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**Treatment Of Inflammation With Glucocorticoids And Angiopoietin-Like 7
(ANGPTL7) Inhibitors**

Reference To Sequence Listing

5 This application includes a Sequence Listing submitted electronically as a text file named 18923806702SEQ, created on February 22, 2022, with a size of 111 kilobytes. The Sequence Listing is incorporated herein by reference.

Field

10 The present disclosure relates generally to the treatment of subjects having inflammation with an Angiopoietin-Like 7 (ANGPTL7) inhibitor and a glucocorticoid, methods of decreasing glucocorticoid-induced ophthalmic conditions in subjects, and methods of identifying subjects having an increased risk of developing glucocorticoid-induced ophthalmic conditions.

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Background

 Glucocorticoids (GCs) are one of the most commonly prescribed medications worldwide for the treatment of a plethora of diseases and conditions. Because of their broad-spectrum anti-inflammatory and immunosuppressive properties, the worldwide market for GC use is estimated to be greater than \$10 billion per year. Approximately 1.2% of the United States population and 0.85% of the United Kingdom population are prescribed therapeutic GCs every year. GCs also remain the mainstay of treatment for a variety of ocular inflammatory diseases involving almost all tissues of the eye, such as eyelids, conjunctiva, cornea, sclera, uvea, retina, and optic nerve. The routes of GC administration in treatment of these disorders can be topical ocular, oral, systemic, intravitreal injection, implants, and periocular injections (including, for example, subconjunctival, subtenon, retrobulbar, and peribulbar). Prolonged GC therapy, however, can be associated with serious, unwanted GC-induced ophthalmic conditions, including development of posterior subcapsular cataracts, the development of GC-induced ocular hypertension (GC-OHT), and iatrogenic open-angle glaucoma. About 40% of individuals exposed to long-term steroids develop steroid-induced ocular hypertension and this risk can increase to about 90% in individuals who already have glaucoma. Thus, decreasing or preventing GC-induced ophthalmic conditions is desirable.

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Summary

The present disclosure provides methods of treating a subject undergoing treatment with a steroid, the methods comprising administering an ANGPTL7 inhibitor to the subject.

5 The present disclosure provides methods of treating a subject having inflammation, the methods comprising administering an ANGPTL7 inhibitor and a glucocorticoid to the subject.

The present disclosure also provides methods of treating a subject having rheumatoid arthritis, the methods comprising administering an ANGPTL7 inhibitor and a glucocorticoid to the subject.

10 The present disclosure also provides methods of treating a subject having Grave's disease, the methods comprising administering an ANGPTL7 inhibitor and a glucocorticoid to the subject.

The present disclosure also provides methods of treating a subject having ophthalmic inflammation, the methods comprising administering an ANGPTL7 inhibitor and a
15 glucocorticoid to the subject.

The present disclosure provides methods of decreasing a steroid-induced ophthalmic condition in a subject treated with a steroid, the methods comprising administering an ANGPTL7 inhibitor to the subject.

20 The present disclosure also provides methods of decreasing a glucocorticoid-induced ophthalmic condition in a subject treated with a glucocorticoid, the methods comprising administering an ANGPTL7 inhibitor to the subject.

The present disclosure provides methods of treating a subject having inflammation and undergoing steroid treatment, the methods comprising administering an ANGPTL7 inhibitor to the subject.

25 The present disclosure also provides methods of treating a subject having inflammation and undergoing glucocorticoid treatment, the methods comprising administering an ANGPTL7 inhibitor to the subject.

The present disclosure also provides methods of treating a subject having rheumatoid arthritis and undergoing glucocorticoid treatment, the methods comprising administering an
30 ANGPTL7 inhibitor to the subject.

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The present disclosure also provides methods of treating a subject having Grave's disease and undergoing glucocorticoid treatment, the methods comprising administering an ANGPTL7 inhibitor to the subject.

5 The present disclosure also provides methods of treating a subject having ophthalmic inflammation and undergoing glucocorticoid treatment, the methods comprising administering an ANGPTL7 inhibitor to the subject.

The present disclosure also provides methods of treating a subject undergoing glucocorticoid treatment, wherein the subject is suffering from inflammation, the methods comprising: determining whether the subject has an ANGPTL7 predicted loss-of-function variant nucleic acid molecule encoding an ANGPTL7 polypeptide by: obtaining or having
10 obtained a biological sample from the subject; and performing or having performed a sequence analysis on the biological sample to determine if the subject has a genotype comprising the ANGPTL7 predicted loss-of-function variant nucleic acid molecule; and administering or continuing to administer to a subject that is ANGPTL7 reference the glucocorticoid in a standard
15 dosage amount, and administering an ANGPTL7 inhibitor to the subject; or administering or continuing to administer to a subject that is heterozygous for the ANGPTL7 predicted loss-of-function variant the glucocorticoid in an amount that is the same as or higher than a standard dosage amount, and administering an ANGPTL7 inhibitor to the subject; or administering or continuing to administer to a subject that is homozygous for the ANGPTL7 predicted loss-of-
20 function variant the glucocorticoid in an amount that is the same as or higher than a standard dosage amount; wherein the presence of a genotype having the ANGPTL7 predicted loss-of-function variant nucleic acid molecule encoding the ANGPTL7 polypeptide indicates the subject has a decreased risk of developing a glucocorticoid-induced ophthalmic condition.

The present disclosure also provides methods of identifying a subject undergoing
25 glucocorticoid treatment having an increased risk for developing a glucocorticoid-induced ophthalmic condition, the method comprising: determining or having determined the presence or absence of an ANGPTL7 predicted loss-of-function variant nucleic acid molecule encoding an ANGPTL7 polypeptide in a biological sample obtained from the subject; wherein: when the subject is ANGPTL7 reference, then the subject has an increased risk for developing the
30 glucocorticoid-induced ophthalmic condition; and when the subject is heterozygous or homozygous for an ANGPTL7 predicted loss-of-function variant, then the subject does not have an increased risk for developing the glucocorticoid-induced ophthalmic condition.

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The present disclosure also provides combinations of a glucocorticoid and an ANGPTL7 inhibitor for use in the treatment of inflammation in a subject identified as having: a genomic nucleic acid molecule having a nucleotide sequence encoding an ANGPTL7 polypeptide, wherein the nucleotide sequence comprises: a thymine at a position corresponding to position 4,291 according to SEQ ID NO:2, or the complement thereof; a thymine at a position corresponding to position 4,287 according to SEQ ID NO:3, or the complement thereof; an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4, or the complement thereof; an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5, or the complement thereof; or a cytosine at a position corresponding to position 4,336 according to SEQ ID NO:6, or the complement thereof; an mRNA molecule having a nucleotide sequence encoding an ANGPTL7 polypeptide, wherein the nucleotide sequence comprises: a uracil at a position corresponding to position 529 according to SEQ ID NO:8, or the complement thereof; a uracil at a position corresponding to position 525 according to SEQ ID NO:9, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:10, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:11, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:12, or the complement thereof; or a cDNA molecule having a nucleotide sequence encoding an ANGPTL7 polypeptide, wherein the nucleotide sequence comprises: a thymine at a position corresponding to position 529 according to SEQ ID NO:14, or the complement thereof; a thymine at a position corresponding to position 525 according to SEQ ID NO:15, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:16, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:17, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18, or the complement thereof.

The present disclosure also provides combinations of a glucocorticoid and an ANGPTL7 inhibitor for use in the preparation of a medicament for treating inflammation in a subject identified as having: a genomic nucleic acid molecule having a nucleotide sequence encoding an ANGPTL7 polypeptide, wherein the nucleotide sequence comprises: a thymine at a position corresponding to position 4,291 according to SEQ ID NO:2, or the complement thereof; a thymine at a position corresponding to position 4,287 according to SEQ ID NO:3, or the complement thereof; an adenine at a position corresponding to position 4,243 according to

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SEQ ID NO:4, or the complement thereof; an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5, or the complement thereof; or a cytosine at a position corresponding to position 4,336 according to SEQ ID NO:6, or the complement thereof; an mRNA molecule having a nucleotide sequence encoding an ANGPTL7 polypeptide, wherein the

5 nucleotide sequence comprises: a uracil at a position corresponding to position 529 according to SEQ ID NO:8, or the complement thereof; a uracil at a position corresponding to position 525 according to SEQ ID NO:9, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:10, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:11, or the complement thereof;

10 or a cytosine at a position corresponding to position 574 according to SEQ ID NO:12, or the complement thereof; or a cDNA molecule having a nucleotide sequence encoding an ANGPTL7 polypeptide, wherein the nucleotide sequence comprises: a thymine at a position corresponding to position 529 according to SEQ ID NO:14, or the complement thereof; a thymine at a position corresponding to position 525 according to SEQ ID NO:15, or the

15 complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:16, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:17, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18, or the complement thereof.

The present disclosure also provides ANGPTL7 inhibitors for use in decreasing or

20 preventing a glucocorticoid-induced ophthalmic condition in a subject undergoing glucocorticoid treatment, wherein the subject is identified as being: a) ANGPTL7 reference for an ANGPTL7 genomic nucleic acid molecule, an ANGPTL7 mRNA molecule, or an ANGPTL7 cDNA molecule; or b) heterozygous for: i) a genomic nucleic acid molecule having a nucleotide sequence encoding an ANGPTL7 polypeptide, wherein the nucleotide sequence comprises: a

25 thymine at a position corresponding to position 4,291 according to SEQ ID NO:2, or the complement thereof; a thymine at a position corresponding to position 4,287 according to SEQ ID NO:3, or the complement thereof; an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4, or the complement thereof; an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5, or the complement thereof; or a cytosine at a

30 position corresponding to position 4,336 according to SEQ ID NO:6, or the complement thereof; ii) an mRNA molecule having a nucleotide sequence encoding an ANGPTL7 polypeptide, wherein the nucleotide sequence comprises: a uracil at a position corresponding to position

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529 according to SEQ ID NO:8, or the complement thereof; a uracil at a position corresponding to position 525 according to SEQ ID NO:9, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:10, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:11, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:12, or the complement thereof; or iii) a cDNA molecule having a nucleotide sequence encoding an ANGPTL7 polypeptide, wherein the nucleotide sequence comprises: a thymine at a position corresponding to position 529 according to SEQ ID NO:14, or the complement thereof; a thymine at a position corresponding to position 525 according to SEQ ID NO:15, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:16, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:17, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18, or the complement thereof.

The present disclosure also provides ANGPTL7 inhibitors for use in the preparation of a medicament for decreasing or preventing a glucocorticoid-induced ophthalmic condition in a subject undergoing glucocorticoid treatment, wherein the subject is identified as being: a) ANGPTL7 reference for an ANGPTL7 genomic nucleic acid molecule, an ANGPTL7 mRNA molecule, or an ANGPTL7 cDNA molecule; or b) heterozygous for: i) a genomic nucleic acid molecule having a nucleotide sequence encoding an ANGPTL7 polypeptide, wherein the nucleotide sequence comprises: a thymine at a position corresponding to position 4,291 according to SEQ ID NO:2, or the complement thereof; a thymine at a position corresponding to position 4,287 according to SEQ ID NO:3, or the complement thereof; an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4, or the complement thereof; an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5, or the complement thereof; or a cytosine at a position corresponding to position 4,336 according to SEQ ID NO:6, or the complement thereof; ii) an mRNA molecule having a nucleotide sequence encoding an ANGPTL7 polypeptide, wherein the nucleotide sequence comprises: a uracil at a position corresponding to position 529 according to SEQ ID NO:8, or the complement thereof; a uracil at a position corresponding to position 525 according to SEQ ID NO:9, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:10, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:11, or the complement thereof; or a cytosine at a position corresponding to position

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574 according to SEQ ID NO:12, or the complement thereof; or iii) a cDNA molecule having a nucleotide sequence encoding an ANGPTL7 polypeptide, wherein the nucleotide sequence comprises: a thymine at a position corresponding to position 529 according to SEQ ID NO:14, or the complement thereof; a thymine at a position corresponding to position 525 according to
5 SEQ ID NO:15, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:16, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:17, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18, or the complement thereof.

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Brief Description Of The Drawings

The accompanying figures, which are incorporated in and constitute a part of this specification, illustrate several features of the present disclosure.

15 The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee.

Figure 1 shows inhibition of dexamethasone-21-acetate (DEX-Ac)-induced ocular hypertension in Angptl7 knockout (KO) mice.

20 Figure 2 depicts effect of ANGPTL7 siRNA on intraocular pressure (IOP) of wild-type mice. Intravitreal injection with 15 µg of ANGPTL7-siRNA significantly lowered IOP in two of six siRNAs tested (n = 6-8/group) compared to the PBS-treated (n = 6) and naïve (no injection, n = 5) groups starting at week 2 and through the end of the study. Error bars represent standard error of the mean (SEM).

25 Figure 3 depicts effect of ANGPTL7 siRNA on ANGPTL7 expression in the limbal ring of wild-type mice *in vivo*. qPCR results from micro-dissected limbal ring showed the highest level of knockdown (> 50%) of ANGPTL7 mRNA with siRNAs #3 and #5 compared to PBS-treated or naïve (no injection) mice, which is consistent with the IOP lowering observed in mice injected with one of these two siRNAs (shown in Figure 1). Error bars represent SEM.

30 Figure 4 depicts effect of ANGPTL7 siRNA on reducing dexamethasone-21-acetate (DEX-Ac)-induced ocular hypertension.

Description

Various terms relating to aspects of the present disclosure are used throughout the specification and claims. Such terms are to be given their ordinary meaning in the art, unless otherwise indicated. Other specifically defined terms are to be construed in a manner
5 consistent with the definitions provided herein.

Unless otherwise expressly stated, it is in no way intended that any method or aspect set forth herein be construed as requiring that its steps be performed in a specific order. Accordingly, where a method claim does not specifically state in the claims or descriptions that the steps are to be limited to a specific order, it is in no way intended that an order be inferred,
10 in any respect. This holds for any possible non-expressed basis for interpretation, including matters of logic with respect to arrangement of steps or operational flow, plain meaning derived from grammatical organization or punctuation, or the number or type of aspects described in the specification.

As used herein, the singular forms “a,” “an” and “the” include plural referents unless
15 the context clearly dictates otherwise.

As used herein, the term “about” means that the recited numerical value is approximate and small variations would not significantly affect the practice of the disclosed embodiments. Where a numerical value is used, unless indicated otherwise by the context, the term “about” means the numerical value can vary by $\pm 10\%$ and remain within the scope of the
20 disclosed embodiments.

As used herein, the term “comprising” may be replaced with “consisting” or “consisting essentially of” in particular embodiments as desired.

As used herein, the term “isolated”, in regard to a nucleic acid molecule or a polypeptide, means that the nucleic acid molecule or polypeptide is in a condition other than its
25 native environment, such as apart from blood and/or animal tissue. In some embodiments, an isolated nucleic acid molecule or polypeptide is substantially free of other nucleic acid molecules or other polypeptides, particularly other nucleic acid molecules or polypeptides of animal origin. In some embodiments, the nucleic acid molecule or polypeptide can be in a highly purified form, i.e., greater than 95% pure or greater than 99% pure. When used in this
30 context, the term “isolated” does not exclude the presence of the same nucleic acid molecule or polypeptide in alternative physical forms, such as dimers or alternatively phosphorylated or derivatized forms.

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As used herein, the terms “nucleic acid”, “nucleic acid molecule”, “nucleic acid sequence”, “polynucleotide”, or “oligonucleotide” can comprise a polymeric form of nucleotides of any length, can comprise DNA and/or RNA, and can be single-stranded, double-stranded, or multiple stranded. One strand of a nucleic acid also refers to its complement.

5 As used herein, the term “subject” includes any animal, including mammals. Mammals include, but are not limited to, farm animals (such as, for example, horse, cow, pig), companion animals (such as, for example, dog, cat), laboratory animals (such as, for example, mouse, rat, rabbits), and non-human primates (such as, for example, apes and monkeys). In some embodiments, the subject is a human. In some embodiments, the subject is a patient under the
10 care of a physician.

 The present disclosure demonstrates that inhibiting ANGPTL7 activity, such as in Angptl7 KO mice, surprisingly and unexpectedly suppresses the GC-mediated increase in ocular hypertension. Thus, it is believed that treatment of subjects undergoing glucocorticoid treatment of, for example, inflammation, with ANGPTL7 inhibitors can decrease or prevent
15 undesirable glucocorticoid-induced ophthalmic conditions. It is believed that no ANGPTL7 inhibitors have any known association with decreasing or preventing undesirable glucocorticoid-induced ophthalmic conditions. Therefore, subjects that are ANGPTL7 reference that have an increased risk of developing glucocorticoid-induced ophthalmic conditions may be treated such that the glucocorticoid-induced ophthalmic conditions are prevented, the
20 symptoms thereof are reduced, and/or development of symptoms is repressed. Accordingly, the present disclosure provides methods of leveraging the identification of ANGPTL7 reference subjects undergoing glucocorticoid treatment to identify or stratify risk in such subjects of developing glucocorticoid-induced ophthalmic conditions such that subjects at risk or subjects with active glucocorticoid-induced ophthalmic conditions may be treated accordingly.

25 For purposes of the present disclosure, any particular subject can be categorized as having one of three ANGPTL7 genotypes: i) ANGPTL7 reference; ii) heterozygous for an ANGPTL7 predicted loss-of-function variant; or iii) homozygous for an ANGPTL7 predicted loss-of-function variant. A subject is ANGPTL7 reference when the subject does not have a copy of an ANGPTL7 predicted loss-of-function variant nucleic acid molecule. A subject is heterozygous
30 for an ANGPTL7 predicted loss-of-function variant when the subject has a single copy of an ANGPTL7 predicted loss-of-function variant nucleic acid molecule. As used herein, an ANGPTL7 predicted loss-of-function variant nucleic acid molecule is any ANGPTL7 nucleic acid molecule

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(such as, a genomic nucleic acid molecule, an mRNA molecule, or a cDNA molecule) encoding an ANGPTL7 polypeptide having a partial loss-of-function, a complete loss-of-function, a predicted partial loss-of-function, or a predicted complete loss-of-function. A subject who has an ANGPTL7 polypeptide having a partial loss-of-function (or predicted partial loss-of-function) is hypomorphic for ANGPTL7. The ANGPTL7 predicted loss-of-function variant nucleic acid molecule can be any nucleic acid molecule encoding an ANGPTL7 Arg177STOP, Gln175His, Phe161Ile, Trp188STOP, Lys192Gln, Arg340His, Arg220His, Asn302Lys, or Arg220Cys. In some embodiments, the ANGPTL7 predicted loss-of-function variant nucleic acid molecule encodes an ANGPTL7 Arg177STOP, Gln175His, Phe161Ile, Trp188STOP, or Lys192Gln. A subject is homozygous for an ANGPTL7 predicted loss-of-function variant when the subject has two copies of an ANGPTL7 predicted loss-of-function variant nucleic acid molecule.

For subjects that are genotyped or determined to be ANGPTL7 reference, such subjects have an increased risk of developing glucocorticoid-induced ophthalmic conditions such as, for example, ocular hypertension, increased intraocular pressure (IOP), pre-glaucoma, glaucoma, decreased corneal hysteresis, and posterior subcapsular cataracts, or any combination thereof. In some embodiments, the IOP is corneal-compensated intraocular pressure (IOPcc). In some embodiments, the IOP is Goldmann-correlated IOP (IOPg). For subjects that are genotyped or determined to be either ANGPTL7 reference or heterozygous for an ANGPTL7 predicted loss-of-function variant, such subjects can be treated with an ANGPTL7 inhibitor.

In any of the embodiments described herein, the glaucoma can be primary open-angle glaucoma, iatrogenic open-angle glaucoma, angle-closure glaucoma, normal-tension glaucoma, congenital glaucoma, neovascular glaucoma, steroid-induced glaucoma, or glaucoma related to ocular trauma.

In any of the embodiments described herein, the ANGPTL7 predicted loss-of-function variant nucleic acid molecule can be any ANGPTL7 nucleic acid molecule (such as, for example, genomic nucleic acid molecule, mRNA molecule, or cDNA molecule) encoding an ANGPTL7 polypeptide having a partial loss-of-function, a complete loss-of-function, a predicted partial loss-of-function, or a predicted complete loss-of-function. For example, the ANGPTL7 predicted loss-of-function variant nucleic acid molecule can be any nucleic acid molecule encoding ANGPTL7 Arg177STOP, Gln175His, Phe161Ile, Trp188STOP, Lys192Gln, Arg340His, Arg220His, Asn302Lys, or Arg220Cys. In some embodiments, the ANGPTL7 predicted loss-of-function

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variant nucleic acid molecule encodes ANGPTL7 Arg177STOP, Gln175His, Phe161Ile, Trp188STOP, or Lys192Gln.

In any of the embodiments described herein, the ANGPTL7 predicted loss-of-function polypeptide can be any ANGPTL7 polypeptide having a partial loss-of-function, a complete loss-of-function, a predicted partial loss-of-function, or a predicted complete loss-of-function. In any of the embodiments described herein, the ANGPTL7 predicted loss-of-function polypeptide can be any of the ANGPTL7 polypeptides described herein including, for example, ANGPTL7 Arg177STOP, Gln175His, Phe161Ile, Trp188STOP, Lys192Gln, Arg340His, Arg220His, Asn302Lys, or Arg220Cys. In some embodiments, the ANGPTL7 predicted loss-of-function polypeptide is ANGPTL7 Arg177STOP, Gln175His, Phe161Ile, Trp188STOP, or Lys192Gln.

In any of the embodiments described herein, the inflammation can be acute inflammation or chronic inflammation. In some embodiments, the acute inflammation is inflammation having a relatively short duration, lasting from about a few minutes to about one to two days. Acute inflammation can be characterized by increased blood flow, exudation of fluid and plasma proteins (edema), and emigration of leukocytes, predominantly neutrophils. In some embodiments, the chronic inflammation is inflammation having a longer duration, such as days to weeks or even longer, and is associated histologically with the presence of lymphocytes and macrophages and with proliferation of blood vessels and connective tissue. In any of the embodiments described herein, the inflammation is associated with rheumatoid arthritis, associated with Grave's disease, or is ophthalmic inflammation. In some embodiments, the inflammation is associated with rheumatoid arthritis. In some embodiments, the inflammation is associated with Grave's disease. In some embodiments, the inflammation is ophthalmic inflammation. In some embodiments, the ophthalmic inflammation is chosen from uveitis, juvenile idiopathic arthritis uveitis, scleritis, blepharitis, conjunctivitis, iritis, and episcleritis, or any combination thereof. In some embodiments, the ophthalmic inflammation is uveitis. In some embodiments, the ophthalmic inflammation is juvenile idiopathic arthritis uveitis. In some embodiments, the ophthalmic inflammation is scleritis. In some embodiments, the ophthalmic inflammation is blepharitis. In some embodiments, the ophthalmic inflammation is conjunctivitis. In some embodiments, the ophthalmic inflammation is iritis. In some embodiments, the ophthalmic inflammation is episcleritis.

In any of the embodiments described herein, the glucocorticoid-induced ophthalmic condition is chosen from ocular hypertension, increased intraocular pressure (IOP), pre-

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glaucoma, glaucoma, decreased corneal hysteresis, and posterior subcapsular cataracts, or any combination thereof. In some embodiments, the glucocorticoid-induced ophthalmic condition is ocular hypertension. In some embodiments, the glucocorticoid-induced ophthalmic condition is increased IOP. In some embodiments, the glucocorticoid-induced ophthalmic condition is pre-glaucoma. In some embodiments, the glucocorticoid-induced ophthalmic condition is glaucoma. In some embodiments, the glucocorticoid-induced ophthalmic condition is decreased corneal hysteresis. In some embodiments, the glucocorticoid-induced ophthalmic condition is posterior subcapsular cataracts.

The present disclosure provides methods of treating a subject undergoing treatment with a steroid, the methods comprising administering an ANGPTL7 inhibitor to the subject.

The present disclosure provides methods of treating a subject having inflammation, the methods comprising administering an ANGPTL7 inhibitor and a glucocorticoid to the subject.

The present disclosure provides methods of treating a subject having rheumatoid arthritis, the methods comprising administering an ANGPTL7 inhibitor and a glucocorticoid to the subject.

The present disclosure provides methods of treating a subject having Grave's disease, the methods comprising administering an ANGPTL7 inhibitor and a glucocorticoid to the subject.

The present disclosure provides methods of treating a subject having ophthalmic inflammation, the methods comprising administering an ANGPTL7 inhibitor and a glucocorticoid to the subject.

The present disclosure provides methods of decreasing a steroid-induced ophthalmic condition in a subject treated with a steroid, the methods comprising administering an ANGPTL7 inhibitor to the subject.

The present disclosure provides methods of decreasing a glucocorticoid-induced ophthalmic condition in a subject treated with a glucocorticoid, the methods comprising administering an ANGPTL7 inhibitor to the subject.

The present disclosure provides methods of treating a subject having inflammation and undergoing steroid treatment, the methods comprising administering an ANGPTL7 inhibitor to the subject.

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The present disclosure provides methods of treating a subject having inflammation and undergoing glucocorticoid treatment, the methods comprising administering an ANGPTL7 inhibitor to the subject.

The present disclosure provides methods of treating a subject having rheumatoid
5 arthritis and undergoing glucocorticoid treatment, the methods comprising administering an ANGPTL7 inhibitor to the subject.

The present disclosure provides methods of treating a subject having Grave's disease and undergoing glucocorticoid treatment, the methods comprising administering an ANGPTL7 inhibitor to the subject.

10 The present disclosure provides methods of treating a subject having ophthalmic inflammation and undergoing glucocorticoid treatment, the methods comprising administering an ANGPTL7 inhibitor to the subject.

In any of the methods described herein, the inflammation can be acute inflammation or chronic inflammation. In some embodiments, the inflammation is acute inflammation. In
15 some embodiments, the inflammation is chronic inflammation. In some embodiments, the inflammation is associated with rheumatoid arthritis, associated with Grave's disease, or is ophthalmic inflammation. In some embodiments, the inflammation is associated with rheumatoid arthritis. In some embodiments, the inflammation is associated with Grave's disease. In some embodiments, the inflammation is ophthalmic inflammation. In some
20 embodiments, the ophthalmic inflammation is chosen from uveitis, juvenile idiopathic arthritis uveitis, scleritis, blepharitis, conjunctivitis, iritis, episcleritis, diabetic macular edema, corneal injury inflammation, ocular surgery pain or inflammation, or any combination thereof. In some embodiments, the ophthalmic inflammation is uveitis. In some embodiments, the ophthalmic inflammation is juvenile idiopathic arthritis uveitis. In some embodiments, the ophthalmic
25 inflammation is scleritis. In some embodiments, the ophthalmic inflammation is blepharitis. In some embodiments, the ophthalmic inflammation is conjunctivitis. In some embodiments, the ophthalmic inflammation is iritis. In some embodiments, the ophthalmic inflammation is episcleritis. In some embodiments, the ophthalmic inflammation is diabetic macular edema. In some embodiments, the ophthalmic inflammation is corneal injury inflammation. In some
30 embodiments, the ophthalmic inflammation is associated with ocular surgery.

In any of the methods described herein, the subject can be undergoing treatment with a steroid or have undergone treatment with a steroid. In some embodiments, such subject can

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have any of the forms of inflammation described herein. Steroids are used after several ophthalmic procedures including, but not limited to, cataract extraction, YAG laser capsulotomy, descemet stripping automated endothelial keratoplasty (DSAEK), lamellar keratoplasty, penetrating keratoplasty, laser in-situ keratomileusis (LASIK), photorefractive keratectomy (PRK), Pars Planar Vitrectomy (PPV), and intralesional injection. In some
5 embodiments, the subject is undergoing or has undergone cataract extraction. In some
embodiments, the subject is undergoing or has undergone YAG laser capsulotomy. In some
embodiments, the subject is undergoing or has undergone DSAEK. In some embodiments, the
subject is undergoing or has undergone lamellar keratoplasty. In some embodiments, the
10 subject is undergoing or has undergone penetrating keratoplasty. In some embodiments, the
subject is undergoing or has undergone LASIK. In some embodiments, the subject is undergoing
or has undergone PRK. In some embodiments, the subject is undergoing or has undergone PPV.
In some embodiments, the subject is undergoing or has undergone intralesional injection.

 In any of the methods described herein, the glucocorticoid-induced ophthalmic
15 condition is chosen from ocular hypertension, increased intraocular pressure (IOP), pre-
glaucoma, glaucoma, decreased corneal hysteresis, and posterior subcapsular cataracts, or any
combination thereof. In some embodiments, the glucocorticoid-induced ophthalmic condition
is ocular hypertension. In some embodiments, the glucocorticoid-induced ophthalmic condition
is increased IOP. In some embodiments, the glucocorticoid-induced ophthalmic condition is
20 pre-glaucoma. In some embodiments, the glucocorticoid-induced ophthalmic condition is
glaucoma. In some embodiments, the glucocorticoid-induced ophthalmic condition is
decreased corneal hysteresis. In some embodiments, the glucocorticoid-induced ophthalmic
condition is posterior subcapsular cataracts.

 In any of the methods described herein, the glucocorticoid is chosen from prednisone,
25 prednisolone, methylprednisolone, dexamethasone, betamethasone, triamcinolone,
beclometasone, fludrocortisone acetate, deoxycorticosterone acetate (DOCA), aldosterone,
budesonide, mometasone furoate, fluticasone propionate, hydrocortisone, cortisone acetate,
and fluticasone furoate, difluprednate ophthalmic, fluorometholone, loteprednol etabonate,
medrysone, rmexolone, fluocinolone acetonide, clobetasol, halobetasol, diflorasone,
30 fluocinonide, flurandrenolide, Neo-Poly-Dex, tobramycin-dexamethasone, difluprednate, or any
combination thereof. In some embodiments, the glucocorticoid is prednisone. In some
embodiments, the glucocorticoid is prednisolone. In some embodiments, the glucocorticoid is

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methyprednisolone. In some embodiments, the glucocorticoid is dexamethasone. In some
embodiments, the glucocorticoid is betamethasone. In some embodiments, the glucocorticoid
is triamcinolone. In some embodiments, the glucocorticoid is beclomethasone. In some
embodiments, the glucocorticoid is fludrocortisone acetate. In some embodiments, the
5 glucocorticoid is DOCA. In some embodiments, the glucocorticoid is aldosterone. In some
embodiments, the glucocorticoid is budesonide. In some embodiments, the glucocorticoid is
mometasone furoate. In some embodiments, the glucocorticoid is fluticasone propionate. In
some embodiments, the glucocorticoid is hydrocortisone. In some embodiments, the
glucocorticoid is cortisone acetate. In some embodiments, the glucocorticoid is fluticasone
10 furoate. In some embodiments, the glucocorticoid is difluprednate ophthalmic. In some
embodiments, the glucocorticoid is fluorometholone. In some embodiments, the glucocorticoid
is loteprednol etabonate. In some embodiments, the glucocorticoid is medrysone. In some
embodiments, the glucocorticoid is rmexolone. In some embodiments, the glucocorticoid is
fluocinolone acetonide. In some embodiments, the glucocorticoid is clobetasol. In some
15 embodiments, the glucocorticoid is halobetasol. In some embodiments, the glucocorticoid is
diflorasone. In some embodiments, the glucocorticoid is fluocinonide. In some embodiments,
the glucocorticoid is flurandrenolide. In some embodiments, the glucocorticoid is Neo-Poly-Dex.
In some embodiments, the glucocorticoid is tobramycin-dexamethasone. In some
embodiments, the glucocorticoid is difluprednate.

20 In any of the methods described herein, the glucocorticoid treatment is treatment with
prednisone, prednisolone, methylprednisolone, dexamethasone, betamethasone,
triamcinolone, beclomethasone, fludrocortisone acetate, DOCA, aldosterone, budesonide,
mometasone furoate, fluticasone propionate, hydrocortisone, cortisone acetate, or fluticasone
furoate, difluprednate ophthalmic, fluorometholone, loteprednol etabonate, medrysone,
25 rmexolone, fluocinolone acetonide, clobetasol, halobetasol, diflorasone, fluocinonide,
flurandrenolide, Neo-Poly-Dex, tobramycin-dexamethasone, difluprednate, or any combination
thereof. In some embodiments, the glucocorticoid treatment is treatment with prednisone. In
some embodiments, the glucocorticoid treatment is treatment with prednisolone. In some
embodiments, the glucocorticoid treatment is treatment with methylprednisolone. In some
30 embodiments, the glucocorticoid treatment is treatment with dexamethasone. In some
embodiments, the glucocorticoid treatment is treatment with betamethasone. In some
embodiments, the glucocorticoid treatment is treatment with triamcinolone. In some

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embodiments, the glucocorticoid treatment is treatment with beclomethasone. In some
embodiments, the glucocorticoid treatment is treatment with fludrocortisone acetate. In some
embodiments, the glucocorticoid treatment is treatment with DOCA. In some embodiments, the
glucocorticoid treatment is treatment with aldosterone. In some embodiments, the
5 glucocorticoid treatment is treatment with budesonide. In some embodiments, the
glucocorticoid treatment is treatment with mometasone furoate. In some embodiments, the
glucocorticoid treatment is treatment with fluticasone propionate. In some embodiments, the
glucocorticoid treatment is treatment with hydrocortisone. In some embodiments, the
glucocorticoid treatment is treatment with cortisone acetate. In some embodiments, the
10 glucocorticoid treatment is treatment with fluticasone furoate. In some embodiments, the
glucocorticoid treatment is treatment with difluprednate ophthalmic. In some embodiments,
the glucocorticoid treatment is treatment with fluorometholone. In some embodiments, the
glucocorticoid treatment is treatment with loteprednol etabonate. In some embodiments, the
glucocorticoid treatment is treatment with medrysone. In some embodiments, the
15 glucocorticoid treatment is treatment with rmexolone. In some embodiments, the
glucocorticoid treatment is treatment with fluocinolone acetonide. In some embodiments, the
glucocorticoid treatment is treatment with clobetasol. In some embodiments, the
glucocorticoid treatment is treatment with halobetasol. In some embodiments, the
glucocorticoid treatment is treatment with diflorasone. In some embodiments, the
20 glucocorticoid treatment is treatment with fluocinonide. In some embodiments, the
glucocorticoid treatment is treatment with flurandrenolide. In some embodiments, the
glucocorticoid treatment is treatment with Neo-Poly-Dex. In some embodiments, the
glucocorticoid treatment is treatment with tobramycin-dexamethasone. In some embodiments,
the glucocorticoid treatment is treatment with difluprednate.

25 In some embodiments, the ANGPTL7 inhibitor comprises an inhibitory nucleic acid
molecule. In some embodiments, the inhibitory nucleic acid molecule comprises an antisense
molecule, a small interfering RNA (siRNA) molecule, or a short hairpin RNA (shRNA) molecule. In
some embodiments, the inhibitory nucleic acid molecule comprises an antisense molecule. In
some embodiments, the inhibitory nucleic acid molecule comprises an siRNA molecule. In some
30 embodiments, the inhibitory nucleic acid molecule comprises an shRNA molecule. Such
inhibitory nucleic acid molecules can be designed to target any region of an ANGPTL7 nucleic
acid molecule, such as an mRNA molecule. In some embodiments, the inhibitory nucleic acid

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molecule hybridizes to a sequence within an ANGPTL7 genomic nucleic acid molecule or mRNA molecule and decreases expression of the ANGPTL7 polypeptide in a cell in the subject. In some embodiments, the ANGPTL7 inhibitor comprises an antisense RNA that hybridizes to an ANGPTL7 genomic nucleic acid molecule or mRNA molecule and decreases expression of the

5 ANGPTL7 polypeptide in a cell in the subject. In some embodiments, the ANGPTL7 inhibitor comprises an siRNA that hybridizes to an ANGPTL7 genomic nucleic acid molecule or mRNA molecule and decreases expression of the ANGPTL7 polypeptide in a cell in the subject. In some

10 embodiments, the ANGPTL7 inhibitor comprises an shRNA that hybridizes to an ANGPTL7 genomic nucleic acid molecule or mRNA molecule and decreases expression of the ANGPTL7 polypeptide in a cell in the subject.

In some embodiments, the antisense nucleic acid molecules comprise or consist of the nucleotide sequences shown in Table 1, Table 2, and Table 3.

Table 1

Sequence	SEQ ID NO:		
AGCUUGAGUCUCUGACAGGG	166	UGACUGAACCUUACGCUUUC	184
UUUUCUCUCUUUCCUUGCUC	167	CUGACUGAACCUUACGCUUU	185
CCUCGCCACUUUGUUGUUU	168	GCUGACUGAACCUUACGCUU	186
GCCUCGCCACUUUGUUGUUU	169	GGCUGACUGAACCUUACGCU	187
GGCCUCGCCACUUUGUUGUU	170	AGGCUGACUGAACCUUACGC	188
GGGCCUCGCCACUUUGUUGU	171	GGUUUGGGUGAGGAAGGCUC	189
AGGGCCUCGCCACUUUGUUG	172	GGGUUUGGGUGAGGAAGGCU	190
GAGGGCCUCGCCACUUUGUU	173	UGUGGGUUUGGGUGAGGAAG	191
UGAGGGCCUCGCCACUUUGU	174	UUGUGGGUUUGGGUGAGGAA	192
UCUGAGGGCCUCGCCACUUU	175	UUUUGUGGGUUUGGGUGAGG	193
UUUCACUCUGAGGGCCUCGC	176	GAAAAUGCAGAGCCAGGUCA	194
CGCUUUCACUCUGAGGGCCU	177	CCACGAUGAAAAUGCAGAGC	195
UACGCUUUCACUCUGAGGGC	178	GCCACGAUGAAAAUGCAGAG	196
UUACGCUUUCACUCUGAGGG	179	AGGCCACGAUGAAAAUGCAG	197
CUUACGCUUUCACUCUGAGG	180	AAAGGCCACGAUGAAAAUGC	198
CCUACGCUUUCACUCUGAG	181	ACAAAGGCCACGAUGAAAAU	199
AACCUACGCUUUCACUCUG	182	UGACAAAGGCCACGAUGAAA	200
GAACCUACGCUUUCACUCU	183	CUGACAAAGGCCACGAUGAA	201
		GCUGACAAAGGCCACGAUGA	202

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GGCUGACAAAGGCCACGAUG	203
ACGCUGGGUGGCUGACAAAG	204
GUGCUUAGAGAGCUUCUGCA	205
UGUGCUUAGAGAGCUUCUGC	206
UUGUGCUUAGAGAGCUUCUG	207
UCUUGUGCUUAGAGAGCUUC	208
GUCUUGUGCUUAGAGAGCUU	209
UGUCUUGUGCUUAGAGAGCU	210
GUGUCUUGUGCUUAGAGAGC	211
GGUGUCUUGUGCUUAGAGAG	212
CUGGUGUCUUGUGCUUAGAG	213
GCUGGUGUCUUGUGCUUAGA	214
UGUGCUGGUGUCUUGUGCUU	215
CUGUGCUGGUGUCUUGUGCU	216
GGCUGUGCUGGUGUCUUGUG	217
CGCUUUGAGCUGUGGCUGUG	218
CCGCUUUGAGCUGUGGCUGU	219
ACCUCCUCACAGCAGUUGGC	220
UCACCUCCUCACAGCAGUUG	221
GUUGGCAACUUGGGCCUUGA	222
GGUUGGCAACUUGGGCCUUG	223
AGGUUGGCAACUUGGGCCUU	224
AAGGUUGGCAACUUGGGCCU	225
UAAGGUUGGCAACUUGGGCC	226
CUAAGGUUGGCAACUUGGGC	227
GCUAAGGUUGGCAACUUGGG	228
UGCUAAGGUUGGCAACUUGG	229
CUGCUAAGGUUGGCAACUUG	230
GCUGCUAAGGUUGGCAACUU	231
GGCUGCUAAGGUUGGCAACU	232
AGGCUGCUAAGGUUGGCAAC	233
CAGGCUGCUAAGGUUGGCAA	234
CAGUUCACUCAGCAGGCUGC	235

UCAGUUCACUCAGCAGGCUG	236
UUCAGUUCACUCAGCAGGCU	237
GUUCAGUUCACUCAGCAGGC	238
CUUGUUCAGUUCACUCAGCA	239
UCUUGUUCAGUUCACUCAGC	240
UUCUUGUUCAGUUCACUCAG	241
GUCCUCUCCUGCUUCUUGU	242
AUGACCACGCUGACCCAGUC	243
UGCAUGACCACGCUGACCCA	244
ACCUGCAUGACCACGCUGAC	245
CACCUGCAUGACCACGCUGA	246
UCACCUGCAUGACCACGCUG	247
AUCACCUGCAUGACCACGCU	248
CUCCAUCACCUGCAUGACCA	249
CGCUUGCUGUUGCUCUCCAG	250
GCGCUUGCUGUUGCUCUCCA	251
CAUGCGCUUGCUGUUGCUCU	252
CCAUGCGCUUGCUGUUGCUC	253
UCCAUGCGCUUGCUGUUGC	254
CUCCAUGCGCUUGCUGUUGC	255
ACUCCAUGCGCUUGCUGUUG	256
GACUCCAUGCGCUUGCUGUU	257
CGACUCCAUGCGCUUGCUGU	258
GGUUGUUAUCUCGGAGUAC	259
UGGUUGUUAUCUCGGAGUA	260
UUGGUUGUUAUCUCGGAGU	261
GCAUGAUGUCAAUUGGUUG	262
AGCUGAUGAUGUCAAUUG	263
AGUGACCGUCUGUGCUGCCU	264
UGAGUGACCGUCUGUGCUGC	265
CUGAGUGACCGUCUGUGCUG	266
UCUGAGUGACCGUCUGUGCU	267
ACUGGUCUCCUACCUGCGG	268

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GACUGGUCUCCUUAACUGCG	269
GGACUGGUCUCCUUAACUGC	270
GAAGCAGUGCUGUAGAUGGG	271
UGUAGAAGCAGUGCUGUAGA	272
AUGUAGAAGCAGUGCUGUAG	273
UAUGUAGAAGCAGUGCUGUA	274
AUAUGUAGAAGCAGUGCUGU	275
GAUAUGUAGAAGCAGUGCUG	276
GGUAUAUGUAGAAGCAGUGC	277
AGGAUAUGUAGAAGCAGUGC	278
CCAGGAUAUGUAGAAGCAGU	279
UGACCAGGAUAUGUAGAAGC	280
GAUGACCAGGAUAUGUAGAA	281
CUGAUGACCAGGAUAUGUAG	282
UCUGAUGACCAGGAUAUGUA	283
GUUCUGAUGACCAGGAUAUG	284
GGUUCUGAUGACCAGGAUAU	285
CAGUAGUGGUUCUGAUGACC	286
CCAGUAGUGGUUCUGAUGAC	287
CCCAGUAGUGGUUCUGAUGA	288
AGUGUACCCACAAAAGAGGC	289
AAGUGUACCCACAAAAGAGG	290
AAAGUGUACCCACAAAAGAG	291
GGAAAGUGUACCCACAAAAG	292
GGGAAAGUGUACCCACAAA	293
AAGGGAAAGUGUACCCACAA	294
CUAAAGGGAAAGUGUACCCA	295
ACUAAAGGGAAAGUGUACCC	296
UACUAAAGGGAAAGUGUACC	297
AGGAAAUACUGCAUAAGCCU	298
GUGAAGGUGUUAGGUAAACU	299
CGUGAAGGUGUUAGGUAAAC	300
CCGUGAAGGUGUUAGGUAAA	301

CCCGUGAAGGUGUUAGGUAA	302
ACCCGUGAAGGUGUUAGGUA	303
GACCCGUGAAGGUGUUAGGU	304
AGACCCGUGAAGGUGUUAGG	305
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GGCUGAAACACUGUGUGGAU	320
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GUAGUAUCUCAGCACUCCAA	322
AUGUAGUAUCUCAGCACUCC	323
CAUGUAGUAUCUCAGCACUC	324
CCAUGUAGUAUCUCAGCACU	325
ACCAUGUAGUAUCUCAGCAC	326
AACCAUGUAGUAUCUCAGCA	327
AAACCAUGUAGUAUCUCAGC	328
CAAACCAUGUAGUAUCUCAG	329
GGCAAACCAUGUAGUAUCUC	330
UUUGGGCAAACCAUGUAGUA	331
CUUUGGGCAAACCAUGUAGU	332
UGCUUCUAAGACUUGCUGGG	333
AACCCUGCUUCUAAGACUUG	334

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UUGAACCCUGCUUCUAAGAC	337
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AGACUUGAACCCUGCUUCUA	339
AAGACUUGAACCCUGCUUCU	340
AAUCAGGAAGACUUGAACCC	341
CAUACAGGAAGACUUGAAC	342
CCAUCAGGAAGACUUGAAC	343
ACCAAUCAGGAAGACUUGAA	344
ACACCAAUCAGGAAGACUUG	345
UACACCAAUCAGGAAGACUU	346
CUACACCAAUCAGGAAGACU	347
GCUACACCAAUCAGGAAGAC	348
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GCUCUUGGUGAGGAAGUAGC	359
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UCUUGAGAUUAGCCUGUCA	366
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UGAGCCAAUGAGAAGAGUUA	400

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CUCUACACUUAACUCUGAGC	403
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UCUCACAGACCAAUUCAGGA	466

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CUGGUUUCAUCUCACAGACC	471
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UUCGCAUGUCUGGUUUCAU	476
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AGUGGCACGGUCAGAUUCCU	494
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UGAGAAAGCCUCCUGUUUGG	509
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GGUGAGAAAGCCUCCUGUUU	511
AUGGUGAGAAAGCCUCCUGU	512
CAGGAUGGUGAGAAAGCCUC	513
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GUGGGAGAGCUGCACUUGAC	516
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UGGUGGGAGAGCUGCACUUG	518
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GAAUGAUGUCCUGGGCAAGA	522
GGAAUGAUGUCCUGGGCAAG	523
GAAUAUAAGGGUAACUGAGC	524
GGGACUACCUACUUAUAGAA	525
AGGGACUACCUACUUAUAGA	526
UGAAAGCACCAACUACUGC	527
GUGAAAGCACCAACUACUG	528
CGUCUUAGUGGUGAAAGCAC	529
UCGUCUUAGUGGUGAAAGCA	530
UUCGUCUUAGUGGUGAAAGC	531
CAUUUCGUCUUAGUGGUGAA	532

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GGACCUUAGAGAGGAGCACC	558
UGGGACCUUAGAGAGGAGCA	559
CUGGGACCUUAGAGAGGAGC	560
CACUGGGACCUUAGAGAGGA	561
GCACUGGGACCUUAGAGAGG	562
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ACUGCACUGGGACCUUAGAG	564
GACCACUGCACUGGGACCUU	565

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GGUGCUUUUCUUGGUGACCA	572
GGGUGCUUUUCUUGGUGACC	573
AGCUUCCUGCCUGCUAUGUC	574
ACAGCCUUUUCUGAUAGGAU	575
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GAAGAGACAGCCUUUUCUGA	577
GGAAGAGACAGCCUUUUCUG	578
AUAGUGGAAGAGACAGCCU	579
GCAUAGUGGAAGAGACAGCC	580
AGCAUAGUGGAAGAGACAGC	581
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AUGAGAGCAUCAGACUGGCC	586
AAUGAGAGCAUCAGACUGGC	587
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UCCUCCCAGAAGUUUUGUUA	589
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ACACUCAGAAGAACCUUUGA	591
AACACUCAGAAGAACCUUUG	592
UAGCACCUCAAAACACUCAG	593
CUAGCACCUCAAAACACUCA	594
UGCCACCUGAGACCAUAAUU	595
ACUGCCACCUGAGACCAUAA	596
UACUGCCACCUGAGACCAUA	597
CAGAGAUGGUGGCUACUGCC	598

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UGUUCAGAGAUGGUGGCUAC	601
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GUUGUUGUUCAGAGAUGGUG	604
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GUCGUGAAUAUCUCAUAGAG	608
CAGUCGUGAAUAUCUCAUAG	609
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GCCACUAUAACAAUUCAGUC	611
CCGCCACUAUAACAAUUCAG	612
CAGACUUCUAGACAGCCGC	613
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UUCAGACUUCUAGACAGCC	615
AUUCAGACUUCUAGACAGC	616
GUCAGAUAGAUUCAGACUUC	617
CUGUCAGAUAGAUUCAGACU	618
UCCUGUCAGAUAGAUUCAGA	619
CUCCUGUCAGAUAGAUUCAG	620
ACUCCUGUCAGAUAGAUUCA	621
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GAUACUCCUGUCAGAUAGAU	623
AGAUACUCCUGUCAGAUAGA	624
CCACGUAACAGAUACUCCUG	625
GCCACGUAACAGAUACUCCU	626
GGCCACGUAACAGAUACUCC	627
GGGCCACGUAACAGAUACUC	628
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GCAGCAGUUGUACCAGUAGC	1191
GUGCAGCAGUUGUACCAGUA	1192

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GAGUAGGUAGAUGCAUGCCA	1232
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AUCAUGUGGAAAAGACAAGC	1304
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GUGUUUUGCCCUCAUAGC	1311
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GGAUUUGUGUUUUGCCCUCA	1313
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AUACCAUUUCCACCUGCCU	1318
UCCAGCCUGGGUCAGUUCCA	1319
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GAUCAGUGCCCUUGGAGUUU	1321
CAGAUCAGUGCCCUUGGAGU	1322
UGAUCGCCAGAUAGCAGUGCC	1323
CUGAUCGCCAGAUAGCAGUGC	1324

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CUGCUGGUGCUUCAUCCUU	1328
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AUGAGAGACUCUGUCCACCU	1332
CAUCCAUGAGAGACUCUGUC	1333

GCAUCCAUGAGAGACUCUGU	1334
GGCAUCCAUGAGAGACUCUG	1335
CCUUGAGCUUGUUUCUJACA	1336
UUCAACCAUUUCCUACAGAC	1337
CCAUCUACCUUCAGUUUUA	1338
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Table 2

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CCAGUCCCGGUAGAAGGAGA	1348
UCCAGUCCCGGUAGAAGGAG	1349
UUCCAGUCCCGGUAGAAGGA	1350
UGCUUCCAGUCCCGGUAGAA	1351
CUGCUUCCAGUCCCGGUAGA	1352
CCUGCUUGUACUGCUUCCAG	1353
CCCUGCUUGUACUGCUUCCA	1354
GAUGCUGCCAAAGCCUGCU	1355
ACGGAUGCUGCCAAAGCCCU	1356
CGGUGGAUGUGUUCGUUCCC	1357
CCGGUGGAUGUGUUCGUUCC	1358
GCCGGUGGAUGUGUUCGUUC	1359
AGCCGGUGGAUGUGUUCGUU	1360
GAGCCGGUGGAUGUGUUCGU	1361
AGAGCCGGUGGAUGUGUUCG	1362

GAGAGCCGGUGGAUGUGUUC	1363
GGAGAGCCGGUGGAUGUGUU	1364
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UCUGGAGAGCCGGUGGAUGU	1366
UGUCUGGAGAGCCGGUGGAU	1367
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UCAGAAUAGGAAUGGCACCC	1371
AUCAGAAUAGGAAUGGCACC	1372
AAUCAGAAUAGGAAUGGCAC	1373
GAAUCAGAAUAGGAAUGGCA	1374
GCAGGAAAACCAUCACAAUG	1375
UGCAGGAAAACCAUCACAAU	1376
UUGCAGGAAAACCAUCACAA	1377
UUACAACUUGCAGGAAAACC	1378
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ACUCCAUUACAACUUGCAGG	1380
AACUCCAUUACAACUUGCAG	1381
CAACUCCAUUACAACUUGCA	1382
CCUCAACUCCAUUACAACUU	1383
UCCUCAACUCCAUUACAACU	1384

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UUCUCAACUCCAUAACAAC	1385	GGCCUUGAUUAGUCUCUCUU	1418
UCUACUCUGGCCUGGGUCUG	1386	UGGCCUUGAUUAGUCUCUCU	1419
UGAAUUUGCUCUACUCUGGC	1387	AUGGCCUUGAUUAGUCUCUC	1420
UUGAAUUUGCUCUACUCUGG	1388	UAUGGCCUUGAUUAGUCUCU	1421
GUUGAAUUUGCUCUACUCUG	1389	AUAUGGCCUUGAUUAGUCUC	1422
UCGGCCAGAGCAGAGACUAG	1390	GAACUUCUUUCCUGAUUCAC	1423
CUCGGCCAGAGCAGAGACUA	1391	UCGAACUUCUUUCCUGAUUC	1424
AAGGACCUCAUGCUCGGCCA	1392	CUCGAACUUCUUUCCUGAUU	1425
AAAGGACCUCAUGCUCGGCC	1393	GCUCGAACUUCUUUCCUGAU	1426
UAAAGGACCUCAUGCUCGGC	1394	GGCUCGAACUUCUUUCCUGA	1427
CUAAAGGACCUCAUGCUCGG	1395	AGGCUCGAACUUCUUUCCUG	1428
CCUAAAGGACCUCAUGCUCG	1396	AAGGCUCGAACUUCUUUCCU	1429
ACCUAAAGGACCUCAUGCUC	1397	CAAGGCUCGAACUUCUUUCC	1430
CACCUAAAGGACCUCAUGCU	1398	ACAAGGCUCGAACUUCUUUC	1431
GCACCUAAAGGACCUCAUGC	1399	AACAAGGCUCGAACUUCUUU	1432
UGCACCUAAAGGACCUCAUG	1400	AAACAAGGCUCGAACUUCUU	1433
UUGCACCUAAAGGACCUCAU	1401	AAAACAAGGCUCGAACUUCU	1434
AUUUGCACCUAAAGGACCUC	1402	GAAAACAAGGCUCGAACUUC	1435
GAUUUGCACCUAAAGGACCU	1403	AGAAAAACAAGGCUCGAACUU	1436
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AAGAUUUUGCACCUAAAGGAC	1405	CCUGGGAAUCAGAAAACAAG	1438
GUAAGAUUUUGCACCUAAAGG	1406	ACCUCCAGUUUACUGUGUUA	1439
GUGAGUGCUUUCAGACCUUC	1407	UUACCUCCAGUUUACUGUGU	1440
AGUGAGUGCUUUCAGACCUU	1408	GUUUACCUCCAGUUUACUGU	1441
UAGUGAGUGCUUUCAGACCU	1409	UGUUUACCUCCAGUUUACUG	1442
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GAUUAUAGUGAGUGCUUUCAG	1411	AGUCCAUAGCCAAACAUCU	1444
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GAGGAUAUAGUGAGUGCUUU	1413	ACAGUCCAUAGCCAAACAUC	1446
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CUAUUUCCUCACUUUCCUG	1417	CCUGACAGUCCAUAGCCAA	1450

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CUCUCCUGACAGUCCCAUAG	1452	CUGUUGAGUUCAUUGCCCAA	1485
UCUCUCCUGACAGUCCCAUA	1453	GCUGUUGAGUUCAUUGCCCA	1486
CCUUCUCUCCUGACAGUCCC	1454	CGAUAGCUGUUGAGUUCAU	1487
GGCUCCAUUUCAUGCUGUCU	1455	GGCGAUAGCUGUUGAGUUCA	1488
AGGCUCCAUUUCAUGCUGUC	1456	AGGCGAUAGCUGUUGAGUUC	1489
GCAGGCUCCAUUUCAUGCUG	1457	GAGGCGAUAGCUGUUGAGUU	1490
GCAGCAGGCUCCAUUUCAUG	1458	AGAGGCGAUAGCUGUUGAGU	1491
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AAAGUGCAGCAGGCUCCAUU	1460	GAAGAGGCGAUAGCUGUUGA	1493
GAAAGUGCAGCAGGCUCCA	1461	GGAAGAGGCGAUAGCUGUUG	1494
AGAAAGUGCAGCAGGCUCCA	1462	AGGAAGAGGCGAUAGCUGUU	1495
AAGAAAGUGCAGCAGGCUCC	1463	CAGGAAGAGGCGAUAGCUGU	1496
UAAAGAAAGUGCAGCAGGCU	1464	CCAGGAAGAGGCGAUAGCUG	1497
UUAAGAAAGUGCAGCAGGC	1465	CCCAGGAAGAGGCGAUAGCU	1498
CUUAAAGAAAGUGCAGCAGG	1466	ACAUUGCCAGUGUAGUCCCC	1499
GCCUUAAGAAAGUGCAGCA	1467	CACAUUGCCAGUGUAGUCC	1500
AGCCUUAAGAAAGUGCAGC	1468	CCACAUUGCCAGUGUAGUUC	1501
AGCAGAGCCUUAAGAAAGU	1469	CCCACAUUGCCAGUGUAGUU	1502
GAGCAGAGCCUUAAGAAAG	1470	AUACUGGAGGGCGUCGUCC	1503
AGGAGCAGAGCCUUAAGAA	1471	GAUACUGGAGGGCGUCGUUC	1504
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UCAGGAGGAGCAGAGCCUUA	1474	UAUGAUACUGGAGGGCGUCG	1507
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UACUCAGCGUAGCGCAGGUU	1477	UGUUGUUUAUGAUACUGGAGG	1510
UAUACUCAGCGUAGCGCAGG	1478	CUGUGUUGUUUAUGAUACUGG	1511
CUAUACUCAGCGUAGCGCAG	1479	GCUGUGUUGUUUAUGAUACUG	1512
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GUUGAGUUCAUUGCCCAAAA	1483	UGAAGGCUUGUGUUGUUUAUGA	1516

