

MODULATORS OF IRF4 EXPRESSION

Sequence Listing

5 The present application is being filed along with a Sequence Listing in electronic format. The Sequence Listing is provided as a file entitled BIOL0332WOSEQ.txt created January 14, 2019, which is 712 kb in size. The information in the electronic format of the sequence listing is incorporated herein by reference in its entirety.

Field

10 The present embodiments provide methods, compounds, and compositions useful for inhibiting IRF4 expression, which can be useful for treating, preventing, or ameliorating a cancer associated with IRF4.

Background

15 Interferon Regulatory Factor 4 (IRF4) is a transcription factor involved in immune responses in normal B and T cells, and is strongly implicated in the development of hematological malignancies, especially multiple myeloma (MM). High IRF4 levels is associated with a poor prognosis of overall survival for MM patients. Upregulation of the cereblon/IRF4 pathway accounts for the failure of lenalidomide treatment, an IMiD approved for MM and B cell malignancies. IRF4 is a component of super enhancer in MM cells in which a positive auto-regulatory loop between the oncogene MYC and IRF4 sustains the survival of MM. IRF4 is also
20 involved in cutaneous anaplastic large cell lymphomas DLBCL, B-cell non-Hodgkin's lymphoma, ALL, adult T cell leukemia/lymphoma (ATLL), and peripheral T cell lymphoma. Despite its role in many cancers, IRF4 is considered an undruggable target by conventional therapeutic approaches.

Summary

25 Certain embodiments provided herein are directed to potent and tolerable compounds and compositions useful for inhibiting IRF4 expression, which can be useful for treating, preventing, ameliorating, or slowing progression of cancer associated with IRF4.

Detailed Description

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 of the embodiments, as claimed. Herein, the use of
30 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.

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, treatises, and GenBank and NCBI reference sequence records are hereby expressly incorporated by reference for the portions of the document discussed herein, as well as in their entirety.

It is understood that the sequence set forth in each SEQ ID NO in the examples contained herein is independent of any modification to a sugar moiety, an internucleoside linkage, or a nucleobase. As such, compounds defined by a SEQ ID NO may comprise, independently, one or more modifications to a sugar moiety, an internucleoside linkage, or a nucleobase. Compounds described by ION number indicate a combination of nucleobase sequence, chemical modification, and motif.

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

“2'-deoxynucleoside” means a nucleoside comprising 2'-H(H) furanosyl sugar moiety, as found in naturally occurring deoxyribonucleic acids (DNA). In certain embodiments, a 2'-deoxynucleoside may comprise a modified nucleobase or may comprise an RNA nucleobase (uracil).

“2'-O-methoxyethyl” (also 2'-MOE and 2'-O(CH₂)₂-OCH₃) refers to an O-methoxy-ethyl modification at the 2' position of a furanosyl ring. A 2'-O-methoxyethyl modified sugar is a modified sugar.

“2'-MOE nucleoside” (also 2'-O-methoxyethyl nucleoside) means a nucleoside comprising a 2'-MOE modified sugar moiety.

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

“3' target site” refers to the nucleotide of a target nucleic acid which is complementary to the 3'-most nucleotide of a particular compound.

“5' target site” refers to the nucleotide of a target nucleic acid which is complementary to the 5'-most nucleotide of a particular compound.

“5-methylcytosine” means a cytosine with a methyl group attached to the 5 position.

“About” means within $\pm 10\%$ of a value. For example, if it is stated, “the compounds affected about 70% inhibition of IRF4”, it is implied that IRF4 levels are inhibited within a range of 60% and 80%.

“Administration” or “administering” refers to routes of introducing a compound or composition provided herein to an individual to perform its intended function. An example of a route of administration that can be used includes, but is not limited to parenteral administration, such as subcutaneous, intravenous, or intramuscular injection or infusion.

“Administered concomitantly” or “co-administration” means administration of two or more compounds in any manner in which the pharmacological effects of both are manifest in the patient. Concomitant administration does not require that both compounds be administered in a single pharmaceutical composition, in the same dosage form, by the same route of administration, or at the same time. The effects of both compounds need not manifest themselves at the same time. The effects need only be overlapping for a period of time and need not be coextensive. Concomitant administration or co-administration encompasses administration in parallel or sequentially.

“Amelioration” refers to an improvement or lessening of at least one indicator, sign, or symptom of an associated disease, disorder, or condition. In certain embodiments, amelioration includes a delay or slowing in the progression or severity of one or more indicators of a condition or disease. The progression or severity of indicators may be determined by subjective or objective measures, which are known to those skilled in the art.

“Animal” refers to a human or non-human animal, including, but not limited to, mice, rats, rabbits, dogs, cats, pigs, and non-human primates, including, but not limited to, monkeys and chimpanzees.

“Antisense activity” means any detectable and/or measurable activity 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 to the target.

“Antisense compound” means a compound comprising an oligonucleotide and optionally one or more additional features, such as a conjugate group or terminal group. Examples of antisense compounds include single-stranded and double-stranded compounds, such as, oligonucleotides, ribozymes, siRNAs, shRNAs, ssRNAs, and occupancy-based compounds.

“Antisense inhibition” means reduction of target nucleic acid levels in the presence of an antisense compound complementary to a target nucleic acid compared to target nucleic acid levels in the absence of the antisense compound.

“Antisense mechanisms” are all those mechanisms involving hybridization of a compound with target nucleic acid, wherein the outcome or effect of the hybridization is either target degradation or target occupancy with concomitant stalling of the cellular machinery involving, for example, transcription or splicing.

“Antisense oligonucleotide” means an oligonucleotide having a nucleobase sequence that is complementary to a target nucleic acid or region or segment thereof. In certain embodiments, an antisense oligonucleotide is specifically hybridizable to a target nucleic acid or region or segment thereof.

“Bicyclic nucleoside” or “BNA” means a nucleoside comprising a bicyclic sugar moiety. “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 in 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.

“Branching group” means a group of atoms having at least 3 positions that are capable of forming covalent linkages to at least 3 groups. In certain embodiments, a branching group provides a plurality of reactive sites for connecting tethered ligands to an oligonucleotide via a conjugate linker and/or a cleavable moiety.

“Cell-targeting moiety” means a conjugate group or portion of a conjugate group that is capable of binding to a particular cell type or particular cell types.

“cEt” or “constrained ethyl” means a bicyclic furanosyl sugar moiety comprising a bridge connecting the 4'-carbon and the 2'-carbon, wherein the bridge has the formula: 4'-CH(CH₃)-O-2'.

“cEt nucleoside” means a nucleoside comprising a cEt modified sugar moiety.

“Chemical modification” in a compound describes the substitutions or changes through chemical reaction, of any of the units in the compound relative to the original state of such unit. “Modified nucleoside” means a nucleoside having, independently, a modified sugar moiety and/or modified nucleobase. “Modified oligonucleotide” means an oligonucleotide comprising at least one modified internucleoside linkage, a modified sugar, and/or a modified nucleobase.

“Chemically distinct region” refers to a region of a compound that is in some way chemically different than another region of the same compound. For example, a region having 2'-O-methoxyethyl nucleotides is chemically distinct from a region having nucleotides without 2'-O-methoxyethyl modifications.

“Chimeric antisense compounds” means antisense compounds that have at least 2 chemically distinct regions, each position having a plurality of subunits.

“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.

“Cleavable bond” means any chemical bond capable of being split. In certain embodiments, a cleavable bond is selected from among: an amide, a polyamide, an ester, an ether, one or both esters of a phosphodiester, a phosphate ester, a carbamate, a di-sulfide, or a peptide.

“Cleavable moiety” means a bond or group of atoms that is cleaved under physiological conditions, for example, inside a cell, an animal, or a human.

“Complementary” in reference to an oligonucleotide means the nucleobase sequence of such oligonucleotide or one or more regions thereof matches the nucleobase sequence of another oligonucleotide or nucleic acid or one or more regions thereof when the two nucleobase sequences are aligned in opposing directions. Nucleobase matches or complementary nucleobases, as described herein, are limited to the following pairs: adenine (A) and thymine (T), adenine (A) and uracil (U), cytosine (C) and guanine (G), and 5-methyl cytosine (^mC) and guanine (G) unless otherwise specified. Complementary oligonucleotides and/or nucleic acids need not have nucleobase complementarity at each nucleoside and may include one or more nucleobase mismatches. By contrast, “fully complementary” or “100% complementary” in reference to oligonucleotides means that such oligonucleotides have nucleobase matches at each nucleoside without any nucleobase mismatches.

“Conjugate group” means a group of atoms that is attached to an oligonucleotide. Conjugate groups include a conjugate moiety and a conjugate linker that attaches the conjugate moiety to the oligonucleotide.

“Conjugate linker” means a group of atoms comprising at least one bond that connects a conjugate moiety to an oligonucleotide.

“Conjugate moiety” means a group of atoms that is attached to an oligonucleotide via a conjugate linker.

“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.

“Designing” or “Designed to” refer to the process of designing a compound that specifically hybridizes with a selected nucleic acid molecule.

“Diluent” means an ingredient in a composition that lacks pharmacological activity, but is pharmaceutically necessary or desirable. For example, the diluent in an injected composition can be a liquid, e.g. saline solution.

“Differently modified” means chemical modifications or chemical substituents that are different from one another, including absence of modifications. Thus, for example, a MOE nucleoside and an unmodified DNA nucleoside are “differently modified,” even though the DNA nucleoside is unmodified. Likewise, DNA and RNA are “differently modified,” even though both are naturally-occurring unmodified nucleosides. Nucleosides that are the same but for comprising different nucleobases are not differently modified. For example, a nucleoside comprising a 2'-OMe modified sugar and an unmodified adenine nucleobase and a nucleoside comprising a 2'-OMe modified sugar and an unmodified thymine nucleobase are not differently modified.

“Dose” means a specified quantity of a compound or pharmaceutical agent provided in a single administration, or in a specified time period. In certain embodiments, a dose may be administered in two or

more boluses, tablets, or injections. For example, in certain embodiments, where subcutaneous administration is desired, the desired dose may require a volume not easily accommodated by a single injection. In such embodiments, two or more injections may be used to achieve the desired dose. In certain embodiments, a dose may be administered in two or more injections to minimize injection site reaction in an individual. In other
5 embodiments, the compound or pharmaceutical agent is administered by infusion over an extended period of time or continuously. Doses may be stated as the amount of pharmaceutical agent per hour, day, week or month.

