

COMPOUNDS AND METHODS FOR MODULATING FACTOR XII

Sequence Listing

The present application is being filed along with a Sequence Listing in electronic format. The Sequence Listing is provided as a file entitled BIOL0369WOSEQ_ST25.txt, created on December 8, 2021, which is 1031 KB in size. The information in the electronic format of the sequence listing is incorporated herein by reference in its entirety.

Field

Provided herein are compounds, methods, and pharmaceutical compositions for reducing an amount of Factor XII (FXII) RNA in a cell or a subject, and in certain instances reducing the amount of FXII protein in a cell or a subject. Such compounds, methods, and pharmaceutical compositions are useful to treat or prevent a thromboembolic condition. Such thromboembolic conditions include myocardial infarction (MI), stroke, limb ischemia and necrosis, and venous thromboembolism (VTE), including deep vein thrombosis (DVT) and pulmonary embolism (PE).

Background

The human *F12* gene encodes FXII protein, a zymogen that circulates in the blood stream. The zymogen is converted to an active enzyme (FXIIa) by plasma kallikrein (PK) or by its unique ability to auto-activate following binding to artificial or biologic surfaces. *In vivo*, FXIIa triggers the kallikrein-kinin system leading to release of bradykinin (BK) which induces microvascular permeability, nitric oxide-mediated vasodilation, hypotension, and inflammatory reactions such as swelling, hyperperfusion, and pain. FXIIa also initiates coagulation via the intrinsic pathway and promotes inflammation via the kallikrein-kinin system comprising, high molecular weight kininogen (HK) and PK.

FXII may contribute to a variety of inflammatory, life-threatening disease conditions, including hereditary angioedema (HAE) and thrombosis. HAE is a rare life-threatening inherited disorder characterized by recurrent episodes of acute swelling in multiple organs because of increased vascular permeability. An excess of FXII activity may trigger excessive BK formation or signaling, thereby contributing to the vascular permeability of hereditary angioedema. Thrombosis is a maladaptive process of vascular occlusion and remains a primary cause of vascular morbidity and mortality associated with myocardial infarction (MI), stroke, limb ischemia and necrosis, and venous thromboembolism (VTE), including deep vein thrombosis (DVT) and pulmonary embolism (PE). VTE is the third leading cause of vascular-related death, after MI and stroke, and is one of the leading causes of death in patients with cancer. While many thromboembolic conditions are due to acquired extrinsic issues, (*e.g.*, surgery, cancer, immobility), other thromboembolic conditions are due to a genetic mutation, (*e.g.*, antiphospholipid syndrome, Factor V Leiden thrombophilia). The most commonly used treatments for thromboembolic conditions (*e.g.*, warfarin, heparin) and newer direct oral anticoagulants all possess significant drawbacks, such as an increased risk of bleeding. It is

therefore an object herein to provide compounds, methods, and pharmaceutical compositions for the treatment and prevention of such thromboembolic conditions.

Summary of the Invention

Provided herein are compounds, methods and pharmaceutical compositions for reducing an amount of FXII RNA, and in certain embodiments reducing the amount or activity of FXII protein in a cell or a subject. In certain embodiments, compounds, methods and pharmaceutical compositions disclosed herein reduce FXII RNA, FXII protein, FXII activity, or a combination thereof, in the blood of a subject. In certain embodiments, the subject has or is at risk for a thromboembolic condition. In certain embodiments, the thromboembolic condition is deep vein thrombosis, venous thrombosis, arterial thrombosis, pulmonary embolism, myocardial infarction, or stroke. In certain embodiments, compounds useful for reducing the amount of FXII RNA, the amount of FXII protein, or FXII activity are oligomeric compounds. In certain embodiments, oligomeric compounds comprise modified oligonucleotides.

Also provided are herein are methods useful for preventing a thromboembolic condition and methods useful for ameliorating a symptom of a thromboembolic condition. Exemplary symptoms of a thromboembolic condition include, but are not limited to, pain, shortness of breath, heart burn, cold sweat, fatigue, lightheadedness, dizziness, swelling, cramping, and death.

Also provided are herein are methods useful for treating hereditary angioedema and methods useful for ameliorating a symptom of hereditary angioedema. Exemplary symptoms of hereditary angioedema include, but are not limited to, swelling, nausea, vomiting, itching, headache, fatigue, abdominal pain, shortness of breath, rhinitis, anaphylaxis, and bronchoconstriction.

Detailed Description of the Invention

It is to be understood that both the foregoing general description and the following detailed description are exemplary and explanatory only and are not restrictive. Herein, the use of the singular includes the plural unless specifically stated otherwise. As used herein, the use of “or” means “and/or” unless stated otherwise. Furthermore, the use of the term “including” as well as other forms, such as “includes” and “included”, is not limiting. Also, terms such as “element” or “component” encompass both elements and components comprising one unit and elements and components that comprise more than one subunit, unless specifically stated otherwise.

The section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described. All documents, or portions of documents, cited in this application, including, but not limited to, patents, patent applications, articles, books, and treatises, are hereby expressly incorporated-by-reference for the portions of the document discussed herein, as well as in their entirety.

Definitions

Unless specific definitions are provided, the nomenclature used in connection with, and the procedures

and techniques of, analytical chemistry, synthetic organic chemistry, and medicinal and pharmaceutical chemistry described herein are those well-known and commonly used in the art. Where permitted, all patents, applications, published applications and other publications and other data referred to throughout in the disclosure are incorporated by reference herein in their entirety.

5 Unless otherwise indicated, the following terms have the following meanings:

DEFINITIONS

As used herein, “2′-deoxynucleoside” means a nucleoside comprising a 2′-H(H) deoxyribosyl sugar moiety. In certain embodiments, a 2′-deoxynucleoside is a 2′-β-D-deoxynucleoside and comprises a 2′-β-D-deoxyribosyl sugar moiety, which has the β-D configuration as found in naturally occurring deoxyribonucleic acids (DNA). In certain embodiments, a 2′-deoxynucleoside may comprise a modified nucleobase or may
10 comprise an RNA nucleobase (uracil).

As used herein, “2′-MOE” or “2′-MOE sugar moiety” means a 2′-OCH₂CH₂OCH₃ group in place of the 2′-OH group of a ribosyl sugar moiety. “MOE” means methoxyethyl. Unless otherwise indicated, a 2′-MOE has the β-D stereochemical configuration.

15 As used herein, “2′-MOE nucleoside” means a nucleoside comprising a 2′-MOE sugar moiety.

As used herein, “2′-OMe” or “2′-O-methyl sugar moiety” means a 2′-OCH₃ group in place of the 2′-OH group of a ribosyl sugar moiety. Unless otherwise indicated, a 2′-OMe has the β-D stereochemical configuration.

As used herein, “2′-OMe nucleoside” means a nucleoside comprising a 2′-OMe sugar moiety.

20 As used herein, “2′-substituted nucleoside” means a nucleoside comprising a 2′-substituted sugar moiety. As used herein, “2′-substituted” in reference to a sugar moiety means a sugar moiety comprising at least one 2′-substituent group other than H or OH.

As used herein, “5-methyl cytosine” means a cytosine modified with a methyl group attached to the 5 position. A 5-methyl cytosine is a modified nucleobase.

25 As used herein, “administering” means providing a pharmaceutical agent to a subject.

As used herein, “ameliorate” in reference to a treatment means improvement in at least one symptom relative to the same symptom in the absence of the treatment. In certain embodiments, amelioration is the reduction in the severity or frequency of a symptom or the delayed onset or slowing of progression in the severity or frequency of a symptom.

30 As used herein, “antisense activity” means any detectable and/or measurable change attributable to the hybridization of an antisense compound to its target nucleic acid. In certain embodiments, antisense activity is a decrease in the amount or expression of a target nucleic acid or protein encoded by such target nucleic acid compared to target nucleic acid levels or target protein levels in the absence of the antisense compound.

35 As used herein, “antisense compound” means an oligomeric compound capable of achieving at least one antisense activity.

As used herein, “bicyclic nucleoside” or “BNA” means a nucleoside comprising a bicyclic sugar moiety.

As used herein, “bicyclic sugar” or “bicyclic sugar moiety” means a modified sugar moiety comprising two rings, wherein the second ring is formed via a bridge connecting two of the atoms of the first ring thereby forming a bicyclic structure. In certain embodiments, the first ring of the bicyclic sugar moiety is a furanosyl moiety. In certain embodiments, the bicyclic sugar moiety does not comprise a furanosyl moiety.

As used herein, “cell-targeting moiety” means a conjugate moiety that interacts with a cell or a portion thereof. In certain embodiments, the cell-targeting moiety binds a receptor on a surface of a cell.

As used herein, “cEt nucleoside” means a nucleoside comprising a cEt modified sugar moiety.

As used herein, “chirally enriched population” means a plurality of molecules of identical molecular formula, wherein the number or percentage of molecules within the population that contain a particular stereochemical configuration at a particular chiral center is greater than the number or percentage of molecules expected to contain the same particular stereochemical configuration at the same particular chiral center within the population if the particular chiral center were stereorandom. Chirally enriched populations of molecules having multiple chiral centers within each molecule may contain one or more stereorandom chiral centers. In certain embodiments, the molecules are modified oligonucleotides. In certain embodiments, the molecules are compounds comprising modified oligonucleotides.

As used herein, “cleavable moiety” means a bond or group of atoms that is cleaved under physiological conditions, for example, inside a cell, a subject, or a human.

As used herein, “complementary” in reference to an oligonucleotide means that at least 70% of the nucleobases of the oligonucleotide or one or more portions thereof and the nucleobases of a target nucleic acid or one or more portions thereof are capable of hydrogen bonding with one another when the nucleobase sequence of the oligonucleotide and the other nucleic acid are aligned in opposing directions. As used herein, complementary nucleobases means nucleobases that are capable of forming hydrogen bonds with one another. Complementary nucleobase pairs include adenine (A) and thymine (T), adenine (A) and uracil (U), cytosine (C) and guanine (G), 5-methyl cytosine (mC) and guanine (G). Complementary oligonucleotides and/or target nucleic acids need not have nucleobase complementarity at each nucleoside. Rather, some mismatches are tolerated. As used herein, “fully complementary” or “100% complementary” in reference to an oligonucleotide, or portion thereof, means that the oligonucleotide, or portion thereof, is complementary to another oligonucleotide or target nucleic acid at each nucleobase of the shorter of the two oligonucleotides, or at each nucleoside if the oligonucleotides are the same length.

As used herein, “conjugate group” means a group of atoms that is directly or indirectly attached to an oligonucleotide. Conjugate groups include a conjugate moiety and a conjugate linker that attaches the conjugate moiety to the oligonucleotide. In certain embodiments, the conjugate moiety comprises a cell-targeting moiety.

As used herein, “conjugate linker” means a single bond or a group of atoms comprising at least one bond that connects a conjugate moiety to an oligonucleotide.

As used herein, “conjugate moiety” means a group of atoms that is attached to an oligonucleotide via a conjugate linker.

5 As used herein, “constrained ethyl” or “cEt” or “cEt modified sugar moiety” means a β -D ribosyl bicyclic sugar moiety wherein the second ring of the bicyclic sugar is formed via a bridge connecting the 4'-carbon and the 2'-carbon of the β -D ribosyl sugar moiety, wherein the bridge has the formula 4'-CH(CH₃)-O-2', and wherein the methyl group of the bridge is in the *S* configuration.

As used herein, “contiguous” in the context of an oligonucleotide refers to nucleosides, nucleobases, sugar moieties, or internucleoside linkages that are immediately adjacent to each other. For example, “contiguous nucleobases” means nucleobases that are immediately adjacent to each other in a sequence.

As used herein, “FXII RNA” is the RNA expression product of a human *F12* gene.

As used herein, “FXII protein” is the protein expression product of a FXII RNA, including zymogen and activated forms FXII protein.

15 As used herein, “gapmer” means an oligonucleotide having a central region positioned between a 5'-region and a 3'-region. Each nucleoside of the 5'-region and the 3'-region comprises a modified sugar moiety. The 3'- and 5'-most nucleosides of the central region are 2'-deoxynucleosides. The “central region” may be referred to as a “gap”, and the “5'-region” and “3'-region” may also be referred to as a “wing.” The hybridization of a gapmer to a target nucleic acid results in RNase H mediated cleavage of the target nucleic acid.

As used herein, “hotspot region” is a range of nucleobases on a target nucleic acid that is amenable to oligomeric compound-mediated reduction of the amount or activity of the target nucleic acid.

As used herein, “hybridization” means the pairing or annealing of complementary oligonucleotides and/or nucleic acids. While not limited to a particular mechanism, the most common mechanism of hybridization involves hydrogen bonding, which may be Watson-Crick, Hoogsteen or reversed Hoogsteen hydrogen bonding, between complementary nucleobases.

As used herein, “identifying a subject at risk for developing a thromboembolic condition” means identifying a subject having been diagnosed with a thromboembolic condition or identifying a subject that has a risk factor for developing a thromboembolic condition.

30 As used herein, “internucleoside linkage” means the covalent linkage between contiguous nucleosides in an oligonucleotide. As used herein, “modified internucleoside linkage” means any internucleoside linkage other than a phosphodiester internucleoside linkage. “Phosphorothioate internucleoside linkage” is a modified internucleoside linkage in which one of the non-bridging oxygen atoms of a phosphodiester internucleoside linkage is replaced with a sulfur atom.

As used herein, “linker-nucleoside” means a nucleoside that links, either directly or indirectly, an oligonucleotide to a conjugate moiety. Linker-nucleosides are located within the conjugate linker of an

oligomeric compound. Linker-nucleosides are not considered part of the oligonucleotide portion of an oligomeric compound even if they are contiguous with the oligonucleotide.

As used herein, “mismatch” or “non-complementary” means a nucleobase of a first oligonucleotide that is not complementary with the corresponding nucleobase of a second oligonucleotide or target nucleic acid when the first and second oligonucleotide are aligned.

As used herein, “motif” means the pattern of unmodified and/or modified sugar moieties, nucleobases, and/or internucleoside linkages, in an oligonucleotide.

As used herein, “non-bicyclic modified sugar moiety” means a modified sugar moiety that comprises a modification, such as a substituent, that does not form a bridge between two atoms of the sugar to form a second ring.

As used herein, “nucleobase” means an unmodified nucleobase or a modified nucleobase. As used herein an “unmodified nucleobase” is adenine (A), thymine (T), cytosine (C), uracil (U), or guanine (G). As used herein, a “modified nucleobase” is a group of atoms other than unmodified A, T, C, U, or G capable of pairing with at least one unmodified nucleobase. A “5-methyl cytosine” is a modified nucleobase. A universal base is a modified nucleobase that can pair with any one of the five unmodified nucleobases. As used herein, “nucleobase sequence” means the order of contiguous nucleobases in a target nucleic acid or oligonucleotide independent of any sugar or internucleoside linkage modification.

As used herein, “nucleoside” means a compound comprising a nucleobase and a sugar moiety. The nucleobase and sugar moiety are each, independently, unmodified or modified. As used herein, “modified nucleoside” means a nucleoside comprising a modified nucleobase and/or a modified sugar moiety. Modified nucleosides include abasic nucleosides, which lack a nucleobase. “Linked nucleosides” are nucleosides that are connected in a contiguous sequence (i.e., no additional nucleosides are presented between those that are linked).

As used herein, “oligomeric compound” means an oligonucleotide and optionally one or more additional features, such as a conjugate group or terminal group. An oligomeric compound may be paired with a second oligomeric compound that is complementary to the first oligomeric compound or may be unpaired. A “singled-stranded oligomeric compound” is an unpaired oligomeric compound. The term “oligomeric duplex” means a duplex formed by two oligomeric compounds having complementary nucleobase sequences. Each oligomeric compound of an oligomeric duplex may be referred to as a “duplexed oligomeric compound.”

As used herein, “oligonucleotide” means a strand of linked nucleosides connected via internucleoside linkages, wherein each nucleoside and internucleoside linkage may be modified or unmodified. Unless otherwise indicated, oligonucleotides consist of 8-50 linked nucleosides. As used herein, “modified oligonucleotide” means an oligonucleotide, wherein at least one nucleoside or internucleoside linkage is modified. As used herein, “unmodified oligonucleotide” means an oligonucleotide that does not comprise any nucleoside modifications or internucleoside modifications.

As used herein, “pharmaceutically acceptable carrier or diluent” means any substance suitable for use in administering to a subject. Certain such carriers enable pharmaceutical compositions to be formulated as, for example, tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspension and lozenges for the oral ingestion by a subject. In certain embodiments, a pharmaceutically acceptable carrier or diluent is sterile water, sterile saline, or sterile buffer solution. In certain embodiments, a pharmaceutically acceptable carrier or diluent is phosphate buffered saline.

As used herein, “pharmaceutically acceptable salts” means physiologically and pharmaceutically acceptable salts of compounds. Pharmaceutically acceptable salts retain the desired biological activity of the parent compound and do not impart undesired toxicological effects thereto.

As used herein, “pharmaceutical composition” means a mixture of substances suitable for administering to a subject. For example, a pharmaceutical composition may comprise an oligomeric compound and a sterile aqueous solution. In certain embodiments, a pharmaceutical composition shows activity in free uptake assay in certain cell lines.

As used herein, “prevent” or “preventing” refers to delaying or forestalling the onset or development of a thromboembolic condition for a period of time or indefinitely.

As used herein, “prodrug” means a therapeutic agent in a form outside the body that is converted to a different form within a subject or cells thereof. Typically, conversion of a prodrug within the subject is facilitated by the action of an enzymes (*e.g.*, endogenous or viral enzyme) or chemicals present in cells or tissues and/or by physiologic conditions.

As used herein, “reducing the amount or activity,” or “inhibiting the amount or activity,” in connection with a gene transcript (RNA) refers to a reduction or blockade of the transcriptional expression or activity relative to the transcriptional expression or activity in an untreated or control sample and does not necessarily indicate a total elimination of transcriptional expression or activity.

As used herein, “reducing the amount or activity,” or “inhibiting the amount or activity,” in connection with a protein refers to a reduction or blockade of the protein’s expression or activity relative to the protein expression or activity in an untreated or control sample and does not necessarily indicate a total elimination of protein expression or activity.

As used herein, “RNA” means an RNA transcript and includes pre-mRNA and mature mRNA unless otherwise specified.

As used herein, “RNAi compound” means an antisense compound that acts, at least in part, through RISC or Ago2 to modulate a target nucleic acid and/or protein encoded by a target nucleic acid. RNAi compounds include, but are not limited to double-stranded siRNA, single-stranded RNA (ssRNA), and microRNA, including microRNA mimics. In certain embodiments, an RNAi compound modulates the amount, activity, and/or splicing of a target nucleic acid. The term RNAi compound excludes antisense compounds that act through RNase H.

As used herein, "self-complementary" in reference to an oligonucleotide means an oligonucleotide that at least partially hybridizes to itself.

As used herein, "standard cell assay" means the assay described in Example 1 and reasonable variations thereof.

5 As used herein, "stereorandom chiral center" in the context of a population of molecules of identical molecular formula means a chiral center having a random stereochemical configuration. For example, in a population of molecules comprising a stereorandom chiral center, the number of molecules having the (*S*) configuration of the stereorandom chiral center may be but is not necessarily the same as the number of molecules having the (*R*) configuration of the stereorandom chiral center. The stereochemical configuration
10 of a chiral center is considered random when it is the result of a synthetic method that is not designed to control the stereochemical configuration. In certain embodiments, a stereorandom chiral center is a stereorandom phosphorothioate internucleoside linkage.

As used herein, "subject" means a human or non-human subject.

As used herein, "sugar moiety" means an unmodified sugar moiety or a modified sugar moiety. As
15 used herein, "unmodified sugar moiety" means a 2'-OH(H) β -D-ribose moiety, as found in RNA (an "unmodified RNA sugar moiety"), or a 2'-H(H) β -D-deoxyribose moiety, as found in DNA (an "unmodified DNA sugar moiety"). Unmodified sugar moieties have one hydrogen at each of the 1', 3', and 4' positions, an oxygen at the 3' position, and two hydrogens at the 5' position. As used herein, "modified sugar moiety" or "modified sugar" means a modified furanosyl sugar moiety or a sugar surrogate.

20 As used herein, "sugar surrogate" means a modified sugar moiety having other than a furanosyl moiety that can link a nucleobase to another group, such as an internucleoside linkage, conjugate group, or terminal group in an oligonucleotide. Modified nucleosides comprising sugar surrogates can be incorporated into one or more positions within an oligonucleotide and such oligonucleotides are capable of hybridizing to complementary oligomeric compounds or target nucleic acids.

25 As used herein, "symptom" means any physical feature or test result that indicates the existence or extent of a disease or disorder. In certain embodiments, a symptom is apparent to a subject or to a medical professional examining or testing said subject.

As used herein, "target nucleic acid" and "target RNA" mean a nucleic acid that an antisense compound is designed to affect.

30 As used herein, "target region" means a portion of a target nucleic acid to which an oligomeric compound is designed to hybridize.

As used herein, "terminal group" means a chemical group or group of atoms that is covalently linked to a terminus of an oligonucleotide.

As used herein, "therapeutically effective amount" means an amount of a pharmaceutical agent that
35 provides a therapeutic benefit to a subject. For example, a therapeutically effective amount improves a symptom of a disease.

As used herein, “thromboembolic condition” means any disease or condition involving a thrombosis or an embolism. A thrombosis is a pathological development of a blood clot, and an embolism occurs when the blood clot migrates to another part of the body and interferes with organ function. Conditions in which a thrombosis and/or an embolism occur are collectively referred to as a thromboembolic condition. Depending on where the blood clot occurs or settles, it may result in a variety of thromboembolic conditions, *e.g.*, deep vein thrombosis (DVT), myocardial infarction (MI), pulmonary embolism (PE), and stroke. In certain embodiments, the thromboembolic condition comprises deep vein thrombosis, venous thrombosis, arterial thrombosis, pulmonary embolism, myocardial infarction, or stroke. Thromboembolic conditions may also be referred to as thromboembolic events or thrombotic events.

10 **CERTAIN EMBODIMENTS**

The present disclosure provides the following non-limiting numbered embodiments:

Embodiment 1. An oligomeric compound comprising a modified oligonucleotide consisting of 12 to 50 linked nucleosides wherein the nucleobase sequence of the modified oligonucleotide is at least 90% complementary to an equal length portion of a FXII RNA, and wherein the modified oligonucleotide comprises at least one modification selected from a modified sugar moiety and a modified internucleoside linkage.

Embodiment 2. An oligomeric compound comprising a modified oligonucleotide consisting of 12 to 50 linked nucleosides and having a nucleobase sequence comprising at least 12, 13, 14, 15, 16, 17, 18, 19, or 20 contiguous nucleobases of any of SEQ ID NOs: 20-5042.

20 Embodiment 3. An oligomeric compound comprising a modified oligonucleotide consisting of 12 to 50 linked nucleosides and having a nucleobase sequence comprising at least 12, 13, 14, 15, 16, 17, or 18 contiguous nucleobases of any of SEQ ID NOs: 3379 and 5006.

Embodiment 4. An oligomeric compound comprising a modified oligonucleotide consisting of 12 to 50 linked nucleosides and having a nucleobase sequence comprising at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, or at least 20 contiguous nucleobases complementary to: an equal length portion of nucleobases 1,899-1,979 of SEQ ID NO: 1; or an equal length portion of nucleobases 2,004-2,045 of SEQ ID NO: 1.

Embodiment 5. An oligomeric compound comprising a modified oligonucleotide consisting of 12 to 50 linked nucleosides and having a nucleobase sequence comprising at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, or at least 18 contiguous nucleobases of a sequence selected from: SEQ ID NOs: 92, 156, 270, 271, 345, 346, 420, 421, 496, 497, 571, 572, 653, 654, 728, 729, 802, 803, 877, 951, 1028, 1103, 1179, 1253, 1330, 1407, 1484, 1560, 1636, 1710, 1711, 1784, 1859, 1860, 1934, 1935, 2008, 2009, 2084, 2085, 2158, 2232, 2233, 2307, 2308, 2393, 2394, 2395, 2396,

2397, 2398, 2461, 2537, 2538, 2614, 2615, 2691, 2692, 2768, 2769, 2845, 2846, 2921, 2922, 2997, 2998, 3073, 3074, 3144, 3145, 3226, 3227, 3303, 3304, 3379, 3380, 3455, 3456, 3531, 3607, 3683, 3759, 3835, 3911, 4948, 4949, 4954, 4955, 4956, 4957, 4961, 4965, 4966, 4967, 4971, 4972, 4976, 4994, 4995, 4996, 4997, 4998, 4999, 5024, 5025, 5026, 5027, 5028, and 5029; or SEQ ID NOs: 95, 159, 162, 163, 164, 165, 347, 422, 498, 573, 953, 1030, 1105, 1255, 1332, 1409, 1486, 1562, 2309, 2463, 2540, 2617, 2694, 2771, 2848, 2924, 3000, 3076, 3147, 3229, 3306, 3382, 3457, 3533, 3609, 3685, 3761, 3837, 3913, 5000, 5001, 5002, 5003, 5004, 5005, 5006, 5031, 5032, 5033, 5034, 5035, 5036, and 5037.

Embodiment 6. The oligomeric compound of any of embodiments 1-5, wherein the modified oligonucleotide has a nucleobase sequence that is at least 80%, 85%, 90%, 95%, or 100% complementary to the nucleobase sequence of any one of SEQ ID NOS: 1-4 when measured across the entire nucleobase sequence of the modified oligonucleotide.

Embodiment 7. The oligomeric compound of any of embodiments 1-6, wherein the modified oligonucleotide comprises at least one modified nucleoside.

Embodiment 8. The oligomeric compound of embodiment 7, wherein the modified oligonucleotide comprises at least one modified nucleoside comprising a modified sugar moiety.

Embodiment 9. The oligomeric compound of embodiment 8, wherein the modified oligonucleotide comprises at least one modified nucleoside comprising a bicyclic sugar moiety.

Embodiment 10. The oligomeric compound of embodiment 9, wherein the modified oligonucleotide comprises at least one modified nucleoside comprising a bicyclic sugar moiety having a 2'-4' bridge, wherein the 2'-4' bridge is selected from -O-CH₂-; and -O-CH(CH₃)-.

Embodiment 11. The oligomeric compound of any of embodiments 8-10, wherein the modified oligonucleotide comprises at least one modified nucleoside comprising a non-bicyclic modified sugar moiety.

Embodiment 12. The oligomeric compound of embodiment 11, wherein the non-bicyclic modified sugar moiety is a 2'-MOE sugar moiety or 2'-OMe sugar moiety.

Embodiment 13. The oligomeric compound of any of embodiments 7-8, wherein the modified oligonucleotide comprises at least one modified nucleoside comprising a sugar surrogate.

Embodiment 14. The oligomeric compound of any of embodiments 1-13, wherein the modified oligonucleotide is a gapmer.

Embodiment 15. The oligomeric compound of any of embodiments 1-14, wherein the modified oligonucleotide has a sugar motif comprising: a 5'-region consisting of 1-6 linked 5'-region nucleosides; a

central region consisting of 6-10 linked central region nucleosides; and a 3'-region consisting of 1-6 linked 3'-region nucleosides, wherein each of the 5'-region nucleosides and each of the 3'-region nucleosides comprises a modified sugar moiety and each of the central region nucleosides comprises a 2'-β-D-deoxyribosyl sugar moiety.

- 5 Embodiment 16. The oligomeric compound of embodiment 15, wherein the 5'-region consists of 3 linked 5'-region nucleosides; the central region consists of 10 linked central region nucleosides; and the 3'-region consists of 3 linked 3'-region nucleosides, and wherein each of the 5'-region nucleosides and each of the 3'-region nucleosides comprises a cEt modified sugar moiety.

- 10 Embodiment 17. The oligomeric compound of any of embodiments 1-16, wherein the modified oligonucleotide comprises at least one modified internucleoside linkage.

Embodiment 18. The oligomeric compound of embodiment 17, wherein each internucleoside linkage of the modified oligonucleotide is a modified internucleoside linkage.

Embodiment 19. The oligomeric compound of embodiment 17 or 18, wherein each internucleoside linkage is a phosphorothioate internucleoside linkage.

- 15 Embodiment 20. The oligomeric compound of embodiment 17 or 18, wherein the modified oligonucleotide comprises at least one phosphodiester internucleoside linkage.

Embodiment 21. The oligomeric compound of embodiment 17, wherein each internucleoside linkage is independently selected from a phosphodiester internucleoside linkage and a phosphorothioate internucleoside linkage.

- 20 Embodiment 22. The oligomeric compound of any of embodiments 1-21, wherein the modified oligonucleotide comprises a modified nucleobase.

Embodiment 23. The oligomeric compound of embodiment 22, wherein the modified nucleobase is a 5-methyl cytosine.

- 25 Embodiment 24. The oligomeric compound of any of embodiments 1-23, wherein the modified oligonucleotide consists of 12-30, 12-22, 12-20, 14-18, 14-20, 15-17, 15-25, 16-20, 18-22 or 18-20 linked nucleosides.

Embodiment 25. The oligomeric compound of any of embodiments 1-23, wherein the modified oligonucleotide consists of 16 linked nucleosides.

- 30 Embodiment 26. The oligomeric compound of any of embodiments 1-25, consisting of the modified oligonucleotide.

Embodiment 27. The oligomeric compound of any of embodiments 1-25, comprising a conjugate group comprising a conjugate moiety and a conjugate linker.

Embodiment 28. The oligomeric compound of embodiment 27, wherein the conjugate linker consists of a single bond.

5 Embodiment 29. The oligomeric compound of embodiment 27, wherein the conjugate linker is cleavable.

Embodiment 30. The oligomeric compound of embodiment 27, wherein the conjugate linker comprises 1-3 linker-nucleosides.

Embodiment 31. The oligomeric compound of 27, wherein the oligomeric compound does not comprise a linker-nucleoside.

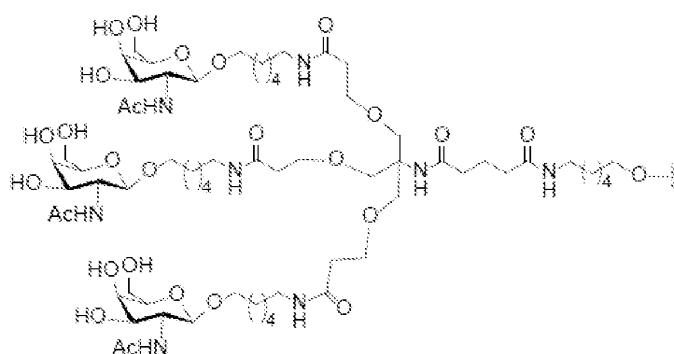
10 Embodiment 32. The oligomeric compound of any of embodiments 28-31, wherein the conjugate group is attached to the modified oligonucleotide at the 5'-end of the modified oligonucleotide.

Embodiment 33. The oligomeric compound of any of embodiments 28-31, wherein the conjugate group is attached to the modified oligonucleotide at the 3'-end of the modified oligonucleotide.

Embodiment 34. The oligomeric compound of any of embodiments 1-33, comprising a terminal group.

15 Embodiment 35. The oligomeric compound of any one of embodiments 1-34, wherein the conjugate group comprises a GalNAc moiety.

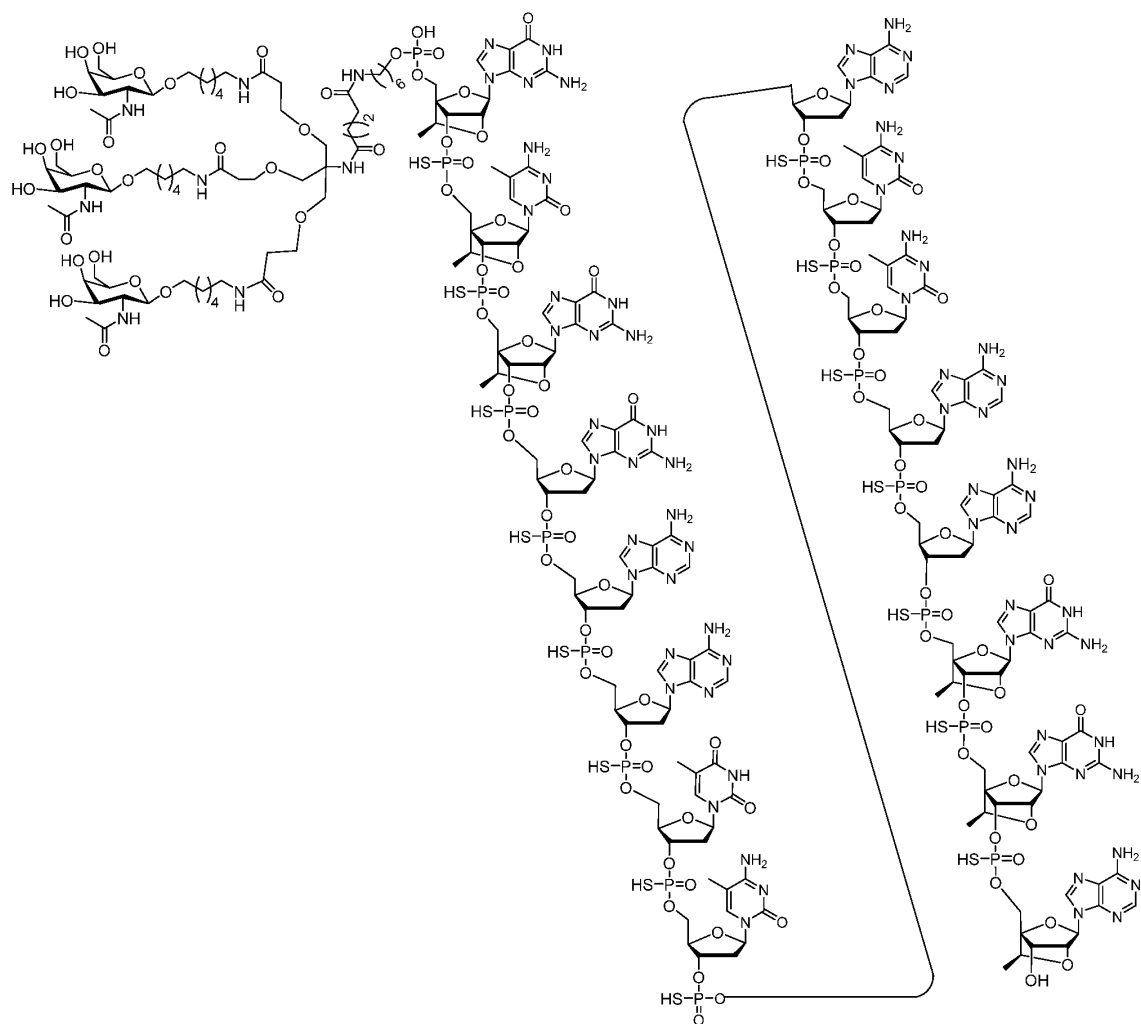
Embodiment 36. The oligomeric compound of anyone of embodiments 1-35, wherein the conjugate group comprises a cell-targeting moiety, a conjugate linker and a cleavable moiety, and wherein the cell-targeting moiety and the conjugate linker together have the following chemical structure:



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Embodiment 37. The oligomeric compound of any of embodiments 1-36, wherein the modified oligonucleotide is a single-stranded modified oligonucleotide.

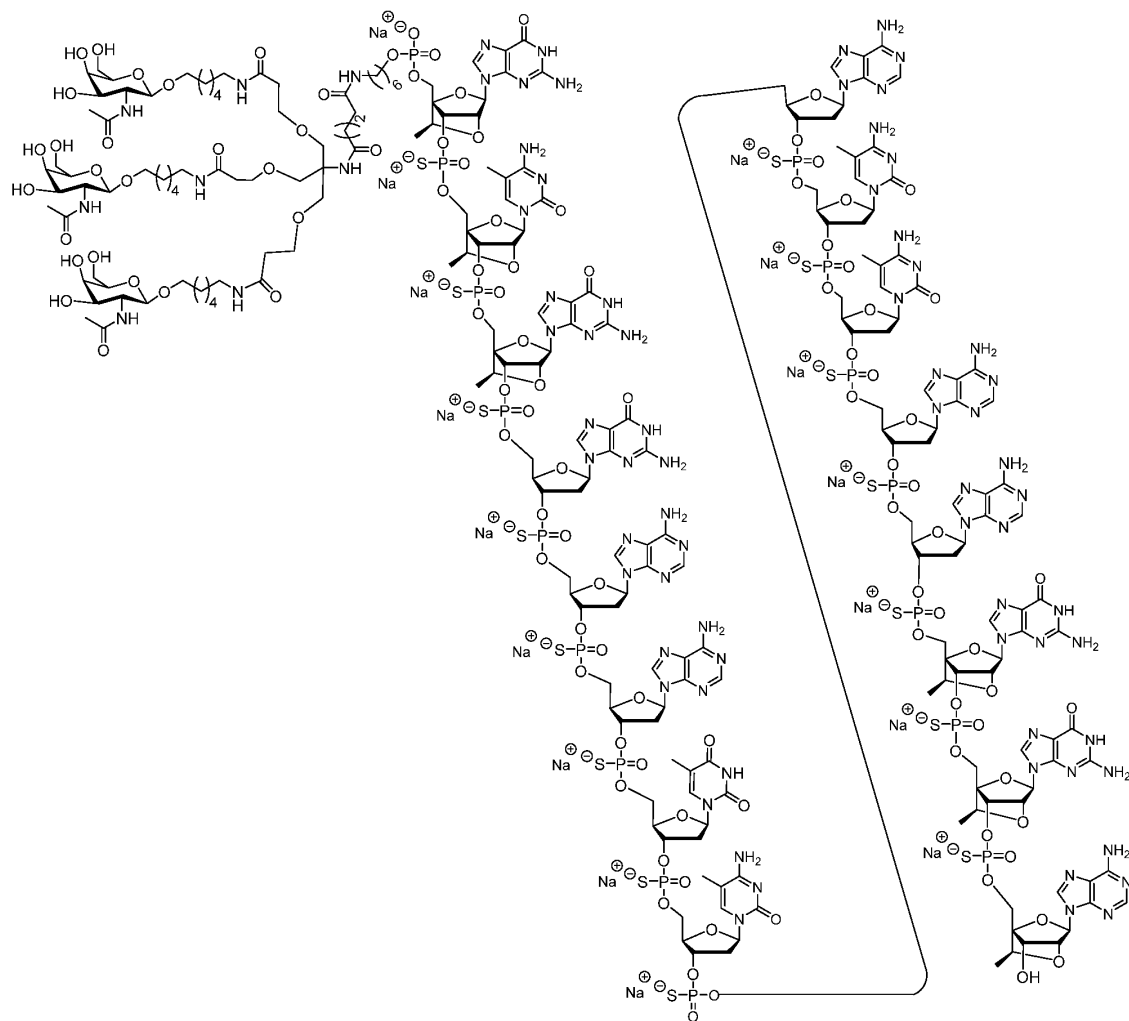
Embodiment 38. An oligomeric compound according to the following chemical structure:



(SEQ ID NO: 3379), or a salt thereof.

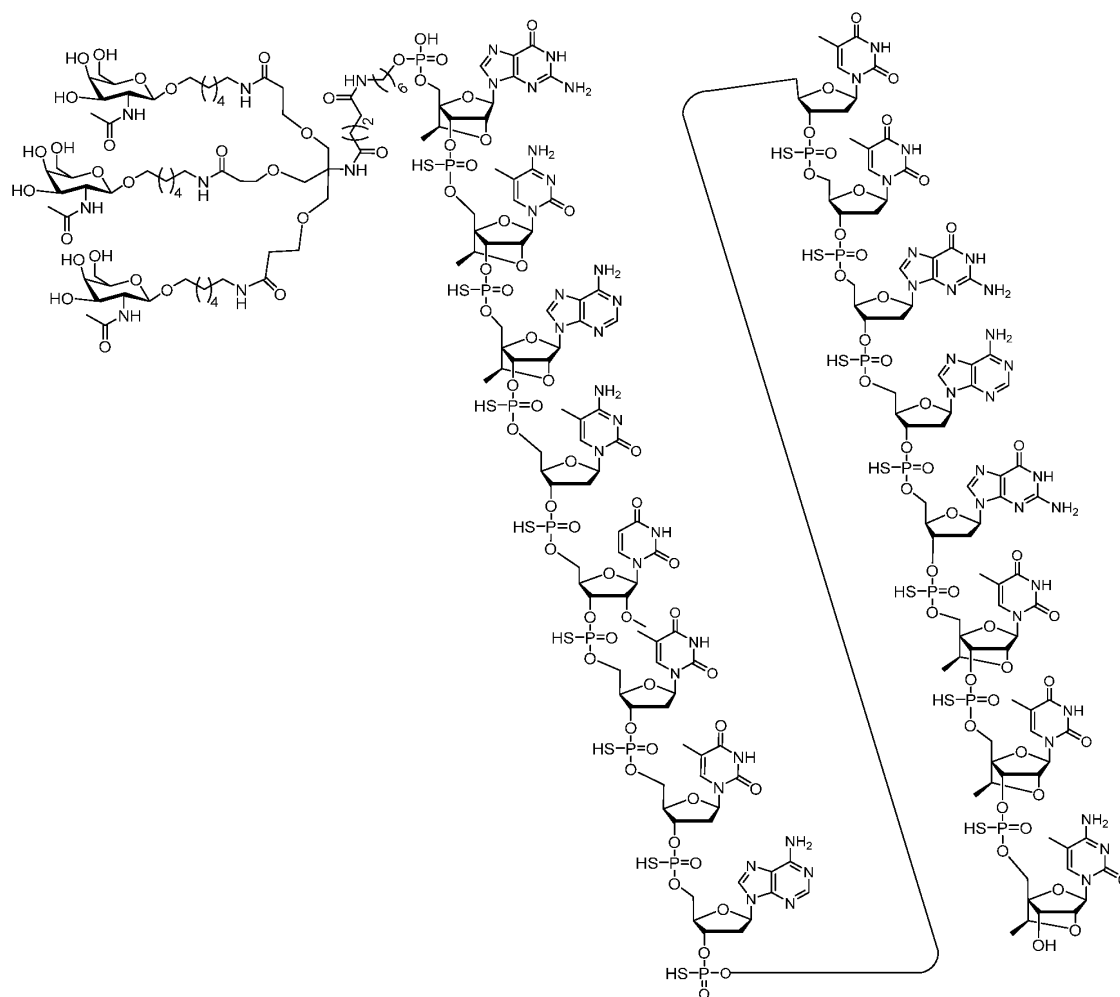
Embodiment 39. The oligomeric compound of embodiment 38, which is the sodium salt or the potassium salt.

Embodiment 40. An oligomeric compound according to the following chemical structure:



(SEQ ID NO: 3379).

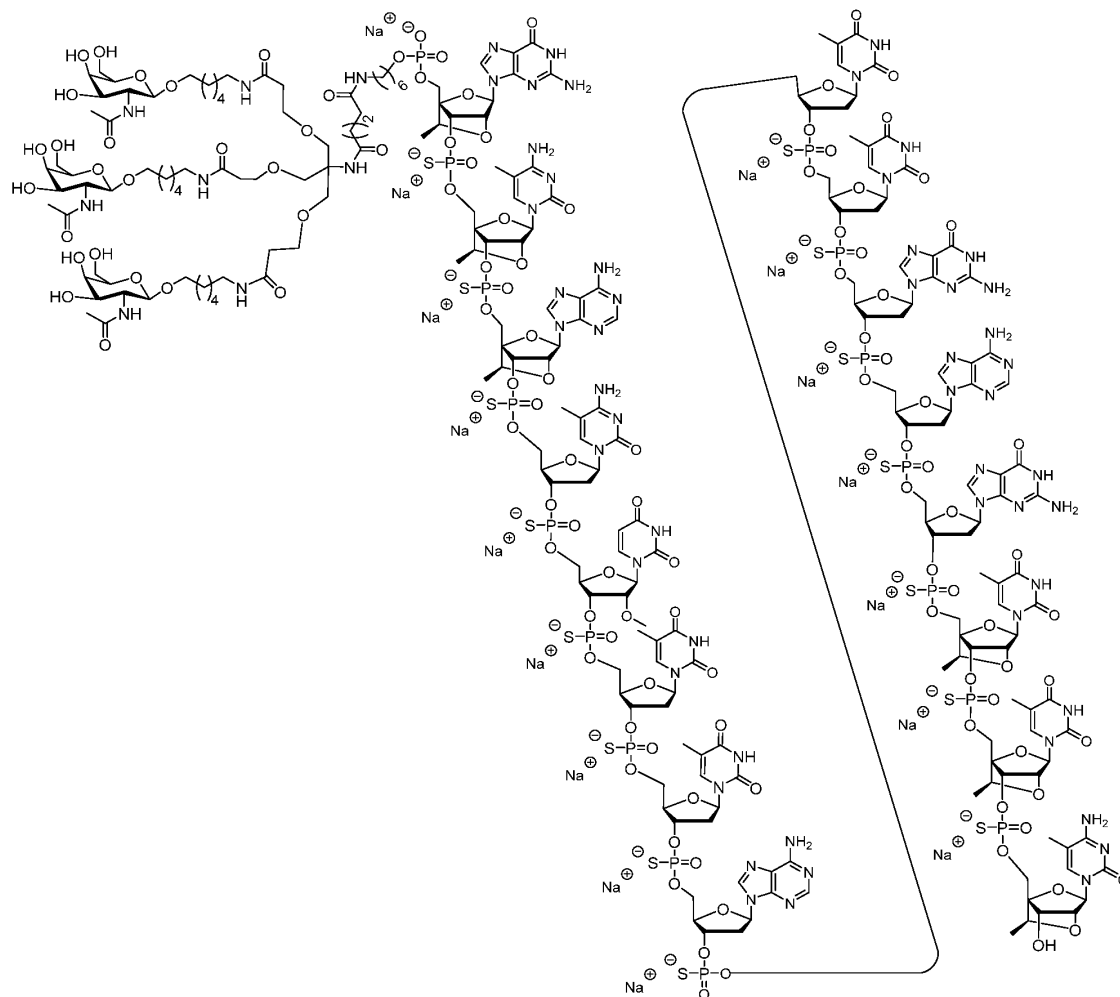
Embodiment 41. An oligomeric compound according to the following chemical structure:



(SEQ ID NO: 5006), or a salt thereof.

Embodiment 42. The oligomeric compound of embodiment 41, which is the sodium salt or the potassium salt.

Embodiment 43. An oligomeric compound according to the following chemical structure:



(SEQ ID NO: 5006).

- 5 Embodiment 44. An oligomeric compound comprising a modified oligonucleotide according to the following chemical notation: (THA- GalNAc₃)_o Gks ^mCks Gks Gds Ads Ads Tds ^mCds Ads ^mCds ^mCds Ads Ads Gks Gks Ak (SEQ ID NO: 3379), wherein:

A = an adenine nucleobase,

mC = a 5-methyl cytosine nucleobase,

10 G = a guanine nucleobase,

T = a thymine nucleobase,

k = a cEt modified sugar moiety,

d = a 2'-β-D-deoxyribosyl sugar moiety,

o = a phosphodiester linkage, and

s = a phosphorothioate internucleoside linkage.

5 Embodiment 45. An oligomeric compound comprising a modified oligonucleotide according to the following chemical notation: (THA- GalNAc₃)_o Gks ^mCks Aks ^mCds Ums Tds Tds Ads Tds Tds Gds Ads Gds Tks Tks mCk (SEQ ID NO: 5006), wherein: A = an adenine nucleobase, mC = a 5-methyl cytosine nucleobase, G = a guanine nucleobase, T = a thymine nucleobase, U = a uracil nucleobase, k = a cEt modified sugar moiety, d = a 2'-β-D-deoxyribosyl sugar moiety, o = a phosphodiester linkage, and s = a phosphorothioate internucleoside linkage.

10 Embodiment 46. An oligomeric duplex comprising the oligomeric compound of any of embodiments 1-36.

Embodiment 47. An antisense compound comprising or consisting of an oligomeric compound of any of embodiments 1-45 or an oligomeric duplex of embodiment 46.

Embodiment 48. A pharmaceutical composition comprising an oligomeric compound of any of embodiments 1-45, an oligomeric duplex of embodiment 46, or an antisense compound of embodiment 47; and a
15 pharmaceutically acceptable carrier or diluent.

Embodiment 49. The pharmaceutical composition of embodiment 48, wherein the pharmaceutically acceptable diluent is phosphate buffered saline.

Embodiment 50. The pharmaceutical composition of embodiment 49, wherein the pharmaceutical composition consists essentially of the modified oligonucleotide and phosphate buffered saline.

20 Embodiment 50. A method comprising administering to a subject a pharmaceutical composition of any of embodiments 48-50.

Embodiment 51. A method of ameliorating or preventing a thromboembolic condition, comprising administering to a subject in need thereof a therapeutically effective amount of a pharmaceutical composition according to any of embodiments 48-50.

25 Embodiment 51. The method of embodiment 52, wherein the thromboembolic condition is selected from myocardial infarction (MI), stroke, limb ischemia and necrosis, venous thromboembolism (VTE), deep vein thrombosis (DVT), and pulmonary embolism (PE).

Embodiment 53. The method of any of embodiments 51-53, wherein at least one symptom of the thromboembolic condition is ameliorated.

Embodiment 54. The method of embodiment 54, wherein the symptom is pain, shortness of breath, heart burn, cold sweat, fatigue, lightheadedness, dizziness, swelling, cramping, and death.

Embodiment 55. The method of any one of embodiments 51-55, comprising identifying the subject as having the thromboembolic condition or as having a risk factor for having the thromboembolic condition.

- 5 Embodiment 56. The method of embodiment 56, wherein the risk factor is surgery, malignancy, pregnancy, aging, use of oral contraceptives, immobility, sepsis, a mechanical heart valve, valvular heart disease, atrial fibrillation, atherosclerosis, antiphospholipid syndrome, an inherited clotting disorder, or an acquired prothrombotic clotting disorder.

- 10 Embodiment 57. A method of ameliorating or preventing hereditary angioedema, comprising administering to a subject in need thereof a therapeutically effective amount of a pharmaceutical composition according to any of embodiments 48-50.

Embodiment 58. A chirally enriched population of oligomeric compounds of any of embodiments 1-45, wherein the population is enriched for oligomeric compounds comprising at least one particular phosphorothioate internucleoside linkage having a particular stereochemical configuration.

- 15 Embodiment 59. The chirally enriched population of embodiment 59, wherein the population is enriched for oligomeric compounds comprising at least one particular phosphorothioate internucleoside linkage having the (*Sp*) configuration.

- Embodiment 60. The chirally enriched population of embodiment 59, wherein the population is enriched for oligomeric compounds comprising at least one particular phosphorothioate internucleoside linkage having the (*Rp*) configuration.
- 20

Embodiment 61. The chirally enriched population of embodiment 59, wherein the population is enriched for oligomeric compounds having a particular, independently selected stereochemical configuration at each phosphorothioate internucleoside linkage.

- Embodiment 62. The chirally enriched population of embodiment 62, wherein the population is enriched for oligomeric compounds having the (*Sp*) configuration at each phosphorothioate internucleoside linkage.
- 25

Embodiment 63. The chirally enriched population of embodiment 62, wherein the population is enriched for oligomeric compounds having the (*Rp*) configuration at each phosphorothioate internucleoside linkage.

- Embodiment 64. The chirally enriched population of embodiment 62, wherein the population is enriched for oligomeric compounds having the (*Rp*) configuration at one particular phosphorothioate internucleoside linkage and the (*Sp*) configuration at each of the remaining phosphorothioate internucleoside linkages.
- 30

Embodiment 65. The chirally enriched population of embodiment 59 or embodiment 62, wherein the population is enriched for oligomeric compounds having at least 3 contiguous phosphorothioate internucleoside linkages in the *Sp*, *Sp*, and *Rp* configurations, in the 5' to 3' direction.

Embodiment 66. A chirally enriched population of oligomeric compounds of any of embodiments 1-45, wherein all of the phosphorothioate internucleoside linkages of the oligomeric compounds are stereorandom.

I. Certain Oligonucleotides

In certain embodiments, provided herein are oligomeric compounds comprising oligonucleotides, which consist of linked nucleosides. Oligonucleotides may be unmodified oligonucleotides (RNA or DNA) or may be modified oligonucleotides. Modified oligonucleotides comprise at least one modification relative to unmodified RNA or DNA. That is, modified oligonucleotides comprise at least one modified nucleoside (comprising a modified sugar moiety and/or a modified nucleobase) and/or at least one modified internucleoside linkage.

A. Certain Modified Nucleosides

Modified nucleosides comprise a modified sugar moiety or a modified nucleobase or both a modified sugar moiety and a modified nucleobase.

1. Certain Sugar Moieties

In certain embodiments, modified sugar moieties are non-bicyclic modified sugar moieties. In certain embodiments, modified sugar moieties are bicyclic or tricyclic sugar moieties. In certain embodiments, modified sugar moieties are sugar surrogates. Such sugar surrogates may comprise one or more substitutions corresponding to those of other types of modified sugar moieties.

In certain embodiments, modified sugar moieties are non-bicyclic modified sugar moieties comprising a furanosyl ring with one or more substituent groups none of which bridges two atoms of the furanosyl ring to form a bicyclic structure. Such non bridging substituents may be at any position of the furanosyl, including but not limited to substituents at the 2', 4', and/or 5' positions. In certain embodiments one or more non-bridging substituent of non-bicyclic modified sugar moieties is branched. Examples of 2'-substituent groups suitable for non-bicyclic modified sugar moieties include but are not limited to: 2'-F, 2'-OCH₃ ("OMe" or "O-methyl"), and 2'-O(CH₂)₂OCH₃ ("MOE"). In certain embodiments, 2'-substituent groups are selected from among: halo, allyl, amino, azido, SH, CN, OCN, CF₃, OCF₃, O-C₁-C₁₀ alkoxy, O-C₁-C₁₀ substituted alkoxy, O-C₁-C₁₀ alkyl, O-C₁-C₁₀ substituted alkyl, S-alkyl, N(R_m)-alkyl, O-alkenyl, S-alkenyl, N(R_m)-alkenyl, O-alkynyl, S-alkynyl, N(R_m)-alkynyl, O-alkylenyl-O-alkyl, alkynyl, alkaryl, aralkyl, O-alkaryl, O-aralkyl, O(CH₂)₂SCH₃, O(CH₂)₂ON(R_m)(R_n) or OCH₂C(=O)-N(R_m)(R_n), where each R_m and R_n is, independently, H, an amino protecting group, or substituted or unsubstituted C₁-C₁₀ alkyl, and the 2'-substituent groups described in Cook et al., U.S. 6,531,584; Cook et al., U.S. 5,859,221; and Cook et al., U.S. 6,005,087. Certain embodiments of these 2'-substituent groups can be further substituted with one or more substituent groups independently selected from among: hydroxyl, amino, alkoxy, carboxy, benzyl, phenyl,

nitro (NO₂), thiol, thioalkoxy, thioalkyl, halogen, alkyl, aryl, alkenyl and alkynyl. Examples of 4'-substituent groups suitable for non-bicyclic modified sugar moieties include but are not limited to alkoxy (*e.g.*, methoxy), alkyl, and those described in Manoharan et al., WO 2015/106128. Examples of 5'-substituent groups suitable for non-bicyclic modified sugar moieties include but are not limited to: 5-methyl (R or S), 5'-vinyl, and 5'-methoxy. In certain embodiments, non-bicyclic modified sugar moieties comprise more than one non-bridging sugar substituent, for example, 2'-F-5'-methyl sugar moieties and the modified sugar moieties and modified nucleosides described in Migawa et al., WO 2008/101157 and Rajeev et al., US2013/0203836.

In certain embodiments, a 2'-substituted non-bicyclic modified nucleoside comprises a sugar moiety comprising a non-bridging 2'-substituent group selected from: F, NH₂, N₃, OCF₃, OCH₃, O(CH₂)₃NH₂, CH₂CH=CH₂, OCH₂CH=CH₂, OCH₂CH₂OCH₃, O(CH₂)₂SCH₃, O(CH₂)₂ON(R_m)(R_n), O(CH₂)₂O(CH₂)₂N(CH₃)₂, and N-substituted acetamide (OCH₂C(=O)-N(R_m)(R_n)), where each R_m and R_n is, independently, H, an amino protecting group, or substituted or unsubstituted C₁-C₁₀ alkyl.

In certain embodiments, a 2'-substituted nucleoside non-bicyclic modified nucleoside comprises a sugar moiety comprising a non-bridging 2'-substituent group selected from: F, OCF₃, OCH₃, OCH₂CH₂OCH₃, O(CH₂)₂SCH₃, O(CH₂)₂ON(CH₃)₂, O(CH₂)₂O(CH₂)₂N(CH₃)₂, and OCH₂C(=O)-N(H)CH₃ ("NMA").

In certain embodiments, a 2'-substituted non-bicyclic modified nucleoside comprises a sugar moiety comprising a non-bridging 2'-substituent group selected from: F, OCH₃, and OCH₂CH₂OCH₃.

Certain modified sugar moieties comprise a substituent that bridges two atoms of the furanosyl ring to form a second ring, resulting in a bicyclic sugar moiety. In certain such embodiments, the bicyclic sugar moiety comprises a bridge between the 4' and the 2' furanose ring atoms. Examples of such 4' to 2' bridging sugar substituents include but are not limited to: 4'-CH₂-2', 4'-(CH₂)₂-2', 4'-(CH₂)₃-2', 4'-CH₂-O-2' ("LNA"), 4'-CH₂-S-2', 4'-(CH₂)₂-O-2' ("ENA"), 4'-CH(CH₃)-O-2' (referred to as "constrained ethyl" or "cEt"), 4'-CH₂-O-CH₂-2', 4'-CH₂-N(R)-2', 4'-CH(CH₂OCH₃)-O-2' ("constrained MOE" or "cMOE") and analogs thereof (*see, e.g.*, Seth et al., U.S. 7,399,845, Bhat et al., U.S. 7,569,686, Swayze et al., U.S. 7,741,457, and Swayze et al., U.S. 8,022,193), 4'-C(CH₃)(CH₃)-O-2' and analogs thereof (*see, e.g.*, Seth et al., U.S. 8,278,283), 4'-CH₂-N(OCH₃)-2' and analogs thereof (*see, e.g.*, Prakash et al., U.S. 8,278,425), 4'-CH₂-O-N(CH₃)-2' (*see, e.g.*, Allerson et al., U.S. 7,696,345 and Allerson et al., U.S. 8,124,745), 4'-CH₂-C(H)(CH₃)-2' (*see, e.g.*, Zhou, *et al.*, *J. Org. Chem.*, 2009, 74, 118-134), 4'-CH₂-C(=CH₂)-2' and analogs thereof (*see e.g.*, Seth et al., U.S. 8,278,426), 4'-C(R_aR_b)-N(R)-O-2', 4'-C(R_aR_b)-O-N(R)-2', 4'-CH₂-O-N(R)-2', and 4'-CH₂-N(R)-O-2', wherein each R, R_a, and R_b is, independently, H, a protecting group, or C₁-C₁₂ alkyl (*see, e.g.* Imanishi et al., U.S. 7,427,672).

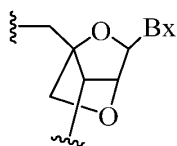
In certain embodiments, such 4' to 2' bridges independently comprise from 1 to 4 linked groups independently selected from: -[C(R_a)(R_b)]_n-, -[C(R_a)(R_b)]_n-O-, -C(R_a)=C(R_b)-, -C(R_a)=N-, -C(=NR_a)-, -C(=O)-, -C(=S)-, -O-, -Si(R_a)₂-, -S(=O)_x-, and -N(R_a)-

wherein: x is 0, 1, or 2; n is 1, 2, 3, or 4; each R_a and R_b is, independently, H, a protecting group, hydroxyl, C_1 - C_{12} alkyl, substituted C_1 - C_{12} alkyl, C_2 - C_{12} alkenyl, substituted C_2 - C_{12} alkenyl, C_2 - C_{12} alkynyl, substituted C_2 - C_{12} alkynyl, C_5 - C_{20} aryl, substituted C_5 - C_{20} aryl, heterocycle radical, substituted heterocycle radical, heteroaryl, substituted heteroaryl, C_5 - C_7 alicyclic radical, substituted C_5 - C_7 alicyclic radical, halogen, OJ₁, NJ₁J₂, SJ₁, N₃, COOJ₁, acyl (C(=O)-H), substituted acyl, CN, sulfonyl (S(=O)₂-J₁), or sulfoxyl (S(=O)-J₁); and

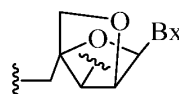
each J₁ and J₂ is, independently, H, C_1 - C_{12} alkyl, substituted C_1 - C_{12} alkyl, C_2 - C_{12} alkenyl, substituted C_2 - C_{12} alkenyl, C_2 - C_{12} alkynyl, substituted C_2 - C_{12} alkynyl, C_5 - C_{20} aryl, substituted C_5 - C_{20} aryl, acyl (C(=O)-H), substituted acyl, a heterocycle radical, a substituted heterocycle radical, C_1 - C_{12} aminoalkyl, substituted C_1 - C_{12} aminoalkyl, or a protecting group.

Additional bicyclic sugar moieties are known in the art, see, for example: Freier *et al.*, *Nucleic Acids Research*, 1997, 25(22), 4429-4443; Alback *et al.*, *J. Org. Chem.*, 2006, 71, 7731-7740; Singh *et al.*, *Chem. Commun.*, 1998, 4, 455-456; Koshkin *et al.*, *Tetrahedron*, 1998, 54, 3607-3630; Kumar *et al.*, *Bioorg. Med. Chem. Lett.*, 1998, 8, 2219-2222; Singh *et al.*, *J. Org. Chem.*, 1998, 63, 10035-10039; Srivastava *et al.*, *J. Am. Chem. Soc.*, 2007, 129, 8362-8379; Wengel *et al.*, U.S. 7,053,207; Imanishi *et al.*, U.S. 6,268,490; Imanishi *et al.*, U.S. 6,770,748; Imanishi *et al.*, U.S. RE44,779; Wengel *et al.*, U.S. 6,794,499; Wengel *et al.*, U.S. 6,670,461; Wengel *et al.*, U.S. 7,034,133; Wengel *et al.*, U.S. 8,080,644; Wengel *et al.*, U.S. 8,034,909; Wengel *et al.*, U.S. 8,153,365; Wengel *et al.*, U.S. 7,572,582; Ramasamy *et al.*, U.S. 6,525,191; Torsten *et al.*, WO 2004/106356; Wengel *et al.*, WO 1999/014226; Seth *et al.*, WO 2007/134181; Seth *et al.*, U.S. 7,547,684; Seth *et al.*, U.S. 7,666,854; Seth *et al.*, U.S. 8,088,746; Seth *et al.*, U.S. 7,750,131; Seth *et al.*, U.S. 8,030,467; Seth *et al.*, U.S. 8,268,980; Seth *et al.*, U.S. 8,546,556; Seth *et al.*, U.S. 8,530,640; Migawa *et al.*, U.S. 9,012,421; Seth *et al.*, U.S. 8,501,805; and U.S. Patent Publication Nos. Allerson *et al.*, US2008/0039618 and Migawa *et al.*, US2015/0191727.

In certain embodiments, bicyclic sugar moieties and nucleosides incorporating such bicyclic sugar moieties are further defined by isomeric configuration. For example, an LNA nucleoside (described herein) may be in the α -L configuration or in the β -D configuration.



LNA (β -D-configuration)
bridge = 4'-CH₂-O-2'



α -L-LNA (α -L-configuration)
bridge = 4'-CH₂-O-2'

α -L-methyleneoxy (4'-CH₂-O-2') or α -L-LNA bicyclic nucleosides have been incorporated into oligonucleotides that showed antisense activity (Frieden *et al.*, *Nucleic Acids Research*, 2003, 31, 6365-6372). Herein, general descriptions of bicyclic nucleosides include both isomeric configurations. When the

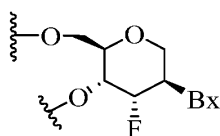
positions of specific bicyclic nucleosides (*e.g.*, LNA or cEt) are identified in exemplified embodiments herein, they are in the β -D configuration, unless otherwise specified.

In certain embodiments, modified sugar moieties comprise one or more non-bridging sugar substituent and one or more bridging sugar substituent (*e.g.*, 5'-substituted and 4'-2' bridged sugars).

5 In certain embodiments, modified sugar moieties are sugar surrogates. In certain such embodiments, the oxygen atom of the sugar moiety is replaced, *e.g.*, with a sulfur, carbon or nitrogen atom. In certain such embodiments, such modified sugar moieties also comprise bridging and/or non-bridging substituents as described herein. For example, certain sugar surrogates comprise a 4'-sulfur atom and a substitution at the 2'-position (*see, e.g.*, Bhat et al., U.S. 7,875,733 and Bhat et al., U.S. 7,939,677) and/or the 5' position.

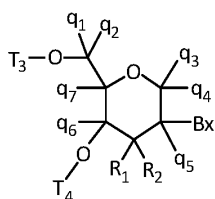
10 In certain embodiments, sugar surrogates comprise rings having other than 5 atoms. For example, in certain embodiments, a sugar surrogate comprises a six-membered tetrahydropyran ("THP"). Such tetrahydropyrans may be further modified or substituted. Nucleosides comprising such modified tetrahydropyrans include but are not limited to hexitol nucleic acid ("HNA"), anitol nucleic acid ("ANA"), manitol nucleic acid ("MNA") (*see, e.g.*, Leumann, *CJ. Bioorg. & Med. Chem.* 2002, 10, 841-854), fluoro

15 HNA:



F-HNA

("F-HNA", *see e.g.* Swayze et al., U.S. 8,088,904; Swayze et al., U.S. 8,440,803; Swayze et al., U.S. 8,796,437; and Swayze et al., U.S. 9,005,906; F-HNA can also be referred to as a F-THP or 3'-fluoro tetrahydropyran), and nucleosides comprising additional modified THP compounds having the formula:



20

wherein, independently, for each of said modified THP nucleoside:

Bx is a nucleobase moiety;

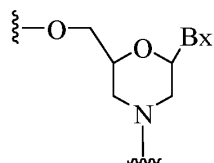
T₃ and T₄ are each, independently, an internucleoside linking group linking the modified THP nucleoside to the remainder of an oligonucleotide or one of T₃ and T₄ is an internucleoside linking group linking the modified THP nucleoside to the remainder of an oligonucleotide and the other of T₃ and T₄ is H, a hydroxyl protecting group, a linked conjugate group, or a 5' or 3'-terminal group;

q₁, q₂, q₃, q₄, q₅, q₆ and q₇ are each, independently, H, C₁-C₆ alkyl, substituted C₁-C₆ alkyl, C₂-C₆ alkenyl, substituted C₂-C₆ alkenyl, C₂-C₆ alkynyl, or substituted C₂-C₆ alkynyl; and

each of R₁ and R₂ is independently selected from among: hydrogen, halogen, substituted or unsubstituted alkoxy, NJ₁J₂, SJ₁, N₃, OC(=X)J₁, OC(=X)NJ₁J₂, NJ₃C(=X)NJ₁J₂, and CN, wherein X is O, S or NJ₁, and each J₁, J₂, and J₃ is, independently, H or C₁-C₆ alkyl.

In certain embodiments, modified THP nucleosides are provided wherein q₁, q₂, q₃, q₄, q₅, q₆ and q₇ are each H. In certain embodiments, at least one of q₁, q₂, q₃, q₄, q₅, q₆ and q₇ is other than H. In certain embodiments, at least one of q₁, q₂, q₃, q₄, q₅, q₆ and q₇ is methyl. In certain embodiments, modified THP nucleosides are provided wherein one of R₁ and R₂ is F. In certain embodiments, R₁ is F and R₂ is H, in certain embodiments, R₁ is methoxy and R₂ is H, and in certain embodiments, R₁ is methoxyethoxy and R₂ is H.

In certain embodiments, sugar surrogates comprise rings having more than 5 atoms and more than one heteroatom. For example, nucleosides comprising morpholino sugar moieties and their use in oligonucleotides have been reported (*see, e.g.*, Braasch et al., *Biochemistry*, 2002, 41, 4503-4510 and Summerton et al., U.S. 5,698,685; Summerton et al., U.S. 5,166,315; Summerton et al., U.S. 5,185,444; and Summerton et al., U.S. 5,034,506). As used here, the term “morpholino” means a sugar surrogate having the following structure:



In certain embodiments, morpholinos may be modified, for example by adding or altering various substituent groups from the above morpholino structure. Such sugar surrogates are referred to herein as “modified morpholinos.”

In certain embodiments, sugar surrogates comprise acyclic moieties. Examples of nucleosides and oligonucleotides comprising such acyclic sugar surrogates include but are not limited to: peptide nucleic acid (“PNA”), acyclic butyl nucleic acid (*see, e.g.*, Kumar et al., *Org. Biomol. Chem.*, 2013, 11, 5853-5865), and nucleosides and oligonucleotides described in Manoharan et al., WO2011/133876.

Many other bicyclic and tricyclic sugar and sugar surrogate ring systems are known in the art that can be used in modified nucleosides.

2. Certain Modified Nucleobases

In certain embodiments, modified oligonucleotides comprise one or more nucleosides comprising an unmodified nucleobase. In certain embodiments, modified oligonucleotides comprise one or more nucleosides comprising a modified nucleobase. In certain embodiments, modified oligonucleotides comprise one or more nucleosides that does not comprise a nucleobase, referred to as an abasic nucleoside.

In certain embodiments, modified nucleobases are selected from: 5-substituted pyrimidines, 6-azapyrimidines, alkyl or alkynyl substituted pyrimidines, alkyl substituted purines, and N-2, N-6 and O-6 substituted purines. In certain embodiments, modified nucleobases are selected from: 2-aminopropyladenine, 5-hydroxymethyl cytosine, xanthine, hypoxanthine, 2-aminoadenine, 6-N-methylguanine, 6-N-methyladenine, 2-propyladenine, 2-thiouracil, 2-thiothymine and 2-thiocytosine, 5-propynyl (-C≡C-CH₃) uracil, 5-propynylcytosine, 6-azouracil, 6-azocytosine, 6-azothymine, 5-ribosyluracil (pseudouracil), 4-thiouracil, 8-halo, 8-amino, 8-thiol, 8-thioalkyl, 8-hydroxyl, 8-aza and other 8-substituted purines, 5-halo, particularly 5-bromo, 5-trifluoromethyl, 5-halouracil, and 5-halocytosine, 7-methylguanine, 7-methyladenine, 2-F-adenine, 2-aminoadenine, 7-deazaguanine, 7-deazaadenine, 3-deazaguanine, 3-deazaadenine, 6-N-benzoyladenine, 2-N-isobutyrylguanine, 4-N-benzoylcytosine, 4-N-benzoyluracil, 5-methyl 4-N-benzoylcytosine, 5-methyl 4-N-benzoyluracil, universal bases, hydrophobic bases, promiscuous bases, size-expanded bases, and fluorinated bases. Further modified nucleobases include tricyclic pyrimidines, such as 1,3-diazaphenoxazine-2-one, 1,3-diazaphenothiazine-2-one and 9-(2-aminoethoxy)-1,3-diazaphenoxazine-2-one (G-clamp). Modified nucleobases may also include those in which the purine or pyrimidine base is replaced with other heterocycles, for example 7-deaza-adenine, 7-deazaguanosine, 2-aminopyridine and 2-pyridone. Further nucleobases include those disclosed in Merigan et al., U.S. 3,687,808, those disclosed in *The Concise Encyclopedia Of Polymer Science And Engineering*, Kroschwitz, J.I., Ed., John Wiley & Sons, 1990, 858-859; Englisch et al., *Angewandte Chemie*, International Edition, 1991, 30, 613; Sanghvi, Y.S., Chapter 15, *Antisense Research and Applications*, Crooke, S.T. and Lebleu, B., Eds., CRC Press, 1993, 273-288; and those disclosed in Chapters 6 and 15, *Antisense Drug Technology*, Crooke S.T., Ed., CRC Press, 2008, 163-166 and 442-443.

Publications that teach the preparation of certain of the above noted modified nucleobases as well as other modified nucleobases include without limitation, Manoharan et al., US2003/0158403; Manoharan et al., US2003/0175906; Dinh et al., U.S. 4,845,205; Spielvogel et al., U.S. 5,130,302; Rogers et al., U.S. 5,134,066; Bischofberger et al., U.S. 5,175,273; Urdea et al., U.S. 5,367,066; Benner et al., U.S. 5,432,272; Matteucci et al., U.S. 5,434,257; Gmeiner et al., U.S. 5,457,187; Cook et al., U.S. 5,459,255; Froehler et al., U.S. 5,484,908; Matteucci et al., U.S. 5,502,177; Hawkins et al., U.S. 5,525,711; Haralambidis et al., U.S. 5,552,540; Cook et al., U.S. 5,587,469; Froehler et al., U.S. 5,594,121; Switzer et al., U.S. 5,596,091; Cook et al., U.S. 5,614,617; Froehler et al., U.S. 5,645,985; Cook et al., U.S. 5,681,941; Cook et al., U.S. 5,811,534; Cook et al., U.S. 5,750,692; Cook et al., U.S. 5,948,903; Cook et al., U.S. 5,587,470; Cook et al., U.S. 5,457,191; Matteucci et al., U.S. 5,763,588; Froehler et al., U.S. 5,830,653; Cook et al., U.S. 5,808,027; Cook et al., 6,166,199; and Matteucci et al., U.S. 6,005,096.

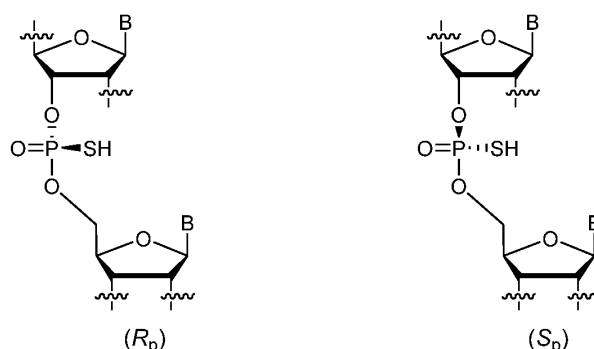
3. Certain Modified Internucleoside Linkages

In certain embodiments, nucleosides of modified oligonucleotides may be linked together using any internucleoside linkage. The two main classes of internucleoside linking groups are defined by the presence or absence of a phosphorus atom. Representative phosphorus-containing internucleoside linkages include but

are not limited to phosphodiester, which contain a phosphodiester bond ("P(O₂)=O") (also referred to as unmodified or naturally occurring linkages), phosphotriesters, methylphosphonates, phosphoramidates, and phosphorothioates, and phosphorodithioates. Representative non-phosphorus containing internucleoside linking groups include but are not limited to methylenemethylimino (-CH₂-N(CH₃)-O-CH₂-), thiodiester, thionocarbamate (-O-C(=O)(NH)-S-); siloxane (-O-SiH₂-O-); and N,N'-dimethylhydrazine (-CH₂-N(CH₃)-N(CH₃)-). Modified internucleoside linkages, compared to naturally occurring phosphate linkages, can be used to alter, typically increase, nuclease resistance of the oligonucleotide. In certain embodiments, internucleoside linkages having a chiral atom can be prepared as a racemic mixture, or as separate enantiomers. Methods of preparation of phosphorous-containing and non-phosphorous-containing internucleoside linkages are well known to those skilled in the art.

Representative internucleoside linkages having a chiral center include but are not limited to alkylphosphonates and phosphorothioates. Modified oligonucleotides comprising internucleoside linkages having a chiral center can be prepared as populations of modified oligonucleotides comprising stereorandom internucleoside linkages, or as populations of modified oligonucleotides comprising phosphorothioate linkages in particular stereochemical configurations. In certain embodiments, populations of modified oligonucleotides comprise phosphorothioate internucleoside linkages wherein all of the phosphorothioate internucleoside linkages are stereorandom. Such modified oligonucleotides can be generated using synthetic methods that result in random selection of the stereochemical configuration of each phosphorothioate linkage. Nonetheless, as is well understood by those of skill in the art, each individual phosphorothioate of each individual oligonucleotide molecule has a defined stereoconfiguration. In certain embodiments, populations of modified oligonucleotides are enriched for modified oligonucleotides comprising one or more particular phosphorothioate internucleoside linkages in a particular, independently selected stereochemical configuration. In certain embodiments, the particular configuration of the particular phosphorothioate linkage is present in at least 65% of the molecules in the population. In certain embodiments, the particular configuration of the particular phosphorothioate linkage is present in at least 70% of the molecules in the population. In certain embodiments, the particular configuration of the particular phosphorothioate linkage is present in at least 80% of the molecules in the population. In certain embodiments, the particular configuration of the particular phosphorothioate linkage is present in at least 90% of the molecules in the population. In certain embodiments, the particular configuration of the particular phosphorothioate linkage is present in at least 99% of the molecules in the population. Such chirally enriched populations of modified oligonucleotides can be generated using synthetic methods known in the art, *e.g.*, methods described in Oka et al., *JACS* 125, 8307 (2003), Wan et al. *Nuc. Acid. Res.* 42, 13456 (2014), and WO 2017/015555. In certain embodiments, a population of modified oligonucleotides is enriched for modified oligonucleotides having at least one indicated phosphorothioate in the (Sp) configuration. In certain embodiments, a population of modified oligonucleotides is enriched for modified oligonucleotides having at least one phosphorothioate in the (Rp) configuration. In certain embodiments, modified oligonucleotides comprising (Rp) and/or (Sp)

phosphorothioates comprise one or more of the following formulas, respectively, wherein "B" indicates a nucleobase:



Unless otherwise indicated, chiral internucleoside linkages of modified oligonucleotides described herein can be stereorandom or in a particular stereochemical configuration.

Neutral internucleoside linkages include, without limitation, phosphotriesters, methylphosphonates, MMI (3'-CH₂-N(CH₃)-O-5'), amide-3 (3'-CH₂-C(=O)-N(H)-5'), amide-4 (3'-CH₂-N(H)-C(=O)-5'), formacetal (3'-O-CH₂-O-5'), methoxypropyl (MOP), and thioformacetal (3'-S-CH₂-O-5'). Further neutral internucleoside linkages include nonionic linkages comprising siloxane (dialkylsiloxane), carboxylate ester, carboxamide, sulfide, sulfonate ester and amides (See for example: *Carbohydrate Modifications in Antisense Research*; Y.S. Sanghvi and P.D. Cook, Eds., ACS Symposium Series 580; Chapters 3 and 4, 40-65). Further neutral internucleoside linkages include nonionic linkages comprising mixed N, O, S and CH₂ component parts.

B. Certain Motifs

In certain embodiments, modified oligonucleotides comprise one or more modified nucleosides comprising a modified sugar moiety. In certain embodiments, modified oligonucleotides comprise one or more modified nucleosides comprising a modified nucleobase. In certain embodiments, modified oligonucleotides comprise one or more modified internucleoside linkage. In such embodiments, the modified, unmodified, and differently modified sugar moieties, nucleobases, and/or internucleoside linkages of a modified oligonucleotide define a pattern or motif. In certain embodiments, the patterns of sugar moieties, nucleobases, and internucleoside linkages are each independent of one another. Thus, a modified oligonucleotide may be described by its sugar motif, nucleobase motif and/or internucleoside linkage motif (as used herein, nucleobase motif describes the modifications to the nucleobases independent of the sequence of nucleobases).

1. Certain Sugar Motifs

In certain embodiments, oligonucleotides comprise one or more type of modified sugar and/or unmodified sugar moiety arranged along the oligonucleotide or portion thereof in a defined pattern or sugar motif. In certain instances, such sugar motifs include but are not limited to any of the sugar modifications discussed herein.

In certain embodiments, modified oligonucleotides have a gapmer motif, which is defined by two external regions or “wings” and a central or internal region or “gap.” The three regions of a gapmer motif (the 5'-wing, the gap, and the 3'-wing) form a contiguous sequence of nucleosides wherein at least some of the sugar moieties of the nucleosides of each of the wings differ from at least some of the sugar moieties of the nucleosides of the gap. Specifically, at least the sugar moieties of the nucleosides of each wing that are closest to the gap (the 3'-most nucleoside of the 5'-wing and the 5'-most nucleoside of the 3'-wing) differ from the sugar moiety of the neighboring gap nucleosides, thus defining the boundary between the wings and the gap (i.e., the wing/gap junction). In certain embodiments, the sugar moieties within the gap are the same as one another. In certain embodiments, the gap includes one or more nucleoside having a sugar moiety that differs from the sugar moiety of one or more other nucleosides of the gap. In certain embodiments, the sugar motifs of the two wings are the same as one another (symmetric gapmer). In certain embodiments, the sugar motif of the 5'-wing differs from the sugar motif of the 3'-wing (asymmetric gapmer).

In certain embodiments, the wings of a gapmer comprise 1-6 nucleosides. In certain embodiments, each nucleoside of each wing of a gapmer comprises a modified sugar moiety. In certain embodiments, at least one nucleoside of each wing of a gapmer comprises a modified sugar moiety. In certain embodiments, at least two nucleosides of each wing of a gapmer comprises a modified sugar moiety. In certain embodiments, at least three nucleosides of each wing of a gapmer comprises a modified sugar moiety. In certain embodiments, at least four nucleosides of each wing of a gapmer comprises a modified sugar moiety. In certain embodiments, at least five nucleosides of each wing of a gapmer comprises a modified sugar moiety.

In certain embodiments, the gap of a gapmer comprises 7-12 nucleosides. In certain embodiments, each nucleoside of the gap of a gapmer comprises a 2'-β-D-deoxyribosyl sugar moiety. In certain embodiments, at least one nucleoside of the gap of a gapmer comprises a modified sugar moiety.

In certain embodiments, the gapmer is a deoxy gapmer. In certain embodiments, the nucleosides on the gap side of each wing/gap junction comprise 2'-β-D-deoxyribosyl sugar moieties and the nucleosides on the wing sides of each wing/gap junction comprise modified sugar moieties. In certain embodiments, each nucleoside of the gap comprises a 2'-β-D-deoxyribosyl sugar moiety. In certain embodiments, each nucleoside of each wing of a gapmer comprises a modified sugar moiety. In certain embodiments, exactly one nucleoside of the gap comprises a modified sugar moiety and each remaining nucleoside of the gap comprises a 2'-β-D-deoxyribosyl sugar moiety.

In certain embodiments, modified oligonucleotides comprise or consist of a portion having a fully modified sugar motif. In such embodiments, each nucleoside of the fully modified portion of the modified oligonucleotide comprises a modified sugar moiety. In certain embodiments, each nucleoside of the entire modified oligonucleotide comprises a modified sugar moiety. In certain embodiments, modified oligonucleotides comprise or consist of a portion having a fully modified sugar motif, wherein each nucleoside within the fully modified portion comprises the same modified sugar moiety, referred to herein as

a uniformly modified sugar motif. In certain embodiments, a fully modified oligonucleotide is a uniformly modified oligonucleotide. In certain embodiments, each nucleoside of a uniformly modified comprises the same 2'-modification.

Herein, the lengths (number of nucleosides) of the three regions of a gapmer may be provided using the notation [# of nucleosides in the 5'-wing] – [# of nucleosides in the gap] – [# of nucleosides in the 3'-wing]. Thus, a 3-10-3 gapmer consists of 3 linked nucleosides in each wing and 10 linked nucleosides in the gap. Where such nomenclature is followed by a specific modification, that modification is the modification in each sugar moiety of each wing and the gap nucleosides comprise 2'-β-D-deoxyribose sugar moieties. Thus, a 5-10-5 MOE gapmer consists of 5 linked 2'-MOE nucleosides in the 5'-wing, 10 linked 2'-β-D-deoxynucleosides in the gap, and 5 linked 2'-MOE nucleosides in the 3'-wing. A 3-10-3 cEt gapmer consists of 3 linked cEt nucleosides in the 5'-wing, 10 linked 2'-β-D-deoxynucleosides in the gap, and 3 linked cEt nucleosides in the 3'-wing. A 5-8-5 gapmer consists of 5 linked nucleosides comprising a modified sugar moiety in the 5'-wing, 8 linked 2'-β-D-deoxynucleosides in the gap, and 5 linked nucleosides comprising a modified sugar moiety in the 3'-wing. A 5-8-5 mixed gapmer has at least two different modified sugar moieties in the 5'- and/or the 3'-wing.

In certain embodiments, modified oligonucleotides are 5-10-5 MOE gapmers. In certain embodiments, modified oligonucleotides are 4-10-6 MOE gapmers. In certain embodiments, modified oligonucleotides are 6-10-4 MOE gapmers. In certain embodiments, modified oligonucleotides are 5-8-5 MOE gapmers. In certain embodiments, modified oligonucleotides are 6-8-4 MOE gapmers. In certain embodiments, modified oligonucleotides are 4-8-6 MOE gapmers. In certain embodiments, modified oligonucleotides are X-Y-Z MOE gapmers, wherein X and Z are independently selected from 1, 2, 3, 4, 5, or 6 and Y is 7, 8, 9, 10, or 11.

2. Certain Nucleobase Motifs

In certain embodiments, oligonucleotides comprise modified and/or unmodified nucleobases arranged along the oligonucleotide or portion thereof in a defined pattern or motif. In certain embodiments, each nucleobase is modified. In certain embodiments, none of the nucleobases are modified. In certain embodiments, each purine or each pyrimidine is modified. In certain embodiments, each adenine is modified. In certain embodiments, each guanine is modified. In certain embodiments, each thymine is modified. In certain embodiments, each uracil is modified. In certain embodiments, each cytosine is modified. In certain embodiments, some or all of the cytosine nucleobases in a modified oligonucleotide are 5-methyl cytosines. In certain embodiments, all of the cytosine nucleobases are 5-methyl cytosines and all of the other nucleobases of the modified oligonucleotide are unmodified nucleobases.

In certain embodiments, modified oligonucleotides comprise a block of modified nucleobases. In certain such embodiments, the block is at the 3'-end of the oligonucleotide. In certain embodiments the block is within 3 nucleosides of the 3'-end of the oligonucleotide. In certain embodiments, the block is at the 5'-

end of the oligonucleotide. In certain embodiments the block is within 3 nucleosides of the 5'-end of the oligonucleotide.

In certain embodiments, oligonucleotides having a gapmer motif comprise a nucleoside comprising a modified nucleobase. In certain such embodiments, one nucleoside comprising a modified nucleobase is in the central gap of an oligonucleotide having a gapmer motif. In certain such embodiments, the sugar moiety of said nucleoside is a 2'-β-D-deoxyribose sugar moiety. In certain embodiments, the modified nucleobase is selected from: a 2-thiopyrimidine and a 5-propynepyrimidine.

3. Certain Internucleoside Linkage Motifs

In certain embodiments, oligonucleotides comprise modified and/or unmodified internucleoside linkages arranged along the oligonucleotide or portion thereof in a defined pattern or motif. In certain embodiments, each internucleoside linking group is a phosphodiester internucleoside linkage ($P(O_2)=O$). In certain embodiments, each internucleoside linking group of a modified oligonucleotide is a phosphorothioate internucleoside linkage ($P(O_2)=S$). In certain embodiments, each internucleoside linkage of a modified oligonucleotide is independently selected from a phosphorothioate internucleoside linkage and phosphodiester internucleoside linkage. In certain embodiments, each phosphorothioate internucleoside linkage is independently selected from a stereorandom phosphorothioate, a (Sp) phosphorothioate, and a (Rp) phosphorothioate. In certain embodiments, the sugar motif of a modified oligonucleotide is a gapmer and the internucleoside linkages within the gap are all modified. In certain such embodiments, some or all of the internucleoside linkages in the wings are unmodified phosphodiester internucleoside linkages. In certain embodiments, the terminal internucleoside linkages are modified. In certain embodiments, the sugar motif of a modified oligonucleotide is a gapmer, and the internucleoside linkage motif comprises at least one phosphodiester internucleoside linkage in at least one wing, wherein the at least one phosphodiester linkage is not a terminal internucleoside linkage, and the remaining internucleoside linkages are phosphorothioate internucleoside linkages. In certain such embodiments, all of the phosphorothioate linkages are stereorandom. In certain embodiments, all of the phosphorothioate linkages in the wings are (Sp) phosphorothioates, and the gap comprises at least one Sp, Sp, Rp motif. In certain embodiments, populations of modified oligonucleotides are enriched for modified oligonucleotides comprising such internucleoside linkage motifs.

In certain embodiments, modified nucleotides have an internucleoside linkage motif of sooooooooooooo, wherein each "s" represents a phosphorothioate internucleoside linkage and each "o" represents a phosphodiester internucleoside linkage. In certain embodiments, modified nucleotides have an internucleoside linkage motif of sooooooooooooo, wherein each "s" represents a phosphorothioate internucleoside linkage and each "o" represents a phosphodiester internucleoside linkage. In certain embodiments, modified nucleotides have an internucleoside linkage motif of sooooooooooooo, wherein each "s" represents a phosphorothioate internucleoside linkage and each "o" represents a phosphodiester internucleoside linkage. In certain embodiments, modified nucleotides have an internucleoside linkage motif of sooooooooooooo, wherein each "s" represents a phosphorothioate internucleoside linkage and each "o" represents a phosphodiester internucleoside linkage.

represents a phosphodiester internucleoside linkage. In certain embodiments, modified nucleotides have an internucleoside linkage motif of sooooooooooooo, wherein each “s” represents a phosphorothioate internucleoside linkage and each “o” represents a phosphodiester internucleoside linkage. In certain embodiments, modified nucleotides have an internucleoside linkage motif of sooooooooooooo, wherein each “s” represents a phosphorothioate internucleoside linkage and each “o” represents a phosphodiester internucleoside linkage.

C. Certain Lengths

It is possible to increase or decrease the length of an oligonucleotide without eliminating activity. For example, in Woolf et al. (Proc. Natl. Acad. Sci. USA 89:7305-7309, 1992), a series of oligonucleotides 13-25 nucleobases in length were tested for their ability to induce cleavage of a target RNA in an oocyte injection model. Oligonucleotides 25 nucleobases in length with 8 or 11 mismatch bases near the ends of the oligonucleotides were able to direct specific cleavage of the target RNA, albeit to a lesser extent than the oligonucleotides that contained no mismatches. Similarly, target specific cleavage was achieved using 13 nucleobase oligonucleotides, including those with 1 or 3 mismatches.

In certain embodiments, oligonucleotides (including modified oligonucleotides) can have any of a variety of ranges of lengths. In certain embodiments, oligonucleotides consist of X to Y linked nucleosides, where X represents the fewest number of nucleosides in the range and Y represents the largest number nucleosides in the range. In certain such embodiments, X and Y are each independently selected from 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and 50; provided that $X \leq Y$. For example, in certain embodiments, oligonucleotides consist of 12 to 13, 12 to 14, 12 to 15, 12 to 16, 12 to 17, 12 to 18, 12 to 19, 12 to 20, 12 to 21, 12 to 22, 12 to 23, 12 to 24, 12 to 25, 12 to 26, 12 to 27, 12 to 28, 12 to 29, 12 to 30, 13 to 14, 13 to 15, 13 to 16, 13 to 17, 13 to 18, 13 to 19, 13 to 20, 13 to 21, 13 to 22, 13 to 23, 13 to 24, 13 to 25, 13 to 26, 13 to 27, 13 to 28, 13 to 29, 13 to 30, 14 to 15, 14 to 16, 14 to 17, 14 to 18, 14 to 19, 14 to 20, 14 to 21, 14 to 22, 14 to 23, 14 to 24, 14 to 25, 14 to 26, 14 to 27, 14 to 28, 14 to 29, 14 to 30, 15 to 16, 15 to 17, 15 to 18, 15 to 19, 15 to 20, 15 to 21, 15 to 22, 15 to 23, 15 to 24, 15 to 25, 15 to 26, 15 to 27, 15 to 28, 15 to 29, 15 to 30, 16 to 17, 16 to 18, 16 to 19, 16 to 20, 16 to 21, 16 to 22, 16 to 23, 16 to 24, 16 to 25, 16 to 26, 16 to 27, 16 to 28, 16 to 29, 16 to 30, 17 to 18, 17 to 19, 17 to 20, 17 to 21, 17 to 22, 17 to 23, 17 to 24, 17 to 25, 17 to 26, 17 to 27, 17 to 28, 17 to 29, 17 to 30, 18 to 19, 18 to 20, 18 to 21, 18 to 22, 18 to 23, 18 to 24, 18 to 25, 18 to 26, 18 to 27, 18 to 28, 18 to 29, 18 to 30, 19 to 20, 19 to 21, 19 to 22, 19 to 23, 19 to 24, 19 to 25, 19 to 26, 19 to 27, 19 to 28, 19 to 29, 19 to 30, 20 to 21, 20 to 22, 20 to 23, 20 to 24, 20 to 25, 20 to 26, 20 to 27, 20 to 28, 20 to 29, 20 to 30, 21 to 22, 21 to 23, 21 to 24, 21 to 25, 21 to 26, 21 to 27, 21 to 28, 21 to 29, 21 to 30, 22 to 23, 22 to 24, 22 to 25, 22 to 26, 22 to 27, 22 to 28, 22 to 29, 22 to 30, 23 to 24, 23 to 25, 23 to 26, 23 to 27, 23 to 28, 23 to 29, 23 to 30, 24 to 25, 24 to 26, 24 to 27, 24 to 28, 24 to 29, 24 to 30, 25 to 26, 25 to 27, 25 to 28, 25 to 29, 25 to 30, 26 to 27, 26 to 28, 26 to 29, 26 to 30, 27 to 28, 27 to 29, 27 to 30, 28 to 29, 28 to 30, or 29 to 30 linked nucleosides.

D. Certain Modified Oligonucleotides

In certain embodiments, the above modifications (sugar, nucleobase, internucleoside linkage) are incorporated into a modified oligonucleotide. In certain embodiments, modified oligonucleotides are characterized by their modification motifs and overall lengths. In certain embodiments, such parameters are each independent of one another. Thus, unless otherwise indicated, each internucleoside linkage of an oligonucleotide having a gapmer sugar motif may be modified or unmodified and may or may not follow the gapmer modification pattern of the sugar modifications. For example, the internucleoside linkages within the wing regions of a sugar gapmer may be the same or different from one another and may be the same or different from the internucleoside linkages of the gap region of the sugar motif. Likewise, such sugar gapmer oligonucleotides may comprise one or more modified nucleobase independent of the gapmer pattern of the sugar modifications. Unless otherwise indicated, all modifications are independent of nucleobase sequence.

E. Certain Populations of Modified Oligonucleotides

Populations of modified oligonucleotides in which all of the modified oligonucleotides of the population have the same molecular formula can be stereorandom populations or chirally enriched populations. All of the chiral centers of all of the modified oligonucleotides are stereorandom in a stereorandom population. In a chirally enriched population, at least one particular chiral center is not stereorandom in the modified oligonucleotides of the population. In certain embodiments, the modified oligonucleotides of a chirally enriched population are enriched for β -D ribosyl sugar moieties, and all of the phosphorothioate internucleoside linkages are stereorandom. In certain embodiments, the modified oligonucleotides of a chirally enriched population are enriched for both β -D ribosyl sugar moieties and at least one, particular phosphorothioate internucleoside linkage in a particular stereochemical configuration.

F. Nucleobase Sequence

In certain embodiments, oligonucleotides (unmodified or modified oligonucleotides) are further described by their nucleobase sequence. In certain embodiments oligonucleotides have a nucleobase sequence that is complementary to a second oligonucleotide or an identified reference nucleic acid, such as a target nucleic acid. In certain such embodiments, a portion of an oligonucleotide has a nucleobase sequence that is complementary to a second oligonucleotide or an identified reference nucleic acid, such as a target nucleic acid. In certain embodiments, the nucleobase sequence of a portion or entire length of an oligonucleotide is at least 50%, at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 95%, or 100% complementary to the second oligonucleotide or nucleic acid, such as a target nucleic acid.

II. Certain Oligomeric Compounds

In certain embodiments, provided herein are oligomeric compounds, which consist of an oligonucleotide (modified or unmodified) and optionally one or more conjugate groups and/or terminal groups. Conjugate groups consist of one or more conjugate moiety and a conjugate linker which links the conjugate moiety to the oligonucleotide. Conjugate groups may be attached to either or both ends of an

oligonucleotide and/or at any internal position. In certain embodiments, conjugate groups are attached to the 2'-position of a nucleoside of a modified oligonucleotide. In certain embodiments, conjugate groups that are attached to either or both ends of an oligonucleotide are terminal groups. In certain such embodiments, conjugate groups or terminal groups are attached at the 3' and/or 5'-end of oligonucleotides. In certain such 5 embodiments, conjugate groups (or terminal groups) are attached at the 3'-end of oligonucleotides. In certain embodiments, conjugate groups are attached near the 3'-end of oligonucleotides. In certain embodiments, conjugate groups (or terminal groups) are attached at the 5'-end of oligonucleotides. In certain embodiments, conjugate groups are attached near the 5'-end of oligonucleotides.

Examples of terminal groups include but are not limited to conjugate groups, capping groups, 10 phosphate moieties, protecting groups, modified or unmodified nucleosides, and two or more nucleosides that are independently modified or unmodified.

A. Certain Conjugate Groups

In certain embodiments, oligonucleotides are covalently attached to one or more conjugate groups. In certain embodiments, conjugate groups modify one or more properties of the attached oligonucleotide, 15 including but not limited to pharmacodynamics, pharmacokinetics, stability, binding, absorption, tissue distribution, cellular distribution, cellular uptake, charge and clearance. In certain embodiments, conjugate groups impart a new property on the attached oligonucleotide, *e.g.*, fluorophores or reporter groups that enable detection of the oligonucleotide. Certain conjugate groups and conjugate moieties have been described previously, for example: cholesterol moiety (Letsinger et al., *Proc. Natl. Acad. Sci. USA*, 1989, 86, 6553-6556), cholic acid (Manoharan et al., *Bioorg. Med. Chem. Lett.*, 1994, 4, 1053-1060), a thioether, *e.g.*, 20 hexyl-S-tritylthiol (Manoharan et al., *Ann. N.Y. Acad. Sci.*, 1992, 660, 306-309; Manoharan et al., *Bioorg. Med. Chem. Lett.*, 1993, 3, 2765-2770), a thiocholesterol (Oberhauser et al., *Nucl. Acids Res.*, 1992, 20, 533-538), an aliphatic chain, *e.g.*, do-decan-diol or undecyl residues (Saison-Behmoaras et al., *EMBO J.*, 1991, 10, 1111-1118; Kabanov et al., *FEBS Lett.*, 1990, 259, 327-330; Svinarchuk et al., *Biochimie*, 1993, 75, 49- 25 54), a phospholipid, *e.g.*, di-hexadecyl-rac-glycerol or triethyl-ammonium 1,2-di-O-hexadecyl-rac-glycero-3-H-phosphonate (Manoharan et al., *Tetrahedron Lett.*, 1995, 36, 3651-3654; Shea et al., *Nucl. Acids Res.*, 1990, 18, 3777-3783), a polyamine or a polyethylene glycol chain (Manoharan et al., *Nucleosides & Nucleotides*, 1995, 14, 969-973), or adamantane acetic acid a palmityl moiety (Mishra et al., *Biochim. Biophys. Acta*, 1995, 1264, 229-237), an octadecylamine or hexylamino-carbonyl-oxycholesterol moiety 30 (Crooke et al., *J. Pharmacol. Exp. Ther.*, 1996, 277, 923-937), a tocopherol group (Nishina et al., *Molecular Therapy Nucleic Acids*, 2015, 4, e220; and Nishina et al., *Molecular Therapy*, 2008, 16, 734-740), or a GalNAc cluster (*e.g.*, WO2014/179620).

1. Conjugate Moieties

Conjugate moieties include, without limitation, intercalators, reporter molecules, polyamines, 35 polyamides, peptides, carbohydrates, vitamin moieties, polyethylene glycols, thioethers, polyethers, cholesterol, thiocholesterols, cholic acid moieties, folate, lipids, phospholipids, biotin, phenazine,

phenanthridine, anthraquinone, adamantane, acridine, fluoresceins, rhodamines, coumarins, fluorophores, and dyes.

In certain embodiments, a conjugate moiety comprises an active drug substance, for example, aspirin, warfarin, phenylbutazone, ibuprofen, suprofen, fen-bufen, ketoprofen, (S)-(+)-pranoprofen, carprofen, dansylsarcosine, 2,3,5-triodobenzoic acid, fingolimod, flufenamic acid, folinic acid, a benzothiadiazide, chlorothiazide, a diazepine, indo-methicin, a barbiturate, a cephalosporin, a sulfa drug, an antidiabetic, an antibacterial or an antibiotic.

2. Conjugate Linkers

Conjugate moieties are attached to oligonucleotides through conjugate linkers. In certain oligomeric compounds, the conjugate linker is a single chemical bond (i.e., the conjugate moiety is attached directly to an oligonucleotide through a single bond). In certain embodiments, the conjugate linker comprises a chain structure, such as a hydrocarbyl chain, or an oligomer of repeating units such as ethylene glycol, nucleosides, or amino acid units.

In certain embodiments, a conjugate linker comprises one or more groups selected from alkyl, amino, oxo, amide, disulfide, polyethylene glycol, ether, thioether, and hydroxylamino. In certain such embodiments, the conjugate linker comprises groups selected from alkyl, amino, oxo, amide and ether groups. In certain embodiments, the conjugate linker comprises groups selected from alkyl and amide groups. In certain embodiments, the conjugate linker comprises groups selected from alkyl and ether groups. In certain embodiments, the conjugate linker comprises at least one phosphorus moiety. In certain embodiments, the conjugate linker comprises at least one phosphate group. In certain embodiments, the conjugate linker includes at least one neutral linking group.

In certain embodiments, conjugate linkers, including the conjugate linkers described above, are bifunctional linking moieties, *e.g.*, those known in the art to be useful for attaching conjugate groups to parent compounds, such as the oligonucleotides provided herein. In general, a bifunctional linking moiety comprises at least two functional groups. One of the functional groups is selected to bind to a particular site on a parent compound and the other is selected to bind to a conjugate group. Examples of functional groups used in a bifunctional linking moiety include but are not limited to electrophiles for reacting with nucleophilic groups and nucleophiles for reacting with electrophilic groups. In certain embodiments, bifunctional linking moieties comprise one or more groups selected from amino, hydroxyl, carboxylic acid, thiol, alkyl, alkenyl, and alkynyl.

Examples of conjugate linkers include but are not limited to pyrrolidine, 8-amino-3,6-dioxaoctanoic acid (ADO), succinimidyl 4-(N-maleimidomethyl) cyclohexane-1-carboxylate (SMCC) and 6-aminohexanoic acid (AHEx or AHA). Other conjugate linkers include but are not limited to substituted or unsubstituted C₁-C₁₀ alkyl, substituted or unsubstituted C₂-C₁₀ alkenyl or substituted or unsubstituted C₂-C₁₀ alkynyl, wherein a nonlimiting list of preferred substituent groups includes hydroxyl, amino, alkoxy, carboxy, benzyl, phenyl, nitro, thiol, thioalkoxy, halogen, alkyl, aryl, alkenyl and alkynyl.

In certain embodiments, conjugate linkers comprise 1-10 linker-nucleosides. In certain embodiments, conjugate linkers comprise 2-5 linker-nucleosides. In certain embodiments, conjugate linkers comprise exactly 3 linker-nucleosides. In certain embodiments, conjugate linkers comprise the TCA motif. In certain embodiments, such linker-nucleosides are modified nucleosides. In certain embodiments such linker-nucleosides comprise a modified sugar moiety. In certain embodiments, linker-nucleosides are unmodified. In certain embodiments, linker-nucleosides comprise an optionally protected heterocyclic base selected from a purine, substituted purine, pyrimidine or substituted pyrimidine. In certain embodiments, a cleavable moiety is a nucleoside selected from uracil, thymine, cytosine, 4-N-benzoylcytosine, 5-methyl cytosine, 4-N-benzoyl-5-methyl cytosine, adenine, 6-N-benzoyladenine, guanine and 2-N-isobutyrylguanine. It is typically desirable for linker-nucleosides to be cleaved from the oligomeric compound after it reaches a target tissue. Accordingly, linker-nucleosides are typically linked to one another and to the remainder of the oligomeric compound through cleavable bonds. In certain embodiments, such cleavable bonds are phosphodiester bonds.

Herein, linker-nucleosides are not considered to be part of the oligonucleotide. Accordingly, in embodiments in which an oligomeric compound comprises an oligonucleotide consisting of a specified number or range of linked nucleosides and/or a specified percent complementarity to a reference nucleic acid and the oligomeric compound also comprises a conjugate group comprising a conjugate linker comprising linker-nucleosides, those linker-nucleosides are not counted toward the length of the oligonucleotide and are not used in determining the percent complementarity of the oligonucleotide for the reference nucleic acid. For example, an oligomeric compound may comprise (1) a modified oligonucleotide consisting of 8-30 nucleosides and (2) a conjugate group comprising 1-10 linker-nucleosides that are contiguous with the nucleosides of the modified oligonucleotide. The total number of contiguous linked nucleosides in such an oligomeric compound is more than 30. Alternatively, an oligomeric compound may comprise a modified oligonucleotide consisting of 8-30 nucleosides and no conjugate group. The total number of contiguous linked nucleosides in such an oligomeric compound is no more than 30. Unless otherwise indicated conjugate linkers comprise no more than 10 linker-nucleosides. In certain embodiments, conjugate linkers comprise no more than 5 linker-nucleosides. In certain embodiments, conjugate linkers comprise no more than 3 linker-nucleosides. In certain embodiments, conjugate linkers comprise no more than 2 linker-nucleosides. In certain embodiments, conjugate linkers comprise no more than 1 linker-nucleoside.

In certain embodiments, it is desirable for a conjugate group to be cleaved from the oligonucleotide. For example, in certain circumstances oligomeric compounds comprising a particular conjugate moiety are better taken up by a particular cell type, but once the oligomeric compound has been taken up, it is desirable that the conjugate group be cleaved to release the unconjugated or parent oligonucleotide. Thus, certain conjugate linkers may comprise one or more cleavable moieties. In certain embodiments, a cleavable moiety is a cleavable bond. In certain embodiments, a cleavable moiety is a group of atoms comprising at least one cleavable bond. In certain embodiments, a cleavable moiety comprises a group of atoms having one, two,

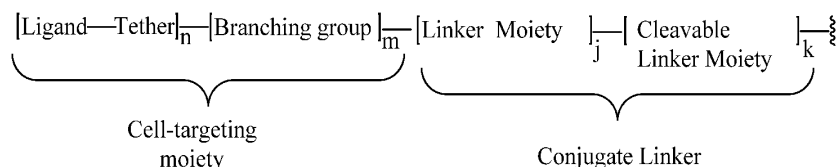
three, four, or more than four cleavable bonds. In certain embodiments, a cleavable moiety is selectively cleaved inside a cell or subcellular compartment, such as a lysosome. In certain embodiments, a cleavable moiety is selectively cleaved by endogenous enzymes, such as nucleases.

In certain embodiments, a cleavable bond is selected from among an amide, an ester, an ether, one or both esters of a phosphodiester, a phosphate ester, a carbamate, and a disulfide. In certain embodiments, a cleavable bond is one or both of the esters of a phosphodiester. In certain embodiments, a cleavable moiety comprises a phosphate or phosphodiester. In certain embodiments, the cleavable moiety is a phosphate or phosphodiester linkage between an oligonucleotide and a conjugate moiety or conjugate group.

In certain embodiments, a cleavable moiety comprises or consists of one or more linker-nucleosides. In certain such embodiments, the one or more linker-nucleosides are linked to one another and/or to the remainder of the oligomeric compound through cleavable bonds. In certain embodiments, such cleavable bonds are unmodified phosphodiester bonds. In certain embodiments, a cleavable moiety is 2'-deoxynucleoside that is attached to either the 3' or 5'-terminal nucleoside of an oligonucleotide by a phosphodiester internucleoside linkage and covalently attached to the remainder of the conjugate linker or conjugate moiety by a phosphate or phosphorothioate linkage. In certain such embodiments, the cleavable moiety is 2'-deoxyadenosine.

3. Cell-Targeting Moieties

In certain embodiments, a conjugate group comprises a cell-targeting moiety. In certain embodiments, a conjugate group has the general formula:



wherein n is from 1 to about 3, m is 0 when n is 1, m is 1 when n is 2 or greater, j is 1 or 0, and k is 1 or 0.

In certain embodiments, n is 1, j is 1 and k is 0. In certain embodiments, n is 1, j is 0 and k is 1. In certain embodiments, n is 1, j is 1 and k is 1. In certain embodiments, n is 2, j is 1 and k is 0. In certain embodiments, n is 2, j is 0 and k is 1. In certain embodiments, n is 2, j is 1 and k is 1. In certain embodiments, n is 3, j is 1 and k is 0. In certain embodiments, n is 3, j is 0 and k is 1. In certain embodiments, n is 3, j is 1 and k is 1.

In certain embodiments, conjugate groups comprise cell-targeting moieties that have at least one tethered ligand. In certain embodiments, cell-targeting moieties comprise two tethered ligands covalently attached to a branching group. In certain embodiments, cell-targeting moieties comprise three tethered ligands covalently attached to a branching group.

In certain embodiments, the cell-targeting moiety comprises a branching group comprising one or more groups selected from alkyl, amino, oxo, amide, disulfide, polyethylene glycol, ether, thioether and

hydroxylamino groups. In certain embodiments, the branching group comprises a branched aliphatic group comprising groups selected from alkyl, amino, oxo, amide, disulfide, polyethylene glycol, ether, thioether and hydroxylamino groups. In certain such embodiments, the branched aliphatic group comprises groups selected from alkyl, amino, oxo, amide and ether groups. In certain such embodiments, the branched aliphatic group comprises groups selected from alkyl, amino and ether groups. In certain such embodiments, the branched aliphatic group comprises groups selected from alkyl and ether groups. In certain embodiments, the branching group comprises a mono or polycyclic ring system.

In certain embodiments, each tether of a cell-targeting moiety comprises one or more groups selected from alkyl, substituted alkyl, ether, thioether, disulfide, amino, oxo, amide, phosphodiester, and polyethylene glycol, in any combination. In certain embodiments, each tether is a linear aliphatic group comprising one or more groups selected from alkyl, ether, thioether, disulfide, amino, oxo, amide, and polyethylene glycol, in any combination. In certain embodiments, each tether is a linear aliphatic group comprising one or more groups selected from alkyl, phosphodiester, ether, amino, oxo, and amide, in any combination. In certain embodiments, each tether is a linear aliphatic group comprising one or more groups selected from alkyl, ether, amino, oxo, and amid, in any combination. In certain embodiments, each tether is a linear aliphatic group comprising one or more groups selected from alkyl, amino, and oxo, in any combination. In certain embodiments, each tether is a linear aliphatic group comprising one or more groups selected from alkyl and oxo, in any combination. In certain embodiments, each tether is a linear aliphatic group comprising one or more groups selected from alkyl and phosphodiester, in any combination. In certain embodiments, each tether comprises at least one phosphorus linking group or neutral linking group. In certain embodiments, each tether comprises a chain from about 6 to about 20 atoms in length. In certain embodiments, each tether comprises a chain from about 10 to about 18 atoms in length. In certain embodiments, each tether comprises about 10 atoms in chain length.

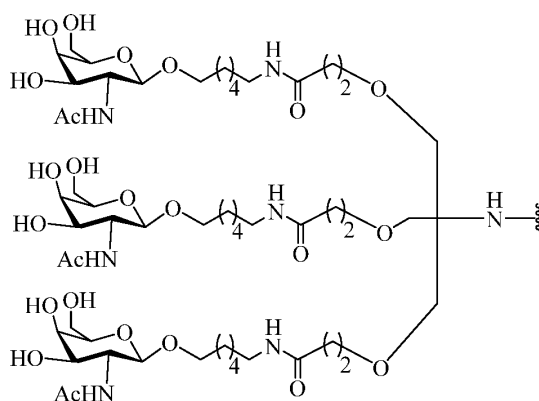
In certain embodiments, each ligand of a cell-targeting moiety has an affinity for at least one type of receptor on a target cell. In certain embodiments, each ligand has an affinity for at least one type of receptor on the surface of a mammalian liver cell. In certain embodiments, each ligand has an affinity for the hepatic asialoglycoprotein receptor (ASGP-R). In certain embodiments, each ligand is a carbohydrate. In certain embodiments, each ligand is, independently selected from galactose, N-acetyl galactosamine (GalNAc), mannose, glucose, glucosamine and fucose. In certain embodiments, each ligand is N-acetyl galactosamine (GalNAc). In certain embodiments, the cell-targeting moiety comprises 3 GalNAc ligands. In certain embodiments, the cell-targeting moiety comprises 2 GalNAc ligands. In certain embodiments, the cell-targeting moiety comprises 1 GalNAc ligand.

In certain embodiments, each ligand of a cell-targeting moiety is a carbohydrate, carbohydrate derivative, modified carbohydrate, polysaccharide, modified polysaccharide, or polysaccharide derivative. In certain such embodiments, the conjugate group comprises a carbohydrate cluster (see, *e.g.*, Maier et al., “Synthesis of Antisense Oligonucleotides Conjugated to a Multivalent Carbohydrate Cluster for Cellular

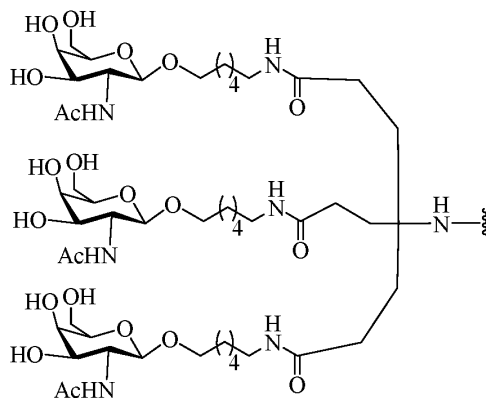
Targeting,” *Bioconjugate Chemistry*, 2003, 14, 18-29, or Rensen et al., “Design and Synthesis of Novel *N*-Acetylgalactosamine-Terminated Glycolipids for Targeting of Lipoproteins to the Hepatic Asialoglycoprotein Receptor,” *J. Med. Chem.* 2004, 47, 5798-5808, which are incorporated herein by reference in their entirety).

In certain such embodiments, each ligand is an amino sugar or a thio sugar. For example, amino sugars may be selected from any number of compounds known in the art, such as sialic acid, α -D-galactosamine, β -muramic acid, 2-deoxy-2-methylamino-L-glucopyranose, 4,6-dideoxy-4-formamido-2,3-di-*O*-methyl-D-mannopyranose, 2-deoxy-2-sulfoamino-D-glucopyranose and *N*-sulfo-D-glucosamine, and *N*-glycoloyl- α -neuraminic acid. For example, thio sugars may be selected from 5-Thio- β -D-glucopyranose, methyl 2,3,4-tri-*O*-acetyl-1-thio-6-*O*-trityl- α -D-glucopyranoside, 4-thio- β -D-galactopyranose, and ethyl 3,4,6,7-tetra-*O*-acetyl-2-deoxy-1,5-dithio- α -D-*gluco*-heptopyranoside.

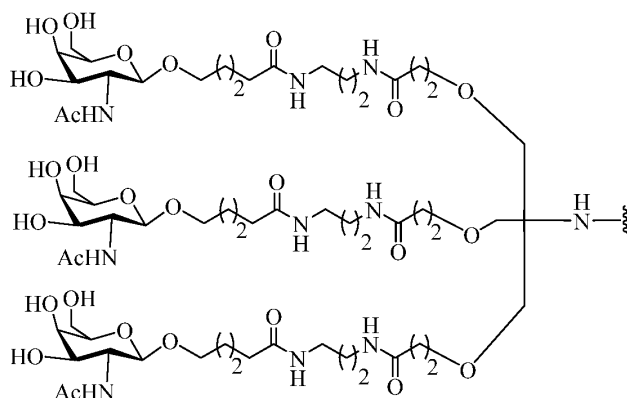
In certain embodiments, conjugate groups comprise a cell-targeting moiety having the formula:



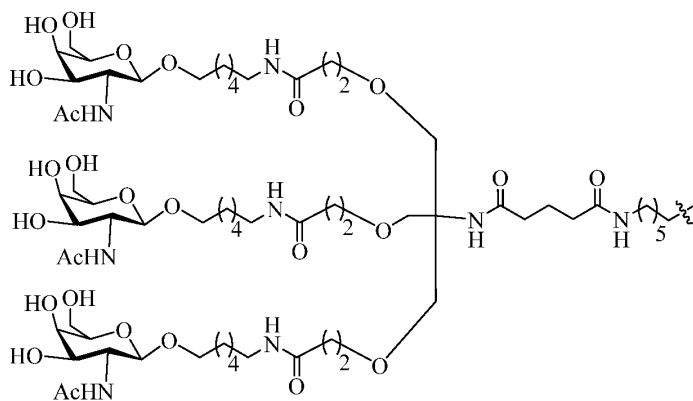
In certain embodiments, conjugate groups comprise a cell-targeting moiety having the formula:



In certain embodiments, conjugate groups comprise a cell-targeting moiety having the formula:

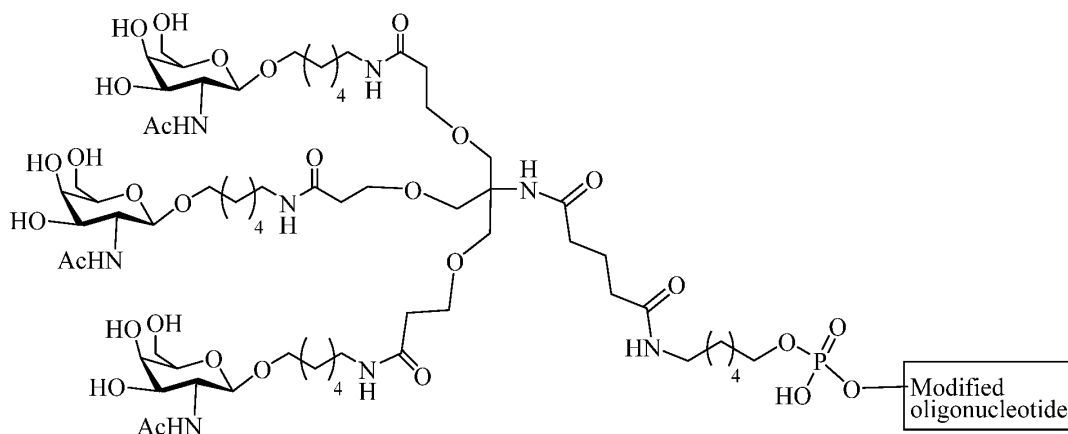


In certain embodiments, compounds described herein comprise a conjugate group described herein as “THA-GalNAc₃”. THA-GalNAc₃ is shown below without the optional cleavable moiety at the end of the linker region:



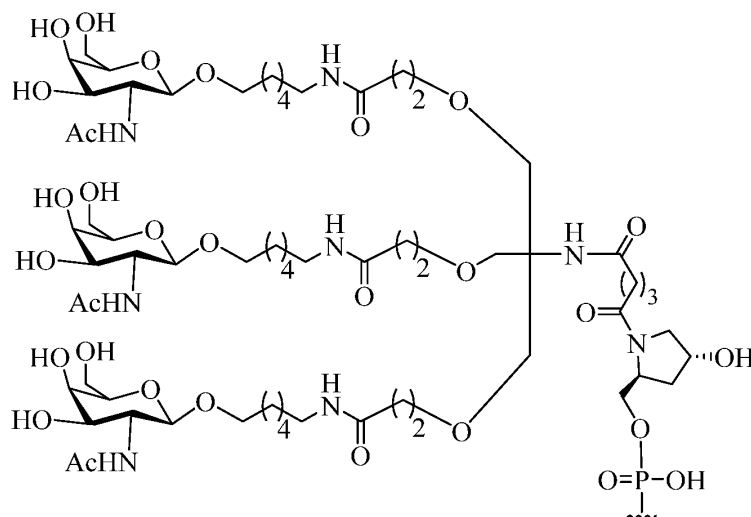
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In certain embodiments, compounds described herein comprise THA-GalNAc₃-phosphate, also represented as (THA-GalNAc₃)_o, having the formula:



10 wherein modified oligonucleotide represents a modified oligonucleotide.

In certain embodiments, compounds described herein comprise a 3'-THA-C6-GalNAc hydroxyproline phosphate, ("HPPO-GalNAc"). 3'- HPPO-GalNAc is represented by the structure below wherein the phosphate group is attached to the 3'-oxygen atom of the 3' nucleoside:



- 5 Representative publications that teach the preparation of certain of the above noted conjugate groups and compounds comprising conjugate groups, tethers, conjugate linkers, branching groups, ligands, cleavable moieties as well as other modifications include without limitation, US 5,994,517, US 6,300,319, US 6,660,720, US 6,906,182, US 7,262,177, US 7,491,805, US 8,106,022, US 7,723,509, US 9,127,276, US 2006/0148740, US 2011/0123520, WO 2013/033230 and WO 2012/037254, Biessen et al., *J. Med. Chem.* 1995, 38, 1846-1852, Lee et al., *Bioorganic & Medicinal Chemistry* 2011, 19, 2494-2500, Rensen et al., *J. Biol. Chem.* 2001, 276, 37577-37584, Rensen et al., *J. Med. Chem.* 2004, 47, 5798-5808, Slidregt et al., *J. Med. Chem.* 1999, 42, 609-618, and Valentijn et al., *Tetrahedron*, 1997, 53, 759-770, each of which is incorporated by reference herein in its entirety.

- 15 In certain embodiments, compounds described herein comprise modified oligonucleotides comprising a gapmer or fully modified motif and a conjugate group comprising at least one, two, or three GalNAc ligands. In certain embodiments compounds described herein comprise a conjugate group found in any of the following references: Lee, *Carbohydr Res*, 1978, 67, 509-514; Connolly et al., *J Biol Chem*, 1982, 257, 939-945; Pavia et al., *Int J Pep Protein Res*, 1983, 22, 539-548; Lee et al., *Biochem*, 1984, 23, 4255-4261; Lee et al., *Glycoconjugate J*, 1987, 4, 317-328; Toyokuni et al., *Tetrahedron Lett*, 1990, 31, 2673-2676; Biessen et al., *J Med Chem*, 1995, 38, 1538-1546; Valentijn et al., *Tetrahedron*, 1997, 53, 759-770; Kim et al., *Tetrahedron Lett*, 1997, 38, 3487-3490; Lee et al., *Bioconjug Chem*, 1997, 8, 762-765; Kato et al., *Glycobiol*, 2001, 11, 821-829; Rensen et al., *J Biol Chem*, 2001, 276, 37577-37584; Lee et al., *Methods Enzymol*, 2003, 362, 38-43; Westerlind et al., *Glycoconj J*, 2004, 21, 227-241; Lee et al., *Bioorg Med Chem Lett*, 2006, 16(19), 5132-5135; Maierhofer et al., *Bioorg Med Chem*, 2007, 15, 7661-7676; Khorev et al.,

- Bioorg Med Chem*, 2008, 16, 5216-5231; Lee et al., *Bioorg Med Chem*, 2011, 19, 2494-2500; Kornilova et al., *Analyt Biochem*, 2012, 425, 43-46; Pujol et al., *Angew Chemie Int Ed Engl*, 2012, 51, 7445-7448; Biessen et al., *J Med Chem*, 1995, 38, 1846-1852; Slidregt et al., *J Med Chem*, 1999, 42, 609-618; Rensen et al., *J Med Chem*, 2004, 47, 5798-5808; Rensen et al., *Arterioscler Thromb Vasc Biol*, 2006, 26, 169-175; van Rosenberg et al., *Gene Ther*, 2004, 11, 457-464; Sato et al., *J Am Chem Soc*, 2004, 126, 14013-14022; Lee et al., *J Org Chem*, 2012, 77, 7564-7571; Biessen et al., *FASEB J*, 2000, 14, 1784-1792; Rajur et al., *Bioconjug Chem*, 1997, 8, 935-940; Duff et al., *Methods Enzymol*, 2000, 313, 297-321; Maier et al., *Bioconjug Chem*, 2003, 14, 18-29; Jayaprakash et al., *Org Lett*, 2010, 12, 5410-5413; Manoharan, *Antisense Nucleic Acid Drug Dev*, 2002, 12, 103-128; Merwin et al., *Bioconjug Chem*, 1994, 5, 612-620; Tomiya et al., *Bioorg Med Chem*, 2013, 21, 5275-5281; International applications WO1998/013381; WO2011/038356; WO1997/046098; WO2008/098788; WO2004/101619; WO2012/037254; WO2011/120053; WO2011/100131; WO2011/163121; WO2012/177947; WO2013/033230; WO2013/075035; WO2012/083185; WO2012/083046; WO2009/082607; WO2009/134487; WO2010/144740; WO2010/148013; WO1997/020563; WO2010/088537; WO2002/043771; WO2010/129709; WO2012/068187; WO2009/126933; WO2004/024757; WO2010/054406; WO2012/089352; WO2012/089602; WO2013/166121; WO2013/165816; U.S. Patents 4,751,219; 8,552,163; 6,908,903; 7,262,177; 5,994,517; 6,300,319; 8,106,022; 7,491,805; 7,491,805; 7,582,744; 8,137,695; 6,383,812; 6,525,031; 6,660,720; 7,723,509; 8,541,548; 8,344,125; 8,313,772; 8,349,308; 8,450,467; 8,501,930; 8,158,601; 7,262,177; 6,906,182; 6,620,916; 8,435,491; 8,404,862; 7,851,615; Published U.S. Patent Application Publications US2011/0097264; US2011/0097265; US2013/0004427; US2005/0164235; US2006/0148740; US2008/0281044; US2010/0240730; US2003/0119724; US2006/0183886; US2008/0206869; US2011/0269814; US2009/0286973; US2011/0207799; US2012/0136042; US2012/0165393; US2008/0281041; US2009/0203135; US2012/0035115; US2012/0095075; US2012/0101148; US2012/0128760; US2012/0157509; US2012/0230938; US2013/0109817; US2013/0121954; US2013/0178512; US2013/0236968; US2011/0123520; US2003/0077829; US2008/0108801; and US2009/0203132; each of which is incorporated by reference in its entirety.

B. Certain Terminal Groups

- In certain embodiments, oligomeric compounds comprise one or more terminal groups. In certain such embodiments, oligomeric compounds comprise a stabilized 5'-phosphate. Stabilized 5'-phosphates include, but are not limited to 5'-phosphanates, including, but not limited to 5'-vinylphosphonates. In certain embodiments, terminal groups comprise one or more abasic nucleosides and/or inverted nucleosides. In certain embodiments, terminal groups comprise one or more 2'-linked nucleosides. In certain such embodiments, the 2'-linked nucleoside is an abasic nucleoside.

III. Oligomeric Duplexes

In certain embodiments, oligomeric compounds described herein comprise an oligonucleotide, having a nucleobase sequence complementary to that of a target nucleic acid. In certain embodiments, an oligomeric compound is paired with a second oligomeric compound to form an oligomeric duplex. Such
5 oligomeric duplexes comprise a first oligomeric compound having a portion complementary to a target nucleic acid and a second oligomeric compound having a portion complementary to the first oligomeric compound. In certain embodiments, the first oligomeric compound of an oligomeric duplex comprises or consists of (1) a modified or unmodified oligonucleotide and optionally a conjugate group and (2) a second
10 modified or unmodified oligonucleotide and optionally a conjugate group. Either or both oligomeric compounds of an oligomeric duplex may comprise a conjugate group. The oligonucleotides of each oligomeric compound of an oligomeric duplex may include non-complementary overhanging nucleosides.

IV. Antisense Activity

In certain embodiments, oligomeric compounds and oligomeric duplexes are capable of hybridizing to a target nucleic acid, resulting in at least one antisense activity; such oligomeric compounds and
15 oligomeric duplexes are antisense compounds. In certain embodiments, antisense compounds have antisense activity when they reduce or inhibit the amount or activity of a target nucleic acid by 25% or more in the standard cell assay. In certain embodiments, antisense compounds selectively affect one or more target nucleic acid. Such antisense compounds comprise a nucleobase sequence that hybridizes to one or more target nucleic acid, resulting in one or more desired antisense activity and does not hybridize to one or more
20 non-target nucleic acid or does not hybridize to one or more non-target nucleic acid in such a way that results in significant undesired antisense activity.

In certain antisense activities, hybridization of an antisense compound to a target nucleic acid results in recruitment of a protein that cleaves the target nucleic acid. For example, certain antisense compounds result in RNase H mediated cleavage of the target nucleic acid. RNase H is a cellular endonuclease that
25 cleaves the RNA strand of an RNA:DNA duplex. The DNA in such an RNA:DNA duplex need not be unmodified DNA. In certain embodiments, described herein are antisense compounds that are sufficiently “DNA-like” to elicit RNase H activity. In certain embodiments, one or more non-DNA-like nucleoside in the gap of a gapmer is tolerated.

In certain antisense activities, an antisense compound or a portion of an antisense compound is
30 loaded into an RNA-induced silencing complex (RISC), ultimately resulting in cleavage of the target nucleic acid. For example, certain antisense compounds result in cleavage of the target nucleic acid by Argonaute. Antisense compounds that are loaded into RISC are RNAi compounds. RNAi compounds may be double-stranded (siRNA) or single-stranded (ssRNA).

In certain embodiments, hybridization of an antisense compound to a target nucleic acid does not
35 result in recruitment of a protein that cleaves that target nucleic acid. In certain embodiments, hybridization

of the antisense compound to the target nucleic acid results in alteration of splicing of the target nucleic acid. In certain embodiments, hybridization of an antisense compound to a target nucleic acid results in inhibition of a binding interaction between the target nucleic acid and a protein or other nucleic acid. In certain embodiments, hybridization of an antisense compound to a target nucleic acid results in alteration of translation of the target nucleic acid.

Antisense activities may be observed directly or indirectly. In certain embodiments, observation or detection of an antisense activity involves observation or detection of a change in an amount of a target nucleic acid or protein encoded by such target nucleic acid, a change in the ratio of splice variants of a nucleic acid or protein and/or a phenotypic change in a cell or subject.

10 V. Certain Target Nucleic Acids

In certain embodiments, oligomeric compounds comprise or consist of an oligonucleotide comprising a portion that is complementary to a target nucleic acid. In certain embodiments, the target nucleic acid is an endogenous RNA molecule. In certain embodiments, the target nucleic acid encodes a protein. In certain such embodiments, the target nucleic acid is selected from: a mature mRNA, and a pre-mRNA, including intronic, exonic and untranslated regions. In certain embodiments, the target RNA is an antisense transcript. In certain embodiments, the target RNA is a mature mRNA. In certain embodiments, the target nucleic acid is a pre-mRNA. In certain such embodiments, the target region is entirely within an intron. In certain embodiments, the target region spans an intron/exon junction. In certain embodiments, the target region is at least 50% within an intron. In certain embodiments, the target nucleic acid is the RNA transcriptional product of a retrogene. In certain embodiments, the target nucleic acid is a non-coding RNA. In certain such embodiments, the target non-coding RNA is selected from: a long non-coding RNA, a short non-coding RNA, an intronic RNA molecule.

A. Complementarity/Mismatches to the Target Nucleic Acid

It is possible to introduce mismatch bases without eliminating activity. For example, Gautschi et al (J. Natl. Cancer Inst. 93:463-471, March 2001) demonstrated the ability of an oligonucleotide having 100% complementarity to the bcl-2 mRNA and having 3 mismatches to the bcl-xL mRNA to reduce the expression of both bcl-2 and bcl-xL *in vitro* and *in vivo*. Furthermore, this oligonucleotide demonstrated potent anti-tumor activity *in vivo*. Maher and Dolnick (Nuc. Acid. Res. 16:3341-3358, 1988) tested a series of tandem 14 nucleobase oligonucleotides, and 28 and 42 nucleobase oligonucleotides comprised of the sequence of two or three of the tandem oligonucleotides, respectively, for their ability to arrest translation of human DHFR in a rabbit reticulocyte assay. Each of the three 14 nucleobase oligonucleotides alone was able to inhibit translation, albeit at a more modest level than the 28 or 42 nucleobase oligonucleotides.

In certain embodiments, oligonucleotides are complementary to the target nucleic acid over the entire length of the oligonucleotide. In certain embodiments, oligonucleotides are 99%, 95%, 90%, 85%, or 80% complementary to the target nucleic acid. In certain embodiments, oligonucleotides are at least 80%

complementary to the target nucleic acid over the entire length of the oligonucleotide and comprise a portion that is 100% or fully complementary to a target nucleic acid. In certain embodiments, the portion of full complementarity is 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, or 24 nucleobases in length.

5 In certain embodiments, oligonucleotides comprise one or more mismatched nucleobases relative to the target nucleic acid. In certain embodiments, antisense activity against the target is reduced by such mismatch, but activity against a non-target is reduced by a greater amount. Thus, in certain embodiments selectivity of the oligonucleotide is improved. In certain embodiments, the mismatch is specifically positioned within an oligonucleotide having a gapmer motif. In certain embodiments, the mismatch is at
10 position 1, 2, 3, 4, 5, 6, 7, or 8 from the 5'-end of the gap region. In certain embodiments, the mismatch is at position 9, 8, 7, 6, 5, 4, 3, 2, 1 from the 3'-end of the gap region. In certain embodiments, the mismatch is at position 1, 2, 3, or 4 from the 5'-end of the wing region. In certain embodiments, the mismatch is at position 4, 3, 2, or 1 from the 3'-end of the wing region.

B. FXII

15 In certain embodiments, oligomeric compounds comprise or consist of an oligonucleotide, or portion thereof, that is complementary to a target nucleic acid, wherein the target nucleic acid is a FXII nucleic acid. In certain embodiments, the FXII nucleic acid has the human FXII mRNA sequence designated herein as SEQ ID NO: 1 (ENSEMBL ID ENST00000253496.3 from ENSEMBL version 99: January 2020). In certain
20 embodiments, the FXII nucleic acid has the human *F12* genomic sequence, designated herein as SEQ ID NO: 2 (ENSEMBL ID ENSG00000131187.9 from ENSEMBL version 99: January 2020, human reference assembly version GRCh38.p13 located on the reverse strand of chromosome 5 from positions 177,402,140 to 177,409,576). In certain embodiments, the FXII nucleic acid has the human *F12* genomic sequence, designated herein as SEQ ID NO: 3 (the complement of GENBANK Accession No. NC_000005.10 truncated
25 from truncated from nucleotides 177399001 to 177413000). In certain embodiments, the FXII nucleic acid has the human FXII mRNA sequence designated herein as SEQ ID NO: 4 (GENBANK Accession No. NM_000505.3).

In certain embodiments, an oligomeric compound complementary to any one of SEQ ID NOS: 1-4 is capable of reducing FXII RNA in a cell. In certain embodiments, an oligomeric compound complementary to any one of SEQ ID NOS: 1-4 is capable of reducing FXII protein in a cell. In certain embodiments, the
30 cell is *in vitro*. In certain embodiments, the cell is in a subject. In certain embodiments, an oligomeric compound complementary to any one of SEQ ID NOS: 1-4 is capable of ameliorating one or more symptoms of a thromboembolic condition when administered to a subject. In certain embodiments, the thromboembolic condition is deep vein thrombosis, venous thrombosis, arterial thrombosis, pulmonary embolism, myocardial infarction, or stroke. In certain embodiments, the symptoms are selected from pain, shortness of breath, heart
35 burn, cold sweat, fatigue, lightheadedness, dizziness, swelling, cramping, and death.

In certain embodiments, an oligomeric compound complementary to any one of SEQ ID NOS: 1-4 is

capable of reducing the detectable amount of FXII RNA *in vitro* by at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, or at least 90%. In certain embodiments, an oligomeric compound complementary to any one of SEQ ID NOS: 1-4 is capable of reducing the detectable amount of FXII protein *in vitro* by at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, or at least 90%. In certain embodiments, an oligomeric compound complementary to any one of SEQ ID NOS: 1-4 is capable of reducing the detectable amount of FXII RNA in a biological sample of a subject by at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, or at least 90%. In certain embodiments, an oligomeric compound complementary to any one of SEQ ID NOS: 1-4 is capable of reducing the detectable amount of FXII protein in a biological sample of a subject by at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, or at least 90%. In certain embodiments, the biological sample comprises blood, plasma/serum, or a cell of the subject.

VI. Certain Pharmaceutical Compositions

In certain embodiments, described herein are pharmaceutical compositions comprising one or more oligomeric compounds. In certain embodiments, the one or more oligomeric compounds each consists of a modified oligonucleotide. In certain embodiments, the pharmaceutical composition comprises a pharmaceutically acceptable diluent or carrier. In certain embodiments, a pharmaceutical composition comprises or consists of a sterile saline solution and one or more oligomeric compound. In certain embodiments, the sterile saline is pharmaceutical grade saline. In certain embodiments, a pharmaceutical composition comprises or consists of one or more oligomeric compound and sterile water. In certain embodiments, the sterile water is pharmaceutical grade water. In certain embodiments, a pharmaceutical composition comprises or consists of one or more oligomeric compound and phosphate-buffered saline (PBS). In certain embodiments, the sterile PBS is pharmaceutical grade PBS. In certain embodiments, a pharmaceutical composition comprises or consists of one or more oligomeric compound and artificial cerebrospinal fluid. In certain embodiments, the artificial cerebrospinal fluid is pharmaceutical grade.

In certain embodiments, a pharmaceutical composition comprises a modified oligonucleotide and artificial cerebrospinal fluid. In certain embodiments, a pharmaceutical composition consists of a modified oligonucleotide and artificial cerebrospinal fluid. In certain embodiments, a pharmaceutical composition consists essentially of a modified oligonucleotide and artificial cerebrospinal fluid. In certain embodiments, the artificial cerebrospinal fluid is pharmaceutical grade.

In certain embodiments, pharmaceutical compositions comprise one or more oligomeric compound and one or more excipients. In certain embodiments, excipients are selected from water, salt solutions, alcohol, polyethylene glycols, gelatin, lactose, amylase, magnesium stearate, talc, silicic acid, viscous paraffin, hydroxymethylcellulose and polyvinylpyrrolidone.

In certain embodiments, oligomeric compounds may be admixed with pharmaceutically acceptable active and/or inert substances for the preparation of pharmaceutical compositions or formulations.

Compositions and methods for the formulation of pharmaceutical compositions depend on a number of criteria, including, but not limited to, route of administration, extent of disease, or dose to be administered.

5 In certain embodiments, pharmaceutical compositions comprising an oligomeric compound encompass any pharmaceutically acceptable salts of the oligomeric compound, esters of the oligomeric compound, or salts of such esters. In certain embodiments, pharmaceutical compositions comprising oligomeric compounds comprising one or more oligonucleotide, upon administration to a subject, including a human, are capable of providing (directly or indirectly) the biologically active metabolite or residue thereof.

10 Accordingly, for example, the disclosure is also drawn to pharmaceutically acceptable salts of oligomeric compounds, prodrugs, pharmaceutically acceptable salts of such prodrugs, and other bioequivalents. Suitable pharmaceutically acceptable salts include, but are not limited to, sodium and potassium salts. In certain embodiments, prodrugs comprise one or more conjugate group attached to an oligonucleotide, wherein the conjugate group is cleaved by endogenous nucleases within the body.

15 Lipid moieties have been used in nucleic acid therapies in a variety of methods. In certain such methods, the nucleic acid, such as an oligomeric compound, is introduced into preformed liposomes or lipoplexes made of mixtures of cationic lipids and neutral lipids. In certain methods, DNA complexes with mono- or poly-cationic lipids are formed without the presence of a neutral lipid. In certain embodiments, a lipid moiety is selected to increase distribution of a pharmaceutical agent to a particular cell or tissue. In

20 certain embodiments, a lipid moiety is selected to increase distribution of a pharmaceutical agent to fat tissue. In certain embodiments, a lipid moiety is selected to increase distribution of a pharmaceutical agent to muscle tissue.

In certain embodiments, pharmaceutical compositions comprise a delivery system. Examples of delivery systems include, but are not limited to, liposomes and emulsions. Certain delivery systems are

25 useful for preparing certain pharmaceutical compositions including those comprising hydrophobic compounds. In certain embodiments, certain organic solvents such as dimethylsulfoxide are used.

In certain embodiments, pharmaceutical compositions comprise one or more tissue-specific delivery molecules designed to deliver the one or more pharmaceutical agents of the present invention to specific tissues or cell types. For example, in certain embodiments, pharmaceutical compositions include liposomes

30 coated with a tissue-specific antibody.

In certain embodiments, pharmaceutical compositions comprise a co-solvent system. Certain of such co-solvent systems comprise, for example, benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. In certain embodiments, such co-solvent systems are used for hydrophobic compounds. A non-limiting example of such a co-solvent system is the VPD co-solvent system, which is a

35 solution of absolute ethanol comprising 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant Polysorbate 80™ and 65% w/v polyethylene glycol 300. The proportions of such co-solvent systems may be

varied considerably without significantly altering their solubility and toxicity characteristics. Furthermore, the identity of co-solvent components may be varied: for example, other surfactants may be used instead of Polysorbate 80™; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, *e.g.*, polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose.

In certain embodiments, pharmaceutical compositions are prepared for oral administration. In certain embodiments, pharmaceutical compositions are prepared for buccal administration. In certain embodiments, a pharmaceutical composition is prepared for administration by injection (*e.g.*, intravenous, subcutaneous, intramuscular, intrathecal (IT), intracerebroventricular (ICV), etc.). In certain of such embodiments, a pharmaceutical composition comprises a carrier and is formulated in aqueous solution, such as water or physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. In certain embodiments, other ingredients are included (*e.g.*, ingredients that aid in solubility or serve as preservatives). In certain embodiments, injectable suspensions are prepared using appropriate liquid carriers, suspending agents and the like. Certain pharmaceutical compositions for injection are presented in unit dosage form, *e.g.*, in ampoules or in multi-dose containers. Certain pharmaceutical compositions for injection are suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents. Certain solvents suitable for use in pharmaceutical compositions for injection include, but are not limited to, lipophilic solvents and fatty oils, such as sesame oil, synthetic fatty acid esters, such as ethyl oleate or triglycerides, and liposomes.

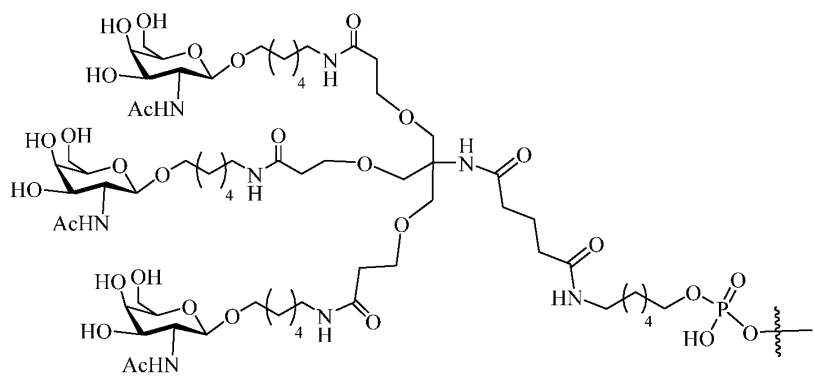
Under certain conditions, certain compounds disclosed herein act as acids. Although such compounds may be drawn or described in protonated (free acid) form, or ionized and in association with a cation (salt) form, aqueous solutions of such compounds exist in equilibrium among such forms. For example, a phosphate linkage of an oligonucleotide in aqueous solution exists in equilibrium among free acid, anion and salt forms. Unless otherwise indicated, compounds described herein are intended to include all such forms. Moreover, certain oligonucleotides have several such linkages, each of which is in equilibrium. Thus, oligonucleotides in solution exist in an ensemble of forms at multiple positions all at equilibrium. The term "oligonucleotide" is intended to include all such forms. Drawn structures necessarily depict a single form. Nevertheless, unless otherwise indicated, such drawings are likewise intended to include corresponding forms. Herein, a structure depicting the free acid of a compound followed by the term "or a salt thereof" expressly includes all such forms that may be fully or partially protonated/de-protonated/in association with a cation. In certain instances, one or more specific cation is identified.

In certain embodiments, modified oligonucleotides or oligomeric compounds are in aqueous solution with sodium. In certain embodiments, modified oligonucleotides or oligomeric compounds are in aqueous solution with potassium. In certain embodiments, modified oligonucleotides or oligomeric compounds are in PBS. In certain embodiments, modified oligonucleotides or oligomeric compounds are in water. In certain such embodiments, the pH of the solution is adjusted with NaOH and/or HCl to achieve a desired pH.

VII. Certain Compositions

1. Compound No. 1194357

In certain embodiments, Compound No. 1194357 is characterized as an oligomeric compound consisting of a conjugate group and a modified oligonucleotide, wherein the conjugate group is a THA-GalNAc₃ that is directly attached to the 5' end of the modified oligonucleotide through a phosphodiester linkage, (THA-GalNAc₃)_o; wherein (THA-GalNAc₃)_o is represented by the following structure:



wherein the modified oligonucleotide is a 3-10-3 cEt gapmer, having a sequence of (from 5' to 3') GCGGAATCACCAAGGA (incorporated herein as SEQ ID NO: 3379); wherein each of nucleosides 1-3 and 14-16 (from 5' to 3') comprise a cEt modified sugar moiety and each of nucleosides 4-13 are 2'-β-D-deoxynucleosides; wherein each internucleoside linkage is a phosphorothioate internucleoside linkage; and wherein each cytosine is a 5-methyl cytosine.

In certain embodiments, Compound No. 1194357 is represented by the following chemical notation: (THA-GalNAc₃)_o Gks ^mCks Gks Gds Ads Ads Tds ^mCds Ads ^mCds ^mCds Ads Ads Gks Gks Ak, wherein:

- 15 A = an adenine nucleobase,
- ^mC = a 5-methyl cytosine nucleobase,
- G = a guanine nucleobase,
- T = a thymine nucleobase,
- k = a cEt modified sugar moiety,
- 20 d = a 2'-β-D-deoxyribose sugar moiety, and
- s = a phosphorothioate internucleoside linkage.