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UGUCCUUGUCCUUGGUGCUG	1520	AACCGGAUAUCAACUGUAC	1553
UUGUCCUUGUCCUUGGUGCU	1521	CAAAACCGGAUAUCAACUG	1554
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CCAAGCAGUUGUCAUUGUCC	1523	ACAAAACCGGAUAUCAAC	1556
UCCAAGCAGUUGUCAUUGUC	1524	GAAAGAAUACAAAACCGGA	1557
UGUCCAAGCAGUUGUCAUUG	1525	GGGUCAGAAAGAAUACCAA	1558
UUGUCCAAGCAGUUGUCAUU	1526	AGGGUCAGAAAGAAUACCAA	1559
CUUGUCCAAGCAGUUGUCAU	1527	ACCAGACAUCAGGUAAGGAG	1560
ACUUGUCCAAGCAGUUGUCA	1528	GACCAGACAUCAGGUAAGGA	1561
CACUUGUCCAAGCAGUUGUC	1529	AGACCAGACAUCAGGUAAGG	1562
ACACUUGUCCAAGCAGUUGU	1530	AUAGACCAGACAUCAGGUA	1563
CACACUUGUCCAAGCAGUUG	1531	GAUAGACCAGACAUCAGGUA	1564
GCACACUUGUCCAAGCAGUU	1532	ACUGUGAUAGACCAGACAUC	1565
UGCACACUUGUCCAAGCAGU	1533	GACUGUGAUAGACCAGACAUC	1566
CACCUUUGCGGAGCUGUGCA	1534	UGACUGUGAUAGACCAGACA	1567
UCACCUUUGCGGAGCUGUGC	1535	UUGACUGUGAUAGACCAGAC	1568
CUCACCUUUGCGGAGCUGUG	1536	GUUGACUGUGAUAGACCAGA	1569
UCUCACCUUUGCGGAGCUGU	1537	AGUUGACUGUGAUAGACCAG	1570
AUCUCACCUUUGCGGAGCUG	1538	AAGUUGACUGUGAUAGACCA	1571
AAUCUCACCUUUGCGGAGCU	1539	GCUAGUAAGUUGACUGUGAU	1572
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UGAGCUUGUACCUGAACUUC	1543	GACCCAGUGCUAGUAAGUUG	1576
UAUGAGCUUGUACCUGAACU	1544	AGACCCAGUGCUAGUAAGUU	1577
UUAUGAGCUUGUACCUGAAC	1545	CAGACCCAGUGCUAGUAAGU	1578
GGAUUAUGAGCUUGUACCUG	1546	ACAGACCCAGUGCUAGUAAG	1579
GGGAUUAUGAGCUUGUACCU	1547	AACAGACCCAGUGCUAGUAA	1580
UGGGAUUAUGAGCUUGUACC	1548	AAACAGACCCAGUGCUAGUA	1581
GUGGGAUUAUGAGCUUGUAC	1549	GAAACAGACCCAGUGCUAGU	1582

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GCCACCUGGCAUGAGAAACA	1584	UGCUCACCCAGGCGGUAGUA	1617
AGCCACCUGGCAUGAGAAAC	1585	GCUUAUUGUGCUCACCCAGG	1618
UAGCCACCUGGCAUGAGAAA	1586	UGC UUAUUGUGCUCACCCAG	1619
AGUAGCCACCUGGCAUGAGA	1587	GUGCUUAUUGUGCUCACCCA	1620
CAGUAGCCACCUGGCAUGAG	1588	CCAGGUGCUUAUUGUGCUCA	1621
GUUGUACCAGUAGCCACCUG	1589	UCCAGGUGCUUAUUGUGCUC	1622
AGUUGUACCAGUAGCCACCU	1590	CCAUCCAGGUGCUUAUUGUG	1623
CAGCAGUUGUACCAGUAGCC	1591	GCCAUCCAGGUGCUUAUUGU	1624
GCAGCAGUUGUACCAGUAGC	1592	UGCCAUCCAGGUGCUUAUUG	1625
GUGCAGCAGUUGUACCAGUA	1593	AUGCCAUCCAGGUGCUUAU	1626
UGUGCAGCAGUUGUACCAGU	1594	GAUGCCAUCCAGGUGCUUAU	1627
CUGUGCAGCAGUUGUACCAG	1595	UGAUGCCAUCCAGGUGCUUA	1628
UCUGUGCAGCAGUUGUACCA	1596	ACCAGGUGAUGCCAUCCAGG	1629
GUCUGUGCAGCAGUUGUACC	1597	UACCAGGUGAUGCCAUCCAG	1630
AGUCUGUGCAGCAGUUGUAC	1598	UAGGUAGAUCCAUGCCAGCC	1631
GAGUCUGUGCAGCAGUUGUA	1599	GUAGGUAGAUCCAUGCCAGC	1632
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UUGGAGUCUGUGCAGCAGUU	1601	GGAGUAGGUAGAUCCAUGCC	1634
GUUGGAGUCUGUGCAGCAGU	1602	GGGAGUAGGUAGAUCCAUGC	1635
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AUUGAGGUUGGAGUCUGUGC	1604	GAGGGAGUAGGUAGAUCCA	1637
CAUUGAGGUUGGAGUCUGUG	1605	UGAGGGAGUAGGUAGAUCCA	1638
CCAUUGAGGUUGGAGUCUGU	1606	UUGAGGGAGUAGGUAGAUCC	1639
GUACACUCCAUUGAGGUUGG	1607	UUUGAGGGAGUAGGUAGAUCC	1640
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GGUAGUACACUCCAUUGAGG	1609	CCGUUUGAGGGAGUAGGUAG	1642
CGGUAGUACACUCCAUUGAG	1610	CCCGUUUGAGGGAGUAGGUA	1643
GCGGUAGUACACUCCAUUGA	1611	ACCCGUUUGAGGGAGUAGGU	1644
GGCGGUAGUACACUCCAUUG	1612	CACCCGUUUGAGGGAGUAGG	1645
AGGCGGUAGUACACUCCAUU	1613	CCACCCGUUUGAGGGAGUAG	1646
CAGGCGGUAGUACACUCCA	1614	UCCACCCGUUUGAGGGAGUA	1647
CCAGGCGGUAGUACACUCCA	1615	AUCUCCACCCGUUUGAGGGA	1648

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UCAUCUCCACCCGUUUGAGG	1650	CUCAGUUUCUGUAUCCGUGC	1667
UUCAUCUCCACCCGUUUGAG	1651	UGUCUCAGUUUCUGUAUCCG	1668
UUUCAUCUCCACCCGUUUGA	1652	UGCCCUCAUCCAGUCUCCAC	1669
UUUUCAUCUCCACCCGUUUG	1653	AUCUGCCCUCAUCCAGUCUC	1670
AUUUUCAUCUCCACCCGUUU	1654	CAUCUGCCCUCAUCCAGUCU	1671
GGCGGAUUUUAUCUCCACC	1655	UCAUCUGCCCUCAUCCAGUC	1672
GGCUUGAAGUCUUCUGGGCG	1656	CCUCAUCUGCCCUCAUCCAG	1673
AAGGCUUGAAGUCUUCUGGG	1657	CUAACACUCUCUCCUGUCC	1674
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CUCCUUUUUAAGGCUUGAAGU	1659	UUCUAACACUCUCUCCUGU	1676
CCUCCUUUUUAAGGCUUGAAG	1660	UAUAGGCUGUUUCUCAGUCC	1677
ACGGCAGCCUCCUUUUAAAG	1661	CCUUGGAGACUUUUUCUUUC	1678
CACGGCAGCCUCCUUUUAAAG	1662	GCUCCUUGGAGACUUUUUCU	1679
CUCCACGGCAGCCUCCUUUU	1663	UGCUCUUGGAGACUUUUUC	1680
UUUCUGUAUCCGUGCUCAC	1664	UUUUGUGCUCCUUGGAGACU	1681
AGUUUCUGUAUCCGUGCUC	1665		

Table 3

Sequence	SEQ ID NO:		
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GCCUCGCCACUUUGUUGUUU	1685	AACCUACGCUUUCACUCUG	1698
GGCCUCGCCACUUUGUUGUU	1686	GAACCUACGCUUUCACUCU	1699
GGGCCUCGCCACUUUGUUGU	1687	UGACUGAACCUUACGCUUUC	1700
AGGGCCUCGCCACUUUGUUG	1688	CUGACUGAACCUUACGCUUU	1701
GAGGGCCUCGCCACUUUGUU	1689	GCUGACUGAACCUUACGCUU	1702
UGAGGGCCUCGCCACUUUGU	1690	GGCUGACUGAACCUUACGCU	1703
UCUGAGGGCCUCGCCACUUU	1691	AGGCUGACUGAACCUUACGC	1704
UUUCACUCUGAGGGCCUCGC	1692	GGUUUGGGUGAGGAAGGCUC	1705
CGCUUUCACUCUGAGGGCCU	1693	GGGUUUGGGUGAGGAAGGCU	1706
UACGCUUUCACUCUGAGGGC	1694	UGUGGGUUUGGGUGAGGAAG	1707
		UUGUGGGUUUGGGUGAGGAA	1708

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UUUUGUGGGUUUGGGUGAGG	1709
GAAAAUGCAGAGCCAGGUCA	1710
CCACGAUGAAAAUGCAGAGC	1711
GCCACGAUGAAAAUGCAGAG	1712
AGGCCACGAUGAAAAUGCAG	1713
AAAGGCCACGAUGAAAAUGC	1714
ACAAAGGCCACGAUGAAAAU	1715
UGACAAAGGCCACGAUGAAA	1716
CUGACAAAGGCCACGAUGAA	1717
GCUGACAAAGGCCACGAUGA	1718
GGCUGACAAAGGCCACGAUG	1719
ACGCUGGGUGGCUGACAAAG	1720
GUGCUUAGAGAGCUUCUGCA	1721
UGUGCUUAGAGAGCUUCUGC	1722
UUGUGCUUAGAGAGCUUCUG	1723
UCUUGUGCUUAGAGAGCUUC	1724
GUCUUGUGCUUAGAGAGCUU	1725
UGUCUUGUGCUUAGAGAGCU	1726
GUGUCUUGUGCUUAGAGAGC	1727
GGUGUCUUGUGCUUAGAGAG	1728
CUGGUGUCUUGUGCUUAGAG	1729
GCUGGUGUCUUGUGCUUAGA	1730
UGUGCUGGUGUCUUGUGCUU	1731
CUGUGCUGGUGUCUUGUGCU	1732
GGCUGUGCUGGUGUCUUGUG	1733
CGCUUUGAGCUGUGGCUGUG	1734
CCGCUUUGAGCUGUGGCUGU	1735
ACCUCCUCACAGCAGUUGGC	1736
UCACCUCCUCACAGCAGUUG	1737
GUUGGCAACUUGGGCCUUGA	1738
GGUUGGCAACUUGGGCCUUG	1739
AGGUUGGCAACUUGGGCCUU	1740
AAGGUUGGCAACUUGGGCCU	1741

UAAGGUUGGCAACUUGGGCC	1742
CUAAGGUUGGCAACUUGGGC	1743
GCUAAGGUUGGCAACUUGGG	1744
UGCUAAGGUUGGCAACUUGG	1745
CUGCUAAGGUUGGCAACUUG	1746
GCUGCUAAGGUUGGCAACUU	1747
GGCUGCUAAGGUUGGCAACU	1748
AGGCUGCUAAGGUUGGCAAC	1749
CAGGCUGCUAAGGUUGGCAA	1750
CAGUUCACUCAGCAGGCUGC	1751
UCAGUUCACUCAGCAGGCUG	1752
UUCAGUUCACUCAGCAGGCU	1753
GUUCAGUUCACUCAGCAGGC	1754
CUUGUUCAGUUCACUCAGCA	1755
UCUUGUUCAGUUCACUCAGC	1756
UUCUUGUUCAGUUCACUCAG	1757
GUCCCUCUCCUGCUUCUUGU	1758
AUGACCACGCUGACCCAGUC	1759
UGCAUGACCACGCUGACCCA	1760
ACCUGCAUGACCACGCUGAC	1761
CACCUGCAUGACCACGCUGA	1762
UCACCUGCAUGACCACGCUG	1763
AUACCUGCAUGACCACGCUC	1764
CUCCAUCACCUGCAUGACCA	1765
CGCUUGCUGUUGCUCUCCAG	1766
GCGCUUGCUGUUGCUCUCCA	1767
CAUGCGCUUGCUGUUGCUCU	1768
CCAUGCGCUUGCUGUUGCUC	1769
UCCAUGCGCUUGCUGUUGCUC	1770
CUCCAUGCGCUUGCUGUUGC	1771
ACUCCAUGCGCUUGCUGUUG	1772
GACUCCAUGCGCUUGCUGUU	1773
CGACUCCAUGCGCUUGCUGU	1774

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GGUUGUUAUCUCGGAGUAC	1775
UGGUUGUUAUCUCGGAGUA	1776
UUGGUUGUUAUCUCGGAGU	1777
GCAUGAUGUCAAUUUGGUUG	1778
AGCUGCAUGAUGUCAAUUUG	1779
AGUGACCGUCUGUGCUGCCU	1780
UGAGUGACCGUCUGUGCUGC	1781
CUGAGUGACCGUCUGUGCUG	1782
UCUGAGUGACCGUCUGUGCU	1783
UCUGCGGAGGUCUGAGUGAC	1784
AUCUGCGGAGGUCUGAGUGA	1785
CAUCUGCGGAGGUCUGAGUG	1786
GCAUCUGCGGAGGUCUGAGU	1787
UGGCAUCUGCGGAGGUCUGA	1788
AUGGCAUCUGCGGAGGUCUG	1789
GAUGGCAUCUGCGGAGGUCU	1790
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GAAGAGCAGUCGUAGAUGGC	1794
GGAAGAGCAGUCGUAGAUGG	1795
GGGAAGAGCAGUCGUAGAUG	1796
AGGGAAGAGCAGUCGUAGAU	1797
GAGGGAAGAGCAGUCGUAGA	1798
GGUAGUUCUUCUGGUAGAGG	1799
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GGAAGUCAUCAGGAGGAAGC	1802
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GCUGCCCAGGAAGUCAUCAG	1804
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AACACCUCCAGUUCAGGGCU	1807

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CUCCGCCUGAAGUCUCCAUG	1810
CCUCCGCCUGAAGUCUCCA	1811
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GUCCCGGUAGAAGGAGACAA	1815
AGUCCCGGUAGAAGGAGACA	1816
CAGUCCCGGUAGAAGGAGAC	1817
CCAGUCCCGGUAGAAGGAGA	1818
UCCAGUCCCGGUAGAAGGAG	1819
UUCAGUCCCGGUAGAAGGA	1820
UGCUUCCAGUCCCGGUAGAA	1821
CUGCUUCCAGUCCCGGUAGA	1822
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CCCUGCUUGUACUGCUUCCA	1824
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UGGAGAGCCGGUGGAUGUGU	1835
UCUGGAGAGCCGGUGGAUGU	1836
UGUCUGGAGAGCCGGUGGAU	1837
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CCUCCAGUCCUCCAUCUCU	1839
UUGCCCUCCAGUCCUCCA	1840

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UACUCAGCGUAGCGCAGGUU	1842
UAUACUCAGCGUAGCGCAGG	1843
CUAUACUCAGCGUAGCGCAG	1844
ACAAAGUGGCUAUACUCAGC	1845
AACAAAGUGGCUAUACUCAG	1846
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UGUUGAGUUCAUUGCCCAAA	1849
CUGUUGAGUUCAUUGCCCAA	1850
GCUGUUGAGUUCAUUGCCCA	1851
CGAUAGCUGUUGAGUUCAUU	1852
GGCGAUAGCUGUUGAGUUCA	1853
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GAAGAGGCGAUAGCUGUUGA	1858
GGAAGAGGCGAUAGCUGUUG	1859
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CCCAGGAAGAGGCGAUAGCU	1863
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CCACAUUGCCAGUGUAGUUC	1866
CCCACAUUGCCAGUGUAGUU	1867
AUACUGGAGGGCGUCGUUCC	1868
GAUACUGGAGGGCGUCGUUC	1869
UGAUACUGGAGGGCGUCGUU	1870
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UAUGAUACUGGAGGGCGUCG	1872
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GUUGUUAUGAUACUGGAGGG	1874
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CUGUGUUGUUAUGAUACUGG	1876
GCUGUGUUGUUAUGAUACUG	1877
GGCUGUGUUGUUAUGAUACU	1878
AGGCUGUGUUGUUAUGAUAC	1879
GAAGGCUGUGUUGUUAUGAU	1880
UGAAGGCUGUGUUGUUAUGA	1881
CUGAAGGCUGUGUUGUUAUG	1882
GCUGAAGGCUGUGUUGUUAU	1883
UGCUGAAGGCUGUGUUGUUA	1884
UGUCCUUGUCCUUGGUGCUG	1885
UUGUCCUUGUCCUUGGUGCU	1886
GCAGUUGUCAUUGUCCUUGU	1887
CCAAGCAGUUGUCAUUGUCC	1888
UCCAAGCAGUUGUCAUUGUC	1889
UGUCCAAGCAGUUGUCAUUG	1890
UUGUCCAAGCAGUUGUCAUU	1891
CUUGUCCAAGCAGUUGUCAU	1892
ACUUGUCCAAGCAGUUGUCA	1893
CACUUGUCCAAGCAGUUGUC	1894
ACACUUGUCCAAGCAGUUGU	1895
CACACUUGUCCAAGCAGUUG	1896
GCACACUUGUCCAAGCAGUU	1897
UGCACACUUGUCCAAGCAGU	1898
CACCUUUGCGGAGCUGUGCA	1899
AGCCACCUUUGCGGAGCUGU	1900
UAGCCACCUUUGCGGAGCUG	1901
GUAGCCACCUUUGCGGAGCU	1902
AGUAGCCACCUUUGCGGAGC	1903
CAGUAGCCACCUUUGCGGAG	1904
CCAGUAGCCACCUUUGCGGA	1905
ACCAGUAGCCACCUUUGCGG	1906

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UACCAGUAGCCACCUUUGCG	1907
GUACCAGUAGCCACCUUUGC	1908
UGUACCAGUAGCCACCUUUG	1909
UUGUACCAGUAGCCACCUUU	1910
GUUGUACCAGUAGCCACCUU	1911
AGUUGUACCAGUAGCCACCU	1912
CAGCAGUUGUACCAGUAGCC	1913
GCAGCAGUUGUACCAGUAGC	1914
GUGCAGCAGUUGUACCAGUA	1915
UGUGCAGCAGUUGUACCAGU	1916
CUGUGCAGCAGUUGUACCAG	1917
UCUGUGCAGCAGUUGUACCA	1918
GUCUGUGCAGCAGUUGUACC	1919
AGUCUGUGCAGCAGUUGUAC	1920
GAGUCUGUGCAGCAGUUGUA	1921
GGAGUCUGUGCAGCAGUUGU	1922
UUGGAGUCUGUGCAGCAGUU	1923
GUUGGAGUCUGUGCAGCAGU	1924
GAGGUUGGAGUCUGUGCAGC	1925
AUUGAGGUUGGAGUCUGUGC	1926
CAUUGAGGUUGGAGUCUGUG	1927
CCAUUGAGGUUGGAGUCUGU	1928
GUACACUCCAUGGAGGUUGG	1929
UAGUACACUCCAUGAGGUU	1930
GGUAGUACACUCCAUGAGG	1931
CGGUAGUACACUCCAUGAG	1932
GCGGUAGUACACUCCAUGA	1933
GGCGGUAGUACACUCCAUG	1934
AGGCGGUAGUACACUCCAUI	1935
CAGGCGGUAGUACACUCCA	1936
CCAGGCGGUAGUACACUCCA	1937
CUCACCCAGGCGGUAGUACA	1938
UGCUCACCCAGGCGGUAGUA	1939

GCUUAUUGUGCUCACCCAGG	1940
UGCUIAUUGUGCUCACCCAG	1941
GUGCUUAUUGUGCUCACCCA	1942
CCAGGUGCUUAUUGUGCUCA	1943
UCCAGGUGCUUAUUGUGCUC	1944
CCAUCCAGGUGCUUAUUGUG	1945
GCCAUCCAGGUGCUUAUUGU	1946
UGCCAUCCAGGUGCUUAUUG	1947
AUGCCAUCCAGGUGCUUAUU	1948
GAUGCCAUCCAGGUGCUUAU	1949
UGAUGCCAUCCAGGUGCUUA	1950
ACCAGGUGAUGCCAUCCAGG	1951
UACCAGGUGAUGCCAUCCAG	1952
UAGGUAGAUGCAUCCAGCC	1953
GUAGGUAGAUGCAUCCAGC	1954
GAGUAGGUAGAUGCAUCCA	1955
GGAGUAGGUAGAUGCAUCC	1956
GGGAGUAGGUAGAUGCAUGC	1957
AGGGAGUAGGUAGAUGCAUG	1958
GAGGGAGUAGGUAGAUGCAU	1959
UGAGGGAGUAGGUAGAUGCA	1960
UUGAGGGAGUAGGUAGAUGCC	1961
UUUGAGGGAGUAGGUAGAUC	1962
CGUUUGAGGGAGUAGGUAGA	1963
CCGUUUGAGGGAGUAGGUAG	1964
CCCGUUUGAGGGAGUAGGUUA	1965
ACCCGUUUGAGGGAGUAGGU	1966
CACCCGUUUGAGGGAGUAGG	1967
CCACCCGUUUGAGGGAGUAG	1968
UCCACCCGUUUGAGGGAGUA	1969
AUCUCCACCCGUUUGAGGGGA	1970
CAUCUCCACCCGUUUGAGGG	1971
UCAUCUCCACCCGUUUGAGG	1972

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UUCAUCUCCACCCGUUUGAG	1973
UUUCAUCUCCACCCGUUUGA	1974
UUUUCAUCUCCACCCGUUUG	1975
AUUUUCAUCUCCACCCGUUU	1976
GGCGGAUUUUCAUCCACC	1977
GGCUUGAAGUCUUCUGGGCG	1978
AAGGCUUGAAGUCUUCUGGG	1979
CCUUUUAAAGGCUUGAAGUCU	1980
CUCCUUUUAAAGGCUUGAAGU	1981
CCUCCUUUUAAAGGCUUGAAG	1982
ACGGCAGCCUCCUUUUAAAG	1983
CACGGCAGCCUCCUUUUAAAG	1984
CUCCACGGCAGCCUCCUUUU	1985
UUUCUGUAUCCGUGCUCCAC	1986
AGUUUCUGUAUCCGUGCUCC	1987
CAGUUUCUGUAUCCGUGCUC	1988
CUCAGUUUCUGUAUCCGUGC	1989
UGUCUCAGUUUCUGUAUCCG	1990
UGCCCUCAUCCAGUCUCCAC	1991
AUCUGCCCUCAUCCAGUCUC	1992
CAUCUGCCCUCAUCCAGUCU	1993
UCAUCUGCCCUCAUCCAGUC	1994
CCUCAUCUGCCCUCAUCCAG	1995
CUAACACUCUCUCCUGUCC	1996
UCUAACACUCUCUCCUGUC	1997
UUCUAACACUCUCUCCUGU	1998
UAUAGGCUGUUUCUGAUCC	1999
CCUUGGAGACUUAUUCUUUC	2000
GCUCCUUGGAGACUUAUUCU	2001
UGCUCUUGGAGACUUAUUC	2002
UUUUGUGCUCCUUGGAGACU	2003
UACUGUAACAUCUUGGUAC	2004
GUUUACUGUAACAUCUUGG	2005

AGGAUGUGGCAGGACCCAGU	2006
AAGGAUGUGGCAGGACCCAG	2007
GAAGGAUGUGGCAGGACCCA	2008
UGAGAAGGAUGUGGCAGGAC	2009
CAGUCUACCACCUUGAGAAG	2010
CACUCAGUCUACCACCUUGA	2011
GGAUCUUGGGCAGAGAGACC	2012
GGGAUCUUGGGCAGAGAGAC	2013
AGGGAUCUUGGGCAGAGAGA	2014
CAGGGAUCUUGGGCAGAGAG	2015
UGUCAGGGAUCUUGGGCAGA	2016
AUGUCAGGGAUCUUGGGCAG	2017
UAUGUCAGGGAUCUUGGGCA	2018
CUAUGUCAGGGAUCUUGGGC	2019
GCUAUGUCAGGGAUCUUGGG	2020
UGCUAUGUCAGGGAUCUUGG	2021
CUGCUAUGUCAGGGAUCUUG	2022
AGCUACUGCUAUGUCAGGGA	2023
AAGCUACUGCUAUGUCAGGG	2024
AAGACAAGCUACUGCUAUGU	2025
CAUGUGGAAAAGACAAGCUA	2026
AUCAUGUGGAAAAGACAAGC	2027
GCCCUACAUAGCCUAAGCC	2028
UUGCCCUACAUAGCCUAAG	2029
UUUGCCCUACAUAGCCUAA	2030
UUUUGCCCUACAUAGCCUA	2031
GUUUUGCCCUACAUAGCCU	2032
UGUUUUGCCCUACAUAGCC	2033
GUGUUUUGCCCUACAUAGC	2034
GAUUUGUGUUUUGCCCUAC	2035
GGAUUUGUGUUUUGCCCUCA	2036
AAGGGAUUUGUGUUUUGCCC	2037
ACUCCUUUCUCUAACACUCA	2038

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CACCUGCCUCCUUCACUCCU	2039	CCUGCUGGUGCUUCAUUCU	2052
UACCAUUUCCACCUGCCUC	2040	ACUCUGUCCACCUCUGCUG	2053
AUACCAUUUCCACCUGCCU	2041	AGAGACUCUGUCCACCUCU	2054
UCCAGCCUGGGUCAGUCCA	2042	AUGAGAGACUCUGUCCACU	2055
UGCAGUGCCUGGAGUUUCC	2043	CAUCCAUGAGAGACUCUGUC	2056
GAUGCAGUGCCUGGAGUUU	2044	GCAUCCAUGAGAGACUCUGU	2057
CAGAUGCAGUGCCUGGAGU	2045	GGCAUCCAUGAGAGACUCUG	2058
UGAUCGCCAGAUGCAGUGCC	2046	CCUUGAGCUUGUUUCUACA	2059
CUGAUCGCCAGAUGCAGUGC	2047	UUCAACCAUUUCCUACAGAC	2060
ACAUGACCAAGGCGAGCAGG	2048	CCAUCUACCUUCAGUUUUA	2061
UACAUGACCAAGGCGAGCAG	2049	ACACCAUCUACCUUCAGUUU	2062
GCUGGUGCUUCAUUCUUUC	2050	AACACCAUCUACCUUCAGUU	2063
CUGCUGGUGCUUCAUUCUU	2051	UAACACCAUCUACCUUCAGU	2064

In some embodiments, the siRNA molecules comprise or consist of the nucleotide sequences (sense and antisense strands) shown in Table 4, Table 5, and Table 6.

Table 4

Sense Sequence	SEQ ID NO:	Antisense Sequence	SEQ ID NO:
AAAGGCUAGCAAAGAGCAA	2065	UUGCUCUUUGCUAGCCUUU	2066
AAGGCUAGCAAAGAGCAAG	2067	CUUGCUCUUUGCUAGCCUU	2068
AGGCUAGCAAAGAGCAAGG	2069	CCUUGCUCUUUGCUAGCCU	2070
GGCUAGCAAAGAGCAAGGA	2071	UCCUUGCUCUUUGCUAGCC	2072
GCUAGCAAAGAGCAAGGAA	2073	UUCCUUGCUCUUUGCUAGC	2074
CAAAGUGGCGAGGCCUCA	2075	UGAGGGCCUCGCCACUUUG	2076
AAAGUGGCGAGGCCUCAG	2077	CUGAGGGCCUCGCCACUUU	2078
AAGUGGCGAGGCCUCAGA	2079	UCUGAGGGCCUCGCCACUU	2080
GCGAGGCCUCAGAGUGAA	2081	UUCACUCUGAGGGCCUCGC	2082
AAAGCGUAAGGUUCAGUCA	2083	UGACUGAACCUUACGCUUU	2084
AAGAGCCUUCUCACCCAA	2085	UUGGGUGAGGAAGGCUCUU	2086
AGAGCCUUCUCACCCAAA	2087	UUUGGGUGAGGAAGGCUCU	2088
AAAAGCCUCUCUCAGCUGU	2089	ACAGCUGAGAGAGGCUUUU	2090
AAAGCCUCUCUCAGCUGUG	2091	CACAGCUGAGAGAGGCUUU	2092
UCAGCUGUGACCUGGCUCU	2093	AGAGCCAGGUCACAGCUGA	2094

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UGACCGGCUUGCAUUUU	2095	AAAAUGCAGAGCCAGGUCA	2096
ACCGGCUUGCAUUUUCA	2097	UGAAAAUGCAGAGCCAGGU	2098
CCUGGCUUGCAUUUUCAU	2099	AUGAAAAUGCAGAGCCAGG	2100
GCUCUGCAUUUUCAUCGUG	2101	CACGAUGAAAAUGCAGAGC	2102
CUCUGCAUUUUCAUCGUGG	2103	CCACGAUGAAAAUGCAGAG	2104
UCUGCAUUUUCAUCGUGGC	2105	GCCACGAUGAAAAUGCAGA	2106
CUGCAUUUUCAUCGUGGCC	2107	GGCCACGAUGAAAAUGCAG	2108
UGCAUUUUCAUCGUGGCCU	2109	AGGCCACGAUGAAAAUGCA	2110
GCAUUUUCAUCGUGGCCUU	2111	AAGGCCACGAUGAAAAUGC	2112
AUUUUCAUCGUGGCCUUUG	2113	CAAAGGCCACGAUGAAAAU	2114
UUUUCAUCGUGGCCUUUGU	2115	ACAAAGGCCACGAUGAAAA	2116
UUUCAUCGUGGCCUUUGUC	2117	GACAAAGGCCACGAUGAAA	2118
UUCAUCGUGGCCUUUGUCA	2119	UGACAAAGGCCACGAUGAA	2120
UCAUCGUGGCCUUUGUCAG	2121	CUGACAAAGGCCACGAUGA	2122
CAUCGUGGCCUUUGUCAGC	2123	GCUGACAAAGGCCACGAUG	2124
AUCGUGGCCUUUGUCAGCC	2125	GGCUGACAAAGGCCACGAU	2126
CCUUUGUCAGCCACCCAGC	2127	GCUGGGUGGCUGACAAAGG	2128
CUUUGUCAGCCACCCAGCG	2129	CGCUGGGUGGCUGACAAAG	2130
UUGUCAGCCACCCAGCGUG	2131	CACGCUGGGUGGCUGACAA	2132
GUGGUCGAGAAGCUCUCU	2133	AGAGAGCUUCUGCAGCCAC	2134
UGGUCGAGAAGCUCUCUA	2135	UAGAGAGCUUCUGCAGCCA	2136
GGCUGCAGAAGCUCUCUAA	2137	UUAGAGAGCUUCUGCAGCC	2138
GCUGCAGAAGCUCUCUAAG	2139	CUUAGAGAGCUUCUGCAGC	2140
CUGCAGAAGCUCUCUAAGC	2141	GCUUAGAGAGCUUCUGCAG	2142
UGCAGAAGCUCUCUAAGCA	2143	UGCUUAGAGAGCUUCUGCA	2144
GCAGAAGCUCUCUAAGCAC	2145	GUGCUUAGAGAGCUUCUGC	2146
CCAGCACAGCCACAGCUCA	2147	UGAGCUGUGGCUGUGCUGG	2148
CAGCACAGCCACAGCUCAA	2149	UUGAGCUGUGGCUGUGCUG	2150
GCACAGCCACAGCUCAAAG	2151	CUUUGAGCUGUGGCUGUGC	2152
CACAGCCACAGCUCAAAGC	2153	GCUUUGAGCUGUGGCUGUG	2154
ACAGCCACAGCUCAAAGCG	2155	CGCUUUGAGCUGUGGCUGU	2156
CAGCCACAGCUCAAAGCGG	2157	CCGCUUUGAGCUGUGGCUG	2158
AGCCACAGCUCAAAGCGGC	2159	GCCGCUUUGAGCUGUGGCU	2160

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GGCCAACUGCUGUGAGGAG	2161	CUCCUCACAGCAGUUGGCC	2162
GCCAACUGCUGUGAGGAGG	2163	CCUCCUCACAGCAGUUGGC	2164
CCAACUGCUGUGAGGAGGU	2165	ACCUCCUCACAGCAGUUGG	2166
CAACUGCUGUGAGGAGGUG	2167	CACCUCCUCACAGCAGUUG	2168
AACUGCUGUGAGGAGGUGA	2169	UCACCUCCUCACAGCAGUU	2170
ACUGCUGUGAGGAGGUGAA	2171	UUCACCUCCUCACAGCAGU	2172
CUCAAGGCCCAAGUUGCCA	2173	UGGCAACUUGGGCCUUGAG	2174
GCCCAAGUUGCCAACCUUA	2175	UAAGGUUGGCAACUUGGC	2176
CCCAAGUUGCCAACCUUAG	2177	CUAAGGUUGGCAACUUGGG	2178
CCAAGUUGCCAACCUUAGC	2179	GCUAAGGUUGGCAACUUGG	2180
CAAGUUGCCAACCUUAGCA	2181	UGCUAAGGUUGGCAACUUG	2182
AAGUUGCCAACCUUAGCAG	2183	CUGCUAAGGUUGGCAACUU	2184
AGUUGCCAACCUUAGCAGC	2185	GCUGCUAAGGUUGGCAACU	2186
GACUGGGUCAGCGUGGUCA	2187	UGACCACGCUGACCCAGUC	2188
ACUGGGUCAGCGUGGUCAU	2189	AUGACCACGCUGACCCAGU	2190
CUGGGUCAGCGUGGUCAUG	2191	CAUGACCACGCUGACCCAG	2192
UGGGUCAGCGUGGUCAUGC	2193	GCAUGACCACGCUGACCCA	2194
GGGUCAGCGUGGUCAUGCA	2195	UGCAUGACCACGCUGACCC	2196
CAGCGUGGUCAUGCAGGUG	2197	CACCUGCAUGACCACGCUG	2198
AGCGUGGUCAUGCAGGUGA	2199	UCACCUGCAUGACCACGCU	2200
GCGUGGUCAUGCAGGUGAU	2201	AUCACCUGCAUGACCACGC	2202
CGUGGUCAUGCAGGUGAUG	2203	CAUCACCUGCAUGACCACG	2204
AGCAAGCGCAUGGAGUCGC	2205	GCGACUCCAUGCGCUUGCU	2206
CAACCAAUUGACAUCAUG	2207	CAUGAUGUCAAUUUGGUUG	2208
ACCAAAUUGACAUCAUGCA	2209	UGCAUGAUGUCAAUUUGGU	2210
UUGACAUCAUGCAGCUGCA	2211	UGCAGCUGCAUGAUGUCAA	2212
CAGGCAGCACAGACGGUCA	2213	UGACCGUCUGUGCUGCCUG	2214
AGGCAGCACAGACGGUCAC	2215	GUGACCGUCUGUGCUGCCU	2216
GGCAGCACAGACGGUCACU	2217	AGUGACCGUCUGUGCUGCC	2218
GCAGCACAGACGGUCACUC	2219	GAGUGACCGUCUGUGCUGC	2220
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UCACUCAGACCUCCGCAGG	2223	CCUGCGGAGGUCUGAGUGA	2224
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CUAUGUAAGUUUACCUAAC	2277	GUUAGGUAAACUACAUAG	2278
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ACCUACAGGGUCUCUUUU	2283	AAAAGAGACCCGUGAAGGU	2284
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AACUCUUCUCAUUGGCUCA	2467	UGAGCCAUUGAGAAGAGUU	2468
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UUCAGGAAGGAUGCGGCU	2517	GAGCCGCAUCCUUCUGAA	2518
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CGGCUCUUAAGGUUCCUC	2529	GAGGAACCUUAAGGAGCCG	2530
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UUAAGGUUCCUCAAUUGUG	2537	CACAAUUGAGGAACCUUAA	2538
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AGCUUCUACUGACUAAGUC	2625	GACUUAGUCAGUAGAAGCU	2626
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CUUGCCCAGGACAUCAUUC	2769	GAAUGAUGUCCUGGGCAAG	2770
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UUUGGCUAUGGGACUGUCA	3889	UGACAGUCCCAUAGCCAAA	3890
UUGGCUAUGGGACUGUCAG	3891	CUGACAGUCCCAUAGCCAA	3892
UGGCUAUGGGACUGUCAGG	3893	CCUGACAGUCCCAUAGCCA	3894
GAGCCUGCUGCACUUUCUU	3895	AAGAAAGUGCAGCAGGCUC	3896
CUGCUGCACUUUCUUUAAG	3897	CUUAAAGAAAGUGCAGCAG	3898
UGCUGCACUUUCUUUAAGG	3899	CCUAAAGAAAGUGCAGCA	3900
GCUGCACUUUCUUUAAGGC	3901	GCCUAAAGAAAGUGCAGC	3902
UGCACUUUCUUUAAGGCUC	3903	GAGCCUAAAGAAAGUGCA	3904
GCACUUUCUUUAAGGCUCU	3905	AGAGCCUAAAGAAAGUGC	3906
CACUUUCUUUAAGGCUCUG	3907	CAGAGCCUAAAGAAAGUG	3908
UUCUUUAAGGCUCUGCUCC	3909	GGAGCAGAGCCUAAAGAA	3910
GCUCUGCUCCUGACAG	3911	CUGUCAGGAGGAGCAGAGC	3912
AGGACUGGGAGGGCAACCU	3913	AGGUUGCCCUCCAGUCCU	3914
GCAACCUGCGCUACGCUGA	3915	UCAGCGUAGCGCAGGUUGC	3916
CAACCUGCGCUACGCUGAG	3917	CUCAGCGUAGCGCAGGUUG	3918
CUGCGCUACGCUGAGUAUA	3919	UAUACUCAGCGUAGCGCAG	3920
UGCGCUACGCUGAGUAUAG	3921	CUAUACUCAGCGUAGCGCA	3922
CUACGCUGAGUAUAGCCAC	3923	GUGGCUAUACUCAGCGUAG	3924
UACGCUGAGUAUAGCCACU	3925	AGUGGCUAUACUCAGCGUA	3926
CACUUUGUUUUGGGCAAUG	3927	CAUUGCCCAAACAAGUG	3928
AACUACACUGGCAAUGUGG	3929	CCACAUUGCCAGUGUAGUU	3930
ACUACACUGGCAAUGUGGG	3931	CCCACAUUGCCAGUGUAGU	3932
AACGACGCCCUCCAGUAUC	3933	GAUACUGGAGGGCGUCGUU	3934
ACGACGCCCUCCAGUAUCA	3935	UGAUACUGGAGGGCGUCGU	3936
CGACGCCCUCCAGUAUCAU	3937	AUGAUACUGGAGGGCGUCG	3938
GACGCCCUCCAGUAUCAUA	3939	UAUGAUACUGGAGGGCGUC	3940
ACGCCCUCCAGUAUCAUAA	3941	UUAUGAUACUGGAGGGCGU	3942

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CGCCUCCAGUAUCAUAAC	3943	GUUAUGAUACUGGAGGGCG	3944
CAAGUGUGCACAGCUCCGC	3945	GCGGAGCUGUGCACACUUG	3946
AAGUGUGCACAGCUCCGCA	3947	UGCGGAGCUGUGCACACUU	3948
AGUGUGCACAGCUCCGCAA	3949	UUGCGGAGCUGUGCACACU	3950
UGCACAGCUCCGCAAAGGU	3951	ACCUUUGCGGAGCUGUGCA	3952
GCACAGCUCCGCAAAGGUG	3953	CACCUUUGCGGAGCUGUGC	3954
CACAGCUCCGCAAAGGUGA	3955	UCACCUUUGCGGAGCUGUG	3956
ACAGCUCCGCAAAGGUGAG	3957	CUCACCUUUGCGGAGCUGU	3958
CAAGCUCAUAAUCCACUU	3959	AAGUGGGAUUAUGAGCUUG	3960
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ACUGUACAGUUGAUUUC	3963	GGAAUAUCAACUGUACAGU	3964
CUGUACAGUUGAUUUCG	3965	CGGAUAUCAACUGUACAG	3966
UGUACAGUUGAUUUCGG	3967	CCGGAUAUCAACUGUACA	3968
GUACAGUUGAUUUCGGU	3969	ACCGGAUAUCAACUGUAC	3970
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CAGUUGAUUUCGGUUUU	3975	AAAACCGGAUAUCAACUG	3976
AGUUGAUUUCGGUUUUUG	3977	CAAACCGGAUAUCAACU	3978
GUUGAUUUCGGUUUUUGG	3979	CCAAACCGGAUAUCAAC	3980
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UGAUUUCGGUUUUUGGUA	3983	UACCAAACCGGAUAUCA	3984
GAUUAUCCGGUUUUUGGUAU	3985	AUACCAAACCGGAUAUC	3986
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UAUCCGGUUUUUGGUAUUC	3989	GAAUACCAAACCGGAUA	3990
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UUCGGUUUUUGGUAUUCU	3993	AAGAAUACCAAACCGGAA	3994
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GGUAUUCUUCUGACCCUG	3999	CAGGGUCAGAAAGAAUACC	4000
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ACUCCUUAACUGAUGUCUG	4003	CAGACAUCAAGGAGU	4004
CUCCUUAACUGAUGUCUGG	4005	CCAGACAUCAAGGAG	4006
UCCUUAACUGAUGUCUGGU	4007	ACCAGACAUCAAGGA	4008

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CCUUACCUGAUGUCUGGUC	4009	GACCAGACAUCAGGUAAGG	4010
CUUACCUGAUGUCUGGUCU	4011	AGACCAGACAUCAGGUAAG	4012
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UACCUGAUGUCUGGUCUAU	4015	AUAGACCAGACAUCAGGUA	4016
ACCUGAUGUCUGGUCUAUC	4017	GAUAGACCAGACAUCAGGU	4018
GAUGUCUGGUCUAUCACAG	4019	CUGUGAUAGACCAGACAUC	4020
AUGUCUGGUCUAUCACAGU	4021	ACUGUGAUAGACCAGACAU	4022
UGUCUGGUCUAUCACAGUC	4023	GACUGUGAUAGACCAGACA	4024
GUCUGGUCUAUCACAGUCA	4025	UGACUGUGAUAGACCAGAC	4026
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CUGGUCUAUCACAGUCAAC	4029	GUUGACUGUGAUAGACCAG	4030
UGGUCUAUCACAGUCAACU	4031	AGUUGACUGUGAUAGACCA	4032
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UAUCACAGUCAACUUACUA	4035	UAGUAAGUUGACUGUGAUA	4036
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ACUUACUAGCACUGGGUCU	4041	AGACCCAGUGCUAGUAAGU	4042
CUUACUAGCACUGGGUCUG	4043	CAGACCCAGUGCUAGUAAG	4044
UUACUAGCACUGGGUCUGU	4045	ACAGACCCAGUGCUAGUAA	4046
UACUAGCACUGGGUCUGUU	4047	AACAGACCCAGUGCUAGUA	4048
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GGGUCUGUUUCUCAUGCCA	4055	UGGCAUGAGAAACAGACCC	4056
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CUCAUGCCAGGUGGCUACU	4069	AGUAGCCACCUGGCAUGAG	4070
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CACAGACUCCAACCUCAAU	4073	AUUGAGGUUGGAGUCUGUG	4074

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ACAGACUCCAACCUCAAUG	4075	CAUUGAGGUUGGAGUCUGU	4076
CAGACUCCAACCUCAAUGG	4077	CCAUUGAGGUUGGAGUCUG	4078
CCAACCUCAAUGGAGUGUA	4079	UACACUCCAUUGAGGUUGG	4080
CAACCUCAAUGGAGUGUAC	4081	GUACACUCCAUUGAGGUUG	4082
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UCAUUGGAGUGUACUACCG	4091	CGGUAGUACACUCCAUUGA	4092
CAUUGGAGUGUACUACCGC	4093	GCGGUAGUACACUCCAUUG	4094
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UAAGCACCUUGGAUGGCAUC	4119	GAUGCCAUCCAGGUGCUUA	4120
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UGGAUGGCAUCACCUUGGUA	4129	UACCAGGUGAUGCCAUCCA	4130
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GGCAUGGAUCUACCUACUC	4133	GAGUAGGUAGAUCCAUGCC	4134
GCAUGGAUCUACCUACUCC	4135	GGAGUAGGUAGAUCCAUGC	4136
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AUGGAUCUACCUACUCCCU	4139	AGGGAGUAGGUAGAUCCA	4140

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GGAUUCUACCUACUCCUCA	4143	UGAGGGAGUAGGUAGAUGC	4144
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AUCUACCUACUCCUCAAA	4147	UUUGAGGGAGUAGGUAGAU	4148
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CCCAGAAGACUUAAGCCU	4153	AGGCUUGAAGUCUUCUGGG	4154
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GAAGACUUAAGCCUUA	4159	UUUAAGGCUUGAAGUCUUC	4160
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ACUUAAGCCUUA	4167	UCCUUUAAGGCUUGAAGU	4168
CUUAAGCCUUA	4169	CUCCUUUAAGGCUUGAAG	4170
UUUAAGCCUUA	4171	CCUCCUUUAAGGCUUGAA	4172
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UUUAAGGAGGCGCCGUG	4177	CACGGCAGCCUCCUUUA	4178
UUAAGGAGGCGCCGUGG	4179	CCACGGCAGCCUCCUUUA	4180
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AAAGGAGGCGCCGUGGAG	4183	CUCCACGGCAGCCUCCUU	4184
GUGGAGCACGGAUACAGAA	4185	UUCUGUAUCCGUGCUCCAC	4186
ACUGGAUGAGGGCAGAU	4187	UCAUCUGCCCUCAUCCAGU	4188
CUGGAUGAGGGCAGAU	4189	CUCAUCUGCCCUCAUCCAG	4190
GGAUGAGGGCAGAU	4191	UCCUCAUCUGCCCUCAUCC	4192
AUGAGGGCAGAU	4193	UGUCCUCAUCUGCCCUCAU	4194
UGAGGGCAGAU	4195	CUGUCCUCAUCUGCCCUCA	4196
AGGGCAGAU	4197	UCCUGUCCUCAUCUGCCCU	4198
GGCAGAU	4199	CUUCCUGUCCUCAUCUGCC	4200
CAGAU	4201	CUCUCCUGUCCUCAUCUG	4202
GAAUAAGUCUCCAAGGAGC	4203	GCUCCUUGGAGACUUAUUC	4204
AAUAAGUCUCCAAGGAGCA	4205	UGCUCCUUGGAGACUUAU	4206

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GUACCAAGGAUGUUACAGU	4209	ACUGUAACAUCUUGGUAC	4210
UACCAAGGAUGUUACAGUA	4211	UACUGUAACAUCUUGGUA	4212
ACCAAGGAUGUUACAGUAA	4213	UUACUGUAACAUCUUGGU	4214
CCAAGGAUGUUACAGUAAA	4215	UUUACUGUAACAUCUUGG	4216
CUGGGUCCUGCCACAUCU	4217	AGGAUGUGGCAGGACCCAG	4218
UGGGUCCUGCCACAUCU	4219	AAGGAUGUGGCAGGACCCA	4220
GGGUCCUGCCACAUCUUC	4221	GAAGGAUGUGGCAGGACCC	4222
GGUCCUGCCACAUCUUCU	4223	AGAAGGAUGUGGCAGGACC	4224
UCCUGCCACAUCUUCUCA	4225	UGAGAAGGAUGUGGCAGGA	4226
CCUGCCACAUCUUCUCA	4227	UUGAGAAGGAUGUGGCAGG	4228
CUGCCACAUCUUCUCAAG	4229	CUUGAGAAGGAUGUGGCAG	4230
CUUCUCAAGGUGGUAGACU	4231	AGUCUACCACCUUGAGAAG	4232
AGGUGGUAGACUGAGUGGG	4233	CCCACUCAGUCUACCACCU	4234
GGUCUCUCUGCCCAAGAUC	4235	GAUCUUGGGCAGAGAGACC	4236
GUCUCUCUGCCCAAGAUCC	4237	GGAUCUUGGGCAGAGAGAC	4238
UCUCUCUGCCCAAGAUCCC	4239	GGGAUCUUGGGCAGAGAGA	4240
UCUGCCCAAGAUCCCUGAC	4241	GUCAGGGAUUCUUGGGCAGA	4242
CUGCCCAAGAUCCCUGACA	4243	UGUCAGGGAUUCUUGGGCAG	4244
UGCCCAAGAUCCCUGACAU	4245	AUGUCAGGGAUUCUUGGGCA	4246
GCCCAAGAUCCCUGACAU	4247	UAUGUCAGGGAUUCUUGGGC	4248
CCCAAGAUCCCUGACAUAG	4249	CUAUGUCAGGGAUUCUUGGG	4250
AUCCCUGACAUAGCAGUAG	4251	CUACUGCUAUGUCAGGGAU	4252
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CCUGACAUAGCAGUAGCUU	4255	AAGCUACUGCUAUGUCAGG	4256
CUGACAUAGCAGUAGCUUG	4257	CAAGCUACUGCUAUGUCAG	4258
UGACAUAGCAGUAGCUUGU	4259	ACAAGCUACUGCUAUGUCA	4260
ACAUAGCAGUAGCUUGUCU	4261	AGACAAGCUACUGCUAUGU	4262
CAUAGCAGUAGCUUGUCUU	4263	AAGACAAGCUACUGCUAUG	4264
GCAGUAGCUUGUCUUUCC	4265	GGAAAAGACAAGCUACUGC	4266
CAGUAGCUUGUCUUUCCA	4267	UGGAAAAGACAAGCUACUG	4268
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GUAGCUUGUCUUUCCACA	4271	UGUGGAAAAGACAAGCUAC	4272

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CUUGUCUUUCCACAUGAU	4273	AUCAUGUGGAAAAGACAAG	4274
UUGUCUUUCCACAUGAUU	4275	AAUCAUGUGGAAAAGACAA	4276
CUUUUCCACAUGAUUUGUC	4277	GACAAAUCAUGUGGAAAAG	4278
UUUUUCCACAUGAUUUGUCU	4279	AGACAAAUCAUGUGGAAAA	4280
UUUCCACAUGAUUUGUCUG	4281	CAGACAAAUCAUGUGGAAA	4282
UUCCACAUGAUUUGUCUGU	4283	ACAGACAAAUCAUGUGGAA	4284
GCUUAGGCUAUGUGAGGGC	4285	GCCCUACAUAAGCCUAGC	4286
AGGCUAUGUGAGGGGAAAA	4287	UUUUGCCCUACAUAAGCCU	4288
AGGAGUGAAGGAGGCAGGU	4289	ACCUGCCUCCUUCACUCCU	4290
GGAGUGAAGGAGGCAGGUG	4291	CACCUGCCUCCUUCACUCC	4292
GAGUGAAGGAGGCAGGUGG	4293	CCACCUGCCUCCUUCACUC	4294
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ACUCCAGGGCAGUCUAUCU	4297	AGAUGCAGUGCCUGGAGU	4298
CUCCAGGGCAGUCUAUCUG	4299	CAGAUGCAGUGCCUGGAG	4300
AGGGCAGUCUAUCUGGCGA	4301	UCGCCAGAUGCAGUGCCU	4302
GGGCAGUCUAUCUGGCGAU	4303	AUCGCCAGAUGCAGUGCCC	4304
GGCAGUCUAUCUGGCGAUC	4305	GAUCGCCAGAUGCAGUGCC	4306
GCAGUCUAUCUGGCGAUC	4307	UGAUCGCCAGAUGCAGUGC	4308
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CCUGCUCGCCUUGGUCAUG	4311	CAUGACCAAGGCGAGCAGG	4312
CUGCUCGCCUUGGUCAUGU	4313	ACAUGACCAAGGCGAGCAG	4314
UGCUCGCCUUGGUCAUGUA	4315	UACAUGACCAAGGCGAGCA	4316
AUGAAGCACCAGCAGGAGG	4317	CCUCCUGCUGGUGCUUCAU	4318
UGAAGCACCAGCAGGAGGU	4319	ACCUCCUGCUGGUGCUUCA	4320
CAGCAGGAGGUGGACAGAG	4321	CUCUGUCCACCUCCUGCUG	4322
AGCAGGAGGUGGACAGAGU	4323	ACUCUGUCCACCUCCUGCU	4324
GCAGGAGGUGGACAGAGUC	4325	GACUCUGUCCACCUCCUGC	4326
CAGGAGGUGGACAGAGUCU	4327	AGACUCUGUCCACCUCCUG	4328
GGAGGUGGACAGAGUCUCU	4329	AGAGACUCUGUCCACCUCC	4330
AGGUGGACAGAGUCUCUCA	4331	UGAGAGACUCUGUCCACCU	4332
UGGACAGAGUCUCUCAUGG	4333	CCAUGAGAGACUCUGUCCA	4334
GGACAGAGUCUCUCAUGGA	4335	UCCAUGAGAGACUCUGUCC	4336
GACAGAGUCUCUCAUGGAU	4337	AUCCAUGAGAGACUCUGUC	4338

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ACAGAGUCUCUCAUGGAUG	4339	CAUCCAUGAGAGACUCUGU	4340
GGAGCUUCCUUUUAAAUUU	4341	AAAUUUAAAAGGAAGCUCC	4342
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ACUGAAGGUAGAUGGUGUU	4345	AACACCAUCUACCUUCAGU	4346
CUGAAGGUAGAUGGUGUUA	4347	UAACACCAUCUACCUUCAG	4348
UGAAGGUAGAUGGUGUUAU	4349	AUAACACCAUCUACCUUCA	4350
GAAGGUAGAUGGUGUUAUA	4351	UAUAACACCAUCUACCUUC	4352
GUAGAUGGUGUUAUAGUUA	4353	UAACUAUAACACCAUCUAC	4354
UGUAAAUAAGCAUCUCACU	4355	AGUGAGAUGCUUAUUUACA	4356
AUAAGCAUCUCACUUUGUA	4357	UACAAAGUGAGAUGCUUAU	4358

Table 5

Sense Sequence	SEQ ID NO:	Antisense Sequence	SEQ ID NO:
AAGUGGCCUUGUCUCCUUC	4359	GAAGGAGACAAGGCCACUU	4360
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GUGGCCUUGUCUCCUUCUA	4363	UAGAAGGAGACAAGGCCAC	4364
CUUGUCUCCUUCUACCGGG	4365	CCCGGUAGAAGGAGACAAG	4366
UUGUCUCCUUCUACCGGGA	4367	UCCCGGUAGAAGGAGACAA	4368
UGUCUCCUUCUACCGGGAC	4369	GUCCCGGUAGAAGGAGACA	4370
GUCUCCUUCUACCGGGACU	4371	AGUCCCGGUAGAAGGAGAC	4372
UUCUACCGGGACUGGAAGC	4373	GCUUCCAGUCCCGGUAGAA	4374
UCUACCGGGACUGGAAGCA	4375	UGCUUCCAGUCCCGGUAGA	4376
CUACCGGGACUGGAAGCAG	4377	CUGCUUCCAGUCCCGGUAG	4378
AGCAGGGCUUUGGCAGCAU	4379	AUGCUGCCAAAGCCUUGCU	4380
AGGGCUUUGGCAGCAUCCG	4381	CGGAUGCUGCCAAAGCCCU	4382
GGGCUUUGGCAGCAUCCGU	4383	ACGGAUGCUGCCAAAGCCC	4384
GGCUUUGGCAGCAUCCGUG	4385	CACGGAUGCUGCCAAAGCC	4386
CAUCCACCGGCUCUCCAGA	4387	UCUGGAGAGCCGGUGGAUG	4388
AUCCACCGGCUCUCCAGAC	4389	GUCUGGAGAGCCGGUGGAU	4390
UCCACCGGCUCUCCAGACA	4391	UGUCUGGAGAGCCGGUGGA	4392
CUGGACCAGUGCCACCACA	4393	UGUGGUGGCACUGGUCCAG	4394
GGGUGCCAUUCCUAUUCUG	4395	CAGAAUAGGAAUGGCACCC	4396
GGUGCCAUUCCUAUUCUGA	4397	UCAGAAUAGGAAUGGCACC	4398