“Dosing regimen” is a combination of doses designed to achieve one or more desired effects.

“Double-stranded antisense compound” means an antisense compound comprising two oligomeric compounds that are complementary to each other and form a duplex, and wherein one of the two said oligomeric
10 compounds comprises an oligonucleotide.

“Effective amount” means the amount of compound sufficient to effectuate a desired physiological outcome in an individual in need of the compound. The effective amount may vary among individuals depending on the health and physical condition of the individual to be treated, the taxonomic group of the individuals to be treated, the formulation of the composition, assessment of the individual’s medical condition,
15 and other relevant factors.

“Efficacy” means the ability to produce a desired effect.

“Expression” includes all the functions by which a gene’s coded information is converted into structures present and operating in a cell. Such structures include, but are not limited to, the products of transcription and translation.

20 “Gapmer” means an oligonucleotide comprising an internal region having a plurality of nucleosides that support RNase H cleavage positioned between external regions having one or more nucleosides, wherein the nucleosides comprising the internal region are chemically distinct from the nucleoside or nucleosides comprising the external regions. The internal region may be referred to as the “gap” and the external regions may be referred to as the “wings.”

25 “Hybridization” means the annealing of 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. In certain embodiments, complementary nucleic acid molecules include, but are not limited to, an antisense compound and a nucleic acid target. In certain embodiments, complementary nucleic acid molecules include,
30 but are not limited to, an oligonucleotide and a nucleic acid target.

“Immediately adjacent” means there are no intervening elements between the immediately adjacent elements of the same kind (e.g. no intervening nucleobases between the immediately adjacent nucleobases).

“Individual” means a human or non-human animal selected for treatment or therapy.

"Inhibiting the expression or activity" refers to a reduction or blockade of the expression or activity relative to the expression of activity in an untreated or control sample and does not necessarily indicate a total elimination of expression or activity.

5 "Internucleoside linkage" means a group or bond that forms a covalent linkage between adjacent nucleosides in an oligonucleotide. "Modified internucleoside linkage" means any internucleoside linkage other than a naturally occurring, phosphate internucleoside linkage. Non-phosphate linkages are referred to herein as modified internucleoside linkages.

"Lengthened oligonucleotides" are those that have one or more additional nucleosides relative to an oligonucleotide disclosed herein, e.g. a parent oligonucleotide.

10 "Linked nucleosides" means adjacent nucleosides linked together by an internucleoside linkage.

"Linker-nucleoside" means a nucleoside that links an oligonucleotide to a conjugate moiety. Linker-nucleosides are located within the conjugate linker of a compound. Linker-nucleosides are not considered part of the oligonucleotide portion of a compound even if they are contiguous with the oligonucleotide.

15 "Mismatch" or "non-complementary" means a nucleobase of a first oligonucleotide that is not complementary to the corresponding nucleobase of a second oligonucleotide or target nucleic acid when the first and second oligonucleotides are aligned. For example, nucleobases including but not limited to a universal nucleobase, inosine, and hypoxanthine, are capable of hybridizing with at least one nucleobase but are still mismatched or non-complementary with respect to nucleobase to which it hybridized. As another example, a nucleobase of a first oligonucleotide that is not capable of hybridizing to the corresponding nucleobase of a
20 second oligonucleotide or target nucleic acid when the first and second oligonucleotides are aligned is a mismatch or non-complementary nucleobase.

"Modulating" refers to changing or adjusting a feature in a cell, tissue, organ or organism. For example, modulating IRF4 RNA can mean to increase or decrease the level of IRF4 RNA and/or IRF4 protein in a cell, tissue, organ or organism. A "modulator" effects the change in the cell, tissue, organ or organism. For example,
25 a IRF4 compound can be a modulator that decreases the amount of IRF4 RNA and/or IRF4 protein in a cell, tissue, organ or organism.

"MOE" means methoxyethyl.

"Monomer" refers to a single unit of an oligomer. Monomers include, but are not limited to, nucleosides and nucleotides.

30 "Motif" means the pattern of unmodified and/or modified sugar moieties, nucleobases, and/or internucleoside linkages, in an oligonucleotide.

"Natural" or "naturally occurring" means found in nature.

“Non-bicyclic modified sugar” or “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.

5 “Nucleic acid” refers to molecules composed of monomeric nucleotides. A nucleic acid includes, but is not limited to, ribonucleic acids (RNA), deoxyribonucleic acids (DNA), single-stranded nucleic acids, and double-stranded nucleic acids.

10 “Nucleobase” means a heterocyclic moiety capable of pairing with a base of another nucleic acid. As used herein a “naturally occurring nucleobase” is adenine (A), thymine (T), cytosine (C), uracil (U), and guanine (G). A “modified nucleobase” is a naturally occurring nucleobase that is chemically modified. A “universal base” or “universal nucleobase” is a nucleobase other than a naturally occurring nucleobase and modified nucleobase, and is capable of pairing with any nucleobase.

“Nucleobase sequence” means the order of contiguous nucleobases in a nucleic acid or oligonucleotide independent of any sugar or internucleoside linkage.

15 “Nucleoside” means a compound comprising a nucleobase and a sugar moiety. The nucleobase and sugar moiety are each, independently, unmodified or modified. “Modified nucleoside” means a nucleoside comprising a modified nucleobase and/or a modified sugar moiety. Modified nucleosides include abasic nucleosides, which lack a nucleobase.

“Oligomeric compound” means a compound comprising a single oligonucleotide and optionally one or more additional features, such as a conjugate group or terminal group.

20 “Oligonucleotide” means a polymer of linked nucleosides each of which can be modified or unmodified, independent one from another. Unless otherwise indicated, oligonucleotides consist of 8-80 linked nucleosides. “Modified oligonucleotide” means an oligonucleotide, wherein at least one sugar, nucleobase, or internucleoside linkage is modified. “Unmodified oligonucleotide” means an oligonucleotide that does not comprise any sugar, nucleobase, or internucleoside modification.

25 “Parent oligonucleotide” means an oligonucleotide whose sequence is used as the basis of design for more oligonucleotides of similar sequence but with different lengths, motifs, and/or chemistries. The newly designed oligonucleotides may have the same or overlapping sequence as the parent oligonucleotide.

30 “Parenteral administration” means administration through injection or infusion. Parenteral administration includes subcutaneous administration, intravenous administration, intramuscular administration, intraarterial administration, intraperitoneal administration, or intracranial administration, e.g. intrathecal or intracerebroventricular administration.

“Pharmaceutically acceptable carrier or diluent” means any substance suitable for use in administering to an individual. For example, a pharmaceutically acceptable carrier can be a sterile aqueous solution, such as PBS or water-for-injection.

5 “Pharmaceutically acceptable salts” means physiologically and pharmaceutically acceptable salts of compounds, such as oligomeric compounds or oligonucleotides, i.e., salts that retain the desired biological activity of the parent compound and do not impart undesired toxicological effects thereto.

“Pharmaceutical agent” means a compound that provides a therapeutic benefit when administered to an individual.

10 “Pharmaceutical composition” means a mixture of substances suitable for administering to an individual. For example, a pharmaceutical composition may comprise one or more compounds or salt thereof and a sterile aqueous solution.

“Phosphorothioate linkage” means a modified phosphate linkage in which one of the non-bridging oxygen atoms is replaced with a sulfur atom. A phosphorothioate internucleoside linkage is a modified internucleoside linkage.

15 “Phosphorus moiety” means a group of atoms comprising a phosphorus atom. In certain embodiments, a phosphorus moiety comprises a mono-, di-, or tri-phosphate, or phosphorothioate.

“Portion” means a defined number of contiguous (i.e., linked) nucleobases of a nucleic acid. In certain embodiments, a portion is a defined number of contiguous nucleobases of a target nucleic acid. In certain embodiments, a portion is a defined number of contiguous nucleobases of an oligomeric compound.

20 “Prevent” refers to delaying or forestalling the onset, development or progression of a disease, disorder, or condition for a period of time from minutes to indefinitely.

“Prodrug” means a compound in a form outside the body which, when administered to an individual, is metabolized to another form within the body or cells thereof. In certain embodiments, the metabolized form is the active, or more active, form of the compound (e.g., drug). Typically conversion of a prodrug within the
25 body is facilitated by the action of an enzyme(s) (e.g., endogenous or viral enzyme) or chemical(s) present in cells or tissues, and/or by physiologic conditions.

“Reduce” means to bring down to a smaller extent, size, amount, or number.

“RefSeq No.” is a unique combination of letters and numbers assigned to a sequence to indicate the sequence is for a particular target transcript (e.g., target gene). Such sequence and information about the target
30 gene (collectively, the gene record) can be found in a genetic sequence database. Genetic sequence_databases include the NCBI Reference Sequence database, GenBank, the European Nucleotide Archive, and the DNA

Data Bank of Japan (the latter three forming the International Nucleotide Sequence Database Collaboration or INSDC).

“Region” is defined as a portion of the target nucleic acid having at least one identifiable structure, function, or characteristic.

5 “RNAi compound” means an antisense compound that acts, at least in part, through RISC or Ago2, but not through RNase H, 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.

“Segments” are defined as smaller or sub-portions of regions within a nucleic acid.

10 “Side effects” means physiological disease and/or conditions attributable to a treatment other than the desired effects. In certain embodiments, side effects include injection site reactions, liver function test abnormalities, renal function abnormalities, liver toxicity, renal toxicity, central nervous system abnormalities, myopathies, and malaise. For example, increased aminotransferase levels in serum may indicate liver toxicity or liver function abnormality. For example, increased bilirubin may indicate liver toxicity or liver function
15 abnormality.

“Single-stranded” in reference to a compound means the compound has only one oligonucleotide. “Self-complementary” means an oligonucleotide that at least partially hybridizes to itself. A compound consisting of one oligonucleotide, wherein the oligonucleotide of the compound is self-complementary, is a single-stranded compound. A single-stranded compound may be capable of binding to a complementary
20 compound to form a duplex.