In certain embodiments, provided is an oligomeric compound comprising a modified oligonucleotide and a conjugate group according to the following chemical notation: (THA-GalNAc₃)_o Gks ^mCks Gks Gds Ads Ads Tds ^mCds Ads ^mCds ^mCds Ads Ads Gks Gks Ak, wherein:

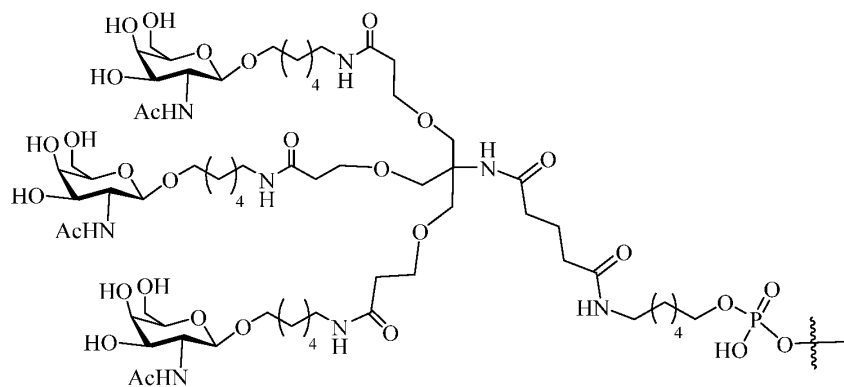
- 25 A = an adenine nucleobase,
- ^mC = a 5-methyl cytosine nucleobase,
- G = a guanine nucleobase,
- T = a thymine nucleobase,

k = a cEt modified sugar moiety,

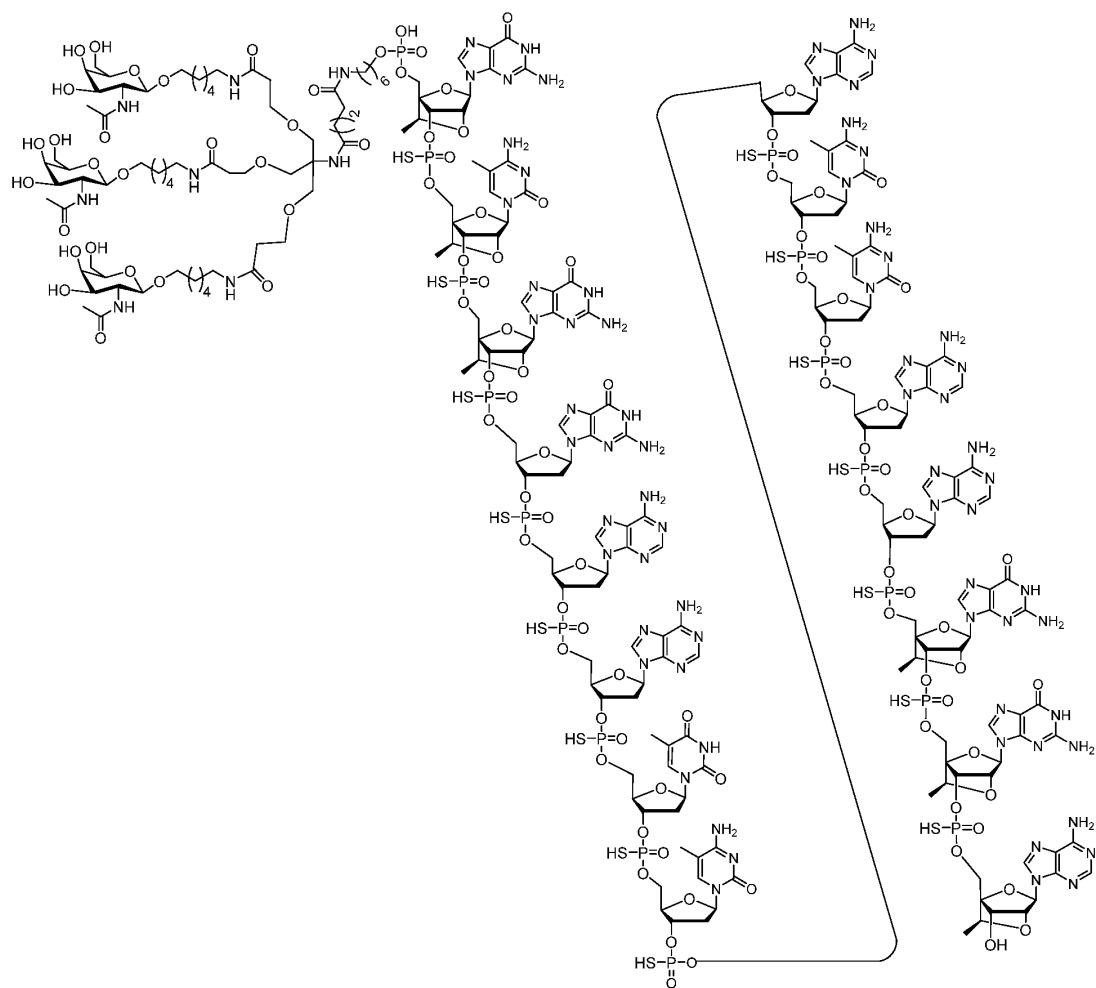
d = a 2'-β-D-deoxyribose sugar moiety, and

s = a phosphorothioate internucleoside linkage;

and wherein (THA-GalNAc)₃o =



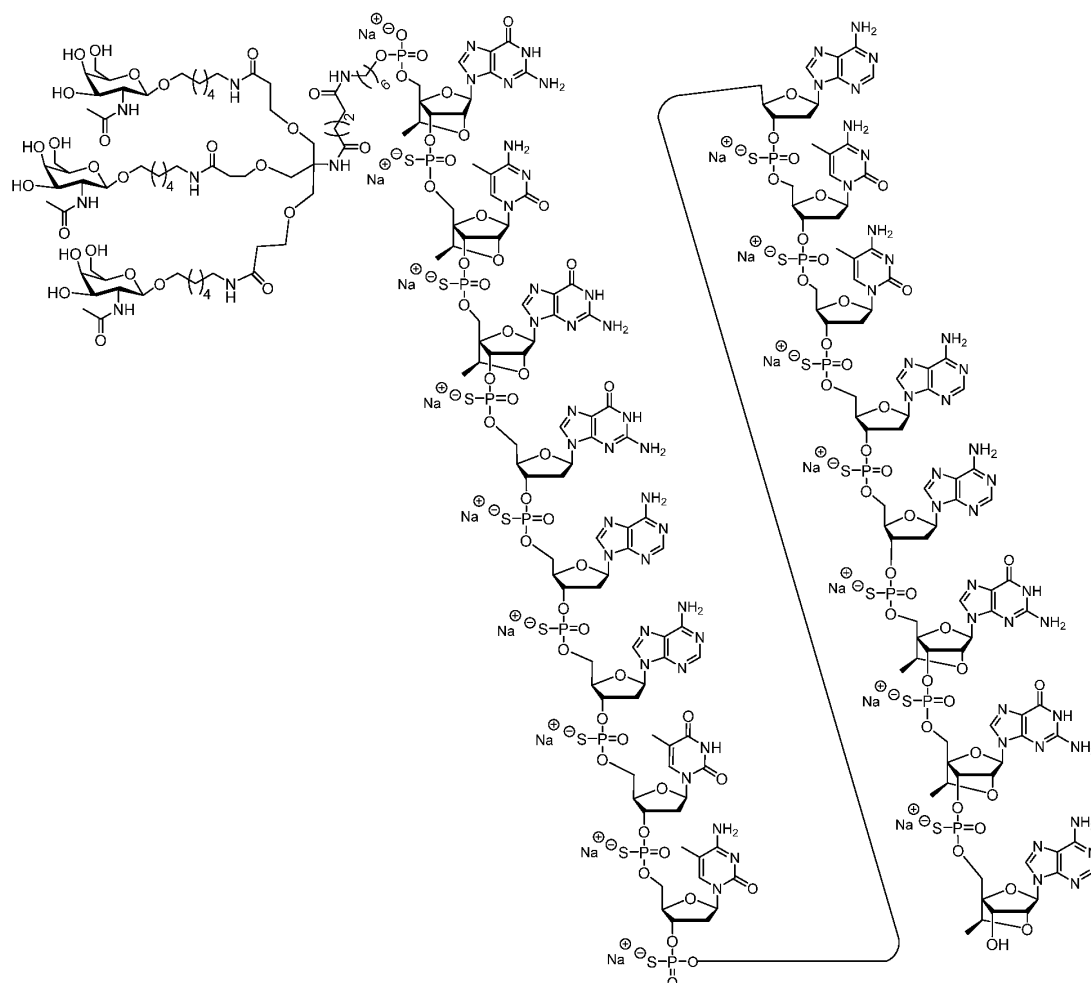
In certain embodiments, Compound No. 1194357 is represented by the following chemical structure:



(SEQ ID NO: 3379).

Structure 1. Compound No. 1194357

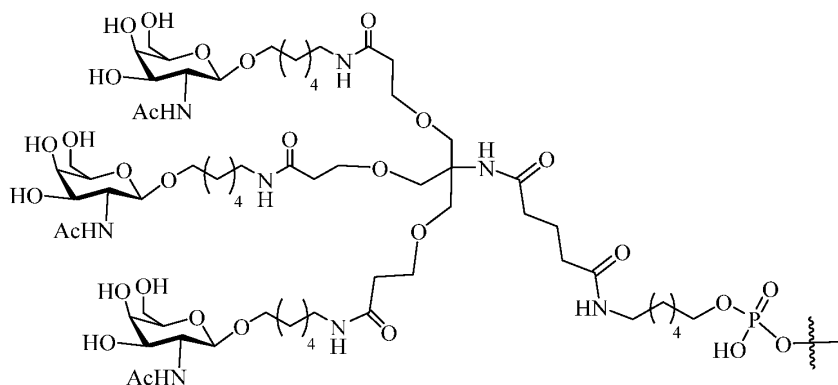
5 In certain embodiments, the sodium salt of Compound No. 1194357 is represented by the following chemical structure:



(SEQ ID NO: 3379).

Structure 2. The sodium salt of Compound No. 1194357**2. Compound No. 1270705**

In certain embodiments, Compound No. 1270705 is characterized as an oligomeric compound
 5 consisting of a conjugate group and a modified oligonucleotide; wherein the conjugate group is a THA-
 GalNAc₃ that is directly attached to the 5' end of the modified oligonucleotide through a phosphodiester
 linkage, (THA- GalNAc₃)_o; wherein (THA- GalNAc₃)_o is represented by the following structure:



wherein the modified oligonucleotide is gapmer, having a sequence of (from 5' to 3')

GCACUTTATTGAGTTC (incorporated herein as SEQ ID NO: 5006); wherein each of nucleosides 1-3 and 14-16 (from 5' to 3') comprise a cEt modified sugar moiety, each of nucleosides 4 and 6-13 are 2'-β-D-deoxynucleosides, and nucleoside 5 comprises a 2'-O-methyl sugar moiety; wherein each internucleoside linkage is a phosphorothioate internucleoside linkage, and wherein each cytosine is a 5-methyl cytosine.

In certain embodiments, Compound No. 1270705 is represented by the following chemical notation: (THA-GalNAc₃)_o Gks ^mCks Aks ^mCds Uys Tds Tds Ads Tds Tds Gds Ads Gds Tks Tks ^mCk, wherein:

A = an adenine nucleobase,

10 ^mC = a 5-methyl cytosine nucleobase,

G = a guanine nucleobase,

T = a thymine nucleobase,

U = a uracil nucleobase,

k = a cEt modified sugar moiety,

15 y = a 2'-O-methyl modified ribosyl sugar moiety,

d = a 2'-β-D-deoxyribosyl sugar moiety, and

s = a phosphorothioate internucleoside linkage.

In certain embodiments, provided is an oligomeric compound comprising a modified oligonucleotide and a conjugate group according to the following chemical notation: (THA-GalNAc₃)_o Gks ^mCks Aks ^mCds Uys Tds Tds Ads Tds Tds Gds Ads Gds Tks Tks ^mCk, wherein:

A = an adenine nucleobase,

^mC = a 5-methyl cytosine nucleobase,

G = a guanine nucleobase,

T = a thymine nucleobase,

25 U = a uracil nucleobase,

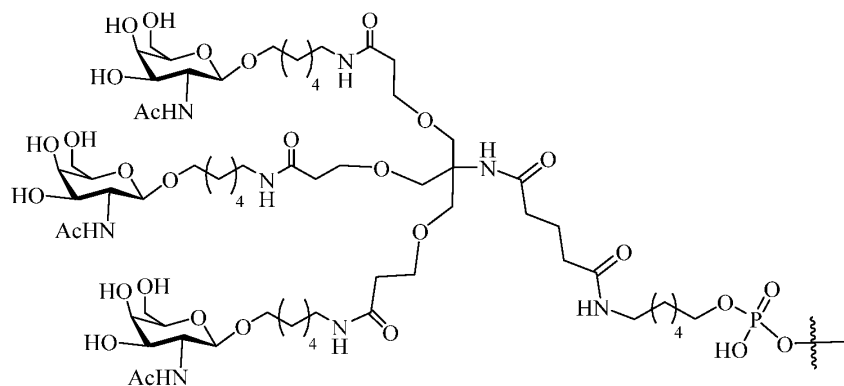
k = a cEt modified sugar moiety,

y = a 2'-O-methyl modified ribosyl sugar moiety,

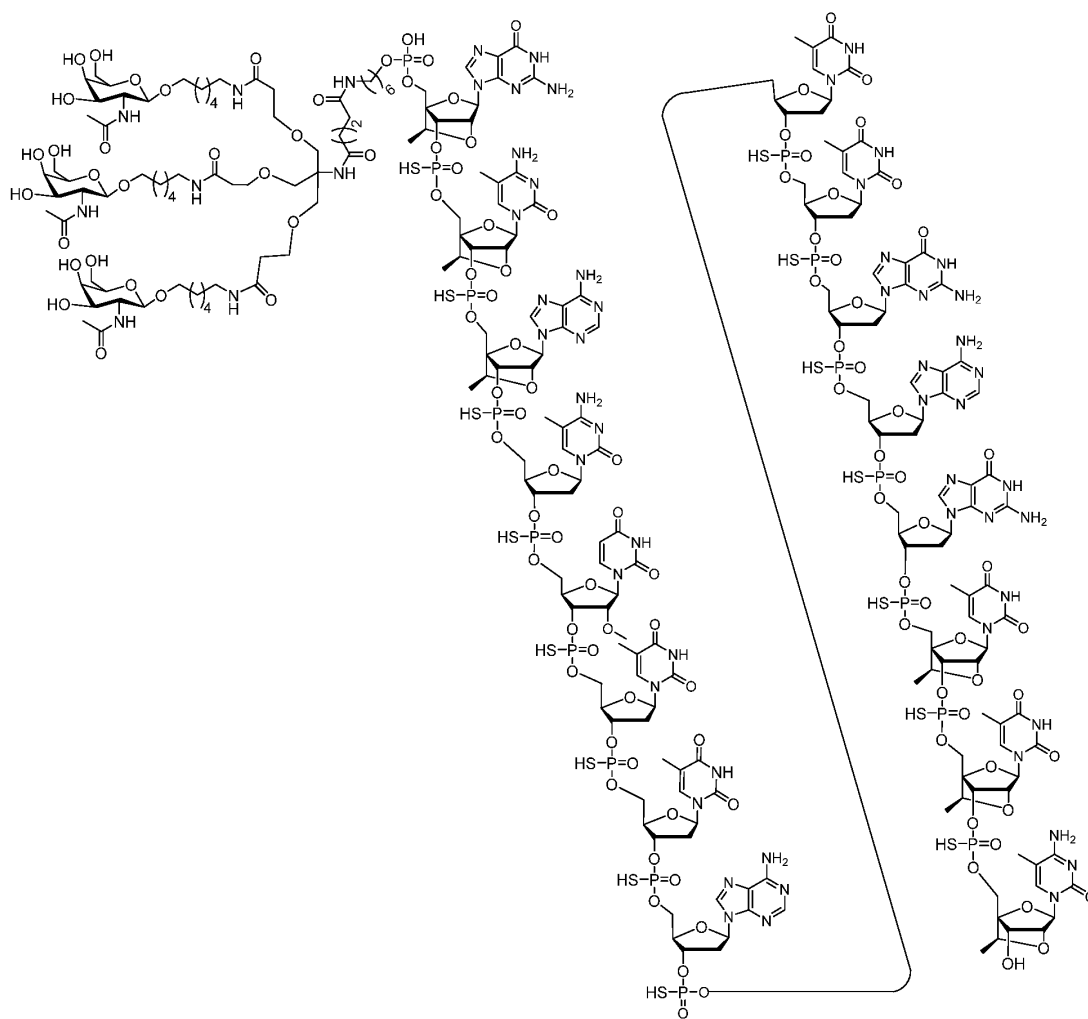
d = a 2'-β-D-deoxyribosyl sugar moiety, and

s = a phosphorothioate internucleoside linkage;

and wherein (THA- GalNAc₃)₀ =



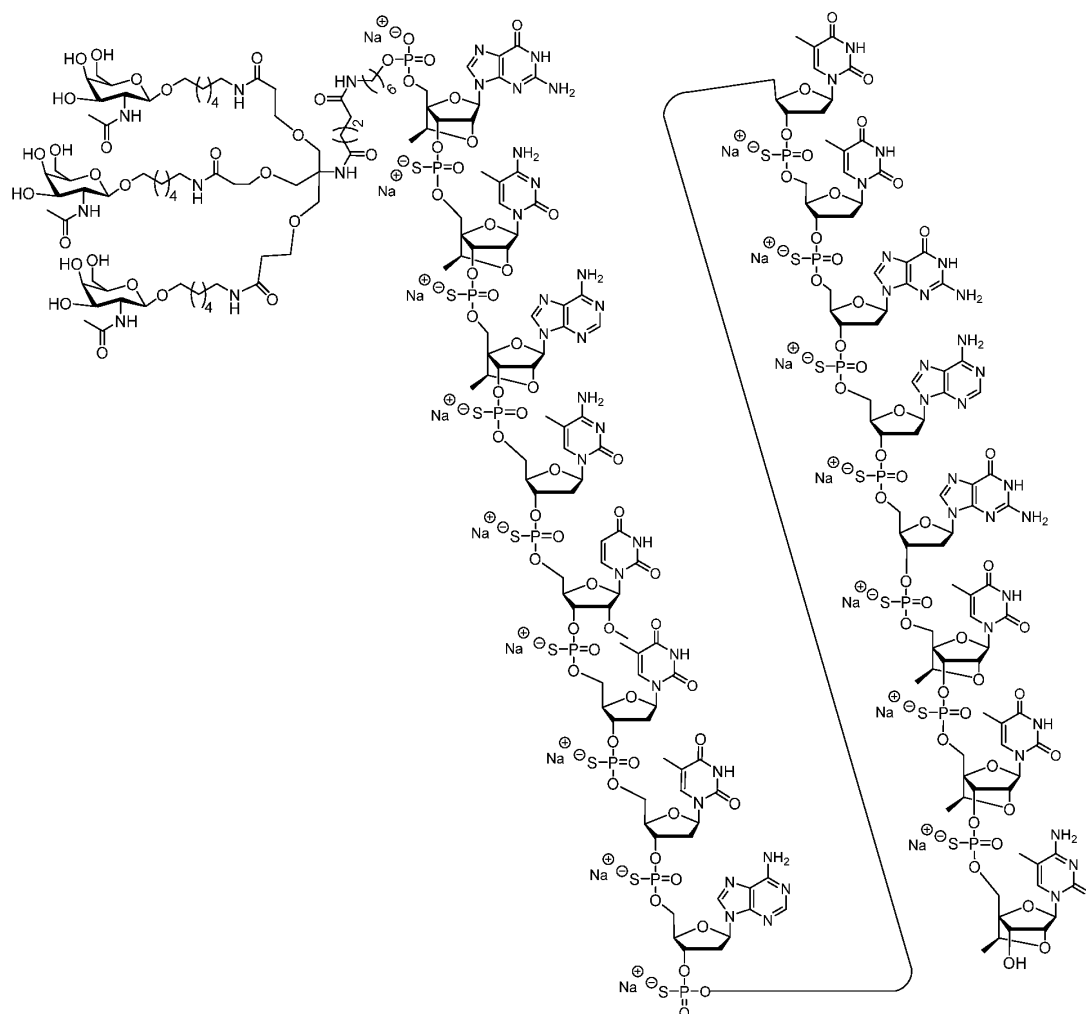
In certain embodiments, Compound No. 1270705 is represented by the following chemical structure:



(SEQ ID NO: 5006).

Structure 3. Compound No. 1270705

In certain embodiments, the sodium salt of Compound No. 1270705 is represented by the following chemical structure:



(SEQ ID NO: 5006).

5 Structure 4. The sodium salt of Compound No. 1270705

VIII. Certain Comparator Compounds

Comparator Compound Nos. 1213029, 1213030, 1213034, and 1358035 (relating to Compound Nos. A-145667, A-145668, A-145676, and A-145669, respectively) were selected as comparator compounds from Example 1 of WO2017/120397 (incorporated herein by reference).

10 In certain embodiments, Compound No. 1213029, a surrogate of which (Compound A-145667) is provided in WO2017/120397, was used as a comparator compound, *see* Example 14. Compound No. 1213029 is a gapmer having a sugar motif of (from 5' to 3') yyyyydddddyyyyy, wherein each "y" represents a 2'-O-methyl sugar moiety and each "d" represents a 2'-β-D-deoxyribosyl sugar moiety; having a

sequence of (from 5' to 3') GAAUACCAAGGAGGGAAAG (SEQ ID NO: 5042), wherein each "C" of the gap is a 5-methyl cytosine; and wherein each internucleoside linkage is a phosphorothioate internucleoside linkage.

5 In certain embodiments, Compound No. 1213030, a surrogate of which (Compound A-145668) is provided in WO2017/120397, was used as a comparator compound, *see* Example 14. Compound No. 1213030 is a gapmer having a sugar motif of (from 5' to 3') yyyyydddddyyyyy, wherein each "y" represents a 2'-O-methyl sugar moiety and each "d" represents a 2'-β-D-deoxyribose sugar moiety; having a sequence of (from 5' to 3') UCUCACTGCGGAATCACCAA (SEQ ID NO: 5041), wherein each "C" of the gap is a 5-methyl cytosine; and wherein each internucleoside linkage is a phosphorothioate internucleoside
10 linkage.

In certain embodiments, Compound No. 1213034, a surrogate of which (Compound A-145676) is provided in WO2017/120397, was used as a comparator compound, *see* Example 14. Compound No. 1213034 is a gapmer having a sugar motif of (from 5' to 3') yyyyydddddyyyyy, wherein each "y" represents a 2'-O-methyl sugar moiety and each "d" represents a 2'-β-D-deoxyribose sugar moiety; having a
15 sequence of (from 5' to 3') CACUUTATTGAGTTCCUGCG (SEQ ID NO: 5039), wherein each "C" of the gap is a 5-methyl cytosine; and wherein each internucleoside linkage is a phosphorothioate internucleoside linkage.

In certain embodiments, Compound No. 1358035, a surrogate of which (Compound A-145669) is provided in WO2017/120397, was used as a comparator compound, *see* Example 14. Compound No.
20 1358035 is a gapmer having a sugar motif of (from 5' to 3') yyyyydddddyyyyy, wherein each "y" represents a 2'-O-methyl sugar moiety and each "d" represents a 2'-β-D-deoxyribose sugar moiety; having a sequence of (from 5' to 3') CCCAGCCACTCTCTCACUG (SEQ ID NO: 5040), wherein each "C" of the gap is a 5-methyl cytosine; and wherein each internucleoside linkage is a phosphorothioate internucleoside linkage.

25 In certain embodiments, compounds described herein are superior relative to comparator compounds described in WO2017/120397 because they demonstrate one or more improved properties, such as *in vitro* activity.

For example, as described herein, certain compounds, including Compound No. 1129485 and Compound No. 1213144, achieved IC₅₀ values of 0.34 and 0.28, respectively, whereas each of comparator
30 compounds Compound No. 1213029, Compound No. 1213030, Compound No. 1213034, and Compound No. 1358035 achieved IC₅₀ values of >10, 8.15, >10, and 8.59, respectively, (*see* Table 154 in Example 14 for IC₅₀ values). Therefore, certain compounds described herein are more potent than comparator compounds Compound No. 1213029, Compound No. 1213030, Compound No. 1213034, and Compound No. 1358035 in a multiple dose assay.

35 Compound No. 1194357 is identical to Compound No. 1129485, with the exception that Compound No. 1194357 comprises a conjugate group, and Compound No. 1270705 is identical to Compound No.

1213144, with the exception that Compound No. 1270705 comprises a conjugate group. Therefore, unconjugated versions of Compound No. 1129485 and Compound No. 1270705 are more active than comparator compounds Compound No. 1213029, Compound No. 1213030, Compound No. 1213034, and Compound No. 1358035 in a multiple dose assay.

5 IX. Certain Hotspot Regions

In certain embodiments, nucleobases in the ranges specified below comprise a hotspot region of FXII nucleic acid. In certain embodiments, modified oligonucleotides that are complementary to a hotspot region of a FXII nucleic acid achieve an average of more than 50% reduction of FXII RNA *in vitro* in a standard cell assay.

10 1. Nucleobases 1,899-1,979 of SEQ ID NO: 1

In certain embodiments, nucleobases 1,899-1,979 of SEQ ID NO: 1 comprise a hotspot region. In certain embodiments, modified oligonucleotides are complementary to a portion of nucleobases 1,899-1,979 of SEQ ID NO: 1. In certain embodiments, modified oligonucleotides are 20 nucleobases in length. In certain embodiments, modified oligonucleotides are 16 nucleobases in length. In certain embodiments, modified oligonucleotides are gapmers. In certain embodiments, the gapmers are MOE gapmers. In certain
15 embodiments, the gapmers are cEt gapmers. In certain embodiments, the internucleoside linkages of the modified oligonucleotides are phosphorothioate internucleoside linkages and phosphodiester internucleoside linkages. In certain embodiments, each internucleoside linkage is a phosphorothioate internucleoside linkage.

The nucleobase sequences of SEQ ID NOs: 92, 156, 270, 271, 345, 346, 420, 421, 496, 497, 571,
20 572, 653, 654, 728, 729, 802, 803, 877, 951, 1028, 1103, 1179, 1253, 1330, 1407, 1484, 1560, 1636, 1710, 1711, 1784, 1859, 1860, 1934, 1935, 2008, 2009, 2084, 2085, 2158, 2232, 2233, 2307, 2308, 2393, 2394, 2395, 2396, 2397, 2398, 2461, 2537, 2538, 2614, 2615, 2691, 2692, 2768, 2769, 2845, 2846, 2921, 2922, 2997, 2998, 3073, 3074, 3144, 3145, 3226, 3227, 3303, 3304, 3379, 3380, 3455, 3456, 3531, 3607, 3683, 3759, 3835, 3911, 4948, 4949, 4954, 4955, 4956, 4957, 4961, 4965, 4966, 4967, 4971, 4972, 4976, 4994,
25 4995, 4996, 4997, 4998, 4999, 5024, 5025, 5026, 5027, 5028, and 5029 are complementary to nucleobases 1,899-1,979 of SEQ ID NO: 1.

The nucleobase sequences of Compound Nos: 1125047, 1125048, 1125049, 1125050, 1125051, 1125074, 1125075, 1125076, 1125077, 1125078, 1129474, 1129475, 1129476, 1129477, 1129478, 1129479, 1129480, 1129481, 1129482, 1129483, 1129484, 1129485, 1129486, 1129487, 1129488, 1129489, 1129490,
30 1129491, 1129492, 1129493, 1129494, 1129495, 1129496, 1129497, 1129498, 1129499, 1129500, 1129501, 1129502, 1129503, 1129504, 1129505, 1129506, 1131681, 1131682, 1131683, 1131684, 1131685, 1131686, 1131687, 1131688, 1131689, 1131690, 1131691, 1131692, 1131693, 1131694, 1131695, 1131696, 1131697, 1131698, 1131699, 1131700, 1131701, 1131702, 1131703, 1131704, 1131705, 1131706, 1131707, 1131708, 1131709, 1131710, 1131711, 1131712, 1131713, 1131714, 1131715, 1131716, 1131717, 1131718, 1131719,
35 1131720, 1131721, 1131722, 1131723, 1131724, 1131725, 1206454, 1206455, 1206456, 1206457, 1206458,

1206459, 1206485, 1206486, 1206487, 1206488, 1206489, 1206490, 1206491, 1206492, 1206505, 1206506, 1206507, 1206508, 1206509, 1206957, 1206958, 1206959, 1206960, 1206961, 1206962, 1206963, 1206964, 1206965, 1206966, 1206967, 1206968, 1206969, 1206970, 1206971, 1206972, 1206973, 1206974, 1206975, 1206976, 1206977, 1206978, 1206979, 1206980, 1206981, 1206982, 1206983, 1206985, 1206986, 1206987, 1206988, 1207098, 1207099, 1207100, 1207101, 1207102, 1207103, 1207104, 1207105, 1207106, 1207107, 1207108, 1207109, 1207110, 1207111, 1207112, 1207113, 1207114, 1207115, 1207116, 1207117, 1207118, 1207120, 1207123, 1207125, 1207127, 1207129, 1207131, 1207133, 1207135, 1207137, 1207139, 1207141, 1207228, 1207229, 1207230, 1207231, 1207232, 1207233, 1207234, 1207235, 1207236, 1207237, 1207238, 1207239, 1207240, 1207241, 1207242, 1207243, 1207244, 1207245, 1207246, 1207247, 1207248, 1207249, 1207250, 1207251, 1207252, 1207253, 1207254, 1207256, 1207257, 1207258, 1207259, 1207345, 1207346, 1207347, 1207348, 1207349, 1207350, 1207351, 1207352, 1207353, 1207354, 1207355, 1207356, 1207357, 1207358, 1207359, 1207360, 1207361, 1207362, 1207363, 1207364, 1207365, 1207366, 1207367, 1207368, 1207369, 1207370, 1207371, 1207372, 1207373, 1207374, 1207375, 1207376, 1207462, 1207463, 1207464, 1207465, 1207466, 1207467, 1207468, 1207469, 1207470, 1207471, 1207472, 1207473, 1207474, 1207475, 1207476, 1207477, 1207478, 1207479, 1207480, 1207481, 1207482, 1207483, 1207484, 1207485, 1207486, 1207487, 1207488, 1207489, 1207490, 1207491, 1207492, 1207493, 1213094, 1213095, 1213096, 1213097, 1213098, 1213099, 1213100, 1213101, 1213102, 1213103, 1213104, 1213105, 1213106, 1213107, 1213108, 1213109, 1213110, 1213111, 1213112, 1213113, 1213114, 1213115, 1213116, 1213117, 1213118, 1213119, 1213120, 1213121, 1213122, 1213123, 1213124, 1213125, 1213211, 1213212, 1213213, 1213214, 1213215, 1213216, 1213217, 1213218, 1213219, 1213220, 1213221, 1213222, 1213223, 1213224, 1213225, 1213226, 1213227, 1213228, 1213229, 1213230, 1213231, 1213232, 1213233, 1213234, 1213235, 1213236, 1213237, 1213238, 1213239, 1213240, 1213241, and 1213242 are complementary to nucleobases 1,899-1,979 of SEQ ID NO: 1.

In certain embodiments, modified oligonucleotides complementary to nucleobases 1,899-1,979 of SEQ ID NO: 1 achieve an average of 78% reduction of F12 mRNA in vitro in the standard cell assay.

2. Nucleobases 2,004-2,045 of SEQ ID NO: 1

In certain embodiments, nucleobases 2,004-2,045 of SEQ ID NO: 1 comprise a hotspot region. In certain embodiments, modified oligonucleotides are complementary to nucleobases 2,004-2,045 of SEQ ID NO: 1.

The nucleobase sequences of SEQ ID NOs: 95, 159, 162, 163, 164, 165, 347, 422, 498, 573, 953, 1030, 1105, 1255, 1332, 1409, 1486, 1562, 2309, 2463, 2540, 2617, 2694, 2771, 2848, 2924, 3000, 3076, 3147, 3229, 3306, 3382, 3457, 3533, 3609, 3685, 3761, 3837, 3913, 5000, 5001, 5002, 5003, 5004, 5005, 5006, 5031, 5032, 5033, 5034, 5035, 5036, and 5037 are complementary to nucleobases 2,004-2,045 of SEQ ID NO: 1.

The modified oligonucleotides of Compound Nos: 462192, 1125101, 1125102, 1125103, 1125104, 1129526, 1129527, 1129528, 1129529, 1129530, 1129531, 1129532, 1129533, 1129534, 1129535, 1129536, 1129537, 1129538, 1129539, 1129540, 1129541, 1129542, 1129543, 1129544, 1129545, 1131745, 1131746,

1131747, 1131748, 1131749, 1131750, 1131751, 1131752, 1131753, 1131754, 1131755, 1131756, 1131757, 1131758, 1131759, 1131760, 1131761, 1131762, 1131763, 1206993, 1206994, 1206995, 1206996, 1206997, 1206998, 1206999, 1207000, 1207001, 1207002, 1207003, 1207004, 1207005, 1207006, 1207007, 1207008, 1207010, 1207011, 1207012, 1207147, 1207148, 1207149, 1207150, 1207151, 1207152, 1207153, 1207154, 1207155, 1207156, 1207157, 1207158, 1207159, 1207160, 1207161, 1207162, 1207163, 1207164, 1207165, 1207166, 1207264, 1207265, 1207266, 1207267, 1207268, 1207269, 1207270, 1207271, 1207272, 1207273, 1207274, 1207275, 1207276, 1207277, 1207278, 1207279, 1207280, 1207281, 1207282, 1207283, 1207381, 1207382, 1207383, 1207384, 1207385, 1207386, 1207387, 1207388, 1207389, 1207390, 1207391, 1207392, 1207393, 1207394, 1207395, 1207396, 1207397, 1207398, 1207399, 1207400, 1207498, 1207499, 1207500, 1207501, 1207502, 1207503, 1207504, 1207505, 1207506, 1207507, 1207508, 1207509, 1207511, 1207512, 1207513, 1207514, 1207515, 1207516, 1207517, 1213130, 1213131, 1213132, 1213133, 1213134, 1213135, 1213136, 1213137, 1213138, 1213139, 1213140, 1213141, 1213142, 1213143, 1213144, 1213145, 1213146, 1213147, 1213148, 1213149, 1213247, 1213248, 1213249, 1213250, 1213251, 1213252, 1213253, 1213254, 1213255, 1213256, 1213257, 1213258, 1213259, 1213260, 1213261, 1213262, 1213263, 1213264, 1213265, and 1213266 are complementary to nucleobases 2,004-2,045 of SEQ ID NO: 1.

In certain embodiments, modified oligonucleotides complementary to nucleobases 2,004-2,045 of SEQ ID NO: 1 achieve an average of 80% reduction of F12 mRNA in vitro in the standard cell assay.

X. Certain Indications

In certain embodiments, methods comprise administering a pharmaceutical composition described herein to a subject with a thromboembolic condition. Thromboembolic conditions include, but are not limited to, myocardial infarction (MI), stroke, limb ischemia and necrosis, and venous thromboembolism (VTE), including deep vein thrombosis (DVT) and pulmonary embolism (PE).

In certain embodiments, methods comprise administering a pharmaceutical composition described herein to a subject having a risk factor for developing a thromboembolic condition. In certain embodiments, the risk factor is genetic, health-associated, or environmental, or a combination thereof. In certain embodiments, the risk factor is surgery, malignancy, pregnancy, aging, use of oral contraceptives, immobility (including travel-related immobility), sepsis, having a mechanical heart valve, valvular heart disease, atrial fibrillation, atherosclerosis, antiphospholipid syndrome, an inherited clotting disorder (*e.g.*, Factor V Leiden), or an acquired prothrombotic clotting disorder. Identifying a subject with a risk factor for developing a thromboembolic condition may be accomplished by evaluating a subject's medical history and/or by conducting standard clinical tests or assessments.

In certain embodiments, methods comprise administering a pharmaceutical composition described herein to a subject who has been identified as in need of anticoagulation therapy. Non-limiting examples of such subjects include a subject undergoing major orthopedic surgery (*e.g.*, hip/knee replacement or hip fracture surgery) and a subject with atrial fibrillation.

Nonlimiting disclosure and incorporation by reference

Each of the literature and patent publications listed herein is incorporated by reference in its entirety.

While certain compounds, compositions and methods described herein have been described with specificity in accordance with certain embodiments, the following examples serve only to illustrate the compounds described herein and are not intended to limit the same. Each of the references, GenBank accession numbers, and the like recited in the present application is incorporated herein by reference in its entirety.

Although the sequence listing accompanying this filing identifies each sequence as either “RNA” or “DNA” as required, in reality, those sequences may be modified with any combination of chemical modifications. One of skill in the art will readily appreciate that such designation as “RNA” or “DNA” to describe modified oligonucleotides is, in certain instances, arbitrary. For example, an oligonucleotide comprising a nucleoside comprising a 2'-OH sugar moiety and a thymine base could be described as a DNA having a modified sugar (2'-OH in place of one 2'-H of DNA) or as an RNA having a modified base (thymine (methylated uracil) in place of an uracil of RNA). Accordingly, nucleic acid sequences provided herein, including, but not limited to those in the sequence listing, are intended to encompass nucleic acids containing any combination of natural or modified RNA and/or DNA, including, but not limited to such nucleic acids having modified nucleobases. By way of further example and without limitation, an oligomeric compound having the nucleobase sequence “ATCGATCG” encompasses any oligomeric compounds having such nucleobase sequence, whether modified or unmodified, including, but not limited to, such compounds comprising RNA bases, such as those having sequence “AUCGAUCG” and those having some DNA bases and some RNA bases such as “AUCGATCG” and oligomeric compounds having other modified nucleobases, such as “AT^mCGAUCG,” wherein ^mC indicates a cytosine base comprising a methyl group at the 5-position.

Certain compounds described herein (*e.g.*, modified oligonucleotides) have one or more asymmetric center and thus give rise to enantiomers, diastereomers, and other stereoisomeric configurations that may be defined, in terms of absolute stereochemistry, as (*R*) or (*S*), as α or β such as for sugar anomers, or as (*D*) or (*L*), such as for amino acids, etc. Compounds provided herein that are drawn or described as having certain stereoisomeric configurations include only the indicated compounds. Compounds provided herein that are drawn or described with undefined stereochemistry include all such possible isomers, including their stereorandom and optically pure forms, unless specified otherwise. Likewise, tautomeric forms of the compounds herein are also included unless otherwise indicated. Unless otherwise indicated, compounds described herein are intended to include corresponding salt forms.

The compounds described herein include variations in which one or more atoms are replaced with a non-radioactive isotope or radioactive isotope of the indicated element. For example, compounds herein that comprise hydrogen atoms encompass all possible deuterium substitutions for each of the ¹H hydrogen atoms. Isotopic substitutions encompassed by the compounds herein include but are not limited to: ²H or ³H in place

of ^1H , ^{13}C or ^{14}C in place of ^{12}C , ^{15}N in place of ^{14}N , ^{17}O or ^{18}O in place of ^{16}O , and ^{33}S , ^{34}S , ^{35}S , or ^{36}S in place of ^{32}S . In certain embodiments, non-radioactive isotopic substitutions may impart new properties on the oligomeric compound that are beneficial for use as a therapeutic or research tool. In certain
 5 embodiments, radioactive isotopic substitutions may make the compound suitable for research or diagnostic purposes such as imaging.

EXAMPLES

The following examples illustrate certain embodiments of the present disclosure and are not limiting. Moreover, where specific embodiments are provided, the inventors have contemplated generic application of those specific embodiments. For example, disclosure of an oligonucleotide having a particular motif provides
 10 reasonable support for additional oligonucleotides having the same or similar motif. And, for example, where a particular high-affinity modification appears at a particular position, other high-affinity modifications at the same position are considered suitable, unless otherwise indicated.

Example 1: Effects of 5-10-5 MOE gapmers on human FXII RNA *in vitro*, single dose

Modified oligonucleotides complementary to an FXII nucleic acid were synthesized and tested for
 15 their effect on FXII RNA levels *in vitro*. The modified oligonucleotides were tested in a series of experiments using culture conditions as indicated. The results for each separate experiment are presented in separate tables below.

The modified oligonucleotides in the tables below are 5-10-5 MOE gapmers (i.e., they have a central region of ten 2'-deoxynucleosides flanked on each side by wings, each comprising five 2'-MOE nucleosides).
 20 The motif for the gapmers is (from 5' to 3'): eeeeeeeeeeeeeee; wherein "d" represents a 2'-β-D-deoxyribose sugar moiety, and "e" represents a 2'-MOE sugar moiety. The internucleoside linkages throughout each modified oligonucleotide are phosphorothioate linkages. All cytosine nucleobases throughout each modified oligonucleotide are 5-methylcytosines.

"Start site" indicates the 5'-most nucleoside of the target sequence to which the modified
 25 oligonucleotide is complementary. "Stop site" indicates the 3'-most nucleoside of the target sequence to which the modified oligonucleotide is complementary. As shown in the tables below, the modified oligonucleotides are 100% complementary to one or more human FXII target sequences, including the human FXII mRNA sequence designated herein as SEQ ID NO: 1 (ENSEMBL ID ENST00000253496.3 from ENSEMBL version 99: January 2020), the human FXII genomic sequence, designated herein as SEQ ID NO:
 30 2 (ENSEMBL ID ENSG00000131187.9 from ENSEML version 99: January 2020), the human FXII genomic sequence, designated herein as SEQ ID NO: 3 (the complement of GENBANK Accession No. NC_000005.10 truncated from truncated from nucleotides 177399001 to 177413000), and the human FXII mRNA sequence designated herein as SEQ ID NO: 4 (GENBANK Accession No. NM_000505.3). 'N/A' indicates that the modified oligonucleotide is not complementary to that particular target sequence with 100%
 35 complementarity.

Cultured Huh7 cells were transfected either with lipofectin, oligofectamine, or by electroporation, as indicated in the tables below. In some cases, Huh7 cells, at a density of 8,000 cells per well, were transfected using lipofectin with 120 nM modified oligonucleotide. In other cases, Huh7 cells, at a density of 5,000 cells per well, were transfected using oligofectamine with 200nM modified oligonucleotide. In other cases, Huh7 cells, at a density of 20,000 cells per well, were transfected using electroporation with 5000nM modified oligonucleotide. After a treatment period of approximately 24 hours, RNA was isolated from the cells and FXII RNA levels were measured by quantitative real-time RTPCR. Either human primer probe set RTS2992 (forward sequence GTCAACACTTTTCGATTCCACCTT, designated herein as SEQ ID NO: 5; reverse sequence TCCCCGGTGACAGTGAGAAC, designated herein as SEQ ID NO: 6; probe sequence AAGCCCCCAAGGAGCATAAGTACAAAGCTG, designated herein as SEQ ID NO: 7) or human primer probe set RTS40528 (forward sequence GTGCACGGATCCTCCATC, designated herein as SEQ ID NO: 8; reverse sequence CAGCTTGGTCCTCACACAC, designated herein as SEQ ID NO: 9; probe sequence AATCACCCCTGGCAGCATCG, designated herein as SEQ ID NO: 10) was used to measure RNA levels. FXII RNA levels were normalized to total RNA content, as measured by RIBOGREEN®. Reduction of FXII RNA is presented in the tables below as percent FXII RNA relative to the amount in untreated control cells (% UTC). The symbol “†” indicates that the modified oligonucleotide is complementary to the target transcript within the amplicon region of the primer probe set. In such instances, additional assays using alternative primer probes must be performed to accurately assess the potency and efficacy of such modified oligonucleotides.

Table 1. Reduction of FXII RNA by 5-10-5 MOE gapmers with full PS internucleoside linkages (Huh7, lipofectin, 120nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC) RTS2992	SEQ ID NO
413577	1	20	1	20	CCAGGAGTCCAGATCAATAG	62	20
413578	67	86	67	86	TCACCAGCAGGAACCCAGG	21	21
413579	92	111	N/A	N/A	GGAATCGAAAGTGTTGACTC	19 [†]	22
413580	159	178	N/A	N/A	GGTGACAGTGAGAACGACTG	6 [†]	23
413581	164	183	3515	3534	TCCCCGGTGACAGTGAGAAC	3 [†]	24
413582	217	236	3568	3587	GGGTACATTTGTGGTACAGC	19	25
413583	227	246	3578	3597	CGGCCCTTGTGGGTACATTT	30	26
413584	237	256	3588	3607	AGGGCCTGGCCGCCCTTGT	67	27
413585	291	310	3798	3817	GTATCCCCATCGCTGGTCCT	14	28
413586	325	344	N/A	N/A	TGCAGTGGTCTTTCACTTTC	19	29
413587	399	418	4207	4226	TTGTGGACAGAGACAGTGGG	27	30
413588	409	428	4217	4236	CAGTGAGGTGTTGTGGACAG	14	31
413589	452	471	4397	4416	AGAAGCTGAGGCTCAAAGCA	38	32

413590	462	481	4407	4426	GAAAAACCGGAGAAGCTGAG	24	33
413591	515	534	4460	4479	TGGCATCTGGCCACAGCTGC	20	34
413592	520	539	4465	4484	TGCACTGGCATCTGGCCACA	33	35
413593	528	547	4473	4492	AGGACCCTTGCACTGGCATC	24	36
413594	538	557	4483	4502	AGTGGGCATCAGGACCCTTG	22	37
413595	548	567	4493	4512	AGCCGCTGGCAGTGGGCATC	57	38
413596	562	581	N/A	N/A	AGGCCTGGCTGGCCAGCCGC	112	39
413597	567	586	N/A	N/A	GCGGCAGGCCTGGCTGGCCA	31	40
413598	572	591	N/A	N/A	TTGGTGCGGCAGGCCTGGCT	48	41
413599	587	606	4671	4690	CCATGGAGGCACGGGTTGGT	19	42
413600	608	627	4692	4711	TCCACCTCTAGGCAGCGACC	19	43
413601	626	645	4710	4729	TGGCACAGGCGGTGGCCCTC	39	44
413602	695	714	4924	4943	CCGCGGCCATCATAGCAGCT	24	45
413603	700	719	4929	4948	TGAGCCCGCGGCCATCATAG	33	46
413604	705	724	4934	4953	GTAGCTGAGCCCGCGGCCAT	28	47
413605	713	732	4942	4961	AGGCCGCGGTAGCTGAGCCC	38	48
413606	718	737	4947	4966	TGGCCAGGCCGCGGTAGCTG	30	49
413607	723	742	4952	4971	GGTCCTGGCCAGGCCGCGGT	23	50
413608	746	765	4975	4994	TGACAGGGCGCACCCGAGAG	33	51
413609	751	770	4980	4999	ACGGCTGACAGGGCGCACCC	28	52
413610	808	827	5037	5056	GTCCCCAGTTCCGCGCTTGC	21	53
413611	818	837	5047	5066	TGGCCGCCAGTCCCCAGTT	29	54
413612	839	858	N/A	N/A	TCCGGGTTCCGGCAGAAGGC	20	55
413613	863	882	5177	5196	AAGCACCAACGGGCGGATGTC	29	56
413614	871	890	5185	5204	TCAGCACGAAGCACACGGG	13	57
413615	978	997	5292	5311	CATGAGTGGGACATGAAGCC	38	58
413616	1119	1138	5538	5557	GAGCCGCTGCCCCGAGCTCA	31	59
413617	1132	1151	5551	5570	ACAGACTCTTGCGGAGCCGC	19	60
413618	1137	1156	5556	5575	CGAAGACAGACTCTTGCGGA	22	61
413619	1142	1161	5561	5580	GTCATCGAAGACAGACTCTT	28	62
413620	1211	1230	5630	5649	TGGCCCCAGTACAGCGCGGC	27	63
413621	1231	1250	5650	5669	GGCTGCCGGCGCAGAACTG	32	64
413622	1236	1255	5655	5674	GATGAGGCTGCCGGCGCAGA	25	65
413623	1283	1302	N/A	N/A	GGCCGGTCCTGCAGGCAGTG	28	66
413624	1304	1323	5964	5983	ACCGTCAGATCCTCGGGTGC	33	67
413625	1379	1398	6039	6058	TGCAAGCGGTAGGAGCGCAC	32	68
413626	1429	1448	N/A	N/A	GGCGCAACAGAGCCAGGTCG	100	69
413627	1455	1474	6198	6217	GCAGCTGCCGTCCGCATCCT	28	70
413628	1466	1485	6209	6228	GACAGGAGCGCGCAGCTGCC	25	71
413629	1492	1511	6235	6254	GCAGGCACACCGGCTGAACG	19	72
413630	1502	1521	6245	6264	GCGCCGCTTGGCAGGCACAC	28	73
413631	1559	1578	6302	6321	TGCAACTGGTGGCCCCAGCC	30	74
413632	1679	1698	6977	6996	CCTGCGCAGAGCATGCCGGG	50	75

413633	1684	1703	6982	7001	GGAACCCTGCGCAGAGCATG	17	76
413634	1689	1708	6987	7006	CTCGAGGAACCCTGCGCAGA	36	77
413635	1695	1714	6993	7012	GCCGCCCTCGAGGAACCCTG	14	78
413636	1743	1762	7131	7150	GTCCTCACACACCAGCGGGC	16	79
413637	1748	1767	7136	7155	GCTTGGTCCTCACACACCAG	18	80
413638	1774	1793	7162	7181	CTTGCAGGGTGAGCCGGCGC	45	81
413639	1779	1798	7167	7186	GATGCCTTGCAGGGTGAGCC	29	82
413640	1809	1828	7197	7216	GCGGTCACCACAGCCCGATC	25	83
413641	1814	1833	7202	7221	TTGTTGCGGTCACCACAGCC	23	84
413642	1820	1839	7208	7227	CCTGGCTTGTTCGCGTCACC	141	85
413643	1839	1858	7227	7246	GGCCACATCGGTGTAGACGC	16	86
413644	1844	1863	7232	7251	TAGTAGGCCACATCGGTGTA	32	87
413645	1849	1868	7237	7256	CCAGGTAGTAGGCCACATCG	21	88
413646	1854	1873	7242	7261	CCAGGCCAGGTAGTAGGCCA	38	89
413647	1859	1878	7247	7266	CGGATCCAGGCCAGGTAGTA	33	90
413648	1891	1910	7279	7298	AGTCCCTGAGCAATCAGGAA	19	91
413649	1901	1920	7289	7308	GGGAAAGATGAGTCCCTGAG	14	92
413650	1992	2011	7380	7399	ATCCTGGCGCGGAGCTGGCC	13	93
413651	2002	2021	7390	7409	TTCTGCGCCATCCTGGCGC	23	94
413652	2012	2031	7400	7419	CTTTATTGAGTTCCTGCGCC	15	95
413653	2022	2041	7410	7429	TTTCAAAGCACTTTATTGAG	11	96
413654	2027	2046	7415	7434	AGCATTTTCAAAGCACTTTA	23	97

Table 2. Reduction of FXII RNA by 5-10-5 MOE gapmers with full PS internucleoside linkages (Huh7, oligofectamine, 200nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC) RTS2992	SEQ ID NO
413627	1455	1474	6198	6217	GCAGCTGCCGTCCGCATCCT	27	70
413633	1684	1703	6982	7001	GGAACCCTGCGCAGAGCATG	41	76
413635	1695	1714	6993	7012	GCCGCCCTCGAGGAACCCTG	34	78
413643	1839	1858	7227	7246	GGCCACATCGGTGTAGACGC	23	86
413648	1891	1910	7279	7298	AGTCCCTGAGCAATCAGGAA	33	91
413649	1901	1920	7289	7308	GGGAAAGATGAGTCCCTGAG	18	92
413652	2012	2031	7400	7419	CTTTATTGAGTTCCTGCGCC	14	95
462131	1128	1147	5547	5566	ACTCTTGCGGAGCCGCTGCC	23	98
462132	1145	1164	5564	5583	CGGGTCATCGAAGACAGACT	39	99
462133	1148	1167	5567	5586	ACGCGGGTCATCGAAGACAG	24	100
462134	1151	1170	5570	5589	ACGACGCGGGTCATCGAAGA	52	101
462135	1154	1173	5573	5592	CCAACGACGCGGGTCATCGA	57	102
462136	1157	1176	5576	5595	CCGCCAACGACGCGGGTCAT	51	103
462137	1160	1179	5579	5598	AGCCCGCCAACGACGCGGGT	59	104

462138	1163	1182	5582	5601	ACCAGCCCGCCAACGACGCG	45	105
462139	1166	1185	5585	5604	GCCACCAGCCCGCCAACGAC	46	106
462140	1202	1221	5621	5640	TACAGCGCGGCGATGTAGGG	44	107
462141	1205	1224	5624	5643	CAGTACAGCGCGGCGATGTA	61	108
462142	1208	1227	5627	5646	CCCCAGTACAGCGCGGCGAT	30	109
462143	1214	1233	5633	5652	CTGTGGCCCCAGTACAGCGC	28	110
462144	1217	1236	5636	5655	AAACTGTGGCCCCAGTACAG	42	111
462145	1223	1242	5642	5661	GCGCAGAAACTGTGGCCCCA	20	112
462146	1226	1245	5645	5664	CCGCGCAGAAACTGTGGCC	41	113
462147	1239	1258	5658	5677	GGCGATGAGGCTGCCGGCGC	22	114
462148	1374	1393	6034	6053	GCGGTAGGAGCGCACGGCCA	32	115
462149	1432	1451	N/A	N/A	GAAGGCGCAACAGAGCCAGG	61	116
462150	1435	1454	N/A	N/A	CCTGAAGGCGCAACAGAGCC	56	117
462151	1438	1457	6181	6200	CCTCCTGAAGGCGCAACAGA	48	118
462152	1444	1463	6187	6206	CCGCATCCTCCTGAAGGCGC	25	119
462153	1447	1466	6190	6209	CGTCCGCATCCTCCTGAAGG	50	120
462154	1450	1469	6193	6212	TGCCGTCCGCATCCTCCTGA	37	121
462155	1453	1472	6196	6215	AGCTGCCGTCCGCATCCTCC	39	122
462156	1454	1473	6197	6216	CAGCTGCCGTCCGCATCCTC	36	123
462157	1456	1475	6199	6218	CGCAGCTGCCGTCCGCATCC	22	124
462158	1457	1476	6200	6219	GCGCAGCTGCCGTCCGCATC	31	125
462159	1458	1477	6201	6220	CGCGCAGCTGCCGTCCGCAT	28	126
462160	1461	1480	6204	6223	GAGCGCGCAGCTGCCGTCCG	41	127
462161	1469	1488	6212	6231	GGCGACAGGAGCGCGCAGCT	25	128
462162	1472	1491	6215	6234	TAAGGCGACAGGAGCGCGCA	41	129
462163	1495	1514	6238	6257	TTGGCAGGCACACCGGCTGA	32	130
462164	1498	1517	6241	6260	CGCTTGGCAGGCACACCGGC	36	131
462165	1518	1537	6261	6280	CTCGGAGGGTCGCGCGGCGC	28	132
462166	1562	1581	6305	6324	CCCTCGAACTGGTGGCCCCA	42	133
462167	1596	1615	6894	6913	CGCCTCCTGCAGGAAGCTGG	33	134
462168	1599	1618	6897	6916	CTGCGCCTCCTGCAGGAAGC	38	135
462169	1602	1621	6900	6919	TACCTGCGCCTCCTGCAGGA	67	136
462170	1682	1701	6980	6999	AACCCTGCGCAGAGCATGCC	28	137
462171	1685	1704	6983	7002	AGGAACCCTGCGCAGAGCAT	36	138
462172	1686	1705	6984	7003	GAGGAACCCTGCGCAGAGCA	27	139
462173	1692	1711	6990	7009	GCCCTCGAGGAACCCTGCGC	38	140
462174	1693	1712	6991	7010	CGCCCTCGAGGAACCCTGCG	39	141
462175	1697	1716	6995	7014	GTGCCGCCCTCGAGGAACCC	44	142
462176	1698	1717	6996	7015	GGTGCCGCCCTCGAGGAACC	19	143
462177	1702	1721	7000	7019	CATCGGTGCCGCCCTCGAGG	50	144
462178	1840	1859	7228	7247	AGGCCACATCGGTGTAGACG	30	145
462179	1841	1860	7229	7248	TAGGCCACATCGGTGTAGAC	36	146
462180	1889	1908	7277	7296	TCCCTGAGCAATCAGGAAAC	31	147
462181	1890	1909	7278	7297	GTCCCTGAGCAATCAGGAAA	29	148
462182	1892	1911	7280	7299	GAGTCCCTGAGCAATCAGGA	39	149

462183	1893	1912	7281	7300	TGAGTCCCTGAGCAATCAGG	16	150
462184	1899	1918	7287	7306	GAAAGATGAGTCCCTGAGCA	34	151
462185	1900	1919	7288	7307	GGAAAGATGAGTCCCTGAGC	24	152
462186	1902	1921	7290	7309	AGGGAAAGATGAGTCCCTGA	25	153
462187	1903	1922	7291	7310	GAGGGAAAGATGAGTCCCTG	24	154
462188	1904	1923	7292	7311	GGAGGGAAAGATGAGTCCCT	21	155
462189	1947	1966	7335	7354	TGCCTTCCATGCCCCAGCCA	17	156
462190	1995	2014	7383	7402	GCCATCCTGGCGCGGAGCTG	23	157
462191	1998	2017	7386	7405	TGCGCCATCCTGGCGCGGAG	50	158
462192	2005	2024	7393	7412	GAGTTCCTGCGCCATCCTGG	13	159
462193	2008	2027	7396	7415	ATTGAGTTCCTGCGCCATCC	17	160
462194	2011	2030	7399	7418	TTTATTGAGTTCCTGCGCCA	22	161
462195	2013	2032	7401	7420	ACTTTATTGAGTTCCTGCGC	16	162
462196	2014	2033	7402	7421	CACTTTATTGAGTTCCTGCG	8	163
462197	2015	2034	7403	7422	GCACTTTATTGAGTTCCTGC	6	164
462198	2018	2037	7406	7425	AAAGCACTTTATTGAGTTCC	7	165
462199	2030	2049	7418	7437	CTCAGCATTTTCAAAGCACT	22	166

Table 3. Reduction of FXII RNA by 5-10-5 MOE gapmers with full PS internucleoside linkages (Huh7, oligofectamine, 200nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC) RTS2992	SEQ ID NO
413582	217	236	3568	3587	GGGTACATTTGTGGTACAGC	42	25
413592	520	539	4465	4484	TGCACTGGCATCTGGCCACA	57	35
413610	808	827	5037	5056	GTCCCCAGTTCCGCGCTTGC	45	53
413611	818	837	5047	5066	TGGCCGCCCAGTCCCCAGTT	77	54
413612	839	858	N/A	N/A	TCCGGGTTCCGGCAGAAGGC	68	55
413652	2012	2031	7400	7419	CTTTATTGAGTTCCTGCGCC	30	95
462056	55	74	55	74	ACCCAGGAGCAGCAGAGCC	58	167
462057	58	77	58	77	GGAACCCAGGAGCAGCAGA	67	168
462058	61	80	61	80	GCAGGAACCCAGGAGCAGC	62	169
462059	64	83	64	83	CCAGCAGGAACCCAGGAGC	76	170
462060	95	114	N/A	N/A	GGTGGAATCGAAAGTGTTGA	65 [†]	171
462061	98	117	N/A	N/A	CAAGGTGGAATCGAAAGTGT	63 [†]	172
462062	137	156	504	523	TGCTCTTCAGCTTTGTACTT	23 [†]	173
462063	140	159	507	526	GTGTGCTCTTCAGCTTTGTA	6 [†]	174
462064	143	162	510	529	ACTGTGTGCTCTTCAGCTTT	10 [†]	175
462065	146	165	N/A	N/A	ACGACTGTGTGCTCTTCAGC	9 [†]	176
462067	155	174	N/A	N/A	ACAGTGAGAACGACTGTGTG	30 [†]	177
462068	167	186	3518	3537	GGCTCCCCGGTGACAGTGAG	13 [†]	178

462069	170	189	3521	3540	CAGGGCTCCCCGGTGACAGT	14 [†]	179
462070	173	192	3524	3543	TGGCAGGGCTCCCCGGTGAC	16 [†]	180
462071	176	195	3527	3546	AAGTGGCAGGGCTCCCCGGT	70 [†]	181
462072	215	234	3566	3585	GTACATTTGTGGTACAGCTG	16	182
462073	216	235	3567	3586	GGTACATTTGTGGTACAGCT	24	183
462074	219	238	3570	3589	GTGGGTACATTTGTGGTACA	38	184
462075	223	242	3574	3593	CCTTGTGGGTACATTTGTGG	48	185
462076	230	249	3581	3600	GGCCGGCCCTTGTGGGTACA	65	186
462077	315	334	3822	3841	TTTCACTTTCTTGGGCTCCA	46	187
462078	318	337	N/A	N/A	GTCTTTCACTTTCTTGGGCT	59	188
462079	321	340	N/A	N/A	GTGGTCTTTCACTTTCTTGG	69	189
462080	448	467	4393	4412	GCTGAGGCTCAAAGCACTTC	42	190
462081	455	474	4400	4419	CGGAGAAGCTGAGGCTCAAA	71	191
462082	458	477	4403	4422	AACCGGAGAAGCTGAGGCTC	60	192
462083	465	484	4410	4429	GTGGAAAAACCGGAGAAGCT	46	193
462084	486	505	4431	4450	TCTATACCATATCTCATTCT	57	194
462085	507	526	4452	4471	GGCCACAGCTGCTTGCTCAG	44	195
462086	518	537	4463	4482	CACTGGCATCTGGCCACAGC	51	196
462087	519	538	4464	4483	GCACTGGCATCTGGCCACAG	62	197
462088	521	540	4466	4485	TTGCACTGGCATCTGGCCAC	37	198
462089	522	541	4467	4486	CTTGCACTGGCATCTGGCCA	55	199
462090	523	542	4468	4487	CCTTGCACTGGCATCTGGCC	81	200
462091	534	553	4479	4498	GGCATCAGGACCCTTGCACT	35	201
462092	541	560	4486	4505	GGCAGTGGGCATCAGGACCC	59	202
462093	544	563	4489	4508	GCTGGCAGTGGGCATCAGGA	85	203
462094	575	594	N/A	N/A	GGGTGGTGCGGCAGGCCTG	68	204
462095	578	597	4662	4681	CACGGGTTGGTGCGGCAGGC	65	205
462096	581	600	4665	4684	AGGCACGGGTTGGTGCGGCA	65	206
462097	584	603	4668	4687	TGGAGGCACGGGTTGGTGCG	105	207
462098	590	609	4674	4693	CCCCCATGGAGGCACGGGTT	32	208
462099	593	612	4677	4696	CGACCCCCATGGAGGCACGG	51	209
462100	596	615	4680	4699	CAGCGACCCCCATGGAGGCA	59	210
462101	599	618	4683	4702	AGGCAGCGACCCCCATGGAG	51	211
462102	602	621	4686	4705	TCTAGGCAGCGACCCCCATG	50	212
462103	605	624	4689	4708	ACCTCTAGGCAGCGACCCCC	59	213
462104	611	630	4695	4714	CCCTCCACCTCTAGGCAGCG	60	214
462105	614	633	4698	4717	TGGCCCTCCACCTCTAGGCA	47	215
462106	620	639	4704	4723	AGGCGGTGGCCCTCCACCTC	73	216
462107	623	642	4707	4726	CACAGGCGGTGGCCCTCCAC	27	217
462108	629	648	4713	4732	CAGTGGCACAGGCGGTGGCC	45	218
462109	632	651	4716	4735	GGGCAGTGGCACAGGCGGTG	54	219
462110	708	727	4937	4956	GCGGTAGCTGAGCCCGCGGC	81	220
462111	726	745	4955	4974	CGTGGTCCTGGCCAGGCCGC	61	221
462112	803	822	5032	5051	CAGTTCGCGCTTGCTCGGC	51	222

462113	806	825	5035	5054	CCCCAGTTCCGCGCTTGCTC	44	223
462114	807	826	5036	5055	TCCCCAGTTCCGCGCTTGCT	69	224
462115	809	828	5038	5057	AGTCCCCAGTTCCGCGCTTG	55	225
462116	810	829	5039	5058	CAGTCCCCAGTTCCGCGCTT	56	226
462117	811	830	5040	5059	CCAGTCCCCAGTTCCGCGCT	40	227
462118	814	833	5043	5062	CGCCCAGTCCCCAGTTCCGC	60	228
462119	817	836	5046	5065	GGCCGCCAGTCCCCAGTTC	57	229
462120	820	839	5049	5068	CGTGGCCGCCAGTCCCCAG	43	230
462121	838	857	N/A	N/A	CCGGGTTCCGGCAGAAGGCG	59	231
462122	841	860	N/A	N/A	TGTCCGGGTTCCGGCAGAAG	95	232
462123	842	861	N/A	N/A	TTGTCCGGGTTCCGGCAGAA	96	233
462124	866	885	5180	5199	ACGAAGCACCACGGGCGGAT	85	234
462125	1002	1021	5316	5335	CTTCGGCGGTGCCGGCTGCG	57	235
462126	1122	1141	5541	5560	GCGGAGCCGCTGCCCGCAGC	80	236
462127	1125	1144	5544	5563	CTTGCGGAGCCGCTGCCCGC	79	237

Table 4. Reduction of FXII RNA by 5-10-5 MOE gapmers with full PS internucleoside linkages (Huh7, electroporation, 5000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC) RTS40528	SEQ ID NO
413612	839	858	N/A	N/A	TCCGGGTTCCGGCAGAAGGC	31	55
462073	216	235	3567	3586	GGTACATTTGTGGTACAGCT	10	183
462192	2005	2024	7393	7412	GAGTTCCTGCGCCATCCTGG	22	159
1124163	32	51	32	51	ATGGCATCCGTCCGTTGGTC	70	238
1124191	78	97	78	97	TGACTCCAAGCTCACCAGCA	79	239
1124219	135	154	502	521	CTCTTCAGCTTTGTACTTAT	60	240
1124245	171	190	3522	3541	GCAGGGCTCCCCGGTGACAG	42	241
1124268	225	244	3576	3595	GCCCTTGTGGGTACATTTGT	79	242
1124296	290	309	3797	3816	TATCCCCATCGCTGGTCCTG	31	243
1124324	331	350	N/A	N/A	GTTTGCTGCAGTGGTCTTTC	25	244
1124352	404	423	4212	4231	AGGTGTTGTGGACAGAGACA	60	245
1124380	446	465	4391	4410	TGAGGCTCAAAGCACTTCTC	43	246
1124407	489	508	4434	4453	AGTTCTATACCATATCTCAT	32	247
1124435	532	551	4477	4496	CATCAGGACCCTTGCACTGG	54	248
1124462	566	585	N/A	N/A	CGGCAGGCCTGGCTGGCCAG	33	249
1124489	606	625	4690	4709	CACCTCTAGGCAGCGACCCC	21	250
1124517	653	672	4737	4756	AAGGCTCCGGTGTAGCCCAC	48	251
1124545	709	728	4938	4957	CGCGGTAGCTGAGCCCGCGG	65	252
1124572	762	781	4991	5010	CTCCGAGGCCACGGCTGAC	39	253
1124620	902	921	5216	5235	TCGCAGTACTCCAGCTCAG	19	254
1124648	993	1012	5307	5326	TGCCGGCTGCGCGGGCATGA	37	255

1124676	1071	1090	5490	5509	CTGCTCCCGCTTCGCCGGCA	79	256
1124704	1116	1135	5535	5554	CCGCTGCCCGCAGCTCAGTG	50	257
1124730	1152	1171	5571	5590	AACGACGCGGGTCATCGAAG	27	258
1124757	1224	1243	5643	5662	GGCGCAGAAACTGTGGCCCC	32	259
1124784	1311	1330	5971	5990	GAGCACCACCGTCAGATCCT	30	260
1124812	1380	1399	6040	6059	GTGCAAGCGGTAGGAGCGCA	48	261
1124839	1459	1478	6202	6221	GCGCGCAGCTGCCGTCCGCA	27	262
1124863	1548	1567	6291	6310	GCCCCAGCCGGCCACCTGGC	149	263
1124890	1578	1597	N/A	N/A	GGCATATTCCTCCGCCCCCT	37	264
1124917	1620	1639	6918	6937	CTCCAGGGAGAGGAACGGTA	116	265
1124943	1746	1765	7134	7153	TTGGTCCTCACACACCAGCG	10 [†]	266
1124970	1793	1812	7181	7200	GATCCCCAGCTGATGATGCC	94	267
1124996	1823	1842	7211	7230	ACGCCTGGCTTGTGCGGTC	24	268
1125021	1870	1889	7258	7277	CGGTGTGCTCCCGGATCCAG	50	269
1125047	1915	1934	7303	7322	GGAATCACCAAGGAGGGAAA	14	270
1125074	1950	1969	7338	7357	TCTTGCCTTCCATGCCCCAG	18	271
1125122	N/A	N/A	94	113	CACTCACCGAAAGTGTTGAC	40	272
1125150	N/A	N/A	178	197	CCACAGGTCATGAGCAGAGG	63	273
1125178	N/A	N/A	274	293	TGCCCTTGTATCCACCCAGT	71	274
1125206	N/A	N/A	368	387	CCCAGAAATGCAGAGATTTC	103	275
1125234	N/A	N/A	457	476	AATCTACAAGGGAGAGAAGA	51	276
1125262	N/A	N/A	603	622	GGCACTAGACTAGACTGCCC	33	277
1125290	N/A	N/A	690	709	CTTAGACACAGCCCATACCC	25	278
1125318	N/A	N/A	859	878	ATTGAAGGCCCTGGCCTCTG	37	279
1125346	N/A	N/A	957	976	TCAAATCCCTCGCCCAGAGT	56	280
1125374	N/A	N/A	1064	1083	CAGGTGATGGGCTGAATACC	123	281
1125402	N/A	N/A	1197	1216	AATTTAGTGTCTGGAAGAAT	44	282
1125430	N/A	N/A	1575	1594	CCCCACCAAGTCAGGCCAC	66	283
1125458	N/A	N/A	1747	1766	TGGACGGACAGAGAGGAGGG	127	284
1125486	N/A	N/A	2123	2142	AGGACCAAACCAGAACTAGG	119	285
1125514	N/A	N/A	2253	2272	TGTCTTCTTCAGAGGAATTG	47	286
1125542	N/A	N/A	2341	2360	GGCTCACAGGAACCTAATAC	36	287
1125570	N/A	N/A	2479	2498	GATTCAGGTGTGTGCTATAG	13	288
1125598	N/A	N/A	2609	2628	GTTTTTCACACTTTGTGCTT	31	289
1125626	N/A	N/A	2734	2753	GGGCATGCACAGAGCAGTGA	47	290
1125654	N/A	N/A	2832	2851	CTCATTCTTCTCTGGTTCTA	32	291
1125682	N/A	N/A	2939	2958	TAGGCACTTAATAATACTTG	51	292
1125710	N/A	N/A	3042	3061	GGAGTCAGATAGCTGGAGTA	163	293
1125738	N/A	N/A	3436	3455	CTCAGGGTCTGGTCAGGAAA	62	294
1125766	N/A	N/A	3631	3650	CAGGCCCTGCTCCAACCTCC	107	295
1125794	N/A	N/A	3743	3762	GAGACAAGGCTTCCCTGCTC	38	296
1125822	N/A	N/A	3889	3908	GATACCAGGAGAGTAATGAG	103	297
1125850	N/A	N/A	4015	4034	AAGCTTGGTTTACCCACCTG	94	298
1125878	N/A	N/A	4122	4141	GAGAGATGGACATGGTGGAA	79	299
1125906	N/A	N/A	4310	4329	CCAGCAACCTATTCTGTAGG	47	300

1125934	N/A	N/A	4535	4554	CTCCCTGGCCCGTTCCCAAC	30	301
1125962	N/A	N/A	4632	4651	AACGCAGTGAGCCACCCCTG	61	302
1125990	N/A	N/A	4859	4878	CTGGGCTCTCCTGCCTCCCT	80	303
1126018	N/A	N/A	5383	5402	TTCCCCCCCCACTTCCTAA	187	304
1126046	N/A	N/A	5751	5770	GAGACGGAGGAGCCGCGGCC	120	305
1126074	N/A	N/A	6158	6177	AACCCGGGCGGAGAGGAGCG	170	306
1126102	N/A	N/A	6373	6392	GGCTTCTTCGCTAACCCTA	111	307
1126130	N/A	N/A	6481	6500	TGAATCCCAGGCCCTGGGAT	73	308
1126158	N/A	N/A	6621	6640	GAGTCGCAGAACCTGGCTCC	84	309
1126186	N/A	N/A	6712	6731	ATTTCATAGGCAAGGAGGCT	53	310
1126214	N/A	N/A	6839	6858	CTTCACACCCCATCTGACAA	82	311
1126242	N/A	N/A	7106	7125	GAATCACCCCTGGGTTCGAAA	43 [†]	312

Table 5. Reduction of FXII RNA by 5-10-5 MOE gapmers with full PS internucleoside linkages (Huh7, electroporation, 5000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC) RTS40528	SEQ ID NO
413643	1839	1858	7227	7246	GGCCACATCGGTGTAGACGC	14	86
462073	216	235	3567	3586	GGTACATTTGTGGTACAGCT	36	183
626671	840	859	N/A	N/A	GTCCGGGTTCCGGCAGAAGG	19	313
1124164	33	52	33	52	CATGGCATCCGTCCGTTGGT	24	314
1124192	79	98	79	98	TTGACTCCAAGCTCACCAGC	95	315
1124220	136	155	503	522	GCTCTTCAGCTTTGTACTTA	93	316
1124246	172	191	3523	3542	GGCAGGGCTCCCCGGTGACA	36	317
1124269	226	245	3577	3596	GGCCCTTGTGGGTACATTTG	34	318
1124297	292	311	3799	3818	AGTATCCCCATCGCTGGTCC	24	319
1124325	332	351	N/A	N/A	TGTTTGCTGCAGTGGTCTTT	92	320
1124353	405	424	4213	4232	GAGGTGTTGTGGACAGAGAC	24	321
1124381	447	466	4392	4411	CTGAGGCTCAAAGCACTTCT	27	322
1124408	493	512	4438	4457	GCTCAGTTCTATACCATATC	18	323
1124436	533	552	4478	4497	GCATCAGGACCCTTGCACTG	78	324
1124463	568	587	N/A	N/A	TGCGGCAGGCCTGGCTGGCC	65	325
1124490	607	626	4691	4710	CCACCTCTAGGCAGCGACCC	17	326
1124518	654	673	4738	4757	GAAGGCTCCGGTGTAGCCCA	75	327
1124546	710	729	4939	4958	CCGCGGTAGCTGAGCCCGCG	170	328
1124573	763	782	4992	5011	CCTCCGAGGCCACGGCTGA	27	329
1124621	903	922	5217	5236	GTCGCAGTACTCCAGCTCA	23	330
1124649	994	1013	5308	5327	GTGCCGGCTGCGCGGGCATG	42	331
1124677	1072	1091	5491	5510	GCTGCTCCCGCTTCGCCGGC	23	332
1124705	1117	1136	5536	5555	GCCGCTGCCCCGAGCTCAGT	40	333
1124731	1153	1172	5572	5591	CAACGACGCGGGTCATCGAA	64	334

1124758	1225	1244	5644	5663	CGGCGCAGAACTGTGGCCC	35	335
1124785	1312	1331	5972	5991	CGAGCACCACCGTCAGATCC	30	336
1124813	1381	1400	6041	6060	CGTGCAAGCGGTAGGAGCGC	18	337
1124840	1460	1479	6203	6222	AGCGCGCAGCTGCCGTCCGC	59	338
1124864	1549	1568	6292	6311	GGCCCCAGCCGGCCACCTGG	54	339
1124891	1579	1598	N/A	N/A	TGGCATATTCCTCCGCCCCC	34	340
1124918	1621	1640	6919	6938	GCTCCAGGGAGAGGAACGGT	84	341
1124944	1747	1766	7135	7154	CTTGGTCTCACACACCAGC	7 [†]	342
1124971	1794	1813	7182	7201	CGATCCCCAGCTGATGATGC	66	343
1125022	1871	1890	7259	7278	ACGGTGTGCTCCCGGATCCA	26	344
1125048	1916	1935	7304	7323	CGGAATCACCAAGGAGGGAA	35	345
1125075	1951	1970	7339	7358	ATCTTGCTTCCATGCCCCA	23	346
1125101	2006	2025	7394	7413	TGAGTTCCTGCGCCATCCTG	7	347
1125123	N/A	N/A	97	116	CAGCACTCACCGAAAGTGTT	67	348
1125151	N/A	N/A	181	200	GACCCACAGGTCATGAGCAG	50	349
1125179	N/A	N/A	277	296	CTGTGCCCTTGATCCACCC	67	350
1125207	N/A	N/A	371	390	CAGCCCAGAAATGCAGAGAT	45	351
1125235	N/A	N/A	460	479	TGGAATCTACAAGGGAGAGA	125	352
1125263	N/A	N/A	606	625	GTAGGCACTAGACTAGACTG	129	353
1125291	N/A	N/A	693	712	GCACTTAGACACAGCCCATA	69	354
1125319	N/A	N/A	862	881	CCCATTGAAGGCCCTGGCCT	38	355
1125347	N/A	N/A	960	979	AACTCAAATCCCTCGCCCAG	77	356
1125375	N/A	N/A	1067	1086	CACCAGGTGATGGGCTGAAT	86	357
1125403	N/A	N/A	1200	1219	GGTAATTTAGTGTCTGGAAG	130	358
1125431	N/A	N/A	1578	1597	CAACCCACCAAGTCAGGCC	74	359
1125459	N/A	N/A	1750	1769	GGATGGACGGACAGAGAGGA	60	360
1125487	N/A	N/A	2126	2145	CCAAGGACCAAACCAGAACT	84	361
1125515	N/A	N/A	2256	2275	CTGTGTCTTCTTCAGAGGAA	50	362
1125543	N/A	N/A	2370	2389	TGTTGGTTGATGAAAATGTT	55	363
1125571	N/A	N/A	2482	2501	CTTGATTACAGGTGTGTGCTA	73	364
1125599	N/A	N/A	2628	2647	TCAGTCTACTTAGTGCAACG	98	365
1125627	N/A	N/A	2739	2758	TTTGTGGGCATGCACAGAGC	31	366
1125655	N/A	N/A	2835	2854	ATCCTCATTTCTTCTTGTT	26	367
1125683	N/A	N/A	2942	2961	AAGTAGGCACTTAATAATAC	73	368
1125711	N/A	N/A	3045	3064	TCAGGAGTCAGATAGCTGGA	100	369
1125739	N/A	N/A	3439	3458	TCCCTCAGGGTCTGGTCAGG	25	370
1125767	N/A	N/A	3637	3656	GTCTCCAGGCCCTGCTCC	77	371
1125795	N/A	N/A	3749	3768	TAGAAAGAGACAAGGCTTCC	102	372
1125823	N/A	N/A	3892	3911	GGTGATAACCAGGAGAGTAAT	93	373
1125851	N/A	N/A	4018	4037	TCCAAGCTTGTTTTACCCAC	38	374
1125879	N/A	N/A	4125	4144	TCTGAGAGATGGACATGGTG	69	375
1125907	N/A	N/A	4313	4332	TATCCAGCAACCTATTCTGT	152	376
1125935	N/A	N/A	4538	4557	CTCCTCCCTGGCCCGTTCCC	64	377
1125963	N/A	N/A	4635	4654	GGGAACGCAGTGAGCCACCC	97	378
1125991	N/A	N/A	4862	4881	AGGCTGGGCTCTCCTGCCTC	105	379

1126019	N/A	N/A	5386	5405	TCCTTCCCCCCCCCACTTCC	37	380
1126047	N/A	N/A	5754	5773	TGGGAGACGGAGGAGCCGCG	87	381
1126075	N/A	N/A	6161	6180	GCTAACCCGGGCGGAGAGGA	36	382
1126103	N/A	N/A	6376	6395	GCGGGCTTCTTCCGCCTAAC	66	383
1126131	N/A	N/A	6484	6503	CAGTGAATCCCAGGCCCTGG	34	384
1126159	N/A	N/A	6624	6643	CCAGAGTCGAGAACCTGGC	34	385
1126187	N/A	N/A	6715	6734	TCAATTTTCATAGGCAAGGAG	28	386
1126215	N/A	N/A	6842	6861	CTTCTTCACACCCCATCTGA	100	387
1126243	N/A	N/A	7109	7128	CCGGAATCACCTGGGTCGG	28 [†]	388

Table 6. Reduction of FXII RNA by 5-10-5 MOE gapmers with full PS internucleoside linkages (Huh7, electroporation, 5000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC) RTS40528	SEQ ID NO
413637	1748	1767	7136	7155	GCTTGGTCTCACACACCAG	12 [†]	80
462073	216	235	3567	3586	GGTACATTTGTGGTACAGCT	20	183
1124193	80	99	80	99	GTTGACTCCAAGCTCACCAG	34	389
1124221	138	157	505	524	GTGCTCTTCAGCTTTGTACT	37	390
1124247	174	193	3525	3544	GTGGCAGGGCTCCCCGGTGA	54	391
1124270	228	247	3579	3598	CCGGCCCTTGTGGGTACATT	51	392
1124298	293	312	3800	3819	CAGTATCCCCATCGCTGGTC	36	393
1124326	333	352	N/A	N/A	GTGTTTGCTGCAGTGGTCTT	56	394
1124354	406	425	4214	4233	TGAGGTGTTGTGGACAGAGA	56	395
1124382	449	468	4394	4413	AGCTGAGGCTCAAAGCACTT	38	396
1124409	494	513	4439	4458	TGCTCAGTTCTATACCATAT	31	397
1124437	535	554	4480	4499	GGGCATCAGGACCCTTGAC	66	398
1124464	569	588	N/A	N/A	GTGCGGCAGGCCTGGCTGGC	70	399
1124491	609	628	4693	4712	CTCCACCTCTAGGCAGCGAC	28	400
1124519	655	674	4739	4758	AGAAGGCTCCGGTGTAGCCC	102	401
1124547	711	730	4940	4959	GCCGCGGTAGCTGAGCCCGC	58	402
1124574	765	784	4994	5013	GGCCTCCGAGGCCACGGCT	44	403
1124597	843	862	N/A	N/A	GTTGTCCGGGTCCGGCAGA	45	404
1124622	904	923	5218	5237	GGTCGCAGTACTCCCAGCTC	42	405
1124650	996	1015	5310	5329	CGGTGCCGGCTGCGCGGGCA	90	406
1124678	1073	1092	5492	5511	GGCTGCTCCCGCTTCGCCGG	92	407
1124706	1118	1137	5537	5556	AGCCGCTGCCCGCAGCTCAG	39	408
1124732	1155	1174	5574	5593	GCCAACGACGCGGGTCATCG	38	409
1124759	1227	1246	5646	5665	GCCGGCGCAGAACTGTGGC	55	410
1124786	1313	1332	5973	5992	CCGAGCACCACCGTCAGATC	40	411
1124814	1399	1418	6059	6078	TGACGGGCGAGAAGGCCTCG	59	412
1124841	1462	1481	6205	6224	GGAGCGCGCAGCTGCCGTCC	44	413

1124865	1550	1569	6293	6312	TGGCCCCAGCCGGCCACCTG	53	414
1124892	1581	1600	6879	6898	GCTGGCATATTCCTCCGCCC	78	415
1124919	1622	1641	6920	6939	CGCTCCAGGGAGAGGAACGG	80	416
1124972	1795	1814	7183	7202	CCGATCCCCAGCTGATGATG	41	417
1124997	1842	1861	7230	7249	GTAGGCCACATCGGTGTAGA	39	418
1125023	1873	1892	7261	7280	AAACGGTGTGCTCCCGGATC	26	419
1125049	1917	1936	7305	7324	GCGGAATCACCAAGGAGGGA	20	420
1125076	1952	1971	7340	7359	AATCTTGCTTCCATGCCCC	22	421
1125102	2007	2026	7395	7414	TTGAGTTCCTGCGCCATCCT	15	422
1125124	N/A	N/A	100	119	CCACAGCACTCACCGAAAGT	102	423
1125152	N/A	N/A	184	203	CTGGACCCACAGGTCATGAG	87	424
1125180	N/A	N/A	280	299	AGGCTGTGCCCTTGTATCCA	109	425
1125208	N/A	N/A	374	393	TCACAGCCCAGAAATGCAGA	82	426
1125236	N/A	N/A	463	482	AGGTGGAATCTACAAGGGAG	100	427
1125264	N/A	N/A	609	628	CAGGTAGGCACTAGACTAGA	81	428
1125292	N/A	N/A	696	715	TGGGCACTTAGACACAGCCC	52	429
1125320	N/A	N/A	865	884	TTGCCCATTGAAGGCCCTGG	39	430
1125348	N/A	N/A	963	982	GAGAACTCAAATCCCTCGCC	50	431
1125376	N/A	N/A	1070	1089	ATGCACCAGGTGATGGGCTG	62	432
1125404	N/A	N/A	1203	1222	GTAGGTAATTTAGTGTCTGG	59	433
1125432	N/A	N/A	1581	1600	ACTCAACCCCAACAGTCAG	52	434
1125460	N/A	N/A	1753	1772	ATGGGATGGACGGACAGAGA	58	435
1125488	N/A	N/A	2129	2148	TTGCCAAGGACCAAAACCAGA	72	436
1125516	N/A	N/A	2259	2278	TGCCTGTGTCTTCTTCAGAG	61	437
1125544	N/A	N/A	2373	2392	TGCTGTTGGTTGATGAAAAT	62	438
1125572	N/A	N/A	2485	2504	ACACTTGATTACAGGTGTGTG	74	439
1125600	N/A	N/A	2634	2653	TCCTTCTCAGTCTACTTAGT	49	440
1125628	N/A	N/A	2742	2761	CCATTTGTGGGCATGCACAG	75	441
1125656	N/A	N/A	2838	2857	TTGATCCTCATTCCTCTCTG	77	442
1125684	N/A	N/A	2950	2969	TTGCCACAAAGTAGGCACTT	51	443
1125712	N/A	N/A	3048	3067	GGTTCAGGAGTCAGATAGCT	66	444
1125740	N/A	N/A	3442	3461	CTGTCCCTCAGGGTCTGGTC	61	445
1125768	N/A	N/A	3640	3659	CATGTCTCCCAGGCCCTGC	73	446
1125796	N/A	N/A	3752	3771	CTGTAGAAAGAGACAAGGCT	59	447
1125824	N/A	N/A	3895	3914	TCTGGTGATACCAGGAGAGT	48	448
1125852	N/A	N/A	4021	4040	GTTTCCAAGCTTGTTTTACC	54	449
1125880	N/A	N/A	4128	4147	TGGTCTGAGAGATGGACATG	59	450
1125908	N/A	N/A	4316	4335	GAGTATCCAGCAACCTATTC	67	451
1125936	N/A	N/A	4541	4560	ACGCTCCTCCCTGGCCCCGTT	60	452
1125964	N/A	N/A	4638	4657	GGAGGGAACGCAGTGAGCCA	127	453
1125992	N/A	N/A	4866	4885	GCCAAGGCTGGGCTCTCCTG	57	454
1126020	N/A	N/A	5389	5408	TCCTCCTTCCCCCCCCCACT	82	455
1126048	N/A	N/A	5757	5776	CGCTGGGAGACGGAGGAGCC	116	456
1126076	N/A	N/A	6164	6183	AGAGCTAACCCGGGCGGAGA	120	457
1126104	N/A	N/A	6379	6398	GTCGCGGGCTTCTCCGCCT	54	458

1126132	N/A	N/A	6487	6506	CAGCAGTGAATCCCAGGCC	96	459
1126160	N/A	N/A	6627	6646	CATCCAGAGTCGCAGAACCT	105	460
1126188	N/A	N/A	6718	6737	AATTCAATTTTCATAGGCAAG	73	461
1126216	N/A	N/A	6845	6864	CGCCTTCTTCACACCCCATC	68	462
1126244	N/A	N/A	7112	7131	CCTCCGGAATCACCTGGGT	31 [†]	463

Table 7. Reduction of FXII RNA by 5-10-5 MOE gapmers with full PS internucleoside linkages (Huh7, electroporation, 5000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC) RTS40528	SEQ ID NO
462073	216	235	3567	3586	GGTACATTTGTGGTACAGCT	15	183
564842	1463	1482	6206	6225	AGGAGCGCGCAGCTGCCGTC	44	464
1124194	82	101	82	101	GTGTTGACTCCAAGCTCACC	63	465
1124222	139	158	506	525	TGTGCTCTTCAGCTTTGTAC	25	466
1124248	175	194	3526	3545	AGTGGCAGGGCTCCCCGGTG	48	467
1124271	229	248	3580	3599	GCCGGCCCTTGTGGGTACAT	49	468
1124299	294	313	3801	3820	ACAGTATCCCCATCGCTGGT	46	469
1124327	334	353	4142	4161	TGTGTTTGCTGCAGTGGTCT	52	470
1124355	407	426	4215	4234	GTGAGGTGTTGTGGACAGAG	110	471
1124383	450	469	4395	4414	AAGCTGAGGCTCAAAGCACT	55	472
1124410	495	514	4440	4459	TTGCTCAGTTCTATACCATA	36	473
1124438	536	555	4481	4500	TGGGCATCAGGACCCTTGCA	51	474
1124465	570	589	N/A	N/A	GGTGCGGCAGGCCTGGCTGG	140	475
1124492	610	629	4694	4713	CCTCCACCTCTAGGCAGCGA	38	476
1124520	656	675	4740	4759	CAGAAGGCTCCGGTGTAGCC	63	477
1124548	712	731	4941	4960	GGCCGCGGTAGCTGAGCCCG	66	478
1124575	766	785	4995	5014	TGGCCTCCGAGGCCACGGC	65	479
1124598	844	863	N/A	N/A	CGTTGTCCGGGTTCCGGCAG	33	480
1124623	905	924	5219	5238	AGGTCGCAGTACTCCCAGCT	47	481
1124651	997	1016	5311	5330	GCGGTGCCGGCTGCGCGGGC	57	482
1124679	1075	1094	5494	5513	GCGGCTGCTCCCGCTTCGCC	45	483
1124707	1120	1139	5539	5558	GGAGCCGCTGCCCGCAGCTC	47	484
1124733	1156	1175	5575	5594	CGCCAACGACGCGGGTCATC	42	485
1124760	1228	1247	5647	5666	TGCCGCGCAGAACTGTGG	64	486
1124787	1314	1333	5974	5993	GCCGAGCACCACCGTCAGAT	36	487
1124815	1400	1419	6060	6079	CTGACGGGCGAGAAGGCCTC	45	488
1124866	1551	1570	6294	6313	GTGGCCCCAGCCGGCCACCT	118	489
1124893	1582	1601	6880	6899	AGCTGGCATATTCCTCCGCC	81	490
1124920	1623	1642	6921	6940	GCGCTCCAGGGAGAGGAACG	79	491
1124945	1749	1768	7137	7156	AGCTTGGTCCTCACACACCA	12 [†]	492
1124973	1796	1815	7184	7203	CCCGATCCCCAGCTGATGAT	39	493

1124998	1843	1862	7231	7250	AGTAGGCCACATCGGTGTAG	31	494
1125024	1874	1893	7262	7281	GAAACGGTGTGCTCCCGGAT	34	495
1125050	1918	1937	7306	7325	TGCGGAATCACCAAGGAGGG	23	496
1125077	1954	1973	7342	7361	ACAATCTTGCCTTCCATGCC	23	497
1125103	2009	2028	7397	7416	TATTGAGTTCCTGCGCCATC	25	498
1125125	N/A	N/A	103	122	TTCCACAGCACTACCGAA	84	499
1125153	N/A	N/A	187	206	CACCTGGACCCACAGGTCAT	110	500
1125181	N/A	N/A	283	302	TGCAGGCTGTGCCCTTGTAT	78	501
1125209	N/A	N/A	377	396	CTCTCACAGCCCAGAAATGC	68	502
1125237	N/A	N/A	466	485	CCAAGGTGGAATCTACAAGG	78	503
1125265	N/A	N/A	612	631	CACCAGGTAGGCACTAGACT	64	504
1125293	N/A	N/A	716	735	CCTGCTCCGAGCCAGGCTCG	74	505
1125321	N/A	N/A	868	887	TCCTTGCCCATTGAAGGCC	65	506
1125349	N/A	N/A	966	985	TTGGAGAACTCAAATCCCTC	66	507
1125377	N/A	N/A	1073	1092	TCCATGCACCAGGTGATGGG	58	508
1125405	N/A	N/A	1206	1225	CATGTAGGTAATTTAGTGTC	90	509
1125433	N/A	N/A	1584	1603	GAGACTCAACCCACCAAGT	88	510
1125461	N/A	N/A	1756	1775	CAGATGGGATGGACGGACAG	65	511
1125489	N/A	N/A	2132	2151	CACTTGCCAAGGACCAAACC	86	512
1125517	N/A	N/A	2262	2281	AATTGCCTGTGTCTTCTTCA	57	513
1125545	N/A	N/A	2376	2395	ATATGCTGTTGGTTGATGAA	55	514
1125573	N/A	N/A	2488	2507	TAGACACTTGATTCAGGTGT	57	515
1125601	N/A	N/A	2637	2656	GTGTCCTTCTCAGTCTACTT	68	516
1125629	N/A	N/A	2745	2764	TGGCCATTTGTGGGCATGCA	54	517
1125657	N/A	N/A	2841	2860	CAGTTGATCCTCATTCTTCT	59	518
1125685	N/A	N/A	2953	2972	CACTTGCCACAAAGTAGGCA	51	519
1125713	N/A	N/A	3051	3070	TTGGGTTTCAGGAGTCAGATA	116	520
1125741	N/A	N/A	3445	3464	GCACTGTCCCTCAGGGTCTG	68	521
1125769	N/A	N/A	3643	3662	GTACATGTCTCCCAGGCCCC	57	522
1125797	N/A	N/A	3755	3774	CACCTGTAGAAAGAGACAAG	148	523
1125825	N/A	N/A	3898	3917	GGGTCTGGTGATACCAGGAG	56	524
1125853	N/A	N/A	4024	4043	CAAGTTTCCAAGCTTGTTTT	53	525
1125881	N/A	N/A	4131	4150	CAGTGGTCTGAGAGATGGAC	56	526
1125909	N/A	N/A	4319	4338	TCCGAGTATCCAGCAACCTA	88	527
1125937	N/A	N/A	4557	4576	CCAGCCTGTCTTCCTGACGC	63	528
1125965	N/A	N/A	4657	4676	GTTGGTGCGGCAGGCTTGGG	60	529
1125993	N/A	N/A	4869	4888	GCAGCCAAGGCTGGGCTCTC	75	530
1126021	N/A	N/A	5392	5411	GGCTCCTCCTTCCCCCCCC	54	531
1126049	N/A	N/A	5760	5779	CTGCGCTGGGAGACGGAGGA	181	532
1126077	N/A	N/A	6167	6186	AACAGAGCTAACC CGGCGG	67	533
1126105	N/A	N/A	6382	6401	AAAGTCGCGGGCTTCTCCG	59	534
1126133	N/A	N/A	6490	6509	TCCCAGCAGTGAATCCCAGG	88	535
1126161	N/A	N/A	6630	6649	ACCCATCCAGAGTCGCAGAA	72	536
1126189	N/A	N/A	6721	6740	ATTAATTCAATTTTCATAGGC	76	537
1126217	N/A	N/A	6862	6881	CCCCTGCGAACACAGAGCGC	105	538

Table 8. Reduction of FXII RNA by 5-10-5 MOE gapmers with full PS internucleoside linkages (Huh7, electroporation, 5000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC) RTS40528	SEQ ID NO
413644	1844	1863	7232	7251	TAGTAGGCCACATCGGTGTA	32	87
462073	216	235	3567	3586	GGTACATTTGTGGTACAGCT	48	183
564822	862	881	5176	5195	AGCACCACGGGCGGATGTCTG	69	539
1124167	36	55	36	55	CCTCATGGCATCCGTCCGTT	42	540
1124195	83	102	83	102	AGTGTGACTCCAAGCTCAC	45	541
1124223	141	160	508	527	TGTGTGCTCTTCAGCTTTGT	32	542
1124249	177	196	3528	3547	GAAGTGGCAGGGCTCCCCGG	54	543
1124272	231	250	3582	3601	TGGCCGGCCCTTGTGGGTAC	141	544
1124300	296	315	3803	3822	AAACAGTATCCCCATCGCTG	66	545
1124328	335	354	4143	4162	CTGTGTTTGCTGCAGTGGTC	38	546
1124356	408	427	4216	4235	AGTGAGGTGTTGTGGACAGA	73	547
1124384	451	470	4396	4415	GAAGCTGAGGCTCAAAGCAC	32	548
1124411	496	515	4441	4460	CTTGCTCAGTTCTATACCAT	52	549
1124439	537	556	4482	4501	GTGGGCATCAGGACCCTTGC	45	550
1124466	571	590	N/A	N/A	TGGTGCGGCAGGCCTGGCTG	146	551
1124493	612	631	4696	4715	GCCCTCCACCTCTAGGCAGC	70	552
1124521	657	676	4741	4760	GCAGAAGGCTCCGGTGTAGC	97	553
1124549	714	733	4943	4962	CAGGCCGCGGTAGCTGAGCC	99	554
1124576	767	786	4996	5015	GTGGCCTCCGAGGCCACCG	78	555
1124624	907	926	5221	5240	CCAGGTCGCACTACTCCAG	51	556
1124652	998	1017	5312	5331	GGCGGTGCCGGCTGCGCGGG	70	557
1124680	1076	1095	5495	5514	GGCGGTGCTCCCGCTTCGC	67	558
1124708	1121	1140	5540	5559	CGGAGCCGCTGCCCCGAGCT	136	559
1124734	1158	1177	5577	5596	CCCGCCAACGACGCGGGTCA	51	560
1124761	1229	1248	5648	5667	CTGCCGCGCAGAACTGTG	54	561
1124788	1315	1334	5975	5994	GGCCGAGCACCACGTCAGA	100	562
1124816	1401	1420	6061	6080	GCTGACGGGCGAGAAGGCCT	70	563
1124842	1464	1483	6207	6226	CAGGAGCGCGCAGCTGCCGT	40	564
1124867	1552	1571	6295	6314	GGTGGCCCCAGCCGGCCACC	66	565
1124894	1583	1602	6881	6900	AAGCTGGCATATTCCTCCGC	80	566
1124921	1657	1676	6955	6974	GGATGGAGGATCCGTGCACG	30 [†]	567
1124946	1750	1769	7138	7157	CAGCTTGGTCCTCACACACC	18 [†]	568
1124974	1797	1816	7185	7204	GCCCGATCCCCAGCTGATGA	43	569
1125025	1876	1895	7264	7283	AGGAAACGGTGTGCTCCCGG	42	570
1125051	1919	1938	7307	7326	CTGCGGAATCACCAAGGAGG	26	571
1125078	1955	1974	7343	7362	CACAATCTTGCCCTCCATGC	37	572
1125104	2010	2029	7398	7417	TTATTGAGTTCCTGCGCCAT	22	573

1125126	N/A	N/A	106	125	TGGTTCACAGCACTCACC	73	574
1125154	N/A	N/A	190	209	AGTCACCTGGACCCACAGGT	78	575
1125182	N/A	N/A	286	305	AAATGCAGGCTGTGCCCTTG	69	576
1125210	N/A	N/A	380	399	TTCTCTCACAGCCCAGAAA	60	577
1125238	N/A	N/A	469	488	TTCCCAAGGTGGAATCTACA	84	578
1125266	N/A	N/A	615	634	TAGCACCAGGTAGGCACTAG	66	579
1125294	N/A	N/A	721	740	AAGCACCTGCTCCGAGCCAG	56	580
1125322	N/A	N/A	871	890	CCTTCCTTGCCCATTGAAGG	60	581
1125350	N/A	N/A	969	988	AGCTTGGAAGAACTCAAATCC	62	582
1125378	N/A	N/A	1076	1095	ATTTCCATGCACCAGGTGAT	62	583
1125406	N/A	N/A	1209	1228	TGGCATGTAGGTAATTTAGT	63	584
1125434	N/A	N/A	1587	1606	TTAGAGACTCAACCCACCA	143	585
1125462	N/A	N/A	1759	1778	ATGCAGATGGGATGGACGGA	167	586
1125490	N/A	N/A	2135	2154	GTGCACTTGCCAAGGACCAA	73	587
1125518	N/A	N/A	2265	2284	GAGAATTGCCTGTGTCTTCT	55	588
1125546	N/A	N/A	2379	2398	ATTATATGCTGTTGGTTGAT	123	589
1125574	N/A	N/A	2513	2532	GCTACCTTAGGGAGAAAGCG	121	590
1125602	N/A	N/A	2640	2659	TGAGTGTCTTCTCAGTCTA	69	591
1125630	N/A	N/A	2748	2767	TCATGGCCATTTGTGGGCAT	89	592
1125658	N/A	N/A	2845	2864	AGTACAGTTGATCCTCATTC	162	593
1125686	N/A	N/A	2956	2975	GAGCACTTGCCACAAAGTAG	91	594
1125714	N/A	N/A	3054	3073	AACTTGCGTTCAGGAGTCAG	105	595
1125742	N/A	N/A	3448	3467	CAGGCACTGTCCCTCAGGGT	141	596
1125770	N/A	N/A	3649	3668	GGCAGGGTACATGTCTCCCA	68	597
1125798	N/A	N/A	3758	3777	GCACACCTGTAGAAAGAGAC	82	598
1125826	N/A	N/A	3916	3935	CAGAAATCCAGGTGTGTGGG	54	599
1125854	N/A	N/A	4027	4046	CTCCAAGTTTCCAAGCTTGG	116	600
1125882	N/A	N/A	4134	4153	CTGCAGTGGTCTGAGAGATG	102	601
1125910	N/A	N/A	4325	4344	CAAGTCTCCGAGTATCCAGC	96	602
1125938	N/A	N/A	4560	4579	CTGCCAGCCTGTCTTCCTGA	80	603
1125966	N/A	N/A	4660	4679	CGGGTTGGTGCGGCAGGCTT	95	604
1125994	N/A	N/A	4875	4894	CCCTGGGCAGCCAAGGCTGG	67	605
1126022	N/A	N/A	5395	5414	CTCGGCTCCTCCTTCCCCC	61	606
1126050	N/A	N/A	5763	5782	AAGCTGCGCTGGGAGACGGA	123	607
1126078	N/A	N/A	6170	6189	CGCAACAGAGCTAACCCGGG	76	608
1126106	N/A	N/A	6385	6404	ACCAAAGTCGCGGGCTTCTT	150	609
1126134	N/A	N/A	6493	6512	GGATCCCAGCAGTGAATCCC	70	610
1126162	N/A	N/A	6633	6652	ACCACCCATCCAGAGTCGCA	60	611
1126190	N/A	N/A	6724	6743	GCCATTAATTCAATTTTCATA	72	612
1126218	N/A	N/A	6865	6884	CCGCCCTGCGAACACAGAG	66	613

Table 9. Reduction of FXII RNA by 5-10-5 MOE gapmers with full PS internucleoside linkages (Huh7, oligofectamine, 200nM modified oligonucleotide)

Compound Number	SEQ ID NO: 3 Start Site	SEQ ID NO: 3 Stop Site	SEQ ID NO: 4 Start Site	SEQ ID NO: 4 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
462200	10845	10864	N/A	N/A	CTTCTCAGCATTTTCAAAGC	63	614
462201	10848	10867	N/A	N/A	TTCCTTCTCAGCATTTTCAA	63	615

Table 10. Reduction of FXII RNA by 5-10-5 MOE gapmers with full PS internucleoside linkages (Huh7, electroporation, 5000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 3 Start Site	SEQ ID NO: 3 Stop Site	SEQ ID NO: 4 Start Site	SEQ ID NO: 4 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1126246	10849	10868	N/A	N/A	TTTCCTTCTCAGCATTTTCA	130	616

5 **Table 11. Reduction of FXII RNA by 5-10-5 MOE gapmers with full PS internucleoside linkages (Huh7, electroporation, 5000nM modified oligonucleotide)**

Compound Number	SEQ ID NO: 3 Start Site	SEQ ID NO: 3 Stop Site	SEQ ID NO: 4 Start Site	SEQ ID NO: 4 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1124165	3458	3477	34	53	TCATGGCATCCGTCCGTTGG	60	617
1126245	10846	10865	N/A	N/A	CCTTCTCAGCATTTTCAAAG	77	618
1124166	3459	3478	35	54	CTCATGGCATCCGTCCGTTG	52	619

Example 2: Effects of 5-10-5 MOE gapmers on human FXII RNA *in vitro*, single dose

Modified oligonucleotides complementary to a FXII nucleic acid were synthesized and tested for their effect on FXII RNA levels *in vitro*. The modified oligonucleotides were tested in a series of experiments using similar culture conditions. The results for each separate experiment are presented in separate tables below.

The modified oligonucleotides in the tables below 5-10-5 MOE gapmers (i.e., they have a central region of ten 2'-deoxynucleosides flanked on each side by wings, each comprising five 2'-MOE nucleosides). The motif for the gapmers is (from 5' to 3'): eeeeeeeeeeeeeee; wherein "d" represents a 2'-β-D-deoxyribose sugar moiety, and "e" represents a 2'-MOE sugar moiety. The internucleoside linkage motif for the gapmers is (from 5' to 3'): sooooooossssoos; wherein "o" represents a phosphodiester internucleoside

linkage and 's' represents a phosphorothioate internucleoside linkage. Each cytosine residue is a 5-methyl cytosine.

“Start site” indicates the 5'-most nucleoside of the target sequence to which the modified oligonucleotide is complementary. “Stop site” indicates the 3'-most nucleoside of the target sequence to which the modified oligonucleotide is complementary. As shown in the tables below, the modified oligonucleotides are 100% complementary to one or more of human FXII target sequences including the human FXII mRNA sequence designated herein as SEQ ID NO: 1 (ENSEMBL ID ENST00000253496.3 from ENSEMBL version 99: January 2020), the human FXII genomic sequence, designated herein as SEQ ID NO: 2 (ENSEMBL ID ENSG00000131187.9 from ENSEMBL version 99: January 2020), the human FXII genomic sequence, designated herein as SEQ ID No. 3 (the complement of GENBANK Accession No. NC_000005.10 truncated from truncated from nucleotides 177399001 to 177413000), and the human FXII mRNA sequence designated herein as SEQ ID No: 4 (GENBANK Accession No. NM_000505.3). 'N/A' indicates that the modified oligonucleotide is not complementary to that particular target sequence with 100% complementarity.

Cultured Huh7 cells, at a density of 20,000 cells per well, were transfected using electroporation with either 5000nM or 2000nM modified oligonucleotide. After a treatment period of approximately 24 hours, RNA was isolated from the cells and FXII RNA levels were measured by quantitative real-time RT-PCR. Human primer probe set RTS40528 (described herein above) was used to measure RNA levels. FXII RNA levels were normalized to total RNA content, as measured by RIBOGREEN®. Reduction of FXII RNA is presented in the tables below as percent FXII RNA relative to the amount in untreated control cells (% UTC). The symbol “†” indicates that the modified oligonucleotide is complementary to the target transcript within the amplicon region of the primer probe set. In such instances, additional assays using alternative primer probes must be performed to accurately assess the potency and efficacy of such modified oligonucleotides.

Table 12. Reduction of FXII RNA by 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages (Huh7, electroporation, 5000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1130742	2	21	2	21	TCCAGGAGTCCAGATCAATA	67	620
1130770	37	56	37	56	CCCTCATGGCATCCGTCCGT	68	621
1130798	84	103	84	103	AAGTGTGACTCCAAGCTCA	90	622
1130826	142	161	509	528	CTGTGTGCTCTTCAGCTTTG	13	623
1130854	178	197	3529	3548	GGAAGTGGCAGGGCTCCCCG	47	624
1130871	216	235	3567	3586	GGTACATTTGTGGTACAGCT	18	183
1130883	232	251	3583	3602	CTGGCCGGCCCTTGTGGGTA	21	625
1130911	297	316	3804	3823	CAAACAGTATCCCCATCGCT	28	626
1130939	338	357	4146	4165	GGGCTGTGTTTGCTGCAGTG	22	627

1130967	410	429	4218	4237	CCAGTGAGGTGTTGTGGACA	68	628
1130995	453	472	4398	4417	GAGAAGCTGAGGCTCAAAGC	38	629
1131023	498	517	4443	4462	TGCTTGCTCAGTTCTATACC	20	630
1131051	538	557	4483	4502	AGTGGGCATCAGGACCCTTG	93	37
1131079	573	592	N/A	N/A	GTTGGTGCGGCAGGCCTGGC	37	631
1131107	613	632	4697	4716	GGCCCTCCACCTCTAGGCAG	28	632
1131135	658	677	4742	4761	CGCAGAAGGCTCCGGTGTAG	54	633
1131163	715	734	4944	4963	CCAGGCCGCGGTAGCTGAGC	40	634
1131191	768	787	4997	5016	GGTGGCCTCCGAGGCCACG	83	635
1131219	864	883	5178	5197	GAAGCACCACGGGCGGATGT	44	636
1131247	908	927	5222	5241	GCCAGGTCGCAGTACTCCCA	19	637
1131275	999	1018	5313	5332	CGGCGGTGCCGGCTGCGCGG	70	638
1131303	1077	1096	5496	5515	AGGCGGCTGCTCCCGCTTCG	38	639
1131331	1123	1142	5542	5561	TGCGGAGCCGCTGCCCGCAG	125	640
1131359	1159	1178	5578	5597	GCCCGCCAACGACGCGGGTC	56	641
1131387	1230	1249	5649	5668	GCTGCCGGCGCAGAACTGT	57	642
1131415	1316	1335	5976	5995	TGGCCGAGCACCACCGTCAG	51	643
1131443	1402	1421	6062	6081	AGCTGACGGGCGAGAAGGCC	36	644
1131471	1465	1484	6208	6227	ACAGGAGCGCGCAGCTGCCG	30	645
1131499	1553	1572	6296	6315	TGGTGGCCCCAGCCGGCCAC	61	646
1131527	1585	1604	6883	6902	GGAAGCTGGCATATTCTCTCC	57	647
1131555	1660	1679	6958	6977	GGAGGATGGAGGATCCGTGC	7 [†]	648
1131583	1751	1770	7139	7158	GCAGCTTGGTCCTCACACAC	8 [†]	649
1131611	1798	1817	7186	7205	AGCCCCGATCCCCAGCTGATG	33	650
1131639	1845	1864	7233	7252	GTAGTAGGCCACATCGGTGT	62	651
1131667	1877	1896	7265	7284	CAGGAAACGGTGTGCTCCCG	28	652
1131695	1921	1940	7309	7328	CACTGCGGAATCACCAAGGA	13	653
1131723	1956	1975	7344	7363	ACACAATCTTGCCCTTCATG	26	654
1131751	2012	2031	7400	7419	CTTTATTGAGTTCTTGCGCC	20	95
1131779	N/A	N/A	109	128	TCCTGGTTCCCACAGCACTC	71	655
1131807	N/A	N/A	193	212	CCTAGTCACCTGGACCCACA	56	656
1131835	N/A	N/A	289	308	CAGAAATGCAGGCTGTGCCC	71	657
1131863	N/A	N/A	386	405	TGCAGCTTCCTCTCACAGCC	120	658
1131891	N/A	N/A	513	532	CCGACTGTGTGCTCTTCAGC	21	659
1131919	N/A	N/A	618	637	ACCTAGCACCAGGTAGGCAC	39	660
1131947	N/A	N/A	724	743	CTCAAGCACCTGCTCCGAGC	54	661
1131975	N/A	N/A	874	893	GATCCTTCCTTGCCCATTGA	122	662
1132003	N/A	N/A	972	991	TGAAGCTTGAGAACTCAAA	76	663
1132031	N/A	N/A	1079	1098	AGCATTTCCATGCACCAGGT	70	664
1132059	N/A	N/A	1212	1231	GCCTGGCATGTAGGTAATTT	60	665
1132087	N/A	N/A	1590	1609	TGCTTAGAGACTCAACCCCA	67	666
1132115	N/A	N/A	1762	1781	AAGATGCAGATGGGATGGAC	79	667
1132143	N/A	N/A	2138	2157	AAAGTGCACCTTGCCAAGGAC	60	668
1132171	N/A	N/A	2268	2287	AATGAGAATTGCCTGTGTCT	41	669
1132199	N/A	N/A	2382	2401	CAGATTATATGCTGTTGGTT	49	670

1132227	N/A	N/A	2516	2535	AAGGCTACCTTAGGGAGAAA	48	671
1132255	N/A	N/A	2643	2662	GAATGAGTGTCTTCTCAGT	46	672
1132283	N/A	N/A	2751	2770	TTTTCATGGCCATTGTGTTGGG	60	673
1132311	N/A	N/A	2848	2867	AATAGTACAGTTGATCCTCA	46	674
1132339	N/A	N/A	2959	2978	GAAGAGCACTTGCCACAAAG	106	675
1132367	N/A	N/A	3060	3079	AAAAAAAACTTGGGTTCAGG	133	676
1132395	N/A	N/A	3451	3470	GCTCAGGCACTGTCCCTCAG	41	677
1132423	N/A	N/A	3652	3671	ACAGGCAGGGTACATGTCTC	45	678
1132451	N/A	N/A	3761	3780	GTAGCACACCTGTAGAAAGA	45	679
1132479	N/A	N/A	3919	3938	GTCCAGAATCCCAGGTGTGT	46	680
1132507	N/A	N/A	4030	4049	CTACTCCAAGTTTCCAAGCT	97	681
1132535	N/A	N/A	4137	4156	TTGCTGCAGTGGTCTGAGAG	36	682
1132563	N/A	N/A	4328	4347	TGCCAAGTCTCCGAGTATCC	56	683
1132591	N/A	N/A	4563	4582	CTCCTGCCAGCCTGTCTTCC	70	684
1132619	N/A	N/A	4763	4782	CAGACCCTCACTCACCACG	67	685
1132647	N/A	N/A	4878	4897	GCTCCCTGGGCAGCCAAGGC	37	686
1132675	N/A	N/A	5398	5417	CCTCTCGGCTCCTCCTTCCC	78	687
1132703	N/A	N/A	5766	5785	TGGAAGCTGCGCTGGGAGAC	122	688
1132731	N/A	N/A	6173	6192	AGGCGCAACAGAGCTAACCC	32	689
1132759	N/A	N/A	6388	6407	GATACCAAAGTCGCGGGCTT	100	690
1132787	N/A	N/A	6512	6531	GTATCCCCAGGAGATTTGGG	66	691
1132815	N/A	N/A	6636	6655	CCCACCACCCATCCAGAGTC	56	692
1132843	N/A	N/A	6727	6746	GGTGCCATTAATTCAATTTC	109	693
1132871	N/A	N/A	6868	6887	CCTCCGCCCTGCGAACACA	55	694

Table 13. Reduction of FXII RNA by 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages
(Huh7, electroporation, 5000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1130743	3	22	3	22	ATCCAGGAGTCCAGATCAAT	48	695
1130771	38	57	38	57	GCCCTCATGGCATCCGTCCG	57	696
1130799	85	104	85	104	AAAGTGTTGACTCCAAGCTC	53	697
1130827	144	163	511	530	GACTGTGTGCTCTTCAGCTT	32	698
1130855	197	216	3548	3567	TGCCGGTGGTACTGGAAGGG	53	699
1130871	216	235	3567	3586	GGTACATTTGTGGTACAGCT	13	183
1130884	233	252	3584	3603	CCTGGCCGGCCCTTGTGGGT	50	700
1130912	298	317	3805	3824	CCAAACAGTATCCCCATCGC	25	701
1130940	357	376	4165	4184	GGTCCCTCCTTTCTGGCAGG	76	702
1130968	411	430	4219	4238	TCCAGTGAGGTGTTGTGGAC	42	703
1130996	456	475	4401	4420	CCGGAAGAAGCTGAGGCTCAA	22	704
1131024	499	518	4444	4463	CTGCTTGCTCAGTTCTATAC	14	705
1131052	539	558	4484	4503	CAGTGGGCATCAGGACCCTT	46	706

1131080	574	593	N/A	N/A	GGTTGGTGCGGCAGGCCTGG	22	707
1131108	615	634	4699	4718	GTGGCCCTCCACCTCTAGGC	62	708
1131136	660	679	4744	4763	GTCGCAGAAGGCTCCGGTGT	64	709
1131164	716	735	4945	4964	GCCAGGCCGCGGTAGCTGAG	46	710
1131192	772	791	5001	5020	GGTAGGTGGCCTCCGAGGCC	52	711
1131220	865	884	5179	5198	CGAAGCACCACGGGCGGATG	95	712
1131248	909	928	5223	5242	TGCCAGGTTCGAGTACTCCC	29	713
1131276	1000	1019	5314	5333	TCGGCGGTGCCGGCTGCGCG	39	714
1131304	1078	1097	5497	5516	AAGGCGGCTGCTCCCGCTTC	78	715
1131332	1124	1143	5543	5562	TTGCGGAGCCGCTGCCCCGCA	65	716
1131360	1161	1180	5580	5599	CAGCCCGCCAACGACGCGGG	62	717
1131388	1232	1251	5651	5670	AGGCTGCCGGCGCAGAACT	34	718
1131416	1317	1336	5977	5996	CTGGCCGAGCACCACCGTCA	13	719
1131444	1405	1424	6065	6084	GGTAGCTGACGGGCGAGAAG	48	720
1131472	1467	1486	6210	6229	CGACAGGAGCGCGCAGCTGC	59	721
1131500	1554	1573	6297	6316	CTGGTGGCCCCAGCCGGCCA	53	722
1131528	1586	1605	6884	6903	AGGAAGCTGGCATATTCCTC	47	723
1131556	1679	1698	6977	6996	CCTGCGCAGAGCATGCCGGG	71 [†]	725
1131584	1752	1771	7140	7159	TGCAGCTTGGTCCTCACACA	17 [†]	724
1131612	1799	1818	7187	7206	CAGCCCGATCCCCAGCTGAT	80	725
1131640	1846	1865	7234	7253	GGTAGTAGGCCACATCGGTG	19	726
1131668	1878	1897	7266	7285	TCAGGAAACGGTGTGCTCCC	46	727
1131696	1922	1941	7310	7329	TCACTGCGGAATCACC AAGG	21	728
1131724	1958	1977	7346	7365	GGACACAATCTTGCCTTCCA	7	729
1131752	2013	2032	7401	7420	ACTTTATTGAGTTCCTGCGC	11	722
1131780	N/A	N/A	112	131	CAATCCTGGTTCCACAGCA	64	730
1131808	N/A	N/A	196	215	CCTCCTAGTCACCTGGACCC	60	731
1131836	N/A	N/A	292	311	CCCCAGAAATGCAGGCTGTG	114	732
1131864	N/A	N/A	389	408	GTCTGCAGCTTCCTCTCACA	56	733
1131892	N/A	N/A	516	535	TTACCGACTGTGTGCTCTTC	18	734
1131920	N/A	N/A	621	640	AAGACCTAGCACCAGGTAGG	58	735
1131948	N/A	N/A	727	746	TATCTCAAGCACCTGCTCCG	25	736
1131976	N/A	N/A	877	896	CTTGATCCTTCCTTGCCCAT	58	737
1132004	N/A	N/A	975	994	AATTGAAGCTTGGAGAACTC	99	738
1132032	N/A	N/A	1082	1101	TAAAGCATTTCATGCACCA	93	739
1132060	N/A	N/A	1215	1234	CATGCCTGGCATGTAGGTAA	53	740
1132088	N/A	N/A	1593	1612	CCATGCTTAGAGACTCAACC	82	741
1132116	N/A	N/A	1765	1784	AAAAAGATGCAGATGGGATG	86	742
1132144	N/A	N/A	2141	2160	GGCAAAGTGCACCTTGCCAAG	85	743
1132172	N/A	N/A	2271	2290	AATAATGAGAATTGCCTGTG	117	744
1132200	N/A	N/A	2385	2404	AACCAGATTATATGCTGTTG	41	745
1132228	N/A	N/A	2519	2538	AAGAAGGCTACCTTAGGGAG	40	746
1132256	N/A	N/A	2646	2665	ATTGAATGAGTGTCTTCTC	50	747
1132284	N/A	N/A	2754	2773	ATGTTTTTCATGGCCATTTGT	45	748
1132312	N/A	N/A	2851	2870	AATAATAGTACAGTTGATCC	62	749

1132340	N/A	N/A	2962	2981	CAGGAAGAGCACTTGCCACA	52	750
1132368	N/A	N/A	3370	3389	CTCTAAAAGTTGGGTTCAGG	51	751
1132396	N/A	N/A	3457	3476	TCAACTGCTCAGGCACTGTC	53	752
1132424	N/A	N/A	3655	3674	AGGACAGGCAGGGTACATGT	51	753
1132452	N/A	N/A	3764	3783	GTGGTAGCACACCTGTAGAA	28	754
1132480	N/A	N/A	3922	3941	TGGGTCCAGAATCCCAGGTG	59	755
1132508	N/A	N/A	4033	4052	TTGCTACTCCAAGTTTCCAA	50	756
1132536	N/A	N/A	4140	4159	TGTTTGCTGCAGTGGTCTGA	21	757
1132564	N/A	N/A	4334	4353	GGACCATGCCAAGTCTCCGA	41	758
1132592	N/A	N/A	4566	4585	GGCCTCCTGCCAGCCTGTCT	49	759
1132620	N/A	N/A	4766	4785	CCCCAGACCCTCACTACCC	90	760
1132648	N/A	N/A	4899	4918	TGGTGTCTGAGGAGAAAGGG	71	761
1132676	N/A	N/A	5401	5420	CGCCCTCTCGGCTCCTCCTT	44	762
1132704	N/A	N/A	5841	5860	CTCCCCGGGAGCTCCGAGAGG	123	763
1132732	N/A	N/A	6176	6195	TGAAGGCGCAACAGAGCTAA	21	764
1132760	N/A	N/A	6394	6413	CGGAACGATACCAAAGTCGC	85	765
1132788	N/A	N/A	6515	6534	CCTGTATCCCCAGGAGATTT	21	766
1132816	N/A	N/A	6639	6658	TCCCCACCACCCATCCAGA	87	767
1132844	N/A	N/A	6730	6749	GGAGGTGCCATTAATTCAAT	46	768
1132872	N/A	N/A	6871	6890	ATTCTCCGCCCTGCGAAC	150	769

Table 14. Reduction of FXII RNA by 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages (Huh7, electroporation, 5000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1130800	89	108	N/A	N/A	ATCGAAAGTGTTGACTCCAA	28	770
1130828	145	164	512	531	CGACTGTGTGCTCTTCAGCT	14	771
1130856	199	218	3550	3569	GCTGCCGGTGGTACTGGAAG	22	772
1130871	216	235	3567	3586	GGTACATTTGTGGTACAGCT	21	773
1130885	234	253	3585	3604	GCCTGGCCGGCCCTTGTGGG	51	773
1130913	304	323	3811	3830	TGGGCTCCAAACAGTATCCC	22	774
1130941	359	378	4167	4186	CAGGTCCCTCCTTTCTGGCA	46	775
1130969	413	432	4221	4240	TTTCCAGTGAGGTGTTGTGG	25	776
1130997	457	476	4402	4421	ACCGGAGAAGCTGAGGCTCA	19	777
1131025	500	519	4445	4464	GCTGCTTGCTCAGTTCTATA	19	778
1131053	540	559	4485	4504	GCAGTGGGCATCAGGACCCT	22	779
1131081	576	595	N/A	N/A	CGGGTTGGTGCAGCAGGCCT	65	780
1131109	616	635	4700	4719	GGTGGCCCTCCACCTCTAGG	38	781
1131137	661	680	4745	4764	CGTCGCAGAAGGCTCCGGTG	94	782
1131165	717	736	4946	4965	GGCCAGGCCGCGGTAGCTGA	35	783
1131193	773	792	5002	5021	CGGTAGGTGGCCTCCGAGGC	30	784
1131221	867	886	5181	5200	CACGAAGCACCACGGGCGGA	38	785

1131249	911	930	5225	5244	TGTGCCAGGTCGCAGTACTC	24	786
1131277	1001	1020	5315	5334	TTCGGCGGTGCCGGCTGCGC	25	787
1131305	1079	1098	5498	5517	GAAGGCGGCTGCTCCCCGTT	39	788
1131333	1126	1145	5545	5564	TCTTGCGGAGCCGCTGCCCG	34	789
1131361	1162	1181	5581	5600	CCAGCCCGCCAACGACGCGG	31	790
1131389	1233	1252	5652	5671	GAGGCTGCCGGCGCAGAAAC	39	791
1131417	1318	1337	5978	5997	CCTGGCCGAGCACCACCGTC	26	792
1131445	1408	1427	6068	6087	GCTGGTAGCTGACGGGCGAG	26	793
1131473	1468	1487	6211	6230	GCGACAGGAGCGCGCAGCTG	21	794
1131501	1555	1574	6298	6317	ACTGGTGGCCCCAGCCGGCC	51	795
1131529	1587	1606	6885	6904	CAGGAAGCTGGCATATTCTT	82	796
1131557	1680	1699	6978	6997	CCCTGCGCAGAGCATGCCGG	28 [†]	797
1131585	1753	1772	7141	7160	CTGCAGCTTGGTCCTCACAC	6 [†]	798
1131613	1800	1819	7188	7207	ACAGCCCGATCCCCAGCTGA	39	799
1131641	1847	1866	7235	7254	AGGTAGTAGGCCACATCGGT	19	800
1131669	1879	1898	7267	7286	ATCAGGAAACGGTGTGCTCC	24	801
1131697	1923	1942	7311	7330	CTCACTGCGGAATCACCAAG	8	802
1131725	1960	1979	7348	7367	TGGGACACAATCTTGCCTTC	12	803
1131753	2014	2033	7402	7421	CACCTTTATTGAGTTCCTGCG	15	163
1131781	N/A	N/A	115	134	GGACAATCCTGGTTCCCA	71	804
1131809	N/A	N/A	199	218	AGGCCTCCTAGTCACCTGGA	58	805
1131837	N/A	N/A	302	321	GGCCCATCTCCCCAGAAAT	50	806
1131865	N/A	N/A	392	411	CTAGTCTGCAGCTTCCTCTC	48	807
1131893	N/A	N/A	519	538	CACCTACCGACTGTGTGCTC	24	808
1131921	N/A	N/A	627	646	GGGCATAAGACCTAGCACCA	46	809
1131949	N/A	N/A	730	749	ACATATCTCAAGCACCTGCT	63	810
1131977	N/A	N/A	880	899	GCTCTTGATCCTTCCTTGCC	54	811
1132005	N/A	N/A	997	1016	AACCTGGTTTCACAGAAGGG	54	812
1132033	N/A	N/A	1085	1104	TTGTAAAGCATTTCCATGCA	37	813
1132061	N/A	N/A	1512	1531	ACTCTAGGTAAATTTTTTTT	86	814
1132089	N/A	N/A	1612	1631	AATGTGCTGGGCCCTCAACGC	49	815
1132117	N/A	N/A	1908	1927	AAGTTGTGTGCCTGTAATCC	50	816
1132145	N/A	N/A	2144	2163	CAAGGCAAAGTGCATTGCC	39	817
1132173	N/A	N/A	2274	2293	GCGAATAATGAGAATTGCCT	38	818
1132201	N/A	N/A	2388	2407	TAAAACCAGATTATATGCTG	67	819
1132229	N/A	N/A	2522	2541	CACAAGAAGGCTACCTTAGG	55	820
1132257	N/A	N/A	2649	2668	CCTATTGAATGAGTGTCTT	48	821
1132285	N/A	N/A	2760	2779	CTTGAAATGTTTTTCATGGCC	59	822
1132313	N/A	N/A	2854	2873	AGTAATAATAGTACAGTTGA	59	823
1132341	N/A	N/A	2965	2984	GGCCAGGAAGAGCACTTGCC	59	824
1132369	N/A	N/A	3373	3392	CTGCTCTAAAAGTTGGGTTC	40	825
1132397	N/A	N/A	3460	3479	TACTCAACTGCTCAGGCACT	34	826
1132425	N/A	N/A	3658	3677	AGAAGGACAGGCAGGGTACA	67	827
1132453	N/A	N/A	3824	3843	CCTTTCACCTTCTTGGGCTC	16	828
1132481	N/A	N/A	3925	3944	GGCTGGGTCCAGAATCCCAG	40	829

1132509	N/A	N/A	4036	4055	ACCTTGCTACTCCAAGTTTC	36	830
1132537	N/A	N/A	4236	4255	CCTTTCTGGCAGTGGTTTCC	20	831
1132565	N/A	N/A	4337	4356	CTAGGACCATGCCAAGTCTC	89	832
1132593	N/A	N/A	4569	4588	CCCGGCCTCCTGCCAGCCTG	40	833
1132621	N/A	N/A	4769	4788	TTGCCCCAGACCCTCACTCA	47	834
1132649	N/A	N/A	4902	4921	CCTTGGTGTCTGAGGAGAAA	59	835
1132677	N/A	N/A	5418	5437	GAATCTAGCTCGCCCGGCGC	58	836
1132705	N/A	N/A	5844	5863	TTCTCCCCGGGAGCTCCGG	65	837
1132733	N/A	N/A	6306	6325	ACCTCGAACTGGTGGCCCC	59	838
1132761	N/A	N/A	6397	6416	ACCCGGAACGATACCAAAGT	61	839
1132789	N/A	N/A	6518	6537	CTCCCTGTATCCCCAGGAGA	77	840
1132817	N/A	N/A	6643	6662	CCCCTCCCCACCACCCATC	46	841
1132845	N/A	N/A	6733	6752	GGAGGAGGTGCCATTAATTC	61	842
1132873	N/A	N/A	6874	6893	CATATTCCTCCGCCCTGCG	90	843

Table 15. Reduction of FXII RNA by 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages
(Huh7, electroporation, 5000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1130745	5	24	5	24	CTATCCAGGAGTCCAGATCA	58	844
1130773	42	61	42	61	CAGAGCCCTCATGGCATCCG	33	845
1130801	90	109	N/A	N/A	AATCGAAAGTGTGACTCCA	33	846
1130829	146	165	N/A	N/A	ACGACTGTGTGCTCTTCAGC	20	846
1130857	200	219	3551	3570	AGCTGCCGGTGGTACTGGAA	43	847
1130871	216	235	3567	3586	GGTACATTTGTGGTACAGCT	18	848
1130886	235	254	3586	3605	GGCCTGGCCGGCCCTTGTGG	49	848
1130914	305	324	3812	3831	TTGGGCTCCAAACAGTATCC	20	849
1130942	361	380	4169	4188	CACAGGTCCCTCCTTTCTGG	62	850
1130970	417	436	4225	4244	GTGGTTTCCAGTGAGGTGTT	19	851
1130998	459	478	4404	4423	AAACCGGAGAAGCTGAGGCT	21	852
1131026	501	520	4446	4465	AGCTGCTTGCTCAGTTCTAT	41	853
1131054	542	561	4487	4506	TGGCAGTGGGCATCAGGACC	60	854
1131082	577	596	N/A	N/A	ACGGGTGGTGCAGGAGGCC	31	855
1131110	617	636	4701	4720	CGGTGGCCCTCCACCTCTAG	44	856
1131138	679	698	N/A	N/A	AGCTTGCCCTTGGTGTCCACG	38	857
1131166	719	738	4948	4967	CTGGCCAGGCCGCGGTAGCT	92	858
1131194	774	793	5003	5022	CCGGTAGGTGGCCTCCGAGG	44	859
1131222	868	887	5182	5201	GCACGAAGCACCACGGGCGG	30	860
1131250	912	931	5226	5245	CTGTGCCAGGTCGAGTACT	38	861
1131278	1003	1022	5317	5336	GCTTCGGCGGTGCCGGCTGC	33	862
1131306	1080	1099	5499	5518	GGAAGGCGGCTGCTCCCGCT	36	863

1131334	1127	1146	5546	5565	CTCTTGCGGAGCCGCTGCCC	46	864
1131362	1164	1183	5583	5602	CACCAGCCCGCCAACGACGC	24	865
1131390	1234	1253	5653	5672	TGAGGCTGCCGGCGCAGAAA	40	866
1131418	1319	1338	5979	5998	TCCTGGCCGAGCACCACCGT	34	867
1131446	1410	1429	6070	6089	GTGCTGGTAGCTGACGGGCG	26	868
1131474	1470	1489	6213	6232	AGGCGACAGGAGCGCGCAGC	21	869
1131502	1556	1575	6299	6318	AACTGGTGGCCCCAGCCGGC	47	870
1131530	1588	1607	6886	6905	GCAGGAAGCTGGCATATTCC	58	871
1131558	1681	1700	6979	6998	ACCCTGCGCAGAGCATGCCG	20 [†]	872
1131586	1755	1774	7143	7162	CTCTGCAGCTTGGTCCTCAC	14 [†]	873
1131614	1801	1820	7189	7208	CACAGCCCGATCCCCAGCTG	38	874
1131642	1848	1867	7236	7255	CAGGTAGTAGGCCACATCGG	35	875
1131670	1881	1900	7269	7288	CAATCAGGAAACGGTGTGCT	47	876
1131698	1924	1943	7312	7331	TCTCACTGCGGAATCACCAA	6	877
1131726	1961	1980	7349	7368	ATGGGACACAATCTTGCCTT	34	878
1131754	2015	2034	7403	7422	GCACTTTATTGAGTTCTGCTC	4	164
1131782	N/A	N/A	118	137	CTGGGACAATCCTGGTTCCC	56	879
1131810	N/A	N/A	202	221	CATAGGCCTCCTAGTCACCT	94	880
1131838	N/A	N/A	305	324	TAAGGCCCATCTCCCCCAGA	41	881
1131866	N/A	N/A	395	414	TTGCTAGTCTGCAGCTTCCT	60	882
1131894	N/A	N/A	523	542	AGGCCACTTACCGACTGTGT	109	883
1131922	N/A	N/A	630	649	CATGGGCATAAGACCTAGCA	65	884
1131950	N/A	N/A	733	752	AGCACATATCTCAAGCACCT	85	885
1131978	N/A	N/A	886	905	AGACAAGCTCTTGATCCTTC	79	886
1132006	N/A	N/A	1000	1019	ATCAACCTGGTTTCACAGAA	48	887
1132034	N/A	N/A	1088	1107	TATTTGTAAAGCATTTCCAT	67	888
1132062	N/A	N/A	1515	1534	CACACTCTAGGTAAATTTTT	59	889
1132090	N/A	N/A	1615	1634	TGGAATGTGCTGGGCCTCAA	59	890
1132118	N/A	N/A	1911	1930	ATGAAGTTGTGTGCCTGTAA	61	891
1132146	N/A	N/A	2147	2166	GTTCAAGGCAAAGTGCACTT	56	892
1132174	N/A	N/A	2277	2296	ATCGCGAATAATGAGAATTG	68	893
1132202	N/A	N/A	2391	2410	ACATAAAACCAGATTATATG	52	894
1132230	N/A	N/A	2525	2544	AAGCACAGAAGGCTACCTT	33	895
1132258	N/A	N/A	2652	2671	TCTCCTATTGAATGAGTGTC	36	896
1132286	N/A	N/A	2765	2784	CAATACTTGAAATGTTTTCA	47	897
1132314	N/A	N/A	2857	2876	GGCAGTAATAATAGTACAGT	38	898
1132342	N/A	N/A	2968	2987	CAAGGCCAGGAAGAGCACTT	76	899
1132370	N/A	N/A	3376	3395	TTTCTGCTCTAAAAGTTGGG	35	900
1132398	N/A	N/A	3463	3482	CTGTACTCAACTGCTCAGGC	60	901
1132426	N/A	N/A	3661	3680	GACAGAAGGACAGGCAGGGT	52	902
1132454	N/A	N/A	3827	3846	GCACCTTTCACTTTCTTGGG	24	903
1132482	N/A	N/A	3945	3964	TATTGTGGAGGGAGAGAAGG	83	904
1132510	N/A	N/A	4039	4058	GTGACCTTGCTACTCCAAGT	74	905
1132538	N/A	N/A	4239	4258	TCACCTTTCTGGCAGTGGTT	44	906
1132566	N/A	N/A	4340	4359	AGTCTAGGACCATGCCAAGT	34	907

1132594	N/A	N/A	4572	4591	CCACCCGGCCTCCTGCCAGC	75	908
1132622	N/A	N/A	4772	4791	TGCTTGCCCCAGACCCTCAC	54	909
1132650	N/A	N/A	4905	4924	TTGCCTTGGTGTCTGAGGAG	44	910
1132678	N/A	N/A	5421	5440	CCGGAATCTAGCTCGCCCGG	50	911
1132706	N/A	N/A	5847	5866	AGCTTCCTCCCCGGGAGCTC	64	912
1132734	N/A	N/A	6309	6328	CCTACCCTCGAACTGGTGGC	61	913
1132762	N/A	N/A	6400	6419	GGCACCCGGAACGATACCAA	63	914
1132790	N/A	N/A	6521	6540	ATTCTCCCTGTATCCCCAGG	58	915
1132818	N/A	N/A	6646	6665	AAACCCCTCCCCCACCACCC	41	916
1132846	N/A	N/A	6752	6771	CTCGCAGCAAGCCCGAAGGG	38	917
1132874	N/A	N/A	6877	6896	TGGCATATTCCTCCGCCCT	49	918

Table 16. Reduction of FXII RNA by 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages
(Huh7, electroporation, 5000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1130746	7	26	7	26	GCCTATCCAGGAGTCCAGAT	29	919
1130774	46	65	46	65	GCAGCAGAGCCCTCATGGCA	22	920
1130802	91	110	N/A	N/A	GAATCGAAAGTGTTGACTCC	40	921
1130830	147	166	N/A	N/A	AACGACTGTGTGCTCTTCAG	9	922
1130858	201	220	3552	3571	CAGCTGCCGGTGGTACTGGA	22	923
1130871	216	235	3567	3586	GGTACATTTGTGGTACAGCT	22	923
1130887	236	255	3587	3606	GGGCCTGGCCGGCCCTTGTG	41	924
1130915	306	325	3813	3832	CTTGGGCTCCAAACAGTATC	26	925
1130943	362	381	4170	4189	ACACAGGTCCCTCCTTTCTG	32	926
1130971	419	438	4227	4246	CAGTGGTTTCCAGTGAGGTG	38	927
1130999	460	479	4405	4424	AAAACCGGAGAAGCTGAGGC	26	928
1131027	502	521	4447	4466	CAGCTGCTTGCTCAGTTCTA	35	929
1131055	543	562	4488	4507	CTGGCAGTGGGCATCAGGAC	33	930
1131083	579	598	4663	4682	GCACGGGTTGGTGCGGCAGG	29	931
1131111	618	637	4702	4721	GCGGTGGCCCTCCACCTCTA	54	932
1131139	680	699	N/A	N/A	CAGCTTGCTTGGTGTCCAC	30	933
1131167	720	739	4949	4968	CCTGGCCAGGCCGCGGTAGC	80	934
1131195	775	794	5004	5023	TCCGGTAGGTGGCCTCCGAG	33	935
1131223	869	888	5183	5202	AGCACGAAGCACACGGGCG	17	936
1131251	913	932	5227	5246	ACTGTGCCAGGTTCGAGTAC	26	937
1131279	1004	1023	5318	5337	GGCTTCGGCGGTGCCGGCTG	24	938
1131307	1081	1100	5500	5519	GGGAAGGCGGCTGCTCCCGC	40	939
1131335	1128	1147	5547	5566	ACTCTTGCGGAGCCGCTGCC	43	940
1131363	1165	1184	5584	5603	CCACCAGCCCGCCAACGACG	59	940
1131391	1235	1254	5654	5673	ATGAGGCTGCCGGCGCAGAA	49	941

1131419	1320	1339	5980	5999	TTCCTGGCCGAGCACCACCG	24	942
1131447	1411	1430	6071	6090	CGTGCTGGTAGCTGACGGGC	25	943
1131475	1471	1490	6214	6233	AAGGCGACAGGAGCGCGCAG	28	944
1131503	1557	1576	6300	6319	GAACTGGTGGCCCCAGCCGG	65	945
1131531	1592	1611	6890	6909	TCCTGCAGGAAGCTGGCATA	88	946
1131559	1683	1702	6981	7000	GAACCCTGCGCAGAGCATGC	56 [†]	947
1131587	1757	1776	7145	7164	CGCTCTGCAGCTTGGTCCTC	19 [†]	948
1131615	1802	1821	7190	7209	CCACAGCCCCGATCCCCAGCT	40	949
1131643	1849	1868	7237	7256	CCAGGTAGTAGGCCACATCG	44	88
1131671	1882	1901	7270	7289	GCAATCAGGAAACGGTGTGC	12	950
1131699	1926	1945	7314	7333	TCTCTCACTGCGGAATCACC	7	951
1131727	1962	1981	7350	7369	AATGGGACACAATCTTGCTC	25	952
1131755	2016	2035	7404	7423	AGCACTTTATTGAGTTCCTG	3	953
1131783	N/A	N/A	121	140	ATCCTGGGACAATCCTGGTT	41	954
1131811	N/A	N/A	205	224	CCACATAGGCCTCCTAGTCA	48	955
1131839	N/A	N/A	308	327	TCTTAAGGCCCATCTCCCCC	46	956
1131867	N/A	N/A	398	417	CTGTTGCTAGTCTGCAGCTT	85	957
1131895	N/A	N/A	526	545	GCCAGGCCACTTACCGACTG	40	958
1131923	N/A	N/A	633	652	GCCCCATGGGCATAAGACCTA	37	959
1131951	N/A	N/A	736	755	AGCAGCACATATCTCAAGCA	68	960
1131979	N/A	N/A	889	908	CAGAGACAAGCTCTTGATCC	44	961
1132007	N/A	N/A	1003	1022	GTTATCAACCTGGTTTCACA	27	962
1132035	N/A	N/A	1097	1116	AAAAGCTAATATTTGTAAAG	42	963
1132063	N/A	N/A	1518	1537	TGCCCACTCTAGGTAAATT	43	964
1132091	N/A	N/A	1618	1637	GGTTGGAATGTGCTGGGCCT	48	965
1132119	N/A	N/A	1914	1933	AGCATGAAGTTGTGTGCCTG	79	966
1132147	N/A	N/A	2150	2169	TTTGTTC AAGGCAAAGTGCA	34	967
1132175	N/A	N/A	2280	2299	ACCATCGCGAATAATGAGAA	32	968
1132203	N/A	N/A	2394	2413	CATACATAAAACCAGATTAT	67	969
1132231	N/A	N/A	2533	2552	TAGTTCCCTAAGCACAAGAAG	98	970
1132259	N/A	N/A	2655	2674	AGCTCTCCTATTGAATGAGT	36	971
1132287	N/A	N/A	2768	2787	AGTCAATACTTGAAATGTTT	84	972
1132315	N/A	N/A	2860	2879	AACGGCAGTAATAATAGTAC	55	973
1132343	N/A	N/A	2971	2990	TCCCAAGGCCAGGAAGAGCA	32	974
1132371	N/A	N/A	3379	3398	CACTTTCTGCTCTAAAAGTT	28	975
1132399	N/A	N/A	3466	3485	CCCCTGTACTCAACTGCTCA	42	976
1132427	N/A	N/A	3664	3683	TTGGACAGAAGGACAGGCAG	58	977
1132455	N/A	N/A	3830	3849	GTAGCACCTTTCACTTTCTT	16	978
1132483	N/A	N/A	3954	3973	TCCAAAGGGTATTGTGGAGG	38	979
1132511	N/A	N/A	4042	4061	CTTGTGACCTTGCTACTCCA	28	980
1132539	N/A	N/A	4242	4261	TCCTCACCTTTCTGGCAGTG	27	981
1132567	N/A	N/A	4343	4362	GAGAGTCTAGGACCATGCCA	80	982
1132595	N/A	N/A	4575	4594	ACACCACCCGGCCTCCTGCC	58	983
1132623	N/A	N/A	4775	4794	TTCTGCTTGCCCCAGACCCT	70	984
1132651	N/A	N/A	4908	4927	AGCTTGCCTTGGTGTCTGAG	19	985

1132679	N/A	N/A	5424	5443	TGGCCGGAATCTAGCTCGCC	61	986
1132707	N/A	N/A	5850	5869	TCCAGCTTCCTCCCCGGGAG	51	987
1132735	N/A	N/A	6312	6331	GTGCCTACCCTCGAACTGGT	45	988
1132763	N/A	N/A	6403	6422	GTAGGCACCCGGAACGATAC	27	989
1132791	N/A	N/A	6524	6543	TCGATTCTCCTGTATCCCC	69	990
1132819	N/A	N/A	6649	6668	CAGAAACCCCTCCCCACCA	50	991
1132847	N/A	N/A	6755	6774	TCTCTCGCAGCAAGCCCGAA	48	992
1132875	N/A	N/A	7010	7029	ACCTGGCAGCATCGGTGCC	29 [†]	993

Table 17. Reduction of FXII RNA by 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages
(Huh7, electroporation, 5000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1130747	10	29	10	29	GCTGCCTATCCAGGAGTCCA	45	994
1130775	47	66	47	66	AGCAGCAGAGCCCTCATGGC	43	995
1130803	93	112	N/A	N/A	TGGAATCGAAAGTGTTGACT	25	996
1130831	148	167	N/A	N/A	GAACGACTGTGTGCTCTTCA	18	997
1130859	203	222	3554	3573	TACAGCTGCCGGTGGTACTG	28	998
1130871	216	235	3567	3586	GGTACATTTGTGGTACAGCT	8	183
1130888	238	257	3589	3608	GAGGGCCTGGCCGGCCCTTG	77	999
1130916	307	326	3814	3833	TCTTGGGCTCCAAACAGTAT	33	1000
1130944	363	382	4171	4190	CACACAGGTCCCTCCTTTCT	53	1001
1130972	420	439	4228	4247	GCAGTGGTTTCCAGTGAGGT	19	1002
1131000	461	480	4406	4425	AAAAACCGGAGAAGCTGAGG	25	1003
1131028	505	524	4450	4469	CCACAGCTGCTTGCTCAGTT	23	1004
1131056	545	564	4490	4509	CGCTGGCAGTGGGCATCAGG	24	1005
1131084	580	599	4664	4683	GGCACGGGTTGGTGCGGCAG	19	1006
1131112	619	638	4703	4722	GGCGGTGGCCCTCCACCTCT	36	1007
1131140	681	700	N/A	N/A	GCAGCTTGCTTGGTGTCCA	21	1008
1131168	721	740	4950	4969	TCCTGGCCAGGCCGCGGTAG	37	1009
1131196	777	796	5006	5025	GTTCCGGTAGGTGGCCTCCG	46	1010
1131224	870	889	5184	5203	CAGCACGAAGCACCACGGGC	35	1011
1131252	914	933	5228	5247	CACTGTGCCAGGTCGCAGTA	60	1012
1131280	1005	1024	5319	5338	AGGCTTCGGCGGTGCCGGCT	31	1013
1131308	1085	1104	5504	5523	GTCAGGGAAGGCGGCTGCTC	25	1014
1131336	1129	1148	5548	5567	GACTCTTGCGGAGCCGCTGC	40	1015
1131364	1167	1186	5586	5605	CGCCACCAGCCCGCCAACGA	43	1016
1131392	1237	1256	5656	5675	CGATGAGGCTGCCGGCGCAG	30	1017
1131420	1322	1341	5982	6001	CGTTCCTGGCCGAGCACCAC	34	1018
1131448	1430	1449	N/A	N/A	AGGCGCAACAGAGCCAGGTC	38	1019
1131476	1473	1492	6216	6235	GTAAGGCGACAGGAGCGCGC	37	1020
1131504	1558	1577	6301	6320	CGAACTGGTGGCCCCAGCCG	76	1021

1131532	1594	1613	6892	6911	CCTCCTGCAGGAAGCTGGCA	112	1022
1131560	1687	1706	6985	7004	CGAGGAACCCTGCGCAGAGC	6 [†]	1023
1131588	1758	1777	7146	7165	GCGCTCTGCAGCTTGGTCCT	16 [†]	1024
1131616	1803	1822	7191	7210	ACCACAGCCCGATCCCCAGC	39	1025
1131644	1850	1869	7238	7257	GCCAGGTAGTAGGCCACATC	34	1026
1131672	1883	1902	7271	7290	AGCAATCAGGAAACGGTGTG	24	1027
1131700	1927	1946	7315	7334	CTCTCTCACTGCGGAATCAC	7	1028
1131728	1963	1982	7351	7370	GAATGGGACACAATCTTGCC	21	1029
1131756	2017	2036	7405	7424	AAGCACTTTATTGAGTTCCT	5	1030
1131784	N/A	N/A	124	143	ACAATCCTGGGACAATCCTG	85	1031
1131812	N/A	N/A	208	227	TTTCCACATAGGCCTCCTAG	42	1032
1131840	N/A	N/A	311	330	TCTTCTTAAGGCCCATCTCC	79	1033
1131868	N/A	N/A	401	420	GATCTGTTGCTAGTCTGCAG	82	1034
1131896	N/A	N/A	529	548	GGAGCCAGGCCACTTACCGA	45	1035
1131924	N/A	N/A	636	655	AGTGCCCATGGGCATAAGAC	52	1036
1131952	N/A	N/A	739	758	GCCAGCAGCACATATCTCAA	55	1037
1131980	N/A	N/A	892	911	TGCCAGAGACAAGCTCTTGA	73	1038
1132008	N/A	N/A	1006	1025	ACTGTTATCAACCTGGTTTC	60	1039
1132036	N/A	N/A	1105	1124	TTCATAATAAAAGCTAATAT	68	1040
1132064	N/A	N/A	1521	1540	ATGTGCCCACTCTAGGTAA	51	1041
1132092	N/A	N/A	1622	1641	CCAGGGTTGGAATGTGCTGG	56	1042
1132120	N/A	N/A	1917	1936	CTGAGCATGAAGTTGTGTGC	44	1043
1132148	N/A	N/A	2166	2185	AAGCTTTTGCCACTATTTTG	36	1044
1132176	N/A	N/A	2283	2302	ATAACCATCGGAATAATGA	50	1045
1132204	N/A	N/A	2397	2416	AATCATACATAAAACCAGAT	75	1046
1132232	N/A	N/A	2536	2555	GTGTAGTTCCTAAGCACAAG	37	1047
1132260	N/A	N/A	2658	2677	TTCAGCTCTCCTATTGAATG	37	1048
1132288	N/A	N/A	2771	2790	CCAAGTCAATACTTGAAATG	42	1049
1132316	N/A	N/A	2863	2882	TAAAACGGCAGTAATAATAG	62	1050
1132344	N/A	N/A	2974	2993	CAGTCCCAAGGCCAGGAAGA	38	1051
1132372	N/A	N/A	3382	3401	AAACACTTTCTGCTCTAAAA	67	1052
1132400	N/A	N/A	3469	3488	CTTCCCCTGTACTCAACTGC	43	1053
1132428	N/A	N/A	3667	3686	TCCTTGGACAGAAGGACAGG	75	1054
1132456	N/A	N/A	3833	3852	TGTGTAGCACCTTTCACCTT	41	1055
1132484	N/A	N/A	3957	3976	ACTTCCAAAGGGTATTGTGG	56	1056
1132512	N/A	N/A	4045	4064	TGCCTTGTGACCTTGCTACT	34	1057
1132540	N/A	N/A	4245	4264	ATCTCCTCACCTTTCTGGCA	82	1058
1132568	N/A	N/A	4346	4365	CAGGAGAGTCTAGGACCATG	78	1059
1132596	N/A	N/A	4578	4597	GGCACACCACCCGGCCTCCT	48	1060
1132624	N/A	N/A	4778	4797	GCCTTCTGCTTGCCCCAGAC	48	1061
1132652	N/A	N/A	4911	4930	AGCAGCTTGCTTGGTGTCT	25	1062
1132680	N/A	N/A	5427	5446	GGCTGGCCGGAATCTAGCTC	69	1063
1132708	N/A	N/A	5853	5872	TGTTCCAGCTTCCTCCCCGG	37	1064
1132736	N/A	N/A	6315	6334	GTTGTGCCTACCCTCGAACT	85	1065
1132764	N/A	N/A	6406	6425	TCTGTAGGCACCCGGAACGA	58	1066

