761 (exon 1), 25,512,059 to 25,512,191 (exon 2), 25,513,476 to 25,513,600 (exon 3), 25,514,752 to 25,514,880 (exon 4), and 25,516,565 to 25,516,681 (exon 5).

Therefore, in some embodiments, the target nucleic acid is ATGATGATATGGAAGAAAAGCACTCTTTGGCCTGTTGTGACTGGGACAGTTGACAGCACCCAGGTGTCCTTTAATGAAAATGCTCTTGACACCAATGCATCCTAGCATCACAGCTTCAGGAAGCCTTCTCAAGTGTGCATGGGGAGTACTATGTCTTTCATCAATAATGAAATCTTCTGATTTG (Exon 1, SEQ ID NO:1).

In some embodiments, the target nucleic acid is TAAGACATGCTGCCAAGAGATGTGCCATTCTATTATAAAAGATCAGTAGCTTCCTTTACCGACGTGTATATTCTATCTAGAACATTGAGCTATGGAAGACTCCCACCTAAGGGAATTAGTTTTACACCTTCAG (Exon 2, SEQ ID NO:2).

In some embodiments, the target nucleic acid is ATAAAGACTGCTGAGAAGAGCACCCTCTGGTGTTGTCACAGAGGCAAGTGCTACCGCACAGGCATGCTGCAGTGAATTTAACTGATCCTCTGTCCCTGCAACCGTTGTTTAAGGATGCTATTCTG (Exon 3, SEQ ID NO:3).

In some embodiments, the target nucleic acid is AAAAGACTGTGGAGGAAGAAAACCCTTTACCCTGTTGTTCAGGGAGAAACTGACACCACTCAACTGCCTGGCACTGAAAATGTGGCATCCAGTCCACTTTACCATCAGTGTTTAAGGAAACCATCTCTG (Exon 4, SEQ ID NO:4).

In some embodiments, the target nucleic acid is ATAAGGATGACTGAGGAAGAGTACTCTTTGGCTTGTTGACACCAGCACAGCTGACACACCCAGATATCTGTTTGGTCTCCTGTGAACTTTCAACCAGGATTTAAGGATGCCACTCTG (Exon 5, SEQ ID NO:5).

In some embodiments, the disclosed ASO has the nucleic acid sequence TAGAGGTGAAGGCCAGGCAC (ASO-1, SEQ ID NO:6).

In some embodiments, the ASO has the nucleic acid sequence GTACTCTTCCTCAGTCATCC (ASO-2, SEQ ID NO:7).

In some embodiments, the disclosed ASO has the nucleic acid sequence TGTCAGTTTCTCCCTGAACA (ASO-3, SEQ ID NO:8).

In some embodiments, the disclosed ASO has the nucleic acid sequence TAGAATGGCACATCTCTTGG (ASO-4, SEQ ID NO:9).

In some embodiments, the disclosed ASO has the nucleic acid sequence GTTTTCTTCCTCCACAGTCT (ASO-6, SEQ ID NO:10).

In some embodiments, the disclosed ASO has the nucleic acid sequence CTGGTGTCAACAAGCCAAAG (ASO-7, SEQ ID NO:11).

Additional ASOs that can target exon 1 of the 3′-end of the *SNORD115* region are provided below in Table 1. Example ASOs that can target exon 2 of the 3′-end of the *SNORD115* are provided below in Table 2. Example ASOs that can target exon 3 of the 3'-end of the *SNORD115* are provided below in Table 3. Example ASOs that can target exon 4 of the 3'-end of the *SNORD115* are provided below in Table 4. Example ASOs that can target exon 5 of the 3'-end of the *SNORD115* are provided below in Table 5.

Table 1. Exon 1 ASOs

Target Sequence (5'→3')	ASO (5'→3')
GAAAAUGCUCUUGACACC (SEQ ID NO:12)	GGTGTCAAGAGCATTTTC (SEQ ID NO:15)
GAAAAUGCUCUUGACACCA (SEQ ID NO:13)	TGGTGTCAAGAGCATTTTC (SEQ ID NO:16)
GAAAAUGCUCUUGACACCAA (SEQ ID NO:14)	TTGGTGTCAAGAGCATTTTC (SEQ ID NO:17)

Table 2. Exon 2 ASOs

Target Sequence (5'→3')	ASO (5'→3')
CAUGCUGCCAAGAGAUGU (SEQ ID NO:18)	ACATCTCTTGGCAGCATG (SEQ ID NO:67)
CAUGCUGCCAAGAGAUGUG (SEQ ID NO:19)	CACATCTCTTGGCAGCATG (SEQ ID NO:68)
CAUGCUGCCAAGAGAUGUGC (SEQ ID NO:20)	GCACATCTCTTGGCAGCATG (SEQ ID NO:69)
AUGCUGCCAAGAGAUGUG (SEQ ID NO:21)	CACATCTCTTGGCAGCAT (SEQ ID NO:70)
AUGCUGCCAAGAGAUGUGC (SEQ ID NO:22)	GCACATCTCTTGGCAGCAT (SEQ ID NO:71)
AUGCUGCCAAGAGAUGUGCC (SEQ ID NO:23)	GGCACATCTCTTGGCAGCAT (SEQ ID NO:72)
UGCUGCCAAGAGAUGUGCC (SEQ ID NO:24)	GGCACATCTCTTGGCAGCA (SEQ ID NO:73)
UGCUGCCAAGAGAUGUGCCA (SEQ ID NO:25)	TGGCACATCTCTTGGCAGCA (SEQ ID NO:74)
GCUGCCAAGAGAUGUGCCA (SEQ ID NO:26)	TGGCACATCTCTTGGCAGC (SEQ ID NO:75)
GCUGCCAAGAGAUGUGCCAU (SEQ ID NO:27)	ATGGCACATCTCTTGGCAGC (SEQ ID NO:76)
CUGCCAAGAGAUGUGCCA (SEQ ID NO:28)	TGGCACATCTCTTGGCAG (SEQ ID NO:77)
CUGCCAAGAGAUGUGCCAU (SEQ ID NO:29)	ATGGCACATCTCTTGGCAG (SEQ ID NO:78)
CUGCCAAGAGAUGUGCCAUU (SEQ ID NO:30)	AATGGCACATCTCTTGGCAG (SEQ ID NO:79)
UGCCAAGAGAUGUGCCAU (SEQ ID NO:31)	ATGGCACATCTCTTGGCA (SEQ ID NO:80)
UGCCAAGAGAUGUGCCAUU (SEQ ID NO:32)	AATGGCACATCTCTTGGCA (SEQ ID NO:81)
UGCCAAGAGAUGUGCCAUUC (SEQ ID NO:33)	GAATGGCACATCTCTTGGCA (SEQ ID NO:82)
GCCAAGAGAUGUGCCAUU (SEQ ID NO:34)	AATGGCACATCTCTTGGC (SEQ ID NO:83)
GCCAAGAGAUGUGCCAUUC (SEQ ID NO:35)	GAATGGCACATCTCTTGGC (SEQ ID NO:84)
GCCAAGAGAUGUGCCAUUCU (SEQ ID NO:36)	AGAATGGCACATCTCTTGGC (SEQ ID NO:85)
CCAAGAGAUGUGCCAUUC (SEQ ID NO:37)	GAATGGCACATCTCTTGG (SEQ ID NO:86)
CCAAGAGAUGUGCCAUUCU (SEQ ID NO:38)	AGAATGGCACATCTCTTGG (SEQ ID NO:87)

CCAAGAGAUGUGCCAUUCUA (SEQ ID NO:39)	TAGAATGGCACATCTCTTGG (SEQ ID NO:88)
CAAGAGAUGUGCCAUUCU (SEQ ID NO:40)	AGAATGGCACATCTCTTG (SEQ ID NO:89)
CAAGAGAUGUGCCAUUCUA (SEQ ID NO:41)	TAGAATGGCACATCTCTTG (SEQ ID NO:90)
CAAGAGAUGUGCCAUUCUAU (SEQ ID NO:42)	ATAGAATGGCACATCTCTTG (SEQ ID NO:91)
UCCUUUACCGACGUGUAU (SEQ ID NO:43)	ATACACGTCGGTAAAGGA (SEQ ID NO:92)
UCCUUUACCGACGUGUAUA (SEQ ID NO:44)	TATACACGTCGGTAAAGGA (SEQ ID NO:93)
UCCUUUACCGACGUGUAUAU (SEQ ID NO:45)	ATATACACGTCGGTAAAGGA (SEQ ID NO:94)
CCUUUACCGACGUGUAUA (SEQ ID NO:46)	TATACACGTCGGTAAAGG (SEQ ID NO:95)
CCUUUACCGACGUGUAUAU (SEQ ID NO:47)	ATATACACGTCGGTAAAGG (SEQ ID NO:96)
CCUUUACCGACGUGUAUAUU (SEQ ID NO:48)	AATATACACGTCGGTAAAGG (SEQ ID NO:97)
ACCGACGUGUAUAUUCUAUC (SEQ ID NO:49)	GATAGAATATACACGTCGGT (SEQ ID NO:98)
CCGACGUGUAUAUUCUAUC (SEQ ID NO:50)	GATAGAATATACACGTCGG (SEQ ID NO:99)
CCGACGUGUAUAUUCUAUCU (SEQ ID NO:51)	AGATAGAATATACACGTCGG (SEQ ID NO:100)
UCUAGAACAUUGAGCUAUGG (SEQ ID NO:52)	CCATAGCTCAATGTTCTAGA (SEQ ID NO:101)
CAUUGAGCUAUGGAAGAC (SEQ ID NO:53)	GTCTTCCATAGCTCAATG (SEQ ID NO:102)
CUAUGGAAGACUCCCACCUA (SEQ ID NO:54)	TAGGTGGGAGTCTTCCATAG (SEQ ID NO:103)
UAUGGAAGACUCCCACCUA (SEQ ID NO:55)	TAGGTGGGAGTCTTCCATA (SEQ ID NO:104)
UAUGGAAGACUCCCACCUAA (SEQ ID NO:56)	TTAGGTGGGAGTCTTCCATA (SEQ ID NO:105)
AUGGAAGACUCCCACCUA (SEQ ID NO:57)	TAGGTGGGAGTCTTCCAT (SEQ ID NO:106)
AUGGAAGACUCCCACCUAA (SEQ ID NO:58)	TTAGGTGGGAGTCTTCCAT (SEQ ID NO:107)
UGGAAGACUCCCACCUAA (SEQ ID NO:59)	TTAGGTGGGAGTCTTCCA (SEQ ID NO:108)
GACUCCCACCUAAGGGAAUU (SEQ ID NO:60)	AATTCCCTTAGGTGGGAGTC (SEQ ID NO:109)
ACUCCCACCUAAGGGAAU (SEQ ID NO:61)	ATTCCCTTAGGTGGGAGT (SEQ ID NO:110)
ACUCCCACCUAAGGGAAUU (SEQ ID NO:62)	AATTCCCTTAGGTGGGAGT (SEQ ID NO:111)
ACUCCCACCUAAGGGAAUUA (SEQ ID NO:63)	TAATTCCCTTAGGTGGGAGT (SEQ ID NO:112)
CUCCCACCUAAGGGAAUU (SEQ ID NO:64)	AATTCCCTTAGGTGGGAG (SEQ ID NO:113)
CUCCCACCUAAGGGAAUUA (SEQ ID NO:65)	TAATTCCCTTAGGTGGGAG (SEQ ID NO:114)
UCCCACCUAAGGGAAUUA (SEQ ID NO:66)	TAATTCCCTTAGGTGGGA (SEQ ID NO:115)

Table 3. Exon 3 ASOs

Target Sequence (5'→3')	ASO (5'→3')
GAUAAAGACUGCUGAGAAGA (SEQ ID NO:116)	TCTTCTCAGCAGTCTTTATC (SEQ ID NO:139)
AUAAAGACUGCUGAGAAGAG (SEQ ID NO:117)	CTCTTCTCAGCAGTCTTTAT (SEQ ID NO:140)
UAAAGACUGCUGAGAAGAGC (SEQ ID NO:118)	GCTCTTCTCAGCAGTCTTTA (SEQ ID NO:141)
AAAGACUGCUGAGAAGAGCA (SEQ ID NO:119)	TGCTCTTCTCAGCAGTCTTT (SEQ ID NO:142)
AAGACUGCUGAGAAGAGCAC (SEQ ID NO:120)	GTGCTCTTCTCAGCAGTCTT (SEQ ID NO:143)
AGACUGCUGAGAAGAGCACC (SEQ ID NO:121)	GGTGCTCTTCTCAGCAGTCT (SEQ ID NO:144)
GACUGCUGAGAAGAGCACCC (SEQ ID NO:122)	GGGTGCTCTTCTCAGCAGTC (SEQ ID NO:145)
CAAGUGCUACCGCACAGGCA (SEQ ID NO:123)	TGCCTGTGCGGTAGCACTTG (SEQ ID NO:146)
AAGUGCUACCGCACAGGCAU (SEQ ID NO:124)	ATGCCTGTGCGGTAGCACTT (SEQ ID NO:147)
AGUGCUACCGCACAGGCAUG (SEQ ID NO:125)	CATGCCTGTGCGGTAGCACT (SEQ ID NO:148)
UGCUACCGCACAGGCAUGCU (SEQ ID NO:126)	AGCATGCCTGTGCGGTAGCA (SEQ ID NO:149)
UACCGCACAGGCAUGCUGCA (SEQ ID NO:127)	TGCAGCATGCCTGTGCGGTA (SEQ ID NO:150)
GCACAGGCAUGCUGCAGUGA (SEQ ID NO:128)	TCACTGCAGCATGCCTGTGC (SEQ ID NO:151)
CACAGGCAUGCUGCAGUGAA (SEQ ID NO:129)	TTCACTGCAGCATGCCTGTG (SEQ ID NO:152)
ACAGGCAUGCUGCAGUGAAU (SEQ ID NO:130)	ATTCACTGCAGCATGCCTGT (SEQ ID NO:153)
CAGGCAUGCUGCAGUGAAUU (SEQ ID NO:131)	AATTCACTGCAGCATGCCTG (SEQ ID NO:154)
AGGCAUGCUGCAGUGAAUUU (SEQ ID NO:132)	AAATTCACTGCAGCATGCCT (SEQ ID NO:155)
GGCAUGCUGCAGUGAAUUUA (SEQ ID NO:133)	TAAATTCACTGCAGCATGCC (SEQ ID NO:156)
GCAUGCUGCAGUGAAUUUAA (SEQ ID NO:134)	TTAAATTCACTGCAGCATGC (SEQ ID NO:157)
CAUGCUGCAGUGAAUUUAAC (SEQ ID NO:135)	GTTAAATTCACTGCAGCATG (SEQ ID NO:158)
GCAGUGAAUUUAACUGAUCC (SEQ ID NO:136)	GGATCAGTTAAATTCACTGC (SEQ ID NO:159)
UCCCUGCAACCGUUGUUUAA (SEQ ID NO:137)	TTAAACAACGGTTGCAGGGA (SEQ ID NO:160)
CCCUGCAACCGUUGUUUAAG (SEQ ID NO:138)	CTTAAACAACGGTTGCAGGG (SEQ ID NO:161)

Table 4. Exon 4 ASOs

Target Sequence (5'→3')	ASO (5'→3')
AAAAGACUGUGGAGGAAGA (SEQ ID NO:162)	TCTTCCTCCACAGTCTTTT (SEQ ID NO:237)
AAAAGACUGUGGAGGAAGAA (SEQ ID NO:163)	TTCTTCCTCCACAGTCTTTT (SEQ ID NO:238)
AAAGACUGUGGAGGAAGAA (SEQ ID NO:164)	TTCTTCCTCCACAGTCTTT (SEQ ID NO:239)
AAAGACUGUGGAGGAAGAAA (SEQ ID NO:165)	TTTCTTCCTCCACAGTCTTT (SEQ ID NO:240)
AAGACUGUGGAGGAAGAAAA (SEQ ID NO:166)	TTTTCTTCCTCCACAGTCTT (SEQ ID NO:241)
AGACUGUGGAGGAAGAAAAC (SEQ ID NO:167)	GTTTTCTTCCTCCACAGTCT (SEQ ID NO:242)
ACUGUGGAGGAAGAAAAC (SEQ ID NO:168)	GTTTTCTTCCTCCACAGT (SEQ ID NO:243)
ACUGUGGAGGAAGAAAACC (SEQ ID NO:169)	GGTTTTCTTCCTCCACAGT (SEQ ID NO:244)
ACUGUGGAGGAAGAAAACCC (SEQ ID NO:170)	GGGTTTTCTTCCTCCACAGT (SEQ ID NO:245)
CUGUGGAGGAAGAAAACC (SEQ ID NO:171)	GGTTTTCTTCCTCCACAG (SEQ ID NO:246)
CUGUGGAGGAAGAAAACCC (SEQ ID NO:172)	GGGTTTTCTTCCTCCACAG (SEQ ID NO:247)
AAAACCCUUUACCCUGUUG (SEQ ID NO:173)	CAACAGGGTAAAGGGTTTT (SEQ ID NO:248)
AAAACCCUUUACCCUGUUGU (SEQ ID NO:174)	ACAACAGGGTAAAGGGTTTT (SEQ ID NO:249)
AAACCCUUUACCCUGUUGUU (SEQ ID NO:175)	AACAACAGGGTAAAGGGTTT (SEQ ID NO:250)
UUGUUCAGGGAGAAACUG (SEQ ID NO:176)	CAGTTTCTCCCTGAACAA (SEQ ID NO:251)
UUGUUCAGGGAGAAACUGAC (SEQ ID NO:177)	GTCAGTTTCTCCCTGAACAA (SEQ ID NO:252)
UGUUCAGGGAGAAACUGA (SEQ ID NO:178)	TCAGTTTCTCCCTGAACA (SEQ ID NO:253)
UGUUCAGGGAGAAACUGAC (SEQ ID NO:179)	GTCAGTTTCTCCCTGAACA (SEQ ID NO:254)
UGUUCAGGGAGAAACUGACA (SEQ ID NO:180)	TGTCAGTTTCTCCCTGAACA (SEQ ID NO:255)
GUUCAGGGAGAAACUGACA (SEQ ID NO:181)	TGTCAGTTTCTCCCTGAAC (SEQ ID NO:256)
UCAGGGAGAAACUGACACCA (SEQ ID NO:182)	TGGTGTCAGTTTCTCCCTGA (SEQ ID NO:257)
CAGGGAGAAACUGACACCA (SEQ ID NO:183)	TGGTGTCAGTTTCTCCCTG (SEQ ID NO:258)
AGGGAGAAACUGACACCA (SEQ ID NO:184)	TGGTGTCAGTTTCTCCCT (SEQ ID NO:259)
AGGGAGAAACUGACACCAC (SEQ ID NO:185)	GTGGTGTCAGTTTCTCCCT (SEQ ID NO:260)
AGGGAGAAACUGACACCACU (SEQ ID NO:186)	AGTGGTGTCAGTTTCTCCCT (SEQ ID NO:261)
GGGAGAAACUGACACCAC (SEQ ID NO:187)	GTGGTGTCAGTTTCTCCC (SEQ ID NO:262)
GGGAGAAACUGACACCACU (SEQ ID NO:188)	AGTGGTGTCAGTTTCTCCC (SEQ ID NO:263)
GGGAGAAACUGACACCACUC (SEQ ID NO:189)	GAGTGGTGTCAGTTTCTCCC (SEQ ID NO:264)
GGAGAAACUGACACCACU (SEQ ID NO:190)	AGTGGTGTCAGTTTCTCC (SEQ ID NO:265)

GGAGAAACUGACACCACUC (SEQ ID NO:191)	GAGTGGTGTCAGTTTCTCC (SEQ ID NO:266)
GGAGAAACUGACACCACUCA (SEQ ID NO:192)	TGAGTGGTGTCAGTTTCTCC (SEQ ID NO:267)
GAGAAACUGACACCACUC (SEQ ID NO:193)	GAGTGGTGTCAGTTTCTC (SEQ ID NO:268)
GAGAAACUGACACCACUCA (SEQ ID NO:194)	TGAGTGGTGTCAGTTTCTC (SEQ ID NO:269)
GAGAAACUGACACCACUCAA (SEQ ID NO:195)	TTGAGTGGTGTCAGTTTCTC (SEQ ID NO:270)
AGAAACUGACACCACUCA (SEQ ID NO:196)	TGAGTGGTGTCAGTTTCT (SEQ ID NO:271)
AGAAACUGACACCACUCAA (SEQ ID NO:197)	TTGAGTGGTGTCAGTTTCT (SEQ ID NO:272)
AGAAACUGACACCACUCAAC (SEQ ID NO:198)	GTTGAGTGGTGTCAGTTTCT (SEQ ID NO:273)
GAAACUGACACCACUCAA (SEQ ID NO:199)	TTGAGTGGTGTCAGTTTC (SEQ ID NO:274)
GAAACUGACACCACUCAAC (SEQ ID NO:200)	GTTGAGTGGTGTCAGTTTC (SEQ ID NO:275)
GAAACUGACACCACUCAACU (SEQ ID NO:201)	AGTTGAGTGGTGTCAGTTTC (SEQ ID NO:276)
AAACUGACACCACUCAAC (SEQ ID NO:202)	GTTGAGTGGTGTCAGTTT (SEQ ID NO:277)
AAACUGACACCACUCAACU (SEQ ID NO:203)	AGTTGAGTGGTGTCAGTTT (SEQ ID NO:278)
AAACUGACACCACUCAACUG (SEQ ID NO:204)	CAGTTGAGTGGTGTCAGTTT (SEQ ID NO:279)
AACUGACACCACUCAACU (SEQ ID NO:205)	AGTTGAGTGGTGTCAGTT (SEQ ID NO:280)
AACUGACACCACUCAACUG (SEQ ID NO:206)	CAGTTGAGTGGTGTCAGTT (SEQ ID NO:281)
AACUGACACCACUCAACUGC (SEQ ID NO:207)	GCAGTTGAGTGGTGTCAGTT (SEQ ID NO:282)
ACUGACACCACUCAACUG (SEQ ID NO:208)	CAGTTGAGTGGTGTCAGT (SEQ ID NO:283)
ACUGACACCACUCAACUGC (SEQ ID NO:209)	GCAGTTGAGTGGTGTCAGT (SEQ ID NO:284)
ACUGACACCACUCAACUGCC (SEQ ID NO:210)	GGCAGTTGAGTGGTGTCAGT (SEQ ID NO:285)
CUGACACCACUCAACUGC (SEQ ID NO:211)	GCAGTTGAGTGGTGTCAG (SEQ ID NO:286)
CUGACACCACUCAACUGCC (SEQ ID NO:212)	GGCAGTTGAGTGGTGTCAG (SEQ ID NO:287)
CUGACACCACUCAACUGCCU (SEQ ID NO:213)	AGGCAGTTGAGTGGTGTCAG (SEQ ID NO:288)
UGACACCACUCAACUGCC (SEQ ID NO:214)	GGCAGTTGAGTGGTGTCA (SEQ ID NO:289)
UGACACCACUCAACUGCCU (SEQ ID NO:215)	AGGCAGTTGAGTGGTGTCA (SEQ ID NO:290)
UGACACCACUCAACUGCCUG (SEQ ID NO:216)	CAGGCAGTTGAGTGGTGTCA (SEQ ID NO:291)
GACACCACUCAACUGCCU (SEQ ID NO:217)	AGGCAGTTGAGTGGTGTC (SEQ ID NO:292)
GACACCACUCAACUGCCUG (SEQ ID NO:218)	CAGGCAGTTGAGTGGTGTC (SEQ ID NO:293)
GACACCACUCAACUGCCUGG (SEQ ID NO:219)	CCAGGCAGTTGAGTGGTGTC (SEQ ID NO:294)
ACACCACUCAACUGCCUG (SEQ ID NO:220)	CAGGCAGTTGAGTGGTGT (SEQ ID NO:295)
ACACCACUCAACUGCCUGG (SEQ ID NO:221)	CCAGGCAGTTGAGTGGTGT (SEQ ID NO:296)

ACACCACUCAACUGCCUGGC (SEQ ID NO:222)	GCCAGGCAGTTGAGTGGTGT (SEQ ID NO:297)
CACCACUCAACUGCCUGGCA (SEQ ID NO:223)	TGCCAGGCAGTTGAGTGGTG (SEQ ID NO:298)
GAAAAUGUGGCAUCCAGU (SEQ ID NO:224)	ACTGGATGCCACATTTTC (SEQ ID NO:299)
AAAAUGUGGCAUCCAGUC (SEQ ID NO:225)	GACTGGATGCCACATTTT (SEQ ID NO:300)
GCAUCCAGUCCACUUUACCA (SEQ ID NO:226)	TGGTAAAGTGGACTGGATGC (SEQ ID NO:301)
CAUCCAGUCCACUUUACC (SEQ ID NO:227)	GGTAAAGTGGACTGGATG (SEQ ID NO:302)
CAUCCAGUCCACUUUACCA (SEQ ID NO:228)	TGGTAAAGTGGACTGGATG (SEQ ID NO:303)
CAUCCAGUCCACUUUACCAU (SEQ ID NO:229)	ATGGTAAAGTGGACTGGATG (SEQ ID NO:304)
AUCCAGUCCACUUUACCA (SEQ ID NO:230)	TGGTAAAGTGGACTGGAT (SEQ ID NO:305)
AUCCAGUCCACUUUACCAU (SEQ ID NO:231)	ATGGTAAAGTGGACTGGAT (SEQ ID NO:306)
AUCCAGUCCACUUUACCAUC (SEQ ID NO:232)	GATGGTAAAGTGGACTGGAT (SEQ ID NO:307)
GUUUAAGGAAACCAUCUCUG (SEQ ID NO:233)	CAGAGATGGTTTCCTTAAAC (SEQ ID NO:308)
UUUAAGGAAACCAUCUCUGG (SEQ ID NO:234)	CCAGAGATGGTTTCCTTAAA (SEQ ID NO:309)
UUAAGGAAACCAUCUCUGG (SEQ ID NO:235)	CCAGAGATGGTTTCCTTAA (SEQ ID NO:310)
UAAGGAAACCAUCUCUGG (SEQ ID NO:236)	CCAGAGATGGTTTCCTTA (SEQ ID NO:311)

Table 5. Exon 5 ASOs

Target Sequence (5'→3')	ASO (5'→3')
AUAAGGAUGACUGAGGAAG (SEQ ID NO:312)	CTTCCTCAGTCATCCTTAT (SEQ ID NO:335)
AUAAGGAUGACUGAGGAAGA (SEQ ID NO:313)	TCTTCCTCAGTCATCCTTAT (SEQ ID NO:336)
UAAGGAUGACUGAGGAAG (SEQ ID NO:314)	CTTCCTCAGTCATCCTTA (SEQ ID NO:337)
UAAGGAUGACUGAGGAAGA (SEQ ID NO:315)	TCTTCCTCAGTCATCCTTA (SEQ ID NO:338)
UAAGGAUGACUGAGGAAGAG (SEQ ID NO:316)	CTCTTCCTCAGTCATCCTTA (SEQ ID NO:339)
AAGGAUGACUGAGGAAGA (SEQ ID NO:317)	TCTTCCTCAGTCATCCTT (SEQ ID NO:340)
AAGGAUGACUGAGGAAGAG (SEQ ID NO:318)	CTCTTCCTCAGTCATCCTT (SEQ ID NO:341)
AAGGAUGACUGAGGAAGAGU (SEQ ID NO:319)	ACTCTTCCTCAGTCATCCTT (SEQ ID NO:342)
AGGAUGACUGAGGAAGAG (SEQ ID NO:320)	CTCTTCCTCAGTCATCCT (SEQ ID NO:343)
AGGAUGACUGAGGAAGAGU (SEQ ID NO:321)	ACTCTTCCTCAGTCATCCT (SEQ ID NO:344)
AGGAUGACUGAGGAAGAGUA (SEQ ID NO:322)	TACTCTTCCTCAGTCATCCT (SEQ ID NO:345)

GGAUGACUGAGGAAGAGU (SEQ ID NO:323)	ACTCTTCCTCAGTCATCC (SEQ ID NO:346)
GGAUGACUGAGGAAGAGUA (SEQ ID NO:324)	TACTCTTCCTCAGTCATCC (SEQ ID NO:347)
GGAUGACUGAGGAAGAGUAC (SEQ ID NO:325)	GTACTCTTCCTCAGTCATCC (SEQ ID NO:348)
GAUGACUGAGGAAGAGUA (SEQ ID NO:326)	TACTCTTCCTCAGTCATC (SEQ ID NO:349)
GAUGACUGAGGAAGAGUAC (SEQ ID NO:327)	GTACTCTTCCTCAGTCATC (SEQ ID NO:350)
GAUGACUGAGGAAGAGUACU (SEQ ID NO:328)	AGTACTCTTCCTCAGTCATC (SEQ ID NO:351)
AUGACUGAGGAAGAGUAC (SEQ ID NO:329)	GTACTCTTCCTCAGTCAT (SEQ ID NO:352)
AUGACUGAGGAAGAGUACU (SEQ ID NO:330)	AGTACTCTTCCTCAGTCAT (SEQ ID NO:353)
AUGACUGAGGAAGAGUACUC (SEQ ID NO:331)	GAGTACTCTTCCTCAGTCAT (SEQ ID NO:354)
UGACUGAGGAAGAGUACU (SEQ ID NO:332)	AGTACTCTTCCTCAGTCA (SEQ ID NO:355)
UGACUGAGGAAGAGUACUC (SEQ ID NO:333)	GAGTACTCTTCCTCAGTCA (SEQ ID NO:356)
UGACUGAGGAAGAGUACUCU (SEQ ID NO:334)	AGAGTACTCTTCCTCAGTCA (SEQ ID NO:357)

The disclosed oligonucleotide is capable of modulating expression of paternal *UBE3A*, in particular induction or up-regulation of paternally expressed UBE3A in neuronal cells. The modulation is achieved by hybridizing to the 5′-end of *UBE3A-AS*. In certain embodiments the oligonucleotide disclosed herein hybridizes to a sub-sequence of the target nucleic acid of SEQ ID NO:1 with a ΔG° below −10 kcal, such as with a ΔG° between −10 to −60 kcal, such as −12 to −40, such as from −15 to −30 kcal or −16 to −27 kcal such as −18 to −25 kcal.