“Sites” are defined as unique nucleobase positions within a target nucleic acid.

“Specifically hybridizable” refers to an oligonucleotide having a sufficient degree of complementarity between the oligonucleotide and a target nucleic acid to induce a desired effect, while exhibiting minimal or no effects on non-target nucleic acids. In certain embodiments, specific hybridization occurs under
25 physiological conditions.

“Specifically inhibit” with reference to a target nucleic acid means to reduce or block expression of the target nucleic acid while exhibiting fewer, minimal, or no effects on non-target nucleic acids. Reduction does not necessarily indicate a total elimination of the target nucleic acid’s expression.

“Standard cell assay” means assay(s) described in the Examples and reasonable variations thereof.

30 “Standard in vivo experiment” means the procedure(s) described in the Example(s) and reasonable variations thereof.

“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 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.

“Sugar moiety” means an unmodified sugar moiety or a modified sugar moiety. “Unmodified sugar moiety” or “unmodified sugar” means a 2’-OH(H) furanosyl moiety, as found in RNA (an “unmodified RNA sugar moiety”), or a 2’-H(H) 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. “Modified sugar moiety” or “modified sugar” means a modified furanosyl sugar moiety or a sugar surrogate. “Modified furanosyl sugar moiety” means a furanosyl sugar comprising a non-hydrogen substituent in place of at least one hydrogen of an unmodified sugar moiety. In certain embodiments, a modified furanosyl sugar moiety is a 2’-substituted sugar moiety. Such modified furanosyl sugar moieties include bicyclic sugars and non-bicyclic sugars.

“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 compounds or nucleic acids.

“Synergy” or “synergize” refers to an effect of a combination that is greater than additive of the effects of each component alone at the same doses.

“IRF4” means any nucleic acid or protein of IRF4. “IRF4 nucleic acid” means any nucleic acid encoding IRF4. For example, in certain embodiments, a IRF4 nucleic acid includes a DNA sequence encoding IRF4, an RNA sequence transcribed from DNA encoding IRF4 (including genomic DNA comprising introns and exons), and an mRNA sequence encoding IRF4. “IRF4 mRNA” means an mRNA encoding a IRF4 protein. The target may be referred to in either upper or lower case.

“IRF4 specific inhibitor” refers to any agent capable of specifically inhibiting IRF4 RNA and/or IRF4 protein expression or activity at the molecular level. For example, IRF4 specific inhibitors include nucleic acids (including antisense compounds), peptides, antibodies, small molecules, and other agents capable of inhibiting the expression of IRF4 RNA and/or IRF4 protein.

“Target gene” refers to a gene encoding a target.

“Targeting” means the specific hybridization of a compound to a target nucleic acid in order to induce a desired effect.

“Target nucleic acid,” “target RNA,” “target RNA transcript” and “nucleic acid target” all mean a nucleic acid capable of being targeted by compounds described herein.

5 “Target region” means a portion of a target nucleic acid to which one or more compounds is targeted.

“Target segment” means the sequence of nucleotides of a target nucleic acid to which a compound is targeted. “5’ target site” refers to the 5’-most nucleotide of a target segment. “3’ target site” refers to the 3’-most nucleotide of a target segment.

10 “Terminal group” means a chemical group or group of atoms that is covalently linked to a terminus of an oligonucleotide.

“Therapeutically effective amount” means an amount of a compound, pharmaceutical agent, or composition that provides a therapeutic benefit to an individual.

“Treat” refers to administering a compound or pharmaceutical composition to an animal in order to effect an alteration or improvement of a disease, disorder, or condition in the animal.

15 *Certain Embodiments*

Certain embodiments provide methods, compounds and compositions for inhibiting IRF4 expression.

20 Certain embodiments provide compounds targeted to a IRF4 nucleic acid. In certain embodiments, the IRF4 nucleic acid has the sequence set forth in RefSeq or GENBANK Accession No. NM_002460.3 or NT_034880.3_TRUNC_328000_354000 (incorporated by reference, disclosed herein as SEQ ID NO: 1 and SEQ ID NO: 2, respectively). In certain embodiments, the compound is an antisense compound or oligomeric compound. In certain embodiments, the compound is single-stranded. In certain embodiments, the compound is double-stranded.

25 Certain embodiments provide a compound comprising a modified oligonucleotide 8 to 80 linked nucleosides in length and having a nucleobase sequence comprising at least 8 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 3-3383. In certain embodiments, the compound is an antisense compound or oligomeric compound. In certain embodiments, the compound is single-stranded. In certain embodiments, the compound is double-stranded. In certain embodiments, the modified oligonucleotide is 10 to 30 linked nucleosides in length.

30 Certain embodiments provide a compound comprising a modified oligonucleotide 9 to 80 linked nucleosides in length and having a nucleobase sequence comprising at least 9 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 3-3383. In certain embodiments, the compound is an antisense compound or oligomeric compound. In certain embodiments, the compound is single-stranded. In certain

embodiments, the compound is double-stranded. In certain embodiments, the modified oligonucleotide is 10 to 30 linked nucleosides in length.

5 Certain embodiments provide a compound comprising a modified oligonucleotide 10 to 80 linked nucleosides in length and having a nucleobase sequence comprising at least 10 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 3-3383. In certain embodiments, the compound is an antisense compound or oligomeric compound. In certain embodiments, the compound is single-stranded. In certain embodiments, the compound is double-stranded. In certain embodiments, the modified oligonucleotide is 10 to 30 linked nucleosides in length.

10 Certain embodiments provide a compound comprising a modified oligonucleotide 11 to 80 linked nucleosides in length and having a nucleobase sequence comprising at least 11 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 3-3383. In certain embodiments, the compound is an antisense compound or oligomeric compound. In certain embodiments, the compound is single-stranded. In certain embodiments, the compound is double-stranded. In certain embodiments, the modified oligonucleotide is 11 to 30 linked nucleosides in length.

15 Certain embodiments provide a compound comprising a modified oligonucleotide 12 to 80 linked nucleosides in length and having a nucleobase sequence comprising at least 12 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 3-3383. In certain embodiments, the compound is an antisense compound or oligomeric compound. In certain embodiments, the compound is single-stranded. In certain embodiments, the compound is double-stranded. In certain embodiments, the modified oligonucleotide is 12 to 20 30 linked nucleosides in length.

Certain embodiments provide a compound comprising a modified oligonucleotide 16 to 80 linked nucleosides in length and having a nucleobase sequence comprising the nucleobase sequence of any one of SEQ ID NOs: 3-3383. In certain embodiments, the compound is an antisense compound or oligomeric compound. In certain embodiments, the compound is single-stranded. In certain embodiments, the compound is double-stranded. In certain embodiments, the modified oligonucleotide is 16 to 30 linked nucleosides in length.

25 Certain embodiments provide a compound comprising a modified oligonucleotide consisting of the nucleobase sequence of any one of SEQ ID NOs: 3-3383. In certain embodiments, the compound is an antisense compound or oligomeric compound. In certain embodiments, the compound is single-stranded. In certain embodiments, the compound is double-stranded.

30 In certain embodiments, a compound comprises a modified oligonucleotide 8 to 80 linked nucleosides in length and having at least an 8, 9, 10, 11, 12, 13, 14, 15, or 16 contiguous nucleobase portion complementary to an equal length portion within the 3'UTR of SEQ ID NO: 1. In certain embodiments, the 3'UTR corresponds to nucleotides 1483 to 5332 of SEQ ID NO: 1. In certain embodiments, a compound comprises a modified oligonucleotide 10 to 30 linked nucleosides in length having a nucleobase sequence at least 85%, at least 90%, at least 95%, or 100% complementary across its entire length to a nucleobase sequence within the 3'UTR of

SEQ ID NO: 1. In certain embodiments, the 3'UTR corresponds to nucleotides 1483 to 5332 of SEQ ID NO: 1. In certain embodiments, a compound comprises a modified oligonucleotide 16 to 30 linked nucleosides in length having a nucleobase sequence at least 85%, at least 90%, at least 95%, or 100% complementary across its entire length to a nucleobase sequence within the 3'UTR of SEQ ID NO: 1. In certain embodiments, the 3'UTR corresponds to nucleotides 1483 to 5332 of SEQ ID NO: 1.

In certain embodiments, a compound comprises a modified oligonucleotide 8 to 80 linked nucleosides in length and having at least an 8, 9, 10, 11, 12, 13, 14, 15, or 16 contiguous nucleobase portion complementary to an equal length portion within nucleotides 4227-4244, 4227-4242, 4228-4243, or 4229-4244 of SEQ ID NO: 1. In certain embodiments, the modified oligonucleotide is 10 to 30 linked nucleosides in length. In certain embodiments, the modified oligonucleotide is 16 to 30 linked nucleosides in length.

In certain embodiments, a compound comprises a modified oligonucleotide 8 to 80 linked nucleosides in length and having at least an 8, 9, 10, 11, 12, 13, 14, 15, or 16 contiguous nucleobase portion complementary to an equal length portion within nucleotides 9667-9682, 11411-11426, or 18090-18105 of SEQ ID NO: 2. In certain embodiments, the modified oligonucleotide is 10 to 30 linked nucleosides in length. In certain embodiments, the modified oligonucleotide is 16 to 30 linked nucleosides in length.

In certain embodiments, a compound comprises a modified oligonucleotide 8 to 80 linked nucleosides in length and complementary within nucleotides 4227-4244, 4227-4242, 4228-4243, or 4229-4244 of SEQ ID NO: 1. In certain embodiments, the modified oligonucleotide is 10 to 30 linked nucleosides in length. In certain embodiments, the modified oligonucleotide is 16 to 30 linked nucleosides in length.

In certain embodiments, a compound comprises a modified oligonucleotide 8 to 80 linked nucleosides in length and complementary within nucleotides 9667-9682, 11411-11426, or 18090-18105 of SEQ ID NO: 2. In certain embodiments, the modified oligonucleotide is 10 to 30 linked nucleosides in length. In certain embodiments, the modified oligonucleotide is 16 to 30 linked nucleosides in length.