1132792	N/A	N/A	6527	6546	AGTTCGATTCTCCCTGTATC	54	1067
1132820	N/A	N/A	6652	6671	AAACAGAAACCCCTCCCCCA	73	1068
1132848	N/A	N/A	6758	6777	TCCTCTCTCGCAGCAAGCCC	57	1069
1132876	N/A	N/A	7013	7032	CTCACCTGGCACGCATCGGT	64 [†]	1070

Table 18. Reduction of FXII RNA by 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages
(Huh7, electroporation, 5000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1130749	12	31	12	31	CAGCTGCCTATCCAGGAGTC	57	1071
1130777	49	68	49	68	GGAGCAGCAGAGCCCTCATG	40	1072
1130805	96	115	N/A	N/A	AGGTGGAATCGAAAGTGTG	34	1073
1130833	151	170	N/A	N/A	TGAGAACGACTGTGTGCTCT	27	1074
1130861	205	224	3556	3575	GGTACAGCTGCCGGTGGTAC	31	1075
1130871	216	235	3567	3586	GGTACATTTGTGGTACAGCT	10	1076
1130890	240	259	3591	3610	CTGAGGGCCTGGCCGGCCCT	40	1077
1130918	310	329	3817	3836	CTTCTTGGGCTCCAAACAG	36	1078
1130946	366	385	4174	4193	GTTACACAGGTCCTCCTT	48	1079
1130974	423	442	4231	4250	CTGGCAGTGGTTTCCAGTGA	28	1080
1131002	464	483	4409	4428	TGGAAAAACCGGAGAAGCTG	22	1081
1131030	508	527	4453	4472	TGGCCACAGCTGCTTGCTCA	48	1082
1131058	547	566	4492	4511	GCCGCTGGCAGTGGGCATCA	42	1083
1131086	583	602	4667	4686	GGAGGCACGGGTGGTGCGG	27	1084
1131114	622	641	4706	4725	ACAGGCGGTGGCCCTCCACC	58	1085
1131142	685	704	4914	4933	CATAGCAGCTTGCCTTGGTG	22	1086
1131170	724	743	4953	4972	TGGTCCTGGCCAGGCCGCGG	77	1087
1131198	796	815	5025	5044	GCGCTTGCTCGGCAGTCACG	18	1088
1131226	873	892	5187	5206	GTTACAGCACGAAGCACCACG	21	1089
1131254	916	935	5230	5249	GGCACTGTGCCAGGTCGCAG	39	1090
1131282	1007	1026	5321	5340	TGAGGCTTCGGCGGTGCCGG	43	1091
1131310	1089	1108	5508	5527	CCTGGTCAGGGAAGGCGGCT	27	1092
1131338	1131	1150	5550	5569	CAGACTCTTGCGGAGCCGCT	22	1093
1131366	1203	1222	5622	5641	GTACAGCGCGCGATGTAGG	41	114
1131394	1239	1258	5658	5677	GGCGATGAGGCTGCCGGCGC	31	1094
1131422	1341	1360	6001	6020	CTCACAGCTGTGGTTACGGC	23	1095
1131450	1433	1452	N/A	N/A	TGAAGGCGCAACAGAGCCAG	46	72
1131478	1492	1511	6235	6254	GCAGGCACACCGGCTGAACG	36	1096
1131506	1560	1579	6303	6322	CTCGAACTGGTGGCCCCAGC	53	1097
1131534	1597	1616	6895	6914	GCGCCTCCTGCAGGAAGCTG	92	1098
1131562	1690	1709	6988	7007	CCTCGAGGAACCTGCGCAG	27 [†]	1099
1131590	1776	1795	7164	7183	GCCTTGCAGGGTGAGCCGGC	43	1100
1131618	1805	1824	7193	7212	TCACCACAGCCCGATCCCCA	40	

1131646	1852	1871	7240	7259	AGGCCAGGTAGTAGGCCACA	63	1101
1131674	1888	1907	7276	7295	CCCTGAGCAATCAGGAAACG	35	1102
1131702	1930	1949	7318	7337	CCACTCTCTCACTGCGGAAT	9	1103
1131730	1984	2003	7372	7391	GCGGAGCTGGCCGCACTGGG	18	1104
1131758	2019	2038	7407	7426	CAAAGCACTTTATTGAGTTC	9	1105
1131786	N/A	N/A	130	149	CCCAGAACAATCCTGGGACA	70	1106
1131814	N/A	N/A	214	233	CTCACCTTTCCACATAGGCC	82	1107
1131842	N/A	N/A	317	336	CCGTTGTCTTCTTAAGGCC	82	1108
1131870	N/A	N/A	407	426	GCCACCGATCTGTTGCTAGT	67	1109
1131898	N/A	N/A	538	557	CCGGGAGGAGGAGCCAGGCC	67	1110
1131926	N/A	N/A	642	661	CACTCTAGTGCCCATGGGCA	83	1111
1131954	N/A	N/A	760	779	CAGGAGCCCAGGTGTGATGG	47	1112
1131982	N/A	N/A	898	917	TTCAGATGCCAGAGACAAGC	54	1113
1132010	N/A	N/A	1012	1031	AGGTTTACTGTTATCAACCT	48	1114
1132038	N/A	N/A	1111	1130	GGTAGTTTCATAATAAAAGC	36	1115
1132066	N/A	N/A	1527	1546	CCTGCTATGTGCCCACTCT	59	1116
1132094	N/A	N/A	1637	1656	GGAGGCTGAGGGAGTCCAGG	90	1117
1132122	N/A	N/A	1923	1942	AATTAGCTGAGCATGAAGTT	54	1118
1132150	N/A	N/A	2172	2191	CTCAATAAGCTTTTGCCACT	57	1119
1132178	N/A	N/A	2289	2308	TAGAACATAACCATCGCGAA	33	1120
1132206	N/A	N/A	2411	2430	ATGTCTTTAAACAGAATCAT	32	1121
1132234	N/A	N/A	2542	2561	AGAGCTGTGTAGTTCCTAAG	65	1122
1132262	N/A	N/A	2664	2683	GCTTGTTTCAGCTCTCCTAT	78	1123
1132290	N/A	N/A	2777	2796	TAACTCCCAAGTCAATACTT	76	1124
1132318	N/A	N/A	2890	2909	TGATCTGAGCCTTGTTTCC	69	1125
1132346	N/A	N/A	2980	2999	AGTCTTCAGTCCCAAGGCCA	71	1126
1132374	N/A	N/A	3388	3407	CATTGAAAACACTTTCTGCT	70	1127
1132402	N/A	N/A	3475	3494	TGAGGACTTCCCCTGTACTC	40	1128
1132430	N/A	N/A	3673	3692	CAGAGTTCCTTGACAGAAG	38	1129
1132458	N/A	N/A	3839	3858	AGGCTGTGTGTAGCACCTTT	54	1130
1132486	N/A	N/A	3963	3982	CTCTGGACTTCCAAAGGGTA	37	1131
1132514	N/A	N/A	4051	4070	CCTACTTGCCTTGTGACCTT	37	1132
1132542	N/A	N/A	4251	4270	CTCCACATCTCCTCACCTTT	39	1133
1132570	N/A	N/A	4352	4371	TGGTCTCAGGAGAGTCTAGG	59	1134
1132598	N/A	N/A	4584	4603	CTTCCTGGCACACCACCCGG	60	1135
1132626	N/A	N/A	4784	4803	GGGCTGGCCTTCTGCTTGCC	36	1136
1132654	N/A	N/A	5070	5089	ACGCGGCGCACCCGGCAGAAG	61	1137
1132682	N/A	N/A	5436	5455	CCCGCGGCCGGCTGGCCGGA	118	1138
1132710	N/A	N/A	5859	5878	ATCCCGTGTTCCAGCTTCCT	67	1139
1132738	N/A	N/A	6321	6340	CTAGCAGTTGTGCCTACCCT	49	1140
1132766	N/A	N/A	6412	6431	ACCCATTCTGTAGGCACCCG	78	1141
1132794	N/A	N/A	6533	6552	AGAGCAAGTTCGATTCTCCC	88	1142
1132822	N/A	N/A	6658	6677	GAGCGGAAACAGAAACCCCT	52	1143
1132850	N/A	N/A	6764	6783	TGCCCTTCCTCTCTCGCAGC	95	1144
1132878	N/A	N/A	7019	7038	TAAGAGCTCACCTGGCACGC	85 [†]	1145

Table 19. Reduction of FXII RNA by 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages
(Huh7, electroporation, 5000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1130748	11	30	11	30	AGCTGCCTATCCAGGAGTCC	62	1146
1130776	48	67	48	67	GAGCAGCAGAGCCCTCATGG	67	1147
1130804	94	113	N/A	N/A	GTGGAATCGAAAGTGTGAC	58	1148
1130832	150	169	N/A	N/A	GAGAACGACTGTGTGCTCTT	12	1149
1130860	204	223	3555	3574	GTACAGCTGCCGGTGGTACT	35	1150
1130871	216	235	3567	3586	GGTACATTTGTGGTACAGCT	16	1151
1130889	239	258	3590	3609	TGAGGGCCTGGCCGGCCCTT	54	1152
1130917	308	327	3815	3834	TTCTTGGGCTCCAAACAGTA	25	1153
1130945	365	384	4173	4192	TTCACACAGGTCCCTCCTTT	37	1154
1130973	421	440	4229	4248	GGCAGTGGTTTCCAGTGAGG	14	1155
1131001	463	482	4408	4427	GGAAAAACCGGAGAAGCTGA	26	1156
1131029	506	525	4451	4470	GCCACAGCTGCTTGCTCAGT	35	1157
1131057	546	565	4491	4510	CCGCTGGCAGTGGGCATCAG	32	1158
1131085	582	601	4666	4685	GAGGCACGGGTGGTGCGGC	32	1159
1131113	621	640	4705	4724	CAGGCGGTGGCCCTCCACCT	25	1160
1131141	682	701	N/A	N/A	AGCAGCTTGCCCTGGTGTCC	29	1161
1131169	722	741	4951	4970	GTCTGGCCAGGCCGCGGTA	42	1162
1131197	778	797	5007	5026	CGTTCCGGTAGGTGGCCTCC	28	1163
1131225	872	891	5186	5205	TTCAGCACGAAGCACCACGG	27	1164
1131253	915	934	5229	5248	GCACTGTGCCAGGTCGCAGT	36	1165
1131281	1006	1025	5320	5339	GAGGCTTCGGCGGTGCCGGC	26	1166
1131309	1087	1106	5506	5525	TGGTCAGGGAAGGCGGCTGC	8	1167
1131337	1130	1149	5549	5568	AGACTCTTGGCGAGCCGCTG	24	1168
1131365	1168	1187	5587	5606	GCGCCACCAGCCCGCCAACG	33	1169
1131393	1238	1257	5657	5676	GCGATGAGGCTGCCGGCGCA	26	1170
1131421	1340	1359	6000	6019	TCACAGCTGTGGTTACGGCG	38	1171
1131449	1431	1450	N/A	N/A	AAGGCGCAACAGAGCCAGGT	55	1172
1131477	1474	1493	6217	6236	CGTAAGGCGACAGGAGCGCG	25	74
1131505	1559	1578	6302	6321	TCGAACTGGTGGCCCCAGCC	86	1173
1131533	1595	1614	6893	6912	GCCTCTGCAGGAAGCTGGC	53	1174
1131561	1688	1707	6986	7005	TCGAGGAACCTGCGCAGAG	21 [†]	1175
1131589	1775	1794	7163	7182	CCTTGCAGGGTGAGCCGGCG	30	1176
1131617	1804	1823	7192	7211	CACCACAGCCCGATCCCCAG	28	1177
1131645	1851	1870	7239	7258	GGCCAGGTAGTAGGCCACAT	63	1178
1131673	1886	1905	7274	7293	CTGAGCAATCAGGAAACGGT	16	1179
1131701	1928	1947	7316	7335	ACTCTCTCACTGCGGAATCA	7	

1131729	1964	1983	7352	7371	GGAATGGGACACAATCTTGC	26	1180
1131757	2018	2037	7406	7425	AAAGCACTTTATTGAGTTCC	3	165
1131785	N/A	N/A	127	146	AGAACAATCCTGGGACAATC	69	1181
1131813	N/A	N/A	211	230	ACCTTTCCACATAGGCCTCC	99	1182
1131841	N/A	N/A	314	333	TTGTCTTCTTAAGGCCCATC	49	1183
1131869	N/A	N/A	404	423	ACCGATCTGTTGCTAGTCTG	72	1184
1131897	N/A	N/A	535	554	GGAGGAGGAGCCAGGCCACT	94	1185
1131925	N/A	N/A	639	658	TCTAGTGCCCATGGGCATAA	38	1186
1131953	N/A	N/A	757	776	GAGCCCAGGTGTGATGGCGC	87	1187
1131981	N/A	N/A	895	914	AGATGCCAGAGACAAGCTCT	49	1188
1132009	N/A	N/A	1009	1028	TTTACTGTTATCAACCTGGT	38	1189
1132037	N/A	N/A	1108	1127	AGTTTCATAATAAAAAGCTAA	83	1190
1132065	N/A	N/A	1524	1543	GCTATGTGCCCACTCTAGG	102	1191
1132093	N/A	N/A	1625	1644	AGTCCAGGGTTGGAATGTGC	80	1192
1132121	N/A	N/A	1920	1939	TAGCTGAGCATGAAGTTGTG	52	1193
1132149	N/A	N/A	2169	2188	AATAAGCTTTTGCCACTATT	59	1194
1132177	N/A	N/A	2286	2305	AACATAACCATCGCGAATAA	53	1195
1132205	N/A	N/A	2400	2419	CAGAATCATACATAAAACCA	45	1196
1132233	N/A	N/A	2539	2558	GCTGTGTAGTTCCTAAGCAC	70	1197
1132261	N/A	N/A	2661	2680	TGTTTCAGCTCTCCTATTGA	53	1198
1132289	N/A	N/A	2774	2793	CTCCCAAGTCAATACTTGAA	93	1199
1132317	N/A	N/A	2870	2889	TTATCTGTAAAACGGCAGTA	38	1200
1132345	N/A	N/A	2977	2996	CTTCAGTCCCAAGGCCAGGA	64	1201
1132373	N/A	N/A	3385	3404	TGAAAACACTTTCTGCTCTA	51	1202
1132401	N/A	N/A	3472	3491	GGACTTCCCCTGTACTCAAC	72	1203
1132429	N/A	N/A	3670	3689	AGTTCCTTGACAGAAGGAC	50	1204
1132457	N/A	N/A	3836	3855	CTGTGTGTAGCACCTTTCAC	73	1205
1132485	N/A	N/A	3960	3979	TGGACTTCCAAAGGGTATTG	39	1206
1132513	N/A	N/A	4048	4067	ACTTGCCCTGTGACCTTGCT	58	1207
1132541	N/A	N/A	4248	4267	CACATCTCCTCACCTTTCTG	98	1208
1132569	N/A	N/A	4349	4368	TCTCAGGAGAGTCTAGGACC	59	1209
1132597	N/A	N/A	4581	4600	CCTGGCACACCACCCGGCCT	70	1210
1132625	N/A	N/A	4781	4800	CTGGCCTTCTGCTTGCCCCA	46	1211
1132653	N/A	N/A	5067	5086	CGGCGCACCGGCAGAAGGCG	37	1212
1132681	N/A	N/A	5430	5449	GCCGGCTGGCCGGAATCTAG	77	1213
1132709	N/A	N/A	5856	5875	CCGTGTTCCAGCTTCCTCCC	160	1214
1132737	N/A	N/A	6318	6337	GCAGTTGTGCCTACCCTCGA	49	1215
1132765	N/A	N/A	6409	6428	CATTCTGTAGGCACCCGGAA	47	1216
1132793	N/A	N/A	6530	6549	GCAAGTTCGATTCTCCCTGT	72	1217
1132821	N/A	N/A	6655	6674	CGGAAACAGAAACCCCTCCC	47	1218
1132849	N/A	N/A	6761	6780	CCTTCCTCTCTCGAGCAAG	59	1219
1132877	N/A	N/A	7016	7035	GAGCTCACCTGGCACGCATC	85 [†]	1220

Table 20. Reduction of FXII RNA by 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages
(Huh7, electroporation, 5000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1130750	13	32	13	32	CCAGCTGCCTATCCAGGAGT	48	1221
1130778	50	69	50	69	AGGAGCAGCAGAGCCCTCAT	38	1222
1130806	97	116	N/A	N/A	AAGGTGGAATCGAAAGTGTT	67	1223
1130834	152	171	N/A	N/A	GTGAGAACGACTGTGTGCTC	20	1224
1130862	206	225	3557	3576	TGGTACAGCTGCCGGTGGTA	26	1225
1130871	216	235	3567	3586	GGTACATTTGTGGTACAGCT	13	183
1130891	241	260	3592	3611	GCTGAGGGCCTGGCCGGCCC	51	1226
1130919	311	330	3818	3837	ACTTTCCTTGGGCTCCAAACA	49	1227
1130947	367	386	4175	4194	TGTTACACAGGTCCCTCCT	28	1228
1130975	426	445	4234	4253	TTTCTGGCAGTGTTTCCAG	24	1229
1131003	469	488	4414	4433	TCTTGTGGAAAAACCGGAGA	36	1230
1131031	509	528	4454	4473	CTGGCCACAGCTGCTTGCTC	46	1231
1131059	549	568	4494	4513	CAGCCGCTGGCAGTGGGCAT	71	1232
1131087	585	604	4669	4688	ATGGAGGCACGGGTTGGTGC	64	1233
1131115	624	643	4708	4727	GCACAGGCGGTGGCCCTCCA	34	1234
1131143	686	705	4915	4934	TCATAGCAGCTTGCCTTGGT	28	1235
1131171	725	744	4954	4973	GTGGTCCTGGCCAGGCCGCG	64	1236
1131199	797	816	5026	5045	CGCGCTTGCTCGGCAGTCAC	17	1237
1131227	874	893	5188	5207	GGTTCAGCACGAAGCACCAC	23	1238
1131255	917	936	5231	5250	TGGCACTGTGCCAGGTCGCA	18	1239
1131283	1008	1027	5322	5341	CTGAGGCTTCGGCGGTGCCG	21	1240
1131311	1090	1109	5509	5528	TCCTGGTCAGGGAAGGCGGC	26	1241
1131339	1132	1151	5551	5570	ACAGACTCTTGCGGAGCCGC	20	60
1131367	1204	1223	5623	5642	AGTACAGCGCGCGATGTAG	42	1242
1131395	1240	1259	5659	5678	GGGCGATGAGGCTGCCGGCG	53	1243
1131423	1342	1361	6002	6021	GCTCACAGCTGTGGTTACGG	19	1244
1131451	1434	1453	N/A	N/A	CTGAAGGCGCAACAGAGCCA	46	1245
1131479	1493	1512	6236	6255	GGCAGGCACACCGGCTGAAC	31	1246
1131507	1561	1580	6304	6323	CCTCGAACTGGTGGCCCCAG	153	1247
1131535	1598	1617	6896	6915	TGCGCCTCCTGCAGGAAGCT	116	1248
1131563	1691	1710	6989	7008	CCCTCGAGGAACCCTGCGCA	23 [†]	1249
1131591	1777	1796	7165	7184	TGCCTTGCAGGGTGAGCCGG	19	1250
1131619	1806	1825	7194	7213	GTCACCACAGCCCGATCCCC	37	1251
1131647	1853	1872	7241	7260	CAGGCCAGGTAGTAGGCCAC	48	1252
1131675	1893	1912	7281	7300	TGAGTCCCTGAGCAATCAGG	19	150
1131703	1932	1951	7320	7339	AGCCACTCTCTCACTGCGGA	24	1253
1131731	1985	2004	7373	7392	CGCGGAGCTGGCCGCACTGG	30	1254
1131759	2020	2039	7408	7427	TCAAAGCACTTTATTGAGTT	11	1255

1131787	N/A	N/A	133	152	CCCCCAGAACAATCCTGGG	80	1256
1131815	N/A	N/A	217	236	GGCCTCACCTTTCCACATAG	66	1257
1131843	N/A	N/A	320	339	CCCCCGTTGTCTTCTTAAGG	47	1258
1131871	N/A	N/A	410	429	CCTGCCACCGATCTGTTGCT	124	1259
1131899	N/A	N/A	541	560	TTCCCGGAGGAGGAGCCAG	46	1260
1131927	N/A	N/A	645	664	GATCACTCTAGTGCCCATGG	48	1261
1131955	N/A	N/A	763	782	TGGCAGGAGCCCAGGTGTGA	66	1262
1131983	N/A	N/A	901	920	GCATTCAGATGCCAGAGACA	77	1263
1132011	N/A	N/A	1015	1034	AAGAGGTTTACTGTTATCAA	55	1264
1132039	N/A	N/A	1114	1133	AAAGGTAGTTTCATAATAAA	44	1265
1132067	N/A	N/A	1530	1549	GGCCCTGCTATGTGCCACAC	93	1266
1132095	N/A	N/A	1640	1659	AGAGGAGGCTGAGGGAGTCC	52	1267
1132123	N/A	N/A	2075	2094	ACCTTTAAGATGCAAATGGG	51	1268
1132151	N/A	N/A	2175	2194	CTGCTCAATAAGCTTTTGCC	54	1269
1132179	N/A	N/A	2292	2311	TTATAGAACATAACCATCGC	68	1270
1132207	N/A	N/A	2426	2445	CATATACTAAATAAAATGTC	99	1271
1132235	N/A	N/A	2545	2564	TGAAGAGCTGTGTAGTTCT	58	1272
1132263	N/A	N/A	2667	2686	GCTGCTTGTTCAGCTCTCC	55	1273
1132291	N/A	N/A	2780	2799	TTGTAACCTCCAAGTCAATA	78	1274
1132319	N/A	N/A	2893	2912	CTCTGATCTGAGCCTTGGTT	95	1275
1132347	N/A	N/A	2983	3002	GTAAGTCTTCAGTCCAAGG	86	1276
1132375	N/A	N/A	3391	3410	GTGCATTGAAAACACTTTCT	41	1277
1132403	N/A	N/A	3478	3497	CTCTGAGGACTTCCCCTGTA	166	1278
1132431	N/A	N/A	3676	3695	AAGCAGAGTTTCCTTGACAG	57	1279
1132459	N/A	N/A	3842	3861	CAGAGGCTGTGTGTAGCACC	76	1280
1132487	N/A	N/A	3966	3985	TCCCTCTGGACTTCCAAAGG	47	1281
1132515	N/A	N/A	4054	4073	GAACCTACTTGCCTTGTGAC	59	1282
1132543	N/A	N/A	4254	4273	GTCCTCCACATCTCCTCACC	47	1283
1132571	N/A	N/A	4355	4374	TAGTGGTCTCAGGAGAGTCT	92	1284
1132599	N/A	N/A	4587	4606	CTCCTTCCTGGCACACCACC	38	1285
1132627	N/A	N/A	4803	4822	GCAAGCCCGTCCCACCTGGG	47	1286
1132655	N/A	N/A	5073	5092	CCCACGCGGCGCACCGGCAG	48	1287
1132683	N/A	N/A	5439	5458	GAGCCCGCGGCCGGCTGGCC	68	1288
1132711	N/A	N/A	5862	5881	CCAATCCCGTGTTCAGCTT	37	1289
1132739	N/A	N/A	6324	6343	CCCCTAGCAGTTGTGCCTAC	138	1290
1132767	N/A	N/A	6415	6434	GCCACCCATTCTGTAGGCAC	59	1291
1132795	N/A	N/A	6536	6555	CCAAGAGCAAGTTCGATTCT	50	1292
1132823	N/A	N/A	6661	6680	GCGGAGCGGAAACAGAAACC	88	1293
1132851	N/A	N/A	6767	6786	TCATGCCCTTCCTCTCTCGC	39	1294
1132879	N/A	N/A	7025	7044	CCGGGCTAAGAGCTCACCTG	59 [†]	1295

Table 21. Reduction of FXII RNA by 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages
(Huh7, electroporation, 5000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1130752	15	34	15	34	GTCCAGCTGCCTATCCAGGA	49	1296
1130780	57	76	57	76	GAACCCCAGGAGCAGCAGAG	72	1297
1130808	103	122	N/A	N/A	CTTCCCAAGGTGGAATCGAA	62	1298
1130836	154	173	N/A	N/A	CAGTGAGAACGACTGTGTGC	41	1299
1130864	208	227	3559	3578	TGTGGTACAGCTGCCGGTGG	42	1300
1130871	216	235	3567	3586	GGTACATTTGTGGTACAGCT	21	183
1130893	254	273	N/A	N/A	GTAGCACACCAGGGCTGAGG	54	1301
1130921	313	332	3820	3839	TCACTTTCTTGGGCTCCAAA	41	1302
1130949	371	390	4179	4198	GGCATGTTACACAGGTCCC	42	1303
1130977	428	447	N/A	N/A	TCTTCTGGCAGTGTTTCC	48	1304
1131005	471	490	4416	4435	ATTCTTGTGGAAAAACCGGA	39	1305
1131033	511	530	4456	4475	ATCTGGCCACAGCTGCTTGC	53	1306
1131061	551	570	4496	4515	GCCAGCCGCTGGCAGTGGGC	58	1307
1131089	588	607	4672	4691	CCCATGGAGGCACGGGTTGG	40	1308
1131117	627	646	4711	4730	GTGGCACAGGCGGTGGCCCT	71	1309
1131145	690	709	4919	4938	GCCATCATAGCAGCTTGCCCT	36	1310
1131173	745	764	4974	4993	GACAGGGCGCACCCGAGAGC	52	1311
1131201	799	818	5028	5047	TCCGCGCTTGCTCGGCAGTC	74	1312
1131229	882	901	5196	5215	CCGGTCGCGGTTACAGCACGA	46	1313
1131257	920	939	5234	5253	GTCTGGCACTGTGCCAGGTC	74	1314
1131285	1011	1030	5325	5344	GGGCTGAGGCTTCGGCGGTG	31	1315
1131313	1092	1111	5511	5530	GTTCTTGGTCAGGGAAGGCG	52	1316
1131341	1134	1153	5553	5572	AGACAGACTCTTGCGGAGCC	37	1317
1131369	1207	1226	5626	5645	CCCAGTACAGCGCGGCGATG	32	1318
1131397	1281	1300	5700	5719	CCGGTCCTGCAGGCAGTGAG	59	1319
1131425	1345	1364	6005	6024	ACGGCTCACAGCTGTGGTTA	49	1320
1131453	1437	1456	6180	6199	CTCCTGAAGGCGCAACAGAG	66	1321
1131481	1496	1515	6239	6258	CTTGGCAGGCACACCGGCTG	24	1322
1131509	1564	1583	N/A	N/A	CCCCCTCGAACTGGTGGCCC	76	1323
1131537	1603	1622	6901	6920	GTACCTGCGCCTCCTGCAGG	126	1324
1131565	1696	1715	6994	7013	TGCCGCCCTCGAGGAACCCT	8 [†]	1325
1131593	1780	1799	7168	7187	TGATGCCTTGCAGGGTGAGC	17	1326
1131621	1808	1827	7196	7215	CGGTCACCACAGCCCGATCC	35	1327
1131649	1856	1875	7244	7263	ATCCAGGCCAGGTAGTAGGC	70	1328
1131677	1895	1914	7283	7302	GATGAGTCCCTGAGCAATCA	35	1329
1131705	1935	1954	7323	7342	CCCAGCCACTCTCTCACTGC	37	1330
1131733	1989	2008	7377	7396	CTGGCGCGGAGCTGGCCGCA	49	1331
1131761	2023	2042	7411	7430	TTTTCAAAGCACTTTATTGA	28	1332

1131789	N/A	N/A	139	158	TAGCGACCCCCCAGAACAAT	101	1333
1131817	N/A	N/A	223	242	CGGGCTGGCCTCACCTTTCC	74	1334
1131845	N/A	N/A	326	345	TACCTCCCCCGTTGTCTTC	105	1335
1131873	N/A	N/A	416	435	TCATAGCCTGCCACCGATCT	77	1336
1131901	N/A	N/A	560	579	ACACATCCCCACCCAAGGGT	61	1337
1131929	N/A	N/A	651	670	GCTCACGATCACTCTAGTGC	44	1338
1131957	N/A	N/A	770	789	GGAAGGCTGGCAGGAGCCCA	81	1339
1131985	N/A	N/A	910	929	GCTTCAGAGGCATTTCAGATG	84	1340
1132013	N/A	N/A	1021	1040	AACCCTAAGAGGTTTACTGT	105	1341
1132041	N/A	N/A	1120	1139	CATCTAAAAGGTAGTTTCAT	90	1342
1132069	N/A	N/A	1536	1555	TTCACAGGCCCTGCTATGTG	101	1343
1132097	N/A	N/A	1667	1686	GGAGAAACTTTTGGGTGTGG	86	1344
1132125	N/A	N/A	2081	2100	AGATGGACCTTTAAGATGCA	79	1345
1132153	N/A	N/A	2181	2200	AAGTACCTGCTCAATAAGCT	61	1346
1132181	N/A	N/A	2299	2318	TGTGATTTTATAGAACATAA	71	1347
1132209	N/A	N/A	2437	2456	AATCAGCAACACATATACTA	73	1348
1132237	N/A	N/A	2551	2570	TCCTGCTGAAGAGCTGTGTA	66	1349
1132265	N/A	N/A	2673	2692	GCTGCTGCTGCTTGTTTCAG	42	1350
1132293	N/A	N/A	2786	2805	TTTTATTTGTAACCCCAAG	100	1351
1132321	N/A	N/A	2899	2918	TAACCACTCTGATCTGAGCC	80	1352
1132349	N/A	N/A	2989	3008	CCTTGGGTAAGTCTTCAGTC	107	1353
1132377	N/A	N/A	3397	3416	GTCGCTGTGCATTGAAAACA	98	1354
1132405	N/A	N/A	3484	3503	CACACTCTCTGAGGACTTCC	83	1355
1132433	N/A	N/A	3682	3701	CTCTCCAAGCAGAGTTCCTT	89	1356
1132461	N/A	N/A	3848	3867	CCACCCAGAGGCTGTGTGT	90	1357
1132489	N/A	N/A	3972	3991	GAACTCTCCCTCTGGACTTC	61	1358
1132517	N/A	N/A	4060	4079	CTTCTTGAACCTACTTGCCT	66	1359
1132545	N/A	N/A	4260	4279	GCCCAGGTCCTCCACATCTC	60	1360
1132573	N/A	N/A	4361	4380	GAGGGATAGTGGTCTCAGGA	76	1361
1132601	N/A	N/A	4593	4612	AGAGCTCTCCTTCCTGGCAC	60	1362
1132629	N/A	N/A	4809	4828	TTCTTGGCAAGCCCGTCCCA	50	1363
1132657	N/A	N/A	5079	5098	CCCAGCCCCACGCGGCGCAC	105	1364
1132685	N/A	N/A	5445	5464	GACGGAGAGCCCGCGGCCGG	109	1365
1132713	N/A	N/A	5868	5887	CGAACCCCAATCCCGTGTTT	81	1366
1132741	N/A	N/A	6330	6349	CCCCTGCCCCTAGCAGTTGT	111	1367
1132769	N/A	N/A	6436	6455	CTCACAACCCATCAGGTCAG	97	1368
1132797	N/A	N/A	6542	6561	AGGGAACCAAGAGCAAGTTC	26	1369
1132825	N/A	N/A	6667	6686	GAATGGGCGGAGCGGAAACA	73	1370
1132853	N/A	N/A	6773	6792	ACCCACTCATGCCCTTCCTC	42	1371
1132881	N/A	N/A	7031	7050	CGCCAACCGGGCTAAGAGCT	82 [†]	1372

Table 22. Reduction of FXII RNA by 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages
(Huh7, electroporation, 5000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1130753	16	35	16	35	GGTCCAGCTGCCTATCCAGG	37	1373
1130781	60	79	60	79	CAGGAACCCCAGGAGCAGCA	65	1374
1130809	104	123	N/A	N/A	GCTTCCCAAGGTGGAATCGA	67	1375
1130837	156	175	N/A	N/A	GACAGTGAGAACGACTGTGT	43	1376
1130865	210	229	3561	3580	TTTGTGGTACAGCTGCCGGT	52	1377
1130871	216	235	3567	3586	GGTACATTTGTGGTACAGCT	20	183
1130894	257	276	N/A	N/A	GTGGTAGCACACCAGGGCTG	19	1378
1130922	314	333	3821	3840	TTCACCTTTCTTGGGCTCCAA	36	1379
1130950	372	391	4180	4199	TGGCATGTTACACAGGTCC	42	1380
1130978	429	448	N/A	N/A	CTCTTTCTGGCAGTGGTTTC	45	1381
1131006	472	491	4417	4436	CATTCTTGTGGAAAAACCGG	22	1382
1131034	512	531	4457	4476	CATCTGGCCACAGCTGCTTG	42	1383
1131062	552	571	4497	4516	GGCCAGCCGCTGGCAGTGGG	87	1384
1131090	589	608	4673	4692	CCCCATGGAGGCACGGGTTG	36	1385
1131118	628	647	4712	4731	AGTGGCACAGGCGGTGGCCC	32	1386
1131146	691	710	4920	4939	GGCCATCATAGCAGCTTGCC	27	1387
1131174	747	766	4976	4995	CTGACAGGGCGCACCCGAGA	49	1388
1131202	800	819	5029	5048	TTCCGCGCTTGCTCGGCAGT	35	1389
1131230	883	902	5197	5216	GCCGGTCGCGGTTACAGCACG	42	1390
1131258	921	940	5235	5254	GGTCTGGCACTGTGCCAGGT	34	1391
1131286	1012	1031	5326	5345	TGGGCTGAGGCTTCGGCGGT	45	1392
1131314	1093	1112	5512	5531	CGTTCCTGGTCAGGGAAGGC	15	1393
1131342	1135	1154	5554	5573	AAGACAGACTCTTGCGGAGC	29	1394
1131370	1209	1228	5628	5647	GCCCCAGTACAGCGCGGCGA	53	1395
1131398	1282	1301	5701	5720	GCCGGTCCTGCAGGCAGTGA	48	1396
1131426	1346	1365	6006	6025	CACGGCTCACAGCTGTGGTT	28	1397
1131454	1439	1458	6182	6201	TCCTCCTGAAGGCGCAACAG	33	1398
1131482	1497	1516	6240	6259	GCTTGGCAGGCACACCGGCT	41	1399
1131510	1565	1584	N/A	N/A	GCCCCCTCGAACTGGTGGCC	49	1400
1131538	1604	1623	6902	6921	GGTACCTGCGCCTCCTGCAG	154	1401
1131566	1699	1718	6997	7016	CGGTGCCGCCCTCGAGGAAC	6 [†]	1402
1131594	1781	1800	7169	7188	ATGATGCCTTGACAGGGTGAG	29	1403
1131622	1810	1829	7198	7217	TGCGGTCACCACAGCCCGAT	37	1404
1131650	1857	1876	7245	7264	GATCCAGGCCAGGTAGTAGG	29	1405
1131678	1896	1915	7284	7303	AGATGAGTCCCTGAGCAATC	32	1406
1131706	1938	1957	7326	7345	TGCCCCAGCCACTCTCTCAC	25	1407
1131734	1990	2009	7378	7397	CCTGGCGCGGAGCTGGCCGC	44	1408
1131762	2024	2043	7412	7431	ATTTTCAAAGCACTTTATTG	32	1409

1131790	N/A	N/A	142	161	TGATAGCGACCCCCCAGAAC	80	1410
1131818	N/A	N/A	229	248	GCCTTCCGGGCTGGCCTCAC	91	1411
1131846	N/A	N/A	329	348	TTCTACCTCCCCCGTTGTC	106	1412
1131874	N/A	N/A	419	438	AAGTCATAGCCTGCCACCGA	105	1413
1131902	N/A	N/A	563	582	CATACACATCCCCACCCAAG	85	1414
1131930	N/A	N/A	654	673	ACAGCTCACGATCACTCTAG	67	1415
1131958	N/A	N/A	773	792	TGAGGAAGGCTGGCAGGAGC	76	1416
1131986	N/A	N/A	913	932	TGGGCTTCAGAGGCATTGAG	50	1417
1132014	N/A	N/A	1024	1043	AACAACCCTAAGAGGTTTAC	62	1418
1132042	N/A	N/A	1123	1142	CTTCATCTAAAAGGTAGTTT	48	1419
1132070	N/A	N/A	1539	1558	TGGTTCACAGGCCCTGCTAT	66	1420
1132098	N/A	N/A	1670	1689	AGAGGAGAACTTTTGGGTG	68	1421
1132126	N/A	N/A	2084	2103	CTGAGATGGACCTTTAAGAT	54	1422
1132154	N/A	N/A	2188	2207	TGGCACAAAGTACCTGCTCA	53	1423
1132182	N/A	N/A	2302	2321	CACTGTGATTTTATAGAACA	65	1424
1132210	N/A	N/A	2440	2459	ATGAATCAGCAACACATATA	58	1425
1132238	N/A	N/A	2554	2573	GCCTCCTGCTGAAGAGCTGT	61	1426
1132266	N/A	N/A	2676	2695	CACGCTGCTGCTGCTTGTTT	75	1427
1132294	N/A	N/A	2789	2808	GAATTTTATTTGTAACCTCCC	84	1428
1132322	N/A	N/A	2902	2921	TGTTAACCCTCTGATCTGA	59	1429
1132350	N/A	N/A	2992	3011	TGACCTTGGGTAAGTCTTCA	93	1430
1132378	N/A	N/A	3400	3419	AAGGTCGCTGTGCATTGAAA	84	1431
1132406	N/A	N/A	3487	3506	CAACACACTCTCTGAGGACT	55	1432
1132434	N/A	N/A	3685	3704	CCTCTCTCCAAGCAGAGTTC	49	1433
1132462	N/A	N/A	3851	3870	AGGCCACCCAGAGGCTGTG	38	1434
1132490	N/A	N/A	3975	3994	CCAGAACTCTCCCTCTGGAC	74	1435
1132518	N/A	N/A	4063	4082	GCCCTTCTTGAACCTACTTG	73	1436
1132546	N/A	N/A	4263	4282	CCCGCCCAGGTCCTCCACAT	59	1437
1132574	N/A	N/A	4364	4383	AAAGAGGGATAGTGGTCTCA	74	1438
1132602	N/A	N/A	4596	4615	CAGAGAGCTCTCCTTCCTGG	81	1439
1132630	N/A	N/A	4812	4831	TCCTTCCTGGCAAGCCCGTC	40	1440
1132658	N/A	N/A	5082	5101	TCACCCAGCCCCACGCGGCG	44	1441
1132686	N/A	N/A	5448	5467	GAGGACGGAGAGCCCGCGGC	75	1442
1132714	N/A	N/A	5871	5890	TCCCGAACCCCAATCCCGTG	83	1443
1132742	N/A	N/A	6333	6352	CTACCCCTGCCCTAGCAGT	70	1444
1132770	N/A	N/A	6439	6458	ATTCTCACAACCCATCAGGT	103	1445
1132798	N/A	N/A	6548	6567	GCCCAGAGGGAACCAAGAGC	85	1446
1132826	N/A	N/A	6670	6689	TTTGAATGGGCGGAGCGGAA	86	1447
1132854	N/A	N/A	6776	6795	TAAACCCACTCATGCCCTTC	87	1448
1132882	N/A	N/A	7057	7076	TTGTGCCTGACGGCCTCGGG	84 [†]	1449

Table 23. Reduction of FXII RNA by 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages
(Huh7, electroporation, 5000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1130751	14	33	14	33	TCCAGCTGCCTATCCAGGAG	65	1450
1130779	51	70	51	70	CAGGAGCAGCAGAGCCCTCA	39	1451
1130807	99	118	N/A	N/A	CCAAGGTGGAATCGAAAGTG	37	1452
1130835	153	172	N/A	N/A	AGTGAGAACGACTGTGTGCT	29	1453
1130863	207	226	3558	3577	GTGGTACAGCTGCCGGTGGT	23	1454
1130871	216	235	3567	3586	GGTACATTTGTGGTACAGCT	8	183
1130892	242	261	3593	3612	GGCTGAGGGCCTGGCCGGCC	54	1455
1130920	312	331	3819	3838	CACTTTCTTGGGCTCCAAAC	17	1456
1130948	370	389	4178	4197	GCATGTTACACAGGTCCCT	36	1457
1130976	427	446	4235	4254	CTTTCTGGCAGTGGTTTCCA	25	1458
1131004	470	489	4415	4434	TTCTTGTGAAAAACCGGAG	28	1459
1131032	510	529	4455	4474	TCTGGCCACAGCTGCTTGCT	26	1460
1131060	550	569	4495	4514	CCAGCCGCTGGCAGTGGGCA	53	1461
1131088	586	605	4670	4689	CATGGAGGCACGGGTTGGTG	89	1462
1131116	625	644	4709	4728	GGCACAGGCGGTGGCCCTCC	47	1463
1131144	688	707	4917	4936	CATCATAGCAGCTTGCCTTG	40	1464
1131172	744	763	4973	4992	ACAGGGCGCACCCGAGAGCG	50	1465
1131200	798	817	5027	5046	CCGCGCTTGCTCGGCAGTCA	31	1466
1131228	876	895	5190	5209	GCGGTTACAGCACGAAGCACC	47	1467
1131256	919	938	5233	5252	TCTGGCACTGTGCCAGGTGCG	43	1468
1131284	1010	1029	5324	5343	GGCTGAGGCTTCGGCGGTGC	27	1469
1131312	1091	1110	5510	5529	TTCTGGTCAGGGAAGGCGG	35	1470
1131340	1133	1152	5552	5571	GACAGACTCTTGCGGAGCCG	19	1471
1131368	1206	1225	5625	5644	CCAGTACAGCGCGCGATGT	17	1472
1131396	1280	1299	5699	5718	CGGTCCTGCAGGCAGTGAGC	26	1473
1131424	1344	1363	6004	6023	CGGCTCACAGCTGTGGTTAC	19	1474
1131452	1436	1455	6179	6198	TCCTGAAGGCGCAACAGAGC	39	1475
1131480	1494	1513	6237	6256	TGGCAGGCACACCGGCTGAA	22	1476
1131508	1563	1582	N/A	N/A	CCCCTCGAACTGGTGGCCCC	132	1477
1131536	1601	1620	6899	6918	ACCTGCGCCTCCTGCAGGAA	108	1478
1131564	1694	1713	6992	7011	CCGCCCTCGAGGAACCCTGC	10 [†]	1479
1131592	1778	1797	7166	7185	ATGCCTTGCAGGGTGAGCCG	24	1480
1131620	1807	1826	7195	7214	GGTCACCACAGCCCGATCCC	23	1481
1131648	1855	1874	7243	7262	TCCAGGCCAGGTAGTAGGCC	81	1482
1131676	1894	1913	7282	7301	ATGAGTCCCTGAGCAATCAG	44	1483
1131704	1933	1952	7321	7340	CAGCCACTCTCTCACTGCGG	11	1484
1131732	1986	2005	7374	7393	GCGCGGAGCTGGCCGCACTG	24	1485
1131760	2021	2040	7409	7428	TTCAAAGCACTTTATTGAGT	6	1486

1131788	N/A	N/A	136	155	CGACCCCCCAGAACAATCCT	54	1487
1131816	N/A	N/A	220	239	GCTGGCCTCACCTTTCCACA	69	1488
1131844	N/A	N/A	323	342	CTCCCCCGTTGTCTTCTTA	87	1489
1131872	N/A	N/A	413	432	TAGCCTGCCACCGATCTGTT	59	1490
1131900	N/A	N/A	557	576	CATCCCCACCCAAGGGTTCC	80	1491
1131928	N/A	N/A	648	667	CACGATCACTCTAGTGCCCA	67	1492
1131956	N/A	N/A	767	786	AGGCTGGCAGGAGCCCAGGT	61	1493
1131984	N/A	N/A	904	923	GAGGCATTGAGATGCCAGAG	101	1494
1132012	N/A	N/A	1018	1037	CCTAAGAGGTTTACTGTTAT	46	1495
1132040	N/A	N/A	1117	1136	CTAAAAGGTAGTTTCATAAT	70	1496
1132068	N/A	N/A	1533	1552	ACAGGCCCTGCTATGTGCCA	67	1497
1132096	N/A	N/A	1647	1666	GGTGAAGAGAGGAGGCTGAG	68	1498
1132124	N/A	N/A	2078	2097	TGGACCTTTAAGATGCAAAT	53	1499
1132152	N/A	N/A	2178	2197	TACCTGCTCAATAAGCTTTT	54	1500
1132180	N/A	N/A	2295	2314	ATTTTATAGAACATAACCAT	125	1501
1132208	N/A	N/A	2430	2449	AACACATATACTAAATAAAA	88	1502
1132236	N/A	N/A	2548	2567	TGCTGAAGAGCTGTGTAGTT	77	1503
1132264	N/A	N/A	2670	2689	GCTGCTGCTTGTTCAGCTC	72	1504
1132292	N/A	N/A	2783	2802	TATTTGTAACCTCCAAGTCA	66	1505
1132320	N/A	N/A	2896	2915	CCACTCTGATCTGAGCCTTG	87	1506
1132348	N/A	N/A	2986	3005	TGGGTAAGTCTTCAGTCCCA	64	1507
1132376	N/A	N/A	3394	3413	GCTGTGCATTGAAAACACTT	32	1508
1132404	N/A	N/A	3481	3500	ACTCTCTGAGGACTTCCCCT	48	1509
1132432	N/A	N/A	3679	3698	TCCAAGCAGAGTTCCTTGGA	102	1510
1132460	N/A	N/A	3845	3864	CCCCAGAGGCTGTGTGTAGC	80	1511
1132488	N/A	N/A	3969	3988	CTCTCCCTCTGGACTTCCAA	52	1512
1132516	N/A	N/A	4057	4076	CTTGAACCTACTTGCCTTGT	53	1513
1132544	N/A	N/A	4257	4276	CAGGTCTCCACATCTCCTC	57	1514
1132572	N/A	N/A	4358	4377	GGATAGTGGTCTCAGGAGAG	82	1515
1132600	N/A	N/A	4590	4609	GCTCTCCTTCCTGGCACACC	73	1516
1132628	N/A	N/A	4806	4825	CTGGCAAGCCCGTCCCACCT	52	1517
1132656	N/A	N/A	5076	5095	AGCCCCACGCGGCGCACCGG	60	1518
1132684	N/A	N/A	5442	5461	GGAGAGCCCGCGGCCGGCTG	72	1519
1132712	N/A	N/A	5865	5884	ACCCCAATCCCGTGTTCCAG	64	1520
1132740	N/A	N/A	6327	6346	CTGCCCTAGCAGTTGTGCC	93	1521
1132768	N/A	N/A	6433	6452	ACAACCCATCAGGTCAGCGC	109	1522
1132796	N/A	N/A	6539	6558	GAACCAAGAGCAAGTTCGAT	67	1523
1132824	N/A	N/A	6664	6683	TGGGCGGAGCGGAAACAGAA	46	1524
1132852	N/A	N/A	6770	6789	CACTCATGCCCTTCCTCTCT	39	1525
1132880	N/A	N/A	7028	7047	CAACCGGGCTAAGAGCTCAC	56 [†]	1526

Table 24. Reduction of FXII RNA by 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages
(Huh7, electroporation, 5000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1130754	18	37	18	37	TTGGTCCAGCTGCCTATCCA	28	1527
1130782	65	84	65	84	ACCAGCAGGAACCCCAGGAG	94	1528
1130810	106	125	473	492	GGGCTTCCCAAGGTGGAATC	19	1529
1130838	157	176	N/A	N/A	TGACAGTGAGAACGACTGTG	33	1530
1130866	211	230	3562	3581	ATTTGTGGTACAGCTGCCGG	23	1531
1130871	216	235	3567	3586	GGTACATTTGTGGTACAGCT	11	183
1130895	258	277	N/A	N/A	GGTGGTAGCACACCAGGGCT	48	1532
1130923	316	335	3823	3842	CTTTCACCTTTCTTGGGCTCC	19	1533
1130951	374	393	4182	4201	CTTGGCATGTTACACACAGGT	26	1534
1130979	430	449	N/A	N/A	TCTCTTTCTGGCAGTGGTTT	17	1535
1131007	473	492	4418	4437	TCATTCTTGTGGAAAAACCG	18	1536
1131035	513	532	4458	4477	GCATCTGGCCACAGCTGCTT	38	1537
1131063	553	572	4498	4517	TGGCCAGCCGCTGGCAGTGG	67	1538
1131091	590	609	4674	4693	CCCCCATGGAGGCACGGGTT	42	208
1131119	630	649	4714	4733	GCAGTGGCACAGGCGGTGGC	30	1539
1131147	693	712	4922	4941	GCGGCCATCATAGCAGCTTG	46	1540
1131175	748	767	4977	4996	GCTGACAGGGCGCACCCGAG	32	1541
1131203	801	820	5030	5049	GTTCCGCGCTTGCTCGGCAG	30	1542
1131231	884	903	5198	5217	AGCCGGTCGCGGTTACACAC	25	1543
1131259	922	941	5236	5255	GGGTCTGGCACTGTGCCAGG	22	1544
1131287	1013	1032	5327	5346	GTGGGCTGAGGCTTCGGCGG	49	1545
1131315	1094	1113	5513	5532	CCGTTCTGGTCAGGGAAGG	46	1546
1131343	1136	1155	5555	5574	GAAGACAGACTCTTGCGGAG	38	1547
1131371	1210	1229	5629	5648	GGCCCCAGTACAGCGCGGCG	54	1548
1131399	1284	1303	N/A	N/A	GGGCCGGTCCTGCAGGCACT	64	1549
1131427	1347	1366	6007	6026	GCACGGCTCACAGCTGTGGT	50	1550
1131455	1440	1459	6183	6202	ATCCTCCTGAAGGCGCAACA	29	1551
1131483	1499	1518	6242	6261	CCGCTTGGCAGGCACACCGG	29	1552
1131511	1566	1585	N/A	N/A	CGCCCCCTCGAACTGGTGGC	126	1553
1131539	1605	1624	6903	6922	CGGTACCTGCGCCTCCTGCA	79	1554
1131567	1700	1719	6998	7017	TCGGTGCCGCCCTCGAGGAA	5 [†]	1555
1131595	1782	1801	7170	7189	GATGATGCCTTGACAGGGTGA	15	1556
1131623	1811	1830	7199	7218	TTGCGGTACACAGCCCGA	32	1557
1131651	1858	1877	7246	7265	GGATCCAGGCCAGGTAGTAG	64	1558
1131679	1897	1916	7285	7304	AAGATGAGTCCCTGAGCAAT	30	1559
1131707	1939	1958	7327	7346	ATGCCCCAGCCACTCTCTCA	24	1560
1131735	1991	2010	7379	7398	TCCTGGCGCGGAGCTGGCCG	25	1561
1131763	2026	2045	7414	7433	GCATTTTCAAAGCACTTTAT	9	1562

1131791	N/A	N/A	145	164	CTGTGATAGCGACCCCCCAG	57	1563
1131819	N/A	N/A	241	260	TCCTCTGCCTGGGCCTTCCG	83	1564
1131847	N/A	N/A	332	351	CCTTTCTACCTCCCCCGTT	78	1565
1131875	N/A	N/A	422	441	TATAAGTCATAGCCTGCCAC	61	1566
1131903	N/A	N/A	566	585	CACCATACACATCCCCACCC	74	1567
1131931	N/A	N/A	657	676	CACACAGCTCACGATCACTC	90	1568
1131959	N/A	N/A	776	795	AACTGAGGAAGGCTGGCAGG	59	1569
1131987	N/A	N/A	919	938	TAAAGCTGGGCTTCAGAGGC	73	1570
1132015	N/A	N/A	1027	1046	CTCAACAACCCCTAAGAGGTT	122	1571
1132043	N/A	N/A	1126	1145	ACCCTTCATCTAAAAGGTAG	42	1572
1132071	N/A	N/A	1542	1561	ATCTGGTTCACAGGCCCTGC	44	1573
1132099	N/A	N/A	1673	1692	GAGAGAGGAGAACTTTTGG	51	1574
1132127	N/A	N/A	2087	2106	GATCTGAGATGGACCTTTAA	68	1575
1132155	N/A	N/A	2191	2210	GTCTGGCACAAGTACCTGC	66	1576
1132183	N/A	N/A	2308	2327	AATGTTCACTGTGATTTTAT	86	1577
1132211	N/A	N/A	2443	2462	TTGATGAATCAGCAACACAT	86	1578
1132239	N/A	N/A	2557	2576	TGAGCCTCCTGCTGAAGAGC	64	1579
1132267	N/A	N/A	2679	2698	CGTCACGCTGCTGCTGCTTG	92	1580
1132295	N/A	N/A	2792	2811	GCTGAATTTTATTTGTAAC	101	1581
1132323	N/A	N/A	2905	2924	CACTGTAAACCACTCTGATC	49	1582
1132351	N/A	N/A	3009	3028	ACAACCTGCTAGCTGTGTGA	65	1583
1132379	N/A	N/A	3403	3422	AAAAAGGTCGCTGTGCATTG	55	1584
1132407	N/A	N/A	3490	3509	GGACAACACACTCTCTGAGG	54	1585
1132435	N/A	N/A	3688	3707	TCCCCTCTCTCCAAGCAGAG	53	1586
1132463	N/A	N/A	3855	3874	CCCCAGGCCACCCAGAGGC	67	1587
1132491	N/A	N/A	3978	3997	TTCCCAGAACTCTCCCTCTG	59	1588
1132519	N/A	N/A	4066	4085	AAGGCCCTTCTTGAACCTAC	50	1589
1132547	N/A	N/A	4266	4285	CACCCCGCCAGGTCCTCCA	99	1590
1132575	N/A	N/A	4387	4406	GCTCAAAGCACTTCTCTGGG	25	1591
1132603	N/A	N/A	4599	4618	CCCCAGAGAGCTCTCCTTCC	76	1592
1132631	N/A	N/A	4816	4835	CTCCTCCTTCTGGCAAGCC	43	1593
1132659	N/A	N/A	5085	5104	GGGTCACCCAGCCCCACGCG	65	1594
1132687	N/A	N/A	5451	5470	GCTGAGGACGGAGAGCCCGC	88	1595
1132715	N/A	N/A	5874	5893	TGCTCCCGAACCCCAATCCC	43	1596
1132743	N/A	N/A	6336	6355	CCCCTACCCCTGCCCCTAGC	65	1597
1132771	N/A	N/A	6442	6461	CACATTCTCACAACCCATCA	72	1598
1132799	N/A	N/A	6566	6585	TGGCCTTTGCAGCCCGGCGC	84	1599
1132827	N/A	N/A	6673	6692	GGATTTGAATGGGCGGAGCG	49	1600
1132855	N/A	N/A	6779	6798	TTGTAAACCCACTCATGCCC	52	1601
1132883	N/A	N/A	7060	7079	GATTTGTGCCTGACGGCCTC	42 [†]	1602

Table 25. Reduction of FXII RNA by 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages
(Huh7, electroporation, 5000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1130783	66	85	66	85	CACCAGCAGGAACCCCAGGA	57	1603
1130811	125	144	492	511	TTGTACTTATGCTCCTTGGG	30	1604
1130839	158	177	N/A	N/A	GTGACAGTGAGAACGACTGT	14	1605
1130867	212	231	3563	3582	CATTTGTGGTACAGCTGCCG	22	1606
1130871	216	235	3567	3586	GGTACATTTGTGGTACAGCT	17	183
1130896	278	297	3785	3804	TGGTCCTGATCAAAGTTGGG	44	1607
1130924	317	336	N/A	N/A	TCTTTCACTTTCTTGGGCTC	30	1608
1130952	375	394	4183	4202	GCTTGGCATGTTACACACAGG	15	1609
1130980	431	450	N/A	N/A	TTCTCTTCTTGGCAGTGTT	44	1610
1131008	474	493	4419	4438	CTCATTCTTGTGGAAAAACC	25	1611
1131036	514	533	4459	4478	GGCATCTGGCCACAGCTGCT	20	1612
1131064	554	573	4499	4518	CTGGCCAGCCGCTGGCAGTG	102	1613
1131092	591	610	4675	4694	ACCCCATGGAGGCACGGGT	45	1614
1131120	631	650	4715	4734	GGCAGTGGCACAGGCGGTGG	20	1615
1131148	696	715	4925	4944	CCCGCGGCCATCATAGCAGC	57	1616
1131176	749	768	4978	4997	GGCTGACAGGGCGCACCCGA	31	1617
1131204	802	821	5031	5050	AGTTCGCGCTTGCTCGGCA	13	1618
1131232	886	905	5200	5219	TCAGCCGGTCGCGGTTTCAGC	39	1619
1131260	974	993	5288	5307	AGTGGGACATGAAGCCTAGG	34	1620
1131288	1060	1079	N/A	N/A	TCGCCGGCAAGGCTCCCGGG	68	1621
1131316	1095	1114	5514	5533	GCCGTTCTTGGTCAGGGAAG	27	1622
1131344	1138	1157	5557	5576	TCGAAGACAGACTCTTGCGG	15	1623
1131372	1212	1231	5631	5650	GTGGCCCCAGTACAGCGCGG	32	1624
1131400	1285	1304	N/A	N/A	CGGGCCGGTCCTGCAGGCAG	34	1625
1131428	1351	1370	6011	6030	TCTGGCACGGCTCACAGCTG	17	1626
1131456	1441	1460	6184	6203	CATCCTCCTGAAGGCGCAAC	51	1627
1131484	1500	1519	6243	6262	GCCGCTTGGCAGGCACACCG	17	1628
1131512	1567	1586	N/A	N/A	CCGCCCCCTCGAACTGGTGG	125	1629
1131540	1609	1628	6907	6926	GGAACGGTACCTGCGCCTCC	62	1630
1131568	1701	1720	6999	7018	ATCGGTGCCGCCCTCGAGGA	43 [†]	1631
1131596	1783	1802	7171	7190	TGATGATGCCTTGCAGGGTG	21	1632
1131624	1812	1831	7200	7219	GTTGCGGTCACCACAGCCCG	20	1633
1131652	1860	1879	7248	7267	CCGGATCCAGGCCAGGTAGT	30	1634
1131680	1898	1917	7286	7305	AAAGATGAGTCCCTGAGCAA	20	1635
1131708	1940	1959	7328	7347	CATGCCCCAGCCACTCTCTC	25	1636
1131736	1993	2012	7381	7400	CATCCTGGCGCGGAGCTGGC	16	1637
1131764	2027	2046	7415	7434	AGCATTTTCAAAGCACTTTA	9	97

1131792	N/A	N/A	148	167	TGGCTGTGATAGCGACCCCC	50	1638
1131820	N/A	N/A	244	263	GTCTCCTCTGCCTGGGCCTT	61	1639
1131848	N/A	N/A	335	354	AACCCTTTCTACCTCCCCC	76	1640
1131876	N/A	N/A	425	444	GACTATAAGTCATAGCCTGC	145	1641
1131904	N/A	N/A	569	588	CTGCACCATAACACATCCCCA	37	1642
1131932	N/A	N/A	660	679	GATCACACAGCTCACGATCA	54	1643
1131960	N/A	N/A	779	798	GGAAACTGAGGAAGGCTGGC	85	1644
1131988	N/A	N/A	922	941	TGATAAAGCTGGGCTTCAGA	69	1645
1132016	N/A	N/A	1031	1050	CCTTCTCAACAACCCTAAGA	59	1646
1132044	N/A	N/A	1129	1148	GGTACCCTTCATCTAAAAGG	56	1647
1132072	N/A	N/A	1545	1564	TCCATCTGGTTCACAGGCC	66	1648
1132100	N/A	N/A	1676	1695	CAAGAGAGAGGAGAACTTT	108	1649
1132128	N/A	N/A	2090	2109	ATGGATCTGAGATGGACCTT	34	1650
1132156	N/A	N/A	2194	2213	AGTGTCTGGCACAAAGTACC	28	1651
1132184	N/A	N/A	2311	2330	TTCAATGTTCACTGTGATTT	52	1652
1132212	N/A	N/A	2446	2465	GCATTGATGAATCAGCAACA	55	1653
1132240	N/A	N/A	2560	2579	CTCTGAGCCTCCTGCTGAAG	33	1654
1132268	N/A	N/A	2697	2716	AGTTAAGGTTCAACAAGGCG	36	1655
1132296	N/A	N/A	2802	2821	GTGCCTACTTGCTGAATTTT	68	1656
1132324	N/A	N/A	2908	2927	AGTCACTGTTAACCACTCTG	41	1657
1132352	N/A	N/A	3012	3031	TCCACAACCTGCTAGCTGTG	29	1658
1132380	N/A	N/A	3406	3425	CTCAAAAAGGTCGCTGTGCA	36	1659
1132408	N/A	N/A	3493	3512	CAGGGACAACACACTCTCTG	86	1660
1132436	N/A	N/A	3691	3710	CAGTCCCCTCTCTCCAAGCA	55	1661
1132464	N/A	N/A	3859	3878	AGAGCCCCAGGCCACCCAG	39	1662
1132492	N/A	N/A	3981	4000	TCCTTCCCAGAACTCTCCCT	53	1663
1132520	N/A	N/A	4069	4088	GCCAAGGCCCTTCTTGAACC	25	1664
1132548	N/A	N/A	4269	4288	CAGCACCCCGCCCAGGTCCT	73	1665
1132576	N/A	N/A	4505	4524	CCCTGGCTGGCCAGCCGCTG	46	1666
1132604	N/A	N/A	4602	4621	CCCCCCCAGAGAGCTCTCCT	120	1667
1132632	N/A	N/A	4819	4838	TCCCTCCTCCTTCCTGGCAA	30	1668
1132660	N/A	N/A	5112	5131	CCGGGAGCCCGGAGCCCTGG	68	1669
1132688	N/A	N/A	5471	5490	AAGGCTGTGGAGGAGCAGGG	69	1670
1132716	N/A	N/A	5877	5896	CCCTGTCTCCCGAACCCCAAT	69	1671
1132744	N/A	N/A	6343	6362	GTCTCCTCCCCTACCCCTGC	63	1672
1132772	N/A	N/A	6445	6464	CTACACATTCTCACAACCCA	57	1673
1132800	N/A	N/A	6569	6588	AGTTGGCCTTTGCAGCCCGG	34	1674
1132828	N/A	N/A	6676	6695	CCAGGATTTGAATGGGCGGA	65	1675
1132856	N/A	N/A	6782	6801	CGCTTGTAACCCACTCATG	51	1676
1132884	N/A	N/A	7063	7082	TGAGATTTGTGCCTGACGGC	126 [†]	1677

Table 26. Reduction of FXII RNA by 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages
(Huh7, electroporation, 5000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1130757	21	40	21	40	CCGTTGGTCCAGCTGCCTAT	42	1678
1130785	69	88	69	88	GCTCACCAGCAGGAACCCCA	25	1679
1130813	127	146	494	513	CTTTGTACTTATGCTCCTTG	55	1680
1130841	161	180	N/A	N/A	CCGGTGACAGTGAGAACGAC	11	1681
1130869	214	233	3565	3584	TACATTTGTGGTACAGCTGC	13	1682
1130871	216	235	3567	3586	GGTACATTTGTGGTACAGCT	10	183
1130898	281	300	3788	3807	CGCTGGTCCTGATCAAAGTT	14	1683
1130926	320	339	N/A	N/A	TGGTCTTTCACTTTCTTGGG	23	1684
1130954	377	396	4185	4204	CCGCTTGGCATGTTACACA	15	1685
1130982	435	454	N/A	N/A	GCACTTCTCTTTCTGGCAGT	21	1686
1131010	476	495	4421	4440	ATCTCATTCTTGTGGAAAAA	29	1687
1131038	517	536	4462	4481	ACTGGCATCTGGCCACAGCT	36	1688
1131066	556	575	4501	4520	GGCTGGCCAGCCGCTGGCAG	51	1689
1131094	594	613	4678	4697	GCGACCCCCATGGAGGCACG	26	1690
1131122	635	654	4719	4738	ACCGGGCAGTGGCACAGGCG	50	1691
1131150	698	717	4927	4946	AGCCCGCGGCCATCATAGCA	56	1692
1131178	751	770	4980	4999	ACGGCTGACAGGGCGCACCC	29	52
1131206	805	824	5034	5053	CCCAGTTCCGCGCTTGCTCG	28	1693
1131234	889	908	5203	5222	AGCTCAGCCGGTCGCGGTTC	25	1694
1131262	976	995	5290	5309	TGAGTGGGACATGAAGCCTA	25	1695
1131290	1062	1081	N/A	N/A	CTTCGCCGGCAAGGCTCCCG	36	1696
1131318	1104	1123	5523	5542	GCTCAGTGGGCCGTTCTTGG	31	1697
1131346	1140	1159	5559	5578	CATCGAAGACAGACTCTTGC	15	1698
1131374	1215	1234	5634	5653	ACTGTGGCCCCAGTACAGCG	22	1699
1131402	1288	1307	N/A	N/A	GTGCGGGCCGGTCTGCAGG	79	1700
1131430	1353	1372	6013	6032	CGTCTGGCACGGCTCACAGC	22	1701
1131458	1443	1462	6186	6205	CGCATCCTCCTGAAGGCGCA	11	1702
1131486	1520	1539	6263	6282	GTCTCGGAGGGTCGCGCGGC	47	1703
1131514	1569	1588	N/A	N/A	CTCCGCCCCCTCGAACTGGT	61	1704
1131542	1612	1631	6910	6929	AGAGGAACGGTACCTGCGCC	155	1705
1131570	1704	1723	7002	7021	CGCATCGGTGCCGCCCTCGA	20 [†]	1706
1131598	1785	1804	7173	7192	GCTGATGATGCCTTGCAGGG	21	1707
1131626	1815	1834	7203	7222	CTTGTTGCGGTCACCACAGC	53	1708
1131654	1862	1881	7250	7269	TCCCGGATCCAGGCCAGGTA	60	1709
1131682	1905	1924	7293	7312	AGGAGGGAAAGATGAGTCCC	17	1710
1131710	1942	1961	7330	7349	TCCATGCCCCAGCCACTCTC	10	1711
1131738	1995	2014	7383	7402	GCCATCCTGGCGCGGAGCTG	21	157

1131766	2029	2048	7417	7436	TCAGCATTTTCAAAGCACTT	9	1712
1131794	N/A	N/A	154	173	GGCTCATGGCTGTGATAGCG	36	1713
1131822	N/A	N/A	250	269	TTGTCTGTCTCCTCTGCCTG	79	1714
1131850	N/A	N/A	341	360	GACCCAAACCCTTTCTACCT	37	1715
1131878	N/A	N/A	431	450	GGAAGTGAAGTATAAGTCATA	68	1716
1131906	N/A	N/A	576	595	GCACACACTGCACCATAACAC	74	1717
1131934	N/A	N/A	666	685	CTCAAGGATCACACAGCTCA	55	1718
1131962	N/A	N/A	835	854	GCATGAATGATGCCCATGAG	85	1719
1131990	N/A	N/A	928	947	CATAAGTGATAAAGCTGGGC	42	1720
1132018	N/A	N/A	1037	1056	GGTTTCCCTTCTCAACAACC	58	1721
1132046	N/A	N/A	1135	1154	ATGGCAGGTACCCTTCATCT	85	1722
1132074	N/A	N/A	1551	1570	GTAAGGTCCATCTGGTTCAC	61	1723
1132102	N/A	N/A	1682	1701	GTAAGGCAAGAGAGAGGAGA	35	1724
1132130	N/A	N/A	2096	2115	ATGGAATGGATCTGAGATG	53	1725
1132158	N/A	N/A	2204	2223	AATGCTGAGCAGTGTCTGGC	59	1726
1132186	N/A	N/A	2317	2336	TGCTAGTTCAATGTTCACTG	31	1727
1132214	N/A	N/A	2452	2471	AGCTTAGCATTGATGAATCA	49	1728
1132242	N/A	N/A	2567	2586	AAATGGCCTCTGAGCCTCCT	67	1729
1132270	N/A	N/A	2703	2722	ATTCCCAGTTAAGGTTCAAC	45	1730
1132298	N/A	N/A	2808	2827	GAGAATGTGCCTACTTGCTG	39	1731
1132326	N/A	N/A	2914	2933	TGTTGAAGTCACTGTTAACC	91	1732
1132354	N/A	N/A	3018	3037	CCTGACTCCACAACCTGCTA	36	1733
1132382	N/A	N/A	3412	3431	CAGACCCTCAAAAAGGTCGC	29	1734
1132410	N/A	N/A	3502	3521	TGAGAACTGCAGGGACAACA	76	1735
1132438	N/A	N/A	3697	3716	CTATCACAGTCCCCTCTCTC	64	1736
1132466	N/A	N/A	3865	3884	GAGGAGAGAGCCCCAGGCCA	51	1737
1132494	N/A	N/A	3987	4006	GACCACTCCTTCCCAGAACT	56	1738
1132522	N/A	N/A	4093	4112	GGGAGCTGAGTCACACAGCT	67	1739
1132550	N/A	N/A	4283	4302	TTGCCCTGTCCCCAGCAC	71	1740
1132578	N/A	N/A	4511	4530	TGCTCACCTGGCTGGCCAG	48	1741
1132606	N/A	N/A	4608	4627	TAAAGACCCCCCAGAGAGC	30	1742
1132634	N/A	N/A	4826	4845	CGCACTCTCCCTCCTCCTTC	51	1743
1132662	N/A	N/A	5146	5165	TCCTGTAGCCACACGACGGG	52	1744
1132690	N/A	N/A	5480	5499	TTCGCCGGCAAGGCTGTGGA	64	1745
1132718	N/A	N/A	5883	5902	GAAGCCCCCTGCTCCCGAAC	26	1746
1132746	N/A	N/A	6349	6368	TCAAAGGTCTCCTCCCCTAC	45	1747
1132774	N/A	N/A	6451	6470	ATTCACCTACACATTCTCAC	82	1748
1132802	N/A	N/A	6575	6594	CGTCCTAGTTGGCCTTTGCA	86	1749
1132830	N/A	N/A	6685	6704	AGAGAAAAGCCAGGATTTGA	93	1750
1132858	N/A	N/A	6802	6821	ATGGACAAAGCTGCTCCAGG	30	1751
1132886	N/A	N/A	7069	7088	TGGACCTGAGATTTGTGCCT	77 [†]	1752

Table 27. Reduction of FXII RNA by 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages
(Huh7, electroporation, 5000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1130784	68	87	68	87	CTCACCAGCAGGAACCCCAG	106	1753
1130812	126	145	493	512	TTTGTACTTATGCTCCTTGG	18	1754
1130840	160	179	N/A	N/A	CGGTGACAGTGAGAACGACT	18	1755
1130868	213	232	3564	3583	ACATTTGTGGTACAGCTGCC	18	1756
1130871	216	235	3567	3586	GGTACATTTGTGGTACAGCT	16	183
1130897	280	299	3787	3806	GCTGGTCCTGATCAAAGTTG	22	1757
1130925	319	338	N/A	N/A	GGTCTTTCACTTTCTTGGGC	16	1758
1130953	376	395	4184	4203	CGCTTGGCATGTTACACAG	40	1759
1130981	434	453	N/A	N/A	CACCTTCTCTTTCTGGCAGTG	15	1760
1131009	475	494	4420	4439	TCTCATTCCTGTGGAAAAAC	18	1761
1131037	516	535	4461	4480	CTGGCATCTGGCCACAGCTG	25	1762
1131065	555	574	4500	4519	GCTGGCCAGCCGCTGGCAGT	131	1763
1131093	592	611	4676	4695	GACCCCCATGGAGGCACGGG	36	1764
1131121	633	652	4717	4736	CGGGCAGTGGCACAGGCGGT	20	1765
1131149	697	716	4926	4945	GCCCCGCGCCATCATAGCAG	35	1766
1131177	750	769	4979	4998	CGGCTGACAGGGCGCACCCG	26	1767
1131205	804	823	5033	5052	CCAGTTCCGCGCTTGCTCGG	26	1768
1131233	888	907	5202	5221	GCTCAGCCGGTCGCGGTTCA	21	1769
1131261	975	994	5289	5308	GAGTGGGACATGAAGCCTAG	24	1770
1131289	1061	1080	N/A	N/A	TTCGCCGGAAGGCTCCCGG	40	1771
1131317	1102	1121	5521	5540	TCAGTGGGCCGTTCTTGGTC	31	1772
1131345	1139	1158	5558	5577	ATCGAAGACAGACTCTTGCG	19	1773
1131373	1213	1232	5632	5651	TGTGGCCCCAGTACAGCGCG	43	1774
1131401	1286	1305	N/A	N/A	GCGGGCCGGTCCTGCAGGCA	28	1775
1131429	1352	1371	6012	6031	GTCTGGCACGGCTCACAGCT	16	1776
1131457	1442	1461	6185	6204	GCATCCTCCTGAAGGCGCAA	24	1777
1131485	1501	1520	6244	6263	CGCCGCTTGGCAGGCACACC	45	1778
1131513	1568	1587	N/A	N/A	TCCGCCCCCTCGAACTGGTG	70	1779
1131541	1610	1629	6908	6927	AGGAACGGTACCTGCGCCTC	66	1780
1131597	1784	1803	7172	7191	CTGATGATGCCTTGCAGGGT	24	1781
1131625	1813	1832	7201	7220	TGTTGCGGTCACCACAGCCC	15	1782
1131653	1861	1880	7249	7268	CCCGGATCCAGGCCAGGTAG	40	1783
1131681	1901	1920	7289	7308	GGGAAAGATGAGTCCCTGAG	19	92
1131709	1941	1960	7329	7348	CCATGCCCCAGCCACTCTCT	18	1784
1131737	1994	2013	7382	7401	CCATCCTGGCGCGGAGCTGG	17	1785
1131765	2028	2047	7416	7435	CAGCATTTTCAAAGCACTTT	39	1786
1131793	N/A	N/A	151	170	TCATGGCTGTGATAGCGACC	80	1787

1131821	N/A	N/A	247	266	TCTGTCTCCTCTGCCTGGGC	91	1788
1131849	N/A	N/A	338	357	CCAAACCCTTTCTACCTCCC	103	1789
1131877	N/A	N/A	428	447	ACTGACTATAAGTCATAGCC	77	1790
1131905	N/A	N/A	572	591	ACACTGCACCATAACACATCC	59	1791
1131933	N/A	N/A	663	682	AAGGATCACACAGCTCACGA	64	1792
1131961	N/A	N/A	832	851	TGAATGATGCCCATGAGACG	33	1793
1131989	N/A	N/A	925	944	AAGTGATAAAGCTGGGCTTC	61	1794
1132017	N/A	N/A	1034	1053	TTCCCTTCTCAACAACCCTA	49	1795
1132045	N/A	N/A	1132	1151	GCAGGTACCCTTCATCTAAA	44	1796
1132073	N/A	N/A	1548	1567	AGGTCCATCTGGTTCACAGG	41	1797
1132101	N/A	N/A	1679	1698	AGGCAAGAGAGAGGAGAAAC	37	1798
1132129	N/A	N/A	2093	2112	GAAATGGATCTGAGATGGAC	65	1799
1132157	N/A	N/A	2201	2220	GCTGAGCAGTGTCTGGCACA	35	1800
1132185	N/A	N/A	2314	2333	TAGTTCAATGTTCACTGTGA	44	1801
1132213	N/A	N/A	2449	2468	TTAGCATTGATGAATCAGCA	46	1802
1132241	N/A	N/A	2564	2583	TGGCCTCTGAGCCTCCTGCT	60	1803
1132269	N/A	N/A	2700	2719	CCCAGTTAAGGTTCAACAAG	62	1804
1132297	N/A	N/A	2805	2824	AATGTGCCTACTTGCTGAAT	77	1805
1132325	N/A	N/A	2911	2930	TGAAGTCACTGTTAACCACT	45	1806
1132353	N/A	N/A	3015	3034	GACTCCACAACCTGCTAGCT	62	1807
1132381	N/A	N/A	3409	3428	ACCCTCAAAAAGGTCGCTGT	58	1808
1132409	N/A	N/A	3499	3518	GAAGTGCAGGGACAACACAC	48	1809
1132437	N/A	N/A	3694	3713	TCACAGTCCCCTCTCTCCAA	63	1810
1132465	N/A	N/A	3862	3881	GAGAGAGCCCCAGGCCACCC	41	1811
1132493	N/A	N/A	3984	4003	CACTCCTTCCCAGAACTCTC	52	1812
1132521	N/A	N/A	4090	4109	AGCTGAGTCACACAGCTGGG	69	1813
1132549	N/A	N/A	4272	4291	CCCCAGCACCCCGCCAGGT	113	1814
1132577	N/A	N/A	4508	4527	TCACCTGGCTGGCCAGCCG	103	1815
1132605	N/A	N/A	4605	4624	AGACCCCCCAGAGAGCTCT	72	1816
1132633	N/A	N/A	4823	4842	ACTCTCCCTCCTCCTTCCTG	42	1817
1132661	N/A	N/A	5115	5134	GCGCCGGGAGCCCGGAGCCC	92	1818
1132689	N/A	N/A	5474	5493	GGCAAGGCTGTGGAGGAGCA	82	1819
1132717	N/A	N/A	5880	5899	GCCCCCTGCTCCCGAACCCC	65	1820
1132745	N/A	N/A	6346	6365	AAGGTCTCCTCCCCCTACCCC	68	1821
1132773	N/A	N/A	6448	6467	CACCTACACATTCTCACAAC	66	1822
1132801	N/A	N/A	6572	6591	CCTAGTTGGCCTTTGCAGCC	67	1823
1132829	N/A	N/A	6679	6698	AAGCCAGGATTTGAATGGGC	50	1824
1132857	N/A	N/A	6799	6818	GACAAAGCTGCTCCAGGCGC	74	1825
1131569	1703	1722	7001	7020	GCATCGGTGCCGCCCTCGAG	8 [†]	1826
1132885	N/A	N/A	7066	7085	ACCTGAGATTTGTGCCTGAC	72 [†]	1827

Table 28. Reduction of FXII RNA by 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages
(Huh7, electroporation, 5000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1130758	22	41	22	41	TCCGTTGGTCCAGCTGCCTA	70	1828
1130786	70	89	70	89	AGCTCACCAGCAGGAACCCC	55	1829
1130814	128	147	495	514	GCTTTGTACTTATGCTCCTT	30	1830
1130842	162	181	N/A	N/A	CCCGGTGACAGTGAGAACGA	43	1831
1130870	215	234	3566	3585	GTACATTTGTGGTACAGCTG	19	182
1130871	216	235	3567	3586	GGTACATTTGTGGTACAGCT	10	183
1130899	282	301	3789	3808	TCGCTGGTCCTGATCAAAGT	30	1832
1130927	322	341	N/A	N/A	AGTGGTCTTTCACTTTCTTG	41	1833
1130955	378	397	4186	4205	GCCGCTTGGCATGTTACACAC	46	1834
1130983	436	455	N/A	N/A	AGCACTTCTCTTTCTGGCAG	14	1835
1131011	478	497	4423	4442	ATATCTCATTCTTGTGGAAG	39	1836
1131039	524	543	4469	4488	CCCTTGCCTGGCATCTGGC	38	1837
1131067	557	576	4502	4521	TGGCTGGCCAGCCGCTGGCA	45	1838
1131095	595	614	4679	4698	AGCGACCCCCATGGAGGCAC	21	1839
1131123	637	656	4721	4740	CCACCGGGCAGTGGCACAGG	42	1840
1131151	699	718	4928	4947	GAGCCCGCGGCCATCATAGC	85	1841
1131179	752	771	4981	5000	CACGGCTGACAGGGCGCACC	94	1842
1131207	808	827	5037	5056	GTCCCCAGTTCCGCGCTTGC	90	53
1131235	891	910	5205	5224	CCAGCTCAGCCGGTCGCGGT	72	1843
1131263	977	996	5291	5310	ATGAGTGGGACATGAAGCCT	51	1844
1131291	1063	1082	N/A	N/A	GCTTCGCCGGAAGGCTCCC	41	1845
1131319	1106	1125	5525	5544	CAGCTCAGTGGGCCGTTCTT	66	1846
1131347	1141	1160	5560	5579	TCATCGAAGACAGACTCTTG	27	1847
1131375	1216	1235	5635	5654	AACTGTGGCCCCAGTACAGC	17	1848
1131403	1289	1308	N/A	N/A	GGTGCGGGCCGGTCCTGCAG	79	1849
1131431	1371	1390	6031	6050	GTAGGAGCGCACGGCCAACG	46	1850
1131459	1445	1464	6188	6207	TCCGCATCCTCCTGAAGGCG	40	1851
1131487	1521	1540	6264	6283	GGTCTCGGAGGGTCGCGCGG	61	1852
1131515	1570	1589	N/A	N/A	CCTCCGCCCCCTCGAACTGG	258	1853
1131543	1613	1632	6911	6930	GAGAGGAACGGTACCTGCGC	80	1854
1131571	1707	1726	7005	7024	GCACGCATCGGTGCCGCCCT	22 [†]	1855
1131599	1786	1805	7174	7193	AGCTGATGATGCCTTGCAGG	25	1856
1131627	1816	1835	7204	7223	GCTTGTTCGGTCACCACAG	21	1857
1131655	1863	1882	7251	7270	CTCCCGGATCCAGGCCAGGT	81	1858
1131683	1906	1925	7294	7313	AAGGAGGGAAAGATGAGTCC	48	1859
1131711	1943	1962	7331	7350	TTCCATGCCCCAGCCACTCT	20	1860
1131739	1996	2015	7384	7403	CGCCATCCTGGCGCGGAGCT	15	1861
1131795	N/A	N/A	157	176	CATGGCTCATGGCTGTGATA	82	1862

1131823	N/A	N/A	253	272	TGGTTGTCTGTCTCCTCTGC	70	1863
1131851	N/A	N/A	344	363	CAAGACCCAAACCCTTTCTA	154	1864
1131879	N/A	N/A	434	453	CAGGGAAGTACTATAAGTC	74	1865
1131907	N/A	N/A	579	598	ACTGCACACACTGCACCATA	78	1866
1131935	N/A	N/A	669	688	GCCCTCAAGGATCACACAGC	80	1867
1131963	N/A	N/A	838	857	GTGGCATGAATGATGCCCAT	153	1868
1131991	N/A	N/A	931	950	GCTCATAAGTGATAAAGCTG	36	1869
1132019	N/A	N/A	1043	1062	CACATGGGTTTCCCTTCTCA	100	1870
1132047	N/A	N/A	1138	1157	GAAATGGCAGGTACCCTTCA	46	1871
1132075	N/A	N/A	1554	1573	AGGGTAAGGTCCATCTGGTT	85	1872
1132103	N/A	N/A	1688	1707	GTTTGGGTAAGGCAAGAGAG	47	1873
1132131	N/A	N/A	2099	2118	TAAATGGAAATGGATCTGAG	37	1874
1132159	N/A	N/A	2207	2226	TGAAATGCTGAGCAGTGTCT	84	1875
1132187	N/A	N/A	2320	2339	GTTTGCTAGTTCAATGTTCA	56	1876
1132215	N/A	N/A	2455	2474	ATCAGCTTAGCATTGATGAA	44	1877
1132243	N/A	N/A	2570	2589	TGGAAATGGCCTCTGAGCCT	52	1878
1132271	N/A	N/A	2706	2725	CACATTCCCAGTTAAGGTTC	30	1879
1132299	N/A	N/A	2811	2830	ATTGAGAATGTGCCTACTTG	87	1880
1132327	N/A	N/A	2917	2936	GAATGTTGAAGTCACTGTTA	74	1881
1132355	N/A	N/A	3021	3040	ACTCCTGACTCCACAACCTG	49	1882
1132383	N/A	N/A	3415	3434	GGACAGACCCTCAAAAAGGT	72	1883
1132411	N/A	N/A	3505	3524	CAGTGAGAACTGCAGGGACA	73	1884
1132439	N/A	N/A	3700	3719	GCCCTATCACAGTCCCCTCT	61	1885
1132467	N/A	N/A	3868	3887	CGGGAGGAGAGAGCCCCAGG	46	1886
1132495	N/A	N/A	3990	4009	TGGGACCACTCCTTCCCAGA	65	1887
1132523	N/A	N/A	4096	4115	GCAGGGAGCTGAGTCACACA	121	1888
1132551	N/A	N/A	4286	4305	GGGTTGCCCTGTCCCCCAG	59	1889
1132579	N/A	N/A	4514	4533	ATCTGCTCACCTGGCTGGC	48	1890
1132607	N/A	N/A	4611	4630	GCCTAAAGACCCCCCAGAG	75	1891
1132635	N/A	N/A	4832	4851	GCTTTCGCACTCTCCCTCC	54	1892
1132663	N/A	N/A	5149	5168	GGTTCCTGTAGCCACACGAC	86	1893
1132691	N/A	N/A	5483	5502	CGCTTCGCCGGCAAGGCTGT	41	1894
1132719	N/A	N/A	5910	5929	CTCAGACCTGGCCACAAGCG	89	1895
1132747	N/A	N/A	6352	6371	TGATCAAAGGTCTCCTCCCC	118	1896
1132775	N/A	N/A	6454	6473	GGGATTCACCTACACATTCT	119	1897
1132803	N/A	N/A	6600	6619	ACACTAGCCCGGAGCGCGGG	62	1898
1132831	N/A	N/A	6688	6707	TCCAGAGAAAAGCCAGGATT	86	1899
1132859	N/A	N/A	6805	6824	ACGATGGACAAAGCTGCTCC	55	1900
1132887	N/A	N/A	7072	7091	CTGTGGACCTGAGATTTGTG	155 [†]	1901

Table 29. Reduction of FXII RNA by 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages
(Huh7, electroporation, 5000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1130759	24	43	24	43	CGTCCGTTGGTCCAGCTGCC	35	1902
1130787	71	90	71	90	AAGCTCACCAGCAGGAACCC	47	1903
1130815	129	148	496	515	AGCTTTGTACTTATGCTCCT	44	1904
1130843	163	182	N/A	N/A	CCCCGGTGACAGTGAGAACG	27	1905
1130871	216	235	3567	3586	GGTACATTTGTGGTACAGCT	17	183
1130872	217	236	3568	3587	GGGTACATTTGTGGTACAGC	23	25
1130900	283	302	3790	3809	ATCGCTGGTCTGTGATCAAAG	22	1906
1130928	323	342	N/A	N/A	CAGTGGTCTTTCACCTTCTT	12	1907
1130956	379	398	4187	4206	GGCCGCTTGGCATGTTTACA	66	1908
1130984	438	457	N/A	N/A	AAAGCACTTCTCTTCTGGC	33	1909
1131012	479	498	4424	4443	CATATCTCATTCTTGTGGAA	38	1910
1131040	525	544	4470	4489	ACCTTGGCACTGGCATCTGG	22	1911
1131068	558	577	4503	4522	CTGGCTGGCCAGCCGCTGGC	26	1912
1131096	597	616	4681	4700	GCAGCGACCCCATGGAGGC	23	1913
1131124	638	657	4722	4741	CCCACCGGGCAGTGGCACAG	45	1914
1131152	701	720	4930	4949	CTGAGCCCGCGGCCATCATA	35	1915
1131180	753	772	4982	5001	CCACGGCTGACAGGGCGCAC	36	1916
1131208	812	831	5041	5060	CCCAGTCCCCAGTTCGCGCG	22	1917
1131236	892	911	5206	5225	CCCAGCTCAGCCGGTCGCGG	71	1918
1131264	979	998	5293	5312	GCATGAGTGGGACATGAAGC	47	1919
1131292	1064	1083	N/A	N/A	CGCTTCGCCGGCAAGGCTCC	55	1920
1131320	1107	1126	5526	5545	GCAGCTCAGTGGGCCGTTCC	71	1921
1131348	1143	1162	5562	5581	GGTCATCGAAGACAGACTCT	22	1922
1131376	1218	1237	5637	5656	GAAACTGTGGCCCCAGTACA	32	1923
1131404	1302	1321	5962	5981	CGTCAGATCCTCGGGTGCGG	29	1924
1131432	1372	1391	6032	6051	GGTAGGAGCGCACGGCCAAC	22	1925
1131460	1446	1465	6189	6208	GTCCGCATCCTCCTGAAGGC	31	1926
1131488	1522	1541	6265	6284	TGGTCTCGGAGGGTCGCGCG	40	1927
1131516	1571	1590	N/A	N/A	TCCTCCGCCCCCTCGAACTG	425	1928
1131544	1614	1633	6912	6931	GGAGAGGAACGGTACCTGCG	87	1929
1131572	1709	1728	7007	7026	TGGCACGCATCGGTGCCGCC	63 [†]	1930
1131600	1787	1806	7175	7194	CAGCTGATGATGCCTTGACG	90	1931
1131628	1817	1836	7205	7224	GGCTTGTTGCGGTCACCACA	40	1932
1131656	1864	1883	7252	7271	GCTCCCGGATCCAGGCCAGG	56	1933
1131684	1907	1926	7295	7314	CAAGGAGGGAAAGATGAGTC	33	1934
1131712	1944	1963	7332	7351	CTTCCATGCCCCAGCCACTC	20	1935
1131740	1997	2016	7385	7404	GCGCCATCCTGGCGCGGAGC	38	1936
1131796	N/A	N/A	160	179	GGCCATGGCTCATGGCTGTG	79	1937

1131824	N/A	N/A	256	275	GTCTGGTTGTCTGTCTCCTC	63	1938
1131852	N/A	N/A	347	366	TCCCAAGACCCAAACCCTTT	57	1939
1131880	N/A	N/A	437	456	AGGCAGGGAACCTGACTATAA	33	1940
1131908	N/A	N/A	582	601	GAGACTGCACACACTGCACC	40	1941
1131936	N/A	N/A	672	691	CCTGCCCTCAAGGATCACAC	45	1942
1131964	N/A	N/A	841	860	TGTGTGGCATGAATGATGCC	85	1943
1131992	N/A	N/A	934	953	CCAGCTCATAAGTGATAAAG	36	1944
1132020	N/A	N/A	1046	1065	CCTCACATGGGTTTCCCTTC	26	1945
1132048	N/A	N/A	1159	1178	TGGCAGAGCTTGAGGAAGGG	31	1946
1132076	N/A	N/A	1557	1576	ACCAGGGTAAGGTCCATCTG	65	1947
1132104	N/A	N/A	1691	1710	CAAGTTTGGGTAAGGCAAGA	40	1948
1132132	N/A	N/A	2102	2121	CAGTAAATGGAAATGGATCT	64	1949
1132160	N/A	N/A	2210	2229	CCATGAAATGCTGAGCAGTG	46	1950
1132188	N/A	N/A	2323	2342	ACTGTTTGCTAGTTCAATGT	25	1951
1132216	N/A	N/A	2458	2477	GCCATCAGCTTAGCATTGAT	38	1952
1132244	N/A	N/A	2573	2592	TTTTGGAAATGGCCTCTGAG	71	1953
1132272	N/A	N/A	2709	2728	TTGCACATTCCCAGTTAAGG	58	1954
1132300	N/A	N/A	2814	2833	TACATTGAGAATGTGCCTAC	116	1955
1132328	N/A	N/A	2920	2939	GTTGAATGTTGAAGTCACTG	47	1956
1132356	N/A	N/A	3024	3043	TAGACTCCTGACTCCACAAC	110	1957
1132384	N/A	N/A	3418	3437	AAAGGACAGACCCTCAAAAA	113	1958
1132412	N/A	N/A	3508	3527	TGACAGTGAGAACTGCAGGG	30	1959
1132440	N/A	N/A	3703	3722	CCTGCCCTATCACAGTCCCC	84	1960
1132468	N/A	N/A	3871	3890	AGGCGGGAGGAGAGAGCCCC	62	1961
1132496	N/A	N/A	3993	4012	AAATGGGACCACTCCTTCCC	41	1962
1132524	N/A	N/A	4099	4118	AGAGCAGGGAGCTGAGTCAC	60	1963
1132552	N/A	N/A	4289	4308	CCAGGGTTGCCCTGTCCCC	190	1964
1132580	N/A	N/A	4517	4536	ACCATCTGCTCACCTGGCT	67	1965
1132608	N/A	N/A	4614	4633	TGGGCCTAAAGACCCCCCA	74	1966
1132636	N/A	N/A	4835	4854	TCTGCTTTCCGCACTCTCCC	36	1967
1132664	N/A	N/A	5152	5171	CCGGGTTCTGTAGCCACAC	53	1968
1132692	N/A	N/A	5702	5721	CGCCGGTCTGCAGGCAGTG	54	1969
1132720	N/A	N/A	5913	5932	GCTCTCAGACCTGGCCACAA	94	1970
1132748	N/A	N/A	6355	6374	CAGTGATCAAAGGTCTCCTC	73	1971
1132776	N/A	N/A	6457	6476	CCTGGGATTACCTACACAT	46	1972
1132804	N/A	N/A	6603	6622	CCCACACTAGCCCGGAGCGC	52	1973
1132832	N/A	N/A	6691	6710	AGGTCCAGAGAAAAGCCAGG	60	1974
1132860	N/A	N/A	6808	6827	CGGACGATGGACAAAGCTGC	37	1975
1132888	N/A	N/A	7075	7094	GCGCTGTGGACCTGAGATTT	87 [†]	1976

Table 30. Reduction of FXII RNA by 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages
(Huh7, electroporation, 5000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1130788	72	91	72	91	CAAGCTCACCAGCAGGAACC	44	1977
1130816	130	149	497	516	CAGCTTTGTACTTATGCTCC	46	1978
1130844	164	183	3515	3534	TCCCCGGTGACAGTGAGAAC	43	24
1130871	216	235	3567	3586	GGTACATTTGTGGTACAGCT	12	183
1130873	218	237	3569	3588	TGGGTACATTTGTGGTACAG	22	1979
1130901	284	303	3791	3810	CATCGCTGGTCCTGATCAAA	26	1980
1130929	324	343	N/A	N/A	GCAGTGGTCTTTCACTTTCT	35	1981
1130957	380	399	4188	4207	GGGCCGCTTGGCATGTTTAC	32	1982
1130985	439	458	N/A	N/A	CAAAGCACTTCTCTTTCTGG	34	1983
1131013	481	500	4426	4445	ACCATATCTCATTCTTGTGG	21	1984
1131041	526	545	4471	4490	GACCCTTGCACTGGCATCTG	27	1985
1131069	559	578	4504	4523	CCTGGCTGGCCAGCCGCTGG	76	1986
1131097	598	617	4682	4701	GGCAGCGACCCCCATGGAGG	24	1987
1131125	640	659	4724	4743	AGCCACCGGGCAGTGGCAC	57	1988
1131153	702	721	4931	4950	GCTGAGCCCCGCGGCCATCAT	36	1989
1131181	754	773	4983	5002	CCCACGGCTGACAGGGCGCA	37	1990
1131209	813	832	5042	5061	GCCCAGTCCCCAGTTCCGCG	41	1991
1131237	893	912	5207	5226	TCCCAGCTCAGCCGGTCGCG	40	1992
1131265	980	999	5294	5313	GGCATGAGTGGGACATGAAG	28	1993
1131293	1065	1084	N/A	N/A	CCGCTTCGCCGGCAAGGCTC	35	1994
1131321	1108	1127	5527	5546	CGCAGCTCAGTGGGCCGTTT	32	1995
1131349	1144	1163	5563	5582	GGGTCATCGAAGACAGACTC	44	1996
1131377	1219	1238	5638	5657	AGAAACTGTGGCCCCAGTAC	46	1997
1131405	1303	1322	5963	5982	CCGTCAGATCCTCGGGTGCG	28	1998
1131433	1373	1392	6033	6052	CGGTAGGAGCGCACGGCCAA	21	1999
1131461	1448	1467	6191	6210	CCGTCCGCATCCTCCTGAAG	42	2000
1131489	1523	1542	6266	6285	GTGGTCTCGGAGGGTCGCGC	41	2001
1131517	1572	1591	N/A	N/A	TTCTCCGCCCCCTCGAACT	194	2002
1131545	1615	1634	6913	6932	GGGAGAGGAACGGTACCTGC	65	2003
1131573	1710	1729	7008	7027	CTGGCACGCATCGGTGCCGC	121 [†]	2004
1131601	1788	1807	7176	7195	CCAGCTGATGATGCCTTGCA	22	2005
1131629	1818	1837	7206	7225	TGGCTTGTTGCGGTCACCAC	26	2006
1131657	1865	1884	7253	7272	TGCTCCCGGATCCAGGCCAG	44	2007
1131685	1908	1927	7296	7315	CCAAGGAGGGAAAGATGAGT	22	2008
1131713	1945	1964	7333	7352	CCTTCCATGCCCCAGCCACT	15	2009
1131741	1999	2018	7387	7406	CTGCGCCATCCTGGCGCGGA	83	2010
1131797	N/A	N/A	163	182	AGAGGCCATGGCTCATGGCT	91	2011

1131825	N/A	N/A	259	278	CCAGTCTGGTTGTCTGTCTC	60	2012
1131853	N/A	N/A	350	369	TCTTCCCAAGACCCAAACCC	65	2013
1131881	N/A	N/A	440	459	AGAAGGCAGGGAAGTACTA	84	2014
1131909	N/A	N/A	585	604	CCTGAGACTGCACACACTGC	56	2015
1131937	N/A	N/A	675	694	TACCCTGCCCTCAAGGATCA	42	2016
1131965	N/A	N/A	844	863	CTCTGTGTGGCATGAATGAT	71	2017
1131993	N/A	N/A	937	956	CACCCAGCTCATAAGTGATA	63	2018
1132021	N/A	N/A	1049	1068	ATACCTCACATGGGTTTCCC	59	2019
1132049	N/A	N/A	1162	1181	CTATGGCAGAGCTTGAGGAA	62	2020
1132077	N/A	N/A	1560	1579	CCCACCAGGGTAAGGTCCAT	54	2021
1132105	N/A	N/A	1694	1713	CACCAAGTTTGGGTAAGGCA	34	2022
1132133	N/A	N/A	2105	2124	GGACAGTAAATGGAAATGGA	45	2023
1132161	N/A	N/A	2219	2238	GAGATAATGCCATGAAATGC	56	2024
1132189	N/A	N/A	2326	2345	AATACTGTTTGCTAGTTCAA	52	2025
1132217	N/A	N/A	2461	2480	AGTGCCATCAGCTTAGCATT	51	2026
1132245	N/A	N/A	2576	2595	GGCTTTTGAAATGGCCTCT	46	2027
1132273	N/A	N/A	2712	2731	AATTTGCACATTCCCAGTTA	64	2028
1132301	N/A	N/A	2817	2836	TTCTACATTGAGAATGTGCC	43	2029
1132329	N/A	N/A	2923	2942	CTTGTTGAATGTTGAAGTCA	50	2030
1132357	N/A	N/A	3027	3046	GAGTAGACTCCTGACTCCAC	73	2031
1132385	N/A	N/A	3421	3440	GGAAAAGGACAGACCCTCAA	72	2032
1132413	N/A	N/A	3511	3530	CGGTGACAGTGAGAACTGCA	32	2033
1132441	N/A	N/A	3706	3725	CACCCTGCCCTATCACAGTC	74	2034
1132469	N/A	N/A	3874	3893	ATGAGGCGGGAGGAGAGAGC	72	2035
1132497	N/A	N/A	3996	4015	GCAAAATGGGACCACTCCTT	42	2036
1132525	N/A	N/A	4102	4121	GGAAGAGCAGGGAGCTGAGT	102	2037
1132553	N/A	N/A	4292	4311	GGCCCAGGGTTGCCCCTGTC	75	2038
1132581	N/A	N/A	4520	4539	CCAACCATCTGCTCACCCCTG	72	2039
1132609	N/A	N/A	4617	4636	CCCTGGGCCTAAAGACCCCC	115	2040
1132637	N/A	N/A	4838	4857	TCATCTGCTTTCCGCACTCT	44	2041
1132665	N/A	N/A	5155	5174	TGTCCGGGTTCTGTAGCCA	43	2042
1132693	N/A	N/A	5705	5724	ACTCGCCGGTCCTGCAGGCA	29	2043
1132721	N/A	N/A	6089	6108	GCCCCACGCACCCAGGTCG	132	2044
1132749	N/A	N/A	6358	6377	ACCCAGTGATCAAAGGTCTC	56	2045
1132777	N/A	N/A	6460	6479	CTACCTGGGATTACCTACA	51	2046
1132805	N/A	N/A	6606	6625	GCTCCCACACTAGCCCGGAG	52	2047
1132833	N/A	N/A	6694	6713	CTGAGGTCCAGAGAAAAGCC	25	2048
1132861	N/A	N/A	6811	6830	GCCCGGACGATGGACAAAGC	86	2049
1132889	N/A	N/A	7091	7110	GGAAACACGCAGCTCAGCGC	87 [†]	2050

Table 31. Reduction of FXII RNA by 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages
(Huh7, electroporation, 5000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (% UTC)	SEQ ID No.
1130761	27	46	27	46	ATCCGTCCGTTGGTCCAGCT	24	2051
1130789	73	92	73	92	CCAAGCTCACCAGCAGGAAC	47	2052
1130817	131	150	498	517	TCAGCTTTGTACTTATGCTC	43	2053
1130845	165	184	3516	3535	CTCCCCGGTGACAGTGAGAA	68	2054
1130871	216	235	3567	3586	GGTACATTTGTGGTACAGCT	16	183
1130874	220	239	3571	3590	TGTGGGTACATTTGTGGTAC	21	2055
1130902	286	305	3793	3812	CCCATCGCTGGTCCTGATCA	25	2056
1130930	326	345	N/A	N/A	CTGCAGTGGTCTTTCACTTT	56	2057
1130958	400	419	4208	4227	GTTGTGGACAGAGACAGTGG	37	2058
1130986	440	459	N/A	N/A	TCAAAGCACTTCTCTTTCTG	41	2059
1131014	484	503	4429	4448	TATACCATATCTCATCTTG	41	2060
1131042	527	546	4472	4491	GGACCCTTGCACTGGCATCT	39	2061
1131070	560	579	N/A	N/A	GCCTGGCTGGCCAGCCGCTG	82	2062
1131098	600	619	4684	4703	TAGGCAGCGACCCCCATGGA	47	2063
1131126	643	662	4727	4746	TGTAGCCCACCGGGCAGTGG	24	2064
1131154	703	722	4932	4951	AGCTGAGCCCGCGGCCATCA	29	2065
1131182	756	775	4985	5004	GGCCACGGCTGACAGGGCG	61	2066
1131210	815	834	5044	5063	CCGCCCAGTCCCCAGTTCCG	27	2067
1131238	894	913	5208	5227	CTCCAGCTCAGCCGGTCGC	66	2068
1131266	989	1008	5303	5322	GGCTGCGCGGGCATGAGTGG	66	2069
1131294	1066	1085	5485	5504	CCCGCTTCGCCGGCAAGGCT	49	2070
1131322	1109	1128	5528	5547	CCGCAGCTCAGTGGGCCGTT	67	2071
1131350	1146	1165	5565	5584	GCGGGTCATCGAAGACAGAC	23	2072
1131378	1220	1239	5639	5658	CAGAACTGTGGCCCCAGTA	51	2073
1131406	1305	1324	5965	5984	CACCGTCAGATCCTCGGGTG	31	2074
1131434	1375	1394	6035	6054	AGCGGTAGGAGCGCACGGCC	24	2075
1131462	1449	1468	6192	6211	GCCGTCCGCATCCTCCTGAA	17	2076
1131490	1524	1543	6267	6286	CGTGGTCTCGGAGGGTCGCG	28	2077
1131518	1573	1592	N/A	N/A	ATTCTCCGCCCCCTCGAAC	238	2078
1131546	1616	1635	6914	6933	AGGGAGAGGAACGGTACCTG	50	2079
1131574	1712	1731	N/A	N/A	CCCTGGCACGCATCGGTGCC	56 [†]	2080
1131602	1789	1808	7177	7196	CCCAGCTGATGATGCCTTGC	45	2081
1131630	1819	1838	7207	7226	CTGGCTTGTTGCGGTACCA	16	2082
1131658	1866	1885	7254	7273	GTGCTCCCGGATCCAGGCCA	32	2083
1131686	1909	1928	7297	7316	ACCAAGGAGGGAAAGATGAG	19	2084
1131714	1946	1965	7334	7353	GCCTTCCATGCCCCAGCCAC	30	2085
1131742	2000	2019	7388	7407	CCTGCGCCATCCTGGCGCGG	113	2086
1131798	N/A	N/A	166	185	AGCAGAGGCCATGGCTCATG	38	2087

1131826	N/A	N/A	262	281	CACCCAGTCTGGTTGTCTGT	71	2088
1131854	N/A	N/A	353	372	ATTTCTTCCCAAGACCCAAA	74	2089
1131882	N/A	N/A	443	462	AGAAGAAGGCAGGGAAGTGA	120	2090
1131910	N/A	N/A	591	610	GACTGCCCTGAGACTGCACA	59	2091
1131938	N/A	N/A	678	697	CCATACCCTGCCCTCAAGGA	46	2092
1131966	N/A	N/A	847	866	GGCCTCTGTGTGGCATGAAT	31	2093
1131994	N/A	N/A	941	960	GAGTCACCCAGCTCATAAGT	80	2094
1132022	N/A	N/A	1052	1071	TGAATACCTCACATGGGTTT	34	2095
1132050	N/A	N/A	1165	1184	GAGCTATGGCAGAGCTTGAG	51	2096
1132078	N/A	N/A	1563	1582	AGGCCACCAAGGTAAGGTC	61	2097
1132106	N/A	N/A	1702	1721	GGATAGGGCACCAAGTTTGG	77	2098
1132134	N/A	N/A	2108	2127	CTAGGACAGTAAATGGAAAT	33	2099
1132162	N/A	N/A	2222	2241	CATGAGATAATGCCATGAAA	50	2100
1132190	N/A	N/A	2329	2348	CCTAATACTGTTTGCTAGTT	36	2101
1132218	N/A	N/A	2464	2483	TATAGTGCCATCAGCTTAGC	43	2102
1132246	N/A	N/A	2579	2598	TTTGGCTTTTGAAATGGCC	29	2103
1132274	N/A	N/A	2715	2734	AAAAATTTGCACATTCCAG	85	2104
1132302	N/A	N/A	2820	2839	TGGTTCTACATTGAGAATGT	76	2105
1132330	N/A	N/A	2926	2945	ATACTTGTTGAATGTTGAAG	52	2106
1132358	N/A	N/A	3030	3049	CTGGAGTAGACTCCTGACTC	62	2107
1132386	N/A	N/A	3424	3443	TCAGGAAAAGGACAGACCCT	36	2108
1132414	N/A	N/A	3514	3533	CCCCGGTGACAGTGAGAACT	33	2109
1132442	N/A	N/A	3709	3728	GCCCACCCTGCCCTATCACA	40	2110
1132470	N/A	N/A	3877	3896	GTAATGAGGCGGGAGGAGAG	46	2111
1132498	N/A	N/A	3999	4018	CCTGCAAAATGGGACCACTC	60	2112
1132526	N/A	N/A	4105	4124	GAAGGAAGAGCAGGGAGCTG	58	2113
1132554	N/A	N/A	4295	4314	GTAGGCCCGGGTTGCCCT	71	2114
1132582	N/A	N/A	4523	4542	TTCCCAACCATCTGCTCACC	72	2115
1132610	N/A	N/A	4620	4639	CACCCCTGGGCCTAAAGACC	79	2116
1132638	N/A	N/A	4841	4860	CTCTCATCTGCTTTCCGCAC	60	2117
1132666	N/A	N/A	5158	5177	CGTTGTCCGGGTTCTGTAG	59	2118
1132694	N/A	N/A	5708	5727	GGTACTCGCCGGTCCTGCAG	37	2119
1132722	N/A	N/A	6111	6130	TCTCTTCCCGTCCCCGCGGG	60	2120
1132750	N/A	N/A	6361	6380	CTAACCAGTGATCAAAGGT	75	2121
1132778	N/A	N/A	6463	6482	ATTCTACCTGGGATTCACCT	34	2122
1132806	N/A	N/A	6609	6628	CTGGCTCCCACTAGCCCG	44	2123
1132834	N/A	N/A	6697	6716	AGGCTGAGGTCCAGAGAAAA	96	2124
1132862	N/A	N/A	6814	6833	GCCGCCCGGACGATGGACAA	97	2125
1132890	N/A	N/A	7094	7113	GTCGGAAACACGCAGCTCAG	90 [†]	2126

Table 32. Reduction of FXII RNA by 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages
(Huh7, electroporation, 5000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (% UTC)	SEQ ID No.
1130762	28	47	28	47	CATCCGTCCGTTGGTCCAGC	46	2127
1130790	74	93	74	93	TCCAAGCTCACCAGCAGGAA	41	2128
1130818	132	151	499	518	TTCAGCTTTGTACTTATGCT	63	2129
1130846	166	185	3517	3536	GCTCCCCGGTGACAGTGAGA	16	2130
1130871	216	235	3567	3586	GGTACATTTGTGGTACAGCT	15	183
1130875	221	240	3572	3591	TTGTGGGTACATTTGTGGTA	31	2131
1130903	287	306	3794	3813	CCCCATCGCTGGTCCTGATC	20	2132
1130931	328	347	N/A	N/A	TGCTGCAGTGGTCTTTCCT	55	2133
1130959	401	420	4209	4228	TGTTGTGGACAGAGACAGTG	67	2134
1130987	443	462	N/A	N/A	GGCTCAAAGCACTTCTCTTT	15	2135
1131015	485	504	4430	4449	CTATACCATATCTCATTCTT	20	2136
1131043	529	548	4474	4493	CAGGACCCTTGCACTGGCAT	38	2137
1131071	561	580	N/A	N/A	GGCCTGGCTGGCCAGCCGCT	114	2138
1131099	601	620	4685	4704	CTAGGCAGCGACCCCCATGG	40	2139
1131127	648	667	4732	4751	TCCGGTGTAGCCACCGGGC	104	2140
1131155	704	723	4933	4952	TAGCTGAGCCCGCGGCCATC	22	2141
1131183	759	778	4988	5007	CGAGGCCACGGCTGACAGG	51	2142
1131211	816	835	5045	5064	GCCGCCAGTCCCCAGTTCC	41	2143
1131239	896	915	5210	5229	TACTCCCAGCTCAGCCGGTC	49	2144
1131267	990	1009	5304	5323	CGGCTGCGCGGGCATGAGTG	71	2145
1131295	1067	1086	5486	5505	TCCCCGTTCCGCGCAAGGC	36	2146
1131323	1110	1129	5529	5548	CCCGCAGCTCAGTGGGCCGT	33	2147
1131351	1147	1166	5566	5585	CGCGGGTCATCGAAGACAGA	39	2148
1131379	1221	1240	5640	5659	GCAGAACTGTGGCCCCAGT	56	2149
1131407	1308	1327	5968	5987	CACCACCGTCAGATCCTCGG	40	2150
1131435	1376	1395	6036	6055	AAGCGGTAGGAGCGCACGGC	25	2151
1131463	1451	1470	6194	6213	CTGCCGTCCGCATCCTCCTG	22	2152
1131491	1542	1561	6285	6304	GCCGGCCACCTGGCAGAGCG	87	2153
1131519	1574	1593	N/A	N/A	TATTCCTCCGCCCCCTCGAA	316	2154
1131547	1617	1636	6915	6934	CAGGGAGAGGAACGGTACCT	116	2155
1131575	1743	1762	7131	7150	GTCCTCACACACCAGCGGGC	14 [†]	79
1131603	1790	1809	7178	7197	CCCCAGCTGATGATGCCTTG	50	2156
1131631	1820	1839	7208	7227	CCTGGCTTGTTGCGGTCACC	38	85
1131659	1867	1886	7255	7274	TGTGCTCCCGGATCCAGGCC	42	2157
1131687	1911	1930	7299	7318	TCACCAAGGAGGGAAAGATG	17	2158
1131715	1947	1966	7335	7354	TGCCCTTCATGCCCCAGCCA	36	156
1131743	2001	2020	7389	7408	TCCTGCGCCATCCTGGCGCG	30	2159
1131799	N/A	N/A	169	188	ATGAGCAGAGGCCATGGCTC	99	2160

1131827	N/A	N/A	265	284	ATCCACCCAGTCTGGTTGTC	89	2161
1131855	N/A	N/A	356	375	GAGATTTCTTCCCAAGACCC	107	2162
1131883	N/A	N/A	446	465	GAGAGAAGAAGGCAGGGAAC	126	2163
1131911	N/A	N/A	594	613	CTAGACTGCCCTGAGACTGC	72	2164
1131939	N/A	N/A	681	700	AGCCCATACCCTGCCCTCAA	38	2165
1131967	N/A	N/A	850	869	CCTGGCCTCTGTGTGGCATG	63	2166
1131995	N/A	N/A	947	966	CGCCCAGAGTCACCCAGCTC	34	2167
1132023	N/A	N/A	1055	1074	GGCTGAATACCTCACATGGG	74	2168
1132051	N/A	N/A	1188	1207	TCTGGAAGAATGAAAGCAAT	62	2169
1132079	N/A	N/A	1566	1585	GTCAGGCCACCAGGGTAAG	47	2170
1132107	N/A	N/A	1705	1724	CAAGGATAGGGCACCAAGTT	56	2171
1132135	N/A	N/A	2114	2133	CCAGAACTAGGACAGTAAAT	52	2172
1132163	N/A	N/A	2225	2244	CTTCATGAGATAATGCCATG	46	2173
1132191	N/A	N/A	2332	2351	GAACCTAATACTGTTTGCTA	27	2174
1132219	N/A	N/A	2467	2486	TGCTATAGTGCCATCAGCTT	60	2175
1132247	N/A	N/A	2582	2601	GGATTTGGCTTTTGGAATG	42	2176
1132275	N/A	N/A	2718	2737	GTGAAAAATTTGCACATTCC	50	2177
1132303	N/A	N/A	2823	2842	CTCTGGTTCTACATTGAGAA	36	2178
1132331	N/A	N/A	2929	2948	ATAATACTTGTTGAATGTTG	39	2179
1132359	N/A	N/A	3033	3052	TAGCTGGAGTAGACTCCTGA	92	2180
1132387	N/A	N/A	3427	3446	TGGTCAGGAAAAGGACAGAC	21	2181
1132415	N/A	N/A	3605	3624	TAGTCTTACCAGGGCTGAGG	50	2182
1132443	N/A	N/A	3734	3753	CTTCCCTGCTCTACCCAGGG	56	2183
1132471	N/A	N/A	3880	3899	AGAGTAATGAGGCGGGAGGA	44	2184
1132499	N/A	N/A	4002	4021	CCACCTGCAAAATGGGACCA	29	2185
1132527	N/A	N/A	4110	4129	TGGTGGAAGGAAGAGCAGGG	90	2186
1132555	N/A	N/A	4298	4317	TCTGTAGGCCCAAGGGTTGCC	73	2187
1132583	N/A	N/A	4526	4545	CCGTTCCCAACCATCTGCTC	42	2188
1132611	N/A	N/A	4623	4642	AGCCACCCCTGGGCCCTAAAG	150	2189
1132639	N/A	N/A	4844	4863	TCCCTCTCATCTGCTTTCCG	26	2190
1132667	N/A	N/A	5374	5393	CCACTTCCTAACCTCCCGGG	129	2191
1132695	N/A	N/A	5711	5730	GCGGGTACTCGCCGGTCCTG	58	2192
1132723	N/A	N/A	6114	6133	AGCTCTCTTCCCGTCCCCGC	67	2193
1132751	N/A	N/A	6364	6383	CGCCTAACCCAGTGATCAAA	91	2194
1132779	N/A	N/A	6472	6491	GGCCCTGGGATTCTACCTGG	50	2195
1132807	N/A	N/A	6612	6631	AACCTGGCTCCCACACTAGC	51	2196
1132835	N/A	N/A	6703	6722	GCAAGGAGGCTGAGGTCCAG	39	2197
1132863	N/A	N/A	6817	6836	CTTGCCGCCCGGACGATGGA	50	2198
1132891	N/A	N/A	7097	7116	TGGGTCGAAACACGCAGCT	115 [†]	2199

Table 33. Reduction of FXII RNA by 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages
(Huh7, electroporation, 5000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (% UTC)	SEQ ID No.
1130763	30	49	30	49	GGCATCCGTCCTGGTCCA	21	2200
1130791	75	94	75	94	CTCCAAGCTCACCAGCAGGA	37	2201
1130819	133	152	500	519	CTTCAGCTTTGTACTTATGC	70	2202
1130847	168	187	3519	3538	GGGCTCCCCGGTGACAGTGA	33	2203
1130871	216	235	3567	3586	GGTACATTTGTGGTACAGCT	14	183
1130876	222	241	3573	3592	CTTGTGGGTACATTTGTGGT	28	2204
1130904	288	307	3795	3814	TCCCCATCGCTGGTCCTGAT	43	2205
1130932	329	348	N/A	N/A	TTGCTGCAGTGGTCTTTCAC	24	2206
1130960	402	421	4210	4229	GTGTTGTGGACAGAGACAGT	34	2207
1130988	444	463	N/A	N/A	AGGCTCAAAGCACTTCTCTT	23	2208
1131016	487	506	4432	4451	TTCTATAACCATATCTCATTC	30	2209
1131044	530	549	4475	4494	TCAGGACCCTTGCACTGGCA	31	2210
1131072	563	582	N/A	N/A	CAGGCCTGGCTGGCCAGCCG	41	2211
1131100	603	622	4687	4706	CTCTAGGCAGCGACCCCCAT	22	2212
1131128	649	668	4733	4752	CTCCGGTGTAGCCACCGGG	44	2213
1131156	706	725	4935	4954	GGTAGCTGAGCCCGCGCCA	29	2214
1131184	760	779	4989	5008	CCGAGGCCACGGCTGACAG	78	2215
1131212	819	838	5048	5067	GTGGCCGCCAGTCCCCAGT	52	2216
1131240	897	916	5211	5230	GTACTCCCAGCTCAGCCGGT	33	2217
1131268	991	1010	5305	5324	CCGGCTGCGCGGCATGAGT	29	2218
1131296	1068	1087	5487	5506	CTCCCGCTTCGCCGCAAGG	35	2219
1131324	1113	1132	5532	5551	CTGCCCGCAGCTCAGTGGGC	53	2220
1131352	1149	1168	5568	5587	GACGCGGGTCATCGAAGACA	30	2221
1131380	1222	1241	5641	5660	CGCAGAACTGTGGCCCCAG	31	2222
1131408	1309	1328	5969	5988	GCACCACCGTCAGATCCTCG	49	2223
1131436	1377	1396	6037	6056	CAAGCGGTAGGAGCGCACGG	33	2224
1131464	1452	1471	6195	6214	GCTGCCGTCCGCATCCTCCT	38	2225
1131492	1544	1563	6287	6306	CAGCCGGCCACCTGGCAGAG	63	2226
1131520	1575	1594	N/A	N/A	ATATTCCTCCGCCCCCTCGA	216	2227
1131548	1618	1637	6916	6935	CCAGGGAGAGGAACGGTACC	119	2228
1131604	1791	1810	7179	7198	TCCCCAGCTGATGATGCCTT	29	2229
1131632	1821	1840	7209	7228	GCCTGGCTTGTGCGGTCAC	27	2230
1131660	1868	1887	7256	7275	GTGTGCTCCCGGATCCAGGC	43	2231
1131688	1913	1932	7301	7320	AATCACCAAGGAGGAAAGA	14	2232
1131716	1948	1967	7336	7355	TTGCCTTCCATGCCCCAGCC	19	2233
1131744	2003	2022	7391	7410	GTTCCTGCGCCATCCTGGCG	7	2234
1131772	N/A	N/A	88	107	CCGAAAGTGTTGACTCCAAG	64	2235
1131800	N/A	N/A	172	191	GTCATGAGCAGAGGCCATGG	43	2236

1131828	N/A	N/A	268	287	TGTATCCACCCAGTCTGGTT	70	2237
1131856	N/A	N/A	359	378	GCAGAGATTTCTTCCCAAGA	53	2238
1131884	N/A	N/A	451	470	CAAGGGAGAGAAGAAGGCAG	75	2239
1131912	N/A	N/A	597	616	AGACTAGACTGCCCTGAGAC	40	2240
1131940	N/A	N/A	684	703	CACAGCCCATAACCCTGCCCT	57	2241
1131968	N/A	N/A	853	872	GGCCCTGGCCTCTGTGTGGC	70	2242
1131996	N/A	N/A	951	970	CCCTCGCCCAGAGTCACCCA	58	2243
1132024	N/A	N/A	1058	1077	ATGGGCTGAATACCTCACAT	44	2244
1132052	N/A	N/A	1191	1210	GTGTCTGGAAGAATGAAAGC	45	2245
1132080	N/A	N/A	1569	1588	CAAGTCAGGCCACCAGGGT	47	2246
1132108	N/A	N/A	1708	1727	AGGCAAGGATAGGGCACCAA	44	2247
1132136	N/A	N/A	2117	2136	AAACCAGAACTAGGACAGTA	52	2248
1132164	N/A	N/A	2228	2247	GGGCTTCATGAGATAATGCC	63	2249
1132192	N/A	N/A	2335	2354	CAGGAACCTAATACTGTTTG	66	2250
1132220	N/A	N/A	2470	2489	GTGTGCTATAGTGCCATCAG	44	2251
1132248	N/A	N/A	2601	2620	CACCTTGTGCTTTTGCTGGG	59	2252
1132276	N/A	N/A	2721	2740	GCAGTGAAAAATTTGCACAT	41	2253
1132304	N/A	N/A	2826	2845	CTTCTCTGGTTCTACATTGA	52	2254
1132332	N/A	N/A	2933	2952	CTTAATAATACTTGTGAAT	56	2255
1132360	N/A	N/A	3036	3055	AGATAGCTGGAGTAGACTCC	57	2256
1132388	N/A	N/A	3430	3449	GTCTGGTCAGGAAAAGGACA	74	2257
1132416	N/A	N/A	3625	3644	CCTGCTCCAACCTCTGCG	27	2258
1132444	N/A	N/A	3737	3756	AGGCTTCCCTGCTCTACCCA	61	2259
1132472	N/A	N/A	3883	3902	AGGAGAGTAATGAGGCGGGA	46	2260
1132500	N/A	N/A	4009	4028	GGTTTACCCACCTGCAAAAT	36	2261
1132528	N/A	N/A	4113	4132	ACATGGTGGAAGGAAGAGCA	35	2262
1132556	N/A	N/A	4301	4320	TATTCTGTAGGCCCAGGGTT	71	2263
1132584	N/A	N/A	4529	4548	GGCCCGTTCCCAACCATCTG	43	2264
1132612	N/A	N/A	4626	4645	GTGAGCCACCCCTGGGCCTA	80	2265
1132640	N/A	N/A	4848	4867	TGCCTCCCTCTCATCTGCTT	74	2266
1132668	N/A	N/A	5377	5396	CCCCACTTCCTAACCTCCC	60	2267
1132696	N/A	N/A	5745	5764	GAGGAGCCGCGGCCCTGGG	70	2268
1132724	N/A	N/A	6117	6136	CCAAGCTCTCTTCCCGTCCC	60	2269
1132752	N/A	N/A	6367	6386	TTCCGCCTAACCCAGTGATC	68	2270
1132780	N/A	N/A	6475	6494	CCAGGCCCTGGGATTCTACC	46	2271
1132808	N/A	N/A	6615	6634	CAGAACCTGGCTCCCACACT	83	2272
1132836	N/A	N/A	6706	6725	TAGGCAAGGAGGCTGAGGTC	80	2273
1132864	N/A	N/A	6820	6839	ACGCTTGCCGCCCCGACGAT	83	2274
1132892	N/A	N/A	7100	7119	CCCTGGGTTCGGAAACACGCA	50 [†]	2275

Table 34. Reduction of FXII RNA by 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages
(Huh7, electroporation, 5000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (% UTC)	SEQ ID No.
1130764	31	50	31	50	TGGCATCCGTCCGTTGGTCC	45	2276
1130792	77	96	77	96	GACTCCAAGCTCACCAGCAG	69	2277
1130820	134	153	501	520	TCTTCAGCTTTGTACTTATG	43	2278
1130848	169	188	3520	3539	AGGGCTCCCCGGTGACAGTG	30	2279
1130871	216	235	3567	3586	GGTACATTTGTGGTACAGCT	17	183
1130877	224	243	3575	3594	CCCTTGTGGGTACATTTGTG	45	2280
1130905	289	308	3796	3815	ATCCCCATCGCTGGTCCTGA	48	2281
1130933	330	349	N/A	N/A	TTTGCTGCAGTGGTCTTTCA	37	2282
1130961	403	422	4211	4230	GGTGTTGTGGACAGAGACAG	43	2283
1130989	445	464	4390	4409	GAGGCTCAAAGCACTTCTCT	32	2284
1131017	488	507	4433	4452	GTTCTATACCATATCTCATT	37	2285
1131045	531	550	4476	4495	ATCAGGACCCTTGCACTGGC	38	2286
1131073	564	583	N/A	N/A	GCAGGCCTGGCTGGCCAGCC	50	2287
1131101	604	623	4688	4707	CCTCTAGGCAGCGACCCCCA	41	2288
1131129	651	670	4735	4754	GGCTCCGGTGTAGCCCACCG	60	2289
1131157	707	726	4936	4955	CGGTAGCTGAGCCCGCGGCC	55	2290
1131185	761	780	4990	5009	TCCGAGGCCCCACGGCTGACA	49	2291
1131213	836	855	N/A	N/A	GGGTTCCGGCAGAAGGCGTG	66	2292
1131241	899	918	5213	5232	CAGTACTCCCAGCTCAGCCG	38	2293
1131269	992	1011	5306	5325	GCCGGCTGCGCGGGCATGAG	51	2294
1131297	1070	1089	5489	5508	TGCTCCCGCTTCGCCGGCAA	30	2295
1131325	1115	1134	5534	5553	CGCTGCCCCGAGCTCAGTGG	45	2296
1131353	1150	1169	5569	5588	CGACGCGGGTCATCGAAGAC	67	2297
1131381	1223	1242	5642	5661	GCGCAGAAACTGTGGCCCCA	47	112
1131409	1310	1329	5970	5989	AGCACCACCGTCAGATCCTC	18	2298
1131437	1378	1397	6038	6057	GCAAGCGGTAGGAGCGCACG	50	2299
1131465	1455	1474	6198	6217	GCAGCTGCCGTCCGCATCCT	45	70
1131493	1547	1566	6290	6309	CCCCAGCCGGCCACCTGGCA	74	2300
1131521	1577	1596	N/A	N/A	GCATATTCTCCGCCCCCTC	148	2301
1131549	1619	1638	6917	6936	TCCAGGGAGAGGAACGGTAC	130	2302
1131577	1745	1764	7133	7152	TGGTCCTCACACACCAGCGG	6 [†]	2303
1131605	1792	1811	7180	7199	ATCCCCAGCTGATGATGCCT	28	2304
1131633	1822	1841	7210	7229	CGCCTGGCTTGTGCGGTCA	34	2305
1131661	1869	1888	7257	7276	GGTGTGCTCCCGGATCCAGG	39	2306
1131689	1914	1933	7302	7321	GAATCACCAAGGAGGGAAAG	21	2307
1131717	1949	1968	7337	7356	CTTGCTTCCATGCCCCAGC	24	2308
1131745	2004	2023	7392	7411	AGTTCCTGCGCCATCCTGGC	25	2309
1131773	N/A	N/A	91	110	TCACCGAAAGTGTTGACTCC	87	2310

1131801	N/A	N/A	175	194	CAGGTCATGAGCAGAGGCCA	70	2311
1131829	N/A	N/A	271	290	CCTTGTATCCACCCAGTCTG	76	2312
1131857	N/A	N/A	365	384	AGAAATGCAGAGATTTCTTC	91	2313
1131885	N/A	N/A	454	473	CTACAAGGGAGAGAAGAAGG	88	2314
1131913	N/A	N/A	600	619	ACTAGACTAGACTGCCCTGA	77	2315
1131941	N/A	N/A	687	706	AGACACAGCCCATACCCTGC	41	2316
1131969	N/A	N/A	856	875	GAAGGCCCTGGCCTCTGTGT	31	2317
1131997	N/A	N/A	954	973	AATCCCTCGCCAGAGTCAC	90	2318
1132025	N/A	N/A	1061	1080	GTGATGGGCTGAATACCTCA	49	2319
1132053	N/A	N/A	1194	1213	TTAGTGTCTGGAAGAATGAA	60	2320
1132081	N/A	N/A	1572	1591	CACCAAGTCAGGCCCACCAG	80	2321
1132109	N/A	N/A	1711	1730	ATTAGGCAAGGATAGGGCAC	32	2322
1132137	N/A	N/A	2120	2139	ACCAAACCAGAACTAGGACA	56	2323
1132165	N/A	N/A	2250	2269	CTTCTTCAGAGGAATTGTCTG	59	2324
1132193	N/A	N/A	2338	2357	TCACAGGAACCTAATACTGT	61	2325
1132221	N/A	N/A	2473	2492	GGTGTGTGCTATAGTGCCAT	59	2326
1132249	N/A	N/A	2604	2623	TCACACTTTGTGCTTTTGCT	35	2327
1132277	N/A	N/A	2724	2743	AGAGCAGTGAAAAATTTGCA	44	2328
1132305	N/A	N/A	2829	2848	ATTCTTCTCTGGTTCTACAT	56	2329
1132333	N/A	N/A	2936	2955	GCACTTAATAATACTTGTTG	41	2330
1132361	N/A	N/A	3039	3058	GTCAGATAGCTGGAGTAGAC	36	2331
1132389	N/A	N/A	3433	3452	AGGGTCTGGTCAGGAAAAGG	47	2332
1132417	N/A	N/A	3628	3647	GCCCCCTGCTCCAACCTCCTCT	63	2333
1132445	N/A	N/A	3740	3759	ACAAGGCTTCCCTGCTCTAC	102	2334
1132473	N/A	N/A	3886	3905	ACCAGGAGAGTAATGAGGCG	47	2335
1132501	N/A	N/A	4012	4031	CTTGTTTTACCCACCTGCAA	59	2336
1132529	N/A	N/A	4116	4135	TGGACATGGTGGAAGGAAGA	94	2337
1132557	N/A	N/A	4304	4323	ACCTATTCTGTAGGCCCAGG	53	2338
1132585	N/A	N/A	4532	4551	CCTGGCCCCGTCCCAACCAT	64	2339
1132613	N/A	N/A	4629	4648	GCAGTGAGCCACCCCTGGGC	72	2340
1132641	N/A	N/A	4851	4870	TCCTGCCTCCCTCTCATCTG	66	2341
1132669	N/A	N/A	5380	5399	CCCCCCCCACTTCCTAACCT	84	2342
1132697	N/A	N/A	5748	5767	ACGGAGGAGCCGCGGCCCT	52	2343
1132725	N/A	N/A	6120	6139	GCCCCAAGCTCTCTTCCCGT	120	2344
1132753	N/A	N/A	6370	6389	TTCTTCCGCCTAACCCAGTG	71	2345
1132781	N/A	N/A	6478	6497	ATCCCAGGCCCTGGGATTCT	79	2346
1132809	N/A	N/A	6618	6637	TCGCAGAACCTGGCTCCAC	60	2347
1132837	N/A	N/A	6709	6728	TCATAGGCAAGGAGGCTGAG	78	2348
1132865	N/A	N/A	6836	6855	CACACCCCATCTGACAACGC	82	2349
1132893	N/A	N/A	7103	7122	TCACCCTGGGTCGGAACAC	73 [†]	2350

Table 35. Reduction of FXII RNA by 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages
(Huh7, electroporation, 5000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1130793	78	97	78	97	TGACTCCAAGCTCACCAGCA	34	239
1130821	135	154	502	521	CTCTTCAGCTTTGTACTTAT	42	240
1130849	171	190	3522	3541	GCAGGGCTCCCCGGTGACAG	34	241
1130871	216	235	3567	3586	GGTACATTTGTGGTACAGCT	11	183
1130878	225	244	3576	3595	GCCCTTGTGGGTACATTTGT	33	242
1130906	290	309	3797	3816	TATCCCCATCGCTGGTCCTG	26	243
1130934	331	350	N/A	N/A	GTTTGCTGCAGTGGTCTTTC	21	244
1130962	404	423	4212	4231	AGGTGTTGTGGACAGAGACA	45	245
1130990	446	465	4391	4410	TGAGGCTCAAAGCACTTCTC	18	246
1131018	489	508	4434	4453	AGTTCTATACCATATCTCAT	13	247
1131046	532	551	4477	4496	CATCAGGACCCTTGCACTGG	26	248
1131074	566	585	N/A	N/A	CGGCAGGCCTGGCTGGCCAG	70	249
1131102	606	625	4690	4709	CACCTCTAGGCAGCGACCCC	28	250
1131130	653	672	4737	4756	AAGGCTCCGGTGTAGCCAC	66	251
1131158	709	728	4938	4957	CGCGGTAGCTGAGCCCGCGG	98	252
1131186	762	781	4991	5010	CTCCGAGGCCACGGCTGAC	40	253
1131214	839	858	N/A	N/A	TCCGGGTTCCGGCAGAAGGC	39	55
1131242	902	921	5216	5235	TCGCAGTACTCCCAGCTCAG	16	254
1131270	993	1012	5307	5326	TGCCGGCTGCGCGGGCATGA	41	255
1131298	1071	1090	5490	5509	CTGCTCCCGCTTCGCCGGCA	27	256
1131326	1116	1135	5535	5554	CCGCTGCCCCGAGCTCAGTG	34	257
1131354	1152	1171	5571	5590	AACGACGCGGGTCATCGAAG	36	258
1131382	1224	1243	5643	5662	GGCGCAGAAACTGTGGCCCC	59	259
1131410	1311	1330	5971	5990	GAGCACCACCGTCAGATCCT	18	260
1131438	1380	1399	6040	6059	GTGCAAGCGGTAGGAGCGCA	40	261
1131466	1459	1478	6202	6221	GCGCGCAGCTGCCGTCCGCA	36	262
1131494	1548	1567	6291	6310	GCCCCAGCCGGCCACCTGGC	62	263
1131522	1578	1597	N/A	N/A	GGCATATTCCTCCGCCCCCT	79	264
1131550	1620	1639	6918	6937	CTCCAGGGAGAGGAACGGTA	74	265
1131578	1746	1765	7134	7153	TTGGTCCTCACACACCAGCG	8 [†]	266
1131606	1793	1812	7181	7200	GATCCCCAGCTGATGATGCC	31	267
1131634	1823	1842	7211	7230	ACGCCTGGCTTGTTGCGGTC	31	268
1131662	1870	1889	7258	7277	CGGTGTGCTCCCGGATCCAG	22	269
1131690	1915	1934	7303	7322	GGAATCACCAAGGAGGGAAA	20	270
1131718	1950	1969	7338	7357	TCTTGCCTTCCATGCCCCAG	17	271
1131746	2005	2024	7393	7412	GAGTTCCTGCGCCATCCTGG	7	159
1131774	N/A	N/A	94	113	CACTCACCGAAAGTGTTGAC	78	272
1131802	N/A	N/A	178	197	CCACAGGTCATGAGCAGAGG	58	273

1131830	N/A	N/A	274	293	TGCCCTTGATCCACCCAGT	97	274
1131858	N/A	N/A	368	387	CCCAGAAATGCAGAGATTTTC	98	275
1131886	N/A	N/A	457	476	AATCTACAAGGGAGAGAAGA	79	276
1131914	N/A	N/A	603	622	GGCACTAGACTAGACTGCCC	67	277
1131942	N/A	N/A	690	709	CTTAGACACAGCCCATACCC	60	278
1131970	N/A	N/A	859	878	ATTGAAGGCCCTGGCCTCTG	62	279
1131998	N/A	N/A	957	976	TCAAATCCCTCGCCCAGAGT	81	280
1132026	N/A	N/A	1064	1083	CAGGTGATGGGCTGAATACC	81	281
1132054	N/A	N/A	1197	1216	AATTTAGTGTCTGGAAGAAT	70	282
1132082	N/A	N/A	1575	1594	CCCCACCAAGTCAGGCCAC	78	283
1132110	N/A	N/A	1747	1766	TGGACGGACAGAGAGGAGGG	71	284
1132138	N/A	N/A	2123	2142	AGGACCAAACCAGAACTAGG	58	285
1132166	N/A	N/A	2253	2272	TGTCTTCTTCAGAGGAATTG	66	286
1132194	N/A	N/A	2341	2360	GGCTCACAGGAACCTAATAC	47	287
1132222	N/A	N/A	2479	2498	GATTCAGGTGTGTGCTATAG	53	288
1132250	N/A	N/A	2609	2628	GTTTTTCACACTTTGTGCTT	51	289
1132278	N/A	N/A	2734	2753	GGGCATGCACAGAGCAGTGA	52	290
1132306	N/A	N/A	2832	2851	CTCATCTTCTCTGGTTCTA	48	291
1132334	N/A	N/A	2939	2958	TAGGCACTTAATAATACTTG	56	292
1132362	N/A	N/A	3042	3061	GGAGTCAGATAGCTGGAGTA	69	293
1132390	N/A	N/A	3436	3455	CTCAGGGTCTGGTCAGGAAA	70	294
1132418	N/A	N/A	3631	3650	CAGGCCCTGCTCCAACCTCC	65	295
1132446	N/A	N/A	3743	3762	GAGACAAGGCTTCCCTGCTC	71	296
1132474	N/A	N/A	3889	3908	GATACCAGGAGAGTAATGAG	55	297
1132502	N/A	N/A	4015	4034	AAGCTTGTTTACCCACCTG	46	298
1132530	N/A	N/A	4122	4141	GAGAGATGGACATGGTGGA	67	299
1132558	N/A	N/A	4310	4329	CCAGCAACCTATTCTGTAGG	56	300
1132586	N/A	N/A	4535	4554	CTCCCTGGCCCGTTCCCAAC	68	301
1132614	N/A	N/A	4632	4651	AACGCAGTGAGCCACCCCTG	32	302
1132642	N/A	N/A	4859	4878	CTGGGCTCTCCTGCCTCCCT	31	303
1132670	N/A	N/A	5383	5402	TTCCCCCCCCCACTTCCTAA	106	304
1132698	N/A	N/A	5751	5770	GAGACGGAGGAGCCGCGGCC	72	305
1132726	N/A	N/A	6158	6177	AACCCGGGCGGAGAGGAGCG	98	306
1132754	N/A	N/A	6373	6392	GGCTTCTTCCGCCTAACCCA	72	307
1132782	N/A	N/A	6481	6500	TGAATCCCAGGCCCTGGGAT	101	308
1132810	N/A	N/A	6621	6640	GAGTCGCAGAACCTGGCTCC	71	309
1132838	N/A	N/A	6712	6731	ATTTTCATAGGCAAGGAGGCT	66	310
1132866	N/A	N/A	6839	6858	CTTCACACCCCATCTGACAA	108	311
1132894	N/A	N/A	7106	7125	GAATCACCCCTGGGTGCGAAA	76 [†]	312

Table 36. Reduction of FXII RNA by 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages
(Huh7, electroporation, 5000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1130794	79	98	79	98	TTGACTCCAAGCTCACCAGC	41	315
1130822	136	155	503	522	GCTCTTCAGCTTTGTACTTA	34	316
1130850	172	191	3523	3542	GGCAGGGCTCCCCGGTGACA	19	317
1130871	216	235	3567	3586	GGTACATTTGTGGTACAGCT	12	183
1130879	226	245	3577	3596	GGCCCTTGTGGGTACATTTG	66	318
1130907	292	311	3799	3818	AGTATCCCCATCGCTGGTCC	19	319
1130935	332	351	N/A	N/A	TGTTTGCTGCAGTGGTCTTT	27	320
1130963	405	424	4213	4232	GAGGTGTTGTGGACAGAGAC	47	321
1130991	447	466	4392	4411	CTGAGGCTCAAAGCACTTCT	29	322
1131019	493	512	4438	4457	GCTCAGTTCTATACCATATC	17	323
1131047	533	552	4478	4497	GCATCAGGACCCTTGCACTG	26	324
1131075	568	587	N/A	N/A	TGCGGCAGGCCTGGCTGGCC	50	325
1131103	607	626	4691	4710	CCACCTCTAGGCAGCGACCC	29	326
1131131	654	673	4738	4757	GAAGGCTCCGGTGTAGCCCA	56	327
1131159	710	729	4939	4958	CCGCGGTAGCTGAGCCCGCG	77	328
1131187	763	782	4992	5011	CCTCCGAGGCCACGGCTGA	47	329
1131215	840	859	N/A	N/A	GTCCGGGTTCCGGCAGAAGG	38	313
1131243	903	922	5217	5236	GTCGCAGTACTCCCAGCTCA	12	330
1131271	994	1013	5308	5327	GTGCCGGCTGCGCGGGCATG	63	331
1131299	1072	1091	5491	5510	GCTGCTCCCGCTTCGCCGGC	26	332
1131327	1117	1136	5536	5555	GCCGCTGCCCCGAGCTCAGT	30	333
1131355	1153	1172	5572	5591	CAACGACGCGGGTCATCGAA	53	334
1131383	1225	1244	5644	5663	CGGCGCAGAACTGTGGCCC	46	335
1131411	1312	1331	5972	5991	CGAGCACCACCGTCAGATCC	17	336
1131439	1381	1400	6041	6060	CGTGCAAGCGGTAGGAGCGC	27	337
1131467	1460	1479	6203	6222	AGCGCGCAGCTGCCGTCCGC	42	338
1131495	1549	1568	6292	6311	GGCCCCAGCCGGCCACCTGG	82	339
1131523	1579	1598	N/A	N/A	TGGCATATTCCTCCGCCCCC	67	340
1131551	1621	1640	6919	6938	GCTCCAGGGAGAGGAACGGT	66	341
1131579	1747	1766	7135	7154	CTTGGTCCTCACACACCAGC	36 [†]	342
1131607	1794	1813	7182	7201	CGATCCCCAGCTGATGATGC	41	343
1131635	1839	1858	7227	7246	GGCCACATCGGTGTAGACGC	18	86
1131663	1871	1890	7259	7278	ACGGTGTGCTCCCGGATCCA	16	344
1131691	1916	1935	7304	7323	CGGAATCACCAAGGAGGGAA	15	345
1131719	1951	1970	7339	7358	ATCTTGCTTCCATGCCCA	28	346
1131747	2006	2025	7394	7413	TGAGTTCTGCGCCATCCTG	17	347
1131775	N/A	N/A	97	116	CAGCACTACCGAAAGTGTT	84	348
1131803	N/A	N/A	181	200	GACCCACAGGTCATGAGCAG	87	349

1131831	N/A	N/A	277	296	CTGTGCCCTTGTATCCACCC	61	350
1131859	N/A	N/A	371	390	CAGCCCAGAAATGCAGAGAT	69	351
1131887	N/A	N/A	460	479	TGGAATCTACAAGGGAGAGA	89	352
1131915	N/A	N/A	606	625	GTAGGCACTAGACTAGACTG	52	353
1131943	N/A	N/A	693	712	GCACTTAGACACAGCCCATA	64	354
1131971	N/A	N/A	862	881	CCCATTGAAGGCCCTGGCCT	49	355
1131999	N/A	N/A	960	979	AACTCAAATCCCTCGCCAG	59	356
1132027	N/A	N/A	1067	1086	CACCAGGTGATGGGCTGAAT	49	357
1132055	N/A	N/A	1200	1219	GGTAATTTAGTGTCTGGAAG	46	358
1132083	N/A	N/A	1578	1597	CAACCCACCAAGTCAGGCC	69	359
1132111	N/A	N/A	1750	1769	GGATGGACGGACAGAGAGGA	63	360
1132139	N/A	N/A	2126	2145	CCAAGGACCAAACCAGAACT	56	361
1132167	N/A	N/A	2256	2275	CTGTGTCTTCTTCAGAGGAA	50	362
1132195	N/A	N/A	2370	2389	TGTTGGTTGATGAAAATGTT	54	363
1132223	N/A	N/A	2482	2501	CTTGATTCAAGGTGTGTGCTA	50	364
1132251	N/A	N/A	2628	2647	TCAGTCTACTTAGTGCAACG	51	365
1132279	N/A	N/A	2739	2758	TTTGTGGGCATGCACAGAGC	53	366
1132307	N/A	N/A	2835	2854	ATCCTCATCTTCTCTGGTT	53	367
1132335	N/A	N/A	2942	2961	AAGTAGGCACTTAATAATAC	67	368
1132363	N/A	N/A	3045	3064	TCAGGAGTCAGATAGCTGGA	77	369
1132391	N/A	N/A	3439	3458	TCCCTCAGGGTCTGGTCAGG	54	370
1132419	N/A	N/A	3637	3656	GTCTCCAGGCCCTGCTCC	56	371
1132447	N/A	N/A	3749	3768	TAGAAAGAGACAAGGCTTCC	61	372
1132475	N/A	N/A	3892	3911	GGTGATAACCAGGAGAGTAAT	47	373
1132503	N/A	N/A	4018	4037	TCCAAGCTTGGTTTACCCAC	38	374
1132531	N/A	N/A	4125	4144	TCTGAGAGATGGACATGGTG	68	375
1132559	N/A	N/A	4313	4332	TATCCAGCAACCTATTCTGT	69	376
1132587	N/A	N/A	4538	4557	CTCCTCCCTGGCCCGTTCCC	70	377
1132615	N/A	N/A	4635	4654	GGGAACGCAGTGAGCCACCC	49	378
1132643	N/A	N/A	4862	4881	AGGCTGGGCTCTCCTGCCTC	75	379
1132671	N/A	N/A	5386	5405	TCCTTCCCCCCCCCACTTCC	92	380
1132699	N/A	N/A	5754	5773	TGGGAGACGGAGGAGCCGCG	61	381
1132727	N/A	N/A	6161	6180	GCTAACCCGGGCGGAGAGGA	101	382
1132755	N/A	N/A	6376	6395	GCGGGCTTCTTCCGCCTAAC	56	383
1132783	N/A	N/A	6484	6503	CAGTGAATCCCAGGCCCTGG	66	384
1132811	N/A	N/A	6624	6643	CCAGAGTCGCAGAACCTGGC	56	385
1132839	N/A	N/A	6715	6734	TCAATTTTCATAGGCAAGGAG	64	386
1132867	N/A	N/A	6842	6861	CTTCTTCACACCCCATCTGA	88	387
1132895	N/A	N/A	7109	7128	CCGGAATCACCCCTGGGTCGG	28 [†]	388