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GUGCAUUCUAUUCUGAU	4399	AUCAGAAUAGGAAUGGCAC	4400
UGCAUUCUAUUCUGAUU	4401	AAUCAGAAUAGGAAUGGCA	4402
AUUCUAUUCUGAUUCAAG	4403	CUUGAAUCAGAAUAGGAAU	4404
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GUAUAUUCAUUGUGAUGGU	4407	ACCAUCACAAUGAAUAUAC	4408
AUUCAUUGUGAUGGUUUUC	4409	GAAAACCAUCACAAUGAAU	4410
UUCAUUGUGAUGGUUUUCC	4411	GGAAAACCAUCACAAUGAA	4412
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GUGAUGGUUUUCCUGCAAG	4415	CUUGCAGGAAAACCAUCAC	4416
UGAUGGUUUUCCUGCAAGU	4417	ACUUGCAGGAAAACCAUCA	4418
AUGGUUUUCCUGCAAGUUG	4419	CAACUUGCAGGAAAACCAU	4420
GGUUUCCUGCAAGUUGUA	4421	UACAACUUGCAGGAAAACC	4422
GUUUUCCUGCAAGUUGUAA	4423	UUACAACUUGCAGGAAAAC	4424
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UUCUGCAAGUUGUAAUGG	4429	CCAUUACAACUUGCAGGAA	4430
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GUUGUAAUGGAGUUGAGGA	4439	UCCUCAACUCCAUUACAAC	4440
CUGCAGGUGGGACAGGAAG	4441	CUUCCUGUCCCACCUGCAG	4442
GCAGGUGGGACAGGAAGAG	4443	CUCUCCUGUCCCACCUGC	4444
CAGGUGGGACAGGAAGAGG	4445	CCUCUCCUGUCCCACCUG	4446
AGGUGGGACAGGAAGAGGC	4447	GCCUCUCCUGUCCCACCU	4448
GGGACAGGAAGAGGCCAGA	4449	UCUGGCCUCUCCUGUCCC	4450
GGACAGGAAGAGGCCAGAC	4451	GUCUGGCCUCUCCUGUCC	4452
GACAGGAAGAGGCCAGACC	4453	GGUCUGGCCUCUCCUGUC	4454
CAGACCCAGGCCAGAGUAG	4455	CUACUCUGGCCUGGGUCUG	4456
AGACCCAGGCCAGAGUAGA	4457	UCUACUCUGGCCUGGGUCU	4458
GACCCAGGCCAGAGUAGAG	4459	CUCUACUCUGGCCUGGGUC	4460
CCCAGGCCAGAGUAGAGCA	4461	UGCUCUACUCUGGCCUGGG	4462
CAGGCCAGAGUAGAGCAA	4463	UUUGCUCUACUCUGGCCUG	4464

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GCCAGAGUAGAGCAAAUUC	4465	GAAUUUGCUCUACUCUGGC	4466
CCAGAGUAGAGCAAAUUCA	4467	UGAAUUUGCUCUACUCUGG	4468
CAGAGUAGAGCAAAUUCAA	4469	UUGAAUUUGCUCUACUCUG	4470
AGAGUAGAGCAAAUUCAAC	4471	GUUGAAUUUGCUCUACUCU	4472
ACACUAGUCUCUGCUCUGG	4473	CCAGAGCAGAGACUAGUGU	4474
CACUAGUCUCUGCUCUGGC	4475	GCCAGAGCAGAGACUAGUG	4476
CUAGUCUCUGCUCUGGCCG	4477	CGGCCAGAGCAGAGACUAG	4478
UAGUCUCUGCUCUGGCCGA	4479	UCGGCCAGAGCAGAGACUA	4480
AGUCUCUGCUCUGGCCGAG	4481	CUCGGCCAGAGCAGAGACU	4482
CUCUGGCCGAGCAUGAGGU	4483	ACCUCAUGCUCGGCCAGAG	4484
UCUGGCCGAGCAUGAGGUC	4485	GACCUCAUGCUCGGCCAGA	4486
UGGCCGAGCAUGAGGUCCU	4487	AGGACCUCAUGCUCGGCCA	4488
GGCCGAGCAUGAGGUCCUU	4489	AAGGACCUCAUGCUCGGCC	4490
GCCGAGCAUGAGGUCCUUU	4491	AAAGGACCUCAUGCUCGGC	4492
CCGAGCAUGAGGUCCUUUA	4493	UAAAGGACCUCAUGCUCGG	4494
CGAGCAUGAGGUCCUUUAG	4495	CUAAAGGACCUCAUGCUCG	4496
GAGCAUGAGGUCCUUUAGG	4497	CCUAAAGGACCUCAUGCUC	4498
AGCAUGAGGUCCUUUAGGU	4499	ACCUAAAGGACCUCAUGCU	4500
GCAUGAGGUCCUUUAGGUG	4501	CACCUAAAGGACCUCAUGC	4502
CAUGAGGUCCUUUAGGUGC	4503	GCACCUAAAGGACCUCAUG	4504
AUGAGGUCCUUUAGGUGCA	4505	UGCACCUAAAGGACCUCAU	4506
UGAGGUCCUUUAGGUGCAA	4507	UUGCACCUAAAGGACCUCA	4508
GAGGUCCUUUAGGUGCAAA	4509	UUUGCACCUAAAGGACCUC	4510
AGGUCCUUUAGGUGCAAAU	4511	AUUUGCACCUAAAGGACCU	4512
GGUCCUUUAGGUGCAAAUC	4513	GAUUUGCACCUAAAGGACC	4514
GUCCUUUAGGUGCAAAUCU	4515	AGAUUUGCACCUAAAGGAC	4516
UCCUUUAGGUGCAAAUCUU	4517	AAGAUUUGCACCUAAAGGA	4518
CCUUUAGGUGCAAAUCUUA	4519	UAAGAUUUGCACCUAAAGG	4520
CUUUAGGUGCAAAUCUUAC	4521	GUAAGAUUUGCACCUAAAG	4522
UUUAGGUGCAAAUCUUACU	4523	AGUAAGAUUUGCACCUAAA	4524
GCAAAUCUUACUGAUACUG	4525	CAGUAUCAGUAAGAUUUGC	4526
UCUUACUGAUACUGUUUGG	4527	CCAAACAGUAUCAGUAAGA	4528
AAAGCACUCACUAUAUCCU	4529	AGGAUAUAGUGAGUGCUUU	4530

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AAGCACUCACUUAUCCUC	4531	GAGGAUUAUGAGUGUCUU	4532
ACUCACUUAUCCUCAUGU	4533	ACAUGAGGAUUAUGUGAGU	4534
UCACUUAUCCUCAUGUUU	4535	AAACAUGAGGAUUAUGUGA	4536
UAUCCUCAUGUUUCUCUUA	4537	UAAGAGAAACAUGAGGAUA	4538
AUCCUCAUGUUUCUCUAC	4539	GUAAGAGAAACAUGAGGAU	4540
UCCUCAUGUUUCUCUACA	4541	UGUAAGAGAAACAUGAGGA	4542
CUCAUGUUUCUCUACAGC	4543	GCUGUAAGAGAAACAUGAG	4544
UCAUGUUUCUCUACAGCA	4545	UGCUGUAAGAGAAACAUGA	4546
UUCUCUACAGCAGCUCUG	4547	CAGAGCUGCUGUAAGAGAA	4548
GCAGCUCUGUGUGGGAUUC	4549	GAAUCCACACAGAGCUGC	4550
ACAUAGCUGCACCUUAUAA	4551	UUAUAAGGUGCAGCUAUGU	4552
CAUAGCUGCACCUUAUAAG	4553	CUUAUAAGGUGCAGCUAUG	4554
AUAGCUGCACCUUAUAAGC	4555	GCUUAUAAGGUGCAGCUAU	4556
UAGCUGCACCUUAUAAGCA	4557	UCUUAUAAGGUGCAGCUA	4558
AGACUAAUCAAGGCCAUUAU	4559	AUAUGGCCUUGAUUAGUCU	4560
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ACUAAUCAAGGCCAUUAUGG	4563	CCUAUGGCCUUGAUUAGU	4564
CUAUAUCAAGGCCAUUAUGGU	4565	ACCAUAUGGCCUUGAUUAG	4566
UAAUCAAGGCCAUUAUGGUG	4567	CACCAUAUGGCCUUGAUUA	4568
AAUCAAGGCCAUUAUGGUGA	4569	UCACCAUAUGGCCUUGAUU	4570
AUCAAGGCCAUUAUGGUGAA	4571	UUCACCAUAUGGCCUUGAU	4572
UCAAGGCCAUUAUGGUGAAU	4573	AUUCACCAUAUGGCCUUGA	4574
CAAGGCCAUUAUGGUGAAUC	4575	GAUUCACCAUAUGGCCUUG	4576
AAGGCCAUUAUGGUGAAUCA	4577	UGAUUCACCAUAUGGCCUU	4578
AAAGAAGUUCGAGCCUUGU	4579	ACAAGGCUCGAACUUCUUU	4580
AAGAAGUUCGAGCCUUGUU	4581	AACAAGGCUCGAACUUCUU	4582
AGAAGUUCGAGCCUUGUUU	4583	AAACAAGGCUCGAACUUCU	4584
GAAGUUCGAGCCUUGUUUU	4585	AAAACAAGGCUCGAACUUC	4586
AAGUUCGAGCCUUGUUUUC	4587	GAAAACAAGGCUCGAACUU	4588
AGUUCGAGCCUUGUUUUCU	4589	AGAAAACAAGGCUCGAACU	4590
GUUCGAGCCUUGUUUUCUG	4591	CAGAAAACAAGGCUCGAAC	4592
UUCGAGCCUUGUUUUCUGA	4593	UCAGAAAACAAGGCUCGAA	4594
UCGAGCCUUGUUUUCUGAU	4595	AUCAGAAAACAAGGCUCGA	4596

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CGAGCCUUGUUUUCUGAUU	4597	AAUCAGAAAACAAGGCUCG	4598
UUCUGAUUCCAGGUUAAC	4599	GUUAACCUGGGAUUCAGAA	4600
AAAAGAUUUUGGCUAUGG	4601	CCAUAGCCAAACAUCUUUU	4602
AAAGAUUUUUGGCUAUGGG	4603	CCCAUAGCCAAACAUCUUU	4604
AAGAUUUUUGGCUAUGGGA	4605	UCCCAUAGCCAAACAUCUU	4606
AGAUGUUUUGGCUAUGGGAC	4607	GUCCCAUAGCCAAACAUCU	4608
GAUGUUUUGGCUAUGGGACU	4609	AGUCCCAUAGCCAAACAUC	4610
UUUGGCUAUGGGACUGUCA	4611	UGACAGUCCCAUAGCCAAA	4612
UUGGCUAUGGGACUGUCAG	4613	CUGACAGUCCCAUAGCCAA	4614
UGGCUAUGGGACUGUCAGG	4615	CCUGACAGUCCCAUAGCCA	4616
GAGCCUGCUGCACUUUCUU	4617	AAGAAAGUGCAGCAGGCUC	4618
CUGCUGCACUUUCUUUAAG	4619	CUUAAAGAAAGUGCAGCAG	4620
UGCUGCACUUUCUUUAAGG	4621	CCUUAAGAAAGUGCAGCA	4622
GCUGCACUUUCUUUAAGGC	4623	GCCUUAAGAAAGUGCAGC	4624
UGCACUUUCUUUAAGGCUC	4625	GAGCCUUAAGAAAGUGC	4626
GCACUUUCUUUAAGGCUCU	4627	AGAGCCUUAAGAAAGUGC	4628
CACUUUCUUUAAGGCUCUG	4629	CAGAGCCUUAAGAAAGUG	4630
UUCUUUAAGGCUCUGCUC	4631	GGAGCAGAGCCUUAAGAA	4632
GCUCUGCUCUCCUGACAG	4633	CUGUCAGGAGGAGCAGAGC	4634
AGGACUGGGAGGGCAACCU	4635	AGGUUGCCCUCCAGUCCU	4636
GCAACCUGCGCUACGCUGA	4637	UCAGCGUAGCGCAGGUUGC	4638
CAACCUGCGCUACGCUGAG	4639	CUCAGCGUAGCGCAGGUUG	4640
CUGCGCUACGCUAGUAUA	4641	UAUACUCAGCGUAGCGCAG	4642
UGCGCUACGCUAGUAUAG	4643	CUAUACUCAGCGUAGCGCA	4644
CUACGCUAGUAUAGCCAC	4645	GUGGCUAUACUCAGCGUAG	4646
UACGCUAGUAUAGCCACU	4647	AGUGGCUAUACUCAGCGUA	4648
CACUUUGUUUUGGGCAAUG	4649	CAUUGCCCAAAACAAGUG	4650
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ACUACACUGGCAAUGUGGG	4653	CCCACAUUGCCAGUGUAGU	4654
AACGACGCCUCCAGUAUC	4655	GAUACUGGAGGGCGUCGUU	4656
ACGACGCCUCCAGUAUCA	4657	UGAUACUGGAGGGCGUCGU	4658
CGACGCCUCCAGUAUCAU	4659	AUGAUACUGGAGGGCGUCG	4660
GACGCCUCCAGUAUCAUA	4661	UAUGAUACUGGAGGGCGUC	4662

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CGCCCUCAGUAUCAUAAAC	4665	GUUAUGAUACUGGAGGGCG	4666
CAAGUGUGCACAGCUCCGC	4667	GCGGAGCUGUGCACACUUG	4668
AAGUGUGCACAGCUCCGCA	4669	UGCGGAGCUGUGCACACUU	4670
AGUGUGCACAGCUCCGCAA	4671	UUGCGGAGCUGUGCACACU	4672
UGCACAGCUCCGCAAAGGU	4673	ACCUUUGCGGAGCUGUGCA	4674
GCACAGCUCCGCAAAGGUG	4675	CACCUUUGCGGAGCUGUGC	4676
CACAGCUCCGCAAAGGUGA	4677	UCACCUUUGCGGAGCUGUG	4678
ACAGCUCCGCAAAGGUGAG	4679	CUCACCUUUGCGGAGCUGU	4680
CAAGCUCAUAAUCCACUU	4681	AAGUGGGAUUUAGAGCUUG	4682
CAUAAUCCACUUGAGGAG	4683	CUCCUCAAGUGGGAUUUAG	4684
ACUGUACAGUUGAUAUUCC	4685	GGAAUAUCAACUGUACAGU	4686
CUGUACAGUUGAUAUUCCG	4687	CGGAUAUCAACUGUACAG	4688
UGUACAGUUGAUAUUCCGG	4689	CCGGAUAUCAACUGUACA	4690
GUACAGUUGAUAUUCCGGU	4691	ACCGGAUAUCAACUGUAC	4692
UACAGUUGAUAUUCCGGUU	4693	AACCGGAUAUCAACUGUA	4694
ACAGUUGAUAUUCCGGUUU	4695	AAACCGGAUAUCAACUGU	4696
CAGUUGAUAUUCCGGUUUU	4697	AAAACCGGAUAUCAACUG	4698
AGUUGAUAUUCCGGUUUUG	4699	CAAAACCGGAUAUCAACU	4700
GUUGAUAUUCCGGUUUUGG	4701	CCAAAACCGGAUAUCAAC	4702
UUGAUAUUCCGGUUUUGGU	4703	ACCAAAACCGGAUAUCAA	4704
UGAUAUUCCGGUUUUGGUA	4705	UACCAAAACCGGAUAUCA	4706
GAUAUUCCGGUUUUGGUAU	4707	AUACCAAAACCGGAUAUC	4708
AUAUCCGGUUUUGGUAUU	4709	AAUACCAAAACCGGAUAU	4710
UAUCCGGUUUUGGUAUUC	4711	GAAUACCAAAACCGGAUA	4712
AUCCGGUUUUGGUAUUCU	4713	AGAAUACCAAAACCGGAU	4714
UCCGGUUUUGGUAUUCUU	4715	AAGAAUACCAAAACCGGAA	4716
GGUUUUGGUAUUCUUUCUG	4717	CAGAAAGAAUACCAAAACC	4718
UUUUGGUAUUCUUUCUGAC	4719	GUCAGAAAGAAUACCAAAA	4720
GGUAUUCUUUCUGACCCUG	4721	CAGGGUCAGAAAGAAUACC	4722
AACUCCUACCGAUGUCU	4723	AGACAUCAGGUAAGGAGUU	4724
ACUCCUACCGAUGUCUG	4725	CAGACAUCAGGUAAGGAGU	4726
CUCCUACCGAUGUCUGG	4727	CCAGACAUCAGGUAAGGAG	4728

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UCCUUACCUGAUGUCUGGU	4729	ACCAGACAUCAGGUAAGGA	4730
CCUUACCUGAUGUCUGGUC	4731	GACCAGACAUCAGGUAAGG	4732
CUUACCUGAUGUCUGGUCU	4733	AGACCAGACAUCAGGUAAG	4734
UUACCUGAUGUCUGGUCUA	4735	UAGACCAGACAUCAGGUAA	4736
UACCUGAUGUCUGGUCUAU	4737	AUAGACCAGACAUCAGGUA	4738
ACCUGAUGUCUGGUCUAUC	4739	GAUAGACCAGACAUCAGGU	4740
GAUGUCUGGUCUAUCACAG	4741	CUGUGAUAGACCAGACAUC	4742
AUGUCUGGUCUAUCACAGU	4743	ACUGUGAUAGACCAGACAU	4744
UGUCUGGUCUAUCACAGUC	4745	GACUGUGAUAGACCAGACA	4746
GUCUGGUCUAUCACAGUCA	4747	UGACUGUGAUAGACCAGAC	4748
UCUGGUCUAUCACAGUCAA	4749	UUGACUGUGAUAGACCAGA	4750
CUGGUCUAUCACAGUCAAC	4751	GUUGACUGUGAUAGACCAG	4752
UGGUCUAUCACAGUCAACU	4753	AGUUGACUGUGAUAGACCA	4754
CUAUCACAGUCAACUUACU	4755	AGUAAGUUGACUGUGAUAG	4756
UAUCACAGUCAACUUACUA	4757	UAGUAAGUUGACUGUGAUA	4758
ACAGUCAACUUACUAGCAC	4759	GUGCUAGUAAGUUGACUGU	4760
AACUUACUAGCACUGGGUC	4761	GACCCAGUGCUAGUAAGUU	4762
ACUUACUAGCACUGGGUCU	4763	AGACCCAGUGCUAGUAAGU	4764
CUUACUAGCACUGGGUCUG	4765	CAGACCCAGUGCUAGUAAG	4766
UUACUAGCACUGGGUCUGU	4767	ACAGACCCAGUGCUAGUAA	4768
UACUAGCACUGGGUCUGUU	4769	AACAGACCCAGUGCUAGUA	4770
ACUAGCACUGGGUCUGUUU	4771	AAACAGACCCAGUGCUAGU	4772
CUGGGUCUGUUUCUCAUGC	4773	GCAUGAGAAACAGACCCAG	4774
UGGGUCUGUUUCUCAUGCC	4775	GGCAUGAGAAACAGACCCA	4776
GGGUCUGUUUCUCAUGCCA	4777	UGGCAUGAGAAACAGACCC	4778
GGUCUGUUUCUCAUGCCAG	4779	CUGGCAUGAGAAACAGACC	4780
UGUUUCUCAUGCCAGGUGG	4781	CCACCUGGCAUGAGAAACA	4782
GUUUUCUCAUGCCAGGUGGC	4783	GCCACCUGGCAUGAGAAAC	4784
UUUCUCAUGCCAGGUGGCU	4785	AGCCACCUGGCAUGAGAAA	4786
UUCUCAUGCCAGGUGGCUA	4787	UAGCCACCUGGCAUGAGAA	4788
UCUCAUGCCAGGUGGCUAC	4789	GUAGCCACCUGGCAUGAGA	4790
CUCAUGCCAGGUGGCUACU	4791	AGUAGCCACCUGGCAUGAG	4792
CAACUGCUGCACAGACUCC	4793	GGAGUCUGUGCAGCAGUUG	4794

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CACAGACUCCAACCUCAAU	4795	AUUGAGGUUGGAGUCUGUG	4796
ACAGACUCCAACCUCAAUG	4797	CAUUGAGGUUGGAGUCUGU	4798
CAGACUCCAACCUCAAUGG	4799	CCAUUGAGGUUGGAGUCUG	4800
CCAACCUCAAUGGAGUGUA	4801	UACACUCCAUUGAGGUUGG	4802
CAACCUCAAUGGAGUGUAC	4803	GUACACUCCAUUGAGGUUG	4804
AACCUCAAUGGAGUGUACU	4805	AGUACACUCCAUUGAGGUU	4806
ACCUCAAUGGAGUGUACUA	4807	UAGUACACUCCAUUGAGGU	4808
CCUCAAUGGAGUGUACUAC	4809	GUAGUACACUCCAUUGAGG	4810
CUCAAUGGAGUGUACUACC	4811	GGUAGUACACUCCAUUGAG	4812
UCAAUGGAGUGUACUACCG	4813	CGGUAGUACACUCCAUUGA	4814
CAAUGGAGUGUACUACCGC	4815	GCGGUAGUACACUCCAUUG	4816
AAUGGAGUGUACUACCGCC	4817	GGCGGUAGUACACUCCAUI	4818
AUGGAGUGUACUACCGCCU	4819	AGGCGGUAGUACACUCCA	4820
UGGAGUGUACUACCGCCUG	4821	CAGGCGGUAGUACACUCCA	4822
GGAGUGUACUACCGCCUGG	4823	CCAGGCGGUAGUACACUCC	4824
GAGUGUACUACCGCCUGGG	4825	CCCAGGCGGUAGUACACUC	4826
AGUGUACUACCGCCUGGGU	4827	ACCCAGGCGGUAGUACACU	4828
GUACUACCGCCUGGGUGAG	4829	CUCACCCAGGCGGUAGUAC	4830
UACUACCGCCUGGGUGAGC	4831	GCUCACCCAGGCGGUAGUA	4832
ACUACCGCCUGGGUGAGCA	4833	UGCUCACCCAGGCGGUAGU	4834
CAUAAGCACCUGGAUGGC	4835	GCCAUCCAGGUGCUUAUUG	4836
AAUAAGCACCUGGAUGGCA	4837	UGCCAUCCAGGUGCUUAUU	4838
AUAAGCACCUGGAUGGCAU	4839	AUGCCAUCCAGGUGCUUAU	4840
UAAGCACCUGGAUGGCAUC	4841	GAUGCCAUCCAGGUGCUUA	4842
AAGCACCUGGAUGGCAUCA	4843	UGAUGCCAUCCAGGUGCUU	4844
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GCACCUGGAUGGCAUCACC	4847	GGUGAUGCCAUCCAGGUGC	4848
CACCUGGAUGGCAUCACCU	4849	AGGUGAUGCCAUCCAGGUG	4850
UGGAUGGCAUCACCUGGUA	4851	UACCAGGUGAUGCCAUCCA	4852
UGGCAUGGAUCUACCUACU	4853	AGUAGGUAGAUCCAUGCCA	4854
GGCAUGGAUCUACCUACUC	4855	GAGUAGGUAGAUCCAUGCC	4856
GCAUGGAUCUACCUACUCC	4857	GGAGUAGGUAGAUCCAUGC	4858
CAUGGAUCUACCUACUCCC	4859	GGGAGUAGGUAGAUCCAUG	4860

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AUGGAUCUACCUACUCCCU	4861	AGGGAGUAGGUAGAUCCA	4862
UGGAUCUACCUACUCCUC	4863	GAGGGAGUAGGUAGAUCCA	4864
GGAUCUACCUACUCCCUCA	4865	UGAGGGAGUAGGUAGAUCC	4866
GAUCUACCUACUCCCUCAA	4867	UUGAGGGAGUAGGUAGAU	4868
AUCUACCUACUCCCUCAA	4869	UUUGAGGGAGUAGGUAGAU	4870
CGCCCAGAAGACUUAAGC	4871	GCUUGAAGUCUUCUGGGCG	4872
GCCCAGAAGACUUAAGCC	4873	GGCUUGAAGUCUUCUGGGC	4874
CCCAGAAGACUUAAGCCU	4875	AGGCUUGAAGUCUUCUGGG	4876
CCAGAAGACUUAAGCCUU	4877	AAGGCUUGAAGUCUUCUGG	4878
CAGAAGACUUAAGCCUUA	4879	UAAGGCUUGAAGUCUUCUG	4880
GAAGACUUAAGCCUUA	4881	UUUAAGGCUUGAAGUCUUC	4882
AAGACUUAAGCCUUA	4883	UUUUAAGGCUUGAAGUCU	4884
AGACUUAAGCCUUA	4885	CUUUUAAGGCUUGAAGUCU	4886
GACUUAAGCCUUA	4887	CCUUUAAGGCUUGAAGUC	4888
ACUUAAGCCUUA	4889	UCCUUUAAGGCUUGAAGU	4890
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UUUAAGCCUUA	4893	CCUCCUUUAAGGCUUGAA	4894
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CUUUAAGGAGGCUGCCGU	4897	ACGGCAGCCUCCUUUAAG	4898
UUUAAGGAGGCUGCCGUG	4899	CACGGCAGCCUCCUUUA	4900
UUAAGGAGGCUGCCGUGG	4901	CCACGGCAGCCUCCUUUA	4902
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AAAGGAGGCUGCCGUGGAG	4905	CUCCACGGCAGCCUCCUU	4906
GUGGAGCACGGAUACAGAA	4907	UUCUGUAUCCGUGCUCCAC	4908
ACUGGAUGAGGGCAGAUGA	4909	UCAUCUGCCCUCAUCCAGU	4910
CUGGAUGAGGGCAGAUGAG	4911	CUCAUCUGCCCUCAUCCAG	4912
GGAUGAGGGCAGAUGAGGA	4913	UCCUCAUCUGCCCUCAUCC	4914
AUGAGGGCAGAUGAGGACA	4915	UGUCCUCAUCUGCCCUCAU	4916
UGAGGGCAGAUGAGGACAG	4917	CUGUCCUCAUCUGCCCUCA	4918
AGGGCAGAUGAGGACAGGA	4919	UCCUGUCCUCAUCUGCCCU	4920
GGCAGAUGAGGACAGGAAG	4921	CUUCCUGUCCUCAUCUGCC	4922
CAGAUGAGGACAGGAAGAG	4923	CUCUCCUGUCCUCAUCUG	4924
GAAUAAGUCUCAAGGAGC	4925	GCUCCUUGGAGACUUAUUC	4926

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AAUAAGUCUCCAAGGAGCA	4927	UGCUCUUGGAGACUUAUU	4928
AUAAGUCUCCAAGGAGCAC	4929	GUGCUCUUGGAGACUUAU	4930

Table 6

Sense Sequence	SEQ ID NO:	Antisense Sequence	SEQ ID NO:
AAAGGCUAGCAAAGAGCAA	4931	UUGCUCUUUGCUAGCCUUU	4932
AAGGCUAGCAAAGAGCAAG	4933	CUUGCUCUUUGCUAGCCUU	4934
AGGCUAGCAAAGAGCAAGG	4935	CCUUGCUCUUUGCUAGCCU	4936
GGCUAGCAAAGAGCAAGGA	4937	UCCUUGCUCUUUGCUAGCC	4938
GCUAGCAAAGAGCAAGGAA	4939	UUCUUGCUCUUUGCUAGC	4940
CAAAGUGGCGAGGCCCUCA	4941	UGAGGGCCUCGCCACUUUG	4942
AAAGUGGCGAGGCCCUAG	4943	CUGAGGGCCUCGCCACUUU	4944
AAGUGGCGAGGCCCUAGA	4945	UCUGAGGGCCUCGCCACUU	4946
GCGAGGCCCUAGAGUGAA	4947	UUCACUCUGAGGGCCUCGC	4948
AAAGCGUAAGGUUCAGUCA	4949	UGACUGAACCUUACGCUUU	4950
AAGAGCCUCCUCACCCAA	4951	UUGGGUGAGGAAGGCUCUU	4952
AGAGCCUCCUCACCCAAA	4953	UUUGGGUGAGGAAGGCUCU	4954
AAAAGCCUCUCUCAGCUGU	4955	ACAGCUGAGAGAGGCUUUU	4956
AAAGCCUCUCUCAGCUGUG	4957	CACAGCUGAGAGAGGCUUU	4958
UCAGCUGUGACCUGGCUCU	4959	AGAGCCAGGUCACAGCUGA	4960
UGACCUGGCUCUGCAUUUU	4961	AAAAUGCAGAGCCAGGUCA	4962
ACCUGGCUCUGCAUUUUCA	4963	UGAAAAUGCAGAGCCAGGU	4964
CCUGGCUCUGCAUUUUCAU	4965	AUGAAAAUGCAGAGCCAGG	4966
GCUCUGCAUUUUCAUCGUG	4967	CACGAUGAAAAUGCAGAGC	4968
CUCUGCAUUUUCAUCGUGG	4969	CCACGAUGAAAAUGCAGAG	4970
UCUGCAUUUUCAUCGUGGC	4971	GCCACGAUGAAAAUGCAGA	4972
CUGCAUUUUCAUCGUGGCC	4973	GGCCACGAUGAAAAUGCAG	4974
UGCAUUUUCAUCGUGGCCU	4975	AGGCCACGAUGAAAAUGCA	4976
GCAUUUUCAUCGUGGCCUU	4977	AAGGCCACGAUGAAAAUGC	4978
AUUUUAUCGUGGCCUUUG	4979	CAAAGGCCACGAUGAAAAU	4980
UUUUUAUCGUGGCCUUUGU	4981	ACAAAGGCCACGAUGAAAA	4982
UUUUAUCGUGGCCUUUGUC	4983	GACAAAGGCCACGAUGAAA	4984
UUUAUCGUGGCCUUUGUCA	4985	UGACAAAGGCCACGAUGAA	4986

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UCAUCGUGGCCUUUGUCAG	4987	CUGACAAAGGCCACGAUGA	4988
CAUCGUGGCCUUUGUCAGC	4989	GCUGACAAAGGCCACGAUG	4990
AUCGUGGCCUUUGUCAGCC	4991	GGCUGACAAAGGCCACGAU	4992
CCUUUGUCAGCCACCCAGC	4993	GCUGGGUGGCUGACAAAGG	4994
CUUUGUCAGCCACCCAGCG	4995	CGCUGGGUGGCUGACAAAG	4996
UUGUCAGCCACCCAGCGUG	4997	CACGCUGGGUGGCUGACAA	4998
GUGGCUGCAGAAGCUCUCU	4999	AGAGAGCUUCUGCAGCCAC	5000
UGGCUGCAGAAGCUCUCUA	5001	UAGAGAGCUUCUGCAGCCA	5002
GGCUGCAGAAGCUCUCUAA	5003	UUAGAGAGCUUCUGCAGCC	5004
GCUGCAGAAGCUCUCUAAG	5005	CUUAGAGAGCUUCUGCAGC	5006
CUGCAGAAGCUCUCUAAGC	5007	GCUUAGAGAGCUUCUGCAG	5008
UGCAGAAGCUCUCUAAGCA	5009	UGC UUAGAGAGCUUCUGCA	5010
GCAGAAGCUCUCUAAGCAC	5011	GUGCUUAGAGAGCUUCUGC	5012
CCAGCACAGCCACAGCUCA	5013	UGAGCUGUGGCUGUGCUGG	5014
CAGCACAGCCACAGCUCAA	5015	UUGAGCUGUGGCUGUGCUG	5016
GCACAGCCACAGCUCAAAG	5017	CUUUGAGCUGUGGCUGUGC	5018
CACAGCCACAGCUCAAAGC	5019	GCUUUGAGCUGUGGCUGUG	5020
ACAGCCACAGCUCAAAGCG	5021	CGCUUUGAGCUGUGGCUGU	5022
CAGCCACAGCUCAAAGCGG	5023	CCGCUUUGAGCUGUGGCUG	5024
AGCCACAGCUCAAAGCGGC	5025	GCCGCUUUGAGCUGUGGCU	5026
GGCCAACUGCUGUGAGGAG	5027	CUCCUCACAGCAGUUGGCC	5028
GCCAACUGCUGUGAGGAGG	5029	CCUCCUCACAGCAGUUGGC	5030
CCAACUGCUGUGAGGAGGU	5031	ACCUCCUCACAGCAGUUGG	5032
CAACUGCUGUGAGGAGGUG	5033	CACCUCCUCACAGCAGUUG	5034
AACUGCUGUGAGGAGGUGA	5035	UCACCUCCUCACAGCAGUU	5036
ACUGCUGUGAGGAGGUGAA	5037	UUCACCUCCUCACAGCAGU	5038
CUCAAGGCCAAGUUGCCA	5039	UGGCAACUUGGGCCUUGAG	5040
GCCAAGUUGCCAACCUUA	5041	UAAGGUUGGCAACUUGGGC	5042
CCAAGUUGCCAACCUUAG	5043	CUAAGGUUGGCAACUUGGG	5044
CCAAGUUGCCAACCUUAGC	5045	GCUAAGGUUGGCAACUUGG	5046
CAAGUUGCCAACCUUAGCA	5047	UGCUAAGGUUGGCAACUUG	5048
AAGUUGCCAACCUUAGCAG	5049	CUGCUAAGGUUGGCAACUU	5050
AGUUGCCAACCUUAGCAGC	5051	GCUGCUAAGGUUGGCAACU	5052

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GACUGGGUCAGCGUGGUCA	5053	UGACCACGCUGACCCAGUC	5054
ACUGGGUCAGCGUGGUCAU	5055	AUGACCACGCUGACCCAGU	5056
CUGGGUCAGCGUGGUCAUG	5057	CAUGACCACGCUGACCCAG	5058
UGGGUCAGCGUGGUCAUGC	5059	GCAUGACCACGCUGACCCA	5060
GGGUCAGCGUGGUCAUGCA	5061	UGCAUGACCACGCUGACCC	5062
CAGCGUGGUCAUGCAGGUG	5063	CACCUGCAUGACCACGCUG	5064
AGCGUGGUCAUGCAGGUGA	5065	UCACCUGCAUGACCACGCU	5066
GCGUGGUCAUGCAGGUGAU	5067	AUACCUGCAUGACCACGC	5068
CGUGGUCAUGCAGGUGAUG	5069	CAUACCUGCAUGACCACG	5070
AGCAAGCGCAUGGAGUCGC	5071	GCGACUCCAUGCGCUUGCU	5072
CAACCAAUUGACAUCAUG	5073	CAUGAUGUCAAUUUGGUUG	5074
ACCAAAUUGACAUCAUGCA	5075	UGCAUGAUGUCAAUUUGGU	5076
UUGACAUCAUGCAGCUGCA	5077	UGCAGCUGCAUGAUGUCAA	5078
CAGGCAGCACAGACGGUCA	5079	UGACCGUCUGUGCUGCCUG	5080
AGGCAGCACAGACGGUCAC	5081	GUGACCGUCUGUGCUGCCU	5082
GGCAGCACAGACGGUCACU	5083	AGUGACCGUCUGUGCUGCC	5084
GCAGCACAGACGGUCACUC	5085	GAGUGACCGUCUGUGCUGC	5086
GUCACUCAGACCUCCGAG	5087	CUGCGGAGGUCUGAGUGAC	5088
UCACUCAGACCUCCGAGCA	5089	UCUGCGGAGGUCUGAGUGA	5090
CACUCAGACCUCCGAGAU	5091	AUCUGCGGAGGUCUGAGUG	5092
ACUCAGACCUCCGAGAUUG	5093	CAUCUGCGGAGGUCUGAGU	5094
CUCAGACCUCCGAGAUUGC	5095	GCAUCUGCGGAGGUCUGAG	5096
UCAGACCUCCGAGAUUGCC	5097	GGCAUCUGCGGAGGUCUGA	5098
CAGACCUCCGAGAUUGCCA	5099	UGGCAUCUGCGGAGGUCUG	5100
GAUGCCAUCUACGACUGCU	5101	AGCAGUCGUAGAUGGCAUC	5102
AUGCCAUCUACGACUGCUC	5103	GAGCAGUCGUAGAUGGCAU	5104
UGCCAUCUACGACUGCUCU	5105	AGAGCAGUCGUAGAUGGCA	5106
GCCAUCUACGACUGCUCUU	5107	AAGAGCAGUCGUAGAUGGC	5108
CCAUCUACGACUGCUCUUC	5109	GAAGAGCAGUCGUAGAUGG	5110
CUACGACUGCUCUUCCUC	5111	GAGGGAAGAGCAGUCGUAG	5112
UACGACUGCUCUUCCUCU	5113	AGAGGGAAGAGCAGUCGUA	5114
AUCUCUGGAGUGUAUAAGC	5115	GCUUAUACACUCCAGAGAU	5116
CUGGAGUGUAUAAGCUUCC	5117	GGAAGCUUAUACACUCCAG	5118

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UGGAGUGUAUAAGCUUCCU	5119	AGGAAGCUUAUACACUCCA	5120
GGAGUGUAUAAGCUUCCUC	5121	GAGGAAGCUUAUACACUCC	5122
GUAUAAGCUUCCUCCUGAU	5123	AUCAGGAGGAAGCUUAUAC	5124
UAUAAGCUUCCUCCUGAUG	5125	CAUCAGGAGGAAGCUUAUA	5126
AUAAGCUUCCUCCUGAUGA	5127	UCAUCAGGAGGAAGCUUAU	5128
AAGCUUCCUCCUGAUGACU	5129	AGUCAUCAGGAGGAAGCUU	5130
AGCUUCCUCCUGAUGACUU	5131	AAGUCAUCAGGAGGAAGCU	5132
GCUUCCUCCUGAUGACUUC	5133	GAAGUCAUCAGGAGGAAGC	5134
CUUCCUCCUGAUGACUUC	5135	GGAAGUCAUCAGGAGGAAG	5136
UUCUCCUGAUGACUUCU	5137	AGGAAGUCAUCAGGAGGAA	5138
ACUUCCUGGGCAGCCUGA	5139	UCAGGGCUGCCAGGAAGU	5140
AGACUUCAGGCGGAGGCUG	5141	CAGCCUCCGCCUGAAGUCU	5142
ACUUCAGGCGGAGGCUGGA	5143	UCCAGCCUCCGCCUGAAGU	5144
GCGGAGGCUGGACCAUCAU	5145	AUGAUGGUCCAGCCUCCGC	5146
CGGAGGCUGGACCAUCAUC	5147	GAUGAUGGUCCAGCCUCCG	5148
GGAGGCUGGACCAUCAUCC	5149	GGAUGAUGGUCCAGCCUCC	5150
AAGUGGCCUUGUCUCCUUC	5151	GAAGGAGACAAGGCCACUU	5152
AGUGGCCUUGUCUCCUUCU	5153	AGAAGGAGACAAGGCCACU	5154
GUGGCCUUGUCUCCUUCUA	5155	UAGAAGGAGACAAGGCCAC	5156
CUUGUCUCCUUCUACCGGG	5157	CCCGGUAGAAGGAGACAAG	5158
UUGUCUCCUUCUACCGGGA	5159	UCCCGGUAGAAGGAGACAA	5160
UGUCUCCUUCUACCGGGAC	5161	GUCCCGGUAGAAGGAGACA	5162
GUCUCCUUCUACCGGGACU	5163	AGUCCCGGUAGAAGGAGAC	5164
UUCUACCGGGACUGGAAGC	5165	GCUUCCAGUCCCGGUAGAA	5166
UCUACCGGGACUGGAAGCA	5167	UGCUCAGUCCCGGUAGA	5168
CUACCGGGACUGGAAGCAG	5169	CUGCUUCCAGUCCCGGUAG	5170
AGCAGGGCUUUGGCAGCAU	5171	AUGCUGCCAAAGCCUGCU	5172
AGGGCUUUGGCAGCAUCCG	5173	CGGAUGCUGCCAAAGCCU	5174
GGGCUUUGGCAGCAUCCGU	5175	ACGGAUGCUGCCAAAGCCC	5176
GGCUUUGGCAGCAUCCGUG	5177	CACGGAUGCUGCCAAAGCC	5178
CAUCCACCGGCUCUCCAGA	5179	UCUGGAGAGCCGGUGGAUG	5180
AUCCACCGGCUCUCCAGAC	5181	GUCUGGAGAGCCGGUGGAU	5182
UCCACCGGCUCUCCAGACA	5183	UGUCUGGAGAGCCGGUGGA	5184

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AGGACUGGGAGGGCAACCU	5185	AGGUUGCCCUCCAGUCCU	5186
GCAACCUGCGCUACGCUGA	5187	UCAGCGUAGCGCAGGUUGC	5188
CAACCUGCGCUACGCUGAG	5189	CUCAGCGUAGCGCAGGUUG	5190
CUGCGCUACGCUAGUAUA	5191	UAUACUCAGCGUAGCGCAG	5192
UGCGCUACGCUAGUAUAG	5193	CUAUACUCAGCGUAGCGCA	5194
CUACGCUAGUAUAGCCAC	5195	GUGGCUAUACUCAGCGUAG	5196
UACGCUAGUAUAGCCACU	5197	AGUGGCUAUACUCAGCGUA	5198
CACUUUGUUUUGGGCAAUG	5199	CAUUGCCCAAAACAAGUG	5200
AACUACACUGGCAAUGUGG	5201	CCACAUUGCCAGUGUAGUU	5202
ACUACACUGGCAAUGUGGG	5203	CCCACAUUGCCAGUGUAGU	5204
AACGACGCCCUCCAGUAUC	5205	GAUACUGGAGGGGCGUCUU	5206
ACGACGCCCUCCAGUAUCA	5207	UGAUACUGGAGGGGCGUCU	5208
CGACGCCCUCCAGUAUCAU	5209	AUGAUACUGGAGGGGCGUCG	5210
GACGCCCUCCAGUAUCAUA	5211	UAUGAUACUGGAGGGGCGUC	5212
ACGCCCUCCAGUAUCAUAA	5213	UUAUGAUACUGGAGGGGCGU	5214
CGCCCUCCAGUAUCAUAAC	5215	GUUAUGAUACUGGAGGGGCG	5216
CAAGUGUGCACAGCUCCGC	5217	GCGGAGCUGUGCACACUUG	5218
AAGUGUGCACAGCUCCGCA	5219	UGCGGAGCUGUGCACACUU	5220
AGUGUGCACAGCUCCGCAA	5221	UUGCGGAGCUGUGCACACU	5222
UGCACAGCUCCGCAAAGGU	5223	ACCUUUGCGGAGCUGUGCA	5224
GCACAGCUCCGCAAAGGUG	5225	CACCUUUGCGGAGCUGUGC	5226
CACAGCUCCGCAAAGGUGG	5227	CCACCUUUGCGGAGCUGUG	5228
ACAGCUCCGCAAAGGUGGC	5229	GCCACCUUUGCGGAGCUGU	5230
CAGCUCCGCAAAGGUGGCU	5231	AGCCACCUUUGCGGAGCUG	5232
AGCUCCGCAAAGGUGGCUA	5233	UAGCCACCUUUGCGGAGCU	5234
GCUCCGCAAAGGUGGCUAC	5235	GUAGCCACCUUUGCGGAGC	5236
CUCCGCAAAGGUGGCUACU	5237	AGUAGCCACCUUUGCGGAG	5238
GCAAAGGUGGCUACUGGUA	5239	UACCAGUAGCCACCUUUGC	5240
CAAAGGUGGCUACUGGUAC	5241	GUACCAGUAGCCACCUUUG	5242
AAAGGUGGCUACUGGUACA	5243	UGUACCAGUAGCCACCUUU	5244
CAACUGCUGCACAGACUCC	5245	GGAGUCUGUGCAGCAGUUG	5246
CACAGACUCCAACCUCAAU	5247	AUUGAGGUUGGAGUCUGUG	5248
ACAGACUCCAACCUCAAUG	5249	CAUUGAGGUUGGAGUCUGU	5250

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CAGACUCCAACCUCAAUGG	5251	CCAUUGAGGUUGGAGUCUG	5252
CCAACCUCAAUGGAGUGUA	5253	UACACUCCAUGAGGUUGG	5254
CAACCUCAAUGGAGUGUAC	5255	GUACACUCCAUGAGGUUG	5256
AACCUCAAUGGAGUGUACU	5257	AGUACACUCCAUGAGGUU	5258
ACCUCAAUGGAGUGUACUA	5259	UAGUACACUCCAUGAGGU	5260
CCUCAAUGGAGUGUACUAC	5261	GUAGUACACUCCAUGAGG	5262
CUCAAUGGAGUGUACUACC	5263	GGUAGUACACUCCAUGAG	5264
UCAAUGGAGUGUACUACCG	5265	CGGUAGUACACUCCAUGA	5266
CAAUGGAGUGUACUACCGC	5267	GCGGUAGUACACUCCAUG	5268
AAUGGAGUGUACUACCGCC	5269	GGCGGUAGUACACUCCAUI	5270
AUGGAGUGUACUACCGCCU	5271	AGGCGGUAGUACACUCCA	5272
UGGAGUGUACUACCGCCUG	5273	CAGGCGGUAGUACACUCCA	5274
GGAGUGUACUACCGCCUGG	5275	CCAGGCGGUAGUACACUCC	5276
GAGUGUACUACCGCCUGGG	5277	CCCAGGCGGUAGUACACUC	5278
AGUGUACUACCGCCUGGGU	5279	ACCCAGGCGGUAGUACACU	5280
GUACUACCGCCUGGGUGAG	5281	CUCACCCAGGCGGUAGUAC	5282
UACUACCGCCUGGGUGAGC	5283	GCUCACCCAGGCGGUAGUA	5284
ACUACCGCCUGGGUGAGCA	5285	UGCUCACCCAGGCGGUAGU	5286
CAUAAGCACCUGGAUGGC	5287	GCCAUCCAGGUGCUUAUUG	5288
AAUAAGCACCUGGAUGGCA	5289	UGCCAUCCAGGUGCUUAUU	5290
AUAAGCACCUGGAUGGCAU	5291	AUGCCAUCCAGGUGCUUAU	5292
UAAGCACCUGGAUGGCAUC	5293	GAUGCCAUCCAGGUGCUUA	5294
AAGCACCUGGAUGGCAUCA	5295	UGAUGCCAUCCAGGUGCUU	5296
AGCACCUGGAUGGCAUCAC	5297	GUGAUGCCAUCCAGGUGCU	5298
GCACCUGGAUGGCAUACCC	5299	GGUGAUGCCAUCCAGGUGC	5300
CACCUGGAUGGCAUACCU	5301	AGGUGAUGCCAUCCAGGUG	5302
UGGAUGGCAUACCUGGUA	5303	UACCAGGUGAUGCCAUCCA	5304
UGGCAUGGAUCUACCUACU	5305	AGUAGGUAGAUCCAUGCCA	5306
GGCAUGGAUCUACCUACUC	5307	GAGUAGGUAGAUCCAUGCC	5308
GCAUGGAUCUACCUACUCC	5309	GGAGUAGGUAGAUCCAUGC	5310
CAUGGAUCUACCUACUCCC	5311	GGGAGUAGGUAGAUCCAUG	5312
AUGGAUCUACCUACUCCCU	5313	AGGGAGUAGGUAGAUCCA	5314
UGGAUCUACCUACUCCCU	5315	GAGGGAGUAGGUAGAUCCA	5316

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GGAUCUACCUACUCCCUCA	5317	UGAGGGAGUAGGUAGAUC	5318
GAUCUACCUACUCCCUCAA	5319	UUGAGGGAGUAGGUAGAUC	5320
AUCUACCUACUCCCUCAAA	5321	UUUGAGGGAGUAGGUAGAU	5322
CGCCAGAAGACUUCAAGC	5323	GCUUGAAGUCUUCUGGGCG	5324
GCCCAGAAGACUUCAAGCC	5325	GGCUUGAAGUCUUCUGGGC	5326
CCCAGAAGACUUCAAGCCU	5327	AGGCUUGAAGUCUUCUGGG	5328
CCAGAAGACUUCAAGCCUU	5329	AAGGCUUGAAGUCUUCUGG	5330
CAGAAGACUUCAAGCCUUA	5331	UAAGGCUUGAAGUCUUCUG	5332
GAAGACUUCAAGCCUUA	5333	UUUAAGGCUUGAAGUCUUC	5334
AAGACUUCAAGCCUUA	5335	UUUUAAGGCUUGAAGUCUU	5336
AGACUUCAAGCCUUA	5337	CUUUUAAGGCUUGAAGUCU	5338
GACUUCAAGCCUUA	5339	CCUUUUAAGGCUUGAAGUC	5340
ACUUCAAGCCUUA	5341	UCCUUUUAAGGCUUGAAGU	5342
CUUCAAGCCUUA	5343	CUCCUUUUAAGGCUUGAAG	5344
UUCAAGCCUUA	5345	CCUCCUUUUAAGGCUUGAA	5346
CCUUA	5347	CGGCAGCCUCCUUUAAGG	5348
CUUUA	5349	ACGGCAGCCUCCUUUAAG	5350
UUUA	5351	CACGGCAGCCUCCUUUA	5352
UUA	5353	CCACGGCAGCCUCCUUUA	5354
UA	5355	UCCACGGCAGCCUCCUUU	5356
AA	5357	CUCCACGGCAGCCUCCUU	5358
GUGGAGCACGGAUACAGAA	5359	UUCUGUAUCCGUGCUCCAC	5360
ACUGGAUGAGGGCAGAU	5361	UCAUCUGCCCUCAUCCAGU	5362
CUGGAUGAGGGCAGAU	5363	CUCAUCUGCCCUCAUCCAG	5364
GGAUGAGGGCAGAU	5365	UCCUCAUCUGCCCUCAUCC	5366
AUGAGGGCAGAU	5367	UGUCCUCAUCUGCCCUCAU	5368
UGAGGGCAGAU	5369	CUGUCCUCAUCUGCCCUCA	5370
AGGGCAGAU	5371	UCCUGUCCUCAUCUGCCCU	5372
GGCAGAU	5373	CUUCCUGUCCUCAUCUGCC	5374
CAGAU	5375	CUCUCCUGUCCUCAUCUG	5376
GAAUAAGUCUCCAAGGAGC	5377	GCUCCUUGGAGACUUAUUC	5378
AAUAAGUCUCCAAGGAGCA	5379	UGCUCUUGGAGACUUAUU	5380
AUAAGUCUCCAAGGAGCAC	5381	GUGCUCCUUGGAGACUUAU	5382

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GUACCAAGGAUGUUACAGU	5383	ACUGUAACAUCUUGGUAC	5384
UACCAAGGAUGUUACAGUA	5385	UACUGUAACAUCUUGGUA	5386
ACCAAGGAUGUUACAGUAA	5387	UUACUGUAACAUCUUGGU	5388
CCAAGGAUGUUACAGUAAA	5389	UUUACUGUAACAUCUUGG	5390
CUGGGUCCUGCCACAUCU	5391	AGGAUGUGGCAGGACCCAG	5392
UGGGUCCUGCCACAUCU	5393	AAGGAUGUGGCAGGACCCA	5394
GGGUCCUGCCACAUCUUC	5395	GAAGGAUGUGGCAGGACCC	5396
GGUCCUGCCACAUCUUCU	5397	AGAAGGAUGUGGCAGGACC	5398
UCCUGCCACAUCUUCUCA	5399	UGAGAAGGAUGUGGCAGGA	5400
CCUGCCACAUCUUCUCAA	5401	UUGAGAAGGAUGUGGCAGG	5402
CUGCCACAUCUUCUCAAG	5403	CUUGAGAAGGAUGUGGCAG	5404
CUUCUCAAGGUGGUAGACU	5405	AGUCUACCACCUUGAGAAG	5406
AGGUGGUAGACUGAGUGGG	5407	CCCACUCAGUCUACCACCU	5408
GGUCUCUCUGCCCAAGAUC	5409	GAUCUUGGGCAGAGAGACC	5410
GUCUCUCUGCCCAAGAUCC	5411	GGAUCUUGGGCAGAGAGAC	5412
UCUCUCUGCCCAAGAUCCC	5413	GGGAUCUUGGGCAGAGAGA	5414
UCUGCCCAAGAUCCUGAC	5415	GUCAGGGAUCUUGGGCAGA	5416
CUGCCCAAGAUCCUGACA	5417	UGUCAGGGAUCUUGGGCAG	5418
UGCCCAAGAUCCUGACAU	5419	AUGUCAGGGAUCUUGGGCA	5420
GCCCAAGAUCCUGACAU	5421	UAUGUCAGGGAUCUUGGGC	5422
CCCAAGAUCCUGACAUAG	5423	CUAUGUCAGGGAUCUUGGG	5424
AUCCUGACAUAGCAGUAG	5425	CUACUGCUAUGUCAGGGAU	5426
CCUGACAUAGCAGUAGCU	5427	AGCUACUGCUAUGUCAGGG	5428
CCUGACAUAGCAGUAGCUU	5429	AAGCUACUGCUAUGUCAGG	5430
CUGACAUAGCAGUAGCUUG	5431	CAAGCUACUGCUAUGUCAG	5432
UGACAUAGCAGUAGCUUGU	5433	ACAAGCUACUGCUAUGUCA	5434
ACAUAGCAGUAGCUUGUCU	5435	AGACAAGCUACUGCUAUGU	5436
CAUAGCAGUAGCUUGUCUU	5437	AAGACAAGCUACUGCUAUG	5438
GCAGUAGCUUGUCUUUUCC	5439	GGAAAAGACAAGCUACUGC	5440
CAGUAGCUUGUCUUUUCCA	5441	UGGAAAAGACAAGCUACUG	5442
AGUAGCUUGUCUUUUCCAC	5443	GUGGAAAAGACAAGCUACU	5444
GUAGCUUGUCUUUUCCACA	5445	UGUGGAAAAGACAAGCUAC	5446
CUUGUCUUUUCCACAUGAU	5447	AUCAUGUGGAAAAGACAAG	5448

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UUGUCUUUCCACAUGAUU	5449	AAUCAUGUGGAAAAGACAA	5450
CUUUUCCACAUGAUUUGUC	5451	GACAAAUCAUGUGGAAAAG	5452
UUUUCCACAUGAUUUGUCU	5453	AGACAAAUCAUGUGGAAAA	5454
UUUCCACAUGAUUUGUCUG	5455	CAGACAAAUCAUGUGGAAA	5456
UUCACAUGAUUUGUCUGU	5457	ACAGACAAAUCAUGUGGAA	5458
GCUUAGGCUAUGUGAGGGC	5459	GCCCUACAUAAGCCUAAGC	5460
AGGCUAUGUGAGGGCAAAA	5461	UUUUGCCCUACAUAAGCCU	5462
AGGAGUGAAGGAGGCAGGU	5463	ACCUGCCUCCUUCACUCCU	5464
GGAGUGAAGGAGGCAGGUG	5465	CACCUGCCUCCUUCACUCC	5466
GAGUGAAGGAGGCAGGUGG	5467	CCACCUGCCUCCUUCACUC	5468
AAUUAUCUUGAGUCUACAC	5469	GUGUAGACUCAAGAUAAUU	5470
ACUCCAGGGCACUGCAUCU	5471	AGAUGCAGUGCCUGGAGU	5472
CUCCAGGGCACUGCAUCUG	5473	CAGAUGCAGUGCCUGGAG	5474
AGGGCACUGCAUCUGGCGA	5475	UCGCCAGAUGCAGUGCCU	5476
GGGCACUGCAUCUGGCGAU	5477	AUCGCCAGAUGCAGUGCCC	5478
GGCACUGCAUCUGGCGAUC	5479	GAUCGCCAGAUGCAGUGCC	5480
GCACUGCAUCUGGCGAUCA	5481	UGAUCGCCAGAUGCAGUGC	5482
CCUGCUCGCCUUGGUCAU	5483	AUGACCAAGGCGAGCAGG	5484
CCUGCUCGCCUUGGUCAUG	5485	CAUGACCAAGGCGAGCAG	5486
CUGCUCGCCUUGGUCAUGU	5487	ACAUGACCAAGGCGAGCAG	5488
UGCUCGCCUUGGUCAUGUA	5489	UACAUGACCAAGGCGAGCA	5490
AUGAAGCACCAGCAGGAGG	5491	CCUCCUGCUGGUGCUUCAU	5492
UGAAGCACCAGCAGGAGGU	5493	ACCUCCUGCUGGUGCUUCA	5494
CAGCAGGAGGUGGACAGAG	5495	CUCUGUCCACCUCCUGCUG	5496
AGCAGGAGGUGGACAGAGU	5497	ACUCUGUCCACCUCCUGCU	5498
GCAGGAGGUGGACAGAGUC	5499	GACUCUGUCCACCUCCUGC	5500
CAGGAGGUGGACAGAGUCU	5501	AGACUCUGUCCACCUCCUG	5502
GGAGGUGGACAGAGUCUCU	5503	AGAGACUCUGUCCACCUCC	5504
AGGUGGACAGAGUCUCUCA	5505	UGAGAGACUCUGUCCACCU	5506
UGGACAGAGUCUCUCAUGG	5507	CCAUGAGAGACUCUGUCCA	5508
GGACAGAGUCUCUCAUGGA	5509	UCCAUGAGAGACUCUGUCC	5510
GACAGAGUCUCUCAUGGAU	5511	AUCCAUGAGAGACUCUGUC	5512
ACAGAGUCUCUCAUGGAUG	5513	CAUCCAUGAGAGACUCUGU	5514

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GGAGCUUCCUUUUAAAUUU	5515	AAAUUUAAAAGGAAGCUCC	5516
AACUGAAGGUAGAUGGUGU	5517	ACACCAUCUACCUUCAGUU	5518
ACUGAAGGUAGAUGGUGUU	5519	AACACCAUCUACCUUCAGU	5520
CUGAAGGUAGAUGGUGUUA	5521	UAACACCAUCUACCUUCAG	5522
UGAAGGUAGAUGGUGUUUAU	5523	AUAACACCAUCUACCUUCA	5524
GAAGGUAGAUGGUGUUUAU	5525	UAUAACACCAUCUACCUUC	5526
GUAGAUGGUGUUUAUGUUA	5527	UAACUAUAACACCAUCUAC	5528
UGUAAAUAAGCAUCUCACU	5529	AGUGAGAUGCUUAUUUACA	5530
AUAAGCAUCUCACUUUGUA	5531	UACAAAGUGAGAUGCUUAU	5532

In some embodiments, the siRNA molecules comprise or consist of the nucleotide sequences (sense and antisense strands) shown in Table 7 and Table 8.