In certain embodiments, a compound comprises a modified oligonucleotide 8 to 80 linked nucleosides in length and having a nucleobase sequence comprising at least an 8, 9, 10, 11, 12, 13, 14, 15, or 16 contiguous nucleobase portion any one of SEQ ID NOs: 2021, 560, 559, 1330, 1540, or 3303. In certain embodiments, the modified oligonucleotide is 10 to 30 linked nucleosides in length. In certain embodiments, the modified oligonucleotide is 16 to 30 linked nucleosides in length.

In certain embodiments, a compound comprises a modified oligonucleotide 16 to 80 linked nucleosides in length and having a nucleobase sequence comprising any one of SEQ ID NOs: 2021, 560, 559, 1330, 1540, or 3303. In certain embodiments, the modified oligonucleotide is 16 to 30 linked nucleosides in length.

In certain embodiments, a compound comprises a modified oligonucleotide 16 linked nucleosides in length having a nucleobase sequence consisting of any one of SEQ ID NOs: 2021, 560, 559, 1330, 1540, or 3303.

In certain embodiments, a compound targeted to IRF4 is ION 935918. Out of over 3,000 compounds that were screened as described in the Examples section below, ION 690890, 935658, 935696, 935762, 935918,

935968, 882800, 1012795, 1014095, and 1014834 emerged as the top lead compounds. In particular, ION 935918 exhibited the best combination of properties in terms of potency and tolerability out of over 3,000 compounds.

5 In certain embodiments, any of the foregoing modified oligonucleotides comprises at least one modified internucleoside linkage, at least one modified sugar, and/or at least one modified nucleobase.

In certain embodiments, any of the foregoing modified oligonucleotides comprises at least one modified sugar. In certain embodiments, at least one modified sugar comprises a 2'-O-methoxyethyl group. In certain embodiments, at least one modified sugar is a bicyclic sugar, such as a 4'-CH(CH₃)-O-2' group, a 4'-CH₂-O-2' group, or a 4'-(CH₂)₂-O-2' group.

10 In certain embodiments, the modified oligonucleotide comprises at least one modified internucleoside linkage, such as a phosphorothioate internucleoside linkage.

In certain embodiments, any of the foregoing modified oligonucleotides comprises at least one modified nucleobase, such as 5-methylcytosine.

In certain embodiments, any of the foregoing modified oligonucleotides comprises:

- 15 a gap segment consisting of linked deoxynucleosides;
 a 5' wing segment consisting of linked nucleosides; and
 a 3' wing segment consisting of linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment and wherein each nucleoside of each wing segment comprises a modified sugar. In certain embodiments, the modified oligonucleotide is 16 to 80 linked nucleosides in length having a nucleobase sequence comprising the sequence recited in any one of SEQ ID NO: 2021, 560, 559, 1330, 1540, or 3303. In certain embodiments, the modified oligonucleotide is 16 to 30 linked nucleosides in length having a nucleobase sequence comprising the sequence recited in any one of SEQ ID NOs: 2021, 560, 559, 1330, 1540, or 3303. In certain embodiments, the modified oligonucleotide is 16 linked nucleosides in length having a nucleobase sequence consisting of the sequence recited in any one of SEQ ID NOs: 2021, 560, 559, 1330, 1540, or 3303.

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In certain embodiments, a compound comprises or consists of a modified oligonucleotide 16-80 linked nucleobases in length having a nucleobase sequence comprising the sequence recited in any one of SEQ ID NOs: 3-3383, wherein the modified oligonucleotide comprises:

- a gap segment consisting of linked deoxynucleosides;
30 a 5' wing segment consisting of linked nucleosides; and
 a 3' wing segment consisting of linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment and wherein each nucleoside of each wing segment comprises a modified sugar. In certain embodiments, the

modified oligonucleotide is 16-30 linked nucleosides in length. In certain embodiments, the modified oligonucleotide is 16 linked nucleosides in length.

In certain embodiments, a compound comprises or consists of a modified oligonucleotide 16-80 linked nucleobases in length having a nucleobase sequence comprising the sequence recited in any one of SEQ ID
5 NOs: 2021, 560, 559, 1330, 1540, or 3303, wherein the modified oligonucleotide comprises:

a gap segment consisting of linked deoxynucleosides;

a 5' wing segment consisting of linked nucleosides; and

a 3' wing segment consisting of linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment and
10 wherein each nucleoside of each wing segment comprises a modified sugar. In certain embodiments, the modified oligonucleotide is 16-30 linked nucleosides in length. In certain embodiments, the modified oligonucleotide is 16 linked nucleosides in length.

In certain embodiments, a compound comprises or consists of a modified oligonucleotide 16-80 linked nucleobases in length having a nucleobase sequence comprising the sequence recited in any one of SEQ ID
15 NOs: 1330 or 3303, wherein the modified oligonucleotide comprises:

a gap segment consisting of ten linked deoxynucleosides;

a 5' wing segment consisting of three linked nucleosides; and

a 3' wing segment consisting of three linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment; wherein
20 each nucleoside of each wing segment comprises a cEt nucleoside; wherein each internucleoside linkage is a phosphorothioate linkage; and wherein each cytosine is a 5-methylcytosine. In certain embodiments, the modified oligonucleotide is 16-30 linked nucleosides in length. In certain embodiments, the modified oligonucleotide is 16 linked nucleosides in length.

In certain embodiments, a compound comprises or consists of a modified oligonucleotide 16-80 linked nucleobases in length having a nucleobase sequence comprising the sequence recited in any one of SEQ ID
25 NOs: 559 or 560, wherein the modified oligonucleotide comprises:

a gap segment consisting of ten linked deoxynucleosides;

a 5' wing segment consisting of one linked nucleoside; and

a 3' wing segment consisting of five linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment; wherein
30 the 5' wing segment comprises a cEt nucleoside; wherein the 3' wing segment comprises a cEt nucleoside, a 2'-O-methoxyethyl nucleoside, a cEt nucleoside, a 2'-O-methoxyethyl nucleoside, and a cEt nucleoside in the

5' to 3' direction; wherein each internucleoside linkage is a phosphorothioate linkage; and wherein each cytosine is a 5-methylcytosine. In certain embodiments, the modified oligonucleotide is 16-30 linked nucleosides in length. In certain embodiments, the modified oligonucleotide is 16 linked nucleosides in length.

5 In certain embodiments, a compound comprises or consists of a modified oligonucleotide 16-80 linked nucleobases in length having a nucleobase sequence comprising the sequence recited in any one of SEQ ID NOs: 1330 or 2021, wherein the modified oligonucleotide comprises:

a gap segment consisting of ten linked deoxynucleosides;

a 5' wing segment consisting of two linked nucleosides; and

a 3' wing segment consisting of four linked nucleosides;

10 wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment; wherein each nucleoside of the 5' wing segment comprises a cEt nucleoside; wherein the 3' wing segment comprises a cEt nucleoside, a 2'-O-methoxyethyl nucleoside, a cEt nucleoside, and a 2'-O-methoxyethyl nucleoside in the 5' to 3' direction; wherein each internucleoside linkage is a phosphorothioate linkage; and wherein each cytosine is a 5-methylcytosine. In certain embodiments, the modified oligonucleotide is 16-30 linked
15 nucleosides in length. In certain embodiments, the modified oligonucleotide is 16 linked nucleosides in length.

In certain embodiments, a compound comprises or consists of a modified oligonucleotide 16-80 linked nucleobases in length having a nucleobase sequence comprising the sequence recited in SEQ ID NO: 560, wherein the modified oligonucleotide comprises:

a gap segment consisting of nine linked deoxynucleosides;

20 a 5' wing segment consisting of two linked nucleosides; and

a 3' wing segment consisting of five linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment; wherein each nucleoside of the 5' wing segment comprises a cEt nucleoside; wherein the 3' wing segment comprises a cEt nucleoside, a 2'-O-methoxyethyl nucleoside, a cEt nucleoside, a 2'-O-methoxyethyl nucleoside, and a cEt
25 nucleoside in the 5' to 3' direction; wherein each internucleoside linkage is a phosphorothioate linkage; and wherein each cytosine is a 5-methylcytosine. In certain embodiments, the modified oligonucleotide is 16-30 linked nucleosides in length. In certain embodiments, the modified oligonucleotide is 16 linked nucleosides in length.

30 In certain embodiments, a compound comprises or consists of a modified oligonucleotide 16-80 linked nucleobases in length having a nucleobase sequence comprising the sequence recited in SEQ ID NOs: 2021, wherein the modified oligonucleotide comprises:

a gap segment consisting of nine linked deoxynucleosides;

a 5' wing segment consisting of two linked nucleosides; and

a 3' wing segment consisting of five linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment; wherein each nucleoside of the 5' wing segment comprises a cEt nucleoside; wherein the 3' wing segment comprises a 2'-O-methoxyethyl nucleoside, a 2'-O-methoxyethyl nucleoside, a 2'-O-methoxyethyl nucleoside, a cEt nucleoside, and a cEt nucleoside in the 5' to 3' direction; wherein each internucleoside linkage is a phosphorothioate linkage; and wherein each cytosine is a 5-methylcytosine. In certain embodiments, the modified oligonucleotide is 16-30 linked nucleosides in length. In certain embodiments, the modified oligonucleotide is 16 linked nucleosides in length.

In certain embodiments, a compound comprises or consists of a modified oligonucleotide 16-80 linked nucleobases in length having a nucleobase sequence comprising the sequence recited in SEQ ID NOs: 1540, wherein the modified oligonucleotide comprises:

a gap segment consisting of nine linked deoxynucleosides;

a 5' wing segment consisting of two linked nucleosides; and

a 3' wing segment consisting of five linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment; wherein each nucleoside of the 5' wing segment comprises a cEt nucleoside; wherein the 3' wing segment comprises a 2'-O-methoxyethyl nucleoside, a 2'-O-methoxyethyl nucleoside, a 2'-O-methoxyethyl nucleoside, a cEt nucleoside, and a cEt nucleoside in the 5' to 3' direction; wherein each internucleoside linkage is a phosphorothioate linkage; and wherein each cytosine is a 5-methylcytosine. In certain embodiments, the modified oligonucleotide is 16-30 linked nucleosides in length. In certain embodiments, the modified oligonucleotide is 16 linked nucleosides in length.