Table 37. Reduction of FXII RNA by 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages
(Huh7, electroporation, 5000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1130795	80	99	80	99	GTTGACTCCAAGCTCACCAG	40	389
1130823	138	157	505	524	GTGCTCTTCAGCTTTGTACT	38	390
1130851	174	193	3525	3544	GTGGCAGGGCTCCCCGGTGA	80	391
1130871	216	235	3567	3586	GGTACATTTGTGGTACAGCT	11	183
1130880	228	247	3579	3598	CCGGCCCTTGTGGGTACATT	42	392
1130908	293	312	3800	3819	CAGTATCCCCATCGCTGGTC	24	393
1130936	333	352	N/A	N/A	GTGTTTGCTGCAGTGGTCTT	32	394
1130964	406	425	4214	4233	TGAGGTGTTGTGGACAGAGA	112	395
1130992	449	468	4394	4413	AGCTGAGGCTCAAAGCACTT	45	396
1131020	494	513	4439	4458	TGCTCAGTTCTATACCATAT	23	397
1131048	535	554	4480	4499	GGGCATCAGGACCCTTGCAC	81	398
1131076	569	588	N/A	N/A	GTGCGGCAGGCCTGGCTGGC	54	399
1131104	609	628	4693	4712	CTCCACCTCTAGGCAGCGAC	45	400
1131132	655	674	4739	4758	AGAAGGCTCCGGTGTAGCCC	69	401
1131160	711	730	4940	4959	GCCGCGGTAGCTGAGCCCGC	97	402
1131188	765	784	4994	5013	GGCCTCCGAGGCCACGGCT	45	403
1131216	843	862	N/A	N/A	GTTGTCCGGGTTCGGCAGA	20	404
1131244	904	923	5218	5237	GGTCGCAGTACTCCCAGCTC	32	405
1131272	996	1015	5310	5329	CGGTGCCGGCTGCGCGGGCA	59	406
1131300	1073	1092	5492	5511	GGCTGCTCCCGCTTCGCCGG	50	407
1131328	1118	1137	5537	5556	AGCCGCTGCCCGCAGCTCAG	83	408
1131356	1155	1174	5574	5593	GCCAACGACGCGGGTCATCG	38	409
1131384	1227	1246	5646	5665	GCCGGCGCAGAACTGTGGC	68	410
1131412	1313	1332	5973	5992	CCGAGCACCACCGTCAGATC	47	411
1131440	1399	1418	6059	6078	TGACGGGCGAGAAGGCCTCG	59	412
1131468	1462	1481	6205	6224	GGAGCGCGCAGCTGCCGTCC	44	413
1131496	1550	1569	6293	6312	TGGCCCCAGCCGGCCACCTG	96	414
1131524	1581	1600	6879	6898	GCTGGCATATTCCTCCGCC	64	415
1131552	1622	1641	6920	6939	CGCTCCAGGGAGAGGAACGG	107	416
1131580	1748	1767	7136	7155	GCTTGGTCCTCACACACCAG	10 [†]	80
1131608	1795	1814	7183	7202	CCGATCCCCAGCTGATGATG	28	417
1131636	1842	1861	7230	7249	GTAGGCCACATCGGTGTAGA	51	418
1131664	1873	1892	7261	7280	AAACGGTGTGCTCCCGGATC	81	419
1131692	1917	1936	7305	7324	GCGGAATCACCAAGGAGGGA	18	420
1131720	1952	1971	7340	7359	AATCTTGCCTTCCATGCCCC	30	421
1131748	2007	2026	7395	7414	TTGAGTTCTGCGCCATCCT	11	422
1131776	N/A	N/A	100	119	CCACAGCACTACCGAAAGT	116	423
1131804	N/A	N/A	184	203	CTGGACCCACAGGTCATGAG	48	424

1131832	N/A	N/A	280	299	AGGCTGTGCCCTTGTATCCA	45	425
1131860	N/A	N/A	374	393	TCACAGCCCAGAAATGCAGA	144	426
1131888	N/A	N/A	463	482	AGGTGGAATCTACAAGGGAG	72	427
1131916	N/A	N/A	609	628	CAGGTAGGCACTAGACTAGA	85	428
1131944	N/A	N/A	696	715	TGGGCACTTAGACACAGCCC	56	429
1131972	N/A	N/A	865	884	TTGCCCATTTGAAGGCCCTGG	60	430
1132000	N/A	N/A	963	982	GAGAACTCAAATCCCTCGCC	77	431
1132028	N/A	N/A	1070	1089	ATGCACCAGGTGATGGGCTG	65	432
1132056	N/A	N/A	1203	1222	GTAGGTAATTTAGTGTCTGG	89	433
1132084	N/A	N/A	1581	1600	ACTCAACCCCAACCAAGTCAG	75	434
1132112	N/A	N/A	1753	1772	ATGGGATGGACGGACAGAGA	60	435
1132140	N/A	N/A	2129	2148	TTGCCAAGGACCAAACCAGA	87	436
1132168	N/A	N/A	2259	2278	TGCCTGTGTCTTCTTCAGAG	51	437
1132196	N/A	N/A	2373	2392	TGCTGTTGGTTGATGAAAAT	51	438
1132224	N/A	N/A	2485	2504	ACACTTGATTGAGGTGTGTG	64	439
1132252	N/A	N/A	2634	2653	TCCTTCTCAGTCTACTTAGT	53	440
1132280	N/A	N/A	2742	2761	CCATTTGTGGGCATGCACAG	60	441
1132308	N/A	N/A	2838	2857	TTGATCCTCATTCTTCTCTG	44	442
1132336	N/A	N/A	2950	2969	TTGCCACAAAGTAGGCACTT	66	443
1132364	N/A	N/A	3048	3067	GGTTCAGGAGTCAGATAGCT	74	444
1132392	N/A	N/A	3442	3461	CTGTCCCTCAGGGTCTGGTC	74	445
1132420	N/A	N/A	3640	3659	CATGTCTCCCAGGCCCTGTC	49	446
1132448	N/A	N/A	3752	3771	CTGTAGAAAGAGACAAGGCT	52	447
1132476	N/A	N/A	3895	3914	TCTGGTGATACCAGGAGAGT	50	448
1132504	N/A	N/A	4021	4040	GTTTCCAAGCTTGTTTACC	61	449
1132532	N/A	N/A	4128	4147	TGGTCTGAGAGATGGACATG	40	450
1132560	N/A	N/A	4316	4335	GAGTATCCAGCAACCTATTC	46	451
1132588	N/A	N/A	4541	4560	ACGCTCCTCCCTGGCCCGTT	85	452
1132616	N/A	N/A	4638	4657	GGAGGGAACGCAGTGAGCCA	83	453
1132644	N/A	N/A	4866	4885	GCCAAGGCTGGGCTCTCCTG	43	454
1132672	N/A	N/A	5389	5408	TCCTCCTTCCCCCCCCCACT	99	455
1132700	N/A	N/A	5757	5776	CGCTGGGAGACGGAGGAGCC	98	456
1132728	N/A	N/A	6164	6183	AGAGCTAACCCGGGCGGAGA	69	457
1132756	N/A	N/A	6379	6398	GTCGCGGGCTTCTTCCGCTT	46	458
1132784	N/A	N/A	6487	6506	CAGCAGTGAATCCCAGGCC	63	459
1132812	N/A	N/A	6627	6646	CATCCAGAGTCGCAGAACCT	48	460
1132840	N/A	N/A	6718	6737	AATTC AATTT CATAGGCAAG	69	461
1132868	N/A	N/A	6845	6864	CGCCTTCTTCACACCCCATC	97	462
1132896	N/A	N/A	7112	7131	CCTCCGGAATCACCCCTGGGT	53 [†]	463

Table 38. Reduction of FXII RNA by 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages
(Huh7, electroporation 5000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1130796	82	101	82	101	GTGTTGACTCCAAGCTCACC	34	465
1130824	139	158	506	525	TGTGCTCTTCAGCTTTGTAC	21	466
1130852	175	194	3526	3545	AGTGGCAGGGCTCCCCGGTG	59	467
1130871	216	235	3567	3586	GGTACATTTGTGGTACAGCT	16	183
1130881	229	248	3580	3599	GCCGGCCCTTGTGGGTACAT	52	468
1130909	294	313	3801	3820	ACAGTATCCCCATCGCTGGT	46	469
1130937	334	353	4142	4161	TGTGTTTGCTGCAGTGGTCT	63	470
1130965	407	426	4215	4234	GTGAGGTGTTGTGGACAGAG	40	471
1130993	450	469	4395	4414	AAGCTGAGGCTCAAAGCACT	37	472
1131021	495	514	4440	4459	TTGCTCAGTTCTATACCATA	16	473
1131049	536	555	4481	4500	TGGGCATCAGGACCCTTGCA	47	474
1131077	570	589	N/A	N/A	GGTGCAGGACGGCCTGGCTGG	52	475
1131105	610	629	4694	4713	CCTCCACCTCTAGGCAGCGA	48	476
1131133	656	675	4740	4759	CAGAAGGCTCCGGTGTAGCC	89	477
1131161	712	731	4941	4960	GGCCGCGGTAGCTGAGCCCG	59	478
1131189	766	785	4995	5014	TGGCCTCCGAGGCCACGGC	75	479
1131217	844	863	N/A	N/A	CGTTGTCCGGGTTCGGGCAG	32	480
1131245	905	924	5219	5238	AGGTCGCAGTACTCCCAGCT	37	481
1131273	997	1016	5311	5330	GCGGTGCCGGCTGCGCGGGC	49	482
1131301	1075	1094	5494	5513	GCGGCTGCTCCCGCTTCGCC	48	483
1131329	1120	1139	5539	5558	GGAGCCGCTGCCCGCAGCTC	51	484
1131357	1156	1175	5575	5594	CGCCAACGACGCGGGTCATC	23	485
1131385	1228	1247	5647	5666	TGCCGGCGCAGAAACTGTGG	61	486
1131413	1314	1333	5974	5993	GCCGAGCACCACCGTCAGAT	35	487
1131441	1400	1419	6060	6079	CTGACGGGCGAGAAGGCCTC	37	488
1131469	1463	1482	6206	6225	AGGAGCGCGCAGCTGCCGTC	77	464
1131497	1551	1570	6294	6313	GTGGCCCCAGCCGGCCACCT	114	489
1131525	1582	1601	6880	6899	AGCTGGCATATTCCTCCGCC	113	490
1131553	1623	1642	6921	6940	GCGCTCCAGGGAGAGGAACG	90	491
1131581	1749	1768	7137	7156	AGCTTGGTCCTCACACACCA	7 [†]	492
1131609	1796	1815	7184	7203	CCCGATCCCCAGCTGATGAT	33	493
1131637	1843	1862	7231	7250	AGTAGGCCACATCGGTGTAG	37	494
1131665	1874	1893	7262	7281	GAAACGGTGTGCTCCCGGAT	36	495
1131693	1918	1937	7306	7325	TGCGGAATCACCAAGGAGGG	11	496
1131721	1954	1973	7342	7361	ACAATCTTGCCTTCCATGCC	25	497
1131749	2009	2028	7397	7416	TATTGAGTTCCTGCGCCATC	13	498
1131777	N/A	N/A	103	122	TTCCCACAGCACTACCGAA	77	499
1131805	N/A	N/A	187	206	CACCTGGACCCACAGGTCAT	88	500

1131833	N/A	N/A	283	302	TGCAGGCTGTGCCCTTGTAT	115	501
1131861	N/A	N/A	377	396	CTCTCACAGCCCAGAAATGC	73	502
1131889	N/A	N/A	466	485	CCAAGGTGGAATCTACAAGG	30	503
1131917	N/A	N/A	612	631	CACCAGGTAGGCACTAGACT	42	504
1131945	N/A	N/A	716	735	CCTGCTCCGAGCCAGGCTCG	62	505
1131973	N/A	N/A	868	887	TCCTTGCCCATTTGAAGGCC	43	506
1132001	N/A	N/A	966	985	TTGGAGAACTCAAATCCCTC	52	507
1132029	N/A	N/A	1073	1092	TCCATGCACCAGGTGATGGG	54	508
1132057	N/A	N/A	1206	1225	CATGTAGGTAATTTAGTGTC	47	509
1132085	N/A	N/A	1584	1603	GAGACTCAACCCACCAAGT	60	510
1132113	N/A	N/A	1756	1775	CAGATGGGATGGACGGACAG	74	511
1132141	N/A	N/A	2132	2151	CACTTGCCAAGGACCAAACC	69	512
1132169	N/A	N/A	2262	2281	AATTGCCTGTGTCTTCTTCA	51	513
1132197	N/A	N/A	2376	2395	ATATGCTGTTGGTTGATGAA	48	514
1132225	N/A	N/A	2488	2507	TAGACACTTGATTCAGGTGT	43	515
1132253	N/A	N/A	2637	2656	GTGTCCTTCTCAGTCTACTT	45	516
1132281	N/A	N/A	2745	2764	TGGCCATTTGTGGGCATGCA	69	517
1132309	N/A	N/A	2841	2860	CAGTTGATCCTCATTCTTCT	57	518
1132337	N/A	N/A	2953	2972	CACTTGCCACAAAGTAGGCA	44	519
1132365	N/A	N/A	3051	3070	TTGGGTTTCAGGAGTCAGATA	73	520
1132393	N/A	N/A	3445	3464	GCACTGTCCCTCAGGGTCTG	47	521
1132421	N/A	N/A	3643	3662	GTACATGTCTCCAGGCCCC	50	522
1132449	N/A	N/A	3755	3774	CACCTGTAGAAAGAGACAAG	58	523
1132477	N/A	N/A	3898	3917	GGGTCTGGTGATACCAGGAG	44	524
1132505	N/A	N/A	4024	4043	CAAGTTTCCAAGCTTGGTTT	29	525
1132533	N/A	N/A	4131	4150	CAGTGGTCTGAGAGATGGAC	46	526
1132561	N/A	N/A	4319	4338	TCCGAGTATCCAGCAACCTA	50	527
1132589	N/A	N/A	4557	4576	CCAGCCTGTCTTCCCTGACGC	67	528
1132617	N/A	N/A	4657	4676	GTGTTGTCGGCAGGCTTGGG	59	529
1132645	N/A	N/A	4869	4888	GCAGCCAAGGCTGGGCTCTC	59	530
1132673	N/A	N/A	5392	5411	GGCTCCTCCTTCCCCCCCC	41	531
1132701	N/A	N/A	5760	5779	CTGCGCTGGGAGACGGAGGA	70	532
1132729	N/A	N/A	6167	6186	AACAGAGCTAACCCGGGCGG	65	533
1132757	N/A	N/A	6382	6401	AAAGTCGCGGGCTTCTTCCG	31	534
1132785	N/A	N/A	6490	6509	TCCCAGCAGTGAATCCCAGG	69	535
1132813	N/A	N/A	6630	6649	ACCCATCCAGAGTCGCAGAA	43	536
1132841	N/A	N/A	6721	6740	ATTAATTCAATTTTCATAGGC	68	537
1132869	N/A	N/A	6862	6881	CCCCTGCGAACACAGAGCGC	59	538

Table 39. Reduction of FXII RNA by 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages
(Huh7, electroporation, 5000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1130797	83	102	83	102	AGTGTGACTCCAAGCTCAC	27	541
1130825	141	160	508	527	TGTGTGCTCTTCAGCTTTGT	14	542
1130853	177	196	3528	3547	GAAGTGGCAGGGCTCCCCGG	33	543
1130871	216	235	3567	3586	GGTACATTTGTGGTACAGCT	9	183
1130882	231	250	3582	3601	TGGCCGGCCCTTGTGGGTAC	23	544
1130910	296	315	3803	3822	AAACAGTATCCCCATCGCTG	36	545
1130938	335	354	4143	4162	CTGTGTTTGCTGCAGTGGTC	13	546
1130966	408	427	4216	4235	AGTGAGGTGTTGTGGACAGA	48	547
1130994	451	470	4396	4415	GAAGCTGAGGCTCAAAGCAC	22	548
1131022	496	515	4441	4460	CTTGCTCAGTTCTATACCAT	23	549
1131050	537	556	4482	4501	GTGGGCATCAGGACCCTTGC	41	550
1131078	571	590	N/A	N/A	TGGTGCGGCAGGCCTGGCTG	33	551
1131106	612	631	4696	4715	GCCCTCCACCTCTAGGCAGC	26	552
1131134	657	676	4741	4760	GCAGAAGGCTCCGGTGTAGC	23	553
1131162	714	733	4943	4962	CAGGCCGCGGTAGCTGAGCC	34	554
1131190	767	786	4996	5015	GTGGCCTCCGAGGCCACGG	50	555
1131218	862	881	5176	5195	AGCACCACGGGCGGATGTCTG	25	539
1131246	907	926	5221	5240	CCAGGTCGCAGTACTCCAG	26	556
1131274	998	1017	5312	5331	GGCGGTGCCGGCTGCGCGGG	71	557
1131302	1076	1095	5495	5514	GGCGGTGCTCCCGCTTCGC	20	558
1131330	1121	1140	5540	5559	CGGAGCCGCTGCCCCGAGCT	33	559
1131358	1158	1177	5577	5596	CCCGCCAACGACGCGGGTCA	19	560
1131386	1229	1248	5648	5667	CTGCCGGCGCAGAACTGTG	46	561
1131414	1315	1334	5975	5994	GGCCGAGCACCACCGTCAGA	32	562
1131442	1401	1420	6061	6080	GCTGACGGGCGAGAAGGCCT	19	563
1131470	1464	1483	6207	6226	CAGGAGCGCGCAGCTGCCGT	33	564
1131498	1552	1571	6295	6314	GGTGGCCCCAGCCGGCCACC	46	565
1131526	1583	1602	6881	6900	AAGCTGGCATATTCCTCCGC	136	566
1131554	1657	1676	6955	6974	GGATGGAGGATCCGTGCACG	15 [†]	567
1131582	1750	1769	7138	7157	CAGCTTGGTCCTCACACACC	11 [†]	568
1131610	1797	1816	7185	7204	GCCCCGATCCCCAGCTGATGA	39	569
1131638	1844	1863	7232	7251	TAGTAGGCCACATCGGTGTA	25	87
1131666	1876	1895	7264	7283	AGGAAACGGTGTGCTCCCGG	31	570
1131694	1919	1938	7307	7326	CTGCGGAATACCAAGGAGG	10	571
1131722	1955	1974	7343	7362	CACAATCTTGCCCTCCATGC	18	572
1131750	2010	2029	7398	7417	TTATTGAGTTCCTGCGCCAT	23	573
1131778	N/A	N/A	106	125	TGGTTCCACAGCACTCACC	42	574
1131806	N/A	N/A	190	209	AGTCACCTGGACCCACAGGT	28	575

1131834	N/A	N/A	286	305	AAATGCAGGCTGTGCCCTTG	33	576
1131862	N/A	N/A	380	399	TTCTCTCACAGCCCAGAAA	41	577
1131890	N/A	N/A	469	488	TTCCCAAGGTGGAATCTACA	74	578
1131918	N/A	N/A	615	634	TAGCACCAGGTAGGCACTAG	45	579
1131946	N/A	N/A	721	740	AAGCACCTGCTCCGAGCCAG	33	580
1131974	N/A	N/A	871	890	CCTTCCTTGCCCATTGAAGG	46	581
1132002	N/A	N/A	969	988	AGCTTGGAGAACTCAAATCC	56	582
1132030	N/A	N/A	1076	1095	ATTTCATGCACCAGGTGAT	58	583
1132058	N/A	N/A	1209	1228	TGGCATGTAGGTAATTTAGT	34	584
1132086	N/A	N/A	1587	1606	TTAGAGACTCAACCCACCA	55	585
1132114	N/A	N/A	1759	1778	ATGCAGATGGGATGGACGGA	48	586
1132142	N/A	N/A	2135	2154	GTGCACTTGCCAAGGACCAA	25	587
1132170	N/A	N/A	2265	2284	GAGAATTGCCTGTGTCTTCT	40	588
1132198	N/A	N/A	2379	2398	ATTATATGCTGTTGGTTGAT	28	589
1132226	N/A	N/A	2513	2532	GCTACCTTAGGGAGAAAGCG	53	590
1132254	N/A	N/A	2640	2659	TGAGTGTCTTCTCAGTCTA	47	591
1132282	N/A	N/A	2748	2767	TCATGGCCATTTGTGGGCAT	46	592
1132310	N/A	N/A	2845	2864	AGTACAGTTGATCCTCATTC	56	593
1132338	N/A	N/A	2956	2975	GAGCACTTGCCACAAAGTAG	30	594
1132366	N/A	N/A	3054	3073	AACTTGGGTTCAGGAGTCAG	42	595
1132394	N/A	N/A	3448	3467	CAGGCACTGTCCCTCAGGGT	32	596
1132422	N/A	N/A	3649	3668	GGCAGGGTACATGTCTCCCA	36	597
1132450	N/A	N/A	3758	3777	GCACACCTGTAGAAAGAGAC	39	598
1132478	N/A	N/A	3916	3935	CAGAATCCCAGGTGTGTGGG	64	599
1132506	N/A	N/A	4027	4046	CTCCAAGTTTCCAAGCTTGG	38	600
1132534	N/A	N/A	4134	4153	CTGCAGTGGTCTGAGAGATG	36	601
1132562	N/A	N/A	4325	4344	CAAGTCTCCGAGTATCCAGC	49	602
1132590	N/A	N/A	4560	4579	CTGCCAGCCTGTCTTCCTGA	30	603
1132618	N/A	N/A	4660	4679	CGGGTTGGTGCAGGAGGCTT	30	604
1132646	N/A	N/A	4875	4894	CCCTGGGCAGCCAAGGCTGG	53	605
1132674	N/A	N/A	5395	5414	CTCGGCTCCTCCTTCCCCC	45	606
1132702	N/A	N/A	5763	5782	AAGCTGCGCTGGGAGACGGA	45	607
1132730	N/A	N/A	6170	6189	CGCAACAGAGCTAACCCGGG	45	608
1132758	N/A	N/A	6385	6404	ACCAAAGTCGCGGGCTTCTT	43	609
1132786	N/A	N/A	6493	6512	GGATCCCAGCAGTGAATCCC	59	610
1132814	N/A	N/A	6633	6652	ACCACCCATCCAGAGTCGCA	44	611
1132842	N/A	N/A	6724	6743	GCCATTAATTCAATTTTCATA	45	612
1132870	N/A	N/A	6865	6884	CCGCCCCTGCGAACACAGAG	44	613

Table 40. Reduction of FXII RNA by 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages
(Huh7, electroporation, 2000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1130868	213	232	3564	3583	ACATTTGTGGTACAGCTGCC	84	1756
1130987	443	462	N/A	N/A	GGCTCAAAGCACTTCTCTTT	93	2135
1131593	1780	1799	7168	7187	TGATGCCTTGCAAGGTGAGC	37	1326
1131694	1919	1938	7307	7326	CTGCGGAATCACCAAGGAGG	57	571
1131701	1928	1947	7316	7335	ACTCTCTCACTGCGGAATCA	42	1179
1131746	2005	2024	7393	7412	GAGTTCCTGCGCCATCCTGG	40	159
1131754	2015	2034	7403	7422	GCACTTTATTGAGTTCCTGC	35	164
1131756	2017	2036	7405	7424	AAGCACTTTATTGAGTTCCT	11	1030
1131757	2018	2037	7406	7425	AAAGCACTTTATTGAGTTCC	36	165
1131763	2026	2045	7414	7433	GCATTTTCAAAGCACTTTAT	41	1562
1131891	N/A	N/A	513	532	CCGACTGTGTGCTCTTCAGC	88	659
1132188	N/A	N/A	2323	2342	ACTGTTTGCTAGTTCAATGT	106	1951
1132271	N/A	N/A	2706	2725	CACATTTCCAGTTAAGGTTC	93	1879
1132505	N/A	N/A	4024	4043	CAAGTTTCCAAGCTTGGTTT	104	525
1132651	N/A	N/A	4908	4927	AGCTTGCTTGGTGTCTGAG	79	985
1132797	N/A	N/A	6542	6561	AGGGAACCAAGAGCAAGTTC	72	1369
1194299	N/A	N/A	2318	2337	TTGCTAGTTCAATGTTCACT	95	2351
1194300	N/A	N/A	2319	2338	TTTGCTAGTTCAATGTTTAC	67	2352
1194301	N/A	N/A	2321	2340	TGTTTGCTAGTTCAATGTTT	102	2353
1194302	N/A	N/A	2322	2341	CTGTTTGCTAGTTCAATGTT	97	2354
1194303	N/A	N/A	2324	2343	TACTGTTTGCTAGTTCAATG	95	2355
1194304	N/A	N/A	2325	2344	ATACTGTTTGCTAGTTCAAT	97	2356
1194305	N/A	N/A	2327	2346	TAATACTGTTTGCTAGTTCA	96	2357
1194306	N/A	N/A	2328	2347	CTAATACTGTTTGCTAGTTT	93	2358
1194307	N/A	N/A	2701	2720	TCCCAGTTAAGGTTCAACAA	99	2359
1194308	N/A	N/A	2702	2721	TTCCCAGTTAAGGTTCAACA	96	2360
1194309	N/A	N/A	2704	2723	CATTTCCCAGTTAAGGTTCAA	79	2361
1194310	N/A	N/A	2705	2724	ACATTCCCAGTTAAGGTTCA	81	2362
1194311	N/A	N/A	2707	2726	GCACATTCCCAGTTAAGGTT	100	2363
1194312	N/A	N/A	2708	2727	TGCACATTCCCAGTTAAGGT	95	2364
1194313	N/A	N/A	2710	2729	TTTGACATTCCCAGTTAAG	92	2365
1194314	N/A	N/A	2711	2730	ATTTGCACATTCCCAGTTAA	105	2366
1194315	N/A	N/A	4019	4038	TTCCAAGCTTGGTTTACCCA	113	2367
1194316	N/A	N/A	4020	4039	TTTCCAAGCTTGGTTTACCC	109	2368
1194317	N/A	N/A	4022	4041	AGTTTCCAAGCTTGGTTTAC	87	2369
1194318	N/A	N/A	4023	4042	AAGTTTCCAAGCTTGGTTTA	84	2370
1194319	N/A	N/A	4025	4044	CCAAGTTTCCAAGCTTGGTT	102	2371
1194320	N/A	N/A	4026	4045	TCCAAGTTTCCAAGCTTGGT	81	2372

1194321	N/A	N/A	4028	4047	ACTCCAAGTTTCCAAGCTTG	95	2373
1194322	N/A	N/A	4029	4048	TACTCCAAGTTTCCAAGCTT	98	2374
1194323	N/A	N/A	4903	4922	GCCTTGGTGTCTGAGGAGAA	83	2375
1194324	N/A	N/A	4904	4923	TGCCTTGGTGTCTGAGGAGA	80	2376
1194325	N/A	N/A	4906	4925	CTTGCTTGGTGTCTGAGGA	75	2377
1194326	N/A	N/A	4907	4926	GCTTGCTTGGTGTCTGAGG	77	2378
1194327	N/A	N/A	4909	4928	CAGCTTGCCTTGGTGTCTGA	78	2379
1194328	N/A	N/A	4910	4929	GCAGCTTGCCTTGGTGTCTG	87	2380
1194329	683	702	4912	4931	TAGCAGCTTGCCTTGGTGTCT	99	2381
1194330	684	703	4913	4932	ATAGCAGCTTGCCTTGGTGT	93	2382
1194331	N/A	N/A	6537	6556	ACCAAGAGCAAGTTCGATTC	60	2383
1194332	N/A	N/A	6538	6557	AACCAAGAGCAAGTTCGATT	56	2384
1194333	N/A	N/A	6540	6559	GGAACCAAGAGCAAGTTCGA	73	2385
1194334	N/A	N/A	6541	6560	GGGAACCAAGAGCAAGTTCG	69	2386
1194335	N/A	N/A	6543	6562	GAGGGAACCAAGAGCAAGTT	74	2387
1194336	N/A	N/A	6544	6563	AGAGGGAACCAAGAGCAAGT	69	2388
1194337	N/A	N/A	6545	6564	CAGAGGGAACCAAGAGCAAG	85	2389
1194338	N/A	N/A	6546	6565	CCAGAGGGAACCAAGAGCAA	68	2390
1194339	N/A	N/A	6547	6566	CCCAGAGGGAACCAAGAGCA	57	2391
1206452	143	162	510	529	ACTGTGTGCTCTTCAGCTTT	78	175
1206453	209	228	3560	3579	TTGTGGTACAGTGCCGGTG	79	2392
1206454	1912	1931	7300	7319	ATCACCAAGGAGGGAAAGAT	53	2393
1206455	1920	1939	7308	7327	ACTGCGGAATCACCAAGGAG	39	2394
1206456	1925	1944	7313	7332	CTCTCACTGCGGAATCACCA	28	2395
1206457	1929	1948	7317	7336	CACTCTCTCACTGCGGAATC	17	2396
1206458	1931	1950	7319	7338	GCCACTCTCTCACTGCGGAA	25	2397
1206459	1934	1953	7322	7341	CCAGCCACTCTCTCACTGCG	42	2398
1206460	N/A	N/A	514	533	ACCGACTGTGTGCTCTTCAG	82	2399
1206461	N/A	N/A	515	534	TACCGACTGTGTGCTCTTCA	90	2400
1206462	N/A	N/A	517	536	CTTACCGACTGTGTGCTCTT	102	2401
1206463	N/A	N/A	518	537	ACTTACCGACTGTGTGCTCT	68	2402
1206464	N/A	N/A	2313	2332	AGTTCAATGTTCACTGTGAT	105	2403
1206465	N/A	N/A	2333	2352	GGAACCTAATACTGTTTGCT	92	2404
1206466	N/A	N/A	2696	2715	GTAAAGGTTCAACAAGGCGT	81	2405
1206467	N/A	N/A	2716	2735	GAAAAATTTGCACATTCCCA	92	2406
1206468	N/A	N/A	4014	4033	AGCTTGGTTTACCCACCTGC	95	2407
1206469	N/A	N/A	4034	4053	CTTGCTACTCCAAGTTTCCA	80	2408
1206470	N/A	N/A	4898	4917	GGTGTCTGAGGAGAAAGGGG	82	2409
1206471	N/A	N/A	6532	6551	GAGCAAGTTCGATTCTCCCT	67	2410
1206472	N/A	N/A	6552	6571	CGGCGCCAGAGGGAACCAA	95	2411

Table 41. Reduction of FXII RNA by 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages
(Huh7, electroporation, 5000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 3 Start Site	SEQ ID NO: 3 Stop Site	SEQ ID NO: 4 Start Site	SEQ ID NO: 4 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1131768	N/A	N/A	2033	2052	TTTCTCAGCATTTTCAAAGC	35	2412
1131767	10843	10862	2031	2050	TCTCAGCATTTTCAAAGCAC	25	2413
1131770	N/A	N/A	2036	2055	TTTTTTCTCAGCATTTTCAA	54	2414
1131771	N/A	N/A	2037	2056	TTTTTTCTCAGCATTTTCA	83	2415
1130767	3458	3477	34	53	TCATGGCATCCGTCCGTTGG	36	617
1130768	3459	3478	35	54	CTCATGGCATCCGTCCGTTG	90	619
1132897	10846	10865	N/A	N/A	CCTTCTCAGCATTTTCAAAG	62	618
1130769	3460	3479	36	55	CCTCATGGCATCCGTCCGTT	22	540
1132898	10849	10868	N/A	N/A	TTTCCTTCTCAGCATTTTCA	61	616

Table 42. Reduction of FXII RNA by 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages
(Huh7, electroporation, 5000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 3 Start Site	SEQ ID NO: 3 Stop Site	SEQ ID NO: 4 Start Site	SEQ ID NO: 4 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1130744	3428	3447	4	23	TATCCAGGAGTCCAGATCAA	61	2416
1130772	3463	3482	39	58	AGCCCTCATGGCATCCGTCC	35	2417
1130755	3443	3462	19	38	GTTGGTCCAGCTGCCTATCC	64	2418
1130756	3444	3463	20	39	CGTTGGTCCAGCTGCCTATC	50	2419
1130760	3450	3469	26	45	TCCGTCCGTTGGTCCAGCTG	37	2420
1130765	3456	3475	32	51	ATGGCATCCGTCCGTTGGTC	43	238
1130766	3457	3476	33	52	CATGGCATCCGTCCGTTGGT	50	314

5 Example 3: Effects of 3-10-3 cET gapmers on human FXII RNA *in vitro*, single dose

Modified oligonucleotides complementary to an FXII nucleic acid were synthesized and tested for their effect on FXII RNA levels *in vitro*. The modified oligonucleotides were tested in a series of experiments using similar culture conditions. The results for each separate experiment are presented in separate tables below.

10 The modified oligonucleotides in the tables below are 3-10-3 cEt gapmers (i.e., they have a central region of ten 2'-deoxynucleosides flanked on each side by wings, each comprising three cEt modified nucleosides). The internucleoside linkages throughout each modified oligonucleotide are phosphorothioate (P=S) linkages. All cytosine nucleobases throughout each modified oligonucleotide are 5-methylcytosines.

15 "Start site" indicates the 5'-most nucleoside of the target sequence to which the modified oligonucleotide is complementary. "Stop site" indicates the 3'-most nucleoside of the target sequence to

which the modified oligonucleotide is complementary. As shown in the tables below, the modified oligonucleotides are 100% complementary to one or more of human FXII target sequences including the human FXII mRNA sequence designated herein as SEQ ID NO: 1 (ENSEMBL ID ENST00000253496.3 from ENSEMBL version 99: January 2020), the human FXII genomic sequence, designated herein as SEQ ID NO: 2 (ENSEMBL ID ENSG00000131187.9 from ENSEMBL version 99: January 2020), the human FXII genomic sequence, designated herein as SEQ ID No. 3 (the complement of GENBANK Accession No. NC_000005.10 truncated from nucleotides 177399001 to 177413000), and the human FXII mRNA sequence designated herein as SEQ ID No: 4 (GENBANK Accession No. NM_000505.3). 'N/A' indicates that the modified oligonucleotide is not complementary to that particular target sequence with 100% complementarity.

Cultured Huh7 cells, at a density of 20,000 cells per well, were transfected using electroporation with either 2000nM or 3000nM modified oligonucleotide. After a treatment period of approximately 24 hours, RNA was isolated from the cells and FXII RNA levels were measured by quantitative real-time RTPCR. Human primer probe set RTS40528 (described herein above) was used to measure RNA levels. FXII RNA levels were normalized to total RNA content, as measured by RIBOGREEN®. Reduction of FXII RNA is presented in the tables below as percent FXII RNA relative to the amount in untreated control cells (% UTC). The symbol “†” indicates that the modified oligonucleotide is complementary to the target transcript within the amplicon region of the primer probe set. In such instances, additional assays using alternative primer probes must be performed to accurately assess the potency and efficacy of such modified oligonucleotides.

Table 43. Reduction of FXII RNA by 3-10-3 cEt gapmers with uniform PS internucleoside linkages (Huh7, electroporation, 3000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (% UTC)	SEQ ID No.
1128712	3	18	3	18	AGGAGTCCAGATCAAT	50	2421
1128732	80	95	80	95	ACTCCAAGCTCACCAG	37	2422
1128752	125	140	492	507	ACTTATGCTCCTTGGG	39	2423
1128772	156	171	N/A	N/A	GTGAGAACGACTGTGT	39	2424
1128792	200	215	3551	3566	GCCGGTGGTACTGGAA	57	2425
1128802	218	233	3569	3584	TACATTTGTGGTACAG	12	2426
1128813	231	246	3582	3597	CGGCCCTTGTGGGTAC	79	2427
1128833	294	309	3801	3816	TATCCCCATCGCTGGT	51	2428
1128853	409	424	4217	4232	GAGGTGTTGTGGACAG	45	2429
1128873	482	497	4427	4442	ATATCTCATTCTTGTG	22	2430
1128893	545	560	4490	4505	GGCAGTGGGCATCAGG	40	2431
1128913	598	613	4682	4697	GCGACCCCATGGAGG	39	2432
1128933	634	649	4718	4733	GCAGTGGCACAGGCGG	36	2433
1128953	664	679	4748	4763	GTCGCAGAAGGCTCCG	64	2434

1128973	713	728	4942	4957	CGCGGTAGCTGAGCCC	68	2435
1128993	759	774	4988	5003	GCCCACGGCTGACAGG	62	2436
1129013	807	822	5036	5051	CAGTTCCGCGCTTGCT	60	2437
1129033	863	878	5177	5192	ACCACGGGCGGATGTC	54	2438
1129053	892	907	5206	5221	GCTCAGCCGGTCGCGG	51	2439
1129073	982	997	5296	5311	CATGAGTGGGACATGA	45	2440
1129093	1043	1058	5357	5372	TCTGGGACTGAGGCGG	33	2441
1129113	1089	1104	5508	5523	GTCAGGGAAGGCGGCT	38	2442
1129133	1129	1144	5548	5563	CTTGCGGAGCCGCTGC	37	2443
1129153	1152	1167	5571	5586	ACGCGGGTCATCGAAG	53	2444
1129173	1209	1224	5628	5643	CAGTACAGCGCGGCGA	35	2445
1129193	1240	1255	5659	5674	GATGAGGCTGCCGCGC	81	2446
1129213	1319	1334	5979	5994	GGCCGAGCACCACCGT	44	2447
1129233	1384	1399	6044	6059	GTGCAAGCGGTAGGAG	76	2448
1129253	1438	1453	6181	6196	CTGAAGGCGCAACAGA	61	2449
1129273	1463	1478	6206	6221	GCGCGCAGCTGCCGTC	39	2450
1129293	1497	1512	6240	6255	GGCAGGCACACCGGCT	93	2451
1129313	1558	1573	6301	6316	CTGGTGGCCCCAGCCG	96	2452
1129333	1580	1595	6878	6893	CATATTCCTCCGCCCC	78	2453
1129353	1619	1634	6917	6932	GGGAGAGGAACGGTAC	126	2454
1129373	1693	1708	6991	7006	CTCGAGGAACCCTGCG	27 [†]	2455
1129393	1748	1763	7136	7151	GGTCCTCACACACCAG	44 [†]	2456
1129413	1798	1813	7186	7201	CGATCCCCAGCTGATG	27	2457
1129433	1839	1854	7227	7242	ACATCGGTGTAGACGC	28	2458
1129453	1866	1881	7254	7269	TCCCGGATCCAGGCCA	41	2459
1129473	1898	1913	7286	7301	ATGAGTCCCTGAGCAA	26	2460
1129493	1931	1946	7319	7334	CTCTCTCACTGCGGAA	15	2461
1129513	1990	2005	7378	7393	GCGCGGAGCTGGCCGC	46	2462
1129533	2011	2026	7399	7414	TTGAGTTCCTGCGCCA	23	2463
1129553	N/A	N/A	97	112	ACTCACCGAAAGTGTT	78	2464
1129573	N/A	N/A	197	212	CCTAGTCACCTGGACC	63	2465
1129593	N/A	N/A	328	343	CCTCCCCCGTTGTCT	49	2466
1129613	N/A	N/A	434	449	GAAGTGAATAAGTC	61	2467
1129633	N/A	N/A	606	621	GCACTAGACTAGACTG	54	2468
1129653	N/A	N/A	652	667	CACGATCACTCTAGTG	51	2469
1129673	N/A	N/A	908	923	GAGGCATTCAGATGCC	61	2470
1129693	N/A	N/A	1055	1070	GAATACCTCACATGGG	86	2471
1129713	N/A	N/A	1557	1572	GGGTAAGGTCCATCTG	61	2472
1129733	N/A	N/A	1709	1724	CAAGGATAGGGCACCA	50	2473
1129753	N/A	N/A	2146	2161	AGGCAAAGTGCACTTG	55	2474
1129773	N/A	N/A	2450	2465	GCATTGATGAATCAGC	47	2475
1129793	N/A	N/A	2527	2542	GCACAAGAAGGCTACC	54	2476
1129813	N/A	N/A	2852	2867	AATAGTACAGTTGATC	54	2477
1129833	N/A	N/A	3048	3063	CAGGAGTCAGATAGCT	64	2478
1129853	N/A	N/A	3652	3667	GCAGGGTACATGTCTC	68	2479

1129873	N/A	N/A	4015	4030	TTGGTTTACCCACCTG	73	2480
1129893	N/A	N/A	4316	4331	ATCCAGCAACCTATTC	67	2481
1129913	N/A	N/A	4360	4375	ATAGTGGTCTCAGGAG	64	2482
1129933	N/A	N/A	4619	4634	CTGGGCCTAAAGACCC	62	2483
1129953	N/A	N/A	5070	5085	GGCGCACCGGCAGAAG	52	2484
1129973	N/A	N/A	5418	5433	CTAGCTCGCCCGGCGC	76	2485
1129993	N/A	N/A	5450	5465	GGACGGAGAGCCCGCG	74	2486
1130013	N/A	N/A	5755	5770	GAGACGGAGGAGCCGC	54	2487
1130033	N/A	N/A	5869	5884	ACCCCAATCCCGTGTT	61	2488
1130053	N/A	N/A	6170	6185	ACAGAGCTAACCCGGG	96	2489
1130073	N/A	N/A	6330	6345	TGCCCCTAGCAGTTGT	65	2490
1130093	N/A	N/A	6389	6404	ACCAAAGTCGCGGGCT	137	2491
1130113	N/A	N/A	6413	6428	CATTCTGTAGGCACCC	83	2492
1130133	N/A	N/A	6538	6553	AAGAGCAAGTTCGATT	51	2493
1130153	N/A	N/A	6624	6639	AGTCGCAGAACCTGGC	49	2494
1130173	N/A	N/A	6676	6691	GATTTGAATGGGCGGA	55	2495
1130193	N/A	N/A	6812	6827	CGGACGATGGACAAAG	64	2496
1130213	N/A	N/A	6876	6891	TATTCCTCCGCCCTG	131	2497
1130233	N/A	N/A	7078	7093	CGCTGTGGACCTGAGA	89 [†]	2498

Table 44. Reduction of FXII RNA by 3-10-3 cEt gapmers with uniform PS internucleoside linkages
(Huh7, electroporation, 3000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (% UTC)	SEQ ID No.
1128713	4	19	4	19	CAGGAGTCCAGATCAA	35	2499
1128733	81	96	81	96	GACTCCAAGCTCACCA	38	2500
1128753	126	141	493	508	TACTTATGCTCCTTGG	35	2501
1128773	157	172	N/A	N/A	AGTGAGAACGACTGTG	31	2502
1128793	201	216	3552	3567	TGCCCGGTGGTACTGGA	41	2503
1128802	218	233	3569	3584	TACATTTGTGGTACAG	18	2426
1128814	233	248	3584	3599	GCCGGCCCTTGTGGGT	55	2504
1128834	295	310	3802	3817	GTATCCCCATCGCTGG	35	2505
1128854	411	426	4219	4234	GTGAGGTGTTGTGGAC	38	2506
1128874	484	499	4429	4444	CCATATCTCATTCTTG	24	2507
1128894	551	566	4496	4511	GCCGCTGGCAGTGGGC	51	2508
1128914	599	614	4683	4698	AGCGACCCCATGGAG	37	2509
1128934	639	654	4723	4738	ACCGGGCAGTGGCACA	46	2510
1128954	665	680	4749	4764	CGTCGCAGAAGGCTCC	45	2511
1128974	714	729	4943	4958	CCGCGGTAGCTGAGCC	90	2512
1128994	761	776	4990	5005	AGGCCCACGGCTGACA	44	2513
1129014	808	823	5037	5052	CCAGTTCCGCGCTTGC	33	2514
1129034	864	879	5178	5193	CACCACGGGCGGATGT	56	2515

1129054	896	911	5210	5225	CCCAGCTCAGCCGGTC	57	2516
1129074	989	1004	5303	5318	GCGCGGGCATGAGTGG	37	2517
1129094	1044	1059	5358	5373	GTCTGGGACTGAGGCG	26	2518
1129114	1090	1105	5509	5524	GGTCAGGGAAGGCGGC	21	2519
1129134	1130	1145	5549	5564	TCTTGCGGAGCCGCTG	38	2520
1129154	1153	1168	5572	5587	GACGCGGGTCATCGAA	47	2521
1129174	1210	1225	5629	5644	CCAGTACAGCGCGGCG	27	2522
1129194	1241	1256	5660	5675	CGATGAGGCTGCCGCG	53	2523
1129214	1320	1335	5980	5995	TGGCCGAGCACCACCG	38	2524
1129234	1385	1400	6045	6060	CGTGCAAGCGGTAGGA	38	2525
1129254	1439	1454	6182	6197	CCTGAAGGCGCAACAG	37	2526
1129274	1464	1479	6207	6222	AGCGCGCAGCTGCCGT	30	2527
1129294	1498	1513	6241	6256	TGGCAGGCACACCGGC	20	2528
1129314	1559	1574	6302	6317	ACTGGTGGCCCCAGCC	73	2529
1129334	1581	1596	6879	6894	GCATATTCCTCCGCCC	83	2530
1129354	1620	1635	6918	6933	AGGGAGAGGAACGGTA	69	2531
1129374	1694	1709	6992	7007	CCTCGAGGAACCTGC	18 [†]	2532
1129394	1749	1764	7137	7152	TGGTCCTCACACACCA	41 [†]	2533
1129414	1800	1815	7188	7203	CCCGATCCCCAGCTGA	47	2534
1129434	1840	1855	7228	7243	CACATCGGTGTAGACG	34	2535
1129454	1867	1882	7255	7270	CTCCCGGATCCAGGCC	47	2536
1129474	1899	1914	7287	7302	GATGAGTCCCTGAGCA	27	2537
1129494	1946	1961	7334	7349	TCCATGCCCCAGCCAC	25	2538
1129514	1991	2006	7379	7394	GGCGCGGAGCTGGCCG	77	2539
1129534	2012	2027	7400	7415	ATTGAGTTCCTGCGCC	15	2540
1129554	N/A	N/A	99	114	GCACTCACCGAAAGTG	78	2541
1129574	N/A	N/A	198	213	TCCTAGTCACCTGGAC	53	2542
1129594	N/A	N/A	329	344	ACCTCCCCCGTTGTC	62	2543
1129614	N/A	N/A	435	450	GGAAGTACTATAAGT	53	2544
1129634	N/A	N/A	607	622	GGCACTAGACTAGACT	64	2545
1129654	N/A	N/A	653	668	TCACGATCACTCTAGT	41	2546
1129674	N/A	N/A	953	968	CTCGCCCAGAGTCACC	72	2547
1129694	N/A	N/A	1056	1071	TGAATACCTCACATGG	48	2548
1129714	N/A	N/A	1558	1573	AGGGTAAGGTCCATCT	35	2549
1129734	N/A	N/A	1710	1725	GCAAGGATAGGGCACC	57	2550
1129754	N/A	N/A	2250	2265	TTCAGAGGAATTGTCTG	52	2551
1129774	N/A	N/A	2452	2467	TAGCATTGATGAATCA	72	2552
1129794	N/A	N/A	2540	2555	GTGTAGTTCCTAAGCA	57	2553
1129814	N/A	N/A	2862	2877	CGGCAGTAATAATAGT	77	2554
1129834	N/A	N/A	3373	3388	TCTAAAAGTTGGGTTC	51	2555
1129854	N/A	N/A	3704	3719	GCCCTATCACAGTCCC	53	2556
1129874	N/A	N/A	4017	4032	GCTTGGTTTACCCACC	70	2557
1129894	N/A	N/A	4318	4333	GTATCCAGCAACCTAT	48	2558
1129914	N/A	N/A	4361	4376	GATAGTGGTCTCAGGA	58	2559
1129934	N/A	N/A	4620	4635	CCTGGGCCTAAAGACC	85	2560

1129954	N/A	N/A	5071	5086	CGGCGCACCGGCAGAA	42	2561
1129974	N/A	N/A	5419	5434	TCTAGCTCGCCCGGCG	61	2562
1129994	N/A	N/A	5451	5466	AGGACGGAGAGCCCCGC	49	2563
1130014	N/A	N/A	5762	5777	GCGCTGGGAGACGGAG	101	2564
1130034	N/A	N/A	5870	5885	AACCCCAATCCCGTGT	54	2565
1130054	N/A	N/A	6171	6186	AACAGAGCTAACCCCGG	62	2566
1130074	N/A	N/A	6331	6346	CTGCCCCCTAGCAGTTG	118	2567
1130094	N/A	N/A	6390	6405	TACCAAAGTCGCGGGC	46	2568
1130114	N/A	N/A	6420	6435	CGCCACCCATTCTGTA	54	2569
1130134	N/A	N/A	6539	6554	CAAGAGCAAGTTCGAT	69	2570
1130154	N/A	N/A	6626	6641	AGAGTCGCAGAACCTG	51	2571
1130174	N/A	N/A	6677	6692	GGATTTGAATGGGCGG	48	2572
1130194	N/A	N/A	6813	6828	CCGGACGATGGACAAA	56	2573
1130214	N/A	N/A	6877	6892	ATATTCCTCCGCCCT	78	2574
1130234	N/A	N/A	7091	7106	ACACGCAGCTCAGCGC	56 [†]	2575

Table 45. Reduction of FXII RNA by 3-10-3 cEt gapmers with uniform PS internucleoside linkages
(Huh7, electroporation, 3000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (% UTC)	SEQ ID No.
1128714	6	21	6	21	TCCAGGAGTCCAGATC	85	2576
1128734	82	97	82	97	TGACTCCAAGCTCACC	30	2577
1128754	127	142	494	509	GTACTTATGCTCCTTG	16	2578
1128774	158	173	N/A	N/A	CAGTGAGAACGACTGT	36	2579
1128794	202	217	3553	3568	CTGCCGGTGGTACTGG	22	2580
1128802	218	233	3569	3584	TACATTTGTGGTACAG	12	2426
1128815	235	250	3586	3601	TGGCCGGCCCTTGTGG	57	2581
1128835	297	312	3804	3819	CAGTATCCCCATCGCT	16	2582
1128855	412	427	4220	4235	AGTGAGGTGTTGTGGA	38	2583
1128875	487	502	4432	4447	ATACCATATCTCATTC	18	2584
1128895	552	567	4497	4512	AGCCGCTGGCAGTGGG	49	2585
1128915	600	615	4684	4699	CAGCGACCCCATGGA	30	2586
1128935	640	655	4724	4739	CACCGGGCAGTGGCAC	32	2587
1128955	679	694	N/A	N/A	TGCCCTGGTGTCCACG	31	2588
1128975	715	730	4944	4959	GCCGCGGTAGCTGAGC	52	2589
1128995	762	777	4991	5006	GAGGCCACGGCTGAC	31	2590
1129015	809	824	5038	5053	CCCAGTTCCGCGCTTG	18	2591
1129035	866	881	5180	5195	AGCACCACGGGCGGAT	26	2592
1129055	897	912	5211	5226	TCCCAGCTCAGCCGGT	27	2593
1129075	990	1005	5304	5319	TGCGCGGCATGAGTG	24	2594
1129095	1060	1075	N/A	N/A	CGGCAAGGCTCCCGGG	35	2595
1129115	1099	1114	5518	5533	GCCGTTCTGGTCAGG	25	2596

1129135	1131	1146	5550	5565	CTCTTGCGGAGCCGCT	22	2597
1129155	1154	1169	5573	5588	CGACGCGGGTCATCGA	58	2598
1129175	1211	1226	5630	5645	CCCAGTACAGCGCGGC	22	2599
1129195	1242	1257	5661	5676	GCGATGAGGCTGCCGG	30	2600
1129215	1321	1336	5981	5996	CTGGCCGAGCACCACC	23	2601
1129235	1399	1414	6059	6074	GGGCGAGAAGGCCTCG	60	2602
1129255	1440	1455	6183	6198	TCCTGAAGGCGCAACA	22	2603
1129275	1465	1480	6208	6223	GAGCGCGCAGCTGCCG	18	2604
1129295	1499	1514	6242	6257	TTGGCAGGCACACCGG	20	2605
1129315	1560	1575	6303	6318	AACTGGTGGCCCCAGC	38	2606
1129335	1582	1597	6880	6895	GGCATATTCCTCCGCC	42	2607
1129355	1621	1636	6919	6934	CAGGGAGAGGAACGGT	43	2608
1129375	1695	1710	6993	7008	CCCTCGAGGAACCCTG	9 [†]	2609
1129395	1750	1765	7138	7153	TTGGTCCTCACACACC	24 [†]	2610
1129415	1801	1816	7189	7204	GCCCGATCCCCAGCTG	33	2611
1129435	1841	1856	7229	7244	CCACATCGGTGTAGAC	20	2612
1129455	1868	1883	7256	7271	GCTCCCGGATCCAGGC	34	2613
1129475	1900	1915	7288	7303	AGATGAGTCCCTGAGC	10	2614
1129495	1947	1962	7335	7350	TTCCATGCCCCAGCCA	20	2615
1129515	1992	2007	7380	7395	TGGCGCGGAGCTGGCC	49	2616
1129535	2013	2028	7401	7416	TATTGAGTTCCTGCGC	8	2617
1129555	N/A	N/A	100	115	AGCACTACCGAAAGT	105	2618
1129575	N/A	N/A	199	214	CTCCTAGTCACCTGGA	80	2619
1129595	N/A	N/A	332	347	TCTACCTCCCCCGTT	117	2620
1129615	N/A	N/A	436	451	GGGAAGTACTATAAG	153	2621
1129635	N/A	N/A	608	623	AGGCACTAGACTAGAC	62	2622
1129655	N/A	N/A	654	669	CTCACGATCACTCTAG	56	2623
1129675	N/A	N/A	955	970	CCCTCGCCCAGAGTCA	58	2624
1129695	N/A	N/A	1059	1074	GGCTGAATACCTCACA	36	2625
1129715	N/A	N/A	1559	1574	CAGGGTAAGGTCCATC	33	2626
1129735	N/A	N/A	1711	1726	GGCAAGGATAGGGCAC	50	2627
1129755	N/A	N/A	2279	2294	CGCGAATAATGAGAAT	64	2628
1129775	N/A	N/A	2457	2472	CAGCTTAGCATTGATG	52	2629
1129795	N/A	N/A	2543	2558	GCTGTGTAGTTCCTAA	56	2630
1129815	N/A	N/A	2863	2878	ACGGCAGTAATAATAG	49	2631
1129835	N/A	N/A	3375	3390	GCTCTAAAAGTTGGGT	60	2632
1129855	N/A	N/A	3764	3779	TAGCACACCTGTAGAA	83	2633
1129875	N/A	N/A	4018	4033	AGCTTGTTTTACCCAC	42	2634
1129895	N/A	N/A	4320	4335	GAGTATCCAGCAACCT	49	2635
1129915	N/A	N/A	4362	4377	GGATAGTGGTCTCAGG	65	2636
1129935	N/A	N/A	4622	4637	CCCCTGGGCCTAAAGA	72	2637
1129955	N/A	N/A	5072	5087	GCGGCGCACCGGCAGA	55	2638
1129975	N/A	N/A	5420	5435	ATCTAGCTCGCCCCGC	37	2639
1129995	N/A	N/A	5452	5467	GAGGACGGAGAGCCCCG	88	2640
1130015	N/A	N/A	5763	5778	TGCGCTGGGAGACGGA	73	2641

1130035	N/A	N/A	5871	5886	GAACCCCAATCCCGTG	49	2642
1130055	N/A	N/A	6172	6187	CAACAGAGCTAACCCG	59	2643
1130075	N/A	N/A	6355	6370	GATCAAAGGTCTCCTC	41	2644
1130095	N/A	N/A	6391	6406	ATACCAAAGTCGCGGG	80	2645
1130115	N/A	N/A	6434	6449	ACCCATCAGGTCAGCG	59	2646
1130135	N/A	N/A	6540	6555	CCAAGAGCAAGTTCGA	47	2647
1130155	N/A	N/A	6627	6642	CAGAGTCGCAGAACCT	48	2648
1130175	N/A	N/A	6678	6693	AGGATTTGAATGGGCG	38	2649
1130195	N/A	N/A	6814	6829	CCCGGACGATGGACAA	68	2650
1130215	N/A	N/A	7015	7030	CACCTGGCACGCATCG	24 [†]	2651
1130235	N/A	N/A	7093	7108	AAACACGCAGCTCAGC	81 [†]	2652

Table 46. Reduction of FXII RNA by 3-10-3 cEt gapmers with uniform PS internucleoside linkages
(Huh7, electroporation, 3000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (% UTC)	SEQ ID No.
1128715	9	24	9	24	CTATCCAGGAGTCCAG	70	2653
1128735	87	102	87	102	AGTGTTGACTCCAAGC	22	2654
1128755	128	143	495	510	TGTACTTATGCTCCTT	23	2655
1128775	159	174	N/A	N/A	ACAGTGAGAACGACTG	48	2656
1128795	210	225	3561	3576	TGGTACAGCTGCCGGT	17	2657
1128802	218	233	3569	3584	TACATTTGTGGTACAG	8	2426
1128816	236	251	3587	3602	CTGGCCGGCCCTTGTG	35	2658
1128836	298	313	3805	3820	ACAGTATCCCCATCGC	16	2659
1128856	413	428	4221	4236	CAGTGAGGTGTTGTGG	34	2660
1128876	489	504	4434	4449	CTATACCATATCTCAT	20	2661
1128896	556	571	4501	4516	GGCCAGCCGCTGGCAG	74	2662
1128916	601	616	4685	4700	GCAGCGACCCCCATGG	19	2663
1128936	641	656	4725	4740	CCACCGGGCAGTGGCA	28	2664
1128956	683	698	4912	4927	AGCTTGCCTTGGTGTC	22	2665
1128976	716	731	4945	4960	GGCCGCGGTAGCTGAG	62	2666
1128996	765	780	4994	5009	TCCGAGGCCACGGCT	30	2667
1129016	810	825	5039	5054	CCCCAGTTCCGCGCTT	36	2668
1129036	867	882	5181	5196	AAGCACCACGGGCGGA	25	2669
1129056	905	920	5219	5234	CGCAGTACTCCCAGCT	20	2670
1129076	991	1006	5305	5320	CTGCGCGGGCATGAGT	23	2671
1129096	1061	1076	N/A	N/A	CCGGCAAGGCTCCCGG	66	2672
1129116	1102	1117	5521	5536	TGGGCCGTTTCTGGTC	31	2673
1129136	1132	1147	5551	5566	ACTCTTGCGGAGCCGC	16	2674
1129156	1156	1171	5575	5590	AACGACGCGGGTCATC	54	2675
1129176	1212	1227	5631	5646	CCCCAGTACAGCGCGG	41	2676
1129196	1243	1258	5662	5677	GGCGATGAGGCTGCCG	79	2677

1129216	1323	1338	5983	5998	TCCTGGCCGAGCACCA	32	2678
1129236	1400	1415	6060	6075	CGGGCGAGAAGGCCTC	46	2679
1129256	1441	1456	6184	6199	CTCCTGAAGGCGCAAC	34	2680
1129276	1467	1482	6210	6225	AGGAGCGCGCAGCTGC	18	2681
1129296	1502	1517	6245	6260	CGCTTGGCAGGCACAC	29	2682
1129316	1561	1576	6304	6319	GAAGTGGTGGCCCCAG	32	2683
1129336	1583	1598	6881	6896	TGGCATATTCTCCGC	37	2684
1129356	1657	1672	6955	6970	GGAGGATCCGTGCACG	3 [†]	2685
1129376	1696	1711	6994	7009	GCCCTCGAGGAACCCT	11 [†]	2686
1129396	1751	1766	7139	7154	CTTGGTCCTCACACAC	9 [†]	2687
1129416	1802	1817	7190	7205	AGCCCGATCCCCAGCT	36	2688
1129436	1842	1857	7230	7245	GCCACATCGGTGTAGA	23	2689
1129456	1876	1891	7264	7279	AACGGTGTGCTCCCGG	17	2690
1129476	1901	1916	7289	7304	AAGATGAGTCCCTGAG	7	2691
1129496	1948	1963	7336	7351	CTTCCATGCCCCAGCC	16	2692
1129516	1993	2008	7381	7396	CTGGCGCGGAGCTGGC	12	2693
1129536	2014	2029	7402	7417	TTATTGAGTTCCTGCG	10	2694
1129556	N/A	N/A	101	116	CAGCACTACCGAAAG	55	2695
1129576	N/A	N/A	204	219	TAGGCCTCCTAGTCAC	57	2696
1129596	N/A	N/A	333	348	TTCTACCTCCCCCGT	92	2697
1129616	N/A	N/A	439	454	GCAGGGAAGTACTAT	143	2698
1129636	N/A	N/A	610	625	GTAGGCACTAGACTAG	52	2699
1129656	N/A	N/A	655	670	GCTCACGATCACTCTA	33	2700
1129676	N/A	N/A	957	972	ATCCCTCGCCCAGAGT	66	2701
1129696	N/A	N/A	1061	1076	TGGGCTGAATACCTCA	52	2702
1129716	N/A	N/A	1560	1575	CCAGGGTAAGGTCCAT	45	2703
1129736	N/A	N/A	1713	1728	TAGGCAAGGATAGGGC	66	2704
1129756	N/A	N/A	2280	2295	TCGCGAATAATGAGAA	38	2705
1129776	N/A	N/A	2459	2474	ATCAGCTTAGCATTGA	55	2706
1129796	N/A	N/A	2628	2643	TCTACTTAGTGCAACG	30	2707
1129816	N/A	N/A	2910	2925	TCACTGTAAACCACTC	52	2708
1129836	N/A	N/A	3376	3391	TGCTCTAAAAGTTGGG	63	2709
1129856	N/A	N/A	3770	3785	GGGTGGTAGCACACCT	55	2710
1129876	N/A	N/A	4019	4034	AAGCTTGGTTTACCCA	49	2711
1129896	N/A	N/A	4321	4336	CGAGTATCCAGCAACC	83	2712
1129916	N/A	N/A	4363	4378	GGGATAGTGGTCTCAG	32	2713
1129936	N/A	N/A	4624	4639	CACCCCTGGGCCTAAA	75	2714
1129956	N/A	N/A	5073	5088	CGCGGCGCACCGGCAG	55	2715
1129976	N/A	N/A	5421	5436	AATCTAGCTCGCCCGG	39	2716
1129996	N/A	N/A	5453	5468	TGAGGACGGAGAGCCC	53	2717
1130016	N/A	N/A	5764	5779	CTGCGCTGGGAGACGG	64	2718
1130036	N/A	N/A	5872	5887	CGAACCCCAATCCCGT	57	2719
1130056	N/A	N/A	6174	6189	CGCAACAGAGCTAACC	43	2720
1130076	N/A	N/A	6360	6375	CCAGTGATCAAAGGTC	71	2721

1130096	N/A	N/A	6392	6407	GATACCAAAGTCGCGG	44	2722
1130116	N/A	N/A	6437	6452	ACAACCCATCAGGTCA	54	2723
1130136	N/A	N/A	6541	6556	ACCAAGAGCAAGTTCG	51	2724
1130156	N/A	N/A	6628	6643	CCAGAGTCGCAGAACC	47	2725
1130176	N/A	N/A	6752	6767	CAGCAAGCCCCGAAGGG	60	2726
1130196	N/A	N/A	6815	6830	GCCCCGACGATGGACA	47	2727
1130216	N/A	N/A	7016	7031	TCACCTGGCACGCATC	32 [†]	2728
1130236	N/A	N/A	7094	7109	GAAACACGCAGCTCAG	74 [†]	2729

Table 47. Reduction of FXII RNA by 3-10-3 cEt gapmers with uniform PS internucleoside linkages
(Huh7, electroporation, 3000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (% UTC)	SEQ ID No.
1128716	11	26	11	26	GCCTATCCAGGAGTCC	73	2730
1128736	89	104	89	104	AAAGTGTTGACTCCAA	21	2731
1128756	129	144	496	511	TTGTACTTATGCTCCT	34	2732
1128776	160	175	N/A	N/A	GACAGTGAGAACGACT	14	2733
1128796	212	227	3563	3578	TGTGGTACAGCTGCCG	11	2734
1128802	218	233	3569	3584	TACATTTGTGGTACAG	7	2426
1128817	238	253	3589	3604	GCCTGGCCGGCCCTTG	46	2735
1128837	299	314	3806	3821	AACAGTATCCCCATCG	30	2736
1128857	414	429	4222	4237	CCAGTGAGGTGTTGTG	29	2737
1128877	492	507	4437	4452	GTTCTATACCATATCT	24	2738
1128897	572	587	N/A	N/A	TGCGGCAGGCCTGGCT	72	2739
1128917	602	617	4686	4701	GGCAGCGACCCCCATG	24	2740
1128937	642	657	4726	4741	CCCACCGGGCAGTGGC	50	2741
1128957	686	701	4915	4930	AGCAGCTTGCCTTGGT	19	2742
1128977	718	733	4947	4962	CAGGCCGCGGTAGCTG	70	2743
1128997	766	781	4995	5010	CTCCGAGGCCACGGC	43	2744
1129017	811	826	5040	5055	TCCCCAGTTCCGCGCT	47	2745
1129037	869	884	5183	5198	CGAAGCACACGGGCG	14	2746
1129057	906	921	5220	5235	TCGCAGTACTCCAGC	15	2747
1129077	993	1008	5307	5322	GGCTGCGCGGGCATGA	26	2748
1129097	1062	1077	N/A	N/A	GCCGGCAAGGCTCCCG	34	2749
1129117	1104	1119	5523	5538	AGTGGGCCGTTCTTGG	23	2750
1129137	1133	1148	5552	5567	GACTCTTGCGGAGCCG	16	2751
1129157	1157	1172	5576	5591	CAACGACGCGGGTCAT	39	2752
1129177	1215	1230	5634	5649	TGGCCCCAGTACAGCG	60	2753
1129197	1244	1259	5663	5678	GGGCGATGAGGCTGCC	67	2754
1129217	1349	1364	6009	6024	ACGGCTCACAGCTGTG	67	2755
1129237	1401	1416	6061	6076	ACGGGCGAGAAGGCCT	51	2756
1129257	1442	1457	6185	6200	CCTCCTGAAGGCGCAA	33	2757

1129277	1468	1483	6211	6226	CAGGAGCGCGCAGCTG	29	2758
1129297	1503	1518	6246	6261	CCGCTTGGCAGGCACA	26	2759
1129317	1562	1577	6305	6320	CGAACTGGTGGCCCCA	35	2760
1129337	1584	1599	6882	6897	CTGGCATATTCCTCCG	47	2761
1129357	1658	1673	6956	6971	TGGAGGATCCGTGCAC	4 [†]	2762
1129377	1697	1712	6995	7010	CGCCCTCGAGGAACCC	13 [†]	2763
1129397	1752	1767	7140	7155	GCTTGGTCCTCACACA	6 [†]	2764
1129417	1803	1818	7191	7206	CAGCCCGATCCCCAGC	24	2765
1129437	1843	1858	7231	7246	GGCCACATCGGTGTAG	45	2766
1129457	1877	1892	7265	7280	AAACGGTGTGCTCCCG	15	2767
1129477	1902	1917	7290	7305	AAAGATGAGTCCCTGA	9	2768
1129497	1949	1964	7337	7352	CCTTCCATGCCCCAGC	4	2769
1129517	1994	2009	7382	7397	CCTGGCGCGGAGCTGG	20	2770
1129537	2016	2031	7404	7419	CTTTATTGAGTTCCTG	4	2771
1129557	N/A	N/A	119	134	GGACAATCCTGGTTCC	55	2772
1129577	N/A	N/A	206	221	CATAGGCCTCCTAGTC	88	2773
1129597	N/A	N/A	334	349	TTTCTACCTCCCCCCG	77	2774
1129617	N/A	N/A	463	478	GGAATCTACAAGGGAG	76	2775
1129637	N/A	N/A	612	627	AGGTAGGCACTAGACT	67	2776
1129657	N/A	N/A	659	674	CACAGCTCACGATCAC	58	2777
1129677	N/A	N/A	958	973	AATCCCTCGCCCAGAG	71	2778
1129697	N/A	N/A	1125	1140	TCATCTAAAAGGTAGT	47	2779
1129717	N/A	N/A	1561	1576	ACCAGGGTAAGGTCCA	56	2780
1129737	N/A	N/A	1716	1731	GATTAGGCAAGGATAG	66	2781
1129757	N/A	N/A	2281	2296	ATCGCGAATAATGAGA	58	2782
1129777	N/A	N/A	2468	2483	TATAGTGCCATCAGCT	60	2783
1129797	N/A	N/A	2629	2644	GTCTACTTAGTGCAAC	64	2784
1129817	N/A	N/A	2912	2927	AGTCACTGTTAACCAC	51	2785
1129837	N/A	N/A	3401	3416	GTCGCTGTGCATTGAA	42	2786
1129857	N/A	N/A	3881	3896	GTAATGAGGCGGGAGG	62	2787
1129877	N/A	N/A	4035	4050	GCTACTCCAAGTTTCC	40	2788
1129897	N/A	N/A	4322	4337	CCGAGTATCCAGCAAC	53	2789
1129917	N/A	N/A	4365	4380	GAGGGATAGTGGTCTC	95	2790
1129937	N/A	N/A	4634	4649	CGCAGTGAGCCACCCC	71	2791
1129957	N/A	N/A	5074	5089	ACGCGGCGCACCGGCA	55	2792
1129977	N/A	N/A	5422	5437	GAATCTAGCTCGCCCCG	78	2793
1129997	N/A	N/A	5482	5497	CGCCGGCAAGGCTGTG	77	2794
1130017	N/A	N/A	5766	5781	AGCTGCGCTGGGAGAC	79	2795
1130037	N/A	N/A	5873	5888	CCGAACCCCAATCCCG	97	2796
1130057	N/A	N/A	6175	6190	GCGCAACAGAGCTAAC	57	2797
1130077	N/A	N/A	6367	6382	GCCTAACCCAGTGATC	95	2798
1130097	N/A	N/A	6393	6408	CGATACCAAAGTCGCG	97	2799
1130117	N/A	N/A	6438	6453	CACAACCCATCAGGTC	57	2800
1130137	N/A	N/A	6567	6582	CCTTTGCAGCCCGGCG	69	2801

1130157	N/A	N/A	6629	6644	TCCAGAGTCGCAGAAC	61	2802
1130177	N/A	N/A	6753	6768	GCAGCAAGCCCGAAGG	65	2803
1130197	N/A	N/A	6816	6831	CGCCCGGACGATGGAC	59	2804
1130217	N/A	N/A	7017	7032	CTCACCTGGCACGCAT	64 [†]	2805
1130237	N/A	N/A	7095	7110	GGAAACACGCAGCTCA	73 [†]	2806

Table 48. Reduction of FXII RNA by 3-10-3 cEt gapmers with uniform PS internucleoside linkages
(Huh7, electroporation, 3000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (% UTC)	SEQ ID No.
1128717	12	27	12	27	TGCCTATCCAGGAGTC	97	2807
1128737	90	105	90	105	GAAAGTGTGACTCCA	24	2808
1128757	131	146	498	513	CTTTGTACTTATGCTC	46	2809
1128777	161	176	N/A	N/A	TGACAGTGAGAACGAC	31	2810
1128797	213	228	3564	3579	TTGTGGTACAGCTGCC	15	2811
1128802	218	233	3569	3584	TACATTTGTGGTACAG	18	2426
1128818	243	258	3594	3609	TGAGGGCCTGGCCGGC	68	2812
1128838	300	315	3807	3822	AAACAGTATCCCCATC	57	2813
1128858	415	430	4223	4238	TCCAGTGAGGTGTTGT	35	2814
1128878	493	508	4438	4453	AGTTCTATACCATATC	15	2815
1128898	581	596	4665	4680	ACGGGTTGGTGC GGCA	44	2816
1128918	603	618	4687	4702	AGGCAGCGACCCCCAT	33	2817
1128938	643	658	4727	4742	GCCCACCGGGCAGTGG	83	2818
1128958	689	704	4918	4933	CATAGCAGCTTGCCTT	17	2819
1128978	720	735	4949	4964	GCCAGGCCGCGGTAGC	63	2820
1128998	767	782	4996	5011	CCTCCGAGGCCACGG	35	2821
1129018	812	827	5041	5056	GTCCCCAGTTCCGCGC	66	2822
1129038	870	885	5184	5199	ACGAAGCACCACGGGC	30	2823
1129058	907	922	5221	5236	GTCGCACTACTCCAG	19	2824
1129078	995	1010	5309	5324	CCGGCTGCGCGGGCAT	33	2825
1129098	1063	1078	N/A	N/A	CGCCGGCAAGGCTCCC	42	2826
1129118	1106	1121	5525	5540	TCAGTGGGCCGTTCCCT	30	2827
1129138	1134	1149	5553	5568	AGACTCTTGCGGAGCC	21	2828
1129158	1158	1173	5577	5592	CCAACGACGCGGGTCA	29	2829
1129178	1220	1235	5639	5654	AACTGTGGCCCCAGTA	42	2830
1129198	1261	1276	5680	5695	CGTCAGCACCCAGCAG	54	2831
1129218	1352	1367	6012	6027	GGCACGGCTCACAGCT	34	2832
1129238	1402	1417	6062	6077	GACGGGCGAGAAGGCC	42	2833
1129258	1443	1458	6186	6201	TCCTCCTGAAGGCGCA	38	2834
1129278	1469	1484	6212	6227	ACAGGAGCGCGCAGCT	37	2835
1129298	1504	1519	6247	6262	GCCGCTTGGCAGGCAC	77	2836
1129318	1563	1578	6306	6321	TCGAACTGGTGGCCCC	76	2837

1129338	1591	1606	6889	6904	CAGGAAGCTGGCATAT	59	2838
1129358	1659	1674	6957	6972	ATGGAGGATCCGTGCA	10 [†]	2839
1129378	1698	1713	6996	7011	CCGCCCTCGAGGAACC	16 [†]	2840
1129398	1753	1768	7141	7156	AGCTTGGTCCTCACAC	22 [†]	2841
1129418	1806	1821	7194	7209	CCACAGCCCCGATCCCC	36	2842
1129438	1844	1859	7232	7247	AGGCCACATCGGTGTA	34	2843
1129458	1878	1893	7266	7281	GAAACGGTGTGCTCCC	21	2844
1129478	1903	1918	7291	7306	GAAAGATGAGTCCCTG	15	2845
1129498	1950	1965	7338	7353	GCCTTCCATGCCCCAG	16	2846
1129518	1995	2010	7383	7398	TCCTGGCGCGGAGCTG	22	2847
1129538	2017	2032	7405	7420	ACTTTATTGAGTTCCT	9	2848
1129558	N/A	N/A	126	141	AATCCTGGGACAATCC	77	2849
1129578	N/A	N/A	207	222	ACATAGGCCTCCTAGT	83	2850
1129598	N/A	N/A	405	420	GATCTGTTGCTAGTCT	77	2851
1129618	N/A	N/A	466	481	GGTGAATCTACAAGG	107	2852
1129638	N/A	N/A	613	628	CAGGTAGGCACTAGAC	76	2853
1129658	N/A	N/A	660	675	ACACAGCTCACGATCA	63	2854
1129678	N/A	N/A	959	974	AAATCCCTCGCCCAGA	62	2855
1129698	N/A	N/A	1132	1147	GTACCCCTTCATCTAAA	83	2856
1129718	N/A	N/A	1562	1577	CACCAGGGTAAGGTCC	64	2857
1129738	N/A	N/A	1717	1732	GGATTAGGCAAGGATA	76	2858
1129758	N/A	N/A	2282	2297	CATCGGAATAATGAG	49	2859
1129778	N/A	N/A	2469	2484	CTATAGTGCCATCAGC	56	2860
1129798	N/A	N/A	2631	2646	CAGTCTACTTAGTGCA	63	2861
1129818	N/A	N/A	2963	2978	GAAGAGCACTTGCCAC	51	2862
1129838	N/A	N/A	3404	3419	AAGGTCGCTGTGCATT	58	2863
1129858	N/A	N/A	3882	3897	AGTAATGAGGCGGGAG	58	2864
1129878	N/A	N/A	4045	4060	TTGTGACCTTGCTACT	50	2865
1129898	N/A	N/A	4323	4338	TCCGAGTATCCAGCAA	68	2866
1129918	N/A	N/A	4366	4381	AGAGGGATAGTGGTCT	88	2867
1129938	N/A	N/A	4635	4650	ACGCAGTGAGCCACCC	43	2868
1129958	N/A	N/A	5075	5090	CACGCGGCGCACCGGC	66	2869
1129978	N/A	N/A	5423	5438	GGAATCTAGCTCGCCC	74	2870
1129998	N/A	N/A	5483	5498	TCGCCGGCAAGGCTGT	80	2871
1130018	N/A	N/A	5772	5787	CGTGGAAGCTGCGCTG	75	2872
1130038	N/A	N/A	5877	5892	GCTCCCGAACCCCAAT	69	2873
1130058	N/A	N/A	6176	6191	GGCGCAACAGAGCTAA	59	2874
1130078	N/A	N/A	6368	6383	CGCCTAACCCAGTGAT	71	2875
1130098	N/A	N/A	6394	6409	ACGATACCAAAGTCGC	68	2876
1130118	N/A	N/A	6457	6472	GGATTACCTACACAT	73	2877
1130138	N/A	N/A	6568	6583	GCCTTTGCAGCCCGGC	98	2878
1130158	N/A	N/A	6630	6645	ATCCAGAGTCGCAGAA	62	2879
1130178	N/A	N/A	6754	6769	CGCAGCAAGCCCGAAG	69	2880
1130198	N/A	N/A	6817	6832	CCGCCCGGACGATGGA	78	2881

1130218	N/A	N/A	7018	7033	GCTCACCTGGCACGCA	98 [†]	2882
1130238	N/A	N/A	7096	7111	CGGAAACACGCAGCTC	79 [†]	2883

Table 49. Reduction of FXII RNA by 3-10-3 cEt gapmers with uniform PS internucleoside linkages
(Huh7, electroporation, 3000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1128738	92	107	N/A	N/A	TCGAAAGTGTGACTC	15	2884
1128758	132	147	499	514	GCTTTGTACTTATGCT	63	2885
1128778	163	178	N/A	N/A	GGTGACAGTGAGAACG	19	2886
1128798	214	229	3565	3580	TTTGTGGTACAGCTGC	28	2887
1128802	218	233	3569	3584	TACATTTGTGGTACAG	16	2426
1128819	245	260	3596	3611	GCTGAGGGCCTGGCCG	59	2888
1128839	301	316	3808	3823	CAAACAGTATCCCCAT	24	2889
1128859	424	439	4232	4247	GCAGTGGTTTCCAGTG	17	2890
1128879	494	509	4439	4454	CAGTTCTATACCATAT	15	2891
1128899	582	597	4666	4681	CACGGGTTGGTGCGGC	33	2892
1128919	604	619	4688	4703	TAGGCAGCGACCCCCA	31	2893
1128939	645	660	4729	4744	TAGCCACCGGGCAGT	40	2894
1128959	690	705	4919	4934	TCATAGCAGCTTGCCCT	22	2895
1128979	744	759	4973	4988	GGCGCACCCGAGAGCG	32	2896
1128999	768	783	4997	5012	GCCTCCGAGGCCACG	46	2897
1129019	813	828	5042	5057	AGTCCCCAGTTCCGCG	39	2898
1129039	871	886	5185	5200	CACGAAGCACCACGGG	16	2899
1129059	908	923	5222	5237	GGTCGCAGTACTCCA	18	2900
1129079	996	1011	5310	5325	GCCGGCTGCGCGGGCA	35	2901
1129099	1064	1079	N/A	N/A	TCGCCGGAAGGCTCC	36	2902
1129119	1107	1122	5526	5541	CTCAGTGGGCCGTTCC	17	2903
1129139	1135	1150	5554	5569	CAGACTCTTGCGGAGC	12	2904
1129159	1159	1174	5578	5593	GCCAACGACGCGGGTC	27	2905
1129179	1222	1237	5641	5656	GAAACTGTGGCCCCAG	18	2906
1129199	1286	1301	5705	5720	GCCGGTCCTGCAGGCA	33	2907
1129219	1353	1368	6013	6028	TGGCACGGCTCACAGC	27	2908
1129239	1403	1418	6063	6078	TGACGGGCGAGAAGGC	47	2909
1129259	1445	1460	6188	6203	CATCCTCCTGAAGGCG	32	2910
1129279	1470	1485	6213	6228	GACAGGAGCGCGCAGC	27	2911
1129299	1505	1520	6248	6263	CGCCGCTTGGCAGGCA	59	2912
1129319	1564	1579	6307	6322	CTCGAACTGGTGGCCC	37	2913
1129339	1592	1607	6890	6905	GCAGGAAGCTGGCATA	72	2914
1129359	1660	1675	6958	6973	GATGGAGGATCCGTGC	11 [†]	2915
1129379	1699	1714	6997	7012	GCCGCCCTCGAGGAAC	6 [†]	2916
1129399	1754	1769	7142	7157	CAGCTTGGTCCTCACA	26 [†]	2917

1129419	1808	1823	7196	7211	CACCACAGCCCGATCC	37	2918
1129439	1845	1860	7233	7248	TAGGCCACATCGGTGT	31	2919
1129459	1879	1894	7267	7282	GGAAACGGTGTGCTCC	41	2920
1129479	1904	1919	7292	7307	GGAAAGATGAGTCCCT	15	2921
1129499	1951	1966	7339	7354	TGCCTTCCATGCCCCA	8	2922
1129519	1996	2011	7384	7399	ATCCTGGCGCGGAGCT	29	2923
1129539	2018	2033	7406	7421	CACTTTATTGAGTTCC	6	2924
1129559	N/A	N/A	138	153	ACCCCCAGAACAATC	45	2925
1129579	N/A	N/A	208	223	CACATAGGCCTCCTAG	24	2926
1129599	N/A	N/A	408	423	ACCGATCTGTTGCTAG	79	2927
1129619	N/A	N/A	469	484	CAAGGTGGAATCTACA	50	2928
1129639	N/A	N/A	614	629	CCAGGTAGGCACTAGA	36	2929
1129659	N/A	N/A	693	708	TTAGACACAGCCCATA	56	2930
1129679	N/A	N/A	960	975	CAAATCCCTCGCCAG	30	2931
1129699	N/A	N/A	1134	1149	AGGTACCCCTTCATCTA	79	2932
1129719	N/A	N/A	1583	1598	TCAACCCCAACCAAGTC	59	2933
1129739	N/A	N/A	1757	1772	ATGGGATGGACGGACA	44	2934
1129759	N/A	N/A	2283	2298	CCATCGCGAATAATGA	50	2935
1129779	N/A	N/A	2470	2485	GCTATAGTGCCATCAG	25	2936
1129799	N/A	N/A	2651	2666	TATTGAATGAGTGTCC	36	2937
1129819	N/A	N/A	2987	3002	GTAAGTCTTCAGTCCC	56	2938
1129839	N/A	N/A	3405	3420	AAAGGTCGCTGTGCAT	58	2939
1129859	N/A	N/A	3883	3898	GAGTAATGAGGCGGGA	55	2940
1129879	N/A	N/A	4058	4073	GAACCTACTTGCCCTTG	42	2941
1129899	N/A	N/A	4324	4339	CTCCGAGTATCCAGCA	28	2942
1129919	N/A	N/A	4367	4382	AAGAGGGATAGTGGTC	48	2943
1129939	N/A	N/A	4636	4651	AACGCAGTGAGCCACC	55	2944
1129959	N/A	N/A	5076	5091	CCACGCGGCGCACCGG	61	2945
1129979	N/A	N/A	5424	5439	CGGAATCTAGCTCGCC	45	2946
1129999	N/A	N/A	5484	5499	TTCGCCGGCAAGGCTG	50	2947
1130019	N/A	N/A	5800	5815	AGAAGGTAGGGCACGG	78	2948
1130039	N/A	N/A	6089	6104	CCACGCACCCAGGTCG	87	2949
1130059	N/A	N/A	6177	6192	AGGCGCAACAGAGCTA	32	2950
1130079	N/A	N/A	6369	6384	CCGCCTAACCCAGTGA	28	2951
1130099	N/A	N/A	6395	6410	AACGATACCAAAGTCG	42	2952
1130119	N/A	N/A	6459	6474	TGGGATTCACCTACAC	94	2953
1130139	N/A	N/A	6576	6591	CCTAGTTGGCCTTTGC	46	2954
1130159	N/A	N/A	6634	6649	ACCCATCCAGAGTCGC	66	2955
1130179	N/A	N/A	6755	6770	TCGCAGCAAGCCCGAA	53	2956
1130199	N/A	N/A	6818	6833	GCCGCCCCGACGATGG	84	2957
1130219	N/A	N/A	7026	7041	GGCTAAGAGCTCACCT	81 [†]	2958
1130239	N/A	N/A	7097	7112	TCGGAAACACGCAGCT	65 [†]	2959

Table 50. Reduction of FXII RNA by 3-10-3 cEt gapmers with uniform PS internucleoside linkages
(Huh7, electroporation, 3000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1128739	93	108	N/A	N/A	ATCGAAAGTGTTGACT	23	2960
1128759	133	148	500	515	AGCTTTGTACTTATGC	13	2961
1128779	164	179	3515	3530	CGGTGACAGTGAGAAC	14	2962
1128799	215	230	3566	3581	ATTTGTGGTACAGCTG	7	2963
1128802	218	233	3569	3584	TACATTTGTGGTACAG	4	2426
1128820	257	272	N/A	N/A	TAGCACACCAGGGCTG	40	2964
1128840	302	317	3809	3824	CCAAACAGTATCCCCA	10	2965
1128860	431	446	4239	4254	CTTTCTGGCAGTGGTT	12	2966
1128880	497	512	4442	4457	GCTCAGTTCTATACCA	2	2967
1128900	583	598	4667	4682	GCACGGGTTGGTGCGG	38	2968
1128920	607	622	4691	4706	CTCTAGGCAGCGACCC	18	2969
1128940	646	661	4730	4745	GTAGCCCACCGGGCAG	33	2970
1128960	691	706	4920	4935	ATCATAGCAGCTTGCC	15	2971
1128980	745	760	4974	4989	GGGCGCACCCGAGAGC	10	2972
1129000	776	791	5005	5020	GGTAGGTGGCCTCCGA	10	2973
1129020	814	829	5043	5058	CAGTCCCCAGTTCCGC	8	2974
1129040	872	887	5186	5201	GCACGAAGCACCACGG	18	2975
1129060	910	925	5224	5239	CAGGTCGCAGTACTCC	24	2976
1129080	998	1013	5312	5327	GTGCCGGCTGCGCGGG	15	2977
1129100	1065	1080	N/A	N/A	TTCGCCGGCAAGGCTC	36	2978
1129120	1108	1123	5527	5542	GCTCAGTGGGCCGTTC	10	2979
1129140	1136	1151	5555	5570	ACAGACTCTTGCGGAG	16	2980
1129160	1160	1175	5579	5594	CGCCAACGACGCGGGT	21	2981
1129180	1223	1238	5642	5657	AGAAACTGTGGCCCCA	10	2982
1129200	1288	1303	N/A	N/A	GGGCCGGTCTGCAGG	15	2983
1129220	1354	1369	6014	6029	CTGGCACGGCTCACAG	23	2984
1129240	1404	1419	6064	6079	CTGACGGGCGAGAAGG	46	2985
1129260	1446	1461	6189	6204	GCATCCTCCTGAAGGC	10	2986
1129280	1471	1486	6214	6229	CGACAGGAGCGCGCAG	39	2987
1129300	1518	1533	6261	6276	GAGGGTCGCGCGGCGC	24	2988
1129320	1565	1580	6308	6323	CCTCGAACTGGTGGCC	48	2989
1129340	1602	1617	6900	6915	TGCGCCTCCTGCAGGA	70	2990
1129360	1662	1677	6960	6975	AGGATGGAGGATCCGT	43 [†]	2991
1129380	1700	1715	6998	7013	TGCCGCCCTCGAGGAA	10 [†]	2992
1129400	1755	1770	7143	7158	GCAGCTTGGTCCTCAC	8 [†]	2993
1129420	1811	1826	7199	7214	GGTCACCACAGCCCGA	9	2994
1129440	1846	1861	7234	7249	GTAGGCCACATCGGTG	12	2995
1129460	1880	1895	7268	7283	AGGAAACGGTGTGCTC	7	2996

1129480	1905	1920	7293	7308	GGGAAAGATGAGTCCC	39	2997
1129500	1952	1967	7340	7355	TTGCCTTCCATGCCCC	4	2998
1129520	1997	2012	7385	7400	CATCCTGGCGCGGAGC	15	2999
1129540	2019	2034	7407	7422	GCACTTTATTGAGTTC	3	3000
1129560	N/A	N/A	139	154	GACCCCCCAGAACAAT	20	3001
1129580	N/A	N/A	216	231	CACCTTTCCACATAGG	44	3002
1129600	N/A	N/A	409	424	CACCGATCTGTTGCTA	77	3003
1129620	N/A	N/A	470	485	CCAAGGTGGAATCTAC	34	3004
1129640	N/A	N/A	615	630	ACCAGGTAGGCACTAG	23	3005
1129660	N/A	N/A	694	709	CTTAGACACAGCCCAT	58	3006
1129680	N/A	N/A	963	978	ACTCAAATCCCTCGCC	23	3007
1129700	N/A	N/A	1136	1151	GCAGGTACCCTTCATC	22	3008
1129720	N/A	N/A	1586	1601	GACTCAACCCCAACAA	32	3009
1129740	N/A	N/A	1758	1773	GATGGGATGGACGGAC	16	3010
1129760	N/A	N/A	2284	2299	ACCATCGCGAATAATG	14	3011
1129780	N/A	N/A	2487	2502	ACTTGATTCAGGTGTG	29	3012
1129800	N/A	N/A	2652	2667	CTATTGAATGAGTGTC	47	3013
1129820	N/A	N/A	2989	3004	GGGTAAGTCTTCAGTC	33	3014
1129840	N/A	N/A	3406	3421	AAAAGGTCGCTGTGCA	49	3015
1129860	N/A	N/A	3884	3899	AGAGTAATGAGGCGGG	27	3016
1129880	N/A	N/A	4059	4074	TGAACCTACTTGCCCTT	21	3017
1129900	N/A	N/A	4325	4340	TCTCCGAGTATCCAGC	34	3018
1129920	N/A	N/A	4529	4544	CGTTCCCAACCATCTG	56	3019
1129940	N/A	N/A	4637	4652	GAACGCAGTGAGCCAC	21	3020
1129960	N/A	N/A	5078	5093	CCCCACGCGGCGCACC	44	3021
1129980	N/A	N/A	5425	5440	CCGGAATCTAGCTCGC	32	3022
1130000	N/A	N/A	5706	5721	CGCCGGTCCTGCAGGC	32	3023
1130020	N/A	N/A	5801	5816	GAGAAGGTAGGGCACG	30	3024
1130040	N/A	N/A	6112	6127	CTTCCCGTCCCCGCGG	45	3025
1130060	N/A	N/A	6178	6193	AAGGCGCAACAGAGCT	19	3026
1130080	N/A	N/A	6370	6385	TCCGCCTAACCCAGTG	76	3027
1130100	N/A	N/A	6396	6411	GAACGATACCAAAGTC	38	3028
1130120	N/A	N/A	6462	6477	ACCTGGGATTACCTA	31	3029
1130140	N/A	N/A	6577	6592	TCCTAGTTGGCCTTTG	23	3030
1130160	N/A	N/A	6659	6674	CGGAAACAGAAACCCC	57	3031
1130180	N/A	N/A	6756	6771	CTCGCAGCAAGCCCGA	46	3032
1130200	N/A	N/A	6819	6834	TGCCGCCCCGGACGATG	26	3033
1130220	N/A	N/A	7028	7043	CGGGCTAAGAGCTCAC	26 [†]	3034
1130240	N/A	N/A	7098	7113	GTCGGAAACACGCAGC	15 [†]	3035

Table 51. Reduction of FXII RNA by 3-10-3 cEt gapmers with uniform PS internucleoside linkages
(Huh7, electroporation, 3000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1128740	94	109	N/A	N/A	AATCGAAAGTGTGAC	55	3036
1128760	143	158	510	525	TGTGCTCTTCAGCTTT	23	3037
1128780	165	180	3516	3531	CCGGTGACAGTGAGAA	29	3038
1128800	216	231	3567	3582	CATTTGTGGTACAGCT	20	3039
1128802	218	233	3569	3584	TACATTTGTGGTACAG	16	2426
1128821	261	276	N/A	N/A	GTGGTAGCACACCAGG	19	3040
1128841	303	318	3810	3825	TCCAAACAGTATCCCC	16	3041
1128861	432	447	N/A	N/A	TCTTTCTGGCAGTGGT	31	3042
1128881	528	543	4473	4488	CCCTTGCACTGGCATC	17	3043
1128901	584	599	4668	4683	GGCACGGGTTGGTGCG	69	3044
1128921	608	623	4692	4707	CCTCTAGGCAGCGACC	32	3045
1128941	648	663	4732	4747	GTGTAGCCCACCGGGC	84	3046
1128961	692	707	4921	4936	CATCATAGCAGCTTGC	28	3047
1128981	746	761	4975	4990	AGGGCGCACCCGAGAG	25	3048
1129001	777	792	5006	5021	CGGTAGGTGGCCTCCG	57	3049
1129021	815	830	5044	5059	CCAGTCCCCAGTTCCG	39	3050
1129041	873	888	5187	5202	AGCACGAAGCACCACG	25	3051
1129061	911	926	5225	5240	CCAGGTCGCAGTACTC	21	3052
1129081	1001	1016	5315	5330	GCGGTGCCGGCTGCGC	73	3053
1129101	1066	1081	5485	5500	CTTCGCCGGCAAGGCT	36	3054
1129121	1112	1127	5531	5546	CGCAGCTCAGTGGGCC	46	3055
1129141	1137	1152	5556	5571	GACAGACTCTTGCGGA	23	3056
1129161	1161	1176	5580	5595	CCGCCAACGACGCGGG	38	3057
1129181	1224	1239	5643	5658	CAGAAACTGTGGCCCC	29	3058
1129201	1289	1304	N/A	N/A	CGGGCCGGTCCTGCAG	58	3059
1129221	1357	1372	6017	6032	CGTCTGGCACGGCTCA	12	3060
1129241	1405	1420	6065	6080	GCTGACGGGCGAGAAG	30	3061
1129261	1448	1463	6191	6206	CCGCATCCTCCTGAAG	46	3062
1129281	1472	1487	6215	6230	GCGACAGGAGCGCGCA	59	3063
1129301	1519	1534	6262	6277	GGAGGGTCGCGCGGCG	61	3064
1129321	1566	1581	6309	6324	CCCTCGAACTGGTGGC	70	3065
1129341	1606	1621	6904	6919	TACCTGCGCCTCCTGC	90	3066
1129361	1663	1678	6961	6976	GAGGATGGAGGATCCG	43 [†]	3067
1129381	1704	1719	7002	7017	TCGGTGCCGCCCTCGA	32 [†]	3068
1129401	1759	1774	7147	7162	CTCTGCAGCTTGGTCC	32 [†]	3069
1129421	1814	1829	7202	7217	TGCGGTCACCACAGCC	22	3070
1129441	1847	1862	7235	7250	AGTAGGCCACATCGGT	13	3071
1129461	1881	1896	7269	7284	CAGGAAACGGTGTGCT	25	3072

1129481	1906	1921	7294	7309	AGGGAAAGATGAGTCC	10	3073
1129501	1954	1969	7342	7357	TCTTGCCCTCCATGCC	14	3074
1129521	1998	2013	7386	7401	CCATCCTGGCGCGGAG	28	3075
1129541	2020	2035	7408	7423	AGCACTTTATTGAGTT	8	3076
1129561	N/A	N/A	140	155	CGACCCCCCAGAACAA	72	3077
1129581	N/A	N/A	229	244	TCCGGGCTGGCCTCAC	81	3078
1129601	N/A	N/A	410	425	CCACCGATCTGTTGCT	56	3079
1129621	N/A	N/A	520	535	TTACCGACTGTGTGCT	30	3080
1129641	N/A	N/A	619	634	TAGCACCAGGTAGGCA	64	3081
1129661	N/A	N/A	697	712	GCACTTAGACACAGCC	88	3082
1129681	N/A	N/A	964	979	AACTCAAATCCCTCGC	70	3083
1129701	N/A	N/A	1137	1152	GGCAGGTACCCTTCAT	151	3084
1129721	N/A	N/A	1590	1605	TAGAGACTCAACCCCA	62	3085
1129741	N/A	N/A	1761	1776	GCAGATGGGATGGACG	42	3086
1129761	N/A	N/A	2285	2300	AACCATCGCGAATAAT	50	3087
1129781	N/A	N/A	2489	2504	ACACTTGATTGAGGTG	49	3088
1129801	N/A	N/A	2653	2668	CCTATTGAATGAGTGT	54	3089
1129821	N/A	N/A	2991	3006	TTGGGTAAGTCTTCAG	51	3090
1129841	N/A	N/A	3407	3422	AAAAAGGTCGCTGTGC	52	3091
1129861	N/A	N/A	3885	3900	GAGAGTAATGAGGCGG	54	3092
1129881	N/A	N/A	4060	4075	TTGAACCTACTTGCCT	62	3093
1129901	N/A	N/A	4326	4341	GTCTCCGAGTATCCAG	106	3094
1129921	N/A	N/A	4532	4547	GCCCGTTCCCAACCAT	63	3095
1129941	N/A	N/A	4639	4654	GGGAACGCAGTGAGCC	47	3096
1129961	N/A	N/A	5080	5095	AGCCCCACGCGGCGCA	112	3097
1129981	N/A	N/A	5426	5441	GCCGGAATCTAGCTCG	49	3098
1130001	N/A	N/A	5707	5722	TCGCCGGTCCTGCAGG	60	3099
1130021	N/A	N/A	5806	5821	GGCGGGAGAAGGTAGG	51	3100
1130041	N/A	N/A	6158	6173	CGGGCGGAGAGGAGCG	118	3101
1130061	N/A	N/A	6310	6325	ACCCTCGAACTGGTGG	45	3102
1130081	N/A	N/A	6371	6386	TTCCGCCTAACCCAGT	113	3103
1130101	N/A	N/A	6397	6412	GGAACGATACCAAAGT	75	3104
1130121	N/A	N/A	6463	6478	TACCTGGGATTACCT	59	3105
1130141	N/A	N/A	6578	6593	GTCCTAGTTGGCCTTT	29	3106
1130161	N/A	N/A	6664	6679	CGGAGCGGAAACAGAA	109	3107
1130181	N/A	N/A	6757	6772	TCTCGCAGCAAGCCCG	99	3108
1130201	N/A	N/A	6823	6838	CGCTTGCCGCCCGGAC	48	3109
1130221	N/A	N/A	7029	7044	CCGGGCTAAGAGCTCA	48 [†]	3110
1130241	N/A	N/A	7099	7114	GGTCGGAAACACGCAG	77 [†]	3111

Table 52. Reduction of FXII RNA by 3-10-3 cEt gapmers with uniform PS internucleoside linkages
(Huh7, electroporation, 3000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1128761	145	160	512	527	TGTGTGCTCTTCAGCT	19	3112
1128781	166	181	3517	3532	CCCGGTGACAGTGAGA	18	3113
1128801	217	232	3568	3583	ACATTTGTGGTACAGC	8	3114
1128802	218	233	3569	3584	TACATTTGTGGTACAG	9	2426
1128862	462	477	4407	4422	AACCGGAGAAGCTGAG	24	3115
1128882	529	544	4474	4489	ACCCTTGCACTGGCAT	32	3116
1128902	585	600	4669	4684	AGGCACGGGTTGGTGC	70	3117
1128922	609	624	4693	4708	ACCTCTAGGCAGCGAC	19	3118
1128942	650	665	4734	4749	CGGTGTAGCCACCGG	67	3119
1128962	693	708	4922	4937	CCATCATAGCAGCTTG	22	3120
1128982	747	762	4976	4991	CAGGGCGCACCCGAGA	27	3121
1129002	778	793	5007	5022	CCGGTAGGTGGCCTCC	32	3122
1129022	823	838	5052	5067	GTGGCCGCCAGTCCC	17	3123
1129042	874	889	5188	5203	CAGCACGAAGCACCAC	21	3124
1129062	912	927	5226	5241	GCCAGGTTCGAGTACT	25	3125
1129082	1003	1018	5317	5332	CGGCGGTGCCGGCTGC	25	3126
1129102	1068	1083	5487	5502	CGCTTCGCCGCAAGG	30	3127
1129122	1113	1128	5532	5547	CCGCAGCTCAGTGGGC	40	3128
1129142	1138	1153	5557	5572	AGACAGACTCTTGCGG	15	3129
1129162	1162	1177	5581	5596	CCCGCCAACGACGCGG	43	3130
1129182	1225	1240	5644	5659	GCAGAACTGTGGCCC	33	3131
1129222	1371	1386	6031	6046	GAGCGCACGGCCAACG	23	3132
1129242	1406	1421	6066	6081	AGCTGACGGGCGAGAA	59	3133
1129262	1449	1464	6192	6207	TCCGCATCCTCCTGAA	55	3134
1129282	1473	1488	6216	6231	GGCGACAGGAGCGCGC	34	3135
1129302	1520	1535	6263	6278	CGGAGGGTCGCGCGGC	65	3136
1129342	1607	1622	6905	6920	GTACCTGCGCCTCCTG	82	3137
1129362	1679	1694	6977	6992	CGCAGAGCATGCCGGG	6 [†]	3138
1129382	1705	1720	7003	7018	ATCGGTGCCGCCCTCG	8 [†]	3139
1129402	1774	1789	7162	7177	CAGGGTGAGCCGGCGC	31	3140
1129422	1815	1830	7203	7218	TTGCGGTCACCACAGC	27	3141
1129442	1848	1863	7236	7251	TAGTAGGCCACATCGG	19	3142
1129462	1882	1897	7270	7285	TCAGGAAACGGTGTGC	18	3143
1129482	1908	1923	7296	7311	GGAGGGAAAGATGAGT	15	3144
1129502	1955	1970	7343	7358	ATCTTGCTTCCATGC	9	3145
1129522	1999	2014	7387	7402	GCCATCCTGGCGCGGA	51	3146
1129542	2021	2036	7409	7424	AAGCACTTTATTGAGT	12	3147
1129562	N/A	N/A	141	156	GCGACCCCCCAGAACA	72	3148

1129582	N/A	N/A	230	245	TTCCGGGCTGGCCTCA	52	3149
1129602	N/A	N/A	411	426	GCCACCGATCTGTTGC	82	3150
1129622	N/A	N/A	521	536	CTTACCGACTGTGTGC	52	3151
1129642	N/A	N/A	623	638	GACCTAGCACCAGGTA	103	3152
1129662	N/A	N/A	699	714	GGGCACTTAGACACAG	55	3153
1129682	N/A	N/A	965	980	GAACTCAAATCCCTCG	49	3154
1129702	N/A	N/A	1138	1153	TGGCAGGTACCCTTCA	62	3155
1129722	N/A	N/A	1591	1606	TTAGAGACTCAACCCC	62	3156
1129742	N/A	N/A	1916	1931	CATGAAGTTGTGTGCC	67	3157
1129762	N/A	N/A	2287	2302	ATAACCATCGCGAATA	36	3158
1129782	N/A	N/A	2490	2505	GACACTTGATTTCAGGT	45	3159
1129802	N/A	N/A	2654	2669	TCCTATTGAATGAGTG	23	3160
1129822	N/A	N/A	3016	3031	TCCACAACCTGCTAGC	74	3161
1129842	N/A	N/A	3408	3423	CAAAAAGGTCGCTGTG	59	3162
1129862	N/A	N/A	3886	3901	GGAGAGTAATGAGGCG	44	3163
1129882	N/A	N/A	4061	4076	CTTGAACCTACTTGCC	50	3164
1129902	N/A	N/A	4328	4343	AAGTCTCCGAGTATCC	61	3165
1129922	N/A	N/A	4534	4549	TGGCCCGTTCCCAACC	46	3166
1129942	N/A	N/A	4805	4820	AAGCCCGTCCACCTG	46	3167
1129962	N/A	N/A	5084	5099	ACCCAGCCCCACGCGG	60	3168
1129982	N/A	N/A	5428	5443	TGGCCGGAATCTAGCT	119	3169
1130002	N/A	N/A	5708	5723	CTCGCCGGTCCTGCAG	54	3170
1130022	N/A	N/A	5823	5838	CGTGGAAGAAGGGTG	78	3171
1130042	N/A	N/A	6159	6174	CCGGGCGGAGAGGAGC	87	3172
1130062	N/A	N/A	6311	6326	TACCCTCGAACTGGTG	69	3173
1130082	N/A	N/A	6373	6388	TCTTCCGCCTAACCCA	74	3174
1130102	N/A	N/A	6398	6413	CGGAACGATACCAAAG	47	3175
1130122	N/A	N/A	6464	6479	CTACCTGGGATTACCC	85	3176
1130142	N/A	N/A	6579	6594	CGTCCTAGTTGGCCTT	33	3177
1130162	N/A	N/A	6665	6680	GCGGAGCGGAAACAGA	67	3178
1130182	N/A	N/A	6759	6774	TCTCTCGCAGCAAGCC	47	3179
1130202	N/A	N/A	6836	6851	CCCCATCTGACAACGC	103	3180
1130222	N/A	N/A	7030	7045	ACCGGGCTAAGAGCTC	69 [†]	3181
1130242	N/A	N/A	7100	7115	GGGTCGGAACACGCA	94 [†]	3182
1128741	95	110	N/A	N/A	GAATCGAAAGTGTGA	28	3183
1128822	263	278	N/A	N/A	GGGTGGTAGCACACCA	36	3184
1128842	327	342	N/A	N/A	CAGTGGTCTTTCACCT	91	3185
1129202	1291	1306	N/A	N/A	TGCGGGCCGGTCCTGC	63	3186
1129322	1567	1582	N/A	N/A	CCCCTCGAACTGGTGG	86	3187

Table 53. Reduction of FXII RNA by 3-10-3 cEt gapmers with uniform PS internucleoside linkages
(Huh7, electroporation, 3000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (% UTC)	SEQ ID No.
1128722	27	42	27	42	GTCCGTTGGTCCAGCT	34	3188
1128742	96	111	N/A	N/A	GGAATCGAAAGTGTTG	19	3189
1128762	146	161	513	528	CTGTGTGCTCTTCAGC	11	3190
1128782	168	183	3519	3534	TCCCCGGTGACAGTGA	16	3191
1128802	218	233	3569	3584	TACATTTGTGGTACAG	7	2426
1128803	219	234	3570	3585	GTACATTTGTGGTACA	41	3192
1128823	278	293	3785	3800	CCTGATCAAAGTTGGG	25	3193
1128843	328	343	N/A	N/A	GCAGTGGTCTTTCAC	34	3194
1128863	463	478	4408	4423	AAACCGGAGAAGCTGA	34	3195
1128883	531	546	4476	4491	GGACCCCTTGCACTGGC	33	3196
1128903	586	601	4670	4685	GAGGCACGGGTTGGTG	33	3197
1128923	610	625	4694	4709	CACCTCTAGGCAGCGA	26	3198
1128943	651	666	4735	4750	CCGGTGTAGCCCACCG	45	3199
1128963	695	710	4924	4939	GGCCATCATAGCAGCT	35	3200
1128983	748	763	4977	4992	ACAGGGCGCACCCGAG	19	3201
1129003	779	794	5008	5023	TCCGGTAGGTGGCCTC	32	3202
1129023	838	853	N/A	N/A	GTTCCGGCAGAAGGCG	20	3203
1129043	877	892	5191	5206	GTTCAGCACGAAGCAC	14	3204
1129063	913	928	5227	5242	TGCCAGGTCGCAGTAC	37	3205
1129083	1004	1019	5318	5333	TCGGCGGTGCCGGCTG	18	3206
1129103	1069	1084	5488	5503	CCGCTTCGCCGCAAG	44	3207
1129123	1114	1129	5533	5548	CCCGCAGCTCAGTGGG	35	3208
1129143	1139	1154	5558	5573	AAGACAGACTCTTGCG	16	3209
1129163	1163	1178	5582	5597	GCCCCCAACGACGCG	39	3210
1129183	1226	1241	5645	5660	CGCAGAACTGTGGCC	36	3211
1129203	1292	1307	N/A	N/A	GTGCGGGCCGGTCCTG	62	3212
1129223	1373	1388	6033	6048	AGGAGCGCACGGCCAA	27	3213
1129243	1411	1426	6071	6086	CTGGTAGCTGACGGGC	24	3214
1129263	1450	1465	6193	6208	GTCCGCATCCTCCTGA	40	3215
1129283	1474	1489	6217	6232	AGGCGACAGGAGCGCG	20	3216
1129303	1521	1536	6264	6279	TCGGAGGGTCGCGCGG	48	3217
1129323	1568	1583	N/A	N/A	CCCCCTCGAACTGGTG	58	3218
1129343	1609	1624	6907	6922	CGGTACCTGCGCCTCC	87	3219
1129363	1680	1695	6978	6993	GCGCAGAGCATGCCGG	44 [†]	3220
1129383	1706	1721	7004	7019	CATCGGTGCCGCCCTC	15 [†]	3221
1129403	1775	1790	7163	7178	GCAGGGTGAGCCGGCG	27	3222
1129423	1817	1832	7205	7220	TGTTGCGGTCACCACA	11	3223

1129443	1849	1864	7237	7252	GTAGTAGGCCACATCG	20	3224
1129463	1883	1898	7271	7286	ATCAGGAAACGGTGTG	38	3225
1129483	1919	1934	7307	7322	GGAATCACCAAGGAGG	5	3226
1129503	1957	1972	7345	7360	CAATCTTGCCTTCCAT	14	3227
1129523	2000	2015	7388	7403	CGCCATCCTGGCGCGG	57	3228
1129543	2022	2037	7410	7425	AAAGCACTTTATTGAG	9	3229
1129563	N/A	N/A	142	157	AGCGACCCCCCAGAAC	42	3230
1129583	N/A	N/A	232	247	CCTTCCGGGCTGGCCT	55	3231
1129603	N/A	N/A	412	427	TGCCACCGATCTGTTG	60	3232
1129623	N/A	N/A	526	541	GGCCACTTACCGACTG	78	3233
1129643	N/A	N/A	624	639	AGACCTAGCACCAGGT	53	3234
1129663	N/A	N/A	701	716	GTGGGCACTTAGACAC	63	3235
1129683	N/A	N/A	1003	1018	TCAACCTGGTTTCACA	20	3236
1129703	N/A	N/A	1139	1154	ATGGCAGGTACCCCTC	21	3237
1129723	N/A	N/A	1592	1607	CTTAGAGACTCAACCC	36	3238
1129743	N/A	N/A	1917	1932	GCATGAAGTTGTGTGC	72	3239
1129763	N/A	N/A	2288	2303	CATAACCATCGCGAAT	29	3240
1129783	N/A	N/A	2494	2509	GTTAGACACTTGATTC	21	3241
1129803	N/A	N/A	2655	2670	CTCCTATTGAATGAGT	64	3242
1129823	N/A	N/A	3031	3046	GAGTAGACTCCTGACT	80	3243
1129843	N/A	N/A	3409	3424	TCAAAAAGGTCGCTGT	64	3244
1129863	N/A	N/A	3895	3910	GTGATACCAGGAGAGT	36	3245
1129883	N/A	N/A	4062	4077	TCTTGAACCTACTTGC	32	3246
1129903	N/A	N/A	4330	4345	CCAAGTCTCCGAGTAT	68	3247
1129923	N/A	N/A	4535	4550	CTGGCCCGTTCCCAAC	41	3248
1129943	N/A	N/A	4808	4823	GGCAAGCCCGTCCAC	21	3249
1129963	N/A	N/A	5148	5163	CTGTAGCCACACGACG	85	3250
1129983	N/A	N/A	5429	5444	CTGGCCGGAATCTAGC	92	3251
1130003	N/A	N/A	5709	5724	ACTCGCCGGTCCTGCA	36	3252
1130023	N/A	N/A	5841	5856	CCGGGAGCTCCGGAGG	69	3253
1130043	N/A	N/A	6160	6175	CCCGGGCGGAGAGGAG	85	3254
1130063	N/A	N/A	6312	6327	CTACCCTCGAACTGGT	52	3255
1130083	N/A	N/A	6375	6390	CTTCTTCCGCCTAACC	51	3256
1130103	N/A	N/A	6399	6414	CCGGAACGATACCAAA	72	3257
1130123	N/A	N/A	6475	6490	GCCCTGGGATTCTACC	54	3258
1130143	N/A	N/A	6600	6615	TAGCCCGGAGCGCGGG	61	3259
1130163	N/A	N/A	6666	6681	GGCGGAGCGGAAACAG	49	3260
1130183	N/A	N/A	6760	6775	CTCTCTCGCAGCAAGC	43	3261
1130203	N/A	N/A	6838	6853	CACCCCATCTGACAAC	45	3262
1130223	N/A	N/A	7031	7046	AACCGGGCTAAGAGCT	62 [†]	3263
1130243	N/A	N/A	7101	7116	TGGGTCGGAAACACGC	33 [†]	3264

Table 54. Reduction of FXII RNA by 3-10-3 cEt gapmers with uniform PS internucleoside linkages
(Huh7, electroporation, 3000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (% UTC)	SEQ ID No.
1128723	29	44	29	44	CCGTCCGTTGGTCCAG	25	3265
1128743	97	112	N/A	N/A	TGGAATCGAAAGTGTT	42	3266
1128763	147	162	514	529	ACTGTGTGCTCTTCAG	20	3267
1128783	169	184	3520	3535	CTCCCCGGTGACAGTG	36	3268
1128802	218	233	3569	3584	TACATTTGTGGTACAG	12	3269
1128804	220	235	3571	3586	GGTACATTTGTGGTAC	39	3269
1128824	279	294	3786	3801	TCCTGATCAAAGTTGG	32	3270
1128844	330	345	N/A	N/A	CTGCAGTGGTCTTTCA	87	3271
1128864	464	479	4409	4424	AAAACCGGAGAAGCTG	32	3272
1128884	535	550	4480	4495	ATCAGGACCCTTGCAC	32	3273
1128904	587	602	4671	4686	GGAGGCACGGGTGGT	41	3274
1128924	612	627	4696	4711	TCCACCTCTAGGCAGC	26	3275
1128944	652	667	4736	4751	TCCGGTGTAGCCCACC	31	3276
1128964	697	712	4926	4941	GCGGCCATCATAGCAG	70	3277
1128984	749	764	4978	4993	GACAGGGCGCACCCGA	28	3278
1129004	780	795	5009	5024	TTCCGGTAGGTGGCCT	38	3279
1129024	839	854	N/A	N/A	GGTTCCGGCAGAAGGC	27	3280
1129044	881	896	5195	5210	CGCGGTTACGACGAA	21	3281
1129064	941	956	5255	5270	GCGCCGCCTGGGTGG	48	3282
1129084	1005	1020	5319	5334	TTCGGCGGTGCCGGCT	17	3283
1129104	1070	1085	5489	5504	CCCGCTTCGCCGGCAA	20	3284
1129124	1115	1130	5534	5549	GCCCCGAGCTCAGTGG	39	3285
1129144	1141	1156	5560	5575	CGAAGACAGACTCTTG	20	3286
1129164	1165	1180	5584	5599	CAGCCCGCCAACGACG	47	3287
1129184	1227	1242	5646	5661	GCGCAGAAACTGTGGC	51	3288
1129204	1302	1317	5962	5977	AGATCCTCGGGTGCGG	22	3289
1129224	1374	1389	6034	6049	TAGGAGCGCACGGCCA	27	3290
1129244	1412	1427	6072	6087	GCTGGTAGCTGACGGG	44	3291
1129264	1452	1467	6195	6210	CCGTCCGCATCCTCCT	24	3292
1129284	1475	1490	6218	6233	AAGGCGACAGGAGCGC	21	3293
1129304	1522	1537	6265	6280	CTCGGAGGGTCGCGCG	26	3294
1129324	1569	1584	N/A	N/A	GCCCCCTCGAACTGGT	110	3295
1129344	1610	1625	6908	6923	ACGGTACCTGCGCCTC	63	3296
1129364	1681	1696	6979	6994	TGCGCAGAGCATGCCG	44 [†]	3297
1129384	1707	1722	7005	7020	GCATCGGTGCCGCCCT	36 [†]	3298
1129404	1776	1791	7164	7179	TGCAGGGTGAGCCGGC	54	3299
1129424	1819	1834	7207	7222	CTTGTTGCGGTACCA	17	3300
1129444	1850	1865	7238	7253	GGTAGTAGGCCACATC	23	3301

1129464	1884	1899	7272	7287	AATCAGGAAACGGTGT	28	3302
1129484	1920	1935	7308	7323	CGGAATCACCAAGGAG	9	3303
1129504	1958	1973	7346	7361	ACAATCTTGCCITCCA	15	3304
1129524	2002	2017	7390	7405	TGCGCCATCCTGGCGC	42	3305
1129544	2023	2038	7411	7426	CAAAGCACTTTATTGA	21	3306
1129564	N/A	N/A	143	158	TAGCGACCCCCAGAA	34	3307
1129584	N/A	N/A	271	286	GTATCCACCCAGTCTG	67	3308
1129604	N/A	N/A	415	430	GCCTGCCACCGATCTG	81	3309
1129624	N/A	N/A	528	543	CAGGCCACTTACCGAC	37	3310
1129644	N/A	N/A	626	641	TAAGACCTAGCACCAG	69	3311
1129664	N/A	N/A	702	717	CGTGGGCACTTAGACA	47	3312
1129684	N/A	N/A	1004	1019	ATCAACCTGGTTTCAC	33	3313
1129704	N/A	N/A	1203	1218	GTAATTTAGTGCTGG	38	3314
1129724	N/A	N/A	1593	1608	GCTTAGAGACTCAACC	60	3315
1129744	N/A	N/A	2082	2097	TGGACCTTTAAGATGC	26	3316
1129764	N/A	N/A	2289	2304	ACATAACCATCGCGAA	45	3317
1129784	N/A	N/A	2499	2514	CGTGTGTTAGACACTT	42	3318
1129804	N/A	N/A	2656	2671	TCTCCTATTGAATGAG	79	3319
1129824	N/A	N/A	3032	3047	GGAGTAGACTCCTGAC	85	3320
1129844	N/A	N/A	3410	3425	CTCAAAAAGGTCGCTG	43	3321
1129864	N/A	N/A	3897	3912	TGGTGATACCAGGAGA	21	3322
1129884	N/A	N/A	4066	4081	CCCTTCTTGAACCTAC	58	3323
1129904	N/A	N/A	4332	4347	TGCCAAGTCTCCGAGT	52	3324
1129924	N/A	N/A	4583	4598	TGGCACACCACCCGGC	51	3325
1129944	N/A	N/A	4809	4824	TGGCAAGCCCGTCCCA	41	3326
1129964	N/A	N/A	5149	5164	CCTGTAGCCACACGAC	61	3327
1129984	N/A	N/A	5433	5448	CCGGCTGGCCGGAATC	63	3328
1130004	N/A	N/A	5710	5725	TACTCGCCGGTCCCTGC	34	3329
1130024	N/A	N/A	5842	5857	CCCGGGAGCTCCGGAG	138	3330
1130044	N/A	N/A	6161	6176	ACCCGGGCGGAGAGGA	38	3331
1130064	N/A	N/A	6313	6328	CCTACCCTCGAACTGG	62	3332
1130084	N/A	N/A	6380	6395	GCGGGCTTCTTCCGCC	103	3333
1130104	N/A	N/A	6400	6415	CCCGGAACGATACCAA	75	3334
1130124	N/A	N/A	6527	6542	CGATTCTCCCTGTATC	34	3335
1130144	N/A	N/A	6602	6617	ACTAGCCCGGAGCGCG	56	3336
1130164	N/A	N/A	6667	6682	GGGCGGAGCGGAAACA	87	3337
1130184	N/A	N/A	6781	6796	GTAAACCCACTCATGC	63	3338
1130204	N/A	N/A	6841	6856	TCACACCCCATCTGAC	52	3339
1130224	N/A	N/A	7032	7047	CAACCGGGCTAAGAGC	74 [†]	3340
1130244	N/A	N/A	7102	7117	CTGGGTCGGAAACACG	57 [†]	3341

Table 55. Reduction of FXII RNA by 3-10-3 cEt gapmers with uniform PS internucleoside linkages
(Huh7, electroporation, 3000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1128744	98	113	N/A	N/A	GTGGAATCGAAAGTGT	37	3342
1128764	148	163	515	530	GACTGTGTGCTCTTCA	12	3343
1128784	170	185	3521	3536	GCTCCCCGGTGACAGT	44	3344
1128802	218	233	3569	3584	TACATTTGTGGTACAG	13	2426
1128805	221	236	3572	3587	GGGTACATTTGTGGTA	35	3345
1128825	284	299	3791	3806	GCTGGTCCTGATCAAA	31	3346
1128845	365	380	4173	4188	CACAGGTCCCTCCTTT	41	3347
1128865	465	480	4410	4425	AAAAACCGGAGAAGCT	57	3348
1128885	536	551	4481	4496	CATCAGGACCCCTTGCA	51	3349
1128905	589	604	4673	4688	ATGGAGGCACGGGTTG	34	3350
1128925	619	634	4703	4718	GTGGCCCTCCACCTCT	37	3351
1128945	653	668	4737	4752	CTCCGGTGTAGCCCAC	51	3352
1128965	698	713	4927	4942	CGCGGCCATCATAGCA	76	3353
1128985	750	765	4979	4994	TGACAGGGCGCACCCG	43	3354
1129005	781	796	5010	5025	GTTCCGGTAGGTGGCC	49	3355
1129025	840	855	N/A	N/A	GGGTTCCGGCAGAAGG	37	3356
1129045	882	897	5196	5211	TCGCGGTTTCAGCACGA	41	3357
1129065	973	988	5287	5302	GACATGAAGCCTAGGG	17	3358
1129085	1006	1021	5320	5335	CTTCGGCGGTGCCGGC	41	3359
1129105	1071	1086	5490	5505	TCCCGCTTCGCCGGCA	35	3360
1129125	1117	1132	5536	5551	CTGCCCCGAGCTCAGT	36	3361
1129145	1142	1157	5561	5576	TCGAAGACAGACTCTT	31	3362
1129165	1168	1183	5587	5602	CACCAGCCCGCCAACG	53	3363
1129185	1228	1243	5647	5662	GGCGCAGAAACTGTGG	42	3364
1129205	1304	1319	5964	5979	TCAGATCCTCGGGTGC	29	3365
1129225	1375	1390	6035	6050	GTAGGAGCGCACGGCC	32	3366
1129245	1413	1428	6073	6088	TGCTGGTAGCTGACGG	36	3367
1129265	1454	1469	6197	6212	TGCCGTCCGCATCCTC	40	3368
1129285	1476	1491	6219	6234	TAAGGCGACAGGAGCG	33	3369
1129305	1523	1538	6266	6281	TCTCGGAGGGTCGCGC	39	3370
1129325	1570	1585	N/A	N/A	CGCCCCCTCGAACTGG	131	3371
1129345	1611	1626	6909	6924	AACGGTACCTGCGCCT	82	3372
1129365	1684	1699	6982	6997	CCCTGCGCAGAGCATG	21 [†]	3373
1129385	1708	1723	7006	7021	CGCATCGGTGCCGCC	17 [†]	3374
1129405	1777	1792	7165	7180	TTGCAGGGTGAGCCGG	40	3375
1129425	1820	1835	7208	7223	GCTTGTTCGGTCACC	27	3376
1129445	1851	1866	7239	7254	AGGTAGTAGGCCACAT	23	3377
1129465	1885	1900	7273	7288	CAATCAGGAAACGGTG	29	3378

1129485	1921	1936	7309	7324	GCGGAATCACCAAGGA	7	3379
1129505	1962	1977	7350	7365	GGACACAATCTTGCCT	34	3380
1129525	2003	2018	7391	7406	CTGCGCCATCCTGGCG	65	3381
1129545	2024	2039	7412	7427	TCAAAGCACTTTATTG	15	3382
1129565	N/A	N/A	144	159	ATAGCGACCCCCCAGA	46	3383
1129585	N/A	N/A	273	288	TTGTATCCACCCAGTC	93	3384
1129605	N/A	N/A	420	435	TCATAGCCTGCCACCG	73	3385
1129625	N/A	N/A	554	569	ACCCAAGGGTTCCCGG	142	3386
1129645	N/A	N/A	629	644	GCATAAGACCTAGCAC	80	3387
1129665	N/A	N/A	725	740	AAGCACCTGCTCCGAG	78	3388
1129685	N/A	N/A	1009	1024	CTGTTATCAACCTGGT	64	3389
1129705	N/A	N/A	1204	1219	GGTAATTTAGTGTCTG	48	3390
1129725	N/A	N/A	1594	1609	TGCTTAGAGACTCAAC	76	3391
1129745	N/A	N/A	2084	2099	GATGGACCTTTAAGAT	72	3392
1129765	N/A	N/A	2290	2305	AACATAACCATCGCGA	55	3393
1129785	N/A	N/A	2513	2528	CCTTAGGGAGAAAGCG	51	3394
1129805	N/A	N/A	2659	2674	AGCTCTCCTATTGAAT	69	3395
1129825	N/A	N/A	3034	3049	CTGGAGTAGACTCCTG	66	3396
1129845	N/A	N/A	3411	3426	CCTCAAAAAGGTCGCT	59	3397
1129865	N/A	N/A	3900	3915	GTCTGGTGATAACCAGG	54	3398
1129885	N/A	N/A	4069	4084	AGGCCCTTCTTGAACC	72	3399
1129905	N/A	N/A	4333	4348	ATGCCAAGTCTCCGAG	68	3400
1129925	N/A	N/A	4584	4599	CTGGCACACCACCCGG	68	3401
1129945	N/A	N/A	4810	4825	CTGGCAAGCCCGTCCC	48	3402
1129965	N/A	N/A	5150	5165	TCCTGTAGCCACACGA	109	3403
1129985	N/A	N/A	5434	5449	GCCGGCTGGCCGGAAT	89	3404
1130005	N/A	N/A	5711	5726	GTA CTGCGCGGTCCTG	76	3405
1130025	N/A	N/A	5843	5858	CCCCGGGAGCTCCGGA	77	3406
1130045	N/A	N/A	6162	6177	AACCCGGGCGGAGAGG	96	3407
1130065	N/A	N/A	6314	6329	GCCTACCCTCGAACTG	85	3408
1130085	N/A	N/A	6381	6396	CGCGGGCTTCTTCCGC	88	3409
1130105	N/A	N/A	6401	6416	ACCCGGAACGATACCA	69	3410
1130125	N/A	N/A	6529	6544	TTCGATTCTCCCTGTA	77	3411
1130145	N/A	N/A	6603	6618	CACTAGCCCGGAGCGC	80	3412
1130165	N/A	N/A	6668	6683	TGGGCGGAGCGGAAAC	80	3413
1130185	N/A	N/A	6783	6798	TTGTAAACCCACTCAT	82	3414
1130205	N/A	N/A	6862	6877	TGCGAACACAGAGCGC	113	3415
1130225	N/A	N/A	7033	7048	CCAACCGGGCTAAGAG	65 [†]	3416
1130245	N/A	N/A	7103	7118	CCTGGGTGCGGAAACAC	80 [†]	3417

Table 56. Reduction of FXII RNA by 3-10-3 cEt gapmers with uniform PS internucleoside linkages
(Huh7, electroporation, 3000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1128745	99	114	N/A	N/A	GGTGGAAATCGAAAGTG	45	3418
1128765	149	164	516	531	CGACTGTGTGCTCTTC	13	3419
1128785	171	186	3522	3537	GGCTCCCCGGTGACAG	37	3420
1128802	218	233	3569	3584	TACATTTGTGGTACAG	14	3421
1128806	222	237	3573	3588	TGGGTACATTTGTGGT	33	3421
1128826	285	300	3792	3807	CGCTGGTCCTGATCAA	23	3422
1128846	366	381	4174	4189	ACACAGGTCCCTCCTT	48	3423
1128866	466	481	4411	4426	GAAAAACCGGAGAAGC	46	3424
1128886	537	552	4482	4497	GCATCAGGACCCTTGC	67	3425
1128906	590	605	4674	4689	CATGGAGGCACGGGTT	29	3426
1128926	623	638	4707	4722	GGCGGTGGCCCTCCAC	38	3427
1128946	654	669	4738	4753	GCTCCGGTGTAGCCCA	69	3428
1128966	699	714	4928	4943	CCGCGGCCATCATAGC	77	3429
1128986	751	766	4980	4995	CTGACAGGGCGCACCC	38	3430
1129006	799	814	5028	5043	CGCTTGCTCGGCAGTC	23	3431
1129026	841	856	N/A	N/A	CGGGTTCCGGCAGAAG	40	3432
1129046	883	898	5197	5212	GTCGCGGTTACGACAG	24	3433
1129066	974	989	5288	5303	GGACATGAAGCCTAGG	23	3434
1129086	1007	1022	5321	5336	GCTTCGGCGGTGCCGG	33	3435
1129106	1073	1088	5492	5507	GCTCCCGCTTCGCCGG	52	3436
1129126	1119	1134	5538	5553	CGCTGCCCCGACGCTCA	31	3437
1129146	1143	1158	5562	5577	ATCGAAGACAGACTCT	25	3438
1129166	1171	1186	5590	5605	CGCCACCAGCCCGCCA	45	3439
1129186	1229	1244	5648	5663	CGGCGCAGAACTGTG	36	3440
1129206	1306	1321	5966	5981	CGTCAGATCCTCGGGT	30	3441
1129226	1377	1392	6037	6052	CGGTAGGAGCGCACGG	25	3442
1129246	1429	1444	N/A	N/A	CAACAGAGCCAGGTCG	36	3443
1129266	1455	1470	6198	6213	CTGCCGTCCGCATCCT	42	3444
1129286	1477	1492	6220	6235	GTAAGGCGACAGGAGC	23	3445
1129306	1524	1539	6267	6282	GTCTCGGAGGGTCGCG	33	3446
1129326	1571	1586	N/A	N/A	CCGCCCCCTCGAACTG	69	3447
1129346	1612	1627	6910	6925	GAACGGTACCTGCGCC	96	3448
1129366	1685	1700	6983	6998	ACCCTGCGCAGAGCAT	19 [†]	3449
1129386	1709	1724	7007	7022	ACGCATCGGTGCCGCC	17 [†]	3450
1129406	1780	1795	7168	7183	GCCTTGACAGGGTGAGC	25	3451
1129426	1821	1836	7209	7224	GGCTTGTTGCGGTCAC	16	3452

1129446	1852	1867	7240	7255	CAGGTAGTAGGCCACA	25	3453
1129466	1888	1903	7276	7291	GAGCAATCAGGAAACG	20	3454
1129486	1922	1937	7310	7325	TGCGGAATCACCAAGG	9	3455
1129506	1964	1979	7352	7367	TGGGACACAATCTTGC	25	3456
1129526	2004	2019	7392	7407	CCTGCGCCATCCTGGC	21	3457
1129546	2031	2046	7419	7434	AGCATTTTCAAAGCAC	51	3458
1129566	N/A	N/A	145	160	GATAGCGACCCCCCAG	53	3459
1129586	N/A	N/A	277	292	GCCCTTGTATCCACCC	80	3460
1129606	N/A	N/A	422	437	AGTCATAGCCTGCCAC	110	3461
1129626	N/A	N/A	555	570	CACCCAAGGGTTCCCG	81	3462
1129646	N/A	N/A	630	645	GGCATAAGACCTAGCA	73	3463
1129666	N/A	N/A	727	742	TCAAGCACCTGCTCCG	53	3464
1129686	N/A	N/A	1010	1025	ACTGTTATCAACCTGG	54	3465
1129706	N/A	N/A	1206	1221	TAGGTAATTTAGTGTC	55	3466
1129726	N/A	N/A	1596	1611	CATGCTTAGAGACTCA	51	3467
1129746	N/A	N/A	2092	2107	GGATCTGAGATGGACC	43	3468
1129766	N/A	N/A	2291	2306	GAACATAACCATCGCG	60	3469
1129786	N/A	N/A	2519	2534	AGGCTACCTTAGGGAG	64	3470
1129806	N/A	N/A	2683	2698	CGTCACGCTGCTGCTG	45	3471
1129826	N/A	N/A	3035	3050	GCTGGAGTAGACTCCT	54	3472
1129846	N/A	N/A	3412	3427	CCCTCAAAAAGGTCGC	71	3473
1129866	N/A	N/A	3956	3971	CAAAGGGTATTGTGGA	48	3474
1129886	N/A	N/A	4306	4321	CTATTCTGTAGGCCCA	62	3475
1129906	N/A	N/A	4343	4358	GTCTAGGACCATGCCA	95	3476
1129926	N/A	N/A	4607	4622	ACCCCCCAGAGAGCT	91	3477
1129946	N/A	N/A	4812	4827	TCCTGGCAAGCCCGTC	37	3478
1129966	N/A	N/A	5157	5172	TCCGGGTTCTGTAGC	60	3479
1129986	N/A	N/A	5436	5451	CGGCCGGCTGGCCGGA	84	3480
1130006	N/A	N/A	5712	5727	GGTACTCGCCGGTCCT	50	3481
1130026	N/A	N/A	5844	5859	TCCCCGGGAGCTCCGG	102	3482
1130046	N/A	N/A	6163	6178	TAACCCGGGCGGAGAG	88	3483
1130066	N/A	N/A	6315	6330	TGCCTACCCTCGAACT	100	3484
1130086	N/A	N/A	6382	6397	TCGCGGGCTTCTTCCG	56	3485
1130106	N/A	N/A	6402	6417	CACCCGGAACGATACC	67	3486
1130126	N/A	N/A	6531	6546	AGTTCGATTCTCCCTG	57	3487
1130146	N/A	N/A	6604	6619	ACACTAGCCCGGAGCG	66	3488
1130166	N/A	N/A	6669	6684	ATGGGCGGAGCGGAAA	108	3489
1130186	N/A	N/A	6784	6799	CTTGTAACCCACTCA	57	3490
1130206	N/A	N/A	6863	6878	CTGCGAACACAGAGCG	100	3491
1130226	N/A	N/A	7034	7049	GCCAACCGGGCTAAGA	134 [†]	3492
1130246	N/A	N/A	7104	7119	CCCTGGGTCGGAAACA	87 [†]	3493

Table 57. Reduction of FXII RNA by 3-10-3 cEt gapmers with uniform PS internucleoside linkages
(Huh7, electroporation, 3000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1128746	101	116	N/A	N/A	AAGGTGGAATCGAAAG	68	3494
1128766	150	165	N/A	N/A	ACGACTGTGTGCTCTT	20	3495
1128786	175	190	3526	3541	GCAGGGCTCCCCGGTG	45	3496
1128802	218	233	3569	3584	TACATTTGTGGTACAG	38	3497
1128807	223	238	3574	3589	GTGGGTACATTTGTGG	57	3497
1128827	287	302	3794	3809	ATCGCTGGTCCTGATC	57	3498
1128847	370	385	4178	4193	GTTACACAGGTCCTT	40	3499
1128867	467	482	4412	4427	GGAAAAACCGGAGAAG	63	3500
1128887	538	553	4483	4498	GGCATCAGGACCCTTG	58	3501
1128907	591	606	4675	4690	CCATGGAGGCACGGGT	50	3502
1128927	624	639	4708	4723	AGGCGGTGGCCCTCCA	69	3503
1128947	655	670	4739	4754	GGCTCCGGTGTAGCCC	97	3504
1128967	700	715	4929	4944	CCCGCGCCATCATAG	100	3505
1128987	752	767	4981	4996	GCTGACAGGGCGCACC	48	3506
1129007	801	816	5030	5045	CGCGCTTGCTCGGCAG	71	3507
1129027	842	857	N/A	N/A	CCGGGTTCGGCAGAA	51	3508
1129047	884	899	5198	5213	GGTCGCGGTTACAGCAC	44	3509
1129067	976	991	5290	5305	TGGGACATGAAGCCTA	61	3510
1129087	1008	1023	5322	5337	GGCTTCGGCGGTGCCG	79	3511
1129107	1079	1094	5498	5513	GCGGCTGCTCCCGCTT	75	3512
1129127	1121	1136	5540	5555	GCCGCTGCCCCGAGCT	59	3513
1129147	1144	1159	5563	5578	CATCGAAGACAGACTC	45	3514
1129167	1202	1217	5621	5636	GCGCGGCGATGTAGGG	57	3515
1129187	1230	1245	5649	5664	CCGGCGCAGAACTGT	73	3516
1129207	1309	1324	5969	5984	CACCGTCAGATCCTCG	52	3517
1129227	1378	1393	6038	6053	GCGGTAGGAGCGCACG	41	3518
1129247	1431	1446	N/A	N/A	CGCAACAGAGCCAGGT	48	3519
1129267	1456	1471	6199	6214	GCTGCCGTCCGCATCC	61	3520
1129287	1478	1493	6221	6236	CGTAAGGCGACAGGAG	36	3521
1129307	1525	1540	6268	6283	GGTCTCGGAGGGTCGC	69	3522
1129327	1572	1587	N/A	N/A	TCCGCCCCCTCGAACT	128	3523
1129347	1613	1628	6911	6926	GGAACGGTACCTGCGC	181	3524
1129367	1686	1701	6984	6999	AACCCCTGCGCAGAGCA	17 [†]	3525
1129387	1710	1725	7008	7023	CACGCATCGGTGCCGC	30 [†]	3526
1129407	1781	1796	7169	7184	TGCCTTGCAGGGTGAG	23	3527
1129427	1822	1837	7210	7225	TGGCTTGTTCGGTCA	59	3528
1129447	1853	1868	7241	7256	CCAGGTAGTAGGCCAC	56	3529
1129467	1892	1907	7280	7295	CCCTGAGCAATCAGGA	48	3530

1129487	1923	1938	7311	7326	CTGCGGAATCACCAAG	30	3531
1129507	1965	1980	7353	7368	ATGGGACACAATCTTG	70	3532
1129527	2005	2020	7393	7408	TCCTGCGCCATCCTGG	33	3533
1129547	2033	2048	7421	7436	TCAGCATTTTCAAAGC	40	3534
1129567	N/A	N/A	146	161	TGATAGCGACCCCCCA	67	3535
1129587	N/A	N/A	279	294	GTGCCCTTGTATCCAC	76	3536
1129607	N/A	N/A	423	438	AAGTCATAGCCTGCCA	115	3537
1129627	N/A	N/A	571	586	GCACCATACACATCCC	57	3538
1129647	N/A	N/A	631	646	GGGCATAAGACCTAGC	76	3539
1129667	N/A	N/A	736	751	GCACATATCTCAAGCA	53	3540
1129687	N/A	N/A	1017	1032	GAGGTTTACTGTTATC	78	3541
1129707	N/A	N/A	1207	1222	GTAGGTAATTTAGTGT	73	3542
1129727	N/A	N/A	1599	1614	CGCCATGCTTAGAGAC	82	3543
1129747	N/A	N/A	2132	2147	TGCCAAGGACCAAACC	72	3544
1129767	N/A	N/A	2292	2307	AGAACATAACCATCGC	63	3545
1129787	N/A	N/A	2520	2535	AAGGCTACCTTAGGGA	94	3546
1129807	N/A	N/A	2697	2712	AAGGTTCAACAAGGCG	61	3547
1129827	N/A	N/A	3036	3051	AGCTGGAGTAGACTCC	75	3548
1129847	N/A	N/A	3469	3484	CCCTGTACTCAACTGC	65	3549
1129867	N/A	N/A	3957	3972	CCAAAGGGTATTGTGG	74	3550
1129887	N/A	N/A	4308	4323	ACCTATTCTGTAGGCC	88	3551
1129907	N/A	N/A	4344	4359	AGTCTAGGACCATGCC	100	3552
1129927	N/A	N/A	4611	4626	AAAGACCCCCCAGAG	116	3553
1129947	N/A	N/A	4837	4852	TGCTTTCGCACTCTC	54	3554
1129967	N/A	N/A	5158	5173	GTCCGGGTTCTGTAG	85	3555
1129987	N/A	N/A	5438	5453	CGCGGCCGGCTGGCCG	89	3556
1130007	N/A	N/A	5713	5728	GGGTACTCGCCGGTCC	62	3557
1130027	N/A	N/A	5862	5877	TCCCGTGTTCCAGCTT	80	3558
1130047	N/A	N/A	6164	6179	CTAACCCGGGCGGAGA	80	3559
1130067	N/A	N/A	6316	6331	GTGCCTACCCTCGAAC	112	3560
1130087	N/A	N/A	6383	6398	GTCGCGGGCTTCTTCC	54	3561
1130107	N/A	N/A	6403	6418	GCACCCGGAACGATAC	80	3562
1130127	N/A	N/A	6532	6547	AAGTTCGATTCTCCCT	70	3563
1130147	N/A	N/A	6605	6620	CACACTAGCCCGGAGC	86	3564
1130167	N/A	N/A	6670	6685	AATGGGCGGAGCGGAA	79	3565
1130187	N/A	N/A	6785	6800	GCTTGTAACCCACTC	73	3566
1130207	N/A	N/A	6865	6880	CCCTGCGAACACAGAG	91	3567
1130227	N/A	N/A	7035	7050	CGCCAACCGGGCTAAG	98 [†]	3568
1130247	N/A	N/A	7105	7120	ACCCTGGGTTCGAAAC	96 [†]	3569

Table 58. Reduction of FXII RNA by 3-10-3 cEt gapmers with uniform PS internucleoside linkages
(Huh7, electroporation, 3000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1128747	102	117	N/A	N/A	CAAGGTGGAATCGAAA	21	3570
1128767	151	166	N/A	N/A	AACGACTGTGTGCTCT	43	3571
1128787	176	191	3527	3542	GGCAGGGCTCCCCGGT	45	3572
1128802	218	233	3569	3584	TACATTTGTGGTACAG	20	2426
1128808	224	239	3575	3590	TGTGGGTACATTTGTG	30	3573
1128828	288	303	3795	3810	CATCGCTGGTCCTGAT	46	3574
1128848	373	388	4181	4196	CATGTTACACAGGTC	31	3575
1128868	468	483	4413	4428	TGGA AAAACCGGAGAA	47	3576
1128888	539	554	4484	4499	GGGCATCAGGACCCTT	69	3577
1128908	592	607	4676	4691	CCCATGGAGGCACGGG	76	3578
1128928	625	640	4709	4724	CAGGCGGTGGCCCTCC	44	3579
1128948	657	672	4741	4756	AAGGCTCCGGTGTAGC	73	3580
1128968	701	716	4930	4945	GCCCGCGGCCATCATA	52	3581
1128988	753	768	4982	4997	GGCTGACAGGGCGCAC	40	3582
1129008	802	817	5031	5046	CCGCGCTTGCTCGGCA	35	3583
1129028	843	858	N/A	N/A	TCCGGGTTCGGCAGA	35	3584
1129048	885	900	5199	5214	CGGTCGCGGTTTACGCA	39	3585
1129068	977	992	5291	5306	GTGGGACATGAAGCCT	31	3586
1129088	1009	1024	5323	5338	AGGCTTCGGCGGTGCC	78	3587
1129108	1082	1097	5501	5516	AAGGCGGCTGCTCCCG	46	3588
1129128	1124	1139	5543	5558	GGAGCCGCTGCCCCGCA	40	3589
1129148	1145	1160	5564	5579	TCATCGAAGACAGACT	36	3590
1129168	1203	1218	5622	5637	AGCGCGGCGATGTAGG	54	3591
1129188	1231	1246	5650	5665	GCCGGCGCAGAAACTG	81	3592
1129208	1311	1326	5971	5986	ACCACCGTCAGATCCT	48	3593
1129228	1379	1394	6039	6054	AGCGGTAGGAGCGCAC	48	3594
1129248	1433	1448	N/A	N/A	GGCGCAACAGAGCCAG	63	3595
1129268	1457	1472	6200	6215	AGCTGCCGTCCGCATC	42	3596
1129288	1492	1507	6235	6250	GCACACCGGCTGAACG	52	3597
1129308	1542	1557	6285	6300	GCCACCTGGCAGAGCG	73	3598
1129328	1573	1588	N/A	N/A	CTCCGCCCCCTCGAAC	135	3599
1129348	1614	1629	6912	6927	AGGAACGGTACCTGCG	127	3600
1129368	1688	1703	6986	7001	GGAACCCTGCGCAGAG	7 [†]	3601
1129388	1711	1726	7009	7024	GCACGCATCGGTGCCG	84 [†]	3602
1129408	1785	1800	7173	7188	ATGATGCCTTGCAGGG	16	3603
1129428	1823	1838	7211	7226	CTGGCTTGTTCGGTC	48	3604
1129448	1854	1869	7242	7257	GCCAGGTAGTAGGCCA	64	3605
1129468	1893	1908	7281	7296	TCCCTGAGCAATCAGG	45	3606

1129488	1924	1939	7312	7327	ACTGCGGAATCACCAA	20	3607
1129508	1967	1982	7355	7370	GAATGGGACACAATCT	63	3608
1129528	2006	2021	7394	7409	TTCTGCGCCATCCTG	35	3609
1129548	N/A	N/A	92	107	CCGAAAGTGTTGACTC	44	3610
1129568	N/A	N/A	147	162	GTGATAGCGACCCCCC	58	3611
1129588	N/A	N/A	323	338	CCCCGTTGTCTTCTTA	80	3612
1129608	N/A	N/A	425	440	ATAAGTCATAGCCTGC	93	3613
1129628	N/A	N/A	598	613	CTAGACTGCCCTGAGA	55	3614
1129648	N/A	N/A	636	651	CCCATGGGCATAAGAC	89	3615
1129668	N/A	N/A	737	752	AGCACATATCTCAAGC	75	3616
1129688	N/A	N/A	1022	1037	CCTAAGAGGTTTACTG	78	3617
1129708	N/A	N/A	1208	1223	TGTAGGTAATTTAGTG	67	3618
1129728	N/A	N/A	1695	1710	CAAGTTTGGGTAAGGC	57	3619
1129748	N/A	N/A	2137	2152	GCACTTGCCAAGGACC	42	3620
1129768	N/A	N/A	2293	2308	TAGAACATAACCATCG	59	3621
1129788	N/A	N/A	2521	2536	GAAGGCTACCTTAGGG	61	3622
1129808	N/A	N/A	2700	2715	GTTAAGGTTCAACAAG	59	3623
1129828	N/A	N/A	3037	3052	TAGCTGGAGTAGACTC	62	3624
1129848	N/A	N/A	3476	3491	GGACTTCCCCTGTACT	70	3625
1129868	N/A	N/A	3958	3973	TCCAAAGGGTATTGTG	64	3626
1129888	N/A	N/A	4309	4324	AACCTATTCTGTAGGC	74	3627
1129908	N/A	N/A	4345	4360	GAGTCTAGGACCATGC	85	3628
1129928	N/A	N/A	4613	4628	CTAAAGACCCCCCAG	77	3629
1129948	N/A	N/A	4840	4855	ATCTGCTTTCCGCACT	23	3630
1129968	N/A	N/A	5159	5174	TGTCCGGGTTCTGTGTA	59	3631
1129988	N/A	N/A	5440	5455	CCCGCGGCCGCTGGC	91	3632
1130008	N/A	N/A	5715	5730	GCGGGTACTCGCCGGT	66	3633
1130028	N/A	N/A	5864	5879	AATCCCCTGTTCCAGC	62	3634
1130048	N/A	N/A	6165	6180	GCTAACCCTGGCGGAG	97	3635
1130068	N/A	N/A	6322	6337	GCAGTTGTGCCTACCC	53	3636
1130088	N/A	N/A	6384	6399	AGTCGCGGGCTTCTTC	78	3637
1130108	N/A	N/A	6405	6420	AGGCACCCGGAACGAT	62	3638
1130128	N/A	N/A	6533	6548	CAAGTTCGATTCTCCC	58	3639
1130148	N/A	N/A	6606	6621	CCACACTAGCCCGGAG	81	3640
1130168	N/A	N/A	6671	6686	GAATGGGCGGAGCGGA	86	3641
1130188	N/A	N/A	6786	6801	CGCTTGTAACCCACT	58	3642
1130208	N/A	N/A	6866	6881	CCCCTGCGAACACAGA	111	3643
1130228	N/A	N/A	7036	7051	GCGCCAACCGGGCTAA	78 [†]	3644
1130248	N/A	N/A	7106	7121	CACCCTGGGTCGGAAA	67 [†]	3645