In some embodiments the disclosed oligonucleotides are capable of increasing the expression of *UBE3A* by least 20% compared to the expression level of *UBE3A* in a neuronal cell treated with saline or a non-targeting oligonucleotide, more preferably by at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 80%, 100%, 120%, 150%, 160%, 170%, 180%, 190%, 200%, 210%, 220%, 230%, 240% or 250% compared to the expression level of *UBE3A* in a neuronal cell treated with saline or a non-targeting oligonucleotide. In some embodiments, the disclosed oligonucleotides are capable of decreasing the level of the *SNHG14* transcript downstream of *SNORD115-45* by at least 20% compared to the level of the *SNHG14* transcript downstream of *SNORD1115-45* in a neuronal cell treated with saline or a non-targeting oligonucleotide, more preferably by at least 30%, 40%, 50%, 60%, 70%, 80%, 90% or 95% compared to the level of the *SNHG14* transcript downstream of *SNORD115-45* in a neuronal cell treated with saline or a non-targeting oligonucleotide.

Target modulation by the disclosed oligonucleotide is triggered by hybridization between a contiguous nucleotide sequence of the oligonucleotide and the target nucleic acid. In some embodiments the disclosed oligonucleotide comprises mismatches between the oligonucleotide and the target nucleic acid. Despite mismatches hybridization to the target nucleic acid may still be sufficient to show a desired modulation of UBE3A expression. Reduced binding affinity resulting from mismatches may advantageously be compensated by increased number of nucleotides in the oligonucleotide and/or an increased number of modified nucleosides capable of increasing the binding affinity to the target, such as 2′ modified nucleosides, including LNA, present within the oligonucleotide sequence.

The disclosed antisense oligonucleotide can have a contiguous nucleotide sequence of 10 to 30 nucleotides in length with at least 90% complementary, such as at least 91%, such as at least 92%, such as at least 93%, such as at least 94%, such as at least 95%, such as at least 96%, such as at least 97%, such as at least 98%, or

100% complementarity to one of five exons located in the 5'-end of *UBE3A-AS* disclosed herein.

Oligonucleotide design refers to the pattern of nucleoside sugar modifications in the oligonucleotide sequence. The disclosed antisense oligonucleotide comprises sugar-modified nucleosides and may also comprise DNA, RNA, or arabino nucleic acid (ANA) nucleosides. In some embodiments, the oligonucleotide comprises sugar-modified nucleosides and DNA nucleosides. In some embodiments, the oligonucleotide comprises sugar-modified nucleosides and RNA nucleosides. In some embodiments, the oligonucleotide comprises sugar-modified nucleosides and ANA nucleosides.

In some embodiments, the oligonucleotide comprises at least 1 modified nucleoside, such as at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15 or at least 16 modified nucleosides. In an embodiment the oligonucleotide comprises from 1 to 10 modified nucleosides, such as from 2 to 9 modified nucleosides, such as from 3 to 8 modified nucleosides, such as from 4 to 7 modified nucleosides, such as 6 or 7 modified nucleosides.

In some embodiments, the oligonucleotide comprises at least one modified internucleoside linkage. In some embodiments, the internucleoside linkages within the contiguous nucleotide sequence are phosphorothioate or boranophosphate internucleoside linkages.

In some embodiments, the disclosed antisense oligonucleotide comprises one or more sugar modified nucleosides, such as 2' sugar modified nucleosides. Preferably the disclosed antisense oligonucleotides comprise one or more LNA nucleosides or 2' sugar modified nucleoside wherein the 2' position is replaced by a substituent independently selected from the group consisting of, –F; –CF_3, –CN, –N_3, –NO, –NO_2, –O–(C_1–C_{10} alkyl), –S–(C_1–C_{10} alkyl), –NH–(C_1–C_{10} alkyl), or –N(C_1–C_{10} alkyl)$_2$; –O–(C_2–C_{10} alkenyl), –S–(C_2–C_{10} alkenyl), –NH–(C_2–C_{10} alkenyl), or –N(C_2–C_{10} alkenyl)$_2$; –O–(C_2–C_{10} alkynyl), –S–(C_2–C_{10} alkynyl), –NH–(C_2–C_{10} alkynyl), –N(C_2–C_{10} alkynyl)$_2$, –O—(C_1–C_{10} alkylene)–O—(C_1–C_{10} alkyl), –O–(C_1–C_{10} alkylene)–NH–(C_1–C_{10} alkyl), –O–(C_1–C_{10} alkylene)–NH(C_1–C_{10} alkyl)$_2$, –NH–(C_1–C_{10} alkylene)–O–(C_1–C_{10} alkyl), and –N(C_1–C_{10} alkyl)–(C_1–C_{10} alkylene)–O–(C_1–C_{10} alkyl) .

In some embodiments, the disclosed oligonucleotides comprises at least one LNA unit, such as 1, 2, 3, 4, 5, 6, 7, or 8 LNA units, such as from 2 to 6 LNA units, such as from 3 to 7 LNA units, 4 to 8 LNA units or 3, 4, 5, 6 or 7 LNA units. In some embodiments, all the modified nucleosides are LNA nucleosides. In some embodiments, LNA comprises a 2′-4′ biradical bridge of −L−, wherein −L− is $-O-CH_2-$, wherein $-CH_2-$ is optionally substituted. In some embodiments, LNA comprises a 2′-4′ biradical bridge of −L−, wherein −L− is $-O-CH_2-$. In some embodiments, LNA comprises a 2′-4′ biradical bridge of −L−, wherein −L− is −O−CH(Et)−. In a further embodiment, the oligonucleotide may comprise both beta-D-oxy-LNA, and one or more of the following LNA units: thio-LNA, amino-LNA, oxy-LNA, and/or ENA in either the beta-D or alpha-L configurations or combinations thereof. In a further embodiment, all LNA cytosine units are 5-methyl-cytosine. In some embodiments, the oligonucleotide or contiguous nucleotide sequence has at least 1 LNA unit at the 5′ end and at least 2 LNA units at the 3′ end of the nucleotide sequence.

In some embodiments, the disclosed oligonucleotide is capable of recruiting RNase H. In some embodiments, the oligonucleotide has a gapmer design or structure also referred herein merely as "Gapmer". In a gapmer structure the oligonucleotide comprises at least three distinct structural regions a 5′-flank, a gap and a 3′-flank, F-G-F′ in ′5->3′ orientation. In this design, flanking regions F and F′ (also termed wing regions) comprise a contiguous stretch of modified nucleosides, which are complementary to the *UBE3A-AS* target nucleic acid, while the gap region, G, comprises a contiguous stretch of nucleotides which are capable of recruiting a nuclease, preferably an endonuclease such as RNase, for example, RNase H, when the oligonucleotide is in duplex with the target nucleic acid. Nucleosides which are capable of recruiting a nuclease, in particular RNase H, can be selected from the group consisting of DNA, alpha-L-oxy-LNA, 2′-Flouro-ANA and UNA. Regions F and F′, flanking the 5′ and 3′ ends of region G, preferably comprise non-nuclease recruiting nucleosides (nucleosides with a 3′ endo structure), more preferably one or more affinity enhancing modified nucleosides. In some embodiments, the 3′ flank comprises at least one LNA nucleoside, preferably at least 2 LNA nucleosides. In some embodiments, the 5′ flank comprises at least one LNA nucleoside. In some embodiments both the 5′ and 3′ flanking regions comprise a LNA nucleoside. In some embodiments all the nucleosides in the flanking regions are LNA nucleosides. In other embodiments, the flanking regions may comprise both LNA nucleosides and other nucleosides (mixed flanks), such as DNA nucleosides and/or non-LNA modified nucleosides, such as 2′ substituted nucleosides. In this case the gap is defined as a contiguous sequence of at least 5 RNase H recruiting nucleosides (nucleosides with a 2′ endo structure, preferably DNA) flanked at the 5′ and 3′ end by an affinity enhancing modified nucleoside, preferably LNA, such as beta-D-oxy-LNA. Consequently, the nucleosides of the 5′ flanking region and the 3′ flanking region which are adjacent to the gap region are modified nucleosides, preferably non-nuclease recruiting nucleosides. In oligonucleotides with mixed flanks where the flanks comprise DNA the 5′ and 3′ nucleosides are modified nucleosides.

Methods for manufacturing the disclosed oligonucleotides are known. In some cases, the method uses phophoramidite chemistry (see for example Caruthers et al, 1987, Methods in Enzymology vol. 154, pages 287-313). In a further embodiment the method further comprises reacting the contiguous nucleotide sequence with a conjugating moiety (ligand).

In some embodiments, oligonucleotide synthesis methodologies are utilized that provide control of stereochemistry at one or more modified internucleoside linkages that include(s) a chiral atom. See, for example, WO2010/064146, WO2014/012081, WO2015/107425, WO2016/079183, WO2016/079181, WO2016/096938, WO2017/194498, and WO2018/177825, which are incorporated by reference for these methodologies.

Those skilled in the art will appreciate that useful nucleic acids provided by the present disclosure include those that store and/or express sequences of oligonucleotides described herein. In some embodiments, such nucleic acids may be or comprise vectors appropriate for delivery into and/or replication and/or expression in a cell (e.g., a microbial cell, for example for production and/or a mammalian cell, for example for treatment). Those skilled in the art are aware of a variety of technologies (e.g., recombinant nucleic acid technologies such as, for instance, that utilize one or more of amplification such as by polymerase chain reaction, cleavage such as by restriction digestion, linkage such as by ligation – whether *in vitro* or *in vivo* e.g., by gap repair, etc.).

Also disclosed are pharmaceutical compositions comprising any of the aforementioned oligonucleotides and/or oligonucleotide conjugates and a pharmaceutically acceptable diluent, carrier, salt and/or adjuvant. A pharmaceutically acceptable diluent includes phosphate-buffered saline (PBS) and pharmaceutically acceptable salts include, but are not limited to, sodium and potassium salts. In some embodiments, the diluent is artificial cerebrospinal fluid (aCSF).

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

Those skilled in the art are aware of a variety of formulation strategies useful for storage and/or administration of nucleic acid therapeutics such as oligonucleotide therapeutics. *See,* for example, Pushpendra et al "Nucleic Acids as Therapeutics" in *From Nucleic Acid Sequences to Molecular Medicines,* ed. Erdmann and Barciszewski, Springer-Verlag, 2012; Juliano "The Delivery of Therapeutic Oligonucleotides" *Nuc. Acids. Res.* 44:6518, 2016; etc.

In some embodiments, the oligonucleotide is formulated as a prodrug. In particular with respect to oligonucleotide conjugates, the conjugate moiety can be cleaved off the oligonucleotide once the prodrug is delivered to the site of action, e.g., the target cell.

Also disclosed are methods for treating or preventing a disease, comprising administering a therapeutically or prophylactically effective amount of an oligonucleotide, an oligonucleotide conjugate or a pharmaceutical composition disclosed herein to a subject suffering from or susceptible to the disease.

Also disclosed is use of the disclosed oligonucleotides for the manufacture of a medicament for the treatment of a disorder as referred to herein, or for a method of the treatment of as a disorder as referred to herein.

The disclosed pharmaceutical compositions may be administered by topical (such as, to the skin, inhalation, ophthalmic or otic) or enteral (such as, orally or through the gastrointestinal tract) or parenteral (such as, intravenous, subcutaneous, intra-muscular, intracerebral, intracerebroventricular or intrathecal) administration. In some embodiments, the disclosed pharmaceutical compositions are administered by a parenteral route including intravenous, intraarterial, subcutaneous, intraperitoneal or intramuscular injection or infusion, intrathecal or intracranial, e.g., intracerebral or intraventricular, administration. In some embodiments, the oligonucleotide is administered by intracerebral or intracerebroventricular injection. In another embodiment the active oligonucleotide or oligonucleotide conjugate is administered intrathecally. In some embodiments, the pharmaceutical composition is administered by intracisternae magna injection.

In some embodiments, AS therapy with pharmaceutical compositions described herein is administered to subject(s) suffering from or susceptible to AS. In some embodiments, a subject has been determined to have genetic characteristic associated with a defect in a maternal *UBE3A* gene. In some embodiments, an AS-associated genetic characteristic is or comprises a maternal deletion. In some embodiments, an AS-associated genetic characteristic is or comprises uniparental disomy. In some embodiments, an AS-associated genetic characteristic is or comprises a *UBE3A* mutation. In some embodiments, an AS-associated genetic characteristic is or comprises an imprinting defect.

In some embodiments, a subject has been determined to have one or more developmental history and/or laboratory finding characteristics that have been associated with AS such as, for example, one or more of:

(i) normal prenatal and birth history with normal head circumference and absence of major birth defects;

(ii) feeding difficulties as a neonate and/or as an infant;

(iii) developmental delay evident by 6-12 months of age, sometimes associated with truncal hypotonus;

(iv) unsteady limb movements and/or increased smiling;

(v) delayed but forward progression of development (no loss of skills);

(vi) normal metabolic, hematologic and chemical laboratory profiles;

(vii) structurally normal brain when assessed using MRI or CT (may have mild cortical atrophy or dysmyelination).

Alternatively or additionally, in some embodiments, a subject has been determined to display one or more clinical features that are consistently associated with AS such as, for example, one or more of:

(i) developmental delay, functionally severe

(ii) movement or balance disorder, usually ataxia of gait and/or tremulous movement of limbs. In some embodiments, such movement disorder can be mild. In some embodiments, such movement disorder may not appear as frank ataxia but can be or involve, for example, forward lurching, unsteadiness, clumsiness, or quick, jerky motion;

(iii) behavioral uniqueness: any combination of frequent laughter/smiling; apparent happy demeanor; easily excitable personality, often with uplifted hand-flapping or waving movements; hypermotoric behavior

(iv) speech impairment, such as for example absent or minimal use of words; alternatively or additionally, receptive and non-verbal communication skills higher than verbal ones.

Alternatively or additionally, in some embodiments, a subject has been determined to display one or more clinical features that are frequently (e.g., about 80% of the time) associated with AS such as, for example, one or more of:

(i) delayed, disproportionate growth in head circumference, usually resulting in microcephaly (≤2 S.D. of normal OFC) by age 2 years. In some embodiments, microcephaly is more pronounced in those with 15q11.2-q13 deletions;

(ii) seizures, onset usually < 3 yrs. of age. In some embodiments, seizure severity may decrease with age but regardless, in some embodiments, the seizure disorder lasts throughout adulthood.

(iv) abnormal EEG, with a characteristic pattern, as is known in the art. In some embodiments, EEG abnormalities can occur in the first 2 years of life and can precede clinical features, and may not be correlated to clinical seizure events.

Alternatively or additionally, in some embodiments, a subject has been determined to display one or more clinical features that are sometimes (e.g., about 20-80% of the time) associated with AS such as, for example, one or more of:

(i) flat occiput

(ii) occipital groove

(iii) protruding tongue

(iv) tongue thrusting; suck/swallowing disorders

(v) feeding problems and/or truncal hypotonia during infancy

(vi) prognathia

(vii) wide mouth, wide-spaced teeth

(viii) frequent drooling

(ix) excessive chewing/mouthing behaviors

(x) strabismus

(xi) hypopigmented skin, light hair and eye color, in some embodiments determined as compared to family, and typically seen only in deletion cases

(xii) hyperactive lower extremity deep tendon reflexes

(xiii) uplifted, flexed arm position especially during ambulation

(xiv) wide-based gait with pronated or valgus-positioned ankles

(xv) increased sensitivity to heat

(xvi) abnormal sleep wake cycles and diminished need for sleep

(xvii) attraction to/fascination with water; fascination with crinkly items such as certain papers and plastics

(xviii) abnormal food related behaviors

(xix) obesity (in the older child)

(xx) scoliosis

(xxi) constipation

In some embodiments, a therapeutic regimen for the treatment of AS with a nucleic acid therapeutic (e.g., an oligonucleotide therapeutic such as an ASO) as described herein is or comprises administration of one or more doses of a pharmaceutical composition that comprises and/or delivers an oligonucleotide as described herein.

In some embodiments, a subject to whom a provided therapeutic regimen is administered is receiving or has received one or more other AS therapeutics including, for example, one or more other nucleic acid therapeutics (e.g., one or more other oligonucleotides that target *UBE3A-AS*). See, for example, WO2014004572A3, US9617539B2, US20170362592A1, and EP2864479B1.

In some embodiments, a subject to whom a provided therapeutic regimen is administered has suffered or is suffering from one or more seizures and/or is receiving or has received anti-seizure therapy. For example. In some embodiments, a subject may have received or be receiving one or more of valproic acid, clonazepam, phenobarbital, topiramate, carbamazepine, lamotrigine, leveltiracetam, phenytoin, zonisamide, ethosuxaminde, gabapentin, felbatame, oxcarbazepine, tranxene, ACTS, nitrazapam, pregabalin, mysoline, vigabatrin, etc. In some particular embodiments, a subject may have received or be receiving one or more of valproic acid, clonazepam, phenobarbital, topiramate, carbamazepine, lamotrigine, and/or levetiracetam.

Alternatively or additionally, in some embodiments, a subject may have received or be receiving dietary therapy such as, for example, a ketogenic diet, low glycemic index therapy, etc.

Still further alternatively or additionally, in some embodiments, a subject may have received or be receiving treatment with a vagal nerve stimulator.

As will be apparent to those skilled in the art reading the present disclosure, provided methods of treatment involve administering one or both of an oligonucleotide as described herein and an additional therapy (e.g., an alternative oligonucleotide and/or anti-epileptic therapy and/or one or more other therapeutic interventions), so that the subject receives combination therapy (e.g., is simultaneously exposed thereto, for example via overlapping dosing etc.). Also disclosed is the use of an oligonucleotide disclosed herein for the manufacture of a medicament wherein the medicament is in a dosage form for intrathecal administration.

Also disclosed is the use of an oligonucleotide disclosed herein for the manufacture of a medicament wherein the medicament is in a dosage form for intracerebral or intraventricular administration.

Also disclosed is the use of an oligonucleotide disclosed herein for the manufacture of a medicament wherein the medicament is in a dosage form for intracerebroventricular administration.

In some embodiments the oligonucleotide disclosed herein is for use in a combination treatment with another therapeutic agent. The therapeutic agent can for example be anticonvulsant medication.

A number of embodiments of the invention have been described. Nevertheless, it will be understood that various modifications may be made without departing from the spirit and scope of the invention. Accordingly, other embodiments are within the scope of the following claims.

EXAMPLES

Example 1:

Results

RNA-sequencing analysis of mouse and human CNS identified a region believed to be important for the stability and/or transcription of *UBE3A-AS*. Further analysis of the region showed low levels of sequence conservation between mouse and human (Figures 1A-1D).

Based on these findings, mouse-specific ASOs were designed to target a specific region in the *Ube3a-AS* transcript (Table 6 and Figure 2A). To test whether ASOs targeting this region reactivate expression of the paternal *Ube3a* allele, primary hippocampal neuronal cultures were generated from the Ube3aYFP reporter mouse model (Ube3a+/YFP; Figure 2B) and treated at 7 days in vitro (DIV) with a control ASO [ASO-C (10 uM, n = 3)], three ASOs targeting *Ube3a-AS* [ASO-1.1, ASO-1.2, ASO-3.1 (1 µM, 5 µM, and 15 µM, n = 3)], and ASO-B (1 µM, 5 µM, and 15 µM, n = 3)]. As a positive control, neurons were also treated with Topotecan [Topo (300 nM, n = 3)] and a negative vehicle control [Veh (1%, n = 3); Figure 2 C]. Three days post-treatment (10 DIV), immunofluorescent imaging was used to quantify paternal Ube3aYFP protein levels in individual cells. Compared to controls (ASO-C and Veh), each treatment substantially increased paternal Ube3aYFP protein levels, with similar levels achieved in ASO-1.1 (15 µM), ASO-3.1 (15 µM), and Topotecan treatments (Figures 2D and 2E).

Human-specific ASOs were then designed to target this region, which included four ASOs targeting non-polymorphic regions in human and regions conserved (100%) with macaque (Rhesus and Cynomolgus) (Table 7 and Figure 3A). Human induced pluripotent stem cell (iPSC) neural precursor cells were differentiated into GABAergic neurons for 14 DIV and then treated with a control ASO [ASO-C (10 µM, n = 3)], Topotecan [Topo (1 µM, n = 2)], and six ASOs targeting *UBE3A-AS* [ASO-1, ASO-2, ASO-3, ASO-4, ASO-5, and ASO-6 (10 µM, n = 3)]. Additionally, an ASO targeting an intronic region downstream of *SNORD109B* was included (ASO-7). Six days post-treatment (20 DIV), RNA was isolated from the neurons and the steady state RNA levels of *UBE3A-AS* and *UBE3A* were estimated relative to the control treatment (Figure 3B). With the exception of ASO-7, each ASO significantly decreased *UBE3A-AS* RNA levels, with ASO-2 and ASO-4 having the largest effect (Table 8 and Figure 3C). *UBE3A* RNA levels also increased after treatment with each ASO (Figure 3D).

The potency of ASO-4 was further examined given its effect on *UBE3A-AS* RNA levels. GABAergic iPSC-derived neurons were treated at 14 DIV with a 10-point ½ log dose response curve of ASO-4 and Topotecan, as a positive control and for comparisons between treatment [1 nM, 3 nM, 10 nM, 30 nM, 100 nM, 300 nM, 1 µM, 3 µM, 10 µM, and 30 µM (ASO-4, n = 6; Topotecan, n = 2)]. At 20 DIV, the steady state RNA levels of *UBE3A-AS* were measured and dose response curves fitted to estimate the IC_{50} and E_{max} (i.e., maximum *UBE3A-AS* inhibition) (Table 9 and Figure 4A). The dose response curves of ASO-4 and Topotecan were significantly different (Parallelism test: $F_{(3,145)} = 11.2$, $p < 0.0001$), thus the relative potencies were not estimated. An equivalence test indicated that the IC_{50} and E_{max} of ASO-4 and Topotecan were not equivalent [ASO-4/Topotecan IC_{50} ratio: = 1.2 (Lower confidence limit = 1.1; Upper confidence limit = 1.3); Emax ratio = -4.1 (Lower confidence limit = -12.9; Upper confidence limit = 4.8)].

The effects of ASO-4 and Topotecan were then examined on the *SNORD116*, *IPW*, *SNORD115*, and *SNORD109A* RNAs, which are located upstream of the ASO-4 target region (see Figure 1A). With the exception of *SNORD116*, ASO-4 had a significant effect on the RNA levels of *IPW*, *SNORD115*, and *SNORD109A/B* but not in a dose dependent manner. In contrast, Topotecan had a significant effect on *SNORD116*, *IPW*, *SNORD115*, and *SNORD109A/B* RNA levels that was dose dependent (Table 10 and Figures 4B-4E). Both ASO-4 and Topotecan increased total *UBE3A* RNA levels in a dose-dependent manner, except for Topotecan at higher concentrations (3 µM, 10 µM, and 30 µM; Figure 4F).

The potency of ASO-4 was further examined in iPSC-derived neurons at a later time point in differentiation. GABAergic iPSC-derived neurons were treated at 59 DIV with a control ASO [ASO-C, 10 µM (n = 3)] and ASO-4 [1 uM, 5 µM, and 10 µM (n = 3)], and the steady state RNA levels of *UBE3A-AS* and *UBE3A* were measured as described above (Figure 4G). Unlike neurons treated with ASO-4 at an earlier time point, the RNA levels of *UBE3A* and *UBE3A-AS* were highly inversely correlated (Figures 4H and 4I). For example, the effect of ASO-4 (10 µM) on *UBE3A-AS* RNA levels was similar between neurons treated at 14 and 59 DIV [20 DIV: *UBE3A-AS*: ↓87% (95% confidence intervals (CI): 80 to 95%); 65 DIV: ↓81% (95% CI: 74 to 88%)], whereas the effect of ASO-4 on *UBE3A* RNA levels was substantially larger in neurons treated at 59 DIV [20 DIV: ↑30% (95% CI: 16 to 44%); 65 DIV: ↑86% (95% CI: 59% to 113%)].

Additional ASOs targeting the 5'-end of *UBE3A-AS* were then designed to optimize the target sequences of ASO-4 (ASO-4.1, ASO-4.2, ASO-4.3, and ASO-4.4) as well as two other target regions, ASO-3 (ASO-3.1 and ASO-3.2) and ASO-6 (ASO-6.1) (Table 11). Additionally, ASO-4 was manufactured at two different vendors for comparative purposes (ASO-4.S, Sigma; ASO-4.I, Integrated DNA Technologies). Human iPSC-derived neurons (GABAergic) were treated at 14 DIV with a 5-point ½ log dose curve of ASO-3.1, ASO-3.2, ASO-4.S, ASO-4.I, ASO-4.1, ASO-4.2, ASO-4.3, ASO-4.4, and ASO-6.1 [30 nM, 100 nM, 300 nM, 1 µM (n = 6)]. At 20 DIV, the IC_{50} and E_{max} of each ASO was estimated as described above (Figure 5 A - B and Table 12). The dose response curves were similar among ASOs (Parallelism test: $F_{(16,513)} = 1.6$, $p = 0.06$), with ASO-4 and ASO-6.1 having the highest relative potency (Table 13). No significant difference was observed between ASO-4.S and ASO-4.I.

The potency of ASO-4 and ASO-6.1 was further examined in iPSC-derived neurons at a later time point in differentiation. GABAergic iPSC-derived neurons were treated at 29 DIV with a 10-point ½ log dose response curve of ASO-4 and ASO-6.1 [1 nM, 3 nM, 10 nM, 30 nM, 100 nM, 300 nM, 1 µM, 3 µM, 10 µM, and 30 µM (n = 3)]. At 35 DIV, the IC_{50} and E_{max} of each ASO was estimated as described above (Figure 5 C-D and Table 14). The dose response curves of ASO-4 and ASO-6.1 were not similar (Parallelism test: $F_{(3,172)} = 22.7$, $p < 0.0001$). An equivalence test indicated that ASO-4 and ASO-6.1 had equivalent potencies but different E_{max} values [ASO-6.1/ASO-4 ratio: $IC_{50} = 1.03$ (Lower confidence limit = 1.0; Upper confidence limit = 1.1); $E_{max} = -1.3$ (Lower confidence limit = -2.6; Upper confidence limit = -0.08)], with ASO-6.1 having the largest inhibition of *UBE3A-AS* levels. The effect of

ASO-4 and ASO-6.1 on *UBE3A* RNA levels was similar, with each treatment increasing RNA levels in dose dependent manner (Figure 5D).

ASO-4 and ASO-6.1 were also examined in glutamatergic iPSC-derived neurons. Glutamatergic iPSC-derived neurons were treated at 14 DIV with a 10-point ½ log dose response curve of ASO-4 and ASO-6.1 [1 nM, 3 nM, 10 nM, 30 nM, 100 nM, 300 nM, 1 µM, 3 µM, 10 µM, and 30 µM (n = 3)]. At 20 DIV, the IC_{50} and E_{max} of each ASO was estimated as described above (Figure 5E-F and Table 15). The dose response curves of ASO-4 and ASO-6.1 were similar and not significantly different (Parallelism test: $F_{(3,165)} = 1.9$, $p = 0.1$), with ASO-6.1 having the highest relative potency (Table 16). As expected, ASO-4 and ASO-6.1 increased *UBE3A* RNA levels in a dose dependent manner (Figure 5F); however, there was a high degree of variation for each concentration that was not attributable to treatment (R^2 = 0.17).

Conclusions

Towards developing a therapy for AS, experiments were conducted to determine whether ASOs targeting a specific region inhibit *Ube3a-AS*/*UBE3A-AS* and reactivate expression of the paternal *Ube3a*/*UBE3A* allele in mouse and human neurons. Altogether, findings show that ASOs targeting this region in mouse and human neurons have potent antisense activity and reverse imprinting of *Ube3a/UBE3A*.

Two of the three ASOs (ASO-1.1 and ASO-3.1) targeting *Ube3a-AS* reactivated expression of the paternal *Ube3a* allele in mouse neurons to a level similar to that achieved by the optimal concentration of Topotecan (300 nM).