In certain embodiments, a compound comprises or consists of a modified oligonucleotide 16-80 linked nucleobases in length having a nucleobase sequence comprising the sequence recited in SEQ ID NOs: 560, wherein the modified oligonucleotide comprises:

a gap segment consisting of nine linked deoxynucleosides;

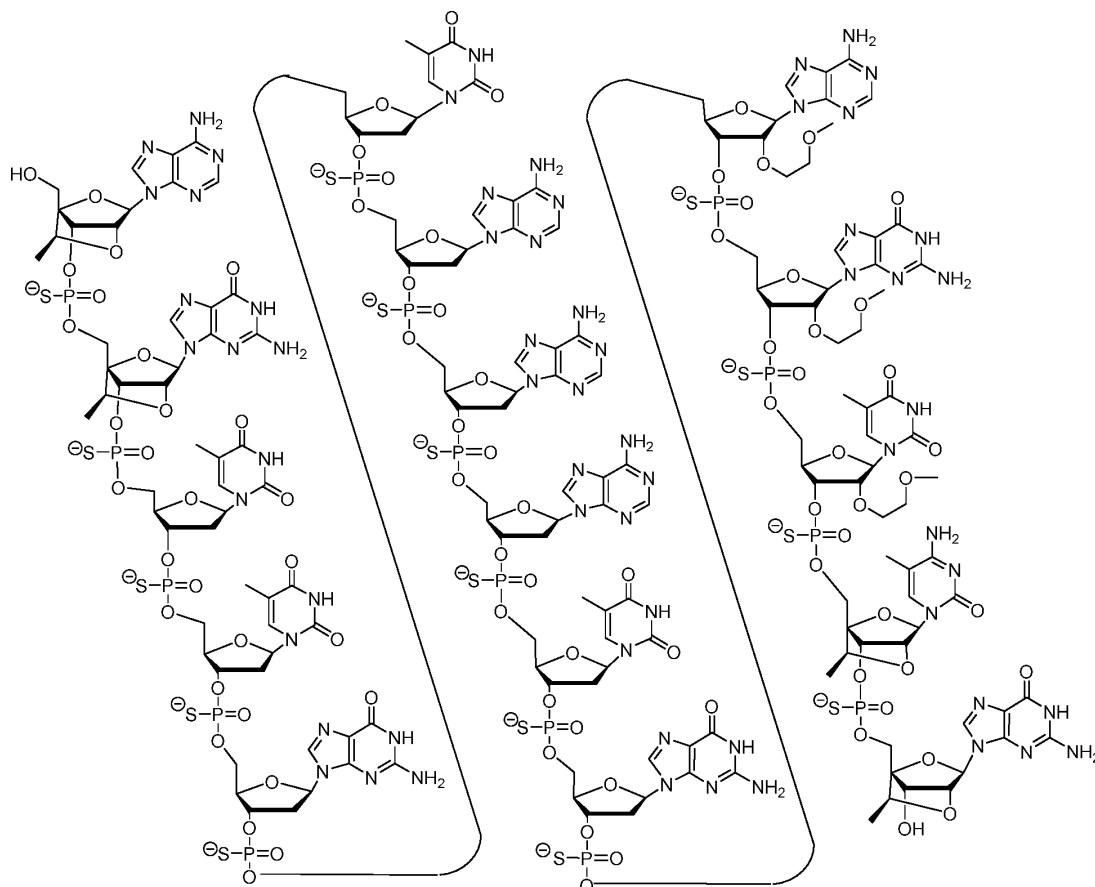
a 5' wing segment consisting of two linked nucleosides; and

a 3' wing segment consisting of five linked nucleosides;

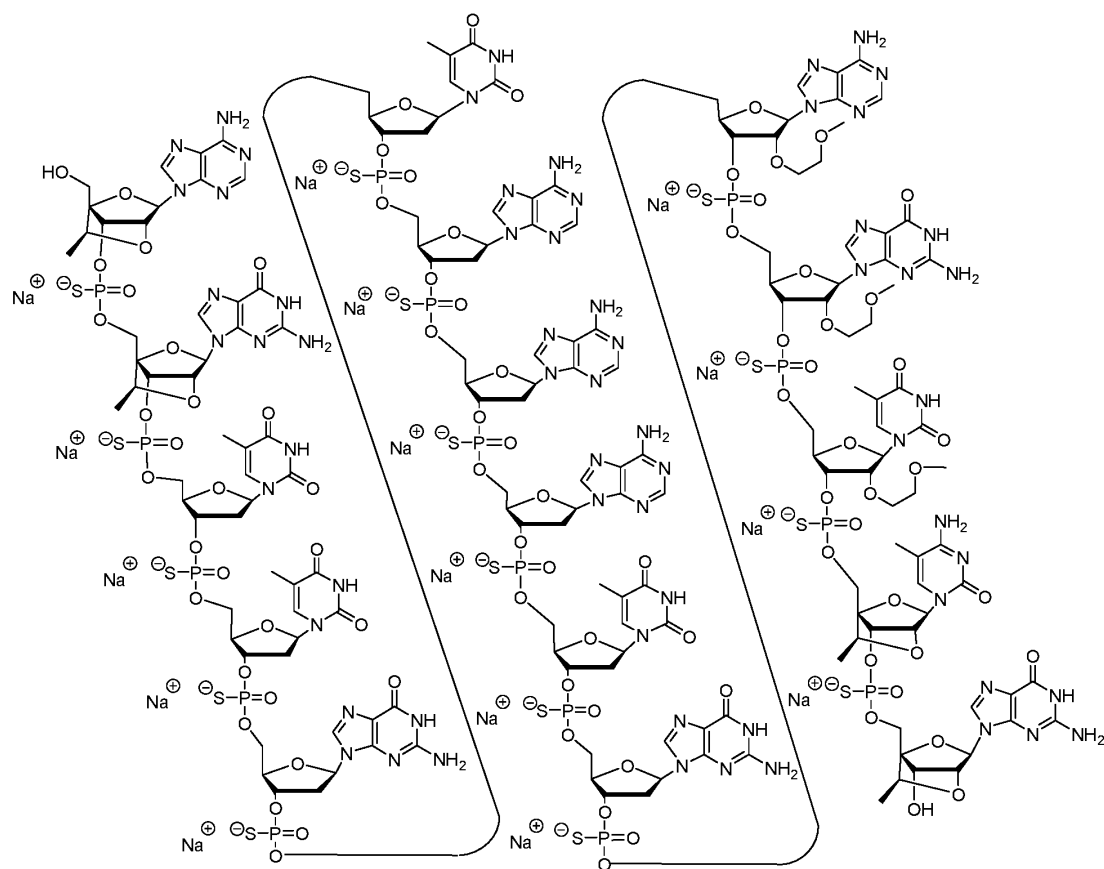
wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment; wherein each nucleoside of the 5' wing segment comprises a cEt nucleoside; wherein the 3' wing segment comprises a 2'-O-methoxyethyl nucleoside, a cEt nucleoside, a 2'-O-methoxyethyl nucleoside, a cEt nucleoside, and a 2'-O-methoxyethyl nucleoside in the 5' to 3' direction; wherein each internucleoside linkage is a phosphorothioate

linkage; and wherein each cytosine is a 5-methylcytosine. In certain embodiments, the modified oligonucleotide is 16-30 linked nucleosides in length. In certain embodiments, the modified oligonucleotide is 16 linked nucleosides in length.

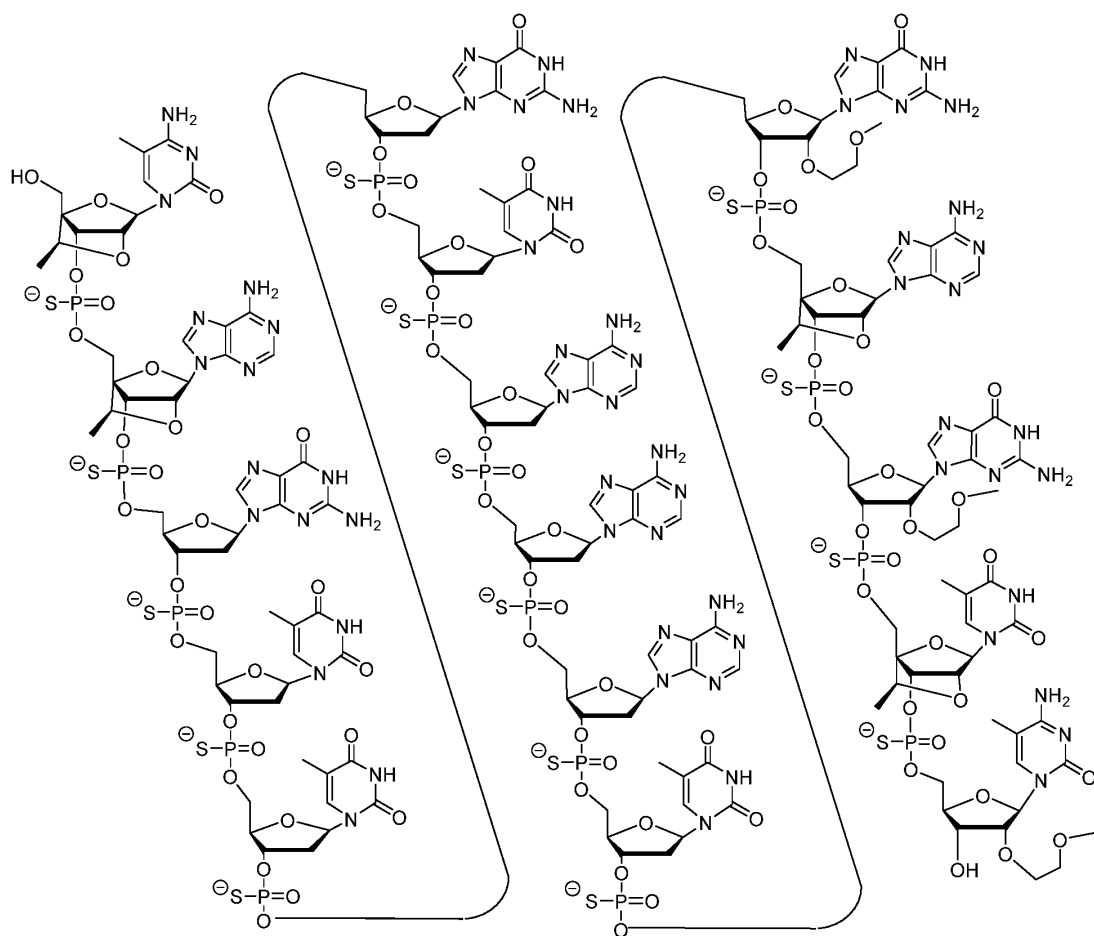
In certain embodiments, a compound comprises or consists of ION 935918 or salt thereof, having the following chemical structure:



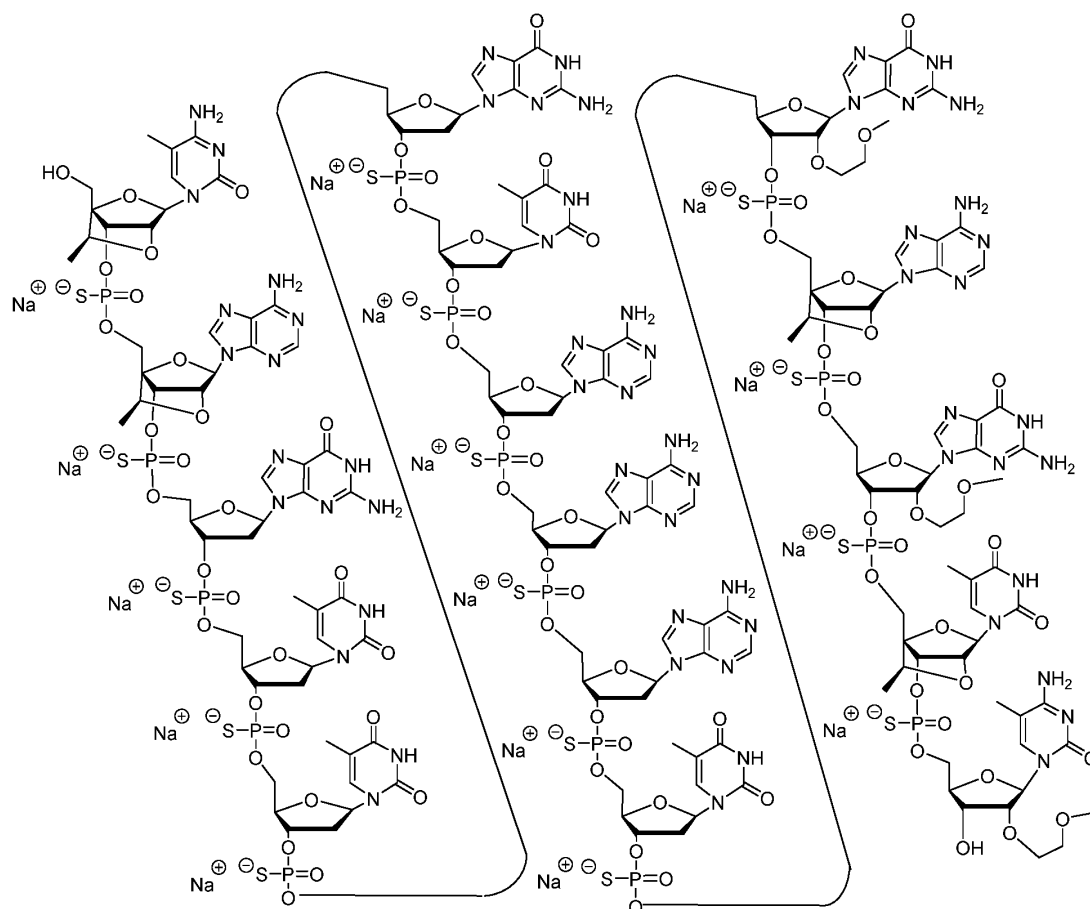
In certain embodiments, a compound comprises or consists of the sodium salt of ION 935918, having the following chemical structure:



In certain embodiments, a compound comprises or consists of ION 935968 or salt thereof, having the following chemical structure:



In certain embodiments, a compound comprises or consists of the sodium salt of ION 935968, having the following chemical structure:



In any of the foregoing embodiments, the compound or oligonucleotide can be at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or 100% complementary to a nucleic acid encoding IRF4.

In any of the foregoing embodiments, the compound can be single-stranded. In certain embodiments, the compound comprises deoxyribonucleotides. In certain embodiments, the compound is double-stranded. In certain embodiments, the compound is double-stranded and comprises ribonucleotides. In any of the foregoing embodiments, the compound can be an antisense compound or oligomeric compound.

In any of the foregoing embodiments, the compound can be 8 to 80, 10 to 30, 12 to 50, 13 to 30, 13 to 50, 14 to 30, 14 to 50, 15 to 30, 15 to 50, 16 to 30, 16 to 50, 17 to 30, 17 to 50, 18 to 22, 18 to 24, 18 to 30, 18 to 50, 19 to 22, 19 to 30, 19 to 50, or 20 to 30 linked nucleosides in length. In certain embodiments, the compound comprises or consists of an oligonucleotide.

In certain embodiments, compounds or compositions provided herein comprise a salt of the modified oligonucleotide. In certain embodiments, the salt is a sodium salt. In certain embodiments, the salt is a potassium salt.

In certain embodiments, the compounds or compositions as described herein are highly tolerable as demonstrated by having at least one of an increase in alanine transaminase (ALT) or aspartate transaminase (AST) value of no more than 4 fold, 3 fold, or 2 fold over saline treated animals or an increase in liver, spleen, or kidney weight of no more than 30%, 20%, 15%, 12%, 10%, 5%, or 2% compared to control treated animals.

5 In certain embodiments, the compounds or compositions as described herein are highly tolerable as demonstrated by having no increase of ALT or AST over control treated animals. In certain embodiments, the compounds or compositions as described herein are highly tolerable as demonstrated by having no increase in liver, spleen, or kidney weight over control animals.

Certain embodiments provide a composition comprising the compound of any of the aforementioned
10 embodiments or salt thereof and at least one of a pharmaceutically acceptable carrier or diluent. In certain embodiments, the composition has a viscosity less than about 40 centipoise (cP), less than about 30 centipoise (cP), less than about 20 centipoise (cP), less than about 15 centipoise (cP), or less than about 10 centipoise (cP). In certain embodiments, the composition having any of the aforementioned viscosities comprises a compound provided herein at a concentration of about 100 mg/mL, about 125 mg/mL, about 150 mg/mL, about 175
15 mg/mL, about 200 mg/mL, about 225 mg/mL, about 250 mg/mL, about 275 mg/mL, or about 300 mg/mL. In certain embodiments, the composition having any of the aforementioned viscosities and/or compound concentrations has a temperature of room temperature or about 20°C, about 21°C, about 22°C, about 23°C, about 24°C, about 25°C, about 26°C, about 27°C, about 28°C, about 29°C, or about 30°C.

Certain Indications

20 Certain embodiments provided herein relate to methods of inhibiting IRF4 expression, which can be useful for treating, preventing, or ameliorating a cancer associated with IRF4 in an individual, by administration of a compound that targets IRF4. In certain embodiments, the compound can be a IRF4 specific inhibitor. In certain embodiments, the compound can be an antisense compound, oligomeric compound, or oligonucleotide targeted to IRF4.

25 Examples of cancers associated with IRF4 treatable, preventable, and/or ameliorable with the methods provided herein include blood cancer, myeloma, multiple myeloma (MM), B cell malignancies, lymphoma, B cell lymphoma, T cell lymphoma, or leukemia. In certain embodiments, the B-cell lymphoma is a non-Hodgkin's B-cell lymphoma. Examples of non-Hodgkin's B-cell lymphoma of certain embodiments that can be treated with compounds provided herein include, but are not limited to, diffuse large B cell lymphoma
30 (DLBCL), activated B-cell lymphoma (ABC-DLBCL), germinal center B-cell lymphoma (GCB DLBCL), follicular lymphoma, mucosa-associated lymphatic tissue lymphoma (MALT), small cell lymphocytic lymphoma, chronic lymphocytic leukemia, mantle cell lymphoma (MCL), Burkitt lymphoma, mediastinal large B cell lymphoma, Waldenström macroglobulinemia, nodal marginal zone B cell lymphoma (NMZL), splenic marginal zone lymphoma (SMZL), intravascular large B-cell lymphoma, primary effusion lymphoma, and

lymphomatoid granulomatosis. In certain embodiments, the T-cell lymphoma that can be treated with compounds provided herein include, but are not limited to, peripheral T-cell lymphoma, adult T cell leukemia/lymphoma (ATLL), and anaplastic large cell lymphoma (ALCL). In certain embodiments, the leukemia that can be treated with compounds provided herein includes, but is not limited to, acute lymphocytic leukemia (ALL).

In certain embodiments, a method of treating, preventing, or ameliorating a cancer associated with IRF4 in an individual comprises administering to the individual a compound comprising a IRF4 specific inhibitor, thereby treating, preventing, or ameliorating the cancer. In certain embodiments, the compound comprises an antisense compound targeted to IRF4. In certain embodiments, the compound comprises an oligonucleotide targeted to IRF4. In certain embodiments, a compound comprises a modified oligonucleotide 8 to 80 linked nucleosides in length and having a nucleobase sequence comprising at least 8 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 3-3383. In certain embodiments, a compound comprises a modified oligonucleotide 16 to 80 linked nucleosides in length and having a nucleobase sequence comprising the nucleobase sequence of any one of SEQ ID NOs: 3-3383. In certain embodiments, a compound comprises a modified oligonucleotide consisting of the nucleobase sequence of any one of SEQ ID NOs: 3-3383. In certain embodiments, a compound comprises a modified oligonucleotide 16 to 80 linked nucleosides in length having a nucleobase sequence comprising any one of SEQ ID NOs: 2021, 560, 559, 1330, 1540, or 3303. In certain embodiments, a compound comprises a modified oligonucleotide having a nucleobase sequence consisting of any one of SEQ ID NOs: 2021, 560, 559, 1330, 1540, or 3303. In any of the foregoing embodiments, the modified oligonucleotide can be 10 to 30 linked nucleosides in length. In certain embodiments, the compound is ION 690890, 935658, 935696, 935762, 935918, 935968, 882800, 1012795, 1014095, and 1014834. In any of the foregoing embodiments, the compound can be single-stranded or double-stranded. In any of the foregoing embodiments, the compound can be an antisense compound or oligomeric compound. In certain embodiments, the compound is administered to the individual parenterally. In certain embodiments, administering the compound inhibits or reduces cancer cell proliferation, tumor growth, or metastasis.