Table 59. Reduction of FXII RNA by 3-10-3 cEt gapmers with uniform PS internucleoside linkages
(Huh7, electroporation, 3000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1128748	103	118	N/A	N/A	CCAAGGTGGAATCGAA	49	3646
1128768	152	167	N/A	N/A	GAACGACTGTGTGCTC	29	3647
1128788	177	192	3528	3543	TGGCAGGGCTCCCCGG	55	3648
1128802	218	233	3569	3584	TACATTTGTGGTACAG	35	2426
1128809	225	240	3576	3591	TTGTGGGTACATTTGT	51	3649
1128829	290	305	3797	3812	CCCATCGCTGGTCCTG	49	3650
1128849	380	395	4188	4203	CGCTTGGCATGTTTAC	41	3651
1128869	469	484	4414	4429	GTGGAAAAACCGGAGA	58	3652
1128889	540	555	4485	4500	TGGGCATCAGGACCCT	79	3653
1128909	593	608	4677	4692	CCCCATGGAGGCACGG	52	3654
1128929	626	641	4710	4725	ACAGGCGGTGGCCCTC	48	3655
1128949	660	675	4744	4759	CAGAAGGCTCCGGTGT	79	3656
1128969	703	718	4932	4947	GAGCCCGCGGCCATCA	68	3657
1128989	754	769	4983	4998	CGGCTGACAGGGCGCA	56	3658
1129009	803	818	5032	5047	TCCGCGCTTGCTCGGC	57	3659
1129029	844	859	N/A	N/A	GTCCGGGTTCGGCAG	51	3660
1129049	886	901	5200	5215	CCGGTCGCGGTTTACG	55	3661
1129069	978	993	5292	5307	AGTGGGACATGAAGCC	41	3662
1129089	1010	1025	5324	5339	GAGGCTTCGGCGGTGC	59	3663
1129109	1083	1098	5502	5517	GAAGGCGGCTGCTCCC	54	3664
1129129	1125	1140	5544	5559	CGGAGCCGCTGCCCCG	70	3665
1129149	1146	1161	5565	5580	GTCATCGAAGACAGAC	58	3666
1129169	1204	1219	5623	5638	CAGCGCGGCGATGTAG	61	3667
1129189	1233	1248	5652	5667	CTGCCGGCGCAGAAAC	65	3668
1129209	1312	1327	5972	5987	CACCACCGTCAGATCC	64	3669
1129229	1380	1395	6040	6055	AAGCGGTAGGAGCGCA	66	3670
1129249	1434	1449	N/A	N/A	AGGCGCAACAGAGCCA	74	3671
1129269	1458	1473	6201	6216	CAGCTGCCGTCCGCAT	55	3672
1129289	1493	1508	6236	6251	GGCACACCGGCTGAAC	56	3673
1129309	1545	1560	6288	6303	CCGGCCACCTGGCAGA	120	3674
1129329	1575	1590	N/A	N/A	TCCTCCGCCCCCTCGA	145	3675
1129349	1615	1630	6913	6928	GAGGAACGGTACCTGC	95	3676
1129369	1689	1704	6987	7002	AGGAACCCTGCGCAGA	20 [†]	3677
1129389	1713	1728	7011	7026	TGGCACGCATCGGTGC	65 [†]	3678
1129409	1788	1803	7176	7191	CTGATGATGCCTTGCA	37	3679
1129429	1824	1839	7212	7227	CCTGGCTTGTTGCGGT	52	3680
1129449	1855	1870	7243	7258	GGCCAGGTAGTAGGCC	88	3681
1129469	1894	1909	7282	7297	GTCCCTGAGCAATCAG	40	3682

1129489	1925	1940	7313	7328	CACTGCGGAATCACCA	29	3683
1129509	1968	1983	7356	7371	GGAATGGGACACAATC	45	3684
1129529	2007	2022	7395	7410	GTTCTGCGCCATCCT	37	3685
1129549	N/A	N/A	93	108	ACCGAAAGTGTTGACT	63	3686
1129569	N/A	N/A	148	163	TGTGATAGCGACCCCC	74	3687
1129589	N/A	N/A	324	339	CCCCCGTTGTCTTCTT	117	3688
1129609	N/A	N/A	426	441	TATAAGTCATAGCCTG	66	3689
1129629	N/A	N/A	600	615	GACTAGACTGCCCTGA	84	3690
1129649	N/A	N/A	637	652	GCCCATGGGCATAAGA	83	3691
1129669	N/A	N/A	744	759	CGCCAGCAGCACATAT	78	3692
1129689	N/A	N/A	1023	1038	CCCTAAGAGGTTTACT	98	3693
1129709	N/A	N/A	1214	1229	CTGGCATGTAGGTAAT	75	3694
1129729	N/A	N/A	1696	1711	CCAAGTTTGGGTAAGG	80	3695
1129749	N/A	N/A	2139	2154	GTGCACTTGCCAAGGA	80	3696
1129769	N/A	N/A	2321	2336	TGCTAGTTCAATGTTC	51	3697
1129789	N/A	N/A	2523	2538	AAGAAGGCTACCTTAG	88	3698
1129809	N/A	N/A	2703	2718	CCAGTTAAGGTTCAAC	64	3699
1129829	N/A	N/A	3038	3053	ATAGCTGGAGTAGACT	80	3700
1129849	N/A	N/A	3495	3510	GGGACAACACACTCTC	68	3701
1129869	N/A	N/A	3963	3978	GGACTTCCAAAGGGTA	66	3702
1129889	N/A	N/A	4310	4325	CAACCTATTCTGTAGG	65	3703
1129909	N/A	N/A	4347	4362	GAGAGTCTAGGACCAT	106	3704
1129929	N/A	N/A	4615	4630	GCCTAAAGACCCCCCCC	88	3705
1129949	N/A	N/A	4844	4859	TCTCATCTGCTTTCCG	35	3706
1129969	N/A	N/A	5160	5175	TTGTCCGGGTTCTGT	67	3707
1129989	N/A	N/A	5443	5458	GAGCCCGCGGCCGGCT	93	3708
1130009	N/A	N/A	5716	5731	GGCGGGTACTCGCCGG	96	3709
1130029	N/A	N/A	5865	5880	CAATCCCGTGTTCCAG	70	3710
1130049	N/A	N/A	6166	6181	AGCTAACCCGGGCGGA	105	3711
1130069	N/A	N/A	6324	6339	TAGCAGTTGTGCCTAC	70	3712
1130089	N/A	N/A	6385	6400	AAGTCGCGGGCTTCTT	93	3713
1130109	N/A	N/A	6407	6422	GTAGGCACCCGGAACG	79	3714
1130129	N/A	N/A	6534	6549	GCAAGTTCGATTCTCC	70	3715
1130149	N/A	N/A	6608	6623	TCCCACACTAGCCCGG	83	3716
1130169	N/A	N/A	6672	6687	TGAATGGGCGGAGCGG	88	3717
1130189	N/A	N/A	6787	6802	GCGCTTGTAACCCAC	91	3718
1130209	N/A	N/A	6867	6882	GCCCCTGCGAACACAG	85	3719
1130229	N/A	N/A	7057	7072	GCCTGACGGCCTCGGG	77 [†]	3720
1130249	N/A	N/A	7107	7122	TCACCCTGGGTCGGAA	86 [†]	3721

Table 60. Reduction of FXII RNA by 3-10-3 cEt gapmers with uniform PS internucleoside linkages
(Huh7, electroporation, 3000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1128749	104	119	N/A	N/A	CCCAAGGTGGAATCGA	63	3722
1128769	153	168	N/A	N/A	AGAACGACTGTGTGCT	33	3723
1128789	178	193	3529	3544	GTGGCAGGGCTCCCCG	44	3724
1128802	218	233	3569	3584	TACATTTGTGGTACAG	24	2426
1128810	226	241	3577	3592	CTTGTGGGTACATTTG	40	3725
1128830	291	306	3798	3813	CCCCATCGCTGGTCCT	40	3726
1128850	381	396	4189	4204	CCGCTTGGCATGTTCA	49	3727
1128870	470	485	4415	4430	TGTGGAAAAACCGGAG	27	3728
1128890	541	556	4486	4501	GTGGGCATCAGGACCC	91	3729
1128910	594	609	4678	4693	CCCCCATGGAGGCACG	63	3730
1128930	627	642	4711	4726	CACAGGCGGTGGCCCT	53	3731
1128950	661	676	4745	4760	GCAGAAAGGCTCCGGTG	118	3732
1128970	706	721	4935	4950	GCTGAGCCCCGCGCCA	61	3733
1128990	755	770	4984	4999	ACGGCTGACAGGGCGC	61	3734
1129010	804	819	5033	5048	TTCCGCGCTTGCTCGG	129	3735
1129030	845	860	N/A	N/A	TGTCCGGGTTCGGCA	52	3736
1129050	887	902	5201	5216	GCCGGTCGCGTTTCAG	47	3737
1129070	979	994	5293	5308	GAGTGGGACATGAAGC	74	3738
1129090	1013	1028	5327	5342	GCTGAGGCTTCGGCGG	52	3739
1129110	1085	1100	5504	5519	GGGAAGGCGGCTGCTC	68	3740
1129130	1126	1141	5545	5560	GCGGAGCCGCTGCCCCG	76	3741
1129150	1147	1162	5566	5581	GGTCATCGAAGACAGA	52	3742
1129170	1206	1221	5625	5640	TACAGCGCGGCGATGT	106	3743
1129190	1236	1251	5655	5670	AGGCTGCCGGCGCAGA	51	3744
1129210	1314	1329	5974	5989	AGCACCACCGTCAGAT	72	3745
1129230	1381	1396	6041	6056	CAAGCGGTAGGAGCGC	61	3746
1129250	1435	1450	N/A	N/A	AAGGCGCAACAGAGCC	60	3747
1129270	1459	1474	6202	6217	GCAGCTGCCGTCCGCA	54	3748
1129290	1494	1509	6237	6252	AGGCACACCGGCTGAA	63	3749
1129310	1546	1561	6289	6304	GCCGGCCACCTGGCAG	93	3750
1129330	1577	1592	N/A	N/A	ATTCCTCCGCCCCCTC	189	3751
1129350	1616	1631	6914	6929	AGAGGAACGGTACCTG	99	3752
1129370	1690	1705	6988	7003	GAGGAACCCTGCGCAG	17 [†]	3753
1129390	1714	1729	7012	7027	CTGGCACGCATCGGTG	30 [†]	3754
1129410	1789	1804	7177	7192	GCTGATGATGCCTTGC	42	3755
1129430	1825	1840	7213	7228	GCCTGGCTTGTTGCGG	60	3756
1129450	1856	1871	7244	7259	AGGCCAGGTAGTAGGC	92	3757
1129470	1895	1910	7283	7298	AGTCCCTGAGCAATCA	53	3758

1129490	1926	1941	7314	7329	TCACTGCGGAATCACC	17	3759
1129510	1984	1999	7372	7387	AGCTGGCCGCACTGGG	36	3760
1129530	2008	2023	7396	7411	AGTTCCTGCGCCATCC	19	3761
1129550	N/A	N/A	94	109	CACCGAAAGTGTTGAC	118	3762
1129570	N/A	N/A	149	164	CTGTGATAGCGACCCC	96	3763
1129590	N/A	N/A	325	340	CCCCCGTTGTCTTCT	118	3764
1129610	N/A	N/A	427	442	CTATAAGTCATAGCCT	139	3765
1129630	N/A	N/A	602	617	TAGACTAGACTGCCCT	78	3766
1129650	N/A	N/A	644	659	CTCTAGTGCCCATGGG	75	3767
1129670	N/A	N/A	866	881	CCCATTGAAGGCCCTG	75	3768
1129690	N/A	N/A	1024	1039	ACCCTAAGAGGTTTAC	106	3769
1129710	N/A	N/A	1522	1537	TGCCACACTCTAGGTA	98	3770
1129730	N/A	N/A	1699	1714	GCACCAAGTTTGGGTA	100	3771
1129750	N/A	N/A	2141	2156	AAGTGCACCTTGCCAAG	107	3772
1129770	N/A	N/A	2376	2391	GCTGTTGGTTGATGAA	85	3773
1129790	N/A	N/A	2524	2539	CAAGAAGGCTACCTTA	146	3774
1129810	N/A	N/A	2708	2723	CATTCCCAGTTAAGGT	85	3775
1129830	N/A	N/A	3039	3054	GATAGCTGGAGTAGAC	108	3776
1129850	N/A	N/A	3609	3624	TAGTCTTACCAGGGCT	82	3777
1129870	N/A	N/A	3995	4010	ATGGGACCACTCCTTC	76	3778
1129890	N/A	N/A	4311	4326	GCAACCTATTCTGTAG	109	3779
1129910	N/A	N/A	4348	4363	GGAGAGTCTAGGACCA	115	3780
1129930	N/A	N/A	4616	4631	GGCCTAAAGACCCCCC	143	3781
1129950	N/A	N/A	5067	5082	GCACCGGCAGAAGGCG	63	3782
1129970	N/A	N/A	5374	5389	TTCCTAACCTCCCGGG	97	3783
1129990	N/A	N/A	5446	5461	GGAGAGCCCGCGGCCG	95	3784
1130010	N/A	N/A	5752	5767	ACGGAGGAGCCGCGGC	62	3785
1130030	N/A	N/A	5866	5881	CCAATCCCGTGTTCCTA	84	3786
1130050	N/A	N/A	6167	6182	GAGCTAACCCGGGCGG	96	3787
1130070	N/A	N/A	6327	6342	CCCTAGCAGTTGTGCC	104	3788
1130090	N/A	N/A	6386	6401	AAAGTCGCGGGCTTCT	92	3789
1130110	N/A	N/A	6409	6424	CTGTAGGCACCCGGAA	164	3790
1130130	N/A	N/A	6535	6550	AGCAAGTTCGATTCTC	80	3791
1130150	N/A	N/A	6621	6636	CGCAGAACCTGGCTCC	95	3792
1130170	N/A	N/A	6673	6688	TTGAATGGGCGGAGCG	126	3793
1130190	N/A	N/A	6809	6824	ACGATGGACAAAGCTG	147	3794
1130210	N/A	N/A	6870	6885	TCCGCCCTGCGAACA	143	3795
1130230	N/A	N/A	7064	7079	GATTTGTGCCTGACGG	93 [†]	3796
1130250	N/A	N/A	7109	7124	AATCACCTGGGTCGG	115 [†]	3797

Table 61. Reduction of FXII RNA by 3-10-3 cEt gapmers with uniform PS internucleoside linkages
(Huh7, electroporation, 3000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1128750	105	120	N/A	N/A	TCCCAAGGTGGAATCG	66	3798
1128770	154	169	N/A	N/A	GAGAACGACTGTGTGC	47	3799
1128790	198	213	3549	3564	CGGTGGTACTGGAAGG	45	3800
1128802	218	233	3569	3584	TACATTTGTGGTACAG	28	3801
1128811	228	243	3579	3594	CCCTTGTGGGTACATT	75	3801
1128831	292	307	3799	3814	TCCCCATCGCTGGTCC	70	3802
1128851	382	397	4190	4205	GCCGCTTGGCATGTTC	53	3803
1128871	472	487	4417	4432	CTTGTGGAAAAACCGG	37	3804
1128891	542	557	4487	4502	AGTGGGCATCAGGACC	64	3805
1128911	595	610	4679	4694	ACCCCCATGGAGGCAC	49	3806
1128931	628	643	4712	4727	GCACAGGCGGTGGCCC	66	3807
1128951	662	677	4746	4761	CGCAGAAGGCTCCGGT	95	3808
1128971	711	726	4940	4955	CGGTAGCTGAGCCCGC	102	3809
1128991	756	771	4985	5000	CACGGCTGACAGGGCG	53	3810
1129011	805	820	5034	5049	GTTCCGCGCTTGCTCG	43	3811
1129031	846	861	N/A	N/A	TTGTCCGGGTTCGGGC	47	3812
1129051	888	903	5202	5217	AGCCGGTCGCGGTTCA	18	3813
1129071	980	995	5294	5309	TGAGTGGGACATGAAG	50	3814
1129091	1014	1029	5328	5343	GGCTGAGGCTTCGGCG	54	3815
1129111	1086	1101	5505	5520	AGGGAAGGCGGCTGCT	44	3816
1129131	1127	1142	5546	5561	TGCGGAGCCGCTGCCC	59	3817
1129151	1150	1165	5569	5584	GCGGGTCATCGAAGAC	52	3818
1129171	1207	1222	5626	5641	GTACAGCGCGGCGATG	57	3819
1129191	1238	1253	5657	5672	TGAGGCTGCCGGCGCA	65	3820
1129211	1315	1330	5975	5990	GAGCACCACCGTCAGA	36	3821
1129231	1382	1397	6042	6057	GCAAGCGGTAGGAGCG	53	3822
1129251	1436	1451	6179	6194	GAAGGCGCAACAGAGC	60	3823
1129271	1460	1475	6203	6218	CGCAGCTGCCGTCCGC	50	3824
1129291	1495	1510	6238	6253	CAGGCACACCGGCTGA	53	3825
1129311	1554	1569	6297	6312	TGGCCCCAGCCGGCCA	78	3826
1129331	1578	1593	N/A	N/A	TATTCCTCCGCCCCCT	140	3827
1129351	1617	1632	6915	6930	GAGAGGAACGGTACCT	120	3828
1129371	1691	1706	6989	7004	CGAGGAACCCTGCGCA	41 [†]	3829
1129391	1746	1761	7134	7149	TCCTCACACACCAGCG	15 [†]	3830
1129411	1790	1805	7178	7193	AGCTGATGATGCCTTG	40	3831
1129431	1826	1841	7214	7229	CGCCTGGCTTGTTGCG	83	3832
1129451	1864	1879	7252	7267	CCGGATCCAGGCCAGG	66	3833
1129471	1896	1911	7284	7299	GAGTCCCTGAGCAATC	43	3834

1129491	1927	1942	7315	7330	CTCACTGCGGAATCAC	21	3835
1129511	1988	2003	7376	7391	GCGGAGCTGGCCGCAC	56	3836
1129531	2009	2024	7397	7412	GAGTTCCTGCGCCATC	18	3837
1129551	N/A	N/A	95	110	TCACCGAAAGTGTTGA	86	3838
1129571	N/A	N/A	150	165	GCTGTGATAGCGACCC	78	3839
1129591	N/A	N/A	326	341	TCCCCCGTTGTCTTC	116	3840
1129611	N/A	N/A	428	443	ACTATAAGTCATAGCC	95	3841
1129631	N/A	N/A	603	618	CTAGACTAGACTGCCC	92	3842
1129651	N/A	N/A	645	660	ACTCTAGTGCCCATGG	86	3843
1129671	N/A	N/A	867	882	GCCCATTGAAGGCCCT	83	3844
1129691	N/A	N/A	1053	1068	ATACCTCACATGGGTT	145	3845
1129711	N/A	N/A	1555	1570	GTAAGGTCCATCTGGT	72	3846
1129731	N/A	N/A	1704	1719	ATAGGGCACCAAGTTT	93	3847
1129751	N/A	N/A	2143	2158	CAAAGTGCACCTTGCCA	73	3848
1129771	N/A	N/A	2445	2460	GATGAATCAGCAACAC	56	3849
1129791	N/A	N/A	2525	2540	ACAAGAAGGCTACCTT	79	3850
1129811	N/A	N/A	2746	2761	CCATTTGTGGGCATGC	64	3851
1129831	N/A	N/A	3040	3055	AGATAGCTGGAGTAGA	87	3852
1129851	N/A	N/A	3610	3625	GTAGTCTTACCAGGGC	72	3853
1129871	N/A	N/A	3996	4011	AATGGGACCACTCCTT	60	3854
1129891	N/A	N/A	4312	4327	AGCAACCTATTCTGTA	95	3855
1129911	N/A	N/A	4349	4364	AGGAGAGTCTAGGACC	116	3856
1129931	N/A	N/A	4617	4632	GGGCCTAAAGACCCCC	94	3857
1129951	N/A	N/A	5068	5083	CGCACCGGCAGAAGGC	75	3858
1129971	N/A	N/A	5375	5390	CTTCCTAACCTCCCGG	76	3859
1129991	N/A	N/A	5448	5463	ACGGAGAGCCCGCGGC	94	3860
1130011	N/A	N/A	5753	5768	GACGGAGGAGCCGCGG	98	3861
1130031	N/A	N/A	5867	5882	CCCAATCCCGTGTTC	76	3862
1130051	N/A	N/A	6168	6183	AGAGCTAACCCGGGCG	91	3863
1130071	N/A	N/A	6328	6343	CCCCTAGCAGTTGTGC	76	3864
1130091	N/A	N/A	6387	6402	CAAAGTCGCGGGCTTC	67	3865
1130111	N/A	N/A	6410	6425	TCTGTAGGCACCCGGA	73	3866
1130131	N/A	N/A	6536	6551	GAGCAAGTTCGATTCT	81	3867
1130151	N/A	N/A	6622	6637	TCGCAGAACCTGGCTC	76	3868
1130171	N/A	N/A	6674	6689	TTTGAATGGGCGGAGC	84	3869
1130191	N/A	N/A	6810	6825	GACGATGGACAAAGCT	82	3870
1130211	N/A	N/A	6871	6886	CTCCGCCCCTGCGAAC	122	3871
1130231	N/A	N/A	7065	7080	AGATTTGTGCCTGACG	84 [†]	3872
1130251	N/A	N/A	7111	7126	GGAATCACCCCTGGGTC	55 [†]	3873

Table 62. Reduction of FXII RNA by 3-10-3 cEt gapmers with uniform PS internucleoside linkages
(Huh7, electroporation, 3000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1128751	107	122	474	489	CTTCCCAAGGTGGAAT	89	3874
1128771	155	170	N/A	N/A	TGAGAACGACTGTGTG	49	3875
1128791	199	214	3550	3565	CCGGTGGTACTGGAAG	55	3876
1128802	218	233	3569	3584	TACATTTGTGGTACAG	12	2426
1128812	229	244	3580	3595	GCCCTTGTGGGTACAT	56	3877
1128832	293	308	3800	3815	ATCCCCATCGCTGGTC	36	3878
1128852	383	398	4191	4206	GGCCGCTTGGCATGTT	54	3879
1128872	480	495	4425	4440	ATCTCATTTCTTGTGGA	32	3880
1128892	543	558	4488	4503	CAGTGGGCATCAGGAC	48	3881
1128912	597	612	4681	4696	CGACCCCCATGGAGGC	36	3882
1128932	630	645	4714	4729	TGGCACAGGCGGTGGC	52	3883
1128952	663	678	4747	4762	TCGCAGAAGGCTCCGG	87	3884
1128972	712	727	4941	4956	GCGGTAGCTGAGCCCG	66	3885
1128992	758	773	4987	5002	CCCACGGCTGACAGGG	73	3886
1129012	806	821	5035	5050	AGTTCCGCGCTTGCTC	34	3887
1129032	862	877	5176	5191	CCACGGGCGGATGTCG	43	3888
1129052	889	904	5203	5218	CAGCCGGTCGCGGTTC	38	3889
1129072	981	996	5295	5310	ATGAGTGGGACATGAA	55	3890
1129092	1016	1031	5330	5345	TGGGCTGAGGCTTCGG	25	3891
1129112	1088	1103	5507	5522	TCAGGGAAGGCGGCTG	45	3892
1129132	1128	1143	5547	5562	TTGCGGAGCCGCTGCC	58	3893
1129152	1151	1166	5570	5585	CGCGGGTCATCGAAGA	44	3894
1129172	1208	1223	5627	5642	AGTACAGCGCGGCGAT	31	3895
1129192	1239	1254	5658	5673	ATGAGGCTGCCGGCGC	43	3896
1129212	1318	1333	5978	5993	GCCGAGCACCACCGTC	40	3897
1129232	1383	1398	6043	6058	TGCAAGCGGTAGGAGC	33	3898
1129252	1437	1452	6180	6195	TGAAGGCGCAACAGAG	44	3899
1129272	1462	1477	6205	6220	CGCGCAGCTGCCGTCC	43	3900
1129292	1496	1511	6239	6254	GCAGGCACACCGGCTG	34	3901
1129312	1556	1571	6299	6314	GGTGGCCCCAGCCGGC	60	3902
1129332	1579	1594	N/A	N/A	ATATTCCTCCGCCCCC	89	3903
1129352	1618	1633	6916	6931	GGAGAGGAACGGTACC	89	3904
1129372	1692	1707	6990	7005	TCGAGGAACCCCTGCGC	46 [†]	3905
1129392	1747	1762	7135	7150	GTCCTCACACACCAGC	5 [†]	3906
1129412	1797	1812	7185	7200	GATCCCCAGCTGATGA	43	3907
1129432	1827	1842	7215	7230	ACGCCTGGCTTGTGTC	43	3908
1129452	1865	1880	7253	7268	CCCGGATCCAGGCCAG	41	3909
1129472	1897	1912	7285	7300	TGAGTCCCTGAGCAAT	24	3910

1129492	1928	1943	7316	7331	TCTCACTGCGGAATCA	14	3911
1129512	1989	2004	7377	7392	CGCGGAGCTGGCCGCA	39	3912
1129532	2010	2025	7398	7413	TGAGTTCCTGCGCCAT	16	3913
1129552	N/A	N/A	96	111	CTCACCGAAAGTGTTG	88	3914
1129572	N/A	N/A	186	201	GGACCCACAGGTCATG	28	3915
1129592	N/A	N/A	327	342	CTCCCCCGTTGTCTT	85	3916
1129612	N/A	N/A	429	444	GACTATAAGTCATAGC	101	3917
1129632	N/A	N/A	604	619	ACTAGACTAGACTGCC	79	3918
1129652	N/A	N/A	649	664	GATCACTCTAGTGCCC	49	3919
1129672	N/A	N/A	889	904	GACAAGCTCTTGATCC	40	3920
1129692	N/A	N/A	1054	1069	AATACCTCACATGGGT	51	3921
1129712	N/A	N/A	1556	1571	GGTAAGGTCCATCTGG	47	3922
1129732	N/A	N/A	1708	1723	AAGGATAGGGCACCAA	53	3923
1129752	N/A	N/A	2145	2160	GGCAAAGTGCACTTGC	80	3924
1129772	N/A	N/A	2449	2464	CATTGATGAATCAGCA	53	3925
1129792	N/A	N/A	2526	2541	CACAAGAAGGCTACCT	69	3926
1129812	N/A	N/A	2806	2821	GTGCCTACTTGCTGAA	72	3927
1129832	N/A	N/A	3041	3056	CAGATAGCTGGAGTAG	39	3928
1129852	N/A	N/A	3647	3662	GTACATGTCTCCCAGG	55	3929
1129872	N/A	N/A	4014	4029	TGGTTTACCCACCTGC	59	3930
1129892	N/A	N/A	4313	4328	CAGCAACCTATTCTGT	88	3931
1129912	N/A	N/A	4350	4365	CAGGAGAGTCTAGGAC	69	3932
1129932	N/A	N/A	4618	4633	TGGGCCTAAAGACCCC	96	3933
1129952	N/A	N/A	5069	5084	GCGCACCGGCAGAAGG	101	3934
1129972	N/A	N/A	5376	5391	ACTTCCTAACCTCCCG	56	3935
1129992	N/A	N/A	5449	5464	GACGGAGAGCCCGCGG	88	3936
1130012	N/A	N/A	5754	5769	AGACGGAGGAGCCGCG	59	3937
1130032	N/A	N/A	5868	5883	CCCCAATCCCGTGTTT	82	3938
1130052	N/A	N/A	6169	6184	CAGAGCTAACCCGGGC	69	3939
1130072	N/A	N/A	6329	6344	GCCCCTAGCAGTTGTG	86	3940
1130092	N/A	N/A	6388	6403	CCAAAGTCGCGGGCTT	54	3941
1130112	N/A	N/A	6412	6427	ATTCTGTAGGCACCCG	46	3942
1130132	N/A	N/A	6537	6552	AGAGCAAGTTCGATTC	51	3943
1130152	N/A	N/A	6623	6638	GTCGCAGAACCTGGCT	60	3944
1130172	N/A	N/A	6675	6690	ATTTGAATGGGCGGAG	44	3945
1130192	N/A	N/A	6811	6826	GGACGATGGACAAAGC	66	3946
1130212	N/A	N/A	6873	6888	TCCTCCGCCCCTGCGA	152	3947
1130232	N/A	N/A	7066	7081	GAGATTTGTGCCTGAC	65 [†]	3948
1130252	N/A	N/A	7112	7127	CGGAATCACCTGGGT	22 [†]	3949

Table 63. Reduction of FXII RNA by 3-10-3 cEt gapmers with uniform PS internucleoside linkages
(Huh7, electroporation, 2000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1128802	218	233	3569	3584	TACATTTGTGGTACAG	124	2426
1129531	2009	2024	7397	7412	GAGTTCCTGCGCCATC	13	3837
1129948	N/A	N/A	4840	4855	ATCTGCTTTCCGCACT	134	3630
1194296	N/A	N/A	4848	4863	TCCCTCTCATCTGCTT	55	3950
1206493	N/A	N/A	4830	4845	CGCACTCTCCCTCCTC	105	3951
1208291	N/A	N/A	130	145	GAACAATCCTGGGACA	84	3952
1208323	N/A	N/A	200	215	CCTCCTAGTCACCTGG	44	3953
1208358	N/A	N/A	269	284	ATCCACCCAGTCTGGT	123	3954
1208388	N/A	N/A	315	330	TCTTCTTAAGGCCCAT	76	3955
1208422	N/A	N/A	407	422	CCGATCTGTTGCTAGT	113	3956
1208453	N/A	N/A	442	457	AAGGCAGGGAAGTAC	91	3957
1208484	N/A	N/A	531	546	AGCCAGGCCACTTACC	123	3958
1208512	N/A	N/A	599	614	ACTAGACTGCCCTGAG	102	3959
1208540	N/A	N/A	632	647	TGGGCATAAGACCTAG	113	3960
1208572	N/A	N/A	662	677	TCACACAGCTCACGAT	77	3961
1208588	N/A	N/A	734	749	ACATATCTCAAGCACC	119	3962
1208601	N/A	N/A	841	856	TGGCATGAATGATGCC	127	3963
1208614	N/A	N/A	887	902	CAAGCTCTTGATCCTT	56	3964
1208627	N/A	N/A	927	942	GTGATAAAGCTGGGCT	101	3965
1208640	N/A	N/A	969	984	TGGAGAACTCAAATCC	52	3966
1208653	N/A	N/A	1015	1030	GGTTTACTGTTATCAA	120	3967
1208666	N/A	N/A	1057	1072	CTGAATACCTCACATG	107	3968
1208679	N/A	N/A	1126	1141	TTCATCTAAAAGGTAG	73	3969
1208692	N/A	N/A	1165	1180	TATGGCAGAGCTTGAG	72	3970
1208705	N/A	N/A	1517	1532	CACTCTAGGTAAATTT	84	3971
1208718	N/A	N/A	1567	1582	AGGCCCACCAGGGTAA	111	3972
1208735	N/A	N/A	1597	1612	CCATGCTTAGAGACTC	83	3973
1208762	N/A	N/A	1690	1705	TTGGGTAAGGCAAGAG	48	3974
1208789	N/A	N/A	1718	1733	GGGATTAGGCAAGGAT	74	3975
1208813	N/A	N/A	1921	1936	CTGAGCATGAAGTTGT	80	3976
1208840	N/A	N/A	2094	2109	ATGGATCTGAGATGGA	52	3977
1208868	N/A	N/A	2126	2141	GGACCAAACCAGAACT	98	3978
1208895	N/A	N/A	2149	2164	TCAAGGCAAAGTGCAC	47	3979
1208918	N/A	N/A	2182	2197	TACCTGCTCAATAAGC	46	3980
1208944	N/A	N/A	2251	2266	CTTCAGAGGAATTGTC	64	3981
1208971	N/A	N/A	2320	2335	GCTAGTTCAATGTTCA	98	3982
1208997	N/A	N/A	2337	2352	GGAACCTAATACTGTT	73	3983
1209023	N/A	N/A	2389	2404	AACCAGATTATATGCT	80	3984

1209048	N/A	N/A	2461	2476	CCATCAGCTTAGCATT	53	3985
1209073	N/A	N/A	2493	2508	TTAGACACTTGATTCA	76	3986
1209100	N/A	N/A	2548	2563	GAAGAGCTGTGTAGTT	95	3987
1209126	N/A	N/A	2647	2662	GAATGAGTGTCTTCT	43	3988
1209152	N/A	N/A	2707	2722	ATTCCCAGTTAAGGTT	78	3989
1209180	N/A	N/A	2750	2765	ATGGCCATTTGTGGGC	98	3990
1209206	N/A	N/A	2785	2800	TTTGTAACCTCCAAGT	80	3991
1209229	N/A	N/A	2817	2832	ACATTGAGAATGTGCC	99	3992
1209253	N/A	N/A	2896	2911	TCTGATCTGAGCCTTG	103	3993
1209277	N/A	N/A	2957	2972	CACTTGCCACAAAGTA	74	3994
1209303	N/A	N/A	3019	3034	GACTCCACAACCTGCT	130	3995
1209329	N/A	N/A	3371	3386	TAAAAGTTGGGTTTCAG	78	3996
1209347	N/A	N/A	3441	3456	CCTCAGGGTCTGGTCA	117	3997
1209360	N/A	N/A	3474	3489	ACTTCCCCTGTACTCA	143	3998
1209373	N/A	N/A	3511	3526	GACAGTGAGAACTGCA	123	3999
1209386	N/A	N/A	3658	3673	GGACAGGCAGGGTACA	76	4000
1209399	N/A	N/A	3703	3718	CCCTATCACAGTCCCC	64	4001
1209412	N/A	N/A	3879	3894	AATGAGGCGGGAGGAG	122	4002
1209425	N/A	N/A	3923	3938	GTCCAGAATCCCAGGT	86	4003
1209438	N/A	N/A	3998	4013	AAAATGGGACCACTCC	144	4004
1209451	N/A	N/A	4034	4049	CTACTCCAAGTTTCCA	71	4005
1209464	N/A	N/A	4067	4082	GCCCTTCTTGAACCTA	88	4006
1209477	N/A	N/A	4269	4284	ACCCCGCCCAGGTCCT	48	4007
1209490	N/A	N/A	4331	4346	GCCAAGTCTCCGAGTA	76	4008
1209503	N/A	N/A	4364	4379	AGGGATAGTGGTCTCA	73	4009
1209516	N/A	N/A	4609	4624	AGACCCCCCAGAGAG	71	4010
1209529	N/A	N/A	4803	4818	GCCCGTCCCACCTGGG	78	4011
1209542	N/A	N/A	5119	5134	GCGCCGGGAGCCCGGA	62	4012
1209555	N/A	N/A	5430	5445	GCTGGCCGGAATCTAG	61	4013
1209568	N/A	N/A	5745	5760	AGCCGCGGCCCTGGG	49	4014
1209581	N/A	N/A	5860	5875	CCGTGTTCCAGCTTCC	53	4015
1209594	N/A	N/A	6095	6110	GCGCCCCACGCACCC	74	4016
1209607	N/A	N/A	6357	6372	GTGATCAAAGGTCTCC	26	4017
1209620	N/A	N/A	6436	6451	CAACCCATCAGGTCAG	41	4018
1209633	N/A	N/A	6474	6489	CCCTGGGATTCTACCT	65	4019
1209646	N/A	N/A	6542	6557	AACCAAGAGCAAGTTC	38	4020
1209659	N/A	N/A	6625	6640	GAGTCGCAGAACCTGG	25	4021
1209672	N/A	N/A	6680	6695	CCAGGATTTGAATGGG	83	4022
1209685	N/A	N/A	6780	6795	TAAACCCACTCATGCC	44	4023
1209698	N/A	N/A	6839	6854	ACACCCCATCTGACAA	63	4024
1209711	N/A	N/A	7027	7042	GGGCTAAGAGCTCACC	88 [†]	4025

Table 64. Reduction of FXII RNA by 3-10-3 cEt gapmers with uniform PS internucleoside linkages
(Huh7 , electroporation, 2000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1128802	218	233	3569	3584	TACATTTGTGGTACAG	88	2426
1129531	2009	2024	7397	7412	GAGTTCCTGCGCCATC	7	3837
1129948	N/A	N/A	4840	4855	ATCTGCTTTCCGCACT	84	3630
1194286	N/A	N/A	4835	4850	CTTTCCGCACTCTCCC	97	4026
1194297	N/A	N/A	4849	4864	CTCCCTCTCATCTGCT	54	4027
1208292	N/A	N/A	131	146	AGAACAATCCTGGGAC	91	4028
1208327	N/A	N/A	201	216	GCCTCCTAGTCACCTG	108	4029
1208361	N/A	N/A	270	285	TATCCACCCAGTCTGG	73	4030
1208392	N/A	N/A	316	331	GTCTTCTTAAGGCCCA	79	4031
1208426	N/A	N/A	413	428	CTGCCACCGATCTGTT	57	4032
1208454	N/A	N/A	460	475	ATCTACAAGGGAGAGA	107	4033
1208487	N/A	N/A	546	561	GTTCCCGGGAGGAGGA	69	4034
1208513	N/A	N/A	601	616	AGACTAGACTGCCCTG	43	4035
1208544	N/A	N/A	633	648	ATGGGCATAAGACCTA	60	4036
1208575	N/A	N/A	664	679	GATCACACAGCTCACG	112	4037
1208589	N/A	N/A	735	750	CACATATCTCAAGCAC	65	4038
1208602	N/A	N/A	842	857	GTGGCATGAATGATGC	94	4039
1208615	N/A	N/A	888	903	ACAAGCTCTTGATCCT	96	4040
1208628	N/A	N/A	928	943	AGTGATAAAGCTGGGC	89	4041
1208641	N/A	N/A	970	985	TTGGAGAACTCAAATC	81	4042
1208654	N/A	N/A	1016	1031	AGGTTTACTGTTATCA	95	4043
1208667	N/A	N/A	1058	1073	GCTGAATACCTCACAT	74	4044
1208680	N/A	N/A	1128	1143	CCTTCATCTAAAAGGT	113	4045
1208693	N/A	N/A	1166	1181	CTATGGCAGAGCTTGA	111	4046
1208706	N/A	N/A	1518	1533	ACACTCTAGGTAAATT	83	4047
1208719	N/A	N/A	1573	1588	CAAGTCAGGCCACCA	168	4048
1208738	N/A	N/A	1598	1613	GCCATGCTTAGAGACT	47	4049
1208764	N/A	N/A	1691	1706	TTTGGGTAAGGCAAGA	53	4050
1208792	N/A	N/A	1751	1766	TGGACGGACAGAGAGG	64	4051
1208816	N/A	N/A	1922	1937	GCTGAGCATGAAGTTG	38	4052
1208843	N/A	N/A	2111	2126	TAGGACAGTAAATGGA	64	4053
1208870	N/A	N/A	2127	2142	AGGACCAAACCAGAAC	125	4054
1208896	N/A	N/A	2151	2166	GTTCAAGGCAAAGTGC	68	4055
1208921	N/A	N/A	2183	2198	GTACCTGCTCAATAAG	102	4056
1208947	N/A	N/A	2266	2281	AATTGCCTGTGTCTTC	47	4057
1208973	N/A	N/A	2322	2337	TTGCTAGTTCAATGTT	60	4058
1209000	N/A	N/A	2338	2353	AGGAACCTAATACTGT	104	4059
1209024	N/A	N/A	2390	2405	AAACCAGATTATATGC	75	4060

1209050	N/A	N/A	2463	2478	TGCCATCAGCTTAGCA	72	4061
1209076	N/A	N/A	2495	2510	TGTTAGACACTTGATT	92	4062
1209101	N/A	N/A	2549	2564	TGAAGAGCTGTGTAGT	83	4063
1209127	N/A	N/A	2648	2663	TGAATGAGTGTCTTC	131	4064
1209155	N/A	N/A	2709	2724	ACATTCCCAGTTAAGG	93	4065
1209183	N/A	N/A	2771	2786	GTCAATACTTGAAATG	88	4066
1209207	N/A	N/A	2786	2801	ATTTGTAACTCCCAAG	108	4067
1209232	N/A	N/A	2818	2833	TACATTGAGAATGTGC	72	4068
1209254	N/A	N/A	2901	2916	ACCACTCTGATCTGAG	70	4069
1209280	N/A	N/A	2962	2977	AAGAGCACTTGCCACA	77	4070
1209305	N/A	N/A	3028	3043	TAGACTCCTGACTCCA	141	4071
1209332	N/A	N/A	3372	3387	CTAAAAGTTGGGTTCA	77	4072
1209348	N/A	N/A	3460	3475	CAACTGCTCAGGCACT	117	4073
1209361	N/A	N/A	3485	3500	ACTCTCTGAGGACTTC	101	4074
1209374	N/A	N/A	3605	3620	CTTACCAGGGCTGAGG	93	4075
1209387	N/A	N/A	3660	3675	AAGGACAGGCAGGGTA	86	4076
1209400	N/A	N/A	3705	3720	TGCCCTATCACAGTCC	96	4077
1209413	N/A	N/A	3880	3895	TAATGAGGCGGGAGGA	106	4078
1209426	N/A	N/A	3949	3964	TATTGTGGAGGGAGAG	131	4079
1209439	N/A	N/A	3999	4014	CAAAATGGGACCACTC	58	4080
1209452	N/A	N/A	4036	4051	TGCTACTCCAAGTTTC	72	4081
1209465	N/A	N/A	4068	4083	GGCCCTTCTTGAACCT	47	4082
1209478	N/A	N/A	4271	4286	GCACCCCGCCCAGGTC	90	4083
1209491	N/A	N/A	4334	4349	CATGCCAAGTCTCCGA	73	4084
1209504	N/A	N/A	4368	4383	AAAGAGGGATAGTGGT	47	4085
1209517	N/A	N/A	4612	4627	TAAAGACCCCCCAGA	95	4086
1209530	N/A	N/A	4804	4819	AGCCCGTCCCACCTGG	97	4087
1209543	N/A	N/A	5146	5161	GTAGCCACACGACGGG	31	4088
1209556	N/A	N/A	5431	5446	GGCTGGCCGGAATCTA	37	4089
1209569	N/A	N/A	5746	5761	GAGCCGCGGCCCTGG	67	4090
1209582	N/A	N/A	5863	5878	ATCCCGTGTTCCAGCT	58	4091
1209595	N/A	N/A	6111	6126	TTCCCGTCCCCGCGGG	82	4092
1209608	N/A	N/A	6359	6374	CAGTGATCAAAGGTCT	34	4093
1209621	N/A	N/A	6439	6454	TCACAACCCATCAGGT	43	4094
1209634	N/A	N/A	6476	6491	GGCCCTGGGATTCTAC	89	4095
1209647	N/A	N/A	6543	6558	GAACCAAGAGCAAGTT	64	4096
1209660	N/A	N/A	6631	6646	CATCCAGAGTCGCAGA	36	4097
1209673	N/A	N/A	6681	6696	GCCAGGATTTGAATGG	84	4098
1209686	N/A	N/A	6782	6797	TGTAAACCCACTCATG	101	4099
1209699	N/A	N/A	6840	6855	CACACCCCATCTGACA	86	4100
1209712	N/A	N/A	7058	7073	TGCCTGACGGCCTCGG	47 [†]	4101

Table 65. Reduction of FXII RNA by 3-10-3 cEt gapmers with uniform PS internucleoside linkages
(Huh7, electroporation, 2000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1128802	218	233	3569	3584	TACATTTGTGGTACAG	102	2426
1129531	2009	2024	7397	7412	GAGTTCCTGCGCCATC	25	3837
1129948	N/A	N/A	4840	4855	ATCTGCTTTCCGCACT	76	3630
1194287	N/A	N/A	4836	4851	GCTTTCCGCACTCTCC	48	4102
1206494	N/A	N/A	4854	4869	CCTGCCTCCCTCTCAT	92	4103
1208296	N/A	N/A	133	148	CCAGAACAATCCTGGG	62	4104
1208328	N/A	N/A	203	218	AGGCCTCCTAGTCACC	56	4105
1208363	N/A	N/A	274	289	CTTGTATCCACCCAGT	79	4106
1208393	N/A	N/A	321	336	CCGTTGTCTTCTTAAG	67	4107
1208427	N/A	N/A	414	429	CCTGCCACCGATCTGT	94	4108
1208458	N/A	N/A	461	476	AATCTACAAGGGAGAG	55	4109
1208489	N/A	N/A	547	562	GGTTCCCGGGAGGAGG	51	4110
1208515	N/A	N/A	605	620	CACTAGACTAGACTGC	69	4111
1208545	N/A	N/A	634	649	CATGGGCATAAGACCT	52	4112
1208577	N/A	N/A	672	687	CCCTCAAGGATCACAC	68	4113
1208590	N/A	N/A	738	753	CAGCACATATCTCAAG	64	4114
1208603	N/A	N/A	862	877	TTGAAGGCCCTGGCCT	45	4115
1208616	N/A	N/A	895	910	GCCAGAGACAAGCTCT	87	4116
1208629	N/A	N/A	932	947	CATAAGTGATAAAGCT	79	4117
1208642	N/A	N/A	975	990	GAAGCTTGGAGAACTC	88	4118
1208655	N/A	N/A	1018	1033	AGAGGTTTACTGTTAT	57	4119
1208668	N/A	N/A	1062	1077	ATGGGCTGAATACCTC	95	4120
1208681	N/A	N/A	1129	1144	CCCTTCATCTAAAAGG	133	4121
1208694	N/A	N/A	1167	1182	GCTATGGCAGAGCTTG	84	4122
1208707	N/A	N/A	1519	1534	CACACTCTAGGTAAAT	76	4123
1208720	N/A	N/A	1574	1589	CCAAGTCAGGCCACC	74	4124
1208739	N/A	N/A	1600	1615	ACGCCATGCTTAGAGA	76	4125
1208766	N/A	N/A	1692	1707	GTTTGGGTAAGGCAAG	60	4126
1208795	N/A	N/A	1756	1771	TGGGATGGACGGACAG	83	4127
1208817	N/A	N/A	1923	1938	AGCTGAGCATGAAGTT	144	4128
1208844	N/A	N/A	2112	2127	CTAGGACAGTAAATGG	73	4129
1208873	N/A	N/A	2129	2144	CAAGGACCAAACCAGA	91	4130
1208898	N/A	N/A	2152	2167	TGTTCAAGGCAAAGTG	72	4131
1208922	N/A	N/A	2190	2205	GCACAAAGTACCTGCT	71	4132
1208948	N/A	N/A	2267	2282	GAATTGCCTGTGTCTT	72	4133
1208976	N/A	N/A	2323	2338	TTTGCTAGTTCAATGT	62	4134
1209001	N/A	N/A	2339	2354	CAGGAACCTAATACTG	61	4135
1209027	N/A	N/A	2442	2457	GAATCAGCAACACATA	85	4136

1209051	N/A	N/A	2465	2480	AGTGCCATCAGCTTAG	111	4137
1209077	N/A	N/A	2496	2511	GTGTTAGACACTTGAT	76	4138
1209104	N/A	N/A	2551	2566	GCTGAAGAGCTGTGTA	74	4139
1209130	N/A	N/A	2649	2664	TTGAATGAGTGTCTT	102	4140
1209156	N/A	N/A	2710	2725	CACATTCCCAGTTAAG	100	4141
1209184	N/A	N/A	2774	2789	CAAGTCAATACTTGAA	50	4142
1209209	N/A	N/A	2803	2818	CCTACTTGCTGAATTT	96	4143
1209234	N/A	N/A	2819	2834	CTACATTGAGAATGTG	55	4144
1209257	N/A	N/A	2902	2917	AACCACTCTGATCTGA	68	4145
1209281	N/A	N/A	2964	2979	GGAAGAGCACTTGCCA	79	4146
1209307	N/A	N/A	3029	3044	GTAGACTCCTGACTCC	79	4147
1209333	N/A	N/A	3374	3389	CTCTAAAAGTTGGGTT	55	4148
1209349	N/A	N/A	3461	3476	TCAACTGCTCAGGCAC	73	4149
1209362	N/A	N/A	3491	3506	CAACACACTCTCTGAG	69	4150
1209375	N/A	N/A	3606	3621	TCTTACCAGGGCTGAG	90	4151
1209388	N/A	N/A	3669	3684	CTTGGACAGAAGGACA	93	4152
1209401	N/A	N/A	3706	3721	CTGCCCTATCACAGTC	65	4153
1209414	N/A	N/A	3887	3902	AGGAGAGTAATGAGGC	80	4154
1209427	N/A	N/A	3950	3965	GTATTGTGGAGGGAGA	70	4155
1209440	N/A	N/A	4003	4018	CCTGCAAAATGGGACC	69	4156
1209453	N/A	N/A	4037	4052	TTGCTACTCCAAGTTT	69	4157
1209466	N/A	N/A	4070	4085	AAGGCCCTTCTTGAAC	62	4158
1209479	N/A	N/A	4272	4287	AGCACCCCGCCCAGGT	73	4159
1209492	N/A	N/A	4335	4350	CCATGCCAAGTCTCCG	87	4160
1209505	N/A	N/A	4369	4384	CAAAGAGGGATAGTGG	92	4161
1209518	N/A	N/A	4623	4638	ACCCCTGGGCCTAAAG	91	4162
1209531	N/A	N/A	4806	4821	CAAGCCCGTCCCACCT	52	4163
1209544	N/A	N/A	5151	5166	TTCCTGTAGCCACACG	50	4164
1209557	N/A	N/A	5432	5447	CGGCTGGCCGGAATCT	46	4165
1209570	N/A	N/A	5747	5762	GGAGCCGCGGCCCTG	62	4166
1209583	N/A	N/A	5876	5891	CTCCCGAACCCCAATC	52	4167
1209596	N/A	N/A	6114	6129	CTCTTCCCGTCCCCGC	53	4168
1209609	N/A	N/A	6362	6377	ACCCAGTGATCAAAGG	40	4169
1209622	N/A	N/A	6440	6455	CTCACAACCCATCAGG	42	4170
1209635	N/A	N/A	6477	6492	AGGCCCTGGGATTCTA	39	4171
1209648	N/A	N/A	6544	6559	GGAACCAAGAGCAAGT	40	4172
1209661	N/A	N/A	6632	6647	CCATCCAGAGTCGCAG	38	4173
1209674	N/A	N/A	6712	6727	CATAGGCAAGGAGGCT	34	4174
1209687	N/A	N/A	6799	6814	AAGCTGCTCCAGGCGC	57	4175
1209700	N/A	N/A	6849	6864	CGCCTTCTTCACACCC	117	4176
1209713	N/A	N/A	7059	7074	GTGCCTGACGGCCTCG	68 [†]	4177

Table 66. Reduction of FXII RNA by 3-10-3 cEt gapmers with uniform PS internucleoside linkages
(Huh7, electroporation, 2000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1128802	218	233	3569	3584	TACATTTGTGGTACAG	99	2426
1129531	2009	2024	7397	7412	GAGTTCCTGCGCCATC	16	3837
1129947	N/A	N/A	4837	4852	TGCTTTCCGCACTCTC	51	3554
1129948	N/A	N/A	4840	4855	ATCTGCTTTCCGCACT	70	3630
1208266	N/A	N/A	98	113	CACTCACCGAAAGTGT	65	4178
1208297	N/A	N/A	136	151	CCCCAGAACAATCCT	84	4179
1208332	N/A	N/A	205	220	ATAGGCCTCCTAGTCA	97	4180
1208366	N/A	N/A	275	290	CCTTGTATCCACCCAG	55	4181
1208397	N/A	N/A	322	337	CCCGTTGTCTTCTTAA	87	4182
1208431	N/A	N/A	417	432	TAGCCTGCCACCGATC	78	4183
1208459	N/A	N/A	462	477	GAATCTACAAGGGAGA	52	4184
1208492	N/A	N/A	556	571	CCACCCAAGGGTTCCC	81	4185
1208516	N/A	N/A	609	624	TAGGCACTAGACTAGA	97	4186
1208549	N/A	N/A	635	650	CCATGGGCATAAGACC	38	4187
1208578	N/A	N/A	674	689	TGCCCTCAAGGATCAC	46	4188
1208591	N/A	N/A	740	755	AGCAGCATATCTCA	95	4189
1208604	N/A	N/A	863	878	ATTGAAGGCCCTGGCC	47	4190
1208617	N/A	N/A	896	911	TGCCAGAGACAAGCTC	43	4191
1208630	N/A	N/A	934	949	CTCATAAGTGATAAAG	58	4192
1208643	N/A	N/A	977	992	TTGAAGCTTGGAGAAC	52	4193
1208656	N/A	N/A	1019	1034	AAGAGGTTTACTGTTA	76	4194
1208669	N/A	N/A	1063	1078	GATGGGCTGAATACCT	51	4195
1208682	N/A	N/A	1130	1145	ACCCTTCATCTAAAAG	56	4196
1208695	N/A	N/A	1168	1183	AGCTATGGCAGAGCTT	98	4197
1208708	N/A	N/A	1520	1535	CCACACTCTAGGTAAA	44	4198
1208721	N/A	N/A	1575	1590	ACCAAGTCAGGCCAC	92	4199
1208742	N/A	N/A	1620	1635	TTGGAATGTGCTGGGC	58	4200
1208768	N/A	N/A	1693	1708	AGTTTGGGTAAGGCAA	62	4201
1208796	N/A	N/A	1759	1774	AGATGGGATGGACGGA	47	4202
1208820	N/A	N/A	1924	1939	TAGCTGAGCATGAAGT	43	4203
1208847	N/A	N/A	2113	2128	ACTAGGACAGTAAATG	50	4204
1208874	N/A	N/A	2130	2145	CCAAGGACCAAACCAG	67	4205
1208899	N/A	N/A	2169	2184	AGCTTTTGCCACTATT	90	4206
1208925	N/A	N/A	2191	2206	GGCACAAAGTACCTGC	71	4207
1208951	N/A	N/A	2269	2284	GAGAATTGCCTGTGTC	92	4208
1208977	N/A	N/A	2325	2340	TGTTTGCTAGTTCAAT	27	4209
1209004	N/A	N/A	2340	2355	ACAGGAACCTAATACT	74	4210
1209028	N/A	N/A	2446	2461	TGATGAATCAGCAACA	59	4211

1209053	N/A	N/A	2467	2482	ATAGTGCCATCAGCTT	50	4212
1209080	N/A	N/A	2498	2513	GTGTGTTAGACACTTG	50	4213
1209105	N/A	N/A	2570	2585	AATGGCCTCTGAGCCT	46	4214
1209131	N/A	N/A	2650	2665	ATTGAATGAGTGTCTT	117	4215
1209159	N/A	N/A	2711	2726	GCACATTCCCAGTTAA	49	4216
1209187	N/A	N/A	2775	2790	CCAAGTCAATACTTGA	45	4217
1209210	N/A	N/A	2804	2819	GCCTACTTGCTGAATT	35	4218
1209236	N/A	N/A	2824	2839	TGGTCTACATTGAGA	93	4219
1209258	N/A	N/A	2903	2918	TAACCACTCTGATCTG	49	4220
1209284	N/A	N/A	2965	2980	AGGAAGAGCACTTGCC	55	4221
1209309	N/A	N/A	3030	3045	AGTAGACTCCTGACTC	49	4222
1209336	N/A	N/A	3377	3392	CTGCTCTAAAAGTTGG	64	4223
1209350	N/A	N/A	3462	3477	CTCAACTGCTCAGGCA	61	4224
1209363	N/A	N/A	3492	3507	ACAACACACTCTCTGA	48	4225
1209376	N/A	N/A	3607	3622	GTCTTACCAGGGCTGA	59	4226
1209389	N/A	N/A	3670	3685	CCTTGGACAGAAGGAC	49	4227
1209402	N/A	N/A	3707	3722	CCTGCCCTATCACAGT	92	4228
1209415	N/A	N/A	3889	3904	CCAGGAGAGTAATGAG	49	4229
1209428	N/A	N/A	3951	3966	GGTATTGTGGAGGGAG	56	4230
1209441	N/A	N/A	4012	4027	GTTTACCCACCTGCAA	39	4231
1209454	N/A	N/A	4038	4053	CTTGCTACTCCAAGTT	108	4232
1209467	N/A	N/A	4073	4088	GCCAAGGCCCTTCTTG	56	4233
1209480	N/A	N/A	4295	4310	GCCCAGGGTTGCCCT	65	4234
1209493	N/A	N/A	4336	4351	ACCATGCCAAGTCTCC	46	4235
1209506	N/A	N/A	4370	4385	ACAAAGAGGGATAGTG	67	4236
1209519	N/A	N/A	4625	4640	CCACCCCTGGGCCTAA	134	4237
1209532	N/A	N/A	4807	4822	GCAAGCCCGTCCCACC	81	4238
1209545	N/A	N/A	5152	5167	GTTCTGTAGCCACAC	23	4239
1209558	N/A	N/A	5435	5450	GGCCGGCTGGCCGGAA	84	4240
1209571	N/A	N/A	5748	5763	AGGAGCCGCGGCCCT	64	4241
1209584	N/A	N/A	5878	5893	TGCTCCCGAACCCCAA	35	4242
1209597	N/A	N/A	6120	6135	CAAGCTCTCTCCCGT	53	4243
1209610	N/A	N/A	6365	6380	CTAACCCAGTGATCAA	29	4244
1209623	N/A	N/A	6443	6458	ATTCTCACAACCCATC	64	4245
1209636	N/A	N/A	6486	6501	GTGAATCCCAGGCCCT	41	4246
1209649	N/A	N/A	6553	6568	CGCCCAGAGGGAACCA	116	4247
1209662	N/A	N/A	6633	6648	CCCATCCAGAGTCGCA	30	4248
1209675	N/A	N/A	6713	6728	TCATAGGCAAGGAGGC	36	4249
1209688	N/A	N/A	6800	6815	AAAGCTGCTCCAGGCG	27	4250
1209701	N/A	N/A	6850	6865	GCGCCTTCTTCACACC	85	4251
1209714	N/A	N/A	7063	7078	ATTTGTGCCTGACGGC	53 [†]	4252

Table 67. Reduction of FXII RNA by 3-10-3 cEt gapmers with uniform PS internucleoside linkages
(Huh7, electroporation, 2000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1128802	218	233	3569	3584	TACATTTGTGGTACAG	29	2426
1129531	2009	2024	7397	7412	GAGTTCCTGCGCCATC	33	3837
1129948	N/A	N/A	4840	4855	ATCTGCTTTCCGCACT	52	3630
1194288	N/A	N/A	4838	4853	CTGCTTTCCGCACTCT	27	4253
1208267	N/A	N/A	104	119	CCACAGCACTCACC GA	128	4254
1208301	N/A	N/A	137	152	CCCCCAGAACAATCC	177	4255
1208333	N/A	N/A	213	228	CTTTCCACATAGGCCT	68	4256
1208370	N/A	N/A	276	291	CCCTTGTATCCACCCA	41	4257
1208398	N/A	N/A	331	346	CTACCTCCCCCGTTG	91	4258
1208432	N/A	N/A	418	433	ATAGCCTGCCACCGAT	116	4259
1208463	N/A	N/A	465	480	GTGGAATCTACAAGGG	34	4260
1208494	N/A	N/A	557	572	CCCACCCAAGGGTTCC	44	4261
1208519	N/A	N/A	616	631	CACCAGGTAGGCACTA	93	4262
1208550	N/A	N/A	638	653	TGCCCATGGGCATAAG	43	4263
1208579	N/A	N/A	685	700	AGCCCATACCTGCCC	77	4264
1208592	N/A	N/A	741	756	CAGCAGCACATATCTC	64	4265
1208605	N/A	N/A	864	879	CATTGAAGGCCCTGGC	90	4266
1208618	N/A	N/A	897	912	ATGCCAGAGACAAGCT	56	4267
1208631	N/A	N/A	935	950	GCTCATAAGTGATAAA	54	4268
1208644	N/A	N/A	1002	1017	CAACCTGGTTTCACAG	32	4269
1208657	N/A	N/A	1020	1035	TAAGAGGTTTACTGTT	44	4270
1208670	N/A	N/A	1066	1081	GGTGATGGGCTGAATA	52	4271
1208683	N/A	N/A	1131	1146	TACCCTTCATCTAAAA	80	4272
1208696	N/A	N/A	1169	1184	GAGCTATGGCAGAGCT	67	4273
1208709	N/A	N/A	1529	1544	TGCTATGTGCCCACT	61	4274
1208722	N/A	N/A	1578	1593	CCCACCAAGTCAGGCC	56	4275
1208744	N/A	N/A	1621	1636	GTTGGAATGTGCTGGG	42	4276
1208771	N/A	N/A	1694	1709	AAGTTTGGGTAAGGCA	81	4277
1208799	N/A	N/A	1760	1775	CAGATGGGATGGACGG	57	4278
1208821	N/A	N/A	2075	2090	TTAAGATGCAAATGGG	31	4279
1208848	N/A	N/A	2115	2130	GAAGTAGGACAGTAAA	40	4280
1208877	N/A	N/A	2131	2146	GCCAAGGACCAAACCA	34	4281
1208901	N/A	N/A	2170	2185	AAGCTTTTGCCACTAT	49	4282
1208926	N/A	N/A	2192	2207	TGGCACAAAGTACCTG	73	4283
1208952	N/A	N/A	2270	2285	TGAGAATTGCCTGTGT	59	4284
1208980	N/A	N/A	2326	2341	CTGTTTGCTAGTTCAA	47	4285
1209005	N/A	N/A	2342	2357	TCACAGGAACCTAATA	101	4286
1209031	N/A	N/A	2447	2462	TTGATGAATCAGCAAC	39	4287

1209054	N/A	N/A	2471	2486	TGCTATAGTGCCATCA	49	4288
1209081	N/A	N/A	2517	2532	GCTACCTTAGGGAGAA	48	4289
1209108	N/A	N/A	2572	2587	GAAATGGCCTCTGAGC	30	4290
1209134	N/A	N/A	2657	2672	CTCTCCTATTGAATGA	18	4291
1209160	N/A	N/A	2713	2728	TTGCACATTCCCAGTT	34	4292
1209188	N/A	N/A	2776	2791	CCCAAGTCAATACTTG	43	4293
1209212	N/A	N/A	2805	2820	TGCCTACTTGCTGAAT	87	4294
1209238	N/A	N/A	2825	2840	CTGGTTCTACATTGAG	20	4295
1209261	N/A	N/A	2905	2920	GTAAACCACTCTGATC	79	4296
1209285	N/A	N/A	2985	3000	AAGTCTTCAGTCCCAA	47	4297
1209312	N/A	N/A	3033	3048	TGGAGTAGACTCCTGA	72	4298
1209337	N/A	N/A	3413	3428	ACCCTCAAAAAGGTCG	45	4299
1209351	N/A	N/A	3463	3478	ACTCAACTGCTCAGGC	87	4300
1209364	N/A	N/A	3493	3508	GACAACACACTCTCTG	44	4301
1209377	N/A	N/A	3608	3623	AGTCTTACCAGGGCTG	88	4302
1209390	N/A	N/A	3673	3688	GTTCTTGGACAGAAG	96	4303
1209403	N/A	N/A	3709	3724	ACCCTGCCCTATCACA	29	4304
1209416	N/A	N/A	3890	3905	ACCAGGAGAGTAATGA	31	4305
1209429	N/A	N/A	3954	3969	AAGGGTATTGTGGAGG	45	4306
1209442	N/A	N/A	4016	4031	CTTGGTTTACCCACCT	49	4307
1209455	N/A	N/A	4041	4056	GACCTTGCTACTCCAA	21	4308
1209468	N/A	N/A	4074	4089	GGCCAAGGCCCTTCTT	128	4309
1209481	N/A	N/A	4298	4313	TAGGCCCAAGGGTTGCC	135	4310
1209494	N/A	N/A	4337	4352	GACCATGCCAAGTCTC	40	4311
1209507	N/A	N/A	4528	4543	GTTCCCAACCATCTGC	42	4312
1209520	N/A	N/A	4631	4646	AGTGAGCCACCCCTGG	91	4313
1209533	N/A	N/A	4813	4828	TTCCTGGCAAGCCCGT	60	4314
1209546	N/A	N/A	5156	5171	CCGGGTTCCTGTAGCC	58	4315
1209559	N/A	N/A	5437	5452	GCGGCCCGCTGGCCGG	56	4316
1209572	N/A	N/A	5749	5764	GAGGAGCCGCGGCCCC	40	4317
1209585	N/A	N/A	5879	5894	CTGCTCCCGAACCCCA	48	4318
1209598	N/A	N/A	6121	6136	CCAAGCTCTCTTCCCG	61	4319
1209611	N/A	N/A	6366	6381	CCTAACCCAGTGATCA	48	4320
1209624	N/A	N/A	6453	6468	TCACCTACACATTCTC	37	4321
1209637	N/A	N/A	6487	6502	AGTGAATCCCAGGCCC	138	4322
1209650	N/A	N/A	6554	6569	GCGCCCAGAGGGAACC	50	4323
1209663	N/A	N/A	6635	6650	CACCCATCCAGAGTCG	51	4324
1209676	N/A	N/A	6714	6729	TTCATAGGCAAGGAGG	45	4325
1209689	N/A	N/A	6803	6818	GACAAAGCTGCTCCAG	99	4326
1209702	N/A	N/A	6864	6879	CCTGCGAACACAGAGC	43	4327
1209715	N/A	N/A	7067	7082	TGAGATTTGTGCCTGA	44 [†]	4328

Table 68. Reduction of FXII RNA by 3-10-3 cEt gapmers with uniform PS internucleoside linkages
(Huh7, electroporation, 2000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1128802	218	233	3569	3584	TACATTTGTGGTACAG	37	2426
1129531	2009	2024	7397	7412	GAGTTCCTGCGCCATC	25	3837
1129948	N/A	N/A	4840	4855	ATCTGCTTTCCGCACT	44	3630
1194289	N/A	N/A	4839	4854	TCTGCTTTCCGCACTC	28	4329
1208271	N/A	N/A	116	131	CAATCCTGGTTCCCAC	68	4330
1208302	N/A	N/A	154	169	CATGGCTGTGATAGCG	73	4331
1208337	N/A	N/A	215	230	ACCTTTCCACATAGGC	81	4332
1208371	N/A	N/A	278	293	TGCCCTTGATCCACC	43	4333
1208402	N/A	N/A	342	357	CCAAACCCCTTCTACC	59	4334
1208435	N/A	N/A	419	434	CATAGCCTGCCACCGA	29	4335
1208464	N/A	N/A	467	482	AGGTGGAATCTACAAG	38	4336
1208497	N/A	N/A	558	573	CCCCACCAAGGGTTC	68	4337
1208520	N/A	N/A	617	632	GCACCAGGTAGGCACT	44	4338
1208554	N/A	N/A	646	661	CACTCTAGTGCCCATG	111	4339
1208580	N/A	N/A	695	710	ACTTAGACACAGCCCA	43	4340
1208593	N/A	N/A	745	760	GCGCCAGCAGCACATA	55	4341
1208606	N/A	N/A	865	880	CCATTGAAGGCCCTGG	39	4342
1208619	N/A	N/A	898	913	GATGCCAGAGACAAGC	26	4343
1208632	N/A	N/A	936	951	AGCTCATAAGTGATAA	73	4344
1208645	N/A	N/A	1005	1020	TATCAACCTGGTTTCA	47	4345
1208658	N/A	N/A	1021	1036	CTAAGAGGTTTACTGT	35	4346
1208671	N/A	N/A	1072	1087	GCACCAGGTGATGGGC	40	4347
1208684	N/A	N/A	1133	1148	GGTACCCTTCATCTAA	121	4348
1208697	N/A	N/A	1200	1215	ATTTAGTGTCTGGAAG	41	4349
1208710	N/A	N/A	1541	1556	GTTCACAGGCCCTGCT	55	4350
1208723	N/A	N/A	1579	1594	CCCCACCAAGTCAGGC	95	4351
1208745	N/A	N/A	1624	1639	AGGGTTGGAATGTGCT	44	4352
1208773	N/A	N/A	1697	1712	ACCAAGTTTGGGTAAG	39	4353
1208800	N/A	N/A	1762	1777	TGCAGATGGGATGGAC	51	4354
1208824	N/A	N/A	2080	2095	GACCTTTAAGATGCAA	40	4355
1208851	N/A	N/A	2116	2131	AGAAGTAGGACAGTAA	33	4356
1208878	N/A	N/A	2133	2148	TTGCCAAGGACCAAAC	36	4357
1208902	N/A	N/A	2171	2186	TAAGCTTTTGCCACTA	29	4358
1208929	N/A	N/A	2193	2208	CTGGCACAAAGTACCT	58	4359
1208955	N/A	N/A	2271	2286	ATGAGAATTGCCTGTG	29	4360
1208981	N/A	N/A	2327	2342	ACTGTTTGCTAGTTCA	44	4361
1209008	N/A	N/A	2375	2390	CTGTTGGTTGATGAAA	83	4362
1209032	N/A	N/A	2448	2463	ATTGATGAATCAGCAA	68	4363

1209057	N/A	N/A	2472	2487	GTGCTATAGTGCCATC	25	4364
1209084	N/A	N/A	2518	2533	GGCTACCTTAGGGAGA	57	4365
1209109	N/A	N/A	2579	2594	GCTTTTGGAAATGGCC	27	4366
1209135	N/A	N/A	2673	2688	CTGCTGCTTGTTTCAG	82	4367
1209163	N/A	N/A	2716	2731	AATTTGCACATTCCCA	71	4368
1209191	N/A	N/A	2777	2792	TCCCAAGTCAATACTT	77	4369
1209213	N/A	N/A	2808	2823	ATGTGCCTACTTGCTG	58	4370
1209240	N/A	N/A	2827	2842	CTCTGGTTCTACATTG	38	4371
1209262	N/A	N/A	2906	2921	TGTTAACCCTCTGAT	106	4372
1209288	N/A	N/A	2986	3001	TAAGTCTTCAGTCCCA	33	4373
1209313	N/A	N/A	3042	3057	TCAGATAGCTGGAGTA	82	4374
1209339	N/A	N/A	3414	3429	GACCCTCAAAAAGGTC	76	4375
1209352	N/A	N/A	3464	3479	TACTCAACTGCTCAGG	47	4376
1209365	N/A	N/A	3494	3509	GGACAACACACTCTCT	73	4377
1209378	N/A	N/A	3611	3626	CGTAGTCTTACCAGGG	27	4378
1209391	N/A	N/A	3678	3693	GCAGAGTTCCTTGAC	22	4379
1209404	N/A	N/A	3713	3728	GCCCACCCTGCCCTAT	83	4380
1209417	N/A	N/A	3891	3906	TACCAGGAGAGTAATG	34	4381
1209430	N/A	N/A	3955	3970	AAAGGGTATTGTGGAG	19	4382
1209443	N/A	N/A	4020	4035	CAAGCTTGTTTACCC	48	4383
1209456	N/A	N/A	4053	4068	TACTTGCTTGAC	42	4384
1209469	N/A	N/A	4075	4090	GGGCCAAGGCCCTTCT	51	4385
1209482	N/A	N/A	4299	4314	GTAGGCCAGGGTTGC	33	4386
1209495	N/A	N/A	4340	4355	TAGGACCATGCCAAGT	39	4387
1209508	N/A	N/A	4530	4545	CCGTTCCAACCATCT	60	4388
1209521	N/A	N/A	4638	4653	GGAACGCAGTGAGCCA	73	4389
1209534	N/A	N/A	4814	4829	CTTCCTGGCAAGCCCG	45	4390
1209547	N/A	N/A	5161	5176	GTTGTCCGGGTTCTG	39	4391
1209560	N/A	N/A	5439	5454	CCGCGGCCGGCTGGCC	42	4392
1209573	N/A	N/A	5756	5771	GGAGACGGAGGAGCCG	71	4393
1209586	N/A	N/A	5885	5900	AGCCCCCTGCTCCCGA	50	4394
1209599	N/A	N/A	6126	6141	GGGCCCCAAGCTCTCT	30	4395
1209612	N/A	N/A	6372	6387	CTCCGCCTAACCAG	36	4396
1209625	N/A	N/A	6456	6471	GATTCACCTACACATT	40	4397
1209638	N/A	N/A	6490	6505	AGCAGTGAATCCCAGG	35	4398
1209651	N/A	N/A	6569	6584	GGCCTTGCAGCCCGG	58	4399
1209664	N/A	N/A	6636	6651	CCACCCATCCAGAGTC	73	4400
1209677	N/A	N/A	6730	6745	GTGCCATTAATTCAAT	61	4401
1209690	N/A	N/A	6804	6819	GGACAAAGCTGCTCCA	75	4402
1209703	N/A	N/A	6868	6883	CGCCCCTGCGAACACA	27	4403
1209716	N/A	N/A	7068	7083	CTGAGATTTGTGCCTG	25 [†]	4404

Table 69. Reduction of FXII RNA by 3-10-3 cEt gapmers with uniform PS internucleoside linkages
(Huh7, electroporation, 2000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1128802	218	233	3569	3584	TACATTTGTGGTACAG	98	2426
1129531	2009	2024	7397	7412	GAGTTCCTGCGCCATC	13	3837
1129948	N/A	N/A	4840	4855	ATCTGCTTTCCGCACT	71	3630
1194290	N/A	N/A	4841	4856	CATCTGCTTTCCGCAC	44	4405
1208272	N/A	N/A	117	132	ACAATCCTGGTTCCCA	40	4406
1208307	N/A	N/A	177	192	GGTCATGAGCAGAGGC	58	4407
1208338	N/A	N/A	217	232	TCACCTTTCCACATAG	59	4408
1208375	N/A	N/A	301	316	ATCTCCCCCAGAAATG	40	4409
1208403	N/A	N/A	343	358	CCCAAACCCCTTCTAC	86	4410
1208436	N/A	N/A	421	436	GTCATAGCCTGCCACC	72	4411
1208468	N/A	N/A	468	483	AAGGTGGAATCTACAA	47	4412
1208498	N/A	N/A	560	575	ATCCCCACCCAAGGGT	53	4413
1208524	N/A	N/A	618	633	AGCACCAGGTAGGCAC	49	4414
1208555	N/A	N/A	648	663	ATCACTCTAGTGCCCA	111	4415
1208581	N/A	N/A	696	711	CACTTAGACACAGCCC	83	4416
1208594	N/A	N/A	834	849	AATGATGCCCATGAGA	40	4417
1208607	N/A	N/A	868	883	TGCCCATTGAAGGCC	60	4418
1208620	N/A	N/A	906	921	GGCATTGAGATGCCAG	108	4419
1208633	N/A	N/A	937	952	CAGCTCATAAGTGATA	55	4420
1208646	N/A	N/A	1006	1021	TTATCAACCTGGTTTC	57	4421
1208659	N/A	N/A	1025	1040	AACCCTAAGAGGTTTA	40	4422
1208672	N/A	N/A	1073	1088	TGCACCAGGTGATGGG	53	4423
1208685	N/A	N/A	1135	1150	CAGGTACCCCTTCATCT	51	4424
1208698	N/A	N/A	1202	1217	TAATTTAGTGTCTGGA	89	4425
1208711	N/A	N/A	1547	1562	CATCTGGTTCACAGGC	53	4426
1208724	N/A	N/A	1580	1595	ACCCACCAAGTCAGG	106	4427
1208748	N/A	N/A	1625	1640	CAGGGTTGGAATGTGC	88	4428
1208775	N/A	N/A	1698	1713	CACCAAGTTTGGGTAA	93	4429
1208802	N/A	N/A	1763	1778	ATGCAGATGGGATGGA	41	4430
1208825	N/A	N/A	2081	2096	GGACCTTTAAGATGCA	44	4431
1208852	N/A	N/A	2117	2132	CAGAACTAGGACAGTA	90	4432
1208881	N/A	N/A	2134	2149	CTTGCCAAGGACCAAA	84	4433
1208905	N/A	N/A	2172	2187	ATAAGCTTTTGCCACT	66	4434
1208930	N/A	N/A	2207	2222	ATGCTGAGCAGTGTCT	30	4435
1208956	N/A	N/A	2277	2292	CGAATAATGAGAATTG	73	4436
1208984	N/A	N/A	2328	2343	TACTGTTTGCTAGTTC	81	4437
1209009	N/A	N/A	2378	2393	ATGCTGTTGGTTGATG	39	4438
1209035	N/A	N/A	2451	2466	AGCATTGATGAATCAG	117	4439

1209058	N/A	N/A	2473	2488	TGTGCTATAGTGCCAT	111	4440
1209085	N/A	N/A	2522	2537	AGAAGGCTACCTTAGG	79	4441
1209111	N/A	N/A	2580	2595	GGCTTTTGAAATGGC	62	4442
1209137	N/A	N/A	2698	2713	TAAGGTTCAACAAGGC	44	4443
1209166	N/A	N/A	2717	2732	AAATTTGCACATTCCC	86	4444
1209192	N/A	N/A	2778	2793	CTCCCAAGTCAATACT	105	4445
1209215	N/A	N/A	2810	2825	GAATGTGCCTACTTGC	42	4446
1209241	N/A	N/A	2851	2866	ATAGTACAGTTGATCC	40	4447
1209265	N/A	N/A	2908	2923	ACTGTTAACCCTCTG	57	4448
1209289	N/A	N/A	2988	3003	GGTAAGTCTTCAGTCC	46	4449
1209316	N/A	N/A	3043	3058	GTCAGATAGCTGGAGT	94	4450
1209340	N/A	N/A	3415	3430	AGACCCTCAAAAAGGT	40	4451
1209353	N/A	N/A	3465	3480	GTACTCAACTGCTCAG	57	4452
1209366	N/A	N/A	3496	3511	AGGGACAACACACTCT	35	4453
1209379	N/A	N/A	3625	3640	CTCCAACCTCTGCG	61	4454
1209392	N/A	N/A	3681	3696	CAAGCAGAGTTCCTTG	62	4455
1209405	N/A	N/A	3745	3760	GACAAGGCTTCCCTGC	106	4456
1209418	N/A	N/A	3892	3907	ATACCAGGAGAGTAAT	51	4457
1209431	N/A	N/A	3959	3974	TTCCAAAGGGTATTGT	41	4458
1209444	N/A	N/A	4021	4036	CCAAGCTTGTTTACC	90	4459
1209457	N/A	N/A	4054	4069	CTACTTGCCTTGTGAC	42	4460
1209470	N/A	N/A	4126	4141	GAGAGATGGACATGGT	44	4461
1209483	N/A	N/A	4301	4316	CTGTAGGCCAGGGTT	44	4462
1209496	N/A	N/A	4341	4356	CTAGGACCATGCCAAG	84	4463
1209509	N/A	N/A	4531	4546	CCCGTTCCCAACCATC	114	4464
1209522	N/A	N/A	4640	4655	AGGGAACGCAGTGAGC	74	4465
1209535	N/A	N/A	4833	4848	TTCCGCACTCTCCCTC	81	4466
1209548	N/A	N/A	5162	5177	CGTTGTCCGGGTTCTT	11	4467
1209561	N/A	N/A	5441	5456	GCCCCGCGCCGGCTGG	39	4468
1209574	N/A	N/A	5757	5772	GGGAGACGGAGGAGCC	76	4469
1209587	N/A	N/A	5886	5901	AAGCCCCCTGCTCCCG	99	4470
1209600	N/A	N/A	6173	6188	GCAACAGAGCTAACCC	52	4471
1209613	N/A	N/A	6374	6389	TTCTTCCGCCTAACCC	31	4472
1209626	N/A	N/A	6460	6475	CTGGGATTACCTACA	58	4473
1209639	N/A	N/A	6491	6506	CAGCAGTGAATCCCAG	66	4474
1209652	N/A	N/A	6574	6589	TAGTTGGCCTTTGCAG	33	4475
1209665	N/A	N/A	6637	6652	ACCACCCATCCAGAGT	54	4476
1209678	N/A	N/A	6736	6751	GAGGAGGTGCCATTAA	37	4477
1209691	N/A	N/A	6805	6820	TGGACAAAGCTGCTCC	57	4478
1209704	N/A	N/A	6869	6884	CCGCCCCTGCGAACAC	48	4479
1209717	N/A	N/A	7069	7084	CCTGAGATTTGTGCCT	88 [†]	4480

Table 70. Reduction of FXII RNA by 3-10-3 cEt gapmers with uniform PS internucleoside linkages
(Huh7, electroporation, 2000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1128802	218	233	3569	3584	TACATTTGTGGTACAG	99	2426
1129531	2009	2024	7397	7412	GAGTTCCTGCGCCATC	11	3837
1129948	N/A	N/A	4840	4855	ATCTGCTTTCCGCACT	43	3630
1194291	N/A	N/A	4842	4857	TCATCTGCTTTCCGCA	55	4481
1208276	N/A	N/A	118	133	GACAATCCTGGTTCCC	81	4482
1208310	N/A	N/A	182	197	CCACAGGTCATGAGCA	44	4483
1208342	N/A	N/A	231	246	CTCCGGGCTGGCCTC	104	4484
1208376	N/A	N/A	309	324	TAAGGCCCATCTCCCC	117	4485
1208407	N/A	N/A	349	364	CCAAGACCCAAACCCT	60	4486
1208438	N/A	N/A	424	439	TAAGTCATAGCCTGCC	71	4487
1208469	N/A	N/A	471	486	CCCAAGGTGGAATCTA	92	4488
1208500	N/A	N/A	570	585	CACCATACACATCCCC	44	4489
1208525	N/A	N/A	620	635	CTAGCACCAGGTAGGC	52	4490
1208559	N/A	N/A	650	665	CGATCACTCTAGTGCC	69	4491
1208582	N/A	N/A	698	713	GGCACTTAGACACAGC	61	4492
1208595	N/A	N/A	835	850	GAATGATGCCCATGAG	65	4493
1208608	N/A	N/A	869	884	TTGCCCATTTGAAGGCC	61	4494
1208621	N/A	N/A	907	922	AGGCATTCAGATGCCA	43	4495
1208634	N/A	N/A	951	966	CGCCCAGAGTCACCCA	58	4496
1208647	N/A	N/A	1007	1022	GTTATCAACCTGGTTT	76	4497
1208660	N/A	N/A	1026	1041	CAACCCTAAGAGGTTT	83	4498
1208673	N/A	N/A	1074	1089	ATGCACCAGGTGATGG	48	4499
1208686	N/A	N/A	1140	1155	AATGGCAGGTACCCTT	64	4500
1208699	N/A	N/A	1205	1220	AGGTAATTTAGTGTCT	96	4501
1208712	N/A	N/A	1550	1565	GTCCATCTGGTTCACA	69	4502
1208725	N/A	N/A	1581	1596	AACCCACCAAGTCAG	55	4503
1208749	N/A	N/A	1629	1644	AGTCCAGGGTTGGAAT	45	4504
1208777	N/A	N/A	1700	1715	GGCACCAAGTTTGGGT	72	4505
1208803	N/A	N/A	1766	1781	AAGATGCAGATGGGAT	99	4506
1208828	N/A	N/A	2083	2098	ATGGACCTTTAAGATG	58	4507
1208855	N/A	N/A	2118	2133	CCAGAACTAGGACAGT	70	4508
1208882	N/A	N/A	2135	2150	ACTTGCCAAGGACCAA	40	4509
1208906	N/A	N/A	2173	2188	AATAAGCTTTTGCCAC	69	4510
1208932	N/A	N/A	2208	2223	AATGCTGAGCAGTGTC	96	4511
1208959	N/A	N/A	2278	2293	GCGAATAATGAGAATT	50	4512
1208985	N/A	N/A	2329	2344	ATACTGTTTGCTAGTT	81	4513
1209012	N/A	N/A	2379	2394	TATGCTGTTGGTTGAT	54	4514
1209036	N/A	N/A	2453	2468	TTAGCATTGATGAATC	50	4515

1209061	N/A	N/A	2482	2497	ATTCAGGTGTGTGCTA	47	4516
1209088	N/A	N/A	2528	2543	AGCACAAGAAGGCTAC	57	4517
1209112	N/A	N/A	2587	2602	GGGATTTGGCTTTTGG	76	4518
1209140	N/A	N/A	2699	2714	TTAAGGTTCAACAAGG	64	4519
1209169	N/A	N/A	2723	2738	AGTGAAAAATTTGCAC	70	4520
1209195	N/A	N/A	2779	2794	ACTCCCAAGTCAATAC	88	4521
1209216	N/A	N/A	2811	2826	AGAATGTGCCTACTTG	37	4522
1209243	N/A	N/A	2853	2868	TAATAGTACAGTTGAT	46	4523
1209266	N/A	N/A	2909	2924	CACTGTTAACCACTCT	84	4524
1209292	N/A	N/A	2990	3005	TGGGTAAGTCTTCAGT	62	4525
1209317	N/A	N/A	3044	3059	AGTCAGATAGCTGGAG	94	4526
1209341	N/A	N/A	3416	3431	CAGACCCTCAAAAAGG	64	4527
1209354	N/A	N/A	3467	3482	CTGTACTCAACTGCTC	47	4528
1209367	N/A	N/A	3497	3512	CAGGGACAACACACTC	61	4529
1209380	N/A	N/A	3648	3663	GGTACATGTCTCCCAG	42	4530
1209393	N/A	N/A	3682	3697	CCAAGCAGAGTTCCTT	74	4531
1209406	N/A	N/A	3758	3773	ACCTGTAGAAAGAGAC	41	4532
1209419	N/A	N/A	3893	3908	GATACCAGGAGAGTAA	70	4533
1209432	N/A	N/A	3960	3975	CTTCCAAAGGGTATTG	79	4534
1209445	N/A	N/A	4022	4037	TCCAAGCTTGTTTAC	99	4535
1209458	N/A	N/A	4055	4070	CCTACTTGCCTTGTGA	67	4536
1209471	N/A	N/A	4130	4145	GTCTGAGAGATGGACA	54	4537
1209484	N/A	N/A	4305	4320	TATTCTGTAGGCCCCAG	38	4538
1209497	N/A	N/A	4342	4357	TCTAGGACCATGCCAA	69	4539
1209510	N/A	N/A	4533	4548	GGCCCGTTCCCAACCA	45	4540
1209523	N/A	N/A	4641	4656	GAGGGAACGCAGTGAG	120	4541
1209536	N/A	N/A	4834	4849	TTTCCGCACTCTCCCT	78	4542
1209549	N/A	N/A	5382	5397	CCCCCACTTCCTAAC	51	4543
1209562	N/A	N/A	5442	5457	AGCCCGCGGCCGCTG	82	4544
1209575	N/A	N/A	5761	5776	CGCTGGGAGACGGAGG	31	4545
1209588	N/A	N/A	5913	5928	TCAGACCTGGCCACAA	45	4546
1209601	N/A	N/A	6326	6341	CCTAGCAGTTGTGCCT	70	4547
1209614	N/A	N/A	6404	6419	GGCACCCGGAACGATA	53	4548
1209627	N/A	N/A	6461	6476	CCTGGGATTCACCTAC	51	4549
1209640	N/A	N/A	6494	6509	TCCCAGCAGTGAATCC	49	4550
1209653	N/A	N/A	6575	6590	CTAGTTGGCCTTTGCA	52	4551
1209666	N/A	N/A	6638	6653	CACCACCCATCCAGAG	47	4552
1209679	N/A	N/A	6758	6773	CTCTCGCAGCAAGCCC	52	4553
1209692	N/A	N/A	6806	6821	ATGGACAAAGCTGCTC	29	4554
1209705	N/A	N/A	6872	6887	CCTCCGCCCTGCGAA	60	4555
1209718	N/A	N/A	7070	7085	ACCTGAGATTTGTGCC	65 [†]	4556

Table 71. Reduction of FXII RNA by 3-10-3 cEt gapmers with uniform PS internucleoside linkages
(Huh7, electroporation, 2000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1128802	218	233	3569	3584	TACATTTGTGGTACAG	35	2426
1129531	2009	2024	7397	7412	GAGTTCCTGCGCCATC	14	3837
1129948	N/A	N/A	4840	4855	ATCTGCTTTCCGCACT	31	3630
1194292	N/A	N/A	4843	4858	CTCATCTGCTTTCCGC	65	4557
1208277	N/A	N/A	121	136	TGGGACAATCCTGGTT	92	4558
1208312	N/A	N/A	183	198	CCCACAGGTCATGAGC	63	4559
1208347	N/A	N/A	233	248	GCCTTCCGGGCTGGCC	57	4560
1208378	N/A	N/A	310	325	TTAAGGCCCATCTCCC	111	4561
1208408	N/A	N/A	358	373	GATTTCTTCCCAAGAC	49	4562
1208439	N/A	N/A	430	445	TGACTATAAGTCATAG	43	4563
1208473	N/A	N/A	472	487	TCCCAAGGTGGAATCT	75	4564
1208502	N/A	N/A	572	587	TGCACCATACACATCC	59	4565
1208529	N/A	N/A	621	636	CCTAGCACCAGGTAGG	40	4566
1208562	N/A	N/A	651	666	ACGATCACTCTAGTGC	78	4567
1208583	N/A	N/A	717	732	GCTCCGAGCCAGGCTC	81	4568
1208596	N/A	N/A	836	851	TGAATGATGCCCATGA	41	4569
1208609	N/A	N/A	872	887	TCCTTGCCCATTGAAG	72	4570
1208622	N/A	N/A	909	924	AGAGGCATTGAGATGC	109	4571
1208635	N/A	N/A	952	967	TCGCCCAGAGTCACCC	55	4572
1208648	N/A	N/A	1008	1023	TGTTATCAACCTGGTT	42	4573
1208661	N/A	N/A	1036	1051	CCCTTCTCAACAACCC	76	4574
1208674	N/A	N/A	1076	1091	CCATGCACCAGGTGAT	52	4575
1208687	N/A	N/A	1141	1156	AAATGGCAGGTACCCT	103	4576
1208700	N/A	N/A	1209	1224	ATGTAGGTAATTTAGT	76	4577
1208713	N/A	N/A	1552	1567	AGGTCCATCTGGTTCA	84	4578
1208726	N/A	N/A	1582	1597	CAACCCCAACCAAGTCA	45	4579
1208752	N/A	N/A	1630	1645	GAGTCCAGGGTTGGAA	26	4580
1208779	N/A	N/A	1703	1718	TAGGGCACCAAGTTTG	27	4581
1208805	N/A	N/A	1913	1928	GAAGTTGTGTGCCTGT	64	4582
1208829	N/A	N/A	2085	2100	AGATGGACCTTTAAGA	34	4583
1208856	N/A	N/A	2119	2134	ACCAGAACTAGGACAG	57	4584
1208884	N/A	N/A	2136	2151	CACCTGCCAAGGACCA	47	4585
1208909	N/A	N/A	2174	2189	CAATAAGCTTTTGCCA	78	4586
1208933	N/A	N/A	2214	2229	CCATGAAATGCTGAGC	29	4587
1208960	N/A	N/A	2286	2301	TAACCATCGCGAATAA	52	4588
1208988	N/A	N/A	2331	2346	TAATACTGTTTGCTAG	48	4589
1209013	N/A	N/A	2384	2399	GATTATATGCTGTTGG	82	4590
1209039	N/A	N/A	2454	2469	CTTAGCATTGATGAAT	51	4591

1209064	N/A	N/A	2484	2499	TGATTCAGGTGTGTGC	75	4592
1209089	N/A	N/A	2537	2552	TAGTTCCTAAGCACAA	32	4593
1209115	N/A	N/A	2614	2629	CGTTTTTCACACTTTG	40	4594
1209142	N/A	N/A	2701	2716	AGTTAAGGTTCAACAA	55	4595
1209170	N/A	N/A	2725	2740	GCAGTGAAAAATTTGC	62	4596
1209196	N/A	N/A	2780	2795	AACTCCCAAGTCAATA	30	4597
1209219	N/A	N/A	2812	2827	GAGAATGTGCCTACTT	40	4598
1209244	N/A	N/A	2864	2879	AACGGCAGTAATAATA	69	4599
1209269	N/A	N/A	2914	2929	GAAGTCACTGTTAACC	65	4600
1209293	N/A	N/A	2993	3008	CCTTGGGTAAAGTCTTC	86	4601
1209320	N/A	N/A	3050	3065	TTCAGGAGTCAGATAG	87	4602
1209342	N/A	N/A	3419	3434	GGACAGACCCTCAAAA	54	4603
1209355	N/A	N/A	3468	3483	CCTGTACTCAACTGCT	36	4604
1209368	N/A	N/A	3498	3513	GCAGGGACAACACACT	53	4605
1209381	N/A	N/A	3650	3665	AGGGTACATGTCTCCC	93	4606
1209394	N/A	N/A	3684	3699	CTCCAAGCAGAGTTCC	56	4607
1209407	N/A	N/A	3760	3775	ACACCTGTAGAAAGAG	58	4608
1209420	N/A	N/A	3894	3909	TGATACCAGGAGAGTA	61	4609
1209433	N/A	N/A	3961	3976	ACTTCCAAAGGGTATT	26	4610
1209446	N/A	N/A	4023	4038	TTCCAAGCTTGTTTA	48	4611
1209459	N/A	N/A	4056	4071	ACCTACTTGCTTGTG	31	4612
1209472	N/A	N/A	4131	4146	GGTCTGAGAGATGGAC	41	4613
1209485	N/A	N/A	4307	4322	CCTATTCTGTAGGCCC	71	4614
1209498	N/A	N/A	4346	4361	AGAGTCTAGGACCATG	50	4615
1209511	N/A	N/A	4577	4592	ACCACCCGGCCTCCTG	71	4616
1209524	N/A	N/A	4642	4657	GGAGGGAACGCAGTGA	113	4617
1209537	N/A	N/A	4909	4924	TTGCCTTGGTGTCTGA	40	4618
1209550	N/A	N/A	5383	5398	CCCCCCCCACTTCCTAA	68	4619
1209563	N/A	N/A	5444	5459	AGAGCCCCGCGCCGGC	79	4620
1209576	N/A	N/A	5767	5782	AAGCTGCGCTGGGAGA	43	4621
1209589	N/A	N/A	5918	5933	CGCTCTCAGACCTGGC	79	4622
1209602	N/A	N/A	6336	6351	TACCCCTGCCCCTAGC	51	4623
1209615	N/A	N/A	6411	6426	TTCTGTAGGCACCCGG	49	4624
1209628	N/A	N/A	6465	6480	TCTACCTGGGATTAC	84	4625
1209641	N/A	N/A	6495	6510	ATCCCAGCAGTGAATC	111	4626
1209654	N/A	N/A	6601	6616	CTAGCCCCGAGCGCGG	66	4627
1209667	N/A	N/A	6660	6675	GCGGAAACAGAAACCC	49	4628
1209680	N/A	N/A	6764	6779	CTTCCTCTCTCGCAGC	60	4629
1209693	N/A	N/A	6807	6822	GATGGACAAAGCTGCT	87	4630
1209706	N/A	N/A	6875	6890	ATTCTCCGCCCTGC	76	4631
1209719	N/A	N/A	7071	7086	GACCTGAGATTTGTGC	98 [†]	4632

Table 72. Reduction of FXII RNA by 3-10-3 cEt gapmers with uniform PS internucleoside linkages
(Huh7, electroporation, 2000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1128802	218	233	3569	3584	TACATTTGTGGTACAG	20	2426
1129531	2009	2024	7397	7412	GAGTTCCTGCGCCATC	8	3837
1129948	N/A	N/A	4840	4855	ATCTGCTTTCCGCACT	21	3630
1129949	N/A	N/A	4844	4859	TCTCATCTGCTTTCCG	27	3706
1208281	N/A	N/A	122	137	CTGGGACAATCCTGGT	104	4633
1208314	N/A	N/A	184	199	ACCCACAGGTCATGAG	28	4634
1208349	N/A	N/A	234	249	GGCCTTCCGGGCTGGC	59	4635
1208379	N/A	N/A	311	326	CTTAAGGCCCATCTCC	37	4636
1208412	N/A	N/A	398	413	TGCTAGTCTGCAGCTT	35	4637
1208443	N/A	N/A	431	446	CTGACTATAAGTCATA	47	4638
1208476	N/A	N/A	517	532	CCGACTGTGTGCTCTT	13	4639
1208504	N/A	N/A	573	588	CTGCACCATACACATC	27	4640
1208530	N/A	N/A	622	637	ACCTAGCACCAGGTAG	85	4641
1208564	N/A	N/A	656	671	AGCTCACGATCACTCT	86	4642
1208584	N/A	N/A	718	733	TGCTCCGAGCCAGGCT	45	4643
1208597	N/A	N/A	837	852	ATGAATGATGCCCATG	35	4644
1208610	N/A	N/A	878	893	GATCCTTCCTTGCCCA	27	4645
1208623	N/A	N/A	913	928	CTTCAGAGGCATTTCAG	65	4646
1208636	N/A	N/A	954	969	CCTCGCCCAGAGTCAC	109	4647
1208649	N/A	N/A	1011	1026	TACTGTTATCAACCTG	40	4648
1208662	N/A	N/A	1046	1061	ACATGGGTTTCCCTTC	52	4649
1208675	N/A	N/A	1078	1093	TTCCATGCACCAGGTG	34	4650
1208688	N/A	N/A	1142	1157	GAAATGGCAGGTACCC	47	4651
1208701	N/A	N/A	1210	1225	CATGTAGGTAATTTAG	21	4652
1208714	N/A	N/A	1554	1569	TAAGGTCCATCTGGTT	92	4653
1208729	N/A	N/A	1584	1599	CTCAACCCACCAAGT	79	4654
1208753	N/A	N/A	1667	1682	AAACTTTTGGGTGTGG	35	4655
1208782	N/A	N/A	1705	1720	GATAGGGCACCAAGTT	85	4656
1208806	N/A	N/A	1915	1930	ATGAAGTTGTGTGCCT	48	4657
1208832	N/A	N/A	2086	2101	GAGATGGACCTTTAAG	38	4658
1208859	N/A	N/A	2122	2137	CAAACCAGAACTAGGA	58	4659
1208887	N/A	N/A	2142	2157	AAAGTGCACCTTGCCAA	29	4660
1208910	N/A	N/A	2175	2190	TCAATAAGCTTTTGCC	31	4661
1208936	N/A	N/A	2215	2230	GCCATGAAATGCTGAG	24	4662
1208963	N/A	N/A	2294	2309	ATAGAACATAACCATC	35	4663
1208989	N/A	N/A	2333	2348	CCTAATACTGTTTGCT	21	4664
1209016	N/A	N/A	2385	2400	AGATTATATGCTGTTG	23	4665
1209040	N/A	N/A	2455	2470	GCTTAGCATTGATGAA	51	4666

1209065	N/A	N/A	2486	2501	CTTGATTCAGGTGTGT	31	4667
1209092	N/A	N/A	2538	2553	GTAGTTCCTAAGCACA	48	4668
1209118	N/A	N/A	2630	2645	AGTCTACTTAGTGCAA	39	4669
1209144	N/A	N/A	2702	2717	CAGTTAAGGTTCAACA	26	4670
1209173	N/A	N/A	2744	2759	ATTTGTGGGCATGCAC	57	4671
1209199	N/A	N/A	2781	2796	TAACCTCCAAGTCAAT	49	4672
1209220	N/A	N/A	2813	2828	TGAGAATGTGCCTACT	24	4673
1209246	N/A	N/A	2865	2880	AAACGGCAGTAATAAT	59	4674
1209270	N/A	N/A	2917	2932	GTTGAAGTCACTGTTA	23	4675
1209296	N/A	N/A	3013	3028	ACAACCTGCTAGCTGT	73	4676
1209321	N/A	N/A	3051	3066	GTTCAGGAGTCAGATA	57	4677
1209343	N/A	N/A	3421	3436	AAGGACAGACCCTCAA	60	4678
1209356	N/A	N/A	3470	3485	CCCCTGTACTCAACTG	64	4679
1209369	N/A	N/A	3499	3514	TGCAGGGACAACACAC	82	4680
1209382	N/A	N/A	3651	3666	CAGGGTACATGTCTCC	39	4681
1209395	N/A	N/A	3686	3701	CTCTCCAAGCAGAGTT	74	4682
1209408	N/A	N/A	3762	3777	GCACACCTGTAGAAAG	54	4683
1209421	N/A	N/A	3896	3911	GGTGATACCAGGAGAG	56	4684
1209434	N/A	N/A	3962	3977	GA CT TCCA AAGGGTAT	57	4685
1209447	N/A	N/A	4025	4040	GTTTCCAAGCTTG GTT	55	4686
1209460	N/A	N/A	4057	4072	AACCTACTTGCCTTGT	28	4687
1209473	N/A	N/A	4242	4257	CACCTTTCTGGCAGTG	56	4688
1209486	N/A	N/A	4317	4332	TATCCAGCAACCTATT	45	4689
1209499	N/A	N/A	4351	4366	TCAGGAGAGTCTAGGA	42	4690
1209512	N/A	N/A	4579	4594	ACACCACCCGGCCTCC	30	4691
1209525	N/A	N/A	4657	4672	GTGCGGCAGGCTTGGG	27	4692
1209538	N/A	N/A	5077	5092	CCCACGCGGCGCACC	57	4693
1209551	N/A	N/A	5404	5419	GCCCTCTCGGCTCCTC	33	4694
1209564	N/A	N/A	5445	5460	GAGAGCCCGCGGCCGG	60	4695
1209577	N/A	N/A	5771	5786	GTGGAAGCTGCGCTGG	30	4696
1209590	N/A	N/A	5919	5934	GCGCTCTCAGACCTGG	111	4697
1209603	N/A	N/A	6352	6367	CAAAGGTCTCCTCCCC	54	4698
1209616	N/A	N/A	6414	6429	CCATTCTGTAGGCACC	25	4699
1209629	N/A	N/A	6468	6483	GATTCTACCTGGGATT	70	4700
1209642	N/A	N/A	6496	6511	GATCCCAGCAGTGAAT	74	4701
1209655	N/A	N/A	6607	6622	CCCACACTAGCCCGGA	80	4702
1209668	N/A	N/A	6661	6676	AGCGGAAACAGAAACC	83	4703
1209681	N/A	N/A	6766	6781	CCCTTCTCTCTCGCA	67	4704
1209694	N/A	N/A	6808	6823	CGATGGACAAAAGCTGC	40	4705
1209707	N/A	N/A	7014	7029	ACCTGGCACGCATCGG	10 [†]	4706
1209720	N/A	N/A	7073	7088	TGGACCTGAGATTTGT	44 [†]	4707

Table 73. Reduction of FXII RNA by 3-10-3 cEt gapmers with uniform PS internucleoside linkages
(Huh7, electroporation, 2000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1128802	218	233	3569	3584	TACATTTGTGGTACAG	42	2426
1129531	2009	2024	7397	7412	GAGTTCCTGCGCCATC	12	3837
1129948	N/A	N/A	4840	4855	ATCTGCTTTCCGCACT	25	3630
1194293	N/A	N/A	4845	4860	CTCTCATCTGCTTTCC	46	4708
1208282	N/A	N/A	124	139	TCCTGGGACAATCCTG	94	4709
1208317	N/A	N/A	185	200	GACCCACAGGTCATGA	41	4710
1208351	N/A	N/A	265	280	ACCCAGTCTGGTTGTC	54	4711
1208382	N/A	N/A	312	327	TCTTAAGGCCCATCTC	78	4712
1208413	N/A	N/A	399	414	TTGCTAGTCTGCAGCT	22	4713
1208444	N/A	N/A	432	447	ACTGACTATAAGTCAT	79	4714
1208478	N/A	N/A	518	533	ACCGACTGTGTGCTCT	26	4715
1208506	N/A	N/A	576	591	ACACTGCACCATACAC	18	4716
1208534	N/A	N/A	625	640	AAGACCTAGCACCAGG	25	4717
1208566	N/A	N/A	657	672	CAGCTCACGATCACTC	40	4718
1208585	N/A	N/A	721	736	ACCTGCTCCGAGCCAG	79	4719
1208598	N/A	N/A	838	853	CATGAATGATGCCCAT	36	4720
1208611	N/A	N/A	881	896	CTTGATCCTTCCTTGC	39	4721
1208624	N/A	N/A	914	929	GCTTCAGAGGCATTCA	45	4722
1208637	N/A	N/A	961	976	TCAAATCCCTCGCCCA	63	4723
1208650	N/A	N/A	1012	1027	TTACTGTTATCAACCT	34	4724
1208663	N/A	N/A	1048	1063	TCACATGGGTTTCCCT	30	4725
1208676	N/A	N/A	1080	1095	ATTTCCATGCACCAGG	105	4726
1208689	N/A	N/A	1143	1158	GGAAATGGCAGGTACC	26	4727
1208702	N/A	N/A	1211	1226	GCATGTAGGTAATTTA	44	4728
1208715	N/A	N/A	1563	1578	CCACCAGGGTAAGGTC	30	4729
1208730	N/A	N/A	1585	1600	ACTCAACCCACCAAG	143	4730
1208756	N/A	N/A	1669	1684	AGAACTTTTGGGTGT	55	4731
1208784	N/A	N/A	1706	1721	GGATAGGGCACCAAGT	110	4732
1208808	N/A	N/A	1918	1933	AGCATGAAGTTGTGTG	68	4733
1208833	N/A	N/A	2087	2102	TGAGATGGACCTTTAA	63	4734
1208860	N/A	N/A	2123	2138	CCAAACCAGAACTAGG	26	4735
1208888	N/A	N/A	2144	2159	GCAAAGTGCACTTGCC	79	4736
1208913	N/A	N/A	2177	2192	GCTCAATAAGCTTTTG	29	4737
1208937	N/A	N/A	2216	2231	TGCCATGAAATGCTGA	32	4738
1208964	N/A	N/A	2316	2331	GTTCAATGTTCACTGT	31	4739
1208992	N/A	N/A	2334	2349	ACCTAATACTGTTTGC	59	4740
1209017	N/A	N/A	2386	2401	CAGATTATATGCTGTT	18	4741
1209043	N/A	N/A	2456	2471	AGCTTAGCATTGATGA	38	4742

1209068	N/A	N/A	2488	2503	CACTTGATTCAGGTGT	66	4743
1209093	N/A	N/A	2539	2554	TGTAGTTCCTAAGCAC	35	4744
1209119	N/A	N/A	2633	2648	CTCAGTCTACTTAGTG	16	4745
1209147	N/A	N/A	2704	2719	CCCAGTTAAGGTTCAA	40	4746
1209174	N/A	N/A	2745	2760	CATTTGTGGGCATGCA	41	4747
1209200	N/A	N/A	2782	2797	GTAACCTCCCAAGTCAA	64	4748
1209247	N/A	N/A	2868	2883	GTAAAACGGCAGTAAT	56	4749
1209273	N/A	N/A	2924	2939	GTTGAATGTTGAAGTC	53	4750
1209297	N/A	N/A	3014	3029	CACAACCTGCTAGCTG	36	4751
1209324	N/A	N/A	3059	3074	AAACTTGGGTTCAGGA	43	4752
1209344	N/A	N/A	3422	3437	AAAGGACAGACCCTCA	55	4753
1209357	N/A	N/A	3471	3486	TCCCCTGTACTCAACT	123	4754
1209370	N/A	N/A	3501	3516	ACTGCAGGGACAACAC	26	4755
1209383	N/A	N/A	3654	3669	AGGCAGGGTACATGTC	55	4756
1209396	N/A	N/A	3700	3715	TATCACAGTCCCCTCT	45	4757
1209409	N/A	N/A	3836	3851	GTGTAGCACCTTTCAC	58	4758
1209422	N/A	N/A	3898	3913	CTGGTGATACCAGGAG	17	4759
1209435	N/A	N/A	3975	3990	AACTCTCCCTCTGGAC	41	4760
1209448	N/A	N/A	4026	4041	AGTTTCCAAGCTTGGT	26	4761
1209461	N/A	N/A	4063	4078	TTCTTGAACCTACTTG	96	4762
1209474	N/A	N/A	4243	4258	TCACCTTTCTGGCAGT	33	4763
1209487	N/A	N/A	4319	4334	AGTATCCAGCAACCTA	42	4764
1209500	N/A	N/A	4352	4367	CTCAGGAGAGTCTAGG	79	4765
1209513	N/A	N/A	4605	4620	CCCCCAGAGAGCTCT	40	4766
1209526	N/A	N/A	4660	4675	TTGGTGCGGCAGGCTT	26	4767
1209539	N/A	N/A	5079	5094	GCCCCACGCGCGCAC	46	4768
1209552	N/A	N/A	5405	5420	CGCCCTCTCGGCTCCT	52	4769
1209565	N/A	N/A	5454	5469	CTGAGGACGGAGAGCC	19	4770
1209578	N/A	N/A	5802	5817	GGAGAAGGTAGGGCAC	101	4771
1209591	N/A	N/A	6090	6105	CCCACGCACCCAGGTC	57	4772
1209604	N/A	N/A	6353	6368	TCAAAGGTCTCCTCCC	100	4773
1209617	N/A	N/A	6416	6431	ACCCATTCTGTAGGCA	73	4774
1209630	N/A	N/A	6469	6484	GGATTCTACCTGGGAT	33	4775
1209643	N/A	N/A	6516	6531	GTATCCCCAGGAGATT	59	4776
1209656	N/A	N/A	6609	6624	CTCCCACACTAGCCCG	91	4777
1209669	N/A	N/A	6662	6677	GAGCGGAAACAGAAAC	75	4778
1209682	N/A	N/A	6777	6792	ACCCACTCATGCCCTT	76	4779
1209695	N/A	N/A	6820	6835	TTGCCGCCCGGACGAT	31	4780
1209708	N/A	N/A	7023	7038	TAAGAGCTCACCTGGC	57 [†]	4781
1209721	N/A	N/A	7079	7094	GCGCTGTGGACCTGAG	37 [†]	4782

Table 74. Reduction of FXII RNA by 3-10-3 cEt gapmers with uniform PS internucleoside linkages
(Huh7, electroporation, 2000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1128802	218	233	3569	3584	TACATTTGTGGTACAG	29	2426
1129531	2009	2024	7397	7412	GAGTTCCTGCGCCATC	18	3837
1129948	N/A	N/A	4840	4855	ATCTGCTTTCCGCACT	54	3630
1194294	N/A	N/A	4846	4861	CCTCTCATCTGCTTTC	27	4783
1208286	N/A	N/A	125	140	ATCCTGGGACAATCCT	50	4784
1208319	N/A	N/A	188	203	CTGGACCCACAGGTCA	42	4785
1208354	N/A	N/A	266	281	CACCCAGTCTGGTTGT	49	4786
1208383	N/A	N/A	313	328	TTCTTAAGGCCCATCT	79	4787
1208417	N/A	N/A	400	415	GTTGCTAGTCTGCAGC	58	4788
1208448	N/A	N/A	433	448	AACTGACTATAAGTCA	25	4789
1208480	N/A	N/A	519	534	TACCGACTGTGTGCTC	49	4790
1208508	N/A	N/A	578	593	ACACACTGCACCATAC	22	4791
1208535	N/A	N/A	627	642	ATAAGACCTAGCACCA	40	4792
1208568	N/A	N/A	658	673	ACAGCTCACGATCACT	30	4793
1208586	N/A	N/A	724	739	AGCACCTGCTCCGAGC	81	4794
1208599	N/A	N/A	839	854	GCATGAATGATGCCCA	55	4795
1208612	N/A	N/A	885	900	AGCTCTTGATCCTTCC	18	4796
1208625	N/A	N/A	915	930	GGCTTCAGAGGCATTC	57	4797
1208638	N/A	N/A	962	977	CTCAAATCCCTCGCCC	27	4798
1208651	N/A	N/A	1013	1028	TTTACTGTTATCAACC	22	4799
1208664	N/A	N/A	1049	1064	CTCACATGGGTTTCCC	52	4800
1208677	N/A	N/A	1122	1137	TCTAAAAGGTAGTTTC	27	4801
1208690	N/A	N/A	1144	1159	GGGAAATGGCAGGTAC	30	4802
1208703	N/A	N/A	1212	1227	GGCATGTAGGTAATTT	44	4803
1208716	N/A	N/A	1564	1579	CCCACCAGGGTAAGGT	147	4804
1208731	N/A	N/A	1589	1604	AGAGACTCAACCCAC	50	4805
1208757	N/A	N/A	1670	1685	GAGAACTTTTGGGTG	19	4806
1208786	N/A	N/A	1714	1729	TTAGGCAAGGATAGGG	79	4807
1208809	N/A	N/A	1919	1934	GAGCATGAAGTTGTGT	73	4808
1208836	N/A	N/A	2088	2103	CTGAGATGGACCTTTA	26	4809
1208863	N/A	N/A	2124	2139	ACCAAACCAGAACTAG	24	4810
1208891	N/A	N/A	2147	2162	AAGGCAAAGTGCCTT	42	4811
1208914	N/A	N/A	2179	2194	CTGCTCAATAAGCTTT	96	4812
1208940	N/A	N/A	2219	2234	TAATGCCATGAAATGC	58	4813
1208967	N/A	N/A	2318	2333	TAGTTCAATGTTCACT	27	4814
1208993	N/A	N/A	2335	2350	AACCTAATACTGTTTG	30	4815
1209020	N/A	N/A	2387	2402	CCAGATTATATGCTGT	40	4816
1209044	N/A	N/A	2458	2473	TCAGCTTAGCATTGAT	52	4817

1209069	N/A	N/A	2491	2506	AGACACTTGATTTCAGG	21	4818
1209096	N/A	N/A	2542	2557	CTGTGTAGTTCCTAAG	28	4819
1209122	N/A	N/A	2639	2654	GTCCCTTCTCAGTCTAC	32	4820
1209148	N/A	N/A	2705	2720	TCCCAGTTAAGGTTCA	22	4821
1209176	N/A	N/A	2747	2762	GCCATTTGTGGGCATG	24	4822
1209203	N/A	N/A	2783	2798	TGTAACCTCCAAGTCA	80	4823
1209224	N/A	N/A	2815	2830	ATTGAGAATGTGCCTA	39	4824
1209249	N/A	N/A	2869	2884	TGTAAAACGGCAGTAA	27	4825
1209274	N/A	N/A	2954	2969	TTGCCACAAAGTAGGC	45	4826
1209299	N/A	N/A	3015	3030	CCACAACCTGCTAGCT	57	4827
1209325	N/A	N/A	3060	3075	AAAACCTTGGGTTCAGG	60	4828
1209345	N/A	N/A	3423	3438	AAAAGGACAGACCCTC	72	4829
1209358	N/A	N/A	3472	3487	TTCCCCTGTACTCAAC	53	4830
1209371	N/A	N/A	3502	3517	AACTGCAGGGACAACA	140	4831
1209384	N/A	N/A	3655	3670	CAGGCAGGGTACATGT	27	4832
1209397	N/A	N/A	3701	3716	CTATCACAGTCCCCTC	39	4833
1209410	N/A	N/A	3872	3887	CGGGAGGAGAGAGCCC	37	4834
1209423	N/A	N/A	3918	3933	GAATCCCAGGTGTGTG	74	4835
1209436	N/A	N/A	3994	4009	TGGGACCACTCCTTCC	48	4836
1209449	N/A	N/A	4027	4042	AAGTTTCCAAGCTTGG	24	4837
1209462	N/A	N/A	4064	4079	CTTCTTGAACCTACTT	38	4838
1209475	N/A	N/A	4265	4280	CGCCCAGGTCCTCCAC	59	4839
1209488	N/A	N/A	4327	4342	AGTCTCCGAGTATCCA	112	4840
1209501	N/A	N/A	4353	4368	TCTCAGGAGAGTCTAG	56	4841
1209514	N/A	N/A	4606	4621	CCCCCCCAGAGAGCTC	20	4842
1209527	N/A	N/A	4765	4780	GACCCTCACTCACCCA	72	4843
1209540	N/A	N/A	5081	5096	CAGCCCCACGCGGCGC	76	4844
1209553	N/A	N/A	5406	5421	GCGCCCTCTCGGCTCC	107	4845
1209566	N/A	N/A	5455	5470	GCTGAGGACGGAGAGC	41	4846
1209579	N/A	N/A	5845	5860	CTCCCCGGGAGCTCCG	68	4847
1209592	N/A	N/A	6091	6106	CCCCACGCACCCAGGT	47	4848
1209605	N/A	N/A	6354	6369	ATCAAAGGTCTCCTCC	30	4849
1209618	N/A	N/A	6421	6436	GCGCCACCCATTCTGT	35	4850
1209631	N/A	N/A	6472	6487	CTGGGATTCTACCTGG	30	4851
1209644	N/A	N/A	6526	6541	GATTCTCCCTGTATCC	69	4852
1209657	N/A	N/A	6616	6631	AACCTGGCTCCACAC	40	4853
1209670	N/A	N/A	6663	6678	GGAGCGGAAACAGAAA	105	4854
1209683	N/A	N/A	6778	6793	AACCCACTCATGCCCT	108	4855
1209696	N/A	N/A	6824	6839	ACGCTTGCCGCCCGGA	32	4856
1209709	N/A	N/A	7024	7039	CTAAGAGCTCACCTGG	82 [†]	4857
1209722	N/A	N/A	7092	7107	AACACGCAGCTCAGCG	63 [†]	4858

Table 75. Reduction of FXII RNA by 3-10-3 cEt gapmers with uniform PS internucleoside linkages
(Huh7, electroporation, 2000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1128802	218	233	3569	3584	TACATTTGTGGTACAG	94	2426
1129531	2009	2024	7397	7412	GAGTTCCTGCGCCATC	12	3837
1129948	N/A	N/A	4840	4855	ATCTGCTTTCCGCACT	45	3630
1194295	N/A	N/A	4847	4862	CCCTCTCATCTGCTTT	46	4859
1208287	N/A	N/A	129	144	AACAATCCTGGGACAA	49	4860
1208322	N/A	N/A	194	209	AGTCACCTGGACCCAC	33	4861
1208356	N/A	N/A	267	282	CCACCCAGTCTGGTTG	76	4862
1208387	N/A	N/A	314	329	CTTCTTAAGGCCCATC	52	4863
1208418	N/A	N/A	402	417	CTGTTGCTAGTCTGCA	72	4864
1208449	N/A	N/A	438	453	CAGGGAAGTACTATA	42	4865
1208483	N/A	N/A	525	540	GCCACTTACCGACTGT	50	4866
1208509	N/A	N/A	585	600	AGACTGCACACACTGC	80	4867
1208539	N/A	N/A	628	643	CATAAGACCTAGCACC	54	4868
1208570	N/A	N/A	661	676	CACACAGCTCACGATC	61	4869
1208587	N/A	N/A	733	748	CATATCTCAAGCACCT	40	4870
1208600	N/A	N/A	840	855	GGCATGAATGATGCCC	56	4871
1208613	N/A	N/A	886	901	AAGCTCTTGATCCTTC	102	4872
1208626	N/A	N/A	925	940	GATAAAGCTGGGCTTC	71	4873
1208639	N/A	N/A	968	983	GGAGAACTCAAATCCC	65	4874
1208652	N/A	N/A	1014	1029	GTTTACTGTTATCAAC	79	4875
1208665	N/A	N/A	1052	1067	TACCTCACATGGGTTT	43	4876
1208678	N/A	N/A	1124	1139	CATCTAAAAGGTAGTT	64	4877
1208691	N/A	N/A	1164	1179	ATGGCAGAGCTTGAGG	50	4878
1208704	N/A	N/A	1213	1228	TGGCATGTAGGTAATT	54	4879
1208717	N/A	N/A	1565	1580	GCCCACCAGGGTAAGG	46	4880
1208734	N/A	N/A	1595	1610	ATGCTTAGAGACTCAA	61	4881
1208760	N/A	N/A	1671	1686	GGAGAACTTTTGGGT	42	4882
1208788	N/A	N/A	1715	1730	ATTAGGCAAGGATAGG	41	4883
1208812	N/A	N/A	1920	1935	TGAGCATGAAGTTGTG	108	4884
1208839	N/A	N/A	2091	2106	GATCTGAGATGGACCT	63	4885
1208865	N/A	N/A	2125	2140	GACCAAACCAGAACTA	69	4886
1208892	N/A	N/A	2148	2163	CAAGGCAAAGTGCCT	65	4887
1208917	N/A	N/A	2181	2196	ACCTGCTCAATAAGCT	58	4888
1208943	N/A	N/A	2226	2241	CATGAGATAATGCCAT	80	4889
1208968	N/A	N/A	2319	2334	CTAGTTCAATGTTTAC	62	4890
1208996	N/A	N/A	2336	2351	GAACCTAATACTGTTT	83	4891
1209021	N/A	N/A	2388	2403	ACCAGATTATATGCTG	43	4892
1209047	N/A	N/A	2460	2475	CATCAGCTTAGCATTG	36	4893

1209072	N/A	N/A	2492	2507	TAGACACTTGATTTCAG	33	4894
1209097	N/A	N/A	2544	2559	AGCTGTGTAGTTCCTA	82	4895
1209123	N/A	N/A	2646	2661	AATGAGTGTCTTCTC	135	4896
1209151	N/A	N/A	2706	2721	TTCCCAGTTAAGGTTC	75	4897
1209177	N/A	N/A	2748	2763	GGCCATTTGTGGGCAT	63	4898
1209204	N/A	N/A	2784	2799	TTGTAACTCCCAAGTC	55	4899
1209227	N/A	N/A	2816	2831	CATTGAGAATGTGCCT	37	4900
1209250	N/A	N/A	2870	2885	CTGTAAAACGGCAGTA	45	4901
1209276	N/A	N/A	2956	2971	ACTTGCCACAAAGTAG	76	4902
1209300	N/A	N/A	3017	3032	CTCCACAACCTGCTAG	32	4903
1209328	N/A	N/A	3370	3385	AAAAGTTGGGTTCAGG	43	4904
1209346	N/A	N/A	3425	3440	GGAAAAGGACAGACCC	35	4905
1209359	N/A	N/A	3473	3488	CTTCCCCTGTACTCAA	72	4906
1209372	N/A	N/A	3503	3518	GAAGTGCAGGGACAAC	62	4907
1209385	N/A	N/A	3656	3671	ACAGGCAGGGTACATG	43	4908
1209398	N/A	N/A	3702	3717	CCTATCACAGTCCCCT	51	4909
1209411	N/A	N/A	3878	3893	ATGAGGCGGGAGGAGA	37	4910
1209424	N/A	N/A	3919	3934	AGAATCCCAGGTGTGT	50	4911
1209437	N/A	N/A	3997	4012	AAATGGGACCACTCCT	114	4912
1209450	N/A	N/A	4028	4043	CAAGTTTCCAAGCTTG	90	4913
1209463	N/A	N/A	4065	4080	CCTTCTTGAACCTACT	65	4914
1209476	N/A	N/A	4266	4281	CCGCCCAGGTCCTCCA	60	4915
1209489	N/A	N/A	4329	4344	CAAGTCTCCGAGTATC	71	4916
1209502	N/A	N/A	4354	4369	GTCTCAGGAGAGTCTA	43	4917
1209515	N/A	N/A	4608	4623	GACCCCCCAGAGAGC	107	4918
1209528	N/A	N/A	4773	4788	TTGCCCCAGACCCTCA	70	4919
1209541	N/A	N/A	5118	5133	CGCCGGGAGCCCGGAG	80	4920
1209554	N/A	N/A	5427	5442	GGCCGGAATCTAGCTC	41	4921
1209567	N/A	N/A	5714	5729	CGGGTACTCGCCGGTC	58	4922
1209580	N/A	N/A	5847	5862	TCCTCCCCGGGAGCTC	64	4923
1209593	N/A	N/A	6094	6109	CGCCCCACGCACCCA	92	4924
1209606	N/A	N/A	6356	6371	TGATCAAAGGTCTCCT	31	4925
1209619	N/A	N/A	6435	6450	AACCCATCAGGTCAGC	43	4926
1209632	N/A	N/A	6473	6488	CCTGGGATTCTACCTG	29	4927
1209645	N/A	N/A	6528	6543	TCGATTCTCCCTGTAT	28	4928
1209658	N/A	N/A	6617	6632	GAACCTGGCTCCCACA	55	4929
1209671	N/A	N/A	6679	6694	CAGGATTTGAATGGGC	31	4930
1209684	N/A	N/A	6779	6794	AAACCCACTCATGCCC	39	4931
1209697	N/A	N/A	6837	6852	ACCCCATCTGACAACG	65	4932
1209710	N/A	N/A	7025	7040	GCTAAGAGCTCACCTG	86 [†]	4933
1209723	N/A	N/A	7108	7123	ATCACCCCTGGGTCGGA	68 [†]	4934

Table 76. Reduction of FXII RNA by 3-10-3 cEt gapmers with uniform PS internucleoside linkages
(Huh7, electroporation, 3000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 3 Start Site	SEQ ID NO: 3 Stop Site	SEQ ID NO: 4 Start Site	SEQ ID NO: 4 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1128718	3437	3452	13	28	CTGCCTATCCAGGAGT	69	4935
1128719	3439	3454	15	30	AGCTGCCTATCCAGGA	33	4936
1128720	3449	3464	25	40	CCGTTGGTCCAGCTGC	22	4937
1128721	3450	3465	26	41	TCCGTTGGTCCAGCTG	49	4938
1128726	3459	3474	35	50	TGGCATCCGTCCGTTG	60	4939
1128727	3460	3475	36	51	ATGGCATCCGTCCGTT	60	4940
1128728	3463	3478	39	54	CTCATGGCATCCGTCC	66	4941
1128729	3464	3479	40	55	CCTCATGGCATCCGTC	85	4942
1128730	3465	3480	41	56	CCCTCATGGCATCCGT	72	4943
1128731	3468	3483	44	59	GAGCCCTCATGGCATC	60	4944

Table 77. Reduction of FXII RNA by 3-10-3 cEt gapmers with uniform PS internucleoside linkages
(Huh7, electroporation, 3000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 3 Start Site	SEQ ID NO: 3 Stop Site	SEQ ID NO: 4 Start Site	SEQ ID NO: 4 Stop Site	Sequence (5' to 3')	FXII (%UTC)	SEQ ID NO
1128724	3455	3470	31	46	ATCCGTCCGTGGTCC	42	4945
1128725	3457	3472	33	48	GCATCCGTCCGTGGT	59	4946

5 Example 4: Effects of modified oligonucleotides with mixed sugar modifications and mixed backbones on human FXII RNA *in vitro*, single dose

Modified oligonucleotides complementary to an FXII nucleic acid were synthesized and tested for their effect on FXII RNA levels *in vitro*. The modified oligonucleotides were tested in a series of experiments using similar culture conditions. The results for each separate experiment are presented in separate tables below.

The chemistry notation column in the tables below specifies the specific chemistry notation for modified oligonucleotides; wherein subscript ‘d’ represents a 2’-β-D-deoxyribose sugar moiety, subscript ‘e’ represents a 2’-MOE sugar moiety, subscript ‘y’ represents a 2’-O-methyl sugar moiety, subscript ‘k’ represents a cEt modified sugar moiety, subscript ‘s’ represents a phosphorothioate internucleoside linkage, subscript ‘o’ represents a phosphodiester internucleoside linkage, and superscript ‘m’ before the cytosine residue (^mC) represents a 5-methyl cytosine.

“Start site” indicates the 5’-most nucleoside of the target sequence to which the modified oligonucleotide is complementary. “Stop site” indicates the 3’-most nucleoside of the target sequence to

which the modified oligonucleotide is complementary. As shown in the tables below, the modified oligonucleotides are 100% complementary to one or more of human FXII target sequences including the human FXII mRNA sequence designated herein as SEQ ID NO: 1 (ENSEMBL ID ENST00000253496.3 from ENSEMBL version 99: January 2020), the human FXII genomic sequence, designated herein as SEQ ID NO: 2 (ENSEMBL ID ENSG00000131187.9 from ENSEMBL version 99: January 2020, human reference assembly version GRCh38.p13 located on the reverse strand of chromosome 5 from positions 177,402,140 to 177,409,576), the human FXII genomic sequence, designated herein as SEQ ID No. 3 (the complement of GENBANK Accession No. NC_000005.10 truncated from truncated from nucleotides 177399001 to 177413000), and the human FXII mRNA sequence designated herein as SEQ ID No: 4 (GENBANK Accession No. NM_000505.3). 'N/A' indicates that the modified oligonucleotide is not complementary to that particular target sequence with 100% complementarity.

Cultured Huh7 cells, at a density of 20,000 cells per well, were transfected using electroporation with either 2000nM or 4000 nM modified oligonucleotide. After a treatment period of approximately 24 hours, RNA was isolated from the cells and FXII RNA levels were measured by quantitative real-time RTPCR. Human primer probe set RTS40528 (described herein above) was used to measure RNA levels. FXII RNA levels were normalized to total RNA content, as measured by RIBOGREEN®. Reduction of FXII RNA is presented in the tables below as percent FXII RNA relative to the amount in untreated control cells (% UTC). The symbol “†” indicates that the modified oligonucleotide is complementary to the target transcript within the amplicon region of the primer probe set. In such instances, additional assays using alternative primer probes must be performed to accurately assess the potency and efficacy of such modified oligonucleotides.