Likewise, each of the human-specific ASOs significantly reduced the steady state RNA levels of *UBE3A-AS* in human iPSC-derived neurons, with higher concentrations of ASO-4 and ASO-6.1 almost completely abolishing expression of *UBE3A-AS*. Given that ASO-4 and ASO-6.1 target regions that are 100% conserved between human and macaque, the efficacy of these ASOs can be examined *in vivo* in either Cynomolgus or Rhesus macaque. Unlike Topotecan, ASO-4 has a small, if any, effect on the upstream *SNORD116*, *IPW*, *SNORD115*, or *SNORD109A/B* RNAs, consistent with the notion that the ASO terminates transcription at or downstream of the target region.

Low concentrations (3 nM) of ASO-4 and ASO-6.1 significantly reduced *UBE3A-AS* RNA levels; however, higher concentrations (≥100 nM) of ASO were necessary to increase *UBE3A* RNA levels. This may reflect a certain threshold required for *UBE3A-AS* to inhibit transcription of *UBE3A*, or a lag between the time that inactivation of *UBE3A-AS* leads to reactivation of paternal *UBE3A*, or the sensitivity of the assay used to quantify *UBE3A* RNA levels.

Collectively, findings suggest that ASOs targeting a candidate region in *UBE3A-AS* almost completely abolishes imprinting of *UBE3A* in neurons and reveals at least two ASOs for future clinical development.

Derivatives of ASO-4 and ASO-6.1 that are comprised of different RNA modifications [2´-hydroxymethyl (2´-OMe), 2´-methoxy-ethyl 2´-MOE, and locked nucleic acid (LNA)] and backbones [phosphorothioate (PS) and phosphodiester (PO)] have also been designed (Table 17).

Table 6. Mouse *Ube3a-AS* Oligonucleotides

ASO	RNA Modification	RNA Backbone	DNA Backbone	Design (5´-3´)	Sequence	SEQ ID
ASO-B	2´-OMe	PS	PS	5-10-5	$C^{O}*C^{O}*A^{O}*G^{O}*C^{O}*c*t*t*g*t*t*g*g*a*t*A^{O}*U^{O}*C^{O}*A^{O}*U^{O}$	SEQ ID NO:358
ASO-1.1	2´-OMe	PS	PS	5-10-5	$C^{O}*C^{O}*A^{O}*C^{O}*A^{O}*t*t*t*c*c*t*c*t*c*a*U^{O}*G^{O}*G^{O}*A^{O}*A^{O}$	SEQ ID NO:359
ASO-1.2	2´-OMe	PS	PS	5-10-5	$G^{O}*A^{O}*G^{O}*U^{O}*G^{O}*t*t*t*g*c*a*a*a*c*c*A^{O}*A^{O}*U^{O}*G^{O}*U^{O}$	SEQ ID NO:360
ASO-3.1	2´-OMe	PS	PS	5-10-5	$U^{O}*G^{O}*U^{O}*U^{O}*U^{O}*c*t*t*t*g*g*t*g*a*t*U^{O}*C^{O}*U^{O}*G^{O}*C^{O}$	SEQ ID NO:361

Capital letter, RNA; lower-case letter, DNA; O, 2´-OMe; PS & *, phosphorothioate

Table 7. Human *UBE3A-AS* Oligonucleotides

ASO	RNA Modification	RNA Backbone	DNA Backbone	Design (5´-3´)	Sequence	SEQ ID
ASO-1	2´-OMe	PS	PS	5-10-5	$U^{O}*A^{O}*G^{O}*A^{O}*G^{O}*g*t*g*a*a*g*g*c*c*a*G^{O}*G^{O}*C^{O}*A^{O}*C^{O}$	SEQ ID NO:362
ASO-2	2´-OMe	PS	PS	5-10-5	$G^{O}*U^{O}*A^{O}*C^{O}*U^{O}*c*t*t*c*c*t*c*a*g*t*C^{O}*A^{O}*U^{O}*C^{O}*C^{O}$	SEQ ID NO:363
ASO-3[C]	2´-OMe	PS	PS	5-10-5	$U^{O}*G^{O}*U^{O}*C^{O}*A^{O}*g*t*t*t*c*t*c*c*c*t*G^{O}*A^{O}*A^{O}*C^{O}*A^{O}$	SEQ ID NO:364
ASO-4[C]	2´-OMe	PS	PS	5-10-5	$U^{O}*A^{O}*G^{O}*A^{O}*A^{O}*t*g*g*c*a*c*a*t*c*t*C^{O}*U^{O}*U^{O}*G^{O}*G^{O}$	SEQ ID NO:365
ASO-5[C]	2´-OMe	PS	PS	5-10-5	$G^{O}*U^{O}*U^{O}*U^{O}*U^{O}*c*t*t*c*c*t*c*c*a*c*A^{O}*G^{O}*U^{O}*C^{O}*U^{O}$	SEQ ID NO:366
ASO-6[C]	2´-OMe	PS	PS	5-10-5	$C^{O}*U^{O}*G^{O}*G^{O}*U^{O}*g*t*c*a*a*c*a*a*g*c*C^{O}*A^{O}*A^{O}*A^{O}*G^{O}$	SEQ ID NO:367

Abbreviations: [C], conserved with macaque & non-polymorphic; capital letter, RNA nucleotide; lower-case letter, DNA nucleotide; [O], 2´-OMe; PS & *, phosphorothioate

Table 8. Analysis of Human ASOs on *UBE3A-AS* and *UBE3A* RNA levels

UBE3A-AS					
ASO 1	ASO 2	Difference	Lower CI	Upper CI	Adj. P
ASO-C	ASO-2	0.89	0.82	0.97	<.0001
ASO-R	ASO-2	0.87	0.80	0.95	<.0001
ASO-C	ASO-4	0.87	0.80	0.95	<.0001
ASO-R	ASO-4	0.85	0.78	0.93	<.0001

ASO-C	ASO-6	0.83	0.75	0.90	<.0001
ASO-R	ASO-6	0.81	0.74	0.89	<.0001
ASO-C	ASO-3	0.79	0.71	0.86	<.0001
ASO-R	ASO-3	0.77	0.70	0.85	<.0001
ASO-C	ASO-5	0.71	0.63	0.78	<.0001
ASO-R	ASO-5	0.69	0.62	0.77	<.0001
ASO-C	Topo	0.66	0.59	0.73	<.0001
ASO-R	Topo	0.64	0.57	0.72	<.0001
ASO-C	ASO-1	0.51	0.43	0.58	<.0001
ASO-R	ASO-1	0.49	0.41	0.56	<.0001
ASO-1	ASO-2	0.38	0.31	0.46	<.0001
ASO-1	ASO-4	0.36	0.29	0.44	<.0001
ASO-1	ASO-6	0.32	0.25	0.40	<.0001
ASO-1	ASO-3	0.28	0.21	0.36	<.0001
Topo	ASO-2	0.23	0.16	0.31	<.0001
Topo	ASO-4	0.21	0.14	0.29	<.0001
ASO-1	ASO-5	0.20	0.13	0.28	<.0001
ASO-5	ASO-2	0.18	0.11	0.26	<.0001
Topo	ASO-6	0.17	0.10	0.24	0.0002
ASO-5	ASO-4	0.16	0.09	0.24	0.0003
ASO-1	Topo	0.15	0.08	0.23	0.0004
Topo	ASO-3	0.13	0.06	0.20	0.0018
ASO-5	ASO-6	0.12	0.04	0.20	0.0035
ASO-3	ASO-2	0.10	0.03	0.18	0.0111
ASO-3	ASO-4	0.08	0.01	0.16	0.0360
ASO-5	ASO-3	0.08	0.00	0.15	0.0381
ASO-6	ASO-2	0.06	-0.01	0.14	0.11
Topo	ASO-5	0.05	-0.02	0.13	0.18
ASO-6	ASO-4	0.04	-0.03	0.12	0.27
ASO-3	ASO-6	0.04	-0.03	0.12	0.28
ASO-4	ASO-2	0.02	-0.06	0.09	0.58

ASO-C	ASO-R	0.02	-0.06	0.09	0.64
UBE3A					
ASO 1	ASO 2	Difference	Lower CI	Upper CI	Adj. P
ASO-4	ASO-C	0.30	0.16	0.44	0.0004
ASO-4	ASO-R	0.29	0.14	0.45	0.001
ASO-2	ASO-C	0.21	0.09	0.34	0.002
ASO-2	ASO-R	0.21	0.07	0.35	0.006
ASO-1	ASO-C	0.18	0.06	0.31	0.007
Topo	ASO-C	0.18	0.04	0.32	0.01
ASO-1	ASO-R	0.18	0.04	0.32	0.02
Topo	ASO-R	0.18	0.03	0.33	0.02
ASO-4	ASO-3	0.17	0.03	0.31	0.02
ASO-5	ASO-C	0.16	0.04	0.29	0.01
ASO-6	ASO-C	0.16	0.04	0.29	0.01
ASO-5	ASO-R	0.16	0.02	0.30	0.03
ASO-6	ASO-R	0.16	0.02	0.30	0.03
ASO-4	ASO-6	0.13	-0.007	0.27	0.06
ASO-4	ASO-5	0.13	-0.007	0.27	0.06
ASO-3	ASO-C	0.13	0.00	0.26	0.04
ASO-3	ASO-R	0.13	-0.015	0.27	0.08
ASO-4	Topo	0.11	-0.04	0.27	0.1
ASO-4	ASO-1	0.11	-0.03	0.25	0.1
ASO-2	ASO-3	0.08	-0.04	0.21	0.2
ASO-4	ASO-2	0.08	-0.06	0.22	0.2
ASO-1	ASO-3	0.05	-0.07	0.18	0.4
Topo	ASO-3	0.05	-0.09	0.19	0.4
ASO-2	ASO-6	0.05	-0.08	0.18	0.4
ASO-2	ASO-5	0.05	-0.08	0.17	0.4
ASO-5	ASO-3	0.03	-0.09	0.16	0.6
ASO-6	ASO-3	0.03	-0.09	0.16	0.6
ASO-2	Topo	0.03	-0.1	0.17	0.7

ASO-2	ASO-1	0.03	-0.01	0.16	0.6
ASO-1	ASO-6	0.02	-0.1	0.15	0.7
Topo	ASO-6	0.02	-0.1	0.16	0.8
ASO-1	ASO-5	0.02	-0.1	0.15	0.7
Topo	ASO-5	0.02	-0.1	0.16	0.8
ASO-R	ASO-C	0.00	-0.1	0.14	0.9
ASO-5	ASO-6	0.00	-0.1	0.13	0.9
ASO-1	Topo	0.00	-0.1	0.14	1.00

Abbreviations: ASO-C, ASO-control; Topo, Topotecan; Adj., Adjusted; CI, 95% confidence interval

Table 9. IC_{50} and E_{max} of ASO-4 and Topotecan

Treatment	IC_{50} Estimate (M)	IC_{50} 95% CI (M)		E_{max} Estimate	E_{max} 95% CI		30 µM (Mean)
ASO-4	6.13E-07	3.47E-07	1.08E-06	-0.06	-0.23	0.10	0.09
Topo	3.37E-08	1.85E-08	6.14E-08	0.26	0.20	0.32	0.21

Full model parameter estimates from 4-parameter logistic regression model (Hill). IC_{50} and confidence intervals represent molar concentration. E_{max} and 30 uM values represent normalized *UBE3A-AS* RNA levels relative to vehicle.

Table 10. Analysis of ASO-4 and Topotecan on *UBE3A*, *SNORD116*, *SNORD115*, *SNORD109A/B*, and *IPW* RNA Levels

Treatment	RNA	DF	DFDen	F Ratio	FDR
ASO-4	UBE3A	9	108	16.5	< 0.0001
	SNORD109A/B	9	104.9	2.6	0.01
	SNORD115	9	108	4.0	0.0002
	SNORD116	9	108	1.74	0.09
	IPW	9	108	4.1	0.0002
Topotecan	UBE3A	9	29	5.6	0.0002
	SNORD109A/B	9	29	28.2	< 0.0001
	SNORD115	9	29	4.60	0.001
	SNORD116	9	29	7.12	< 0.0001
	IPW	9	29	49.8	< 0.0001

Least squares linear regression. Abbreviations: DF, degrees of freedom; DFDen, degrees of freedom density

Table 11. Optimized Human *UBE3A-AS* Antisense Oligonucleotides

ASO	RNA Modification	RNA Backbone	DNA Backbone	Design (5´-3´)	Sequence	SEQ ID
ASO-3.1[C]	2´-OMe	PS	PS	4-10-5	G^{O}*U^{O}*U^{O}*G^{O}*a*g*t*g*g*t*g*t*c*a*G^{O}*U^{O}*U^{O}*U^{O}*C^{O}	SEQ ID NO:368
ASO-3.2[C]	2´-OMe	PS	PS	4-10-4	U^{O}*U^{O}*G^{O}*A^{O}*g*t*g*g*t*g*t*c*a*g*U^{O}*U^{O}*U^{O}*C^{O}	SEQ ID NO:369
ASO-6.1[C]	2´-OMe	PS	PS	4-10-4	C^{O}*U^{O}*G^{O}*G^{O}*t*g*t*c*a*a*c*a*a*g*C^{O}*C^{O}*A^{O}*A^{O}	SEQ ID NO:370
ASO-4.1[C]	2´-OMe	PS	PS	5-10-5	A^{O}*U^{O}*A^{O}*G^{O}*A^{O}*a*t*g*g*c*a*c*a*t*c*U^{O}*C^{O}*U^{O}*U^{O}*G^{O}	SEQ ID NO:371
ASO-4.2[C]	2´-OMe	PS	PS	4-10-5	A^{O}*G^{O}*A^{O}*A^{O}*t*g*g*c*a*c*a*t*c*t*C^{O}*U^{O}*U^{O}*G^{O}*G^{O}	SEQ ID NO:372
ASO-4.3[C]	2´-OMe	PS	PS	4-10-5	U^{O}*A^{O}*G^{O}*A^{O}*a*t*g*g*c*a*c*a*t*c*U^{O}*C^{O}*U^{O}*U^{O}*G^{O}	SEQ ID NO:373
ASO-4.4[C]	2´-OMe	PS	PS	4-10-4	A^{O}*G^{O}*A^{O}*A^{O}*t*g*g*c*a*c*a*t*c*t*C^{O}*U^{O}*U^{O}*G^{O}	SEQ ID NO:374

[C], conserved with macaque & non-polymorphic; capital letter, RNA nucleotide; lower-case letter, DNA nucleotide; O, 2´-OMe; PS & *, phosphorothioate

Table 12. IC_{50} and E_{max} of Optimized ASO Target Sequences

Group	IC_{50} Estimate	IC_{50} 95% CI (M)		3 µM (Mean)
6.1	5.20E-07	3.33E-07	8.11E-07	0.23
4.0	1.06E-06	9.31E-07	1.21E-06	0.29
4.2	1.08E-06	8.62E-07	1.35E-06	0.31
3.2	1.88E-06	1.39E-06	2.56E-06	0.44
4.3	2.03E-06	1.67E-06	2.47E-06	0.40
4.4	2.11E-06	1.73E-06	2.59E-06	0.44
4.1	2.27E-06	1.92E-06	2.68E-06	0.42
3.1	2.98E-06	2.45E-06	3.62E-06	0.51

Full model parameter estimates from 3-parameter logistic regression model. IC_{50} and confidence intervals represent molar concentration. E_{max} (3 uM) values represent normalized *UBE3A-AS* RNA levels relative to vehicle.

Table 13. Relative Potency of Optimized ASOs

ASO	IC_{50} (M)	Relative Potency	Std. Error
ASO 3.1	2.81E-06	0.53	0.059
ASO 3.2	1.85E-06	0.81	0.086
ASO 4.1	2.25E-06	0.66	0.072
ASO 4.2	1.24E-06	1.21	0.13
ASO 4.3	1.96E-06	0.76	0.081
ASO 4.4	2.04E-06	0.73	0.079
ASO 6.1	7.20E-07	2.07	0.21
ASO 4.I	8.28E-07	1.80	0.19
ASO 4.S	1.49E-06	1	0

Parallel model parameter estimates from 3-parameter logistic regression model. Potency represents molar concentration. Abbreviations: M, molar; Std. Error, standard error of mean.

Table 14. IC_{50} and E_{max} of ASO-4 and ASO-6.1 in GABAergic iPSC Neurons

ASO	IC_{50} Estimate	IC_{50} 95% CI (M)		E_{max} Estimate	E_{max} 95% CI		30 µM (Mean)
ASO-4	7.77E-07	6.86E-07	8.79E-07	0.08	0.05	0.11	0.11
ASO-6.1	5.17E-07	3.41E-07	7.82E-07	-0.11	-0.22	0.01	0.06

Full model parameter estimates from 4-parameter logistic regression model (Hill). IC_{50} and confidence intervals represent molar concentration. E_{max} and 30 uM values represent normalized *UBE3A-AS* RNA levels relative to vehicle.

Table 15. IC_{50} and E_{max} of ASO-4 and ASO-6.1 in Glutamatergic iPSC Neurons

ASO	IC_{50} Estimate	IC_{50} 95% CI (M)		E_{max} Estimate	E_{max} 95% CI		30 µM (Mean)
ASO-4	1.21E-04	1.12E-13	1.32E+05	-1.45	-9.01	6.12	0.17
ASO-6.1	2.44E-07	2.39E-08	2.50E-06	-0.27	-1.24	0.70	0.04

Full model parameter estimates from 4-parameter logistic regression model (Hill). IC_{50} and confidence intervals represent molar concentration. E_{max} and 30 uM values represent normalized *UBE3A-AS* RNA levels relative to vehicle.

Table 16. Relative Potency of ASO-4 and ASO-6.1 in Glutamatergic Neurons

ASO	IC_{50} (M)	Relative Potency	Std. Error
ASO-4	3.06E-06	1	0
ASO-6.1	7.8E-07	3.89	0.72

Parallel model parameter estimates from 4 Parameter logistic regression model. Abbreviations: M, molar

Table 17. Derivatives of ASO-4 and ASO-6.1

ASO	RNA Mod.	Backbone	PO linkages	Design (5'-3')	Sequence (5´-3´)	SEQ ID
ASO-4.0.PS.O	OMe	PS	0	5-10-5	$U^{O}*A^{O}*G^{O}*A^{O}*A^{O}*t*g*g*c*a*c*a*t*c*t*C^{O}*U^{O}*U^{O}*G^{O}*G^{O}$	SEQ ID NO:375
ASO-4.0.PO-1.O	OMe	PS/PO	2	5-10-5	$U^{O}*A^{O}*G^{O}*A^{O}*A^{O}-t*g*g*c*a*c*a*t*c*t-C^{O}*U^{O}*U^{O}*G^{O}*G^{O}$	SEQ ID NO:376
ASO-4.0.PO-2.O	OMe	PS/PO	0	5-10-5	$U^{O}*A^{O}-G^{O}*A^{O}-A^{O}*t-g*g-c*a-c*a-t*c-t*C^{O}-U^{O}*U^{O}-G^{O}*G^{O}$	SEQ ID NO:377
ASO-4.0.PS.M	MOE	PS	0	5-10-5	$T^{M}*A^{M}*G^{M}*A^{M}*A^{M}*t*g*g*c*a*c*a*t*c*t*5mC^{M}*T^{M}*T^{M}*G^{M}*G^{M}$	SEQ ID NO:378
ASO-4.0.PO-1.M	MOE	PS/PO	2	5-10-5	$T^{M}*A^{M}*G^{M}*A^{M}*A^{M}-t*g*g*c*a*c*a*t*c*t-5mC^{M}*T^{M}*T^{M}*G^{M}*G^{M}$	SEQ ID NO:379
ASO-4.0.PO-2.M	MOE	PS/PO	9	5-10-5	$T^{M}*A^{M}-G^{M}*A^{M}-A^{M}*t-g*g-c*a-c*a-t*c-t*5mC^{M}-T^{M}*T^{M}-G^{M}*G^{M}$	SEQ ID NO:380
ASO-4.4.PS.L	LNA	PS	0	3-11-4	$A^{L}*G^{L}*A^{L}*a*t*g*g*c*a*c*a*t*c*t*5mC^{L}*T^{L}*T^{L}*G^{L}$	SEQ ID NO:381
ASO-4.4.PO-1.L	LNA	PS/PO	2	3-11-4	$A^{L}*G^{L}*A^{L}-a*t*g*g*c*a*c*a*t*c*t-5mC^{L}*T^{L}*T^{L}*G^{L}$	SEQ ID NO:382
ASO-4.4.PO-2.L	LNA	PS/PO	8	3-11-4	$A^{L}*G^{L}-A^{L}*a-t*g-g*c-a*c-a*t-c*t-5mC^{L}*T^{L}-T^{L}*G^{L}$	SEQ ID NO:383
ASO-6.1.PS.O	OMe	PS	0	4-10-4	$C^{O}*U^{O}*G^{O}*G^{O}*t*g*t*c*a*a*c*a*a*g*C^{O}*C^{O}*A^{O}*A^{O}$	SEQ ID NO:384
ASO-6.1.PO-1.O	OMe	PS/PO	2	4-10-4	$C^{O}*U^{O}*G^{O}*G^{O}-t*g*t*c*a*a*c*a*a*g-C^{O}*C^{O}*A^{O}*A^{O}$	SEQ ID NO:385
ASO-6.1.PO-2.O	OMe	PS/PO	8	4-10-4	$C^{O}*U^{O}-G^{O}*G^{O}-t*g-t*c-a*a-c*a-a*g-C^{O}*C^{O}-A^{O}*A^{O}$	SEQ ID NO:386
ASO-6.1.PS.M	MOE	PS	0	4-10-4	$5mC^{M}*T^{M}*G^{M}*G^{M}*t*g*t*c*a*a*c*a*a*g*5mC^{M}*5mC^{M}*A^{M}*A^{M}$	SEQ ID NO:387
ASO-6.1.PO-1.M	MOE	PS/PO	2	4-10-4	$5mC^{M}*T^{M}*G^{M}*G^{M}-t*g*t*c*a*a*c*a*a*g-5mC^{M}*5mC^{M}*A^{M}*A^{M}$	SEQ ID NO:388
ASO-6.1.PO-2.M	MOE	PS/PO	8	4-10-4	$5mC^{M}*T^{M}-G^{M}*G^{M}-t*g-t*c-a*a-c*a-a*g-5mC^{M}*5mC^{M}-A^{M}*A^{M}$	SEQ ID NO:389
ASO-6.1.PS.L	LNA	PS	0	3-10-4	$T^{L}*G^{L}*G^{L}*t*g*t*c*a*a*c*a*a*g*5mC^{L}*5mC^{L}*A^{L}*A^{L}$	SEQ ID NO:390
ASO-6.1.PO-1.L	LNA	PS/PO	2	3-10-4	$T^{L}*G^{L}*G^{L}-t*g*t*c*a*a*c*a*a*g-5mC^{L}*5mC^{L}*A^{L}*A^{L}$	SEQ ID NO:391
ASO-6.1.PO-2.L	LNA	PS/PO	8	3-10-4	$T^{L}*G^{L}-G^{L}*t-g*t-c*a-a*c-a*a-g*5mC^{L}-5mC^{L}-A^{L}*A^{L}$	SEQ ID NO:392

Capital letter, RNA; lower-case letter, DNA. 5mC, 5-methylcytosine. Superscript: O, 2´-OMe; M, 2´-MOE; L, LNA. PS & *, phosphorothioate; PO & -, phosphodiester

Materials and Methods

Antisense oligonucleotide design

Antisense oligonucleotides (ASOs) were designed using Soligo (Software for Statistical Folding of Nucleic Acids and Studies of Regulatory RNAs). Briefly, candidate ASOs (20- 18mer) with the lowest binding site disruption energy and free binding energy were identified for each target sequence and then inspected for motifs with increased effectiveness. ASOs were further filtered based on accessibility within predicted lowest free energy centroid secondary structure of target sequence generated by Soligo. In some instances, secondary structure models were compared using lowest free energy structures generated by RNAfold and Mfold.

Human ASOs were filtered using the following criteria: 1) target sequence was polymorphic [dbSNP138, dbSNP150, and 1000 Genomes Phase 3 Integrated Variant Calls (SNV, INDEL, and SV)]; 2) target sequence was not 100% conserved with Rhesus and Cynomolgus macaque; 3) target sequence was located upstream of retained *Snord115/SNORD115* snoRNA (per exon). Remaining ASOs were then ranked by free energy (<= -8 kcal/mol), average unpaired probability for target site nucleotides, binding site disruption energy (low>high), location within secondary structure (Ensembl Centroid), and presence/absence of sequence motifs associated with high/low effectiveness.

Mouse primary hippocampal neurons

Primary cultures of hippocampal neurons were generated from P0-P1 pups (*Ube3a*$^{m+/p+}$ and *Ube3a*$^{m+/pYFP}$) by crossing *Ube3a*$^{m+/pYFP}$ males with wild-type C57BL/6J females. Genotypes were determined using methods described previously. Briefly, hippocampal neurons were cultured in Neurobasal A medium (Invitrogen, San Diego, CA) supplemented with B27 (Invitrogen) and penicillin/streptomycin (Invitrogen) on 96-well optical bottom plates coated with poly-D-Lysine (152028, Thermo Fisher Scientific) and laminin (23017-01, Thermo Fisher Scientific). Cultures were maintained at 37°C in 5% CO_2 until use.

Mouse Neuron Imaging

Mouse primary hippocampal neurons were fixed at 10 DIV (3 days post treatment) with 4% paraformaldehyde. The cultures were then washed twice with 1X PBS, fixed in 4% paraformaldehyde in PBS for 15 min, and then washed three times in 1X PBS. The cells were blocked in 0.3% Triton-X100 in PBS (T-PBS) plus 5% goat or donkey serum for 1-2 hr at room temperature with gentle agitation. Cells were incubated with anti-GFP [Novus Biologicals, NB 600-308 (rabbit)] and anti-NeuN (Millipore, 05-557 (mouse)] antibodies for 24 hr at 4°C with gentle agitation. Cells were washed 3 times in 0.1% Tween 20 1X PBS for 15 min each and then incubated with anti-rabbit 488 (Jackson ImmunoResearch, 111-545-144) and anti-mouse Cy3 (Jackson ImmunoResearch, 115-165-166) secondary antibodies for 24 hr at 4°C in the dark. Cells were then washed 4 times in 0.1% Tween 20 1X PBS for 15 min each. Nuclei were labeled using Hoechst stain (Thermo Fisher Scientific) at a dilution of 1:1000 in the third wash.

Plates were imaged using the Cytation 5 and Gen5 Image+ software (BioTek, Winooski, VT). Briefly, a 4X inverted objective was used to generate montage images of each well by acquiring 5x4 autofocused images with overlapping tiles for automatic image stitching. The filters used were DAPI (377,477), GFP (469, 525), and RFP (531, 593). Exposure time and gain were adjusted for each plate using the negative and positive controls. Auto-focus was performed on nuclei (Hoechst stain, DAPI) for each well, with the same focal height used for the GFP and RFP filters. Images were stitched together by Gen5 Image+ software.

Single cell image analysis was performed using IN Cell Developer 6.0 (GE Healthcare Life Sciences, Pittsburgh, PA). Briefly, individual track masks were generated for either nuclei (Hoechst stain, DAPI) or mature neurons (NeuN, RFP) by optimizing inclusion and exclusion parameters based on size and intensity of randomly selected cells in the acquired images. The mean and median intensity values of GFP were then acquired within the boundaries of the selected mask, generating intensity values for Ube3aYFP within each cell.

Human induced pluripotent stem cell derived neurons

GABAergic and glutamatergic induced pluripotent stem cell (iPSC) derived neural precursor cells (NRC-100-010-001and GNC-301-030-001, Cellular Dynamics International, Madison WI) were differentiated into neurons according to the manufactures protocol. Briefly, neural precursor cells were thawed and resuspended in chemically defined medium and added to sterile-culture plates coated with poly-D-lysine and laminin. The medium was replaced 24 hr after plating and then one-half of the medium was replaced every 3-5 days afterwards.

RNA Isolation

For cultured iPSC-derived neurons, RNA isolation and cDNA synthesis were performed using the Cell-to-CT kit (Thermo Fisher Scientific) in a lysate volume of 55 µl.

Analysis of RNA levels

The steady state RNA levels of target transcripts were measured using TaqMan quantitative reverse-transcription PCR (qRT-PCR) assays. Total reaction volume was 10 uL, including 2 µl of cDNA, 1X Gene Expression Master mix (4369016, Thermo Fisher Scientific, Waltham, MA), and 1X TaqMan primer assay (Thermo Fisher Scientific). Cycling conditions were 2 minutes at 50°C, 10 minutes at 95°C, and 40 cycles of 15 seconds at 95°C and 1 minute at 60°C, with readings taken at the 60°C step of every cycle. Reactions were run on a BIO-RAD T1000 CFX96 thermocycler (Bio-Rad Laboratories, Hercules CA), with internal control (*PPIA*, Hs99999904_m1, Thermo Fisher Scientific) and target [*UBE3A-AS*, Hs01372957_m1; SNORD116-11, Hs04275268_gH; SNORD115, Hs04275288_gH; IPW, Hs03455409_s1; SNORD109A/B, AP47WVR (Thermo Fisher Scientific); *UBE3A*: forward ATATGTGGAAGCCGGAATCT (SEQ ID NO:500); reverse: CCCAGAACTCCCTAATCAGAA (SEQ ID NO:501); and, probe: ATGACGGTGGCTATACCAGG (SEQ ID NO:502)] reactions performed together. Data was retrieved and analyzed with the BIORAD CFX Maestro software (Bio-Rad Laboratories). Samples with internal control Cq values ≥ 30 were filtered. Quality of data was visually inspected to identify discrepancies between technical and/or plate replicates. Measurements for inferential statistics and descriptive statistics consist of $\Delta\Delta$Cq values ($2^{-\Delta\Delta Cq} = 2^{-(Cq[target] - Cq[internal\ control]) - (Cq[target] - Cq[internal\ control])}$).