Table 7

Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:
ACACUCCUUGUGUCUAUAGA	5533	UCUAUAGACACAAGGAAGUGUCG	5534
GUACCAGAAGAACUACCGAAA	5535	UUUCGGUAGUUCUUCUGGUACAG	5536
UACCAGAAGAACUACCGAAUA	5537	UAUUCGGUAGUUCUUCUGGUACA	5538
CUGUGACAUGGAAACUUCAGA	5539	UCUGAAGUUCCAUGUCACAGAA	5540
CAGAAGAACUACCGAAUCUCA	5541	UGAGAUUCGGUAGUUCUUCUGGU	5542
AGAAGAACUACCGAAUCUCUA	5543	UAGAGAUUCGGUAGUUCUUCUGG	5544
GACAGUAUAAGCAAGGGUUUA	5545	UAAACCCUUGCUUAUACUGUCUC	5546
GAAGAACUACCGAAUCUCUGA	5547	UCAGAGAUUCGGUAGUUCUUCUG	5548
UGUGACAUGGAAACUUCAGGA	5549	UCCUGAAGUUCCAUGUCACAGA	5550
GUCUCCUUCUACCAAGACUGA	5551	UCAGUCUUGGUAGAAGGAGACAA	5552
ACUCUGAGAUGAACCAACCAGA	5553	UCUGGUUGUUAUCUCAGAGUAC	5554
AGACAGUAUAAGCAAGGGUUA	5555	UAACCCUUGCUUAUACUGUCUCC	5556
ACAGUAUAAGCAAGGGUUUGA	5557	UCAAACCCUUGCUUAUACUGUCU	5558
UUGGGCAAUGAACUGAACAGA	5559	UCUGUUCAGUUCUUAUGCCCAACG	5560
GCCAACUAUCCCUCAAACGA	5561	UCGUUUGAGGGAAUAGUUGGCUC	5562
CCGAGAGCAAGUACUCUGAGA	5563	UCUCAGAGUACUUGCUCUCGGCA	5564

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CAUAACAACACCGUCUUCAGA	5565	UCUGAAGACGGUGUUGUUAUGGU	5566
UGUACCAGAAGAACUACCGAA	5567	UUCGGUAGUUCUUCUGGUACAGG	5568
UGACAUGGAAACUUCAGGAGA	5569	UCUCCUGAAGUUUCCAUGUCACA	5570
CUGCAGAAGCCUCAUAAACGA	5571	UCGUUUUAUGAGGCUUCUGCAGCC	5572
GCAGAAGCCUCAUAAACGCAA	5573	UUGCGUUUAUGAGGCUUCUGCAG	5574
UGCCGAGAGCAAGUACUCUGA	5575	UCAGAGUACUUGCUCUCGGCAGU	5576

Table 8

Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:
CUUGGAAGGAAAGCUAUAGGU	5577	ACCUAUAGCUUUCUCCAAGCC	5578
UAUAGGCUACCAUUCAGCUU	5579	AAGCUGAAUGGGUAGCCUAUAGC	5580
GAGACUCAAGCUUUGAGAAAU	5581	AUUUCUCAAGCUUGAGUCUCUG	5582
GCUAGCAAAGAGCAAGGAAAU	5583	AUUUCCUUGCUCUUUGCUAGCCU	5584
AAGAGAGAAAACAACAAGUU	5585	AACUUUGUUGUUUUCUCUCUUUC	5586
GUGGCGAGGCCUCAGAGUGU	5587	ACACUCUGAGGGCCUCGCCACUU	5588
CAGAGUGAAAGCGUAAGGUUU	5589	AAACCUUACGCUUUCACUCUGAG	5590
CGUAAGGUUCAGUCAGCCUGU	5591	ACAGGCUGACUGAACCUUACGCU	5592
CUGCAGCUUUGCAGACCUCAU	5593	AUGAGGUCUGCAAAGCUGCAGCA	5594
CUCAGCUGGGCAUCUCCAGAU	5595	AUCUGGAGAUGCCCAGCUGAGGU	5596
UGAAGGAAGAGCCUUCUCAU	5597	AUGAGGAAGGCUCUCCUUCAGG	5598
CACCCAAACCCACAAAAGAUU	5599	AAUCUUUUGUGGGUUUGGGUGAG	5600
GCCUCUCUCAGCUGUGACCUU	5601	AAGGUCACAGCUGAGAGAGGCUU	5602
UGGCUCUGCAUUUUCUUCGUU	5603	AACGAUGAAAUGCAGAGCCAGG	5604
UUUCAUCGUGGCCUUUGUCAU	5605	AUGACAAAGGCCACGAUGAAAAU	5606
CUGCAGAAGCUCUCUAAGCAU	5607	AUGCUUAGAGAGCUUCUGCAGCC	5608
AAGCACAAGACACCAGCACAU	5609	AUGUGCUGGUGUCUUGUGCUUAG	5610
CCAGCACAGCCACAGCUCAAU	5611	AUUGAGCUGUGGCUGUGCUGGUG	5612

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CAGCUCAAAGCGGCCAACUGU	5613	ACAGUUGGCCGCUUUGAGCUGUG	5614
GCCAACUGCUGUGAGGAGGUU	5615	AACCUCCUCACAGCAGUUGGCCG	5616
GAGGAGGUGAAGGAGCUAAU	5617	AUUGAGCUCCUUCACCUCCUCAC	5618
GGAGCUCAAGGCCCAAGUUGU	5619	ACAACUUGGGCCUUGAGCUCCU	5620
CCAAGUUGCCAACCUUAGCAU	5621	AUGCUAAGGUUGGCAACUUGGGC	5622
CUUAGCAGCCUGCUGAGUGAU	5623	AUCACUCAGCAGGCUGCUAAGGU	5624
GCUGAGUGAACUGAACAAGAU	5625	AUCUUGUUCAGUUCACUCAGCAG	5626
UGAACAAAGAAGCAGGAGAGGU	5627	ACCUCUCCUGCUUCUUGUUCAGU	5628
GACUGGGUCAGCGUGGUCAUU	5629	AAUGACCACGCUGACCCAGUCCC	5630
GUGGUCAUGCAGGUGAUGGAU	5631	AUCCAUCACCUGCAUGACCACGC	5632
GUGAUGGAGCUGGAGAGCAAU	5633	AUUGCUCUCCAGCUCCAUCACCU	5634
GGAGAGCAACAGCAAGCGCAU	5635	AUGCGCUUGCUGUUGCUCUCCAG	5636
AUGGAGUCGCGGCCUCACAGAU	5637	AUCUGUGAGCCGCGACUCCAUGC	5638
CUCACAGAUGCUGAGAGCAAU	5639	AUUGCUCUCAGCAUCUGUGAGCC	5640
GAGCAAGUACUCCGAGAUGAU	5641	AUCAUCUCGGAGUACUUGCUCUC	5642
CGAGAUGAACAAACAAAUUGU	5643	ACA AUUUGGUUGUUCAUCUCGGA	5644
ACCAAAUUGACAUCAUGCAGU	5645	ACUGCAUGAUGUCAAUUUGGUUG	5646
CAGCUGCAGGCAGCACAGACU	5647	AGUCUGUGCUGCCUGCAGCUGCA	5648
AGCACAGACGGUCACUCAGAU	5649	AUCUGAGUGACCGUCUGUGCUGC	5650
UCACUCAGACCUCCGCAGAUU	5651	AAUCUGCGGAGGUCUGAGUGACC	5652
CGCAGAUGCCAUUCACGACUU	5653	AAGUCGUAGAUGGCAUCUGCGGA	5654
UACGACUGCUCUUCCCUUAU	5655	AUAGAGGGAAGAGCAGUCGUAGA	5656
UCCCUUACACAGAAGAACUAU	5657	AUAGUUCUUCUGGUAGAGGGAAG	5658
GAAGAACUACCGCAUCUCUGU	5659	ACAGAGAUGCAGGUAGUUCUUCUG	5660
UCUCUGGAGUGUAUAAGCUUU	5661	AAAGCUUAUACACUCCAGAGAUG	5662
CUUCCUCCUGAUGACUCCUU	5663	AAGGAAGUCAUCAGGAGGAAGCU	5664
AGCCCUGAACUGGAGGUGUUU	5665	AAACACCUCCAGUUCAGGGCUGC	5666

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GGAGGUGUUCUGUGACAUGGU	5667	ACCAUGUCACAGAACACCUCCAG	5668
GUGACAUGGAGACUUCAGGCU	5669	AGCCUGAAGUCUCCAUGUCACAG	5670
UCAGGCGGAGGCUUGGACCAU	5671	AAUGGUCCAGCCUCCGCCUGAAG	5672
GACCAUCAUCCAGAGACGAAU	5673	AUUCGUCUCUGGAUGAUGGUCCA	5674
GUGGCCUUGUCUCCUUCUACU	5675	AGUAGAAGGAGACAAGGCCACUU	5676
UCCUUCUACCGGGACUGGAAU	5677	AUUCAGUCCCGGUAGAAGGAGA	5678
GGACUGGAAGCAGUACAAGCU	5679	AGCUUGUACUGCUUCCAGUCCCG	5680
GGGCUUUGGCAGCAUCCGUGU	5681	ACACGGAUGCUGCCAAAGCCCUG	5682
AACGAACACAUCCACCGGCUU	5683	AAGCCGGUGGAUGUGUUCGUUCC	5684
CCGGCUCUCCAGACAGCCAAU	5685	AUUGGCUGUCUGGAGAGCCGGUG	5686
AGCCAACCCGGCUGCGUGUAU	5687	AUACACGCAGCCGGGUUGGCUGU	5688
CUGCGUGUAGAGAUGGAGGAU	5689	AUCCUCCAUCUCUACACGCAGCC	5690
GAGGACUGGGAGGGCAACCUU	5691	AAGGUUGCCUCCAGUCCUCCA	5692
GGCAACCUGCGCUACGCUGAU	5693	AUCAGCGUAGCGCAGGUUGCCCU	5694
UACGCUGAGUAUAGCCACUUU	5695	AAAGUGGCUAUACUCAGCGUAGC	5696
UAGCCACUUUGUUUUGGGCAU	5697	AUGCCCAAACAAAGUGGCUAUA	5698
UUUGGGCAUUAACUACAACU	5699	AUGUUGAGUUAUUGCCCAAAC	5700
AACAGCUAUCGCCUCUCCUU	5701	AAGGAAGAGGCGAUAGCUGUUGA	5702
GAACUACACUGGCAAUGUGGU	5703	ACCACAUUGCCAGUGUAGUUCCC	5704
CCUCCAGUAUCAUAACAACU	5705	AUGUUGUUAUGAUACUGGAGGGC	5706
AGCCUUCAGCACCAAGGACAU	5707	AUGUCCUUGGUGCUGAAGGCUGU	5708
AAGGACAAGGACAAUGACAAU	5709	AUUGUCAUUGUCCUUGUCCUUGG	5710
UGACAACUGCUUGGACAAGUU	5711	AACUUGUCCAAGCAGUUGUCAUU	5712
UGGACAAGUGUGCACAGCUCU	5713	AGAGCUGUGCACACUUGUCCAAG	5714
GCUCCGCAAAGGUGGCUACUU	5715	AAGUAGCCACCUUUGCGGAGCUG	5716
UGGCUACUGGUACAACUGCUU	5717	AAGCAGUUGUACCAGUAGCCACC	5718
GCACAGACUCCAACCUCAAUU	5719	AAUUGAGGUUGGAGUCUGUGCAG	5720

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AACCUCAAUGGAGUGUACUUAU	5721	AUAGUACACUCCAUUGAGGUUUG	5722
ACUACCGCCUGGGUGAGCACU	5723	AGUGCUCACCCAGGCGGUAGUAC	5724
GGUGAGCACAAUAAGCACCUU	5725	AAGGUGCUUAUUGUGCUCACCCA	5726
UGGAUGGCAUCACCUGGUAUU	5727	AAUACCAGGUGAUGCCAUCAGG	5728
ACCUGGUAUGGCUGGCAUGGU	5729	ACCAUGCCAGCCAUACCAGGUGA	5730
CUGGCAUGGAUCUACCUACUU	5731	AAGUAGGUAGAUGCAUGCCAGCC	5732
UACCUACUCCCUCAAACGGGU	5733	ACCCGUUUGAGGGAGUAGGUAGA	5734
ACGGGUGGAGAUGAAAAUCCU	5735	AGGAUUUUAUCUCCACCCGUUU	5736
CCCAGAAGACUUAAGCCUUU	5737	AAAGGCUUGAAGUCUUCUGGGCG	5738
UCAAGCCUAAAAAGGAGGCUU	5739	AAGCCUCCUUUUAAGGCUUGAAG	5740
AGCACGGAUACAGAAACUGAU	5741	AUCAGUUUCUGUAUCCGUGCUCC	5742
GAGACACGUGGAGACUGGAUU	5743	AAUCCAGUCUCCACGUGUCUCAG	5744
AGACUGGAUGAGGGCAGAUGU	5745	ACAUCUGCCCUCAUCCAGUCUCC	5746
GGCAGAUGAGGACAGGAAGAU	5747	AUCUUCCUGUCCUCAUCUGCCCU	5748
CAGGAAGAGAGUGUUAGAAAU	5749	AUUUCUAAACACUCUCUCCUGUC	5750
GAAAGGGUAGGACUGAGAAAU	5751	AUUUCUCAGUCCUACCCUUUCUA	5752
ACUGAGAAACAGCCUAUAAUU	5753	AAUUAUAGGCUGUUUCUCAGUCC	5754
UCUCCAAAGAAAGAAUAAGUU	5755	AACUUAUUCUUCUUCUUGGAGAUU	5756
UAAGUCUCCAAGGAGCACAAU	5757	AUUGUGCUCUUGGAGACUUAUU	5758
UCAUAUGUACCAAGGAUGUUU	5759	AAACAUCUUGGUACAUAUGAUU	5760
AAGGAUGUUACAGUAAACAGU	5761	ACUGUUUACUGUAACAUCUUGG	5762
ACAGGAUGAACUAUUUAAACU	5763	AGUUUAAAUAAGUUAUCCUGUUU	5764
AUUUAAACCCACUGGGUCCUU	5765	AAGGACCCAGUGGGUUUAAAUAG	5766
UGCCACAUCUUCUCAAGGUU	5767	AACCUUGAGAAGGAUGUGGCAGG	5768
UCUCAAGGUGGUAGACUGAGU	5769	ACUCAGUCUACCACUUGAGAAG	5770
UCUCUCUGCCCAAGAUCUCCUU	5771	AAGGGAUCUUGGGCAGAGAGACC	5772
UCCUGACAUAGCAGUAGCUU	5773	AAGCUACUGCUAUGUCAGGGAUC	5774

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GCAGUAGCUUGUCUUUUCCA	5775	AUGGAAAAGACAAGCUACUGCUA	5776
UCUUUUCCACAUGAUUUGUCU	5777	AGACAAAUCAUGUGGAAAAGACA	5778
AUUUUGUCUGUGAAAGAAAAUU	5779	AAUUUUCUUUCACAGACAAAUCA	5780
AGAUCGUUUUAUCUAUUUUUCU	5781	AGAAAAUAGAUAAAACGAUCUCA	5782
UCUACGGCUUAGGCUAUGUGU	5783	ACACAUAGCCUAAGCCGUAGAGA	5784
GUGAGGGGCAAAACACAAAU	5785	AGAUUUGUGUUUUGCCCUACAU	5786
ACACAAAUCCCUUUGCUAAAU	5787	AUUUAGCAAAGGGAUUUGUGUUU	5788
ACCAUAUUAUUUUGAUUCUCU	5789	AGAGAAUCAAAAUAAUAUGGUUC	5790
CUCAAAGGAUAGGCCUUUGAU	5791	AUCAAGGCCUAUCCUUUGAGAA	5792
GCCUUUGAGUGUUAGAGAAAU	5793	AUUUCUCUAACACUCAAGGCCU	5794
GAGAAAGGAGUGAAGGAGGCU	5795	AGCCUCCUUCACUCCUUUCUCUA	5796
AGGUGGGAAUUGGUUUUUUU	5797	AAGAAUACCAUUUCCACCUGC	5798
CAGUGAAAUUAUCUUGAGUCU	5799	AGACUCAAGAUAAUUUCACUGGA	5800
UUGAGUCUACACAUUUAUUUU	5801	AAAAUUAUGUGUAGACUCAAGA	5802
AAUUGUUCGGCUGGAACUGAU	5803	AUCAGUUCAGCCGAACAAUUUU	5804
UGACCCAGGCUGGACUUGCGU	5805	ACGCAAGUCCAGCCUGGGUCAGU	5806
GAGGAAACUCCAGGGCACUGU	5807	ACAGUGCCCUGGAGUUUCCUCCC	5808
GCACUGCAUCUGGCGAUCAGU	5809	ACUGAUCGCCAGAUGCAGUGCCC	5810
GCGAUCAGACUCUGAGCACUU	5811	AAGUGCUCAGAGUCUGAUCGCA	5812
CGCCUUGGUCAUGUACAGCAU	5813	AUGCUGUACAUGACCAAGGCGAG	5814
CAGCACUGAAAGGAAUGAAGU	5815	ACUUAUUCUUUCAGUGCUGUA	5816
GGAUUGAAGCACCAGCAGGAU	5817	AUCCUGCUGGUGCUUCAUUCUU	5818
CAGCAGGAGGUGGACAGAGUU	5819	AACUCUGUCCACCUCUGCUGGU	5820
GGACAGAGUCUCUCAUGGAUU	5821	AAUCCAUGAGAGACUCUGUCCAC	5822
CUCAUGGAUGCCGGCACAAAU	5823	AUUUGUGCCGGCAUCCAUGAGAG	5824
GCACAAACUGCCUUAAAAUU	5825	AAUUUUAAAGGCAGUUUUGUGCCG	5826
UAGUUAUACAGGUUAUUCUU	5827	AAGAUUAACUGUAUUAACUAUG	5828

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CUUUGUAAGAAACAAGCUCAU	5829	AUGAGCUUGUUUCUACAAAGUA	5830
GGAGCUUCCUUUUAAAUUUUU	5831	AAAAUUUAAAAGGAAGCUCCUU	5832
CUGUAGGAAUUGGUUGAAAAU	5833	AUUUUCAACCAUUUCCUACAGAC	5834
GUUGAAAACUGAAGGUAGAUU	5835	AAUCUACCUUCAGUUUUAACCA	5836
AAGGUAGAUGGUGUUAUAGUU	5837	AACUUAACACCAUCUACCUUCA	5838
GUAAAUAAGCAUCUCACUUUU	5839	AAAAGUGAGAUGCUUAUUUACAG	5840
UGGUUUUGUUUUAACAUUCU	5841	AGAAUGUUUAAAACAAAACCACA	5842
AACAUUCAACGUUUCUUUUCU	5843	AGAAAAGAAACGUUGAAUGUUUA	5844
CUUUUCCUUCUACAAUAAACU	5845	AGUUUAUUGUAGAAGGAAAAGAA	5846

The inhibitory nucleic acid molecules disclosed herein can comprise RNA, DNA, or both RNA and DNA. The inhibitory nucleic acid molecules can also be linked or fused to a heterologous nucleic acid sequence, such as in a vector, or a heterologous label. For example,

5 the inhibitory nucleic acid molecules disclosed herein can be within a vector or as an exogenous donor sequence comprising the inhibitory nucleic acid molecule and a heterologous nucleic acid sequence. The inhibitory nucleic acid molecules can also be linked or fused to a heterologous label. The label can be directly detectable (such as, for example, fluorophore) or indirectly detectable (such as, for example, hapten, enzyme, or fluorophore quencher). Such labels can be

10 detectable by spectroscopic, photochemical, biochemical, immunochemical, or chemical means. Such labels include, for example, radiolabels, pigments, dyes, chromogens, spin labels, and fluorescent labels. The label can also be, for example, a chemiluminescent substance; a metal-containing substance; or an enzyme, where there occurs an enzyme-dependent secondary generation of signal. The term "label" can also refer to a "tag" or hapten that can

15 bind selectively to a conjugated molecule such that the conjugated molecule, when added subsequently along with a substrate, is used to generate a detectable signal. For example, biotin can be used as a tag along with an avidin or streptavidin conjugate of horseradish peroxidase (HRP) to bind to the tag, and examined using a calorimetric substrate (such as, for example, tetramethylbenzidine (TMB)) or a fluorogenic substrate to detect the presence of

20 HRP. Exemplary labels that can be used as tags to facilitate purification include, but are not limited to, myc, HA, FLAG or 3XFLAG, 6XHis or polyhistidine, glutathione-S-transferase (GST),

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maltose binding protein, an epitope tag, or the Fc portion of immunoglobulin. Numerous labels include, for example, particles, fluorophores, haptens, enzymes and their calorimetric, fluorogenic and chemiluminescent substrates and other labels.

The disclosed inhibitory nucleic acid molecules can comprise, for example, nucleotides or non-natural or modified nucleotides, such as nucleotide analogs or nucleotide substitutes. Such nucleotides include a nucleotide that contains a modified base, sugar, or phosphate group, or that incorporates a non-natural moiety in its structure. Examples of non-natural nucleotides include, but are not limited to, dideoxynucleotides, biotinylated, aminated, deaminated, alkylated, benzylated, and fluorophor-labeled nucleotides.

The inhibitory nucleic acid molecules disclosed herein can also comprise one or more nucleotide analogs or substitutions. A nucleotide analog is a nucleotide which contains a modification to either the base, sugar, or phosphate moieties. Modifications to the base moiety include, but are not limited to, natural and synthetic modifications of A, C, G, and T/U, as well as different purine or pyrimidine bases such as, for example, pseudouridine, uracil-5-yl, hypoxanthin-9-yl (I), and 2-aminoadenin-9-yl. Modified bases include, but are not limited to, 5-methylcytosine (5-me-C), 5-hydroxymethyl cytosine, xanthine, hypoxanthine, 2-aminoadenine, 6-methyl and other alkyl derivatives of adenine and guanine, 2-propyl and other alkyl derivatives of adenine and guanine, 2-thiouracil, 2-thiothymine and 2-thiocytosine, 5-halouracil and cytosine, 5-propynyl uracil and cytosine, 6-azo uracil, cytosine and thymine, 5-uracil (pseudouracil), 4-thiouracil, 8-halo, 8-amino, 8-thiol, 8-thioalkyl, 8-hydroxyl and other 8-substituted adenines and guanines, 5-halo (such as, for example, 5-bromo), 5-trifluoromethyl and other 5-substituted uracils and cytosines, 7-methylguanine, 7-methyladenine, 8-azaguanine, 8-azaadenine, 7-deazaguanine, 7-deazaadenine, 3-deazaguanine, and 3-deazaadenine.

Nucleotide analogs can also include modifications of the sugar moiety. Modifications to the sugar moiety include, but are not limited to, natural modifications of the ribose and deoxy ribose as well as synthetic modifications. Sugar modifications include, but are not limited to, the following modifications at the 2' position: OH; F; O-, S-, or N-alkyl; O-, S-, or N-alkenyl; O-, S- or N-alkynyl; or O-alkyl-O-alkyl, wherein the alkyl, alkenyl, and alkynyl may be substituted or unsubstituted C₁₋₁₀alkyl or C₂₋₁₀alkenyl, and C₂₋₁₀alkynyl. Exemplary 2' sugar modifications also include, but are not limited to, -O[(CH₂)_nO]_mCH₃, -O(CH₂)_nOCH₃, -O(CH₂)_nNH₂, -O(CH₂)_nCH₃,

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-O(CH₂)_n-ONH₂, and -O(CH₂)_nON[(CH₂)_nCH₃]₂, where n and m, independently, are from 1 to about 10. Other modifications at the 2' position include, but are not limited to, C₁₋₁₀alkyl, substituted lower alkyl, alkaryl, aralkyl, O-alkaryl or O-aralkyl, SH, SCH₃, OCN, Cl, Br, CN, CF₃, OCF₃, SOCH₃, SO₂CH₃, ONO₂, NO₂, N₃, NH₂, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, an RNA cleaving group, a reporter group, an intercalator, a group for improving the pharmacokinetic properties of an oligonucleotide, or a group for improving the pharmacodynamic properties of an oligonucleotide, and other substituents having similar properties. Similar modifications may also be made at other positions on the sugar, particularly the 3' position of the sugar on the 3' terminal nucleotide or in 2'-5' linked oligonucleotides and the 5' position of 5' terminal nucleotide. Modified sugars can also include those that contain modifications at the bridging ring oxygen, such as CH₂ and S. Nucleotide sugar analogs can also have sugar mimetics, such as cyclobutyl moieties in place of the pentofuranosyl sugar.

Nucleotide analogs can also be modified at the phosphate moiety. Modified phosphate moieties include, but are not limited to, those that can be modified so that the linkage between two nucleotides contains a phosphorothioate, chiral phosphorothioate, phosphorodithioate, phosphotriester, aminoalkylphosphotriester, methyl and other alkyl phosphonates including 3'-alkylene phosphonate and chiral phosphonates, phosphinates, phosphoramidates including 3'-amino phosphoramidate and aminoalkylphosphoramidates, thionophosphoramidates, thionoalkylphosphonates, thionoalkylphosphotriesters, and boranophosphates. These phosphate or modified phosphate linkage between two nucleotides can be through a 3'-5' linkage or a 2'-5' linkage, and the linkage can contain inverted polarity such as 3'-5' to 5'-3' or 2'-5' to 5'-2'. Various salts, mixed salts, and free acid forms are also included. Nucleotide substitutes also include peptide nucleic acids (PNAs).

In some embodiments, the antisense nucleic acid molecules are gapmers, whereby the first one to seven nucleotides at the 5' and 3' ends each have 2'-methoxyethyl (2'-MOE) modifications. In some embodiments, the first five nucleotides at the 5' and 3' ends each have 2'-MOE modifications. In some embodiments, the first one to seven nucleotides at the 5' and 3' ends are RNA nucleotides. In some embodiments, the first five nucleotides at the 5' and 3' ends are RNA nucleotides. In some embodiments, each of the backbone linkages between the nucleotides is a phosphorothioate linkage.

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In some embodiments, the siRNA molecules have termini modifications. In some embodiments, the 5' end of the antisense strand is phosphorylated. In some embodiments, 5'-phosphate analogs that cannot be hydrolyzed, such as 5'-(E)-vinyl-phosphonate are used.

In some embodiments, the siRNA molecules have backbone modifications. In some
 5 embodiments, the modified phosphodiester groups that link consecutive ribose nucleosides
 have been shown to enhance the stability and *in vivo* bioavailability of siRNAs. The non-ester
 groups (-OH, =O) of the phosphodiester linkage can be replaced with sulfur, boron, or acetate
 to give phosphorothioate, boranophosphate, and phosphonoacetate linkages. In addition,
 substituting the phosphodiester group with a phosphotriester can facilitate cellular uptake of
 10 siRNAs and retention on serum components by eliminating their negative charge. In some
 embodiments, the siRNA molecules have sugar modifications. In some embodiments, the
 sugars are deprotonated (reaction catalyzed by exo- and endonucleases) whereby the 2'-
 hydroxyl can act as a nucleophile and attack the adjacent phosphorous in the phosphodiester
 bond. Such alternatives include 2'-O-methyl, 2'-O-methoxyethyl, and 2'-fluoro modifications.

15 In some embodiments, the siRNA molecules have base modifications. In some
 embodiments, the bases can be substituted with modified bases such as pseudouridine, 5'-
 methylcytidine, N6-methyladenosine, inosine, and N7-methylguanosine.

In some embodiments, the siRNA molecules are conjugated to lipids. Lipids can be
 conjugated to the 5' or 3' termini of siRNA to improve their *in vivo* bioavailability by allowing
 20 them to associate with serum lipoproteins. Representative lipids include, but are not limited to,
 cholesterol and vitamin E, and fatty acids, such as palmitate and tocopherol.

In some embodiments, a representative siRNA has the following formula:

Sense: mN*mN*/i2FN/mN/i2FN/mN/i2FN/mN/i2FN/mN/i2FN/mN/i2FN/mN/
 i2FN/*mN*/32FN/
 25 Antisense: /52FN/*i2FN/*mN/i2FN/mN/i2FN/mN/i2FN/mN/i2FN/mN/i2FN/mN/
 i2FN/mN/i2FN/mN*N*N

wherein: "N" is the base; "2F" is a 2'-F modification; "m" is a 2'-O-methyl modification,
 "I" is an internal base; and "*" is a phosphorothioate backbone linkage.

The present disclosure also provides vectors comprising any one or more of the
 30 inhibitory nucleic acid molecules disclosed herein. In some embodiments, the vectors comprise
 any one or more of the inhibitory nucleic acid molecules disclosed herein and a heterologous
 nucleic acid. The vectors can be viral or nonviral vectors capable of transporting a nucleic acid

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molecule. In some embodiments, the vector is a plasmid or cosmid (such as, for example, a circular double-stranded DNA into which additional DNA segments can be ligated). In some embodiments, the vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Expression vectors include, but are not limited to, plasmids, cosmids, retroviruses, adenoviruses, adeno-associated viruses (AAV), plant viruses such as cauliflower mosaic virus and tobacco mosaic virus, yeast artificial chromosomes (YACs), Epstein-Barr (EBV)-derived episomes, and other expression vectors known in the art.

The present disclosure also provides compositions comprising any one or more of the inhibitory nucleic acid molecules disclosed herein. In some embodiments, the composition is a pharmaceutical composition. In some embodiments, the compositions comprise a carrier and/or excipient. Examples of carriers include, but are not limited to, poly(lactic acid) (PLA) microspheres, poly(D,L-lactic-co-glycolic-acid) (PLGA) microspheres, liposomes, micelles, inverse micelles, lipid cochleates, and lipid microtubules. A carrier may comprise a buffered salt solution such as PBS, HBSS, etc.

In some embodiments, the ANGPTL7 inhibitor comprises an anti-ANGPTL7 antibody. Antibodies that are specific to ANGPTL7 are described, for example, in U.S. Patent Application Publication Nos. US 2013/0022983 and US 2020/0399640, and in Comes et al., *Genes Cells*, 2011, 16, 243–259; Xu et al., *FASEB J.*, 2020, 34, 13548-13560, and Kuchtey et al., *Invest. Ophthalmol. Vis. Sci.*, 2008, 49, 3438-3448.

In some embodiments, the ANGPTL7 inhibitor comprises a nuclease agent that induces one or more nicks or double-strand breaks at a recognition sequence(s) or a DNA-binding protein that binds to a recognition sequence within an ANGPTL7 genomic nucleic acid molecule. The recognition sequence can be located within a coding region of the ANGPTL7 gene, or within regulatory regions that influence the expression of the gene. A recognition sequence of the DNA-binding protein or nuclease agent can be located in an intron, an exon, a promoter, an enhancer, a regulatory region, or any non-protein coding region. The recognition sequence can include or be proximate to the start codon of the ANGPTL7 gene. For example, the recognition sequence can be located about 10, about 20, about 30, about 40, about 50, about 100, about 200, about 300, about 400, about 500, or about 1,000 nucleotides from the start codon. As another example, two or more nuclease agents can be used, each targeting a nuclease recognition sequence including or proximate to the start codon. As another example, two nuclease agents can be used, one targeting a nuclease recognition sequence including or

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proximate to the start codon, and one targeting a nuclease recognition sequence including or proximate to the stop codon, wherein cleavage by the nuclease agents can result in deletion of the coding region between the two nuclease recognition sequences. Any nuclease agent that induces a nick or double-strand break into a desired recognition sequence can be used in the methods and compositions disclosed herein. Any DNA-binding protein that binds to a desired recognition sequence can be used in the methods and compositions disclosed herein.

Suitable nuclease agents and DNA-binding proteins for use herein include, but are not limited to, zinc finger protein or zinc finger nuclease (ZFN) pair, Transcription Activator-Like Effector (TALE) protein or Transcription Activator-Like Effector Nuclease (TALEN), or Clustered Regularly Interspersed Short Palindromic Repeats (CRISPR)/CRISPR-associated (Cas) systems. The length of the recognition sequence can vary, and includes, for example, recognition sequences that are about 30-36 bp for a zinc finger protein or ZFN pair, about 15-18 bp for each ZFN, about 36 bp for a TALE protein or TALEN, and about 20 bp for a CRISPR/Cas guide RNA.

In some embodiments, CRISPR/Cas systems can be used to modify an ANGPTL7 genomic nucleic acid molecule within a cell. The methods and compositions disclosed herein can employ CRISPR-Cas systems by utilizing CRISPR complexes (comprising a guide RNA (gRNA) complexed with a Cas protein) for site-directed cleavage of ANGPTL7 nucleic acid molecules.

Cas proteins generally comprise at least one RNA recognition or binding domain that can interact with gRNAs. Cas proteins can also comprise nuclease domains (such as, for example, DNase or RNase domains), DNA binding domains, helicase domains, protein-protein interaction domains, dimerization domains, and other domains. Suitable Cas proteins include, for example, a wild type Cas9 protein and a wild type Cpf1 protein (such as, for example, FnCpf1). A Cas protein can have full cleavage activity to create a double-strand break in an ANGPTL7 genomic nucleic acid molecule or it can be a nickase that creates a single-strand break in an ANGPTL7 genomic nucleic acid molecule. Additional examples of Cas proteins include, but are not limited to, Cas1, Cas1B, Cas2, Cas3, Cas4, Cas5, Cas5e (CasD), Cas6, Cas6e, Cas6f, Cas7, Cas8a1, Cas8a2, Cas8b, Cas8c, Cas9 (Csn1 or Csx12), Cas10, Cas10d, CasF, CasG, CasH, Csy1, Csy2, Csy3, Cse1 (CasA), Cse2 (CasB), Cse3 (CasE), Cse4 (CasC), Csc1, Csc2, Csa5, Csn2, Csm2, Csm3, Csm4, Csm5, Csm6, Cmr1, Cmr3, Cmr4, Cmr5, Cmr6, Csb1, Csb2, Csb3, Csx17, Csx14, Csx10, Csx16, CsaX, Csx3, Csx1, Csx15, Csf1, Csf2, Csf3, Csf4, and Cu1966, and homologs or modified versions thereof. Cas proteins can also be operably linked to heterologous polypeptides as fusion proteins. For example, a Cas protein can be fused to a cleavage domain,

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an epigenetic modification domain, a transcriptional activation domain, or a transcriptional repressor domain. Cas proteins can be provided in any form. For example, a Cas protein can be provided in the form of a protein, such as a Cas protein complexed with a gRNA. Alternately, a Cas protein can be provided in the form of a nucleic acid molecule encoding the Cas protein,
5 such as an RNA or DNA.

In some embodiments, targeted genetic modifications of an ANGPTL7 genomic nucleic acid molecules can be generated by contacting a cell with a Cas protein and one or more gRNAs that hybridize to one or more gRNA recognition sequences within a target genomic locus in the ANGPTL7 genomic nucleic acid molecule. For example, a gRNA recognition sequence can be
10 located within a region of SEQ ID NO:1. The gRNA recognition sequence can also include or be proximate to a position corresponding to: position 4,291, position 4,287, position 4,243, position 4,325, or position 4,336 according to SEQ ID NO:1. For example, the gRNA recognition sequence can be located from about 1000, from about 500, from about 400, from about 300, from about 200, from about 100, from about 50, from about 45, from about 40, from about 35,
15 from about 30, from about 25, from about 20, from about 15, from about 10, or from about 5 nucleotides of a position corresponding to: position 4,291, position 4,287, position 4,243, position 4,325, or position 4,336 according to SEQ ID NO:1. The gRNA recognition sequence can include or be proximate to the start codon of an ANGPTL7 genomic nucleic acid molecule or the stop codon of an ANGPTL7 genomic nucleic acid molecule. For example, the gRNA recognition
20 sequence can be located from about 10, from about 20, from about 30, from about 40, from about 50, from about 100, from about 200, from about 300, from about 400, from about 500, or from about 1,000 nucleotides of the start codon or the stop codon.

The gRNA recognition sequences within a target genomic locus in an ANGPTL7 genomic nucleic acid molecule are located near a Protospacer Adjacent Motif (PAM) sequence,
25 which is a 2-6 base pair DNA sequence immediately following the DNA sequence targeted by the Cas9 nuclease. The canonical PAM is the sequence 5'-NGG-3' where "N" is any nucleobase followed by two guanine ("G") nucleobases. gRNAs can transport Cas9 to anywhere in the genome for gene editing, but no editing can occur at any site other than one at which Cas9 recognizes PAM. In addition, 5'-NGA-3' can be a highly efficient non-canonical PAM for human
30 cells. Generally, the PAM is about 2-6 nucleotides downstream of the DNA sequence targeted by the gRNA. The PAM can flank the gRNA recognition sequence. In some embodiments, the gRNA recognition sequence can be flanked on the 3' end by the PAM. In some embodiments,

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the gRNA recognition sequence can be flanked on the 5' end by the PAM. For example, the cleavage site of Cas proteins can be about 1 to about 10, about 2 to about 5 base pairs, or three base pairs upstream or downstream of the PAM sequence. In some embodiments (such as when Cas9 from *S. pyogenes* or a closely related Cas9 is used), the PAM sequence of the non-complementary strand can be 5'-NGG-3', where N is any DNA nucleotide and is immediately 3' of the gRNA recognition sequence of the non-complementary strand of the target DNA. As such, the PAM sequence of the complementary strand would be 5'-CCN-3', where N is any DNA nucleotide and is immediately 5' of the gRNA recognition sequence of the complementary strand of the target DNA.

10 A gRNA is an RNA molecule that binds to a Cas protein and targets the Cas protein to a specific location within an ANGPTL7 genomic nucleic acid molecule. An exemplary gRNA is a gRNA effective to direct a Cas enzyme to bind to or cleave an ANGPTL7 genomic nucleic acid molecule, wherein the gRNA comprises a DNA-targeting segment that hybridizes to a gRNA recognition sequence within the ANGPTL7 genomic nucleic acid molecule that includes or is proximate to a position corresponding to: position 4,291, position 4,287, position 4,243, position 4,325, or position 4,336 according to SEQ ID NO:1. For example, a gRNA can be selected such that it hybridizes to a gRNA recognition sequence that is located from about 5, from about 10, from about 15, from about 20, from about 25, from about 30, from about 35, from about 40, from about 45, from about 50, from about 100, from about 200, from about 300, from about 400, from about 500, or from about 1,000 nucleotides of a position corresponding to: position 4,291, position 4,287, position 4,243, position 4,325, or position 4,336 according to SEQ ID NO:1. Other exemplary gRNAs comprise a DNA-targeting segment that hybridizes to a gRNA recognition sequence present within an ANGPTL7 genomic nucleic acid molecule that includes or is proximate to the start codon or the stop codon. For example, a gRNA can be selected such that it hybridizes to a gRNA recognition sequence that is located from about 5, from about 10, from about 15, from about 20, from about 25, from about 30, from about 35, from about 40, from about 45, from about 50, from about 100, from about 200, from about 300, from about 400, from about 500, or from about 1,000 nucleotides of the start codon or located from about 5, from about 10, from about 15, from about 20, from about 25, from about 30, from about 35, from about 40, from about 45, from about 50, from about 100, from about 200, from about 300, from about 400, from about 500, or from about 1,000 nucleotides of the stop codon. Suitable gRNAs can comprise from about 17 to about 25

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nucleotides, from about 17 to about 23 nucleotides, from about 18 to about 22 nucleotides, or from about 19 to about 21 nucleotides. In some embodiments, the gRNAs can comprise 20 nucleotides.

Examples of suitable gRNA recognition sequences located within the ANGPTL7

5 reference gene are set forth in Tables 9-17 as SEQ ID NOs:25-165.

Table 9: Guide RNA Recognition Sequences Near ANGPTL7 Arg177Stop Variation

Strand	Guide RNA Recognition Sequence	SEQ ID NO:
+	CTGCAGGGACAGGAACAGGTTGG	25
+	CAGAGTATCCCCTCTGCTTCAGG	26
+	GGCTCTGCAGGGACAGGAACAGG	27
+	GCTTCAGGTGTTCTGTGACATGG	28
+	TGCAGGGACAGGAACAGGTTGGG	29
+	TCTACTGGCTCTGCAGGGACAGG	30
-	CCTTCTACCGGGACTGGAAGCAG	31
-	CCGTGGGGACTTCTGGCTGGGGA	32
-	CCGGGACTGGAAGCAGTACAAGC	33
-	CCTTGTCTCCTTCTACCGGGACT	34
-	CCACCGGCTCTCCAGACAGCCAA	35
-	CCGGCTCTCCAGACAGCCAACCC	36
+	TGGAGACTTCAGGCGGAGGCTGG	37
+	TGTGACATGGAGACTTCAGGCGG	38
+	TTCTGTGACATGGAGACTTCAGG	39
+	GACATGGAGACTTCAGGCGGAGG	40
-	CCATGACTGGACCAAGTGCCACCA	41
-	CCCGGCTGCGTGTAGAGATGGAG	42
-	CCGGCTGCGTGTAGAGATGGAGG	43
-	CCAACCCGGCTGCGTGTAGAGAT	44
-	CCAGGGGCCCCATGACTGGACCA	45
-	CCCCATGACTGGACCAAGTGCCAC	46

Table 10: Guide RNA Recognition Sequences Near ANGPTL7 Gln175His Variation

Strand	Guide RNA Recognition Sequence	SEQ ID NO:
-	CTGCTTCCAGTCCCGGTAGAAGG	47
+	TTGTCTCCTTCTACCGGGACTGG	48
+	GCGGGAGTGCACACATCTACTGG	49
+	GGACTGGAAGCAGTACAAGCAGG	50
+	GACATGGAGACTTCAGGCGGAGG	40
+	GTGGCCTTGTCTCCTTCTACCGG	51
+	TGGAGACTTCAGGCGGAGGCTGG	37
-	TACTCTGGTGAGGGACTTGCAGG	52
-	ACTCTGGTGAGGGACTTGCAGGG	53
-	GCTTGTACTGCTTCCAGTCCCGG	53
-	AGTCCCGGTAGAAGGAGACAAGG	55
+	CACACATCTACTGGCTCTGCAGG	56
-	CAAGGCCACTTTTTCGTCTATGG	57
+	GACTGGAAGCAGTACAAGCAGGG	58
-	GCAGAGGGGATACTCTGGTGAGG	59
+	CAGAGTATCCCCTCTGCTTCAGG	26
+	TTCTGTGACATGGAGACTTCAGG	39
-	CTCTGGTGAGGGACTTGCAGGGG	60
-	CAGAGGGGATACTCTGGTGAGGG	61
-	ACTTTTTCGTCTATGGATGATGG	62
+	TGGCCTTGTCTCCTTCTACCGGG	63
+	AAGCAGTACAAGCAGGGCTTTGG	64
+	GCTTCAGGTGTTCTGTGACATGG	28
-	CTGAAGCAGAGGGGATACTCTGG	65
-	TCACAGAACACCTGAAGCAGAGG	66
+	ACACATCTACTGGCTCTGCAGGG	67
+	ATCATCCATAGACGAAAAAGTGG	68
+	TGTGACATGGAGACTTCAGGCGG	38
+	TCTACTGGCTCTGCAGGGACAGG	30

Table 11: Guide RNA Recognition Sequences Near ANGPTL7 Arg220His Variation

Strand	Guide RNA Recognition Sequence	SEQ ID NO:
+	ATGACCGCGTACAACTCCGGGGG	69
+	CATGACCGCGTACAACTCCGGGG	70
-	GGCACCCCGGAGTTGTACGCGG	71
-	GAGTTGTACGCGGTCATGTGTGG	72
+	ACATGACCGCGTACAACTCCGGG	73
+	CACATGACCGCGTACAACTCCGG	74
-	TTGTACGCGGTCATGTGTGGTGG	75
+	TTGTCTCCTTCTACCGGGACTGG	48
-	CTGCTTCCAGTCCCGGTAGAAGG	47
+	TGGGGAACGAACACATCCACCGG	76
+	GGAAGCAGTACAAGCAGG	50
-	GGTGGCACTGGTCCAGTCATGGG	77
-	CAGAATAGGAATGGCACCCCGG	78
-	GTGGCACTGGTCCAGTCATGGGG	79
-	GCGGTCATGTGTGGTGGCACTGG	80
-	TGGTGGCACTGGTCCAGTCATGG	81
+	GTGGCCTTGTCTCCTTCTACCGG	51
+	GCAGCATCCGTGGGGACTTCTGG	82
+	CATCCGTGGGGACTTCTGGCTGG	83
-	GCTTGACTGCTTCCAGTCCCGG	54
-	AGTCCCGGTAGAAGGAGACAAGG	55
+	GGCTCTCAGACAGCCAACCCGG	84
+	ATCCGTGGGGACTTCTGGCTGGG	85
+	GACTGGAAGCAGTACAAGCAGGG	58
-	TTGGCTGTCTGGAGAGCCGGTGG	86
-	TGGTCCAGTCATGGGGCCCCTGG	86
-	GATTTGTCTTGAATCAGAATAGG	88
+	AACCCGGCTGCATGTAGAGATGG	89
-	CTCCATCTCTACATGCAGCCGGG	90

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+	TGGCCTTGTCTCCTTCTACCGGG	63
+	AAGCAGTACAAGCAGGGCTTTGG	64
+	TAGAGATGGAGGTAAGCACAAAGG	91
+	TCCGTGGGGACTTCTGGCTGGGG	92

Table 12: Guide RNA Recognition Sequences Near ANGPTL7 Arg220Cys Variation

Strand	Guide RNA Recognition Sequence	SEQ ID NO:
+	ATGACCGCGTACAACCTCCGGGGG	69
+	CATGACCGCGTACAACCTCCGGGG	70
-	GGCACCCCGGAGTTGTACGCGG	71
-	GAGTTGTACGCGGTCATGTGTGG	72
+	ACATGACCGCGTACAACCTCCGGG	73
+	CACATGACCGCGTACAACCTCCGG	74
-	TTGTACGCGGTCATGTGTGGTGG	75
+	TTGTCTCCTTCTACCGGGACTGG	48
-	CTGCTTCCAGTCCCGGTAGAAGG	47
+	TGGGGAACGAACACATCCACCGG	76
+	GGACTGGAAGCAGTACAAGCAGG	50
-	GGTGGCACTGGTCCAGTCATGGG	77
-	CAGAATAGGAATGGCACCCCGG	78
-	GTGGCACTGGTCCAGTCATGGGG	79
-	GCGGTCATGTGTGGTGGCACTGG	80
-	TGGTGGCACTGGTCCAGTCATGG	81
+	CATCCGTGGGGACTTCTGGCTGG	83
+	GCAGCATCCGTGGGGACTTCTGG	82
+	GTGGCCTTGTCTCCTTCTACCGG	51
-	GCTTGTAAGTCTTCCAGTCCCGG	54
+	GGCTCTCCAGACAGCCAACCCGG	84
-	AGTCCCGGTAGAAGGAGACAAGG	55
+	ATCCGTGGGGACTTCTGGCTGGG	85
+	GAAGTGAAGCAGTACAAGCAGGG	58

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-	TGGTCCAGTCATGGGGCCCTGG	87
-	TTGGCTGTCTGGAGAGCCGGTGG	86
-	GATTTGTCTTGAATCAGAATAGG	88
-	ATCTCTACACACAGCCGGGTTGG	93
+	AAGCAGTACAAGCAGGGCTTTGG	64
+	TGGCCTTGTCTCCTTCTACCGGG	63
+	TAGAGATGGAGGTAAGCACAAGG	91
+	TCCGTGGGGACTTCTGGCTGGGG	92
+	AACCCGGCTGTGTGTAGAGATGG	94
-	CCTCCATCTCTACACACAGCCGG	95

Table 13: Guide RNA Recognition Sequences Near ANGPTL7 Asn302Lys Variation

Strand	Guide RNA Recognition Sequence	SEQ ID NO:
+	CAATGGAGTGTAACCGCCTGG	96
+	AATGGAGTGTAACCGCCTGGG	97
+	TACCTACTCCCTCAAACGGGTGG	98
-	TTTCATCTCCACCCGTTTGAGGG	99
+	ACAGTCAACTTACTAGCACTGGG	100
-	TTTTCATCTCCACCCGTTTGAGG	101
+	GGGTGAGCACAATAAGCACCTGG	102
+	ATGGCATCACCTGGTATGGCTGG	103
-	CTCCACCCGTTTGAGGGAGTAGG	104
-	GGTGCTTATTGTGCTCACCCAGG	105
+	CTAACTCCTTACCTGATGTCTGG	106
+	CACAGTCAACTTACTAGCACTGG	107
-	CAGTTGTACAGTAGCCACCTGG	108
-	GATAGACCAGACATCAGGTAAGG	109
-	TCAGGTAAGGAGTTAGAGCCAGG	110
+	GATCTACCTACTCCCTCAAACGG	111
-	AGATCCATGCCAGCCATACCAGG	112

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-	GCTTATTGTGCTCACCCAGGCGG	113
-	CATACCAGGTGATGCCATCCAGG	114
+	ATCTACCTACTCCCTCAAACGGG	115
-	ACTGTGATAGACCAGACATCAGG	116
+	TTCTCATGCCAGGTGGCTACTGG	117
+	CTGGATGGCATCACCTGGTATGG	118
+	AGCACCTGGATGGCATCACCTGG	119
+	ATCACCTGGTATGGCTGGCATGG	120
-	GTAGTACACTCCATTGAGTTTGG	121
+	GAGCACAATAAGCACCTGGATGG	122
-	CAGGTAAGGAGTTAGAGCCAGGG	123
+	CTGGGTCTGTTTCTCATGCCAGG	124
+	TTTGGTATTCTTTCTGACCCTGG	125
-	GTCAGAAAGAATACCAAAACCGG	126
+	GGTCTGTTTCTCATGCCAGGTGG	127

Table 14: Guide RNA Recognition Sequences Near ANGPTL7 Arg340His Variation

Strand	Guide RNA Recognition Sequence	SEQ ID NO:
+	CAATGGAGTGTAACCGCCTGG	96
+	AATGGAGTGTAACCGCCTGGG	97
-	GGCGGTAGTACACTCCATTGAGG	128
+	TACCTACTCCCTCAAACGGGTGG	98
-	GTAGTACACTCCATTGAGGTTGG	129
-	TTTCATCTCCACCCGTTTGAGGG	99
-	TTTTATCTCCACCCGTTTGAGG	101
+	GGGTGAGCACAATAAGCACCTGG	102
+	ATGGCATCACCTGGTATGGCTGG	103
-	GGTGCTTATTGTGCTCACCCAGG	105
-	CTCCACCCGTTTGAGGGAGTAGG	104
-	GTTTCTGTATCCGTGCTCCACGG	130
+	AAACTGAGACACGTGGAGACTGG	131

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-	GCTTATTGTGCTCAGGCGG	113
+	GATCTACCTACTCCCTCAAACGG	111
-	AGATCCATGCCAGCCATACCAGG	112
+	GCCTTAAAAGGAGGCTGCCGTGG	132
-	CATACCAGGTGATGCCATCCAGG	114
+	ATCTACCTACTCCCTCAAACGGG	115
+	GACACGTGGAGACTGGATGAGGG	133
-	TCCACGGCAGCCTCCTTTAAGG	134
+	CTGGATGGCATCACCTGGTATGG	118
+	AGCACCTGGATGGCATCACCTGG	119
+	ATCACCTGGTATGGCTGGCATGG	120
+	TGCACAGACTCCAACCTCAATGG	135
+	GAGCACAATAAGCACCTGGATGG	122
+	AGACACGTGGAGACTGGATGAGG	136
+	AGACTTCAAGCCTTAAAAGGAGG	137
-	TTTAAGGCTTGAAGTCTTCTGGG	138
-	AAGGCTTGAAGTCTTCTGGGTGG	139
-	TTTTAAGGCTTGAAGTCTTCTGG	140
+	GATACAGAACTGAGACACGTGG	141
+	AAGGAGGCTGCCGTGGAGCACGG	142
+	AGAAGACTTCAAGCCTTAAAAGG	143

Table 15: Guide RNA Recognition Sequences Near ANGPTL7 Phe161Ile Variation

Strand	Guide RNA Recognition Sequence	SEQ ID NO:
-	ACAGAACACCTGAAGCAGAGGGG	144
-	ACAGAACACCTGAAGCAGAGGGG	145
-	CACAGAACACCTGAAGCAGAGGG	146
+	CAGAGTATCCCCTCTGCTTCAGG	147
-	ACTCTGGTGAGGGACTTGCAGGG	148
-	TACTCTGGTGAGGGACTTGCAGG	149
-	GCAGAGGGGATACTCTGGTGAGG	150

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+	GCTTCAGGTGTTCTGTGACATGG	151
-	CAGAGGGGATACTCTGGTGAGGG	152

Table 16: Guide RNA Recognition Sequences Near ANGPTL7 Trp188STOP Variation

Strand	Guide RNA Recognition Sequence	SEQ ID NO:
+	TTGTCTCCTTCTACCGGGACTGG	153
+	GTGGCCTTGTCTCCTTCTACCGG	154
+	TGGCCTTGTCTCCTTCTACCGGG	155
+	GACTGGAAGCAGTACAAGCAGGG	156
+	GGACTGGAAGCAGTACAAGCAGG	157
-	CTGCTTCCAGTCCCGGTAGAAGG	158
-	GCTTGTAAGTCTTCCAGTCCCGG	159
-	AGTCCCGGTAGAAGGAGACAAGG	160

Table 17: Guide RNA Recognition Sequences Near ANGPTL7 Lys192Gln Variation

Strand	Guide RNA Recognition Sequence	SEQ ID NO:
+	GACTGGAAGCAGTACAAGCAGGG	156
+	GGACTGGAAGCAGTACAAGCAGG	157
-	GGACTGGAAGCAGTACAAGC	159
+	AAGCAGTACAAGCAGGGCTTTGG	161
+	CAGGGCTTTGGCAGCATCCGTGG	162
+	AGGGCTTTGGCAGCATCCGTGGG	163
+	GGGCTTTGGCAGCATCCGTGGGG	164
-	TCCCCAGCCAGAAGTCCCCACGG	165

5

The Cas protein and the gRNA form a complex, and the Cas protein cleaves the target ANGPTL7 genomic nucleic acid molecule. The Cas protein can cleave the nucleic acid molecule at a site within or outside of the nucleic acid sequence present in the target ANGPTL7 genomic nucleic acid molecule to which the DNA-targeting segment of a gRNA will bind. For example, formation of a CRISPR complex (comprising a gRNA hybridized to a gRNA recognition sequence and complexed with a Cas protein) can result in cleavage of one or both strands in or near (such

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as, for example, within 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 50, or more base pairs from) the nucleic acid sequence present in the ANGPTL7 genomic nucleic acid molecule to which a DNA-targeting segment of a gRNA will bind.