Table 78. Reduction of FXII RNA (Huh7, electroporation, 4000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence with Chemistry notation (5' to 3')	FXII (%UTC)	SEQ ID NO
1129531	2009	2024	7397	7412	G _{ks} A _{ks} G _{ks} T _{ds} T _{ds} ^m C _{ds} ^m C _{ds} T _{ds} G _{ds} ^m C _{ds} G _{ds} ^m C _{ds} ^m C _{ds} A _{ks} T _{ks} ^m C _k	44	3837
1206480	1782	1797	7170	7185	A _{ks} T _{ks} G _{ks} ^m C _{ds} ^m C _{ds} T _{ds} T _{ds} G _{ds} ^m C _{ds} A _{ds} G _{ds} G _{ds} G _{ds} T _{ks} G _{ks} A _k	60	4947
1206486	1915	1930	7303	7318	T _{ks} ^m C _{ks} A _{ks} ^m C _{ds} ^m C _{ds} A _{ds} A _{ds} G _{ds} G _{ds} A _{ds} G _{ds} G _{ds} G _{ds} A _{ks} A _{ks} A _k	59	4948
1206491	1934	1949	7322	7337	^m C _{ks} ^m C _{ks} A _{ks} ^m C _{ds} T _{ds} ^m C _{ds} T _{ds} ^m C _{ds} T _{ds} ^m C _{ds} A _{ds} ^m C _{ds} T _{ds} G _{ks} ^m C _{ks} G _k	64	4949
1206495	141	156	508	523	T _{ks} G _{ks} ^m C _{ks} T _{ds} ^m C _{ds} T _{ds} T _{ds} ^m C _{ds} A _{ds} G _{ds} ^m C _{ds} T _{ds} T _{ds} T _{ks} G _{ks} T _k	64	4950
1206901	144	159	511	526	G _{ks} T _{es} G _{ks} T _{ds} G _{ds} ^m C _{ds} T _{ds} ^m C _{ds} T _{ds} T _{ds} ^m C _{ds} dsA _{ds} G _{es} ^m C _{es} T _{ks} T _k	81	4951
1206909	152	167	N/A	N/A	G _{ks} A _{es} A _{ks} ^m C _{ds} G _{ds} A _{ds} ^m C _{ds} T _{ds} G _{ds} T _{ds} G _{ds} dsT _{ds} G _{es} ^m C _{es} T _{ks} ^m C _k	53	3647

1206917	209	224	3560	3575	$G_{ks}G_{es}T_{ks}A_{ds}{}^mC_{ds}A_{ds}G_{ds}{}^mC_{ds}T_{ds}G_{ds}{}^mC_{ds}{}^mC_{ds}G_{es}G_{es}T_{ks}G_k$	42	4952
1206925	217	232	3568	3583	$A_{ks}{}^mC_{es}A_{ks}T_{ds}T_{ds}T_{ds}G_{ds}T_{ds}G_{ds}G_{ds}T_{ds}A_{ds}{}^mC_{es}A_{es}G_{ks}{}^mC_k$	64	3114
1206933	1777	1792	7165	7180	$T_{ks}T_{es}G_{ks}{}^mC_{ds}A_{ds}G_{ds}G_{ds}G_{ds}T_{ds}G_{ds}A_{ds}G_{ds}{}^mC_{es}{}^mC_{es}G_{ks}G_k$	62	3375
1206941	1785	1800	7173	7188	$A_{ks}T_{es}G_{ks}A_{ds}T_{ds}G_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}T_{ds}G_d{}^mC_{ds}A_{es}G_{es}G_{ks}G_k$	57	3603
1206949	1793	1808	7181	7196	${}^mC_{ks}{}^mC_{es}{}^mC_{ks}A_{ds}G_{ds}{}^mC_{ds}T_{ds}G_{ds}A_{ds}T_{ds}G_{ds}A_{ds}T_{es}G_{es}{}^mC_{ks}{}^mC_k$	64	4953
1206957	1899	1914	7287	7302	$G_{ks}A_{es}T_{ks}G_{ds}A_{ds}G_{ds}T_{ds}{}^mC_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}G_{ds}A_{es}G_{es}{}^mC_{ks}A_k$	47	2537
1206965	1914	1929	7302	7317	${}^mC_{ks}A_{es}{}^mC_{ks}{}^mC_{ds}A_{ds}A_{ds}G_{ds}G_{ds}A_{ds}G_{ds}G_{ds}A_{es}A_{es}A_{ks}G_k$	60	4954
1206973	1922	1937	7310	7325	$T_{ks}G_{es}{}^mC_{ks}G_{ds}G_{ds}A_{ds}A_{ds}T_{ds}{}^mC_{ds}A_{ds}{}^mC_{ds}{}^mC_{ds}A_{es}G_{ks}G_k$	62	3455
1206981	1930	1945	7318	7333	$T_{ks}{}^mC_{es}T_{ks}{}^mC_{ds}T_{ds}{}^mC_{ds}A_{ds}{}^mC_{ds}T_{ds}G_{ds}{}^mC_{ds}G_{ds}G_{es}A_{es}A_{ks}T_k$	50	4955
1206989	2000	2015	7388	7403	${}^mC_{ks}G_{es}{}^mC_{ks}{}^mC_{ds}A_{ds}T_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}G_{ds}G_{ds}{}^mC_{ds}G_{es}{}^mC_{es}G_{ks}G_k$	91	3228
1206997	2008	2023	7396	7411	$A_{ks}G_{es}T_{ks}T_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}G_{ds}{}^mC_{ds}G_{ds}{}^mC_{ds}{}^mC_{ds}A_{es}T_{es}{}^mC_{ks}{}^mC_k$	38	3761
1207005	2017	2032	7405	7420	$A_{ks}{}^mC_{es}T_{ks}T_{ds}T_{ds}A_{ds}T_{ds}T_{ds}G_{ds}A_{ds}G_{ds}T_{ds}T_{es}{}^mC_{es}{}^mC_{ks}T_k$	41	2848
1207013	2031	2046	7419	7434	$A_{ks}G_{es}{}^mC_{ks}A_{ds}T_{ds}T_{ds}T_{ds}T_{ds}{}^mC_{ds}A_{ds}A_d{}^mC_{ds}G_{es}{}^mC_{es}A_{ks}{}^mC_k$	106	3458
1207032	147	162	514	529	$A_{ks}{}^mC_{ks}T_{ds}G_{ds}T_{ds}G_{ds}T_{ds}G_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}T_{es}T_{es}{}^mC_{es}A_{ks}G_k$	51	3267
1207040	155	170	N/A	N/A	$T_{ks}G_{ks}A_{ds}G_{ds}A_{ds}A_{ds}{}^mC_{ds}G_{ds}A_{ds}{}^mC_{ds}T_{ds}G_{es}T_{es}G_{es}T_{ks}G_k$	71	3875
1207048	212	227	3563	3578	$T_{ks}G_{ks}T_{ds}G_{ds}G_{ds}T_{ds}A_{ds}{}^mC_{ds}A_{ds}G_{ds}{}^mC_d{}^mC_{es}G_{es}{}^mC_{es}{}^mC_{ks}G_k$	63	2734
1207056	220	235	3571	3586	$G_{ks}G_{ks}T_{ds}A_{ds}{}^mC_{ds}A_{ds}T_{ds}T_{ds}T_{ds}G_{ds}T_{ds}G_{es}G_{es}T_{es}A_{ks}{}^mC_k$	66	3269
1207064	1780	1795	7168	7183	$G_{ks}{}^mC_{ks}{}^mC_{ds}T_{ds}T_{ds}G_{ds}{}^mC_{ds}A_{ds}G_{ds}G_{ds}G_{ds}T_{es}G_{es}A_{es}G_{ks}{}^mC_k$	58	3451
1207085	1788	1803	7176	7191	${}^mC_{ks}T_{ks}G_{ds}A_{ds}T_{ds}G_{ds}A_{ds}T_{ds}G_{ds}{}^mC_{ds}{}^mC_{ds}T_{es}T_{es}G_{es}{}^mC_{ks}A_k$	61	3679
1207093	1894	1909	7282	7297	$G_{ks}T_{ks}{}^mC_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}G_{ds}A_{ds}G_{ds}{}^mC_{ds}A_{ds}A_{es}T_{es}{}^mC_{es}A_{ks}G_k$	56	3682
1207101	1902	1917	7290	7305	$A_{ks}A_{ks}A_{ds}G_{ds}A_{ds}T_{ds}G_{ds}A_{ds}G_{ds}T_{ds}{}^mC_{ds}{}^mC_{es}{}^mC_{es}T_{es}G_{ks}A_k$	48	2768
1207109	1917	1932	7305	7320	$A_{ks}A_{ks}T_{ds}{}^mC_{ds}A_{ds}{}^mC_{ds}{}^mC_{ds}A_{ds}A_{ds}G_{ds}G_{ds}A_{es}G_{es}G_{es}G_{ks}A_k$	42	4956
1207117	1925	1940	7313	7328	${}^mC_{ks}A_{ks}{}^mC_{ds}T_{ds}G_{ds}{}^mC_{ds}G_{ds}G_{ds}A_{ds}A_{ds}T_{ds}{}^mC_{es}A_{es}{}^mC_{es}{}^mC_{ks}A_k$	56	3683
1207133	1933	1948	7321	7336	${}^mC_{ks}A_{ks}{}^mC_{ds}T_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}A_d{}^mC_{ds}T_{es}G_{es}{}^mC_{es}G_{ks}G_k$	33	4957
1207146	2003	2018	7391	7406	${}^mC_{ks}T_{ks}G_{ds}{}^mC_{ds}G_{ds}{}^mC_{ds}{}^mC_{ds}A_{ds}T_{ds}{}^mC_{ds}{}^mC_{ds}T_{es}G_{es}G_{es}{}^mC_{ks}G_k$	76	3381
1207154	2011	2026	7399	7414	$T_{ks}T_{ks}G_{ds}A_{ds}G_{ds}T_{ds}T_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}G_{ds}{}^mC_{es}G_{es}{}^mC_{es}{}^mC_{ks}A_k$	48	2463

1207162	2020	2035	7408	7423	$A_{ks}G_{ks}{}^mC_{ds}A_{ds}{}^mC_{ds}T_{ds}T_{ds}T_{ds}A_{ds}T_{ds}T_{ds}$ $G_{es}A_{es}G_{es}T_{ks}T_k$	55	3076
1207170	142	157	509	524	$G_{ks}T_{ks}G_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}T_{ds}T_{ds}{}^mC_{ds}A_{ds}G_{ds}$ ${}^mC_{es}T_{ks}T_{es}T_{ks}G_e$	47	4958
1207178	150	165	N/A	N/A	$A_{ks}{}^mC_{ks}G_{ds}A_{ds}{}^mC_{ds}T_{ds}G_{ds}T_{ds}G_{ds}T_{ds}G_{ds}$ ${}^mC_{es}T_{ks}{}^mC_{es}T_{ks}T_e$	50	3495
1207186	158	173	N/A	N/A	${}^mC_{ks}A_{ks}G_{ds}T_{ds}G_{ds}A_{ds}G_{ds}A_{ds}A_{ds}{}^mC_{ds}G_{ds}$ ${}^mC_{es}T_{ks}G_{ks}T_e$	78	2579
1207194	215	230	3566	3581	$A_{ks}T_{ks}T_{ds}T_{ds}G_{ds}T_{ds}G_{ds}G_{ds}T_{ds}A_{ds}{}^mC_{ds}$ $A_{es}G_{ks}{}^mC_{es}T_{ks}G_e$	70	2963
1207202	223	238	3574	3589	$G_{ks}T_{ks}G_{ds}G_{ds}G_{ds}T_{ds}A_{ds}{}^mC_{ds}A_{ds}T_{ds}T_{ds}$ $T_{es}G_{ks}T_{es}G_{ks}G_e$	36	3497
1207210	1783	1798	7171	7186	$G_{ks}A_{ks}T_{ds}G_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}T_{ds}G_{ds}{}^mC_{ds}$ $A_{ds}G_{es}G_{ks}G_{es}T_{ks}G_e$	39	4959
1207218	1791	1806	7179	7194	${}^mC_{ks}A_{ks}G_{ds}{}^mC_{ds}T_{ds}G_{ds}A_{ds}T_{ds}G_{ds}A_{ds}T_d$ ${}^mC_{es}T_{ks}{}^mC_{es}T_{ks}T_e$	89	4960
1207226	1897	1912	7285	7300	$T_{ks}G_{ks}A_{ds}G_{ds}T_{ds}{}^mC_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}G_{ds}$ $A_{ds}G_{es}{}^mC_{ks}A_{es}A_{ks}T_e$	65	3910
1207234	1905	1920	7293	7308	$G_{ks}G_{ks}G_{ds}A_{ds}A_{ds}A_{ds}G_{ds}A_{ds}T_{ds}G_{ds}A_{ds}$ $G_{es}T_{ks}{}^mC_{es}{}^mC_{ks}{}^mC_e$	68	2997
1207242	1920	1935	7308	7323	${}^mC_{ks}G_{ks}G_{ds}A_{ds}A_{ds}T_{ds}{}^mC_{ds}A_{ds}{}^mC_{ds}{}^mC_d$ ${}^mC_{es}A_{es}G_{ks}G_{es}A_{ks}G_e$	26	3303
1207250	1928	1943	7316	7331	$T_{ks}{}^mC_{ks}T_{ds}{}^mC_{ds}A_{ds}{}^mC_{ds}T_{ds}G_{ds}{}^mC_{ds}G_{ds}$ $G_{ds}A_{es}A_{ks}T_{es}{}^mC_{ks}A_e$	31	3911
1207258	1936	1951	7324	7339	$A_{ks}G_{ks}{}^mC_{ds}{}^mC_{ds}A_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}$ ${}^mC_{es}A_{ks}{}^mC_{es}T_{ks}G_e$	29	4961
1207266	2006	2021	7394	7409	$T_{ks}T_{ks}{}^mC_{ds}{}^mC_{ds}T_{ds}G_{ds}{}^mC_{ds}G_{ds}{}^mC_{ds}{}^mC_d$ ${}^mC_{es}T_{es}{}^mC_{ks}{}^mC_{es}T_{ks}G_e$	70	3609
1207274	2014	2029	7402	7417	$T_{ks}T_{ks}A_{ds}T_{ds}T_{ds}G_{ds}A_{ds}G_{ds}T_{ds}T_{ds}{}^mC_{ds}{}^mC_{ds}$ ${}^mC_{es}T_{ks}G_{es}{}^mC_{ks}G_e$	54	2694
1207282	2023	2038	7411	7426	${}^mC_{ks}A_{ks}A_{ds}A_{ds}G_{ds}{}^mC_{ds}A_{ds}{}^mC_{ds}T_{ds}T_{ds}$ $T_{ds}A_{es}T_{ks}T_{es}G_{ks}A_e$	68	3306
1207290	145	160	512	527	$T_{ks}G_{ks}T_{ds}G_{ds}T_{ds}G_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}T_{ds}T_{ds}$ ${}^mC_{ks}A_{es}G_{ks}{}^mC_{es}T_k$	74	3112
1207298	153	168	N/A	N/A	$A_{ks}G_{ks}A_{ds}A_{ds}{}^mC_{ds}G_{ds}A_{ds}{}^mC_{ds}T_{ds}G_{ds}T_{ds}$ ${}^mC_{es}T_{ks}G_{ks}{}^mC_{es}T_k$	52	3723
1207306	210	225	3561	3576	$T_{ks}G_{ks}G_{ds}T_{ds}A_{ds}{}^mC_{ds}A_{ds}G_{ds}{}^mC_{ds}T_{ds}G_d$ ${}^mC_{ks}{}^mC_{es}G_{ks}G_{es}T_k$	91	2657
1207314	218	233	3569	3584	$T_{ks}A_{ks}{}^mC_{ds}A_{ds}T_{ds}T_{ds}T_{ds}G_{ds}T_{ds}G_{ds}G_{ds}$ $T_{ks}A_{es}{}^mC_{ks}A_{es}G_k$	66	2426
1207322	1778	1793	7166	7181	${}^mC_{ks}T_{ks}T_{ds}G_{ds}{}^mC_{ds}A_{ds}G_{ds}G_{ds}G_{ds}T_{ds}G_d$ ${}^mC_{es}A_{es}{}^mC_{ks}{}^mC_{es}G_k$	59	4962
1207330	1786	1801	7174	7189	$G_{ks}A_{ks}T_{ds}G_{ds}A_{ds}T_{ds}G_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}T_d$ ${}^mC_{es}A_{ks}G_{es}G_k$	53	4963
1207338	1892	1907	7280	7295	${}^mC_{ks}{}^mC_{ks}{}^mC_{ds}T_{ds}G_{ds}A_{ds}G_{ds}{}^mC_{ds}A_{ds}A_d$ ${}^mC_{es}T_{ds}{}^mC_{ks}A_{es}G_{ks}G_{es}A_k$	74	3530
1207346	1900	1915	7288	7303	$A_{ks}G_{ks}A_{ds}T_{ds}G_{ds}A_{ds}G_{ds}T_{ds}{}^mC_{ds}{}^mC_{ds}{}^mC_{ds}$ ${}^mC_{es}T_{ks}G_{es}A_{ks}G_{es}{}^mC_k$	76	2614
1207354	1915	1930	7303	7318	$T_{ks}{}^mC_{ks}A_{ds}{}^mC_{ds}{}^mC_{ds}A_{ds}A_{ds}G_{ds}G_{ds}A_{ds}$ $G_{ds}G_{ks}G_{es}A_{ks}A_{es}A_k$	44	4948
1207362	1923	1938	7311	7326	${}^mC_{ks}T_{ks}G_{ds}{}^mC_{ds}G_{ds}G_{ds}A_{ds}A_{ds}T_{ds}{}^mC_{ds}$ $A_{ds}{}^mC_{ks}{}^mC_{es}A_{ks}A_{es}G_k$	46	3531

1207370	1931	1946	7319	7334	${}^m\text{C}_{ks}\text{T}_{ks}{}^m\text{C}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}\text{A}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}$ ${}_s\text{G}_{ds}{}^m\text{C}_{ks}\text{G}_{es}\text{G}_{ks}\text{A}_{es}\text{A}_{ks}$	41	2461
1207378	2001	2016	7389	7404	$\text{G}_{ks}{}^m\text{C}_{ks}\text{G}_{ds}{}^m\text{C}_{ds}{}^m\text{C}_{ds}\text{A}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}$ ${}_s\text{G}_{ds}\text{G}_{ks}{}^m\text{C}_{es}\text{G}_{ks}{}^m\text{C}_{es}\text{G}_{ks}$	80	4964
1207386	2009	2024	7397	7412	$\text{G}_{ks}\text{A}_{ks}\text{G}_{ds}\text{T}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}$ $\text{G}_{ds}{}^m\text{C}_{ks}{}^m\text{C}_{es}\text{A}_{ks}\text{T}_{es}{}^m\text{C}_{ks}$	71	3837
1207394	2018	2033	7406	7421	${}^m\text{C}_{ks}\text{A}_{ks}{}^m\text{C}_{ds}\text{T}_{ds}\text{T}_{ds}\text{T}_{ds}\text{A}_{ds}\text{T}_{ds}\text{T}_{ds}\text{G}_{ds}\text{A}_{ds}$ $\text{G}_{ks}\text{T}_{es}\text{T}_{ks}{}^m\text{C}_{es}{}^m\text{C}_{ks}$	47	2924
1207402	2033	2048	7421	7436	$\text{T}_{ks}{}^m\text{C}_{ks}\text{A}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}\text{A}_{ds}\text{T}_{ds}\text{T}_{ds}\text{T}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}$ ${}_s\text{A}_{ks}\text{A}_{es}\text{A}_{ks}\text{G}_{es}{}^m\text{C}_{ks}$	32	3534
1207410	148	163	515	530	$\text{G}_{ks}\text{A}_{ks}{}^m\text{C}_{ks}\text{T}_{ds}\text{G}_{ds}\text{T}_{ds}\text{G}_{ds}\text{T}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}$ ${}_s{}^m\text{C}_{ds}\text{T}_{ks}\text{T}_{ks}{}^m\text{C}_{ks}\text{A}_{es}$	64	3343
1207418	156	171	N/A	N/A	$\text{G}_{ks}\text{T}_{ks}\text{G}_{ks}\text{A}_{ds}\text{G}_{ds}\text{A}_{ds}\text{A}_{ds}{}^m\text{C}_{ds}\text{G}_{ds}\text{A}_{ds}{}^m\text{C}_{ds}$ ${}_s\text{T}_{ds}\text{G}_{ks}\text{T}_{ks}\text{G}_{ks}\text{T}_{es}$	88	2424
1207426	213	228	3564	3579	$\text{T}_{ks}\text{T}_{ks}\text{G}_{ks}\text{T}_{ds}\text{G}_{ds}\text{G}_{ds}\text{T}_{ds}\text{A}_{ds}{}^m\text{C}_{ds}\text{A}_{ds}\text{G}_{ds}$ ${}_s{}^m\text{C}_{ds}\text{T}_{ks}\text{G}_{ks}{}^m\text{C}_{ks}{}^m\text{C}_{es}$	54	2811
1207434	221	236	3572	3587	$\text{G}_{ks}\text{G}_{ks}\text{G}_{ks}\text{T}_{ds}\text{A}_{ds}{}^m\text{C}_{ds}\text{A}_{ds}\text{T}_{ds}\text{T}_{ds}\text{T}_{ds}\text{G}_{ds}$ $\text{T}_{ds}\text{G}_{ks}\text{G}_{ks}\text{T}_{ks}\text{A}_{es}$	63	3345
1207442	1781	1796	7169	7184	$\text{T}_{ks}\text{G}_{ks}{}^m\text{C}_{ks}{}^m\text{C}_{ds}\text{T}_{ds}\text{T}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}\text{A}_{ds}\text{G}_{ds}$ $\text{G}_{ds}\text{G}_{ds}\text{T}_{ks}\text{G}_{ks}\text{A}_{ks}\text{G}_{es}$	70	3527
1207450	1789	1804	7177	7192	$\text{G}_{ks}{}^m\text{C}_{ks}\text{T}_{ks}\text{G}_{ds}\text{A}_{ds}\text{T}_{ds}\text{G}_{ds}\text{A}_{ds}\text{T}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}$ ${}_s{}^m\text{C}_{ds}\text{T}_{ks}\text{T}_{ks}\text{G}_{ks}{}^m\text{C}_{es}$	67	3755
1207458	1895	1910	7283	7298	$\text{A}_{ks}\text{G}_{ks}\text{T}_{ks}{}^m\text{C}_{ds}{}^m\text{C}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}\text{G}_{ds}\text{A}_{ds}\text{G}_{ds}{}^m$ $\text{C}_{ds}\text{A}_{ds}\text{A}_{ks}\text{T}_{ks}{}^m\text{C}_{ks}\text{A}_{es}$	51	3758
1207466	1903	1918	7291	7306	$\text{G}_{ks}\text{A}_{ks}\text{A}_{ks}\text{A}_{ds}\text{G}_{ds}\text{A}_{ds}\text{T}_{ds}\text{G}_{ds}\text{A}_{ds}\text{G}_{ds}\text{T}_{ds}{}^m$ $\text{C}_{ds}{}^m\text{C}_{ks}{}^m\text{C}_{ks}\text{T}_{ks}\text{G}_{es}$	36	2845
1207474	1918	1933	7306	7321	$\text{G}_{ks}\text{A}_{ks}\text{A}_{ks}\text{T}_{ds}{}^m\text{C}_{ds}\text{A}_{ds}{}^m\text{C}_{ds}{}^m\text{C}_{ds}\text{A}_{ds}\text{A}_{ds}$ $\text{G}_{ds}\text{G}_{ds}\text{A}_{ks}\text{G}_{ks}\text{G}_{ks}\text{G}_{es}$	36	4965
1207482	1926	1941	7314	7329	$\text{T}_{ks}{}^m\text{C}_{ks}\text{A}_{ks}{}^m\text{C}_{ds}\text{T}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}\text{G}_{ds}\text{G}_{ds}\text{A}_{ds}$ $\text{A}_{ds}\text{T}_{ds}{}^m\text{C}_{ks}\text{A}_{ks}{}^m\text{C}_{ks}{}^m\text{C}_{es}$	50	3759
1207490	1934	1949	7322	7337	${}^m\text{C}_{ks}{}^m\text{C}_{ks}\text{A}_{ks}{}^m\text{C}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}{}^m$ $\text{C}_{ds}\text{A}_{ds}{}^m\text{C}_{ds}\text{T}_{ks}\text{G}_{ks}{}^m\text{C}_{ks}\text{G}_{es}$	38	4949
1207498	2004	2019	7392	7407	${}^m\text{C}_{ks}{}^m\text{C}_{ks}\text{T}_{ks}\text{G}_{ds}{}^m\text{C}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}{}^m\text{C}_{ds}\text{A}_{ds}\text{T}_{ds}$ ${}_s{}^m\text{C}_{ds}{}^m\text{C}_{ds}\text{T}_{ks}\text{G}_{ks}\text{G}_{ks}{}^m\text{C}_{es}$	54	3457
1207506	2012	2027	7400	7415	$\text{A}_{ks}\text{T}_{ks}\text{T}_{ks}\text{G}_{ds}\text{A}_{ds}\text{G}_{ds}\text{T}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}$ $\text{G}_{ds}{}^m\text{C}_{ks}\text{G}_{ks}{}^m\text{C}_{ks}{}^m\text{C}_{es}$	66	2540
1207514	2021	2036	7409	7424	$\text{A}_{ks}\text{A}_{ks}\text{G}_{ks}{}^m\text{C}_{ds}\text{A}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}\text{T}_{ds}\text{T}_{ds}\text{A}_{ds}\text{T}_{ds}$ ${}_s\text{T}_{ds}\text{G}_{ks}\text{A}_{ks}\text{G}_{ks}\text{T}_{es}$	42	3147

Table 79. Reduction of FXII RNA (Huh7, electroporation, 4000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence and Chemistry notation (5' to 3')	FXII (%UTC)	SEQ ID NO
1129531	2009	2024	7397	7412	$\text{G}_{ks}\text{A}_{ks}\text{G}_{ks}\text{T}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}$ $\text{G}_{ds}{}^m\text{C}_{ds}{}^m\text{C}_{ds}\text{A}_{ks}\text{T}_{ks}{}^m\text{C}_{ks}$	21	3837
1206475	142	157	509	524	$\text{G}_{ks}\text{T}_{ks}\text{G}_{ks}{}^m\text{C}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}\text{A}_{ds}\text{G}_{ds}$ ${}_s{}^m\text{C}_{ds}\text{T}_{ds}\text{T}_{ks}\text{T}_{ks}\text{G}_{ks}$	32	4958
1206487	1916	1931	7304	7319	$\text{A}_{ks}\text{T}_{ks}{}^m\text{C}_{ks}\text{A}_{ds}{}^m\text{C}_{ds}{}^m\text{C}_{ds}\text{A}_{ds}\text{A}_{ds}\text{G}_{ds}\text{G}_{ds}$ $\text{A}_{ds}\text{G}_{ds}\text{G}_{ds}\text{G}_{ks}\text{A}_{ks}\text{A}_{ks}$	33	4966

1206492	1935	1950	7323	7338	$G_{ks}^m C_{ks}^m C_{ks}^m A_{ds}^m C_{ds}^m T_{ds}^m C_{ds}^m T_{ds}^m C_{ds}^m T_d$ $s^m C_{ds}^m A_{ds}^m C_{ds}^m T_{ks}^m G_{ks}^m C_k^m$	5	4967
1206500	1783	1798	7171	7186	$G_{ks}^m A_{ks}^m T_{ks}^m G_{ds}^m C_{ds}^m C_{ds}^m T_{ds}^m T_{ds}^m G_{ds}^m C_{ds}^m$ $A_{ds}^m G_{ds}^m G_{ds}^m G_{ks}^m T_{ks}^m G_k^m$	22	4959
1206902	145	160	512	527	$T_{ks}^m G_{es}^m T_{ks}^m G_{ds}^m T_{ds}^m G_{ds}^m C_{ds}^m T_{ds}^m C_{ds}^m T_{ds}^m T_{ds}^m$ $m C_{ds}^m A_{es}^m G_{es}^m C_{ks}^m T_k^m$	33	3112
1206910	153	168	N/A	N/A	$A_{ks}^m G_{es}^m A_{ks}^m A_{ds}^m C_{ds}^m G_{ds}^m A_{ds}^m C_{ds}^m T_{ds}^m G_{ds}^m T$ $ds^m G_{ds}^m T_{es}^m G_{es}^m C_{ks}^m T_k^m$	39	3723
1206918	210	225	3561	3576	$T_{ks}^m G_{es}^m G_{ks}^m T_{ds}^m A_{ds}^m C_{ds}^m A_{ds}^m G_{ds}^m C_{ds}^m T_{ds}^m G_d$ $s^m C_{ds}^m C_{es}^m G_{es}^m G_{ks}^m T_k^m$	45	2657
1206926	218	233	3569	3584	$T_{ks}^m A_{es}^m C_{ks}^m A_{ds}^m T_{ds}^m T_{ds}^m T_{ds}^m G_{ds}^m T_{ds}^m G_{ds}^m G_{ds}^m$ $T_{ds}^m A_{es}^m C_{es}^m A_{ks}^m G_k^m$	17	2426
1206934	1778	1793	7166	7181	$m C_{ks}^m T_{es}^m T_{ks}^m G_{ds}^m C_{ds}^m A_{ds}^m G_{ds}^m G_{ds}^m T_{ds}^m G_d$ $s^m A_{ds}^m G_{es}^m C_{es}^m C_{ks}^m G_k^m$	31	4962
1206942	1786	1801	7174	7189	$G_{ks}^m A_{es}^m T_{ks}^m G_{ds}^m A_{ds}^m T_{ds}^m G_{ds}^m C_{ds}^m C_{ds}^m T_{ds}^m T_d$ $s^m G_{ds}^m C_{es}^m A_{es}^m G_{ks}^m G_k^m$	24	4963
1206950	1892	1907	7280	7295	$m C_{ks}^m C_{es}^m C_{ks}^m T_{ds}^m G_{ds}^m A_{ds}^m G_{ds}^m C_{ds}^m A_{ds}^m A_{ds}^m$ $T_{ds}^m C_{ds}^m A_{es}^m G_{es}^m G_{ks}^m A_k^m$	47	3530
1206958	1900	1915	7288	7303	$A_{ks}^m G_{es}^m A_{ks}^m T_{ds}^m G_{ds}^m A_{ds}^m G_{ds}^m T_{ds}^m C_{ds}^m C_{ds}^m m$ $C_{ds}^m T_{ds}^m G_{es}^m A_{es}^m G_{ks}^m C_k^m$	24	2614
1206966	1915	1930	7303	7318	$T_{ks}^m C_{es}^m A_{ks}^m C_{ds}^m C_{ds}^m A_{ds}^m A_{ds}^m G_{ds}^m G_{ds}^m A_{ds}^m$ $G_{ds}^m G_{ds}^m G_{es}^m A_{es}^m A_{ks}^m A_k^m$	24	4948
1206974	1923	1938	7311	7326	$m C_{ks}^m T_{es}^m G_{ks}^m C_{ds}^m G_{ds}^m G_{ds}^m A_{ds}^m A_{ds}^m T_{ds}^m C_{ds}^m$ $A_{ds}^m C_{ds}^m C_{es}^m A_{es}^m A_{ks}^m G_k^m$	15	3531
1206982	1931	1946	7319	7334	$m C_{ks}^m T_{es}^m C_{ks}^m T_{ds}^m C_{ds}^m T_{ds}^m C_{ds}^m A_{ds}^m C_{ds}^m T_d$ $s^m G_{ds}^m C_{ds}^m G_{es}^m G_{es}^m A_{ks}^m A_k^m$	17	2461
1206990	2001	2016	7389	7404	$G_{ks}^m C_{es}^m G_{ks}^m C_{ds}^m C_{ds}^m A_{ds}^m T_{ds}^m C_{ds}^m C_{ds}^m T$ $ds^m G_{ds}^m G_{ds}^m C_{es}^m G_{es}^m C_{ks}^m G_k^m$	73	4964
1206998	2009	2024	7397	7412	$G_{ks}^m A_{es}^m G_{ks}^m T_{ds}^m T_{ds}^m C_{ds}^m C_{ds}^m T_{ds}^m G_{ds}^m C_{ds}^m$ $G_{ds}^m C_{ds}^m C_{es}^m A_{es}^m T_{ks}^m C_k^m$	21	3837
1207006	2018	2033	7406	7421	$m C_{ks}^m A_{es}^m C_{ks}^m T_{ds}^m T_{ds}^m T_{ds}^m A_{ds}^m T_{ds}^m T_{ds}^m G_{ds}^m A_{ds}^m$ $G_{ds}^m T_{es}^m T_{es}^m C_{ks}^m C_k^m$	20	2924
1207014	2033	2048	7421	7436	$T_{ks}^m C_{es}^m A_{ks}^m G_{ds}^m C_{ds}^m A_{ds}^m T_{ds}^m T_{ds}^m T_{ds}^m T_{ds}^m C$ $ds^m A_{ds}^m A_{es}^m A_{es}^m G_{ks}^m C_k^m$	44	3534
1207033	148	163	515	530	$G_{ks}^m A_{ks}^m C_{ds}^m T_{ds}^m G_{ds}^m T_{ds}^m G_{ds}^m T_{ds}^m G_{ds}^m C_{ds}^m T_d$ $s^m C_{es}^m T_{es}^m T_{es}^m C_{ks}^m A_k^m$	11	3343
1207041	156	171	N/A	N/A	$G_{ks}^m T_{ks}^m G_{ds}^m A_{ds}^m G_{ds}^m A_{ds}^m A_{ds}^m C_{ds}^m G_{ds}^m A_{ds}^m C$ $ds^m T_{es}^m G_{es}^m T_{es}^m G_{ks}^m T_k^m$	48	2424
1207049	213	228	3564	3579	$T_{ks}^m T_{ks}^m G_{ds}^m T_{ds}^m G_{ds}^m G_{ds}^m T_{ds}^m A_{ds}^m C_{ds}^m A_{ds}^m G_{ds}^m$ $m C_{es}^m T_{es}^m G_{es}^m C_{ks}^m C_k^m$	25	2811
1207057	221	236	3572	3587	$G_{ks}^m G_{ks}^m G_{ds}^m T_{ds}^m A_{ds}^m C_{ds}^m A_{ds}^m T_{ds}^m T_{ds}^m T_{ds}^m G_{ds}^m$ $T_{es}^m G_{es}^m G_{es}^m T_{ks}^m A_k^m$	47	3345
1207071	1781	1796	7169	7184	$T_{ks}^m G_{ks}^m C_{ds}^m C_{ds}^m T_{ds}^m T_{ds}^m G_{ds}^m C_{ds}^m A_{ds}^m G_{ds}^m$ $G_{ds}^m G_{es}^m T_{es}^m G_{es}^m A_{ks}^m G_k^m$	35	3527
1207086	1789	1804	7177	7192	$G_{ks}^m C_{ks}^m T_{ds}^m G_{ds}^m A_{ds}^m T_{ds}^m G_{ds}^m A_{ds}^m T_{ds}^m G_{ds}^m C_d$ $s^m C_{es}^m T_{es}^m T_{es}^m G_{ks}^m C_k^m$	24	3755
1207094	1895	1910	7283	7298	$A_{ks}^m G_{ks}^m T_{ds}^m C_{ds}^m C_{ds}^m C_{ds}^m T_{ds}^m G_{ds}^m A_{ds}^m G_{ds}^m m$ $C_{ds}^m A_{es}^m A_{es}^m T_{es}^m C_{ks}^m A_k^m$	36	3758
1207102	1903	1918	7291	7306	$G_{ks}^m A_{ks}^m A_{ds}^m G_{ds}^m A_{ds}^m T_{ds}^m G_{ds}^m A_{ds}^m G_{ds}^m T_{ds}^m m$ $C_{es}^m C_{es}^m C_{es}^m T_{ks}^m G_k^m$	28	2845
1207110	1918	1933	7306	7321	$G_{ks}^m A_{ks}^m A_{ds}^m T_{ds}^m C_{ds}^m A_{ds}^m C_{ds}^m C_{ds}^m A_{ds}^m A_{ds}^m$ $G_{ds}^m G_{es}^m A_{es}^m G_{es}^m G_{ks}^m G_k^m$	24	4965

1207118	1926	1941	7314	7329	$T_{ks} {}^mC_{ks} A_{ds} {}^mC_{ds} T_{ds} G_{ds} {}^mC_{ds} G_{ds} G_{ds} A_{ds}$ $A_{ds} T_{es} {}^mC_{es} A_{es} {}^mC_{ks} {}^mC_k$	12	3759
1207135	1934	1949	7322	7337	${}^mC_{ks} {}^mC_{ks} A_{ds} {}^mC_{ds} T_{ds} {}^mC_{ds} T_{ds} {}^mC_{ds} T_{ds} {}^m$ $C_{ds} A_{ds} {}^mC_{es} T_{es} G_{es} {}^mC_{ks} G_k$	16	4949
1207147	2004	2019	7392	7407	${}^mC_{ks} {}^mC_{ks} T_{ds} G_{ds} {}^mC_{ds} G_{ds} {}^mC_{ds} {}^mC_{ds} A_{ds} T$ $ds {}^mC_{ds} {}^mC_{es} T_{es} G_{es} G_{ks} {}^mC_k$	29	3457
1207155	2012	2027	7400	7415	$A_{ks} T_{ks} T_{ds} G_{ds} A_{ds} G_{ds} T_{ds} T_{ds} {}^mC_{ds} {}^mC_{ds} T_{ds}$ $G_{es} {}^mC_{es} G_{es} {}^mC_{ks} {}^mC_k$	33	2540
1207163	2021	2036	7409	7424	$A_{ks} A_{ks} G_{ds} {}^mC_{ds} A_{ds} {}^mC_{ds} T_{ds} T_{ds} T_{ds} A_{ds} T_d$ $s T_{es} G_{es} A_{es} G_{ks} T_k$	22	3147
1207171	143	158	510	525	$T_{ks} G_{ks} T_{ds} G_{ds} {}^mC_{ds} T_{ds} {}^mC_{ds} T_{ds} T_{ds} {}^mC_{ds} A$ $ds G_{es} {}^mC_{ks} T_{es} T_{ks} T_e$	49	3037
1207179	151	166	N/A	N/A	$A_{ks} A_{ks} {}^mC_{ds} G_{ds} A_{ds} {}^mC_{ds} T_{ds} G_{ds} T_{ds} G_{ds} T_d$ $s G_{es} {}^mC_{ks} T_{es} {}^mC_{ks} T_e$	43	3571
1207187	208	223	3559	3574	$G_{ks} T_{ks} A_{ds} {}^mC_{ds} A_{ds} G_{ds} {}^mC_{ds} T_{ds} G_{ds} {}^mC_{ds} {}^m$ $C_{ds} G_{es} G_{ks} T_{es} G_{ks} G_e$	45	4968
1207195	216	231	3567	3582	${}^mC_{ks} A_{ks} T_{ds} T_{ds} T_{ds} G_{ds} T_{ds} G_{ds} G_{ds} T_{ds} A_{ds}$ ${}^mC_{es} A_{ks} G_{es} {}^mC_{ks} T_e$	26	3039
1207203	1776	1791	7164	7179	$T_{ks} G_{ks} {}^mC_{ds} A_{ds} G_{ds} G_{ds} G_{ds} T_{ds} G_{ds} A_{ds} G_{ds}$ ${}^mC_{es} {}^mC_{ks} G_{es} G_{ks} {}^mC_e$	68	3299
1207211	1784	1799	7172	7187	$T_{ks} G_{ks} A_{ds} T_{ds} G_{ds} {}^mC_{ds} {}^mC_{ds} T_{ds} T_{ds} G_{ds} {}^mC$ $ds A_{es} G_{ks} G_{es} G_{ks} T_e$	46	4969
1207219	1792	1807	7180	7195	${}^mC_{ks} {}^mC_{ks} A_{ds} G_{ds} {}^mC_{ds} T_{ds} G_{ds} A_{ds} T_{ds} G_{ds}$ $A_{ds} T_{es} G_{ks} {}^mC_{es} {}^mC_{ks} T_e$	39	4970
1207227	1898	1913	7286	7301	$A_{ks} T_{ks} G_{ds} A_{ds} G_{ds} T_{ds} {}^mC_{ds} {}^mC_{ds} {}^mC_{ds} T_{ds}$ $G_{ds} A_{es} G_{ks} {}^mC_{es} A_{ks} A_e$	31	2460
1207235	1906	1921	7294	7309	$A_{ks} G_{ks} G_{ds} G_{ds} A_{ds} A_{ds} A_{ds} G_{ds} A_{ds} T_{ds} G_{ds}$ $A_{es} G_{ks} T_{es} {}^mC_{ks} {}^mC_e$	46	3073
1207243	1921	1936	7309	7324	$G_{ks} {}^mC_{ks} G_{ds} G_{ds} A_{ds} A_{ds} T_{ds} {}^mC_{ds} A_{ds} {}^mC_{ds}$ ${}^mC_{ds} A_{es} A_{ks} G_{es} G_{ks} A_e$	26	3379
1207251	1929	1944	7317	7332	${}^mC_{ks} T_{ks} {}^mC_{ds} T_{ds} {}^mC_{ds} A_{ds} {}^mC_{ds} T_{ds} G_{ds} {}^mC_d$ $s G_{ds} G_{es} A_{ks} A_{es} T_{ks} {}^mC_e$	11	4971
1207259	1937	1952	7325	7340	${}^mC_{ks} A_{ks} G_{ds} {}^mC_{ds} {}^mC_{ds} A_{ds} {}^mC_{ds} T_{ds} {}^mC_{ds} T$ $ds {}^mC_{ds} T_{es} {}^mC_{ks} A_{es} {}^mC_{ks} T_e$	20	4972
1207267	2007	2022	7395	7410	$G_{ks} T_{ks} T_{ds} {}^mC_{ds} {}^mC_{ds} T_{ds} G_{ds} {}^mC_{ds} G_{ds} {}^mC_{ds}$ ${}^mC_{ds} A_{es} T_{ks} {}^mC_{es} {}^mC_{ks} T_e$	32	3685
1207275	2016	2031	7404	7419	${}^mC_{ks} T_{ks} T_{ds} T_{ds} A_{ds} T_{ds} T_{ds} G_{ds} A_{ds} G_{ds} T_{ds}$ $T_{es} {}^mC_{ks} {}^mC_{es} T_{ks} G_e$	10	2771
1207283	2024	2039	7412	7427	$T_{ks} {}^mC_{ks} A_{ds} A_{ds} A_{ds} G_{ds} {}^mC_{ds} A_{ds} {}^mC_{ds} T_{ds}$ $T_{ds} T_{es} A_{ks} T_{es} T_{ks} G_e$	24	3382
1207291	146	161	513	528	${}^mC_{ks} T_{ks} G_{ds} T_{ds} G_{ds} T_{ds} G_{ds} {}^mC_{ds} T_{ds} {}^mC_{ds} T$ $ds T_{ks} {}^mC_{es} A_{ks} G_{es} {}^mC_k$	29	3190
1207299	154	169	N/A	N/A	$G_{ks} A_{ks} G_{ds} A_{ds} A_{ds} {}^mC_{ds} G_{ds} A_{ds} {}^mC_{ds} T_{ds} G$ $ds T_{ks} G_{es} T_{ks} G_{es} {}^mC_k$	56	3799
1207307	211	226	3562	3577	$G_{ks} T_{ks} G_{ds} G_{ds} T_{ds} A_{ds} {}^mC_{ds} A_{ds} G_{ds} {}^mC_{ds} T_d$ $s G_{ks} {}^mC_{es} {}^mC_{ks} G_{es} G_k$	36	4973
1207315	219	234	3570	3585	$G_{ks} T_{ks} A_{ds} {}^mC_{ds} A_{ds} T_{ds} T_{ds} T_{ds} G_{ds} T_{ds} G_{ds}$ $G_{ks} T_{es} A_{ks} {}^mC_{es} A_k$	88	3192
1207323	1779	1794	7167	7182	${}^mC_{ks} {}^mC_{ks} T_{ds} T_{ds} G_{ds} {}^mC_{ds} A_{ds} G_{ds} G_{ds} G_{ds}$ $T_{ds} G_{ks} A_{es} G_{ks} {}^mC_{es} {}^mC_k$	41	4974
1207331	1787	1802	7175	7190	$T_{ks} G_{ks} A_{ds} T_{ds} G_{ds} A_{ds} T_{ds} G_{ds} {}^mC_{ds} {}^mC_{ds} T_d$ $s T_{ks} G_{es} {}^mC_{ks} A_{es} G_k$	35	4975

1207339	1893	1908	7281	7296	$T_{ks}^m C_{ks}^m C_{ds}^m T_{ds} G_{ds} A_{ds} G_{ds}^m C_{ds} A_{ds}$ $A_{ds} T_{ks}^m C_{es} A_{ks} G_{es} G_k$	44	3606
1207347	1901	1916	7289	7304	$A_{ks} A_{ks} G_{ds} A_{ds} T_{ds} G_{ds} A_{ds} G_{ds} T_{ds}^m C_{ds}^m C_{ds}^m C_{ks} T_{es} G_{ks} A_{es} G_k$	37	2691
1207355	1916	1931	7304	7319	$A_{ks} T_{ks}^m C_{ds} A_{ds}^m C_{ds}^m C_{ds} A_{ds} A_{ds} G_{ds} G_{ds}$ $A_{ds} G_{ks} G_{es} G_{ks} A_{es} A_k$	41	4966
1207363	1924	1939	7312	7327	$A_{ks}^m C_{ks} T_{ds} G_{ds}^m C_{ds} G_{ds} G_{ds} A_{ds} A_{ds} T_{ds}^m$ $C_{ds} A_{ks}^m C_{es}^m C_{ks} A_{es} A_k$	22	3607
1207371	1932	1947	7320	7335	$A_{ks}^m C_{ks} T_{ds}^m C_{ds} T_{ds}^m C_{ds} T_{ds}^m C_{ds} A_{ds}^m C_d$ $s T_{ds} G_{ks}^m C_{es} G_{ks} G_{es} A_k$	22	4976
1207379	2002	2017	7390	7405	$T_{ks} G_{ks}^m C_{ds} G_{ds}^m C_{ds}^m C_{ds} A_{ds} T_{ds}^m C_{ds}^m C_{ds}^m C_{ds} G_{ks} G_{es}^m C_{ks} G_{es}^m C_k$	96	3305
1207387	2010	2025	7398	7413	$T_{ks} G_{ks} A_{ds} G_{ds} T_{ds} T_{ds}^m C_{ds}^m C_{ds} T_{ds} G_{ds}^m C_{ds}^m C_{ds}^m C_{ks} T_{es}^m C_{ks} A_{es} T_k$	24	3913
1207395	2019	2034	7407	7422	$G_{ks}^m C_{ks} A_{ds}^m C_{ds} T_{ds} T_{ds} T_{ds} A_{ds} T_{ds} T_{ds} G_{ds}$ $A_{ks} G_{es} T_{ks} T_{es}^m C_k$	26	3000
1207403	141	156	508	523	$T_{ks} G_{ks}^m C_{ks} T_{ds}^m C_{ds} T_{ds} T_{ds}^m C_{ds} A_{ds} G_{ds}^m$ $C_{ds} T_{ds} T_{ks} T_{ks} G_{ks} T_e$	38	4950
1207411	149	164	516	531	$^m C_{ks} G_{ks} A_{ks}^m C_{ds} T_{ds} G_{ds} T_{ds} G_{ds} T_{ds} G_{ds}^m$ $C_{ds} T_{ds}^m C_{ks} T_{ks} T_{ks}^m C_e$	24	3419
1207419	157	172	N/A	N/A	$A_{ks} G_{ks} T_{ks} G_{ds} A_{ds} G_{ds} A_{ds} A_{ds}^m C_{ds} G_{ds} A_{ds}$ $^m C_{ds} T_{ks} G_{ks} T_{ks} G_e$	25	2502
1207427	214	229	3565	3580	$T_{ks} T_{ks} T_{ks} G_{ds} T_{ds} G_{ds} G_{ds} T_{ds} A_{ds}^m C_{ds} A_{ds}$ $G_{ds}^m C_{ks} T_{ks} G_{ks}^m C_e$	31	2887
1207435	222	237	3573	3588	$T_{ks} G_{ks} G_{ks} G_{ds} T_{ds} A_{ds}^m C_{ds} A_{ds} T_{ds} T_{ds} T_{ds}$ $G_{ds} T_{ks} G_{ks} G_{ks} T_e$	53	3421
1207443	1782	1797	7170	7185	$A_{ks} T_{ks} G_{ks}^m C_{ds}^m C_{ds} T_{ds} T_{ds} G_{ds}^m C_{ds} A_{ds}$ $G_{ds} G_{ds} G_{ks} T_{ks} G_{ks} A_e$	46	4947
1207451	1790	1805	7178	7193	$A_{ks} G_{ks}^m C_{ks} T_{ds} G_{ds} A_{ds} T_{ds} G_{ds} A_{ds} T_{ds} G_{ds}$ $^m C_{ds}^m C_{ks} T_{ks} T_{ks} G_e$	49	3831
1207459	1896	1911	7284	7299	$G_{ks} A_{ks} G_{ks} T_{ds}^m C_{ds}^m C_{ds}^m C_{ds} T_{ds} G_{ds} A_{ds}$ $G_{ds}^m C_{ds} A_{ks} A_{ks} T_{ks}^m C_e$	33	3834
1207467	1904	1919	7292	7307	$G_{ks} G_{ks} A_{ks} A_{ds} A_{ds} G_{ds} A_{ds} T_{ds} G_{ds} A_{ds} G_{ds}$ $T_{ds}^m C_{ks}^m C_{ks}^m C_{ks} T_e$	38	2921
1207475	1919	1934	7307	7322	$G_{ks} G_{ks} A_{ks} A_{ds} T_{ds}^m C_{ds} A_{ds}^m C_{ds}^m C_{ds} A_{ds}$ $A_{ds} G_{ds} G_{ks} A_{ks} G_{ks} G_e$	16	3226
1207483	1927	1942	7315	7330	$^m C_{ks} T_{ks}^m C_{ks} A_{ds}^m C_{ds} T_{ds} G_{ds}^m C_{ds} G_{ds} G_{ds}$ $A_{ds} A_{ds} T_{ks}^m C_{ks} A_{ks}^m C_e$	22	3835
1207491	1935	1950	7323	7338	$G_{ks}^m C_{ks}^m C_{ks} A_{ds}^m C_{ds} T_{ds}^m C_{ds} T_{ds}^m C_{ds} T_d$ $s^m C_{ds} A_{ds}^m C_{ks} T_{ks} G_{ks}^m C_e$	22	4967
1207499	2005	2020	7393	7408	$T_{ks}^m C_{ks}^m C_{ks} T_{ds} G_{ds}^m C_{ds} G_{ds}^m C_{ds}^m C_{ds} A_{ds}$ $ds T_{ds}^m C_{ds}^m C_{ks} T_{ks} G_{ks} G_e$	21	3533
1207507	2013	2028	7401	7416	$T_{ks} A_{ks} T_{ks} T_{ds} G_{ds} A_{ds} G_{ds} T_{ds} T_{ds}^m C_{ds}^m C_{ds}$ $T_{ds} G_{ks}^m C_{ks} G_{ks}^m C_e$	26	2617
1207515	2022	2037	7410	7425	$A_{ks} A_{ks} A_{ks} G_{ds}^m C_{ds} A_{ds}^m C_{ds} T_{ds} T_{ds} T_{ds} A_d$ $s T_{ds} T_{ks} G_{ks} A_{ks} G_e$	21	3229

Table 80. Reduction of FXII RNA (Huh7, electroporation, 4000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence and Chemistry notation (5' to 3')	FXII (%UTC)	SEQ ID NO
1129531	2009	2024	7397	7412	G _{ks} A _{ks} G _{ks} T _{ds} T _{ds} ^m C _{ds} ^m C _{ds} T _{ds} G _{ds} ^m C _{ds} G _{ds} ^m C _{ds} ^m C _{ds} A _{ks} T _{ks} ^m C _k	19	3837
1206476	144	159	511	526	G _{ks} T _{ks} G _{ks} T _{ds} G _{ds} ^m C _{ds} T _{ds} ^m C _{ds} T _{ds} T _{ds} ^m C _{ds} dsA _{ds} G _{ds} ^m C _{ks} T _{ks} T _k	24	4951
1206481	1784	1799	7172	7187	T _{ks} G _{ks} A _{ks} T _{ds} G _{ds} ^m C _{ds} ^m C _{ds} T _{ds} T _{ds} G _{ds} ^m C _{ds} dsA _{ds} G _{ds} G _{ks} G _{ks} T _k	42	4969
1206505	1917	1932	7305	7320	A _{ks} A _{ks} T _{ks} ^m C _{ds} A _{ds} ^m C _{ds} ^m C _{ds} A _{ds} A _{ds} G _{ds} G _{ds} A _{ds} G _{ds} G _{ks} G _{ks} A _k	27	4956
1206508	1936	1951	7324	7339	A _{ks} G _{ks} ^m C _{ks} ^m C _{ds} A _{ds} ^m C _{ds} T _{ds} ^m C _{ds} T _{ds} ^m C _{ds} dsT _{ds} ^m C _{ds} A _{ds} ^m C _{ks} T _{ks} G _k	9	4961
1206903	146	161	513	528	^m C _{ks} T _{es} G _{ks} T _{ds} G _{ds} T _{ds} G _{ds} ^m C _{ds} T _{ds} ^m C _{ds} T _{ds} dsT _{ds} ^m C _{es} A _{es} G _{ks} ^m C _k	14	3190
1206911	154	169	N/A	N/A	G _{ks} A _{es} G _{ks} A _{ds} A _{ds} ^m C _{ds} G _{ds} A _{ds} ^m C _{ds} T _{ds} G _{ds} dsT _{ds} G _{es} T _{es} G _{ks} ^m C _k	29	3799
1206919	211	226	3562	3577	G _{ks} T _{es} G _{ks} G _{ds} T _{ds} A _{ds} ^m C _{ds} A _{ds} G _{ds} ^m C _{ds} T _{ds} sG _{ds} ^m C _{es} ^m C _{es} G _{ks} G _k	24	4973
1206927	219	234	3570	3585	G _{ks} T _{es} A _{ks} ^m C _{ds} A _{ds} T _{ds} T _{ds} T _{ds} G _{ds} T _{ds} G _{ds} G _{ds} T _{es} A _{es} ^m C _{ks} A _k	27	3192
1206935	1779	1794	7167	7182	^m C _{ks} ^m C _{es} T _{ks} T _{ds} G _{ds} ^m C _{ds} A _{ds} G _{ds} G _{ds} G _{ds} T _{ds} G _{ds} A _{es} G _{es} ^m C _{ks} ^m C _k	51	4974
1206943	1787	1802	7175	7190	T _{ks} G _{es} A _{ks} T _{ds} G _{ds} A _{ds} T _{ds} G _{ds} ^m C _{ds} ^m C _{ds} T _{ds} sT _{ds} G _{es} ^m C _{es} A _{ks} G _k	36	4975
1206951	1893	1908	7281	7296	T _{ks} ^m C _{es} ^m C _{ks} ^m C _{ds} T _{ds} G _{ds} A _{ds} G _{ds} ^m C _{ds} A _{ds} A _{ds} T _{ds} ^m C _{es} A _{es} G _{ks} G _k	46	3606
1206959	1901	1916	7289	7304	A _{ks} A _{es} G _{ks} A _{ds} T _{ds} G _{ds} A _{ds} G _{ds} T _{ds} ^m C _{ds} ^m C _{ds} ds ^m C _{ds} T _{es} G _{es} A _{ks} G _k	34	2691
1206967	1916	1931	7304	7319	A _{ks} T _{es} ^m C _{ks} A _{ds} ^m C _{ds} ^m C _{ds} A _{ds} A _{ds} G _{ds} G _{ds} A _{ds} G _{ds} G _{es} G _{es} A _{ks} A _k	14	4966
1206975	1924	1939	7312	7327	A _{ks} ^m C _{es} T _{ks} G _{ds} ^m C _{ds} G _{ds} G _{ds} A _{ds} A _{ds} T _{ds} ^m C _{ds} A _{ds} ^m C _{es} ^m C _{es} A _{ks} A _k	13	3607
1206983	1932	1947	7320	7335	A _{ks} ^m C _{es} T _{ks} ^m C _{ds} T _{ds} ^m C _{ds} T _{ds} ^m C _{ds} A _{ds} ^m C _d sT _{ds} G _{ds} ^m C _{es} G _{es} G _{ks} A _k	9	4976
1206991	2002	2017	7390	7405	T _{ks} G _{es} ^m C _{ks} G _{ds} ^m C _{ds} ^m C _{ds} A _{ds} T _{ds} ^m C _{ds} ^m C _{ds} dsT _{ds} G _{ds} G _{es} ^m C _{es} G _{ks} ^m C _k	64	3305
1206999	2010	2025	7398	7413	T _{ks} G _{es} A _{ks} G _{ds} T _{ds} T _{ds} ^m C _{ds} ^m C _{ds} T _{ds} G _{ds} ^m C _{ds} dsG _{ds} ^m C _{es} ^m C _{es} A _{ks} T _k	12	3913
1207007	2019	2034	7407	7422	G _{ks} ^m C _{es} A _{ks} ^m C _{ds} T _{ds} T _{ds} T _{ds} A _{ds} T _{ds} T _{ds} G _{ds} A _{ds} G _{es} T _{es} T _{ks} ^m C _k	7	3000
1207026	141	156	508	523	T _{ks} G _{ks} ^m C _{ds} T _{ds} ^m C _{ds} T _{ds} T _{ds} ^m C _{ds} A _{ds} G _{ds} ^m C _{ds} T _{es} T _{es} T _{es} G _{ks} T _k	49	4950
1207034	149	164	516	531	^m C _{ks} G _{ks} A _{ds} ^m C _{ds} T _{ds} G _{ds} T _{ds} G _{ds} T _{ds} G _{ds} ^m C _{ds} T _{es} ^m C _{es} T _{es} T _{ks} ^m C _k	36	3419
1207042	157	172	N/A	N/A	A _{ks} G _{ks} T _{ds} G _{ds} A _{ds} G _{ds} A _{ds} A _{ds} ^m C _{ds} G _{ds} A _{ds} ^m C _{es} T _{es} G _{es} T _{ks} G _k	42	2502

1207050	214	229	3565	3580	$T_{ks}T_{ks}T_{ds}G_{ds}T_{ds}G_{ds}G_{ds}T_{ds}A_{ds}{}^mC_{ds}A_{ds}$ $G_{es}{}^mC_{es}T_{es}G_{ks}{}^mC_k$	43	2887
1207058	222	237	3573	3588	$T_{ks}G_{ks}G_{ds}G_{ds}T_{ds}A_{ds}{}^mC_{ds}A_{ds}T_{ds}T_{ds}T_{ds}$ $G_{es}T_{es}G_{es}G_{ks}T_k$	25	3421
1207078	1782	1797	7170	7185	$A_{ks}T_{ks}G_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}T_{ds}G_{ds}{}^mC_{ds}A_{ds}$ $G_{ds}G_{es}G_{es}T_{es}G_{ks}A_k$	52	4947
1207087	1790	1805	7178	7193	$A_{ks}G_{ks}{}^mC_{ds}T_{ds}G_{ds}A_{ds}T_{ds}G_{ds}A_{ds}T_{ds}G_{ds}$ ${}^mC_{es}{}^mC_{es}T_{es}T_{ks}G_k$	42	3831
1207095	1896	1911	7284	7299	$G_{ks}A_{ks}G_{ds}T_{ds}{}^mC_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}G_{ds}A_{ds}$ $G_{ds}{}^mC_{es}A_{es}A_{es}T_{ks}{}^mC_k$	25	3834
1207103	1904	1919	7292	7307	$G_{ks}G_{ks}A_{ds}A_{ds}A_{ds}G_{ds}A_{ds}T_{ds}G_{ds}A_{ds}G_{ds}$ $T_{es}{}^mC_{es}{}^mC_{es}{}^mC_{ks}T_k$	31	2921
1207111	1919	1934	7307	7322	$G_{ks}G_{ks}A_{ds}A_{ds}T_{ds}{}^mC_{ds}A_{ds}{}^mC_{ds}{}^mC_{ds}A_{ds}$ $A_{ds}G_{es}G_{es}A_{es}G_{ks}G_k$	9	3226
1207120	1927	1942	7315	7330	${}^mC_{ks}T_{ks}{}^mC_{ds}A_{ds}{}^mC_{ds}T_{ds}G_{ds}{}^mC_{ds}G_{ds}G_{ds}$ $A_{ds}A_{es}T_{es}{}^mC_{es}A_{ks}{}^mC_k$	10	3835
1207137	1935	1950	7323	7338	$G_{ks}{}^mC_{ks}{}^mC_{ds}A_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}T_d$ ${}^mC_{ds}A_{es}{}^mC_{es}T_{es}G_{ks}{}^mC_k$	19	4967
1207148	2005	2020	7393	7408	$T_{ks}{}^mC_{ks}{}^mC_{ds}T_{ds}G_{ds}{}^mC_{ds}G_{ds}{}^mC_{ds}{}^mC_{ds}A$ $_{ds}T_{ds}{}^mC_{es}{}^mC_{es}T_{es}G_{ks}G_k$	13	3533
1207156	2013	2028	7401	7416	$T_{ks}A_{ks}T_{ds}T_{ds}G_{ds}A_{ds}G_{ds}T_{ds}T_{ds}{}^mC_{ds}{}^mC_{ds}$ $T_{es}G_{es}{}^mC_{es}G_{ks}{}^mC_k$	9	2617
1207164	2022	2037	7410	7425	$A_{ks}A_{ks}A_{ds}G_{ds}{}^mC_{ds}A_{ds}{}^mC_{ds}T_{ds}T_{ds}T_{ds}A_d$ $_{s}T_{es}T_{es}G_{es}A_{ks}G_k$	5	3229
1207172	144	159	511	526	$G_{ks}T_{ks}G_{ds}T_{ds}G_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}T_{ds}T_{ds}{}^mC$ $_{ds}A_{es}G_{ks}{}^mC_{es}T_{ks}T_e$	14	4951
1207180	152	167	N/A	N/A	$G_{ks}A_{ks}A_{ds}{}^mC_{ds}G_{ds}A_{ds}{}^mC_{ds}T_{ds}G_{ds}T_{ds}G$ $_{ds}T_{es}G_{ks}{}^mC_{es}T_{ks}{}^mC_e$	32	3647
1207188	209	224	3560	3575	$G_{ks}G_{ks}T_{ds}A_{ds}{}^mC_{ds}A_{ds}G_{ds}{}^mC_{ds}T_{ds}G_{ds}{}^m$ $C_{ds}{}^mC_{es}G_{ks}G_{es}T_{ks}G_e$	23	4952
1207196	217	232	3568	3583	$A_{ks}{}^mC_{ks}A_{ds}T_{ds}T_{ds}G_{ds}T_{ds}G_{ds}G_{ds}T_{ds}$ $A_{es}{}^mC_{ks}A_{es}G_{ks}{}^mC_e$	13	3114
1207204	1777	1792	7165	7180	$T_{ks}T_{ks}G_{ds}{}^mC_{ds}A_{ds}G_{ds}G_{ds}G_{ds}T_{ds}G_{ds}A_{ds}$ $G_{es}{}^mC_{ks}{}^mC_{es}G_{ks}G_e$	50	3375
1207212	1785	1800	7173	7188	$A_{ks}T_{ks}G_{ds}A_{ds}T_{ds}G_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}T_{ds}G_d$ ${}^mC_{es}A_{ks}G_{es}G_{ks}G_e$	25	3603
1207220	1793	1808	7181	7196	${}^mC_{ks}{}^mC_{ks}{}^mC_{ds}A_{ds}G_{ds}{}^mC_{ds}T_{ds}G_{ds}A_{ds}T_{ds}$ $G_{ds}A_{es}T_{ks}G_{es}{}^mC_{ks}{}^mC_e$	26	4953
1207228	1899	1914	7287	7302	$G_{ks}A_{ks}T_{ds}G_{ds}A_{ds}G_{ds}T_{ds}{}^mC_{ds}{}^mC_{ds}{}^mC_{ds}$ $T_{ds}G_{es}A_{ks}G_{es}{}^mC_{ks}A_e$	6	2537
1207236	1914	1929	7302	7317	${}^mC_{ks}A_{ks}{}^mC_{ds}{}^mC_{ds}A_{ds}A_{ds}G_{ds}G_{ds}A_{ds}G_{ds}$ $G_{ds}G_{es}A_{ks}A_{es}A_{ks}G_e$	12	4954
1207244	1922	1937	7310	7325	$T_{ks}G_{ks}{}^mC_{ds}G_{ds}G_{ds}A_{ds}A_{ds}T_{ds}{}^mC_{ds}A_{ds}{}^m$ $C_{ds}{}^mC_{es}A_{ks}A_{es}G_{ks}G_e$	17	3455
1207252	1930	1945	7318	7333	$T_{ks}{}^mC_{ks}T_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}A_{ds}{}^mC_{ds}T_{ds}G_{ds}$ ${}^mC_{ds}G_{es}G_{ks}A_{es}A_{ks}T_e$	16	4955
1207260	2000	2015	7388	7403	${}^mC_{ks}G_{ks}{}^mC_{ds}{}^mC_{ds}A_{ds}T_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}G$ $_{ds}G_{ds}{}^mC_{es}G_{ks}{}^mC_{es}G_{ks}G_e$	77	3228
1207268	2008	2023	7396	7411	$A_{ks}G_{ks}T_{ds}T_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}G_{ds}{}^mC_{ds}G_{ds}{}^m$ $C_{ds}{}^mC_{es}A_{ks}T_{es}{}^mC_{ks}{}^mC_e$	18	3761
1207276	2017	2032	7405	7420	$A_{ks}{}^mC_{ks}T_{ds}T_{ds}T_{ds}A_{ds}T_{ds}T_{ds}G_{ds}A_{ds}G_{ds}$ $T_{es}T_{ks}{}^mC_{es}{}^mC_{ks}T_e$	8	2848

1207284	2031	2046	7419	7434	$A_{ks}G_{ks}{}^mC_{ds}A_{ds}T_{ds}T_{ds}T_{ds}T_{ds}{}^mC_{ds}A_{ds}A_{ds}$ $sA_{es}G_{ks}{}^mC_{es}A_{ks}{}^mC_e$	20	3458
1207292	147	162	514	529	$A_{ks}{}^mC_{ks}T_{ds}G_{ds}T_{ds}G_{ds}T_{ds}G_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}$ $T_{ks}T_{es}{}^mC_{ks}A_{es}G_{ks}$	36	3267
1207300	155	170	N/A	N/A	$T_{ks}G_{ks}A_{ds}G_{ds}A_{ds}A_{ds}{}^mC_{ds}G_{ds}A_{ds}{}^mC_{ds}T_{ds}$ $dsG_{ks}T_{es}G_{ks}T_{es}G_{ks}$	25	3875
1207308	212	227	3563	3578	$T_{ks}G_{ks}T_{ds}G_{ds}G_{ds}T_{ds}A_{ds}{}^mC_{ds}A_{ds}G_{ds}{}^mC_{ds}$ $sT_{ks}G_{es}{}^mC_{ks}{}^mC_{es}G_{ks}$	18	2734
1207316	220	235	3571	3586	$G_{ks}G_{ks}T_{ds}A_{ds}{}^mC_{ds}A_{ds}T_{ds}T_{ds}T_{ds}G_{ds}T_{ds}$ $G_{ks}G_{es}T_{ks}A_{es}{}^mC_{ks}$	49	3269
1207324	1780	1795	7168	7183	$G_{ks}{}^mC_{ks}{}^mC_{ds}T_{ds}T_{ds}G_{ds}{}^mC_{ds}A_{ds}G_{ds}G_{ds}$ $G_{ds}T_{ks}G_{es}A_{ks}G_{es}{}^mC_{ks}$	47	3451
1207332	1788	1803	7176	7191	${}^mC_{ks}T_{ks}G_{ds}A_{ds}T_{ds}G_{ds}A_{ds}T_{ds}G_{ds}{}^mC_{ds}{}^mC_{ds}$ $C_{ds}T_{ks}T_{es}G_{ks}{}^mC_{es}A_{ks}$	29	3679
1207340	1894	1909	7282	7297	$G_{ks}T_{ks}{}^mC_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}G_{ds}A_{ds}G_{ds}{}^mC_{ds}$ $A_{ds}A_{ks}T_{es}{}^mC_{ks}A_{es}G_{ks}$	57	3682
1207348	1902	1917	7290	7305	$A_{ks}A_{ks}A_{ds}G_{ds}A_{ds}T_{ds}G_{ds}A_{ds}G_{ds}T_{ds}{}^mC_{ds}$ ${}^mC_{ks}{}^mC_{es}T_{ks}G_{es}A_{ks}$	32	2768
1207356	1917	1932	7305	7320	$A_{ks}A_{ks}T_{ds}{}^mC_{ds}A_{ds}{}^mC_{ds}{}^mC_{ds}A_{ds}A_{ds}G_{ds}$ $G_{ds}A_{ks}G_{es}G_{ks}G_{es}A_{ks}$	57	4956
1207364	1925	1940	7313	7328	${}^mC_{ks}A_{ks}{}^mC_{ds}T_{ds}G_{ds}{}^mC_{ds}G_{ds}G_{ds}A_{ds}A_{ds}$ $T_{ds}{}^mC_{ks}A_{es}{}^mC_{ks}{}^mC_{es}A_{ks}$	14	3683
1207372	1933	1948	7321	7336	${}^mC_{ks}A_{ks}{}^mC_{ds}T_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}A_{ds}$ $s{}^mC_{ds}T_{ks}G_{es}{}^mC_{ks}G_{es}G_{ks}$	20	4957
1207380	2003	2018	7391	7406	${}^mC_{ks}T_{ks}G_{ds}{}^mC_{ds}G_{ds}{}^mC_{ds}{}^mC_{ds}A_{ds}T_{ds}{}^mC_{ds}$ $ds{}^mC_{ds}T_{ks}G_{es}G_{ks}{}^mC_{es}G_{ks}$	50	3381
1207388	2011	2026	7399	7414	$T_{ks}T_{ks}G_{ds}A_{ds}G_{ds}T_{ds}T_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}G_{ds}$ ${}^mC_{ks}G_{es}{}^mC_{ks}{}^mC_{es}A_{ks}$	27	2463
1207396	2020	2035	7408	7423	$A_{ks}G_{ks}{}^mC_{ds}A_{ds}{}^mC_{ds}T_{ds}T_{ds}T_{ds}A_{ds}T_{ds}T_{ds}$ $G_{ks}A_{es}G_{ks}T_{es}T_{ks}$	17	3076
1207404	142	157	509	524	$G_{ks}T_{ks}G_{ks}{}^mC_{ds}T_{ds}{}^mC_{ds}T_{ds}T_{ds}{}^mC_{ds}A_{ds}G_{ds}$ $ds{}^mC_{ds}T_{ks}T_{ks}T_{ks}G_{es}$	33	4958
1207412	150	165	N/A	N/A	$A_{ks}{}^mC_{ks}G_{ks}A_{ds}{}^mC_{ds}T_{ds}G_{ds}T_{ds}G_{ds}T_{ds}G_{ds}$ $s{}^mC_{ds}T_{ks}{}^mC_{ks}T_{ks}T_{es}$	24	3495
1207420	158	173	N/A	N/A	${}^mC_{ks}A_{ks}G_{ks}T_{ds}G_{ds}A_{ds}G_{ds}A_{ds}A_{ds}{}^mC_{ds}G_{ds}$ $dsA_{ds}{}^mC_{ks}T_{ks}G_{ks}T_{es}$	20	2579
1207428	215	230	3566	3581	$A_{ks}T_{ks}T_{ks}T_{ds}G_{ds}T_{ds}G_{ds}G_{ds}T_{ds}A_{ds}{}^mC_{ds}$ $A_{ds}G_{ks}{}^mC_{ks}T_{ks}G_{es}$	27	2963
1207436	223	238	3574	3589	$G_{ks}T_{ks}G_{ks}G_{ds}G_{ds}T_{ds}A_{ds}{}^mC_{ds}A_{ds}T_{ds}T_{ds}$ $T_{ds}G_{ks}T_{ks}G_{ks}G_{es}$	25	3497
1207444	1783	1798	7171	7186	$G_{ks}A_{ks}T_{ks}G_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}T_{ds}G_{ds}{}^mC_{ds}$ $A_{ds}G_{ds}G_{ks}G_{ks}T_{ks}G_{es}$	43	4959
1207452	1791	1806	7179	7194	${}^mC_{ks}A_{ks}G_{ks}{}^mC_{ds}T_{ds}G_{ds}A_{ds}T_{ds}G_{ds}A_{ds}T_{ds}$ $sG_{ds}{}^mC_{ks}{}^mC_{ks}T_{ks}T_{es}$	24	4960
1207460	1897	1912	7285	7300	$T_{ks}G_{ks}A_{ks}G_{ds}T_{ds}{}^mC_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}G_{ds}$ $A_{ds}G_{ds}{}^mC_{ks}A_{ks}A_{ks}T_{es}$	36	3910
1207468	1905	1920	7293	7308	$G_{ks}G_{ks}G_{ks}A_{ds}A_{ds}G_{ds}A_{ds}T_{ds}G_{ds}A_{ds}$ $G_{ds}T_{ks}{}^mC_{ks}{}^mC_{ks}{}^mC_{es}$	54	2997
1207476	1920	1935	7308	7323	${}^mC_{ks}G_{ks}G_{ks}A_{ds}A_{ds}T_{ds}{}^mC_{ds}A_{ds}{}^mC_{ds}{}^mC_{ds}$ $sA_{ds}A_{ds}G_{ks}G_{ks}A_{ks}G_{es}$	22	3303
1207484	1928	1943	7316	7331	$T_{ks}{}^mC_{ks}T_{ks}{}^mC_{ds}A_{ds}{}^mC_{ds}T_{ds}G_{ds}{}^mC_{ds}G_{ds}$ $G_{ds}A_{ds}A_{ks}T_{ks}{}^mC_{ks}A_{es}$	9	3911

1207492	1936	1951	7324	7339	$A_{ks}G_{ks}{}^mC_{ks}{}^mC_{ds}A_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}$	40	4961
1207500	2006	2021	7394	7409	$T_{ks}T_{ks}{}^mC_{ks}{}^mC_{ds}T_{ds}G_{ds}{}^mC_{ds}G_{ds}{}^mC_{ds}{}^mC_d$	33	3609
1207508	2014	2029	7402	7417	$sA_{ds}T_{ds}{}^mC_{ks}{}^mC_{ks}T_{ks}G_e$	17	2694
1207516	2023	2038	7411	7426	$T_{ks}T_{ks}A_{ks}T_{ds}T_{ds}G_{ds}A_{ds}G_{ds}T_{ds}T_{ds}{}^mC_{ds}{}^mC_{ds}T_{ks}G_{ks}{}^mC_{ks}G_e$	5	3306

Table 81. Reduction of FXII RNA (Huh7, electroporation, 4000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence and Chemistry notation (5' to 3')	FXII (%UTC)	SEQ ID NO
1129531	2009	2024	7397	7412	$G_{ks}A_{ks}G_{ks}T_{ds}T_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}G_{ds}{}^mC_{ds}G_d$ ${}_s{}^mC_{ds}{}^mC_{ds}A_{ks}T_{ks}{}^mC_k$	13	3837
1206496	208	223	3559	3574	$G_{ks}T_{ks}A_{ks}{}^mC_{ds}A_{ds}G_{ds}{}^mC_{ds}T_{ds}G_{ds}{}^mC_{ds}{}^m$ $C_{ds}G_{ds}G_{ds}T_{ks}G_{ks}G_k$	27	4968
1206501	1786	1801	7174	7189	$G_{ks}A_{ks}T_{ks}G_{ds}A_{ds}T_{ds}G_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}T_{ds}$ $G_{ds}{}^mC_{ds}A_{ks}G_{ks}G_k$	48	4963
1206506	1918	1933	7306	7321	$G_{ks}A_{ks}A_{ks}T_{ds}{}^mC_{ds}A_{ds}{}^mC_{ds}{}^mC_{ds}A_{ds}A_{ds}G$ $_{ds}G_{ds}A_{ds}G_{ks}G_{ks}G_k$	10	4965
1206509	1937	1952	7325	7340	${}^mC_{ks}A_{ks}G_{ks}{}^mC_{ds}{}^mC_{ds}A_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}T_{ds}$ ${}^mC_{ds}T_{ds}{}^mC_{ds}A_{ks}{}^mC_{ks}T_k$	6	4972
1206904	147	162	514	529	$A_{ks}{}^mC_{es}T_{ks}G_{ds}T_{ds}G_{ds}T_{ds}G_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}$ $T_{ds}T_{es}{}^mC_{es}A_{ks}G_k$	23	3267
1206912	155	170	N/A	N/A	$T_{ks}G_{es}A_{ks}G_{ds}A_{ds}A_{ds}{}^mC_{ds}G_{ds}A_{ds}{}^mC_{ds}T_{ds}$ $G_{ds}T_{es}G_{es}T_{ks}G_k$	23	3875
1206920	212	227	3563	3578	$T_{ks}G_{es}T_{ks}G_{ds}G_{ds}T_{ds}A_{ds}{}^mC_{ds}A_{ds}G_{ds}{}^mC_{ds}$ $T_{ds}G_{es}{}^mC_{es}{}^mC_{ks}G_k$	13	2734
1206928	220	235	3571	3586	$G_{ks}G_{es}T_{ks}A_{ds}{}^mC_{ds}A_{ds}T_{ds}T_{ds}T_{ds}G_{ds}T_{ds}G$ $_{ds}G_{es}T_{es}A_{ks}{}^mC_k$	45	3269
1206936	1780	1795	7168	7183	$G_{ks}{}^mC_{es}{}^mC_{ks}T_{ds}T_{ds}G_{ds}{}^mC_{ds}A_{ds}G_{ds}G_{ds}G_d$ ${}_sT_{ds}G_{es}A_{es}G_{ks}{}^mC_k$	48	3451
1206944	1788	1803	7176	7191	${}^mC_{ks}T_{es}G_{ks}A_{ds}T_{ds}G_{ds}A_{ds}T_{ds}G_{ds}{}^mC_{ds}{}^mC_d$ ${}_sT_{ds}T_{es}G_{es}{}^mC_{ks}A_k$	46	3679
1206952	1894	1909	7282	7297	$G_{ks}T_{es}{}^mC_{ks}{}^mC_{ds}{}^mC_{ds}T_{ds}G_{ds}A_{ds}G_{ds}{}^mC_{ds}$ $A_{ds}A_{ds}T_{es}{}^mC_{es}A_{ks}G_k$	19	3682
1206960	1902	1917	7290	7305	$A_{ks}A_{es}A_{ks}G_{ds}A_{ds}T_{ds}G_{ds}A_{ds}G_{ds}T_{ds}{}^mC_{ds}{}^m$ $C_{ds}{}^mC_{es}T_{es}G_{ks}A_k$	17	2768
1206968	1917	1932	7305	7320	$A_{ks}A_{es}T_{ks}{}^mC_{ds}A_{ds}{}^mC_{ds}{}^mC_{ds}A_{ds}A_{ds}G_{ds}G$ $_{ds}A_{ds}G_{es}G_{es}G_{ks}A_k$	41	4956
1206976	1925	1940	7313	7328	${}^mC_{ks}A_{es}{}^mC_{ks}T_{ds}G_{ds}{}^mC_{ds}G_{ds}G_{ds}A_{ds}A_{ds}T_d$ ${}_s{}^mC_{ds}A_{es}{}^mC_{es}{}^mC_{ks}A_k$	29	3683
1206984	1933	1948	7321	7336	${}^mC_{ks}A_{es}{}^mC_{ks}T_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}A_{ds}$ ${}^mC_{ds}T_{ds}G_{es}{}^mC_{es}G_{ks}G_k$	N.D	4957
1206992	2003	2018	7391	7406	${}^mC_{ks}T_{es}G_{ks}{}^mC_{ds}G_{ds}{}^mC_{ds}{}^mC_{ds}A_{ds}T_{ds}{}^mC_{ds}$ ${}^mC_{ds}T_{ds}G_{es}G_{es}{}^mC_{ks}G_k$	77	3381
1207000	2011	2026	7399	7414	$T_{ks}T_{es}G_{ks}A_{ds}G_{ds}T_{ds}T_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}G_{ds}{}^m$ $C_{ds}G_{es}{}^mC_{es}{}^mC_{ks}A_k$	11	2463
1207008	2020	2035	7408	7423	$A_{ks}G_{es}{}^mC_{ks}A_{ds}{}^mC_{ds}T_{ds}T_{ds}T_{ds}A_{ds}T_{ds}T_{ds}$ $G_{ds}A_{es}G_{es}T_{ks}T_k$	5	3076
1207027	142	157	509	524	$G_{ks}T_{ks}G_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}T_{ds}T_{ds}{}^mC_{ds}A_{ds}G_d$ ${}^mC_{es}T_{es}T_{es}T_{ks}G_k$	40	4958

1207035	150	165	N/A	N/A	$A_{ks}^m C_{ks} G_{ds} A_{ds}^m C_{ds} T_{ds} G_{ds} T_{ds} G_{ds} T_{ds} G_{ds}$ $^m C_{es} T_{es} ^m C_{es} T_{ks} T_k$	35	3495
1207043	158	173	N/A	N/A	$^m C_{ks} A_{ks} G_{ds} T_{ds} G_{ds} A_{ds} G_{ds} A_{ds} A_{ds} ^m C_{ds} G_{ds}$ $A_{es} ^m C_{es} T_{es} G_{ks} T_k$	36	2579
1207051	215	230	3566	3581	$A_{ks} T_{ks} T_{ds} T_{ds} G_{ds} T_{ds} G_{ds} T_{ds} A_{ds} ^m C_{ds} A_{es} G_{es} ^m C_{es} T_{ks} G_k$	43	2963
1207059	223	238	3574	3589	$G_{ks} T_{ks} G_{ds} G_{ds} G_{ds} T_{ds} A_{ds} ^m C_{ds} A_{ds} T_{ds} T_{es} G_{es} T_{es} G_{ks} G_k$	25	3497
1207079	1783	1798	7171	7186	$G_{ks} A_{ks} T_{ds} G_{ds} ^m C_{ds} ^m C_{ds} T_{ds} T_{ds} G_{ds} ^m C_{ds} A_{ds}$ $^s G_{es} G_{es} G_{es} T_{ks} G_k$	37	4959
1207088	1791	1806	7179	7194	$^m C_{ks} A_{ks} G_{ds} ^m C_{ds} T_{ds} G_{ds} A_{ds} T_{ds} G_{ds} A_{ds} T_{ds}$ $G_{es} ^m C_{es} ^m C_{es} T_{ks} T_k$	40	4960
1207096	1897	1912	7285	7300	$T_{ks} G_{ks} A_{ds} G_{ds} T_{ds} ^m C_{ds} ^m C_{ds} ^m C_{ds} T_{ds} G_{ds} A_{ds}$ $^s G_{es} ^m C_{es} A_{es} A_{ks} T_k$	27	3910
1207104	1905	1920	7293	7308	$G_{ks} G_{ks} G_{ds} A_{ds} A_{ds} A_{ds} G_{ds} A_{ds} T_{ds} G_{ds} A_{ds} G_{es} T_{es} ^m C_{es} ^m C_{ks} ^m C_k$	31	2997
1207112	1920	1935	7308	7323	$^m C_{ks} G_{ks} G_{ds} A_{ds} A_{ds} T_{ds} ^m C_{ds} A_{ds} ^m C_{ds} ^m C_{ds}$ $A_{ds} A_{es} G_{es} G_{es} A_{ks} G_k$	19	3303
1207123	1928	1943	7316	7331	$T_{ks} ^m C_{ks} T_{ds} ^m C_{ds} A_{ds} ^m C_{ds} T_{ds} G_{ds} ^m C_{ds} G_{ds}$ $G_{ds} A_{es} A_{es} T_{es} ^m C_{ks} A_k$	7	3911
1207139	1936	1951	7324	7339	$A_{ks} G_{ks} ^m C_{ds} ^m C_{ds} A_{ds} ^m C_{ds} T_{ds} ^m C_{ds} T_{ds} ^m C_{ds}$ $T_{ds} ^m C_{es} A_{es} ^m C_{es} T_{ks} G_k$	7	4961
1207149	2006	2021	7394	7409	$T_{ks} T_{ks} ^m C_{ds} ^m C_{ds} T_{ds} G_{ds} ^m C_{ds} G_{ds} ^m C_{ds} ^m C_{ds}$ $A_{ds} T_{es} ^m C_{es} ^m C_{es} T_{ks} G_k$	13	3609
1207157	2014	2029	7402	7417	$T_{ks} T_{ks} A_{ds} T_{ds} T_{ds} G_{ds} A_{ds} G_{ds} T_{ds} T_{ds} ^m C_{ds} ^m$ $C_{es} T_{es} G_{es} ^m C_{ks} G_k$	15	2694
1207165	2023	2038	7411	7426	$^m C_{ks} A_{ks} A_{ds} G_{ds} ^m C_{ds} A_{ds} ^m C_{ds} T_{ds} T_{ds} T_d$ $^s A_{es} T_{es} T_{es} G_{ks} A_k$	18	3306
1207173	145	160	512	527	$T_{ks} G_{ks} T_{ds} G_{ds} T_{ds} G_{ds} ^m C_{ds} T_{ds} ^m C_{ds} T_{ds} T_{ds} ^m$ $C_{es} A_{ks} G_{es} ^m C_{ks} T_e$	12	3112
1207181	153	168	N/A	N/A	$A_{ks} G_{ks} A_{ds} A_{ds} ^m C_{ds} G_{ds} A_{ds} ^m C_{ds} T_{ds} G_{ds} T_{ds}$ $G_{es} T_{ks} G_{es} ^m C_{ks} T_e$	53	3723
1207189	210	225	3561	3576	$T_{ks} G_{ks} G_{ds} T_{ds} A_{ds} ^m C_{ds} A_{ds} G_{ds} ^m C_{ds} T_{ds} G_{ds}$ $^m C_{es} ^m C_{ks} G_{es} G_{ks} T_e$	30	2657
1207197	218	233	3569	3584	$T_{ks} A_{ks} ^m C_{ds} A_{ds} T_{ds} T_{ds} T_{ds} G_{ds} T_{ds} G_{ds} T_e$ $^s A_{ks} ^m C_{es} A_{ks} G_e$	14	2426
1207205	1778	1793	7166	7181	$^m C_{ks} T_{ks} T_{ds} G_{ds} ^m C_{ds} A_{ds} G_{ds} G_{ds} T_{ds} G_{ds}$ $A_{es} G_{ks} ^m C_{es} ^m C_{ks} G_e$	48	4962
1207213	1786	1801	7174	7189	$G_{ks} A_{ks} T_{ds} G_{ds} A_{ds} T_{ds} G_{ds} ^m C_{ds} ^m C_{ds} T_{ds} T_{ds}$ $G_{es} ^m C_{ks} A_{es} G_{ks} G_e$	16	4963
1207221	1892	1907	7280	7295	$^m C_{ks} ^m C_{ks} ^m C_{ds} T_{ds} G_{ds} A_{ds} G_{ds} ^m C_{ds} A_{ds} A_{ds}$ $T_{ds} ^m C_{es} A_{ks} G_{es} G_{ks} A_e$	53	3530
1207229	1900	1915	7288	7303	$A_{ks} G_{ks} A_{ds} T_{ds} G_{ds} A_{ds} G_{ds} T_{ds} ^m C_{ds} ^m C_{ds} ^m C_d$ $^s T_{es} G_{ks} A_{es} G_{ks} ^m C_e$	14	2614
1207237	1915	1930	7303	7318	$T_{ks} ^m C_{ks} A_{ds} ^m C_{ds} ^m C_{ds} A_{ds} A_{ds} G_{ds} G_{ds} A_{ds} G_{ds}$ $^s G_{es} G_{ks} A_{es} A_{ks} A_e$	30	4948
1207245	1923	1938	7311	7326	$^m C_{ks} T_{ks} G_{ds} ^m C_{ds} G_{ds} G_{ds} A_{ds} A_{ds} T_{ds} ^m C_{ds} A_d$ $^s ^m C_{es} ^m C_{ks} A_{es} A_{ks} G_e$	11	3531
1207253	1931	1946	7319	7334	$^m C_{ks} T_{ks} ^m C_{ds} T_{ds} ^m C_{ds} T_{ds} ^m C_{ds} A_{ds} ^m C_{ds} T_{ds}$ $G_{ds} ^m C_{es} G_{ks} G_{es} A_{ks} A_e$	9	2461
1207261	2001	2016	7389	7404	$G_{ks} ^m C_{ks} G_{ds} ^m C_{ds} ^m C_{ds} A_{ds} T_{ds} ^m C_{ds} ^m C_{ds} T_{ds}$ $G_{ds} G_{es} ^m C_{ks} G_{es} ^m C_{ks} G_e$	56	4964
1207269	2009	2024	7397	7412	$G_{ks} A_{ks} G_{ds} T_{ds} T_{ds} ^m C_{ds} ^m C_{ds} T_{ds} G_{ds} ^m C_{ds} G_d$ $^s ^m C_{es} ^m C_{ks} A_{es} T_{ks} ^m C_e$	11	3837
1207277	2018	2033	7406	7421	$^m C_{ks} A_{ks} ^m C_{ds} T_{ds} T_{ds} A_{ds} T_{ds} T_{ds} G_{ds} A_{ds}$ $G_{es} T_{ks} T_{es} ^m C_{ks} ^m C_e$	6	2924

1207285	2033	2048	7421	7436	$T_{ks} {}^mC_{ks} A_{ds} G_{ds} {}^mC_{ds} A_{ds} T_{ds} T_{ds} T_{ds} {}^mC_{ds}$ $A_{es} A_{ks} A_{es} G_{ks} {}^mC_e$	36	3534
1207293	148	163	515	530	$G_{ks} A_{ks} {}^mC_{ds} T_{ds} G_{ds} T_{ds} G_{ds} T_{ds} G_{ds} {}^mC_{ds} T_{ds}$ ${}^mC_{ks} T_{es} T_{ks} {}^mC_{es} A_{ks}$	12	3343
1207301	156	171	N/A	N/A	$G_{ks} T_{ks} G_{ds} A_{ds} G_{ds} A_{ds} {}^mC_{ds} G_{ds} A_{ds} {}^mC_{ds}$ $T_{ks} G_{es} T_{ks} G_{es} T_{ks}$	29	2424
1207309	213	228	3564	3579	$T_{ks} T_{ks} G_{ds} T_{ds} G_{ds} G_{ds} T_{ds} A_{ds} {}^mC_{ds} A_{ds} G_{ds} {}^m$ $C_{ks} T_{es} G_{ks} {}^mC_{es} {}^mC_{ks}$	21	2811
1207317	221	236	3572	3587	$G_{ks} G_{ks} G_{ds} T_{ds} A_{ds} {}^mC_{ds} A_{ds} T_{ds} T_{ds} T_{ds} G_{ds} T$ ${}_{ks} G_{es} G_{ks} T_{es} A_{ks}$	46	3345
1207325	1781	1796	7169	7184	$T_{ks} G_{ks} {}^mC_{ds} {}^mC_{ds} T_{ds} T_{ds} G_{ds} {}^mC_{ds} A_{ds} G_{ds} G_{ds}$ ${}_{ks} G_{es} T_{es} G_{ks} A_{es} G_{ks}$	28	3527
1207333	1789	1804	7177	7192	$G_{ks} {}^mC_{ks} T_{ds} G_{ds} A_{ds} T_{ds} G_{ds} A_{ds} T_{ds} G_{ds} {}^mC_{ds}$ ${}^mC_{ks} T_{es} T_{ks} G_{es} {}^mC_{ks}$	26	3755
1207341	1895	1910	7283	7298	$A_{ks} G_{ks} T_{ds} {}^mC_{ds} {}^mC_{ds} {}^mC_{ds} T_{ds} G_{ds} A_{ds} G_{ds} {}^m$ $C_{ds} A_{ks} A_{es} T_{ks} {}^mC_{es} A_{ks}$	27	3758
1207349	1903	1918	7291	7306	$G_{ks} A_{ks} A_{ds} A_{ds} G_{ds} A_{ds} T_{ds} G_{ds} A_{ds} G_{ds} T_{ds} {}^m$ $C_{ks} {}^mC_{es} {}^mC_{ks} T_{es} G_{ks}$	29	2845
1207357	1918	1933	7306	7321	$G_{ks} A_{ks} A_{ds} T_{ds} {}^mC_{ds} A_{ds} {}^mC_{ds} {}^mC_{ds} A_{ds} A_{ds} G$ ${}_{ds} G_{ks} A_{es} G_{ks} G_{es} G_{ks}$	35	4965
1207365	1926	1941	7314	7329	$T_{ks} {}^mC_{ks} A_{ds} {}^mC_{ds} T_{ds} G_{ds} {}^mC_{ds} G_{ds} G_{ds} A_{ds} A_{ds}$ ${}_{ks} T_{ks} {}^mC_{es} A_{ks} {}^mC_{es} {}^mC_{ks}$	10	3759
1207373	1934	1949	7322	7337	${}^mC_{ks} {}^mC_{ks} A_{ds} {}^mC_{ds} T_{ds} {}^mC_{ds} T_{ds} {}^mC_{ds} T_{ds} {}^mC_{ds}$ ${}_{ds} A_{ds} {}^mC_{ks} T_{es} G_{ks} {}^mC_{es} G_{ks}$	23	4949
1207381	2004	2019	7392	7407	${}^mC_{ks} {}^mC_{ks} T_{ds} G_{ds} {}^mC_{ds} G_{ds} {}^mC_{ds} {}^mC_{ds} A_{ds} T_{ds}$ ${}^mC_{ds} {}^mC_{ks} T_{es} G_{ks} G_{es} {}^mC_{ks}$	9	3457
1207389	2012	2027	7400	7415	$A_{ks} T_{ks} T_{ds} G_{ds} A_{ds} G_{ds} T_{ds} T_{ds} {}^mC_{ds} {}^mC_{ds} T_{ds}$ $G_{ks} {}^mC_{es} G_{ks} {}^mC_{es} {}^mC_{ks}$	44	2540
1207397	2021	2036	7409	7424	$A_{ks} A_{ks} G_{ds} {}^mC_{ds} A_{ds} {}^mC_{ds} T_{ds} T_{ds} T_{ds} A_{ds} T_{ds}$ $T_{ks} G_{es} A_{ks} G_{es} T_{ks}$	22	3147
1207405	143	158	510	525	$T_{ks} G_{ks} T_{ks} G_{ds} {}^mC_{ds} T_{ds} {}^mC_{ds} T_{ds} T_{ds} {}^mC_{ds} A_{ds}$ $G_{ds} {}^mC_{ks} T_{ks} T_{ks} T_{es}$	29	3037
1207413	151	166	N/A	N/A	$A_{ks} A_{ks} {}^mC_{ks} G_{ds} A_{ds} {}^mC_{ds} T_{ds} G_{ds} T_{ds} G_{ds} T_{ds}$ $G_{ds} {}^mC_{ks} T_{ks} {}^mC_{ks} T_{es}$	24	3571
1207421	208	223	3559	3574	$G_{ks} T_{ks} A_{ks} {}^mC_{ds} A_{ds} G_{ds} {}^mC_{ds} T_{ds} G_{ds} {}^mC_{ds} {}^m$ $C_{ds} G_{ds} G_{ks} T_{ks} G_{ks} G_{es}$	25	4968
1207429	216	231	3567	3582	${}^mC_{ks} A_{ks} T_{ks} T_{ds} T_{ds} G_{ds} T_{ds} G_{ds} G_{ds} T_{ds} A_{ds} {}^m$ $C_{ds} A_{ks} G_{ks} {}^mC_{ks} T_{es}$	14	3039
1207437	1776	1791	7164	7179	$T_{ks} G_{ks} {}^mC_{ks} A_{ds} G_{ds} G_{ds} G_{ds} T_{ds} G_{ds} A_{ds} G_{ds} {}^m$ $C_{ds} {}^mC_{ks} G_{ks} G_{ks} {}^mC_e$	37	3299
1207445	1784	1799	7172	7187	$T_{ks} G_{ks} A_{ks} T_{ds} G_{ds} {}^mC_{ds} {}^mC_{ds} T_{ds} T_{ds} G_{ds} {}^mC_{ds}$ ${}_{ds} A_{ds} G_{ks} G_{ks} G_{ks} T_{es}$	36	4969
1207453	1792	1807	7180	7195	${}^mC_{ks} {}^mC_{ks} A_{ks} G_{ds} {}^mC_{ds} T_{ds} G_{ds} A_{ds} T_{ds} G_{ds} A_{ds}$ ${}_{ds} T_{ds} G_{ks} {}^mC_{ks} {}^mC_{ks} T_{es}$	28	4970
1207461	1898	1913	7286	7301	$A_{ks} T_{ks} G_{ks} A_{ds} G_{ds} T_{ds} {}^mC_{ds} {}^mC_{ds} {}^mC_{ds} T_{ds} G_{ds}$ ${}_{ds} A_{ds} G_{ks} {}^mC_{ks} A_{ks} A_{es}$	21	2460
1207469	1906	1921	7294	7309	$A_{ks} G_{ks} G_{ks} G_{ds} A_{ds} A_{ds} A_{ds} G_{ds} A_{ds} T_{ds} G_{ds} A$ ${}_{ds} G_{ks} T_{ks} {}^mC_{ks} {}^mC_e$	15	3073
1207477	1921	1936	7309	7324	$G_{ks} {}^mC_{ks} G_{ks} G_{ds} A_{ds} A_{ds} T_{ds} {}^mC_{ds} A_{ds} {}^mC_{ds} {}^m$ $C_{ds} A_{ds} A_{ks} G_{ks} G_{ks} A_{es}$	15	3379
1207485	1929	1944	7317	7332	${}^mC_{ks} T_{ks} {}^mC_{ks} T_{ds} {}^mC_{ds} A_{ds} {}^mC_{ds} T_{ds} G_{ds} {}^mC_{ds}$ $G_{ds} G_{ds} A_{ks} A_{ks} T_{ks} {}^mC_e$	12	4971
1207493	1937	1952	7325	7340	${}^mC_{ks} A_{ks} G_{ks} {}^mC_{ds} {}^mC_{ds} A_{ds} {}^mC_{ds} T_{ds} {}^mC_{ds} T_{ds}$ ${}^mC_{ds} T_{ds} {}^mC_{ks} A_{ks} {}^mC_{ks} T_{es}$	14	4972
1207501	2007	2022	7395	7410	$G_{ks} T_{ks} T_{ks} {}^mC_{ds} {}^mC_{ds} T_{ds} G_{ds} {}^mC_{ds} G_{ds} {}^mC_{ds} {}^m$ $C_{ds} A_{ds} T_{ks} {}^mC_{ks} {}^mC_{ks} T_{es}$	21	3685

1207509	2016	2031	7404	7419	${}^m\text{C}_{\text{ks}}\text{T}_{\text{ks}}\text{T}_{\text{ks}}\text{T}_{\text{ds}}\text{A}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}\text{G}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{d}}$ ${}_s{}^m\text{C}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{T}_{\text{ks}}\text{G}_{\text{e}}$	8	2771
1207517	2024	2039	7412	7427	$\text{T}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{A}_{\text{ks}}\text{A}_{\text{ds}}\text{A}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{d}}$ ${}_s\text{T}_{\text{ds}}\text{A}_{\text{ks}}\text{T}_{\text{ks}}\text{T}_{\text{ks}}\text{G}_{\text{e}}$	11	3382

Table 82. Reduction of FXII RNA (Huh7, electroporation, 4000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence and Chemistry notation (5' to 3')	FXII (%UTC)	SEQ ID NO
1129531	2009	2024	7397	7412	$\text{G}_{\text{ks}}\text{A}_{\text{ks}}\text{G}_{\text{ks}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}$ $\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ks}}\text{T}_{\text{ks}}{}^m\text{C}_{\text{k}}$	12	3837
1206479	209	224	3560	3575	$\text{G}_{\text{ks}}\text{G}_{\text{ks}}\text{T}_{\text{ks}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}{}^m$ $\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{G}_{\text{ds}}\text{G}_{\text{ks}}\text{T}_{\text{ks}}\text{G}_{\text{k}}$	20	4952
1206502	1787	1802	7175	7190	$\text{T}_{\text{ks}}\text{G}_{\text{ks}}\text{A}_{\text{ks}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}$ ${}_s\text{T}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ks}}\text{A}_{\text{ks}}\text{G}_{\text{k}}$	27	4975
1206507	1929	1944	7317	7332	${}^m\text{C}_{\text{ks}}\text{T}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}{}^m$ $\text{C}_{\text{ds}}\text{G}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}\text{A}_{\text{ks}}\text{T}_{\text{ks}}{}^m\text{C}_{\text{k}}$	11	4971
1206897	2001	2016	7389	7404	$\text{G}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{G}_{\text{ks}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}$ $\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{G}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{G}_{\text{k}}$	41	4964
1206905	148	163	515	530	$\text{G}_{\text{ks}}\text{A}_{\text{es}}{}^m\text{C}_{\text{ks}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}$ ${}_s{}^m\text{C}_{\text{ds}}\text{T}_{\text{es}}\text{T}_{\text{es}}{}^m\text{C}_{\text{ks}}\text{A}_{\text{k}}$	10	3343
1206913	156	171	N/A	N/A	$\text{G}_{\text{ks}}\text{T}_{\text{es}}\text{G}_{\text{ks}}\text{A}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}{}^m$ $\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{es}}\text{T}_{\text{es}}\text{G}_{\text{ks}}\text{T}_{\text{k}}$	21	2424
1206921	213	228	3564	3579	$\text{T}_{\text{ks}}\text{T}_{\text{es}}\text{G}_{\text{ks}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{G}_{\text{ds}}\text{T}_{\text{ds}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}\text{G}_{\text{d}}$ ${}_s{}^m\text{C}_{\text{ds}}\text{T}_{\text{es}}\text{G}_{\text{es}}{}^m\text{C}_{\text{ks}}{}^m\text{C}_{\text{k}}$	21	2811
1206929	221	236	3572	3587	$\text{G}_{\text{ks}}\text{G}_{\text{es}}\text{G}_{\text{ks}}\text{T}_{\text{ds}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{d}}$ ${}_s\text{T}_{\text{ds}}\text{G}_{\text{es}}\text{G}_{\text{es}}\text{T}_{\text{ks}}\text{A}_{\text{k}}$	22	3345
1206937	1781	1796	7169	7184	$\text{T}_{\text{ks}}\text{G}_{\text{es}}{}^m\text{C}_{\text{ks}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}\text{G}_{\text{ds}}$ $\text{G}_{\text{ds}}\text{G}_{\text{ds}}\text{T}_{\text{es}}\text{G}_{\text{es}}\text{A}_{\text{ks}}\text{G}_{\text{k}}$	58	3527
1206945	1789	1804	7177	7192	$\text{G}_{\text{ks}}{}^m\text{C}_{\text{es}}\text{T}_{\text{ks}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}{}^m$ $\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{es}}\text{T}_{\text{es}}\text{G}_{\text{ks}}{}^m\text{C}_{\text{k}}$	23	3755
1206953	1895	1910	7283	7298	$\text{A}_{\text{ks}}\text{G}_{\text{es}}\text{T}_{\text{ks}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}\text{G}_{\text{ds}}$ ${}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}\text{A}_{\text{es}}\text{T}_{\text{es}}{}^m\text{C}_{\text{ks}}\text{A}_{\text{k}}$	8	3758
1206961	1903	1918	7291	7306	$\text{G}_{\text{ks}}\text{A}_{\text{es}}\text{A}_{\text{ks}}\text{A}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}\text{G}_{\text{ds}}\text{T}_{\text{ds}}$ ${}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{es}}{}^m\text{C}_{\text{es}}\text{T}_{\text{ks}}\text{G}_{\text{k}}$	17	2845
1206969	1918	1933	7306	7321	$\text{G}_{\text{ks}}\text{A}_{\text{es}}\text{A}_{\text{ks}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}\text{A}_{\text{d}}$ ${}_s\text{G}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{es}}\text{G}_{\text{es}}\text{G}_{\text{ks}}\text{G}_{\text{k}}$	18	4965
1206977	1926	1941	7314	7329	$\text{T}_{\text{ks}}{}^m\text{C}_{\text{es}}\text{A}_{\text{ks}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{G}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}$ $\text{A}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{es}}\text{A}_{\text{es}}{}^m\text{C}_{\text{ks}}{}^m\text{C}_{\text{k}}$	12	3759
1206985	1934	1949	7322	7337	${}^m\text{C}_{\text{ks}}{}^m\text{C}_{\text{es}}\text{A}_{\text{ks}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}{}^m$ $\text{C}_{\text{ds}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{es}}\text{G}_{\text{es}}{}^m\text{C}_{\text{ks}}\text{G}_{\text{k}}$	13	4949
1206993	2004	2019	7392	7407	${}^m\text{C}_{\text{ks}}{}^m\text{C}_{\text{es}}\text{T}_{\text{ks}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}$ $\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{es}}\text{G}_{\text{es}}\text{G}_{\text{ks}}{}^m\text{C}_{\text{k}}$	7	3457
1207001	2012	2027	7400	7415	$\text{A}_{\text{ks}}\text{T}_{\text{es}}\text{T}_{\text{ks}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}\text{G}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}$ ${}_s\text{G}_{\text{ds}}{}^m\text{C}_{\text{es}}\text{G}_{\text{es}}{}^m\text{C}_{\text{ks}}{}^m\text{C}_{\text{k}}$	28	2540
1207009	2021	2036	7409	7424	$\text{A}_{\text{ks}}\text{A}_{\text{es}}\text{G}_{\text{ks}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}\text{A}_{\text{ds}}\text{T}_{\text{ds}}\text{T}$ ${}_s\text{G}_{\text{es}}\text{A}_{\text{es}}\text{G}_{\text{ks}}\text{T}_{\text{k}}$	N.D	3147
1207028	143	158	510	525	$\text{T}_{\text{ks}}\text{G}_{\text{ks}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}$ $\text{A}_{\text{ds}}\text{G}_{\text{es}}{}^m\text{C}_{\text{es}}\text{T}_{\text{es}}\text{T}_{\text{ks}}\text{T}_{\text{k}}$	72	3037

1207036	151	166	N/A	N/A	$A_{ks}A_{ks}{}^mC_{ds}G_{ds}A_{ds}{}^mC_{ds}T_{ds}G_{ds}T_{ds}G_{ds}$ $T_{ds}G_{es}{}^mC_{es}T_{es}{}^mC_{ks}T_k$	19	3571
1207044	208	223	3559	3574	$G_{ks}T_{ks}A_{ds}{}^mC_{ds}A_{ds}G_{ds}{}^mC_{ds}T_{ds}G_{ds}{}^mC_{ds}$ ${}^mC_{ds}G_{es}G_{es}T_{es}G_{ks}G_k$	58	4968
1207052	216	231	3567	3582	${}^mC_{ks}A_{ks}T_{ds}T_{ds}T_{ds}G_{ds}T_{ds}G_{ds}G_{ds}T_{ds}A_d$ ${}_s{}^mC_{es}A_{es}G_{es}{}^mC_{ks}T_k$	24	3039
1207060	1776	1791	7164	7179	$T_{ks}G_{ks}{}^mC_{ds}A_{ds}G_{ds}G_{ds}G_{ds}T_{ds}G_{ds}A_{ds}G$ ${}_ds{}^mC_{es}{}^mC_{es}G_{es}G_{ks}{}^mC_k$	26	3299
1207081	1784	1799	7172	7187	$T_{ks}G_{ks}A_{ds}T_{ds}G_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}T_{ds}G_{ds}{}^m$ $C_{ds}A_{es}G_{es}G_{es}G_{ks}T_k$	39	4969
1207089	1792	1807	7180	7195	${}^mC_{ks}{}^mC_{ks}A_{ds}G_{ds}{}^mC_{ds}T_{ds}G_{ds}A_{ds}T_{ds}G_{ds}$ $A_{ds}T_{es}G_{es}{}^mC_{es}{}^mC_{ks}T_k$	45	4970
1207097	1898	1913	7286	7301	$A_{ks}T_{ks}G_{ds}A_{ds}G_{ds}T_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}$ $G_{ds}A_{es}G_{es}{}^mC_{es}A_{ks}A_k$	14	2460
1207105	1906	1921	7294	7309	$A_{ks}G_{ks}G_{ds}G_{ds}A_{ds}A_{ds}A_{ds}G_{ds}A_{ds}T_{ds}G_d$ ${}_sA_{es}G_{es}T_{es}{}^mC_{ks}{}^mC_k$	25	3073
1207113	1921	1936	7309	7324	$G_{ks}{}^mC_{ks}G_{ds}G_{ds}A_{ds}A_{ds}T_{ds}{}^mC_{ds}A_{ds}{}^mC_d$ ${}_s{}^mC_{ds}A_{es}A_{es}G_{es}G_{ks}A_k$	8	3379
1207125	1929	1944	7317	7332	${}^mC_{ks}T_{ks}{}^mC_{ds}T_{ds}{}^mC_{ds}A_{ds}{}^mC_{ds}T_{ds}G_{ds}{}^m$ $C_{ds}G_{ds}G_{es}A_{es}A_{es}T_{ks}{}^mC_k$	9	4971
1207141	1937	1952	7325	7340	${}^mC_{ks}A_{ks}G_{ds}{}^mC_{ds}{}^mC_{ds}A_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}$ $T_{ds}{}^mC_{ds}T_{es}{}^mC_{es}A_{es}{}^mC_{ks}T_k$	28	4972
1207150	2007	2022	7395	7410	$G_{ks}T_{ks}T_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}G_{ds}{}^mC_{ds}G_{ds}{}^mC$ ${}_ds{}^mC_{ds}A_{es}T_{es}{}^mC_{es}{}^mC_{ks}T_k$	21	3685
1207158	2016	2031	7404	7419	${}^mC_{ks}T_{ks}T_{ds}T_{ds}A_{ds}T_{ds}T_{ds}G_{ds}A_{ds}G_{ds}T_{ds}$ $T_{es}{}^mC_{es}{}^mC_{es}T_{ks}G_k$	27	2771
1207166	2024	2039	7412	7427	$T_{ks}{}^mC_{ks}A_{ds}A_{ds}A_{ds}G_{ds}{}^mC_{ds}A_{ds}{}^mC_{ds}T_{ds}$ $T_{ds}T_{es}A_{es}T_{es}T_{ks}G_k$	22	3382
1207174	146	161	513	528	${}^mC_{ks}T_{ks}G_{ds}T_{ds}G_{ds}T_{ds}G_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}$ $T_{ds}T_{es}{}^mC_{ks}A_{es}G_{ks}{}^mC_e$	28	3190
1207182	154	169	N/A	N/A	$G_{ks}A_{ks}G_{ds}A_{ds}A_{ds}{}^mC_{ds}G_{ds}A_{ds}{}^mC_{ds}T_{ds}$ $G_{ds}T_{es}G_{ks}T_{es}G_{ks}{}^mC_e$	16	3799
1207190	211	226	3562	3577	$G_{ks}T_{ks}G_{ds}G_{ds}T_{ds}A_{ds}{}^mC_{ds}A_{ds}G_{ds}{}^mC_{ds}$ $T_{ds}G_{es}{}^mC_{ks}{}^mC_{es}G_{ks}G_e$	5	4973
1207198	219	234	3570	3585	$G_{ks}T_{ks}A_{ds}{}^mC_{ds}A_{ds}T_{ds}T_{ds}T_{ds}G_{ds}T_{ds}G_d$ ${}_sG_{es}T_{ks}A_{es}{}^mC_{ks}A_e$	48	3192
1207206	1779	1794	7167	7182	${}^mC_{ks}{}^mC_{ks}T_{ds}T_{ds}G_{ds}{}^mC_{ds}A_{ds}G_{ds}G_{ds}G_{ds}$ $T_{ds}G_{es}A_{ks}G_{es}{}^mC_{ks}{}^mC_e$	36	4974
1207214	1787	1802	7175	7190	$T_{ks}G_{ks}A_{ds}T_{ds}G_{ds}A_{ds}T_{ds}G_{ds}{}^mC_{ds}{}^mC_{ds}T$ ${}_dsT_{es}G_{ks}{}^mC_{es}A_{ks}G_e$	26	4975
1207222	1893	1908	7281	7296	$T_{ks}{}^mC_{ks}{}^mC_{ds}{}^mC_{ds}T_{ds}G_{ds}A_{ds}G_{ds}{}^mC_{ds}A$ ${}_dsA_{ds}T_{es}{}^mC_{ks}A_{es}G_{ks}G_e$	35	3606
1207230	1901	1916	7289	7304	$A_{ks}A_{ks}G_{ds}A_{ds}T_{ds}G_{ds}A_{ds}G_{ds}T_{ds}{}^mC_{ds}{}^m$ $C_{ds}{}^mC_{es}T_{ks}G_{es}A_{ks}G_e$	7	2691
1207238	1916	1931	7304	7319	$A_{ks}T_{ks}{}^mC_{ds}A_{ds}{}^mC_{ds}{}^mC_{ds}A_{ds}A_{ds}G_{ds}G_d$ ${}_sA_{ds}G_{es}G_{ks}G_{es}A_{ks}A_e$	32	4966
1207246	1924	1939	7312	7327	$A_{ks}{}^mC_{ks}T_{ds}G_{ds}{}^mC_{ds}G_{ds}G_{ds}A_{ds}A_{ds}T_{ds}{}^m$ $C_{ds}A_{es}{}^mC_{ks}{}^mC_{es}A_{ks}A_e$	17	3607
1207254	1932	1947	7320	7335	$A_{ks}{}^mC_{ks}T_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}A_{ds}{}^m$ $C_{ds}T_{ds}G_{es}{}^mC_{ks}G_{es}G_{ks}A_e$	18	4976
1207262	2002	2017	7390	7405	$T_{ks}G_{ks}{}^mC_{ds}G_{ds}{}^mC_{ds}{}^mC_{ds}A_{ds}T_{ds}{}^mC_{ds}{}^m$ $C_{ds}T_{ds}G_{es}G_{ks}{}^mC_{es}G_{ks}{}^mC_e$	37	3305

1207270	2010	2025	7398	7413	$T_{ks}G_{ks}A_{ds}G_{ds}T_{ds}T_{ds}^mC_{ds}^mC_{ds}T_{ds}G_{ds}^m$ $C_{ds}G_{es}^mC_{ks}^mC_{es}A_{ks}T_e$	21	3913
1207278	2019	2034	7407	7422	$G_{ks}^mC_{ks}A_{ds}^mC_{ds}T_{ds}T_{ds}T_{ds}A_{ds}T_{ds}T_{ds}G$ $_{ds}A_{es}G_{ks}T_{es}T_{ks}^mC_e$	7	3000
1207286	141	156	508	523	$T_{ks}G_{ks}^mC_{ds}T_{ds}^mC_{ds}T_{ds}T_{ds}^mC_{ds}A_{ds}G_{ds}$ $^mC_{ds}T_{ks}T_{es}T_{ks}G_{es}T_k$	27	4950
1207294	149	164	516	531	$^mC_{ks}G_{ks}A_{ds}^mC_{ds}T_{ds}G_{ds}T_{ds}G_{ds}T_{ds}G_{ds}^m$ $C_{ds}T_{ks}^mC_{es}T_{ks}T_{es}^mC_k$	21	3419
1207302	157	172	N/A	N/A	$A_{ks}G_{ks}T_{ds}G_{ds}A_{ds}G_{ds}A_{ds}A_{ds}^mC_{ds}G_{ds}A$ $_{ds}^mC_{ks}T_{es}G_{ks}T_{es}G_k$	38	2502
1207310	214	229	3565	3580	$T_{ks}T_{ks}T_{ds}G_{ds}T_{ds}G_{ds}G_{ds}T_{ds}A_{ds}^mC_{ds}A_d$ $_sG_{ks}^mC_{es}T_{ks}G_{es}^mC_k$	26	2887
1207318	222	237	3573	3588	$T_{ks}G_{ks}G_{ds}G_{ds}T_{ds}A_{ds}^mC_{ds}A_{ds}T_{ds}T_{ds}T_d$ $_sG_{ks}T_{es}G_{ks}G_{es}T_k$	30	3421
1207326	1782	1797	7170	7185	$A_{ks}T_{ks}G_{ds}^mC_{ds}^mC_{ds}T_{ds}T_{ds}G_{ds}^mC_{ds}A_{ds}$ $G_{ds}G_{ks}G_{es}T_{ks}G_{es}A_k$	34	4947
1207334	1790	1805	7178	7193	$A_{ks}G_{ks}^mC_{ds}T_{ds}G_{ds}A_{ds}T_{ds}G_{ds}A_{ds}T_{ds}G_d$ $_s^mC_{ks}^mC_{es}T_{ks}T_{es}G_k$	32	3831
1207342	1896	1911	7284	7299	$G_{ks}A_{ks}G_{ds}T_{ds}^mC_{ds}^mC_{ds}^mC_{ds}T_{ds}G_{ds}A_{ds}$ $G_{ds}^mC_{ks}A_{es}A_{ks}T_{es}^mC_k$	33	3834
1207350	1904	1919	7292	7307	$G_{ks}G_{ks}A_{ds}A_{ds}A_{ds}G_{ds}A_{ds}T_{ds}G_{ds}A_{ds}G_d$ $_sT_{ks}^mC_{es}^mC_{ks}^mC_{es}T_k$	54	2921
1207358	1919	1934	7307	7322	$G_{ks}G_{ks}A_{ds}A_{ds}T_{ds}^mC_{ds}A_{ds}^mC_{ds}^mC_{ds}A_d$ $_sA_{ds}G_{ks}G_{es}A_{ks}G_{es}G_k$	8	3226
1207366	1927	1942	7315	7330	$^mC_{ks}T_{ks}^mC_{ds}A_{ds}^mC_{ds}T_{ds}G_{ds}^mC_{ds}G_{ds}G$ $_{ds}A_{ds}A_{ks}T_{es}^mC_{ks}A_{es}^mC_k$	13	3835
1207374	1935	1950	7323	7338	$G_{ks}^mC_{ks}^mC_{ds}A_{ds}^mC_{ds}T_{ds}^mC_{ds}T_{ds}^mC_{ds}$ $T_{ds}^mC_{ds}A_{ks}^mC_{es}T_{ks}G_{es}^mC_k$	31	4967
1207382	2005	2020	7393	7408	$T_{ks}^mC_{ks}^mC_{ds}T_{ds}G_{ds}^mC_{ds}G_{ds}^mC_{ds}^mC_{ds}$ $A_{ds}T_{ds}^mC_{ks}^mC_{es}T_{ks}G_{es}G_k$	27	3533
1207390	2013	2028	7401	7416	$T_{ks}A_{ks}T_{ds}T_{ds}G_{ds}A_{ds}G_{ds}T_{ds}T_{ds}^mC_{ds}^mC$ $_{ds}T_{ks}G_{es}^mC_{ks}G_{es}^mC_k$	38	2617
1207398	2022	2037	7410	7425	$A_{ks}A_{ks}A_{ds}G_{ds}^mC_{ds}A_{ds}^mC_{ds}T_{ds}T_{ds}T_{ds}$ $A_{ds}T_{ks}T_{es}G_{ks}A_{es}G_k$	24	3229
1207406	144	159	511	526	$G_{ks}T_{ks}G_{ks}T_{ds}G_{ds}^mC_{ds}T_{ds}^mC_{ds}T_{ds}T_{ds}^m$ $C_{ds}A_{ds}G_{ks}^mC_{ks}T_{ks}T_e$	6	4951
1207414	152	167	N/A	N/A	$G_{ks}A_{ks}A_{ks}^mC_{ds}G_{ds}A_{ds}^mC_{ds}T_{ds}G_{ds}T_{ds}$ $G_{ds}T_{ds}G_{ks}^mC_{ks}T_{ks}^mC_e$	19	3647
1207422	209	224	3560	3575	$G_{ks}G_{ks}T_{ks}A_{ds}^mC_{ds}A_{ds}G_{ds}^mC_{ds}T_{ds}G_{ds}^m$ $C_{ds}^mC_{ds}G_{ks}G_{ks}T_{ks}G_e$	44	4952
1207430	217	232	3568	3583	$A_{ks}^mC_{ks}A_{ks}T_{ds}T_{ds}T_{ds}G_{ds}T_{ds}G_{ds}G_{ds}T_d$ $_sA_{ds}^mC_{ks}A_{ks}G_{ks}^mC_e$	12	3114
1207438	1777	1792	7165	7180	$T_{ks}T_{ks}G_{ks}^mC_{ds}A_{ds}G_{ds}G_{ds}G_{ds}T_{ds}G_{ds}A_d$ $_sG_{ds}^mC_{ks}^mC_{ks}G_{ks}G_e$	40	3375
1207446	1785	1800	7173	7188	$A_{ks}T_{ks}G_{ks}A_{ds}T_{ds}G_{ds}^mC_{ds}^mC_{ds}T_{ds}T_{ds}G$ $_{ds}^mC_{ds}A_{ks}G_{ks}G_{ks}G_e$	16	3603
1207454	1793	1808	7181	7196	$^mC_{ks}^mC_{ks}^mC_{ks}A_{ds}G_{ds}^mC_{ds}T_{ds}G_{ds}A_{ds}T$ $_{ds}G_{ds}A_{ds}T_{ks}G_{ks}^mC_{ks}^mC_e$	11	4953
1207462	1899	1914	7287	7302	$G_{ks}A_{ks}T_{ks}G_{ds}A_{ds}G_{ds}T_{ds}^mC_{ds}^mC_{ds}^mC_{ds}$ $T_{ds}G_{ds}A_{ks}G_{ks}^mC_{ks}A_e$	15	2537
1207470	1914	1929	7302	7317	$^mC_{ks}A_{ks}^mC_{ks}^mC_{ds}A_{ds}A_{ds}G_{ds}G_{ds}A_{ds}G_d$ $_sG_{ds}G_{ds}A_{ks}A_{ks}A_{ks}G_e$	40	4954

1207478	1922	1937	7310	7325	$T_{ks}G_{ks}^mC_{ks}G_{ds}G_{ds}A_{ds}A_{ds}T_{ds}^mC_{ds}A_{ds}^m$ $C_{ds}^mC_{ds}A_{ks}A_{ks}G_{ks}G_e$	16	3455
1207486	1930	1945	7318	7333	$T_{ks}^mC_{ks}T_{ks}^mC_{ds}T_{ds}^mC_{ds}A_{ds}^mC_{ds}T_{ds}G_d$ $s^mC_{ds}G_{ds}G_{ks}A_{ks}A_{ks}T_e$	22	4955
1207494	2000	2015	7388	7403	$^mC_{ks}G_{ks}^mC_{ks}^mC_{ds}A_{ds}T_{ds}^mC_{ds}^mC_{ds}T_{ds}$ $G_{ds}G_{ds}^mC_{ds}G_{ks}^mC_{ks}G_{ks}G_e$	39	3228
1207502	2008	2023	7396	7411	$A_{ks}G_{ks}T_{ks}T_{ds}^mC_{ds}^mC_{ds}T_{ds}G_{ds}^mC_{ds}G_{ds}$ $^mC_{ds}^mC_{ds}A_{ks}T_{ks}^mC_{ks}^mC_e$	22	3761
1207518	2031	2046	7419	7434	$A_{ks}G_{ks}^mC_{ks}A_{ds}T_{ds}T_{ds}T_{ds}T_{ds}^mC_{ds}A_{ds}A$ $dsA_{ds}G_{ks}^mC_{ks}A_{ks}^mC_e$	13	3458

Table 83. Reduction of FXII RNA (Huh7, electroporation, 4000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence and Chemistry notation (5' to 3')	FXII (%UTC)	SEQ ID NO
1129531	2009	2024	7397	7412	$G_{ks}A_{ks}G_{ks}T_{ds}T_{ds}^mC_{ds}^mC_{ds}T_{ds}G_{ds}^mC_d$ $sG_{ds}^mC_{ds}^mC_{ds}A_{ks}T_{ks}^mC_k$	8	3837
1206488	1930	1945	7318	7333	$T_{ks}^mC_{ks}T_{ks}^mC_{ds}T_{ds}^mC_{ds}A_{ds}^mC_{ds}T_{ds}G$ $ds^mC_{ds}G_{ds}G_{ds}A_{ks}A_{ks}T_k$	10	4955
1206497	211	226	3562	3577	$G_{ks}T_{ks}G_{ks}G_{ds}T_{ds}A_{ds}^mC_{ds}A_{ds}G_{ds}^mC_{ds}$ $T_{ds}G_{ds}^mC_{ds}^mC_{ks}G_{ks}G_k$	7	4973
1206503	1792	1807	7180	7195	$^mC_{ks}^mC_{ks}A_{ks}G_{ds}^mC_{ds}T_{ds}G_{ds}A_{ds}T_{ds}G_d$ $sA_{ds}T_{ds}G_{ds}^mC_{ks}^mC_{ks}T_k$	35	4970
1206898	141	156	508	523	$T_{ks}G_{es}^mC_{ks}T_{ds}^mC_{ds}T_{ds}T_{ds}^mC_{ds}A_{ds}G_{ds}$ $^mC_{ds}T_{ds}T_{es}T_{es}G_{ks}T_k$	18	4950
1206906	149	164	516	531	$^mC_{ks}G_{es}A_{ks}^mC_{ds}T_{ds}G_{ds}T_{ds}G_{ds}T_{ds}G_{ds}$ $^mC_{ds}T_{ds}^mC_{es}T_{es}T_{ks}^mC_k$	5	3419
1206914	157	172	N/A	N/A	$A_{ks}G_{es}T_{ks}G_{ds}A_{ds}G_{ds}A_{ds}A_{ds}^mC_{ds}G_{ds}$ $A_{ds}^mC_{ds}T_{es}G_{es}T_{ks}G_k$	14	2502
1206922	214	229	3565	3580	$T_{ks}T_{es}T_{ks}G_{ds}T_{ds}G_{ds}G_{ds}T_{ds}A_{ds}^mC_{ds}A_d$ $sG_{ds}^mC_{es}T_{es}G_{ks}^mC_k$	22	2887
1206930	222	237	3573	3588	$T_{ks}G_{es}G_{ks}G_{ds}T_{ds}A_{ds}^mC_{ds}A_{ds}T_{ds}T_d$ $sG_{ds}T_{es}G_{es}G_{ks}T_k$	11	3421
1206938	1782	1797	7170	7185	$A_{ks}T_{es}G_{ks}^mC_{ds}^mC_{ds}T_{ds}T_{ds}G_{ds}^mC_{ds}A_d$ $sG_{ds}G_{ds}G_{es}T_{es}G_{ks}A_k$	27	4947
1206946	1790	1805	7178	7193	$A_{ks}G_{es}^mC_{ks}T_{ds}G_{ds}A_{ds}T_{ds}G_{ds}A_{ds}T_{ds}G$ $ds^mC_{ds}^mC_{es}T_{es}T_{ks}G_k$	32	3831
1206954	1896	1911	7284	7299	$G_{ks}A_{es}G_{ks}T_{ds}^mC_{ds}^mC_{ds}^mC_{ds}T_{ds}G_{ds}A_d$ $sG_{ds}^mC_{ds}A_{es}A_{es}T_{ks}^mC_k$	16	3834
1206962	1904	1919	7292	7307	$G_{ks}G_{es}A_{ks}A_{ds}A_{ds}G_{ds}A_{ds}T_{ds}G_{ds}A_{ds}G_d$ $sT_{ds}^mC_{es}^mC_{es}^mC_{ks}T_k$	16	2921
1206970	1919	1934	7307	7322	$G_{ks}G_{es}A_{ks}A_{ds}T_{ds}^mC_{ds}A_{ds}^mC_{ds}^mC_{ds}A$ $dsA_{ds}G_{ds}G_{es}A_{es}G_{ks}G_k$	7	3226
1206978	1927	1942	7315	7330	$^mC_{ks}T_{es}^mC_{ks}A_{ds}^mC_{ds}T_{ds}G_{ds}^mC_{ds}G_{ds}$ $G_{ds}A_{ds}A_{ds}T_{es}^mC_{es}A_{ks}^mC_k$	7	3835
1206986	1935	1950	7323	7338	$G_{ks}^mC_{es}^mC_{ks}A_{ds}^mC_{ds}T_{ds}^mC_{ds}T_{ds}^mC_{ds}$ $T_{ds}^mC_{ds}A_{ds}^mC_{es}T_{es}G_{ks}^mC_k$	8	4967

1206994	2005	2020	7393	7408	$T_{ks}^m C_{es}^m C_{ks} T_{ds} G_{ds}^m C_{ds} G_{ds}^m C_{ds}^m C_{ds}$ $A_{ds} T_{ds}^m C_{ds}^m C_{es} T_{es} G_{ks} G_k$	10	3533
1207002	2013	2028	7401	7416	$T_{ks} A_{es} T_{ks} T_{ds} G_{ds} A_{ds} G_{ds} T_{ds} T_{ds}^m C_{ds}^m$ $C_{ds} T_{ds} G_{es}^m C_{es} G_{ks}^m C_k$	19	2617
1207010	2022	2037	7410	7425	$A_{ks} A_{es} A_{ks} G_{ds}^m C_{ds} A_{ds}^m C_{ds} T_{ds} T_{ds} T_{ds}$ $A_{ds} T_{ds} T_{es} G_{es} A_{ks} G_k$	3	3229
1207029	144	159	511	526	$G_{ks} T_{ks} G_{ds} T_{ds} G_{ds}^m C_{ds} T_{ds}^m C_{ds} T_{ds} T_{ds}^m$ $C_{ds} A_{es} G_{es}^m C_{es} T_{ks} T_k$	11	4951
1207037	152	167	N/A	N/A	$G_{ks} A_{ks} A_{ds}^m C_{ds} G_{ds} A_{ds}^m C_{ds} T_{ds} G_{ds} T_{ds}$ $G_{ds} T_{es} G_{es}^m C_{es} T_{ks}^m C_k$	14	3647
1207045	209	224	3560	3575	$G_{ks} G_{ks} T_{ds} A_{ds}^m C_{ds} A_{ds} G_{ds}^m C_{ds} T_{ds} G_{ds}$ $^m C_{ds}^m C_{es} G_{es} G_{es} T_{ks} G_k$	5	4952
1207053	217	232	3568	3583	$A_{ks}^m C_{ks} A_{ds} T_{ds} T_{ds} T_{ds} G_{ds} T_{ds} G_{ds} T_{ds}$ $A_{es}^m C_{es} A_{es} G_{ks}^m C_k$	12	3114
1207061	1777	1792	7165	7180	$T_{ks} T_{ks} G_{ds}^m C_{ds} A_{ds} G_{ds} G_{ds} G_{ds} T_{ds} G_{ds} A_{ds}$ $G_{es}^m C_{es}^m C_{es} G_{ks} G_k$	20	3375
1207082	1785	1800	7173	7188	$A_{ks} T_{ks} G_{ds} A_{ds} T_{ds} G_{ds}^m C_{ds}^m C_{ds} T_{ds} T_{ds}$ $G_{ds}^m C_{es} A_{es} G_{es} G_{ks} G_k$	15	3603
1207090	1793	1808	7181	7196	$^m C_{ks}^m C_{ks}^m C_{ds} A_{ds} G_{ds}^m C_{ds} T_{ds} G_{ds} A_{ds}$ $T_{ds} G_{ds} A_{es} T_{es} G_{es}^m C_{ks}^m C_k$	52	4953
1207098	1899	1914	7287	7302	$G_{ks} A_{ks} T_{ds} G_{ds} A_{ds} G_{ds} T_{ds}^m C_{ds}^m C_{ds}^m C_d$ $s T_{ds} G_{es} A_{es} G_{es}^m C_{ks} A_k$	12	2537
1207106	1914	1929	7302	7317	$^m C_{ks} A_{ks}^m C_{ds}^m C_{ds} A_{ds} A_{ds} G_{ds} G_{ds} A_{ds} G_{ds}$ $G_{ds} G_{es} A_{es} A_{es} A_{ks} G_k$	13	4954
1207114	1922	1937	7310	7325	$T_{ks} G_{ks}^m C_{ds} G_{ds} G_{ds} A_{ds} A_{ds} T_{ds}^m C_{ds} A_{ds}$ $^m C_{ds}^m C_{es} A_{es} A_{es} G_{ks} G_k$	11	3455
1207127	1930	1945	7318	7333	$T_{ks}^m C_{ks} T_{ds}^m C_{ds} T_{ds}^m C_{ds} A_{ds}^m C_{ds} T_{ds} G_{ds}$ $^m C_{ds} G_{es} G_{es} A_{es} A_{ks} T_k$	12	4955
1207142	2000	2015	7388	7403	$^m C_{ks} G_{ks}^m C_{ds}^m C_{ds} A_{ds} T_{ds}^m C_{ds}^m C_{ds} T_{ds}$ $G_{ds} G_{ds}^m C_{es} G_{es}^m C_{es} G_{ks} G_k$	24	3228
1207151	2008	2023	7396	7411	$A_{ks} G_{ks} T_{ds} T_{ds}^m C_{ds}^m C_{ds} T_{ds} G_{ds}^m C_{ds} G_d$ $s^m C_{ds}^m C_{es} A_{es} T_{es}^m C_{ks}^m C_k$	19	3761
1207159	2017	2032	7405	7420	$A_{ks}^m C_{ks} T_{ds} T_{ds} T_{ds} A_{ds} T_{ds} T_{ds} G_{ds} A_{ds} G_{ds}$ $ds T_{es} T_{es}^m C_{es}^m C_{ks} T_k$	4	2848
1207167	2031	2046	7419	7434	$A_{ks} G_{ks}^m C_{ds} A_{ds} T_{ds} T_{ds} T_{ds} T_{ds}^m C_{ds} A_{ds}$ $A_{ds} A_{es} G_{es}^m C_{es} A_{ks}^m C_k$	20	3458
1207175	147	162	514	529	$A_{ks}^m C_{ks} T_{ds} G_{ds} T_{ds} G_{ds} T_{ds} G_{ds}^m C_{ds} T_{ds}$ $^m C_{ds} T_{es} T_{ks}^m C_{es} A_{ks} G_e$	13	3267
1207183	155	170	N/A	N/A	$T_{ks} G_{ks} A_{ds} G_{ds} A_{ds} A_{ds}^m C_{ds} G_{ds} A_{ds}^m C_{ds}$ $T_{ds} G_{es} T_{ks} G_{es} T_{ks} G_e$	26	3875
1207191	212	227	3563	3578	$T_{ks} G_{ks} T_{ds} G_{ds} G_{ds} T_{ds} A_{ds}^m C_{ds} A_{ds} G_{ds}^m$ $C_{ds} T_{es} G_{ks}^m C_{es}^m C_{ks} G_e$	11	2734
1207199	220	235	3571	3586	$G_{ks} G_{ks} T_{ds} A_{ds}^m C_{ds} A_{ds} T_{ds} T_{ds} T_{ds} G_{ds} T_{ds}$ $ds G_{es} G_{ks} T_{es} A_{ks}^m C_e$	14	3269
1207207	1780	1795	7168	7183	$G_{ks}^m C_{ks}^m C_{ds} T_{ds} T_{ds} G_{ds}^m C_{ds} A_{ds} G_{ds} G_d$ $s G_{ds} T_{es} G_{ks} A_{es} G_{ks}^m C_e$	22	3451
1207215	1788	1803	7176	7191	$^m C_{ks} T_{ks} G_{ds} A_{ds} T_{ds} G_{ds} A_{ds} T_{ds} G_{ds}^m C_{ds}$ $^m C_{ds} T_{es} T_{ks} G_{es}^m C_{ks} A_e$	12	3679
1207223	1894	1909	7282	7297	$G_{ks} T_{ks}^m C_{ds}^m C_{ds}^m C_{ds} T_{ds} G_{ds} A_{ds} G_{ds}^m$ $C_{ds} A_{ds} A_{es} T_{ks}^m C_{es} A_{ks} G_e$	27	3682
1207231	1902	1917	7290	7305	$A_{ks} A_{ks} A_{ds} G_{ds} A_{ds} T_{ds} G_{ds} A_{ds} G_{ds} T_{ds}^m$ $C_{ds}^m C_{es}^m C_{ks} T_{es} G_{ks} A_e$	19	2768

1207239	1917	1932	7305	7320	$A_{ks}A_{ks}T_{ds}{}^mC_{ds}A_{ds}{}^mC_{ds}{}^mC_{ds}A_{ds}A_{ds}G_{ds}G_{ds}A_{es}G_{ks}G_{es}G_{ks}A_e$	14	4956
1207247	1925	1940	7313	7328	${}^mC_{ks}A_{ks}{}^mC_{ds}T_{ds}G_{ds}{}^mC_{ds}G_{ds}G_{ds}A_{ds}A_{ds}T_{ds}{}^mC_{es}A_{ks}{}^mC_{es}{}^mC_{ks}A_e$	11	3683
1207255	1933	1948	7321	7336	${}^mC_{ks}A_{ks}{}^mC_{ds}T_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}A_{ds}{}^mC_{ds}T_{es}G_{ks}{}^mC_{es}G_{ks}G_e$	N.D.	4957
1207263	2003	2018	7391	7406	${}^mC_{ks}T_{ks}G_{ds}{}^mC_{ds}G_{ds}{}^mC_{ds}{}^mC_{ds}A_{ds}T_{ds}{}^mC_{ds}{}^mC_{ds}T_{es}G_{ks}G_{es}{}^mC_{ks}G_e$	30	3381
1207271	2011	2026	7399	7414	$T_{ks}T_{ks}G_{ds}A_{ds}G_{ds}T_{ds}T_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}G_{ds}{}^mC_{es}G_{ks}{}^mC_{es}{}^mC_{ks}A_e$	9	2463
1207279	2020	2035	7408	7423	$A_{ks}G_{ks}{}^mC_{ds}A_{ds}{}^mC_{ds}T_{ds}T_{ds}T_{ds}A_{ds}T_{ds}T_{ds}G_{es}A_{ks}G_{es}T_{ks}T_e$	6	3076
1207287	142	157	509	524	$G_{ks}T_{ks}G_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}T_{ds}T_{ds}{}^mC_{ds}A_{ds}G_{ds}{}^mC_{ks}T_{es}T_{ks}T_{es}G_k$	15	4958
1207295	150	165	N/A	N/A	$A_{ks}{}^mC_{ks}G_{ds}A_{ds}{}^mC_{ds}T_{ds}G_{ds}T_{ds}G_{ds}T_{ds}G_{ds}{}^mC_{ks}T_{es}{}^mC_{ks}T_{es}T_k$	13	3495
1207303	158	173	N/A	N/A	${}^mC_{ks}A_{ks}G_{ds}T_{ds}G_{ds}A_{ds}G_{ds}A_{ds}A_{ds}{}^mC_{ds}G_{ds}A_{ks}{}^mC_{es}T_{ks}G_{es}T_k$	31	2579
1207311	215	230	3566	3581	$A_{ks}T_{ks}T_{ds}T_{ds}G_{ds}T_{ds}G_{ds}G_{ds}T_{ds}A_{ds}{}^mC_{ds}A_{ks}G_{es}{}^mC_{ks}T_{es}G_k$	30	2963
1207319	223	238	3574	3589	$G_{ks}T_{ks}G_{ds}G_{ds}G_{ds}T_{ds}A_{ds}{}^mC_{ds}A_{ds}T_{ds}T_{ds}T_{ks}G_{es}T_{ks}G_{es}G_k$	19	3497
1207327	1783	1798	7171	7186	$G_{ks}A_{ks}T_{ds}G_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}T_{ds}G_{ds}{}^mC_{ds}A_{ds}G_{ks}G_{es}G_{ks}T_{es}G_k$	66	4959
1207335	1791	1806	7179	7194	${}^mC_{ks}A_{ks}G_{ds}{}^mC_{ds}T_{ds}G_{ds}A_{ds}T_{ds}G_{ds}A_{ds}T_{ds}G_{ks}{}^mC_{es}{}^mC_{ks}T_{es}T_k$	24	4960
1207343	1897	1912	7285	7300	$T_{ks}G_{ks}A_{ds}G_{ds}T_{ds}{}^mC_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}G_{ds}A_{ds}G_{ks}{}^mC_{es}A_{ks}A_{es}T_k$	20	3910
1207351	1905	1920	7293	7308	$G_{ks}G_{ks}G_{ds}A_{ds}A_{ds}A_{ds}G_{ds}A_{ds}T_{ds}G_{ds}A_{ds}G_{ks}T_{es}{}^mC_{ks}{}^mC_{es}{}^mC_k$	10	2997
1207359	1920	1935	7308	7323	${}^mC_{ks}G_{ks}G_{ds}A_{ds}A_{ds}T_{ds}{}^mC_{ds}A_{ds}{}^mC_{ds}{}^mC_{ds}A_{ds}A_{ks}G_{es}G_{ks}A_{es}G_k$	18	3303
1207367	1928	1943	7316	7331	$T_{ks}{}^mC_{ks}T_{ds}{}^mC_{ds}A_{ds}{}^mC_{ds}T_{ds}G_{ds}{}^mC_{ds}G_{ds}G_{ds}A_{ks}A_{es}T_{ks}{}^mC_{es}A_k$	4	3911
1207375	1936	1951	7324	7339	$A_{ks}G_{ks}{}^mC_{ds}{}^mC_{ds}A_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}T_{es}{}^mC_{ks}A_{es}{}^mC_{ks}T_{es}G_k$	10	4961
1207383	2006	2021	7394	7409	$T_{ks}T_{ks}{}^mC_{ds}{}^mC_{ds}T_{ds}G_{ds}{}^mC_{ds}G_{ds}{}^mC_{ds}{}^mC_{ds}A_{ds}T_{ks}{}^mC_{es}{}^mC_{ks}T_{es}G_k$	20	3609
1207391	2014	2029	7402	7417	$T_{ks}T_{ks}A_{ds}T_{ds}T_{ds}G_{ds}A_{ds}G_{ds}T_{ds}T_{ds}{}^mC_{ds}{}^mC_{ks}T_{es}G_{ks}{}^mC_{es}G_k$	28	2694
1207399	2023	2038	7411	7426	${}^mC_{ks}A_{ks}A_{ds}A_{ds}G_{ds}{}^mC_{ds}A_{ds}{}^mC_{ds}T_{ds}T_{ds}T_{ds}A_{ks}T_{es}T_{ks}G_{es}A_k$	13	3306
1207407	145	160	512	527	$T_{ks}G_{ks}T_{ks}G_{ds}T_{ds}G_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}T_{ds}T_{ds}{}^mC_{ds}A_{ks}G_{ks}{}^mC_{ks}T_e$	6	3112
1207415	153	168	N/A	N/A	$A_{ks}G_{ks}A_{ks}A_{ds}{}^mC_{ds}G_{ds}A_{ds}{}^mC_{ds}T_{ds}G_{ds}T_{ds}G_{ds}T_{ks}G_{ks}{}^mC_{ks}T_e$	19	3723
1207423	210	225	3561	3576	$T_{ks}G_{ks}G_{ks}T_{ds}A_{ds}{}^mC_{ds}A_{ds}G_{ds}{}^mC_{ds}T_{ds}G_{ds}{}^mC_{ds}{}^mC_{ks}G_{ks}G_{ks}T_e$	23	2657
1207431	218	233	3569	3584	$T_{ks}A_{ks}{}^mC_{ks}A_{ds}T_{ds}T_{ds}T_{ds}G_{ds}T_{ds}G_{ds}G_{ds}T_{ds}A_{ks}{}^mC_{ks}A_{ks}G_e$	18	2426
1207439	1778	1793	7166	7181	${}^mC_{ks}T_{ks}T_{ks}G_{ds}{}^mC_{ds}A_{ds}G_{ds}G_{ds}T_{ds}G_{ds}A_{ds}G_{ks}{}^mC_{ks}{}^mC_{ks}G_e$	26	4962

1207447	1786	1801	7174	7189	$G_{ks}A_{ks}T_{ks}G_{ds}A_{ds}T_{ds}G_{ds}^mC_{ds}^mC_{ds}T_{ds}$ $T_{ds}G_{ds}^mC_{ks}A_{ks}G_{ks}G_e$	7	4963
1207455	1892	1907	7280	7295	$^mC_{ks}^mC_{ks}^mC_{ks}T_{ds}G_{ds}A_{ds}G_{ds}^mC_{ds}A_{ds}$ $A_{ds}T_{ds}^mC_{ds}A_{ks}G_{ks}G_{ks}A_e$	18	3530
1207463	1900	1915	7288	7303	$A_{ks}G_{ks}A_{ks}T_{ds}G_{ds}A_{ds}G_{ds}T_{ds}^mC_{ds}^mC_{ds}$ $^mC_{ds}T_{ds}G_{ks}A_{ks}G_{ks}^mC_e$	14	2614
1207471	1915	1930	7303	7318	$T_{ks}^mC_{ks}A_{ks}^mC_{ds}^mC_{ds}A_{ds}A_{ds}G_{ds}G_{ds}A$ $_{ds}G_{ds}G_{ds}G_{ks}A_{ks}A_{ks}A_e$	24	4948
1207479	1923	1938	7311	7326	$^mC_{ks}T_{ks}G_{ks}^mC_{ds}G_{ds}G_{ds}A_{ds}A_{ds}T_{ds}^mC_d$ $sA_{ds}^mC_{ds}^mC_{ks}A_{ks}A_{ks}G_e$	11	3531
1207487	1931	1946	7319	7334	$^mC_{ks}T_{ks}^mC_{ks}T_{ds}^mC_{ds}T_{ds}^mC_{ds}A_{ds}^mC_{ds}$ $T_{ds}G_{ds}^mC_{ds}G_{ks}G_{ks}A_{ks}A_e$	6	2461
1207495	2001	2016	7389	7404	$G_{ks}^mC_{ks}G_{ks}^mC_{ds}^mC_{ds}A_{ds}T_{ds}^mC_{ds}^mC_{ds}$ $T_{ds}G_{ds}G_{ds}^mC_{ks}G_{ks}^mC_{ks}G_e$	116	4964
1207503	2009	2024	7397	7412	$G_{ks}A_{ks}G_{ks}T_{ds}T_{ds}^mC_{ds}^mC_{ds}T_{ds}G_{ds}^mC_d$ $sG_{ds}^mC_{ds}^mC_{ks}A_{ks}T_{ks}^mC_e$	9	3837
1207511	2018	2033	7406	7421	$^mC_{ks}A_{ks}^mC_{ks}T_{ds}T_{ds}T_{ds}A_{ds}T_{ds}T_{ds}G_{ds}$ $A_{ds}G_{ds}T_{ks}T_{ks}^mC_{ks}^mC_e$	11	2924
1207519	2033	2048	7421	7436	$T_{ks}^mC_{ks}A_{ks}G_{ds}^mC_{ds}A_{ds}T_{ds}T_{ds}T_{ds}T_{ds}^m$ $C_{ds}A_{ds}A_{ks}A_{ks}G_{ks}^mC_e$	20	3534

Table 84. Reduction of FXII RNA (Huh7, electroporation, 4000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence and Chemistry notation (5' to 3')	FXII (%UTC)	SEQ ID NO
1129491	1927	1942	7315	7330	$^mC_{ks}T_{ks}^mC_{ks}A_{ds}^mC_{ds}T_{ds}G_{ds}^mC_{ds}G_{ds}G_{ds}$ $A_{ds}A_{ds}T_{ds}^mC_{ks}A_{ks}^mC_k$	14	3835
1129531	2009	2024	7397	7412	$G_{ks}A_{ks}G_{ks}T_{ds}T_{ds}^mC_{ds}^mC_{ds}T_{ds}G_{ds}^mC_{ds}$ $G_{ds}^mC_{ds}^mC_{ds}A_{ks}T_{ks}^mC_k$	7	3837
1206489	1932	1947	7320	7335	$A_{ks}^mC_{ks}T_{ks}^mC_{ds}T_{ds}^mC_{ds}T_{ds}^mC_{ds}A_{ds}^mC_d$ $sT_{ds}G_{ds}^mC_{ds}G_{ks}G_{ks}A_k$	5	4976
1206498	1778	1793	7166	7181	$^mC_{ks}T_{ks}T_{ks}G_{ds}^mC_{ds}A_{ds}G_{ds}G_{ds}T_{ds}G_d$ $sA_{ds}G_{ds}^mC_{ks}^mC_{ks}G_k$	24	4962
1206504	1793	1808	7181	7196	$^mC_{ks}^mC_{ks}^mC_{ks}A_{ds}G_{ds}^mC_{ds}T_{ds}G_{ds}A_{ds}T_{ds}$ $G_{ds}A_{ds}T_{ds}G_{ks}^mC_{ks}^mC_k$	29	4953
1206899	142	157	509	524	$G_{ks}T_{es}G_{ks}^mC_{ds}T_{ds}^mC_{ds}T_{ds}T_{ds}^mC_{ds}A_{ds}G$ $_{ds}^mC_{ds}T_{es}T_{es}T_{ks}G_k$	8	4958
1206907	150	165	N/A	N/A	$A_{ks}^mC_{es}G_{ks}A_{ds}^mC_{ds}T_{ds}G_{ds}T_{ds}G_{ds}T_{ds}G_d$ $s^mC_{ds}T_{es}^mC_{es}T_{ks}T_k$	20	3495
1206915	158	173	N/A	N/A	$^mC_{ks}A_{es}G_{ks}T_{ds}G_{ds}A_{ds}G_{ds}A_{ds}A_{ds}^mC_{ds}G$ $_{ds}A_{ds}^mC_{es}T_{es}G_{ks}T_k$	25	2579
1206923	215	230	3566	3581	$A_{ks}T_{es}T_{ks}T_{ds}G_{ds}T_{ds}G_{ds}T_{ds}A_{ds}^mC_{ds}$ $A_{ds}G_{es}^mC_{es}T_{ks}G_k$	23	2963
1206931	223	238	3574	3589	$G_{ks}T_{es}G_{ks}G_{ds}G_{ds}T_{ds}A_{ds}^mC_{ds}A_{ds}T_{ds}T_{ds}$ $T_{ds}G_{es}T_{es}G_{ks}G_k$	23	3497
1206939	1783	1798	7171	7186	$G_{ks}A_{es}T_{ks}G_{ds}^mC_{ds}^mC_{ds}T_{ds}T_{ds}G_{ds}^mC_{ds}$ $A_{ds}G_{ds}G_{es}G_{es}T_{ks}G_k$	32	4959
1206947	1791	1806	7179	7194	$^mC_{ks}A_{es}G_{ks}^mC_{ds}T_{ds}G_{ds}A_{ds}T_{ds}G_{ds}A_{ds}T_d$ $sG_{ds}^mC_{es}^mC_{es}T_{ks}T_k$	41	4960

1206955	1897	1912	7285	7300	$T_{ks}G_{es}A_{ks}G_{ds}T_{ds}{}^mC_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}G_{ds}$ $A_{ds}G_{ds}{}^mC_{es}A_{es}A_{ks}T_k$	25	3910
1206963	1905	1920	7293	7308	$G_{ks}G_{es}G_{ks}A_{ds}A_{ds}A_{ds}G_{ds}A_{ds}T_{ds}G_{ds}A_{ds}$ $G_{ds}T_{es}{}^mC_{es}{}^mC_{ks}{}^mC_k$	43	2997
1206971	1920	1935	7308	7323	${}^mC_{ks}G_{es}G_{ks}A_{ds}A_{ds}T_{ds}{}^mC_{ds}A_{ds}{}^mC_{ds}{}^mC_{ds}$ $A_{ds}A_{ds}G_{es}G_{es}A_{ks}G_k$	7	3303
1206979	1928	1943	7316	7331	$T_{ks}{}^mC_{es}T_{ks}{}^mC_{ds}A_{ds}{}^mC_{ds}T_{ds}G_{ds}{}^mC_{ds}G_{ds}$ $G_{ds}A_{ds}A_{es}T_{es}{}^mC_{ks}A_k$	15	3911
1206987	1936	1951	7324	7339	$A_{ks}G_{es}{}^mC_{ks}{}^mC_{ds}A_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}$ ${}^mC_{ds}T_{ds}{}^mC_{ds}A_{es}{}^mC_{es}T_{ks}G_k$	8	4961
1206995	2006	2021	7394	7409	$T_{ks}T_{es}{}^mC_{ks}{}^mC_{ds}T_{ds}G_{ds}{}^mC_{ds}G_{ds}{}^mC_{ds}{}^mC_d$ $A_{ds}T_{ds}{}^mC_{es}{}^mC_{es}{}^mC_{es}T_{ks}G_k$	30	3609
1207003	2014	2029	7402	7417	$T_{ks}T_{es}A_{ks}T_{ds}T_{ds}G_{ds}A_{ds}G_{ds}T_{ds}{}^mC_{ds}{}^mC_{ds}$ $C_{ds}T_{es}G_{es}{}^mC_{ks}G_k$	16	2694
1207011	2023	2038	7411	7426	${}^mC_{ks}A_{es}A_{ks}A_{ds}G_{ds}{}^mC_{ds}A_{ds}{}^mC_{ds}T_{ds}T_{ds}$ $T_{ds}A_{ds}T_{es}T_{es}G_{ks}A_k$	25	3306
1207030	145	160	512	527	$T_{ks}G_{ks}T_{ds}G_{ds}T_{ds}G_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}T_{ds}T_{ds}$ ${}^mC_{es}A_{es}G_{es}{}^mC_{ks}T_k$	7	3112
1207038	153	168	N/A	N/A	$A_{ks}G_{ks}A_{ds}A_{ds}{}^mC_{ds}G_{ds}A_{ds}{}^mC_{ds}T_{ds}G_{ds}T_{ds}$ ${}^mC_{es}T_{es}G_{es}{}^mC_{ks}T_k$	15	3723
1207046	210	225	3561	3576	$T_{ks}G_{ks}G_{ds}T_{ds}A_{ds}{}^mC_{ds}A_{ds}G_{ds}{}^mC_{ds}T_{ds}G_d$ ${}^mC_{es}{}^mC_{es}G_{es}G_{ks}T_k$	18	2657
1207054	218	233	3569	3584	$T_{ks}A_{ks}{}^mC_{ds}A_{ds}T_{ds}T_{ds}T_{ds}G_{ds}T_{ds}G_{ds}G_{ds}$ $T_{es}A_{es}{}^mC_{es}A_{ks}G_k$	27	2426
1207062	1778	1793	7166	7181	${}^mC_{ks}T_{ks}T_{ds}G_{ds}{}^mC_{ds}A_{ds}G_{ds}G_{ds}T_{ds}G_d$ $A_{es}G_{es}{}^mC_{es}{}^mC_{ks}G_k$	31	4962
1207083	1786	1801	7174	7189	$G_{ks}A_{ks}T_{ds}G_{ds}A_{ds}T_{ds}G_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}T_d$ ${}^mC_{es}A_{es}G_{ks}G_k$	18	4963
1207091	1892	1907	7280	7295	${}^mC_{ks}{}^mC_{ks}{}^mC_{ds}T_{ds}G_{ds}A_{ds}G_{ds}{}^mC_{ds}A_{ds}A_d$ ${}^mC_{es}A_{es}G_{es}G_{ks}A_k$	48	3530
1207099	1900	1915	7288	7303	$A_{ks}G_{ks}A_{ds}T_{ds}G_{ds}A_{ds}G_{ds}T_{ds}{}^mC_{ds}{}^mC_{ds}{}^mC_{ds}$ $C_{ds}T_{es}G_{es}A_{es}G_{ks}{}^mC_k$	18	2614
1207107	1915	1930	7303	7318	$T_{ks}{}^mC_{ks}A_{ds}{}^mC_{ds}{}^mC_{ds}A_{ds}A_{ds}G_{ds}G_{ds}A_{ds}$ $G_{ds}G_{es}G_{es}A_{es}A_{ks}A_k$	20	4948
1207115	1923	1938	7311	7326	${}^mC_{ks}T_{ks}G_{ds}{}^mC_{ds}G_{ds}G_{ds}A_{ds}A_{ds}T_{ds}{}^mC_{ds}$ $A_{ds}{}^mC_{es}{}^mC_{es}A_{es}A_{ks}G_k$	10	3531
1207129	1931	1946	7319	7334	${}^mC_{ks}T_{ks}{}^mC_{ds}T_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}A_{ds}{}^mC_{ds}T_d$ ${}^mC_{es}G_{es}G_{es}A_{ks}A_k$	8	2461
1207144	2001	2016	7389	7404	$G_{ks}{}^mC_{ks}G_{ds}{}^mC_{ds}{}^mC_{ds}A_{ds}T_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}$ ${}^mC_{es}G_{es}{}^mC_{es}{}^mC_{ks}G_k$	74	4964
1207152	2009	2024	7397	7412	$G_{ks}A_{ks}G_{ds}T_{ds}T_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}G_{ds}{}^mC_{ds}$ $G_{ds}{}^mC_{es}{}^mC_{es}A_{es}T_{ks}{}^mC_k$	16	3837
1207160	2018	2033	7406	7421	${}^mC_{ks}A_{ks}{}^mC_{ds}T_{ds}T_{ds}T_{ds}A_{ds}T_{ds}T_{ds}G_{ds}A_{ds}$ $G_{es}T_{es}T_{es}{}^mC_{ks}{}^mC_k$	8	2924
1207168	2033	2048	7421	7436	$T_{ks}{}^mC_{ks}A_{ds}G_{ds}{}^mC_{ds}A_{ds}T_{ds}T_{ds}T_{ds}T_{ds}{}^mC_{ds}$ ${}^mC_{es}A_{es}A_{es}G_{ks}{}^mC_k$	29	3534
1207176	148	163	515	530	$G_{ks}A_{ks}{}^mC_{ds}T_{ds}G_{ds}T_{ds}G_{ds}T_{ds}G_{ds}{}^mC_{ds}T_d$ ${}^mC_{es}T_{ks}T_{es}{}^mC_{ks}A_e$	16	3343
1207184	156	171	N/A	N/A	$G_{ks}T_{ks}G_{ds}A_{ds}G_{ds}A_{ds}A_{ds}{}^mC_{ds}G_{ds}A_{ds}{}^mC_{ds}$ ${}^mC_{es}T_{ks}T_{es}G_{ks}T_e$	18	2424
1207192	213	228	3564	3579	$T_{ks}T_{ks}G_{ds}T_{ds}G_{ds}G_{ds}T_{ds}A_{ds}{}^mC_{ds}A_{ds}G_{ds}$ ${}^mC_{es}T_{ks}G_{es}{}^mC_{ks}{}^mC_e$	25	2811

1207200	221	236	3572	3587	$G_{ks}G_{ks}G_{ds}T_{ds}A_{ds}^mC_{ds}A_{ds}T_{ds}T_{ds}G_{ds}$ $T_{es}G_{ks}G_{es}T_{ks}A_e$	51	3345
1207208	1781	1796	7169	7184	$T_{ks}G_{ks}^mC_{ds}^mC_{ds}T_{ds}T_{ds}G_{ds}^mC_{ds}A_{ds}G_{ds}$ $G_{ds}G_{es}T_{ks}G_{es}A_{ks}G_e$	45	3527
1207216	1789	1804	7177	7192	$G_{ks}^mC_{ks}T_{ds}G_{ds}A_{ds}T_{ds}G_{ds}A_{ds}T_{ds}G_{ds}^mC_d$ $s^mC_{es}T_{ks}T_{es}G_{ks}^mC_e$	17	3755
1207224	1895	1910	7283	7298	$A_{ks}G_{ks}T_{ds}^mC_{ds}^mC_{ds}^mC_{ds}T_{ds}G_{ds}A_{ds}G_{ds}^m$ $C_{ds}A_{es}A_{ks}T_{es}^mC_{ks}A_e$	18	3758
1207232	1903	1918	7291	7306	$G_{ks}A_{ks}A_{ds}A_{ds}G_{ds}A_{ds}T_{ds}G_{ds}A_{ds}G_{ds}T_{ds}^m$ $C_{es}^mC_{ks}^mC_{es}T_{ks}G_e$	13	2845
1207240	1918	1933	7306	7321	$G_{ks}A_{ks}A_{ds}T_{ds}^mC_{ds}A_{ds}^mC_{ds}^mC_{ds}A_{ds}A_{ds}$ $G_{ds}G_{es}A_{ks}G_{es}G_{ks}G_e$	18	4965
1207248	1926	1941	7314	7329	$T_{ks}^mC_{ks}A_{ds}^mC_{ds}T_{ds}G_{ds}^mC_{ds}G_{ds}A_{ds}$ $A_{ds}T_{es}^mC_{ks}A_{es}^mC_{ks}^mC_e$	6	3759
1207256	1934	1949	7322	7337	$^mC_{ks}^mC_{ks}A_{ds}^mC_{ds}T_{ds}^mC_{ds}T_{ds}^mC_{ds}T_{ds}^m$ $C_{ds}A_{ds}^mC_{es}T_{ks}G_{es}^mC_{ks}G_e$	19	4949
1207264	2004	2019	7392	7407	$^mC_{ks}^mC_{ks}T_{ds}G_{ds}^mC_{ds}G_{ds}^mC_{ds}^mC_{ds}A_{ds}T$ $ds^mC_{ds}^mC_{es}T_{ks}G_{es}G_{ks}^mC_e$	18	3457
1207272	2012	2027	7400	7415	$A_{ks}T_{ks}T_{ds}G_{ds}A_{ds}G_{ds}T_{ds}T_{ds}^mC_{ds}^mC_{ds}T_{ds}$ $G_{es}^mC_{ks}G_{es}^mC_{ks}^mC_e$	22	2540
1207280	2021	2036	7409	7424	$A_{ks}A_{ks}G_{ds}^mC_{ds}A_{ds}^mC_{ds}T_{ds}T_{ds}T_{ds}A_{ds}T_d$ $s^mT_{es}G_{ks}A_{es}G_{ks}T_e$	9	3147
1207288	143	158	510	525	$T_{ks}G_{ks}T_{ds}G_{ds}^mC_{ds}T_{ds}^mC_{ds}T_{ds}T_{ds}^mC_{ds}A$ $dsG_{ks}^mC_{es}T_{ks}T_{es}T_k$	12	3037
1207296	151	166	N/A	N/A	$A_{ks}A_{ks}^mC_{ds}G_{ds}A_{ds}^mC_{ds}T_{ds}G_{ds}T_{ds}G_{ds}T_d$ $s^mG_{ks}^mC_{es}T_{ks}^mC_{es}T_k$	33	3571
1207304	208	223	3559	3574	$G_{ks}T_{ks}A_{ds}^mC_{ds}A_{ds}G_{ds}^mC_{ds}T_{ds}G_{ds}^mC_{ds}^m$ $C_{ds}G_{ks}G_{es}T_{ks}G_{es}G_k$	21	4968
1207312	216	231	3567	3582	$^mC_{ks}A_{ks}T_{ds}T_{ds}T_{ds}G_{ds}T_{ds}G_{ds}G_{ds}T_{ds}A_{ds}$ $^mC_{ks}A_{es}G_{ks}^mC_{es}T_k$	6	3039
1207320	1776	1791	7164	7179	$T_{ks}G_{ks}^mC_{ds}A_{ds}G_{ds}G_{ds}G_{ds}T_{ds}G_{ds}A_{ds}G_{ds}$ $^mC_{ks}^mC_{es}G_{ks}G_{es}^mC_k$	58	3299
1207328	1784	1799	7172	7187	$T_{ks}G_{ks}A_{ds}T_{ds}G_{ds}^mC_{ds}^mC_{ds}T_{ds}T_{ds}G_{ds}^mC$ $dsA_{ks}G_{es}G_{ks}G_{es}T_k$	42	4969
1207336	1792	1807	7180	7195	$^mC_{ks}^mC_{ks}A_{ds}G_{ds}^mC_{ds}T_{ds}G_{ds}A_{ds}T_{ds}G_{ds}$ $A_{ds}T_{ks}G_{es}^mC_{ks}^mC_{es}T_k$	25	4970
1207344	1898	1913	7286	7301	$A_{ks}T_{ks}G_{ds}A_{ds}G_{ds}T_{ds}^mC_{ds}^mC_{ds}^mC_{ds}T_{ds}$ $G_{ds}A_{ks}G_{es}^mC_{ks}A_{es}A_k$	30	2460
1207352	1906	1921	7294	7309	$A_{ks}G_{ks}G_{ds}G_{ds}A_{ds}A_{ds}A_{ds}G_{ds}A_{ds}T_{ds}G_{ds}$ $A_{ks}G_{es}T_{ks}^mC_{es}^mC_k$	18	3073
1207360	1921	1936	7309	7324	$G_{ks}^mC_{ks}G_{ds}G_{ds}A_{ds}A_{ds}T_{ds}^mC_{ds}A_{ds}^mC_{ds}$ $^mC_{ds}A_{ks}A_{es}G_{ks}G_{es}A_k$	6	3379
1207368	1929	1944	7317	7332	$^mC_{ks}T_{ks}^mC_{ds}T_{ds}^mC_{ds}A_{ds}^mC_{ds}T_{ds}G_{ds}^mC_d$ $s^mG_{ds}G_{ks}A_{es}A_{ks}T_{es}^mC_k$	16	4971
1207376	1937	1952	7325	7340	$^mC_{ks}A_{ks}G_{ds}^mC_{ds}^mC_{ds}A_{ds}^mC_{ds}T_{ds}^mC_{ds}T$ $ds^mC_{ds}T_{ks}^mC_{es}A_{ks}^mC_{es}T_k$	11	4972
1207384	2007	2022	7395	7410	$G_{ks}T_{ks}T_{ds}^mC_{ds}T_{ds}G_{ds}^mC_{ds}G_{ds}^mC_{ds}$ $^mC_{ds}A_{ks}T_{es}^mC_{ks}^mC_{es}T_k$	15	3685
1207392	2016	2031	7404	7419	$^mC_{ks}T_{ks}T_{ds}T_{ds}A_{ds}T_{ds}T_{ds}G_{ds}A_{ds}G_{ds}T_{ds}$ $T_{ks}^mC_{es}^mC_{ks}T_{es}G_k$	11	2771
1207400	2024	2039	7412	7427	$T_{ks}^mC_{ks}A_{ds}A_{ds}A_{ds}G_{ds}^mC_{ds}A_{ds}^mC_{ds}T_{ds}$ $T_{ds}T_{ks}A_{es}T_{ks}T_{es}G_k$	21	3382