Example 2: Identification of ASO target region

Analysis of RNA-sequencing data generated from mouse tissues and cells revealed a region located between the 3'-end of the *Snord115* cluster and 5'-end of the *Ube3a* antisense (*Ube3a-AS*) transcript containing genetic elements believed to be important for processing of the *Snord115* host-gene transcript and transcription of *Ube3a-AS* (Figures 6A - 6D). Analysis of RNA-sequencing data generated from human tissues revealed a region located between the 3'-end of the *SNORD115* cluster and *SNORD109B* (Figures 7A - 7G) that contained elements similar to those observed in mouse; however, comparative analysis of this region indicated that there was little to no sequence conservation between human and rodents.

Materials and Methods

RNA-sequencing

RNA was isolated using Qiagen RNAeasy Plus (74136, Qiagen, Hilden, Germany). RNA concentration was determined using Qubit Fluorometric Quantitation (Thermo Fisher Scientific) and RNA quality was assessed using a 4200 Agilent TapeStation (Agilent, Santa Clara, CA). RNA-sequencing libraries were generated using the Illumina TruSeq Stranded Total RNA kit (20020597, Illumina, Inc., San Diego, CA) according to the manufacturer's protocol. 75 base-pair pairedend sequencing was performed using a NextSeq 500 (Illumina, San Diego, CA) at the Texas A&M Institute for Genome Sciences and Society Genomics core. Raw sequencing reads were processed using CASAVA. The resulting FASTQ sequences were examined using FASTQC.

FASTQ sequences were aligned to the human reference assembly (hg19) using Hisat2 (version 2.1.0), with the following settings: --fr. Aligned SAM sequences were then converted to binary BAM sequences, indexed, and sorted using Samtools. BAM files from individual samples were merged and indexed using Samtools. Aligned sequences were filtered using the view command in Samtools to remove non-uniquely aligned reads (quality > 1).

A transcript assembly was generated for merged samples using Stringtie (version 1.3.4.d), with the following options: (stranded) --rf -f 0 -j 2. Single exon transcripts were excluded from the assembled transcripts using gffread (GFF utilities, Johns Hopkins University, Center for Computational Biology).

Example 3: Identification of lead ASOs

Eighteen ASOs targeting the ASO-4 and ASO-6.1 target sequences and consisting of different backbone designs and RNA modifications were designed to identify potential lead ASOs (Table 17). Normal iPSC derived-neurons (GABAergic) were treated with a 10-point ½ log dose response curve of each ASO to compare the IC_{50} and E_{max} values. Neural precursor cells were differentiated into neurons for at 18 DIV and then treated with a 10-point ½ log dose response ASOs [1 nM, 3 nM, 10 nM, 30 nM, 100 nM, 300 nM, 1 μM, 3 μM, 10 μM, and 30 μM (n = 2)]. At 24 DIV, the steady state RNA levels of *UBE3A-AS* were measured and dose response curves fitted as described above (Figure 8A and Table 18). The dose response curves were significantly different (Parallelism test: $F_{(51,606)} = 7.86$; $p < 0.0001$; $R^2 = 0.90$), thus relative potencies were not estimated. Hierarchical clustering of the fitted curves revealed 3 Clusters of ASOs, with Cluster 1 representing the 9 most potent ASOs (Figures 8B and 8C). Analysis of Cluster 1 indicated that the ASOs had similar curves (Parallelism test: $F_{(24,299)} = 1.01$; $p = 0.5$; $R^2 = 0.93$), and that ASO-4.4.PS.L was at least 3-times as potent as the other ASOs (Table 19). Further analysis, however, indicated that ASO-4.4.PS.L, ASO-6.1.PS.M, and ASO-6.1.PO-1.M had equivalent IC_{50} values, whereas the other ASOs were slightly less potent (Table 20). Based on the relative potencies and internal selection criteria, ASO-4.4.PS.L and ASO-6.1.PO-1.O were investigated further.

Table 18. IC_{50} and E_{max} of Candidate ASOs

ASO	IC_{50} (M)	IC_{50} 95% CI (M)		E_{max}	E_{max} 95% CI		30 µM (Mean)	Cluster
ASO-4.4.PS.L	2.66E-08	3.66E-09	1.93E-07	0.0	-0.23	0.23	0.05	1
ASO-6.1.PS.M	1.47E-07	6.80E-08	3.19E-07	-0.05	-0.21	0.12	0.02	1
ASO-6.1.PO-1.M	1.66E-07	7.15E-08	3.84E-07	-0.02	-0.20	0.16	0.04	1
ASO-4.4.PO-1.L	2.26E-07	8.95E-08	5.71E-07	0.04	-0.17	0.25	0.1	1
ASO-4.0.PO-1.M	2.78E-07	1.52E-07	5.08E-07	0.02	-0.11	0.15	0.05	1
ASO-4.0.PS.M	3.00E-07	1.80E-07	5.00E-07	0.05	-0.06	0.15	0.05	1
ASO-6.1.PO-1.O	3.15E-07	7.98E-08	1.24E-06	-0.1	-0.50	0.26	0.04	1
ASO-6.1.PS.L	3.62E-07	1.37E-07	9.57E-07	-0.07	-0.32	0.18	0.04	1
ASO-6.1.PS.O	5.32E-07	1.20E-07	2.36E-06	-0.2	-0.67	0.29	0.05	1
ASO-6.1.PO-2.L	7.34E-07	5.35E-08	1.01E-05	0.3	-0.11	0.76	0.4	2
ASO-4.0.PO-1.O	7.66E-07	3.70E-07	1.59E-06	0.05	-0.12	0.23	0.1	2
ASO-4.0.PS.O	1.27E-06	5.13E-07	3.13E-06	0.06	-0.20	0.31	0.1	2
ASO-6.1.PO-1.L	1.89E-06	4.42E-07	8.06E-06	0.03	-0.34	0.39	0.2	2
ASO-4.0.PO-2.O	1.30E-04	1.65E-17	1.03E+09	-0.3	-9.51	8.94	0.6	2
ASO-6.1.PO-2.M	2.69E-04	9.85E-16	7.37E+07	-1.2	-13.16	10.77	0.3	2
ASO-4.4.PO-2.L	3.27E+01	0	Inf	-2.7	-577	571	0.6	3
ASO-4.0.PO-2.M	1.14E+05	0	Inf	-76	-74,958.	74,805	0.5	3
ASO-6.1.PO-2.O	1.93E+10	0	Inf	-5569	-85,963,650	85,952,510	0.3	3

Full model parameter estimates from 4-parameter logistic regression model (Hill). IC50 and confidence intervals represent molar concentration. Emax and 30 uM values represent normalized UBE3A-AS RNA levels relative to vehicle.
Abbreviations: Inf, infinity; 95% CI, 95% confidence intervals

Table 19. Relative potency of ASOs in Cluster 1

ASO	IC_{50} (M)	Relative Potency	Std Error
ASO-4.4.PS.L	5.03E-08	1	0
ASO-6.1.PS.M	1.53E-07	0.3	0.08
ASO-6.1.PO-1.M	1.77E-07	0.3	0.07
ASO-6.1.PO-1.O	1.99E-07	0.3	0.06
ASO-4.0.PS.M	2.62E-07	0.2	0.05
ASO-4.0.PO-1.M	2.78E-07	0.2	0.04
ASO-6.1.PS.L	2.81E-07	0.2	0.04
ASO-4.4.PO-1.L	3.22E-07	0.2	0.04
ASO-6.1.PS.O	4.32E-07	0.1	0.03

Parallel model parameter estimates from 4 Parameter logistic regression model (Hill).
Abbreviations: M, molar; Std, standard

Table 20. Equivalence of ASOs in Cluster 1 Relative to ASO-4.4.PS.L

ASO	ASO	IC_{50} Ratio	Lower and Upper Confidence Limits		Limit Exceeded
ASO-4.4.PS.L	ASO-6.1.PO-1.M	0.90	0.81	0.98	Equivalent
	ASO-6.1.PS.M	0.90	0.82	0.98	Equivalent
	ASO-4.0.PO-1.M	0.87	0.79	0.94	Lower
	ASO-4.0.PS.M	0.86	0.79	0.94	Lower
	ASO-4.4.PO-1.L	0.88	0.79	0.96	Lower
	ASO-6.1.PO-1.O	0.86	0.77	0.95	Lower
	ASO-6.1.PS.L	0.85	0.77	0.93	Lower
	ASO-6.1.PS.O	0.83	0.73	0.92	Lower

Two one-sided Tests

Materials and Methods

Methods were similar to those described in Example 2 unless noted otherwise.

Example 4: Pharmacodynamic analysis of ASO-6.1-PO-1.O and ASO-4.4.PS.L in Angelman syndrome iPSC neurons

The potencies of ASO-6.1.PS.O and ASO-4.4.PS.L were then examined in iPSC derived-neurons from an Angelman syndrome patient with a maternal derived deletion of the 15q11-q13 region. Induced pluripotent stem cells were differentiated into neurons and then treated with a 10-point ½ log dose response curve of ASO-6.1.PO-1.O and ASO-4.4.PS.L [1 nM, 3 nM, 10 nM, 30 nM, 100 nM, 300 nM, 1 µM, 3 µM, 10 µM, and 30 µM (n = 3)]. Six days following treatment, the steady state RNA levels of *UBE3A-AS* were measured and dose response curves were fitted as described above (Figure 9A). The dose response curves were similar between ASOs (Parallelism test: $F_{(3,132)} = 1.07$, $p = 0.4$, $R^2 = 0.82$), with ASO-4.4.PS.L (437 nM) being approximately 2.7-fold more potent than ASO-6.1.PO-1.O (1.22 uM). The IC_{50} values were equivalent [ASO-6.1.PO-1.O /ASO-4.4.PS.L IC_{50} ratio: = 0.96 (Lower confidence limit = 0.9; Upper confidence limit = 1.0)]. The E_{max} values were similar (30 µM: ASO-4.4.PS.L = 0.01 ± 0.0007; ASO-6.1.PO-1.O = 0.05 ± 0.004) but not considered equivalent due to the confidence intervals [ASO-6.1.PO-1.O /ASO-4.4.PS.L E_{max} ratio: = -9.1 (Lower confidence limit = -224; Upper confidence limit = 205)].

Materials and Methods

Methods were similar to those described in Example 2 unless noted otherwise.

Angelman syndrome induced pluripotent stem cells derived neurons

Angelman syndrome iPS cells (AG1-0 iPSCs) (ECN001, Kerafast, Boston, MA) were co-cultured on irradiated murine embryonic fibroblasts in human embryonic stem cell medium [DMEM/F12 (11330-057, Gibco Biosciences, Dublin, Ireland), 20% Knockout Serum Replacement (10828-028, Thermo Fisher Scientific), 1X Non-essential amino acids, 2 mM L-glutamine, 7 µl/mL 2-Mercaptoethanol, and 4 µg/mL basic Fibroblast Growth Factor]. For the first passage, AG1-0 cells were passaged according to the product manual for PluriSTEM Human ES/iPS Medium (SCM130, Millipore Sigma, Burlington, MA), which is feeder-free and utilizes Dispase II (SCM133, Millipore Sigma) to dissociate cells. Matrigel™ hESC-qualified Matrix (354277, Corning BD Biosciences, Corning, NY) was used as an extracellular matrix. At the second passage, the matrix was switched to vitronectin (CC130, Millipore Sigma). During subsequent passages, areas of differentiation were manually removed until differentiated cells represented approximately < 5% of the colonies. After four subsequent passages, AG1-0 cells were differentiated using the Millipore ES/iPS Neurogenesis Kit (SCR603, SCM110, and SCM111) but lacking vitronectin as an extracellular matrix. The initial passage was performed with EZ-LiFT (SCM139, Millipore Sigma) to obtain high quality iPS cells. Neural progenitor cells were frozen at stage zero (P_0) and subsequently thawed for differentiation. Differentiation was performed on sterile culture plates coated with poly-D-lysine (10 µg/mL) and laminin [10 µg/mL (23017-015, Gibco) in differentiation medium (SCM111) for 10 days of differentiation. In some instances, cells were differentiated in Cellular Dynamics Maintenance Medium (NRM-100-121-001, Cellular Dynamics International, Madison, WI).

Example 5: Expression analysis of the PWS polycistronic transcript in Angelman syndrome iPSC neurons treated with ASO-6.1-PO-1.O and ASO-4.4.PS.L

To determine whether ASO-4.4.PS.L and ASO-6.1.PO-1.O affect the levels of RNA transcripts encoded by the PWS polycistronic transcript, RNA-sequencing was performed on AS iPS cells treated with each ASO and the steady state RNA levels of *SNURF*, *SNRPN*, the *SNORD116* host-gene transcript (*SNHG116*), the *SNORD116* snoRNAs, *IPW*, the *SNORD115* host-gene transcript (*SNHG115*), the *SNORD115* snoRNAs, and *UBE3A-AS* were quantified. *UBE3A* steady state RNA levels were also measured. Angelman syndrome iPS cells were differentiated into neurons as described above and then treated with vehicle (1% H2O, n = 3), ASO-4.4.PS.L (30 u µM, n = 3) and ASO-6.1.PO-1.O (30 µM, n = 3). Six days post-treatment, RNA RNA-sequencing was performed on total RNA (rRNA depleted) isolated from the cultures. To generate annotations of the *SNHG116*, *SNHG115*, and *UBE3A-AS* transcripts, a transcriptome was assembled from the vehicle RNA-seq data and then incorporated into the reference gene annotation. Relative to vehicle, the steady state RNA levels of *SNURF*, *SNRPN*, *SNHG116*, the *SNORD116* snoRNAs, and the *SNORD115* snoRNAs were similar and not significantly different. ASO-4.4.PS.L, but not ASO-6.1.PO-1.O, reduced *IPW* levels (1.5-fold), but the effect was not significant. ASO-6.1.PO-1.O and ASO-4.4.PS.L significantly reduced *SNHG115* and *UBE3A-AS* RNA levels. ASO-6.1.PO-1.O and ASO-4.4.PS.L had a similar effect on *SNHG115* levels; however, ASO-4.4.PS.L had a much larger effect on *UBE3A-AS* RNA levels than ASO-6.1.PO-1.O (ASO-4.4.PS.L: -6.1-fold change; ASO-6.1.PO-1.O: -2.8-fold change). ASO treatment increased *UBE3A* RNA levels by approximately 1.2-fold, but the effect was not significant (Figure 10 and Table 21).

Table 21. Effect of ASO Treatment on RNA Levels of PWS Polycistronic Transcripts and *UBE3A*

Gene	Treatment	Difference	Std Error	t Ratio	Adjusted P
SNURF	ASO-6.1.PO-1.O	-0.53	0.51	-1.02	0.5
	ASO-4.4.PS.L	0.49	0.51	0.96	0.6
SNRPN	ASO-6.1.PO-1.O	0.03	0.11	0.30	0.9
	ASO-4.4.PS.L	-0.02	0.11	-0.16	1.0
SNHG116	ASO-6.1.PO-1.O	-0.07	0.10	-0.75	0.7
	ASO-4.4.PS.L	-0.24	0.10	-2.49	0.08
SNORD116	ASO-6.1.PO-1.O	-0.04	0.46	-0.08	1.0
	ASO-4.4.PS.L	0.27	0.45	0.60	0.8
IPW	ASO-6.1.PO-1.O	0.18	0.37	0.49	0.8
	ASO-4.4.PS.L	-0.49	0.37	-1.33	0.4
SNH115G	ASO-6.1.PO-1.O	-0.55	0.09	-5.92	0.002
	ASO-4.4.PS.L	-0.58	0.09	-6.33	0.001
SNORD115	ASO-6.1.PO-1.O	0.24	0.52	0.45	0.8
	ASO-4.4.PS.L	-0.26	0.49	-0.54	0.8
UBE3A-AS	ASO-6.1.PO-1.O	-1.48	0.06	-24.17	< 0.0001
	ASO-4.4.PS.L	-1.94	0.06	-31.56	< 0.0001
UBE3A	ASO-6.1.PO-1.O	0.74	0.48	1.53	0.3
	ASO-4.4.PS.L	0.90	0.48	1.88	0.2

One way ANOVA with Dunnett's multiple comparison test relative to vehicle.

Materials and Methods

Methods were similar to those described in Example 4 unless noted otherwise.

Differential expression analysis of PWS RNAs

Normalized FPKM (fragments per thousand per million) values of the RefSeq gene annotation will be estimated using Cuffnorm with the default settings and the following option: -u. The FPKM values of each gene annotation was determined for each sample from the output file and used for descriptive and inferential statistics.

Example 6: Pharmacodynamic analysis of ASO-6.1-PO-1.O and ASO-4.4.PS.L in Cynomolgus macaque

The ASO-4 and ASO-6 target regions are conserved across several non-human primate (NHP) species, thus enabling both safety and efficacy studies in a large animal model. To examine the efficacy of ASO-4.4.PS.L and ASO-6.1.PO-1.O in the central nervous system (CNS), ASOs were delivered to Cynomolgus macaques by intrathecal lumbar puncture. Animals were administered a single bolus injection of vehicle (0.9% saline, n = 5), ASO-6.1.PO-1.O (10 mg, n = 3), and ASO.4.4.PS.L (10 mg, n = 3). Twenty-eight days following treatment, central nervous (CNS) tissues were collected and the steady state RNA levels of *UBE3A-AS* were measured. Overall, ASO-4.4.PS.L had a larger effect on *UBE3A-AS* RNA levels than ASO-6.1.PO-1.O (Table 22). ASO-4.4.PS.L reduced *UBE3A-AS* RNA in most CNS regions, with large effects in temporal lobe, primary motor cortex, pons, medulla, hippocampus, globus pallidus, frontal cortex (corona radiata), prefrontal cortex, and lumbar spinal cord. Similarly, ASO-6.1.PO-1.O reduced *UBE3A-AS* RNA levels in most CNS regions, with large effects observed in pons, oculomotor nucleus, and lumbar spinal cord (Figure 11 and Table 23).

Table 22. Effect Size of ASO Treatment on *UBE3A-AS* RNA Levels in CNS

Treatment	Treatment*	Cohen's d	95% Confidence Intervals		FDR
Vehicle	ASO-4.4.PS.L	1.4	1.0	1.8	2.3E-10
ASO-6.1.PO-1.O	ASO-4.4.PS.L	1.0	0.6	1.5	6.4E-06
Vehicle	ASO-6.1.PO-1.O	0.3	-0.06	0.7	0.09

Students t-test with FDR adjusted P values
Cohen's d effect sizes: 0.2, small; 0.5, medium; 0.8, large; 1.2, very large
Abbreviations: FDR, false discovery rate

Table 23. Effect of ASO Treatment on *UBE3A-AS* RNA Levels in CNS Regions

CNS Region	ASO	Difference	Std Error	t Ratio	Adjusted P
Caudate Nucleus	ASO-6.1.PO-1.O	0.10	0.22	0.46	0.9
	ASO-4.4.PS.L	-0.21	0.22	-0.94	0.6
Cerebellum	ASO-6.1.PO-1.O	-0.11	0.09	-1.15	0.5
	ASO-4.4.PS.L	-0.05	0.09	-0.53	0.8
Frontal cortex	ASO-6.1.PO-1.O	0.01	0.27	0.04	0.9
	ASO-4.4.PS.L	-0.71	0.27	-2.66	0.05
Frontal Cortex (Corona radiata)	ASO-6.1.PO-1.O	-0.08	0.22	-0.34	0.9
	ASO-4.4.PS.L	-0.62	0.22	-2.79	0.04
Globus Pallidus	ASO-6.1.PO-1.O	0.10	0.24	0.40	0.9
	ASO-4.4.PS.L	-0.38	0.24	-1.54	0.3
Hippocampus	ASO-6.1.PO-1.O	-0.19	0.21	-0.91	0.6
	ASO-4.4.PS.L	-0.57	0.21	-2.66	0.05

Spinal Cord (Lumbar)	ASO-6.1.PO-1.O	-0.32	0.20	-1.63	0.2
	ASO-4.4.PS.L	-0.87	0.20	-4.46	0.004
Medulla	ASO-6.1.PO-1.O	-0.24	0.20	-1.16	0.45
	ASO-4.4.PS.L	-0.32	0.20	-1.59	0.3
Oculomotor Nucleus	ASO-6.1.PO-1.O	-0.37	0.29	-1.27	0.4
	ASO-4.4.PS.L	-0.18	0.29	-0.62	0.8
Pons	ASO-6.1.PO-1.O	-0.27	0.21	-1.30	0.4
	ASO-4.4.PS.L	-0.47	0.21	-2.25	0.1
Motor Cortex	ASO-6.1.PO-1.O	-0.19	0.30	-0.65	0.8
	ASO-4.4.PS.L	-0.59	0.30	-1.99	0.1
Putamen	ASO-6.1.PO-1.O	0.07	0.15	0.44	0.9
	ASO-4.4.PS.L	-0.04	0.15	-0.25	0.9
Temporal Lobe	ASO-6.1.PO-1.O	0.13	0.25	0.54	0.8
	ASO-4.4.PS.L	-0.59	0.25	-2.39	0.08
Thalamus	ASO-6.1.PO-1.O	-0.02	0.14	-0.14	0.9
	ASO-4.4.PS.L	-0.20	0.14	-1.46	0.3
One way ANOVA with Dunnett's multiple comparison test relative to vehicle.					

Materials and Methods

Administration of ASOs

NHP studies were performed at Northern Biomedical Research and Charles River Laboratories using protocols approved by the institutions respective Institutional Animal Care and Use Committees. Male and female Cynomolgus macaques (Macaca fascicularis) weighing 2- 4 kg were anesthetized and single 1 mL dose of ASO or vehicle was administered via intrathecal lumbar puncture. The dosing solution was prepared by dissolution of lyophilized ASO in the vehicle control article (0.9% sodium chloride) and was filtered through a 0.2-μm filter. CNS and spinal cord samples were harvested, and the CNS was sectioned into 4-mm coronal slices. Tissue samples were flash frozen and stored at -80°C until RNA isolation.

RNA isolation

A 4mm tissue punch was taken from each region of interest of which approximately half was used for RNA isolation. RNA isolation was performed using the Qiagen RNeasy Plus Mini kit (74136, Qiagen) with tissue disruption and lysis performed with 5 mm stainless steel beads in a TissueLyser II. The RNA was eluted in two volumes of 30 μl water, for a total elution volume of 60 μl. RNA was quantified using the Qubit with the RNA XR assay (Q33224, Thermo Fisher Scientific). cDNA was synthesized from 2 μg of input RNA using the High Capacity RNA-to-cDNA kit (4387406, Thermo Fisher Scientific) in a total reaction volume of 50 μl.

Analysis of UBE3A-AS RNA levels in tissues

Cynomolgus macaque *UBE3A-AS* RNA levels were estimated using SYBR Green quantitative reverse-transcription PCR (qRT-PCR). Total reaction volume was 10 μl, including 2 μl of cDNA, 1X PowerUp SYBR Green Master mix (A25741, Thermo Fisher Scientific), and 500 nM of each primer (forward and reverse). Cycling conditions were 2 minutes at 50°C, 2 minutes at 95°C, and 40 cycles of 15 seconds at 95°C and 1 minute at 60°C, with readings taken at the 60°C step of every cycle. Reactions were run on a BIO-RAD T1000 CFX96 thermocycler, with internal control (*PPIA*, forward: GTCTCCTTCGAGCTGTTTGC (SEQ ID NO:503); reverse: CCTTTCTCTCCAGTGCTCAGA (SEQ ID NO:504)) and target (*UBE3A-AS*, forward: CCTGTGAACTTTCAACCAGGA (SEQ ID NO:505); reverse: GGATCAGACTCCAGGCCTTC (SEQ ID NO:506)) reactions performed separately. Data was retrieved and initial analysis was done with the BIORAD CFX Maestro software, with in depth statistical analyses performed with Excel and JMP.

Example 7: ASOs targeting exonic boundaries of spliced *UBE3A-AS* transcripts

In some embodiments, the target sequence is an exonic boundary involving *UBE3A-AS* exons 1-5 and *SNORD109B* exons 1-2. Target sequences consist of 38 nucleotides (19 nucleotides of each exon) centered on the exonic boundary of each exon (19 nucleotides representing the 5′ and 3′-ends of adjacent exons). There were 12 segments of sequences, with exonic boundaries involving segments 1-2, 2-3, 3-4, 5-6, 7-8, 9-10, and 11-12. The chromosomal coordinates are provided in Table 24. A single merged junction sequence was created that shows the spliced exons (|, exonic junction) and intervening exonic sequences ([]). ASOs (20-, 19, and 18-mer) targeting the exonic junctions are provided in Table 25.