Such methods can result, for example, in an ANGPTL7 genomic nucleic acid molecule in which a region of SEQ ID NO:1 is disrupted, the start codon is disrupted, the stop codon is disrupted, or the coding sequence is disrupted or deleted. Optionally, the cell can be further contacted with one or more additional gRNAs that hybridize to additional gRNA recognition sequences within the target genomic locus in the ANGPTL7 genomic nucleic acid molecule. By contacting the cell with one or more additional gRNAs (such as, for example, a second gRNA that hybridizes to a second gRNA recognition sequence), cleavage by the Cas protein can create two or more double-strand breaks or two or more single-strand breaks.

In any of the embodiments described herein, the subject can also be treated with a therapeutic agent that treats or inhibits an ophthalmic condition. Such therapeutic agents include, but are not limited to, a prostaglandin, a beta blocker, an alpha-adrenergic agonist, a carbonic anhydrase inhibitor, a rho kinase inhibitor, or a miotic or cholinergic agent. In some embodiments, the therapeutic agent that treats or inhibits the ophthalmic condition is a prostaglandin. In some embodiments, the prostaglandin is XALATAN® (latanoprost), TRAVATAN Z® (travoprost), ZIOPTAN® (tafluprost), LUMIGAN® (bimatoprost), or VYZULTA® (latanoprostene bunod). In some embodiments, the prostaglandin is latanoprost, travoprost, tafluprost, bimatoprost, or latanoprostene bunod. In some embodiments, the therapeutic agent that treats or inhibits the ophthalmic condition is a beta blocker. In some embodiments, the beta blocker is BETIMOL®, ISTALOL®, or TIMOPTIC® (timolol) or BETOPTIC® (betaxolol). In some embodiments, the beta blocker is timolol or betaxolol. In some embodiments, the therapeutic agent that treats or inhibits the ophthalmic condition is an alpha-adrenergic agonist. In some embodiments, the alpha-adrenergic agonist is IOPIDINE® (apraclonidine) or ALPHAGAN® or QOLIANA® (brimonidine). In some embodiments, the alpha-adrenergic agonist is apraclonidine or brimonidine. In some embodiments, the therapeutic agent that treats or inhibits the ophthalmic condition is a carbonic anhydrase inhibitor. In some embodiments, the carbonic anhydrase inhibitor is TRUSOPT® (dorzolamide) or AZOPT® (brinzolamide). In some embodiments, the carbonic anhydrase inhibitor is dorzolamide or brinzolamide. In some embodiments, the therapeutic agent that treats or inhibits the ophthalmic condition is a rho kinase inhibitor. In some embodiments, the rho kinase inhibitor is RHOPRESSA® (netarsudil). In

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some embodiments, the rho kinase inhibitor is netarsudil. In some embodiments, the therapeutic agent that treats or inhibits the ophthalmic condition is a miotic or cholinergic agent. In some embodiments, the miotic or cholinergic agent is ISOPTO® Carpine (pilocarpine). In some embodiments, the miotic or cholinergic agent is pilocarpine.

5 In some embodiments, the methods of treatment further comprise detecting the presence or absence of an ANGPTL7 predicted loss-of-function variant nucleic acid molecule encoding an ANGPTL7 polypeptide in a biological sample from the subject. As used throughout the present disclosure, “an ANGPTL7 predicted loss-of-function variant nucleic acid molecule” is any ANGPTL7 nucleic acid molecule (such as, for example, genomic nucleic acid molecule,
10 mRNA molecule, or cDNA molecule) encoding an ANGPTL7 polypeptide having a partial loss-of-function, a complete loss-of-function, a predicted partial loss-of-function, or a predicted complete loss-of-function.

 The present disclosure also provides methods of treating a subject undergoing glucocorticoid treatment. In some embodiments, the subject is suffering from inflammation. In
15 some embodiments, the methods comprise determining whether the subject has an ANGPTL7 predicted loss-of-function variant nucleic acid molecule encoding an ANGPTL7 polypeptide. In some embodiments, the determining step comprises obtaining or having obtained a biological sample from the subject, and performing or having performed a sequence analysis on the biological sample to determine if the subject has a genotype comprising the ANGPTL7 predicted
20 loss-of-function variant nucleic acid molecule. In some embodiments, the methods comprise administering or continuing to administer to a subject that is ANGPTL7 reference the glucocorticoid in a standard dosage amount, and administering an ANGPTL7 inhibitor to the subject. In some embodiments, the methods comprise administering or continuing to administer to a subject that is heterozygous for the ANGPTL7 predicted loss-of-function variant
25 the glucocorticoid in an amount that is the same as or higher than a standard dosage amount, and administering an ANGPTL7 inhibitor to the subject. In some embodiments, the methods comprise administering or continuing to administer to a subject that is homozygous for the ANGPTL7 predicted loss-of-function variant the glucocorticoid in an amount that is the same as or higher than a standard dosage amount. The presence of a genotype having the ANGPTL7
30 predicted loss-of-function variant nucleic acid molecule encoding the ANGPTL7 polypeptide indicates the subject has a decreased risk of developing a glucocorticoid-induced ophthalmic

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condition. In some embodiments, the subject is ANGPTL7 reference. In some embodiments, the subject is heterozygous for the ANGPTL7 predicted loss-of-function variant.

In some embodiments, the subject is ANGPTL7 reference, and the subject is administered or continued to be administered the glucocorticoid in a standard dosage amount, and is administered an ANGPTL7 inhibitor. In some embodiments, the subject is heterozygous for an ANGPTL7 predicted loss-of-function variant, and the subject is administered or continued to be administered the glucocorticoid in an amount that is the same as or higher than a standard dosage amount, and is administered an ANGPTL7 inhibitor. In some embodiments, the subject is homozygous for an ANGPTL7 predicted loss-of-function variant, and the subject is administered or continued to be administered the glucocorticoid in an amount that is the same as or higher than a standard dosage amount.

Detecting the presence or absence of an ANGPTL7 predicted loss-of-function variant nucleic acid molecule in a biological sample from a subject and/or determining whether a subject has an ANGPTL7 predicted loss-of-function variant nucleic acid molecule can be carried out by any of the methods described herein. In some embodiments, these methods can be carried out *in vitro*. In some embodiments, these methods can be carried out *in situ*. In some embodiments, these methods can be carried out *in vivo*. In any of these embodiments, the nucleic acid molecule can be present within a cell obtained from the subject.

The present disclosure also provides methods of treating a subject undergoing glucocorticoid treatment. In some embodiments, the subject is suffering from inflammation. In some embodiments, the methods comprise determining whether the subject has an ANGPTL7 predicted loss-of-function variant polypeptide. In some embodiments, the determining step comprises obtaining or having obtained a biological sample from the subject, and performing or having performed an assay on the biological sample to determine if the subject has an ANGPTL7 predicted loss-of-function variant polypeptide. In some embodiments, the methods comprise administering or continuing to administer to a subject that does not have an ANGPTL7 predicted loss-of-function variant polypeptide the glucocorticoid in a standard dosage amount, and administering an ANGPTL7 inhibitor to the subject. In some embodiments, the methods comprise administering or continuing to administer to a subject that has the ANGPTL7 predicted loss-of-function variant polypeptide the glucocorticoid in an amount that is the same as or higher than a standard dosage amount. The presence of an ANGPTL7 predicted loss-of-function variant polypeptide indicates the subject does not have an increased risk of developing

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a glucocorticoid-induced ophthalmic condition. In some embodiments, the subject has an ANGPTL7 predicted loss-of-function variant polypeptide. In some embodiments, the subject does not have an ANGPTL7 predicted loss-of-function variant polypeptide.

5 Detecting the presence or absence of an ANGPTL7 predicted loss-of-function polypeptide in a biological sample from a subject and/or determining whether a subject has an ANGPTL7 predicted loss-of-function polypeptide can be carried out by any of the methods described herein. In some embodiments, these methods can be carried out *in vitro*. In some
10 embodiments, these methods can be carried out *in situ*. In some embodiments, these methods can be carried out *in vivo*. In any of these embodiments, the polypeptide can be present within a cell obtained from the subject.

In some embodiments, the dose of the glucocorticoids can be increased by about 10%, by about 20%, by about 30%, by about 40%, by about 50%, by about 60%, by about 70%, by about 80%, or by about 90% for subjects that are heterozygous or homozygous for an ANGPTL7 predicted loss-of-function variant (i.e., a higher than the standard dosage amount) compared to
15 subjects that are ANGPTL7 reference (who may receive a standard dosage amount). In some embodiments, the dose of the glucocorticoids can be increased by about 10%, by about 20%, by about 30%, by about 40%, or by about 50%. In addition, the dose of glucocorticoids in subjects that are heterozygous or homozygous for an ANGPTL7 predicted loss-of-function variant can be administered more frequently compared to subjects that are ANGPTL7 reference.

20 Administration of the glucocorticoids and/or ANGPTL7 inhibitors can be repeated, for example, after one day, two days, three days, five days, one week, two weeks, three weeks, one month, five weeks, six weeks, seven weeks, eight weeks, two months, or three months. The repeated administration can be at the same dose or at a different dose. The administration can be repeated once, twice, three times, four times, five times, six times, seven times, eight times,
25 nine times, ten times, or more. For example, according to certain dosage regimens a subject can receive therapy for a prolonged period of time such as, for example, 6 months, 1 year, or more.

Administration of the glucocorticoids and/or ANGPTL7 inhibitors can occur by any suitable route including, but not limited to, parenteral, intravenous, oral, subcutaneous, intra-
30 arterial, intracranial, intrathecal, intraperitoneal, topical, intranasal, or intramuscular. Pharmaceutical compositions for administration are desirably sterile and substantially isotonic and manufactured under GMP conditions. Pharmaceutical compositions can be provided in unit

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dosage form (i.e., the dosage for a single administration). Pharmaceutical compositions can be formulated using one or more physiologically and pharmaceutically acceptable carriers, diluents, excipients or auxiliaries. The formulation depends on the route of administration chosen. The term "pharmaceutically acceptable" means that the carrier, diluent, excipient, or
5 auxiliary is compatible with the other ingredients of the formulation and not substantially deleterious to the recipient thereof.

Administration of the glucocorticoids and/or ANGPTL7 inhibitors can be administered in a single dosage form or as separate dosage forms. When administered as separate dosage forms, the glucocorticoids can be administered concurrently with or sequentially to ANGPTL7
10 inhibitors. In some embodiments, the glucocorticoids and ANGPTL7 inhibitors are administered concurrently. In some embodiments, the glucocorticoids and ANGPTL7 inhibitors are administered sequentially. For example, in some embodiments, the glucocorticoids can be administered prior to the ANGPTL7 inhibitors. In some embodiments, the ANGPTL7 inhibitors are administered prior to the glucocorticoids.

15 The terms "treat", "treating", and "treatment" and "prevent", "preventing", and "prevention" as used herein referring to inflammation, refer to eliciting the desired biological response, such as a therapeutic and prophylactic effect, respectively. In some embodiments, a therapeutic effect comprises one or more of a decrease/reduction in inflammation, a decrease/reduction in the severity of inflammation (such as, for example, a reduction or
20 inhibition of development of inflammation), a decrease/reduction in symptoms and inflammation-related effects, delaying the onset of symptoms and inflammation-related effects, reducing the severity of symptoms of inflammation-related effects, reducing the severity of an acute episode, reducing the number of symptoms and inflammation-related effects, reducing the latency of symptoms and inflammation-related effects, an amelioration of
25 symptoms and inflammation-related effects, reducing secondary symptoms, reducing secondary infections, preventing relapse to inflammation, decreasing the number or frequency of relapse episodes, increasing latency between symptomatic episodes, increasing time to sustained progression, speeding recovery, and/or increasing efficacy of or decreasing resistance to alternative therapeutics, following administration of the glucocorticoid or composition
30 comprising the glucocorticoid. A prophylactic effect may comprise a complete or partial avoidance/inhibition or a delay of inflammation development/progression (such as, for example, a complete or partial avoidance/inhibition or a delay) following administration of a

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therapeutic protocol. Treatment of inflammation encompasses the treatment of subjects already diagnosed as having any form of inflammation at any clinical stage or manifestation, the delay of the onset or evolution or aggravation or deterioration of the symptoms or signs of inflammation, and/or preventing and/or reducing the severity of inflammation.

- 5 The terms “treat”, “treating”, and “treatment” and “prevent”, “preventing”, and “prevention” as used herein referring to glucocorticoid-induced ophthalmic conditions, refer to eliciting the desired biological response, such as a therapeutic and prophylactic effect, respectively. In some embodiments, a therapeutic effect comprises one or more of a decrease/reduction in a glucocorticoid-induced ophthalmic condition, a decrease/reduction in
- 10 the severity of a glucocorticoid-induced ophthalmic condition (such as, for example, a reduction or inhibition of development of a glucocorticoid-induced ophthalmic condition), a decrease/reduction in symptoms and a glucocorticoid-induced ophthalmic condition-related effects, delaying the onset of symptoms and a glucocorticoid-induced ophthalmic condition-related effects, reducing the severity of symptoms of a glucocorticoid-induced ophthalmic
- 15 condition-related effects, reducing the severity of an acute episode, reducing the number of symptoms and a glucocorticoid-induced ophthalmic condition-related effects, reducing the latency of symptoms and a glucocorticoid-induced ophthalmic condition-related effects, an amelioration of symptoms and a glucocorticoid-induced ophthalmic condition-related effects, reducing secondary symptoms, preventing relapse to a glucocorticoid-induced ophthalmic
- 20 condition, decreasing the number or frequency of relapse episodes, increasing latency between symptomatic episodes, increasing time to sustained progression, speeding recovery, and/or increasing efficacy of or decreasing resistance to alternative therapeutics, following administration of the ANGPTL7 inhibitor or composition comprising the ANGPTL7 inhibitor. A prophylactic effect may comprise a complete or partial avoidance/inhibition or a delay of a
- 25 glucocorticoid-induced ophthalmic condition development/progression (such as, for example, a complete or partial avoidance/inhibition or a delay) following administration of an ANGPTL7 inhibitor. Treatment of a glucocorticoid-induced ophthalmic condition encompasses the treatment of subjects already diagnosed as having any form of a glucocorticoid-induced ophthalmic condition at any clinical stage or manifestation, the delay of the onset or evolution
- 30 or aggravation or deterioration of the symptoms or signs of a glucocorticoid-induced ophthalmic condition, and/or preventing and/or reducing the severity of a glucocorticoid-induced ophthalmic condition.

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The present disclosure also provides methods of identifying a subject undergoing glucocorticoid treatment having an increased risk for developing a glucocorticoid-induced ophthalmic condition. In some embodiments, the methods comprise determining or having determined the presence or absence of an ANGPTL7 predicted loss-of-function variant nucleic acid molecule encoding an ANGPTL7 polypeptide in a biological sample obtained from the subject. When the subject is ANGPTL7 reference, then the subject has an increased risk for developing the glucocorticoid-induced ophthalmic condition. When the subject is heterozygous or homozygous for an ANGPTL7 predicted loss-of-function variant, then the subject does not have an increased risk for developing the glucocorticoid-induced ophthalmic condition.

Having a single copy of an ANGPTL7 predicted loss-of-function variant nucleic acid molecule is more protective of a subject undergoing glucocorticoid treatment from developing a glucocorticoid-induced ophthalmic condition than having no copies of an ANGPTL7 predicted loss-of-function variant nucleic acid molecule. Without intending to be limited to any particular theory or mechanism of action, it is believed that a single copy of an ANGPTL7 predicted loss-of-function variant nucleic acid molecule (i.e., heterozygous for an ANGPTL7 predicted loss-of-function variant) is protective of a subject undergoing glucocorticoid treatment from developing a glucocorticoid-induced ophthalmic condition, and it is also believed that having two copies of an ANGPTL7 predicted loss-of-function variant nucleic acid molecule (i.e., homozygous for an ANGPTL7 predicted loss-of-function variant nucleic acid molecule) may be more protective of a subject undergoing glucocorticoid treatment from developing a glucocorticoid-induced ophthalmic condition, relative to a subject with a single copy. Thus, in some embodiments, a single copy of an ANGPTL7 predicted loss-of-function variant nucleic acid molecule may not be completely protective, but instead, may be partially or incompletely protective of a subject undergoing glucocorticoid treatment from developing a glucocorticoid-induced ophthalmic condition. While not desiring to be bound by any particular theory, there may be additional factors or molecules involved in the development of a glucocorticoid-induced ophthalmic condition that are still present in a subject having a single copy of an ANGPTL7 predicted loss-of-function variant nucleic acid molecule, thus resulting in less than complete protection from the development of a glucocorticoid-induced ophthalmic condition.

In some embodiments, the subject can have inflammation. In some embodiments, the inflammation can be acute inflammation or chronic inflammation. In some embodiments, the inflammation is acute inflammation. In some embodiments, the inflammation is chronic

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inflammation. In some embodiments, the inflammation is associated with rheumatoid arthritis, associated with Grave's disease, or is ophthalmic inflammation. In some embodiments, the inflammation is associated with rheumatoid arthritis. In some embodiments, the inflammation is associated with Grave's disease. In some embodiments, the inflammation is ophthalmic

5 inflammation. In some embodiments, the ophthalmic inflammation is chosen from uveitis, juvenile idiopathic arthritis uveitis, scleritis, blepharitis, conjunctivitis, iritis, and episcleritis, or any combination thereof. In some embodiments, the ophthalmic inflammation is uveitis. In some embodiments, the ophthalmic inflammation is juvenile idiopathic arthritis uveitis. In some embodiments, the ophthalmic inflammation is scleritis. In some embodiments, the

10 ophthalmic inflammation is blepharitis. In some embodiments, the ophthalmic inflammation is conjunctivitis. In some embodiments, the ophthalmic inflammation is iritis. In some embodiments, the ophthalmic inflammation is episcleritis.

In some embodiments, the glucocorticoid-induced ophthalmic condition is chosen from ocular hypertension, increased intraocular pressure (IOP), pre-glaucoma, glaucoma,

15 decreased corneal hysteresis, and posterior subcapsular cataracts, or any combination thereof. In some embodiments, the glucocorticoid-induced ophthalmic condition is ocular hypertension. In some embodiments, the glucocorticoid-induced ophthalmic condition is increased IOP. In some embodiments, the glucocorticoid-induced ophthalmic condition is pre-glaucoma. In some embodiments, the glucocorticoid-induced ophthalmic condition is glaucoma. In some

20 embodiments, the glucocorticoid-induced ophthalmic condition is decreased corneal hysteresis. In some embodiments, the glucocorticoid-induced ophthalmic condition is posterior subcapsular cataracts.

In some embodiments, the glucocorticoid treatment is treatment with prednisone, prednisolone, methylprednisolone, dexamethasone, betamethasone, triamcinolone,

25 beclometasone, fludrocortisone acetate, DOCA, aldosterone, budesonide, mometasone furoate, fluticasone propionate, hydrocortisone, cortisone acetate, or fluticasone furoate, difluprednate ophthalmic, fluorometholone, loteprednol etabonate, medrysone, rmexolone, fluocinolone acetonide, clobetasol, halobetasol, diflorasone, fluocinonide, flurandrenolide, Neo-Poly-Dex, tobramycin-dexamethasone, difluprednate, or any combination thereof. In some

30 embodiments, the glucocorticoid treatment is treatment with prednisone. In some embodiments, the glucocorticoid treatment is treatment with prednisolone. In some embodiments, the glucocorticoid treatment is treatment with methylprednisolone. In some

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embodiments, the glucocorticoid treatment is treatment with dexamethasone. In some
embodiments, the glucocorticoid treatment is treatment with betamethasone. In some
embodiments, the glucocorticoid treatment is treatment with triamcinolone. In some
embodiments, the glucocorticoid treatment is treatment with beclomethasone. In some
5 embodiments, the glucocorticoid treatment is treatment with fludrocortisone acetate. In some
embodiments, the glucocorticoid treatment is treatment with DOCA. In some embodiments,
the glucocorticoid treatment is treatment with aldosterone. In some embodiments, the
glucocorticoid treatment is treatment with budesonide. In some embodiments, the
glucocorticoid treatment is treatment with mometasone furoate. In some embodiments, the
10 glucocorticoid treatment is treatment with fluticasone propionate. In some embodiments, the
glucocorticoid treatment is treatment with hydrocortisone. In some embodiments, the
glucocorticoid treatment is treatment with cortisone acetate. In some embodiments, the
glucocorticoid treatment is treatment with fluticasone furoate. In some embodiments, the
glucocorticoid treatment is treatment with difluprednate ophthalmic. In some embodiments,
15 the glucocorticoid treatment is treatment with fluorometholone. In some embodiments, the
glucocorticoid treatment is treatment with loteprednol etabonate. In some embodiments, the
glucocorticoid treatment is treatment with medrysone. In some embodiments, the
glucocorticoid treatment is treatment with rmexolone. In some embodiments, the
glucocorticoid treatment is treatment with fluocinolone acetonide. In some embodiments, the
20 glucocorticoid treatment is treatment with clobetasol. In some embodiments, the
glucocorticoid treatment is treatment with halobetasol. In some embodiments, the
glucocorticoid treatment is treatment with diflorasone. In some embodiments, the
glucocorticoid treatment is treatment with fluocinonide. In some embodiments, the
glucocorticoid treatment is treatment with flurandrenolide. In some embodiments, the
25 glucocorticoid treatment is treatment with Neo-Poly-Dex. In some embodiments, the
glucocorticoid treatment is treatment with tobramycin-dexamethasone. In some embodiments,
the glucocorticoid treatment is treatment with difluprednate.

Determining whether a subject has an ANGPTL7 predicted loss-of-function variant
nucleic acid molecule in a biological sample from the subject and/or determining whether a
30 subject has an ANGPTL7 predicted loss-of-function variant nucleic acid molecule can be carried
out by any of the methods described herein. In some embodiments, these methods can be
carried out *in vitro*. In some embodiments, these methods can be carried out *in situ*. In some

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embodiments, these methods can be carried out *in vivo*. In any of these embodiments, the nucleic acid molecule can be present within a cell obtained from the subject.

In some embodiments, when a subject is identified as having an increased risk of developing a glucocorticoid-induced ophthalmic condition, the subject is further treated with an ANGPTL7 inhibitor, as described herein. For example, when the subject is ANGPTL7
5 reference, and therefore has an increased risk for developing a glucocorticoid-induced ophthalmic condition, the subject is administered an ANGPTL7 inhibitor. In some embodiments, when the subject is heterozygous for an ANGPTL7 predicted loss-of-function variant nucleic acid molecule, the subject is administered an ANGPTL7 inhibitor. In some embodiments, the
10 subject is ANGPTL7 reference. In some embodiments, the subject is heterozygous for an ANGPTL7 predicted loss-of-function variant.

The present disclosure also provides methods of detecting the presence or absence of an ANGPTL7 predicted loss-of-function variant genomic nucleic acid molecule in a biological sample from a subject, and/or an ANGPTL7 predicted loss-of-function variant mRNA molecule
15 in a biological sample from a subject, and/or an ANGPTL7 predicted loss-of-function variant cDNA molecule produced from an mRNA molecule in a biological sample from a subject. It is understood that gene sequences within a population and mRNA molecules encoded by such genes can vary due to polymorphisms such as single-nucleotide polymorphisms. The sequences provided herein for the ANGPTL7 variant genomic nucleic acid molecule, ANGPTL7 variant
20 mRNA molecule, and ANGPTL7 variant cDNA molecule are only exemplary sequences. Other sequences for the ANGPTL7 variant genomic nucleic acid molecule, variant mRNA molecule, and variant cDNA molecule are also possible.

The biological sample can be derived from any cell, tissue, or biological fluid from the subject. The biological sample may comprise any clinically relevant tissue such as, for example,
25 a bone marrow sample, a tumor biopsy, a fine needle aspirate, or a sample of bodily fluid, such as blood, gingival crevicular fluid, plasma, serum, lymph, ascitic fluid, cystic fluid, or urine. In some embodiments, the sample comprises a buccal swab. The biological sample used in the methods disclosed herein can vary based on the assay format, nature of the detection method, and the tissues, cells, or extracts that are used as the sample. A biological sample can be
30 processed differently depending on the assay being employed. For example, when detecting any ANGPTL7 variant nucleic acid molecule, preliminary processing designed to isolate or enrich the biological sample for the ANGPTL7 variant nucleic acid molecule can be employed. A variety

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of techniques may be used for this purpose. When detecting the level of any ANGPTL7 variant mRNA molecule, different techniques can be used to enrich the biological sample with mRNA molecules. Various methods to detect the presence or level of an mRNA molecule or the presence of a particular variant genomic DNA locus can be used.

5 In some embodiments, detecting an ANGPTL7 predicted loss-of-function variant nucleic acid molecule in a subject comprises assaying or analyzing a biological sample obtained from the subject to determine whether an ANGPTL7 genomic nucleic acid molecule in the biological sample, an ANGPTL7 mRNA molecule in the biological sample, and/or an ANGPTL7 cDNA molecule produced from an mRNA molecule in the biological sample, comprises one or
10 more variations that cause a loss-of-function (partial or complete) or are predicted to cause a loss-of-function (partial or complete).

 In some embodiments, the methods of detecting the presence or absence of an ANGPTL7 predicted loss-of-function variant nucleic acid molecule (such as, for example, a genomic nucleic acid molecule, an mRNA molecule, and/or a cDNA molecule produced from an
15 mRNA molecule) in a subject, comprise performing an assay on a biological sample obtained from the subject. The assay determines whether a nucleic acid molecule in the biological sample comprises a particular nucleotide sequence.

 In some embodiments, the nucleotide sequence comprises: a thymine at a position corresponding to position 4,291 according to SEQ ID NO:2 (for genomic nucleic acid molecules);
20 a uracil at a position corresponding to position 529 according to SEQ ID NO:8 (for mRNA molecules); or a thymine at a position corresponding to position 529 according to SEQ ID NO:14 (for cDNA molecules obtained from mRNA molecules).

 In some embodiments, the nucleotide sequence comprises: a thymine at a position corresponding to position 4,287 according to SEQ ID NO:3 (for genomic nucleic acid molecules);
25 a uracil at a position corresponding to position 525 according to SEQ ID NO:9 (for mRNA molecules); or a thymine at a position corresponding to position 525 according to SEQ ID NO:15 (for cDNA molecules obtained from mRNA molecules).

 In some embodiments, the nucleotide sequence comprises: an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4 (for genomic nucleic acid molecules);
30 an adenine at a position corresponding to position 481 according to SEQ ID NO:10 (for mRNA molecules); or an adenine at a position corresponding to position 481 according to SEQ ID NO:16 (for cDNA molecules obtained from mRNA molecules).

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In some embodiments, the nucleotide sequence comprises: an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5 (for genomic nucleic acid molecules); an adenine at a position corresponding to position 563 according to SEQ ID NO:11 (for mRNA molecules); or an adenine at a position corresponding to position 563 according to SEQ ID NO:17 (for cDNA molecules obtained from mRNA molecules).

In some embodiments, the nucleotide sequence comprises: a cytosine at a position corresponding to position 4,336 according to SEQ ID NO:6 (for genomic nucleic acid molecules); a cytosine at a position corresponding to position 574 according to SEQ ID NO:12 (for mRNA molecules); or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18 (for cDNA molecules obtained from mRNA molecules).

In some embodiments, the nucleotide sequence comprises: a thymine at a position corresponding to position 4,291 according to SEQ ID NO:2, or the complement thereof; a thymine at a position corresponding to position 4,287 according to SEQ ID NO:3, or the complement thereof; an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4, or the complement thereof; an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5, or the complement thereof; or a cytosine at a position corresponding to position 4,336 according to SEQ ID NO:6, or the complement thereof.

In some embodiments, the nucleotide sequence comprises: a uracil at a position corresponding to position 529 according to SEQ ID NO:8, or the complement thereof; a uracil at a position corresponding to position 525 according to SEQ ID NO:9, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:10, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:11, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:12, or the complement thereof.

In some embodiments, the nucleotide sequence comprises: a thymine at a position corresponding to position 529 according to SEQ ID NO:14, or the complement thereof; a thymine at a position corresponding to position 525 according to SEQ ID NO:15, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:16, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:17, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18, or the complement thereof.

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In some embodiments, the biological sample comprises a cell or cell lysate. Such methods can further comprise, for example, obtaining a biological sample from the subject comprising an ANGPTL7 genomic nucleic acid molecule or mRNA molecule, and if mRNA, optionally reverse transcribing the mRNA into cDNA. Such assays can comprise, for example
5 determining the identity of these positions of the particular ANGPTL7 nucleic acid molecule. In some embodiments, the method is an *in vitro* method.

In some embodiments, the determining step, detecting step, or sequence analysis comprises sequencing at least a portion of the nucleotide sequence of the ANGPTL7 genomic nucleic acid molecule, the ANGPTL7 mRNA molecule, or the ANGPTL7 cDNA molecule produced
10 from the mRNA molecule in the biological sample, wherein the sequenced portion comprises one or more variations that cause a loss-of-function (partial or complete) or are predicted to cause a loss-of-function (partial or complete).

In some embodiments, the determining step, detecting step, or sequence analysis comprises sequencing at least a portion of: the nucleotide sequence of the ANGPTL7 genomic
15 nucleic acid molecule in the biological sample, wherein the sequenced portion comprises a position corresponding to position 4,291 according to SEQ ID NO:2, or the complement thereof; the nucleotide sequence of the ANGPTL7 mRNA molecule in the biological sample, wherein the sequenced portion comprises a position corresponding to position 529 according to SEQ ID NO:8, or the complement thereof; and/or the nucleotide sequence of the ANGPTL7 cDNA
20 molecule produced from the mRNA in the biological sample, wherein the sequenced portion comprises a position corresponding to position 529 according to SEQ ID NO:14, or the complement thereof. When the sequenced portion of the ANGPTL7 nucleic acid molecule in the biological sample comprises: a thymine at a position corresponding to position 4,291 according to SEQ ID NO:2, a uracil at a position corresponding to position 529 according to SEQ ID NO:8,
25 or a thymine at a position corresponding to position 529 according to SEQ ID NO:14, then the ANGPTL7 nucleic acid molecule in the biological sample is an ANGPTL7 predicted loss-of-function variant nucleic acid molecule.

In some embodiments, the determining step, detecting step, or sequence analysis comprises sequencing at least a portion of: the nucleotide sequence of the ANGPTL7 genomic
30 nucleic acid molecule in the biological sample, wherein the sequenced portion comprises a position corresponding to position 4,287 according to SEQ ID NO:3, or the complement thereof; the nucleotide sequence of the ANGPTL7 mRNA molecule in the biological sample, wherein the

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sequenced portion comprises a position corresponding to position 525 according to SEQ ID NO:9, or the complement thereof; and/or the nucleotide sequence of the ANGPTL7 cDNA molecule produced from the mRNA in the biological sample, wherein the sequenced portion comprises a position corresponding to position 525 according to SEQ ID NO:15, or the
5 complement thereof. When the sequenced portion of the ANGPTL7 nucleic acid molecule in the biological sample comprises: a thymine at a position corresponding to position 4,287 according to SEQ ID NO:3, a uracil at a position corresponding to position 525 according to SEQ ID NO:9, or a thymine at a position corresponding to position 525 according to SEQ ID NO:15, then the ANGPTL7 nucleic acid molecule in the biological sample is an ANGPTL7 predicted loss-of-
10 function variant nucleic acid molecule.

In some embodiments, the determining step, detecting step, or sequence analysis comprises sequencing at least a portion of: the nucleotide sequence of the ANGPTL7 genomic nucleic acid molecule in the biological sample, wherein the sequenced portion comprises a position corresponding to position 4,243 according to SEQ ID NO:4, or the complement thereof;
15 the nucleotide sequence of the ANGPTL7 mRNA molecule in the biological sample, wherein the sequenced portion comprises a position corresponding to position 481 according to SEQ ID NO:10, or the complement thereof; and/or the nucleotide sequence of the ANGPTL7 cDNA molecule produced from the mRNA in the biological sample, wherein the sequenced portion comprises a position corresponding to position 481 according to SEQ ID NO:16, or the
20 complement thereof. When the sequenced portion of the ANGPTL7 nucleic acid molecule in the biological sample comprises: an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4, an adenine at a position corresponding to position 481 according to SEQ ID NO:10, or an adenine at a position corresponding to position 481 according to SEQ ID NO:16, then the ANGPTL7 nucleic acid molecule in the biological sample is an ANGPTL7
25 predicted loss-of-function variant nucleic acid molecule.

In some embodiments, the determining step, detecting step, or sequence analysis comprises sequencing at least a portion of: the nucleotide sequence of the ANGPTL7 genomic nucleic acid molecule in the biological sample, wherein the sequenced portion comprises a position corresponding to position 4,325 according to SEQ ID NO:5, or the complement thereof;
30 the nucleotide sequence of the ANGPTL7 mRNA molecule in the biological sample, wherein the sequenced portion comprises a position corresponding to position 563 according to SEQ ID NO:11, or the complement thereof; and/or the nucleotide sequence of the ANGPTL7 cDNA

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molecule produced from the mRNA in the biological sample, wherein the sequenced portion comprises a position corresponding to position 563 according to SEQ ID NO:17, or the complement thereof. When the sequenced portion of the ANGPTL7 nucleic acid molecule in the biological sample comprises: an adenine at a position corresponding to position 4,325

- 5 according to SEQ ID NO:5, an adenine at a position corresponding to position 563 according to SEQ ID NO:11, or an adenine at a position corresponding to position 563 according to SEQ ID NO:17, then the ANGPTL7 nucleic acid molecule in the biological sample is an ANGPTL7 predicted loss-of-function variant nucleic acid molecule.

- In some embodiments, the determining step, detecting step, or sequence analysis
- 10 comprises sequencing at least a portion of: the nucleotide sequence of the ANGPTL7 genomic nucleic acid molecule in the biological sample, wherein the sequenced portion comprises a position corresponding to position 4,336 according to SEQ ID NO:6, or the complement thereof; the nucleotide sequence of the ANGPTL7 mRNA molecule in the biological sample, wherein the sequenced portion comprises a position corresponding to position 574 according to SEQ ID
- 15 NO:12, or the complement thereof; and/or the nucleotide sequence of the ANGPTL7 cDNA molecule produced from the mRNA in the biological sample, wherein the sequenced portion comprises a position corresponding to position 574 according to SEQ ID NO:18, or the complement thereof. When the sequenced portion of the ANGPTL7 nucleic acid molecule in the biological sample comprises: a cytosine at a position corresponding to position 4,336 according
- 20 to SEQ ID NO:6, a cytosine at a position corresponding to position 574 according to SEQ ID NO:12, or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18, then the ANGPTL7 nucleic acid molecule in the biological sample is an ANGPTL7 predicted loss-of-function variant nucleic acid molecule.

- In some embodiments, the determining step, detecting step, or sequence analysis
- 25 comprises sequencing at least a portion of the nucleotide sequence of the ANGPTL7 genomic nucleic acid molecule in the biological sample, wherein the sequenced portion comprises a position corresponding to: position 4,291 according to SEQ ID NO:2, or the complement thereof; position 4,287 according to SEQ ID NO:3, or the complement thereof; position 4,243 according to SEQ ID NO:4, or the complement thereof; position 4,325 according to SEQ ID NO:5,
- 30 or the complement thereof; or position 4,336 according to SEQ ID NO:6, or the complement thereof. When the sequenced portion of the ANGPTL7 nucleic acid molecule in the biological sample comprises: i) a thymine at a position corresponding to position 4,291 according to SEQ

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ID NO:2, a thymine at a position corresponding to position 4,287 according to SEQ ID NO:3, an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4, an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5, or a cytosine at a position corresponding to position 4,336 according to SEQ ID NO:6, then the ANGPTL7 nucleic acid molecule in the biological sample is an ANGPTL7 predicted loss-of-function variant nucleic acid molecule.

In some embodiments, the determining step, detecting step, or sequence analysis comprises sequencing at least a portion of the nucleotide sequence of the ANGPTL7 mRNA molecule in the biological sample, wherein the sequenced portion comprises a position corresponding to: position 529 according to SEQ ID NO:8, or the complement thereof; position 525 according to SEQ ID NO:9, or the complement thereof; position 481 according to SEQ ID NO:10, or the complement thereof; position 563 according to SEQ ID NO:11, or the complement thereof; or position 574 according to SEQ ID NO:12, or the complement thereof. When the sequenced portion of the ANGPTL7 nucleic acid molecule in the biological sample comprises: a uracil at a position corresponding to position 529 according to SEQ ID NO:8, a uracil at a position corresponding to position 525 according to SEQ ID NO:9, an adenine at a position corresponding to position 481 according to SEQ ID NO:10, an adenine at a position corresponding to position 563 according to SEQ ID NO:11, or a cytosine at a position corresponding to position 574 according to SEQ ID NO:12, then the ANGPTL7 nucleic acid molecule in the biological sample is an ANGPTL7 predicted loss-of-function variant nucleic acid molecule.

In some embodiments, the determining step, detecting step, or sequence analysis comprises sequencing at least a portion of the nucleotide sequence of the ANGPTL7 cDNA molecule produced from the mRNA molecule in the biological sample, wherein the sequenced portion comprises a position corresponding to: position 529 according to SEQ ID NO:14, or the complement thereof; position 525 according to SEQ ID NO:15, or the complement thereof; position 481 according to SEQ ID NO:16, or the complement thereof; position 563 according to SEQ ID NO:17, or the complement thereof; or position 574 according to SEQ ID NO:18, or the complement thereof. When the sequenced portion of the ANGPTL7 nucleic acid molecule in the biological sample comprises: a thymine at a position corresponding to position 529 according to SEQ ID NO:14, a thymine at a position corresponding to position 525 according to SEQ ID NO:15, an adenine at a position corresponding to position 481 according to SEQ ID NO:16, an

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adenine at a position corresponding to position 563 according to SEQ ID NO:17, or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18, then the ANGPTL7 nucleic acid molecule in the biological sample is an ANGPTL7 predicted loss-of-function variant nucleic acid molecule.

5 In some embodiments, the determining step, detecting step, or sequence analysis comprises: a) contacting the biological sample with a primer hybridizing to a portion of the nucleotide sequence of the ANGPTL7: genomic nucleic acid molecule that is proximate to a position corresponding to position 4,291 according to SEQ ID NO:2; mRNA molecule that is proximate to a position corresponding to position 529 according to SEQ ID NO:8; and/or cDNA
10 molecule that is proximate to a position corresponding to position 529 according to SEQ ID NO:14; b) extending the primer at least through the position of the nucleotide sequence of the ANGPTL7: genomic nucleic acid molecule corresponding to position 4,291 according to SEQ ID NO:2; mRNA molecule corresponding to position 529 according to SEQ ID NO:8; and/or cDNA molecule corresponding to position 529 according to SEQ ID NO:14; and c) determining
15 whether the extension product of the primer comprises: a thymine at a position corresponding to position 4,291 according to SEQ ID NO:2, a uracil at a position corresponding to position 529 according to SEQ ID NO:8, and/or a thymine at a position corresponding to position 529 according to SEQ ID NO:14.

 In some embodiments, the determining step, detecting step, or sequence analysis
20 comprises: a) contacting the biological sample with a primer hybridizing to a portion of the nucleotide sequence of the ANGPTL7: genomic nucleic acid molecule that is proximate to a position corresponding to position 4,287 according to SEQ ID NO:3; mRNA molecule that is proximate to a position corresponding to position 525 according to SEQ ID NO:9; and/or cDNA molecule that is proximate to a position corresponding to position 525 according to SEQ ID
25 NO:15; b) extending the primer at least through the position of the nucleotide sequence of the ANGPTL7: genomic nucleic acid molecule corresponding to position 4,287 according to SEQ ID NO:3; mRNA molecule corresponding to position 525 according to SEQ ID NO:9; and/or cDNA molecule corresponding to position 525 according to SEQ ID NO:15; and c) determining whether the extension product of the primer comprises: a thymine at a position corresponding
30 to position 4,287 according to SEQ ID NO:3, a uracil at a position corresponding to position 525 according to SEQ ID NO:9, and/or a thymine at a position corresponding to position 525 according to SEQ ID NO:15.

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In some embodiments, the determining step, detecting step, or sequence analysis comprises: a) contacting the biological sample with a primer hybridizing to a portion of the nucleotide sequence of the ANGPTL7: genomic nucleic acid molecule that is proximate to a position corresponding to position 4,243 according to SEQ ID NO:4; mRNA molecule that is proximate to a position corresponding to position 481 according to SEQ ID NO:10; and/or cDNA molecule that is proximate to a position corresponding to position 481 according to SEQ ID NO:16; b) extending the primer at least through the position of the nucleotide sequence of the ANGPTL7: genomic nucleic acid molecule corresponding to position 4,243 according to SEQ ID NO:4; mRNA molecule corresponding to position 481 according to SEQ ID NO:10; and/or cDNA molecule corresponding to position 481 according to SEQ ID NO:16; and c) determining whether the extension product of the primer comprises: an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4, an adenine at a position corresponding to position 481 according to SEQ ID NO:10, and/or an adenine at a position corresponding to position 481 according to SEQ ID NO:16.

In some embodiments, the determining step, detecting step, or sequence analysis comprises: a) contacting the biological sample with a primer hybridizing to a portion of the nucleotide sequence of the ANGPTL7: genomic nucleic acid molecule that is proximate to a position corresponding to position 4,325 according to SEQ ID NO:5; mRNA molecule that is proximate to a position corresponding to position 563 according to SEQ ID NO:11; and/or cDNA molecule that is proximate to a position corresponding to position 563 according to SEQ ID NO:17; b) extending the primer at least through the position of the nucleotide sequence of the ANGPTL7: genomic nucleic acid molecule corresponding to position 4,325 according to SEQ ID NO:5; mRNA molecule corresponding to position 563 according to SEQ ID NO:11; and/or cDNA molecule corresponding to position 563 according to SEQ ID NO:17; and c) determining whether the extension product of the primer comprises: an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5, an adenine at a position corresponding to position 563 according to SEQ ID NO:11, and/or an adenine at a position corresponding to position 563 according to SEQ ID NO:17.

In some embodiments, the determining step, detecting step, or sequence analysis comprises: a) contacting the biological sample with a primer hybridizing to a portion of the nucleotide sequence of the ANGPTL7: genomic nucleic acid molecule that is proximate to a position corresponding to position 4,336 according to SEQ ID NO:6; mRNA molecule that is

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proximate to a position corresponding to position 574 according to SEQ ID NO:12; and/or cDNA molecule that is proximate to a position corresponding to position 574 according to SEQ ID NO:18; b) extending the primer at least through the position of the nucleotide sequence of the ANGPTL7: genomic nucleic acid molecule corresponding to position 4,336 according to SEQ ID NO:6; mRNA molecule corresponding to position 574 according to SEQ ID NO:12; and/or cDNA molecule corresponding to position 574 according to SEQ ID NO:18; and c) determining whether the extension product of the primer comprises: a cytosine at a position corresponding to position 4,336 according to SEQ ID NO:6, a cytosine at a position corresponding to position 574 according to SEQ ID NO:12, and/or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18.

In some embodiments, the determining step, detecting step, or sequence analysis comprises: a) contacting the biological sample with a primer hybridizing to a portion of the nucleotide sequence of the ANGPTL7 genomic nucleic acid molecule that is proximate to a position corresponding to: position 4,291 according to SEQ ID NO:2, position 4,287 according to SEQ ID NO:3, position 4,243 according to SEQ ID NO:4, position 4,325 according to SEQ ID NO:5, or position 4,336 according to SEQ ID NO:6; b) extending the primer at least through the position of the nucleotide sequence of the ANGPTL7 genomic nucleic acid molecule corresponding to: position 4,291 according to SEQ ID NO:2, position 4,287 according to SEQ ID NO:3, position 4,243 according to SEQ ID NO:4, position 4,325 according to SEQ ID NO:5, or position 4,336 according to SEQ ID NO:6; and c) determining whether the extension product of the primer comprises: a thymine at a position corresponding to position 4,291 according to SEQ ID NO:2, a thymine at a position corresponding to position 4,287 according to SEQ ID NO:3, an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4, an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5, or a cytosine at a position corresponding to position 4,336 according to SEQ ID NO:6.

In some embodiments, the determining step, detecting step, or sequence analysis comprises: a) contacting the biological sample with a primer hybridizing to a portion of the nucleotide sequence of the ANGPTL7 mRNA molecule that is proximate to a position corresponding to: position 529 according to SEQ ID NO:8, position 525 according to SEQ ID NO:9, position 481 according to SEQ ID NO:10; position 563 according to SEQ ID NO:11, or position 574 according to SEQ ID NO:12; b) extending the primer at least through the position of the nucleotide sequence of the ANGPTL7 mRNA molecule corresponding to: position 529

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according to SEQ ID NO:8, position 525 according to SEQ ID NO:9, position 481 according to SEQ ID NO:10, position 563 according to SEQ ID NO:11, or position 574 according to SEQ ID NO:12; and c) determining whether the extension product of the primer comprises: a uracil at a position corresponding to position 529 according to SEQ ID NO:8, a uracil at a position
5 corresponding to position 525 according to SEQ ID NO:9, an adenine at a position corresponding to position 481 according to SEQ ID NO:10, an adenine at a position corresponding to position 563 according to SEQ ID NO:11, or a cytosine at a position corresponding to position 574 according to SEQ ID NO:12.

In some embodiments, the determining step, detecting step, or sequence analysis
10 comprises: a) contacting the biological sample with a primer hybridizing to a portion of the nucleotide sequence of the ANGPTL7 cDNA molecule that is proximate to a position corresponding to: position 529 according to SEQ ID NO:14, position 525 according to SEQ ID NO:15, position 481 according to SEQ ID NO:16, position 563 according to SEQ ID NO:17, or position 574 according to SEQ ID NO:18; b) extending the primer at least through the position
15 of the nucleotide sequence of the ANGPTL7 cDNA molecule corresponding to: position 529 according to SEQ ID NO:14, position 525 according to SEQ ID NO:15, position 481 according to SEQ ID NO:16, position 563 according to SEQ ID NO:17, or position 574 according to SEQ ID NO:18, and c) determining whether the extension product of the primer comprises: a thymine at a position corresponding to position 529 according to SEQ ID NO:14, a thymine at a position
20 corresponding to position 525 according to SEQ ID NO:15, an adenine at a position corresponding to position 481 according to SEQ ID NO:16, an adenine at a position corresponding to position 563 according to SEQ ID NO:17, or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18.

In some embodiments, the assay comprises sequencing the entire nucleic acid
25 molecule. In some embodiments, only an ANGPTL7 genomic nucleic acid molecule is analyzed. In some embodiments, only an ANGPTL7 mRNA is analyzed. In some embodiments, only an ANGPTL7 cDNA obtained from ANGPTL7 mRNA is analyzed.

In some embodiments, the determining step, detecting step, or sequence analysis
30 comprises: a) amplifying at least a portion of the nucleic acid molecule that encodes the ANGPTL7 polypeptide, wherein the amplified portion comprises: a thymine at a position corresponding to position 4,291 according to SEQ ID NO:2, or the complement thereof; a uracil at a position corresponding to position 529 according to SEQ ID NO:8, or the complement

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thereof; and/or a thymine at a position corresponding to position 529 according to SEQ ID NO:14, or the complement thereof; b) labeling the amplified nucleic acid molecule with a detectable label; c) contacting the labeled nucleic acid molecule with a support comprising an alteration-specific probe, wherein the alteration-specific probe comprises a nucleotide
5 sequence which hybridizes under stringent conditions to the nucleic acid sequence of the amplified nucleic acid molecule comprising: a thymine at a position corresponding to position 4,291 according to SEQ ID NO:2, or the complement thereof; a uracil at a position corresponding to position 529 according to SEQ ID NO:8, or the complement thereof; and/or a thymine at a position corresponding to position 529 according to SEQ ID NO:14, or the
10 complement thereof; and d) detecting the detectable label.

In some embodiments, the determining step, detecting step, or sequence analysis comprises: a) amplifying at least a portion of the nucleic acid molecule that encodes the ANGPTL7 polypeptide, wherein the amplified portion comprises: a thymine at a position corresponding to position 4,287 according to SEQ ID NO:3, or the complement thereof; a uracil
15 at a position corresponding to position 525 according to SEQ ID NO:9, or the complement thereof; and/or a thymine at a position corresponding to position 525 according to SEQ ID NO:15, or the complement thereof; b) labeling the amplified nucleic acid molecule with a detectable label; c) contacting the labeled nucleic acid molecule with a support comprising an alteration-specific probe, wherein the alteration-specific probe comprises a nucleotide
20 sequence which hybridizes under stringent conditions to the nucleic acid sequence of the amplified nucleic acid molecule comprising: a thymine at a position corresponding to position 4,287 according to SEQ ID NO:3, or the complement thereof; a uracil at a position corresponding to position 525 according to SEQ ID NO:9, or the complement thereof; and/or a thymine at a position corresponding to position 525 according to SEQ ID NO:15, or the
25 complement thereof; and d) detecting the detectable label.

In some embodiments, the determining step, detecting step, or sequence analysis comprises: a) amplifying at least a portion of the nucleic acid molecule that encodes the ANGPTL7 polypeptide, wherein the amplified portion comprises: an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4, or the complement thereof; an
30 adenine at a position corresponding to position 481 according to SEQ ID NO:10, or the complement thereof; and/or an adenine at a position corresponding to position 481 according to SEQ ID NO:16, or the complement thereof; b) labeling the amplified nucleic acid molecule

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with a detectable label; c) contacting the labeled nucleic acid molecule with a support comprising an alteration-specific probe, wherein the alteration-specific probe comprises a nucleotide sequence which hybridizes under stringent conditions to the nucleic acid sequence of the amplified nucleic acid molecule comprising: an adenine at a position corresponding to
5 position 4,243 according to SEQ ID NO:4, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:10, or the complement thereof; and/or an adenine at a position corresponding to position 481 according to SEQ ID NO:16, or the complement thereof; and d) detecting the detectable label.

In some embodiments, the determining step, detecting step, or sequence analysis
10 comprises: a) amplifying at least a portion of the nucleic acid molecule that encodes the ANGPTL7 polypeptide, wherein the amplified portion comprises: an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:11, or the complement thereof; and/or an adenine at a position corresponding to position 563 according
15 to SEQ ID NO:17, or the complement thereof; b) labeling the amplified nucleic acid molecule with a detectable label; c) contacting the labeled nucleic acid molecule with a support comprising an alteration-specific probe, wherein the alteration-specific probe comprises a nucleotide sequence which hybridizes under stringent conditions to the nucleic acid sequence of the amplified nucleic acid molecule comprising: an adenine at a position corresponding to
20 position 4,325 according to SEQ ID NO:5, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:11, or the complement thereof; and/or an adenine at a position corresponding to position 563 according to SEQ ID NO:17, or the complement thereof; and d) detecting the detectable label.

In some embodiments, the determining step, detecting step, or sequence analysis
25 comprises: a) amplifying at least a portion of the nucleic acid molecule that encodes the ANGPTL7 polypeptide, wherein the amplified portion comprises: a cytosine at a position corresponding to position 4,336 according to SEQ ID NO:6, or the complement thereof; a cytosine at a position corresponding to position 574 according to SEQ ID NO:12, or the complement thereof; and/or a cytosine at a position corresponding to position 574 according
30 to SEQ ID NO:18, or the complement thereof; b) labeling the amplified nucleic acid molecule with a detectable label; c) contacting the labeled nucleic acid molecule with a support comprising an alteration-specific probe, wherein the alteration-specific probe comprises a

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nucleotide sequence which hybridizes under stringent conditions to the nucleic acid sequence of the amplified nucleic acid molecule comprising: a cytosine at a position corresponding to position 4,336 according to SEQ ID NO:6, or the complement thereof; a cytosine at a position corresponding to position 574 according to SEQ ID NO:12, or the complement thereof; and/or a
5 cytosine at a position corresponding to position 574 according to SEQ ID NO:18, or the complement thereof; and d) detecting the detectable label.

In some embodiments, the determining step, detecting step, or sequence analysis comprises: a) amplifying at least a portion of the nucleic acid molecule that encodes the ANGPTL7 polypeptide, wherein the amplified portion comprises: a thymine at a position
10 corresponding to position 4,291 according to SEQ ID NO:2, or the complement thereof; a thymine at a position corresponding to position 4,287 according to SEQ ID NO:3, or the complement thereof; an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4, or the complement thereof; an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5, or the complement thereof; or a cytosine at a position
15 corresponding to position 4,336 according to SEQ ID NO:6, or the complement thereof; b) labeling the amplified nucleic acid molecule with a detectable label; c) contacting the labeled nucleic acid molecule with a support comprising an alteration-specific probe, wherein the alteration-specific probe comprises a nucleotide sequence which hybridizes under stringent conditions to the nucleic acid sequence of the amplified nucleic acid molecule comprising: a
20 thymine at a position corresponding to position 4,291 according to SEQ ID NO:2, or the complement thereof; a thymine at a position corresponding to position 4,287 according to SEQ ID NO:3, or the complement thereof; an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4, or the complement thereof; an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5, or the complement thereof; or a cytosine at a
25 position corresponding to position 4,336 according to SEQ ID NO:6, or the complement thereof; and d) detecting the detectable label.

In some embodiments, the determining step, detecting step, or sequence analysis comprises: a) amplifying at least a portion of the nucleic acid molecule that encodes the ANGPTL7 polypeptide, wherein the amplified portion comprises: a uracil at a position
30 corresponding to position 529 according to SEQ ID NO:8, or the complement thereof; a uracil at a position corresponding to position 525 according to SEQ ID NO:9, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:10, or the

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complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:11, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:12, or the complement thereof; b) labeling the amplified nucleic acid molecule with a detectable label; c) contacting the labeled nucleic acid molecule with a support
5 comprising an alteration-specific probe, wherein the alteration-specific probe comprises a nucleotide sequence which hybridizes under stringent conditions to the nucleic acid sequence of the amplified nucleic acid molecule comprising: a uracil at a position corresponding to position 529 according to SEQ ID NO:8, or the complement thereof; a uracil at a position corresponding to position 525 according to SEQ ID NO:9, or the complement thereof; an
10 adenine at a position corresponding to position 481 according to SEQ ID NO:10, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:11, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:12, or the complement thereof; and d) detecting the detectable label.

In some embodiments, the determining step, detecting step, or sequence analysis
15 comprises: a) amplifying at least a portion of the nucleic acid molecule that encodes the ANGPTL7 polypeptide, wherein the amplified portion comprises: a thymine at a position corresponding to position 529 according to SEQ ID NO:14, or the complement thereof; a thymine at a position corresponding to position 525 according to SEQ ID NO:15, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ
20 ID NO:16, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:17, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18, or the complement thereof; b)
labeling the amplified nucleic acid molecule with a detectable label; c) contacting the labeled nucleic acid molecule with a support comprising an alteration-specific probe, wherein the
25 alteration-specific probe comprises a nucleotide sequence which hybridizes under stringent conditions to the nucleic acid sequence of the amplified nucleic acid molecule comprising: a thymine at a position corresponding to position 529 according to SEQ ID NO:14, or the complement thereof; a thymine at a position corresponding to position 525 according to SEQ ID NO:15, or the complement thereof; an adenine at a position corresponding to position 481
30 according to SEQ ID NO:16, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:17, or the complement thereof; or a cytosine at a

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position corresponding to position 574 according to SEQ ID NO:18, or the complement thereof; and d) detecting the detectable label.

In some embodiments, the nucleic acid molecule is mRNA and the determining step further comprises reverse-transcribing the mRNA into a cDNA prior to the amplifying step.