In certain embodiments, a method of treating or ameliorating cancer comprises administering to the individual a compound comprising a IRF4 specific inhibitor, thereby treating or ameliorating the cancer. In certain embodiments, the cancer is a blood cancer, myeloma, multiple myeloma (MM), B cell malignancy, lymphoma, B cell lymphoma, T cell lymphoma, or leukemia. In certain embodiments, the B-cell lymphoma is a non-Hodgkin's B-cell lymphoma. Examples of non-Hodgkin's B-cell lymphoma of certain embodiments that can be treated with compounds provided herein include, but are not limited to, diffuse large B cell lymphoma (DLBCL), activated B-cell lymphoma (ABC-DLBCL), germinal center B-cell lymphoma (GCB DLBCL), follicular lymphoma, mucosa-associated lymphatic tissue lymphoma (MALT), small cell lymphocytic

lymphoma, chronic lymphocytic leukemia, mantle cell lymphoma (MCL), Burkitt lymphoma, mediastinal large B cell lymphoma, Waldenström macroglobulinemia, nodal marginal zone B cell lymphoma (NMZL), splenic marginal zone lymphoma (SMZL), intravascular large B-cell lymphoma, primary effusion lymphoma, and lymphomatoid granulomatosis. In certain embodiments, the T-cell lymphoma that can be treated with compounds provided herein include, but are not limited to, peripheral T-cell lymphoma, adult T cell leukemia/lymphoma (ATLL), and anaplastic large cell lymphoma (ALCL). In certain embodiments, the leukemia that can be treated with compounds provided herein includes, but is not limited to, acute lymphocytic leukemia (ALL). In certain embodiments, the compound comprises an antisense compound targeted to IRF4. In certain embodiments, the compound comprises an oligonucleotide targeted to IRF4. In certain embodiments, the compound comprises a modified oligonucleotide 8 to 80 linked nucleosides in length and having a nucleobase sequence comprising at least 8 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 3-3383. In certain embodiments, the compound comprises a modified oligonucleotide 16 to 80 linked nucleosides in length and having a nucleobase sequence comprising the nucleobase sequence of any one of SEQ ID NOs: 3-3383. In certain embodiments, the compound comprises a modified oligonucleotide consisting of the nucleobase sequence of any one of SEQ ID NOs: 3-3383. In certain embodiments, the compound comprises a modified oligonucleotide of 16 to 80 linked nucleosides in length having a nucleobase sequence comprising any one of SEQ ID NOs: 2021, 560, 559, 1330, 1540, or 3303. In certain embodiments, the compound comprises a modified oligonucleotide having a nucleobase sequence consisting of any one of SEQ ID NOs: 2021, 560, 559, 1330, 1540, or 3303. In any of the foregoing embodiments, the modified oligonucleotide can be 10 to 30 linked nucleosides in length. In certain embodiments, the compound is ION 690890, 935658, 935696, 935762, 935918, 935968, 882800, 1012795, 1014095, and 1014834. In any of the foregoing embodiments, the compound can be single-stranded or double-stranded. In any of the foregoing embodiments, the compound can be an antisense compound or oligomeric compound. In certain embodiments, the compound is administered to the individual parenterally. In certain embodiments, administering the compound inhibits or reduces cancer cell proliferation, tumor growth, or metastasis. In certain embodiments, the individual is identified as having or at risk of having a cancer associated with IRF4.

In certain embodiments, a method of inhibiting expression of IRF4 in an individual having, or at risk of having, a cancer associated with IRF4 comprises administering to the individual a compound comprising a IRF4 specific inhibitor, thereby inhibiting expression of IRF4 in the individual. In certain embodiments, administering the compound inhibits expression of IRF4 in the bone marrow, lymphoid tissue, or lymph node. In certain embodiments, the individual has, or is at risk of having blood cancer, myeloma, multiple myeloma (MM), B cell malignancies, lymphoma, B cell lymphoma, T cell lymphoma, or leukemia. In certain embodiments, the B-cell lymphoma is a non-Hodgkin's B-cell lymphoma. Examples of non-Hodgkin's B-cell lymphoma of certain embodiments that can be treated with compounds provided herein include, but are not limited to, diffuse large B cell lymphoma (DLBCL), activated B-cell lymphoma (ABC-DLBCL), germinal

center B-cell lymphoma (GCB DLBCL), follicular lymphoma, mucosa-associated lymphatic tissue lymphoma (MALT), small cell lymphocytic lymphoma, chronic lymphocytic leukemia, mantle cell lymphoma (MCL), Burkitt lymphoma, mediastinal large B cell lymphoma, Waldenström macroglobulinemia, nodal marginal zone B cell lymphoma (NMZL), splenic marginal zone lymphoma (SMZL), intravascular large B-cell lymphoma, primary effusion lymphoma, and lymphomatoid granulomatosis. In certain embodiments, the T-cell lymphoma that can be treated with compounds provided herein include, but are not limited to, peripheral T-cell lymphoma, adult T cell leukemia/lymphoma (ATLL), and anaplastic large cell lymphoma (ALCL). In certain embodiments, the leukemia that can be treated with compounds provided herein includes, but is not limited to, acute lymphocytic leukemia (ALL). In certain embodiments, the compound comprises an antisense compound targeted to IRF4. In certain embodiments, the compound comprises an oligonucleotide targeted to IRF4. In certain embodiments, the compound comprises a modified oligonucleotide 8 to 80 linked nucleosides in length and having a nucleobase sequence comprising at least 8 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 3-3383. In certain embodiments, the compound comprises a modified oligonucleotide 16 to 80 linked nucleosides in length and having a nucleobase sequence comprising the nucleobase sequence of any one of SEQ ID NOs: 3-3383. In certain embodiments, the compound comprises a modified oligonucleotide consisting of the nucleobase sequence of any one of SEQ ID NOs: 3-3383. In certain embodiments, the compound comprises a modified oligonucleotide of 16 to 80 linked nucleosides in length having a nucleobase sequence comprising any one of SEQ ID NOs: 2021, 560, 559, 1330, 1540, or 3303. In certain embodiments, the compound comprises a modified oligonucleotide having a nucleobase sequence consisting of any one of SEQ ID NOs: 2021, 560, 559, 1330, 1540, or 3303. In any of the foregoing embodiments, the modified oligonucleotide can be 10 to 30 linked nucleosides in length. In certain embodiments, the compound is ION 690890, 935658, 935696, 935762, 935918, 935968, 882800, 1012795, 1014095, and 1014834. In any of the foregoing embodiments, the compound can be single-stranded or double-stranded. In any of the foregoing embodiments, the compound can be an antisense compound or oligomeric compound. In certain embodiments, the compound is administered to the individual parenterally. In certain embodiments, administering the compound inhibits or reduces cancer cell proliferation, tumor growth, or metastasis. In certain embodiments, the individual is identified as having or at risk of having a cancer associated with IRF4.

In certain embodiments, a method of inhibiting expression of IRF4 in a cell comprises contacting the cell with a compound comprising a IRF4 specific inhibitor, thereby inhibiting expression of IRF4 in the cell. In certain embodiments, the cell is a cancer cell. In certain embodiments, the cell is a bone marrow, lymphoid tissue, or lymph node cell. In certain embodiments, the cell is in the bone marrow, lymphoid tissue, or lymph node. In certain embodiments, the cell is in the bone marrow, lymphoid tissue, or lymph node of an individual who has, or is at risk of having cancer, such as blood cancer, myeloma, multiple myeloma (MM), B cell malignancies, lymphoma, B cell lymphoma, T cell lymphoma, or leukemia. In certain embodiments, the compound comprises an antisense compound targeted to IRF4. In certain embodiments, the compound

comprises an oligonucleotide targeted to IRF4. In certain embodiments, the compound comprises a modified oligonucleotide 8 to 80 linked nucleosides in length and having a nucleobase sequence comprising at least 8 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 3-3383. In certain embodiments, the compound comprises a modified oligonucleotide 16 to 80 linked nucleosides in length and having a nucleobase sequence comprising the nucleobase sequence of any one of SEQ ID NOs: 3-3383. In certain embodiments, the compound comprises a modified oligonucleotide consisting of the nucleobase sequence of any one of SEQ ID NOs: 3-3383. In certain embodiments, the compound comprises a modified oligonucleotide of 16 to 80 linked nucleosides in length having a nucleobase sequence comprising any one of SEQ ID NOs: 2021, 560, 559, 1330, 1540, or 3303. In certain embodiments, the compound comprises a modified oligonucleotide having a nucleobase sequence consisting of any one of SEQ ID NOs: 2021, 560, 559, 1330, 1540, or 3303. In any of the foregoing embodiments, the modified oligonucleotide can be 10 to 30 linked nucleosides in length. In certain embodiments, the compound is ION 690890, 935658, 935696, 935762, 935918, 935968, 882800, 1012795, 1014095, and 1014834. In any of the foregoing embodiments, the compound can be single-stranded or double-stranded. In any of the foregoing embodiments, the compound can be an antisense compound or oligomeric compound.