Merged junction-sequence

AATGAAATCTTCTGATTTG|TAAGACATGCTGCCAAGAG[]ATTAGTTTTACACCTTCAG|GATAAAGACTGCTGAGAAG[]GTTTAAGGATGCTATTCTG|AAAAGACTGTGGAGGAAGA[]TTAAGGAAACCATCTCTGG|GATAAGGATGACTGAGGAA[]ATTTAAGGATGCCACTCTG|GTTAAAAGCTGAAACAACT[]GAAACTTCAGGGAAAAGAG|AAGGCCTGGAATCTGATCC (SEQ ID NO:489).

| = 3′-5′ exonic junction

[] = intervening exonic sequence

Table 24. Chromosome 15 coordinates of targeted exonic junctions			
Segment	Start	End	Exonic Region
1	25,511,743	25,511,761	3′
2	25,512,059	25,512,079	5′
3	25,512,175	25,512,191	3′
4	25,513,475	25,513,493	5′
5	25,513,582	25,513,600	3′
6	25,514,752	25,514,770	5′
7	25,514,863	25,514,881	3′
8	25,516,564	25,516,582	5′
9	25,516,663	25,516,681	3′
10	25,522,514	25,522,532	5′
11	25,522,537	25,522,556	3′
12	25,523,994	25,524,012	5′
Human chromosome 15 coordinates (hg19 reference assembly)			

Table 25. List of Junction ASOs and corresponding target regions

ASO size	Target Sequence (5'-3')		ASO sequence (5'-3')	
20-mer	GAAACCAUCUCUGGGAUAAG	SEQ ID NO:393	CTTATCCCAGAGATGGTTTC	SEQ ID NO:441
	AAACCAUCUCUGGGAUAAGG	SEQ ID NO:394	CCTTATCCCAGAGATGGTTT	SEQ ID NO:442
	AACCAUCUCUGGGAUAAGGA	SEQ ID NO:395	TCCTTATCCCAGAGATGGTT	SEQ ID NO:443
	ACCAUCUCUGGGAUAAGGAU	SEQ ID NO:396	ATCCTTATCCCAGAGATGGT	SEQ ID NO:444
	CCAUCUCUGGGAUAAGGAUG	SEQ ID NO:397	CATCCTTATCCCAGAGATGG	SEQ ID NO:445
	CAUCUCUGGGAUAAGGAUGA	SEQ ID NO:398	TCATCCTTATCCCAGAGATG	SEQ ID NO:446
	AUCUCUGGGAUAAGGAUGAC	SEQ ID NO:399	GTCATCCTTATCCCAGAGAT	SEQ ID NO:447
	UCUCUGGGAUAAGGAUGACU	SEQ ID NO:400	AGTCATCCTTATCCCAGAGA	SEQ ID NO:448
	CUCUGGGAUAAGGAUGACUG	SEQ ID NO:401	CAGTCATCCTTATCCCAGAG	SEQ ID NO:449
	UCUGGGAUAAGGAUGACUGA	SEQ ID NO:402	TCAGTCATCCTTATCCCAGA	SEQ ID NO:450
	CUGGGAUAAGGAUGACUGAG	SEQ ID NO:403	CTCAGTCATCCTTATCCCAG	SEQ ID NO:451
	UGGGAUAAGGAUGACUGAGG	SEQ ID NO:404	CCTCAGTCATCCTTATCCCA	SEQ ID NO:452
	GGGAUAAGGAUGACUGAGGA	SEQ ID NO:405	TCCTCAGTCATCCTTATCCC	SEQ ID NO:453
	GGAUAAGGAUGACUGAGGAA	SEQ ID NO:406	TTCCTCAGTCATCCTTATCC	SEQ ID NO:454
	GCUGAAACAACUGAAACUUC	SEQ ID NO:407	GAAGTTTCAGTTGTTTCAGC	SEQ ID NO:455
	GAAACAACUGAAACUUCAGG	SEQ ID NO:408	CCTGAAGTTTCAGTTGTTTC	SEQ ID NO:456
	AAACAACUGAAACUUCAGGG	SEQ ID NO:409	CCCTGAAGTTTCAGTTGTTT	SEQ ID NO:457
	AACAACUGAAACUUCAGGGA	SEQ ID NO:410	TCCCTGAAGTTTCAGTTGTT	SEQ ID NO:458
	ACAACUGAAACUUCAGGGAA	SEQ ID NO:411	TTCCCTGAAGTTTCAGTTGT	SEQ ID NO:459
	CAACUGAAACUUCAGGGAAA	SEQ ID NO:412	TTTCCCTGAAGTTTCAGTTG	SEQ ID NO:460
	ACUGAAACUUCAGGGAAAAG	SEQ ID NO:413	CTTTTCCCTGAAGTTTCAGT	SEQ ID NO:461
19-mer	AACCAUCUCUGGGAUAAGG	SEQ ID NO:414	CCTTATCCCAGAGATGGTT	SEQ ID NO:462
	ACCAUCUCUGGGAUAAGGA	SEQ ID NO:415	TCCTTATCCCAGAGATGGT	SEQ ID NO:463
	CCAUCUCUGGGAUAAGGAU	SEQ ID NO:416	ATCCTTATCCCAGAGATGG	SEQ ID NO:464
	CAUCUCUGGGAUAAGGAUG	SEQ ID NO:417	CATCCTTATCCCAGAGATG	SEQ ID NO:465
	AUCUCUGGGAUAAGGAUGA	SEQ ID NO:418	TCATCCTTATCCCAGAGAT	SEQ ID NO:466
	UCUCUGGGAUAAGGAUGAC	SEQ ID NO:419	GTCATCCTTATCCCAGAGA	SEQ ID NO:467
	CUCUGGGAUAAGGAUGACU	SEQ ID NO:420	AGTCATCCTTATCCCAGAG	SEQ ID NO:468

	UCUGGGAUAAGGAUGACUG	SEQ ID NO:421	CAGTCATCCTTATCCCAGA	SEQ ID NO:469
	CUGGGAUAAGGAUGACUGA	SEQ ID NO:422	TCAGTCATCCTTATCCCAG	SEQ ID NO:470
	UGGGAUAAGGAUGACUGAG	SEQ ID NO:423	CTCAGTCATCCTTATCCCA	SEQ ID NO:471
	GGGAUAAGGAUGACUGAGG	SEQ ID NO:424	CCTCAGTCATCCTTATCCC	SEQ ID NO:472
	GGAUAAGGAUGACUGAGGA	SEQ ID NO:425	TCCTCAGTCATCCTTATCC	SEQ ID NO:473
	AACAACUGAAACUUCAGGG	SEQ ID NO:426	CCCTGAAGTTTCAGTTGTT	SEQ ID NO:474
	ACAACUGAAACUUCAGGGA	SEQ ID NO:427	TCCCTGAAGTTTCAGTTGT	SEQ ID NO:475
	CAACUGAAACUUCAGGGAA	SEQ ID NO:428	TTCCCTGAAGTTTCAGTTG	SEQ ID NO:476
	CAACUGAAACUUCAGGGAA	SEQ ID NO:429	TTCCCTGAAGTTTCAGTTG	SEQ ID NO:477
18-mer	CCAUCUCUGGGAUAAGGA	SEQ ID NO:430	TCCTTATCCCAGAGATGG	SEQ ID NO:478
	CAUCUCUGGGAUAAGGAU	SEQ ID NO:431	ATCCTTATCCCAGAGATG	SEQ ID NO:479
	AUCUCUGGGAUAAGGAUG	SEQ ID NO:432	CATCCTTATCCCAGAGAT	SEQ ID NO:480
	UCUCUGGGAUAAGGAUGA	SEQ ID NO:433	TCATCCTTATCCCAGAGA	SEQ ID NO:481
	CUCUGGGAUAAGGAUGAC	SEQ ID NO:434	GTCATCCTTATCCCAGAG	SEQ ID NO:482
	UCUGGGAUAAGGAUGACU	SEQ ID NO:435	AGTCATCCTTATCCCAGA	SEQ ID NO:483
	CUGGGAUAAGGAUGACUG	SEQ ID NO:436	CAGTCATCCTTATCCCAG	SEQ ID NO:484
	UGGGAUAAGGAUGACUGA	SEQ ID NO:437	TCAGTCATCCTTATCCCA	SEQ ID NO:485
	GGGAUAAGGAUGACUGAG	SEQ ID NO:438	CTCAGTCATCCTTATCCC	SEQ ID NO:486
	GGAUAAGGAUGACUGAGG	SEQ ID NO:439	CCTCAGTCATCCTTATCC	SEQ ID NO:487
	ACAACUGAAACUUCAGGG	SEQ ID NO:440	CCCTGAAGTTTCAGTTGT	SEQ ID NO:488

Example 8: siRNA, shRNA, and CRISPR guide RNAs targeting UBE3a-AS exons 1-5

As noted above, in some embodiments, the disclosed oligonucleotide is a functional nucleic acid, such as a siRNA, shRNA, or nuclease gRNA, that inhibits, mutates, or deletes the target nucleic acid sequence.

Examples of siRNA targeting UBE3a-AS exons 1-5 are provided in Table 26. Examples of shRNA targeting UBE3a-AS exons 1-5 are provided in Table 27. Examples of gRNA targeting UBE3a-AS exons 1-5 are provided in Table 28.

Table. 26 siRNA targeting UBE3a-AS exons 1-5

Target sequence		siRNA	
CCCAGGUGUCCUUUAAUGAA	SEQ ID NO:507	TTCATTAAAGGACACCTGGG	SEQ ID NO:538
CCAGGUGUCCUUUAAUGAAA	SEQ ID NO:508	TTTCATTAAAGGACACCTGG	SEQ ID NO:539
UGAAAAUGCUCUUGACACCA	SEQ ID NO:509	TGGTGTCAAGAGCATTTTCA	SEQ ID NO:540
GAAAAUGCUCUUGACACCAA	SEQ ID NO:510	TTGGTGTCAAGAGCATTTTC	SEQ ID NO:541
AAAUGCUCUUGACACCAAUG	SEQ ID NO:511	CATTGGTGTCAAGAGCATTT	SEQ ID NO:542
AGAUCAGUAGCUUCCUUUAC	SEQ ID NO:512	GTAAAGGAAGCTACTGATCT	SEQ ID NO:543
UCAGUAGCUUCCUUUACCGA	SEQ ID NO:513	TCGGTAAAGGAAGCTACTGA	SEQ ID NO:544
UCUAGAACAUUGAGCUAUGG	SEQ ID NO:514	CCATAGCTCAATGTTCTAGA	SEQ ID NO:545
CUAGAACAUUGAGCUAUGGA	SEQ ID NO:515	TCCATAGCTCAATGTTCTAG	SEQ ID NO:546
AACAUUGAGCUAUGGAAGAC	SEQ ID NO:516	GTCTTCCATAGCTCAATGTT	SEQ ID NO:547
ACAUUGAGCUAUGGAAGACU	SEQ ID NO:517	AGTCTTCCATAGCTCAATGT	SEQ ID NO:548
CUAUGGAAGACUCCCACCUA	SEQ ID NO:518	TAGGTGGGAGTCTTCCATAG	SEQ ID NO:549
UAUGGAAGACUCCCACCUAA	SEQ ID NO:519	TTAGGTGGGAGTCTTCCATA	SEQ ID NO:550
CAAGUGCUACCGCACAGGCA	SEQ ID NO:520	TGCCTGTGCGGTAGCACTTG	SEQ ID NO:551
AAGUGCUACCGCACAGGCAU	SEQ ID NO:521	ATGCCTGTGCGGTAGCACTT	SEQ ID NO:552
UACCGCACAGGCAUGCUGCA	SEQ ID NO:522	TGCAGCATGCCTGTGCGGTA	SEQ ID NO:553
CAGGCAUGCUGCAGUGAAUU	SEQ ID NO:523	AATTCACTGCAGCATGCCTG	SEQ ID NO:554
AGGCAUGCUGCAGUGAAUUU	SEQ ID NO:524	AAATTCACTGCAGCATGCCT	SEQ ID NO:555
ACCGUUGUUUAAGGAUGCUA	SEQ ID NO:525	TAGCATCCTTAAACAACGGT	SEQ ID NO:556
CCGUUGUUUAAGGAUGCUAU	SEQ ID NO:526	ATAGCATCCTTAAACAACGG	SEQ ID NO:557
CUGUGGAGGAAGAAAACCCU	SEQ ID NO:527	AGGGTTTTCTTCCTCCACAG	SEQ ID NO:558
AAGAAAACCCUUUACCCUGU	SEQ ID NO:528	ACAGGGTAAAGGGTTTTCTT	SEQ ID NO:559
AGAAAACCCUUUACCCUGUU	SEQ ID NO:529	AACAGGGTAAAGGGTTTTCT	SEQ ID NO:560
CUCAACUGCCUGGCACUGAA	SEQ ID NO:530	TTCAGTGCCAGGCAGTTGAG	SEQ ID NO:561
AACUGCCUGGCACUGAAAAU	SEQ ID NO:531	ATTTTCAGTGCCAGGCAGTT	SEQ ID NO:562
ACUGCCUGGCACUGAAAAUG	SEQ ID NO:532	CATTTTCAGTGCCAGGCAGT	SEQ ID NO:563
GUGUUUAAGGAAACCAUCUC	SEQ ID NO:533	GAGATGGTTTCCTTAAACAC	SEQ ID NO:564
GUUUAAGGAAACCAUCUCUG	SEQ ID NO:534	CAGAGATGGTTTCCTTAAAC	SEQ ID NO:565
AGGAAACCAUCUCUGAUAAG	SEQ ID NO:535	CTTATCAGAGATGGTTTCCT	SEQ ID NO:566

UCUUUGGCUUGUUGACACCA	SEQ ID NO:536	TGGTGTCAACAAGCCAAAGA	SEQ ID NO:567
CUUUGGCUUGUUGACACCAG	SEQ ID NO:537	CTGGTGTCAACAAGCCAAAG	SEQ ID NO:568

Table 27. shRNA targeting UBE3a-AS exons 1-5

GGTGCCATTCTATTATAAAtaacctgacccattaTTTATAATAGAATGGCACCTTTTT	SEQ ID NO:569
GCTTTCATCAATAATGAAAtaacctgacccattaTTTCATTATTGATGAAAGCTTTTT	SEQ ID NO:570
GGTCTTTCATCAATAATGAtaacctgacccattaTCATTATTGATGAAAGACCTTTTT	SEQ ID NO:571
GAAATCTTCTGATTTGTAAtaacctgacccattaTTACAAATCAGAAGATTTCTTTTT	SEQ ID NO:572
GCACCTAAGGGAATTAGTAtaacctgacccattaTACTAATTCCCTTAGGTGCTTTTT	SEQ ID NO:573
GTTTCAACCAGGATTTAAAtaacctgacccattaTTTAAATCCTGGTTGAAACTTTTT	SEQ ID NO:574
GCTTTCAACCAGGATTTAAtaacctgacccattaTTAAATCCTGGTTGAAAGCTTTTT	SEQ ID NO:575
GGAGATGTGCCATTCTATAtaacctgacccattaTATAGAATGGCACATCTCCTTTTT	SEQ ID NO:576
GTCTTTCATCAATAATGAAtaacctgacccattaTTCATTATTGATGAAAGACTTTTT	SEQ ID NO:577
GATCAATAATGAAATCTTAtaacctgacccattaTAAGATTTCATTATTGATCTTTTT	SEQ ID NO:578
GTGTCTTTCATCAATAATAtaacctgacccattaTATTATTGATGAAAGACACTTTTT	SEQ ID NO:579
GCAATAATGAAATCTTCTAtaacctgacccattaTAGAAGATTTCATTATTGCTTTTT	SEQ ID NO:580
GCATGCTGCAGTGAATTTAtaacctgacccattaTAAATTCACTGCAGCATGCTTTTT	SEQ ID NO:581
GGAAATCTTCTGATTTGTAtaacctgacccattaTACAAATCAGAAGATTTCCTTTTT	SEQ ID NO:582
GGTATATTCTATCTAGAAAtaacctgacccattaTTTCTAGATAGAATATACCTTTTT	SEQ ID NO:583
GTGCTGCAGTGAATTTAAAtaacctgacccattaTTTAAATTCACTGCAGCACTTTTT	SEQ ID NO:584
GTGTGCCATTCTATTATAAtaacctgacccattaTTATAATAGAATGGCACACTTTTT	SEQ ID NO:585
GTTACCATCAGTGTTTAAAtaacctgacccattaTTTAAACACTGATGGTAACTTTTT	SEQ ID NO:586
GCCTGCAACCGTTGTTTAAtaacctgacccattaTTAAACAACGGTTGCAGGCTTTTT	SEQ ID NO:587
GTATGTCTTTCATCAATAAtaacctgacccattaTTATTGATGAAAGACATACTTTTT	SEQ ID NO:588

Table 28. CRISPR Guide RNAs targeting UBE3a-AS exons 1-5

Strand	Sequence	SEQ ID	PAM
-	ACACTGATGGTAAAGTGGAC	SEQ ID NO:589	TGG
-	TAGAATATACACGTCGGTAA	SEQ ID NO:590	AGG
-	TCAACTGTCCCAGTCACAAC	SEQ ID NO:591	AGG
-	TCTAGATAGAATATACACGT	SEQ ID NO:592	CGG
-	TCTAGATAGAATATACACGT	SEQ ID NO:593	CGG
-	CTCCCCATGCACACTTGAGA	SEQ ID NO:594	AGG
-	CATCCTTAAACAACGGTTGC	SEQ ID NO:595	AGG
-	GGTGTAAAACTAATTCCCTT	SEQ ID NO:596	AGG
-	AACAACGGTTGCAGGGACAG	SEQ ID NO:597	AGG
+	TATGGAAGACTCCCACCTAA	SEQ ID NO:598	GGG
+	CTATGGAAGACTCCCACCTA	SEQ ID NO:599	AGG
+	AAGCCTTCTCAAGTGTGCAT	SEQ ID NO:600	GGG
+	CTATCTAGAACATTGAGCTA	SEQ ID NO:601	TGG
+	ACCCTCTGGTGTTGTCACAG	SEQ ID NO:602	AGG
+	AACCCTTTACCCTGTTGTTC	SEQ ID NO:603	AGG

Unless defined otherwise, all technical and scientific terms used herein have the same meanings as commonly understood by one of skill in the art to which the disclosed invention belongs. Publications cited herein and the materials for which they are cited are specifically incorporated by reference.

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

WHAT IS CLAIMED IS:

1. An antisense oligonucleotide comprising a contiguous nucleotide sequence of 10 to 30 nucleotides in length with at least 98% complementarity to a contiguous portion of nucleic acid sequence SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, or SEQ ID NO:5.
2. The oligonucleotide of claim 1, wherein the oligonucleotide comprises a sequence selected from the group consisting of SEQ ID NO: 6, 7, 8, 9, 10, or 11.
3. The oligonucleotide of claim 1 or 2, comprising one or more modified nucleosides.
4. The oligonucleotide of claim 3, wherein the one or more modified nucleosides is a 2′ sugar modified nucleoside.
5. The oligonucleotide of claim 4, wherein the one or more 2′ sugar modified nucleoside is independently selected from the group consisting of 2′-O-alkyl-RNA, 2′-O-methyl-RNA, 2′-alkoxy-RNA, 2′-O-methoxyethyl-RNA, 2′-amino-DNA, 2′-fluoro-DNA, arabino nucleic acid (ANA), 2′-fluoro-ANA and LNA nucleosides.
6. The oligonucleotide of claim 5, wherein the one or more modified nucleoside is a LNA nucleoside.
7. The oligonucleotide of claim 1, wherein the oligonucleotide comprises at least one modified internucleoside linkage.
8. The oligonucleotide of claim 7, wherein the internucleoside linkages within the contiguous nucleotide sequence are phosphorothioate internucleoside linkages.
9. The oligonucleotide of claim 1, wherein the oligonucleotide is capable of recruiting RNase H.
10. The oligonucleotide of claim 9, wherein the oligonucleotide is a gapmer.
11. The oligonucleotide of claim 10, wherein the oligonucleotide has a nucleic acid sequence selected from the group consisting of SEQ ID NOs:362 to 392.
12. A pharmaceutical composition comprising one or more of the oligonucleotides of any one of claims 1 to 11 and a pharmaceutically acceptable diluent, solvent, carrier, salt and/or adjuvant.
13. A method for treating or preventing Angelman syndrome in a subject comprising administering a therapeutically or prophylactically effective amount of the composition of claim 12 to a subject suffering from or susceptible to Angelman syndrome.

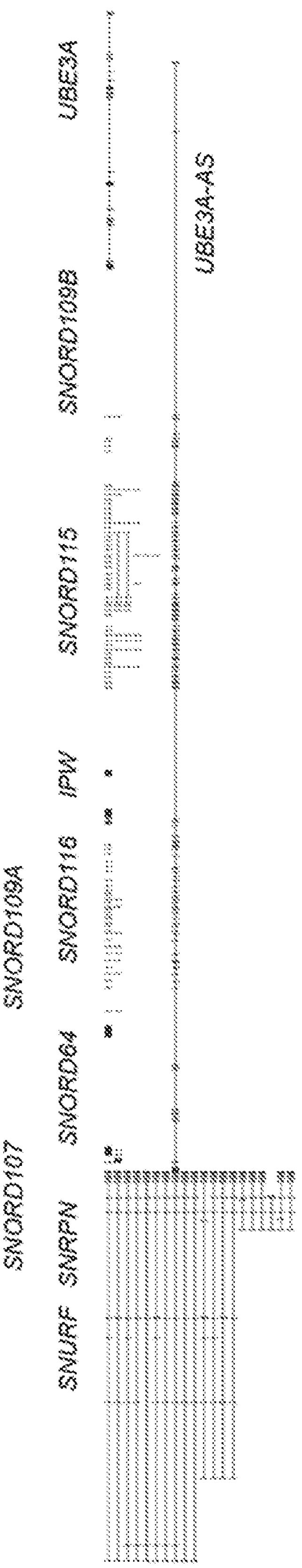


FIG. 1A

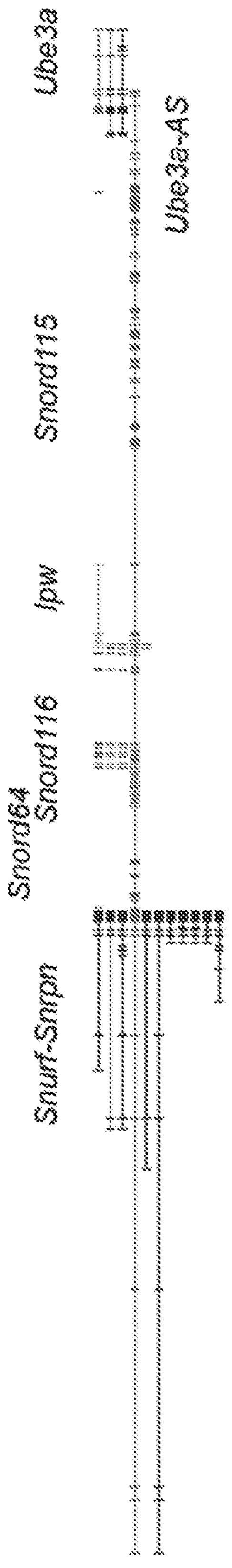


FIG. 1B

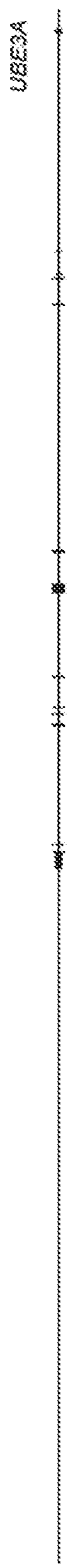


FIG. 1C

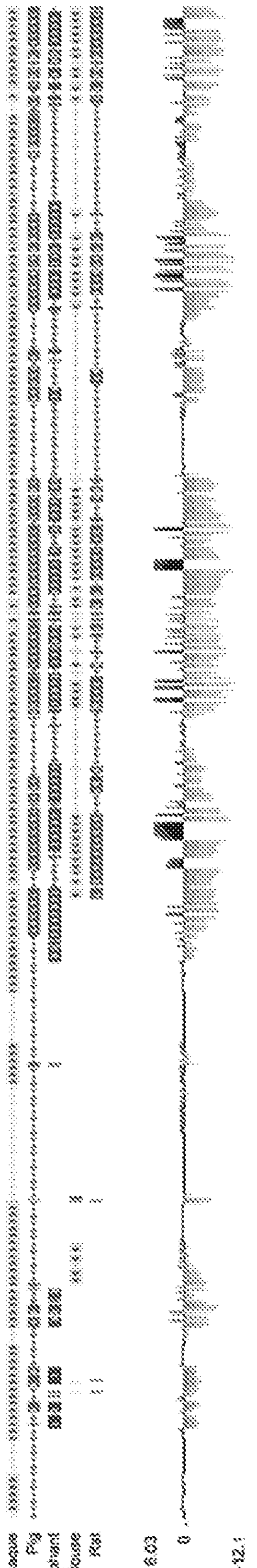

Macaque
Pig
Elephant
Mouse
Rat
6.03
0
-12.1

FIG. 1D

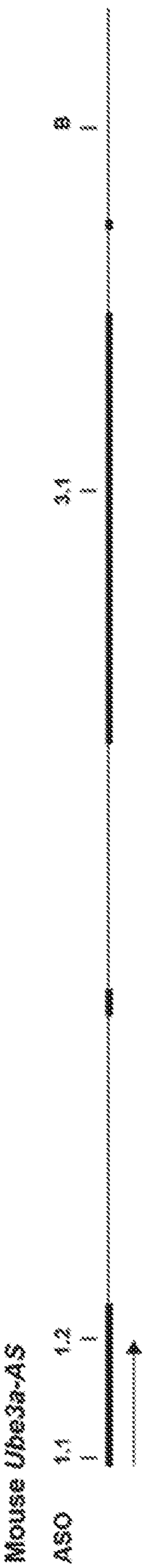

Mouse Ube3a-AS
ASO
1.1
1.2
3.1
8

FIG. 2A

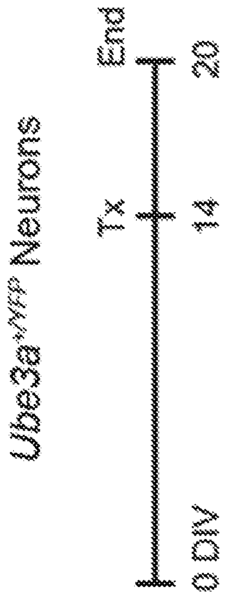

Ube3a+/YFP Neurons
Tx
End
0 DIV
14
20

FIG. 2C

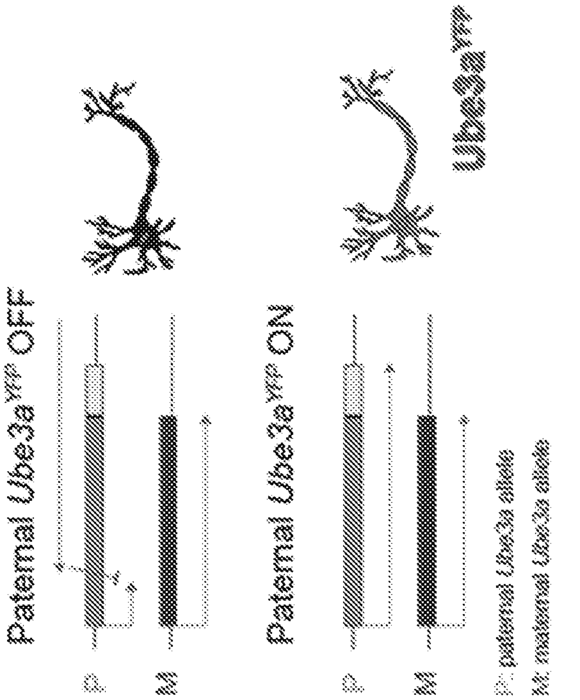

Paternal Ube3a YFP OFF
P
M
Paternal Ube3a YFP ON
P
M
P: paternal Ube3a allele
M: maternal Ube3a allele
Ube3a YFP

FIG. 2B

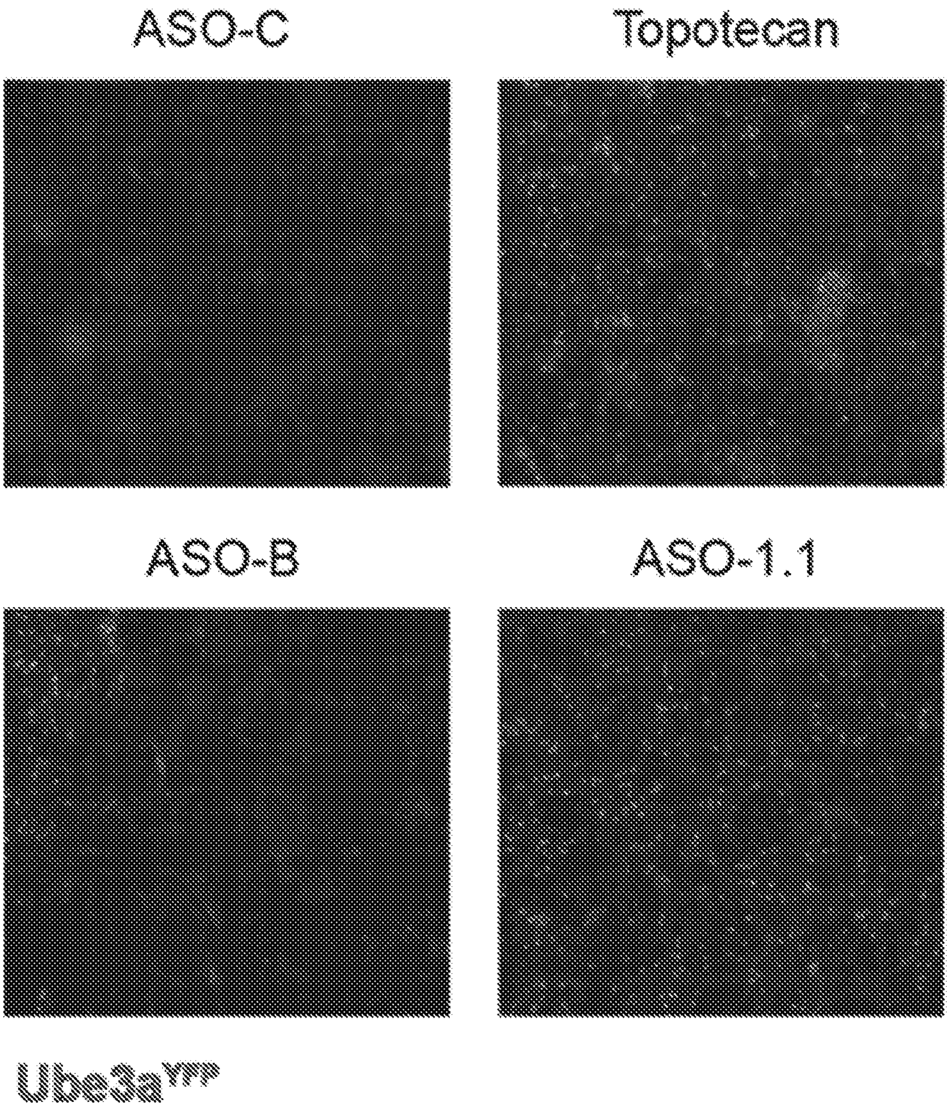


FIG. 2D

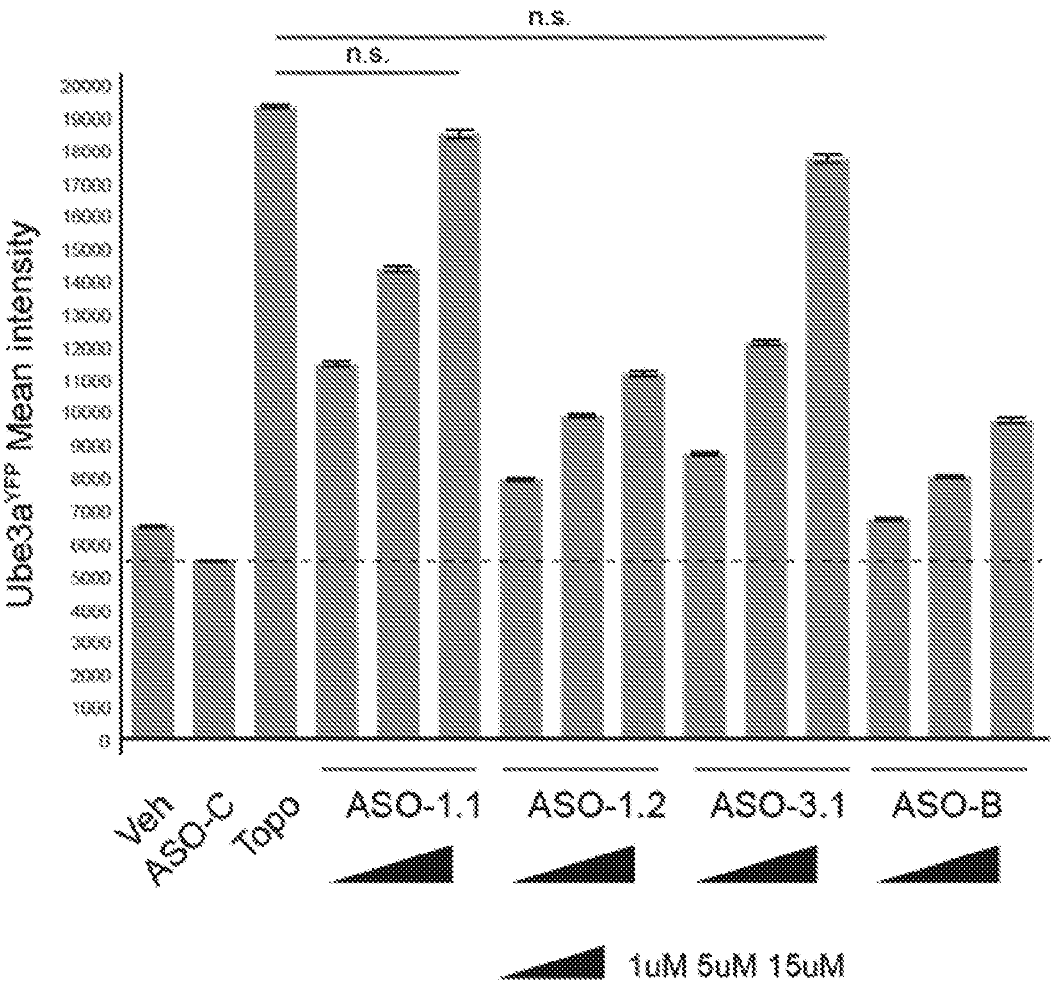

n.s.
n.s.
Ube3a^{YFP} Mean intensity
20000
19000
18000
17000
16000
15000
14000
13000
12000
11000
10000
9000
8000
7000
6000
5000
4000
3000
2000
1000
0
Veh
ASO-C
Topo
ASO-1.1
ASO-1.2
ASO-3.1
ASO-B
1uM 5uM 15uM