5 In some embodiments, the determining step, detecting step, or sequence analysis comprises: contacting the nucleic acid molecule in the biological sample with an alteration-specific probe comprising a detectable label, wherein the alteration-specific probe comprises a nucleotide sequence which hybridizes under stringent conditions to the nucleotide sequence of the amplified nucleic acid molecule comprising: a thymine at a position corresponding to
10 position 4,291 according to SEQ ID NO:2, or the complement thereof; a uracil at a position corresponding to position 529 according to SEQ ID NO:8, or the complement thereof; and/or a thymine at a position corresponding to position 529 according to SEQ ID NO:14, or the complement thereof; and detecting the detectable label.

In some embodiments, the determining step, detecting step, or sequence analysis
15 comprises: contacting the nucleic acid molecule in the biological sample with an alteration-specific probe comprising a detectable label, wherein the alteration-specific probe comprises a nucleotide sequence which hybridizes under stringent conditions to the nucleotide sequence of the amplified nucleic acid molecule comprising: a thymine at a position corresponding to position 4,287 according to SEQ ID NO:3, or the complement thereof; a uracil at a position
20 corresponding to position 525 according to SEQ ID NO:9, or the complement thereof; and/or a thymine at a position corresponding to position 525 according to SEQ ID NO:15, or the complement thereof; and detecting the detectable label.

In some embodiments, the determining step, detecting step, or sequence analysis comprises: contacting the nucleic acid molecule in the biological sample with an alteration-
25 specific probe comprising a detectable label, wherein the alteration-specific probe comprises a nucleotide sequence which hybridizes under stringent conditions to the nucleotide sequence of the amplified nucleic acid molecule comprising: an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:10, or the complement thereof; and/or
30 an adenine at a position corresponding to position 481 according to SEQ ID NO:16, or the complement thereof; and detecting the detectable label.

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In some embodiments, the determining step, detecting step, or sequence analysis comprises: contacting the nucleic acid molecule in the biological sample with an alteration-specific probe comprising a detectable label, wherein the alteration-specific probe comprises a nucleotide sequence which hybridizes under stringent conditions to the nucleotide sequence of
5 the amplified nucleic acid molecule comprising: an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:11, or the complement thereof; and/or an adenine at a position corresponding to position 563 according to SEQ ID NO:17, or the complement thereof; and detecting the detectable label.

10 In some embodiments, the determining step, detecting step, or sequence analysis comprises: contacting the nucleic acid molecule in the biological sample with an alteration-specific probe comprising a detectable label, wherein the alteration-specific probe comprises a nucleotide sequence which hybridizes under stringent conditions to the nucleotide sequence of the amplified nucleic acid molecule comprising: a cytosine at a position corresponding to
15 position 4,336 according to SEQ ID NO:6, or the complement thereof; a cytosine at a position corresponding to position 574 according to SEQ ID NO:12, or the complement thereof; and/or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18, or the complement thereof; and detecting the detectable label.

In some embodiments, the determining step, detecting step, or sequence analysis
20 comprises: contacting the nucleic acid molecule in the biological sample with an alteration-specific probe comprising a detectable label, wherein the alteration-specific probe comprises a nucleotide sequence which hybridizes under stringent conditions to the nucleotide sequence of the amplified nucleic acid molecule comprising: a thymine at a position corresponding to position 4,291 according to SEQ ID NO:2, or the complement thereof; a thymine at a position
25 corresponding to position 4,287 according to SEQ ID NO:3, or the complement thereof; an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4, or the complement thereof; an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5, or the complement thereof; or a cytosine at a position corresponding to position 4,336 according to SEQ ID NO:6, or the complement thereof; and detecting the detectable
30 label.

In some embodiments, the determining step, detecting step, or sequence analysis comprises: contacting the nucleic acid molecule in the biological sample with an alteration-

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specific probe comprising a detectable label, wherein the alteration-specific probe comprises a nucleotide sequence which hybridizes under stringent conditions to the nucleotide sequence of the amplified nucleic acid molecule comprising: a uracil at a position corresponding to position 529 according to SEQ ID NO:8, or the complement thereof; a uracil at a position corresponding to position 525 according to SEQ ID NO:9, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:10, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:11, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:12, or the complement thereof; and detecting the detectable label.

10 In some embodiments, the determining step, detecting step, or sequence analysis comprises: contacting the nucleic acid molecule in the biological sample with an alteration-specific probe comprising a detectable label, wherein the alteration-specific probe comprises a nucleotide sequence which hybridizes under stringent conditions to the nucleotide sequence of the amplified nucleic acid molecule comprising: a thymine at a position corresponding to position 529 according to SEQ ID NO:14, or the complement thereof; a thymine at a position corresponding to position 525 according to SEQ ID NO:15, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:16, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:17, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18, or the complement thereof; and detecting the detectable label.

Alteration-specific polymerase chain reaction techniques can be used to detect mutations such as SNPs in a nucleic acid sequence. Alteration-specific primers can be used because the DNA polymerase will not extend when a mismatch with the template is present.

25 In some embodiments, the nucleic acid molecule in the sample is mRNA and the mRNA is reverse-transcribed into a cDNA prior to the amplifying step. In some embodiments, the nucleic acid molecule is present within a cell obtained from the subject.

In some embodiments, the assay comprises contacting the biological sample with a primer or probe, such as an alteration-specific primer or alteration-specific probe, that specifically hybridizes to an ANGPTL7 variant genomic sequence, variant mRNA sequence, or variant cDNA sequence and not the corresponding ANGPTL7 reference sequence under stringent conditions, and determining whether hybridization has occurred.

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In some embodiments, the assay comprises RNA sequencing (RNA-Seq). In some embodiments, the assays also comprise reverse transcribing mRNA into cDNA, such as by the reverse transcriptase polymerase chain reaction (RT-PCR).

In some embodiments, the methods utilize probes and primers of sufficient nucleotide
5 length to bind to the target nucleotide sequence and specifically detect and/or identify a polynucleotide comprising an ANGPTL7 variant genomic nucleic acid molecule, variant mRNA molecule, or variant cDNA molecule. The hybridization conditions or reaction conditions can be determined by the operator to achieve this result. The nucleotide length may be any length
10 that is sufficient for use in a detection method of choice, including any assay described or exemplified herein. Such probes and primers can hybridize specifically to a target nucleotide sequence under high stringency hybridization conditions. Probes and primers may have complete nucleotide sequence identity of contiguous nucleotides within the target nucleotide sequence, although probes differing from the target nucleotide sequence and that retain the ability to specifically detect and/or identify a target nucleotide sequence may be designed by
15 conventional methods. Probes and primers can have about 80%, about 85%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or 100% sequence identity or complementarity with the nucleotide sequence of the target nucleic acid molecule.

In some embodiments, to determine whether an ANGPTL7 nucleic acid molecule
20 (genomic nucleic acid molecule, mRNA molecule, or cDNA molecule), or complement thereof, within a biological sample comprises a nucleotide sequence comprising a thymine at a position corresponding to position 4,291 according to SEQ ID NO:2 (genomic nucleic acid molecule), a uracil at a position corresponding to position 529 according to SEQ ID NO:8 (mRNA molecule), or a thymine at a position corresponding to position 529 according to SEQ ID NO:14 (cDNA
25 molecule), the biological sample can be subjected to an amplification method using a primer pair that includes a first primer derived from the 5' flanking sequence adjacent to a thymine at a position corresponding to position 4,291 according to SEQ ID NO:2, a uracil at a position corresponding to position 529 according to SEQ ID NO:8, or a thymine at a position corresponding to position 529 according to SEQ ID NO:14, and a second primer derived from
30 the 3' flanking sequence adjacent to a thymine at a position corresponding to position 4,291 according to SEQ ID NO:2, a uracil at a position corresponding to position 529 according to SEQ ID NO:8, or a thymine at a position corresponding to position 529 according to SEQ ID NO:14 to

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produce an amplicon that is indicative of the presence of the SNP at positions encoding a thymine at a position corresponding to position 4,291 according to SEQ ID NO:2, a uracil at a position corresponding to position 529 according to SEQ ID NO:8, or a thymine at a position corresponding to position 529 according to SEQ ID NO:14. In some embodiments, the amplicon
5 may range in length from the combined length of the primer pairs plus one nucleotide base pair to any length of amplicon producible by a DNA amplification protocol. This distance can range from one nucleotide base pair up to the limits of the amplification reaction, or about twenty thousand nucleotide base pairs. Optionally, the primer pair flanks a region including positions comprising a thymine at a position corresponding to position 4,291 according to SEQ ID NO:2, a
10 uracil at a position corresponding to position 529 according to SEQ ID NO:8, or a thymine at a position corresponding to position 529 according to SEQ ID NO:14, and at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more nucleotides on each side of positions comprising a thymine at a position corresponding to position 4,291 according to SEQ ID NO:2, a uracil at a position corresponding to position 529 according to SEQ ID NO:8, or a thymine at a position corresponding to position
15 529 according to SEQ ID NO:14.

In some embodiments, to determine whether an ANGPTL7 nucleic acid molecule (genomic nucleic acid molecule, mRNA molecule, or cDNA molecule), or complement thereof, within a biological sample comprises a nucleotide sequence comprising a thymine at a position corresponding to position 4,287 according to SEQ ID NO:3 (genomic nucleic acid molecule), a
20 uracil at a position corresponding to position 525 according to SEQ ID NO:9 (mRNA molecule), or a thymine at a position corresponding to position 525 according to SEQ ID NO:15 (cDNA molecule), the biological sample can be subjected to an amplification method using a primer pair that includes a first primer derived from the 5' flanking sequence adjacent to a thymine at a position corresponding to position 4,287 according to SEQ ID NO:3, a uracil at a position
25 corresponding to position 525 according to SEQ ID NO:9, or a thymine at a position corresponding to position 525 according to SEQ ID NO:15, and a second primer derived from the 3' flanking sequence adjacent to a thymine at a position corresponding to position 4,287 according to SEQ ID NO:3, a uracil at a position corresponding to position 525 according to SEQ ID NO:9, or a thymine at a position corresponding to position 525 according to SEQ ID NO:15 to
30 produce an amplicon that is indicative of the presence of the SNP at positions encoding a thymine at a position corresponding to position 4,287 according to SEQ ID NO:3, a uracil at a position corresponding to position 525 according to SEQ ID NO:9, or a thymine at a position

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corresponding to position 525 according to SEQ ID NO:15. In some embodiments, the amplicon may range in length from the combined length of the primer pairs plus one nucleotide base pair to any length of amplicon producible by a DNA amplification protocol. This distance can range from one nucleotide base pair up to the limits of the amplification reaction, or about twenty
5 thousand nucleotide base pairs. Optionally, the primer pair flanks a region including positions comprising a thymine at a position corresponding to position 4,287 according to SEQ ID NO:3, a uracil at a position corresponding to position 525 according to SEQ ID NO:9, or a thymine at a position corresponding to position 525 according to SEQ ID NO:15, and at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more nucleotides on each side of positions comprising a thymine at a position
10 corresponding to position 4,287 according to SEQ ID NO:3, a uracil at a position corresponding to position 525 according to SEQ ID NO:9, or a thymine at a position corresponding to position 525 according to SEQ ID NO:15.

In some embodiments, to determine whether an ANGPTL7 nucleic acid molecule (genomic nucleic acid molecule, mRNA molecule, or cDNA molecule), or complement thereof,
15 within a biological sample comprises a nucleotide sequence comprising an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4 (genomic nucleic acid molecule), an adenine at a position corresponding to position 481 according to SEQ ID NO:10 (mRNA molecule), or an adenine at a position corresponding to position 481 according to SEQ ID NO:16 (cDNA molecule), the biological sample can be subjected to an amplification method using a
20 primer pair that includes a first primer derived from the 5' flanking sequence adjacent to an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4, an adenine at a position corresponding to position 481 according to SEQ ID NO:10, or an adenine at a position corresponding to position 481 according to SEQ ID NO:16, and a second primer derived from the 3' flanking sequence adjacent to an adenine at a position corresponding to position 4,243
25 according to SEQ ID NO:4, an adenine at a position corresponding to position 481 according to SEQ ID NO:10, or an adenine at a position corresponding to position 481 according to SEQ ID NO:16 to produce an amplicon that is indicative of the presence of the SNP at positions encoding an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4, an adenine at a position corresponding to position 481 according to SEQ ID NO:10, or an adenine
30 at a position corresponding to position 481 according to SEQ ID NO:16. In some embodiments, the amplicon may range in length from the combined length of the primer pairs plus one nucleotide base pair to any length of amplicon producible by a DNA amplification protocol. This

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distance can range from one nucleotide base pair up to the limits of the amplification reaction, or about twenty thousand nucleotide base pairs. Optionally, the primer pair flanks a region including positions comprising an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4, an adenine at a position corresponding to position 481 according to
5 SEQ ID NO:10, or an adenine at a position corresponding to position 481 according to SEQ ID NO:16, and at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more nucleotides on each side of positions comprising an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4, an adenine at a position corresponding to position 481 according to SEQ ID NO:10, or an adenine at a position corresponding to position 481 according to SEQ ID NO:16.

10 In some embodiments, to determine whether an ANGPTL7 nucleic acid molecule (genomic nucleic acid molecule, mRNA molecule, or cDNA molecule), or complement thereof, within a biological sample comprises a nucleotide sequence comprising an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5 (genomic nucleic acid molecule), an adenine at a position corresponding to position 563 according to SEQ ID NO:11 (mRNA
15 molecule), or an adenine at a position corresponding to position 563 according to SEQ ID NO:17 (cDNA molecule), the biological sample can be subjected to an amplification method using a primer pair that includes a first primer derived from the 5' flanking sequence adjacent to an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5, an adenine at a position corresponding to position 563 according to SEQ ID NO:11, or an adenine at a position
20 corresponding to position 563 according to SEQ ID NO:17, and a second primer derived from the 3' flanking sequence adjacent to an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5, an adenine at a position corresponding to position 563 according to SEQ ID NO:11, or an adenine at a position corresponding to position 563 according to SEQ ID NO:17 to produce an amplicon that is indicative of the presence of the SNP at positions
25 encoding an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5, an adenine at a position corresponding to position 563 according to SEQ ID NO:11, or an adenine at a position corresponding to position 563 according to SEQ ID NO:17. In some embodiments, the amplicon may range in length from the combined length of the primer pairs plus one nucleotide base pair to any length of amplicon producible by a DNA amplification protocol. This
30 distance can range from one nucleotide base pair up to the limits of the amplification reaction, or about twenty thousand nucleotide base pairs. Optionally, the primer pair flanks a region including positions comprising an adenine at a position corresponding to position 4,325

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according to SEQ ID NO:5, an adenine at a position corresponding to position 563 according to SEQ ID NO:11, or an adenine at a position corresponding to position 563 according to SEQ ID NO:17, and at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more nucleotides on each side of positions comprising an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5,
5 an adenine at a position corresponding to position 563 according to SEQ ID NO:11, or an adenine at a position corresponding to position 563 according to SEQ ID NO:17.

In some embodiments, to determine whether an ANGPTL7 nucleic acid molecule (genomic nucleic acid molecule, mRNA molecule, or cDNA molecule), or complement thereof, within a biological sample comprises a nucleotide sequence comprising a cytosine at a position
10 corresponding to position 4,336 according to SEQ ID NO:6 (genomic nucleic acid molecule), a cytosine at a position corresponding to position 574 according to SEQ ID NO:12 (mRNA molecule), or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18 (cDNA molecule), the biological sample can be subjected to an amplification method using a primer pair that includes a first primer derived from the 5' flanking sequence adjacent to a
15 cytosine at a position corresponding to position 4,336 according to SEQ ID NO:6, a cytosine at a position corresponding to position 574 according to SEQ ID NO:12, or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18, and a second primer derived from the 3' flanking sequence adjacent to a cytosine at a position corresponding to position 4,336 according to SEQ ID NO:6, a cytosine at a position corresponding to position 574 according to
20 SEQ ID NO:12, or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18 to produce an amplicon that is indicative of the presence of the SNP at positions encoding a cytosine at a position corresponding to position 4,336 according to SEQ ID NO:6, a cytosine at a position corresponding to position 574 according to SEQ ID NO:12, or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18. In some embodiments, the
25 amplicon may range in length from the combined length of the primer pairs plus one nucleotide base pair to any length of amplicon producible by a DNA amplification protocol. This distance can range from one nucleotide base pair up to the limits of the amplification reaction, or about twenty thousand nucleotide base pairs. Optionally, the primer pair flanks a region including positions comprising a cytosine at a position corresponding to position 4,336 according to SEQ
30 ID NO:6, a cytosine at a position corresponding to position 574 according to SEQ ID NO:12, or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18, and at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more nucleotides on each side of positions comprising a cytosine at a

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position corresponding to position 4,336 according to SEQ ID NO:6, a cytosine at a position corresponding to position 574 according to SEQ ID NO:12, or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18.

Similar amplicons can be generated from the mRNA and/or cDNA sequences. PCR primer pairs can be derived from a known sequence, for example, by using computer programs intended for that purpose, such as the PCR primer analysis tool in Vector NTI version 10 (Informax Inc., Bethesda Md.); PrimerSelect (DNASTAR Inc., Madison, Wis.); and Primer3 (Version 0.4.0.COPYRGT., 1991, Whitehead Institute for Biomedical Research, Cambridge, Mass.). Additionally, the sequence can be visually scanned and primers manually identified using known guidelines.

Illustrative examples of nucleic acid sequencing techniques include, but are not limited to, chain terminator (Sanger) sequencing and dye terminator sequencing. Other methods involve nucleic acid hybridization methods other than sequencing, including using labeled primers or probes directed against purified DNA, amplified DNA, and fixed cell preparations (fluorescence in situ hybridization (FISH)). In some methods, a target nucleic acid molecule may be amplified prior to or simultaneous with detection. Illustrative examples of nucleic acid amplification techniques include, but are not limited to, polymerase chain reaction (PCR), ligase chain reaction (LCR), strand displacement amplification (SDA), and nucleic acid sequence based amplification (NASBA). Other methods include, but are not limited to, ligase chain reaction, strand displacement amplification, and thermophilic SDA (tSDA).

In hybridization techniques, stringent conditions can be employed such that a probe or primer will specifically hybridize to its target. In some embodiments, a polynucleotide primer or probe under stringent conditions will hybridize to its target sequence to a detectably greater degree than to other non-target sequences, such as, at least 2-fold, at least 3-fold, at least 4-fold, or more over background, including over 10-fold over background. In some embodiments, a polynucleotide primer or probe under stringent conditions will hybridize to its target nucleotide sequence to a detectably greater degree than to other nucleotide sequences by at least 2-fold. In some embodiments, a polynucleotide primer or probe under stringent conditions will hybridize to its target nucleotide sequence to a detectably greater degree than to other nucleotide sequences by at least 3-fold. In some embodiments, a polynucleotide primer or probe under stringent conditions will hybridize to its target nucleotide sequence to a detectably greater degree than to other nucleotide sequences by at least 4-fold. In some

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embodiments, a polynucleotide primer or probe under stringent conditions will hybridize to its target nucleotide sequence to a detectably greater degree than to other nucleotide sequences by over 10-fold over background. Stringent conditions are sequence-dependent and will be different in different circumstances.

- 5 Appropriate stringency conditions which promote DNA hybridization, for example, 6X sodium chloride/sodium citrate (SSC) at about 45°C., followed by a wash of 2X SSC at 50°C, are known or can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. Typically, stringent conditions for hybridization and detection will be those in which the salt concentration is less than about 1.5 M Na⁺ ion, typically about 0.01 to 1.0 M
- 10 Na⁺ ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (such as, for example, 10 to 50 nucleotides) and at least about 60°C for longer probes (such as, for example, greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. Optionally, wash buffers may comprise about 0.1% to about 1% SDS. Duration of hybridization is generally less
- 15 than about 24 hours, usually about 4 to about 12 hours. The duration of the wash time will be at least a length of time sufficient to reach equilibrium.

- The present disclosure also provides methods of detecting the presence of an ANGPTL7 predicted loss-of-function polypeptide comprising performing an assay on a biological sample obtained from the subject to determine whether an ANGPTL7 polypeptide in the
- 20 subject contains one or more variations that causes the polypeptide to have a loss-of-function (partial or complete) or predicted loss-of-function (partial or complete). The ANGPTL7 predicted loss-of-function polypeptide can be any of the ANGPTL7 variant polypeptides described herein. In some embodiments, the methods detect the presence of ANGPTL7 Arg177STOP, Gln175His, Phe161Ile, Trp188STOP, Lys192Gln, Arg340His, Arg220His, Asn302Lys,
- 25 or Arg220Cys. In some embodiments, the methods detect the presence of ANGPTL7 Arg177STOP, Gln175His, Phe161Ile, Trp188STOP, or Lys192Gln.

- In some embodiments, the methods comprise performing an assay on a sample obtained from a subject to determine whether an ANGPTL7 polypeptide in the sample terminates at position 176 and does not comprise amino acids at positions corresponding to
- 30 positions 177 to 346 according to SEQ ID NO:19. In some embodiments, the methods comprise performing an assay on a sample obtained from a subject to determine whether an ANGPTL7 polypeptide in the sample comprises a histidine at a position corresponding to position 175

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according to SEQ ID NO:21. In some embodiments, the methods comprise performing an assay on a sample obtained from a subject to determine whether an ANGPTL7 polypeptide in the sample comprises an isoleucine at a position corresponding to position 161 according to SEQ ID NO:22. In some embodiments, the methods comprise performing an assay on a sample
5 obtained from a subject to determine whether an ANGPTL7 polypeptide in the sample comprises terminates at position 187 and does not comprise amino acids at positions corresponding to positions 188 to 346 according to SEQ ID NO:19. In some embodiments, the methods comprise performing an assay on a sample obtained from a subject to determine whether an ANGPTL7 polypeptide in the sample comprises a glutamine at a position
10 corresponding to position 192 according to SEQ ID NO:24.

In some embodiments, the determining step comprises sequencing at least a portion of the polypeptide that comprises a position corresponding to position 175 according to SEQ ID NO:21 or SEQ ID NO:19. In some embodiments, the determining step comprises sequencing at least a portion of the polypeptide that comprises a position corresponding to position 161
15 according to SEQ ID NO:22 or SEQ ID NO:19. In some embodiments, the determining step comprises sequencing at least a portion of the polypeptide that comprises a position corresponding to position 192 according to SEQ ID NO:24 or SEQ ID NO:19.

In some embodiments, the determining step comprises sequencing at least a portion of the ANGPTL7 polypeptide that may comprise positions corresponding to any positions that are C-terminal to position 176 according to SEQ ID NO:20. If amino acids are detected in the ANGPTL7 polypeptide at positions corresponding to positions 177 to 346 according to SEQ ID NO:19, then such ANGPTL7 polypeptide is an NGPTL7 reference polypeptide. An absence of positions 177 to 346 according to SEQ ID NO:19 in the ANGPTL7 polypeptide indicates that the ANGPTL7 polypeptide terminates at position 176 according to SEQ ID NO:20 and is an ANGPTL7
25 predicted loss-of-function polypeptide.

In some embodiments, the determining step comprises sequencing at least a portion of the ANGPTL7 polypeptide that may comprise positions corresponding to any positions that are C-terminal to position 187 according to SEQ ID NO:23. If amino acids are detected in the ANGPTL7 polypeptide at positions corresponding to positions 188 to 346 according to SEQ ID
30 NO:19, then such ANGPTL7 polypeptide is an NGPTL7 reference polypeptide. An absence of positions 188 to 346 according to SEQ ID NO:19 in the ANGPTL7 polypeptide indicates that the

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ANGPTL7 polypeptide terminates at position 187 according to SEQ ID NO:23 and is an ANGPTL7 predicted loss-of-function polypeptide.

In some embodiments, the determining step comprises an immunoassay for detecting at least a portion of the polypeptide that comprises a position corresponding to position 175 according to SEQ ID NO:21 or SEQ ID NO:19. In some embodiments, the determining step comprises an immunoassay for detecting at least a portion of the polypeptide that comprises a position corresponding to position 161 according to SEQ ID NO:22 or SEQ ID NO:19. In some embodiments, the determining step comprises an immunoassay for detecting at least a portion of the polypeptide that comprises a position corresponding to position 192 according to SEQ ID NO:24 or SEQ ID NO:19.

In some embodiments, the determining step comprises an immunoassay for detecting at least a portion of the ANGPTL7 polypeptide that may comprise positions corresponding to any positions that are C-terminal to position 176 according to SEQ ID NO:20. If amino acids are detected in the ANGPTL7 polypeptide at positions corresponding to positions 177 to 346 according to SEQ ID NO:19, then such ANGPTL7 polypeptide is an NGPTL7 reference polypeptide. An absence of positions 177 to 346 according to SEQ ID NO:19 in the ANGPTL7 polypeptide indicates that the ANGPTL7 polypeptide terminates at position 176 according to SEQ ID NO:20 and is an ANGPTL7 predicted loss-of-function polypeptide.

In some embodiments, the determining step comprises an immunoassay for detecting at least a portion of the ANGPTL7 polypeptide that may comprise positions corresponding to any positions that are C-terminal to position 187 according to SEQ ID NO:23. If amino acids are detected in the ANGPTL7 polypeptide at positions corresponding to positions 188 to 346 according to SEQ ID NO:19, then such ANGPTL7 polypeptide is an NGPTL7 reference polypeptide. An absence of positions 188 to 346 according to SEQ ID NO:19 in the ANGPTL7 polypeptide indicates that the ANGPTL7 polypeptide terminates at position 187 according to SEQ ID NO:23 and is an ANGPTL7 predicted loss-of-function polypeptide.

In some embodiments, when the subject does not have an ANGPTL7 predicted loss-of-function polypeptide, the subject has an increased risk for developing a glucocorticoid-induced ophthalmic condition. In some embodiments, when the subject has an ANGPTL7 predicted loss-of-function polypeptide, the subject has a decreased risk for developing a glucocorticoid-induced ophthalmic condition.

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The present disclosure also provides isolated nucleic acid molecules that hybridize to ANGPTL7 variant genomic nucleic acid molecules, ANGPTL7 variant mRNA molecules, and/or ANGPTL7 variant cDNA molecules (such as any of the genomic variant nucleic acid molecules, mRNA variant molecules, and cDNA variant molecules disclosed herein). In some embodiments, the isolated nucleic acid molecules hybridize to a portion of the ANGPTL7 nucleic acid molecule that includes a position corresponding to: position 4,291 according to SEQ ID NO:2, position 529 according to SEQ ID NO:8, or position 529 according to SEQ ID NO:14. In some embodiments, the isolated nucleic acid molecules hybridize to a portion of the ANGPTL7 nucleic acid molecule that includes a position corresponding to: position 4,287 according to SEQ ID NO:3, position 525 according to SEQ ID NO:9, or position 525 according to SEQ ID NO:15. In some embodiments, the isolated nucleic acid molecules hybridize to a portion of the ANGPTL7 nucleic acid molecule that includes a position corresponding to: position 4,243 according to SEQ ID NO:4, position 481 according to SEQ ID NO:10, or position 481 according to SEQ ID NO:16. In some embodiments, the isolated nucleic acid molecules hybridize to a portion of the ANGPTL7 nucleic acid molecule that includes a position corresponding to: position 4,325 according to SEQ ID NO:5, position 563 according to SEQ ID NO:11, or position 563 according to SEQ ID NO:17. In some embodiments, the isolated nucleic acid molecules hybridize to a portion of the ANGPTL7 nucleic acid molecule that includes a position corresponding to: position 4,336 according to SEQ ID NO:6, position 574 according to SEQ ID NO:12, or position 574 according to SEQ ID NO:18.

In some embodiments, such isolated nucleic acid molecules comprise or consist of at least about 5, at least about 8, at least about 10, at least about 11, at least about 12, at least about 13, at least about 14, at least about 15, at least about 16, at least about 17, at least about 18, at least about 19, at least about 20, at least about 21, at least about 22, at least about 23, at least about 24, at least about 25, at least about 30, at least about 35, at least about 40, at least about 45, at least about 50, at least about 55, at least about 60, at least about 65, at least about 70, at least about 75, at least about 80, at least about 85, at least about 90, at least about 95, at least about 100, at least about 200, at least about 300, at least about 400, at least about 500, at least about 600, at least about 700, at least about 800, at least about 900, at least about 1000, at least about 2000, at least about 3000, at least about 4000, or at least about 5000 nucleotides. In some embodiments, such isolated nucleic acid molecules comprise or consist of at least about 5, at least about 8, at least about 10, at least about 11, at least about 12, at least about 13, at least about 14, at least about 15, at least about 16, at least about 17, at least about

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18, at least about 19, at least about 20, at least about 21, at least about 22, at least about 23, at least about 24, or at least about 25 nucleotides. In some embodiments, the isolated nucleic acid molecules comprise or consist of at least about 18 nucleotides. In some embodiments, the isolated nucleic acid molecules comprise or consists of at least about 15 nucleotides. In some
5 embodiments, the isolated nucleic acid molecules consist of or comprise from about 10 to about 35, from about 10 to about 30, from about 10 to about 25, from about 12 to about 30, from about 12 to about 28, from about 12 to about 24, from about 15 to about 30, from about 15 to about 25, from about 18 to about 30, from about 18 to about 25, from about 18 to about 24, or from about 18 to about 22 nucleotides. In some
10 embodiments, the isolated nucleic acid molecules consist of or comprise from about 18 to about 30 nucleotides. In some embodiments, the isolated nucleic acid molecules comprise or consist of at least about 15 nucleotides to at least about 35 nucleotides.

 In some embodiments, such isolated nucleic acid molecules hybridize to ANGPTL7 variant nucleic acid molecules (such as genomic nucleic acid molecules, mRNA molecules,
15 and/or cDNA molecules) under stringent conditions. Such nucleic acid molecules can be used, for example, as probes, primers, alteration-specific probes, or alteration-specific primers as described or exemplified herein, and include, without limitation primers, probes, antisense RNAs, shRNAs, and siRNAs, each of which is described in more detail elsewhere herein, and can be used in any of the methods described herein.

20 In some embodiments, the isolated nucleic acid molecules hybridize to at least about 15 contiguous nucleotides of a nucleic acid molecule that is at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or 100% identical to
25 ANGPTL7 variant genomic nucleic acid molecules, ANGPTL7 variant mRNA molecules, and/or ANGPTL7 variant cDNA molecules. In some embodiments, the isolated nucleic acid molecules consist of or comprise from about 15 to about 100 nucleotides, or from about 15 to about 35 nucleotides. In some embodiments, the isolated nucleic acid molecules consist of or comprise from about 15 to about 100 nucleotides. In some embodiments, the isolated nucleic acid molecules consist of or comprise from about 15 to about 35 nucleotides.

30 In some embodiments, the isolated alteration-specific probes or alteration-specific primers comprise at least about 15 nucleotides, wherein the alteration-specific probe or alteration-specific primer comprises a nucleotide sequence which is complementary to a

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portion of a nucleotide sequence encoding an ANGPTL7 polypeptide, wherein the portion comprises a position corresponding to: position 4,291 according to SEQ ID NO:2, or the complement thereof; position 529 according to SEQ ID NO:8, or the complement thereof; or position 529 according to SEQ ID NO:14, or the complement thereof. In some embodiments, the alteration-specific probe or alteration-specific primer comprises a nucleotide sequence which is complementary to a portion of a nucleotide sequence comprising positions corresponding to: positions 4,291 to 4,293 according to SEQ ID NO:2, or the complement thereof; positions 529 to 531 according to SEQ ID NO:8, or the complement thereof; and/or positions 529 to 531 according to SEQ ID NO:14, or the complement thereof.

10 In some embodiments, the isolated alteration-specific probes or alteration-specific primers comprise at least about 15 nucleotides, wherein the alteration-specific probe or alteration-specific primer comprises a nucleotide sequence which is complementary to a portion of a nucleotide sequence encoding an ANGPTL7 polypeptide, wherein the portion comprises a position corresponding to: position 4,287 according to SEQ ID NO:3, or the complement thereof; position 525 according to SEQ ID NO:9, or the complement thereof; or position 525 according to SEQ ID NO:15, or the complement thereof. In some embodiments, the alteration-specific probe or alteration-specific primer comprises a nucleotide sequence which is complementary to a portion of a nucleotide sequence comprising positions corresponding to: positions 4,285 to 4,287 according to SEQ ID NO:3, or the complement thereof; positions 523 to 525 according to SEQ ID NO:9, or the complement thereof; and/or positions 523 to 525 according to SEQ ID NO:15, or the complement thereof.

25 In some embodiments, the isolated alteration-specific probes or alteration-specific primers comprise at least about 15 nucleotides, wherein the alteration-specific probe or alteration-specific primer comprises a nucleotide sequence which is complementary to a portion of a nucleotide sequence encoding an ANGPTL7 polypeptide, wherein the portion comprises a position corresponding to: position 4,243 according to SEQ ID NO:4, or the complement thereof; position 481 according to SEQ ID NO:10, or the complement thereof; or position 481 according to SEQ ID NO:16, or the complement thereof. In some embodiments, the alteration-specific probe or alteration-specific primer comprises a nucleotide sequence which is complementary to a portion of a nucleotide sequence comprising positions corresponding to: positions 4,243 to 4,245 according to SEQ ID NO:4, or the complement

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thereof; positions 481 to 483 according to SEQ ID NO:10, or the complement thereof; and/or positions 481 to 483 according to SEQ ID NO:16, or the complement thereof.

In some embodiments, the isolated alteration-specific probes or alteration-specific primers comprise at least about 15 nucleotides, wherein the alteration-specific probe or alteration-specific primer comprises a nucleotide sequence which is complementary to a portion of a nucleotide sequence encoding an ANGPTL7 polypeptide, wherein the portion comprises a position corresponding to: position 4,325 according to SEQ ID NO:5, or the complement thereof; position 563 according to SEQ ID NO:11, or the complement thereof; or position 563 according to SEQ ID NO:17, or the complement thereof. In some embodiments, the alteration-specific probe or alteration-specific primer comprises a nucleotide sequence which is complementary to a portion of a nucleotide sequence comprising positions corresponding to: positions 4,324 to 4,326 according to SEQ ID NO:5, or the complement thereof; positions 562 to 564 according to SEQ ID NO:11, or the complement thereof; and/or positions 562 to 564 according to SEQ ID NO:17, or the complement thereof.

In some embodiments, the isolated alteration-specific probes or alteration-specific primers comprise at least about 15 nucleotides, wherein the alteration-specific probe or alteration-specific primer comprises a nucleotide sequence which is complementary to a portion of a nucleotide sequence encoding an ANGPTL7 polypeptide, wherein the portion comprises a position corresponding to: position 4,336 according to SEQ ID NO:6, or the complement thereof; position 574 according to SEQ ID NO:12, or the complement thereof; or position 574 according to SEQ ID NO:18, or the complement thereof. In some embodiments, the alteration-specific probe or alteration-specific primer comprises a nucleotide sequence which is complementary to a portion of a nucleotide sequence comprising positions corresponding to: positions 4,336 to 4,338 according to SEQ ID NO:6, or the complement thereof; positions 574 to 576 according to SEQ ID NO:12, or the complement thereof; and/or positions 574 to 576 according to SEQ ID NO:18, or the complement thereof.

In some embodiments, the alteration-specific probes and alteration-specific primers comprise DNA. In some embodiments, the alteration-specific probes and alteration-specific primers comprise RNA.

In some embodiments, the probes and primers described herein (including alteration-specific probes and alteration-specific primers) have a nucleotide sequence that specifically hybridizes to any of the nucleic acid molecules disclosed herein, or the complement thereof. In

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some embodiments, the probes and primers specifically hybridize to any of the nucleic acid molecules disclosed herein under stringent conditions.

In some embodiments, the primers, including alteration-specific primers, can be used in second generation sequencing or high throughput sequencing. In some instances, the primers, including alteration-specific primers, can be modified. In particular, the primers can comprise various modifications that are used at different steps of, for example, Massive Parallel Signature Sequencing (MPSS), Polony sequencing, and 454 Pyrosequencing. Modified primers can be used at several steps of the process, including biotinylated primers in the cloning step and fluorescently labeled primers used at the bead loading step and detection step. Polony sequencing is generally performed using a paired-end tags library wherein each molecule of DNA template is about 135 bp in length. Biotinylated primers are used at the bead loading step and emulsion PCR. Fluorescently labeled degenerate nonamer oligonucleotides are used at the detection step. An adaptor can contain a 5'-biotin tag for immobilization of the DNA library onto streptavidin-coated beads.

The probes and primers described herein can be used to detect a nucleotide variation within any of the ANGPTL7 variant genomic nucleic acid molecules, ANGPTL7 variant mRNA molecules, and/or ANGPTL7 variant cDNA molecules disclosed herein. The primers described herein can be used to amplify the ANGPTL7 variant genomic nucleic acid molecules, ANGPTL7 variant mRNA molecules, or ANGPTL7 variant cDNA molecules, or a fragment thereof.

The present disclosure also provides pairs of primers comprising any of the primers described above. For example, if one of the primers' 3'-ends hybridizes to a cytosine at a position corresponding to position 4,291 according to SEQ ID NO:1 (rather than a thymine) in a particular ANGPTL7 nucleic acid molecule, then the presence of the amplified fragment would indicate the presence of an ANGPTL7 reference genomic nucleic acid molecule. Conversely, if one of the primers' 3'-ends hybridizes to a thymine at a position corresponding to position 4,291 according to SEQ ID NO:2 (rather than a cytosine) in a particular ANGPTL7 nucleic acid molecule, then the presence of the amplified fragment would indicate the presence of the ANGPTL7 variant genomic nucleic acid molecule. In some embodiments, the nucleotide of the primer complementary to the thymine at a position corresponding to position 4,291 according to SEQ ID NO:2 can be at the 3' end of the primer. In addition, if one of the primers' 3'-ends hybridizes to a cytosine at a position corresponding to position 529 according to SEQ ID NO:7 (rather than a uracil) in a particular ANGPTL7 nucleic acid molecule, then the presence of the

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amplified fragment would indicate the presence of an ANGPTL7 reference mRNA molecule. Conversely, if one of the primers' 3'-ends hybridizes to a uracil at a position corresponding to position 529 according to SEQ ID NO:8 (rather than a cytosine) in a particular ANGPTL7 mRNA molecule, then the presence of the amplified fragment would indicate the presence of the

5 ANGPTL7 variant mRNA molecule. In some embodiments, the nucleotide of the primer complementary to the uracil at a position corresponding to position 529 according to SEQ ID NO:8 can be at the 3' end of the primer. In addition, if one of the primers' 3'-ends hybridizes to a cytosine at a position corresponding to position 529 according to SEQ ID NO:13 (rather than a thymine) in a particular ANGPTL7 nucleic acid molecule, then the presence of the amplified

10 fragment would indicate the presence of an ANGPTL7 reference cDNA molecule. Conversely, if one of the primers' 3'-ends hybridizes to a thymine at a position corresponding to position 529 according to SEQ ID NO:14 (rather than a cytosine) in a particular ANGPTL7 cDNA molecule, then the presence of the amplified fragment would indicate the presence of the ANGPTL7 variant cDNA molecule. In some embodiments, the nucleotide of the primer complementary to

15 the thymine at a position corresponding to position 529 according to SEQ ID NO:14 can be at the 3' end of the primer.

The present disclosure also provides pairs of primers comprising any of the primers described above. For example, if one of the primers' 3'-ends hybridizes to a guanine at a position corresponding to position 4,287 according to SEQ ID NO:1 (rather than a thymine) in a

20 particular ANGPTL7 nucleic acid molecule, then the presence of the amplified fragment would indicate the presence of an ANGPTL7 reference genomic nucleic acid molecule. Conversely, if one of the primers' 3'-ends hybridizes to a thymine at a position corresponding to position 4,287 according to SEQ ID NO:3 (rather than a guanine) in a particular ANGPTL7 nucleic acid molecule, then the presence of the amplified fragment would indicate the presence of the

25 ANGPTL7 variant genomic nucleic acid molecule. In some embodiments, the nucleotide of the primer complementary to the thymine at a position corresponding to position 4,287 according to SEQ ID NO:3 can be at the 3' end of the primer. In addition, if one of the primers' 3'-ends hybridizes to a guanine at a position corresponding to position 525 according to SEQ ID NO:7 (rather than a uracil) in a particular ANGPTL7 nucleic acid molecule, then the presence of the

30 amplified fragment would indicate the presence of an ANGPTL7 reference mRNA molecule. Conversely, if one of the primers' 3'-ends hybridizes to a uracil at a position corresponding to position 525 according to SEQ ID NO:9 (rather than a guanine) in a particular ANGPTL7 mRNA

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molecule, then the presence of the amplified fragment would indicate the presence of the ANGPTL7 variant mRNA molecule. In some embodiments, the nucleotide of the primer complementary to the uracil at a position corresponding to position 525 according to SEQ ID NO:9 can be at the 3' end of the primer. In addition, if one of the primers' 3'-ends hybridizes to a guanine at a position corresponding to position 525 according to SEQ ID NO:13 (rather than a thymine) in a particular ANGPTL7 nucleic acid molecule, then the presence of the amplified fragment would indicate the presence of an ANGPTL7 reference cDNA molecule. Conversely, if one of the primers' 3'-ends hybridizes to a thymine at a position corresponding to position 525 according to SEQ ID NO:15 (rather than a guanine) in a particular ANGPTL7 cDNA molecule, then the presence of the amplified fragment would indicate the presence of the ANGPTL7 variant cDNA molecule. In some embodiments, the nucleotide of the primer complementary to the thymine at a position corresponding to position 525 according to SEQ ID NO:15 can be at the 3' end of the primer.

The present disclosure also provides pairs of primers comprising any of the primers described above. For example, if one of the primers' 3'-ends hybridizes to a thymine at a position corresponding to position 4,243 according to SEQ ID NO:1 (rather than an adenine) in a particular ANGPTL7 nucleic acid molecule, then the presence of the amplified fragment would indicate the presence of an ANGPTL7 reference genomic nucleic acid molecule. Conversely, if one of the primers' 3'-ends hybridizes to an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4 (rather than a thymine) in a particular ANGPTL7 nucleic acid molecule, then the presence of the amplified fragment would indicate the presence of the ANGPTL7 variant genomic nucleic acid molecule. In some embodiments, the nucleotide of the primer complementary to the adenine at a position corresponding to position 4,243 according to SEQ ID NO:4 can be at the 3' end of the primer. In addition, if one of the primers' 3'-ends hybridizes to a uracil at a position corresponding to position 481 according to SEQ ID NO:7 (rather than an adenine) in a particular ANGPTL7 nucleic acid molecule, then the presence of the amplified fragment would indicate the presence of an ANGPTL7 reference mRNA molecule. Conversely, if one of the primers' 3'-ends hybridizes to an adenine at a position corresponding to position 481 according to SEQ ID NO:10 (rather than a uracil) in a particular ANGPTL7 mRNA molecule, then the presence of the amplified fragment would indicate the presence of the ANGPTL7 variant mRNA molecule. In some embodiments, the nucleotide of the primer complementary to the adenine at a position corresponding to position 481 according to SEQ ID

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NO:10 can be at the 3' end of the primer. In addition, if one of the primers' 3'-ends hybridizes to a thymine at a position corresponding to position 481 according to SEQ ID NO:13 (rather than an adenine) in a particular ANGPTL7 nucleic acid molecule, then the presence of the amplified fragment would indicate the presence of an ANGPTL7 reference cDNA molecule.

- 5 Conversely, if one of the primers' 3'-ends hybridizes to an adenine at a position corresponding to position 481 according to SEQ ID NO:16 (rather than a thymine) in a particular ANGPTL7 cDNA molecule, then the presence of the amplified fragment would indicate the presence of the ANGPTL7 variant cDNA molecule. In some embodiments, the nucleotide of the primer complementary to the adenine at a position corresponding to position 481 according to SEQ ID
10 NO:16 can be at the 3' end of the primer.

- The present disclosure also provides pairs of primers comprising any of the primers described above. For example, if one of the primers' 3'-ends hybridizes to a guanine at a position corresponding to position 4,325 according to SEQ ID NO:1 (rather than an adenine) in a particular ANGPTL7 nucleic acid molecule, then the presence of the amplified fragment would
15 indicate the presence of an ANGPTL7 reference genomic nucleic acid molecule. Conversely, if one of the primers' 3'-ends hybridizes to an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5 (rather than a guanine) in a particular ANGPTL7 nucleic acid molecule, then the presence of the amplified fragment would indicate the presence of the ANGPTL7 variant genomic nucleic acid molecule. In some embodiments, the nucleotide of the
20 primer complementary to the adenine at a position corresponding to position 4,325 according to SEQ ID NO:5 can be at the 3' end of the primer. In addition, if one of the primers' 3'-ends hybridizes to a guanine at a position corresponding to position 563 according to SEQ ID NO:7 (rather than an adenine) in a particular ANGPTL7 nucleic acid molecule, then the presence of the amplified fragment would indicate the presence of an ANGPTL7 reference mRNA molecule.
25 Conversely, if one of the primers' 3'-ends hybridizes to an adenine at a position corresponding to position 563 according to SEQ ID NO:11 (rather than a guanine) in a particular ANGPTL7 mRNA molecule, then the presence of the amplified fragment would indicate the presence of the ANGPTL7 variant mRNA molecule. In some embodiments, the nucleotide of the primer complementary to the adenine at a position corresponding to position 563 according to SEQ ID
30 NO:11 can be at the 3' end of the primer. In addition, if one of the primers' 3'-ends hybridizes to a guanine at a position corresponding to position 563 according to SEQ ID NO:13 (rather than an adenine) in a particular ANGPTL7 nucleic acid molecule, then the presence of the amplified

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fragment would indicate the presence of an ANGPTL7 reference cDNA molecule. Conversely, if one of the primers' 3'-ends hybridizes to an adenine at a position corresponding to position 563 according to SEQ ID NO:17 (rather than a guanine) in a particular ANGPTL7 cDNA molecule, then the presence of the amplified fragment would indicate the presence of the ANGPTL7
5 variant cDNA molecule. In some embodiments, the nucleotide of the primer complementary to the adenine at a position corresponding to position 563 according to SEQ ID NO:17 can be at the 3' end of the primer.

The present disclosure also provides pairs of primers comprising any of the primers described above. For example, if one of the primers' 3'-ends hybridizes to an adenine at a
10 position corresponding to position 4,336 according to SEQ ID NO:1 (rather than a cytosine) in a particular ANGPTL7 nucleic acid molecule, then the presence of the amplified fragment would indicate the presence of an ANGPTL7 reference genomic nucleic acid molecule. Conversely, if one of the primers' 3'-ends hybridizes to a cytosine at a position corresponding to position 4,336 according to SEQ ID NO:6 (rather than an adenine) in a particular ANGPTL7 nucleic acid
15 molecule, then the presence of the amplified fragment would indicate the presence of the ANGPTL7 variant genomic nucleic acid molecule. In some embodiments, the nucleotide of the primer complementary to the cytosine at a position corresponding to position 4,336 according to SEQ ID NO:6 can be at the 3' end of the primer. In addition, if one of the primers' 3'-ends hybridizes to an adenine at a position corresponding to position 574 according to SEQ ID NO:7
20 (rather than a cytosine) in a particular ANGPTL7 nucleic acid molecule, then the presence of the amplified fragment would indicate the presence of an ANGPTL7 reference mRNA molecule. Conversely, if one of the primers' 3'-ends hybridizes to a cytosine at a position corresponding to position 574 according to SEQ ID NO:12 (rather than an adenine) in a particular ANGPTL7 mRNA molecule, then the presence of the amplified fragment would indicate the presence of the
25 ANGPTL7 variant mRNA molecule. In some embodiments, the nucleotide of the primer complementary to the cytosine at a position corresponding to position 574 according to SEQ ID NO:12 can be at the 3' end of the primer. In addition, if one of the primers' 3'-ends hybridizes to an adenine at a position corresponding to position 574 according to SEQ ID NO:13 (rather than a cytosine) in a particular ANGPTL7 nucleic acid molecule, then the presence of the
30 amplified fragment would indicate the presence of an ANGPTL7 reference cDNA molecule. Conversely, if one of the primers' 3'-ends hybridizes to a cytosine at a position corresponding to position 574 according to SEQ ID NO:18 (rather than an adenine) in a particular ANGPTL7 cDNA

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molecule, then the presence of the amplified fragment would indicate the presence of the ANGPTL7 variant cDNA molecule. In some embodiments, the nucleotide of the primer complementary to the cytosine at a position corresponding to position 574 according to SEQ ID NO:18 can be at the 3' end of the primer.

5 In the context of the present disclosure "specifically hybridizes" means that the probe or primer (such as, for example, the alteration-specific probe or alteration-specific primer) does not hybridize to a nucleic acid sequence encoding an ANGPTL7 reference genomic nucleic acid molecule, an ANGPTL7 reference mRNA molecule, and/or an ANGPTL7 reference cDNA molecule.

10 In some embodiments, the probes (such as, for example, an alteration-specific probe) comprise a label. In some embodiments, the label is a fluorescent label, a radiolabel, or biotin.

 The present disclosure also provides supports comprising a substrate to which any one or more of the probes disclosed herein is attached. Solid supports are solid-state substrates or supports with which molecules, such as any of the probes disclosed herein, can be associated. A
15 form of solid support is an array. Another form of solid support is an array detector. An array detector is a solid support to which multiple different probes have been coupled in an array, grid, or other organized pattern. A form for a solid-state substrate is a microtiter dish, such as a standard 96-well type. In some embodiments, a multiwell glass slide can be employed that normally contains one array per well.

20 The nucleotide sequence of an ANGPTL7 reference genomic nucleic acid molecule is set forth in SEQ ID NO:1. Referring to SEQ ID NO:1, position 4,291 is a cytosine. Referring to SEQ ID NO:1, position 4,287 is a guanine. Referring to SEQ ID NO:1, position 4,243 is a thymine. Referring to SEQ ID NO:1, position 4,325 is a guanine. Referring to SEQ ID NO:1, position 4,336 is an adenine.

25 A variant genomic nucleic acid molecule of ANGPTL7 exists, wherein the cytosine at position 4,291 is replaced with a thymine. The nucleotide sequence of this ANGPTL7 variant genomic nucleic acid molecule is set forth in SEQ ID NO:2.

 Another variant genomic nucleic acid molecule of ANGPTL7 exists, wherein the guanine at position 4,287 is replaced with a thymine. The nucleotide sequence of this ANGPTL7
30 variant genomic nucleic acid molecule is set forth in SEQ ID NO:3.

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Another variant genomic nucleic acid molecule of ANGPTL7 exists, wherein the thymine at position 4,243 is replaced with an adenine. The nucleotide sequence of this ANGPTL7 variant genomic nucleic acid molecule is set forth in SEQ ID NO:4.

Another variant genomic nucleic acid molecule of ANGPTL7 exists, wherein the
5 guanine at position 4,325 is replaced with an adenine. The nucleotide sequence of this ANGPTL7 variant genomic nucleic acid molecule is set forth in SEQ ID NO:5.

Another variant genomic nucleic acid molecule of ANGPTL7 exists, wherein the adenine at position 4,336 is replaced with a cytosine. The nucleotide sequence of this ANGPTL7 variant genomic nucleic acid molecule is set forth in SEQ ID NO:6.

10 The nucleotide sequence of an ANGPTL7 reference mRNA molecule is set forth in SEQ ID NO:7. Referring to SEQ ID NO:7, position 529 is a cytosine. Referring to SEQ ID NO:7, position 525 is a guanine. Referring to SEQ ID NO:7, position 481 is a uracil. Referring to SEQ ID NO:7, position 563 is a guanine. Referring to SEQ ID NO:7, position 574 is an adenine.

A variant mRNA molecule of ANGPTL7 exists, wherein the cytosine at position 529 is
15 replaced with a uracil. The nucleotide sequence of this ANGPTL7 variant mRNA molecule is set forth in SEQ ID NO:8.

Another variant mRNA molecule of ANGPTL7 exists, wherein the guanine at position 525 is replaced with a uracil. The nucleotide sequence of this ANGPTL7 variant mRNA molecule is set forth in SEQ ID NO:9.

20 Another variant mRNA molecule of ANGPTL7 exists, wherein the uracil at position 481 is replaced with an adenine. The nucleotide sequence of this ANGPTL7 variant mRNA molecule is set forth in SEQ ID NO:10.

Another variant mRNA molecule of ANGPTL7 exists, wherein the guanine at position 563 is replaced with an adenine. The nucleotide sequence of this ANGPTL7 variant mRNA
25 molecule is set forth in SEQ ID NO:11.

Another variant mRNA molecule of ANGPTL7 exists, wherein the adenine at position 574 is replaced with a cytosine. The nucleotide sequence of this ANGPTL7 variant mRNA molecule is set forth in SEQ ID NO:12.

The nucleotide sequence of an ANGPTL7 reference cDNA molecule is set forth in SEQ
30 ID NO:13. Referring to SEQ ID NO:13, position 529 is a cytosine. Referring to SEQ ID NO:13, position 525 is a guanine. Referring to SEQ ID NO:13, position 481 is a thymine. Referring to

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SEQ ID NO:13, position 563 is a guanine. Referring to SEQ ID NO:13, position 574 is an adenine. Referring to SEQ ID NO:13, position 574 is an adenine.

A variant cDNA molecule of ANGPTL7 exists, wherein the cytosine at position 529 is replaced with a thymine. The nucleotide sequence of this ANGPTL7 variant cDNA molecule is set forth in SEQ ID NO:14.

Another variant cDNA molecule of ANGPTL7 exists, wherein the guanine at position 525 is replaced with a thymine. The nucleotide sequence of this ANGPTL7 variant cDNA molecule is set forth in SEQ ID NO:15.

Another variant cDNA molecule of ANGPTL7 exists, wherein the thymine at position 481 is replaced with an adenine. The nucleotide sequence of this ANGPTL7 variant cDNA molecule is set forth in SEQ ID NO:16.

Another variant cDNA molecule of ANGPTL7 exists, wherein the guanine at position 563 is replaced with an adenine. The nucleotide sequence of this ANGPTL7 variant cDNA molecule is set forth in SEQ ID NO:17.

Another variant cDNA molecule of ANGPTL7 exists, wherein the adenine at position 574 is replaced with a cytosine. The nucleotide sequence of this ANGPTL7 variant cDNA molecule is set forth in SEQ ID NO:18.

The genomic nucleic acid molecules, mRNA molecules, and cDNA molecules can be from any organism. For example, the genomic nucleic acid molecules, mRNA molecules, and cDNA molecules can be human or an ortholog from another organism, such as a non-human mammal, a rodent, a mouse, or a rat. It is understood that gene sequences within a population can vary due to polymorphisms such as single-nucleotide polymorphisms. The examples provided herein are only exemplary sequences. Other sequences are also possible.

Also provided herein are functional polynucleotides that can interact with the disclosed nucleic acid molecules. Examples of functional polynucleotides include, but are not limited to, antisense molecules, aptamers, ribozymes, triplex forming molecules, and external guide sequences. The functional polynucleotides can act as effectors, inhibitors, modulators, and stimulators of a specific activity possessed by a target molecule, or the functional polynucleotides can possess a *de novo* activity independent of any other molecules.

The isolated nucleic acid molecules disclosed herein can comprise RNA, DNA, or both RNA and DNA. The isolated nucleic acid molecules can also be linked or fused to a heterologous nucleic acid sequence, such as in a vector, or a heterologous label. For example, the isolated

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nucleic acid molecules disclosed herein can be within a vector or as an exogenous donor sequence comprising the isolated nucleic acid molecule and a heterologous nucleic acid sequence. The isolated nucleic acid molecules can also be linked or fused to a heterologous label. The label can be directly detectable (such as, for example, fluorophore) or indirectly
5 detectable (such as, for example, hapten, enzyme, or fluorophore quencher). Such labels can be detectable by spectroscopic, photochemical, biochemical, immunochemical, or chemical means. Such labels include, for example, radiolabels, pigments, dyes, chromogens, spin labels, and fluorescent labels. The label can also be, for example, a chemiluminescent substance; a metal-containing substance; or an enzyme, where there occurs an enzyme-dependent
10 secondary generation of signal. The term "label" can also refer to a "tag" or hapten that can bind selectively to a conjugated molecule such that the conjugated molecule, when added subsequently along with a substrate, is used to generate a detectable signal. For example, biotin can be used as a tag along with an avidin or streptavidin conjugate of horseradish peroxidase (HRP) to bind to the tag, and examined using a calorimetric substrate (such as, for
15 example, tetramethylbenzidine (TMB)) or a fluorogenic substrate to detect the presence of HRP. Exemplary labels that can be used as tags to facilitate purification include, but are not limited to, myc, HA, FLAG or 3XFLAG, 6XHis or polyhistidine, glutathione-S-transferase (GST), maltose binding protein, an epitope tag, or the Fc portion of immunoglobulin. Numerous labels include, for example, particles, fluorophores, haptens, enzymes and their calorimetric,
20 fluorogenic and chemiluminescent substrates and other labels.