1207408	146	161	513	528	${}^m\text{C}_{\text{ks}}\text{T}_{\text{ks}}\text{G}_{\text{ks}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ks}}\text{A}_{\text{ks}}\text{G}_{\text{ks}}{}^m\text{C}_{\text{e}}$	20	3190
1207416	154	169	N/A	N/A	$\text{G}_{\text{ks}}\text{A}_{\text{ks}}\text{G}_{\text{ks}}\text{A}_{\text{ds}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ks}}\text{T}_{\text{ks}}\text{G}_{\text{ks}}{}^m\text{C}_{\text{e}}$	24	3799
1207424	211	226	3562	3577	$\text{G}_{\text{ks}}\text{T}_{\text{ks}}\text{G}_{\text{ks}}\text{G}_{\text{ds}}\text{T}_{\text{ds}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{d}}\text{s}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{G}_{\text{ks}}\text{G}_{\text{e}}$	41	4973
1207432	219	234	3570	3585	$\text{G}_{\text{ks}}\text{T}_{\text{ks}}\text{A}_{\text{ks}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{G}_{\text{ds}}\text{T}_{\text{ks}}\text{A}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{A}_{\text{e}}$	50	3192
1207440	1779	1794	7167	7182	${}^m\text{C}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{T}_{\text{ks}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}\text{G}_{\text{ds}}\text{G}_{\text{ds}}\text{G}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ks}}\text{G}_{\text{ks}}{}^m\text{C}_{\text{ks}}{}^m\text{C}_{\text{e}}$	34	4974
1207448	1787	1802	7175	7190	$\text{T}_{\text{ks}}\text{G}_{\text{ks}}\text{A}_{\text{ks}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{d}}\text{s}\text{T}_{\text{ds}}\text{G}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{A}_{\text{ks}}\text{G}_{\text{e}}$	25	4975
1207456	1893	1908	7281	7296	$\text{T}_{\text{ks}}{}^m\text{C}_{\text{ks}}{}^m\text{C}_{\text{ks}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}\text{A}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ks}}\text{A}_{\text{ks}}\text{G}_{\text{ks}}\text{G}_{\text{e}}$	21	3606
1207464	1901	1916	7289	7304	$\text{A}_{\text{ks}}\text{A}_{\text{ks}}\text{G}_{\text{ks}}\text{A}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}\text{G}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ks}}\text{A}_{\text{ks}}\text{G}_{\text{e}}$	22	2691
1207472	1916	1931	7304	7319	$\text{A}_{\text{ks}}\text{T}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}\text{A}_{\text{ds}}\text{G}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}\text{G}_{\text{ds}}\text{G}_{\text{ks}}\text{G}_{\text{ks}}\text{A}_{\text{ks}}\text{A}_{\text{e}}$	10	4966
1207480	1924	1939	7312	7327	$\text{A}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{T}_{\text{ks}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{G}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}\text{A}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{A}_{\text{ks}}\text{A}_{\text{e}}$	2	3607
1207488	1932	1947	7320	7335	$\text{A}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{T}_{\text{ks}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{d}}\text{s}\text{T}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ks}}\text{G}_{\text{ks}}\text{G}_{\text{ks}}\text{A}_{\text{e}}$	6	4976
1207496	2002	2017	7390	7405	$\text{T}_{\text{ks}}\text{G}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{G}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{G}_{\text{ks}}{}^m\text{C}_{\text{e}}$	73	3305
1207504	2010	2025	7398	7413	$\text{T}_{\text{ks}}\text{G}_{\text{ks}}\text{A}_{\text{ks}}\text{G}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{A}_{\text{ks}}\text{T}_{\text{e}}$	5	3913
1207512	2019	2034	7407	7422	$\text{G}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{A}_{\text{ks}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}\text{A}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}\text{G}_{\text{ks}}\text{T}_{\text{ks}}\text{T}_{\text{ks}}{}^m\text{C}_{\text{e}}$	3	3000

Table 85. Reduction of FXII RNA (Huh7, electroporation, 4000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 2 Stop Site	SEQ ID NO: 1 Start Site	SEQ ID NO: 2 Stop Site	Sequence and Chemistry notation (5' to 3')	FXII (%UTC)	SEQ ID NO
1129531	2009	2024	7397	7412	$\text{G}_{\text{ks}}\text{A}_{\text{ks}}\text{G}_{\text{ks}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ks}}\text{T}_{\text{ks}}{}^m\text{C}_{\text{k}}$	15	3837
1129532	2010	2025	7398	7413	$\text{T}_{\text{ks}}\text{G}_{\text{ks}}\text{A}_{\text{ks}}\text{G}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ks}}\text{A}_{\text{ks}}\text{T}_{\text{k}}$	7	3913
1206485	1914	1929	7302	7317	${}^m\text{C}_{\text{ks}}\text{A}_{\text{ks}}{}^m\text{C}_{\text{ks}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}\text{A}_{\text{ds}}\text{G}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}\text{G}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}\text{A}_{\text{ks}}\text{A}_{\text{ks}}\text{G}_{\text{k}}$	27	4954
1206490	1933	1948	7321	7336	${}^m\text{C}_{\text{ks}}\text{A}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{d}}\text{s}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ks}}\text{G}_{\text{ks}}\text{G}_{\text{k}}$	6	4957
1206499	1779	1794	7167	7182	${}^m\text{C}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{T}_{\text{ks}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}\text{G}_{\text{ds}}\text{G}_{\text{ds}}\text{G}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}\text{G}_{\text{ks}}{}^m\text{C}_{\text{ks}}{}^m\text{C}_{\text{k}}$	36	4974
1206900	143	158	510	525	$\text{T}_{\text{ks}}\text{G}_{\text{es}}\text{T}_{\text{ks}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{es}}\text{T}_{\text{es}}\text{T}_{\text{ks}}\text{T}_{\text{k}}$	24	3037
1206908	151	166	N/A	N/A	$\text{A}_{\text{ks}}\text{A}_{\text{es}}{}^m\text{C}_{\text{ks}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{T}_{\text{d}}\text{s}\text{G}_{\text{ds}}{}^m\text{C}_{\text{es}}\text{T}_{\text{es}}{}^m\text{C}_{\text{ks}}\text{T}_{\text{k}}$	12	3571
1206916	208	223	3559	3574	$\text{G}_{\text{ks}}\text{T}_{\text{es}}\text{A}_{\text{ks}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{G}_{\text{ds}}\text{G}_{\text{es}}\text{T}_{\text{es}}\text{G}_{\text{ks}}\text{G}_{\text{k}}$	32	4968

1206924	216	231	3567	3582	${}^m\text{C}_{ks}\text{A}_{es}\text{T}_{ks}\text{T}_{ds}\text{T}_{ds}\text{G}_{ds}\text{T}_{ds}\text{G}_{ds}\text{G}_{ds}\text{T}_{ds}\text{A}_{ds}$ ${}^m\text{C}_{ds}\text{A}_{es}\text{G}_{es}{}^m\text{C}_{ks}\text{T}_k$	26	3039
1206932	1776	1791	7164	7179	$\text{T}_{ks}\text{G}_{es}{}^m\text{C}_{ks}\text{A}_{ds}\text{G}_{ds}\text{G}_{ds}\text{G}_{ds}\text{T}_{ds}\text{G}_{ds}\text{A}_{ds}\text{G}_{ds}$ ${}^m\text{C}_{ds}{}^m\text{C}_{es}\text{G}_{es}\text{G}_{ks}{}^m\text{C}_k$	40	3299
1206940	1784	1799	7172	7187	$\text{T}_{ks}\text{G}_{es}\text{A}_{ks}\text{T}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}\text{T}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}$ $\text{A}_{ds}\text{G}_{es}\text{G}_{es}\text{G}_{ks}\text{T}_k$	25	4969
1206948	1792	1807	7180	7195	${}^m\text{C}_{ks}{}^m\text{C}_{es}\text{A}_{ks}\text{G}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}\text{G}_{ds}\text{A}_{ds}\text{T}_{ds}\text{G}_{ds}$ $\text{A}_{ds}\text{T}_{ds}\text{G}_{es}{}^m\text{C}_{es}{}^m\text{C}_{ks}\text{T}_k$	24	4970
1206956	1898	1913	7286	7301	$\text{A}_{ks}\text{T}_{es}\text{G}_{ks}\text{A}_{ds}\text{G}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}{}^m\text{C}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}$ $\text{G}_{ds}\text{A}_{ds}\text{G}_{es}{}^m\text{C}_{es}\text{A}_{ks}\text{A}_k$	16	2460
1206964	1906	1921	7294	7309	$\text{A}_{ks}\text{G}_{es}\text{G}_{ks}\text{G}_{ds}\text{A}_{ds}\text{A}_{ds}\text{A}_{ds}\text{G}_{ds}\text{A}_{ds}\text{T}_{ds}\text{G}_{ds}$ $\text{A}_{ds}\text{G}_{es}\text{T}_{es}{}^m\text{C}_{ks}{}^m\text{C}_k$	21	3073
1206972	1921	1936	7309	7324	$\text{G}_{ks}{}^m\text{C}_{es}\text{G}_{ks}\text{G}_{ds}\text{A}_{ds}\text{A}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}\text{A}_{ds}{}^m\text{C}_{ds}$ ${}^m\text{C}_{ds}\text{A}_{ds}\text{A}_{es}\text{G}_{es}\text{G}_{ks}\text{A}_k$	15	3379
1206980	1929	1944	7317	7332	${}^m\text{C}_{ks}\text{T}_{es}{}^m\text{C}_{ks}\text{T}_{ds}{}^m\text{C}_{ds}\text{A}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}\text{G}_{ds}{}^m\text{C}_d$ $\text{G}_{ds}\text{G}_{ds}\text{A}_{es}\text{A}_{es}\text{T}_{ks}{}^m\text{C}_k$	8	4971
1206988	1937	1952	7325	7340	${}^m\text{C}_{ks}\text{A}_{es}\text{G}_{ks}{}^m\text{C}_{ds}{}^m\text{C}_{ds}\text{A}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}$ ${}^m\text{C}_{ds}\text{T}_{ds}{}^m\text{C}_{es}\text{A}_{es}{}^m\text{C}_{ks}\text{T}_k$	15	4972
1206996	2007	2022	7395	7410	$\text{G}_{ks}\text{T}_{es}\text{T}_{ks}{}^m\text{C}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}$ ${}^m\text{C}_{ds}\text{A}_{ds}\text{T}_{es}{}^m\text{C}_{es}{}^m\text{C}_{ks}\text{T}_k$	10	3685
1207004	2016	2031	7404	7419	${}^m\text{C}_{ks}\text{T}_{es}\text{T}_{ks}\text{T}_{ds}\text{A}_{ds}\text{T}_{ds}\text{T}_{ds}\text{G}_{ds}\text{A}_{ds}\text{G}_{ds}\text{T}_{ds}$ $\text{T}_{ds}{}^m\text{C}_{es}{}^m\text{C}_{es}\text{T}_{ks}\text{G}_k$	7	2771
1207012	2024	2039	7412	7427	$\text{T}_{ks}{}^m\text{C}_{es}\text{A}_{ks}\text{A}_{ds}\text{A}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}\text{A}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}$ $\text{T}_{ds}\text{T}_{ds}\text{A}_{es}\text{T}_{es}\text{T}_{ks}\text{G}_k$	14	3382
1207031	146	161	513	528	${}^m\text{C}_{ks}\text{T}_{ks}\text{G}_{ds}\text{T}_{ds}\text{G}_{ds}\text{T}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}$ $\text{T}_{es}{}^m\text{C}_{es}\text{A}_{es}\text{G}_{ks}{}^m\text{C}_k$	24	3190
1207039	154	169	N/A	N/A	$\text{G}_{ks}\text{A}_{ks}\text{G}_{ds}\text{A}_{ds}\text{A}_{ds}{}^m\text{C}_{ds}\text{G}_{ds}\text{A}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}\text{G}_{ds}$ $\text{T}_{es}\text{G}_{es}\text{T}_{es}\text{G}_{ks}{}^m\text{C}_k$	14	3799
1207047	211	226	3562	3577	$\text{G}_{ks}\text{T}_{ks}\text{G}_{ds}\text{G}_{ds}\text{T}_{ds}\text{A}_{ds}{}^m\text{C}_{ds}\text{A}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}\text{T}_d$ $\text{G}_{es}{}^m\text{C}_{es}{}^m\text{C}_{es}\text{G}_{ks}\text{G}_k$	18	4973
1207055	219	234	3570	3585	$\text{G}_{ks}\text{T}_{ks}\text{A}_{ds}{}^m\text{C}_{ds}\text{A}_{ds}\text{T}_{ds}\text{T}_{ds}\text{T}_{ds}\text{G}_{ds}\text{T}_{ds}\text{G}_{ds}$ $\text{G}_{es}\text{T}_{es}\text{A}_{es}{}^m\text{C}_{ks}\text{A}_k$	65	3192
1207063	1779	1794	7167	7182	${}^m\text{C}_{ks}{}^m\text{C}_{ks}\text{T}_{ds}\text{T}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}\text{A}_{ds}\text{G}_{ds}\text{G}_{ds}\text{G}_{ds}$ $\text{T}_{ds}\text{G}_{es}\text{A}_{es}\text{G}_{es}{}^m\text{C}_{ks}{}^m\text{C}_k$	32	4974
1207084	1787	1802	7175	7190	$\text{T}_{ks}\text{G}_{ks}\text{A}_{ds}\text{T}_{ds}\text{G}_{ds}\text{A}_{ds}\text{T}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}{}^m\text{C}_{ds}\text{T}_d$ $\text{T}_{es}\text{G}_{es}{}^m\text{C}_{es}\text{A}_{ks}\text{G}_k$	15	4975
1207092	1893	1908	7281	7296	$\text{T}_{ks}{}^m\text{C}_{ks}{}^m\text{C}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}\text{G}_{ds}\text{A}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}\text{A}_{ds}$ $\text{A}_{ds}\text{T}_{es}{}^m\text{C}_{es}\text{A}_{es}\text{G}_{ks}\text{G}_k$	29	3606
1207100	1901	1916	7289	7304	$\text{A}_{ks}\text{A}_{ks}\text{G}_{ds}\text{A}_{ds}\text{T}_{ds}\text{G}_{ds}\text{A}_{ds}\text{G}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}{}^m\text{C}_{ds}$ $\text{T}_{es}{}^m\text{C}_{es}\text{T}_{es}\text{G}_{es}\text{A}_{ks}\text{G}_k$	16	2691
1207108	1916	1931	7304	7319	$\text{A}_{ks}\text{T}_{ks}{}^m\text{C}_{ds}\text{A}_{ds}{}^m\text{C}_{ds}{}^m\text{C}_{ds}\text{A}_{ds}\text{A}_{ds}\text{G}_{ds}\text{G}_{ds}$ $\text{A}_{ds}\text{G}_{es}\text{G}_{es}\text{G}_{es}\text{A}_{ks}\text{A}_k$	9	4966
1207116	1924	1939	7312	7327	$\text{A}_{ks}{}^m\text{C}_{ks}\text{T}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}\text{G}_{ds}\text{G}_{ds}\text{A}_{ds}\text{A}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}$ $\text{C}_{ds}\text{A}_{es}{}^m\text{C}_{es}{}^m\text{C}_{es}\text{A}_{ks}\text{A}_k$	10	3607
1207131	1932	1947	7320	7335	$\text{A}_{ks}{}^m\text{C}_{ks}\text{T}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}\text{A}_{ds}{}^m\text{C}_d$ $\text{T}_{ds}\text{T}_{ds}\text{G}_{es}\text{G}_{es}{}^m\text{C}_{es}\text{G}_{es}\text{G}_{ks}\text{A}_k$	6	4976
1207145	2002	2017	7390	7405	$\text{T}_{ks}\text{G}_{ks}{}^m\text{C}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}{}^m\text{C}_{ds}\text{A}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}{}^m\text{C}_{ds}$ $\text{T}_{ds}\text{G}_{es}\text{G}_{es}{}^m\text{C}_{es}\text{G}_{ks}{}^m\text{C}_k$	46	3305
1207153	2010	2025	7398	7413	$\text{T}_{ks}\text{G}_{ks}\text{A}_{ds}\text{G}_{ds}\text{T}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}$ $\text{T}_{es}\text{G}_{es}{}^m\text{C}_{es}{}^m\text{C}_{es}\text{A}_{ks}\text{T}_k$	13	3913
1207161	2019	2034	7407	7422	$\text{G}_{ks}{}^m\text{C}_{ks}\text{A}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}\text{T}_{ds}\text{T}_{ds}\text{A}_{ds}\text{T}_{ds}\text{T}_{ds}\text{G}_{ds}$ $\text{A}_{es}\text{G}_{es}\text{T}_{es}\text{T}_{ks}{}^m\text{C}_k$	17	3000

1207169	141	156	508	523	$T_{ks}G_{ks}{}^mC_{ds}T_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}A_{ds}G_{ds}{}^m$ $C_{ds}T_{es}T_{ks}T_{es}G_{ks}T_e$	33	4950
1207177	149	164	516	531	${}^mC_{ks}G_{ks}A_{ds}{}^mC_{ds}T_{ds}G_{ds}T_{ds}G_{ds}T_{ds}G_{ds}{}^m$ $C_{ds}T_{es}{}^mC_{ks}T_{es}T_{ks}{}^mC_e$	17	3419
1207185	157	172	N/A	N/A	$A_{ks}G_{ks}T_{ds}G_{ds}A_{ds}G_{ds}A_{ds}{}^mC_{ds}G_{ds}A_{ds}$ ${}^mC_{es}T_{ks}G_{es}T_{ks}G_e$	15	2502
1207193	214	229	3565	3580	$T_{ks}T_{ks}T_{ds}G_{ds}T_{ds}G_{ds}G_{ds}T_{ds}A_{ds}{}^mC_{ds}A_{ds}$ $G_{es}{}^mC_{ks}T_{es}G_{ks}{}^mC_e$	17	2887
1207201	222	237	3573	3588	$T_{ks}G_{ks}G_{ds}G_{ds}T_{ds}A_{ds}{}^mC_{ds}A_{ds}T_{ds}T_{ds}T_{ds}$ $G_{es}T_{ks}G_{es}G_{ks}T_e$	25	3421
1207209	1782	1797	7170	7185	$A_{ks}T_{ks}G_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}T_{ds}G_{ds}{}^mC_{ds}A_{ds}$ $G_{ds}G_{es}G_{ks}T_{es}G_{ks}A_e$	26	4947
1207217	1790	1805	7178	7193	$A_{ks}G_{ks}{}^mC_{ds}T_{ds}G_{ds}A_{ds}T_{ds}G_{ds}A_{ds}T_{ds}G_{ds}$ ${}^mC_{es}{}^mC_{ks}T_{es}T_{ks}G_e$	22	3831
1207225	1896	1911	7284	7299	$G_{ks}A_{ks}G_{ds}T_{ds}{}^mC_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}G_{ds}A_{ds}$ $G_{ds}{}^mC_{es}A_{ks}A_{es}T_{ks}{}^mC_e$	7	3834
1207233	1904	1919	7292	7307	$G_{ks}G_{ks}A_{ds}A_{ds}A_{ds}G_{ds}A_{ds}T_{ds}G_{ds}A_{ds}G_{ds}$ $T_{es}{}^mC_{ks}{}^mC_{es}{}^mC_{ks}T_e$	31	2921
1207241	1919	1934	7307	7322	$G_{ks}G_{ks}A_{ds}A_{ds}T_{ds}{}^mC_{ds}A_{ds}{}^mC_{ds}{}^mC_{ds}A_{ds}$ $A_{ds}G_{es}G_{ks}A_{es}G_{ks}G_e$	21	3226
1207249	1927	1942	7315	7330	${}^mC_{ks}T_{ks}{}^mC_{ds}A_{ds}{}^mC_{ds}T_{ds}G_{ds}{}^mC_{ds}G_{ds}G_{ds}$ $A_{ds}A_{es}T_{ks}{}^mC_{es}A_{ks}{}^mC_e$	12	3835
1207257	1935	1950	7323	7338	$G_{ks}{}^mC_{ks}{}^mC_{ds}A_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}T_d$ ${}^mC_{ds}A_{es}{}^mC_{ks}T_{es}G_{ks}{}^mC_e$	25	4967
1207265	2005	2020	7393	7408	$T_{ks}{}^mC_{ks}{}^mC_{ds}T_{ds}G_{ds}{}^mC_{ds}G_{ds}{}^mC_{ds}{}^mC_{ds}A$ ${}^mC_{ds}T_{ds}{}^mC_{es}{}^mC_{ks}T_{es}G_{ks}G_e$	24	3533
1207273	2013	2028	7401	7416	$T_{ks}A_{ks}T_{ds}T_{ds}G_{ds}A_{ds}G_{ds}T_{ds}T_{ds}{}^mC_{ds}{}^mC_{ds}$ $T_{es}G_{ks}{}^mC_{es}G_{ks}{}^mC_e$	21	2617
1207281	2022	2037	7410	7425	$A_{ks}A_{ks}A_{ds}G_{ds}{}^mC_{ds}A_{ds}{}^mC_{ds}T_{ds}T_{ds}T_{ds}A_d$ ${}^mC_{es}T_{ks}G_{es}A_{ks}G_e$	21	3229
1207289	144	159	511	526	$G_{ks}T_{ks}G_{ds}T_{ds}G_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}T_{ds}T_{ds}{}^mC$ ${}^mC_{ds}A_{ks}G_{es}{}^mC_{ks}T_{es}T_k$	20	4951
1207297	152	167	N/A	N/A	$G_{ks}A_{ks}A_{ds}{}^mC_{ds}G_{ds}A_{ds}{}^mC_{ds}T_{ds}G_{ds}T_{ds}G$ ${}^mC_{ds}T_{ks}G_{es}{}^mC_{ks}T_{es}{}^mC_k$	23	3647
1207305	209	224	3560	3575	$G_{ks}G_{ks}T_{ds}A_{ds}{}^mC_{ds}A_{ds}G_{ds}{}^mC_{ds}T_{ds}G_{ds}{}^m$ $C_{ds}{}^mC_{ks}G_{es}G_{ks}T_{es}G_k$	23	4952
1207313	217	232	3568	3583	$A_{ks}{}^mC_{ks}A_{ds}T_{ds}T_{ds}T_{ds}G_{ds}T_{ds}G_{ds}G_{ds}T_{ds}$ $A_{ks}{}^mC_{es}A_{ks}G_{es}{}^mC_k$	12	3114
1207321	1777	1792	7165	7180	$T_{ks}T_{ks}G_{ds}{}^mC_{ds}A_{ds}G_{ds}G_{ds}G_{ds}T_{ds}G_{ds}A_{ds}$ $G_{ks}{}^mC_{es}{}^mC_{ks}G_{es}G_k$	36	3375
1207329	1785	1800	7173	7188	$A_{ks}T_{ks}G_{ds}A_{ds}T_{ds}G_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}T_{ds}G_d$ ${}^mC_{ks}A_{es}G_{ks}G_{es}G_k$	21	3603
1207337	1793	1808	7181	7196	${}^mC_{ks}{}^mC_{ks}{}^mC_{ds}A_{ds}G_{ds}{}^mC_{ds}T_{ds}G_{ds}A_{ds}T_{ds}$ $G_{ds}A_{ks}T_{es}G_{ks}{}^mC_{es}{}^mC_k$	53	4953
1207345	1899	1914	7287	7302	$G_{ks}A_{ks}T_{ds}G_{ds}A_{ds}G_{ds}T_{ds}{}^mC_{ds}{}^mC_{ds}{}^mC_{ds}$ $T_{ds}G_{ks}A_{es}G_{ks}{}^mC_{es}A_k$	12	2537
1207353	1914	1929	7302	7317	${}^mC_{ks}A_{ks}{}^mC_{ds}{}^mC_{ds}A_{ds}A_{ds}G_{ds}G_{ds}A_{ds}G_{ds}$ $G_{ds}G_{ks}A_{es}A_{ks}A_{es}G_k$	22	4954
1207361	1922	1937	7310	7325	$T_{ks}G_{ks}{}^mC_{ds}G_{ds}G_{ds}A_{ds}A_{ds}T_{ds}{}^mC_{ds}A_{ds}{}^m$ $C_{ds}{}^mC_{ks}A_{es}A_{ks}G_{es}G_k$	11	3455
1207369	1930	1945	7318	7333	$T_{ks}{}^mC_{ks}T_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}A_{ds}{}^mC_{ds}T_{ds}G_{ds}$ ${}^mC_{ds}G_{ks}G_{es}A_{ks}A_{es}T_k$	13	4955

1207377	2000	2015	7388	7403	${}^m\text{C}_{\text{ks}}\text{G}_{\text{ks}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ks}}\text{G}_{\text{es}}{}^m\text{C}_{\text{ks}}\text{G}_{\text{es}}\text{G}_{\text{k}}$	42	3228
1207385	2008	2023	7396	7411	$\text{A}_{\text{ks}}\text{G}_{\text{ks}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ks}}\text{A}_{\text{es}}\text{T}_{\text{ks}}{}^m\text{C}_{\text{es}}{}^m\text{C}_{\text{k}}$	14	3761
1207393	2017	2032	7405	7420	$\text{A}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}\text{A}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}\text{G}_{\text{ds}}\text{T}_{\text{ks}}\text{T}_{\text{es}}{}^m\text{C}_{\text{ks}}{}^m\text{C}_{\text{es}}\text{T}_{\text{k}}$	7	2848
1207401	2031	2046	7419	7434	$\text{A}_{\text{ks}}\text{G}_{\text{ks}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}\text{A}_{\text{d}}\text{s}_{\text{A}}\text{G}_{\text{es}}{}^m\text{C}_{\text{ks}}\text{A}_{\text{es}}{}^m\text{C}_{\text{k}}$	10	3458
1207409	147	162	514	529	$\text{A}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{T}_{\text{ks}}\text{G}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{A}_{\text{ks}}\text{G}_{\text{e}}$	21	3267
1207417	155	170	N/A	N/A	$\text{T}_{\text{ks}}\text{G}_{\text{ks}}\text{A}_{\text{ks}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{T}_{\text{ks}}\text{G}_{\text{ks}}\text{T}_{\text{ks}}\text{G}_{\text{e}}$	35	3875
1207425	212	227	3563	3578	$\text{T}_{\text{ks}}\text{G}_{\text{ks}}\text{T}_{\text{ks}}\text{G}_{\text{ds}}\text{G}_{\text{ds}}\text{T}_{\text{ds}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{d}}\text{s}_{\text{T}}\text{G}_{\text{ds}}\text{G}_{\text{ks}}{}^m\text{C}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{G}_{\text{e}}$	30	2734
1207433	220	235	3571	3586	$\text{G}_{\text{ks}}\text{G}_{\text{ks}}\text{T}_{\text{ks}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{G}_{\text{ks}}\text{T}_{\text{ks}}\text{A}_{\text{ks}}{}^m\text{C}_{\text{e}}$	23	3269
1207441	1780	1795	7168	7183	$\text{G}_{\text{ks}}{}^m\text{C}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}\text{G}_{\text{ds}}\text{G}_{\text{ds}}\text{G}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ks}}\text{A}_{\text{ks}}\text{G}_{\text{ks}}{}^m\text{C}_{\text{e}}$	26	3451
1207449	1788	1803	7176	7191	${}^m\text{C}_{\text{ks}}\text{T}_{\text{ks}}\text{G}_{\text{ks}}\text{A}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ks}}\text{G}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{A}_{\text{e}}$	25	3679
1207457	1894	1909	7282	7297	$\text{G}_{\text{ks}}\text{T}_{\text{ks}}{}^m\text{C}_{\text{ks}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}\text{A}_{\text{ds}}\text{T}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{A}_{\text{ks}}\text{G}_{\text{e}}$	25	3682
1207465	1902	1917	7290	7305	$\text{A}_{\text{ks}}\text{A}_{\text{ks}}\text{A}_{\text{ks}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}\text{G}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ks}}\text{T}_{\text{ks}}\text{G}_{\text{ks}}\text{A}_{\text{e}}$	13	2768
1207473	1917	1932	7305	7320	$\text{A}_{\text{ks}}\text{A}_{\text{ks}}\text{T}_{\text{ks}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}\text{A}_{\text{ds}}\text{G}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}\text{G}_{\text{ks}}\text{G}_{\text{ks}}\text{A}_{\text{e}}$	23	4956
1207481	1925	1940	7313	7328	${}^m\text{C}_{\text{ks}}\text{A}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{G}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}\text{A}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ks}}{}^m\text{C}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{A}_{\text{e}}$	4	3683
1207489	1933	1948	7321	7336	${}^m\text{C}_{\text{ks}}\text{A}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{d}}\text{s}_{\text{T}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{G}_{\text{ks}}\text{G}_{\text{e}}$	12	4957
1207497	2003	2018	7391	7406	${}^m\text{C}_{\text{ks}}\text{T}_{\text{ks}}\text{G}_{\text{ks}}{}^m\text{C}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ks}}\text{G}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{G}_{\text{e}}$	45	3381
1207505	2011	2026	7399	7414	$\text{T}_{\text{ks}}\text{T}_{\text{ks}}\text{G}_{\text{ks}}\text{A}_{\text{ds}}\text{G}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{G}_{\text{ks}}{}^m\text{C}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{A}_{\text{e}}$	7	2463
1207513	2020	2035	7408	7423	$\text{A}_{\text{ks}}\text{G}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}\text{A}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ks}}\text{G}_{\text{ks}}\text{T}_{\text{ks}}\text{T}_{\text{e}}$	4	3076

Table 86. Reduction of FXII RNA (Huh7, electroporation, 2000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence and Chemistry notation (5' to 3')	FXII (%UTC)	SEQ ID NO
1128769	153	168	N/A	N/A	$\text{A}_{\text{ks}}\text{G}_{\text{ks}}\text{A}_{\text{ks}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{T}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{T}_{\text{k}}$	19	3723
1128802	218	233	3569	3584	$\text{T}_{\text{ks}}\text{A}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{A}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{G}_{\text{ds}}\text{T}_{\text{ds}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{ks}}\text{A}_{\text{ks}}\text{G}_{\text{k}}$	108	2426
1128870	470	485	4415	4430	$\text{T}_{\text{ks}}\text{G}_{\text{ks}}\text{T}_{\text{ks}}\text{G}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}\text{A}_{\text{ds}}\text{A}_{\text{ds}}\text{A}_{\text{ds}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{G}_{\text{ds}}\text{G}_{\text{ks}}\text{A}_{\text{ks}}\text{G}_{\text{k}}$	31	3728
1129485	1921	1936	7309	7324	$\text{G}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{G}_{\text{ks}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}\text{A}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}\text{A}_{\text{ds}}\text{G}_{\text{ks}}\text{G}_{\text{ks}}\text{A}_{\text{k}}$	20	3379

1129491	1927	1942	7315	7330	${}^m\text{C}_{ks}\text{T}_{ks}{}^m\text{C}_{ks}\text{A}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}\text{G}_{ds}\text{G}_{ds}$ $\text{A}_{ds}\text{A}_{ds}\text{T}_{ds}{}^m\text{C}_{ks}\text{A}_{ks}{}^m\text{C}_k$	17	3835
1129492	1928	1943	7316	7331	$\text{T}_{ks}{}^m\text{C}_{ks}\text{T}_{ks}{}^m\text{C}_{ds}\text{A}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}\text{G}_{ds}$ $\text{G}_{ds}\text{A}_{ds}\text{A}_{ds}\text{T}_{ks}{}^m\text{C}_{ks}\text{A}_k$	7	3911
1129531	2009	2024	7397	7412	$\text{G}_{ks}\text{A}_{ks}\text{G}_{ks}\text{T}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}$ $\text{G}_{ds}{}^m\text{C}_{ds}{}^m\text{C}_{ds}\text{A}_{ks}\text{T}_{ks}{}^m\text{C}_k$	17	3837
1129532	2010	2025	7398	7413	$\text{T}_{ks}\text{G}_{ks}\text{A}_{ks}\text{G}_{ds}\text{T}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}$ $\text{G}_{ds}{}^m\text{C}_{ds}{}^m\text{C}_{ks}\text{A}_{ks}\text{T}_k$	6	3913
1129538	2017	2032	7405	7420	$\text{A}_{ks}{}^m\text{C}_{ks}\text{T}_{ks}\text{T}_{ds}\text{T}_{ds}\text{A}_{ds}\text{T}_{ds}\text{T}_{ds}\text{G}_{ds}\text{A}_{ds}\text{G}_{ds}$ $\text{T}_{ds}\text{T}_{ds}{}^m\text{C}_{ks}{}^m\text{C}_{ks}\text{T}_k$	7	2848
1129540	2019	2034	7407	7422	$\text{G}_{ks}{}^m\text{C}_{ks}\text{A}_{ks}{}^m\text{C}_{ds}\text{T}_{ds}\text{T}_{ds}\text{T}_{ds}\text{A}_{ds}\text{T}_{ds}\text{T}_{ds}\text{G}_{ds}$ $\text{A}_{ds}\text{G}_{ds}\text{T}_{ks}\text{T}_{ks}{}^m\text{C}_k$	3	3000
1129579	N/A	N/A	208	223	${}^m\text{C}_{ks}\text{A}_{ks}{}^m\text{C}_{ks}\text{A}_{ds}\text{T}_{ds}\text{A}_{ds}\text{G}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}{}^m\text{C}_d$ $\text{T}_{ds}{}^m\text{C}_{ds}{}^m\text{C}_{ds}\text{T}_{ks}\text{A}_{ks}\text{G}_k$	55	2926
1129714	N/A	N/A	1558	1573	$\text{A}_{ks}\text{G}_{ks}\text{G}_{ks}\text{G}_{ds}\text{T}_{ds}\text{A}_{ds}\text{A}_{ds}\text{G}_{ds}\text{G}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}$ ${}^m\text{C}_{ds}\text{A}_{ds}\text{T}_{ks}{}^m\text{C}_{ks}\text{T}_k$	63	2549
1129740	N/A	N/A	1758	1773	$\text{G}_{ks}\text{A}_{ks}\text{T}_{ks}\text{G}_{ds}\text{G}_{ds}\text{G}_{ds}\text{A}_{ds}\text{T}_{ds}\text{G}_{ds}\text{G}_{ds}\text{A}_{ds}{}^m$ $\text{C}_{ds}\text{G}_{ds}\text{G}_{ks}\text{A}_{ks}{}^m\text{C}_k$	69	3010
1129760	N/A	N/A	2284	2299	$\text{A}_{ks}{}^m\text{C}_{ks}{}^m\text{C}_{ks}\text{A}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}\text{G}_{ds}\text{A}_d$ $\text{A}_{ds}\text{T}_{ds}\text{A}_{ds}\text{A}_{ks}\text{T}_{ks}\text{G}_k$	44	3011
1129773	N/A	N/A	2450	2465	$\text{G}_{ks}{}^m\text{C}_{ks}\text{A}_{ks}\text{T}_{ds}\text{T}_{ds}\text{G}_{ds}\text{A}_{ds}\text{T}_{ds}\text{G}_{ds}\text{A}_{ds}\text{A}_{ds}$ $\text{T}_{ds}{}^m\text{C}_{ds}\text{A}_{ks}\text{G}_{ks}{}^m\text{C}_k$	28	2475
1129779	N/A	N/A	2470	2485	$\text{G}_{ks}{}^m\text{C}_{ks}\text{T}_{ks}\text{A}_{ds}\text{T}_{ds}\text{A}_{ds}\text{G}_{ds}\text{T}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}{}^m$ $\text{C}_{ds}\text{A}_{ds}\text{T}_{ds}{}^m\text{C}_{ks}\text{A}_{ks}\text{G}_k$	27	2936
1129802	N/A	N/A	2654	2669	$\text{T}_{ks}{}^m\text{C}_{ks}{}^m\text{C}_{ks}\text{T}_{ds}\text{A}_{ds}\text{T}_{ds}\text{T}_{ds}\text{G}_{ds}\text{A}_{ds}\text{A}_{ds}\text{T}_{ds}$ $\text{G}_{ds}\text{A}_{ds}\text{G}_{ks}\text{T}_{ks}\text{G}_k$	33	3160
1129948	N/A	N/A	4840	4855	$\text{A}_{ks}\text{T}_{ks}{}^m\text{C}_{ks}\text{T}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}\text{T}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}{}^m$ $\text{C}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}\text{A}_{ks}{}^m\text{C}_{ks}\text{T}_k$	51	3630
1129949	N/A	N/A	4844	4859	$\text{T}_{ks}{}^m\text{C}_{ks}\text{T}_{ks}{}^m\text{C}_{ds}\text{A}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}$ $\text{T}_{ds}\text{T}_{ds}\text{T}_{ds}{}^m\text{C}_{ks}{}^m\text{C}_{ks}\text{G}_k$	24	3706
1130060	N/A	N/A	6178	6193	$\text{A}_{ks}\text{A}_{ks}\text{G}_{ks}\text{G}_{ds}{}^m\text{C}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}\text{A}_{ds}\text{A}_{ds}{}^m\text{C}_{ds}$ $\text{A}_{ds}\text{G}_{ds}\text{A}_{ds}\text{G}_{ks}{}^m\text{C}_{ks}\text{T}_k$	22	3026
1130240	N/A	N/A	7098	7113	$\text{G}_{ks}\text{T}_{ks}{}^m\text{C}_{ks}\text{G}_{ds}\text{G}_{ds}\text{A}_{ds}\text{A}_{ds}\text{A}_{ds}{}^m\text{C}_{ds}\text{A}_{ds}{}^m$ $\text{C}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}\text{A}_{ks}\text{G}_{ks}{}^m\text{C}_k$	47 [†]	3035
1213035	141	156	508	523	$\text{T}_{ks}\text{G}_{ks}{}^m\text{C}_{ks}\text{T}_{ds}\text{C}_{ys}\text{T}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}\text{A}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}$ $\text{T}_{ds}\text{T}_{ds}\text{T}_{ks}\text{G}_{ks}\text{T}_k$	40	4950
1213036	142	157	509	524	$\text{G}_{ks}\text{T}_{ks}\text{G}_{ks}{}^m\text{C}_{ds}\text{U}_{ys}{}^m\text{C}_{ds}\text{T}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}\text{A}_{ds}$ $\text{G}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}\text{T}_{ks}\text{T}_{ks}\text{G}_k$	28	4977
1213037	143	158	510	525	$\text{T}_{ks}\text{G}_{ks}\text{T}_{ks}\text{G}_{ds}\text{C}_{ys}\text{T}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}\text{A}_{ds}$ $\text{G}_{ds}{}^m\text{C}_{ds}\text{T}_{ks}\text{T}_{ks}\text{T}_k$	46	3037
1213038	144	159	511	526	$\text{G}_{ks}\text{T}_{ks}\text{G}_{ks}\text{T}_{ds}\text{G}_{ys}{}^m\text{C}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}$ $\text{dsA}_{ds}\text{G}_{ds}{}^m\text{C}_{ks}\text{T}_{ks}\text{T}_k$	33	4951
1213039	145	160	512	527	$\text{T}_{ks}\text{G}_{ks}\text{T}_{ks}\text{G}_{ds}\text{U}_{ys}\text{G}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}\text{T}_{ds}$ ${}^m\text{C}_{ds}\text{A}_{ds}\text{G}_{ks}{}^m\text{C}_{ks}\text{T}_k$	91	4978
1213040	146	161	513	528	${}^m\text{C}_{ks}\text{T}_{ks}\text{G}_{ks}\text{T}_{ds}\text{G}_{ys}\text{T}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}$ $\text{T}_{ds}{}^m\text{C}_{ds}\text{A}_{ks}\text{G}_{ks}{}^m\text{C}_k$	35	3190
1213041	147	162	514	529	$\text{A}_{ks}{}^m\text{C}_{ks}\text{T}_{ks}\text{G}_{ds}\text{U}_{ys}\text{G}_{ds}\text{T}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}{}^m$ $\text{C}_{ds}\text{T}_{ds}\text{T}_{ds}{}^m\text{C}_{ks}\text{A}_{ks}\text{G}_k$	27	4979
1213042	148	163	515	530	$\text{G}_{ks}\text{A}_{ks}{}^m\text{C}_{ks}\text{T}_{ds}\text{G}_{ys}\text{T}_{ds}\text{G}_{ds}\text{T}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}\text{T}_d$ $\text{s}{}^m\text{C}_{ds}\text{T}_{ds}\text{T}_{ks}{}^m\text{C}_{ks}\text{A}_k$	50	3343
1213043	149	164	516	531	${}^m\text{C}_{ks}\text{G}_{ks}\text{A}_{ks}{}^m\text{C}_{ds}\text{U}_{ys}\text{G}_{ds}\text{T}_{ds}\text{G}_{ds}\text{T}_{ds}\text{G}_{ds}{}^m$ $\text{C}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}\text{T}_{ks}\text{T}_{ks}{}^m\text{C}_k$	65	4980

1213044	150	165	N/A	N/A	$A_{ks} {}^mC_{ks} G_{ks} A_{ds} C_{ys} T_{ds} G_{ds} T_{ds} G_{ds} T_{ds} G_{ds}$ ${}^mC_{ds} T_{ds} {}^mC_{ks} T_{ks} T_k$	52	3495
1213045	151	166	N/A	N/A	$A_{ks} A_{ks} {}^mC_{ks} G_{ds} A_{ys} {}^mC_{ds} T_{ds} G_{ds} T_{ds} G_{ds} T_d$ $s G_{ds} {}^mC_{ds} T_{ks} {}^mC_{ks} T_k$	47	3571
1213046	152	167	N/A	N/A	$G_{ks} A_{ks} A_{ks} {}^mC_{ds} G_{ys} A_{ds} {}^mC_{ds} T_{ds} G_{ds} T_{ds} G$ $ds T_{ds} G_{ds} {}^mC_{ks} T_{ks} {}^mC_k$	77	3647
1213047	153	168	N/A	N/A	$A_{ks} G_{ks} A_{ks} A_{ds} C_{ys} G_{ds} A_{ds} {}^mC_{ds} T_{ds} G_{ds} T_{ds}$ $G_{ds} T_{ds} G_{ks} {}^mC_{ks} T_k$	42	3723
1213048	154	169	N/A	N/A	$G_{ks} A_{ks} G_{ks} A_{ds} A_{ys} {}^mC_{ds} G_{ds} A_{ds} {}^mC_{ds} T_{ds} G$ $ds T_{ds} G_{ds} T_{ks} G_{ks} {}^mC_k$	61	3799
1213049	155	170	N/A	N/A	$T_{ks} G_{ks} A_{ks} G_{ds} A_{ys} A_{ds} {}^mC_{ds} G_{ds} A_{ds} {}^mC_{ds} T$ $ds G_{ds} T_{ds} G_{ks} T_{ks} G_k$	42	3875
1213050	156	171	N/A	N/A	$G_{ks} T_{ks} G_{ks} A_{ds} G_{ys} A_{ds} A_{ds} {}^mC_{ds} G_{ds} A_{ds} {}^mC$ $ds T_{ds} G_{ds} T_{ks} G_{ks} T_k$	35	2424
1213051	157	172	N/A	N/A	$A_{ks} G_{ks} T_{ks} G_{ds} A_{ys} G_{ds} A_{ds} A_{ds} {}^mC_{ds} G_{ds} A_{ds}$ ${}^mC_{ds} T_{ds} G_{ks} T_{ks} G_k$	69	2502
1213052	158	173	N/A	N/A	${}^mC_{ks} A_{ks} G_{ks} T_{ds} G_{ys} A_{ds} G_{ds} A_{ds} A_{ds} {}^mC_{ds} G$ $ds A_{ds} {}^mC_{ds} T_{ks} G_{ks} T_k$	54	2579
1213053	208	223	3559	3574	$G_{ks} T_{ks} A_{ks} {}^mC_{ds} A_{ys} G_{ds} {}^mC_{ds} T_{ds} G_{ds} {}^mC_{ds} {}^m$ $C_{ds} G_{ds} G_{ds} T_{ks} G_{ks} G_k$	33	4968
1213054	209	224	3560	3575	$G_{ks} G_{ks} T_{ks} A_{ds} C_{ys} A_{ds} G_{ds} {}^mC_{ds} T_{ds} G_{ds} {}^mC$ $ds {}^mC_{ds} G_{ds} G_{ks} T_{ks} G_k$	33	4952
1213055	210	225	3561	3576	$T_{ks} G_{ks} G_{ks} T_{ds} A_{ys} {}^mC_{ds} A_{ds} G_{ds} {}^mC_{ds} T_{ds} G_d$ $s {}^mC_{ds} {}^mC_{ds} G_{ks} G_{ks} T_k$	26	2657
1213056	211	226	3562	3577	$G_{ks} T_{ks} G_{ks} G_{ds} U_{ys} A_{ds} {}^mC_{ds} A_{ds} G_{ds} {}^mC_{ds} T$ $ds G_{ds} {}^mC_{ds} {}^mC_{ks} G_{ks} G_k$	34	4981
1213057	212	227	3563	3578	$T_{ks} G_{ks} T_{ks} G_{ds} G_{ys} T_{ds} A_{ds} {}^mC_{ds} A_{ds} G_{ds} {}^mC_d$ $s T_{ds} G_{ds} {}^mC_{ks} {}^mC_{ks} G_k$	78	2734
1213058	213	228	3564	3579	$T_{ks} T_{ks} G_{ks} T_{ds} G_{ys} G_{ds} T_{ds} A_{ds} {}^mC_{ds} A_{ds} G_{ds}$ ${}^mC_{ds} T_{ds} G_{ks} {}^mC_{ks} {}^mC_k$	29	2811
1213059	214	229	3565	3580	$T_{ks} T_{ks} T_{ks} G_{ds} U_{ys} G_{ds} G_{ds} T_{ds} A_{ds} {}^mC_{ds} A_{ds}$ $G_{ds} {}^mC_{ds} T_{ks} G_{ks} {}^mC_k$	44	4982
1213060	215	230	3566	3581	$A_{ks} T_{ks} T_{ks} T_{ds} G_{ys} T_{ds} G_{ds} G_{ds} T_{ds} A_{ds} {}^mC_{ds}$ $A_{ds} G_{ds} {}^mC_{ks} T_{ks} G_k$	44	2963
1213061	216	231	3567	3582	${}^mC_{ks} A_{ks} T_{ks} T_{ds} U_{ys} G_{ds} T_{ds} G_{ds} G_{ds} T_{ds} A_{ds}$ ${}^mC_{ds} A_{ds} G_{ks} {}^mC_{ks} T_k$	36	4983
1213062	217	232	3568	3583	$A_{ks} {}^mC_{ks} A_{ks} T_{ds} U_{ys} T_{ds} G_{ds} T_{ds} G_{ds} G_{ds} T_{ds}$ $A_{ds} {}^mC_{ds} A_{ks} G_{ks} {}^mC_k$	75	4984
1213063	218	233	3569	3584	$T_{ks} A_{ks} {}^mC_{ks} A_{ds} U_{ys} T_{ds} T_{ds} G_{ds} T_{ds} G_{ds} G_{ds}$ $T_{ds} A_{ds} {}^mC_{ks} A_{ks} G_k$	55	4985
1213064	219	234	3570	3585	$G_{ks} T_{ks} A_{ks} {}^mC_{ds} A_{ys} T_{ds} T_{ds} T_{ds} G_{ds} T_{ds} G_{ds}$ $G_{ds} T_{ds} A_{ks} {}^mC_{ks} A_k$	38	3192
1213065	220	235	3571	3586	$G_{ks} G_{ks} T_{ks} A_{ds} C_{ys} A_{ds} T_{ds} T_{ds} T_{ds} G_{ds} T_{ds} G$ $ds G_{ds} T_{ks} A_{ks} {}^mC_k$	54	3269
1213066	221	236	3572	3587	$G_{ks} G_{ks} G_{ks} T_{ds} A_{ys} {}^mC_{ds} A_{ds} T_{ds} T_{ds} T_{ds} G_{ds}$ $T_{ds} G_{ds} G_{ks} T_{ks} A_k$	24	3345
1213067	222	237	3573	3588	$T_{ks} G_{ks} G_{ks} G_{ds} U_{ys} A_{ds} {}^mC_{ds} A_{ds} T_{ds} T_{ds} T_{ds}$ $G_{ds} T_{ds} G_{ks} G_{ks} T_k$	31	4986
1213068	223	238	3574	3589	$G_{ks} T_{ks} G_{ks} G_{ds} G_{ys} T_{ds} A_{ds} {}^mC_{ds} A_{ds} T_{ds} T_{ds}$ $T_{ds} G_{ds} T_{ks} G_{ks} G_k$	63	3497
1213069	1776	1791	7164	7179	$T_{ks} G_{ks} {}^mC_{ks} A_{ds} G_{ys} G_{ds} G_{ds} T_{ds} G_{ds} A_{ds} G_{ds}$ ${}^mC_{ds} {}^mC_{ds} G_{ks} G_{ks} {}^mC_k$	26	3299

1213070	1777	1792	7165	7180	$T_{ks}T_{ks}G_{ks}^mC_{ds}A_{ys}G_{ds}G_{ds}G_{ds}T_{ds}G_{ds}A_{ds}$ $G_{ds}^mC_{ds}^mC_{ks}G_{ks}G_k$	38	3375
1213071	1778	1793	7166	7181	$^mC_{ks}T_{ks}T_{ks}G_{ds}C_{ys}A_{ds}G_{ds}G_{ds}G_{ds}T_{ds}G_{ds}$ $A_{ds}G_{ds}^mC_{ks}^mC_{ks}G_k$	24	4962
1213072	1779	1794	7167	7182	$^mC_{ks}^mC_{ks}T_{ks}T_{ds}G_{ys}^mC_{ds}A_{ds}G_{ds}G_{ds}G_{ds}$ $T_{ds}G_{ds}A_{ds}G_{ks}^mC_{ks}^mC_k$	41	4974
1213073	1780	1795	7168	7183	$G_{ks}^mC_{ks}^mC_{ks}T_{ds}U_{ys}G_{ds}^mC_{ds}A_{ds}G_{ds}G_{ds}$ $G_{ds}T_{ds}G_{ds}A_{ks}G_{ks}^mC_k$	25	4987
1213074	1781	1796	7169	7184	$T_{ks}G_{ks}^mC_{ks}^mC_{ds}U_{ys}T_{ds}G_{ds}^mC_{ds}A_{ds}G_{ds}$ $G_{ds}G_{ds}T_{ds}G_{ks}A_{ks}G_k$	16	4988
1213075	1782	1797	7170	7185	$A_{ks}T_{ks}G_{ks}^mC_{ds}C_{ys}T_{ds}T_{ds}G_{ds}^mC_{ds}A_{ds}G_d$ $sG_{ds}G_{ds}T_{ks}G_{ks}A_k$	26	4947
1213076	1783	1798	7171	7186	$G_{ks}A_{ks}T_{ks}G_{ds}C_{ys}^mC_{ds}T_{ds}T_{ds}G_{ds}^mC_{ds}A_d$ $sG_{ds}G_{ds}G_{ks}T_{ks}G_k$	23	4959
1213077	1784	1799	7172	7187	$T_{ks}G_{ks}A_{ks}T_{ds}G_{ys}^mC_{ds}^mC_{ds}T_{ds}T_{ds}G_{ds}^mC$ $dsA_{ds}G_{ds}G_{ks}G_{ks}T_k$	17	4969
1213078	1785	1800	7173	7188	$A_{ks}T_{ks}G_{ks}A_{ds}U_{ys}G_{ds}^mC_{ds}^mC_{ds}T_{ds}T_{ds}G_d$ $s^mC_{ds}A_{ds}G_{ks}G_{ks}G_k$	25	4989
1213079	1786	1801	7174	7189	$G_{ks}A_{ks}T_{ks}G_{ds}A_{ys}T_{ds}G_{ds}^mC_{ds}^mC_{ds}T_{ds}T_d$ $sG_{ds}^mC_{ds}A_{ks}G_{ks}G_k$	24	4963
1213080	1787	1802	7175	7190	$T_{ks}G_{ks}A_{ks}T_{ds}G_{ys}A_{ds}T_{ds}G_{ds}^mC_{ds}^mC_{ds}T_d$ $sT_{ds}G_{ds}^mC_{ks}A_{ks}G_k$	34	4975
1213081	1788	1803	7176	7191	$^mC_{ks}T_{ks}G_{ks}A_{ds}U_{ys}G_{ds}A_{ds}T_{ds}G_{ds}^mC_{ds}^m$ $C_{ds}T_{ds}T_{ds}G_{ks}^mC_{ks}A_k$	19	4990
1213082	1789	1804	7177	7192	$G_{ks}^mC_{ks}T_{ks}G_{ds}A_{ys}T_{ds}G_{ds}A_{ds}T_{ds}G_{ds}^mC_d$ $s^mC_{ds}T_{ds}T_{ks}G_{ks}^mC_k$	50	3755
1213083	1790	1805	7178	7193	$A_{ks}G_{ks}^mC_{ks}T_{ds}G_{ys}A_{ds}T_{ds}G_{ds}A_{ds}T_{ds}G_{ds}$ $^mC_{ds}^mC_{ds}T_{ks}T_{ks}G_k$	59	3831
1213084	1791	1806	7179	7194	$^mC_{ks}A_{ks}G_{ks}^mC_{ds}U_{ys}G_{ds}A_{ds}T_{ds}G_{ds}A_{ds}T$ $dsG_{ds}^mC_{ds}^mC_{ks}T_{ks}T_k$	35	4991
1213085	1792	1807	7180	7195	$^mC_{ks}^mC_{ks}A_{ks}G_{ds}C_{ys}T_{ds}G_{ds}A_{ds}T_{ds}G_{ds}A$ $dsT_{ds}G_{ds}^mC_{ks}^mC_{ks}T_k$	31	4970
1213086	1793	1808	7181	7196	$^mC_{ks}^mC_{ks}^mC_{ks}A_{ds}G_{ys}^mC_{ds}T_{ds}G_{ds}A_{ds}T_{ds}$ $G_{ds}A_{ds}T_{ds}G_{ks}^mC_{ks}^mC_k$	39	4953
1213087	1892	1907	7280	7295	$^mC_{ks}^mC_{ks}^mC_{ks}T_{ds}G_{ys}A_{ds}G_{ds}^mC_{ds}A_{ds}A_d$ $sT_{ds}^mC_{ds}A_{ds}G_{ks}G_{ks}A_k$	27	3530
1213088	1893	1908	7281	7296	$T_{ks}^mC_{ks}^mC_{ks}^mC_{ds}U_{ys}G_{ds}A_{ds}G_{ds}^mC_{ds}A_d$ $sA_{ds}T_{ds}^mC_{ds}A_{ks}G_{ks}G_k$	43	4992
1213089	1894	1909	7282	7297	$G_{ks}T_{ks}^mC_{ks}^mC_{ds}C_{ys}T_{ds}G_{ds}A_{ds}G_{ds}^mC_{ds}$ $A_{ds}A_{ds}T_{ds}^mC_{ks}A_{ks}G_k$	22	3682
1213090	1895	1910	7283	7298	$A_{ks}G_{ks}T_{ks}^mC_{ds}C_{ys}^mC_{ds}T_{ds}G_{ds}A_{ds}G_{ds}^m$ $C_{ds}A_{ds}A_{ds}T_{ks}^mC_{ks}A_k$	29	3758
1213091	1896	1911	7284	7299	$G_{ks}A_{ks}G_{ks}T_{ds}C_{ys}^mC_{ds}^mC_{ds}T_{ds}G_{ds}A_{ds}G$ $ds^mC_{ds}A_{ds}A_{ks}T_{ks}^mC_k$	33	3834
1213092	1897	1912	7285	7300	$T_{ks}G_{ks}A_{ks}G_{ds}U_{ys}^mC_{ds}^mC_{ds}^mC_{ds}T_{ds}G_{ds}$ $A_{ds}G_{ds}^mC_{ds}A_{ks}A_{ks}T_k$	38	4993

Table 87. Reduction of FXII RNA (Huh7, electroporation, 2000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence and Chemistry notation (5' to 3')	FXII (%UTC)	SEQ ID NO
1128769	153	168	N/A	N/A	A _{ks} G _{ks} A _{ks} A _{ds} ^m C _{ds} G _{ds} A _{ds} ^m C _{ds} T _{ds} G _{ds} T _{ds} G _{ds} T _{ds} G _{ds} T _{ds} G _{ks} ^m C _{ks} T _k	63	3723
1128802	218	233	3569	3584	T _{ks} A _{ks} ^m C _{ks} A _{ds} T _{ds} T _{ds} T _{ds} G _{ds} T _{ds} G _{ds} G _{ds} T _{ds} A _{ds} ^m C _{ks} A _{ks} G _k	90	2426
1128870	470	485	4415	4430	T _{ks} G _{ks} T _{ks} G _{ds} G _{ds} A _{ds} A _{ds} A _{ds} A _{ds} ^m C _{ds} ^m C _{ds} G _{ds} G _{ks} A _{ks} G _k	44	3728
1129409	1788	1803	7176	7191	^m C _{ks} T _{ks} G _{ks} A _{ds} T _{ds} G _{ds} A _{ds} T _{ds} G _{ds} ^m C _{ds} ^m C _{ds} T _{ds} T _{ds} G _{ks} ^m C _{ks} A _k	7	3679
1129486	1922	1937	7310	7325	T _{ks} G _{ks} ^m C _{ks} G _{ds} G _{ds} A _{ds} A _{ds} T _{ds} ^m C _{ds} A _{ds} ^m C _{ds} ^m C _{ds} A _{ds} A _{ks} G _{ks} G _k	11	3455
1129489	1925	1940	7313	7328	^m C _{ks} A _{ks} ^m C _{ks} T _{ds} G _{ds} ^m C _{ds} G _{ds} G _{ds} A _{ds} A _{ds} T _{ds} ^m C _{ds} A _{ds} ^m C _{ks} ^m C _{ks} A _k	21	3683
1129491	1927	1942	7315	7330	^m C _{ks} T _{ks} ^m C _{ks} A _{ds} ^m C _{ds} T _{ds} G _{ds} ^m C _{ds} G _{ds} G _{ds} A _{ds} A _{ds} T _{ds} ^m C _{ks} A _{ks} ^m C _k	54	3835
1129531	2009	2024	7397	7412	G _{ks} A _{ks} G _{ks} T _{ds} T _{ds} ^m C _{ds} ^m C _{ds} T _{ds} G _{ds} ^m C _{ds} G _{ds} ^m C _{ds} A _{ks} T _{ks} ^m C _k	9	3837
1129532	2010	2025	7398	7413	T _{ks} G _{ks} A _{ks} G _{ds} T _{ds} T _{ds} ^m C _{ds} ^m C _{ds} T _{ds} G _{ds} ^m C _{ds} G _{ds} ^m C _{ds} ^m C _{ks} A _{ks} T _k	16	3913
1129540	2019	2034	7407	7422	G _{ks} ^m C _{ks} A _{ks} ^m C _{ds} T _{ds} T _{ds} T _{ds} A _{ds} T _{ds} T _{ds} G _{ds} A _{ds} G _{ds} T _{ks} T _{ks} ^m C _k	19	3000
1129572	N/A	N/A	186	201	G _{ks} G _{ks} A _{ks} ^m C _{ds} ^m C _{ds} ^m C _{ds} A _{ds} ^m C _{ds} A _{ds} G _d _s G _{ds} T _{ds} ^m C _{ds} A _{ks} T _{ks} G _k	47	3915
1129857	N/A	N/A	3881	3896	G _{ks} T _{ks} A _{ks} A _{ds} T _{ds} G _{ds} A _{ds} G _{ds} G _{ds} ^m C _{ds} G _{ds} G _{ds} G _{ds} A _{ks} G _{ks} G _k	48	2787
1129938	N/A	N/A	4635	4650	A _{ks} ^m C _{ks} G _{ks} ^m C _{ds} A _{ds} G _{ds} T _{ds} G _{ds} A _{ds} G _{ds} ^m C _{ds} ^m C _{ds} A _{ds} ^m C _{ks} ^m C _{ks} ^m C _k	62	2868
1129948	N/A	N/A	4840	4855	A _{ks} T _{ks} ^m C _{ks} T _{ds} G _{ds} ^m C _{ds} T _{ds} T _{ds} T _{ds} ^m C _{ds} ^m C _{ds} G _{ds} ^m C _{ds} A _{ks} ^m C _{ks} T _k	34	3630
1129949	N/A	N/A	4844	4859	T _{ks} ^m C _{ks} T _{ks} ^m C _{ds} A _{ds} T _{ds} ^m C _{ds} T _{ds} G _{ds} ^m C _{ds} T _{ds} T _{ds} ^m C _{ks} ^m C _{ks} G _k	41	3706
1130010	N/A	N/A	5752	5767	A _{ks} ^m C _{ks} G _{ks} G _{ds} A _{ds} G _{ds} A _{ds} G _{ds} ^m C _{ds} ^m C _{ds} G _{ds} ^m C _{ds} G _{ks} G _{ks} ^m C _k	29	3785
1130142	N/A	N/A	6579	6594	^m C _{ks} G _{ks} T _{ks} ^m C _{ds} ^m C _{ds} T _{ds} A _{ds} G _{ds} T _{ds} T _{ds} G _{ds} ^m C _{ds} ^m C _{ks} T _{ks} T _k	32	3177
1130215	N/A	N/A	7015	7030	^m C _{ks} A _{ks} ^m C _{ks} ^m C _{ds} T _{ds} G _{ds} G _{ds} ^m C _{ds} A _{ds} ^m C _{ds} G _{ds} ^m C _{ds} A _{ds} T _{ks} ^m C _{ks} G _k	41 [†]	2651
1130251	N/A	N/A	7111	7126	G _{ks} G _{ks} A _{ks} A _{ds} T _{ds} ^m C _{ds} A _{ds} ^m C _{ds} ^m C _{ds} ^m C _d _s T _{ds} G _{ds} G _{ds} G _{ks} T _{ks} ^m C _k	30 [†]	3873
1130252	N/A	N/A	7112	7127	^m C _{ks} G _{ks} G _{ks} A _{ds} A _{ds} T _{ds} ^m C _{ds} A _{ds} ^m C _{ds} ^m C _d _s ^m C _{ds} T _{ds} G _{ds} G _{ks} G _{ks} T _k	15 [†]	3949
1213093	1898	1913	7286	7301	A _{ks} T _{ks} G _{ks} A _{ds} G _{ys} T _{ds} ^m C _{ds} ^m C _{ds} ^m C _{ds} T _{ds} G _{ds} A _{ds} G _{ds} ^m C _{ks} A _{ks} A _k	42	2460
1213094	1899	1914	7287	7302	G _{ks} A _{ks} T _{ks} G _{ds} A _{ys} G _{ds} T _{ds} ^m C _{ds} ^m C _{ds} ^m C _{ds} T _{ds} G _{ds} A _{ds} G _{ks} ^m C _{ks} A _k	18	2537

1213095	1900	1915	7288	7303	$A_{ks}G_{ks}A_{ks}T_{ds}G_{ys}A_{ds}G_{ds}T_{ds}^mC_{ds}^mC_{ds}^m$ $C_{ds}T_{ds}G_{ds}A_{ks}G_{ks}^mC_k$	13	2614
1213096	1901	1916	7289	7304	$A_{ks}A_{ks}G_{ks}A_{ds}U_{ys}G_{ds}A_{ds}G_{ds}T_{ds}^mC_{ds}^mC$ $ds^mC_{ds}T_{ds}G_{ks}A_{ks}G_k$	28	4994
1213097	1902	1917	7290	7305	$A_{ks}A_{ks}A_{ks}G_{ds}A_{ys}T_{ds}G_{ds}A_{ds}G_{ds}T_{ds}^mC_{ds}$ $^mC_{ds}^mC_{ds}T_{ks}G_{ks}A_k$	19	2768
1213098	1903	1918	7291	7306	$G_{ks}A_{ks}A_{ks}A_{ds}G_{ys}A_{ds}T_{ds}G_{ds}A_{ds}G_{ds}T_{ds}^m$ $C_{ds}^mC_{ds}^mC_{ks}T_{ks}G_k$	36	2845
1213099	1904	1919	7292	7307	$G_{ks}G_{ks}A_{ks}A_{ds}A_{ys}G_{ds}A_{ds}T_{ds}G_{ds}A_{ds}G_{ds}$ $T_{ds}^mC_{ds}^mC_{ks}^mC_{ks}T_k$	25	2921
1213100	1905	1920	7293	7308	$G_{ks}G_{ks}G_{ks}A_{ds}A_{ys}A_{ds}G_{ds}A_{ds}T_{ds}G_{ds}A_{ds}$ $G_{ds}T_{ds}^mC_{ks}^mC_{ks}^mC_k$	26	2997
1213101	1906	1921	7294	7309	$A_{ks}G_{ks}G_{ks}A_{ys}A_{ds}A_{ds}G_{ds}A_{ds}T_{ds}G_{ds}$ $A_{ds}G_{ds}T_{ks}^mC_{ks}^mC_k$	24	3073
1213102	1914	1929	7302	7317	$^mC_{ks}A_{ks}^mC_{ks}^mC_{ds}A_{ys}A_{ds}G_{ds}G_{ds}A_{ds}G_{ds}$ $G_{ds}G_{ds}A_{ds}A_{ks}A_{ks}G_k$	34	4954
1213103	1915	1930	7303	7318	$T_{ks}^mC_{ks}A_{ks}^mC_{ds}C_{ys}A_{ds}A_{ds}G_{ds}G_{ds}A_{ds}G$ $dsG_{ds}G_{ds}A_{ks}A_{ks}A_k$	41	4948
1213104	1916	1931	7304	7319	$A_{ks}T_{ks}^mC_{ks}A_{ds}C_{ys}^mC_{ds}A_{ds}A_{ds}G_{ds}G_{ds}A$ $dsG_{ds}G_{ds}G_{ks}A_{ks}A_k$	41	4966
1213105	1917	1932	7305	7320	$A_{ks}A_{ks}T_{ks}^mC_{ds}A_{ys}^mC_{ds}^mC_{ds}A_{ds}A_{ds}G_{ds}$ $G_{ds}A_{ds}G_{ds}G_{ks}G_{ks}A_k$	21	4956
1213106	1918	1933	7306	7321	$G_{ks}A_{ks}A_{ks}T_{ds}C_{ys}A_{ds}^mC_{ds}^mC_{ds}A_{ds}A_{ds}G$ $dsG_{ds}A_{ds}G_{ks}G_{ks}G_k$	23	4965
1213107	1919	1934	7307	7322	$G_{ks}G_{ks}A_{ks}A_{ds}U_{ys}^mC_{ds}A_{ds}^mC_{ds}^mC_{ds}A_{ds}$ $A_{ds}G_{ds}G_{ds}A_{ks}G_{ks}G_k$	18	4995
1213108	1920	1935	7308	7323	$^mC_{ks}G_{ks}G_{ks}A_{ds}A_{ys}T_{ds}^mC_{ds}A_{ds}^mC_{ds}^mC_d$ $sA_{ds}A_{ds}G_{ds}G_{ks}A_{ks}G_k$	28	3303
1213109	1921	1936	7309	7324	$G_{ks}^mC_{ks}G_{ks}G_{ds}A_{ys}A_{ds}T_{ds}^mC_{ds}A_{ds}^mC_{ds}$ $^mC_{ds}A_{ds}A_{ds}G_{ks}G_{ks}A_k$	37	3379
1213110	1922	1937	7310	7325	$T_{ks}G_{ks}^mC_{ks}G_{ds}G_{ys}A_{ds}A_{ds}T_{ds}^mC_{ds}A_{ds}^m$ $C_{ds}^mC_{ds}A_{ds}A_{ks}G_{ks}G_k$	20	3455
1213111	1923	1938	7311	7326	$^mC_{ks}T_{ks}G_{ks}^mC_{ds}G_{ys}G_{ds}A_{ds}A_{ds}T_{ds}^mC_{ds}$ $A_{ds}^mC_{ds}^mC_{ds}A_{ks}A_{ks}G_k$	12	3531
1213112	1924	1939	7312	7327	$A_{ks}^mC_{ks}T_{ks}G_{ds}C_{ys}G_{ds}G_{ds}A_{ds}A_{ds}T_{ds}^mC$ $dsA_{ds}^mC_{ds}^mC_{ks}A_{ks}A_k$	20	3607
1213113	1925	1940	7313	7328	$^mC_{ks}A_{ks}^mC_{ks}T_{ds}G_{ys}^mC_{ds}G_{ds}G_{ds}A_{ds}A_{ds}$ $T_{ds}^mC_{ds}A_{ds}^mC_{ks}^mC_{ks}A_k$	29	3683
1213114	1926	1941	7314	7329	$T_{ks}^mC_{ks}A_{ks}^mC_{ds}U_{ys}G_{ds}^mC_{ds}G_{ds}G_{ds}A_{ds}$ $A_{ds}T_{ds}^mC_{ds}A_{ks}^mC_{ks}^mC_k$	30	4996
1213115	1927	1942	7315	7330	$^mC_{ks}T_{ks}^mC_{ks}A_{ds}C_{ys}T_{ds}G_{ds}^mC_{ds}G_{ds}G_{ds}$ $A_{ds}A_{ds}T_{ds}^mC_{ks}A_{ks}^mC_k$	18	3835
1213116	1928	1943	7316	7331	$T_{ks}^mC_{ks}T_{ks}^mC_{ds}A_{ys}^mC_{ds}T_{ds}G_{ds}^mC_{ds}G_{ds}$ $G_{ds}A_{ds}A_{ds}T_{ks}^mC_{ks}A_k$	28	3911
1213117	1929	1944	7317	7332	$^mC_{ks}T_{ks}^mC_{ks}T_{ds}C_{ys}A_{ds}^mC_{ds}T_{ds}G_{ds}^mC_{ds}$ $G_{ds}G_{ds}A_{ds}A_{ks}T_{ks}^mC_k$	26	4971
1213118	1930	1945	7318	7333	$T_{ks}^mC_{ks}T_{ks}^mC_{ds}U_{ys}^mC_{ds}A_{ds}^mC_{ds}T_{ds}G_{ds}$ $^mC_{ds}G_{ds}G_{ds}A_{ks}A_{ks}T_k$	19	4997
1213119	1931	1946	7319	7334	$^mC_{ks}T_{ks}^mC_{ks}T_{ds}C_{ys}T_{ds}^mC_{ds}A_{ds}^mC_{ds}T_{ds}$ $G_{ds}^mC_{ds}G_{ds}G_{ks}A_{ks}A_k$	52	2461
1213120	1932	1947	7320	7335	$A_{ks}^mC_{ks}T_{ks}^mC_{ds}U_{ys}^mC_{ds}T_{ds}^mC_{ds}A_{ds}^mC$ $dsT_{ds}G_{ds}^mC_{ds}G_{ks}G_{ks}A_k$	10	4998

1213121	1933	1948	7321	7336	${}^mC_{ks}A_{ks}{}^mC_{ks}T_{ds}C_{ys}T_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}A_{ds}$ ${}^mC_{ds}T_{ds}G_{ds}{}^mC_{ks}G_{ks}G_k$	34	4957
1213122	1934	1949	7322	7337	${}^mC_{ks}{}^mC_{ks}A_{ks}{}^mC_{ds}U_{ys}{}^mC_{ds}T_{ds}{}^mC_{ds}T_{ds}{}^m$ $C_{ds}A_{ds}{}^mC_{ds}T_{ds}G_{ks}{}^mC_{ks}G_k$	19	4999
1213123	1935	1950	7323	7338	$G_{ks}{}^mC_{ks}{}^mC_{ks}A_{ds}C_{ys}T_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}T_{ds}$ ${}^mC_{ds}A_{ds}{}^mC_{ds}T_{ks}G_{ks}{}^mC_k$	33	4967
1213124	1936	1951	7324	7339	$A_{ks}G_{ks}{}^mC_{ks}{}^mC_{ds}A_{ys}{}^mC_{ds}T_{ds}{}^mC_{ds}T_{ds}{}^mC$ ${}_{ds}T_{ds}{}^mC_{ds}A_{ds}{}^mC_{ks}T_{ks}G_k$	14	4961
1213125	1937	1952	7325	7340	${}^mC_{ks}A_{ks}G_{ks}{}^mC_{ds}C_{ys}A_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}T_{ds}$ ${}^mC_{ds}T_{ds}{}^mC_{ds}A_{ks}{}^mC_{ks}T_k$	42	4972
1213126	2000	2015	7388	7403	${}^mC_{ks}G_{ks}{}^mC_{ks}{}^mC_{ds}A_{ys}T_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}G$ ${}_{ds}G_{ds}{}^mC_{ds}G_{ds}{}^mC_{ks}G_{ks}G_k$	53	3228
1213127	2001	2016	7389	7404	$G_{ks}{}^mC_{ks}G_{ks}{}^mC_{ds}C_{ys}A_{ds}T_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}$ $G_{ds}G_{ds}{}^mC_{ds}G_{ks}{}^mC_{ks}G_k$	34	4964
1213128	2002	2017	7390	7405	$T_{ks}G_{ks}{}^mC_{ks}G_{ds}C_{ys}{}^mC_{ds}A_{ds}T_{ds}{}^mC_{ds}{}^mC_{ds}$ $T_{ds}G_{ds}G_{ds}{}^mC_{ks}G_{ks}{}^mC_k$	61	3305
1213129	2003	2018	7391	7406	${}^mC_{ks}T_{ks}G_{ks}{}^mC_{ds}G_{ys}{}^mC_{ds}{}^mC_{ds}A_{ds}T_{ds}{}^mC$ ${}_{ds}{}^mC_{ds}T_{ds}G_{ds}G_{ks}{}^mC_{ks}G_k$	114	3381
1213130	2004	2019	7392	7407	${}^mC_{ks}{}^mC_{ks}T_{ks}G_{ds}C_{ys}G_{ds}{}^mC_{ds}{}^mC_{ds}A_{ds}T_{ds}$ ${}^mC_{ds}{}^mC_{ds}T_{ds}G_{ks}G_{ks}{}^mC_k$	24	3457
1213131	2005	2020	7393	7408	$T_{ks}{}^mC_{ks}{}^mC_{ks}T_{ds}G_{ys}{}^mC_{ds}G_{ds}{}^mC_{ds}{}^mC_{ds}A$ ${}_{ds}T_{ds}{}^mC_{ds}{}^mC_{ds}T_{ks}G_{ks}G_k$	35	3533
1213132	2006	2021	7394	7409	$T_{ks}T_{ks}{}^mC_{ks}{}^mC_{ds}U_{ys}G_{ds}{}^mC_{ds}G_{ds}{}^mC_{ds}{}^mC$ ${}_{ds}A_{ds}T_{ds}{}^mC_{ds}{}^mC_{ks}T_{ks}G_k$	29	5000
1213133	2007	2022	7395	7410	$G_{ks}T_{ks}T_{ks}{}^mC_{ds}C_{ys}T_{ds}G_{ds}{}^mC_{ds}G_{ds}{}^mC_{ds}{}^m$ $C_{ds}A_{ds}T_{ds}{}^mC_{ks}{}^mC_{ks}T_k$	33	3685
1213134	2008	2023	7396	7411	$A_{ks}G_{ks}T_{ks}T_{ds}C_{ys}{}^mC_{ds}T_{ds}G_{ds}{}^mC_{ds}G_{ds}{}^m$ $C_{ds}{}^mC_{ds}A_{ds}T_{ks}{}^mC_{ks}{}^mC_k$	33	3761
1213135	2009	2024	7397	7412	$G_{ks}A_{ks}G_{ks}T_{ds}U_{ys}{}^mC_{ds}{}^mC_{ds}T_{ds}G_{ds}{}^mC_{ds}$ $G_{ds}{}^mC_{ds}{}^mC_{ds}A_{ks}T_{ks}{}^mC_k$	9	5001
1213136	2010	2025	7398	7413	$T_{ks}G_{ks}A_{ks}G_{ds}U_{ys}T_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}G_{ds}{}^m$ $C_{ds}G_{ds}{}^mC_{ds}{}^mC_{ks}A_{ks}T_k$	20	5002
1213137	2011	2026	7399	7414	$T_{ks}T_{ks}G_{ks}A_{ds}G_{ys}T_{ds}T_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}G_{ds}$ ${}^mC_{ds}G_{ds}{}^mC_{ks}{}^mC_{ks}A_k$	17	2463
1213138	2012	2027	7400	7415	$A_{ks}T_{ks}T_{ks}G_{ds}A_{ys}G_{ds}T_{ds}T_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}$ $G_{ds}{}^mC_{ds}G_{ks}{}^mC_{ks}{}^mC_k$	17	2540
1213139	2013	2028	7401	7416	$T_{ks}A_{ks}T_{ks}T_{ds}G_{ys}A_{ds}G_{ds}T_{ds}T_{ds}{}^mC_{ds}{}^mC_{ds}$ $T_{ds}G_{ds}{}^mC_{ks}G_{ks}{}^mC_k$	26	2617
1213140	2014	2029	7402	7417	$T_{ks}T_{ks}A_{ks}T_{ds}U_{ys}G_{ds}A_{ds}G_{ds}T_{ds}T_{ds}{}^mC_{ds}$ ${}^mC_{ds}T_{ds}G_{ks}{}^mC_{ks}G_k$	25	5003
1213141	2016	2031	7404	7419	${}^mC_{ks}T_{ks}T_{ks}T_{ds}A_{ys}T_{ds}T_{ds}G_{ds}A_{ds}G_{ds}T_{ds}$ $T_{ds}{}^mC_{ds}{}^mC_{ks}T_{ks}G_k$	22	2771
1213142	2017	2032	7405	7420	$A_{ks}{}^mC_{ks}T_{ks}T_{ds}U_{ys}A_{ds}T_{ds}T_{ds}G_{ds}A_{ds}G_{ds}$ $T_{ds}T_{ds}{}^mC_{ks}{}^mC_{ks}T_k$	30	5004
1213143	2018	2033	7406	7421	${}^mC_{ks}A_{ks}{}^mC_{ks}T_{ds}U_{ys}T_{ds}A_{ds}T_{ds}T_{ds}G_{ds}A_d$ ${}_sG_{ds}T_{ds}T_{ks}{}^mC_{ks}{}^mC_k$	25	5005
1213144	2019	2034	7407	7422	$G_{ks}{}^mC_{ks}A_{ks}{}^mC_{ds}U_{ys}T_{ds}T_{ds}A_{ds}T_{ds}T_{ds}G_d$ ${}_sA_{ds}G_{ds}T_{ks}T_{ks}{}^mC_k$	10	5006
1213145	2020	2035	7408	7423	$A_{ks}G_{ks}{}^mC_{ks}A_{ds}C_{ys}T_{ds}T_{ds}T_{ds}A_{ds}T_{ds}T_{ds}$ $G_{ds}A_{ds}G_{ks}T_{ks}T_k$	20	3076
1213146	2021	2036	7409	7424	$A_{ks}A_{ks}G_{ks}{}^mC_{ds}A_{ys}{}^mC_{ds}T_{ds}T_{ds}T_{ds}A_{ds}T_d$ ${}_cT_{ds}G_{ds}A_{ks}G_{ks}T_k$	11	3147

1213147	2022	2037	7410	7425	$A_{ks}A_{ks}A_{ks}G_{ds}C_{ys}A_{ds}^mC_{ds}T_{ds}T_{ds}T_{ds}A_{ds}$ $T_{ds}T_{ds}G_{ks}A_{ks}G_k$	15	3229
1213148	2023	2038	7411	7426	$^mC_{ks}A_{ks}A_{ks}A_{ds}G_{ys}^mC_{ds}A_{ds}^mC_{ds}T_{ds}T_{ds}$ $T_{ds}A_{ds}T_{ds}T_{ks}G_{ks}A_k$	34	3306
1213149	2024	2039	7412	7427	$T_{ks}^mC_{ks}A_{ks}A_{ds}A_{ys}G_{ds}^mC_{ds}A_{ds}^mC_{ds}T_{ds}$ $T_{ds}T_{ds}A_{ds}T_{ks}T_{ks}G_k$	35	3382
1213150	2031	2046	7419	7434	$A_{ks}G_{ks}^mC_{ks}A_{ds}U_{ys}T_{ds}T_{ds}T_{ds}^mC_{ds}A_{ds}A_d$ $sA_{ds}G_{ds}^mC_{ks}A_{ks}^mC_k$	41	5007
1213151	2033	2048	7421	7436	$T_{ks}^mC_{ks}A_{ks}G_{ds}C_{ys}A_{ds}T_{ds}T_{ds}T_{ds}T_{ds}^mC_{ds}$ $A_{ds}A_{ds}A_{ks}G_{ks}^mC_k$	23	3534

Table 88. Reduction of FXII RNA (Huh7, electroporation, 2000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Chemistry notation (5' to 3')	FXII (%UTC)	SEQ ID NO
1128769	153	168	N/A	N/A	$A_{ks}G_{ks}A_{ks}A_{ds}^mC_{ds}G_{ds}A_{ds}^mC_{ds}T_{ds}G_{ds}T_{ds}G_{ds}T_{ds}G_{ks}^mC_{ks}T_k$	41	3723
1128802	218	233	3569	3584	$T_{ks}A_{ks}^mC_{ks}A_{ds}T_{ds}T_{ds}T_{ds}G_{ds}T_{ds}G_{ds}G_{ds}$ $T_{ds}A_{ds}^mC_{ks}A_{ks}G_k$	N/A	2426
1128870	470	485	4415	4430	$T_{ks}G_{ks}T_{ks}G_{ds}G_{ds}A_{ds}A_{ds}A_{ds}A_{ds}A_{ds}^mC_{ds}$ $^mC_{ds}G_{ds}G_{ks}A_{ks}G_k$	31	3728
1129491	1927	1942	7315	7330	$^mC_{ks}T_{ks}^mC_{ks}A_{ds}^mC_{ds}T_{ds}G_{ds}^mC_{ds}G_{ds}G_{ds}$ $A_{ds}A_{ds}T_{ds}^mC_{ks}A_{ks}^mC_k$	16	3835
1129510	1984	1999	7372	7387	$A_{ks}G_{ks}^mC_{ks}T_{ds}G_{ds}G_{ds}^mC_{ds}^mC_{ds}G_{ds}^mC_d$ $sA_{ds}^mC_{ds}T_{ds}G_{ks}G_{ks}G_k$	29	3760
1129530	2008	2023	7396	7411	$A_{ks}G_{ks}T_{ks}T_{ds}^mC_{ds}^mC_{ds}T_{ds}G_{ds}^mC_{ds}G_{ds}^m$ $C_{ds}^mC_{ds}A_{ds}T_{ks}^mC_{ks}^mC_k$	80	3761
1129531	2009	2024	7397	7412	$G_{ks}A_{ks}G_{ks}T_{ds}T_{ds}^mC_{ds}^mC_{ds}T_{ds}G_{ds}^mC_{ds}$ $G_{ds}^mC_{ds}^mC_{ds}A_{ks}T_{ks}^mC_k$	29	3837
1129532	2010	2025	7398	7413	$T_{ks}G_{ks}A_{ks}G_{ds}T_{ds}T_{ds}^mC_{ds}^mC_{ds}T_{ds}G_{ds}^mC_{ds}$ $G_{ds}^mC_{ds}^mC_{ks}A_{ks}T_k$	19	3913
1129540	2019	2034	7407	7422	$G_{ks}^mC_{ks}A_{ks}^mC_{ds}T_{ds}T_{ds}T_{ds}A_{ds}T_{ds}T_{ds}G_{ds}$ $A_{ds}G_{ds}T_{ks}T_{ks}^mC_k$	48	3000
1129683	N/A	N/A	1003	1018	$T_{ks}^mC_{ks}A_{ks}A_{ds}^mC_{ds}^mC_{ds}T_{ds}G_{ds}G_{ds}T_{ds}T_{ds}$ $T_{ds}^mC_{ds}A_{ks}^mC_{ks}A_k$	64	3236
1129703	N/A	N/A	1139	1154	$A_{ks}T_{ks}G_{ks}G_{ds}^mC_{ds}A_{ds}G_{ds}G_{ds}T_{ds}A_{ds}^mC_{ds}$ $^mC_{ds}^mC_{ds}T_{ks}T_{ks}^mC_k$	32	3237
1129715	N/A	N/A	1559	1574	$^mC_{ks}A_{ks}G_{ks}G_{ds}G_{ds}T_{ds}A_{ds}A_{ds}G_{ds}G_{ds}T_{ds}$ $^mC_{ds}^mC_{ds}A_{ks}T_{ks}^mC_k$	52	2626
1129783	N/A	N/A	2494	2509	$G_{ks}T_{ks}T_{ks}A_{ds}G_{ds}A_{ds}^mC_{ds}A_{ds}^mC_{ds}T_{ds}T_d$ $sG_{ds}A_{ds}T_{ks}T_{ks}^mC_k$	104	3241
1129796	N/A	N/A	2628	2643	$T_{ks}^mC_{ks}T_{ks}A_{ds}^mC_{ds}T_{ds}T_{ds}A_{ds}G_{ds}T_{ds}G_{ds}$ $^mC_{ds}A_{ds}A_{ks}^mC_{ks}G_k$	57	2707
1129877	N/A	N/A	4035	4050	$G_{ks}^mC_{ks}T_{ks}A_{ds}^mC_{ds}T_{ds}^mC_{ds}^mC_{ds}A_{ds}A_{ds}$ $G_{ds}T_{ds}T_{ds}T_{ks}^mC_{ks}^mC_k$	66	2788
1129916	N/A	N/A	4363	4378	$G_{ks}G_{ks}G_{ks}A_{ds}T_{ds}A_{ds}G_{ds}T_{ds}G_{ds}G_{ds}T_{ds}^m$ $C_{ds}T_{ds}^mC_{ks}A_{ks}G_k$	103	2713
1129938	N/A	N/A	4635	4650	$A_{ks}^mC_{ks}G_{ks}^mC_{ds}A_{ds}G_{ds}T_{ds}G_{ds}A_{ds}G_{ds}^m$ $C_{ds}^mC_{ds}A_{ds}^mC_{ks}^mC_{ks}^mC_k$	52	2868

1129943	N/A	N/A	4808	4823	$G_{ks}G_{ks}{}^mC_{ks}A_{ds}A_{ds}G_{ds}{}^mC_{ds}{}^mC_{ds}{}^mC_{ds}G_d$ $sT_{ds}{}^mC_{ds}{}^mC_{ds}{}^mC_{ks}A_{ks}{}^mC_k$	63	3249
1129948	N/A	N/A	4840	4855	$A_{ks}T_{ks}{}^mC_{ks}T_{ds}G_{ds}{}^mC_{ds}T_{ds}T_{ds}T_{ds}{}^mC_{ds}{}^m$ $C_{ds}G_{ds}{}^mC_{ds}A_{ks}{}^mC_{ks}T_k$	108	3630
1129949	N/A	N/A	4844	4859	$T_{ks}{}^mC_{ks}T_{ks}{}^mC_{ds}A_{ds}T_{ds}{}^mC_{ds}T_{ds}G_{ds}{}^mC_{ds}$ $T_{ds}T_{ds}T_{ds}{}^mC_{ks}{}^mC_{ks}G_k$	81	3706
1213152	141	156	508	523	$T_{ks}G_{ks}{}^mC_{ks}T_{ds}{}^mC_{ds}U_{ys}T_{ds}{}^mC_{ds}A_{ds}G_{ds}{}^m$ $C_{ds}T_{ds}T_{ds}T_{ks}G_{ks}T_k$	72	5008
1213153	142	157	509	524	$G_{ks}T_{ks}G_{ks}{}^mC_{ds}T_{ds}C_{ys}T_{ds}T_{ds}{}^mC_{ds}A_{ds}G_d$ $s{}^mC_{ds}T_{ds}T_{ks}T_{ks}G_k$	29	4958
1213154	143	158	510	525	$T_{ks}G_{ks}T_{ks}G_{ds}{}^mC_{ds}U_{ys}{}^mC_{ds}T_{ds}T_{ds}{}^mC_{ds}A$ $dsG_{ds}{}^mC_{ds}T_{ks}T_{ks}T_k$	75	5009
1213155	144	159	511	526	$G_{ks}T_{ks}G_{ks}T_{ds}G_{ds}C_{ys}T_{ds}{}^mC_{ds}T_{ds}T_{ds}{}^mC_{ds}$ $A_{ds}G_{ds}{}^mC_{ks}T_{ks}T_k$	70	4951
1213156	145	160	512	527	$T_{ks}G_{ks}T_{ks}G_{ds}T_{ds}G_{ys}{}^mC_{ds}T_{ds}{}^mC_{ds}T_{ds}T_{ds}$ ${}^mC_{ds}A_{ds}G_{ks}{}^mC_{ks}T_k$	35	3112
1213157	146	161	513	528	${}^mC_{ks}T_{ks}G_{ks}T_{ds}G_{ds}U_{ys}G_{ds}{}^mC_{ds}T_{ds}{}^mC_{ds}T$ $dsT_{ds}{}^mC_{ds}A_{ks}G_{ks}{}^mC_k$	60	5010
1213158	147	162	514	529	$A_{ks}{}^mC_{ks}T_{ks}G_{ds}T_{ds}G_{ys}T_{ds}G_{ds}{}^mC_{ds}T_{ds}{}^mC$ $dsT_{ds}T_{ds}{}^mC_{ks}A_{ks}G_k$	56	3267
1213160	149	164	516	531	${}^mC_{ks}G_{ks}A_{ks}{}^mC_{ds}T_{ds}G_{ys}T_{ds}G_{ds}T_{ds}G_{ds}{}^m$ $C_{ds}T_{ds}{}^mC_{ds}T_{ks}T_{ks}{}^mC_k$	61	3419
1213161	150	165	N/A	N/A	$A_{ks}{}^mC_{ks}G_{ks}A_{ds}{}^mC_{ds}U_{ys}G_{ds}T_{ds}G_{ds}T_{ds}G$ $ds{}^mC_{ds}T_{ds}{}^mC_{ks}T_{ks}T_k$	36	5011
1213162	151	166	N/A	N/A	$A_{ks}A_{ks}{}^mC_{ks}G_{ds}A_{ds}C_{ys}T_{ds}G_{ds}T_{ds}G_{ds}T_{ds}$ $G_{ds}{}^mC_{ds}T_{ks}{}^mC_{ks}T_k$	97	3571
1213163	152	167	N/A	N/A	$G_{ks}A_{ks}A_{ks}{}^mC_{ds}G_{ds}A_{ys}{}^mC_{ds}T_{ds}G_{ds}T_{ds}G$ $dsT_{ds}G_{ds}{}^mC_{ks}T_{ks}{}^mC_k$	50	3647
1213164	153	168	N/A	N/A	$A_{ks}G_{ks}A_{ks}A_{ds}{}^mC_{ds}G_{ys}A_{ds}{}^mC_{ds}T_{ds}G_{ds}T$ $dsG_{ds}T_{ds}G_{ks}{}^mC_{ks}T_k$	99	3723
1213165	154	169	N/A	N/A	$G_{ks}A_{ks}G_{ks}A_{ds}A_{ds}C_{ys}G_{ds}A_{ds}{}^mC_{ds}T_{ds}G_{ds}$ $T_{ds}G_{ds}T_{ks}G_{ks}{}^mC_k$	132	3799
1213166	155	170	N/A	N/A	$T_{ks}G_{ks}A_{ks}G_{ds}A_{ds}A_{ys}{}^mC_{ds}G_{ds}A_{ds}{}^mC_{ds}T$ $dsG_{ds}T_{ds}G_{ks}T_{ks}G_k$	70	3875
1213167	156	171	N/A	N/A	$G_{ks}T_{ks}G_{ks}A_{ds}G_{ds}A_{ys}A_{ds}{}^mC_{ds}G_{ds}A_{ds}{}^mC$ $dsT_{ds}G_{ds}T_{ks}G_{ks}T_k$	45	2424
1213168	157	172	N/A	N/A	$A_{ks}G_{ks}T_{ks}G_{ds}A_{ds}G_{ys}A_{ds}A_{ds}{}^mC_{ds}G_{ds}A_{ds}$ ${}^mC_{ds}T_{ds}G_{ks}T_{ks}G_k$	112	2502
1213169	158	173	N/A	N/A	${}^mC_{ks}A_{ks}G_{ks}T_{ds}G_{ds}A_{ys}G_{ds}A_{ds}A_{ds}{}^mC_{ds}G$ $dsA_{ds}{}^mC_{ds}T_{ks}G_{ks}T_k$	73	2579
1213170	208	223	3559	3574	$G_{ks}T_{ks}A_{ks}{}^mC_{ds}A_{ds}G_{ys}{}^mC_{ds}T_{ds}G_{ds}{}^mC_{ds}{}^m$ $C_{ds}G_{ds}G_{ds}T_{ks}G_{ks}G_k$	47	4968
1213171	209	224	3560	3575	$G_{ks}G_{ks}T_{ks}A_{ds}{}^mC_{ds}A_{ys}G_{ds}{}^mC_{ds}T_{ds}G_{ds}{}^m$ $C_{ds}{}^mC_{ds}G_{ds}G_{ks}T_{ks}G_k$	22	4952
1213173	211	226	3562	3577	$G_{ks}T_{ks}G_{ks}G_{ds}T_{ds}A_{ys}{}^mC_{ds}A_{ds}G_{ds}{}^mC_{ds}T_d$ $sG_{ds}{}^mC_{ds}{}^mC_{ks}G_{ks}G_k$	112	4973
1213174	212	227	3563	3578	$T_{ks}G_{ks}T_{ks}G_{ds}G_{ds}U_{ys}A_{ds}{}^mC_{ds}A_{ds}G_{ds}{}^mC$ $dsT_{ds}G_{ds}{}^mC_{ks}{}^mC_{ks}G_k$	72	5012
1213175	213	228	3564	3579	$T_{ks}T_{ks}G_{ks}T_{ds}G_{ds}G_{ys}T_{ds}A_{ds}{}^mC_{ds}A_{ds}G_{ds}$ ${}^mC_{ds}T_{ds}G_{ks}{}^mC_{ks}{}^mC_k$	46	2811
1213176	214	229	3565	3580	$T_{ks}T_{ks}T_{ks}G_{ds}T_{ds}G_{ys}G_{ds}T_{ds}A_{ds}{}^mC_{ds}A_{ds}$ $G_{ds}{}^mC_{ds}T_{ks}G_{ks}{}^mC_k$	62	2887

1213177	215	230	3566	3581	$A_{ks}T_{ks}T_{ks}T_{ds}G_{ds}U_{ys}G_{ds}G_{ds}T_{ds}A_{ds}{}^mC_{ds}$ $A_{ds}G_{ds}{}^mC_{ks}T_{ks}G_k$	45	5013
1213178	216	231	3567	3582	${}^mC_{ks}A_{ks}T_{ks}T_{ds}T_{ds}G_{ys}T_{ds}G_{ds}G_{ds}T_{ds}A_{ds}$ ${}^mC_{ds}A_{ds}G_{ks}{}^mC_{ks}T_k$	33	3039
1213179	217	232	3568	3583	$A_{ks}{}^mC_{ks}A_{ks}T_{ds}T_{ds}U_{ys}G_{ds}T_{ds}G_{ds}G_{ds}T_{ds}$ $A_{ds}{}^mC_{ds}A_{ks}G_{ks}{}^mC_k$	49	5014
1213180	218	233	3569	3584	$T_{ks}A_{ks}{}^mC_{ks}A_{ds}T_{ds}U_{ys}T_{ds}G_{ds}T_{ds}G_{ds}G_{ds}$ $T_{ds}A_{ds}{}^mC_{ks}A_{ks}G_k$	26	5015
1213181	219	234	3570	3585	$G_{ks}T_{ks}A_{ks}{}^mC_{ds}A_{ds}U_{ys}T_{ds}T_{ds}G_{ds}T_{ds}G_{ds}$ $G_{ds}T_{ds}A_{ks}{}^mC_{ks}A_k$	50	5016
1213182	220	235	3571	3586	$G_{ks}G_{ks}T_{ks}A_{ds}{}^mC_{ds}A_{ys}T_{ds}T_{ds}T_{ds}G_{ds}T_{ds}$ $G_{ds}G_{ds}T_{ks}A_{ks}{}^mC_k$	46	3269
1213183	221	236	3572	3587	$G_{ks}G_{ks}G_{ks}T_{ds}A_{ds}C_{ys}A_{ds}T_{ds}T_{ds}T_{ds}G_{ds}T_{ds}$ $G_{ds}G_{ks}T_{ks}A_k$	117	3345
1213184	222	237	3573	3588	$T_{ks}G_{ks}G_{ks}G_{ds}T_{ds}A_{ys}{}^mC_{ds}A_{ds}T_{ds}T_{ds}T_{ds}$ $G_{ds}T_{ds}G_{ks}G_{ks}T_k$	N/A	3421
1213185	223	238	3574	3589	$G_{ks}T_{ks}G_{ks}G_{ds}G_{ds}U_{ys}A_{ds}{}^mC_{ds}A_{ds}T_{ds}T_{ds}$ $T_{ds}G_{ds}T_{ks}G_{ks}G_k$	63	5017
1213186	1776	1791	7164	7179	$T_{ks}G_{ks}{}^mC_{ks}A_{ds}G_{ds}G_{ys}G_{ds}T_{ds}G_{ds}A_{ds}G_{ds}$ ${}^mC_{ds}{}^mC_{ds}G_{ks}G_{ks}{}^mC_k$	149	3299
1213187	1777	1792	7165	7180	$T_{ks}T_{ks}G_{ks}{}^mC_{ds}A_{ds}G_{ys}G_{ds}G_{ds}T_{ds}G_{ds}A_{ds}$ $G_{ds}{}^mC_{ds}{}^mC_{ks}G_{ks}G_k$	98	3375
1213188	1778	1793	7166	7181	${}^mC_{ks}T_{ks}T_{ks}G_{ds}{}^mC_{ds}A_{ys}G_{ds}G_{ds}G_{ds}T_{ds}G_{ds}$ $sA_{ds}G_{ds}{}^mC_{ks}{}^mC_{ks}G_k$	71	4962
1213189	1779	1794	7167	7182	${}^mC_{ks}{}^mC_{ks}T_{ks}T_{ds}G_{ds}C_{ys}A_{ds}G_{ds}G_{ds}G_{ds}T_{ds}$ $sG_{ds}A_{ds}G_{ks}{}^mC_{ks}{}^mC_k$	40	4974
1213190	1780	1795	7168	7183	$G_{ks}{}^mC_{ks}{}^mC_{ks}T_{ds}T_{ds}G_{ys}{}^mC_{ds}A_{ds}G_{ds}G_{ds}$ $G_{ds}T_{ds}G_{ds}A_{ks}G_{ks}{}^mC_k$	53	3451
1213192	1782	1797	7170	7185	$A_{ks}T_{ks}G_{ks}{}^mC_{ds}{}^mC_{ds}U_{ys}T_{ds}G_{ds}{}^mC_{ds}A_{ds}$ $G_{ds}G_{ds}G_{ds}T_{ks}G_{ks}A_k$	107	5018
1213193	1783	1798	7171	7186	$G_{ks}A_{ks}T_{ks}G_{ds}{}^mC_{ds}C_{ys}T_{ds}T_{ds}G_{ds}{}^mC_{ds}A_{ds}$ $sG_{ds}G_{ds}G_{ks}T_{ks}G_k$	54	4959
1213194	1784	1799	7172	7187	$T_{ks}G_{ks}A_{ks}T_{ds}G_{ds}C_{ys}{}^mC_{ds}T_{ds}T_{ds}G_{ds}{}^mC_{ds}$ $sA_{ds}G_{ds}G_{ks}G_{ks}T_k$	28	4969
1213195	1785	1800	7173	7188	$A_{ks}T_{ks}G_{ks}A_{ds}T_{ds}G_{ys}{}^mC_{ds}{}^mC_{ds}T_{ds}T_{ds}G_{ds}$ $s{}^mC_{ds}A_{ds}G_{ks}G_{ks}G_k$	53	3603
1213196	1786	1801	7174	7189	$G_{ks}A_{ks}T_{ks}G_{ds}A_{ds}U_{ys}G_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}T_{ds}$ $sG_{ds}{}^mC_{ds}A_{ks}G_{ks}G_k$	73	5019
1213197	1787	1802	7175	7190	$T_{ks}G_{ks}A_{ks}T_{ds}G_{ds}A_{ys}T_{ds}G_{ds}{}^mC_{ds}{}^mC_{ds}T_{ds}$ $sT_{ds}G_{ds}{}^mC_{ks}A_{ks}G_k$	43	4975
1213198	1788	1803	7176	7191	${}^mC_{ks}T_{ks}G_{ks}A_{ds}T_{ds}G_{ys}A_{ds}T_{ds}G_{ds}{}^mC_{ds}{}^m$ $C_{ds}T_{ds}T_{ds}G_{ks}{}^mC_{ks}A_k$	65	3679
1213199	1789	1804	7177	7192	$G_{ks}{}^mC_{ks}T_{ks}G_{ds}A_{ds}U_{ys}G_{ds}A_{ds}T_{ds}G_{ds}{}^mC_{ds}$ ${}^mC_{ds}T_{ds}T_{ks}G_{ks}{}^mC_k$	80	5020
1213200	1790	1805	7178	7193	$A_{ks}G_{ks}{}^mC_{ks}T_{ds}G_{ds}A_{ys}T_{ds}G_{ds}A_{ds}T_{ds}G_{ds}$ ${}^mC_{ds}{}^mC_{ds}T_{ks}T_{ks}G_k$	49	3831
1213201	1791	1806	7179	7194	${}^mC_{ks}A_{ks}G_{ks}{}^mC_{ds}T_{ds}G_{ys}A_{ds}T_{ds}G_{ds}A_{ds}T_{ds}$ $sG_{ds}{}^mC_{ds}{}^mC_{ks}T_{ks}T_k$	83	4960
1213202	1792	1807	7180	7195	${}^mC_{ks}{}^mC_{ks}A_{ks}G_{ds}{}^mC_{ds}U_{ys}G_{ds}A_{ds}T_{ds}G_{ds}$ $A_{ds}T_{ds}G_{ds}{}^mC_{ks}{}^mC_{ks}T_k$	44	5021
1213203	1793	1808	7181	7196	${}^mC_{ks}{}^mC_{ks}{}^mC_{ks}A_{ds}G_{ds}C_{ys}T_{ds}G_{ds}A_{ds}T_{ds}$ $G_{ds}A_{ds}T_{ds}G_{ks}{}^mC_{ks}{}^mC_k$	42	4953

1213204	1892	1907	7280	7295	${}^m\text{C}_{\text{ks}}{}^m\text{C}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ys}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}\text{A}_{\text{d}}$ $\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}\text{G}_{\text{ks}}\text{G}_{\text{ks}}\text{A}_{\text{k}}$	53	3530
1213205	1893	1908	7281	7296	$\text{T}_{\text{ks}}{}^m\text{C}_{\text{ks}}{}^m\text{C}_{\text{ks}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ys}}\text{A}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}$ $\text{A}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ks}}\text{G}_{\text{ks}}\text{G}_{\text{k}}$	104	3606
1213206	1894	1909	7282	7297	$\text{G}_{\text{ks}}\text{T}_{\text{ks}}{}^m\text{C}_{\text{ks}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{U}_{\text{ys}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{d}}$ $\text{A}_{\text{ds}}\text{A}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ks}}\text{A}_{\text{ks}}\text{G}_{\text{k}}$	45	5022
1213207	1895	1910	7283	7298	$\text{A}_{\text{ks}}\text{G}_{\text{ks}}\text{T}_{\text{ks}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{C}_{\text{ys}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}\text{G}_{\text{ds}}{}^m$ $\text{C}_{\text{ds}}\text{A}_{\text{ds}}\text{A}_{\text{ds}}\text{T}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{A}_{\text{k}}$	36	3758
1213208	1896	1911	7284	7299	$\text{G}_{\text{ks}}\text{A}_{\text{ks}}\text{G}_{\text{ks}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{C}_{\text{ys}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}\text{G}$ $\text{ds}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}\text{A}_{\text{ks}}\text{T}_{\text{ks}}{}^m\text{C}_{\text{k}}$	62	3834
1213209	1897	1912	7285	7300	$\text{T}_{\text{ks}}\text{G}_{\text{ks}}\text{A}_{\text{ks}}\text{G}_{\text{ds}}\text{T}_{\text{ds}}\text{C}_{\text{ys}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{d}}$ $\text{sG}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ks}}\text{A}_{\text{ks}}\text{T}_{\text{k}}$	46	3910

Table 89. Reduction of FXII RNA (Huh7, electroporation, 2000nM modified oligonucleotide)

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence and Chemistry notation (5' to 3')	FXII (%UTC)	SEQ ID NO
1128769	153	168	N/A	N/A	$\text{A}_{\text{ks}}\text{G}_{\text{ks}}\text{A}_{\text{ks}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{T}$ $\text{dsG}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{T}_{\text{k}}$	84	3723
1128796	212	227	3563	3578	$\text{T}_{\text{ks}}\text{G}_{\text{ks}}\text{T}_{\text{ks}}\text{G}_{\text{ds}}\text{G}_{\text{ds}}\text{T}_{\text{ds}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{d}}$ $\text{sT}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{G}_{\text{k}}$	103	2734
1128802	218	233	3569	3584	$\text{T}_{\text{ks}}\text{A}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{A}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{G}_{\text{ds}}$ $\text{T}_{\text{ds}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{ks}}\text{A}_{\text{ks}}\text{G}_{\text{k}}$	97	2426
1128870	470	485	4415	4430	$\text{T}_{\text{ks}}\text{G}_{\text{ks}}\text{T}_{\text{ks}}\text{G}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}\text{A}_{\text{ds}}\text{A}_{\text{ds}}\text{A}_{\text{ds}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{ds}}$ ${}^m\text{C}_{\text{ds}}\text{G}_{\text{ds}}\text{G}_{\text{ks}}\text{A}_{\text{ks}}\text{G}_{\text{k}}$	60	3728
1129221	1357	1372	6017	6032	${}^m\text{C}_{\text{ks}}\text{G}_{\text{ks}}\text{T}_{\text{ks}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{ds}}$ $\text{G}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{A}_{\text{k}}$	19	3060
1129407	1781	1796	7169	7184	$\text{T}_{\text{ks}}\text{G}_{\text{ks}}{}^m\text{C}_{\text{ks}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}\text{G}_{\text{ds}}$ $\text{G}_{\text{ds}}\text{G}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ks}}\text{A}_{\text{ks}}\text{G}_{\text{k}}$	12	3527
1129472	1897	1912	7285	7300	$\text{T}_{\text{ks}}\text{G}_{\text{ks}}\text{A}_{\text{ks}}\text{G}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}$ $\text{A}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ks}}\text{A}_{\text{ks}}\text{T}_{\text{k}}$	18	3910
1129488	1924	1939	7312	7327	$\text{A}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{T}_{\text{ks}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{G}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}\text{A}_{\text{ds}}\text{T}_{\text{ds}}{}^m$ $\text{C}_{\text{ds}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ks}}\text{A}_{\text{ks}}\text{A}_{\text{k}}$	5	3607
1129491	1927	1942	7315	7330	${}^m\text{C}_{\text{ks}}\text{T}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{G}_{\text{ds}}\text{G}_{\text{ds}}$ $\text{A}_{\text{ds}}\text{A}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ks}}\text{A}_{\text{ks}}{}^m\text{C}_{\text{k}}$	15	3835
1129531	2009	2024	7397	7412	$\text{G}_{\text{ks}}\text{A}_{\text{ks}}\text{G}_{\text{ks}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}$ $\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ks}}\text{T}_{\text{ks}}{}^m\text{C}_{\text{k}}$	12	3837
1129532	2010	2025	7398	7413	$\text{T}_{\text{ks}}\text{G}_{\text{ks}}\text{A}_{\text{ks}}\text{G}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}$ $\text{dsG}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ks}}\text{A}_{\text{ks}}\text{T}_{\text{k}}$	11	3913
1129533	2011	2026	7399	7414	$\text{T}_{\text{ks}}\text{T}_{\text{ks}}\text{G}_{\text{ks}}\text{A}_{\text{ds}}\text{G}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}$ ${}^m\text{C}_{\text{ds}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{A}_{\text{k}}$	8	2463
1129540	2019	2034	7407	7422	$\text{G}_{\text{ks}}{}^m\text{C}_{\text{ks}}\text{A}_{\text{ks}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}\text{A}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}$ $\text{A}_{\text{ds}}\text{G}_{\text{ds}}\text{T}_{\text{ks}}\text{T}_{\text{ks}}{}^m\text{C}_{\text{k}}$	4	3000
1129542	2021	2036	7409	7424	$\text{A}_{\text{ks}}\text{A}_{\text{ks}}\text{G}_{\text{ks}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}\text{A}_{\text{ds}}\text{T}_{\text{d}}$ $\text{sT}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ks}}\text{G}_{\text{ks}}\text{T}_{\text{k}}$	17	3147
1129565	N/A	N/A	144	159	$\text{A}_{\text{ks}}\text{T}_{\text{ks}}\text{A}_{\text{ks}}\text{G}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{d}}$ $\text{s}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{A}_{\text{ks}}\text{G}_{\text{ks}}\text{A}_{\text{k}}$	82	3383
1129744	N/A	N/A	2082	2097	$\text{T}_{\text{ks}}\text{G}_{\text{ks}}\text{G}_{\text{ks}}\text{A}_{\text{ds}}{}^m\text{C}_{\text{ds}}{}^m\text{C}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}\text{A}_{\text{ds}}\text{A}_{\text{d}}$ $\text{sG}_{\text{ds}}\text{A}_{\text{ds}}\text{T}_{\text{ks}}\text{G}_{\text{ks}}{}^m\text{C}_{\text{k}}$	75	3316

1129864	N/A	N/A	3897	3912	$T_{ks}G_{ks}G_{ks}T_{ds}G_{ds}A_{ds}T_{ds}A_{ds}^mC_{ds}^mC_{ds}A_{ds}$ $sG_{ds}G_{ds}A_{ks}G_{ks}A_{ks}$	74	3322
1129946	N/A	N/A	4812	4827	$T_{ks}^mC_{ks}^mC_{ks}T_{ds}G_{ds}G_{ds}^mC_{ds}A_{ds}A_{ds}G_{ds}^m$ $C_{ds}^mC_{ds}^mC_{ds}G_{ks}T_{ks}^mC_{ks}$	119	3478
1129948	N/A	N/A	4840	4855	$A_{ks}T_{ks}^mC_{ks}T_{ds}G_{ds}^mC_{ds}T_{ds}T_{ds}T_{ds}^mC_{ds}^m$ $C_{ds}G_{ds}^mC_{ds}A_{ks}^mC_{ks}T_{ks}$	77	3630
1129949	N/A	N/A	4844	4859	$T_{ks}^mC_{ks}T_{ks}^mC_{ds}A_{ds}T_{ds}^mC_{ds}T_{ds}G_{ds}^mC_{ds}$ $T_{ds}T_{ds}T_{ds}^mC_{ks}^mC_{ks}G_{ks}$	84	3706
1213210	1898	1913	7286	7301	$A_{ks}T_{ks}G_{ks}A_{ds}G_{ds}U_{ys}^mC_{ds}^mC_{ds}^mC_{ds}T_{ds}$ $G_{ds}A_{ds}G_{ds}^mC_{ks}A_{ks}A_{ks}$	40	5023
1213211	1899	1914	7287	7302	$G_{ks}A_{ks}T_{ks}G_{ds}A_{ds}G_{ys}T_{ds}^mC_{ds}^mC_{ds}^mC_{ds}$ $T_{ds}G_{ds}A_{ds}G_{ks}^mC_{ks}A_{ks}$	27	2537
1213212	1900	1915	7288	7303	$A_{ks}G_{ks}A_{ks}T_{ds}G_{ds}A_{ys}G_{ds}T_{ds}^mC_{ds}^mC_{ds}^m$ $C_{ds}T_{ds}G_{ds}A_{ks}G_{ks}^mC_{ks}$	24	2614
1213213	1901	1916	7289	7304	$A_{ks}A_{ks}G_{ks}A_{ds}T_{ds}G_{ys}A_{ds}G_{ds}T_{ds}^mC_{ds}^mC_{ds}$ $ds^mC_{ds}T_{ds}G_{ks}A_{ks}G_{ks}$	19	2691
1213214	1902	1917	7290	7305	$A_{ks}A_{ks}A_{ks}G_{ds}A_{ds}U_{ys}G_{ds}A_{ds}G_{ds}T_{ds}^mC_{ds}$ $^mC_{ds}^mC_{ds}T_{ks}G_{ks}A_{ks}$	31	5024
1213215	1903	1918	7291	7306	$G_{ks}A_{ks}A_{ks}A_{ds}G_{ds}A_{ys}T_{ds}G_{ds}A_{ds}G_{ds}T_{ds}^m$ $C_{ds}^mC_{ds}^mC_{ks}T_{ks}G_{ks}$	23	2845
1213216	1904	1919	7292	7307	$G_{ks}G_{ks}A_{ks}A_{ds}A_{ds}G_{ys}A_{ds}T_{ds}G_{ds}A_{ds}G_{ds}$ $T_{ds}^mC_{ds}^mC_{ks}^mC_{ks}T_{ks}$	39	2921
1213217	1905	1920	7293	7308	$G_{ks}G_{ks}G_{ks}A_{ds}A_{ds}A_{ys}G_{ds}A_{ds}T_{ds}G_{ds}A_{ds}$ $G_{ds}T_{ds}^mC_{ks}^mC_{ks}^mC_{ks}$	55	2997
1213218	1906	1921	7294	7309	$A_{ks}G_{ks}G_{ks}G_{ds}A_{ds}A_{ys}A_{ds}G_{ds}A_{ds}T_{ds}G_{ds}$ $A_{ds}G_{ds}T_{ks}^mC_{ks}^mC_{ks}$	18	3073
1213219	1914	1929	7302	7317	$^mC_{ks}A_{ks}^mC_{ks}^mC_{ds}A_{ds}A_{ys}G_{ds}G_{ds}A_{ds}G_{ds}$ $G_{ds}G_{ds}A_{ds}A_{ks}A_{ks}G_{ks}$	31	4954
1213220	1915	1930	7303	7318	$T_{ks}^mC_{ks}A_{ks}^mC_{ds}^mC_{ds}A_{ys}A_{ds}G_{ds}G_{ds}A_{ds}$ $G_{ds}G_{ds}G_{ds}A_{ks}A_{ks}A_{ks}$	9	4948
1213221	1916	1931	7304	7319	$A_{ks}T_{ks}^mC_{ks}A_{ds}^mC_{ds}C_{ys}A_{ds}A_{ds}G_{ds}G_{ds}A_{ds}$ $dsG_{ds}G_{ds}G_{ks}A_{ks}A_{ks}$	31	4966
1213222	1917	1932	7305	7320	$A_{ks}A_{ks}T_{ks}^mC_{ds}A_{ds}C_{ys}^mC_{ds}A_{ds}A_{ds}G_{ds}G_{ds}$ $dsA_{ds}G_{ds}G_{ks}G_{ks}A_{ks}$	44	4956
1213223	1918	1933	7306	7321	$G_{ks}A_{ks}A_{ks}T_{ds}^mC_{ds}A_{ys}^mC_{ds}^mC_{ds}A_{ds}A_{ds}$ $G_{ds}G_{ds}A_{ds}G_{ks}G_{ks}G_{ks}$	28	4965
1213224	1919	1934	7307	7322	$G_{ks}G_{ks}A_{ks}A_{ds}T_{ds}C_{ys}A_{ds}^mC_{ds}^mC_{ds}A_{ds}A_{ds}$ $dsG_{ds}G_{ds}A_{ks}G_{ks}G_{ks}$	21	3226
1213225	1920	1935	7308	7323	$^mC_{ks}G_{ks}G_{ks}A_{ds}A_{ds}U_{ys}^mC_{ds}A_{ds}^mC_{ds}^mC_{ds}$ $sA_{ds}A_{ds}G_{ds}G_{ks}A_{ks}G_{ks}$	33	5025
1213226	1921	1936	7309	7324	$G_{ks}^mC_{ks}G_{ks}G_{ds}A_{ds}A_{ys}T_{ds}^mC_{ds}A_{ds}^mC_{ds}$ $^mC_{ds}A_{ds}A_{ds}G_{ks}G_{ks}A_{ks}$	21	3379
1213227	1922	1937	7310	7325	$T_{ks}G_{ks}^mC_{ks}G_{ds}G_{ds}A_{ys}A_{ds}T_{ds}^mC_{ds}A_{ds}^m$ $C_{ds}^mC_{ds}A_{ds}A_{ks}G_{ks}G_{ks}$	8	3455
1213228	1923	1938	7311	7326	$^mC_{ks}T_{ks}G_{ks}^mC_{ds}G_{ds}G_{ys}A_{ds}A_{ds}T_{ds}^mC_{ds}$ $A_{ds}^mC_{ds}^mC_{ds}A_{ks}A_{ks}G_{ks}$	17	3531
1213229	1924	1939	7312	7327	$A_{ks}^mC_{ks}T_{ks}G_{ds}^mC_{ds}G_{ys}G_{ds}A_{ds}A_{ds}T_{ds}^m$ $C_{ds}A_{ds}^mC_{ds}^mC_{ks}A_{ks}A_{ks}$	12	3607
1213230	1925	1940	7313	7328	$^mC_{ks}A_{ks}^mC_{ks}T_{ds}G_{ds}C_{ys}G_{ds}G_{ds}A_{ds}A_{ds}T_{ds}$ $ds^mC_{ds}A_{ds}^mC_{ks}^mC_{ks}A_{ks}$	22	3683
1213231	1926	1941	7314	7329	$T_{ks}^mC_{ks}A_{ks}^mC_{ds}T_{ds}G_{ys}^mC_{ds}G_{ds}G_{ds}A_{ds}$ $A_{ds}T_{ds}^mC_{ds}A_{ks}^mC_{ks}^mC_{ks}$	23	3759

1213232	1927	1942	7315	7330	${}^m\text{C}_{ks}\text{T}_{ks}{}^m\text{C}_{ks}\text{A}_{ds}{}^m\text{C}_{ds}\text{U}_{ys}\text{G}_{ds}{}^m\text{C}_{ds}\text{G}_{ds}\text{G}_{ds}$ $\text{A}_{ds}\text{A}_{ds}\text{T}_{ds}{}^m\text{C}_{ks}\text{A}_{ks}{}^m\text{C}_k$	11	5026
1213233	1928	1943	7316	7331	$\text{T}_{ks}{}^m\text{C}_{ks}\text{T}_{ks}{}^m\text{C}_{ds}\text{A}_{ds}\text{C}_{ys}\text{T}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}\text{G}_{ds}$ $\text{G}_{ds}\text{A}_{ds}\text{A}_{ds}\text{T}_{ks}{}^m\text{C}_{ks}\text{A}_k$	16	3911
1213234	1929	1944	7317	7332	${}^m\text{C}_{ks}\text{T}_{ks}{}^m\text{C}_{ks}\text{T}_{ds}{}^m\text{C}_{ds}\text{A}_{ys}{}^m\text{C}_{ds}\text{T}_{ds}\text{G}_{ds}{}^m\text{C}_d$ $\text{G}_{ds}\text{G}_{ds}\text{A}_{ds}\text{A}_{ks}\text{T}_{ks}{}^m\text{C}_k$	11	4971
1213235	1930	1945	7318	7333	$\text{T}_{ks}{}^m\text{C}_{ks}\text{T}_{ks}{}^m\text{C}_{ds}\text{T}_{ds}\text{C}_{ys}\text{A}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}\text{G}_{ds}{}^m$ $\text{C}_{ds}\text{G}_{ds}\text{G}_{ds}\text{A}_{ks}\text{A}_{ks}\text{T}_k$	11	4955
1213236	1931	1946	7319	7334	${}^m\text{C}_{ks}\text{T}_{ks}{}^m\text{C}_{ks}\text{T}_{ds}{}^m\text{C}_{ds}\text{U}_{ys}{}^m\text{C}_{ds}\text{A}_{ds}{}^m\text{C}_{ds}\text{T}_d$ $\text{G}_{ds}{}^m\text{C}_{ds}\text{G}_{ds}\text{G}_{ks}\text{A}_{ks}\text{A}_k$	34	5027
1213237	1932	1947	7320	7335	$\text{A}_{ks}{}^m\text{C}_{ks}\text{T}_{ks}{}^m\text{C}_{ds}\text{T}_{ds}\text{C}_{ys}\text{T}_{ds}{}^m\text{C}_{ds}\text{A}_{ds}{}^m\text{C}_{ds}$ $\text{T}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}\text{G}_{ks}\text{G}_{ks}\text{A}_k$	20	4976
1213238	1933	1948	7321	7336	${}^m\text{C}_{ks}\text{A}_{ks}{}^m\text{C}_{ks}\text{T}_{ds}{}^m\text{C}_{ds}\text{U}_{ys}{}^m\text{C}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}\text{A}_{ds}$ $\text{G}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}\text{G}_{ds}{}^m\text{C}_{ks}\text{G}_{ks}\text{G}_k$	26	5028
1213239	1934	1949	7322	7337	${}^m\text{C}_{ks}{}^m\text{C}_{ks}\text{A}_{ks}{}^m\text{C}_{ds}\text{T}_{ds}\text{C}_{ys}\text{T}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}{}^m\text{C}_d$ $\text{A}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}\text{G}_{ks}{}^m\text{C}_{ks}\text{G}_k$	18	4949
1213240	1935	1950	7323	7338	$\text{G}_{ks}{}^m\text{C}_{ks}{}^m\text{C}_{ks}\text{A}_{ds}{}^m\text{C}_{ds}\text{U}_{ys}{}^m\text{C}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}$ $\text{G}_{ds}{}^m\text{C}_{ds}\text{A}_{ds}{}^m\text{C}_{ds}\text{T}_{ks}\text{G}_{ks}{}^m\text{C}_k$	32	5029
1213241	1936	1951	7324	7339	$\text{A}_{ks}\text{G}_{ks}{}^m\text{C}_{ks}{}^m\text{C}_{ds}\text{A}_{ds}\text{C}_{ys}\text{T}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}$ $\text{T}_{ds}{}^m\text{C}_{ds}\text{A}_{ds}{}^m\text{C}_{ks}\text{T}_{ks}\text{G}_k$	28	4961
1213242	1937	1952	7325	7340	${}^m\text{C}_{ks}\text{A}_{ks}\text{G}_{ks}{}^m\text{C}_{ds}{}^m\text{C}_{ds}\text{A}_{ys}{}^m\text{C}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}$ $\text{G}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}\text{A}_{ks}{}^m\text{C}_{ks}\text{T}_k$	55	4972
1213243	2000	2015	7388	7403	${}^m\text{C}_{ks}\text{G}_{ks}{}^m\text{C}_{ks}{}^m\text{C}_{ds}\text{A}_{ds}\text{U}_{ys}{}^m\text{C}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}\text{G}_{ds}$ $\text{G}_{ds}{}^m\text{C}_{ds}\text{G}_{ds}{}^m\text{C}_{ks}\text{G}_{ks}\text{G}_k$	92	5030
1213244	2001	2016	7389	7404	$\text{G}_{ks}{}^m\text{C}_{ks}\text{G}_{ks}{}^m\text{C}_{ds}{}^m\text{C}_{ds}\text{A}_{ys}\text{T}_{ds}{}^m\text{C}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}$ $\text{G}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}\text{G}_{ks}{}^m\text{C}_{ks}\text{G}_k$	92	4964
1213245	2002	2017	7390	7405	$\text{T}_{ks}\text{G}_{ks}{}^m\text{C}_{ks}\text{G}_{ds}{}^m\text{C}_{ds}\text{C}_{ys}\text{A}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}{}^m\text{C}_{ds}$ $\text{T}_{ds}\text{G}_{ds}\text{G}_{ds}{}^m\text{C}_{ks}\text{G}_{ks}{}^m\text{C}_k$	71	3305
1213246	2003	2018	7391	7406	${}^m\text{C}_{ks}\text{T}_{ks}\text{G}_{ks}{}^m\text{C}_{ds}\text{G}_{ds}\text{C}_{ys}{}^m\text{C}_{ds}\text{A}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}$ ${}^m\text{C}_{ds}\text{T}_{ds}\text{G}_{ds}\text{G}_{ks}{}^m\text{C}_{ks}\text{G}_k$	54	3381
1213247	2004	2019	7392	7407	${}^m\text{C}_{ks}{}^m\text{C}_{ks}\text{T}_{ks}\text{G}_{ds}{}^m\text{C}_{ds}\text{G}_{ys}{}^m\text{C}_{ds}{}^m\text{C}_{ds}\text{A}_{ds}\text{T}_{ds}$ $\text{G}_{ds}{}^m\text{C}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}\text{G}_{ks}\text{G}_{ks}{}^m\text{C}_k$	54	3457
1213248	2005	2020	7393	7408	$\text{T}_{ks}{}^m\text{C}_{ks}{}^m\text{C}_{ks}\text{T}_{ds}\text{G}_{ds}\text{C}_{ys}\text{G}_{ds}{}^m\text{C}_{ds}{}^m\text{C}_{ds}\text{A}_{ds}$ $\text{T}_{ds}{}^m\text{C}_{ds}{}^m\text{C}_{ds}\text{T}_{ks}\text{G}_{ks}\text{G}_k$	21	3533
1213249	2006	2021	7394	7409	$\text{T}_{ks}\text{T}_{ks}{}^m\text{C}_{ks}{}^m\text{C}_{ds}\text{T}_{ds}\text{G}_{ys}{}^m\text{C}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}{}^m\text{C}_d$ $\text{A}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}{}^m\text{C}_{ks}\text{T}_{ks}\text{G}_k$	64	3609
1213250	2007	2022	7395	7410	$\text{G}_{ks}\text{T}_{ks}\text{T}_{ks}{}^m\text{C}_{ds}{}^m\text{C}_{ds}\text{U}_{ys}\text{G}_{ds}{}^m\text{C}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}$ ${}^m\text{C}_{ds}\text{A}_{ds}\text{T}_{ds}{}^m\text{C}_{ks}{}^m\text{C}_{ks}\text{T}_k$	30	5031
1213251	2008	2023	7396	7411	$\text{A}_{ks}\text{G}_{ks}\text{T}_{ks}\text{T}_{ds}{}^m\text{C}_{ds}\text{C}_{ys}\text{T}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}\text{G}_{ds}{}^m$ $\text{C}_{ds}{}^m\text{C}_{ds}\text{A}_{ds}\text{T}_{ks}{}^m\text{C}_{ks}{}^m\text{C}_k$	21	3761
1213252	2009	2024	7397	7412	$\text{G}_{ks}\text{A}_{ks}\text{G}_{ks}\text{T}_{ds}\text{T}_{ds}\text{C}_{ys}{}^m\text{C}_{ds}\text{T}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}\text{G}_d$ ${}^m\text{C}_{ds}{}^m\text{C}_{ds}\text{A}_{ks}\text{T}_{ks}{}^m\text{C}_k$	24	3837
1213253	2010	2025	7398	7413	$\text{T}_{ks}\text{G}_{ks}\text{A}_{ks}\text{G}_{ds}\text{T}_{ds}\text{U}_{ys}{}^m\text{C}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}\text{G}_{ds}{}^m$ $\text{C}_{ds}\text{G}_{ds}{}^m\text{C}_{ds}{}^m\text{C}_{ks}\text{A}_{ks}\text{T}_k$	17	5032
1213254	2011	2026	7399	7414	$\text{T}_{ks}\text{T}_{ks}\text{G}_{ks}\text{A}_{ds}\text{G}_{ds}\text{U}_{ys}\text{T}_{ds}{}^m\text{C}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}\text{G}_d$ ${}^m\text{C}_{ds}\text{G}_{ds}{}^m\text{C}_{ks}{}^m\text{C}_{ks}\text{A}_k$	30	5033
1213255	2012	2027	7400	7415	$\text{A}_{ks}\text{T}_{ks}\text{T}_{ks}\text{G}_{ds}\text{A}_{ds}\text{G}_{ys}\text{T}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}$ $\text{G}_{ds}{}^m\text{C}_{ds}\text{G}_{ks}{}^m\text{C}_{ks}{}^m\text{C}_k$	20	2540
1213256	2013	2028	7401	7416	$\text{T}_{ks}\text{A}_{ks}\text{T}_{ks}\text{T}_{ds}\text{G}_{ds}\text{A}_{ys}\text{G}_{ds}\text{T}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}{}^m\text{C}_{ds}$ $\text{T}_{ds}\text{G}_{ds}{}^m\text{C}_{ks}\text{G}_{ks}{}^m\text{C}_k$	26	2617
1213257	2014	2029	7402	7417	$\text{T}_{ks}\text{T}_{ks}\text{A}_{ks}\text{T}_{ds}\text{T}_{ds}\text{G}_{ys}\text{A}_{ds}\text{G}_{ds}\text{T}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}{}^m$ $\text{C}_{ds}\text{T}_{ds}\text{G}_{ks}{}^m\text{C}_{ks}\text{G}_k$	21	2694

1213258	2016	2031	7404	7419	${}^m\text{C}_{ks}\text{T}_{ks}\text{T}_{ks}\text{T}_{ds}\text{A}_{ds}\text{U}_{ys}\text{T}_{ds}\text{G}_{ds}\text{A}_{ds}\text{G}_{ds}\text{T}_{ds}$ $\text{T}_{ds}{}^m\text{C}_{ds}{}^m\text{C}_{ks}\text{T}_{ks}\text{G}_k$	19	5034
1213259	2017	2032	7405	7420	$\text{A}_{ks}{}^m\text{C}_{ks}\text{T}_{ks}\text{T}_{ds}\text{T}_{ds}\text{A}_{ys}\text{T}_{ds}\text{T}_{ds}\text{G}_{ds}\text{A}_{ds}\text{G}_{ds}$ $\text{T}_{ds}\text{T}_{ds}{}^m\text{C}_{ks}{}^m\text{C}_{ks}\text{T}_k$	2	2848
1213260	2018	2033	7406	7421	${}^m\text{C}_{ks}\text{A}_{ks}{}^m\text{C}_{ks}\text{T}_{ds}\text{T}_{ds}\text{U}_{ys}\text{A}_{ds}\text{T}_{ds}\text{T}_{ds}\text{G}_{ds}\text{A}_d$ ${}_s\text{G}_{ds}\text{T}_{ds}\text{T}_{ks}{}^m\text{C}_{ks}{}^m\text{C}_k$	2	5035
1213261	2019	2034	7407	7422	$\text{G}_{ks}{}^m\text{C}_{ks}\text{A}_{ks}{}^m\text{C}_{ds}\text{T}_{ds}\text{U}_{ys}\text{T}_{ds}\text{A}_{ds}\text{T}_{ds}\text{T}_{ds}\text{G}_d$ ${}_s\text{A}_{ds}\text{G}_{ds}\text{T}_{ks}\text{T}_{ks}{}^m\text{C}_k$	12	5036
1213262	2020	2035	7408	7423	$\text{A}_{ks}\text{G}_{ks}{}^m\text{C}_{ks}\text{A}_{ds}{}^m\text{C}_{ds}\text{U}_{ys}\text{T}_{ds}\text{T}_{ds}\text{A}_{ds}\text{T}_{ds}\text{T}_d$ ${}_s\text{G}_{ds}\text{A}_{ds}\text{G}_{ks}\text{T}_{ks}\text{T}_k$	4	5037
1213263	2021	2036	7409	7424	$\text{A}_{ks}\text{A}_{ks}\text{G}_{ks}{}^m\text{C}_{ds}\text{A}_{ds}\text{C}_{ys}\text{T}_{ds}\text{T}_{ds}\text{T}_{ds}\text{A}_{ds}\text{T}_{ds}$ $\text{T}_{ds}\text{G}_{ds}\text{A}_{ks}\text{G}_{ks}\text{T}_k$	19	3147
1213264	2022	2037	7410	7425	$\text{A}_{ks}\text{A}_{ks}\text{A}_{ks}\text{G}_{ds}{}^m\text{C}_{ds}\text{A}_{ys}{}^m\text{C}_{ds}\text{T}_{ds}\text{T}_{ds}\text{T}_{ds}\text{A}_d$ ${}_s\text{T}_{ds}\text{T}_{ds}\text{G}_{ks}\text{A}_{ks}\text{G}_k$	11	3229
1213265	2023	2038	7411	7426	${}^m\text{C}_{ks}\text{A}_{ks}\text{A}_{ks}\text{A}_{ds}\text{G}_{ds}\text{C}_{ys}\text{A}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}\text{T}_{ds}\text{T}_d$ ${}_s\text{A}_{ds}\text{T}_{ds}\text{T}_{ks}\text{G}_{ks}\text{A}_k$	19	3306
1213266	2024	2039	7412	7427	$\text{T}_{ks}{}^m\text{C}_{ks}\text{A}_{ks}\text{A}_{ds}\text{A}_{ds}\text{G}_{ys}{}^m\text{C}_{ds}\text{A}_{ds}{}^m\text{C}_{ds}\text{T}_{ds}$ $\text{T}_{ds}\text{T}_{ds}\text{A}_{ds}\text{T}_{ks}\text{T}_{ks}\text{G}_k$	54	3382
1213267	2031	2046	7419	7434	$\text{A}_{ks}\text{G}_{ks}{}^m\text{C}_{ks}\text{A}_{ds}\text{T}_{ds}\text{U}_{ys}\text{T}_{ds}\text{T}_{ds}{}^m\text{C}_{ds}\text{A}_{ds}\text{A}_d$ ${}_s\text{A}_{ds}\text{G}_{ds}{}^m\text{C}_{ks}\text{A}_{ks}{}^m\text{C}_k$	23	5038
1213268	2033	2048	7421	7436	$\text{T}_{ks}{}^m\text{C}_{ks}\text{A}_{ks}\text{G}_{ds}{}^m\text{C}_{ds}\text{A}_{ys}\text{T}_{ds}\text{T}_{ds}\text{T}_{ds}{}^m\text{C}$ ${}_ds\text{A}_{ds}\text{A}_{ds}\text{A}_{ks}\text{G}_{ks}{}^m\text{C}_k$	20	3534

Example 5: Dose-dependent reduction of human FXII RNA by modified oligonucleotides *in vitro*

Certain modified oligonucleotides described in the studies above exhibiting significant *in vitro* inhibition of FXII RNA were selected and tested at various doses in HepG2 cells.

The modified oligonucleotides were tested in a series of experiments using the same culture conditions. The results for each experiment are presented in separate tables shown below. Cultured HepG2 cells at a density of 10,000 cells per well were transfected using lipofectin with modified oligonucleotides diluted to different concentrations as specified in the tables below. After a treatment period of approximately 24 hours, FXII RNA levels were measured as previously described using the Human FXII primer-probe set RTS2976_MGB (forward sequence CCGGGAGCACACCGTTT, designated herein as SEQ ID NO: 11; reverse sequence GGAATCACCAAGGAGGGAAAG, designated herein as SEQ ID NO: 12; probe sequence CTGATTGCTCAGGGACT, designated herein as SEQ ID NO: 13). FXII RNA levels were normalized to total RNA, as measured by RIBOGREEN®. Reduction of FXII RNA is presented in the tables below as percent FXII RNA relative to the amount in untreated control cells (% UTC).

The half maximal inhibitory concentration (IC₅₀) of each modified oligonucleotide was calculated using a linear regression on a log/linear plot of the data in excel and is also presented in the tables below.

Table 90. Dose-dependent reduction of human FXII RNA by modified oligonucleotides

Compound Number	FXII (% UTC)						IC50 (μM)
	5 nM	9 nM	19 nM	38 nM	75 nM	150 nM	
413627	74	57	45	30	22	18	0.02
413631	77	66	46	36	27	11	0.02

413632	80	64	53	42	27	21	0.02
413636	87	71	58	44	28	21	0.03
413637	85	66	56	36	24	15	0.02
413642	72	57	42	32	17	11	0.01
413643	75	50	37	25	18	13	0.01
413644	81	77	54	39	29	18	0.03
413645	80	69	51	35	28	21	0.02
413652	77	62	46	32	21	12	0.02

Example 6: Dose-dependent reduction of human FXII RNA by modified oligonucleotides *in vitro*

Certain modified oligonucleotides described in the studies above exhibiting significant *in vitro* inhibition of FXII RNA were selected and tested at various doses in Huh7 cells.

The modified oligonucleotides were tested in a series of experiments using the same culture conditions. The results for each experiment are presented in separate tables shown below. Cultured Huh7 cells at a density of 5,000 cells per well were transfected using oligofectamine with modified oligonucleotides diluted to different concentrations as specified in the tables below. After a treatment period of approximately 24 hours, FXII RNA levels were measured as previously described using the Human FXII primer-probe set RTS2992. FXII RNA levels were normalized to total RNA, as measured by RIBOGREEN®. Reduction of FXII RNA is presented in the tables below as percent FXII RNA relative to the amount in untreated control cells (% UTC).

The half maximal inhibitory concentration (IC₅₀) of each modified oligonucleotide was calculated using a linear regression on a log/linear plot of the data in excel and is also presented in the tables below. The symbol “†” indicates that the modified oligonucleotide is complementary to the target transcript within the amplicon region of the primer probe set. In such instances, additional assays using alternative primer probes must be performed to accurately assess the potency and efficacy of such modified oligonucleotides.

Table 91. Dose-dependent reduction of human FXII RNA by modified oligonucleotides

Compound Number	FXII (% UTC)					
	14 nM	28 nM	55 nM	110 nM	220 nM	IC ₅₀ μM
462145	87	68	48	37	20	0.06
462147	80	66	43	34	28	0.056
462176	95	79	67	56	31	0.113
462183	76	64	52	39	24	0.058
462189	56	60	37	25	22	0.028
462190	72	67	52	34	26	0.056
462192	53	44	32	15	22	0.015
462193	86	75	48	43	27	0.072
462195	50	42	35	19	23	0.013
462196	53	31	36	17	19	0.012
462197	46	40	31	17	15	< 14 nM

462198	42	34	32	27	19	< 14 nM
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Table 92. Dose-dependent reduction of human FXII RNA by modified oligonucleotides

Compound Number	FXII (% UTC)					
	14 nM	28 nM	55 nM	110 nM	220 nM	IC ₅₀ μ M
462072	80	55	40	26	12	0.041
462073	81	47	30	22	23	0.035
462098	89	89	57	38	19	0.075
462107	90	88	54	58	32	0.109
462131	69	61	68	42	34	0.08
462188	95	84	52	46	41	0.106
462194	73	63	50	40	49	0.087
462199	50	46	44	28	31	0.016
462064†	73	62	32	16	13	N/A
462065†	66	48	41	13	4	N/A
462068†	56	52	29	15	8	N/A
462069†	81	57	53	21	10	N/A

Example 7: Dose-dependent reduction of human FXII RNA by modified oligonucleotides *in vitro*

Certain modified oligonucleotides described in the studies above exhibiting significant *in vitro* inhibition of FXII RNA were selected and tested at various doses in Huh7 cells.

- 5 The modified oligonucleotides were tested in a series of experiments using the same culture conditions. The results for each experiment are presented in separate tables shown below. Cultured Huh7 cells at a density of 20,000 cells per well were transfected using electroporation with modified oligonucleotides diluted to different concentrations as specified in the tables below. After a treatment period of approximately 24 hours, FXII RNA levels were measured as previously described using the Human FXII primer-probe set RTS40528.
- 10 FXII RNA levels were normalized to total RNA, as measured by RIBOGREEN®. Reduction of FXII RNA is presented in the tables below as percent FXII RNA relative to the amount in untreated control cells (% UTC).

The half maximal inhibitory concentration (IC₅₀) of each modified oligonucleotide was calculated using a linear regression on a log/linear plot of the data in excel and is also presented in the tables below.