FIG. 2E

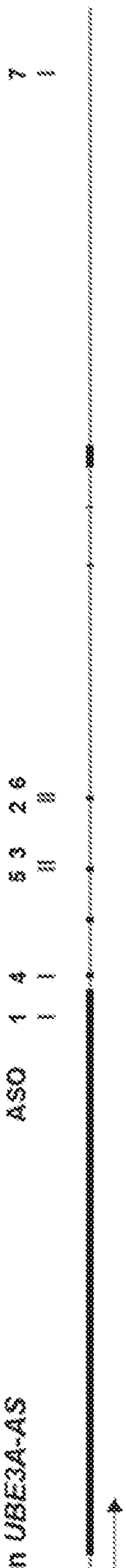

Human UBE3A-AS
ASO
1
4
5 3
2 6
7

FIG. 3A

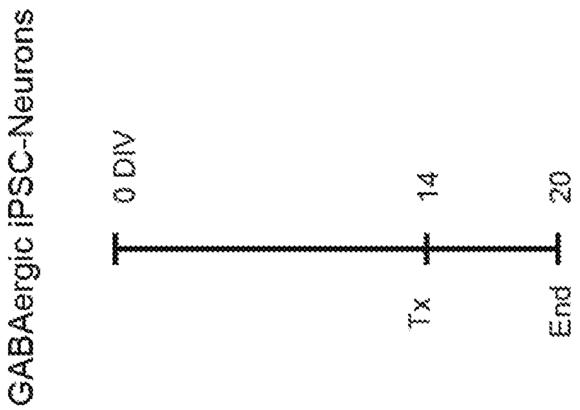

GABAergic iPSC-Neurons
0 DIV
Tx
14
End
20

FIG. 3B

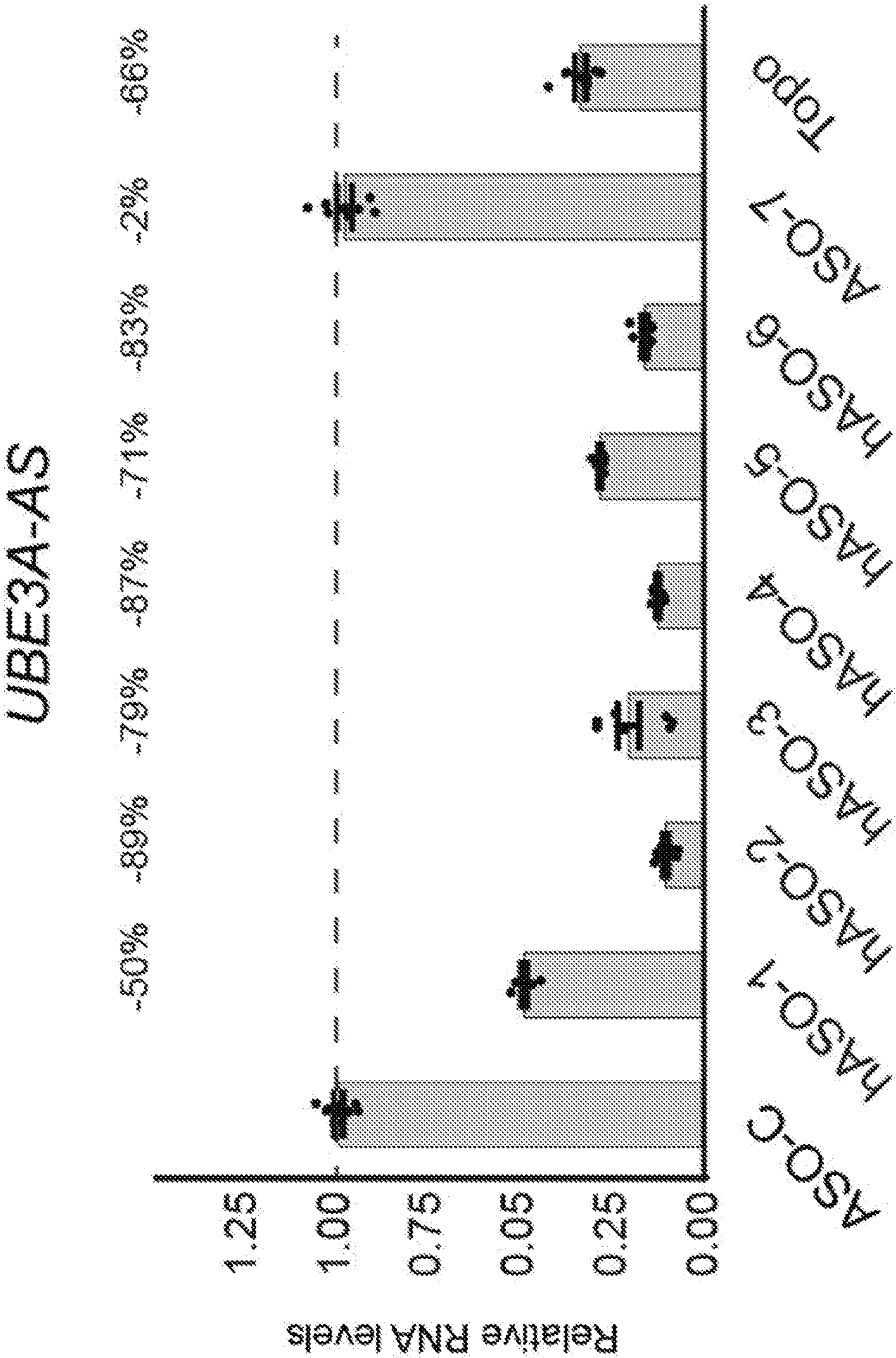

UBE3A-AS
-50%
-89%
-79%
-87%
-71%
-83%
-2%
-66%
1.25
1.00
0.75
0.05
0.25
0.00
Relative RNA levels
ASO-C
hASO-1
hASO-2
hASO-3
hASO-4
hASO-5
hASO-6
ASO-7
Topo

FIG. 3C

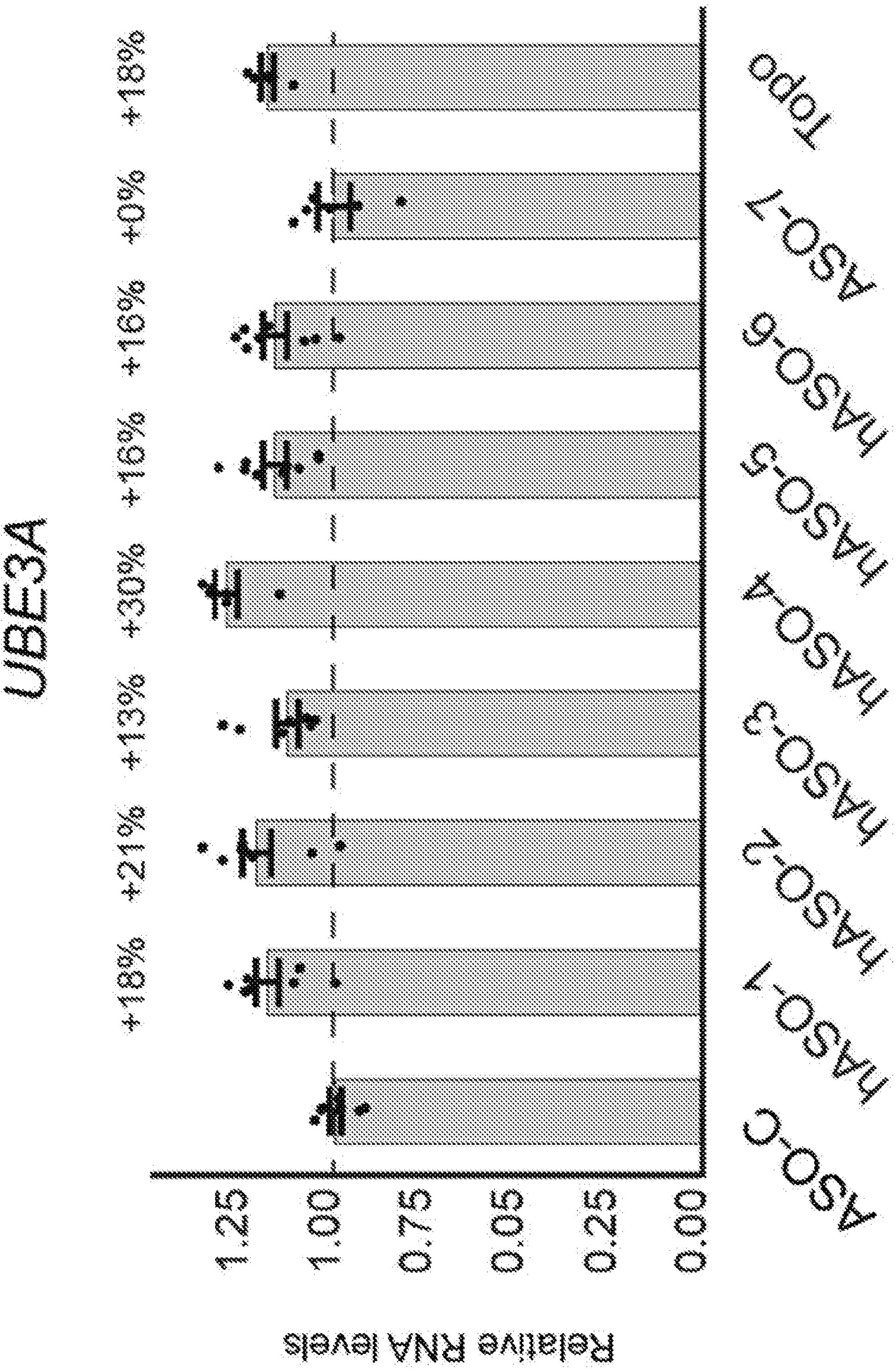

UBE3A
Relative RNA levels
0.00
0.25
0.05
0.75
1.00
1.25
ASO-C
hASO-1
hASO-2
hASO-3
hASO-4
hASO-5
hASO-6
ASO-7
Topo
+18%
+21%
+13%
+30%
+16%
+16%
+0%
+18%

FIG. 3D

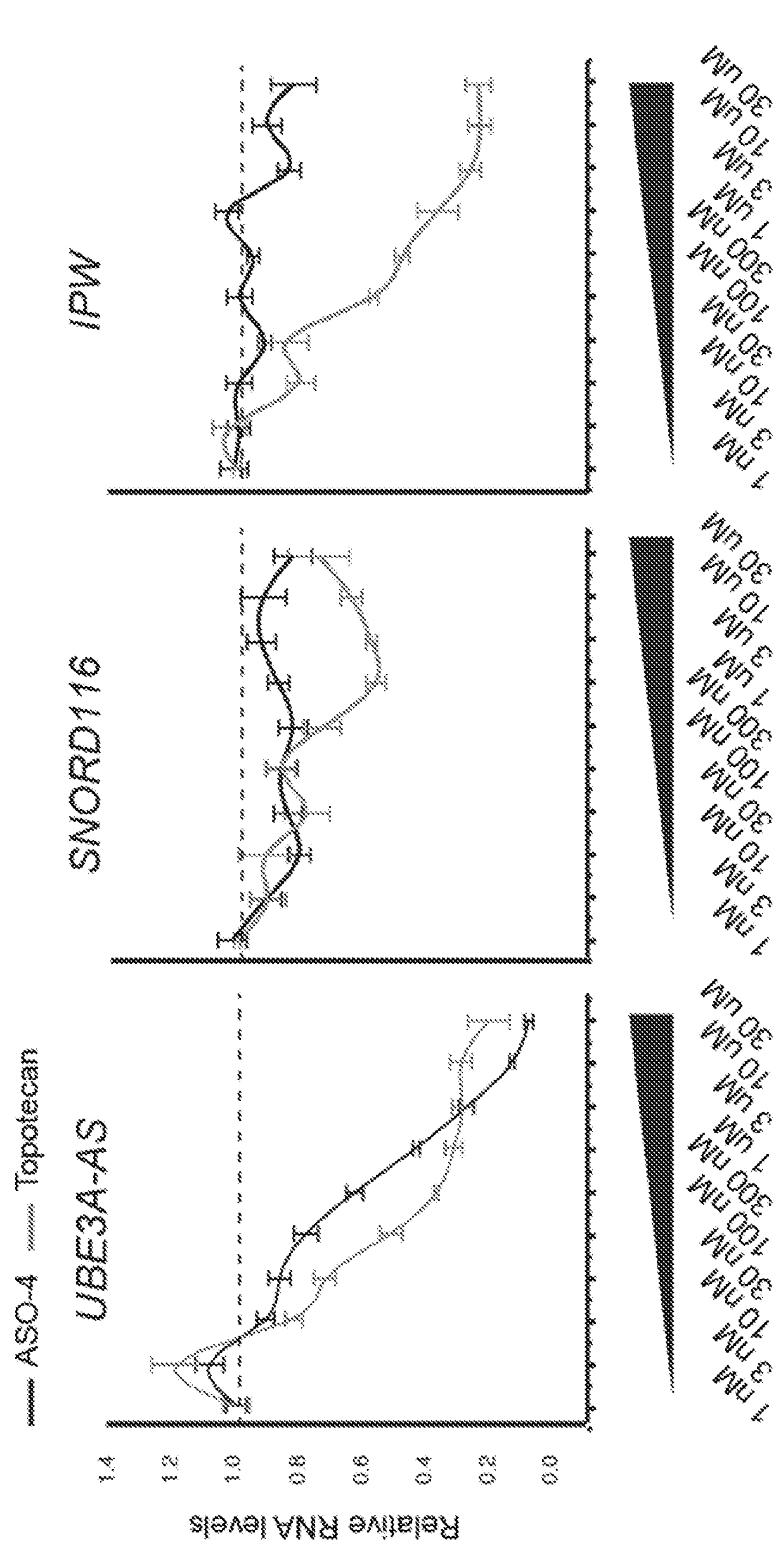


FIG. 4A

FIG. 4B

FIG. 4C

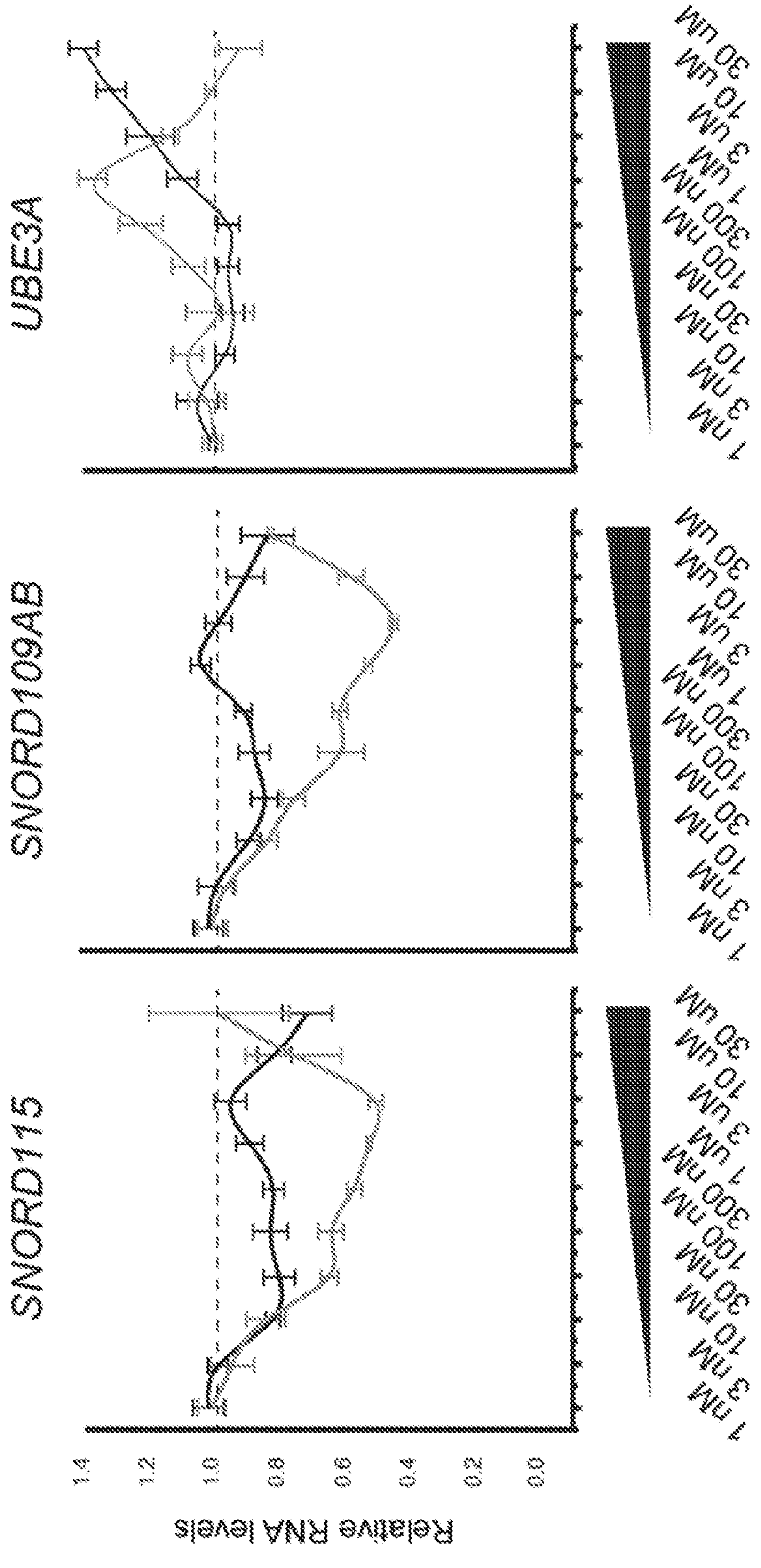


FIG. 4D

FIG. 4E

FIG. 4F

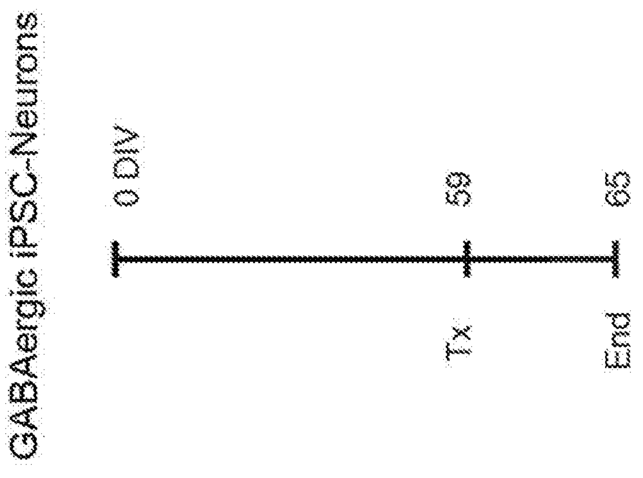


FIG. 4G

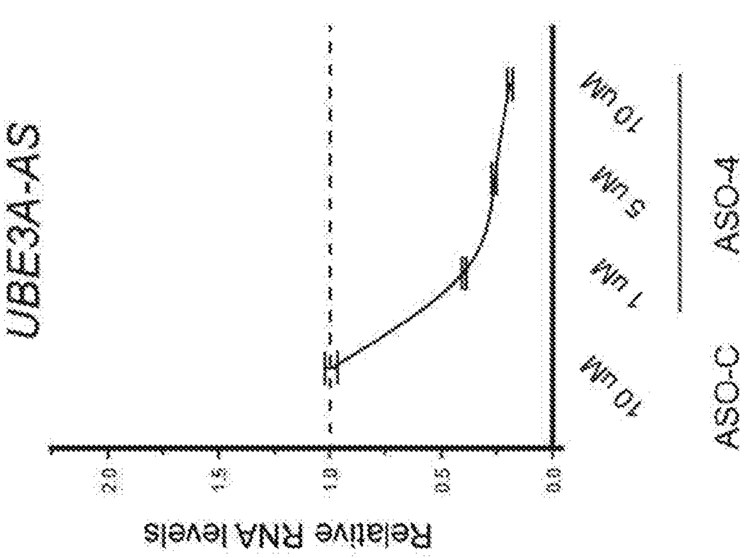


FIG. 4H

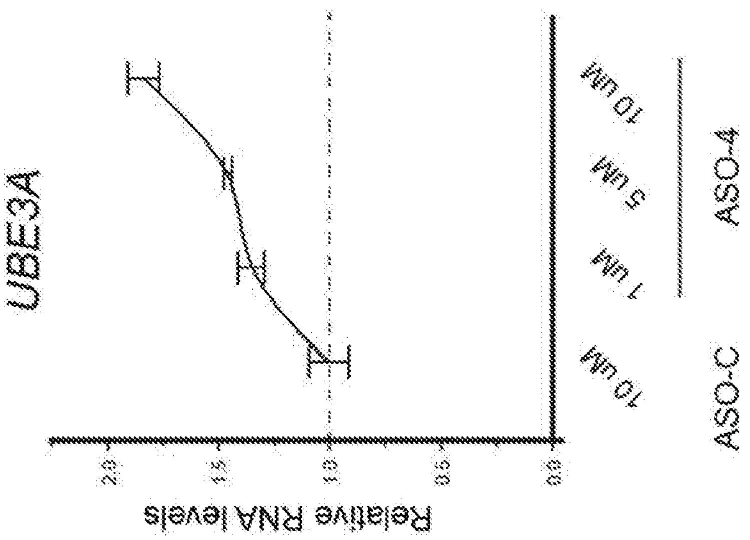


FIG. 4I

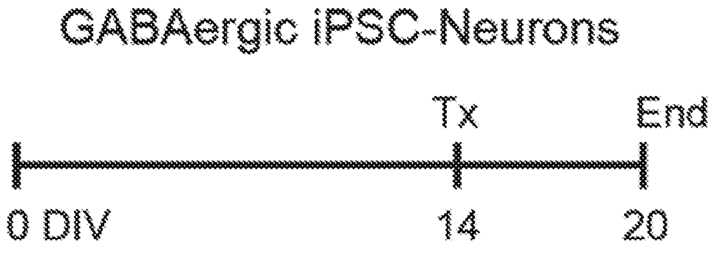

GABAergic iPSC-Neurons
Tx
End
0 DIV
14
20

FIG. 5A

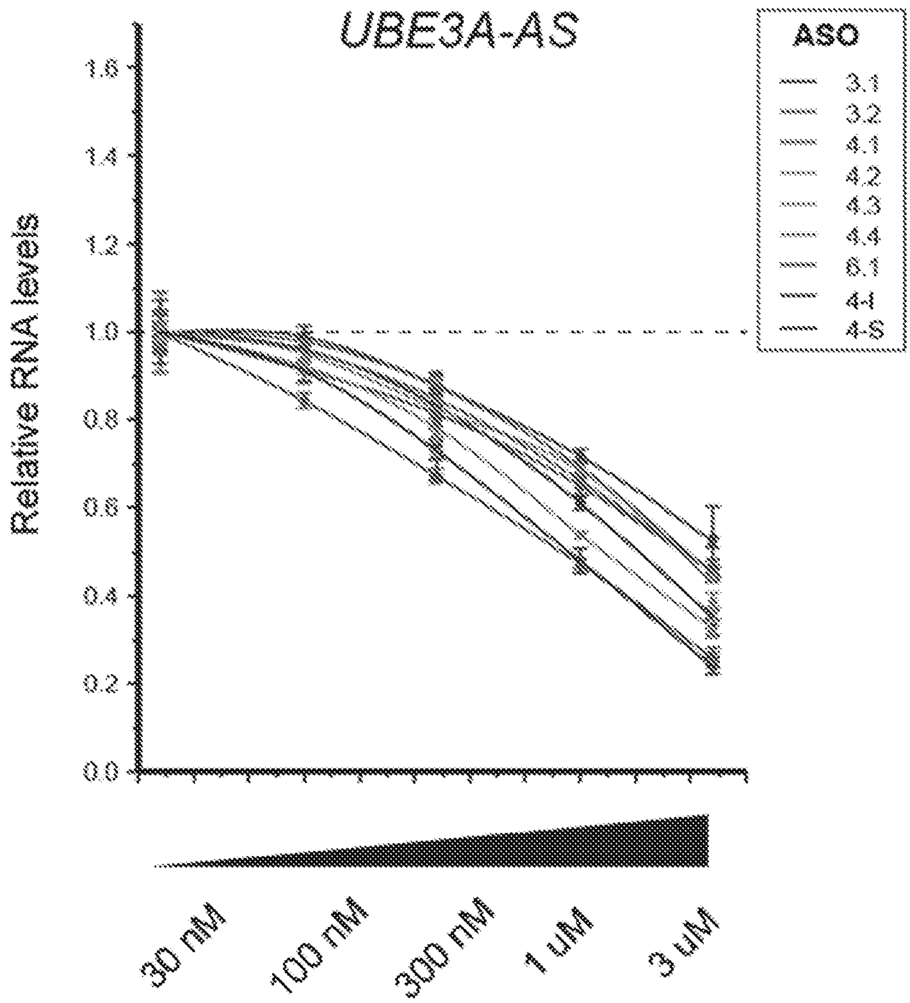

UBE3A-AS
Relative RNA levels
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ASO
3.1
3.2
4.1
4.2
4.3
4.4
6.1
4-I
4-S
30 nM
100 nM
300 nM
1 uM
3 uM