The disclosed nucleic acid molecules can comprise, for example, nucleotides or non-natural or modified nucleotides, such as nucleotide analogs or nucleotide substitutes. Such nucleotides include a nucleotide that contains a modified base, sugar, or phosphate group, or that incorporates a non-natural moiety in its structure. Examples of non-natural nucleotides
25 include, but are not limited to, dideoxynucleotides, biotinylated, aminated, deaminated, alkylated, benzylated, and fluorophore-labeled nucleotides.

The nucleic acid molecules disclosed herein can also comprise one or more nucleotide analogs or substitutions. A nucleotide analog is a nucleotide which contains a modification to either the base, sugar, or phosphate moieties. Modifications to the base moiety include, but
30 are not limited to, natural and synthetic modifications of A, C, G, and T/U, as well as different purine or pyrimidine bases such as, for example, pseudouridine, uracil-5-yl, hypoxanthin-9-yl (I), and 2-aminoadenin-9-yl. Modified bases include, but are not limited to, 5-methylcytosine (5-

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me-C), 5-hydroxymethyl cytosine, xanthine, hypoxanthine, 2-aminoadenine, 6-methyl and other alkyl derivatives of adenine and guanine, 2-propyl and other alkyl derivatives of adenine and guanine, 2-thiouracil, 2-thiothymine and 2-thiocytosine, 5-halouracil and cytosine, 5-propynyl uracil and cytosine, 6-azo uracil, cytosine and thymine, 5-uracil (pseudouracil), 4-thiouracil, 8-halo, 8-amino, 8-thiol, 8-thioalkyl, 8-hydroxyl and other 8-substituted adenines and guanines, 5-halo (such as, for example, 5-bromo), 5-trifluoromethyl and other 5-substituted uracils and cytosines, 7-methylguanine, 7-methyladenine, 8-azaguanine, 8-azaadenine, 7-deazaguanine, 7-deazaadenine, 3-deazaguanine, and 3-deazaadenine.

10 Nucleotide analogs can also include modifications of the sugar moiety. Modifications to the sugar moiety include, but are not limited to, natural modifications of the ribose and deoxy ribose as well as synthetic modifications. Sugar modifications include, but are not limited to, the following modifications at the 2' position: OH; F; O-, S-, or N-alkyl; O-, S-, or N-alkenyl; O-, S- or N-alkynyl; or O-alkyl-O-alkyl, wherein the alkyl, alkenyl, and alkynyl may be substituted or
15 unsubstituted C₁₋₁₀alkyl or C₂₋₁₀alkenyl, and C₂₋₁₀alkynyl. Exemplary 2' sugar modifications also include, but are not limited to, -O[(CH₂)_nO]_mCH₃, -O(CH₂)_nOCH₃, -O(CH₂)_nNH₂, -O(CH₂)_nCH₃, -O(CH₂)_n-ONH₂, and -O(CH₂)_nON[(CH₂)_nCH₃]₂, where n and m, independently, are from 1 to about 10. Other modifications at the 2' position include, but are not limited to, C₁₋₁₀alkyl, substituted lower alkyl, alkaryl, aralkyl,
20 O-alkaryl or O-aralkyl, SH, SCH₃, OCN, Cl, Br, CN, CF₃, OCF₃, SOCH₃, SO₂CH₃, ONO₂, NO₂, N₃, NH₂, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, an RNA cleaving group, a reporter group, an intercalator, a group for improving the pharmacokinetic properties of an oligonucleotide, or a group for improving the pharmacodynamic properties of an oligonucleotide, and other substituents having similar properties. Similar modifications may
25 also be made at other positions on the sugar, particularly the 3' position of the sugar on the 3' terminal nucleotide or in 2'-5' linked oligonucleotides and the 5' position of 5' terminal nucleotide. Modified sugars can also include those that contain modifications at the bridging ring oxygen, such as CH₂ and S. Nucleotide sugar analogs can also have sugar mimetics, such as cyclobutyl moieties in place of the pentofuranosyl sugar.

30 Nucleotide analogs can also be modified at the phosphate moiety. Modified phosphate moieties include, but are not limited to, those that can be modified so that the linkage between two nucleotides contains a phosphorothioate, chiral phosphorothioate, phosphorodithioate,

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phosphotriester, aminoalkylphosphotriester, methyl and other alkyl phosphonates including 3'-alkylene phosphonate and chiral phosphonates, phosphinates, phosphoramidates including 3'-amino phosphoramidate and aminoalkylphosphoramidates, thionophosphoramidates, thionoalkylphosphonates, thionoalkylphosphotriesters, and boranophosphates. These
5 phosphate or modified phosphate linkage between two nucleotides can be through a 3'-5' linkage or a 2'-5' linkage, and the linkage can contain inverted polarity such as 3'-5' to 5'-3' or 2'-5' to 5'-2'. Various salts, mixed salts, and free acid forms are also included. Nucleotide substitutes also include peptide nucleic acids (PNAs).

The present disclosure also provides vectors comprising any one or more of the nucleic
10 acid molecules disclosed herein. In some embodiments, the vectors comprise any one or more of the nucleic acid molecules disclosed herein and a heterologous nucleic acid. The vectors can be viral or nonviral vectors capable of transporting a nucleic acid molecule. In some embodiments, the vector is a plasmid or cosmid (such as, for example, a circular double-stranded DNA into which additional DNA segments can be ligated). In some embodiments, the
15 vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Expression vectors include, but are not limited to, plasmids, cosmids, retroviruses, adenoviruses, adeno-associated viruses (AAV), plant viruses such as cauliflower mosaic virus and tobacco mosaic virus, yeast artificial chromosomes (YACs), Epstein-Barr (EBV)-derived episomes, and other expression vectors known in the art.

Desired regulatory sequences for mammalian host cell expression can include, for
20 example, viral elements that direct high levels of polypeptide expression in mammalian cells, such as promoters and/or enhancers derived from retroviral LTRs, cytomegalovirus (CMV) (such as, for example, CMV promoter/enhancer), Simian Virus 40 (SV40) (such as, for example, SV40 promoter/enhancer), adenovirus, (such as, for example, the adenovirus major late promoter
25 (AdMLP)), polyoma and strong mammalian promoters such as native immunoglobulin and actin promoters. Methods of expressing polypeptides in bacterial cells or fungal cells (such as, for example, yeast cells) are also well known. A promoter can be, for example, a constitutively active promoter, a conditional promoter, an inducible promoter, a temporally restricted promoter (such as, for example, a developmentally regulated promoter), or a spatially
30 restricted promoter (such as, for example, a cell-specific or tissue-specific promoter).

Percent identity (or percent complementarity) between particular stretches of nucleotide sequences within nucleic acid molecules or amino acid sequences within

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polypeptides can be determined routinely using BLAST programs (basic local alignment search tools) and PowerBLAST programs (Altschul et al., J. Mol. Biol., 1990, 215, 403-410; Zhang and Madden, Genome Res., 1997, 7, 649-656) or by using the Gap program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, Madison Wis.), using default settings, which uses the algorithm of Smith and Waterman (Adv. Appl. Math., 1981, 2, 482-489). Herein, if reference is made to percent sequence identity, the higher percentages of sequence identity are preferred over the lower ones.

The present disclosure also provides compositions comprising any one or more of the isolated nucleic acid molecules, genomic nucleic acid molecules, mRNA molecules, and/or cDNA molecules disclosed herein. In some embodiments, the composition is a pharmaceutical composition. In some embodiments, the compositions comprise a carrier and/or excipient. Examples of carriers include, but are not limited to, poly(lactic acid) (PLA) microspheres, poly(D,L-lactic-co-glycolic-acid) (PLGA) microspheres, liposomes, micelles, inverse micelles, lipid cochleates, and lipid microtubules. A carrier may comprise a buffered salt solution such as PBS, HBSS, etc.

As used herein, the phrase "corresponding to" or grammatical variations thereof when used in the context of the numbering of a particular nucleotide or nucleotide sequence or position refers to the numbering of a specified reference sequence when the particular nucleotide or nucleotide sequence is compared to a reference sequence (such as, for example, SEQ ID NO:1, SEQ ID NO:7, or SEQ ID NO:13). In other words, the residue (such as, for example, nucleotide or amino acid) number or residue (such as, for example, nucleotide or amino acid) position of a particular polymer is designated with respect to the reference sequence rather than by the actual numerical position of the residue within the particular nucleotide or nucleotide sequence. For example, a particular nucleotide sequence can be aligned to a reference sequence by introducing gaps to optimize residue matches between the two sequences. In these cases, although the gaps are present, the numbering of the residue in the particular nucleotide or nucleotide sequence is made with respect to the reference sequence to which it has been aligned.

For example, a nucleic acid molecule comprising a nucleotide sequence encoding an ANGPTL7 polypeptide, wherein the nucleotide sequence comprises a thymine at a position corresponding to position 4,291 according to SEQ ID NO:2 means that if the nucleotide sequence of the ANGPTL7 genomic nucleic acid molecule is aligned to the sequence of SEQ ID

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NO:2, the ANGPTL7 sequence has a thymine residue at the position that corresponds to position 4,291 of SEQ ID NO:2. The same applies for mRNA molecules comprising a nucleotide sequence encoding an ANGPTL7 polypeptide, wherein the nucleotide sequence comprises a uracil at a position corresponding to position 529 according to SEQ ID NO:8, and cDNA

5 molecules comprising a nucleotide sequence encoding an ANGPTL7 polypeptide, wherein the nucleotide sequence comprises a thymine at a position corresponding to position 529 according to SEQ ID NO:14. In other words, these phrases refer to a nucleic acid molecule encoding an ANGPTL7 polypeptide, wherein the genomic nucleic acid molecule has a nucleotide sequence that comprises a thymine residue that is homologous to the thymine residue at position 4,291
10 of SEQ ID NO:2 (or wherein the mRNA molecule has a nucleotide sequence that comprises a uracil residue that is homologous to the uracil residue at position 529 of SEQ ID NO:8, or wherein the cDNA molecule has a nucleotide sequence that comprises a thymine residue that is homologous to the thymine residue at position 529 of SEQ ID NO:14). Herein, the polypeptide produced from such nucleic acid molecules is referred to herein as "Arg177STOP."

15 As described herein, a position within an ANGPTL7 genomic nucleic acid molecule that corresponds to position 4,291 according to SEQ ID NO:2, for example, can be identified by performing a sequence alignment between the nucleotide sequence of a particular ANGPTL7 nucleic acid molecule and the nucleotide sequence of SEQ ID NO:2. A variety of computational algorithms exist that can be used for performing a sequence alignment to identify a nucleotide
20 position that corresponds to, for example, position 4,291 in SEQ ID NO:2. For example, by using the NCBI BLAST algorithm (Altschul et al., Nucleic Acids Res., 1997, 25, 3389-3402) or CLUSTALW software (Sievers and Higgins, Methods Mol. Biol., 2014, 1079, 105-116) sequence alignments may be performed. However, sequences can also be aligned manually.

The amino acid sequence of an ANGPTL7 reference polypeptide is set forth in SEQ ID
25 NO:19. Referring to SEQ ID NO:19, the ANGPTL7 reference polypeptide is 346 amino acids in length. Referring to SEQ ID NO:19, position 175 is a glutamine. Referring to SEQ ID NO:19, position 177 is an arginine. Referring to SEQ ID NO:19, position 161 is a phenylalanine. Referring to SEQ ID NO:19, position 188 is a tryptophan. Referring to SEQ ID NO:19, position 192 is a lysine.

30 A variant polypeptide of ANGPTL7 exists (Arg177STOP), the amino acid sequence of which is set forth in SEQ ID NO:20. Referring to SEQ ID NO:20, the ANGPTL7 variant polypeptide terminates at position 176. Thus, this variant is 176 amino acids in length. Referring to SEQ ID

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NO:20, the ANGPTL7 variant polypeptide does not contain amino acids at positions corresponding to positions 177 to 346 of SEQ ID NO:19.

Another variant polypeptide of ANGPTL7 exists (Gln175His), the amino acid sequence of which is set forth in SEQ ID NO:21. Referring to SEQ ID NO:21, the ANGPTL7 variant
5 polypeptide is 346 amino acids in length. Referring to SEQ ID NO:21, position 175 is a histidine.

Another variant polypeptide of ANGPTL7 exists (Phe161Ile), the amino acid sequence of which is set forth in SEQ ID NO:22. Referring to SEQ ID NO:22, the ANGPTL7 variant polypeptide is 346 amino acids in length. Referring to SEQ ID NO:22, position 161 is an isoleucine.

10 A variant polypeptide of ANGPTL7 exists (Trp188STOP), the amino acid sequence of which is set forth in SEQ ID NO:23. Referring to SEQ ID NO:23, the ANGPTL7 variant polypeptide terminates at position 187. Thus, this variant is 187 amino acids in length. Referring to SEQ ID NO:23, the ANGPTL7 variant polypeptide does not contain amino acids at positions corresponding to positions 188 to 346 of SEQ ID NO:19.

15 Another variant polypeptide of ANGPTL7 exists (Lys192Gln), the amino acid sequence of which is set forth in SEQ ID NO:24. Referring to SEQ ID NO:24, the ANGPTL7 variant polypeptide is 346 amino acids in length. Referring to SEQ ID NO:24, position 192 is a glutamine.

The present disclosure also provides combinations of a glucocorticoid and an ANGPTL7
20 inhibitor for use in the treatment of inflammation. The present disclosure also provides combinations of a glucocorticoid and an ANGPTL7 inhibitor for use in the preparation of a medicament for treating inflammation. In any of the embodiments described herein, the subject is identified as having any of the ANGPTL7 variant nucleic acid molecules and/or polypeptides described herein. The glucocorticoid can be any of the glucocorticoids described
25 herein. The ANGPTL7 inhibitors can be any of the ANGPTL7 inhibitors described herein. The combinations of a glucocorticoid and an ANGPTL7 inhibitor can be used to treat or prevent a glucocorticoid-induced ophthalmic condition in a subject who is undergoing or will be undergoing glucocorticoid treatment, such as for inflammation.

The present disclosure also provides ANGPTL7 inhibitors for use in decreasing or
30 preventing a glucocorticoid-induced ophthalmic condition in a subject undergoing glucocorticoid treatment. The present disclosure also provides ANGPTL7 inhibitors for use in the preparation of a medicament for decreasing or preventing a glucocorticoid-induced

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ophthalmic condition in a subject undergoing glucocorticoid treatment. In any of the embodiments described herein, the subject is identified as having any of the ANGPTL7 variant nucleic acid molecules and/or polypeptides described herein. The glucocorticoid treatment can be treatment with any of the glucocorticoids described herein. The ANGPTL7 inhibitors can be
5 any of the ANGPTL7 inhibitors described herein. The glucocorticoid-induced ophthalmic condition can be any of the glucocorticoid-induced ophthalmic conditions described herein.

In any of the embodiments described herein, the subject is identified as having a genomic nucleic acid molecule having a nucleotide sequence encoding an ANGPTL7 polypeptide, wherein the nucleotide sequence comprises: a thymine at a position
10 corresponding to position 4,291 according to SEQ ID NO:2, or the complement thereof; a thymine at a position corresponding to position 4,287 according to SEQ ID NO:3, or the complement thereof; an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4, or the complement thereof; an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5, or the complement thereof; or a cytosine at a position
15 corresponding to position 4,336 according to SEQ ID NO:6, or the complement thereof. In any of the embodiments described herein, the subject is identified as having an mRNA molecule having a nucleotide sequence encoding an ANGPTL7 polypeptide, wherein the nucleotide sequence comprises: a uracil at a position corresponding to position 529 according to SEQ ID NO:8, or the complement thereof; a uracil at a position corresponding to position 525
20 according to SEQ ID NO:9, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:10, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:11, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:12, or the complement thereof. In any of the embodiments described herein, the subject is identified as
25 having a cDNA molecule having a nucleotide sequence encoding an ANGPTL7 polypeptide, wherein the nucleotide sequence comprises: a thymine at a position corresponding to position 529 according to SEQ ID NO:14, or the complement thereof; a thymine at a position corresponding to position 525 according to SEQ ID NO:15, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:16, or the
30 complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:17, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18, or the complement thereof.

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In some embodiments, the subject can have inflammation. In some embodiments, the inflammation can be acute inflammation or chronic inflammation. In some embodiments, the inflammation is acute inflammation. In some embodiments, the inflammation is chronic inflammation. In some embodiments, the inflammation is associated with rheumatoid arthritis, associated with Grave's disease, or is ophthalmic inflammation. In some embodiments, the inflammation is associated with rheumatoid arthritis. In some embodiments, the inflammation is associated with Grave's disease. In some embodiments, the inflammation is ophthalmic inflammation. In some embodiments, the ophthalmic inflammation is chosen from uveitis, juvenile idiopathic arthritis uveitis, scleritis, blepharitis, conjunctivitis, iritis, and episcleritis, or any combination thereof. In some embodiments, the ophthalmic inflammation is uveitis. In some embodiments, the ophthalmic inflammation is juvenile idiopathic arthritis uveitis. In some embodiments, the ophthalmic inflammation is scleritis. In some embodiments, the ophthalmic inflammation is blepharitis. In some embodiments, the ophthalmic inflammation is conjunctivitis. In some embodiments, the ophthalmic inflammation is iritis. In some embodiments, the ophthalmic inflammation is episcleritis.

In some embodiments, the glucocorticoid-induced ophthalmic condition is chosen from ocular hypertension, increased intraocular pressure (IOP), pre-glaucoma, glaucoma, decreased corneal hysteresis, and posterior subcapsular cataracts, or any combination thereof. In some embodiments, the glucocorticoid-induced ophthalmic condition is ocular hypertension. In some embodiments, the glucocorticoid-induced ophthalmic condition is increased IOP. In some embodiments, the glucocorticoid-induced ophthalmic condition is pre-glaucoma. In some embodiments, the glucocorticoid-induced ophthalmic condition is glaucoma. In some embodiments, the glucocorticoid-induced ophthalmic condition is decreased corneal hysteresis. In some embodiments, the glucocorticoid-induced ophthalmic condition is posterior subcapsular cataracts.

In some embodiments, the glucocorticoid treatment is treatment with prednisone, prednisolone, methylprednisolone, dexamethasone, betamethasone, triamcinolone, beclometasone, fludrocortisone acetate, DOCA, aldosterone, budesonide, mometasone furoate, fluticasone propionate, hydrocortisone, cortisone acetate, or fluticasone furoate, difluprednate ophthalmic, fluorometholone, loteprednol etabonate, medrysone, rmexolone, fluocinolone acetonide, clobetasol, halobetasol, diflorasone, fluocinonide, flurandrenolide, Neo-Poly-Dex, tobramycin-dexamethasone, difluprednate, or any combination thereof. In some

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embodiments, the glucocorticoid treatment is treatment with prednisone. In some
embodiments, the glucocorticoid treatment is treatment with prednisolone. In some
embodiments, the glucocorticoid treatment is treatment with methylprednisolone. In some
embodiments, the glucocorticoid treatment is treatment with dexamethasone. In some
5 embodiments, the glucocorticoid treatment is treatment with betamethasone. In some
embodiments, the glucocorticoid treatment is treatment with triamcinolone. In some
embodiments, the glucocorticoid treatment is treatment with beclomethasone. In some
embodiments, the glucocorticoid treatment is treatment with fludrocortisone acetate. In some
embodiments, the glucocorticoid treatment is treatment with DOCA. In some embodiments,
10 the glucocorticoid treatment is treatment with aldosterone. In some embodiments, the
glucocorticoid treatment is treatment with budesonide. In some embodiments, the
glucocorticoid treatment is treatment with mometasone furoate. In some embodiments, the
glucocorticoid treatment is treatment with fluticasone propionate. In some embodiments, the
glucocorticoid treatment is treatment with hydrocortisone. In some embodiments, the
15 glucocorticoid treatment is treatment with cortisone acetate. In some embodiments, the
glucocorticoid treatment is treatment with fluticasone furoate. In some embodiments, the
glucocorticoid treatment is treatment with difluprednate ophthalmic. In some embodiments,
the glucocorticoid treatment is treatment with fluorometholone. In some embodiments, the
glucocorticoid treatment is treatment with loteprednol etabonate. In some embodiments, the
20 glucocorticoid treatment is treatment with medrysone. In some embodiments, the
glucocorticoid treatment is treatment with rmexolone. In some embodiments, the
glucocorticoid treatment is treatment with fluocinolone acetonide. In some embodiments, the
glucocorticoid treatment is treatment with clobetasol. In some embodiments, the
glucocorticoid treatment is treatment with halobetasol. In some embodiments, the
25 glucocorticoid treatment is treatment with diflorasone. In some embodiments, the
glucocorticoid treatment is treatment with fluocinonide. In some embodiments, the
glucocorticoid treatment is treatment with flurandrenolide. In some embodiments, the
glucocorticoid treatment is treatment with Neo-Poly-Dex. In some embodiments, the
glucocorticoid treatment is treatment with tobramycin-dexamethasone. In some embodiments,
30 the glucocorticoid treatment is treatment with difluprednate.

In some embodiments, the ANGPTL7 inhibitor comprises an inhibitory nucleic acid
molecule. In some embodiments, the inhibitory nucleic acid molecule comprises an antisense

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nucleic acid molecule, an siRNA, or an shRNA that hybridizes to an ANGPTL7 nucleic acid molecule. In some embodiments, the inhibitory nucleic acid molecule comprises an antisense nucleic acid molecule. In some embodiments, the inhibitory nucleic acid molecule comprises an siRNA. In some embodiments, the inhibitory nucleic acid molecule comprises an shRNA.

5 In some embodiments, the ANGPTL7 inhibitor comprises a Cas protein and gRNA that hybridizes to a gRNA recognition sequence within an ANGPTL7 genomic nucleic acid molecule. In some embodiments, the Cas protein is Cas9 or Cpf1. In some embodiments, the gRNA recognition sequence includes or is proximate to a position corresponding to: position 4,291 according to SEQ ID NO:1, position 4,287 according to SEQ ID NO:1, position 4,243 according to
10 SEQ ID NO:1, position 4,325 according to SEQ ID NO:1, or position 4,336 according to SEQ ID NO:1. In some embodiments, the gRNA recognition sequence is located from about 1000, from about 500, from about 400, from about 300, from about 200, from about 100, from about 50, from about 45, from about 40, from about 35, from about 30, from about 25, from about 20, from about 15, from about 10, or from about 5 nucleotides of a position corresponding to:
15 position 4,291 according to SEQ ID NO:1, position 4,287 according to SEQ ID NO:1, position 4,243 according to SEQ ID NO:1, position 4,325 according to SEQ ID NO:1, or position 4,336 according to SEQ ID NO:1. In some embodiments, a PAM sequence is about 2 to about 6 nucleotides downstream of the gRNA recognition sequence. In some embodiments, the gRNA comprises from about 17 nucleotides to about 23 nucleotides. In some embodiments, the gRNA
20 recognition sequence comprises a nucleotide sequence according to any one of SEQ ID NOs:25-165.

All patent documents, websites, other publications, accession numbers and the like cited above or below are incorporated by reference in their entirety for all purposes to the same extent as if each individual item were specifically and individually indicated to be so
25 incorporated by reference. If different versions of a sequence are associated with an accession number at different times, the version associated with the accession number at the effective filing date of this application is meant. The effective filing date means the earlier of the actual filing date or filing date of a priority application referring to the accession number if applicable. Likewise, if different versions of a publication, website or the like are published at different
30 times, the version most recently published at the effective filing date of the application is meant unless otherwise indicated. Any feature, step, element, embodiment, or aspect of the present disclosure can be used in combination with any other feature, step, element,

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embodiment, or aspect unless specifically indicated otherwise. Although the present disclosure has been described in some detail by way of illustration and example for purposes of clarity and understanding, it will be apparent that certain changes and modifications may be practiced within the scope of the appended claims.

5 The following examples are provided to describe the embodiments in greater detail. They are intended to illustrate, not to limit, the claimed embodiments. The following examples provide those of ordinary skill in the art with a disclosure and description of how the compounds, compositions, articles, devices and/or methods described herein are made and evaluated, and are intended to be purely exemplary and are not intended to limit the scope of
10 any claims. Efforts have been made to ensure accuracy with respect to numbers (such as, for example, amounts, temperature, etc.), but some errors and deviations may be accounted for. Unless indicated otherwise, parts are parts by weight, temperature is in °C or is at ambient temperature, and pressure is at or near atmospheric.

15 **Examples**

Example 1: ANGPTL7 KO Mice Inhibit DEX-Ac-Induced Ocular Hypertension in Mice

Weekly periocular CF injections of DEX-Ac in both eyes in ANGPTL7 WT mice significantly elevated IOP in (see, Figure 1). IOP measurements of DEX-Ac-treated (n=18) versus vehicle-treated (n=6) mice show IOP elevation from week 1 to 6; **p < 0.01, ***p < 0.001,
20 ****p < 0.0001. In contrast, weekly periocular CF injections of DEX-Ac in both eyes in ANGPTL7 KO mice did not elevate IOP (see, Figure 1). IOP measurements of DEX-Ac-treated (n=20) versus vehicle-treated (n=12) ANGPTL7 KO mice showed no effect in IOP elevation from week 1 to week 6.

25 **Example 2: *In Vivo* Evaluation of ANGPTL7 siRNA in Wild-Type Mice**

dsRNA were assessed for their ability to reduce the level of ANGPTL7 RNAs and/or reduce IOP *in vivo* in wild-type mice.

Six different siRNAs targeting ANGPTL7 (siRNA #1-6; see below) were tested in C57BL/6J wild-type mice and IOP was monitored over time. C57BL/6J mice were each
30 intravitreally injected with 15 µg of an siRNA or PBS control. Animals in the naïve group received no injection. Six weeks later, animals were sacrificed, eyes were collected, and limbal rings were carefully micro-dissected. qPCR was performed on limbal rings dissected from

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mouse eyes enriched for the trabecular meshwork (TM) for ANGPTL7 expression. The data were expressed as percent message remaining relative to the baseline value, and presented as mean $\pm$ standard error of the mean (SEM).

5	Duplex #	sense strand sequence	antisense strand sequence
	#1	UUGGGCAAUGAACUGAACAGA (SEQ ID NO: 5559)	UCUGUUCAGUUCAUUGCCCAACG (SEQ ID NO: 5560)
	#2	GUACCAGAAGAACUACCGAAA (SEQ ID NO: 5535)	UUUCGGUAGUUCUUCUGGUACAG (SEQ ID NO: 5536)
10	#3	AGACAGUAUAAGCAAGGGUUA (SEQ ID NO: 5555)	UAACCCUUGCUUAUACUGUCUCC (SEQ ID NO: 5556)
	#4	GCAGAAGCCUCAUAAACGCAA (SEQ ID NO: 5573)	UUGCGUUUAUGAGGCUUCUGCAG (SEQ ID NO: 5574)
	#5	ACACUCCUUGUGUCUAUAGA (SEQ ID NO: 5533)	UCUAUAGACACAAGGAAGUGUCG (SEQ ID NO: 5534)
15	#6	CUGCAGAAGCCUCAUAAACGA (SEQ ID NO: 5571)	UCGUUUUAUGAGGCUUCUGCAGCC (SEQ ID NO: 5572)

The results of the *in vivo* evaluation are shown in Figures 2 and 3. As shown in Figure 2, IOP was significantly lowered 2 weeks post-injection in mice treated with two of the six siRNAs (siRNA #3 and #5, n = 6-8/group) compared to the PBS-treated (n = 6) or naïve (no injection, n = 5) groups. Naïve and PBS-treated animals maintained their IOPs at baseline for the duration of the study (weeks 0-6). In contrast, in mice treated with siRNA#3 and #5, IOP was lowered by 2-4 mmHg starting at week 2 compared to PBS-treated or naïve mice, and remained lowered through the end of the study (i.e., 6 weeks).

As shown in Figure 3, in qPCR of the limbal ring tissue harvested at the end of the study (i.e., 6 weeks after the siRNA administration), the highest level of knockdown (> 50%) of ANGPTL7 mRNA was observed with siRNAs #3 and #5 compared to PBS-treated or naïve mice. Such mRNA knockdown effect is consistent with the lowering of IOP observed in mice injected with one of these two siRNAs. The results suggest that inhibition of ANGPTL7 expression also lowers IOP, and demonstrate the ability of the exemplary dsRNA agents to reduce the ANGPTL7 expression and also lower IOP *in vivo*.

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Example 3: In vivo Knock Down of ANGPTL7 by siRNA in Wild Type Mice Inhibits Steroid-Induced and other types of TM-stress Related IOP Elevation in Glaucoma

dsRNA were further assessed for their ability to reduce steroid induced IOP *in vivo* in wild-type mice. Weekly periocular CF injections of DEX-Ac suspension to both eyes caused DEX-induced OHT with sustained and significantly elevated IOP in WT mice. Mice were divided into following groups as shown in Figure 4: a) Vehicle (n=4), b) Vehicle + PBS (n=6), c) DEX-Ac (n=12), d) DEX-Ac + siRNA#3 (n=14), and e) DEX-Ac + siRNA#5 (n=14). IOP elevation was rapid and significantly higher in DEX-Ac-treated mice compared with vehicle-treated mice starting 6-days post-injection. DEX-Ac treated mice in group c developed DEX-induced OHT with sustained and significantly elevated IOP throughout the study. At Day 22, siRNA targeting ANGPTL7 (#3 and #5) were intravitreally injected into groups: d and e (DEX-Ac + siRNA#3 and DEX-Ac + siRNA#5) and IOP measurements continued to be recorded. In groups d and e, IOPs were significantly reduced and returned to baseline IOP within one week as compared with DEX-Ac treated group (c). The IOP remained at baseline throughout the study even though these mice continued to receive weekly DEX-Ac treatment.

Various modifications of the described subject matter, in addition to those described herein, will be apparent to those skilled in the art from the foregoing description. Such modifications are also intended to fall within the scope of the appended claims. Each reference (including, but not limited to, journal articles, U.S. and non-U.S. patents, patent application publications, international patent application publications, gene bank accession numbers, and the like) cited in the present application is incorporated herein by reference in its entirety and for all purposes.

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What is Claimed is:

1. A method of treating a subject having inflammation, the method comprising administering an Angiopoietin-Like 7 (ANGPTL7) inhibitor and a glucocorticoid to the subject.
2. A method of treating a subject having rheumatoid arthritis, the method comprising
5 administering an Angiopoietin-Like 7 (ANGPTL7) inhibitor and a glucocorticoid to the subject.
3. A method of treating a subject having Grave's disease, the method comprising administering an Angiopoietin-Like 7 (ANGPTL7) inhibitor and a glucocorticoid to the subject.
4. A method of treating a subject having ophthalmic inflammation, the method comprising administering an Angiopoietin-Like 7 (ANGPTL7) inhibitor and a glucocorticoid to
10 the subject.
5. The method according to claim 4, wherein the ophthalmic inflammation is chosen from uveitis, juvenile idiopathic arthritis uveitis, scleritis, blepharitis, conjunctivitis, iritis, and episcleritis, or any combination thereof.
6. A method of decreasing a glucocorticoid-induced ophthalmic condition in a subject
15 treated with a glucocorticoid, the method comprising administering an Angiopoietin-Like 7 (ANGPTL7) inhibitor to the subject.
7. The method according to claim 6, wherein the glucocorticoid-induced ophthalmic condition is chosen from ocular hypertension, increased intraocular pressure (IOP), pre-glaucoma, glaucoma, decreased corneal hysteresis, and posterior subcapsular cataracts, or any
20 combination thereof.
8. A method of treating a subject having inflammation and undergoing glucocorticoid treatment, the method comprising administering an Angiopoietin-Like 7 (ANGPTL7) inhibitor to the subject.
9. A method of treating a subject having rheumatoid arthritis and undergoing
25 glucocorticoid treatment, the method comprising administering an Angiopoietin-Like 7 (ANGPTL7) inhibitor to the subject.
10. A method of treating a subject having Grave's disease and undergoing glucocorticoid treatment, the method comprising administering an Angiopoietin-Like 7 (ANGPTL7) inhibitor to the subject.
- 30 11. A method of treating a subject having ophthalmic inflammation and undergoing glucocorticoid treatment, the method comprising administering an Angiopoietin-Like 7 (ANGPTL7) inhibitor to the subject.

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12. The method according to claim 11, wherein the ophthalmic inflammation is chosen from uveitis, juvenile idiopathic arthritis uveitis, scleritis, blepharitis, conjunctivitis, iritis, and episcleritis, or any combination thereof.
13. The method according to any one of claims 1 to 7, wherein the glucocorticoid is chosen
5 from prednisone, prednisolone, methylprednisolone, dexamethasone, betamethasone, triamcinolone, beclometasone, fludrocortisone acetate, deoxycorticosterone acetate (DOCA), aldosterone, budesonide, mometasone furoate, fluticasone propionate, hydrocortisone, cortisone acetate, and fluticasone furoate, or any combination thereof.
14. The method according to any one of claims 8 to 12, wherein the glucocorticoid
10 treatment is treatment with prednisone, prednisolone, methylprednisolone, dexamethasone, betamethasone, triamcinolone, beclometasone, fludrocortisone acetate, DOCA, aldosterone, budesonide, mometasone furoate, fluticasone propionate, hydrocortisone, cortisone acetate, or fluticasone furoate, difluprednate ophthalmic, fluorometholone, loteprednol etabonate, medrysone, rmexolone, fluocinolone acetonide, clobetasol, halobetasol, diflorasone,
15 fluocinonide, flurandrenolide, Neo-Poly-Dex, tobramycin-dexamethasone, difluprednate, or any combination thereof.
15. The method according to any one of claims 1 to 14, wherein the ANGPTL7 inhibitor comprises an inhibitory nucleic acid molecule.
16. The method according to claim 14, wherein the inhibitory nucleic acid molecule
20 comprises an antisense nucleic acid molecule, a small interfering RNA (siRNA), or a short hairpin RNA (shRNA) that hybridizes to an ANGPTL7 nucleic acid molecule.
17. The method according to any one of claims 1 to 14, wherein the ANGPTL7 inhibitor comprises a Cas protein and guide RNA (gRNA) that hybridizes to a gRNA recognition sequence within an ANGPTL7 genomic nucleic acid molecule.
- 25 18. The method according to claim 17, wherein the Cas protein is Cas9 or Cpf1.
19. The method according to claim 17 or claim 18, wherein the gRNA recognition sequence includes or is proximate to a position corresponding to: position 4,291 according to SEQ ID NO:1, position 4,287 according to SEQ ID NO:1, position 4,243 according to SEQ ID NO:1, position 4,325 according to SEQ ID NO:1, or position 4,336 according to SEQ ID NO:1.
- 30 20. The method according to claim 17 or claim 18, wherein the gRNA recognition sequence is located from about 1000, from about 500, from about 400, from about 300, from about 200, from about 100, from about 50, from about 45, from about 40, from about 35, from about 30,

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from about 25, from about 20, from about 15, from about 10, or from about 5 nucleotides of a position corresponding to: position 4,291 according to SEQ ID NO:1, position 4,287 according to SEQ ID NO:1, position 4,243 according to SEQ ID NO:1, position 4,325 according to SEQ ID NO:1, or position 4,336 according to SEQ ID NO:1.

5 21. The method according to claim 17 or claim 18, wherein a Protospacer Adjacent Motif (PAM) sequence is about 2 to about 6 nucleotides downstream of the gRNA recognition sequence.

22. The method according to any one of claims 17 to 21, wherein the gRNA comprises from about 17 nucleotides to about 23 nucleotides.

10 23. The method according to any one of claims 17 to 21, wherein the gRNA recognition sequence comprises a nucleotide sequence according to any one of SEQ ID NOs:25-165.

24. The method according to any one of claims 1 to 23, further comprising detecting the presence or absence of an ANGPTL7 predicted loss-of-function variant nucleic acid molecule encoding an ANGPTL7 polypeptide in a biological sample from the subject.

15 25. The method according to claim 24, wherein the ANGPTL7 predicted loss-of-function variant nucleic acid molecule is a nucleic acid molecule encoding Arg177STOP, Gln175His, Phe161Ile, Trp188STOP, Lys192Gln, Arg340His, Arg220His, Asn302Lys, or Arg220Cys.

26. The method according to claim 24, wherein the ANGPTL7 predicted loss-of-function variant nucleic acid molecule is a nucleic acid molecule encoding Arg177STOP, Gln175His,

20 Phe161Ile, Trp188STOP, or Lys192Gln.

27. The method according to claim 26, wherein the ANGPTL7 predicted loss-of-function variant nucleic acid molecule is:

a genomic nucleic acid molecule having a nucleotide sequence comprising: a thymine at a position corresponding to position 4,291 according to SEQ ID NO:2; a thymine at a position
25 corresponding to position 4,287 according to SEQ ID NO:3; an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4; an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5; or a cytosine at a position corresponding to position 4,336 according to SEQ ID NO:6;

an mRNA molecule having a nucleotide sequence comprising: a uracil at a position
30 corresponding to position 529 according to SEQ ID NO:8; a uracil at a position corresponding to position 525 according to SEQ ID NO:9; an adenine at a position corresponding to position 481 according to SEQ ID NO:10; an adenine at a position corresponding to position 563 according to

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SEQ ID NO:11; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:12; or

a cDNA molecule produced from an mRNA molecule in the biological sample, wherein the cDNA molecule has a nucleotide sequence comprising: a thymine at a position

- 5 corresponding to position 529 according to SEQ ID NO:14; a thymine at a position corresponding to position 525 according to SEQ ID NO:15; an adenine at a position corresponding to position 481 according to SEQ ID NO:16; an adenine at a position corresponding to position 563 according to SEQ ID NO:17; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18.

- 10 28. The method according to any one of claims 24 to 27, wherein the detecting step is carried out *in vitro*.

29. The method according to any one of claims 24 to 28, wherein the detecting step comprises sequencing at least a portion of the nucleotide sequence of the ANGPTL7 genomic nucleic acid molecule in the biological sample, wherein the sequenced portion comprises a
15 position corresponding to: position 4,291 according to SEQ ID NO:2, or the complement thereof; position 4,287 according to SEQ ID NO:3, or the complement thereof; position 4,243 according to SEQ ID NO:4, or the complement thereof; position 4,325 according to SEQ ID NO:5, or the complement thereof; or position 4,336 according to SEQ ID NO:6, or the complement thereof;

- 20 wherein when the sequenced portion of the ANGPTL7 genomic nucleic acid molecule comprises: a thymine at a position corresponding to position 4,291 according to SEQ ID NO:2, a thymine at a position corresponding to position 4,287 according to SEQ ID NO:3, an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4, an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5, or a cytosine at a position
25 corresponding to position 4,336 according to SEQ ID NO:6, then the ANGPTL7 genomic nucleic acid molecule in the biological sample is an ANGPTL7 predicted loss-of-function variant genomic nucleic acid molecule.

30. The method according to any one of claims 24 to 28, wherein the detecting step comprises sequencing at least a portion of the nucleotide sequence of the ANGPTL7 mRNA
30 molecule in the biological sample, wherein the sequenced portion comprises a position corresponding to: position 529 according to SEQ ID NO:8, or the complement thereof; position 525 according to SEQ ID NO:9, or the complement thereof; position 481 according to SEQ ID

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NO:10, or the complement thereof; position 563 according to SEQ ID NO:11, or the complement thereof; or position 574 according to SEQ ID NO:12, or the complement thereof;

wherein when the sequenced portion of the ANGPTL7 mRNA molecule comprises: a uracil at a position corresponding to position 529 according to SEQ ID NO:8, a uracil at a

- 5 position corresponding to position 525 according to SEQ ID NO:9, an adenine at a position corresponding to position 481 according to SEQ ID NO:10, an adenine at a position corresponding to position 563 according to SEQ ID NO:11, or a cytosine at a position corresponding to position 574 according to SEQ ID NO:12, then the ANGPTL7 mRNA molecule in the biological sample is an ANGPTL7 predicted loss-of-function variant mRNA molecule.

- 10 31. The method according to any one of claims 24 to 28, wherein the detecting step comprises sequencing at least a portion of the nucleotide sequence of the ANGPTL7 cDNA molecule produced from an mRNA molecule in the biological sample, wherein the sequenced portion comprises a position corresponding to: position 529 according to SEQ ID NO:14, or the complement thereof; position 525 according to SEQ ID NO:15, or the complement thereof;
- 15 position 481 according to SEQ ID NO:16, or the complement thereof; position 563 according to SEQ ID NO:17, or the complement thereof; or position 574 according to SEQ ID NO:18, or the complement thereof;

wherein when the sequenced portion of the ANGPTL7 cDNA molecule comprises: a thymine at a position corresponding to position 529 according to SEQ ID NO:14, a thymine at a

20 position corresponding to position 525 according to SEQ ID NO:15, an adenine at a position corresponding to position 481 according to SEQ ID NO:16, an adenine at a position corresponding to position 563 according to SEQ ID NO:17, or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18, then the ANGPTL7 cDNA molecule in the biological sample is an ANGPTL7 predicted loss-of-function variant cDNA molecule.

- 25 32. The method according to any one of claims 24 to 28, wherein the detecting step comprises:

a) contacting the biological sample with a primer hybridizing to a portion of the nucleotide sequence of the ANGPTL7 genomic nucleic acid molecule that is proximate to a position corresponding to: position 4,291 according to SEQ ID NO:2, position 4,287 according to

30 SEQ ID NO:3, position 4,243 according to SEQ ID NO:4, position 4,325 according to SEQ ID NO:5, or position 4,336 according to SEQ ID NO:6;

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b) extending the primer at least through the position of the nucleotide sequence of the ANGPTL7 genomic nucleic acid molecule corresponding to: position 4,291 according to SEQ ID NO:2, position 4,287 according to SEQ ID NO:3, position 4,243 according to SEQ ID NO:4, position 4,325 according to SEQ ID NO:5, or position 4,336 according to SEQ ID NO:6; and

5 c) determining whether the extension product of the primer comprises: a thymine at a position corresponding to position 4,291 according to SEQ ID NO:2, a thymine at a position corresponding to position 4,287 according to SEQ ID NO:3, an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4, an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5, or a cytosine at a position
10 corresponding to position 4,336 according to SEQ ID NO:6.

33. The method according to any one of claims 24 to 28, wherein the detecting step comprises:

a) contacting the biological sample with a primer hybridizing to a portion of the nucleotide sequence of the ANGPTL7 mRNA molecule that is proximate to a position
15 corresponding to: position 529 according to SEQ ID NO:8, position 525 according to SEQ ID NO:9, position 481 according to SEQ ID NO:10, position 563 according to SEQ ID NO:11, or position 574 according to SEQ ID NO:12;

b) extending the primer at least through the position of the nucleotide sequence of the ANGPTL7 mRNA molecule corresponding to: position 529 according to SEQ ID NO:8, position
20 525 according to SEQ ID NO:9, position 481 according to SEQ ID NO:10, position 563 according to SEQ ID NO:11, or position 574 according to SEQ ID NO:12; and

c) determining whether the extension product of the primer comprises: a uracil at a position corresponding to position 529 according to SEQ ID NO:8, a uracil at a position corresponding to position 525 according to SEQ ID NO:9, an adenine at a position
25 corresponding to position 481 according to SEQ ID NO:10, an adenine at a position corresponding to position 563 according to SEQ ID NO:11, or a cytosine at a position corresponding to position 574 according to SEQ ID NO:12.

34. The method according to any one of claims 24 to 28, wherein the detecting step comprises:

30 a) contacting the biological sample with a primer hybridizing to a portion of the nucleotide sequence of the ANGPTL7 cDNA molecule produced from the mRNA molecule in the biological sample that is proximate to a position corresponding to: position 529 according to

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SEQ ID NO:14, position 525 according to SEQ ID NO:15, position 481 according to SEQ ID NO:16, position 563 according to SEQ ID NO:17, or position 574 according to SEQ ID NO:18;

b) extending the primer at least through the position of the nucleotide sequence of the ANGPTL7 cDNA molecule corresponding to: position 529 according to SEQ ID NO:14, position
5 525 according to SEQ ID NO:15, position 481 according to SEQ ID NO:16, position 563 according to SEQ ID NO:17, or position 574 according to SEQ ID NO:18; and

c) determining whether the extension product of the primer comprises: a thymine at a position corresponding to position 529 according to SEQ ID NO:14, a thymine at a position corresponding to position 525 according to SEQ ID NO:15, an adenine at a position
10 corresponding to position 481 according to SEQ ID NO:16, an adenine at a position corresponding to position 563 according to SEQ ID NO:17, or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18.

35. The method according to any one of claims 29 to 34, wherein the detecting step comprises sequencing the entire nucleic acid molecule.

15 36. The method according to any one of claims 24 to 28, wherein the detecting step comprises:

a) amplifying at least a portion of the genomic nucleic acid molecule that encodes the ANGPTL7 polypeptide, wherein the portion comprises: a thymine at a position corresponding to position 4,291 according to SEQ ID NO:2, or the complement thereof; a thymine at a position
20 corresponding to position 4,287 according to SEQ ID NO:3, or the complement thereof; an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4, or the complement thereof; an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5, or the complement thereof; or a cytosine at a position corresponding to position 4,336 according to SEQ ID NO:6, or the complement thereof;

25 b) labeling the amplified nucleic acid molecule with a detectable label;

c) contacting the labeled nucleic acid molecule with a support comprising an alteration-specific probe, wherein the alteration-specific probe comprises a nucleotide sequence which hybridizes under stringent conditions to the nucleic acid sequence of the amplified nucleic acid molecule comprising: a thymine at a position corresponding to position
30 4,291 according to SEQ ID NO:2, or the complement thereof; a thymine at a position corresponding to position 4,287 according to SEQ ID NO:3, or the complement thereof; an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4, or the

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complement thereof; an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5, or the complement thereof; or a cytosine at a position corresponding to position 4,336 according to SEQ ID NO:6, or the complement thereof; and

d) detecting the detectable label.

- 5 37. The method according to any one of claims 24 to 28, wherein the detecting step comprises:

a) amplifying at least a portion of the mRNA molecule that encodes the ANGPTL7 polypeptide, wherein the portion comprises: a uracil at a position corresponding to position 529 according to SEQ ID NO:8, or the complement thereof; a uracil at a position corresponding to position 525 according to SEQ ID NO:9, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:10, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:11, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:12, or the complement thereof;

15 b) labeling the amplified nucleic acid molecule with a detectable label;

c) contacting the labeled nucleic acid molecule with a support comprising an alteration-specific probe, wherein the alteration-specific probe comprises a nucleotide sequence which hybridizes under stringent conditions to the nucleic acid sequence of the amplified nucleic acid molecule comprising: a uracil at a position corresponding to position 529 according to SEQ ID NO:8, or the complement thereof; a uracil at a position corresponding to position 525 according to SEQ ID NO:9, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:10, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:11, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:12, or the complement thereof; and

d) detecting the detectable label.

38. The method according to any one of claims 24 to 28, wherein the detecting step comprises:

a) amplifying at least a portion of the cDNA molecule that encodes the ANGPTL7 polypeptide, wherein the portion comprises: a thymine at a position corresponding to position 529 according to SEQ ID NO:14, or the complement thereof; a thymine at a position corresponding to position 525 according to SEQ ID NO:15, or the complement thereof; an

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adenine at a position corresponding to position 481 according to SEQ ID NO:16, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:17, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18, or the complement thereof;

- 5 b) labeling the amplified nucleic acid molecule with a detectable label;
- c) contacting the labeled nucleic acid molecule with a support comprising an alteration-specific probe, wherein the alteration-specific probe comprises a nucleotide sequence which hybridizes under stringent conditions to the nucleic acid sequence of the amplified nucleic acid molecule comprising: a thymine at a position
- 10 529 according to SEQ ID NO:14, or the complement thereof; a thymine at a position corresponding to position 525 according to SEQ ID NO:15, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:16, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:17, or the complement thereof; or a cytosine at a position corresponding to position 574
- 15 according to SEQ ID NO:18, or the complement thereof; and
- d) detecting the detectable label.

39. The method according to claim 38, wherein the nucleic acid molecule in the sample is mRNA and the mRNA is reverse-transcribed into cDNA prior to the amplifying step.

40. The method according to any one of claims 24 to 28, wherein the detecting step
- 20 comprises:
- contacting the genomic nucleic acid molecule in the biological sample with an alteration-specific probe comprising a detectable label, wherein the alteration-specific probe comprises a nucleotide sequence which hybridizes under stringent conditions to the nucleotide sequence of the amplified nucleic acid molecule comprising: a thymine at a position
- 25 corresponding to position 4,291 according to SEQ ID NO:2, or the complement thereof; a thymine at a position corresponding to position 4,287 according to SEQ ID NO:3, or the complement thereof; an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4, or the complement thereof; an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5, or the complement thereof; or a cytosine at a position
- 30 corresponding to position 4,336 according to SEQ ID NO:6, or the complement thereof; and
- detecting the detectable label.

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41. The method according to any one of claims 24 to 28, wherein the detecting step comprises:

contacting the mRNA molecule in the biological sample with an alteration-specific probe comprising a detectable label, wherein the alteration-specific probe comprises a
5 nucleotide sequence which hybridizes under stringent conditions to the nucleotide sequence of the amplified nucleic acid molecule comprising: a uracil at a position corresponding to position 529 according to SEQ ID NO:8, or the complement thereof; a uracil at a position corresponding to position 525 according to SEQ ID NO:9, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:10, or the complement thereof; an
10 adenine at a position corresponding to position 563 according to SEQ ID NO:11, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:12, or the complement thereof; and
detecting the detectable label.

42. The method according to any one of claims 24 to 28, wherein the detecting step
15 comprises:

contacting the cDNA molecule produced from the mRNA molecule in the biological sample with an alteration-specific probe comprising a detectable label, wherein the alteration-specific probe comprises a nucleotide sequence which hybridizes under stringent conditions to the nucleotide sequence of the amplified nucleic acid molecule comprising: a thymine at a
20 position corresponding to position 529 according to SEQ ID NO:14, or the complement thereof; a thymine at a position corresponding to position 525 according to SEQ ID NO:15, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:16, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:17, or the complement thereof; or a cytosine at a position
25 corresponding to position 574 according to SEQ ID NO:18, or the complement thereof; and
detecting the detectable label.

43. A method of treating a subject undergoing glucocorticoid treatment, wherein the subject is suffering from inflammation, the method comprising:

determining whether the subject has an Angiopoietin-Like 7 (ANGPTL7) predicted loss-
30 of-function variant nucleic acid molecule encoding an ANGPTL7 polypeptide by:
obtaining or having obtained a biological sample from the subject;
and

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performing or having performed a sequence analysis on the biological sample to determine if the subject has a genotype comprising the ANGPTL7 predicted loss-of-function variant nucleic acid molecule; and

administering or continuing to administer to a subject that is ANGPTL7 reference the
5 glucocorticoid in a standard dosage amount, and administering an ANGPTL7 inhibitor to the subject; or

administering or continuing to administer to a subject that is heterozygous for the ANGPTL7 predicted loss-of-function variant the glucocorticoid in an amount that is the same as or higher than a standard dosage amount, and administering an ANGPTL7 inhibitor to the
10 subject; or

administering or continuing to administer to a subject that is homozygous for the ANGPTL7 predicted loss-of-function variant the glucocorticoid in an amount that is the same as or higher than a standard dosage amount;

wherein the presence of a genotype having the ANGPTL7 predicted loss-of-function
15 variant nucleic acid molecule encoding the ANGPTL7 polypeptide indicates the subject has a decreased risk of developing a glucocorticoid-induced ophthalmic condition.

44. The method according to claim 43, wherein the subject is ANGPTL7 reference, and the subject is administered or continued to be administered the glucocorticoid in a standard dosage amount, and is administered an ANGPTL7 inhibitor.

20 45. The method according to claim 43, wherein the subject is heterozygous for an ANGPTL7 predicted loss-of-function variant, and the subject is administered or continued to be administered the glucocorticoid in an amount that is the same as or higher than a standard dosage amount, and is administered an ANGPTL7 inhibitor.

46. The method according to claim 43, wherein the subject is homozygous for an ANGPTL7
25 predicted loss-of-function variant, and the subject is administered or continued to be administered the glucocorticoid in an amount that is the same as or higher than a standard dosage amount.

47. The method according to any one of claims 43 to 46, wherein the ANGPTL7 predicted loss-of-function variant nucleic acid molecule is a nucleic acid molecule encoding Arg177STOP,
30 Gln175His, Phe161Ile, Trp188STOP, Lys192Gln, Arg340His, Arg220His, Asn302Lys, or Arg220Cys.

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48. The method according to any one of claims 43 to 46, wherein the ANGPTL7 predicted loss-of-function variant nucleic acid molecule is a nucleic acid molecule encoding Arg177STOP, Gln175His, Phe161Ile, Trp188STOP, or Lys192Gln.

49. The method according to claim 48, wherein the ANGPTL7 predicted loss-of-function
5 variant nucleic acid molecule is:

a genomic nucleic acid molecule having a nucleotide sequence comprising: a thymine at a position corresponding to position 4,291 according to SEQ ID NO:2; a thymine at a position corresponding to position 4,287 according to SEQ ID NO:3; an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4; an adenine at a position
10 corresponding to position 4,325 according to SEQ ID NO:5; or a cytosine at a position corresponding to position 4,336 according to SEQ ID NO:6;

an mRNA molecule having a nucleotide sequence comprising: a uracil at a position corresponding to position 529 according to SEQ ID NO:8; a uracil at a position corresponding to position 525 according to SEQ ID NO:9; an adenine at a position corresponding to position 481
15 according to SEQ ID NO:10; an adenine at a position corresponding to position 563 according to SEQ ID NO:11; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:12; or

a cDNA molecule produced from an mRNA molecule in the biological sample, wherein the cDNA molecule has a nucleotide sequence comprising: a thymine at a position
20 corresponding to position 529 according to SEQ ID NO:14; a thymine at a position corresponding to position 525 according to SEQ ID NO:15; an adenine at a position corresponding to position 481 according to SEQ ID NO:16; an adenine at a position corresponding to position 563 according to SEQ ID NO:17; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18.

25 50. The method according to any one of claims 43 to 49, wherein the determining step is carried out *in vitro*.

51. The method according to any one of claims 43 to 50, wherein the sequence analysis comprises sequencing at least a portion of the nucleotide sequence of the ANGPTL7 genomic nucleic acid molecule in the biological sample, wherein the sequenced portion comprises a
30 position corresponding to: position 4,291 according to SEQ ID NO:2, or the complement thereof; position 4,287 according to SEQ ID NO:3, or the complement thereof; position 4,243 according to SEQ ID NO:4, or the complement thereof; position 4,325 according to SEQ ID NO:5,

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or the complement thereof; or position 4,336 according to SEQ ID NO:6, or the complement thereof;

wherein when the sequenced portion of the ANGPTL7 genomic nucleic acid molecule comprises: a thymine at a position corresponding to position 4,291 according to SEQ ID NO:2, a
5 thymine at a position corresponding to position 4,287 according to SEQ ID NO:3, an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4, an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5, or a cytosine at a position corresponding to position 4,336 according to SEQ ID NO:6, then the ANGPTL7 genomic nucleic acid molecule in the biological sample is an ANGPTL7 predicted loss-of-function variant
10 genomic nucleic acid molecule.

52. The method according to any one of claims 43 to 50, wherein the sequence analysis comprises sequencing at least a portion of the nucleotide sequence of the ANGPTL7 mRNA molecule in the biological sample, wherein the sequenced portion comprises a position corresponding to: position 529 according to SEQ ID NO:8, or the complement thereof; position
15 525 according to SEQ ID NO:9, or the complement thereof; position 481 according to SEQ ID NO:10, or the complement thereof; position 563 according to SEQ ID NO:11, or the complement thereof; or position 574 according to SEQ ID NO:12, or the complement thereof;

wherein when the sequenced portion of the ANGPTL7 mRNA molecule comprises: a uracil at a position corresponding to position 529 according to SEQ ID NO:8, a uracil at a
20 position corresponding to position 525 according to SEQ ID NO:9, an adenine at a position corresponding to position 481 according to SEQ ID NO:10, an adenine at a position corresponding to position 563 according to SEQ ID NO:11, or a cytosine at a position corresponding to position 574 according to SEQ ID NO:12, then the ANGPTL7 mRNA molecule in the biological sample is an ANGPTL7 predicted loss-of-function variant mRNA molecule.