Table 93. Dose-dependent reduction of human FXII RNA by modified oligonucleotides

Compound Number	FXII (% UTC)				IC ₅₀ μ M
	47 nM	188 nM	750 nM	3000 nM	
1128754	94	82	66	37	1.6
1128802	81	54	38	16	0.3
1128835	92	83	57	37	1.3
1128873	91	75	63	42	1.8
1128874	93	67	41	17	0.5

1128875	93	76	60	36	1.3
1129015	93	71	44	30	0.7
1129094	81	66	42	24	0.5
1129114	92	64	50	23	0.6
1129294	86	55	55	30	0.6
1129473	84	63	37	22	0.4
1129475	76	50	28	15	0.2
1129476	70	44	40	22	0.2
1129493	81	48	23	11	0.2
1129494	87	85	45	26	0.7
1129533	65	54	21	21	0.2
1129534	77	46	36	17	0.2
1129535	80	64	32	25	0.4
1129536	85	47	30	25	0.3

Table 94. Dose-dependent reduction of human FXII RNA by modified oligonucleotides

Compound Number	FXII (% UTC)				IC ₅₀ μ M
	47 nM	188 nM	750 nM	3000 nM	
1128795	84	63	38	28	0.5
1128796	66	50	21	12	0.2
1128797	86	71	37	24	0.5
1128802	86	62	37	15	0.4
1128836	80	67	44	30	0.6
1128878	85	74	50	27	0.7
1128958	92	94	74	42	> 3.0
1129058	94	54	45	28	0.5
1129136	77	68	62	32	1.0
1129477	96	56	39	26	0.5
1129478	98	65	37	22	0.5
1129496	88	76	70	45	2.8
1129497	100	75	43	17	0.6
1129498	80	69	43	32	0.6
1129499	77	65	31	26	0.4
1129516	82	43	38	32	0.3
1129537	69	57	21	16	0.2
1129538	55	38	18	11	0.1
1129539	45	22	14	7	< 0.04

Table 95. Dose-dependent reduction of human FXII RNA by modified oligonucleotides

Compound Number	FXII (% UTC)				IC ₅₀ μ M
	47 nM	188 nM	750 nM	3000 nM	
1128738	88	72	56	32	0.9
1128799	92	68	58	22	0.7

1128802	104	73	40	23	0.6
1128879	81	76	33	23	0.5
1128880	97	72	39	25	0.6
1128980	112	85	62	42	1.7
1129000	118	97	65	38	1.7
1129020	106	92	52	35	1.2
1129039	84	63	45	24	0.5
1129119	108	77	65	35	1.3
1129139	78	58	44	19	0.4
1129180	97	88	40	34	0.9
1129420	88	69	47	33	0.8
1129460	86	60	39	24	0.4
1129479	98	58	36	17	0.4
1129481	79	63	42	31	0.5
1129500	82	64	44	18	0.4
1129540	48	28	19	11	< 0.04
1129541	64	36	17	10	0.1

Table 96. Dose-dependent reduction of human FXII RNA by modified oligonucleotides

Compound Number	FXII (% UTC)				IC ₅₀ μ M
	47 nM	188 nM	750 nM	3000 nM	
1128762	73	63	37	21	0.3
1128801	99	56	35	18	0.4
1128802	97	65	37	14	0.4
1128821	78	55	57	21	0.5
1128841	106	91	73	36	1.9
1128881	80	66	42	27	0.5
1129022	122	100	80	46	2.9
1129043	112	98	57	31	1.2
1129142	98	79	48	20	0.7
1129221	63	49	28	14	0.1
1129423	99	72	36	29	0.6
1129441	78	45	27	12	0.2
1129462	95	70	64	25	0.9
1129482	84	63	70	29	1.0
1129483	69	33	14	8	0.1
1129501	95	66	35	14	0.4
1129502	93	73	49	19	0.6
1129542	66	34	24	12	0.1
1129543	89	44	30	17	0.3

Table 97. Dose-dependent reduction of human FXII RNA by modified oligonucleotides

Compound Number	FXII (% UTC)				IC ₅₀ μ M
	47 nM	188 nM	750 nM	3000 nM	
1128763	80	57	37	22	0.3
1128764	73	42	26	12	0.2
1128802	68	58	32	19	0.2
1129044	88	69	43	26	0.6
1129065	85	60	36	15	0.4
1129084	87	70	47	23	0.6
1129104	103	87	54	40	1.4
1129143	81	65	40	24	0.4
1129144	98	68	45	30	0.7
1129424	95	59	39	24	0.5
1129445	83	54	40	20	0.4
1129484	61	40	22	15	0.1
1129485	55	39	21	10	0.1
1129486	57	38	21	9	0.1
1129503	114	110	86	43	> 3.0
1129504	100	71	43	26	0.7
1129544	82	46	33	18	0.3
1129545	70	54	32	15	0.2
1129864	89	66	53	31	0.8

Table 98. Dose-dependent reduction of human FXII RNA by modified oligonucleotides

Compound Number	FXII (% UTC)				IC ₅₀ μ M
	47 nM	188 nM	750 nM	3000 nM	
1128747	99	95	60	38	1.6
1128765	76	48	29	11	0.2
1128766	49	52	36	17	0.1
1128768	65	53	34	25	0.2
1128802	83	55	41	15	0.3
1128808	98	85	67	31	1.4
1128848	79	59	47	18	0.4
1129227	81	60	39	31	0.5
1129287	72	72	34	18	0.3
1129407	59	51	44	27	0.2
1129408	61	58	40	25	0.2
1129426	81	68	46	19	0.5
1129466	84	55	48	29	0.5
1129487	71	56	23	35	0.3
1129488	59	49	26	11	0.1
1129489	58	42	16	15	0.1
1129526	96	79	64	33	1.3

1129527	69	58	31	19	0.2
1129948	84	65	45	27	0.5

Table 99. Dose-dependent reduction of human FXII RNA by modified oligonucleotides

Compound Number	FXII (% UTC)				IC ₅₀ μ M
	47 nM	188 nM	750 nM	3000 nM	
1128769	49	37	24	19	< 0.04
1128802	67	49	25	12	0.2
1128810	75	77	43	29	0.6
1128830	117	72	33	29	0.7
1128870	49	36	38	18	< 0.04
1129051	88	71	52	33	0.9
1129092	86	66	43	27	0.6
1129211	76	54	57	19	0.4
1129409	60	32	34	13	0.1
1129472	70	35	42	18	0.2
1129490	58	29	13	6	0.1
1129491	52	31	22	7	< 0.04
1129492	62	26	10	9	0.1
1129510	55	42	42	14	0.1
1129529	73	50	44	21	0.3
1129530	66	34	24	9	0.1
1129531	48	42	32	10	< 0.04
1129532	55	27	13	8	< 0.04
1129949	84	98	56	42	2.0

Table 100. Dose-dependent reduction of human FXII RNA by modified oligonucleotides

Compound Number	FXII (%UTC)				IC ₅₀ μ M
	78nM	313 nM	1250 nM	5000 nM	
1130826	88	63	43	14	0.7
1130828	73	56	37	23	0.5
1130871	65	28	19	18	0.1
1130883	94	57	44	21	0.8
1131023	89	64	42	22	0.8
1131024	92	68	43	31	1.1
1131247	107	105	54	34	2.3
1131416	81	67	39	23	0.7
1131640	97	64	45	20	0.9
1131695	78	54	33	21	0.5
1131696	100	45	34	14	0.6
1131697	70	46	31	7	0.3
1131724	96	60	36	37	1.0
1131725	83	64	45	17	0.7
1131751	88	54	34	15	0.5
1131752	75	49	40	21	0.5

1131753	61	38	20	8	0.1
1131891	80	46	37	13	0.4
1131892	77	84	61	33	2.1

Table 101. Dose-dependent reduction of human FXII RNA by modified oligonucleotides

Compound Number	FXII (%UTC)				IC ₅₀ μ M
	78nM	313 nM	1250 nM	5000 nM	
1130829	78	62	28	18	0.5
1130830	92	49	26	25	0.6
1130871	75	53	27	15	0.4
1130914	100	86	73	43	4.2
1130970	88	84	63	39	3.0
1130997	87	73	57	24	1.2
1130998	92	76	61	45	3.4
1131025	71	76	42	20	0.7
1131053	84	85	55	32	1.8
1131473	90	74	35	19	0.8
1131474	94	77	55	36	1.9
1131641	82	69	43	23	0.8
1131671	61	49	35	21	0.3
1131698	88	87	48	14	1.0
1131699	73	43	24	11	0.3
1131754	48	22	14	7	< 0.1
1131755	61	41	18	5	0.2
1132453	96	74	55	23	1.2
1132537	88	65	46	22	0.9

Table 102. Dose-dependent reduction of human FXII RNA by modified oligonucleotides

Compound Number	FXII (%UTC)				IC ₅₀ μ M
	78 nM	313 nM	1250 nM	5000 nM	
1130831	68	50	20	11	0.3
1130832	77	55	35	21	0.5
1130858	80	88	55	35	2.0
1130871	72	37	24	16	0.2
1130973	85	61	45	22	0.8
1131084	85	95	49	27	1.5
1131198	85	68	38	24	0.8
1131223	91	53	41	16	0.6
1131309	87	64	34	42	1.1
1131310	86	62	51	28	1.1
1131700	67	45	29	9	0.2
1131701	55	48	26	5	0.2
1131702	96	42	16	9	0.4

1131730	93	64	38	32	1.0
1131756	39	13	13	5	< 0.1
1131757	54	27	14	10	< 0.1
1131758	73	58	25	9	0.4
1132455	88	74	59	33	1.8
1132651	76	76	55	38	2.0

Table 103. Dose-dependent reduction of human FXII RNA by modified oligonucleotides

Compound Number	FXII (% UTC)				IC ₅₀ μ M
	78 nM	313 nM	1250 nM	5000 nM	
1130871	65	52	30	22	0.3
1130894	72	66	50	38	1.3
1131006	100	92	68	47	4.8
1131146	84	91	56	37	2.4
1131199	76	75	54	22	1.0
1131255	83	65	53	19	0.9
1131314	77	71	61	34	1.9
1131337	70	81	57	36	2.1
1131423	74	64	40	21	0.6
1131426	98	87	81	44	> 5.0
1131481	91	66	43	28	1.0
1131593	66	51	37	26	0.4
1131673	93	63	45	35	1.2
1131704	96	45	39	19	0.6
1131706	93	80	62	40	2.7
1131759	62	67	40	23	0.5
1131760	87	71	55	40	2.0
1131761	89	75	60	29	1.6
1132797	100	75	77	54	> 5.0

Table 104. Dose-dependent reduction of human FXII RNA by modified oligonucleotides

Compound Number	FXII (% UTC)				IC ₅₀ μ M
	78 nM	313nM	1250 nM	5000 nM	
1130839	141	86	58	32	2.0
1130871	57	34	22	9	0.1
1130920	89	83	76	23	2.1
1130952	94	71	49	29	1.3
1130979	81	84	68	34	2.7
1131007	104	73	61	43	2.6
1131120	108	68	44	42	1.6
1131204	71	50	27	26	0.4
1131340	92	78	63	27	1.7
1131344	88	69	44	35	1.2

1131368	87	79	63	41	3.0
1131424	74	79	47	33	1.3
1131428	99	64	47	21	0.9
1131480	82	60	57	17	0.8
1131484	85	67	46	24	0.9
1131595	67	48	35	23	0.3
1131736	79	78	40	14	0.7
1131763	49	38	22	15	< 0.1
1131764	59	44	25	15	0.2

Table 105. Dose-dependent reduction of human FXII RNA by modified oligonucleotides

Compound Number	FXII (% UTC)				IC ₅₀ μ M
	78 nM	313 nM	1250 nM	5000 nM	
1130840	76	69	46	27	0.9
1130868	54	49	33	13	0.2
1130870	76	57	48	18	0.6
1130871	72	41	29	18	0.3
1130925	70	60	31	19	0.4
1130981	86	62	42	23	0.8
1130983	88	62	43	29	0.9
1131009	92	91	50	35	1.9
1131036	83	72	59	32	1.7
1131095	74	59	31	34	0.6
1131375	91	89	67	46	4.9
1131429	75	61	45	24	0.7
1131624	72	56	49	22	0.6
1131625	61	72	43	22	0.6
1131627	91	58	42	20	0.7
1131711	94	100	53	30	1.9
1131737	79	62	42	19	0.6
1131739	94	80	58	31	1.8
1131767	82	50	42	34	0.8

Table 106. Dose-dependent reduction of human FXII RNA by modified oligonucleotides

Compound Number	FXII (% UTC)				IC ₅₀ μ M
	78 nM	313 nM	1250 nM	5000 nM	
1130871	59	39	23	11	0.1
1130872	77	59	31	38	0.7
1130900	57	50	51	23	0.3
1130928	76	53	57	55	> 5.0
1131013	75	58	25	16	0.4
1131040	61	57	43	23	0.4
1131096	82	70	39	35	1.1

1131208	102	80	57	33	1.9
1131347	86	67	63	31	1.7
1131348	74	67	42	29	0.8
1131432	61	45	34	22	0.2
1131433	91	63	28	20	0.6
1131599	70	61	37	23	0.5
1131601	88	58	49	34	1.1
1131630	93	54	42	20	0.7
1131712	73	54	32	22	0.4
1131713	101	66	33	27	0.9
1132188	89	75	69	41	3.4
1132271	80	76	68	48	> 5.0

Table 107. Dose-dependent reduction of human FXII RNA by modified oligonucleotides

Compound Number	FXII (% UTC)				IC ₅₀ μ M
	78 nM	313 nM	1250 nM	5000 nM	
1130763	91	71	50	44	2.1
1130846	64	56	42	37	0.6
1130871	63	41	19	16	0.2
1130874	69	74	40	24	0.7
1130903	119	90	65	35	2.4
1130987	66	39	27	17	0.2
1131015	80	84	65	33	2.4
1131126	66	77	51	28	1.1
1131155	87	79	61	31	1.9
1131350	79	66	46	30	1.0
1131434	83	56	40	23	0.6
1131462	73	73	56	34	1.6
1131463	98	104	77	45	> 5.0
1131686	71	53	48	29	0.7
1131687	78	60	42	29	0.8
1131688	74	57	34	23	0.5
1131716	100	58	43	23	0.9
1131744	78	67	32	58	2.2
1132387	104	96	77	51	> 5.0

Table 108. Dose-dependent reduction of human FXII RNA by modified oligonucleotides

Compound Number	FXII (% UTC)				IC ₅₀ μ M
	78 nM	313 nM	1250 nM	5000 nM	
1130871	69.8	45.8	26.5	23.1	0.3
1130988	76.2	74.4	49.9	24.9	1.0
1131018	92.2	62.8	43.5	20.2	0.8
1131019	90.5	78.4	36.3	20.4	0.9

1131100	90.3	69.0	47.3	29.5	1.2
1131242	85.1	59.3	45.8	19.2	0.7
1131243	84.3	70.1	49.8	23.1	1.0
1131409	85.6	82.4	46.3	26.1	1.2
1131411	95.8	87.5	48.1	39.4	2.0
1131605	77.7	80.7	44.5	25.8	1.0
1131635	80.9	50.2	44.3	28.5	0.7
1131663	80.0	74.7	44.0	17.3	0.8
1131689	92.7	72.3	64.7	27.1	1.6
1131691	76.5	55.0	35.1	16.4	0.5
1131717	85.2	58.3	39.3	23.6	0.7
1131718	94.4	63.5	47.4	33.6	1.2
1131745	73.3	49.4	32.1	25.7	0.4
1131746	81.7	54.2	39.0	15.6	0.5
1131747	69.9	48.1	33.6	18.1	0.3

Table 109. Dose-dependent reduction of human FXII RNA by modified oligonucleotides

Compound Number	FXII (% UTC)				IC ₅₀ μ M
	78 nM	313 nM	1250 nM	5000 nM	
1130824	86	73	56	29	1.4
1130825	111	78	49	42	2.0
1130871	76	39	26	17	0.3
1130908	76	65	51	28	1.0
1130938	97	77	57	19	1.2
1131020	79	62	47	15	0.6
1131021	77	72	51	27	1.1
1131216	78	87	56	55	> 5.0
1131357	90	84	64	38	2.8
1131608	100	70	51	30	1.4
1131692	70	63	33	22	0.5
1131693	63	41	29	18	0.2
1131694	79	57	21	16	0.4
1131720	92	63	72	27	1.7
1131721	92	85	67	40	3.3
1131722	106	95	56	40	2.6
1131748	75	57	53	20	0.7
1131749	90	66	47	25	1.0
1132505	85	78	50	36	1.7

Table 110. Dose-dependent reduction of human FXII RNA by modified oligonucleotides

Compound Number	FXII (% UTC)				IC ₅₀ μ M
	78 nM	313 nM	1250 nM	5000 nM	
413643	71	57	28	26	0.4

462073	94	68	30	23	0.8
462192	64	50	41	16	0.3
626671	101	98	74	45	> 5.0
1124324	97	87	102	52	> 5.0
1124408	103	74	50	22	1.2
1124489	86	84	75	56	> 5.0
1124490	98	83	58	44	3.0
1124620	91	74	55	33	1.6
1124621	93	74	45	21	1.0
1124677	112	83	66	48	3.8
1124813	102	86	55	39	2.3
1124996	93	62	49	32	1.2
1125047	72	63	59	24	1.0
1125074	92	70	56	39	2.0
1125075	100	94	58	51	> 5.0
1125101	120	108	50	43	2.7
1125102	105	61	57	45	2.3
1125570	115	113	115	81	> 5.0

Table 111. Dose-dependent reduction of human FXII RNA by modified oligonucleotides

Compound Number	FXII (%UTC)				IC ₅₀ μ M
	78 nM	313 nM	1250 nM	5000 nM	
413644	129	90	69	36	2.6
462073	117	78	46	36	1.6
1124222	490	74	81	51	> 5.0
1124223	93	84	66	51	> 5.0
1124328	129	93	82	42	4.0
1124384	80	101	79	59	> 5.0
1124491	76	78	52	35	1.6
1124598	100	87	91	51	> 5.0
1124842	105	93	65	56	> 5.0
1124998	122	77	67	41	2.7
1125023	96	91	53	36	2.1
1125049	105	91	56	43	2.7
1125050	100	78	67	29	1.9
1125051	80	58	39	19	0.6
1125076	103	96	83	51	> 5.0
1125077	106	99	74	42	4.4
1125078	94	92	87	40	> 5.0
1125103	99	116	65	37	3.5
1125104	115	94	49	55	3.5

Table 112. Dose-dependent reduction of human FXII RNA by modified oligonucleotides

Compound Number	FXII (% UTC)				IC ₅₀ μ M
	63nM	250 nM	1000 nM	4000 nM	
1129531	78	53	26	11	0.3
1206486	82	65	51	31	0.9
1206977	92	69	50	23	0.8
1206981	79	66	45	25	0.7
1207005	67	41	17	13	0.2
1207007	51	31	15	6	< 0.1
1207009	90	65	38	26	0.7
1207111	87	56	44	22	0.6
1207113	92	73	45	26	0.9
1207133	72	48	29	18	0.3
1207164	77	76	52	36	1.3
1207228	87	65	53	37	1.2
1207230	106	77	63	60	> 4.0
1207244	91	57	46	24	0.7
1207276	63	39	11	11	0.1
1207362	75	71	48	20	0.6
1207366	94	53	38	24	0.6
1207370	68	55	39	21	0.3
1207394	61	39	22	11	0.1

Table 113. Dose-dependent reduction of human FXII RNA by modified oligonucleotides

Compound Number	FXII (%UTC)				IC ₅₀ μ M
	63 nM	250 nM	1000 nM	4000 nM	
1129531	92	47	28	14	0.4
1206487	82	68	54	29	1
1206497	99	70	58	31	1.3
1206970	77	54	35	12	0.4
1206978	93	63	35	15	0.5
1206986	91	71	52	36	1.3
1207010	76	51	17	7	0.2
1207106	84	65	49	19	0.7
1207125	91	52	28	8	0.4
1207159	71	36	14	6	0.2
1207190	78	61	59	31	1
1207247	101	70	28	16	0.6
1207254	71	49	29	18	0.3
1207255	71	49	28	21	0.3
1207271	113	80	55	29	1.3
1207278	46	36	11	4	< 0.1
1207279	66	38	23	10	0.2

1207358	78	61	43	17	0.5
1207367	79	48	30	9	0.3

Table 114. Dose-dependent reduction of human FXII RNA by modified oligonucleotides

Compound Number	FXII (%UTC)				IC ₅₀ μ M
	63 nM	250 nM	1000 nM	4000 nM	
1129531	57	40	17	7	0.1
1206490	72	42	35	24	0.3
1206492	73	60	46	22	0.5
1206980	68	51	34	13	0.3
1206996	76	54	30	20	0.4
1207004	66	57	41	30	0.4
1207006	47	19	10	7	< 0.1
1207118	73	53	31	14	0.3
1213120	60	45	24	15	0.1
1213135	70	53	31	23	0.3
1213144	42	20	25	6	< 0.1
1213220	58	53	41	33	0.3
1213227	78	72	40	27	0.7
1213234	80	64	44	25	0.6
1213235	66	59	30	18	0.3
1213259	52	29	16	9	< 0.1
1213260	51	35	13	13	< 0.1
1213262	56	27	18	9	< 0.1
1213264	77	46	18	9	0.2

Table 115. Dose-dependent reduction of human FXII RNA by modified oligonucleotides

Compound Number	FXII (% UTC)				IC ₅₀ μ M
	63 nM	250 nM	1000 nM	4000 nM	
1129531	77	44	20	20	0.2
1206489	83	53	35	21	0.4
1206509	97	89	72	33	2.3
1206971	84	65	38	22	0.6
1206972	69	70	49	21	0.6
1206984	64	51	37	25	0.3
1206987	70	82	64	47	> 4.0
1207008	58	37	18	14	0.1
1207123	96	73	59	26	1.1
1207131	79	57	45	27	0.6
1207139	86	66	54	24	0.9
1207160	53	27	13	11	< 0.1
1207161	53	31	16	13	< 0.1
1207248	83	58	43	31	0.7

1207277	42	28	12	6	< 0.1
1207312	85	75	39	23	0.7
1207360	80	48	39	22	0.4
1207381	79	85	61	46	3.6
1207393	58	38	17	7	0.1

Table 116. Dose-dependent reduction of human FXII RNA by modified oligonucleotides

Compound Number	FXII (% UTC)				IC ₅₀ μ M
	63 nM	250 nM	1000 nM	4000 nM	
1128802	88	57	36	17	0.5
1129531	68	44	30	14	0.2
1208476	71	62	35	23	0.4
1208506	80	80	77	67	> 4.0
1208689	84	76	66	76	> 4.0
1208937	92	85	83	69	> 4.0
1209017	80	73	72	59	> 4.0
1209119	80	66	72	59	> 4.0
1209422	94	90	54	61	> 4.0
1209543	91	94	83	76	> 4.0
1209545	88	82	71	70	> 4.0
1209565	98	95	70	78	> 4.0
1209576	82	83	68	60	> 4.0
1209607	93	88	74	85	> 4.0
1209615	97	83	68	71	> 4.0
1209616	82	76	70	60	> 4.0
1209630	92	86	83	71	> 4.0
1209659	91	98	67	57	> 4.0
1209674	99	81	81	70	> 4.0

Table 117. Dose-dependent reduction of human FXII RNA by modified oligonucleotides

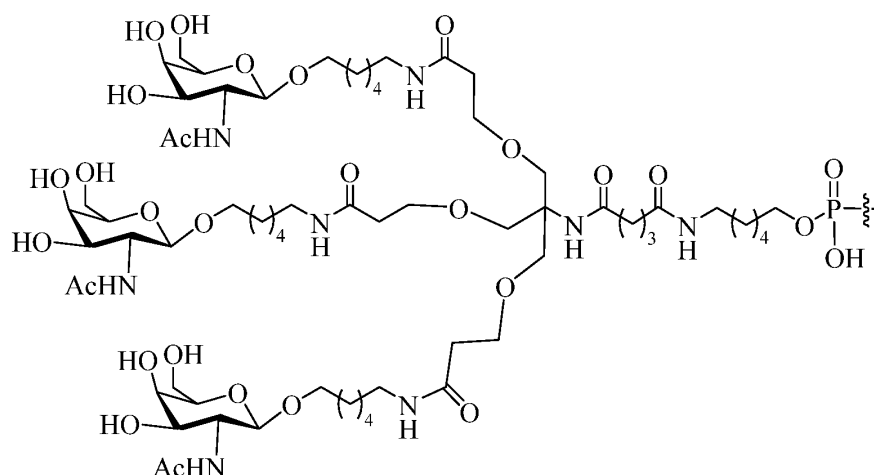
Compound Number	FXII (%UTC)				IC ₅₀ μ M
	63 nM	250 nM	1000 nM	4000 nM	
1128802	82	55	38	16	0.4
1129531	77	38	29	9	0.2
1208612	83	79	63	58	> 4.0
1208757	84	76	74	69	> 4.0
1208977	76	75	76	43	> 4.0
1209134	81	78	75	72	> 4.0
1209238	76	73	68	71	> 4.0
1209391	91	100	89	78	> 4.0
1209430	84	77	73	54	> 4.0
1209455	77	74	71	71	> 4.0
1209514	76	77	70	73	> 4.0

1209547	89	78	58	35	1.6
1209548	81	74	59	35	1.5
1209605	103	100	78	80	> 4.0
1209624	89	90	75	70	> 4.0
1209645	105	85	79	62	> 4.0
1209670	115	96	82	85	> 4.0
1209688	78	75	80	76	> 4.0
1209692	88	97	89	71	> 4.0

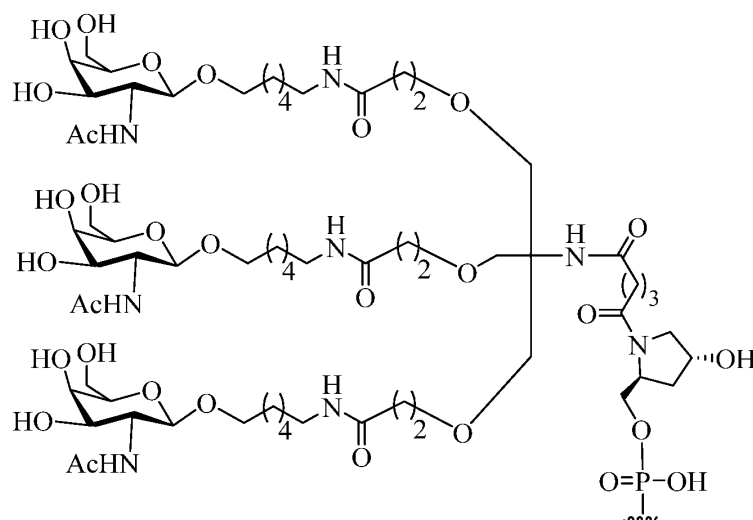
Example 8: Design of oligomeric compounds complementary to a human FXII nucleic acid

Oligomeric compounds were designed as indicated in the tables below. Modified oligonucleotides described in the Examples above (parent compounds) were further modified by either adding a THA-C6-GalNAc3 conjugate (designated as [THA-GalNAc] in the table below) at the 5' end of the modified

- 5 oligonucleotide, or by adding a 3'-THA-C6-GalNAc hydroxyproline PO conjugate (designated as 3'- HPPO-GalNAc in the tables below), at the 3'-end of the modified oligonucleotide. THA-GalNAc is represented by the structure below wherein the phosphate group is attached to the 5'-oxygen atom of the 5' nucleoside:



- 10 3'- HPPO-GalNAc is represented by the structure below wherein the phosphate group is attached to the 3'- oxygen atom of the 3' nucleoside:



The chemistry notation column in the tables below specifies the specific chemistry notation for modified oligonucleotides; wherein subscript ‘d’ represents a 2’-β-D-deoxyribosyl sugar moiety, subscript ‘e’ represents a 2’-MOE sugar moiety, subscript ‘y’ represents a 2’-O-methyl sugar moiety, subscript ‘k’ represents a cEt modified sugar moiety, subscript ‘s’ represents a phosphorothioate internucleoside linkage, subscript ‘o’ represents a phosphodiester internucleoside linkage, and superscript ‘m’ before the cytosine residue (^mC) represents a 5-methyl cytosine.

Table 118. Design of GalNAc conjugated modified oligonucleotides complementary to human FXII

Compound No.	Parent Compound No.	Sequence and Chemistry notation (5' to 3')	SEQ ID No.
1194343	1128769	THA-GalNAc-oA _{ks} G _{ks} A _{ks} A _{ds} ^m C _{ds} G _{ds} A _{ds} ^m C _{ds} T _{ds} G _{ds} T _{ds} G _{ds} T _{ds} G _{ks} ^m C _{ks} T _k	3723
1194345	1128801	THA-GalNAc-oA _{ks} ^m C _{ks} A _{ks} T _{ds} T _{ds} T _{ds} G _{ds} T _{ds} G _{ds} G _{ds} T _{ds} A _{ds} ^m C _{ds} A _{ks} G _{ks} ^m C _k	3114
1194346	1128802	THA-GalNAc-oT _{ks} A _{ks} ^m C _{ks} A _{ds} T _{ds} T _{ds} T _{ds} G _{ds} T _{ds} G _{ds} G _{ds} T _{ds} A _{ds} ^m C _{ks} A _{ks} G _k	2426
1194347	1128870	THA-GalNAc-oT _{ks} G _{ks} T _{ks} G _{ds} G _{ds} A _{ds} A _{ds} A _{ds} A _{ds} ^m C _{ds} ^m C _{ds} G _{ds} G _{ks} A _{ks} G _k	3728
1194348	1129221	THA-GalNAc-o ^m C _{ks} G _{ks} T _{ks} ^m C _{ds} T _{ds} G _{ds} G _{ds} ^m C _{ds} A _{ds} ^m C _{ds} G _{ds} G _{ds} ^m C _{ds} T _{ks} ^m C _{ks} A _k	3060
1194349	1129287	THA-GalNAc-o ^m C _{ks} G _{ks} T _{ks} A _{ds} A _{ds} G _{ds} G _{ds} ^m C _{ds} G _{ds} A _{ds} ^m C _{ds} A _{ds} G _{ds} G _{ks} A _{ks} G _k	3521
1194350	1129407	THA-GalNAc-oT _{ks} G _{ks} ^m C _{ks} ^m C _{ds} T _{ds} T _{ds} G _{ds} ^m C _{ds} A _{ds} G _{ds} G _{ds} G _{ds} T _{ds} G _{ks} A _{ks} G _k	3527
1194357	1129485	THA-GalNAc-oG _{ks} ^m C _{ks} G _{ks} G _{ds} A _{ds} A _{ds} T _{ds} ^m C _{ds} A _{ds} ^m C _{ds} ^m C _{ds} A _{ds} A _{ds} G _{ks} G _{ks} A _k	3379
1194358	1129486	THA-GalNAc-oT _{ks} G _{ks} ^m C _{ks} G _{ds} G _{ds} A _{ds} A _{ds} T _{ds} ^m C _{ds} A _{ds} ^m C _{ds} ^m C _{ds} A _{ds} A _{ks} G _{ks} G _k	3455
1194359	1129487	THA-GalNAc-o ^m C _{ks} T _{ks} G _{ks} ^m C _{ds} G _{ds} G _{ds} A _{ds} A _{ds} T _{ds} ^m C _{ds} A _{ds} ^m C _{ds} ^m C _{ds} A _{ks} A _{ks} G _k	3531
1194360	1129488	THA-GalNAc-oA _{ks} ^m C _{ks} T _{ks} G _{ds} ^m C _{ds} G _{ds} G _{ds} A _{ds} A _{ds} T _{ds} ^m C _{ds} A _{ds} ^m C _{ds} ^m C _{ks} A _{ks} A _k	3607
1194361	1129489	THA-GalNAc-o ^m C _{ks} A _{ks} ^m C _{ks} T _{ds} G _{ds} ^m C _{ds} G _{ds} G _{ds} A _{ds} A _{ds} T _{ds} ^m C _{ds} A _{ds} ^m C _{ks} ^m C _{ks} A _k	3683
1194363	1129492	THA-GalNAc-oT _{ks} ^m C _{ks} T _{ks} ^m C _{ds} A _{ds} ^m C _{ds} T _{ds} G _{ds} ^m C _{ds} G _{ds} G _{ds} A _{ds} A _{ds} T _{ks} ^m C _{ks} A _k	3911
1194370	1129534	THA-GalNAc-oA _{ks} T _{ks} T _{ks} G _{ds} A _{ds} G _{ds} T _{ds} T _{ds} ^m C _{ds} ^m C _{ds} T _{ds} G _{ds} ^m C _{ds} G _{ks} ^m C _{ks} ^m C _k	2540
1194371	1129538	THA-GalNAc-oA _{ks} ^m C _{ks} T _{ks} T _{ds} T _{ds} A _{ds} T _{ds} T _{ds} G _{ds} A _{ds} G _{ds} T _{ds} T _{ds} ^m C _{ks} ^m C _{ks} T _k	2848

1194372	1129540	THA-GalNAc- _o G _{ks} ^m C _{ks} A _{ks} ^m C _{ds} T _{ds} T _{ds} T _{ds} A _{ds} T _{ds} T _{ds} G _{ds} A _{ds} G _{ds} T _{ks} T _{ks} ^m C _k	3000
1194373	1129542	THA-GalNAc- _o A _{ks} A _{ks} G _{ks} ^m C _{ds} A _{ds} ^m C _{ds} T _{ds} T _{ds} T _{ds} A _{ds} T _{ds} T _{ds} G _{ds} A _{ks} G _{ks} T _k	3147
1194374	1129543	THA-GalNAc- _o A _{ks} A _{ks} A _{ks} G _{ds} ^m C _{ds} A _{ds} ^m C _{ds} T _{ds} T _{ds} T _{ds} A _{ds} T _{ds} T _{ds} G _{ks} A _{ks} G _k	3229
1194375	1129544	THA-GalNAc- _o ^m C _{ks} A _{ks} A _{ks} A _{ds} G _{ds} ^m C _{ds} A _{ds} ^m C _{ds} T _{ds} T _{ds} T _{ds} A _{ds} T _{ds} T _{ks} G _{ks} A _k	3306
1194376	1129545	THA-GalNAc- _o T _{ks} ^m C _{ks} A _{ks} A _{ds} A _{ds} G _{ds} ^m C _{ds} A _{ds} ^m C _{ds} T _{ds} T _{ds} T _{ds} A _{ds} T _{ks} T _{ks} G _k	3382
1194377	1129947	THA-GalNAc- _o T _{ks} G _{ks} ^m C _{ks} T _{ds} T _{ds} T _{ds} ^m C _{ds} ^m C _{ds} G _{ds} ^m C _{ds} A _{ds} ^m C _{ds} T _{ds} ^m C _{ks} T _{ks} ^m C _k	3554
1194378	1130831	THA-GalNAc- _o G _{es} A _{eo} A _{eo} ^m C _{eo} G _{eo} A _{ds} ^m C _{ds} T _{ds} G _{ds} T _{ds} G _{ds} T _{ds} G _{ds} ^m C _{ds} T _{ds} ^m C _{eo} T _{eo} T _{es} ^m C _{es} A _e	997
1194379	1130868	THA-GalNAc- _o A _{es} ^m C _{eo} A _{eo} T _{eo} T _{eo} T _{ds} G _{ds} T _{ds} G _{ds} G _{ds} T _{ds} A _{ds} ^m C _{ds} A _{ds} G _{ds} ^m C _{eo} T _{eo} G _{es} ^m C _{es} ^m C _e	1756
1194380	1130871	THA-GalNAc- _o G _{es} G _{eo} T _{eo} A _{eo} ^m C _{eo} A _{ds} T _{ds} T _{ds} G _{ds} T _{ds} G _{ds} G _{ds} T _{ds} A _{ds} ^m C _{eo} A _{eo} G _{es} ^m C _{es} T _e	183
1194381	1130900	THA-GalNAc- _o A _{es} T _{eo} ^m C _{eo} G _{eo} ^m C _{eo} T _{ds} G _{ds} G _{ds} T _{ds} ^m C _{ds} ^m C _{ds} T _{ds} G _{ds} A _{ds} T _{ds} ^m C _{eo} A _{eo} A _e _s A _{es} G _e	1906
1194382	1130925	THA-GalNAc- _o G _{es} G _{eo} T _{eo} ^m C _{eo} T _{eo} T _{ds} T _{ds} ^m C _{ds} A _{ds} ^m C _{ds} T _{ds} T _{ds} ^m C _{ds} T _{ds} T _{eo} G _{eo} G _{es} G _{es} ^m C _e	1758
1194383	1130987	THA-GalNAc- _o G _{es} G _{eo} ^m C _{eo} T _{eo} ^m C _{eo} A _{ds} A _{ds} A _{ds} G _{ds} ^m C _{ds} A _{ds} ^m C _{ds} T _{ds} T _{ds} ^m C _{ds} T _{eo} ^m C _{eo} T _{es} T _{es} T _e	2135
1194384	1131013	THA-GalNAc- _o A _{es} ^m C _{eo} ^m C _{eo} A _{eo} T _{eo} A _{ds} T _{ds} ^m C _{ds} T _{ds} ^m C _{ds} A _{ds} T _{ds} T _{ds} ^m C _{ds} T _{ds} T _{eo} G _{eo} T _{es} G _{es} G _e	1984
1194385	1131040	THA-GalNAc- _o A _{es} ^m C _{eo} ^m C _{eo} ^m C _{eo} T _{eo} T _{ds} G _{ds} ^m C _{ds} A _{ds} ^m C _{ds} T _{ds} G _{ds} G _{ds} ^m C _{ds} A _{ds} T _{eo} ^m C _{eo} T _{es} G _{es} G _e	1911
1194387	1131204	THA-GalNAc- _o A _{es} G _{eo} T _{eo} T _{eo} ^m C _{eo} ^m C _{ds} G _{ds} ^m C _{ds} G _{ds} ^m C _{ds} T _{ds} T _{ds} G _{ds} ^m C _{ds} T _{ds} ^m C _{eo} G _{eo} G _{es} ^m C _{es} A _e	1618
1194388	1131432	THA-GalNAc- _o G _{es} G _{eo} T _{eo} A _{eo} G _{eo} G _{ds} A _{ds} G _{ds} ^m C _{ds} G _{ds} ^m C _{ds} A _{ds} ^m C _{ds} G _{ds} G _{ds} ^m C _{eo} ^m C _{eo} A _{es} A _{es} ^m C _e	1925
1194389	1131593	THA-GalNAc- _o T _{es} G _{eo} A _{eo} T _{eo} G _{eo} ^m C _{ds} ^m C _{ds} T _{ds} T _{ds} G _{ds} ^m C _{ds} A _{ds} G _{ds} G _{ds} T _{eo} G _{eo} A _{es} G _{es} ^m C _e	1326
1194390	1131595	THA-GalNAc- _o G _{es} A _{eo} T _{eo} G _{eo} A _{eo} T _{ds} G _{ds} ^m C _{ds} ^m C _{ds} T _{ds} T _{ds} G _{ds} ^m C _{ds} A _{ds} G _{ds} G _{eo} G _{eo} T _{es} G _{es} A _e	1556
1194391	1131671	THA-GalNAc- _o G _{es} ^m C _{eo} A _{eo} A _{eo} T _{eo} ^m C _{ds} A _{ds} G _{ds} G _{ds} A _{ds} A _{ds} ^m C _{ds} G _{ds} G _{ds} T _{eo} G _{eo} T _{es} G _{es} ^m C _e	950
1194392	1131693	THA-GalNAc- _o T _{es} G _{eo} ^m C _{eo} G _{eo} G _{eo} A _{ds} A _{ds} T _{ds} ^m C _{ds} A _{ds} ^m C _{ds} ^m C _{ds} A _{ds} A _{ds} G _{ds} G _{eo} A _{eo} G _{es} G _{es} G _e	496
1194393	1131694	THA-GalNAc- _o ^m C _{es} T _{eo} G _{eo} ^m C _{eo} G _{eo} G _{ds} A _{ds} A _{ds} T _{ds} ^m C _{ds} A _{ds} ^m C _{ds} ^m C _{ds} A _{ds} A _{ds} G _{eo} G _{eo} A _{es} G _{es} G _e	571
1194394	1131697	THA-GalNAc- _o ^m C _{es} T _{eo} ^m C _{eo} A _{eo} ^m C _{eo} T _{ds} G _{ds} ^m C _{ds} G _{ds} G _{ds} A _{ds} A _{ds} T _{ds} ^m C _{ds} A _{ds} ^m C _{eo} ^m C _{eo} A _{es} A _{es} G _e	802
1194395	1131699	THA-GalNAc- _o T _{es} ^m C _{eo} T _{eo} ^m C _{eo} T _{eo} ^m C _{ds} A _{ds} ^m C _{ds} T _{ds} G _{ds} ^m C _{ds} G _{ds} G _{ds} A _{ds} A _{ds} T _{eo} ^m C _{eo} A _{es} ^m C _{es} ^m C _e	951
1194396	1131700	THA-GalNAc- _o ^m C _{es} T _{eo} ^m C _{eo} T _{eo} ^m C _{eo} T _{ds} ^m C _{ds} A _{ds} ^m C _{ds} T _{ds} G _{ds} ^m C _{ds} G _{ds} G _{ds} A _{ds} A _{eo} T _{eo} ^m C _{es} A _{es} ^m C _e	1028
1194397	1131701	THA-GalNAc- _o A _{es} ^m C _{eo} T _{eo} ^m C _{eo} T _{eo} ^m C _{ds} T _{ds} ^m C _{ds} A _{ds} ^m C _{ds} T _{ds} G _{ds} ^m C _{ds} G _{ds} G _{ds} A _{eo} A _{eo} T _{es} ^m C _{es} A _e	1179
1194398	1131702	THA-GalNAc- _o ^m C _{es} ^m C _{eo} A _{eo} ^m C _{eo} T _{eo} ^m C _{ds} T _{ds} ^m C _{ds} T _{ds} ^m C _{ds} A _{ds} ^m C _{ds} T _{ds} G _{ds} ^m C _{ds} G _{eo} G _e _o A _{es} A _{es} T _e	1103
1194399	1131712	THA-GalNAc- _o ^m C _{es} T _{eo} T _{eo} ^m C _{eo} ^m C _{eo} A _{ds} T _{ds} G _{ds} ^m C _{ds} ^m C _{ds} ^m C _{ds} A _{ds} G _{ds} ^m C _{ds} ^m C _{eo} A _{eo} ^m C _{es} T _{es} ^m C _e	1935
1194400	1131745	THA-GalNAc- _o A _{es} G _{eo} T _{eo} T _{eo} ^m C _{eo} ^m C _{ds} T _{ds} G _{ds} ^m C _{ds} G _{ds} ^m C _{ds} ^m C _{ds} A _{ds} T _{ds} ^m C _{ds} ^m C _{eo} T _{eo} G _{es} G _{es} ^m C _e	2309
1194401	1131747	THA-GalNAc- _o T _{es} G _{eo} A _{eo} G _{eo} T _{eo} T _{ds} ^m C _{ds} ^m C _{ds} T _{ds} G _{ds} ^m C _{ds} G _{ds} ^m C _{ds} ^m C _{ds} A _{ds} T _{eo} ^m C _{eo} ^m C _{es} T _{es} G _e	347
1194402	1131753	THA-GalNAc- _o ^m C _{es} A _{eo} ^m C _{eo} T _{eo} T _{eo} T _{ds} A _{ds} T _{ds} T _{ds} G _{ds} A _{ds} G _{ds} T _{ds} T _{ds} ^m C _{ds} ^m C _{eo} T _{eo} G _{es} ^m C _{es} G _e	163

1194403	1131754	THA-GalNAC-o-G _{es} ^m C _{eo} A _{eo} ^m C _{eo} T _{eo} T _{ds} T _{ds} A _{ds} T _{ds} T _{ds} G _{ds} A _{ds} G _{ds} T _{ds} T _{ds} ^m C _{eo} ^m C _{eo} T _{es} G _{es} ^m C _e	164
1194404	1131755	THA-GalNAC-o-A _{es} G _{eo} ^m C _{eo} A _{eo} ^m C _{eo} T _{ds} T _{ds} T _{ds} A _{ds} T _{ds} T _{ds} G _{ds} A _{ds} G _{ds} T _{ds} T _{eo} ^m C _{eo} ^m C _{es} T _{es} G _e	953
1194405	1131756	THA-GalNAC-o-A _{es} A _{eo} G _{eo} ^m C _{eo} A _{eo} ^m C _{ds} T _{ds} T _{ds} T _{ds} A _{ds} T _{ds} T _{ds} G _{ds} A _{ds} G _{ds} T _{eo} T _{eo} ^m C _{es} ^m C _{es} T _e	1030
1194406	1131757	THA-GalNAC-o-A _{es} A _{eo} A _{eo} G _{eo} ^m C _{eo} A _{ds} ^m C _{ds} T _{ds} T _{ds} T _{ds} A _{ds} T _{ds} T _{ds} G _{ds} A _{ds} G _{eo} T _{eo} T _{es} ^m C _e s ^m C _e	165
1194407	1131758	THA-GalNAC-o- ^m C _{es} A _{eo} A _{eo} A _{eo} G _{eo} ^m C _{ds} A _{ds} ^m C _{ds} T _{ds} T _{ds} T _{ds} A _{ds} T _{ds} T _{ds} G _{ds} A _{ds} G _{eo} T _{es} T _e s ^m C _e	1105
1194408	1131763	THA-GalNAC-o-G _{es} ^m C _{eo} A _{eo} T _{eo} T _{eo} T _{ds} T _{ds} ^m C _{ds} A _{ds} A _{ds} A _{ds} G _{ds} ^m C _{ds} A _{ds} ^m C _{ds} T _{eo} T _{eo} T _{es} A _{es} T _e	1562
1194409	1131764	THA-GalNAC-o-A _{es} G _{eo} ^m C _{eo} A _{eo} T _{eo} T _{ds} T _{ds} ^m C _{ds} A _{ds} A _{ds} A _{ds} G _{ds} ^m C _{ds} A _{ds} ^m C _{eo} T _{eo} T _{es} T _{es} A _e	97
1194410	1131891	THA-GalNAC-o- ^m C _{es} ^m C _{eo} G _{eo} A _{eo} ^m C _{eo} T _{ds} G _{ds} T _{ds} G _{ds} T _{ds} G _{ds} ^m C _{ds} T _{ds} ^m C _{ds} T _{ds} T _{eo} ^m C _{eo} A _{es} G _{es} ^m C _e	659
1194411	1132187	THA-GalNAC-o-G _{es} T _{eo} T _{eo} T _{eo} G _{eo} ^m C _{ds} T _{ds} A _{ds} G _{ds} T _{ds} T _{ds} ^m C _{ds} A _{ds} A _{ds} T _{ds} G _{eo} T _{eo} T _{es} ^m C _{es} A _e	1876
1194412	1132188	THA-GalNAC-o-A _{es} ^m C _{eo} T _{eo} G _{eo} T _{eo} T _{ds} T _{ds} G _{ds} ^m C _{ds} T _{ds} A _{ds} G _{ds} T _{ds} T _{ds} ^m C _{ds} A _{eo} A _{eo} T _{es} G _e s ^m T _e	1951
1194413	1132189	THA-GalNAC-o-A _{es} A _{eo} T _{eo} A _{eo} ^m C _{eo} T _{ds} G _{ds} T _{ds} T _{ds} G _{ds} ^m C _{ds} T _{ds} A _{ds} G _{ds} T _{eo} T _{eo} ^m C _{es} A _e s ^m A _e	2025
1194415	1132270	THA-GalNAC-o-A _{es} T _{eo} T _{eo} ^m C _{eo} ^m C _{eo} ^m C _{ds} A _{ds} G _{ds} T _{ds} T _{ds} A _{ds} A _{ds} G _{ds} G _{ds} T _{ds} T _{eo} ^m C _{eo} A _{es} A _{es} ^m C _e	1730
1194416	1132271	THA-GalNAC-o- ^m C _{es} A _{eo} ^m C _{eo} A _{eo} T _{eo} T _{ds} ^m C _{ds} ^m C _{ds} ^m C _{ds} A _{ds} G _{ds} T _{ds} T _{ds} A _{ds} A _{ds} G _{eo} G _{eo} T _e s ^m T _{es} ^m C _e	1879
1194417	1132272	THA-GalNAC-o-T _{es} T _{eo} G _{eo} ^m C _{eo} A _{eo} ^m C _{ds} A _{ds} T _{ds} T _{ds} ^m C _{ds} ^m C _{ds} ^m C _{ds} A _{ds} G _{ds} T _{ds} T _{eo} A _{eo} A _{es} G _{es} G _e	1954
1194419	1132504	THA-GalNAC-o-G _{es} T _{eo} T _{eo} T _{eo} ^m C _{eo} ^m C _{ds} A _{ds} A _{ds} G _{ds} ^m C _{ds} T _{ds} T _{ds} G _{ds} G _{ds} T _{ds} T _{eo} A _{es} ^m C _{es} ^m C _e	449
1194420	1132505	THA-GalNAC-o- ^m C _{es} A _{eo} A _{eo} G _{eo} T _{eo} T _{ds} T _{ds} ^m C _{ds} ^m C _{ds} A _{ds} A _{ds} G _{ds} ^m C _{ds} T _{ds} T _{ds} G _{eo} G _{eo} T _{es} T _{es} T _e	525
1194421	1132506	THA-GalNAC-o- ^m C _{es} T _{eo} ^m C _{eo} ^m C _{eo} A _{eo} A _{ds} G _{ds} T _{ds} T _{ds} T _{ds} ^m C _{ds} ^m C _{ds} A _{ds} A _{ds} G _{ds} ^m C _{eo} T _{eo} T _{es} G _{es} G _e	600
1194423	1132650	THA-GalNAC-o-T _{es} T _{eo} G _{eo} ^m C _{eo} ^m C _{eo} T _{ds} T _{ds} G _{ds} G _{ds} T _{ds} G _{ds} T _{ds} ^m C _{ds} T _{ds} G _{ds} A _{eo} G _{eo} G _{es} A _e s ^m G _e	910
1194424	1132651	THA-GalNAC-o-A _{es} G _{eo} ^m C _{eo} T _{eo} T _{eo} G _{ds} ^m C _{ds} ^m C _{ds} T _{ds} T _{ds} G _{ds} G _{ds} T _{ds} G _{ds} T _{ds} ^m C _{eo} T _{eo} G _{es} A _{es} G _e	985
1194425	1132652	THA-GalNAC-o-A _{es} G _{eo} ^m C _{eo} A _{eo} G _{eo} ^m C _{ds} T _{ds} T _{ds} G _{ds} ^m C _{ds} ^m C _{ds} T _{ds} T _{ds} G _{ds} G _{ds} T _{eo} G _{eo} T _{es} m ^m C _{es} T _e	1062
1194426	1132796	THA-GalNAC-o-G _{es} A _{eo} A _{eo} ^m C _{eo} ^m C _{eo} A _{ds} A _{ds} G _{ds} A _{ds} G _{ds} ^m C _{ds} A _{ds} A _{ds} G _{ds} T _{ds} T _{eo} ^m C _{eo} G _{es} A _{es} T _e	1523
1194427	1132797	THA-GalNAC-o-A _{es} G _{eo} G _{eo} G _{eo} A _{eo} A _{ds} ^m C _{ds} ^m C _{ds} A _{ds} A _{ds} G _{ds} A _{ds} G _{ds} ^m C _{ds} A _{ds} A _{eo} G _{eo} T _{es} T _{es} ^m C _e	1369
1194429	1194286	THA-GalNAC-o- ^m C _{ks} T _{ks} T _{ks} T _{ds} ^m C _{ds} ^m C _{ds} G _{ds} ^m C _{ds} A _{ds} ^m C _{ds} T _{ds} ^m C _{ds} T _{ds} ^m C _{ks} ^m C _{ks} ^m C _k	4026
1194430	1194287	THA-GalNAC-o-G _{ks} ^m C _{ks} T _{ks} T _{ds} T _{ds} ^m C _{ds} ^m C _{ds} G _{ds} ^m C _{ds} A _{ds} ^m C _{ds} T _{ds} ^m C _{ds} T _{ks} ^m C _{ks} ^m C _k	4102
1194483	1129948	A _{ks} T _{ks} ^m C _{ks} T _{ds} G _{ds} ^m C _{ds} T _{ds} T _{ds} ^m C _{ds} ^m C _{ds} G _{ds} ^m C _{ds} A _{ks} ^m C _{ks} T _k -3'-HPPO-GalNAC	3630
1194484	1129949	T _{ks} ^m C _{ks} T _{ks} ^m C _{ds} A _{ds} T _{ds} ^m C _{ds} T _{ds} G _{ds} ^m C _{ds} T _{ds} T _{ds} T _{ds} ^m C _{ks} ^m C _{ks} G _k -3'-HPPO-GalNAC	3706
1194486	1128769	A _{ks} G _{ks} A _{ks} A _{ds} ^m C _{ds} G _{ds} A _{ds} ^m C _{ds} T _{ds} G _{ds} T _{ds} G _{ds} T _{ds} G _{ks} ^m C _{ks} T _k -3'-HPPO-GalNAC	3723
1194487	1128796	T _{ks} G _{ks} T _{ks} G _{ds} G _{ds} T _{ds} A _{ds} ^m C _{ds} A _{ds} G _{ds} ^m C _{ds} T _{ds} G _{ds} ^m C _{ks} ^m C _{ks} G _k -3'-HPPO-GalNAC	2734
1194488	1128801	A _{ks} ^m C _{ks} A _{ks} T _{ds} T _{ds} T _{ds} G _{ds} T _{ds} G _{ds} G _{ds} T _{ds} A _{ds} ^m C _{ds} A _{ks} G _{ks} ^m C _k -3'-HPPO-GalNAC	3114
1194489	1128802	T _{ks} A _{ks} ^m C _{ks} A _{ds} T _{ds} T _{ds} T _{ds} G _{ds} T _{ds} G _{ds} G _{ds} T _{ds} A _{ds} ^m C _{ks} A _{ks} G _k -3'-HPPO-GalNAC	2426

1194490	1128870	$T_{ks}G_{ks}T_{ks}G_{ds}G_{ds}A_{ds}A_{ds}A_{ds}A_{ds}A_{ds}^mC_{ds}^mC_{ds}G_{ds}G_{ks}A_{ks}G_{k-3}'$ - HPPO-GalNAc	3728
1194491	1129221	$^mC_{ks}G_{ks}T_{ks}^mC_{ds}T_{ds}G_{ds}G_{ds}^mC_{ds}A_{ds}^mC_{ds}G_{ds}G_{ds}^mC_{ds}T_{ks}^mC_{ks}A_{k-3}'$ - HPPO-GalNAc	3060
1194492	1129287	$^mC_{ks}G_{ks}T_{ks}A_{ds}A_{ds}G_{ds}G_{ds}^mC_{ds}G_{ds}A_{ds}^mC_{ds}A_{ds}G_{ds}G_{ks}A_{ks}G_{k-3}'$ - HPPO-GalNAc	3521
1194493	1129407	$T_{ks}G_{ks}^mC_{ks}^mC_{ds}T_{ds}T_{ds}G_{ds}^mC_{ds}A_{ds}G_{ds}G_{ds}T_{ds}G_{ks}A_{ks}G_{k-3}'$ - HPPO-GalNAc	3527
1194494	1129408	$A_{ks}T_{ks}G_{ks}A_{ds}T_{ds}G_{ds}^mC_{ds}^mC_{ds}T_{ds}T_{ds}G_{ds}^mC_{ds}A_{ds}G_{ks}G_{ks}G_{k-3}'$ - HPPO-GalNAc	3603
1194495	1129409	$^mC_{ks}T_{ks}G_{ks}A_{ds}T_{ds}G_{ds}A_{ds}T_{ds}G_{ds}^mC_{ds}^mC_{ds}T_{ds}T_{ds}G_{ks}^mC_{ks}A_{k-3}'$ - HPPO-GalNAc	3679
1194496	1129441	$A_{ks}G_{ks}T_{ks}A_{ds}G_{ds}G_{ds}^mC_{ds}^mC_{ds}A_{ds}^mC_{ds}A_{ds}T_{ds}^mC_{ds}G_{ks}G_{ks}T_{k-3}'$ - HPPO-GalNAc	3071
1194497	1129472	$T_{ks}G_{ks}A_{ks}G_{ds}T_{ds}^mC_{ds}^mC_{ds}^mC_{ds}T_{ds}G_{ds}A_{ds}G_{ds}^mC_{ds}A_{ks}A_{ks}T_{k-3}'$ - HPPO-GalNAc	3910
1194498	1129476	$A_{ks}A_{ks}G_{ks}A_{ds}T_{ds}G_{ds}A_{ds}G_{ds}T_{ds}^mC_{ds}^mC_{ds}^mC_{ds}T_{ds}G_{ks}A_{ks}G_{k-3}'$ - HPPO-GalNAc	2691
1194499	1129483	$G_{ks}G_{ks}A_{ks}A_{ds}T_{ds}^mC_{ds}A_{ds}^mC_{ds}^mC_{ds}A_{ds}A_{ds}G_{ds}G_{ds}A_{ks}G_{ks}G_{k-3}'$ - HPPO-GalNAc	3226
1194500	1129485	$G_{ks}^mC_{ks}G_{ks}G_{ds}A_{ds}A_{ds}T_{ds}^mC_{ds}A_{ds}^mC_{ds}^mC_{ds}A_{ds}A_{ds}G_{ks}G_{ks}A_{k-3}'$ - HPPO-GalNAc	3379
1194501	1129486	$T_{ks}G_{ks}^mC_{ks}G_{ds}G_{ds}A_{ds}A_{ds}T_{ds}^mC_{ds}A_{ds}^mC_{ds}^mC_{ds}A_{ds}A_{ks}G_{ks}G_{k-3}'$ - HPPO-GalNAc	3455
1194502	1129487	$^mC_{ks}T_{ks}G_{ks}^mC_{ds}G_{ds}G_{ds}A_{ds}A_{ds}T_{ds}^mC_{ds}A_{ds}^mC_{ds}^mC_{ds}A_{ks}A_{ks}G_{k-3}'$ - HPPO-GalNAc	3531
1194503	1129488	$A_{ks}^mC_{ks}T_{ks}G_{ds}^mC_{ds}G_{ds}G_{ds}A_{ds}A_{ds}T_{ds}^mC_{ds}A_{ds}^mC_{ds}^mC_{ks}A_{ks}A_{k-3}'$ - HPPO-GalNAc	3607
1194504	1129489	$^mC_{ks}A_{ks}^mC_{ks}T_{ds}G_{ds}^mC_{ds}G_{ds}G_{ds}A_{ds}A_{ds}T_{ds}^mC_{ds}A_{ds}^mC_{ks}^mC_{ks}A_{k-3}'$ - HPPO-GalNAc	3683
1194505	1129491	$^mC_{ks}T_{ks}^mC_{ks}A_{ds}^mC_{ds}T_{ds}G_{ds}^mC_{ds}G_{ds}G_{ds}A_{ds}A_{ds}T_{ds}^mC_{ks}A_{ks}^mC_{k-3}'$ - HPPO-GalNAc	3835
1194506	1129492	$T_{ks}^mC_{ks}T_{ks}^mC_{ds}A_{ds}^mC_{ds}T_{ds}G_{ds}^mC_{ds}G_{ds}G_{ds}A_{ds}A_{ds}T_{ks}^mC_{ks}A_{k-3}'$ - HPPO-GalNAc	3911
1194507	1129510	$A_{ks}G_{ks}^mC_{ks}T_{ds}G_{ds}G_{ds}^mC_{ds}^mC_{ds}G_{ds}^mC_{ds}A_{ds}^mC_{ds}T_{ds}G_{ks}G_{ks}G_{k-3}'$ - HPPO-GalNAc	3760
1194508	1129527	$T_{ks}^mC_{ks}^mC_{ks}T_{ds}G_{ds}^mC_{ds}G_{ds}^mC_{ds}^mC_{ds}A_{ds}T_{ds}^mC_{ds}^mC_{ds}T_{ks}G_{ks}G_{k-3}'$ - HPPO-GalNAc	3533
1194509	1129530	$A_{ks}G_{ks}T_{ks}T_{ds}^mC_{ds}^mC_{ds}T_{ds}G_{ds}^mC_{ds}G_{ds}^mC_{ds}^mC_{ds}A_{ds}T_{ks}^mC_{ks}^mC_{k-3}'$ - HPPO-GalNAc	3761
1194510	1129531	$G_{ks}A_{ks}G_{ks}T_{ds}T_{ds}^mC_{ds}^mC_{ds}T_{ds}G_{ds}^mC_{ds}G_{ds}^mC_{ds}^mC_{ds}A_{ks}T_{ks}^mC_{k-3}'$ - HPPO-GalNAc	3837
1194512	1129533	$T_{ks}T_{ks}G_{ks}A_{ds}G_{ds}T_{ds}T_{ds}^mC_{ds}^mC_{ds}T_{ds}G_{ds}^mC_{ds}G_{ds}^mC_{ks}^mC_{ks}A_{k-3}'$ - HPPO-GalNAc	2463
1194513	1129534	$A_{ks}T_{ks}T_{ks}G_{ds}A_{ds}G_{ds}T_{ds}T_{ds}^mC_{ds}^mC_{ds}T_{ds}G_{ds}^mC_{ds}G_{ks}^mC_{ks}^mC_{k-3}'$ - HPPO-GalNAc	2540
1194514	1129538	$A_{ks}^mC_{ks}T_{ks}T_{ds}T_{ds}A_{ds}T_{ds}T_{ds}G_{ds}A_{ds}G_{ds}T_{ds}T_{ds}^mC_{ks}^mC_{ks}T_{k-3}'$ - HPPO-GalNAc	2848
1194515	1129540	$G_{ks}^mC_{ks}A_{ks}^mC_{ds}T_{ds}T_{ds}A_{ds}T_{ds}T_{ds}G_{ds}A_{ds}G_{ds}T_{ks}T_{ks}^mC_{k-3}'$ - HPPO-GalNAc	3000
1194516	1129542	$A_{ks}A_{ks}G_{ks}^mC_{ds}A_{ds}^mC_{ds}T_{ds}T_{ds}T_{ds}A_{ds}T_{ds}T_{ds}G_{ds}A_{ks}G_{ks}T_{k-3}'$ - HPPO-GalNAc	3147
1194517	1129543	$A_{ks}A_{ks}A_{ks}G_{ds}^mC_{ds}A_{ds}^mC_{ds}T_{ds}T_{ds}T_{ds}A_{ds}T_{ds}T_{ds}G_{ks}A_{ks}G_{k-3}'$ - HPPO-GalNAc]	3229
1194518	1129544	$^mC_{ks}A_{ks}A_{ks}A_{ds}G_{ds}^mC_{ds}A_{ds}^mC_{ds}T_{ds}T_{ds}T_{ds}A_{ds}T_{ds}T_{ks}G_{ks}A_{k-3}'$ - HPPO-GalNAc	3306
1194519	1129545	$T_{ks}^mC_{ks}A_{ks}A_{ds}A_{ds}G_{ds}^mC_{ds}A_{ds}^mC_{ds}T_{ds}T_{ds}T_{ds}A_{ds}T_{ks}T_{ks}G_{k-3}'$ - HPPO-GalNAc	3382
1194520	1129947	$T_{ks}G_{ks}^mC_{ks}T_{ds}T_{ds}T_{ds}^mC_{ds}G_{ds}^mC_{ds}A_{ds}^mC_{ds}T_{ds}^mC_{ks}T_{ks}^mC_{k-3}'$ - HPPO-GalNAc	3554
1194572	1194286	$^mC_{ks}T_{ks}T_{ks}T_{ds}^mC_{ds}^mC_{ds}G_{ds}^mC_{ds}A_{ds}^mC_{ds}T_{ds}^mC_{ks}^mC_{ks}^mC_{k-3}'$ - HPPO-GalNAc	4026
1194573	1194287	$G_{ks}^mC_{ks}T_{ks}T_{ds}T_{ds}^mC_{ds}G_{ds}^mC_{ds}A_{ds}^mC_{ds}T_{ds}^mC_{ds}T_{ks}^mC_{ks}^mC_{k-3}'$ - HPPO-GalNAc	4102
1194574	1194288	$^mC_{ks}T_{ks}G_{ks}^mC_{ds}T_{ds}T_{ds}T_{ds}^mC_{ds}^mC_{ds}G_{ds}^mC_{ds}A_{ds}^mC_{ds}T_{ks}^mC_{ks}T_{k-3}'$ - HPPO-GalNAc	4253
1194575	1194289	$T_{ks}^mC_{ks}T_{ks}G_{ds}^mC_{ds}T_{ds}T_{ds}T_{ds}^mC_{ds}^mC_{ds}G_{ds}^mC_{ds}A_{ds}^mC_{ks}T_{ks}^mC_{k-3}'$ - HPPO-GalNAc	4329
1194576	1194290	$^mC_{ks}A_{ks}T_{ks}^mC_{ds}T_{ds}G_{ds}^mC_{ds}T_{ds}T_{ds}T_{ds}^mC_{ds}^mC_{ds}G_{ds}^mC_{ks}A_{ks}^mC_{k-3}'$ - HPPO-GalNAc	4405
1194578	1194292	$^mC_{ks}T_{ks}^mC_{ks}A_{ds}T_{ds}^mC_{ds}T_{ds}G_{ds}^mC_{ds}T_{ds}T_{ds}T_{ds}^mC_{ds}^mC_{ks}G_{ks}^mC_{k-3}'$ - HPPO-GalNAc	4557
1194579	1194293	$^mC_{ks}T_{ks}^mC_{ks}T_{ds}^mC_{ds}A_{ds}T_{ds}^mC_{ds}T_{ds}G_{ds}^mC_{ds}T_{ds}T_{ds}T_{ks}^mC_{ks}^mC_{k-3}'$ - HPPO-GalNAc	4708

1194580	1194294	^m C _{ks} ^m C _{ks} T _{ks} ^m C _{ds} T _{ds} ^m C _{ds} A _{ds} T _{ds} ^m C _{ds} T _{ds} G _{ds} ^m C _{ds} T _{ds} T _{ks} T _{ks} ^m C _k -3'- HPPO-GalNAc	4783
1194581	1194295	^m C _{ks} ^m C _{ks} ^m C _{ks} T _{ds} ^m C _{ds} T _{ds} ^m C _{ds} A _{ds} T _{ds} ^m C _{ds} T _{ds} G _{ds} ^m C _{ds} T _{ks} T _{ks} T _k -3'- HPPO-GalNAc	4859
1194582	1194296	T _{ks} ^m C _{ks} ^m C _{ks} ^m C _{ds} T _{ds} ^m C _{ds} T _{ds} ^m C _{ds} A _{ds} T _{ds} ^m C _{ds} T _{ds} G _{ds} ^m C _{ks} T _{ks} T _k -3'- HPPO-GalNAc	3950
1194583	1194297	^m C _{ks} T _{ks} ^m C _{ks} ^m C _{ds} ^m C _{ds} T _{ds} ^m C _{ds} T _{ds} ^m C _{ds} A _{ds} T _{ds} ^m C _{ds} T _{ds} G _{ds} ^m C _{ks} T _k -3'- HPPO-GalNAc	4027
1270699	1207006	THA-GalNAc- _o ^m C _{ks} A _{es} ^m C _{ks} T _{ds} T _{ds} T _{ds} A _{ds} T _{ds} T _{ds} G _{ds} A _{ds} G _{ds} T _{es} T _{es} ^m C _{ks} ^m C _k	2924
1270700	1207007	THA-GalNAc- _o G _{ks} ^m C _{es} A _{ks} ^m C _{ds} T _{ds} T _{ds} T _{ds} A _{ds} T _{ds} T _{ds} G _{ds} A _{ds} G _{es} T _{es} T _{es} ^m C _k	3000
1270701	1207160	THA-GalNAc- _o ^m C _{ks} A _{ks} ^m C _{ds} T _{ds} T _{ds} T _{ds} A _{ds} T _{ds} T _{ds} G _{ds} A _{ds} G _{es} T _{es} T _{es} ^m C _{ks} ^m C _k	2924
1270702	1207161	THA-GalNAc- _o G _{ks} ^m C _{ks} A _{ds} ^m C _{ds} T _{ds} T _{ds} T _{ds} A _{ds} T _{ds} T _{ds} G _{ds} A _{es} G _{es} T _{es} T _{es} ^m C _k	3000
1270703	1207277	THA-GalNAc- _o ^m C _{ks} A _{ks} ^m C _{ds} T _{ds} T _{ds} T _{ds} A _{ds} T _{ds} T _{ds} G _{ds} A _{ds} G _{es} T _{es} T _{es} ^m C _{ks} ^m C _e	2924
1270705	1213144	THA-GalNAc- _o G _{ks} ^m C _{ks} A _{ks} ^m C _{ds} U _{ys} T _{ds} T _{ds} A _{ds} T _{ds} T _{ds} G _{ds} A _{ds} G _{ds} T _{ks} T _{ks} ^m C _k	5006
1270707	1213260	THA-GalNAc- _o ^m C _{ks} A _{ks} ^m C _{ks} T _{ds} T _{ds} U _{ys} A _{ds} T _{ds} T _{ds} G _{ds} A _{ds} G _{ds} T _{ds} T _{ks} ^m C _{ks} ^m C _k	5035
1270710	1207393	THA-GalNAc- _o A _{ks} ^m C _{ks} T _{ds} T _{ds} T _{ds} A _{ds} T _{ds} T _{ds} G _{ds} A _{ds} G _{ds} T _{ks} T _{es} ^m C _{ks} ^m C _{es} T _k	2848
1270712	1207394	THA-GalNAc- _o ^m C _{ks} A _{ks} ^m C _{ds} T _{ds} T _{ds} T _{ds} A _{ds} T _{ds} T _{ds} G _{ds} A _{ds} G _{ks} T _{es} T _{es} ^m C _{es} ^m C _k	2924
1270714	1207279	THA-GalNAc- _o A _{ks} G _{ks} ^m C _{ds} A _{ds} ^m C _{ds} T _{ds} T _{ds} T _{ds} A _{ds} T _{ds} T _{ds} G _{es} A _{ks} G _{es} T _{ks} T _e	3076
1270715	1207159	THA-GalNAc- _o A _{ks} ^m C _{ks} T _{ds} T _{ds} T _{ds} A _{ds} T _{ds} T _{ds} G _{ds} A _{ds} G _{ds} T _{es} T _{es} ^m C _{es} ^m C _{ks} T _k	2848
1270716	1207005	THA-GalNAc- _o A _{ks} ^m C _{es} T _{ks} T _{ds} T _{ds} A _{ds} T _{ds} T _{ds} G _{ds} A _{ds} G _{ds} T _{ds} T _{es} ^m C _{es} ^m C _{ks} T _k	2848

Example 9: Design of oligomeric compounds complementary to a human FXII nucleic acid

Modified oligonucleotides were designed as indicated in the tables below. The chemistry notation column in the tables below specifies the specific chemistry notation for modified oligonucleotides; wherein subscript 'd' represents a 2'-β-D-deoxyribose sugar moiety, subscript 'e' represents a 2'-MOE sugar moiety, subscript 'y' represents a 2'-O-methyl sugar moiety, subscript 'k' represents a cET modified sugar moiety, subscript 's' represents a phosphorothioate internucleoside linkage, subscript 'o' represents a phosphodiester internucleoside linkage, and superscript 'm' before the cytosine residue (^mC) represents a 5-methyl cytosine.

"Start site" indicates the 5'-most nucleoside of the target sequence to which the modified oligonucleotide is complementary. "Stop site" indicates the 3'-most nucleoside of the target sequence to which the modified oligonucleotide is complementary. As shown in the tables below, the modified oligonucleotides are complementary to either the human FXII mRNA, designated herein as SEQ ID NO: 1 (described herein above) or to the human FXII genomic sequence, designated herein as SEQ ID NO: 2 (described herein above) or to both. 'N/A' indicates that the modified oligonucleotide is not complementary to that particular target sequence with 100% complementarity.

Table 119. 5-10-5 2'-O-methyl modified oligonucleotides complementary to human FXII

Compound Number	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Sequence and Chemistry notation (5' to 3')	SEQ ID No.
1213034	2014	2033	7402	7421	C _{ys} A _{ys} C _{ys} U _{ys} U _{ys} T _{ds} A _{ds} T _{ds} T _{ds} G _{ds} A _{ds} G _{ds} T _{ds} T _{ds} ^m C _{ds} C _{ys} U _{ys} G _{ys} C _{ys} G _y	5039

1358035	1936	1955	7324	7343	C _{ys} C _{ys} C _{ys} C _{ys} A _{ys} G _{ds} ^m C _{ds} ^m C _{ds} A _{ds} ^m C _{ds} T _{ds} ^m C _{ds} T _{ds} ^m C _{ds} T _{ds} C _{ys} A _{ys} C _{ys} U _{ys} G _y	5040
1213030	1924	1943	7312	7331	U _{ys} C _{ys} U _{ys} C _{ys} A _{ys} ^m C _{ds} T _{ds} G _{ds} ^m C _{ds} G _{ds} G _{ds} A _{ds} A _{ds} T _{ds} ^m C _{ds} A _{ys} C _{ys} C _{ys} A _{ys} A _y	5041
1213029	1914	1933	7302	7321	G _{ys} A _{ys} A _{ys} U _{ys} C _{ys} A _{ds} ^m C _{ds} ^m C _{ds} A _{ds} A _{ds} G _{ds} G _{ds} A _{ds} G _{ds} G _{ds} G _{ys} A _{ys} A _{ys} A _{ys} G _y	5042

Example 10: Tolerability of modified oligonucleotides targeting human FXII in CD-1 mice

CD-1 mice are a multipurpose mouse model frequently utilized for safety and efficacy testing. The mice were treated with modified oligonucleotides selected from studies described above and evaluated for changes in the levels of various plasma chemistry markers.

5 Study 1

Groups of four 7-to-8-week-old male CD-1 mice were injected subcutaneously once a week for six weeks (for a total of 6 treatments) with 80 mg/kg of modified oligonucleotides. One group of four male CD-1 mice was injected with saline. Mice were euthanized 72 hours following the final administration.

To evaluate the effect of modified oligonucleotides on liver and kidney function, plasma levels of aspartate aminotransferase (AST), alanine aminotransferase (ALT), total bilirubin (TBIL), blood urea nitrogen (BUN), creatinine (CRT) and albumin were measured using an automated clinical chemistry analyzer (Hitachi Olympus AU400c, Melville, NY). The results are presented in the table below. Modified oligonucleotides that caused changes in the levels of any of the liver or kidney function markers outside the expected range for modified oligonucleotides were excluded in further studies.

15 Table 120. Plasma chemistry markers in male CD-1 mice

Compound No.	AST (IU/L)	ALT (IU/L)	TBIL (mg/dL)	BUN (mg/dL)	CRT (mg/dL)	Albumin (mg/dL)
saline	51	33	0.27	25	0.05	2.82
1194378	603	1124	0.34	27	0.07	2.61
1194379	255	740	0.25	22	0.04	2.65
1194380	62	58	0.17	26	0.08	2.84
1194381	368	375	0.18	24	0.09	2.83
1194382	380	423	0.21	25	0.08	2.67
1194383	72	104	0.15	25	0.06	2.54
1194384	66	41	0.17	23	0.05	2.70
1194385	1287	1501	0.24	27	0.08	2.10
1194387	157	239	0.26	27	0.06	2.69
1194388	68	48	0.17	24	0.07	2.77
1194389	69	53	0.16	25	0.06	2.75
1194390	870	1395	0.22	26	0.08	2.84
1194391	49	40	0.17	23	0.07	2.81

1194392	62	56	0.16	27	0.07	2.75
1194393	51	39	0.16	22	0.07	2.58
1194394	99	106	0.20	24	0.07	2.84
1194395	71	112	0.13	24	0.05	2.53
1194396	1614	1954	1.81	18	0.03	2.54
1194397	678	836	0.20	17	0.06	2.62
1194398	713	867	0.20	23	0.07	2.76
1194399	548	393	0.26	26	0.07	2.84
1194400	854	1165	0.66	22	0.07	2.78
1194401	457	1201	0.23	27	0.05	2.76

Body weights of CD-1 mice were measured at days 1 and 40, and the average body weight for each group is presented in the table below. Liver, kidney and spleen weights were measured at the end of the study and are presented in the table below. Modified oligonucleotides that caused any changes in organ weights outside the expected range for modified oligonucleotides were excluded from further studies.

5

Table 121. Body and organ weights (in grams)

Compound No.	Body Weight (g)		Liver (g)	Kidney (g)	Spleen (g)
	Day 1	Day 40			
saline	31	36	2.0	0.6	0.1
1194378	32	39	2.6	0.6	0.1
1194379	32	38	2.7	0.6	0.1
1194380	32	38	2.6	0.6	0.1
1194381	32	40	2.8	0.6	0.1
1194382	32	38	2.5	0.6	0.1
1194383	31	36	2.2	0.5	0.1
1194384	32	40	2.2	0.6	0.1
1194385	31	39	3.0	0.6	0.1
1194387	30	37	2.2	0.5	0.3
1194388	31	38	2.5	0.6	0.2
1194389	30	37	2.3	0.6	0.1
1194390	32	38	3.2	0.6	0.1
1194391	30	37	2.4	0.6	0.1
1194392	32	38	2.2	0.6	0.1
1194393	31	38	2.0	0.6	0.1
1194394	31	37	2.1	0.6	0.1
1194395	32	37	2.4	0.6	0.1
1194396	31	35	2.0	0.6	0.1
1194397	32	40	2.8	0.6	0.1

1194398	32	38	3.0	0.6	0.2
1194399	32	38	2.9	0.6	0.2
1194400	31	38	3.2	0.6	0.1
1194401	33	41	2.6	0.6	0.2

Study 2

Groups of four 7-to-8-week-old male CD-1 mice were injected subcutaneously once a week for six weeks (for a total of 6 treatments) with 80 mg/kg of modified oligonucleotides. One group of four male CD-1 mice was injected with saline. Mice were euthanized 72 hours following the final administration.

- 5 To evaluate the effect of modified oligonucleotides on liver and kidney function, plasma levels of aspartate aminotransferase (AST), alanine aminotransferase (ALT), total bilirubin (TBIL), blood urea nitrogen (BUN), creatinine (CRT) and albumin were measured using an automated clinical chemistry analyzer (Hitachi Olympus AU400c, Melville, NY). The results are presented in the table below. Modified oligonucleotides that caused changes in the levels of any of the liver or kidney function markers outside the
- 10 expected range for modified oligonucleotides were excluded in further studies.

Table 122. Plasma chemistry markers in male CD-1 mice

Compound No.	AST (IU/L)	ALT (IU/L)	TBIL (mg/dL)	BUN (mg/dL)	CRT (mg/dL)	Albumin (mg/dL)
saline	70	68	0.16	22	0.09	2.84
1194402	66	66	0.17	24	0.09	2.73
1194403	67	64	0.15	26	0.09	2.64
1194404	77	82	0.17	25	0.10	2.91
1194405	100	155	0.14	25	0.07	2.53
1194406	95	84	0.15	25	0.07	2.60
1194407	94	69	0.11	19	0.07	2.56
1194408	111	137	0.15	26	0.06	2.54
1194409	134	102	0.16	25	0.06	2.69
1194410	344	385	0.18	28	0.08	2.53
1194411	321	242	0.15	22	0.08	2.53
1194412	227	333	0.17	25	0.06	2.49
1194413	110	61	0.16	24	0.10	2.79
1194415	143	132	0.13	25	0.08	2.39
1194416	73	107	0.11	21	0.06	2.43
1194417	488	672	0.24	23	0.05	2.43
1194419	72	60	0.14	28	0.08	2.64
1194420	104	86	0.15	26	0.09	2.72
1194421	548	502	0.26	26	0.12	2.99
1194423	255	443	0.11	25	0.04	1.54
1194424	325	423	0.14	26	0.09	2.48

1194425	447	490	0.18	25	0.10	2.95
1194426	320	298	0.21	26	0.10	2.80
1194427	147	194	0.18	22	0.08	2.75

Body weights of CD-1 mice were measured at days 1 and 39, and the average body weight for each group is presented in the table below. Liver, kidney and spleen weights were measured at the end of the study and are presented in the table below. Modified oligonucleotides that caused any changes in organ weights outside the expected range for modified oligonucleotides were excluded from further studies.

5

Table 123. Body and organ weights (in grams)

Compound No.	Body Weight (g)		Liver (g)	Kidney (g)	Spleen (g)
	Day 1	Day 39			
Saline	33	38	2.0	0.6	0.1
1194402	35	41	2.3	0.6	0.1
1194403	32	37	2.2	0.5	0.1
1194404	33	39	2.4	0.6	0.2
1194405	35	41	2.7	0.6	0.1
1194406	34	43	2.7	0.7	0.1
1194407	32	38	2.1	0.6	0.1
1194408	33	39	2.6	0.7	0.2
1194409	32	39	2.7	0.6	0.1
1194410	35	41	2.9	0.6	0.2
1194411	35	41	2.9	0.6	0.1
1194412	32	38	2.7	0.6	0.2
1194413	32	39	2.3	0.6	0.1
1194415	33	37	2.2	0.6	0.2
1194416	34	39	2.3	0.6	0.1
1194417	35	41	2.3	0.6	0.2
1194419	33	37	2.1	0.5	0.1
1194420	33	38	2.2	0.6	0.1
1194421	37	42	2.7	0.6	0.1
1194423	33	39	2.7	0.6	0.2
1194424	33	41	2.8	0.6	0.2
1194425	37	41	2.0	0.6	0.1
1194426	35	41	2.7	0.6	0.2
1194427	34	41	2.9	0.6	0.1

Study 3

Groups of two 8-to-10-week-old male CD-1 mice were injected subcutaneously once (for a total of 1 treatment) with 50 mg/kg of modified oligonucleotides. One group of two male CD-1 mice was injected with saline. Mice were euthanized 4 days following administration.

To evaluate the effect of modified oligonucleotides on liver and kidney function, plasma levels of aspartate aminotransferase (AST), alanine aminotransferase (ALT), total bilirubin (TBIL), blood urea nitrogen (BUN), creatinine (CRT) and albumin were measured using an automated clinical chemistry analyzer (Hitachi Olympus AU400c, Melville, NY). The results are presented in the table below. Assays include two animals in a group, except where the symbol “†” indicates that only 1 animal was used for a specific assay. Modified oligonucleotides that caused changes in the levels of any of the liver or kidney function markers outside the expected range for modified oligonucleotides were excluded in further studies.

Table 124. Plasma chemistry markers in male CD-1 mice

Compound No.	AST (IU/L)	ALT (IU/L)	TBIL (mg/dL)	BUN (mg/dL)	CRT (mg/dL)	Albumin (mg/dL)
saline	81	63	0.13	18	0.12	2.5
1194483	1073	1351	0.78	19	0.13	2.58
1194484	5261	6171	4.19	15	0.13	2.46
1194486	112	115	0.17	19	0.14	2.85
1194487 [†]	2747	3998	5.21	16	0.2	2.91
1194488	68	46	0.14	25	0.14	2.92
1194489	43	38	0.16	23	0.13	2.48
1194490	61	62	0.13	21	0.13	2.74
1194491	59	77	0.16	21	0.16	2.85
1194492	47	26	0.13	23	0.14	2.59
1194493	114	141	0.15	21	0.15	2.77
1194494 [†]	2255	3189	3.49	25	0.09	2.25
1194495	3848	3311	1.48	19	0.15	2.56
1194496	839	3491	2.8	21	0.14	2.37
1194497	3145	3724	0.77	20	0.17	2.53
1194498	229	251	0.17	15	0.12	2.14
1194499	519	464	0.93	26	0.18	2.85
1194500	58	52	0.16	21	0.12	2.61
1194501	60	30	0.13	21	0.14	2.69
1194502	45	30	0.15	21	0.14	2.61
1194503	57	38	0.14	19	0.14	2.68
1194504	47	53	0.15	20	0.13	2.63
1194505 [†]	109	183	0.15	23	0.16	3.06
1194506	63	96	0.14	25	0.13	2.86
1194507	124	198	0.16	22	0.14	2.41
1194508	1291	797	0.3	17	0.14	2.81
1194509	6147	5321	3.17	18	0.18	2.99
1194510	322	505	0.21	19	0.15	2.83
1194512 [†]	2308	5902	1.98	18	0.09	2.52
1194513	87	112	0.21	20	0.14	2.42
1194514	60	63	0.13	19	0.14	2.52
1194515	90	116	0.14	23	0.13	2.52
1194516	54	47	0.15	21	0.16	2.62

1194517	102	102	0.14	17	0.16	2.54
1194518	78	83	0.15	22	0.13	2.62
1194519	43	32	0.19	19	0.12	2.66
1194520	84	61	0.12	20	0.15	2.56
1194572	148	153	0.14	22	0.11	2.54
1194573	71	50	0.16	18	0.14	2.6
1194574 [†]	324	428	0.11	25	0.13	2.77
1194575 [†]	6483	7128	6.54	27	0.14	2.39
1194576	2701	1943	6.15	30	0.32	2.44
1194578	N/A	1182 [†]	5.22	85	0.69	2.63
1194579	4055	6429	4.34	25	0.18	2.83
1194580 [†]	3302	4048	6.96	24	0.2	2.51
1194581	6176	6185	5.21	22	0.21	3.23
1194582	1160 [†]	16 [†]	3.86	32	0.32	3.31
1194583 [†]	N/A	N/A	5.19	27	0.19	3.44

Study 4

Groups of four 7-to-8-week-old male CD-1 mice were injected subcutaneously once per week for 6 weeks (for a total of 6 treatments) with 40 mg/kg of modified oligonucleotides. One group of four male CD-1 mice was injected with saline. Mice were euthanized 2 days following final administration.

- 5 To evaluate the effect of modified oligonucleotides on liver and kidney function, plasma levels of aspartate aminotransferase (AST), alanine aminotransferase (ALT), total bilirubin (TBIL), blood urea nitrogen (BUN), creatinine (CRT) and albumin were measured using an automated clinical chemistry analyzer (Hitachi Olympus AU400c, Melville, NY). The results are presented in the table below. Assays include four animals in a group, except where the symbol “[†]” indicates that 3 animals or less was used for a
- 10 specific assay. Modified oligonucleotides that caused changes in the levels of any of the liver or kidney function markers outside the expected range for modified oligonucleotides were excluded in further studies.

Table 125. Plasma chemistry markers in male CD-1 mice

Compound No.	AST (IU/L)	ALT (IU/L)	TBIL (mg/dL)	BUN (mg/dL)	CRT (mg/dL)	Albumin (mg/dL)
saline	74	57	0.24	20	0.11	3.07
1194343	767	1036	0.41	16	0.10	2.87
1194345	165	163	0.20	23	0.12	2.75
1194346	826	955	0.25	25	0.16	3.06
1194347	965	1210	0.22	23	0.12	3.01
1194348	1886	3635	0.55	24	0.15	3.15
1194349	140	209	0.19	22	0.12	2.75
1194350	1342	1861	0.24	23	0.13	2.72
1194357	66	46	0.13	25	0.14	2.61
1194358	54	59	0.16	24	0.15	2.99
1194359	132	202	0.16	22	0.11	2.66
1194360	119	263	0.15	19	0.08	2.57

1194361	596	740	0.21	27	0.09	2.83
1194363 [†]	441	604	0.19	22	0.11	3.08
1194370	502	572	0.16	21	0.09	2.74
1194371	58	53	0.18	22	0.09	2.85
1194372	510	646	0.27	21	0.09	2.88
1194373	677	963	0.24	20	0.08	2.87
1194374	1530	2506	0.20	23	0.09	2.99
1194375	544	815	0.18	19	0.09	2.81
1194376	251	490	0.16	19	0.06	2.54
1194377	438	704	0.18	23	0.09	2.75
1194429	1282	1188	0.36	21	0.06	2.80
1194430	558	820	0.18	20	0.11	2.87

Body weights of CD-1 mice were measured at days 1 and 35, and the average body weight for each group is presented in the table below. Liver, kidney and spleen weights were measured at the end of the study and are presented in the table below. Modified oligonucleotides that caused any changes in organ weights outside the expected range for modified oligonucleotides were excluded from further studies.

5

Table 126. Body and organ weights (in grams)

Compound No.	Body Weight (g)		Liver (g)	Kidney (g)	Spleen (g)
	Day 1	Day 35			
Saline	31	39	2.0	0.6	0.1
1194343	31	37	2.3	0.5	0.1
1194345	33	40	2.6	0.5	0.1
1194346	30	36	2.8	0.5	0.1
1194347	34	39	3.1	0.6	0.2
1194348	33	37	3.2	0.5	0.1
1194349	32	38	2.6	0.5	0.1
1194350	32	39	3.3	0.6	0.2
1194357	31	36	2.2	0.5	0.2
1194358	33	39	2.6	0.5	0.1
1194359	31	36	2.3	0.5	0.1
1194360	31	36	2.3	0.5	0.2
1194361	33	37	2.7	0.5	0.1
1194363	31	35	3.4	0.5	0.2
1194370	32	36	2.1	0.5	0.2
1194371	32	38	2.1	0.5	0.1
1194372	31	36	2.3	0.5	0.1
1194373	32	36	2.3	0.5	0.1
1194374	32	38	3.1	0.6	0.2
1194375	31	37	2.9	0.5	0.2
1194376	31	37	2.3	0.5	0.1
1194377	33	39	2.8	0.5	0.2

1194429	31	36	2.7	0.5	0.3
1194430	32	36	2.5	0.4	0.1

Example 11: Tolerability of modified oligonucleotides targeting human FXII in Sprague-Dawley rats

Sprague-Dawley rats are a multipurpose model used for safety and efficacy evaluations. The rats were treated with Ionis modified oligonucleotides described in the Examples above and evaluated for changes in the levels of various plasma chemistry markers.

5 Study 1

Groups of 4 Sprague-Dawley rats each were weekly injected subcutaneously with 80 mg/kg of Ionis oligonucleotide for 6 weeks (total 6 doses). The rats were euthanized; and organs, urine and plasma were harvested for further analysis 3 days after the last dose.

Plasma chemistry markers

10 To evaluate the effect of Ionis oligonucleotides on hepatic function, plasma levels of transaminases were measured using an automated clinical chemistry analyzer (Hitachi Olympus AU400c, Melville, NY). Plasma levels of ALT (alanine transaminase) and AST (aspartate transaminase) were measured and the results are presented in the table below expressed in IU/L. Plasma levels of total bilirubin (TBIL), creatinine (CREA), albumin (ALB), and Blood Urea Nitrogen (BUN) were also measured using the same clinical
15 chemistry analyzer and the results are also presented in the table below. Ionis modified oligonucleotides that caused changes in the levels of any markers of liver function outside the expected range for modified oligonucleotides were excluded in further studies. In some cases, where less than 4 samples were available in a group, the compounds are marked with the symbol “†”.

Table 127. Plasma chemistry markers in Sprague-Dawley rats

Compound No.	AST (IU/L)	ALT (IU/L)	TBIL (mg/dL)	BUN (mg/dL)	CREA (mg/dL)	ALB (mg/dL)
Saline	68	41	0.16	17	0.21	3.13
1194380	89	56	0.28	19	0.26	3.03
1194383	198	158	0.22	17	0.22	3.18
1194384 [†]	52	24	0.12	17	0.18	2.93
1194388	244	80	0.34	17	0.15	2.22
1194389	157	103	0.20	27	0.59	3.31
1194392	64	29	0.18	18	0.20	3.18
1194393	59	32	0.15	16	0.23	3.19
1194394	58	28	0.12	17	0.20	3.03
1194395	154	83	0.20	17	0.23	2.99
1194402	82	64	0.17	19	0.20	3.23
1194403	68	37	0.17	16	0.22	3.13

20 Blood obtained from rat groups at week 6 were sent to IDEXX BioResearch for measurement of blood cell counts. Counts taken include red blood cell (RBC) count, white blood cell (WBC) count, hemoglobin (HGB), hematocrit (HCT), Mean corpuscular volume (MCV), mean corpuscular hemoglobin

(MCH), mean corpuscular hemoglobin concentration (MCHC), and individual white blood cell counts, such as that of monocytes (MON), neutrophils (NEU), lymphocytes (LYM), and platelets (PLT). The results are presented in the tables below. Ionis oligonucleotides that caused changes in the blood cell count outside the expected range for modified oligonucleotides were excluded in further studies.

5

Table 128. Blood Cell Count in Sprague-Dawley Rats

Compound No.	WBC (/nL)	RBC (/pL)	HGB (g/dL)	HCT (%)	MCV (fL)	MCH (pg)	MCHC (%)	NEU (%)	LYM (%)	MON (%)	PLT (/nL)
Saline	11	8	15	44	52	18	35	17	78	4	786
1194380	5	9	15	44	52	18	34	16	77	5	981
1194383	10	9	17	48	51	18	35	12	80	5	916
1194384	8	9	15	44	51	18	35	15	79	4	958
1194388	6	5	10	34	68	21	31	19	74	6	229
1194389	10	9	16	44	52	18	36	16	79	4	1080
1194392	7	8	15	44	53	18	35	13	83	3	792
1194393	7	9	16	46	53	18	35	19	74	5	714
1194394	5	8	14	41	54	18	34	8	88	2	513
1194395	10	9	15	42	49	17	35	13	80	5	792
1194402	8	9	16	45	50	17	35	9	86	3	800
1194403	6	9	15	44	51	18	35	17	78	4	939

To evaluate the effect of Ionis oligonucleotides on kidney function, urinary levels of micro total protein (MTP) and creatinine were measured using an automated clinical chemistry analyzer (Hitachi Olympus AU400c, Melville, NY). The ratios of MTP to creatinine (MTP/C ratio) are presented in the table below. Ionis oligonucleotides that caused changes in the levels of the ratio outside the expected range for modified oligonucleotides were excluded in further studies.

10

Table 129. MTP to creatinine ratio in Sprague-Dawley rats

Compound No.	MTP/C Ratio
saline	1.7
1194380	1.9
1194383	2.5
1194384	2.5
1194388	2.4
1194389	1.9
1194392	1.6
1194393	1.7
1194394	1.9
1194395	1.9
1194402	2.0
1194403	1.8

Body weights of rats were measured at days 1 and 38, and the average body weight for each group is presented in the table below. Liver, spleen and kidney weights were measured at the end of the study, and are presented in the table below. Ionis oligonucleotides that caused any changes in organ weights outside the expected range for modified oligonucleotides were excluded from further studies.

5

Table 130. Body and organ weights (g)

Compound No.	Body Weight (g)		Liver Weight (g)	Kidney Weight (g)	Spleen Weight (g)
	Day 1	Day 38			
Saline	266	424	18	3.4	1.0
1194380	255	378	17	3.1	1.1
1194383	260	370	16	3.3	1.2
1194384	256	396	17	3.5	1.4
1194388	256	346	27	3.4	4.8
1194389	257	398	18	3.3	1.4
1194392	256	387	19	3.3	1.5
1194393	245	363	16	2.8	1.0
1194394	265	389	18	3.5	1.9
1194395	264	377	14	3.2	1.3
1194402	249	335	13	2.7	1.1
1194403	260	387	16	3.4	1.1

Study 2

Groups of 4 Sprague-Dawley rats each were weekly injected subcutaneously with 80 mg/kg of Ionis oligonucleotide for 6 weeks (total 6 doses). The rats were euthanized; and organs, urine and plasma were harvested for further analysis 3 days after the last dose.

10 *Plasma chemistry markers*

To evaluate the effect of Ionis oligonucleotides on hepatic function, plasma levels of transaminases were measured using an automated clinical chemistry analyzer (Hitachi Olympus AU400c, Melville, NY). Plasma levels of ALT (alanine transaminase) and AST (aspartate transaminase) were measured and the results are presented in the table below expressed in IU/L. Plasma levels of total bilirubin (TBIL), creatinine (CREA), albumin (ALB), and Blood Urea Nitrogen (BUN) were also measured using the same clinical chemistry analyzer and the results are also presented in the table below. Ionis modified oligonucleotides that caused changes in the levels of any markers of liver function outside the expected range for modified oligonucleotides were excluded in further studies. In some cases, where less than 4 samples were available in a group, the compounds are marked with the symbol “†”.

20

Table 131. Plasma chemistry markers in Sprague-Dawley rats

Compound No.	AST (IU/L)	ALT (IU/L)	TBIL (mg/dL)	BUN (mg/dL)	CREA (mg/dL)	ALB (mg/dL)
Saline	81	49	0.16	15	0.22	3.11
1194404	99	47.5	0.22	18.375	0.28	3.21
1194405	853	783	0.28	19	0.30	3.32

1194406	96	50	0.16	16	0.21	3.40
1194407	71	34	0.15	17	0.24	3.20
1194408	223	179	0.23	16	0.24	3.49 [†]
1194409	169	133	0.24	17	0.22	3.30
1194413 [†]	209	167	0.28	17	0.21	3.27
1194415	61	41	0.14	17	0.21	3.44
1194416 [†]	91	57	0.16	17	0.22	3.47
1194419	105	48	0.16	15	0.23	3.32
1194420	84	52	0.13	16	0.22	3.36
1194427	113	71	0.18	14	0.22	3.65 [†]

Blood obtained from rat groups at week 6 were sent to IDEXX BioResearch for measurement of blood cell counts. Counts taken include red blood cell (RBC) count, white blood cell (WBC) count, hemoglobin (HGB), hematocrit (HCT), Mean corpuscular volume (MCV), mean corpuscular hemoglobin (MCH), mean corpuscular hemoglobin concentration (MCHC), and individual white blood cell counts, such as that of monocytes (MON), neutrophils (NEU), lymphocytes (LYM), and platelets (PLT). The results are presented in the tables below. Ionis oligonucleotides that caused changes in the blood cell count outside the expected range for modified oligonucleotides were excluded in further studies.

Table 132. Blood Cell Count in Sprague-Dawley Rats

Compound No.	WBC (/nL)	RBC (/pL)	HGB (g/dL)	HCT (%)	MCV (fL)	MCH (pg)	MCHC (%)	NEU (%)	LYM (%)	MON (%)	PLT (/nL)
Saline	12	8	15	43	55	19	35	17	78	5	882
1194404	13	8	15	43	53	19	35	10	86	4	868
1194405	10	9	16	44	52	18	35	10	77	12	909
1194406	11	8	15	44	52	18	35	11	82	6	867
1194407	11	8	15	44	54	19	35	12	83	4	817
1194408	9	8	16	45	54	19	35	14	78	7	918
1194409	10	8	15	43	55	19	35	8	86	6	735
1194413 [†]	8	8	15	44	55	19	35	12	79	8	798
1194415	8	8	16	45	54	19	35	10	82	7	855
1194416	9	8	16	45	53	19	35	10	83	6	1093
1194419	5	8	15	42	54	19	35	11	81	8	813
1194420	8	9	16	45	53	19	35	13	80	5	835
1194427	12	8	16	47	56	19	35	13	80	6	1003

To evaluate the effect of Ionis oligonucleotides on kidney function, urinary levels of micro total protein (MTP) and creatinine were measured using an automated clinical chemistry analyzer (Hitachi Olympus AU400c, Melville, NY). The ratios of MTP to creatinine (MTP/C ratio) are presented in the table below. Ionis oligonucleotides that caused changes in the levels of the ratio outside the expected range for modified oligonucleotides were excluded in further studies.

Table 133. MTP to creatinine ratio in Sprague-Dawley rats

Compound No.	MTP/C Ratio
saline	0.8
1194404	1.1
1194405	1.6
1194406	1.5
1194407	1.8
1194408	1.9
1194409	1.5
1194413	1.4
1194415	2.0
1194416	1.4
1194419	2.0
1194420	2.3
1194427	2.6

Body weights of rats were measured at days 1 and 35, and the average body weight for each group is presented in the table below. Liver, spleen and kidney weights were measured at the end of the study, and are presented in the table below. Ionis oligonucleotides that caused any changes in organ weights outside the expected range for modified oligonucleotides were excluded from further studies.

Table 134. Body and organ weights (g)

Compound No.	Body Weight (g)		Liver Weight (g)	Kidney Weight (g)	Spleen Weight (g)
	Day 1	Day 35			
Saline	219	433	17	3.8	4.4
1194404	213	391	15	3.3	5.5
1194405	210	357	16	3.3	4.4
1194406	218	388	16	3.6	4.7
1194407	227	410	17	3.9	5.0
1194408	222	390	15	3.6	4.8
1194409	216	376	16	3.7	5.3
1194413 [†]	207	399	17	4.0	4.2
1194415	220	382	15	3.5	3.9
1194416	218	369	13	3.3	4.7
1194419	218	388	16	3.2	3.6
1194420	219	392	16	3.6	4.6
1194427	204	375	15	3.2	4.0

Study 3

Groups of 4 Sprague-Dawley rats each were weekly injected subcutaneously with 40 mg/kg of Ionis oligonucleotide for 6 weeks (total 6 doses). A group of 4 rats were treated subcutaneously with 80 mg/kg of Compound No. 1194391. The rats were euthanized; and organs, urine and plasma were harvested for further analysis 2 days after the last dose.

Plasma chemistry markers

To evaluate the effect of Ionis oligonucleotides on hepatic function, plasma levels of transaminases were measured using an automated clinical chemistry analyzer (Hitachi Olympus AU400c, Melville, NY). Plasma levels of ALT (alanine transaminase) and AST (aspartate transaminase) were measured and the results are presented in the table below expressed in IU/L. Plasma levels of total bilirubin (TBIL), creatinine (CREA), albumin (ALB), and Blood Urea Nitrogen (BUN) were also measured using the same clinical chemistry analyzer and the results are also presented in the table below. Ionis modified oligonucleotides that caused changes in the levels of any markers of liver function outside the expected range for modified oligonucleotides were excluded in further studies.

Table 135. Plasma chemistry markers in Sprague-Dawley rats

Compound No.	AST (IU/L)	ALT (IU/L)	TBIL (mg/dL)	BUN (mg/dL)	CREA(mg/dL)	ALB (mg/dL)
Saline	65	52	0.16	15	0.23	3.31
1194345	122	52	0.15	19	0.25	2.81
1194349	59	38	0.16	16	0.27	3.54
1194357	78	50	0.16	16	0.28	3.67
1194358	82	51	0.18	16	0.29	3.88
1194359	70	41	0.15	15	0.28	3.65
1194360	269	92	0.35	20	0.27	2.66
1194371	125	85	0.20	17	0.25	2.74
1194377	1054	319	1.04	16	0.35	3.18
1194430	1195	379	1.04	16	0.26	3.39
1194391	83	65	0.17	15	0.21	3.39

Blood obtained from rat groups at week 6 were sent to IDEXX BioResearch for measurement of blood cell counts. Counts taken include red blood cell (RBC) count, white blood cell (WBC) count, hemoglobin (HGB), hematocrit (HCT), Mean corpuscular volume (MCV), mean corpuscular hemoglobin (MCH), mean corpuscular hemoglobin concentration (MCHC), and individual white blood cell counts, such as that of monocytes (MON), neutrophils (NEU), lymphocytes (LYM), and platelets (PLT). The results are presented in the tables below. Ionis oligonucleotides that caused changes in the blood cell count outside the expected range for modified oligonucleotides were excluded in further studies.

Table 136. Blood Cell Count in Sprague-Dawley Rats

Compound No.	WBC (/nL)	RBC (/pL)	HGB (g/dL)	HCT (%)	MCV (fL)	MCH (pg)	MCHC (%)	NEU (%)	LYM (%)	MON (%)	PLT (/nL)
Saline	9	8	16	47	58	19	34	16	81	2	749
1194345	12	7	14	42	61	20	33	9	87	3	687
1194349	10	8	15	45	55	19	34	21	75	3	921
1194357	9	8	16	47	57	19	34	10	86	3	814
1194358	11	9	16	47	55	19	34	13	82	4	1020
1194359	10	8	15	45	55	19	34	13	82	3	887

1194360	16	8	13	38	50	17	34	10	84	6	733
1194371	9	8	14	43	56	18	33	19	74	5	910
1194377	9	8	15	43	56	19	34	17	76	6	917
1194430	13	8	14	42	56	19	34	20	73	7	1241
1194391	8	8	16	46	58	20	34	22	74	3	803

To evaluate the effect of Ionis oligonucleotides on kidney function, urinary levels of micro total protein (MTP) and creatinine were measured using an automated clinical chemistry analyzer (Hitachi Olympus AU400c, Melville, NY). The ratios of MTP to creatinine (MTP/C ratio) are presented in the table below. Ionis oligonucleotides that caused changes in the levels of the ratio outside the expected range for modified oligonucleotides were excluded in further studies.

Table 137. MTP to creatinine ratio in Sprague-Dawley rats

Compound No.	MTP/C Ratio
saline	1.1
1194345	1.8
1194349	2.9
1194357	2.1
1194358	1.6
1194359	1.8
1194360	1.7
1194371	1.2
1194377	2.4
1194430	2.2
1194391	1.4

Body weights of rats were measured at days 1 and 38, and the average body weight for each group is presented in the table below. Liver, spleen and kidney weights were measured at the end of the study, and are presented in the table below. Ionis oligonucleotides that caused any changes in organ weights outside the expected range for modified oligonucleotides were excluded from further studies.

Table 138. Body and organ weights (g)

Compound No.	Body Weight (g)		Liver Weight (g)	Kidney Weight (g)	Spleen Weight (g)
	Day 1	Day 38			
Saline	237	450	17	3.5	0.8
1194345	249	446	20	3.8	2.3
1194349	232	425	19	3.2	1.2
1194357	235	409	17	3.6	1.2
1194358	240	396	16	3.3	1.2
1194359	249	414	15	3.4	1.1
1194360	239	385	15	3.5	1.8
1194371	235	422	19	3.5	1.4
1194377	243	376	10	3.0	1.4
1194391	233	414	16	3.3	0.8

1194430	243	406	13	3.7	1.5
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Study 4

Groups of 4 Sprague-Dawley rats each were weekly injected subcutaneously with 40 mg/kg of Ionis oligonucleotide for 6 weeks (total 6 doses). The rats were euthanized; and organs, urine and plasma were harvested for further analysis 3 days after the last dose.

5 *Plasma chemistry markers*

To evaluate the effect of Ionis oligonucleotides on hepatic function, plasma levels of transaminases were measured using an automated clinical chemistry analyzer (Hitachi Olympus AU400c, Melville, NY). Plasma levels of ALT (alanine transaminase) and AST (aspartate transaminase) were measured and the results are presented in the table below expressed in IU/L. Plasma levels of total bilirubin (TBIL), creatinine (CREA), albumin (ALB), and Blood Urea Nitrogen (BUN) were also measured using the same clinical chemistry analyzer and the results are also presented in the table below. Ionis modified oligonucleotides that caused changes in the levels of any markers of liver function outside the expected range for modified oligonucleotides were excluded in further studies.

Table 139. Plasma chemistry markers in Sprague-Dawley rats

Compound No.	AST (IU/L)	ALT (IU/L)	TBIL (mg/dL)	BUN (mg/dL)	CREA(mg/dL)	ALB (mg/dL)
Saline	61	43	0.1	16	0.3	3.4
1270699	86	63	0.2	17	0.3	3.7
1270700	195	157	0.3	17	0.4	3.6
1270701	83	47	0.2	15	0.3	3.6
1270703	113	61	0.2	25	0.4	3.5
1270705	254	246	0.2	17	0.3	3.5
1270707	213	196	0.2	18	0.3	3.6
1270710	130	61	0.1	17	0.3	3.5
1270712	119	80	0.2	17	0.3	3.6
1270714	112	70	0.2	22	0.3	3.3
1270715	337	198	0.3	19	0.3	3.5
1270716	195	92	0.2	15	0.3	3.6

Blood obtained from rat groups at week 6 were sent to IDEXX BioResearch for measurement of blood cell counts. Counts taken include red blood cell (RBC) count, white blood cell (WBC) count, hemoglobin (HGB), hematocrit (HCT), Mean corpuscular volume (MCV), mean corpuscular hemoglobin (MCH), mean corpuscular hemoglobin concentration (MCHC), and individual white blood cell counts, such as that of monocytes (MON), neutrophils (NEU), lymphocytes (LYM), and platelets (PLT). The results are presented in the tables below. Ionis oligonucleotides that caused changes in the blood cell count outside the expected range for modified oligonucleotides were excluded in further studies.

Table 140. Blood Cell Count in Sprague-Dawley Rats

Compound No.	WBC (/nL)	RBC (/pL)	HGB (g/dL)	HCT (%)	MCV (fL)	MCH (pg)	MCH C (%)	NEU (%)	LYM (%)	MON (%)	PLT (/nL)
Saline	6	9	16	47	54	18	33	15	78	6	804
1270699	7	9	15	45	52	18	34	11	82	6	717
1270700	11	9	15	44	51	18	35	10	83	6	813
1270701	8	9	15	44	51	18	34	13	80	6	814
1270703	9	8	14	43	54	18	33	19	73	6	757
1270705	9	9	15	45	51	18	34	15	76	8	799
1270707	10	9	16	45	52	18	35	10	81	8	939
1270710	13	8	13	39	49	17	34	12	81	6	778
1270712	7	8	14	42	51	17	34	21	69	8	780
1270714	9	9	16	44	50	18	36	19	72	8	754
1270715	13	8	14	42	51	17	34	11	83	5	865
1270716	8	8	14	42	51	17	34	11	80	8	738

To evaluate the effect of Ionis oligonucleotides on kidney function, urinary levels of micro total protein (MTP) and creatinine were measured using an automated clinical chemistry analyzer (Hitachi Olympus AU400c, Melville, NY). The ratios of MTP to creatinine (MTP/C ratio) are presented in the table below. Ionis oligonucleotides that caused changes in the levels of the ratio outside the expected range for modified oligonucleotides were excluded in further studies.

Table 141. MTP to creatinine ratio in Sprague-Dawley rats

Compound No.	MTP/C Ratio
saline	1.0
1270699	2.5
1270700	1.0
1270701	1.6
1270703	1.3
1270705	1.2
1270707	1.8
1270710	2.6
1270712	1.2
1270714	0.9
1270715	3.1
1270716	2.5

Body weights of rats were measured at days 1 and 35, and the average body weight for each group is presented in the table below. Liver, spleen and kidney weights were measured at the end of the study, and are presented in the table below. Ionis oligonucleotides that caused any changes in organ weights outside the expected range for modified oligonucleotides were excluded from further studies.

Table 142. Body and organ weights (g)

Compound No.	Body Weight (g)		Liver Weight (g)	Kidney Weight (g)	Spleen Weight (g)
	Day 1	Day 35			
Saline	469	529	18	4.0	0.8
1270699	484	511	22	4.3	1.6
1270700	496	507	19	4.0	1.4
1270701	469	513	19	4.4	1.2
1270703	491	509	19	4.6	1.4
1270705	499	527	21	4.7	1.6
1270707	486	500	21	4.5	1.7
1270710	499	540	22	4.6	1.5
1270712	500	552	17	4.5	1.4
1270714	504	548	17	4.8	1.2
1270715	474	494	19	4.0	1.7
1270716	477	501	17	4.2	1.5

Example 12: Activity of modified oligonucleotides complementary to human FXII in transgenic mice, single dose

A transgenic mouse model was developed in-house using the Fosmid NCBI Clone DB ID: ABC12-49040200E6. The clone was digested at AgeI and NdeI restriction sites to produce a region containing the entire ~23kb portion of human *F12* gene, including regions 12kb upstream and 4kb downstream of the *F12* gene. The gene fragment was introduced into fertilized eggs from C57Bl/6 mice by pronuclear injection to produce FXII founder lines. Line 16459 was used in the experiments described herein. Human FXII RNA expression is found in the liver and circulating protein is found in plasma.

STUDY 1

Treatment

The transgenic mice were divided into groups of 2 female mice each for modified oligonucleotide treatment. Groups received subcutaneous injections of modified oligonucleotide at a dose of 2.5 mg/kg twice a week for two weeks (4 treatments). One group of two mice received subcutaneous injections of PBS twice a week for two weeks (4 treatments). The PBS-injected group served as the control group to which oligonucleotide-treated groups were compared.

RNA analysis

48 hours after the last treatment, mice were sacrificed and RNA was extracted from liver for real-time RTPCR analysis of FXII RNA expression. Human FXII primer probe sets RTS2992 (described herein above) and RTS40528 (described herein above) were used to measure human FXII RNA levels. FXII RNA levels were normalized to total RNA content, as measured by RIBOGREEN®. Reduction of FXII RNA is presented in the tables below as percent FXII RNA relative to the amount in PBS control animals (%control).

Table 143. Reduction of human FXII RNA in transgenic mice

Compound No.	FXII RNA (% control) in liver	
	RTS2992	RTS40528
PBS	100	100
1194343	2	9
1194347	15	20

Protein Analysis

Human FXII protein levels in plasma were determined using an Abcam FXII ELISA kit (ab192144). Reduction of FXII protein is presented in the tables below as percent FXII protein relative to the amount in PBS control animals (%control).

Table 144. Reduction of human FXII protein in transgenic mice

Compound No.	FXII protein (% control) in plasma
PBS	100
1194343	0.3
1194347	17

STUDY 2*Treatment*

The transgenic mice were divided into groups of 4 mice (2 male and 2 female) each for modified oligonucleotide treatment. Groups received subcutaneous injections of modified oligonucleotide at a dose of 1.5 mg/kg twice a week for two weeks (4 treatments). One group of four mice (2 male and 2 female) received subcutaneous injections of PBS twice a week for two weeks (4 treatments). The PBS-injected group served as the control group to which oligonucleotide-treated groups were compared.

RNA analysis

48 hours after the last treatment, mice were sacrificed and RNA was extracted from liver for real-time RTPCR analysis of FXII RNA expression. Human FXII primer probe sets RTS2992 (described herein above) and RTS40528 (described herein above) were used to measure human FXII RNA levels. FXII RNA levels were normalized to total RNA content, as measured by RIBOGREEN®. Reduction of FXII RNA is presented in the tables below as percent FXII RNA relative to the amount in PBS treated animals (% control).

Table 145. Reduction of human FXII RNA in transgenic mice

Compound No.	FXII RNA (% control) in liver	
	RTS2992	RTS40528
PBS	100	100
1194380	32	36
1194383	52	58
1194384	32	35
1194389	54	76
1194391	45	57
1194392	48	68

1194393	37	40
1194394	31	41
1194395	21	35
1194402	22	27
1194403	12	10
1194404	17	17
1194406	31	40
1194407	56	76
1194408	21	23
1194409	22	20
1194413	82	80
1194415	83	111
1194416	81	96
1194419	45	54
1194420	61	53
1194427	90	71
1194345	14	12
1194349	10	9
1194357	3	3
1194358	3	2
1194359	6	4
1194360	5	4
1194371	5	6
1194377	12	12
1194430	21	22

Protein Analysis

Human FXII protein levels in plasma were determined using an Abcam FXII ELISA kit (ab192144). Reduction of FXII protein is presented in the tables below as percent FXII protein relative to the amount in PBS treated animals (% control).

5

Table 146. Reduction of human FXII protein in transgenic mice

Compound No.	FXII protein (% control) in plasma
PBS	100
1194380	23
1194383	41
1194384	24
1194389	56
1194391	36
1194392	38
1194393	27
1194394	20
1194395	12
1194402	14
1194403	4

1194404	9
1194406	23
1194407	42
1194408	16
1194409	15
1194413	61
1194415	80
1194416	72
1194419	42
1194420	61
1194427	87
1194345	11
1194349	3
1194357	1
1194358	0
1194359	1
1194360	2
1194371	1
1194377	9
1194430	20

Example 13: Activity of modified oligonucleotides complementary to human FXII in transgenic mice, multiple dose

A transgenic mouse model was developed in-house using the Fosmid NCBI Clone DB ID: ABC12-49040200E6. The clone was digested at AgeI and NdeI restriction sites to produce a region containing the entire ~23kb portion of human *F12* gene, including regions 12kb upstream and 4kb downstream of the *F12* gene. The gene fragment was introduced into fertilized eggs from C57Bl/6 mice by pronuclear injection to produce FXII founder lines. Line 16459 was used in the experiments described herein. Human FXII RNA expression is found in the liver and circulating protein is found in plasma.

STUDY 1

10 *Treatment*

The transgenic mice were divided into groups of 2 female mice each for modified oligonucleotide treatment. Groups received subcutaneous injections of modified oligonucleotide at doses indicated in the table below twice a week for two weeks (4 treatments). One group of two mice received subcutaneous injections of PBS twice a week for two weeks (4 treatments). The PBS-injected group served as the control group to which oligonucleotide-treated groups were compared.

15

RNA analysis

48 hours after the last treatment, mice were sacrificed and RNA was extracted from liver for real-time RTPCR analysis of FXII RNA expression. Human FXII primer probe set RTS2992 (described herein above) was used to measure human FXII RNA levels. FXII RNA levels were normalized to total RNA

content, as measured by RIBOGREEN®. Reduction of FXII RNA is presented in the tables below as percent FXII RNA relative to the amount in PBS treated animals (% control).

Table 147. Reduction of human FXII RNA in transgenic mice

Compound No.	Concentration (mpk)	RTS2992	
		FXII RNA (% control) in liver	ED50 (mpk)
1194347	0.32	75	1.292
	0.8	59	
	2	50	
	5	14	

Protein Analysis

- 5 Human FXII protein levels in plasma were determined using an Abcam FXII ELISA kit (ab192144). Reduction of FXII protein is presented in the tables below as percent FXII protein relative to the amount in PBS treated animals (% control).

Table 148. Reduction of human FXII protein in transgenic mice

Compound No.	Concentration (mpk)	FXII protein (% control) in plasma	ED50 (mpk)
1194347	0.32	78	1.073
	0.8	64	
	2	31	
	5	11	

STUDY 2

10 *Treatment*

The transgenic mice were divided into groups of four mice (2 male and 2 female) each for modified oligonucleotide treatment. Groups received subcutaneous injections of modified oligonucleotide at doses indicated in the table below twice a week for two weeks (4 treatments). One group of four mice (2 male and 2 female) received subcutaneous injections of PBS twice a week for two weeks (4 treatments). The PBS-

15 injected group served as the control group to which oligonucleotide-treated groups were compared.

RNA analysis

- 48 hours after the last treatment, mice were sacrificed and RNA was extracted from liver for real-time RTPCR analysis of FXII RNA expression. Human FXII primer probe set RTS2992 (described herein above) was used to measure human FXII RNA levels. FXII RNA levels were normalized to total RNA
- 20 content, as measured by RIBOGREEN®. Reduction of FXII RNA is presented in the tables below as percent FXII RNA relative to the amount in PBS treated animals (% control).

Table 149. Reduction of human FXII RNA in transgenic mice

Compound No.	Concentration (mpk)	FXII RNA (% control) in liver (RTS2992)	ED50 (mpk)
1194357	0.08	60	0.07514
	0.1	33	
	0.2	27	
	0.3	14	
	0.6	8	
	0.9	4	
1194349	0.1	60	0.4603
	0.3	61	
	0.9	25	
1194358	0.1	47	0.08653
	0.3	18	
	0.9	9	
1194359	0.1	80	0.1997
	0.3	36	
	0.9	9	
1194371	0.1	114	0.2737
	0.3	35	
	0.9	10	
1194377	0.1	91	0.5223
	0.3	70	
	0.9	28	
1270699	0.1	79	0.1731
	0.3	31	
	0.9	6	
1270700	0.1	57	0.1211
	0.3	21	
	0.9	4	
1270701	0.1	38	0.1871
	0.3	41	
	0.9	6	
1270702	0.1	59	0.1816
	0.3	22	
	0.9	6	
1270703	0.08	76	0.2228
	0.2	71	
	0.6	11	
1270705	0.08	62	0.113
	0.2	33	

	0.6	12	
1270707	0.08	82	0.2085
	0.2	57	
	0.6	14	
1270710	0.08	92	0.265
	0.2	61	
	0.6	19	
1270712	0.08	92	0.3297
	0.2	63	
	0.6	14	
1270714	0.08	57	0.3936
	0.2	47	
	0.6	25	
1270715	0.08	69	0.3242
	0.2	57	
	0.6	20	
1270716	0.08	58	0.3093
	0.2	52	
	0.6	20	

Protein Analysis

Human FXII protein levels in plasma were determined using an Abcam FXII ELISA kit (ab192144). Reduction of FXII protein is presented in the tables below as percent FXII protein relative to the amount in PBS treated animals (% control).

5

Table 150. Reduction of human FXII protein in transgenic mice

Compound No.	Concentration (mpk)	FXII protein (% control) in plasma	ED50 (mpk)
1194357	0.08	67	0.065
	0.1	43	
	0.2	25	
	0.3	15	
	0.6	3	
	0.9	6	
1194349	0.1	84	0.2799
	0.3	48	
	0.9	13	
1194358	0.1	52	0.09148
	0.3	20	
	0.9	5	

1194359	0.1	53	0.0959
	0.3	22	
	0.9	3	
1194371	0.1	65	0.1356
	0.3	29	
	0.9	3	
1194377	0.1	80	0.2882
	0.3	50	
	0.9	16	
1270699	0.1	62	0.1153
	0.3	22	
	0.9	4	
1270700	0.1	53	0.08752
	0.3	17	
	0.9	1	
1270701	0.1	42	0.08131
	0.3	27	
	0.9	5	
1270702	0.1	65	0.1331
	0.3	27	
	0.9	4	
1270703	0.08	79	0.1572
	0.2	41	
	0.6	7	
1270705	0.08	66	0.1174
	0.2	36	
	0.6	7	
1270707	0.08	77	0.1668
	0.2	46	
	0.6	8	
1270710	0.08	86	0.2288
	0.2	56	
	0.6	13	
1270712	0.08	86	0.2467
	0.2	58	
	0.6	16	
1270714	0.08	93	0.3053
	0.2	62	
	0.6	24	
1270715	0.08	89	0.3739
	0.2	62	
	0.6	37	

1270716	0.08	89	0.3447
	0.2	71	
	0.6	25	

STUDY 3

Treatment

The transgenic mice were divided into groups of four mice (2 male and 2 female) each for modified oligonucleotide treatment. Groups received subcutaneous injections of modified oligonucleotide at doses indicated in the table below twice a week for two weeks (4 treatments). One group of four mice (2 male and 2 female) received subcutaneous injections of PBS twice a week for two weeks (4 treatments). The PBS-injected group served as the control group to which oligonucleotide-treated groups were compared.

RNA analysis

72 hours after the last treatment, mice were sacrificed and RNA was extracted from liver for real-time RTPCR analysis of FXII RNA expression. Human FXII primer probe sets RTS2992 (described herein above) was used to measure human FXII RNA levels. FXII RNA levels were normalized to total RNA content, as measured by RIBOGREEN®. Reduction of FXII RNA is presented in the tables below as percent FXII RNA relative to the amount in PBS treated animals (% control).

Table 151. Reduction of human FXII RNA in transgenic mice

Compound No.	Concentration (mpk)	RTS2992	
		FXII RNA (% control) in liver	ED50 (mpk)
1194371	0.075	94	0.2457
	0.15	57	
	0.3	47	
	0.6	22	
	1.2	10	

Example 14: Effect of modified oligonucleotides on human FXII mRNA *in vitro*, multiple doses

Modified oligonucleotides selected from the examples above were tested at various doses in Huh7 cells. Cultured Huh7 cells at a density of 20,000 cells per well were transfected by electroporation with various concentrations of modified oligonucleotide as specified in the table below. After a treatment period of approximately 24 hours, total RNA was isolated from the cells, and FXII mRNA levels were measured by quantitative real-time RTPCR. Human FXII primer probe set RTS40528 (described herein above) was used to measure RNA levels. FXII levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Reduction of FXII RNA is presented in the tables below as percent FXII RNA relative to the amount in untreated control cells (% UTC). The half maximal inhibitory concentration (IC₅₀) of each modified

oligonucleotide was calculated in GraphPad Prism using the log (inhibitor) vs. normalized response – variable slope method.

Four comparator compounds from WO 2017/120397 were added to the study. These include Compound Nos. 1213034, 1358035, 1213030 and 1213029 designated as A-145676, A-145669, A-145668, and A-145667 respectively in WO 2017/120397.

Table 152. Dose-dependent reduction of human FXII RNA by modified oligonucleotides

Compound No.	FXII RNA (%UTC)					IC50 (μM)
	10μM	2μM	0.4μM	0.08μM	0.016μM	
1129485	7	15	44	81	98	0.34
1129486	8	18	51	96	97	0.48
1207006	8	10	28	52	84	0.1
1207160	17	18	30	58	65	0.09
1207161	12	20	27	68	83	0.17
1207277	6	9	29	59	84	0.13
1207279	12	29	45	80	95	0.43
1207393	7	14	26	63	83	0.14
1213260	12	18	26	62	87	0.15
1213144	8	25	37	71	95	0.28
Comparator Compounds						
1213030	43	84	132	132	94	8.15
1213034	69	116	139	127	92	>10
1213029	63	123	146	130	98	>10
1358035	43	93	127	121	104	8.59

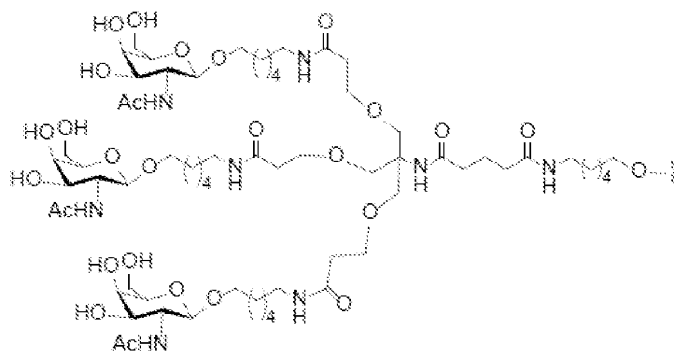
CLAIMS:

1. An oligomeric compound comprising a modified oligonucleotide consisting of 12 to 50 linked nucleosides wherein the nucleobase sequence of the modified oligonucleotide is at least 90% complementary to an equal length portion of a FXII RNA, and wherein the modified oligonucleotide comprises at least one modification selected from a modified sugar moiety and a modified internucleoside linkage.
2. An oligomeric compound comprising a modified oligonucleotide consisting of 12 to 50 linked nucleosides and having a nucleobase sequence comprising at least 12, 13, 14, 15, 16, 17, 18, 19, or 20 contiguous nucleobases of any of SEQ ID NOs: 20-5042.
3. An oligomeric compound comprising a modified oligonucleotide consisting of 12 to 50 linked nucleosides and having a nucleobase sequence comprising at least 12, 13, 14, 15, 16, 17, or 18 contiguous nucleobases of any of SEQ ID NOs: 3379 and 5006.
4. An oligomeric compound comprising a modified oligonucleotide consisting of 12 to 50 linked nucleosides and having a nucleobase sequence comprising at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, or at least 20 contiguous nucleobases complementary to:
 - an equal length portion of nucleobases 1,899-1,979 of SEQ ID NO: 1; or
 - an equal length portion of nucleobases 2,004-2,045 of SEQ ID NO: 1.
5. An oligomeric compound comprising a modified oligonucleotide consisting of 12 to 50 linked nucleosides and having a nucleobase sequence comprising at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, or at least 18 contiguous nucleobases of a sequence selected from:
 - SEQ ID NOs: 92, 156, 270, 271, 345, 346, 420, 421, 496, 497, 571, 572, 653, 654, 728, 729, 802, 803, 877, 951, 1028, 1103, 1179, 1253, 1330, 1407, 1484, 1560, 1636, 1710, 1711, 1784, 1859, 1860, 1934, 1935, 2008, 2009, 2084, 2085, 2158, 2232, 2233, 2307, 2308, 2393, 2394, 2395, 2396, 2397, 2398, 2461, 2537, 2538, 2614, 2615, 2691, 2692, 2768, 2769, 2845, 2846, 2921, 2922, 2997, 2998, 3073, 3074, 3144, 3145, 3226, 3227, 3303, 3304, 3379, 3380, 3455, 3456, 3531, 3607, 3683, 3759, 3835, 3911, 4948, 4949, 4954, 4955, 4956, 4957, 4961, 4965, 4966, 4967, 4971, 4972, 4976, 4994, 4995, 4996, 4997, 4998, 4999, 5024, 5025, 5026, 5027, 5028, and 5029; or
 - SEQ ID NOs: 95, 159, 162, 163, 164, 165, 347, 422, 498, 573, 953, 1030, 1105, 1255, 1332, 1409, 1486, 1562, 2309, 2463, 2540, 2617, 2694, 2771, 2848, 2924, 3000, 3076, 3147, 3229, 3306, 3382, 3457, 3533, 3609, 3685, 3761, 3837, 3913, 5000, 5001, 5002, 5003, 5004, 5005, 5006, 5031, 5032, 5033, 5034, 5035, 5036, and 5037.
6. The oligomeric compound of any of claims 1-5, wherein the modified oligonucleotide has a nucleobase sequence that is at least 80%, 85%, 90%, 95%, or 100% complementary to the nucleobase sequence of

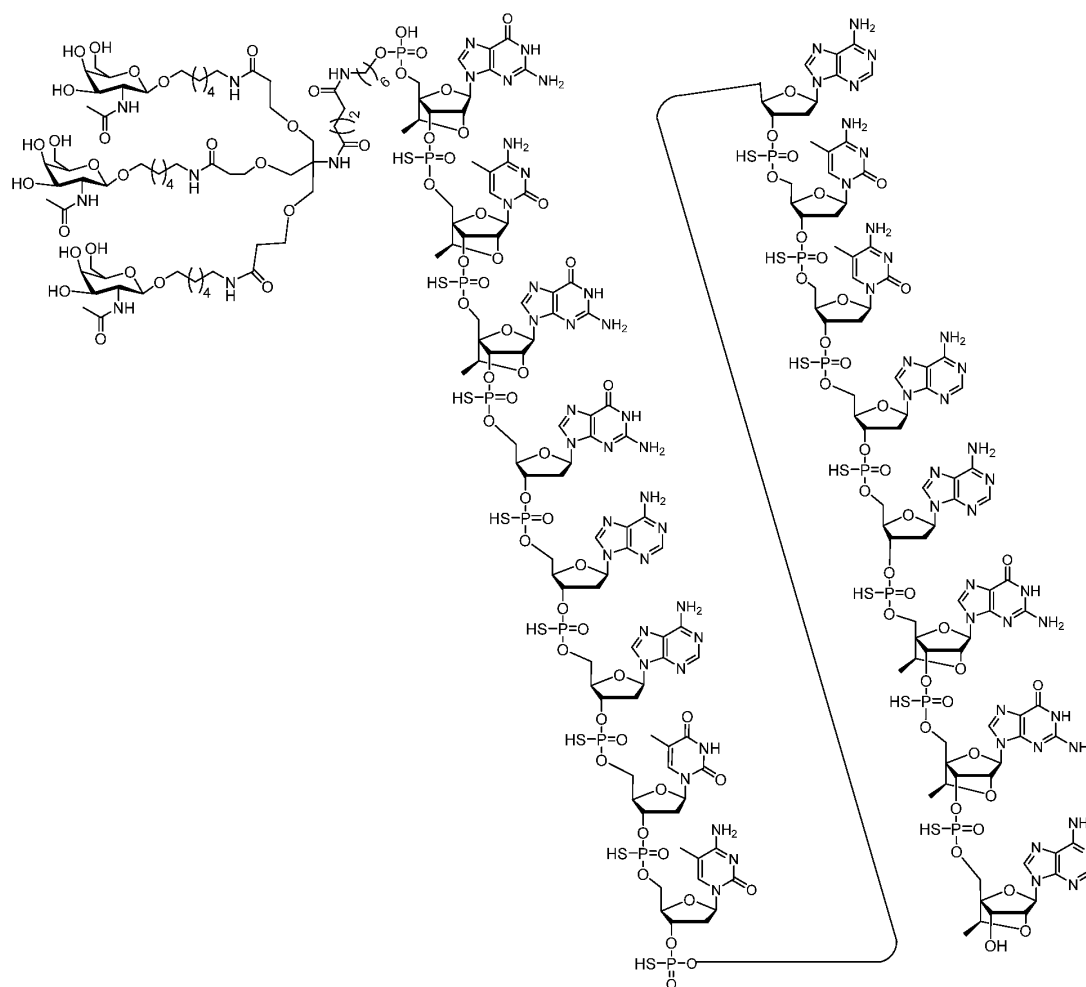
any one of SEQ ID NOS: 1-4 when measured across the entire nucleobase sequence of the modified oligonucleotide.

7. The oligomeric compound of any of claims 1-6, wherein the modified oligonucleotide comprises at least one modified nucleoside.
8. The oligomeric compound of claim 7, wherein the modified oligonucleotide comprises at least one modified nucleoside comprising a modified sugar moiety.
9. The oligomeric compound of claim 8, wherein the modified oligonucleotide comprises at least one modified nucleoside comprising a bicyclic sugar moiety.
10. The oligomeric compound of claim 9, wherein the modified oligonucleotide comprises at least one modified nucleoside comprising a bicyclic sugar moiety having a 2'-4' bridge, wherein the 2'-4' bridge is selected from -O-CH₂-; and -O-CH(CH₃)-.
11. The oligomeric compound of any of claims 8-10, wherein the modified oligonucleotide comprises at least one modified nucleoside comprising a non-bicyclic modified sugar moiety.
12. The oligomeric compound of claim 11, wherein the non-bicyclic modified sugar moiety is a 2'-MOE sugar moiety or 2'-OMe sugar moiety.
13. The oligomeric compound of any of claims 7-8, wherein the modified oligonucleotide comprises at least one modified nucleoside comprising a sugar surrogate.
14. The oligomeric compound of any of claims 1-13, wherein the modified oligonucleotide is a gapmer.
15. The oligomeric compound of any of claims 1-14, wherein the modified oligonucleotide has a sugar motif comprising:
 - a 5'-region consisting of 1-6 linked 5'-region nucleosides;
 - a central region consisting of 6-10 linked central region nucleosides; and
 - a 3'-region consisting of 1-6 linked 3'-region nucleosides,wherein each of the 5'-region nucleosides and each of the 3'-region nucleosides comprises a modified sugar moiety and each of the central region nucleosides comprises a 2'-β-D-deoxyribosyl sugar moiety.
16. The oligomeric compound of claim 15, wherein
 - the 5'-region consists of 3 linked 5'-region nucleosides;
 - the central region consists of 10 linked central region nucleosides; and
 - the 3'-region consists of 3 linked 3'-region nucleosides, andwherein each of the 5'-region nucleosides and each of the 3'-region nucleosides comprises a cEt modified sugar moiety.
17. The oligomeric compound of any of claims 1-16, wherein the modified oligonucleotide comprises at least one modified internucleoside linkage.
18. The oligomeric compound of claim 17, wherein each internucleoside linkage of the modified oligonucleotide is a modified internucleoside linkage.

19. The oligomeric compound of claim 17 or 18, wherein each internucleoside linkage is a phosphorothioate internucleoside linkage.
20. The oligomeric compound of claim 17 or 18, wherein the modified oligonucleotide comprises at least one phosphodiester internucleoside linkage.
21. The oligomeric compound of claim 17, wherein each internucleoside linkage is independently selected from a phosphodiester internucleoside linkage or a phosphorothioate internucleoside linkage.
22. The oligomeric compound of any of claims 1-21, wherein the modified oligonucleotide comprises a modified nucleobase.
23. The oligomeric compound of claim 22, wherein the modified nucleobase is a 5-methyl cytosine.
24. The oligomeric compound of any of claims 1-23, wherein the modified oligonucleotide consists of 12-30, 12-22, 12-20, 14-18, 14-20, 15-17, 15-25, 16-20, 18-22 or 18-20 linked nucleosides.
25. The oligomeric compound of any of claims 1-23, wherein the modified oligonucleotide consists of 16 linked nucleosides.
26. The oligomeric compound of any of claims 1-25, consisting of the modified oligonucleotide.
27. The oligomeric compound of any of claims 1-25, comprising a conjugate group comprising a conjugate moiety and a conjugate linker.
28. The oligomeric compound of claim 27, wherein the conjugate linker consists of a single bond.
29. The oligomeric compound of claim 27, wherein the conjugate linker is cleavable.
30. The oligomeric compound of claim 27, wherein the conjugate linker comprises 1-3 linker-nucleosides.
31. The oligomeric compound of 27, wherein the oligomeric compound does not comprise a linker-nucleoside.
32. The oligomeric compound of claim 27, wherein the conjugate linker is a phosphate.
33. The oligomeric compound of any of claims 29-32, wherein the conjugate group is attached to the modified oligonucleotide at the 5'-end of the modified oligonucleotide.
34. The oligomeric compound of any of claims 29-32, wherein the conjugate group is attached to the modified oligonucleotide at the 3'-end of the modified oligonucleotide.
35. The oligomeric compound of any of claims 1-34, comprising a terminal group.
36. The oligomeric compound of any one of claims 1-35, wherein the conjugate group comprises a GalNAc moiety.
37. The oligomeric compound of anyone of claims 1-36, wherein the conjugate group comprises a cell-targeting moiety, a conjugate linker and a cleavable moiety, and wherein the cell-targeting moiety and the conjugate linker together have the following chemical structure:

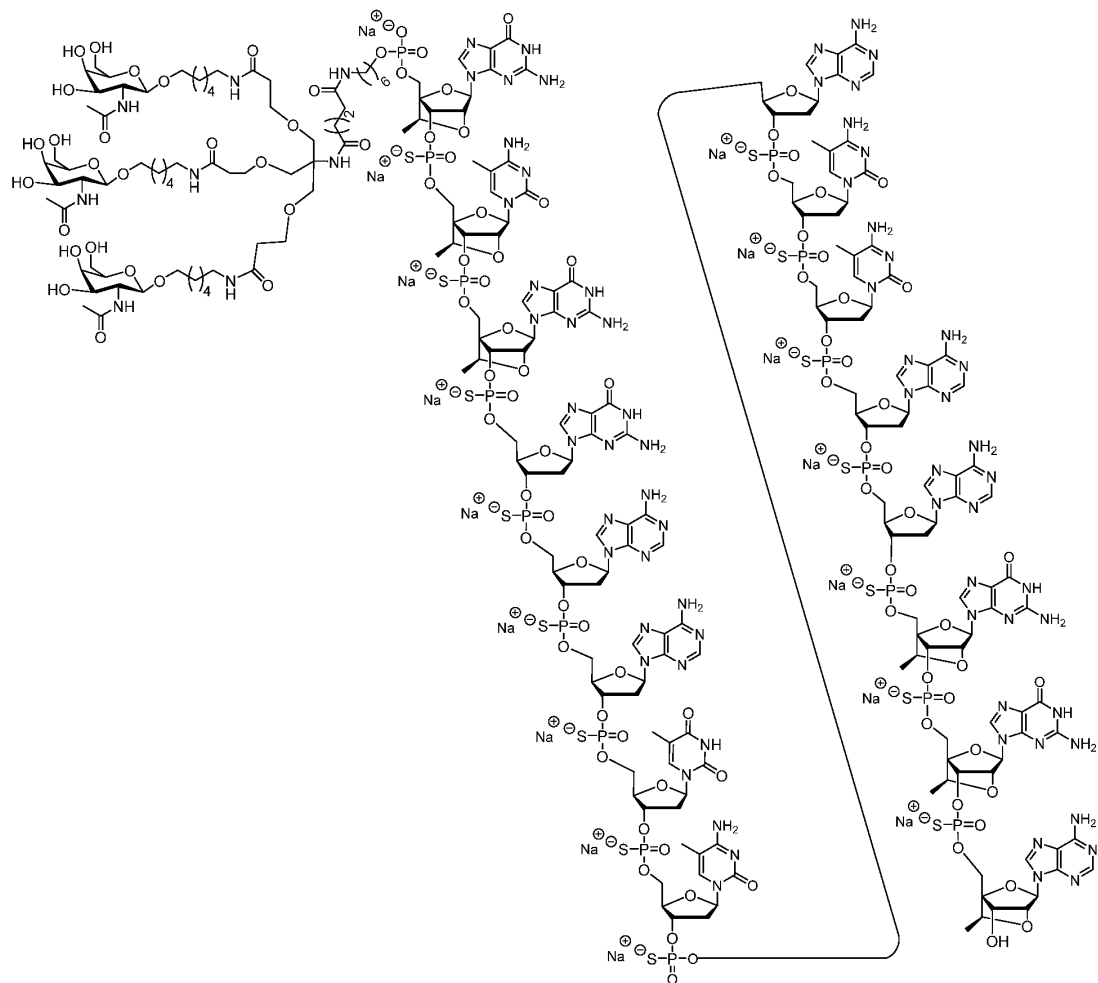


38. The oligomeric compound of any of claims 1-37 wherein the modified oligonucleotide is a single-stranded modified oligonucleotide.
39. An oligomeric compound according to the following chemical structure:



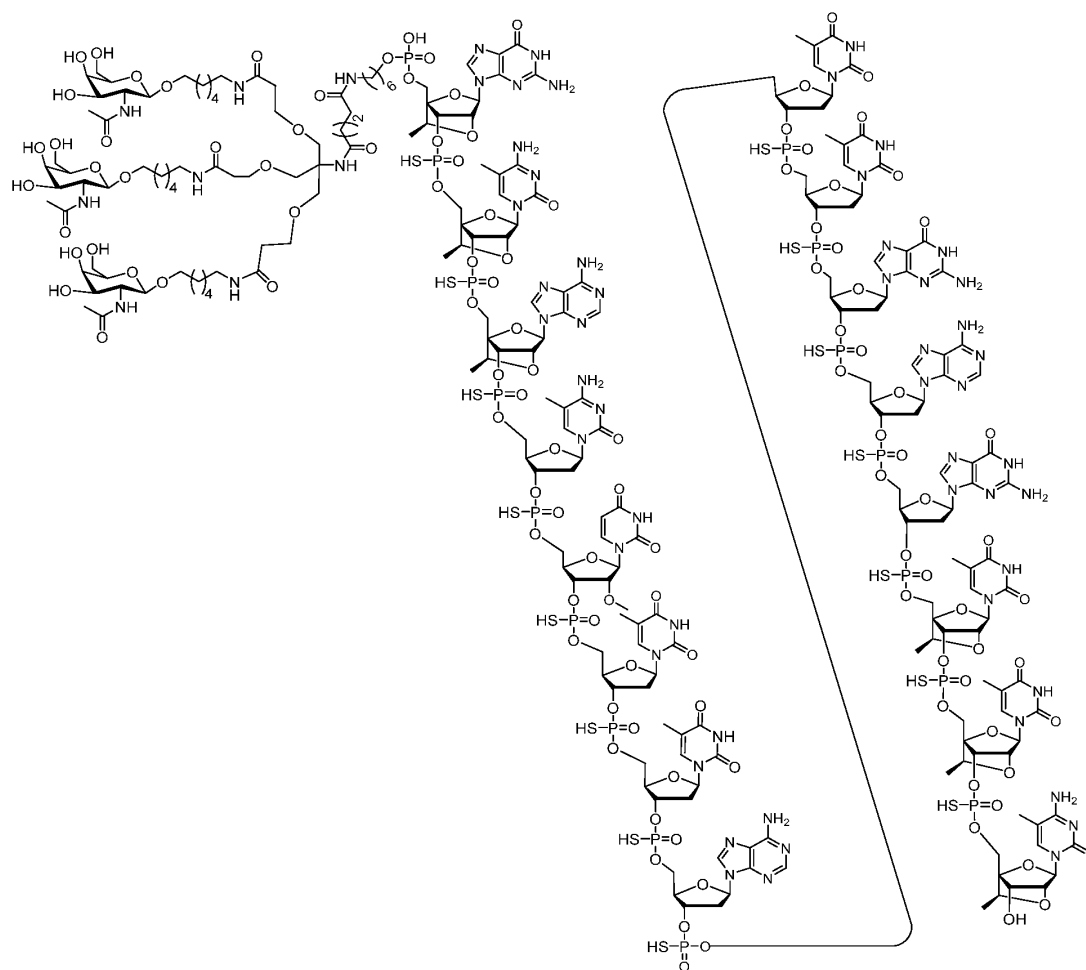
(SEQ ID NO: 3379), or a salt thereof.

40. The oligomeric compound of claim 39, which is the sodium salt or the potassium salt.
41. An oligomeric compound according to the following chemical structure:



(SEQ ID NO: 3379).

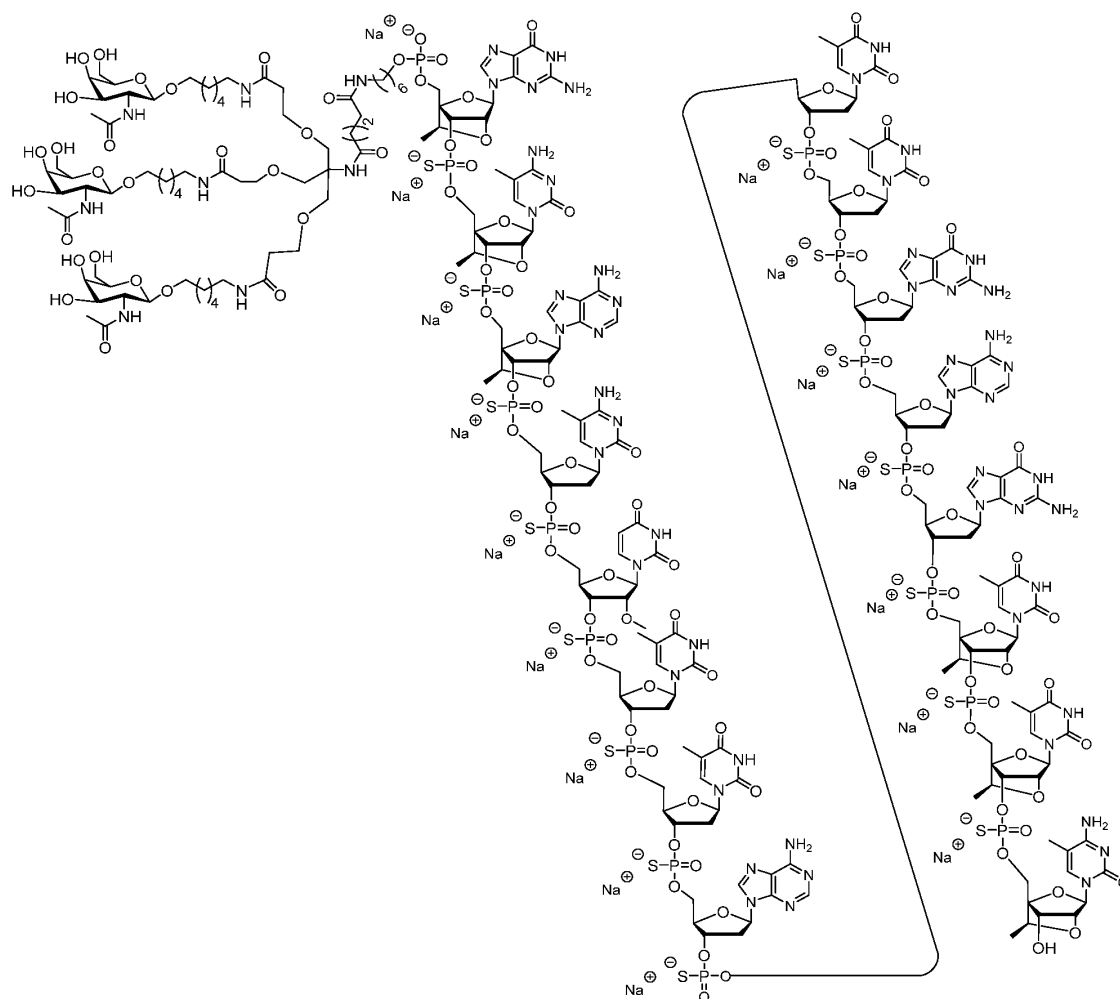
42. An oligomeric compound according to the following chemical structure:



(SEQ ID NO: 5006), or a salt thereof.

43. The oligomeric compound of claim 42, which is the sodium salt or the potassium salt.

44. An oligomeric compound according to the following chemical structure:



(SEQ ID NO: 5006).

45. An oligomeric compound comprising a modified oligonucleotide according to the following chemical notation: (THA- GalNAc₃)_o Gks ^mCks Gks Gds Ads Ads Tds ^mCds Ads ^mCds ^mCds Ads Ads Gks Gks Ak (SEQ ID NO: 3379), wherein:

- A = an adenine nucleobase,
- mC = a 5-methyl cytosine nucleobase,
- G = a guanine nucleobase,
- T = a thymine nucleobase,
- k = a cEt modified sugar moiety,
- d = a 2'-β-D-deoxyribsyl sugar moiety,
- o = a phosphodiester linkage, and

s = a phosphorothioate internucleoside linkage.

46. An oligomeric compound comprising a modified oligonucleotide according to the following chemical notation: (THA- GalNAc₃)_o Gks ^mCks Aks ^mCds Uys Tds Tds Ads Tds Tds Gds Ads Gds Tks Tks mCk (SEQ ID NO: 5006), wherein:

A = an adenine nucleobase,

mC = a 5-methyl cytosine nucleobase,

G = a guanine nucleobase,

T = a thymine nucleobase,

U = a uracil nucleobase,

k = a cEt modified sugar moiety,

y = a 2'-O-methyl modified ribosyl sugar moiety,

d = a 2'-β-D-deoxyribosyl sugar moiety,

o = a phosphodiester linkage, and

s = a phosphorothioate internucleoside linkage.

47. An oligomeric duplex comprising a first oligomeric compound and a second oligomeric compound comprising a second modified oligonucleotide, wherein the first oligomeric compound is an oligomeric compound of any of claims 1 to 37.
48. The oligomeric duplex of claim 47, wherein the second oligomeric compound comprises a second modified oligonucleotide consisting of 8 to 80 linked nucleosides, and wherein the nucleobase sequence of the second modified oligonucleotide comprises a complementary region of at least 8 nucleobases that is at least 90% complementary to an equal length portion of the first modified oligonucleotide.
49. The oligomeric duplex of claim 47 or 48, wherein the modified oligonucleotide of the first oligomeric compound comprises a 5'-stabilized phosphate group.
50. The oligomeric duplex of claim 49, wherein the stabilized phosphate group comprises a cyclopropyl phosphonate or a vinyl phosphonate.
51. The oligomeric duplex of any of claims 47 to 50, wherein at least one nucleoside of the second modified oligonucleotide comprises a modified sugar moiety.
52. The oligomeric duplex of claim 51, wherein the modified sugar moiety of the second modified oligonucleotide comprises a bicyclic sugar moiety.
53. The oligomeric duplex of claim 52, wherein the bicyclic sugar moiety of the second modified oligonucleotide comprises a 2'-4' bridge selected from -O-CH₂-; and -O-CH(CH₃)-.
54. The oligomeric duplex of claim 51, wherein the modified sugar moiety of the second modified oligonucleotide comprises a non-bicyclic modified sugar moiety.
55. The oligomeric duplex of claim 54, wherein the non-bicyclic modified sugar moiety of the second modified oligonucleotide is a 2'-MOE sugar moiety, a 2'-F sugar moiety, or 2'-OMe sugar moiety.

56. The oligomeric duplex of any of claims 47 to 55, wherein at least one nucleoside of the second modified oligonucleotide comprises a sugar surrogate.
57. The oligomeric duplex of any of claims 47 to 56, wherein at least one internucleoside linkage of the second modified oligonucleotide is a modified internucleoside linkage.
58. The oligomeric duplex of claim 57, wherein at least one modified internucleoside linkage of the second modified oligonucleotide is a phosphorothioate internucleoside linkage.
59. The oligomeric duplex of any of claims 47 to 58, wherein at least one internucleoside linkage of the second modified oligonucleotide is a phosphodiester internucleoside linkage.
60. The oligomeric duplex of any of claims 47 to 59, wherein each internucleoside linkage of the second modified oligonucleotide is independently selected from a phosphodiester or a phosphorothioate internucleoside linkage.
61. The oligomeric duplex of any of claims 47 to 60, wherein the second modified oligonucleotide comprises at least one modified nucleobase.
62. The oligomeric duplex of claim 61, wherein the modified nucleobase of the second modified oligonucleotide is 5-methylcytosine.
63. The oligomeric duplex of any of claims 47 to 62, wherein the second modified oligonucleotide comprises a conjugate group.
64. The oligomeric duplex of claim 63, wherein the conjugate group comprises a conjugate linker and a conjugate moiety.
65. The oligomeric duplex of claim 63 or 64, wherein the conjugate group is attached to the second modified oligonucleotide at the 5'-end of the second modified oligonucleotide.
66. The oligomeric duplex of claim 63 or 64, wherein the conjugate group is attached to the second modified oligonucleotide at the 3'-end of the second modified oligonucleotide.
67. The oligomeric duplex of any of claims 63 to 66, wherein the conjugate group comprises a GalNAc₃.
68. The oligomeric duplex of any of claims 47 to 62, wherein the second modified oligonucleotide comprises a terminal group.
69. The oligomeric duplex of claim 68, wherein the terminal group is an abasic sugar moiety.
70. The oligomeric duplex of any of claims 47 to 69, wherein the second modified oligonucleotide consists of 10 to 25, 10 to 30, 10 to 50, 12 to 20, 12 to 25, 12 to 30, 12 to 50, 13 to 20, 13 to 25, 13 to 30, 13 to 50, 14 to 20, 14 to 25, 14 to 30, 14 to 50, 15 to 20, 15 to 25, 15 to 30, 15 to 50, 16 to 18, 16 to 20, 16 to 25, 16 to 30, 16 to 50, 17 to 20, 17 to 25, 17 to 30, 17 to 50, 18 to 20, 18 to 25, 18 to 30, 18 to 50, 19 to 20, 19 to 25, 19 to 30, 19 to 50, 20 to 25, 20 to 30, 20 to 50, 21 to 25, 21 to 30, 21 to 50, 22 to 25, 22 to 30, 22 to 50, 23 to 25, 23 to 30, or 23 to 50 linked nucleosides.
71. An antisense compound comprising or consisting of an oligomeric compound of any of claims 1-37 or an oligomeric duplex of claims 47-70.

72. A chirally enriched population of oligomeric compounds of any of claims 1-46, wherein the population is enriched for oligomeric compounds comprising at least one particular phosphorothioate internucleoside linkage having a particular stereochemical configuration.
73. The chirally enriched population of claim 72, wherein the population is enriched for oligomeric compounds comprising at least one particular phosphorothioate internucleoside linkage having the (*Sp*) configuration.
74. The chirally enriched population of claim 72, wherein the population is enriched for oligomeric compounds comprising at least one particular phosphorothioate internucleoside linkage having the (*Rp*) configuration.
75. The chirally enriched population of claim 72, wherein the population is enriched for oligomeric compounds having a particular, independently selected stereochemical configuration at each phosphorothioate internucleoside linkage
76. The chirally enriched population of claim 72, wherein the population is enriched for oligomeric compounds having the (*Sp*) configuration at each phosphorothioate internucleoside linkage.
77. The chirally enriched population of claim 72, wherein the population is enriched for oligomeric compounds having the (*Rp*) configuration at each phosphorothioate internucleoside linkage.
78. The chirally enriched population of claim 72, wherein the population is enriched for oligomeric compounds having the (*Rp*) configuration at one particular phosphorothioate internucleoside linkage and the (*Sp*) configuration at each of the remaining phosphorothioate internucleoside linkages.
79. The chirally enriched population of any one of claims 72-74, wherein the population is enriched for oligomeric compounds having at least 3 contiguous phosphorothioate internucleoside linkages in the *Sp*, *Sp*, and *Rp* configurations, in the 5' to 3' direction.
80. A population of oligomeric compounds of any of claims 1-46, wherein all of the phosphorothioate internucleoside linkages of the oligomeric compounds are stereorandom.
81. A pharmaceutical composition comprising an oligomeric compound of any of claims 1-46, an oligomeric duplex of any one of claims 47-70, an antisense compound of claim 71, or a population of any one of claims 72-80; and a pharmaceutically acceptable carrier or diluent.
82. The pharmaceutical composition of claim 81, wherein the pharmaceutically acceptable diluent is phosphate buffered saline.
83. The pharmaceutical composition of claim 82, wherein the pharmaceutical composition consists or consists essentially of the modified oligonucleotide and phosphate buffered saline.
84. A method comprising administering to a subject a pharmaceutical composition of any of claims 81-83.
85. A method of ameliorating or preventing a thromboembolic condition, comprising administering to a subject in need thereof a therapeutically effective amount of a pharmaceutical composition according to any of claims 81-83.

86. The method of claim 85, wherein the thromboembolic condition is selected from myocardial infarction (MI), stroke, limb ischemia and necrosis, venous thromboembolism (VTE), deep vein thrombosis (DVT), and pulmonary embolism (PE).
87. The method of any of claims 84-86, wherein at least one symptom of the thromboembolic condition is ameliorated.
88. The method of claim 87, wherein the symptom is pain, shortness of breath, heart burn, cold sweat, fatigue, lightheadedness, dizziness, swelling, cramping, and death.
89. The method of any one of claims 84-88, further comprising identifying the subject as having the thromboembolic condition or as having a risk factor for having the thromboembolic condition.
90. The method of claim 89, wherein the risk factor is surgery, malignancy, pregnancy, aging, use of oral contraceptives, immobility, sepsis, a mechanical heart valve, valvular heart disease, atrial fibrillation, atherosclerosis, antiphospholipid syndrome, an inherited clotting disorder, or an acquired prothrombotic clotting disorder.
91. A method of ameliorating or preventing hereditary angioedema, comprising administering to a subject in need thereof a therapeutically effective amount of a pharmaceutical composition according to any of claims 81-83.
92. The oligomeric compound of any of claims 1-46, the oligomeric duplex of any one of claims 47-70, the antisense compound of claim 71, or the population of any one of claims 72-80, for use in therapy.
93. The oligomeric compound of any of claims 1-46, the oligomeric duplex of any one of claims 47-70, the antisense compound of claim 71, or the population of any one of claims 72-80, for use in ameliorating or preventing a thromboembolic condition.
94. The oligomeric compound of any of claims 1-46, the oligomeric duplex of any one of claims 47-70, the antisense compound of claim 71, or the population of any one of claims 72-80, for use in ameliorating or preventing hereditary angioedema.