FIG. 5B

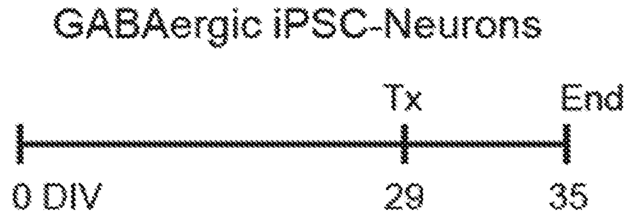

GABAergic iPSC-Neurons
Tx
End
0 DIV
29
35

FIG. 5C

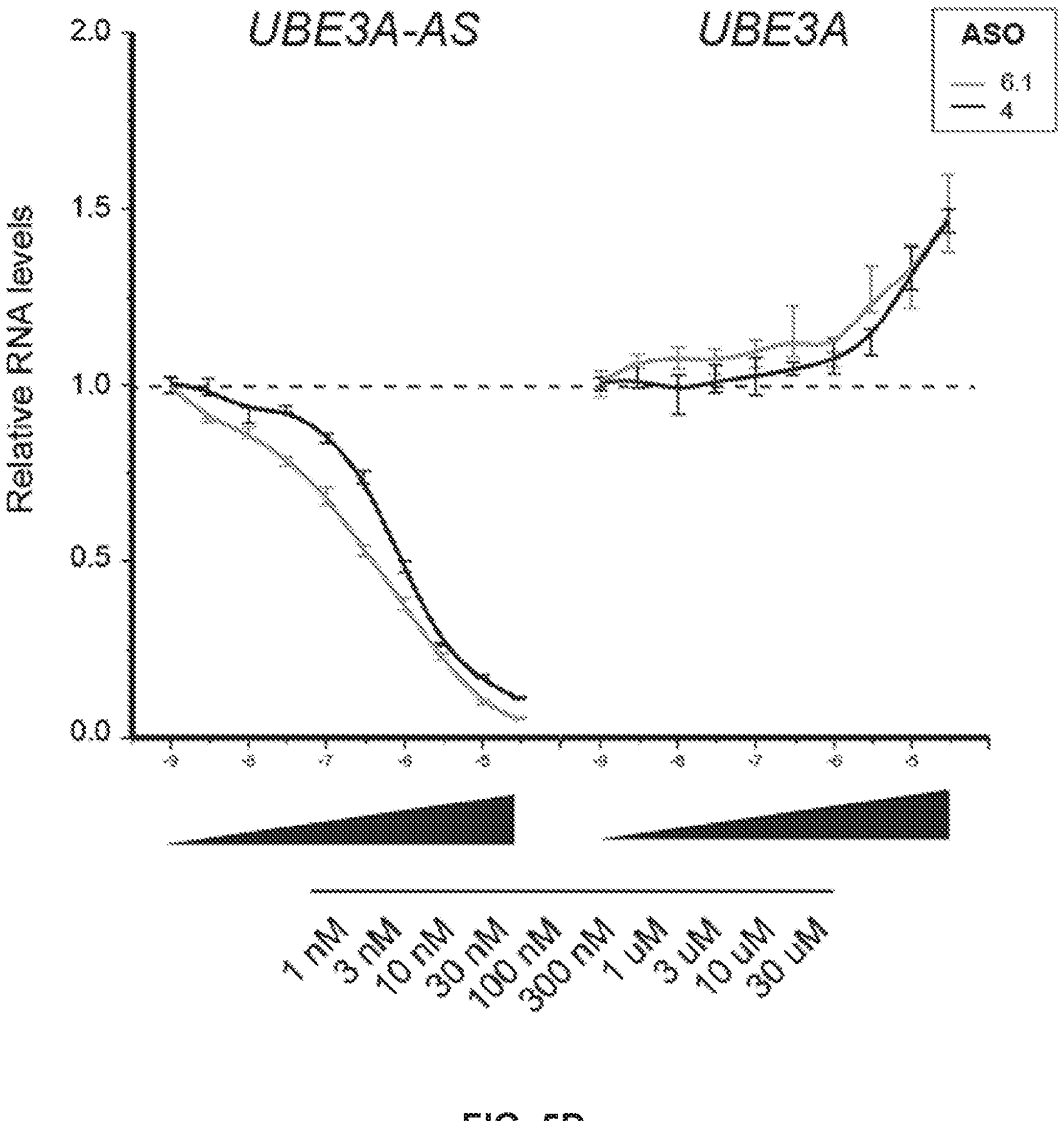

UBE3A-AS
UBE3A
ASO
6.1
4
Relative RNA levels
2.0
1.5
1.0
0.5
0.0
1 nM
3 nM
10 nM
30 nM
100 nM
300 nM
1 uM
3 uM
10 uM
30 uM

FIG. 5D

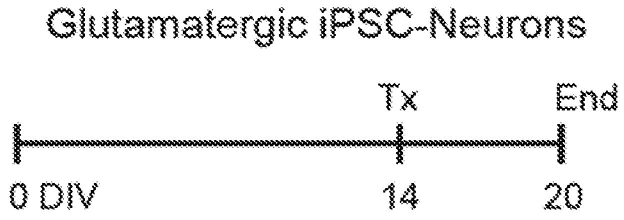

Glutamatergic iPSC-Neurons
Tx
End
0 DIV
14
20

FIG. 5E

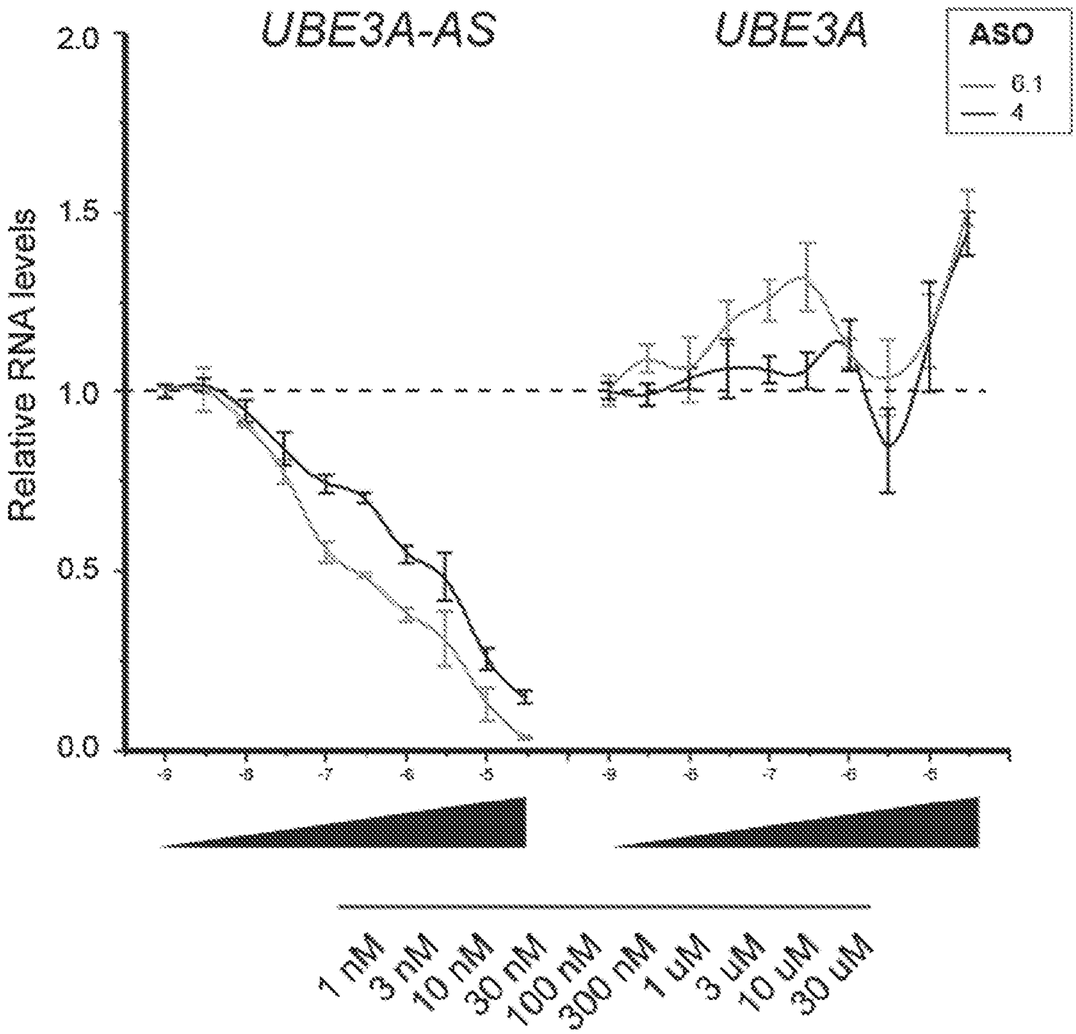

UBE3A-AS
UBE3A
ASO
6.1
4
Relative RNA levels
2.0
1.5
1.0
0.5
0.0
1 nM
3 nM
10 nM
30 nM
100 nM
300 nM
1 uM
3 uM
10 uM
30 uM

FIG. 5F

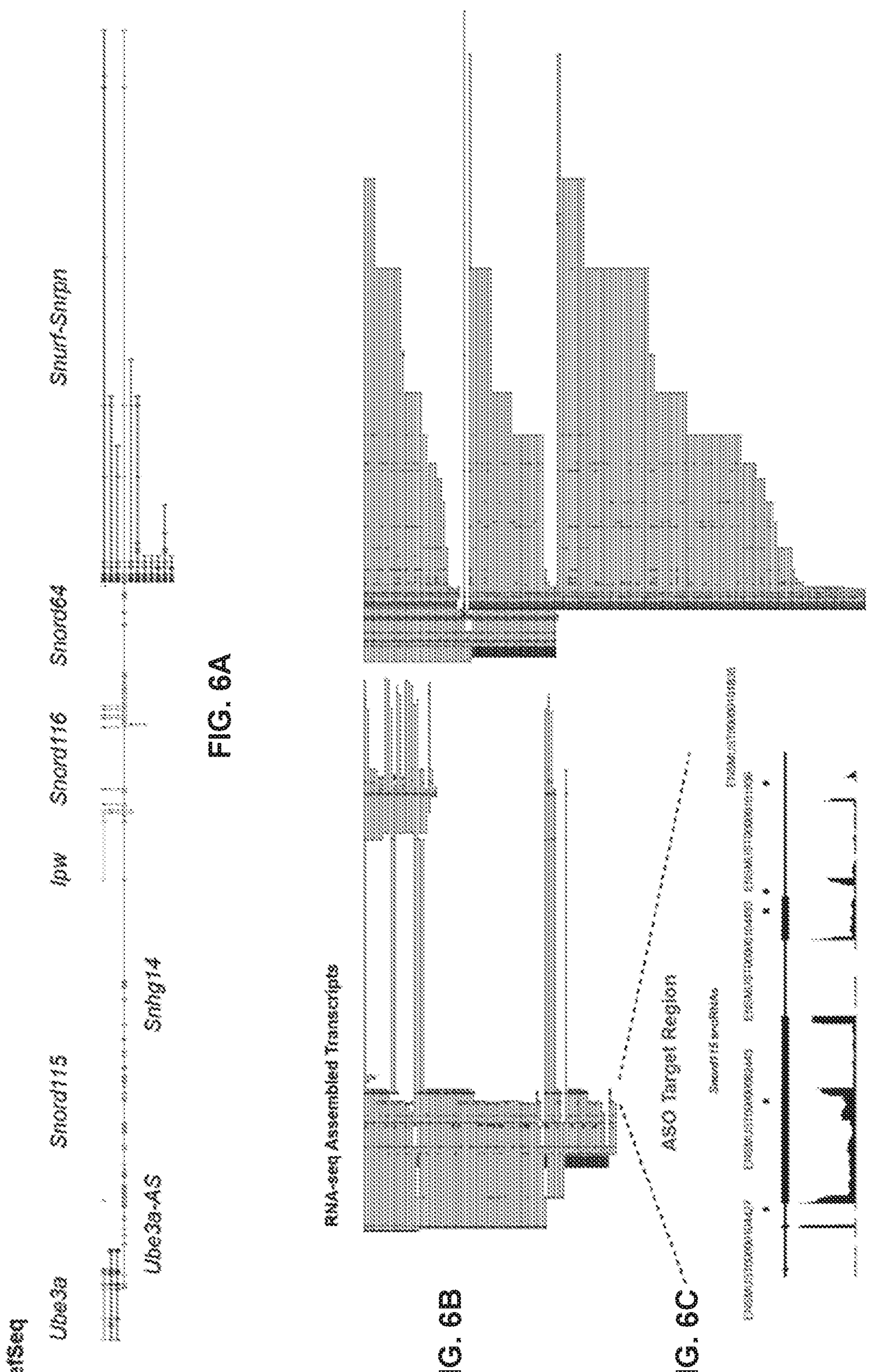


FIG. 6A

FIG. 6B

FIG. 6C

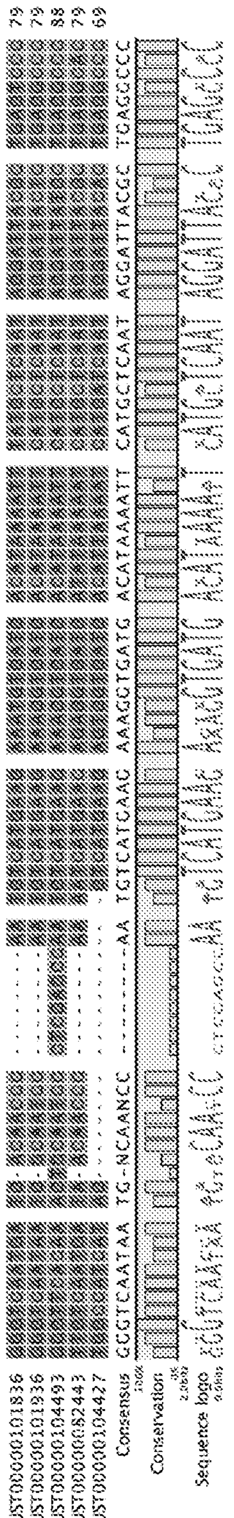

C Box
C'-Box
D Box
Snord115_ENSMUST00000101836
Snord115_ENSMUST00000101936
Snord115_ENSMUST00000104493
Snord115_ENSMUST00000082443
Snord115_ENSMUST00000104427
Consensus
Conservation
Sequence logo
GCGTCAATAA TG-NCAANCC ---------AA TGTCATCAAC AAAGCTGATG ACATAAAATT CATGCTCAAT AGGATTACGC TGAGGCCC
79
79
88
79
69

FIG. 6D

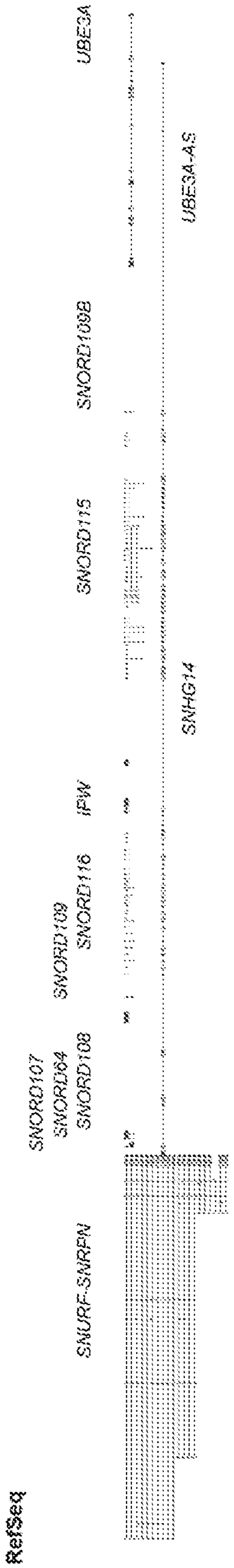

RefSeq
SNURF-SNRPN
SNORD107
SNORD64
SNORD108
SNORD109
SNORD116
IPW
SNORD115
SNHG14
SNORD109B
UBE3A-AS
UBE3A

FIG. 7A

RNA-seq Assembled Transcripts

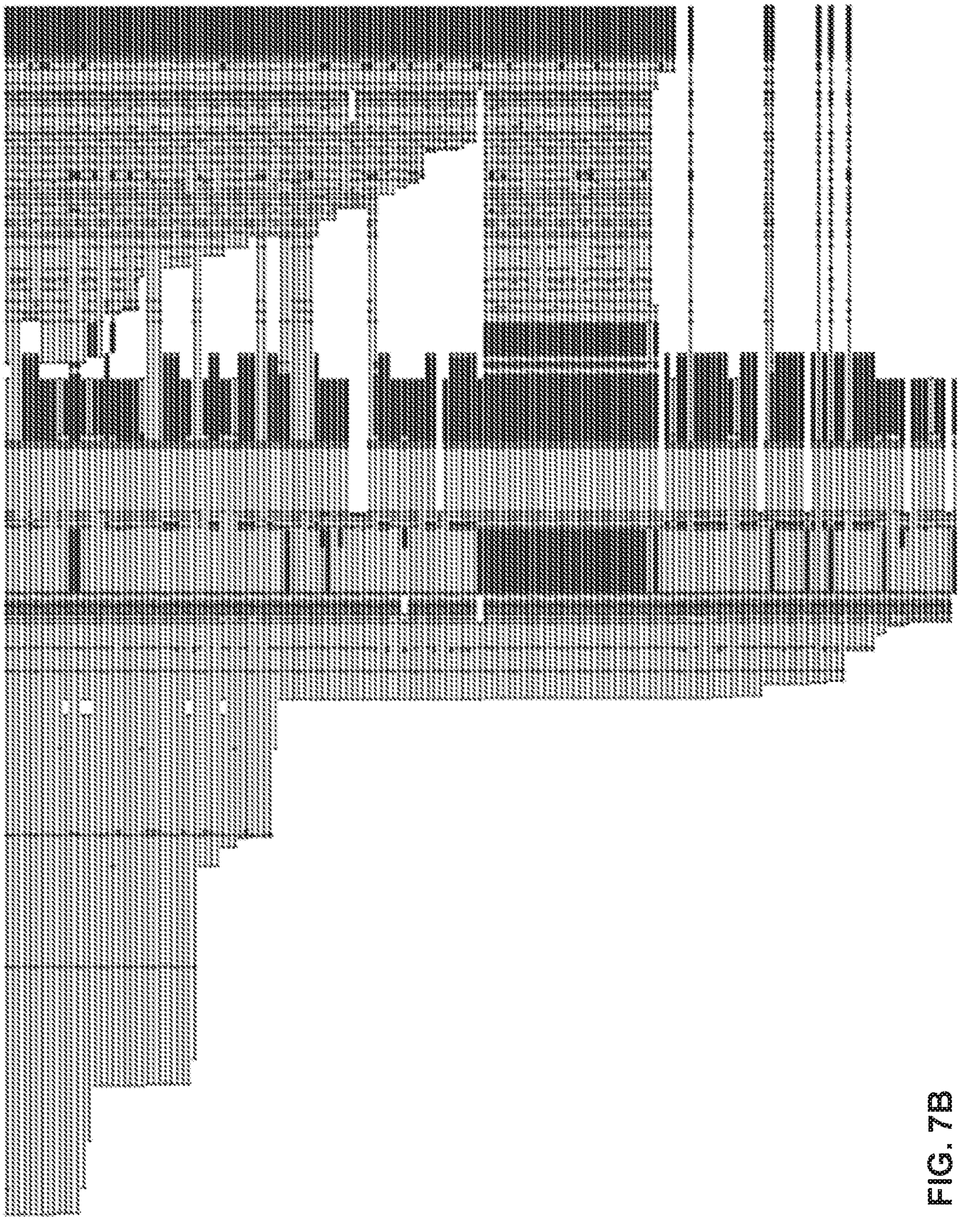


FIG. 7B

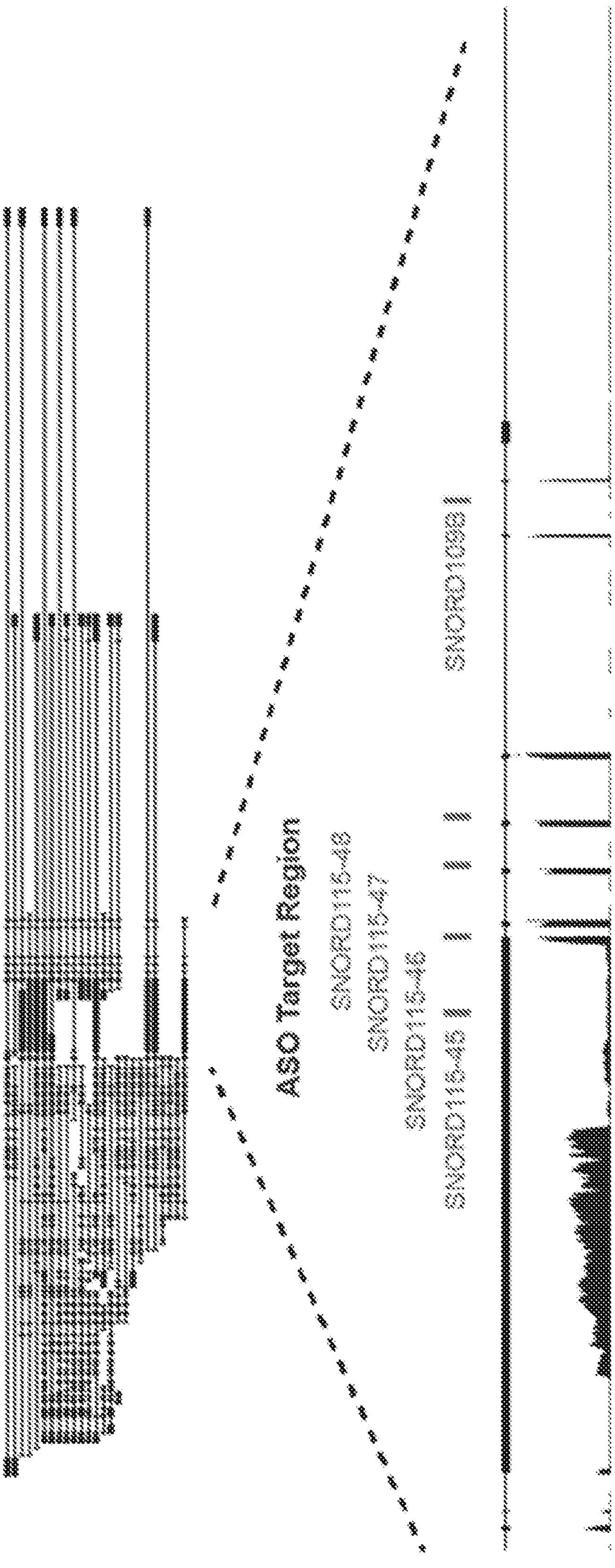
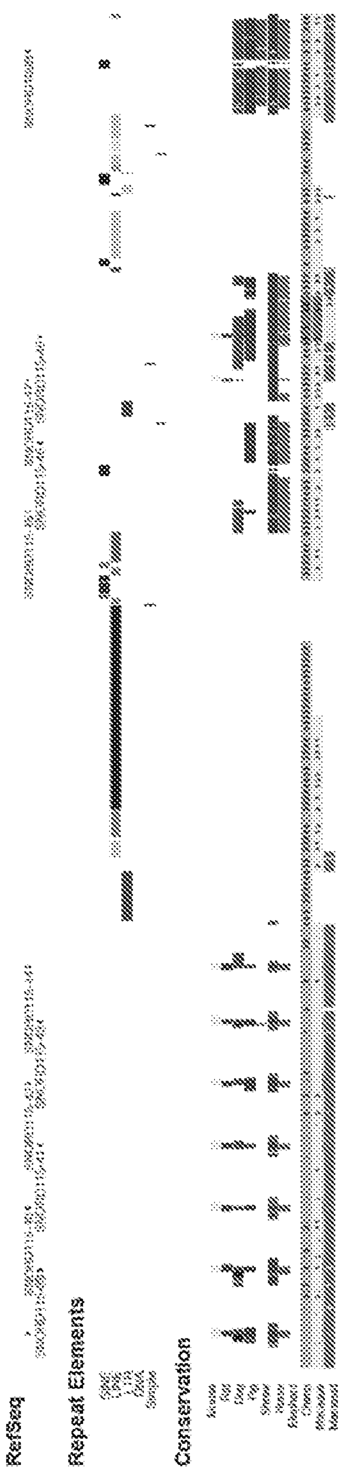

ASO Target Region
SNORD116-48
SNORD116-47
SNORD116-46
SNORD116-45
SNORD109B

FIG. 7C

FIG. 7D

FIG. 7E

FIG. 7F



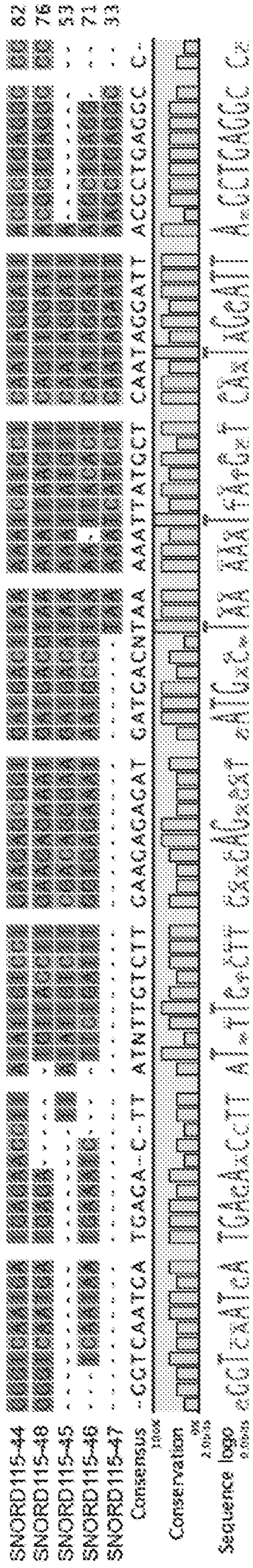


FIG. 7G

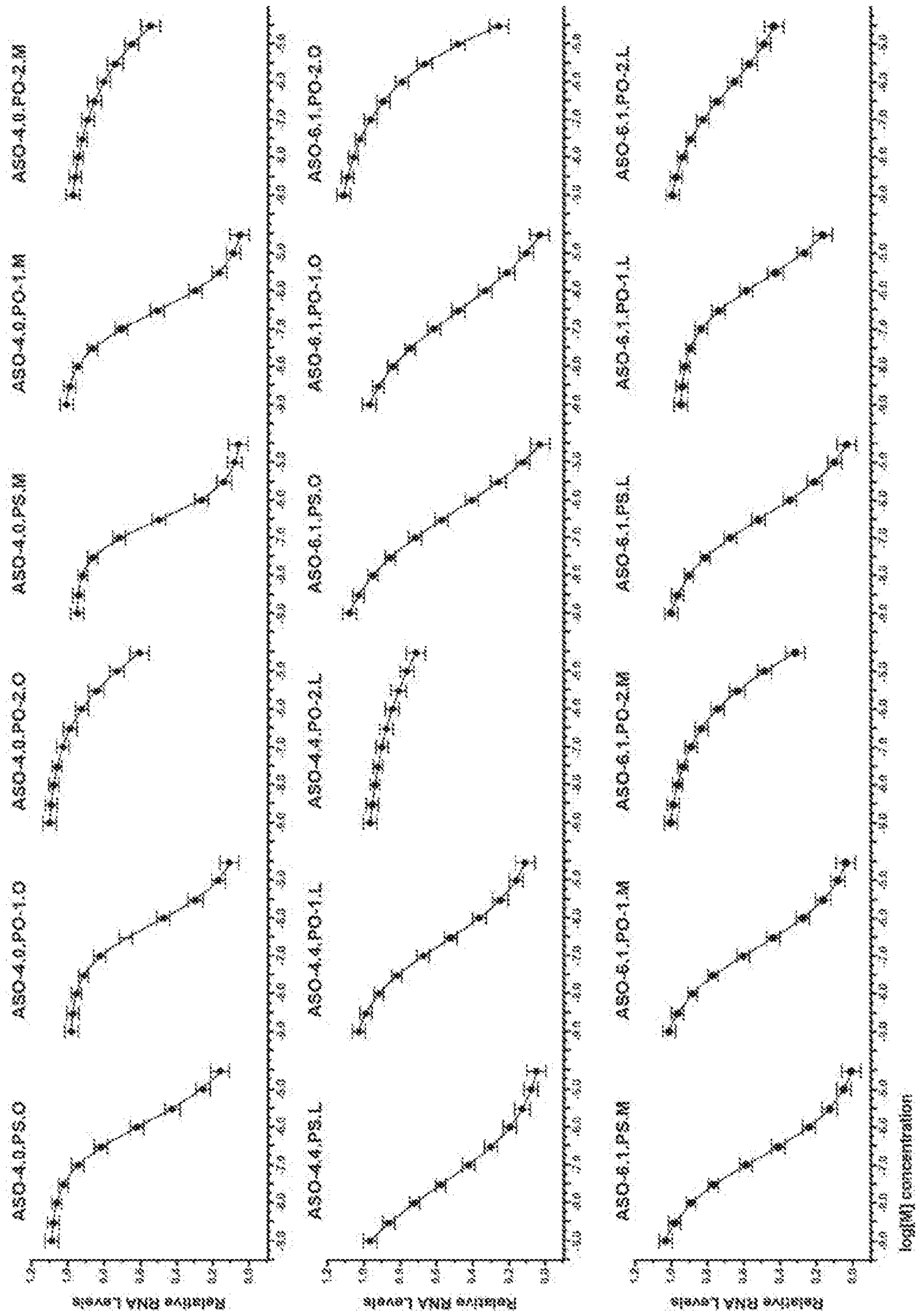

ASO-4.0.PS.O
ASO-4.0.PO-1.O
ASO-4.0.PO-2.O
ASO-4.0.PS.M
ASO-4.0.PO-1.M
ASO-4.0.PO-2.M
ASO-4.4.PS.L
ASO-4.4.PO-1.L
ASO-4.4.PO-2.L
ASO-6.1.PS.O
ASO-6.1.PO-1.O
ASO-6.1.PO-2.O
ASO-6.1.PS.M
ASO-6.1.PO-1.M
ASO-6.1.PO-2.M
ASO-6.1.PS.L
ASO-6.1.PO-1.L
ASO-6.1.PO-2.L
Relative RNA Levels
log[M] concentration