25 53. The method according to any one of claims 43 to 50, wherein the sequence analysis comprises sequencing at least a portion of the nucleotide sequence of the ANGPTL7 cDNA molecule produced from an mRNA molecule in the biological sample, wherein the sequenced portion comprises a position corresponding to: position 529 according to SEQ ID NO:14, or the complement thereof; position 525 according to SEQ ID NO:15, or the complement thereof;
30 position 481 according to SEQ ID NO:16, or the complement thereof; position 563 according to SEQ ID NO:17, or the complement thereof; or position 574 according to SEQ ID NO:18, or the complement thereof;

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wherein when the sequenced portion of the ANGPTL7 cDNA molecule comprises: a thymine at a position corresponding to position 529 according to SEQ ID NO:14, a thymine at a position corresponding to position 525 according to SEQ ID NO:15, an adenine at a position corresponding to position 481 according to SEQ ID NO:16, an adenine at a position corresponding to position 563 according to SEQ ID NO:17, or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18, then the ANGPTL7 cDNA molecule in the biological sample is an ANGPTL7 predicted loss-of-function variant cDNA molecule.

54. The method according to any one of claims 43 to 50, wherein the sequence analysis comprises:

10 a) contacting the biological sample with a primer hybridizing to a portion of the nucleotide sequence of the ANGPTL7 genomic nucleic acid molecule that is proximate to a position corresponding to: position 4,291 according to SEQ ID NO:2, position 4,287 according to SEQ ID NO:3, position 4,243 according to SEQ ID NO:4, position 4,325 according to SEQ ID NO:5, or position 4,336 according to SEQ ID NO:6;

15 b) extending the primer at least through the position of the nucleotide sequence of the ANGPTL7 genomic nucleic acid molecule corresponding to: position 4,291 according to SEQ ID NO:2, position 4,287 according to SEQ ID NO:3, position 4,243 according to SEQ ID NO:4, position 4,325 according to SEQ ID NO:5, or position 4,336 according to SEQ ID NO:6; and

c) determining whether the extension product of the primer comprises: a thymine at a position corresponding to position 4,291 according to SEQ ID NO:2, a thymine at a position corresponding to position 4,287 according to SEQ ID NO:3, an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4, an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5, or a cytosine at a position corresponding to position 4,336 according to SEQ ID NO:6.

25 55. The method according to any one of claims 43 to 50, wherein the sequence analysis comprises:

a) contacting the biological sample with a primer hybridizing to a portion of the nucleotide sequence of the ANGPTL7 mRNA molecule that is proximate to a position corresponding to: position 529 according to SEQ ID NO:8, position 525 according to SEQ ID NO:9, position 481 according to SEQ ID NO:10, position 563 according to SEQ ID NO:11, or position 574 according to SEQ ID NO:12;

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b) extending the primer at least through the position of the nucleotide sequence of the ANGPTL7 mRNA molecule corresponding to: position 529 according to SEQ ID NO:8, position 525 according to SEQ ID NO:9, position 481 according to SEQ ID NO:10, position 563 according to SEQ ID NO:11, or position 574 according to SEQ ID NO:12; and

- 5 c) determining whether the extension product of the primer comprises: a uracil at a position corresponding to position 529 according to SEQ ID NO:8, a uracil at a position corresponding to position 525 according to SEQ ID NO:9, an adenine at a position corresponding to position 481 according to SEQ ID NO:10, an adenine at a position corresponding to position 563 according to SEQ ID NO:11, or a cytosine at a position
10 corresponding to position 574 according to SEQ ID NO:12.

56. The method according to any one of claims 43 to 50, wherein the sequence analysis comprises:

- a) contacting the biological sample with a primer hybridizing to a portion of the nucleotide sequence of the ANGPTL7 cDNA molecule produced from the mRNA molecule in the
15 biological sample that is proximate to a position corresponding to: position 529 according to SEQ ID NO:14, position 525 according to SEQ ID NO:15, position 481 according to SEQ ID NO:16, position 563 according to SEQ ID NO:17, or position 574 according to SEQ ID NO:18;

- b) extending the primer at least through the position of the nucleotide sequence of the ANGPTL7 cDNA molecule corresponding to: position 529 according to SEQ ID NO:14, position
20 525 according to SEQ ID NO:15, position 481 according to SEQ ID NO:16, position 563 according to SEQ ID NO:17, or position 574 according to SEQ ID NO:18; and

- c) determining whether the extension product of the primer comprises: a thymine at a position corresponding to position 529 according to SEQ ID NO:14, a thymine at a position corresponding to position 525 according to SEQ ID NO:15, an adenine at a position
25 corresponding to position 481 according to SEQ ID NO:16, an adenine at a position corresponding to position 563 according to SEQ ID NO:17, or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18.

57. The method according to any one of claims 51 to 56, wherein the sequence analysis comprises sequencing the entire nucleic acid molecule.

- 30 58. The method according to any one of claims 43 to 50, wherein the sequence analysis comprises:

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- a) amplifying at least a portion of the genomic nucleic acid molecule that encodes the ANGPTL7 polypeptide, wherein the portion comprises: a thymine at a position corresponding to position 4,291 according to SEQ ID NO:2, or the complement thereof; a thymine at a position corresponding to position 4,287 according to SEQ ID NO:3, or the complement thereof; an
- 5 adenine at a position corresponding to position 4,243 according to SEQ ID NO:4, or the complement thereof; an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5, or the complement thereof; or a cytosine at a position corresponding to position 4,336 according to SEQ ID NO:6, or the complement thereof;
- b) labeling the amplified nucleic acid molecule with a detectable label;
- 10 c) contacting the labeled nucleic acid molecule with a support comprising an alteration-specific probe, wherein the alteration-specific probe comprises a nucleotide sequence which hybridizes under stringent conditions to the nucleic acid sequence of the amplified nucleic acid molecule comprising: a thymine at a position corresponding to position 4,291 according to SEQ ID NO:2, or the complement thereof; a thymine at a position
- 15 corresponding to position 4,287 according to SEQ ID NO:3, or the complement thereof; an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4, or the complement thereof; an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5, or the complement thereof; or a cytosine at a position corresponding to position 4,336 according to SEQ ID NO:6, or the complement thereof; and
- 20 d) detecting the detectable label.
59. The method according to any one of claims 43 to 50, wherein the sequence analysis comprises:
- a) amplifying at least a portion of the mRNA molecule that encodes the ANGPTL7 polypeptide, wherein the portion comprises: a uracil at a position corresponding to position
- 25 529 according to SEQ ID NO:8, or the complement thereof; a uracil at a position corresponding to position 525 according to SEQ ID NO:9, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:10, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:11, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ
- 30 ID NO:12, or the complement thereof;
- b) labeling the amplified nucleic acid molecule with a detectable label;

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- c) contacting the labeled nucleic acid molecule with a support comprising an alteration-specific probe, wherein the alteration-specific probe comprises a nucleotide sequence which hybridizes under stringent conditions to the nucleic acid sequence of the amplified nucleic acid molecule comprising: a uracil at a position corresponding to position 529 according to SEQ ID NO:8, or the complement thereof; a uracil at a position corresponding to position 525 according to SEQ ID NO:9, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:10, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:11, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:12, or the complement thereof; and
- d) detecting the detectable label.
60. The method according to any one of claims 43 to 50, wherein the sequence analysis comprises:
- a) amplifying at least a portion of the cDNA molecule that encodes the ANGPTL7 polypeptide, wherein the portion comprises: a thymine at a position corresponding to position 529 according to SEQ ID NO:14, or the complement thereof; a thymine at a position corresponding to position 525 according to SEQ ID NO:15, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:16, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:17, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18, or the complement thereof;
- b) labeling the amplified nucleic acid molecule with a detectable label;
- c) contacting the labeled nucleic acid molecule with a support comprising an alteration-specific probe, wherein the alteration-specific probe comprises a nucleotide sequence which hybridizes under stringent conditions to the nucleic acid sequence of the amplified nucleic acid molecule comprising: a thymine at a position corresponding to position 529 according to SEQ ID NO:14, or the complement thereof; a thymine at a position corresponding to position 525 according to SEQ ID NO:15, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:16, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:17, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18, or the complement thereof; and

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d) detecting the detectable label.

61. The method according to claim 60, wherein the nucleic acid molecule in the sample is mRNA and the mRNA is reverse-transcribed into cDNA prior to the amplifying step.

62. The method according to any one of claims 43 to 50, wherein the sequence analysis
5 comprises:

contacting the genomic nucleic acid molecule in the biological sample with an alteration-specific probe comprising a detectable label, wherein the alteration-specific probe comprises a nucleotide sequence which hybridizes under stringent conditions to the nucleotide sequence of the amplified nucleic acid molecule comprising: a thymine at a position
10 corresponding to position 4,291 according to SEQ ID NO:2, or the complement thereof; a thymine at a position corresponding to position 4,287 according to SEQ ID NO:3, or the complement thereof; an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4, or the complement thereof; an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5, or the complement thereof; or a cytosine at a position
15 corresponding to position 4,336 according to SEQ ID NO:6, or the complement thereof; and detecting the detectable label.

63. The method according to any one of claims 43 to 50, wherein the sequence analysis comprises:

contacting the mRNA molecule in the biological sample with an alteration-specific
20 probe comprising a detectable label, wherein the alteration-specific probe comprises a nucleotide sequence which hybridizes under stringent conditions to the nucleotide sequence of the amplified nucleic acid molecule comprising: a uracil at a position corresponding to position 529 according to SEQ ID NO:8, or the complement thereof; a uracil at a position corresponding to position 525 according to SEQ ID NO:9, or the complement thereof; an adenine at a position
25 corresponding to position 481 according to SEQ ID NO:10, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:11, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:12, or the complement thereof; and detecting the detectable label.

30 64. The method according to any one of claims 43 to 50, wherein the sequence analysis comprises:

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contacting the cDNA molecule produced from the mRNA molecule in the biological sample with an alteration-specific probe comprising a detectable label, wherein the alteration-specific probe comprises a nucleotide sequence which hybridizes under stringent conditions to the nucleotide sequence of the amplified nucleic acid molecule comprising: a thymine at a position corresponding to position 529 according to SEQ ID NO:14, or the complement thereof;
5 a thymine at a position corresponding to position 525 according to SEQ ID NO:15, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:16, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:17, or the complement thereof; or a cytosine at a position
10 corresponding to position 574 according to SEQ ID NO:18, or the complement thereof; and detecting the detectable label.

65. The method according to any one of claims 51 to 64, wherein the nucleic acid molecule is present within a cell obtained from the subject.

66. The method according to any one of claims 43 to 65, wherein the subject has
15 rheumatoid arthritis, Grave's disease, or ophthalmic inflammation.

67. The method according to claim 66, wherein the ophthalmic inflammation is chosen from uveitis, juvenile idiopathic arthritis uveitis, scleritis, blepharitis, conjunctivitis, iritis, and episcleritis, or any combination thereof.

68. The method according to any one of claims 43 to 67, wherein the glucocorticoid is
20 chosen from prednisone, prednisolone, methylprednisolone, dexamethasone, betamethasone, triamcinolone, beclometasone, fludrocortisone acetate, deoxycorticosterone acetate (DOCA), aldosterone, budesonide, mometasone furoate, fluticasone propionate, hydrocortisone, cortisone acetate, and fluticasone furoate, or any combination thereof.

69. The method according to any one of claims 43 to 68, wherein the ANGPTL7 inhibitor
25 comprises an inhibitory nucleic acid molecule.

70. The method according to claim 69, wherein the inhibitory nucleic acid molecule comprises an antisense nucleic acid molecule, a small interfering RNA (siRNA), or a short hairpin RNA (shRNA) that hybridizes to an ANGPTL7 nucleic acid molecule.

71. The method according to any one of claims 43 to 68, wherein the ANGPTL7 inhibitor
30 comprises a Cas protein and guide RNA (gRNA) that hybridizes to a gRNA recognition sequence within an ANGPTL7 genomic nucleic acid molecule.

72. The method according to claim 71, wherein the Cas protein is Cas9 or Cpf1.

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73. The method according to claim 71 or claim 72, wherein the gRNA recognition sequence includes or is proximate to a position corresponding to: position 4,291 according to SEQ ID NO:1, position 4,287 according to SEQ ID NO:1, position 4,243 according to SEQ ID NO:1, position 4,325 according to SEQ ID NO:1, or position 4,336 according to SEQ ID NO:1.
- 5 74. The method according to claim 71 or claim 72, wherein the gRNA recognition sequence is located from about 1000, from about 500, from about 400, from about 300, from about 200, from about 100, from about 50, from about 45, from about 40, from about 35, from about 30, from about 25, from about 20, from about 15, from about 10, or from about 5 nucleotides of a position corresponding to: position 4,291 according to SEQ ID NO:1, position 4,287 according to
- 10 SEQ ID NO:1, position 4,243 according to SEQ ID NO:1, position 4,325 according to SEQ ID NO:1, or position 4,336 according to SEQ ID NO:1.
75. The method according to claim 71 or claim 72, wherein a Protospacer Adjacent Motif (PAM) sequence is about 2 to about 6 nucleotides downstream of the gRNA recognition sequence.
- 15 76. The method according to any one of claims 71 to 75, wherein the gRNA comprises from about 17 nucleotides to about 23 nucleotides.
77. The method according to any one of claims 71 to 75, wherein the gRNA recognition sequence comprises a nucleotide sequence according to any one of SEQ ID NOs:25-165.
78. A method of identifying a subject undergoing glucocorticoid treatment having an
- 20 increased risk for developing a glucocorticoid-induced ophthalmic condition, the method comprising:
- determining or having determined the presence or absence of an Angiopoietin-Like 7 (ANGPTL7) predicted loss-of-function variant nucleic acid molecule encoding an ANGPTL7 polypeptide in a biological sample obtained from the subject;
- 25 wherein:
- when the subject is ANGPTL7 reference, then the subject has an increased risk for developing the glucocorticoid-induced ophthalmic condition; and
- when the subject is heterozygous or homozygous for an ANGPTL7 predicted loss-of-function variant, then the subject does not have an increased risk for
- 30 developing the glucocorticoid-induced ophthalmic condition.
79. The method according to claim 78, wherein the subject has rheumatoid arthritis, Grave's disease, or ophthalmic inflammation.

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80. The method according to claim 79, wherein the ophthalmic inflammation is chosen from uveitis, juvenile idiopathic arthritis uveitis, scleritis, blepharitis, conjunctivitis, iritis, and episcleritis, or any combination thereof.

81. The method according to any one of claims 78 to 80, wherein the glucocorticoid treatment is treatment with the glucocorticoid treatment is treatment with prednisone, prednisolone, methylprednisolone, dexamethasone, betamethasone, triamcinolone, beclometasone, fludrocortisone acetate, DOCA, aldosterone, budesonide, mometasone furoate, fluticasone propionate, hydrocortisone, cortisone acetate, or fluticasone furoate, difluprednate ophthalmic, fluorometholone, loteprednol etabonate, medrysone, rmexolone, fluocinolone acetonide, clobetasol, halobetasol, diflorasone, fluocinonide, flurandrenolide, Neo-Poly-Dex, tobramycin-dexamethasone, difluprednate, or any combination thereof.

82. The method according to any one of claims 78 to 81, wherein the ANGPTL7 predicted loss-of-function variant nucleic acid molecule is a nucleic acid molecule encoding Arg177STOP, Gln175His, Phe161Ile, Trp188STOP, Lys192Gln, Arg340His, Arg220His, Asn302Lys, or Arg220Cys.

83. The method according to any one of claims 78 to 81, wherein the ANGPTL7 predicted loss-of-function variant nucleic acid molecule is a nucleic acid molecule encoding Arg177STOP, Gln175His, Phe161Ile, Trp188STOP, or Lys192Gln.

84. The method according to claim 83, wherein the ANGPTL7 predicted loss-of-function variant nucleic acid molecule is:

a genomic nucleic acid molecule having a nucleotide sequence comprising: a thymine at a position corresponding to position 4,291 according to SEQ ID NO:2; a thymine at a position corresponding to position 4,287 according to SEQ ID NO:3; an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4; an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5; or a cytosine at a position corresponding to position 4,336 according to SEQ ID NO:6;

an mRNA molecule having a nucleotide sequence comprising: a uracil at a position corresponding to position 529 according to SEQ ID NO:8; a uracil at a position corresponding to position 525 according to SEQ ID NO:9; an adenine at a position corresponding to position 481 according to SEQ ID NO:10; an adenine at a position corresponding to position 563 according to SEQ ID NO:11; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:12; or

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a cDNA molecule produced from an mRNA molecule in the biological sample, wherein the cDNA molecule has a nucleotide sequence comprising: a thymine at a position corresponding to position 529 according to SEQ ID NO:14; a thymine at a position corresponding to position 525 according to SEQ ID NO:15; an adenine at a position
5 corresponding to position 481 according to SEQ ID NO:16; an adenine at a position corresponding to position 563 according to SEQ ID NO:17; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18.

85. The method according to any one of claims 78 to 84, wherein the determining step is carried out *in vitro*.

- 10 86. The method according to any one of claims 78 to 85, wherein the determining step comprises sequencing at least a portion of the nucleotide sequence of the ANGPTL7 genomic nucleic acid molecule in the biological sample, wherein the sequenced portion comprises a position corresponding to: position 4,291 according to SEQ ID NO:2, or the complement thereof; position 4,287 according to SEQ ID NO:3, or the complement thereof; position 4,243
15 according to SEQ ID NO:4, or the complement thereof; position 4,325 according to SEQ ID NO:5, or the complement thereof; or position 4,336 according to SEQ ID NO:6, or the complement thereof;

- wherein when the sequenced portion of the ANGPTL7 genomic nucleic acid molecule comprises: a thymine at a position corresponding to position 4,291 according to SEQ ID NO:2, a
20 thymine at a position corresponding to position 4,287 according to SEQ ID NO:3, an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4, an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5, or a cytosine at a position corresponding to position 4,336 according to SEQ ID NO:6, then the ANGPTL7 genomic nucleic acid molecule in the biological sample is an ANGPTL7 predicted loss-of-function variant
25 genomic nucleic acid molecule.

87. The method according to any one of claims 78 to 85, wherein the determining step comprises sequencing at least a portion of the nucleotide sequence of the ANGPTL7 mRNA molecule in the biological sample, wherein the sequenced portion comprises a position corresponding to: position 529 according to SEQ ID NO:8, or the complement thereof; position
30 525 according to SEQ ID NO:9, or the complement thereof; position 481 according to SEQ ID NO:10, or the complement thereof; position 563 according to SEQ ID NO:11, or the complement thereof; or position 574 according to SEQ ID NO:12, or the complement thereof;

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wherein when the sequenced portion of the ANGPTL7 mRNA molecule comprises: a uracil at a position corresponding to position 529 according to SEQ ID NO:8, a uracil at a position corresponding to position 525 according to SEQ ID NO:9, an adenine at a position corresponding to position 481 according to SEQ ID NO:10, an adenine at a position
5 corresponding to position 563 according to SEQ ID NO:11, or a cytosine at a position corresponding to position 574 according to SEQ ID NO:12, then the ANGPTL7 mRNA molecule in the biological sample is an ANGPTL7 predicted loss-of-function variant mRNA molecule.

88. The method according to any one of claims 78 to 85, wherein the determining step comprises sequencing at least a portion of the nucleotide sequence of the ANGPTL7 cDNA
10 molecule produced from an mRNA molecule in the biological sample, wherein the sequenced portion comprises a position corresponding to: position 529 according to SEQ ID NO:14, or the complement thereof; position 525 according to SEQ ID NO:15, or the complement thereof; position 481 according to SEQ ID NO:16, or the complement thereof; position 563 according to SEQ ID NO:17, or the complement thereof; or position 574 according to SEQ ID NO:18, or the
15 complement thereof;

wherein when the sequenced portion of the ANGPTL7 cDNA molecule comprises: a thymine at a position corresponding to position 529 according to SEQ ID NO:14, a thymine at a position corresponding to position 525 according to SEQ ID NO:15, an adenine at a position corresponding to position 481 according to SEQ ID NO:16, an adenine at a position
20 corresponding to position 563 according to SEQ ID NO:17, or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18, then the ANGPTL7 cDNA molecule in the biological sample is an ANGPTL7 predicted loss-of-function variant cDNA molecule.

89. The method according to any one of claims 78 to 85, wherein the determining step comprises:
25 a) contacting the biological sample with a primer hybridizing to a portion of the nucleotide sequence of the ANGPTL7 genomic nucleic acid molecule that is proximate to a position corresponding to: position 4,291 according to SEQ ID NO:2, position 4,287 according to SEQ ID NO:3, position 4,243 according to SEQ ID NO:4, position 4,325 according to SEQ ID NO:5, or position 4,336 according to SEQ ID NO:6;
30 b) extending the primer at least through the position of the nucleotide sequence of the ANGPTL7 genomic nucleic acid molecule corresponding to: position 4,291 according to SEQ ID

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NO:2, position 4,287 according to SEQ ID NO:3, position 4,243 according to SEQ ID NO:4, position 4,325 according to SEQ ID NO:5, or position 4,336 according to SEQ ID NO:6; and

c) determining whether the extension product of the primer comprises: a thymine at a position corresponding to position 4,291 according to SEQ ID NO:2, a thymine at a position
5 corresponding to position 4,287 according to SEQ ID NO:3, an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4, an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5, or a cytosine at a position corresponding to position 4,336 according to SEQ ID NO:6.

90. The method according to any one of claims 78 to 85, wherein the determining step
10 comprises:

a) contacting the biological sample with a primer hybridizing to a portion of the nucleotide sequence of the ANGPTL7 mRNA molecule that is proximate to a position corresponding to: position 529 according to SEQ ID NO:8, position 525 according to SEQ ID NO:9, position 481 according to SEQ ID NO:10, position 563 according to SEQ ID NO:11, or
15 position 574 according to SEQ ID NO:12;

b) extending the primer at least through the position of the nucleotide sequence of the ANGPTL7 mRNA molecule corresponding to: position 529 according to SEQ ID NO:8, position 525 according to SEQ ID NO:9, position 481 according to SEQ ID NO:10, position 563 according to SEQ ID NO:11, or position 574 according to SEQ ID NO:12; and

c) determining whether the extension product of the primer comprises: a uracil at a position corresponding to position 529 according to SEQ ID NO:8, a uracil at a position corresponding to position 525 according to SEQ ID NO:9, an adenine at a position corresponding to position 481 according to SEQ ID NO:10, an adenine at a position corresponding to position 563 according to SEQ ID NO:11, or a cytosine at a position
25 corresponding to position 574 according to SEQ ID NO:12.

91. The method according to any one of claims 78 to 85, wherein the determining step comprises:

a) contacting the biological sample with a primer hybridizing to a portion of the nucleotide sequence of the ANGPTL7 cDNA molecule produced from the mRNA molecule in the
30 biological sample that is proximate to a position corresponding to: position 529 according to SEQ ID NO:14, position 525 according to SEQ ID NO:15, position 481 according to SEQ ID NO:16, position 563 according to SEQ ID NO:17, or position 574 according to SEQ ID NO:18;

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b) extending the primer at least through the position of the nucleotide sequence of the ANGPTL7 cDNA molecule corresponding to: position 529 according to SEQ ID NO:14, position 525 according to SEQ ID NO:15, position 481 according to SEQ ID NO:16, position 563 according to SEQ ID NO:17, or position 574 according to SEQ ID NO:18; and

- 5 c) determining whether the extension product of the primer comprises: a thymine at a position corresponding to position 529 according to SEQ ID NO:14, a thymine at a position corresponding to position 525 according to SEQ ID NO:15, an adenine at a position corresponding to position 481 according to SEQ ID NO:16, an adenine at a position corresponding to position 563 according to SEQ ID NO:17, or a cytosine at a position
10 corresponding to position 574 according to SEQ ID NO:18.

92. The method according to any one of claims 86 to 91, wherein the determining step comprises sequencing the entire nucleic acid molecule.

93. The method according to any one of claims 78 to 85, wherein the determining step comprises:

- 15 a) amplifying at least a portion of the genomic nucleic acid molecule that encodes the ANGPTL7 polypeptide, wherein the portion comprises: a thymine at a position corresponding to position 4,291 according to SEQ ID NO:2, or the complement thereof; a thymine at a position corresponding to position 4,287 according to SEQ ID NO:3, or the complement thereof; an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4, or the
20 complement thereof; an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5, or the complement thereof; or a cytosine at a position corresponding to position 4,336 according to SEQ ID NO:6, or the complement thereof;

b) labeling the amplified nucleic acid molecule with a detectable label;

- c) contacting the labeled nucleic acid molecule with a support comprising an
25 alteration-specific probe, wherein the alteration-specific probe comprises a nucleotide sequence which hybridizes under stringent conditions to the nucleic acid sequence of the amplified nucleic acid molecule comprising: a thymine at a position corresponding to position 4,291 according to SEQ ID NO:2, or the complement thereof; a thymine at a position corresponding to position 4,287 according to SEQ ID NO:3, or the complement thereof; an
30 adenine at a position corresponding to position 4,243 according to SEQ ID NO:4, or the complement thereof; an adenine at a position corresponding to position 4,325 according to

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SEQ ID NO:5, or the complement thereof; or a cytosine at a position corresponding to position 4,336 according to SEQ ID NO:6, or the complement thereof; and

d) detecting the detectable label.

94. The method according to any one of claims 78 to 85, wherein the determining step
5 comprises:

a) amplifying at least a portion of the mRNA molecule that encodes the ANGPTL7 polypeptide, wherein the portion comprises: a uracil at a position corresponding to position 529 according to SEQ ID NO:8, or the complement thereof; a uracil at a position corresponding to position 525 according to SEQ ID NO:9, or the complement thereof; an adenine at a position
10 corresponding to position 481 according to SEQ ID NO:10, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:11, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:12, or the complement thereof;

b) labeling the amplified nucleic acid molecule with a detectable label;

15 c) contacting the labeled nucleic acid molecule with a support comprising an alteration-specific probe, wherein the alteration-specific probe comprises a nucleotide sequence which hybridizes under stringent conditions to the nucleic acid sequence of the amplified nucleic acid molecule comprising: a uracil at a position corresponding to position 529 according to SEQ ID NO:8, or the complement thereof; a uracil at a position corresponding to position 525 according to SEQ ID NO:9, or the complement thereof; an adenine at a position
20 corresponding to position 481 according to SEQ ID NO:10, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:11, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:12, or the complement thereof; and

25 d) detecting the detectable label.

95. The method according to any one of claims 78 to 85, wherein the determining step comprises:

a) amplifying at least a portion of the cDNA molecule that encodes the ANGPTL7 polypeptide, wherein the portion comprises: a thymine at a position corresponding to position 529 according to SEQ ID NO:14, or the complement thereof; a thymine at a position
30 corresponding to position 525 according to SEQ ID NO:15, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:16, or the

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complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:17, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18, or the complement thereof;

b) labeling the amplified nucleic acid molecule with a detectable label;

5 c) contacting the labeled nucleic acid molecule with a support comprising an alteration-specific probe, wherein the alteration-specific probe comprises a nucleotide sequence which hybridizes under stringent conditions to the nucleic acid sequence of the amplified nucleic acid molecule comprising: a thymine at a position corresponding to position 529 according to SEQ ID NO:14, or the complement thereof; a thymine at a position
10 corresponding to position 525 according to SEQ ID NO:15, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:16, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:17, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18, or the complement thereof; and

15 d) detecting the detectable label.

96. The method according to claim 95, wherein the nucleic acid molecule in the sample is mRNA and the mRNA is reverse-transcribed into cDNA prior to the amplifying step.

97. The method according to any one of claims 78 to 85, wherein the determining step comprises:

20 contacting the genomic nucleic acid molecule in the biological sample with an alteration-specific probe comprising a detectable label, wherein the alteration-specific probe comprises a nucleotide sequence which hybridizes under stringent conditions to the nucleotide sequence of the amplified nucleic acid molecule comprising: a thymine at a position corresponding to position 4,291 according to SEQ ID NO:2, or the complement thereof; a
25 thymine at a position corresponding to position 4,287 according to SEQ ID NO:3, or the complement thereof; an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4, or the complement thereof; an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5, or the complement thereof; or a cytosine at a position corresponding to position 4,336 according to SEQ ID NO:6, or the complement thereof; and
30 detecting the detectable label.

98. The method according to any one of claims 78 to 85, wherein the determining step comprises:

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contacting the mRNA molecule in the biological sample with an alteration-specific probe comprising a detectable label, wherein the alteration-specific probe comprises a nucleotide sequence which hybridizes under stringent conditions to the nucleotide sequence of the amplified nucleic acid molecule comprising: a uracil at a position corresponding to position 529 according to SEQ ID NO:8, or the complement thereof; a uracil at a position corresponding to position 525 according to SEQ ID NO:9, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:10, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:11, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:12, or the complement thereof; and

detecting the detectable label.

99. The method according to any one of claims 78 to 85, wherein the determining step comprises:

contacting the cDNA molecule produced from the mRNA molecule in the biological sample with an alteration-specific probe comprising a detectable label, wherein the alteration-specific probe comprises a nucleotide sequence which hybridizes under stringent conditions to the nucleotide sequence of the amplified nucleic acid molecule comprising: a thymine at a position corresponding to position 529 according to SEQ ID NO:14, or the complement thereof; a thymine at a position corresponding to position 525 according to SEQ ID NO:15, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:16, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:17, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18, or the complement thereof; and detecting the detectable label.

100. The method according to any one of claims 78 to 99, wherein the nucleic acid molecule is present within a cell obtained from the subject.

101. The method according to any one of claims 78 to 100, wherein the subject is ANGPTL7 reference, and the subject is administered or continued to be administered the glucocorticoid in a standard dosage amount, and is further administered an ANGPTL7 inhibitor.

102. The method according to any one of claims 78 to 100, wherein the subject is heterozygous for an ANGPTL7 predicted loss-of-function variant, and the subject is

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administered or continued to be administered the glucocorticoid in an amount that is the same as or higher than a standard dosage amount, and is further administered an ANGPTL7 inhibitor.

103. The method according to any one of claims 78 to 100, wherein the subject is homozygous for an ANGPTL7 predicted loss-of-function variant, and the subject is administered
5 or continued to be administered the glucocorticoid in an amount that is the same as or higher than a standard dosage amount.

104. The method according to claim 101 or claim 102, wherein the ANGPTL7 inhibitor comprises an inhibitory nucleic acid molecule.

105. The method according to claim 104, wherein the inhibitory nucleic acid molecule
10 comprises an antisense nucleic acid molecule, a small interfering RNA (siRNA), or a short hairpin RNA (shRNA) that hybridizes to an ANGPTL7 nucleic acid molecule.

106. The method according to claim 101 or claim 102, wherein the ANGPTL7 inhibitor comprises a Cas protein and guide RNA (gRNA) that hybridizes to a gRNA recognition sequence within an ANGPTL7 genomic nucleic acid molecule.

15 107. The method according to claim 106, wherein the Cas protein is Cas9 or Cpf1.

108. The method according to claim 106 or claim 107, wherein the gRNA recognition sequence includes or is proximate to a position corresponding to: position 4,291 according to SEQ ID NO:1, position 4,287 according to SEQ ID NO:1, position 4,243 according to SEQ ID NO:1, position 4,325 according to SEQ ID NO:1, or position 4,336 according to SEQ ID NO:1.

20 109. The method according to claim 106 or claim 107, wherein the gRNA recognition sequence is located from about 1000, from about 500, from about 400, from about 300, from about 200, from about 100, from about 50, from about 45, from about 40, from about 35, from about 30, from about 25, from about 20, from about 15, from about 10, or from about 5 nucleotides of a position corresponding to: position 4,291 according to SEQ ID NO:1, position
25 4,287 according to SEQ ID NO:1, position 4,243 according to SEQ ID NO:1, position 4,325 according to SEQ ID NO:1, or position 4,336 according to SEQ ID NO:1.

110. The method according to claim 106 or claim 107, wherein a Protospacer Adjacent Motif (PAM) sequence is about 2 to about 6 nucleotides downstream of the gRNA recognition sequence.

30 111. The method according to any one of claims 106 to 110, wherein the gRNA comprises from about 17 nucleotides to about 23 nucleotides.

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112. The method according to any one of claims 106 to 110, wherein the gRNA recognition sequence comprises a nucleotide sequence according to any one of SEQ ID NOs:25-165.

113. A combination of a glucocorticoid and an Angiopoietin-Like 7 (ANGPTL7) inhibitor for use in the treatment of inflammation in a subject identified as having:

- 5 a genomic nucleic acid molecule having a nucleotide sequence encoding an ANGPTL7 polypeptide, wherein the nucleotide sequence comprises: a thymine at a position corresponding to position 4,291 according to SEQ ID NO:2, or the complement thereof; a thymine at a position corresponding to position 4,287 according to SEQ ID NO:3, or the complement thereof; an adenine at a position corresponding to position 4,243 according to
10 SEQ ID NO:4, or the complement thereof; an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5, or the complement thereof; or a cytosine at a position corresponding to position 4,336 according to SEQ ID NO:6, or the complement thereof;
- a mRNA molecule having a nucleotide sequence encoding an ANGPTL7 polypeptide, wherein the nucleotide sequence comprises: a uracil at a position corresponding to position
15 529 according to SEQ ID NO:8, or the complement thereof; a uracil at a position corresponding to position 525 according to SEQ ID NO:9, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:10, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:11, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ
20 ID NO:12, or the complement thereof; or
- a cDNA molecule having a nucleotide sequence encoding an ANGPTL7 polypeptide, wherein the nucleotide sequence comprises: a thymine at a position corresponding to position 529 according to SEQ ID NO:14, or the complement thereof; a thymine at a position corresponding to position 525 according to SEQ ID NO:15, or the complement thereof; an
25 adenine at a position corresponding to position 481 according to SEQ ID NO:16, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:17, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18, or the complement thereof.

114. A combination of a glucocorticoid and an Angiopoietin-Like 7 (ANGPTL7) inhibitor for
30 use in the preparation of a medicament for treating inflammation in a subject identified as having:

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a genomic nucleic acid molecule having a nucleotide sequence encoding an ANGPTL7 polypeptide, wherein the nucleotide sequence comprises: a thymine at a position corresponding to position 4,291 according to SEQ ID NO:2, or the complement thereof; a thymine at a position corresponding to position 4,287 according to SEQ ID NO:3, or the complement thereof; an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4, or the complement thereof; an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5, or the complement thereof; or a cytosine at a position corresponding to position 4,336 according to SEQ ID NO:6, or the complement thereof;

an mRNA molecule having a nucleotide sequence encoding an ANGPTL7 polypeptide, wherein the nucleotide sequence comprises: a uracil at a position corresponding to position 529 according to SEQ ID NO:8, or the complement thereof; a uracil at a position corresponding to position 525 according to SEQ ID NO:9, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:10, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:11, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:12, or the complement thereof; or

a cDNA molecule having a nucleotide sequence encoding an ANGPTL7 polypeptide, wherein the nucleotide sequence comprises: a thymine at a position corresponding to position 529 according to SEQ ID NO:14, or the complement thereof; a thymine at a position corresponding to position 525 according to SEQ ID NO:15, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:16, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:17, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18, or the complement thereof.

115. The method according to claim 113 or claim 114, wherein the subject has rheumatoid arthritis, Grave's disease, or ophthalmic inflammation.

116. The method according to claim 115, wherein the ophthalmic inflammation is chosen from uveitis, juvenile idiopathic arthritis uveitis, scleritis, blepharitis, conjunctivitis, iritis, and episcleritis, or any combination thereof.

117. The method according to any one of claims 113 to 116, wherein the glucocorticoid is chosen from prednisone, prednisolone, methylprednisolone, dexamethasone, betamethasone, triamcinolone, beclometasone, fludrocortisone acetate, deoxycorticosterone acetate (DOCA),

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aldosterone, budesonide, mometasone furoate, fluticasone propionate, hydrocortisone, cortisone acetate, and fluticasone furoate, or any combination thereof.

118. The method according to any one of claims 113 to 117, wherein the ANGPTL7 inhibitor comprises an inhibitory nucleic acid molecule.

5 119. The method according to claim 118, wherein the inhibitory nucleic acid molecule comprises an antisense nucleic acid molecule, a small interfering RNA (siRNA), or a short hairpin RNA (shRNA) that hybridizes to an ANGPTL7 nucleic acid molecule.

120. The method according to any one of claims 113 to 117, wherein the ANGPTL7 inhibitor comprises a Cas protein and guide RNA (gRNA) that hybridizes to a gRNA recognition sequence
10 within an ANGPTL7 genomic nucleic acid molecule.

121. The method according to claim 120, wherein the Cas protein is Cas9 or Cpf1.

122. The method according to claim 120 or claim 121, wherein the gRNA recognition sequence includes or is proximate to a position corresponding to: position 4,291 according to SEQ ID NO:1, position 4,287 according to SEQ ID NO:1, position 4,243 according to SEQ ID NO:1,
15 position 4,325 according to SEQ ID NO:1, or position 4,336 according to SEQ ID NO:1.

123. The method according to claim 120 or claim 121, wherein the gRNA recognition sequence is located from about 1000, from about 500, from about 400, from about 300, from about 200, from about 100, from about 50, from about 45, from about 40, from about 35, from about 30, from about 25, from about 20, from about 15, from about 10, or from about 5
20 nucleotides of a position corresponding to: position 4,291 according to SEQ ID NO:1, position 4,287 according to SEQ ID NO:1, position 4,243 according to SEQ ID NO:1, position 4,325 according to SEQ ID NO:1, or position 4,336 according to SEQ ID NO:1.

124. The method according to claim 120 or claim 121, wherein a Protospacer Adjacent Motif (PAM) sequence is about 2 to about 6 nucleotides downstream of the gRNA recognition
25 sequence.

125. The method according to any one of claims 120 to 124, wherein the gRNA comprises from about 17 nucleotides to about 23 nucleotides.

126. The method according to any one of claims 120 to 124, wherein the gRNA recognition sequence comprises a nucleotide sequence according to any one of SEQ ID NOs:25-165.

30 127. An Angiopoietin-Like 7 (ANGPTL7) inhibitor for use in decreasing or preventing a glucocorticoid-induced ophthalmic condition in a subject undergoing glucocorticoid treatment, wherein the subject is identified as being:

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a) ANGPTL7 reference for an ANGPTL7 genomic nucleic acid molecule, an ANGPTL7 mRNA molecule, or an ANGPTL7 cDNA molecule; or

b) heterozygous for: i) a genomic nucleic acid molecule having a nucleotide sequence encoding an ANGPTL7 polypeptide, wherein the nucleotide sequence comprises: a thymine at a position corresponding to position 4,291 according to SEQ ID NO:2, or the complement thereof; a thymine at a position corresponding to position 4,287 according to SEQ ID NO:3, or the complement thereof; an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4, or the complement thereof; an adenine at a position corresponding to position 4,325 according to SEQ ID NO:5, or the complement thereof; or a cytosine at a position corresponding to position 4,336 according to SEQ ID NO:6, or the complement thereof; ii) an mRNA molecule having a nucleotide sequence encoding an ANGPTL7 polypeptide, wherein the nucleotide sequence comprises: a uracil at a position corresponding to position 529 according to SEQ ID NO:8, or the complement thereof; a uracil at a position corresponding to position 525 according to SEQ ID NO:9, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:10, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:11, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:12, or the complement thereof; or iii) a cDNA molecule having a nucleotide sequence encoding an ANGPTL7 polypeptide, wherein the nucleotide sequence comprises: a thymine at a position corresponding to position 529 according to SEQ ID NO:14, or the complement thereof; a thymine at a position corresponding to position 525 according to SEQ ID NO:15, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:16, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:17, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18, or the complement thereof.

128. An Angiopoietin-Like 7 (ANGPTL7) inhibitor for use in the preparation of a medicament for decreasing or preventing a glucocorticoid-induced ophthalmic condition in a subject undergoing glucocorticoid treatment, wherein the subject is identified as being:

a) ANGPTL7 reference for an ANGPTL7 genomic nucleic acid molecule, an ANGPTL7 mRNA molecule, or an ANGPTL7 cDNA molecule; or

b) heterozygous for: i) a genomic nucleic acid molecule having a nucleotide sequence encoding an ANGPTL7 polypeptide, wherein the nucleotide sequence comprises: a thymine at a

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- position corresponding to position 4,291 according to SEQ ID NO:2, or the complement thereof; a thymine at a position corresponding to position 4,287 according to SEQ ID NO:3, or the complement thereof; an adenine at a position corresponding to position 4,243 according to SEQ ID NO:4, or the complement thereof; an adenine at a position corresponding to position
- 5 4,325 according to SEQ ID NO:5, or the complement thereof; or a cytosine at a position corresponding to position 4,336 according to SEQ ID NO:6, or the complement thereof; ii) an mRNA molecule having a nucleotide sequence encoding an ANGPTL7 polypeptide, wherein the nucleotide sequence comprises: a uracil at a position corresponding to position 529 according to SEQ ID NO:8, or the complement thereof; a uracil at a position corresponding to position 525
- 10 according to SEQ ID NO:9, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:10, or the complement thereof; an adenine at a position corresponding to position 563 according to SEQ ID NO:11, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:12, or the complement thereof; or iii) a cDNA molecule having a nucleotide sequence encoding an
- 15 ANGPTL7 polypeptide, wherein the nucleotide sequence comprises: a thymine at a position corresponding to position 529 according to SEQ ID NO:14, or the complement thereof; a thymine at a position corresponding to position 525 according to SEQ ID NO:15, or the complement thereof; an adenine at a position corresponding to position 481 according to SEQ ID NO:16, or the complement thereof; an adenine at a position corresponding to position 563
- 20 according to SEQ ID NO:17, or the complement thereof; or a cytosine at a position corresponding to position 574 according to SEQ ID NO:18, or the complement thereof.
129. The method according to claim 127 or claim 128, wherein the subject has inflammation, rheumatoid arthritis, Grave's disease, or ophthalmic inflammation.
130. The method according to claim 129, wherein the ophthalmic inflammation is chosen
- 25 from uveitis, juvenile idiopathic arthritis uveitis, scleritis, blepharitis, conjunctivitis, iritis, and episcleritis, or any combination thereof.
131. The method according to any one of claims 127 to 128, wherein the glucocorticoid treatment is treatment with the glucocorticoid treatment is treatment with prednisone, prednisolone, methylprednisolone, dexamethasone, betamethasone, triamcinolone,
- 30 beclometasone, fludrocortisone acetate, DOCA, aldosterone, budesonide, mometasone furoate, fluticasone propionate, hydrocortisone, cortisone acetate, or fluticasone furoate, difluprednate ophthalmic, fluorometholone, loteprednol etabonate, medrysone, rmexolone,

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fluocinolone acetonide, clobetasol, halobetasol, diflorasone, fluocinonide, flurandrenolide, Neo-Poly-Dex, tobramycin-dexamethasone, difluprednate, or any combination thereof.

132. The method according to any one of claims 127 to 131, wherein the ANGPTL7 inhibitor comprises an inhibitory nucleic acid molecule.

5 133. The method according to claim 132, wherein the inhibitory nucleic acid molecule comprises an antisense nucleic acid molecule, a small interfering RNA (siRNA), or a short hairpin RNA (shRNA) that hybridizes to an ANGPTL7 nucleic acid molecule.

134. The method according to any one of claims 127 to 131, wherein the ANGPTL7 inhibitor comprises a Cas protein and guide RNA (gRNA) that hybridizes to a gRNA recognition sequence
10 within an ANGPTL7 genomic nucleic acid molecule.

135. The method according to claim 134, wherein the Cas protein is Cas9 or Cpf1.

136. The method according to claim 134 or claim 135, wherein the gRNA recognition sequence includes or is proximate to a position corresponding to: position 4,291 according to SEQ ID NO:1, position 4,287 according to SEQ ID NO:1, position 4,243 according to SEQ ID NO:1,
15 position 4,325 according to SEQ ID NO:1, or position 4,336 according to SEQ ID NO:1.

137. The method according to claim 134 or claim 135, wherein the gRNA recognition sequence is located from about 1000, from about 500, from about 400, from about 300, from about 200, from about 100, from about 50, from about 45, from about 40, from about 35, from about 30, from about 25, from about 20, from about 15, from about 10, or from about 5
20 nucleotides of a position corresponding to: position 4,291 according to SEQ ID NO:1, position 4,287 according to SEQ ID NO:1, position 4,243 according to SEQ ID NO:1, position 4,325 according to SEQ ID NO:1, or position 4,336 according to SEQ ID NO:1.

138. The method according to claim 134 or claim 135, wherein a Protospacer Adjacent Motif (PAM) sequence is about 2 to about 6 nucleotides downstream of the gRNA recognition
25 sequence.

139. The method according to any one of claims 134 to 138, wherein the gRNA comprises from about 17 nucleotides to about 23 nucleotides.

140. The method according to any one of claims 134 to 138, wherein the gRNA recognition sequence comprises a nucleotide sequence according to any one of SEQ ID NOs:25-165.

30 141. A method of treating a subject having inflammation, the method comprising administering an Angiopoietin-Like 7 (ANGPTL7) inhibitor and a glucocorticoid to the subject, wherein the ANGPTL7 inhibitor is a double stranded ribonucleic acid (dsRNA) inhibitory nucleic

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acid molecule for inhibiting expression of ANGPTL7, wherein the dsRNA inhibitory nucleic acid molecule comprises a sense strand and an antisense strand forming a double stranded region, wherein the antisense strand comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, from one of the antisense sequences listed in any one of Tables 4, 5, 6, 7, or 8, and wherein the sense strand comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, from a sense sequence listed in any one of Tables 4, 5, 6, 7, or 8 that corresponds to the antisense sequence.

142. The method according to claim 141, wherein the sense strand comprises AGACAGUAUAAGCAAGGGUUA and the antisense strand comprises UAACCCUUGCUUAUACUGUCUCC, or the sense strand comprises ACACUCCUUGUGUCUAUAGA and the antisense strand comprises UCUAUAGACACAAGGAAGUGUCG.

143. A method of treating a subject having rheumatoid arthritis, the method comprising administering an Angiopoietin-Like 7 (ANGPTL7) inhibitor and a glucocorticoid to the subject, wherein the ANGPTL7 inhibitor is a double stranded ribonucleic acid (dsRNA) inhibitory nucleic acid molecule for inhibiting expression of ANGPTL7, wherein the dsRNA inhibitory nucleic acid molecule comprises a sense strand and an antisense strand forming a double stranded region, wherein the antisense strand comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, from one of the antisense sequences listed in any one of Tables 4, 5, 6, 7, or 8, and wherein the sense strand comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, from a sense sequence listed in any one of Tables 4, 5, 6, 7, or 8 that corresponds to the antisense sequence.

144. The method according to claim 143, wherein the sense strand comprises AGACAGUAUAAGCAAGGGUUA and the antisense strand comprises UAACCCUUGCUUAUACUGUCUCC, or the sense strand comprises ACACUCCUUGUGUCUAUAGA and the antisense strand comprises UCUAUAGACACAAGGAAGUGUCG.

145. A method of treating a subject having Grave's disease, the method comprising administering an Angiopoietin-Like 7 (ANGPTL7) inhibitor and a glucocorticoid to the subject, wherein the ANGPTL7 inhibitor is a double stranded ribonucleic acid (dsRNA) inhibitory nucleic

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acid molecule for inhibiting expression of ANGPTL7, wherein the dsRNA inhibitory nucleic acid molecule comprises a sense strand and an antisense strand forming a double stranded region, wherein the antisense strand comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, from one of the antisense sequences listed in any one of Tables 4, 5, 6, 7, or 8, and wherein the sense strand comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, from a sense sequence listed in any one of Tables 4, 5, 6, 7, or 8 that corresponds to the antisense sequence.

146. The method according to claim 145, wherein the sense strand comprises AGACAGUAUAAGCAAGGGUUA and the antisense strand comprises UAACCCUUGCUUAUACUGUCUCC, or the sense strand comprises ACACUCCUUGUGUCUAUAGA and the antisense strand comprises UCUAUAGACACAAGGAAGUGUCG.

147. A method of treating a subject having ophthalmic inflammation, the method comprising administering an Angiopoietin-Like 7 (ANGPTL7) inhibitor and a glucocorticoid to the subject, wherein the ANGPTL7 inhibitor is a double stranded ribonucleic acid (dsRNA) inhibitory nucleic acid molecule for inhibiting expression of ANGPTL7, wherein the dsRNA inhibitory nucleic acid molecule comprises a sense strand and an antisense strand forming a double stranded region, wherein the antisense strand comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, from one of the antisense sequences listed in any one of Tables 4, 5, 6, 7, or 8, and wherein the sense strand comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, from a sense sequence listed in any one of Tables 4, 5, 6, 7, or 8 that corresponds to the antisense sequence.

148. The method according to claim 147, wherein the sense strand comprises AGACAGUAUAAGCAAGGGUUA and the antisense strand comprises UAACCCUUGCUUAUACUGUCUCC, or the sense strand comprises ACACUCCUUGUGUCUAUAGA and the antisense strand comprises UCUAUAGACACAAGGAAGUGUCG.

149. The method according to claim 147 or claim 148, wherein the ophthalmic inflammation is chosen from uveitis, juvenile idiopathic arthritis uveitis, scleritis, blepharitis, conjunctivitis, iritis, and episcleritis, or any combination thereof.

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150. A method of decreasing a glucocorticoid-induced ophthalmic condition in a subject treated with a glucocorticoid, the method comprising administering an Angiopoietin-Like 7 (ANGPTL7) inhibitor to the subject, wherein the ANGPTL7 inhibitor is a double stranded ribonucleic acid (dsRNA) inhibitory nucleic acid molecule for inhibiting expression of ANGPTL7,
- 5 wherein the dsRNA inhibitory nucleic acid molecule comprises a sense strand and an antisense strand forming a double stranded region, wherein the antisense strand comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, from one of the antisense sequences listed in any one of Tables 4, 5, 6, 7, or 8, and wherein the sense strand comprises a nucleotide sequence comprising at least 15 contiguous nucleotides,
- 10 with 0, 1, 2, or 3 mismatches, from a sense sequence listed in any one of Tables 4, 5, 6, 7, or 8 that corresponds to the antisense sequence.
151. The method according to claim 150, wherein the sense strand comprises AGACAGUAUAAGCAAGGGUUA and the antisense strand comprises UAACCCUUGCUUAUACUGUCUCC, or the sense strand comprises
- 15 ACACUCCUUGUGUCUAUAGA and the antisense strand comprises UCUAUAGACACAAGGAAGUGUCG.
152. The method according to claim 150 or claim 151, wherein the glucocorticoid-induced ophthalmic condition is chosen from ocular hypertension, increased intraocular pressure (IOP), pre-glaucoma, glaucoma, decreased corneal hysteresis, and posterior subcapsular cataracts, or
- 20 any combination thereof.
153. A method of treating a subject having inflammation and undergoing glucocorticoid treatment, the method comprising administering an Angiopoietin-Like 7 (ANGPTL7) inhibitor to the subject, wherein the ANGPTL7 inhibitor is a double stranded ribonucleic acid (dsRNA) inhibitory nucleic acid molecule for inhibiting expression of ANGPTL7, wherein the dsRNA
- 25 inhibitory nucleic acid molecule comprises a sense strand and an antisense strand forming a double stranded region, wherein the antisense strand comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, from one of the antisense sequences listed in any one of Tables 4, 5, 6, 7, or 8, and wherein the sense strand comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, 1, 2, or
- 30 3 mismatches, from a sense sequence listed in any one of Tables 4, 5, 6, 7, or 8 that corresponds to the antisense sequence.

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154. The method according to claim 153, wherein the sense strand comprises AGACAGUAUAAGCAAGGGUUA and the antisense strand comprises UAACCCUUGCUUAUACUGUCUCC, or the sense strand comprises ACACUCCUUGUGUCUAUAGA and the antisense strand comprises

5 UCUAUAGACACAAGGAAGUGUCG.

155. A method of treating a subject having rheumatoid arthritis and undergoing glucocorticoid treatment, the method comprising administering an Angiopoietin-Like 7 (ANGPTL7) inhibitor to the subject, wherein the ANGPTL7 inhibitor is a double stranded ribonucleic acid (dsRNA) inhibitory nucleic acid molecule for inhibiting expression of ANGPTL7,
10 wherein the dsRNA inhibitory nucleic acid molecule comprises a sense strand and an antisense strand forming a double stranded region, wherein the antisense strand comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, from one of the antisense sequences listed in any one of Tables 4, 5, 6, 7, or 8, and wherein the sense strand comprises a nucleotide sequence comprising at least 15 contiguous nucleotides,
15 with 0, 1, 2, or 3 mismatches, from a sense sequence listed in any one of Tables 4, 5, 6, 7, or 8 that corresponds to the antisense sequence.

156. The method according to claim 155, wherein the sense strand comprises AGACAGUAUAAGCAAGGGUUA and the antisense strand comprises UAACCCUUGCUUAUACUGUCUCC, or the sense strand comprises
20 ACACUCCUUGUGUCUAUAGA and the antisense strand comprises UCUAUAGACACAAGGAAGUGUCG.

157. A method of treating a subject having Grave's disease and undergoing glucocorticoid treatment, the method comprising administering an Angiopoietin-Like 7 (ANGPTL7) inhibitor to the subject, wherein the ANGPTL7 inhibitor is a double stranded ribonucleic acid (dsRNA)
25 inhibitory nucleic acid molecule for inhibiting expression of ANGPTL7, wherein the dsRNA inhibitory nucleic acid molecule comprises a sense strand and an antisense strand forming a double stranded region, wherein the antisense strand comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, from one of the antisense sequences listed in any one of Tables 4, 5, 6, 7, or 8, and wherein the sense strand
30 comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, from a sense sequence listed in any one of Tables 4, 5, 6, 7, or 8 that corresponds to the antisense sequence.

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158. The method according to claim 157, wherein the sense strand comprises AGACAGUAUAAGCAAGGGUUA and the antisense strand comprises UAACCCUUGCUUAUACUGUCUCC, or the sense strand comprises ACACUCCUUGUGUCUAUAGA and the antisense strand comprises

5 UCUAUAGACACAAGGAAGUGUCG.

159. A method of treating a subject having ophthalmic inflammation and undergoing glucocorticoid treatment, the method comprising administering an Angiopoietin-Like 7 (ANGPTL7) inhibitor to the subject, wherein the ANGPTL7 inhibitor is a double stranded ribonucleic acid (dsRNA) inhibitory nucleic acid molecule for inhibiting expression of ANGPTL7, wherein the dsRNA inhibitory nucleic acid molecule comprises a sense strand and an antisense strand forming a double stranded region, wherein the antisense strand comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, from one of the antisense sequences listed in any one of Tables 4, 5, 6, 7, or 8, and wherein the sense strand comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, from a sense sequence listed in any one of Tables 4, 5, 6, 7, or 8 that corresponds to the antisense sequence.

160. The method according to claim 159, wherein the sense strand comprises AGACAGUAUAAGCAAGGGUUA and the antisense strand comprises UAACCCUUGCUUAUACUGUCUCC, or the sense strand comprises ACACUCCUUGUGUCUAUAGA and the antisense strand comprises UCUAUAGACACAAGGAAGUGUCG.

161. The method according to claim 159 or claim 160, wherein the ophthalmic inflammation is chosen from uveitis, juvenile idiopathic arthritis uveitis, scleritis, blepharitis, conjunctivitis, iritis, and episcleritis, or any combination thereof.

162. The method according to any one of claims 141 to 161, wherein the glucocorticoid is chosen from prednisone, prednisolone, methylprednisolone, dexamethasone, betamethasone, triamcinolone, beclometasone, fludrocortisone acetate, deoxycorticosterone acetate (DOCA), aldosterone, budesonide, mometasone furoate, fluticasone propionate, hydrocortisone, cortisone acetate, and fluticasone furoate, or any combination thereof.

163. The method according to any one of claims 153 to 161, wherein the glucocorticoid treatment is treatment with prednisone, prednisolone, methylprednisolone, dexamethasone, betamethasone, triamcinolone, beclometasone, fludrocortisone acetate, DOCA, aldosterone,

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budesonide, mometasone furoate, fluticasone propionate, hydrocortisone, cortisone acetate, or fluticasone furoate, difluprednate ophthalmic, fluorometholone, loteprednol etabonate, medrysone, rmexolone, fluocinolone acetonide, clobetasol, halobetasol, diflorasone, fluocinonide, flurandrenolide, Neo-Poly-Dex, tobramycin-dexamethasone, difluprednate, or any
5 combination thereof.