FIG. 8A

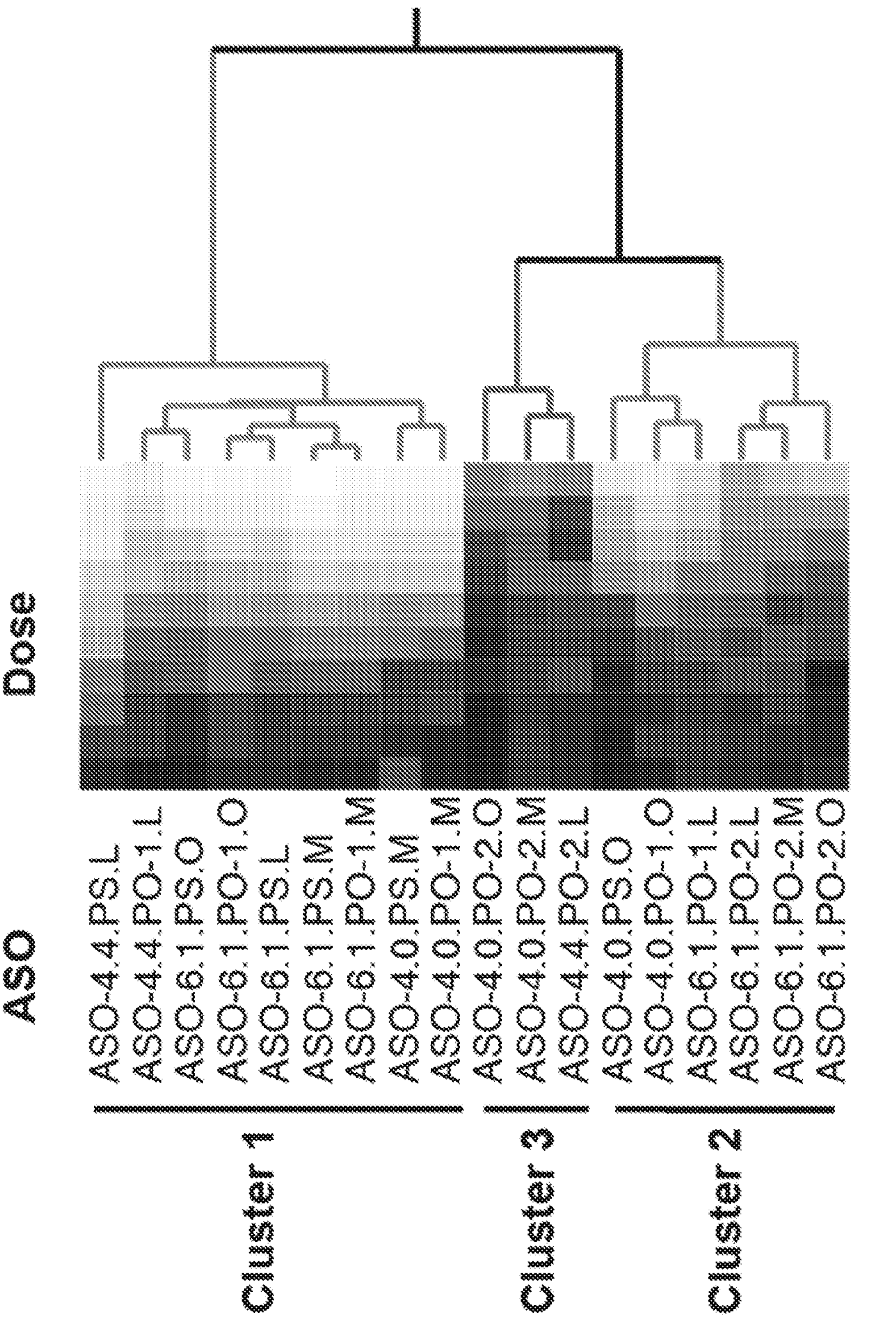

ASO
Dose
ASO-4.4.PS.L
ASO-4.4.PO-1.L
ASO-6.1.PS.O
ASO-6.1.PO-1.O
ASO-6.1.PS.L
ASO-6.1.PS.M
ASO-6.1.PO-1.M
ASO-4.0.PS.M
ASO-4.0.PO-1.M
ASO-4.0.PO-2.O
ASO-4.0.PO-2.M
ASO-4.4.PO-2.L
ASO-4.0.PS.O
ASO-4.0.PO-1.O
ASO-6.1.PO-1.L
ASO-6.1.PO-2.L
ASO-6.1.PO-2.M
ASO-6.1.PO-2.O
Cluster 1
Cluster 3
Cluster 2

FIG. 8B

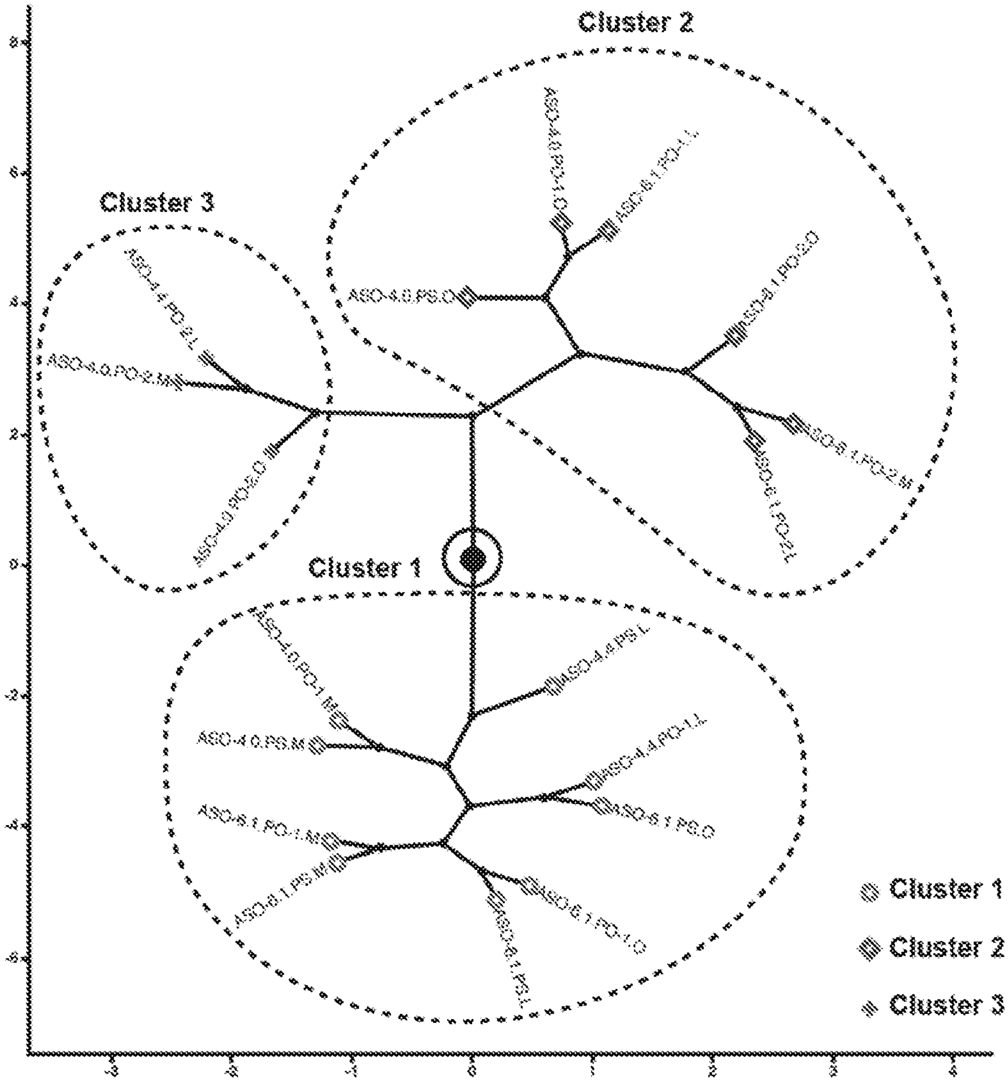

Cluster 1
Cluster 2
Cluster 3
ASO-4.0.PS.O
ASO-6.1.PO-1.L
ASO-6.1.PO-2.O
ASO-6.1.PO-2.M
ASO-4.0.PO-2.M
ASO-4.4.PS.L
ASO-4.0.PO-1.M
ASO-4.0.PS.M
ASO-4.4.PO-1.L
ASO-6.1.PS.O
ASO-6.1.PO-1.M
ASO-6.1.PS.M
ASO-6.1.PO-1.O
ASO-6.1.PS.L
-3
-2
-1
0
1
2
3
4
8
6
4
2
0
-2
-4
-6

FIG. 8C

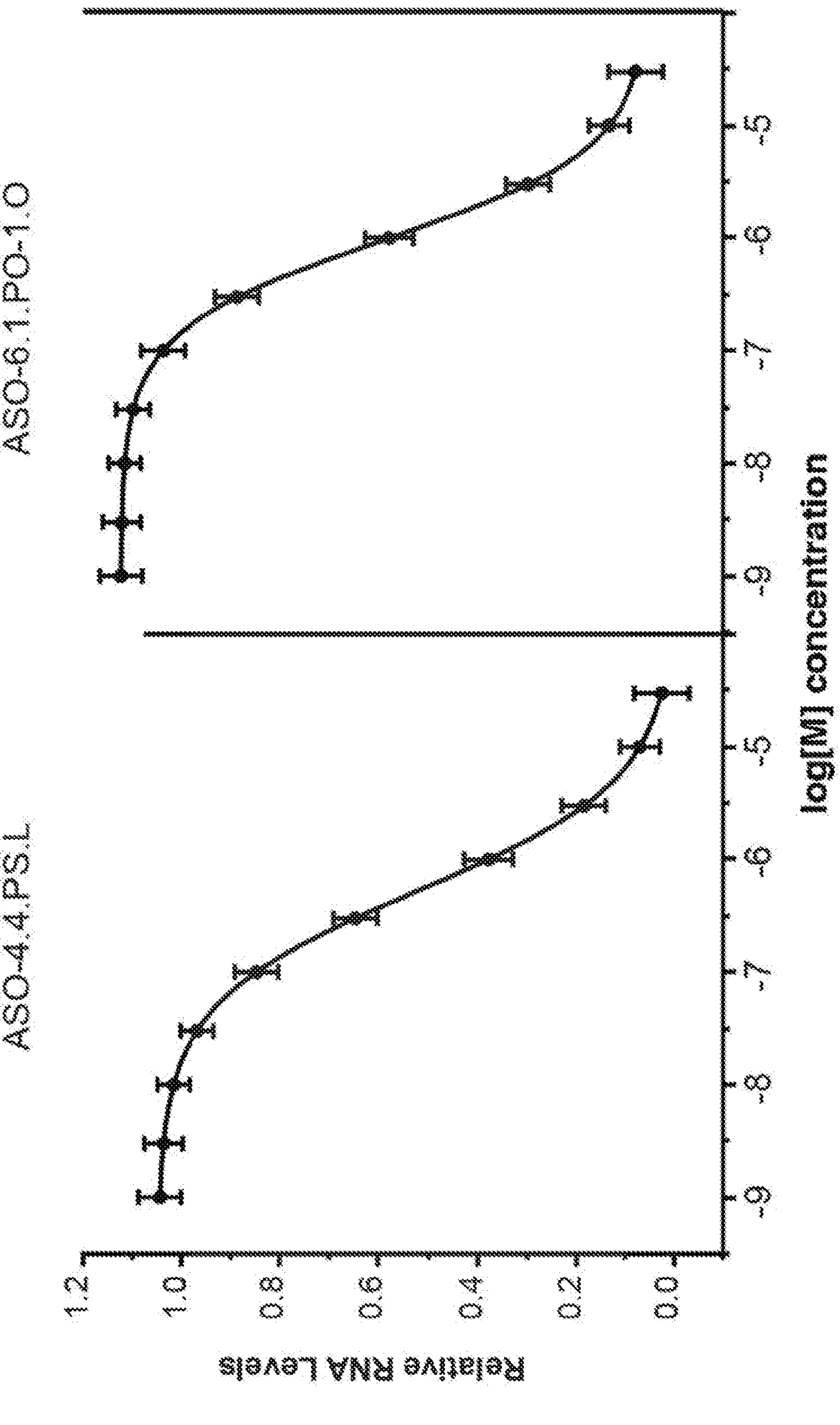

ASO-4.4.PS.L
ASO-6.1.PO-1.O
Relative RNA Levels
1.2
1.0
0.8
0.6
0.4
0.2
0.0
-9
-8
-7
-6
-5
log[M] concentration

FIG. 9

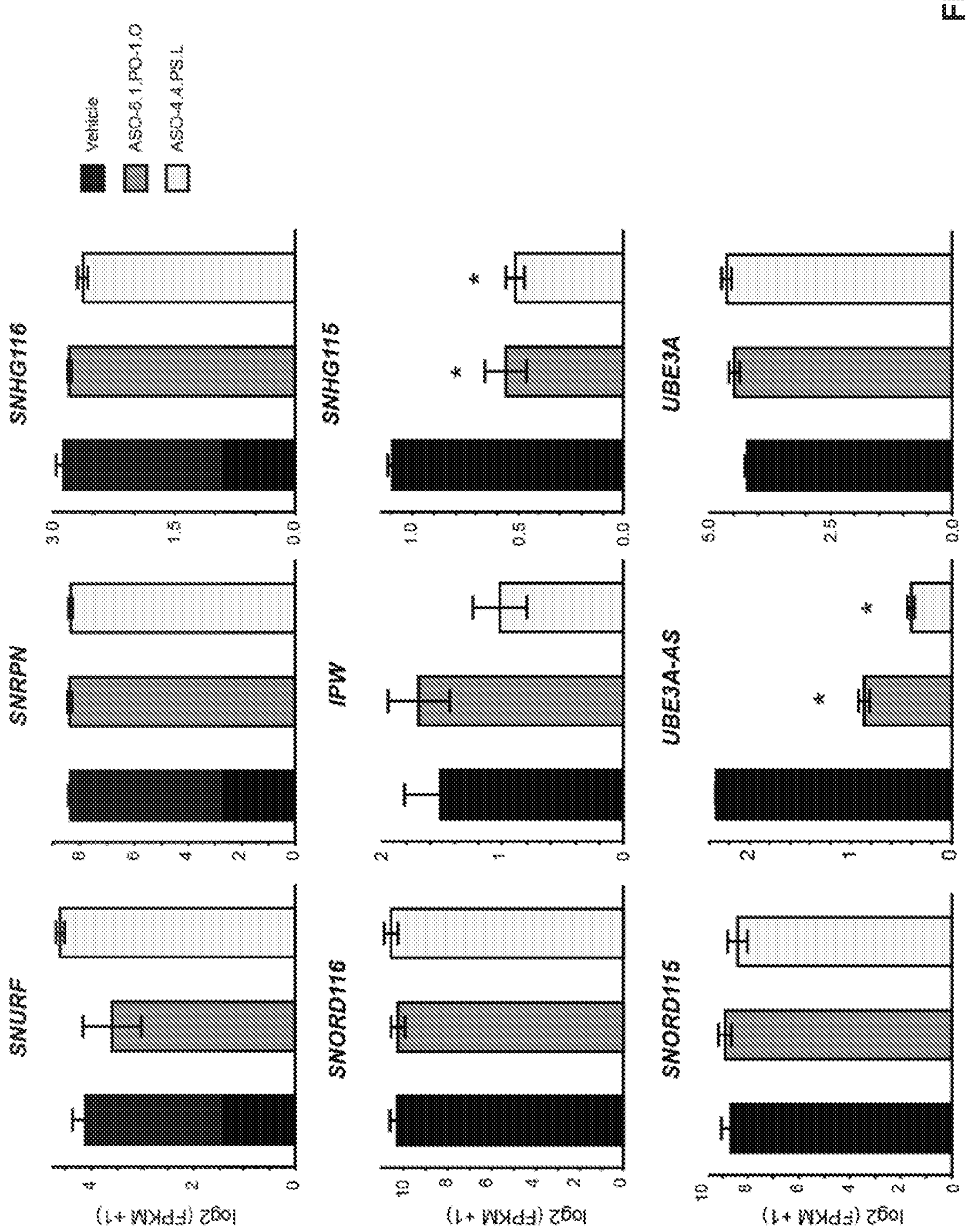

SNURF
SNRPN
SNHG116
SNORD116
IPW
SNHG115
SNORD115
UBE3A-AS
UBE3A
log2 (FPKM +1)
Vehicle
ASO-6.1.PO-1.O
ASO-4.4.PS.L
*

FIG. 10

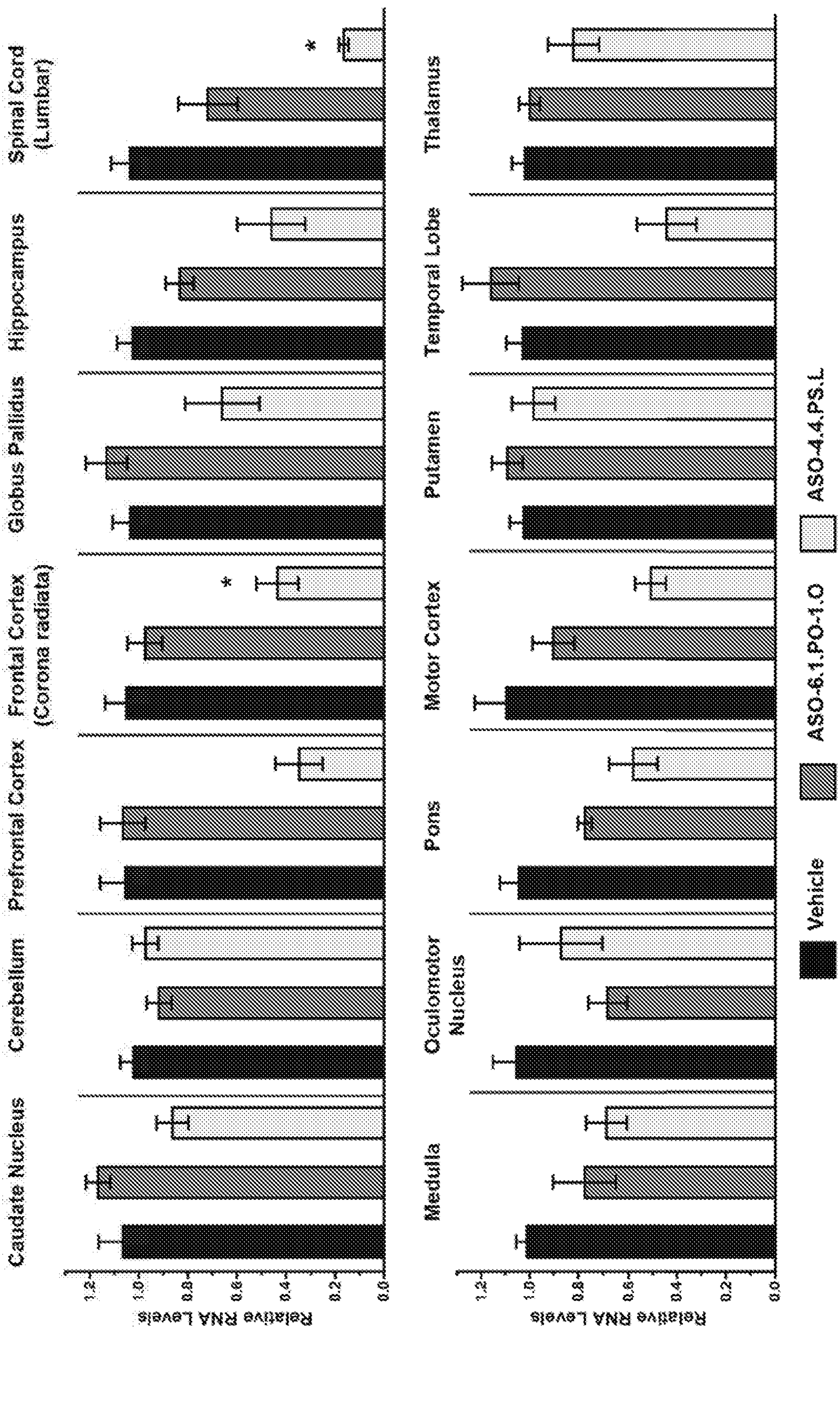

Caudate Nucleus
Cerebellum
Prefrontal Cortex
Frontal Cortex (Corona radiata)
Globus Pallidus
Hippocampus
Spinal Cord (Lumbar)
Medulla
Oculomotor Nucleus
Pons
Motor Cortex
Putamen
Temporal Lobe
Thalamus
Relative RNA Levels
1.2
1.0
0.8
0.6
0.4
0.2
0.0
*
*
Vehicle
ASO-6.1.PO-1.O
ASO-4.4.PS.L

FIG. 11

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 18/63416

A. CLASSIFICATION OF SUBJECT MATTER
IPC(8) - C12N 15/11; A61K 48/00; C07H 21/04; C12N 15/00 (2019.01)
CPC - C12N 15/113; A61K 48/00; C12N 2310/14; C12N 2310/11; C12N 15/00; C12N 15/8; C12N 2800/10

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
See Search History Document

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
See Search History Document

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
See Search History Document

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US 2015/0191723 A1 (ISIS PHARMACEUTICALS, INC. et al.) 09 July 2015 (09.07.2015), Abstract, para [0011], [0014], [0032], [0047], [0048], [0062], [0064], [0082], [0109], [0114], [0131], [0143],[0146], [0147], [0148], [0149], [0164], [0206], [0271], [0346], and SEQ ID NO: 2 (615382 nt), the region between nucleotides 442785-442968, 442308-442289, and 443266-443398	1-11
A	MENG et al., Towards a therapy for Angelman syndrome by reduction of a long non-coding RNA. Nature. 2015, Vol. 518(7539), p. 409-12. PDF File: pg 1-20. Entire Documentation, especially Abstract; pg 1; and pg 4, last para	1-11
A	BUREL et al., Hepatotoxicity of high affinity gapmer antisense oligonucleotides is mediated by RNase H1 dependent promiscuous reduction of very long pre-mRNA transcripts. Nucleic Acids Res. 2016, Vol. 44(5), p. 2093-109. Entire Documentation, especially Abstract; pg 2093, col 2; pg 2094, col 2, last para; pg 2095, col 1, para 1, and Table 1; and pg 2096, Table 2	1-11

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:
"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier application or patent but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
01 February 2019	10 MAY 2019

Name and mailing address of the ISA/US	Authorized officer:
Mail Stop PCT, Attn: ISA/US, Commissioner for Patents P.O. Box 1450, Alexandria, Virginia 22313-1450 Facsimile No. 571-273-8300	Lee W. Young PCT Helpdesk: 571-272-4300 PCT OSP: 571-272-7774

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☒ Claims Nos.: 12-13
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Groups I+, Claims 1-11, directed to an antisense oligonucleotide comprising a contiguous nucleotide sequence of 10 to 30 nucleotides in length. The oligonucleotide will be searched to the extent that the oligonucleotide encompasses SEQ ID NO: 6 or SEQ ID NO: 362; or the oligonucleotide comprising a contiguous nucleotide sequence of 10 to 30 nucleotides in length with at least 98% complementarity to a contiguous portion of nucleic acid sequence SEQ ID NO:1. It is believed that claims 1-2 (in part), 3-10, and 11 (in part) encompass this first named invention, and thus these claims will be searched without fee to the extent that they encompass the oligonucleotide encompasses SEQ ID NO: 6 or SEQ ID NO: 362; or the oligonucleotide comprising a contiguous nucleotide sequence of 10 to 30 nucleotides in length with at least 98% complementarity to a contiguous portion of nucleic acid sequence SEQ ID NO: 1.

************************Continued in the extra sheet**********************************

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-2 (in part), 3-10, and 11 (in part), limited to SEQ ID NO: 1, SEQ ID NO: 6, SEQ ID NO: 362

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.

Continuation of:
Box No III (unity of invention is lacking)

(Continuation of Groups I+) Additional oligonucleotide will be searched upon the payment of additional fees. Applicants must specify the claims that encompass any additionally elected oligonucleotides. Applicants must further indicate, if applicable, the claims which encompass the first named invention, if different than what was indicated above for this group. Failure to clearly identify how any paid additional invention fees are to be applied to the "+" group(s) will result in only the first claimed invention to be searched. An exemplary election would be the oligonucleotide encompasses SEQ ID NO: 7 or SEQ ID NO: 363; or the oligonucleotide comprising a contiguous nucleotide sequence of 10 to 30 nucleotides in length with at least 98% complementarity to a contiguous portion of nucleic acid sequence SEQ ID NO: 5 [claims 1-2 (in part), (3-10), 11 (in part)]. [Please Note: 1) This Application does not provide a clear description for the association of SEQ ID NO: 6 or SEQ ID NO: 7 with any one of SEQ ID NOs: 1-5. Therefore, there is no association between searching SEQ ID NO: 1 and SEQ ID NO: 6 or SEQ ID NO: 362; 2) the association of SEQ ID NO: 7 with SEQ ID NO: 5 is determined by manual comparison of a complementary strand of SEQ ID NO: 7 with SEQ ID NOs: 1-5, to obtain SEQ ID NO: 7 is complementary to the nucleotides between 5-24 of SEQ ID NO: 5; Specification: pg 19, ln 19-21, SEQ ID NO: 5; and ln 25, SEQ ID NO: 7]

The inventions listed as Groups I+ do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

Special Technical Feature
Among Groups I+, each SEQ ID NO represents a structurally different nucleotide sequence.

Common Technical Features
The inventions of Groups I+ share the technical features of an antisense oligonucleotide comprising a contiguous nucleotide sequence of 10 to 30 nucleotides in length with at least 98% complementarity to a contiguous portion of nucleic acid sequence of a selected SEQ ID NO, such as SEQ ID NO: 1 (part of claim 1); and
--part of the inventions of Groups I+ (claim 11) further shares the technical feature of wherein the oligonucieotide comprising one or more modified nucleosides (claim 3, or part of claim 11; because claim 11 contains modified oligonucieotides associated with SEQ ID NOs: 6-7; Specification: pg 19, ln 23-25; pg 41, Table 7).

However, these shared technical features do not represent a contribution over prior art as being anticipated by US 2015/0191723 A1 to ISIS PHARMACEUTICALS, INC. et al. (hereinafter 'Isis_Pharm') as follows:

Isis_Pharm discloses an antisense oligonucleotide comprising a contiguous nucleotide sequence of 10 to 30 nucleotides in length (Abstract - 'compounds for inhibiting UBE3A-ATS, the endogenous antisense transcript of ubiquitin protein ligase E3A (UBE3A)'; para [0114] - 'antisense compound can comprise an oligonucleotide consisting of 12 to 30 linked nucleosides')
--with at least 98% complementarity to a contiguous portion of nucleic acid sequence of SEQ ID NO: 1 (Abstract; para [0114] - 'antisense compound can comprise an oligonucleotide consisting of 12 to 30 linked nucleosides, wherein the oligonucleotide is at least 85% complementary to a UBE3A-ATS nucleic acid sequence'; para [0109] - 'antisense compound targeted to UBE3A-ATS... UBE3A-ATS comprises a nucleic acid sequence at least 85% identical to...SEQ ID NO: 2', wherein SEQ ID NO: 2 consisting of 615382 nucleosides and comprising a region between nucleosides 442785-442968, that is 100% identical to the claimed SEQ ID NO: 1).

Isis_Pharm further discloses wherein the oligonucieotide comprising one or more modified nucleosides (para 0047] - 'Fully modified motif...refers to an antisense compound comprising a contiguous sequence of nucleosides wherein essentially each nucleoside is a sugar modified nucleoside having uniform modification').

Without a shared special technical feature, the inventions lack unity with one another.

Groups I+ therefore lack unity under PCT Rule 13 because they do not share a same or corresponding special technical feature.

Continuation of item 4: Claims 12-13 are not drafted in accordance with the second and third sentences of Rule 6.4 (a). These claims are improper multiple dependent claims.

Note:

I) This Application does not provide a clear description for the association of each of SEQ ID NOs: 6-11 with any one of SEQ ID NOs: 1-5 (Specification; pg 19, ln 2-33; pg 21-27, Table 1-5). According to the Specification, SEQ ID NOs: 1-5 are sequences of exons 1-5, respectively (Specification: pg 19, ln 2-21). However, based on the sequence search results, SEQ ID NO: 6 is located at the 5', upstream of SEQ ID NO: 1 (exon 1); as evident by US 2015/0191723 A1 to ISIS PHARMACEUTICALS, INC. et al. (hereinafter 'ISIS_PHARM': para [0109] - 'antisense compound targeted to UBE3A-ATS... UBE3A-ATS comprises a nucleic acid sequence at least 85% identical to...SEQ ID NO: 2', wherein SEQ ID NO: 2 consisting of 615382 nucleosides and comprising a region between 442785-442968, that is 100% identical to the claimed SEQ ID NO: 1; and comprising a region between 442308-442289, that is 100% identical to the claimed SEQ ID NO: 6, which is located at the 5', upstream of SEQ ID NO: 1).

The SEQ ID NO: 6 is located at the 5', upstream of SEQ ID NO: 1, is supported by a further sequence search of the claimed SEQ ID NO: 2 (exon 2; Specification: pg 19, ln 7-9), which is located at the 3', downstream of SEQ ID NO: 1, as evident by ISIS_PHARM (para [0109] - 'antisense compound targeted to UBE3A-ATS... UBE3A-ATS comprises a nucleic acid sequence at least 85% identical to...SEQ ID NO: 2', wherein SEQ ID NO: 2 consisting of 615382 nucleosides and comprising a region between 442785-442968, that is 100% identical to the claimed SEQ ID NO: 1, and comprising a region between nucleosides 443266-443398, that is100% to the claimed SEQ ID NO: 2).