In certain embodiments, a method of reducing or inhibiting cancer cell proliferation, tumor growth, or metastasis of an individual having, or at risk of having, a cancer associated with IRF4 comprises administering to the individual a compound comprising a IRF4 specific inhibitor, thereby reducing or inhibiting cancer cell proliferation, tumor growth, or metastasis in the individual. In certain embodiments, the individual has, or is at risk of having, blood cancer, myeloma, multiple myeloma (MM), B cell malignancies, lymphoma, B cell lymphoma, T cell lymphoma, or leukemia. Examples of cancers associated with IRF4 treatable, preventable, and/or ameliorable with the methods provided herein include blood cancer, myeloma, multiple myeloma (MM), B cell malignancies, lymphoma, B cell lymphoma, T cell lymphoma, or leukemia. In certain embodiments, the B-cell lymphoma is a non-Hodgkin's B-cell lymphoma. Examples of non-Hodgkin's B-cell lymphoma of certain embodiments that can be treated with compounds provided herein include, but are not limited to, diffuse large B cell lymphoma (DLBCL), activated B-cell lymphoma (ABC-DLBCL), germinal center B-cell lymphoma (GCB DLBCL), follicular lymphoma, mucosa-associated lymphatic tissue lymphoma (MALT), small cell lymphocytic lymphoma, chronic lymphocytic leukemia, mantle cell lymphoma (MCL), Burkitt lymphoma, mediastinal large B cell lymphoma, Waldenström macroglobulinemia, nodal marginal zone B cell lymphoma (NMZL), splenic marginal zone lymphoma (SMZL), intravascular large B-cell lymphoma, primary effusion lymphoma, and lymphomatoid granulomatosis. In certain embodiments, the T-cell lymphoma that can be treated with compounds provided herein include, but are not limited to, peripheral T-cell lymphoma, adult T cell leukemia/lymphoma (ATLL), and anaplastic large cell lymphoma (ALCL). In certain embodiments, the leukemia that can be treated with compounds provided herein includes, but is not limited to, acute lymphocytic leukemia (ALL). In certain embodiments, the compound comprises an antisense compound targeted to IRF4.

In certain embodiments, the compound comprises an oligonucleotide targeted to IRF4. In certain embodiments, the compound comprises a modified oligonucleotide 8 to 80 linked nucleosides in length and having a nucleobase sequence comprising at least 8 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 3-3383. In certain embodiments, the compound comprises a modified oligonucleotide 16 to 80 linked nucleosides in length and having a nucleobase sequence comprising the nucleobase sequence of any one of SEQ ID NOs: 3-3383. In certain embodiments, the compound comprises a modified oligonucleotide consisting of the nucleobase sequence of any one of SEQ ID NOs: 3-3383. In certain embodiments, the compound comprises a modified oligonucleotide of 16 to 80 linked nucleosides in length having a nucleobase sequence comprising any one of SEQ ID NOs: 2021, 560, 559, 1330, 1540, or 3303. In certain embodiments, the compound comprises a modified oligonucleotide having a nucleobase sequence consisting of any one of SEQ ID NOs: 2021, 560, 559, 1330, 1540, or 3303. In any of the foregoing embodiments, the modified oligonucleotide can be 10 to 30 linked nucleosides in length. In certain embodiments, the compound is ION 690890, 935658, 935696, 935762, 935918, 935968, 882800, 1012795, 1014095, and 1014834. In any of the foregoing embodiments, the compound can be single-stranded or double-stranded. In any of the foregoing embodiments, the compound can be an antisense compound or oligomeric compound. In certain embodiments, the compound is administered to the individual parenterally. In certain embodiments, the individual is identified as having or at risk of having a cancer associated with IRF4.

Certain embodiments are drawn to a compound comprising a IRF4 specific inhibitor for use in treating cancer. In certain embodiments, the cancer is a blood cancer, myeloma, multiple myeloma (MM), B cell malignancy, lymphoma, B cell lymphoma, T cell lymphoma, or leukemia. In certain embodiments, the B-cell lymphoma is a non-Hodgkin's B-cell lymphoma. Examples of non-Hodgkin's B-cell lymphoma of certain embodiments that can be treated with compounds provided herein include, but are not limited to, diffuse large B cell lymphoma (DLBCL), activated B-cell lymphoma (ABC-DLBCL), germinal center B-cell lymphoma (GCB DLBCL), follicular lymphoma, mucosa-associated lymphatic tissue lymphoma (MALT), small cell lymphocytic lymphoma, chronic lymphocytic leukemia, mantle cell lymphoma (MCL), Burkitt lymphoma, mediastinal large B cell lymphoma, Waldenström macroglobulinemia, nodal marginal zone B cell lymphoma (NMZL), splenic marginal zone lymphoma (SMZL), intravascular large B-cell lymphoma, primary effusion lymphoma, and lymphomatoid granulomatosis. In certain embodiments, the T-cell lymphoma that can be treated with compounds provided herein include, but are not limited to, peripheral T-cell lymphoma, adult T cell leukemia/lymphoma (ATLL), and anaplastic large cell lymphoma (ALCL). In certain embodiments, the leukemia that can be treated with compounds provided herein includes, but is not limited to, acute lymphocytic leukemia (ALL). In certain embodiments, the compound comprises an antisense compound targeted to IRF4. In certain embodiments, the compound comprises an oligonucleotide targeted to IRF4. In certain embodiments, the compound comprises a modified oligonucleotide 8 to 80 linked nucleosides in length and having a nucleobase sequence comprising at least 8 contiguous nucleobases of any of the nucleobase sequences of SEQ

ID NOs: 3-3383. In certain embodiments, the compound comprises a modified oligonucleotide 16 to 80 linked nucleosides in length and having a nucleobase sequence comprising the nucleobase sequence of any one of SEQ ID NOs: 3-3383. In certain embodiments, the compound comprises a modified oligonucleotide consisting of the nucleobase sequence of any one of SEQ ID NOs: 3-3383. In certain embodiments, the compound
5 comprises a modified oligonucleotide of 16 to 80 linked nucleosides in length having a nucleobase sequence comprising any one of SEQ ID NOs: 2021, 560, 559, 1330, 1540, or 3303. In certain embodiments, the compound comprises a modified oligonucleotide having a nucleobase sequence consisting of any one of SEQ ID NOs: 2021, 560, 559, 1330, 1540, or 3303. In any of the foregoing embodiments, the modified oligonucleotide can be 10 to 30 linked nucleosides in length. In certain embodiments, the compound is ION
10 690890, 935658, 935696, 935762, 935918, 935968, 882800, 1012795, 1014095, and 1014834. In any of the foregoing embodiments, the compound can be single-stranded or double-stranded. In any of the foregoing embodiments, the compound can be an antisense compound or oligomeric compound.

Certain embodiments are drawn to a compound comprising a IRF4 specific inhibitor for use in reducing or inhibiting cancer cell proliferation, tumor growth, or metastasis in an individual having cancer. In certain
15 embodiments, the cancer is a blood cancer, myeloma, multiple myeloma (MM), B cell malignancy, lymphoma, B cell lymphoma, T cell lymphoma, or leukemia. In certain embodiments, the compound comprises an antisense compound targeted to IRF4. In certain embodiments, the compound comprises an oligonucleotide targeted to IRF4. In certain embodiments, the compound comprises a modified oligonucleotide 8 to 80 linked nucleosides in length and having a nucleobase sequence comprising at least 8 contiguous nucleobases of any
20 of the nucleobase sequences of SEQ ID NOs: 3-3383. In certain embodiments, the compound comprises a modified oligonucleotide 16 to 80 linked nucleosides in length and having a nucleobase sequence comprising the nucleobase sequence of any one of SEQ ID NOs: 3-3383. In certain embodiments, the compound comprises a modified oligonucleotide consisting of the nucleobase sequence of any one of SEQ ID NOs: 3-3383. In certain embodiments, the compound comprises a modified oligonucleotide of 16 to 80 linked nucleosides in length
25 having a nucleobase sequence comprising any one of SEQ ID NOs: 2021, 560, 559, 1330, 1540, or 3303. In certain embodiments, the compound comprises a modified oligonucleotide having a nucleobase sequence consisting of any one of SEQ ID NOs: 2021, 560, 559, 1330, 1540, or 3303. In any of the foregoing embodiments, the modified oligonucleotide can be 10 to 30 linked nucleosides in length. In certain embodiments, the compound is ION 690890, 935658, 935696, 935762, 935918, 935968, 882800, 1012795,
30 1014095, and 1014834. In any of the foregoing embodiments, the compound can be single-stranded or double-stranded. In any of the foregoing embodiments, the compound can be an antisense compound or oligomeric compound.

Certain embodiments are drawn to use of a compound comprising a IRF4 specific inhibitor for the manufacture or preparation of a medicament for treating cancer. Certain embodiments are drawn to use of a

compound comprising a IRF4 specific inhibitor for the preparation of a medicament for treating a cancer associated with IRF4. In certain embodiments, the cancer is a blood cancer, myeloma, multiple myeloma (MM), B cell malignancy, lymphoma, B cell lymphoma, T cell lymphoma, or leukemia. In certain embodiments, the B-cell lymphoma is a non-Hodgkin's B-cell lymphoma. Examples of non-Hodgkin's B-cell lymphoma of certain embodiments that can be treated with compounds provided herein include, but are not limited to, diffuse large B cell lymphoma (DLBCL), activated B-cell lymphoma (ABC-DLBCL), germinal center B-cell lymphoma (GCB DLBCL), follicular lymphoma, mucosa-associated lymphatic tissue lymphoma (MALT), small cell lymphocytic lymphoma, chronic lymphocytic leukemia, mantle cell lymphoma (MCL), Burkitt lymphoma, mediastinal large B cell lymphoma, Waldenström macroglobulinemia, nodal marginal zone B cell lymphoma (NMZL), splenic marginal zone lymphoma (SMZL), intravascular large B-cell lymphoma, primary effusion lymphoma, and lymphomatoid granulomatosis. In certain embodiments, the T-cell lymphoma that can be treated with compounds provided herein include, but are not limited to, peripheral T-cell lymphoma, adult T cell leukemia/lymphoma (ATLL), and anaplastic large cell lymphoma (ALCL). In certain embodiments, the leukemia that can be treated with compounds provided herein includes, but is not limited to, acute lymphocytic leukemia (ALL). In certain embodiments, the compound comprises an antisense compound targeted to IRF4. In certain embodiments, the compound comprises an oligonucleotide targeted to IRF4. In certain embodiments, the compound comprises a modified oligonucleotide 8 to 80 linked nucleosides in length and having a nucleobase sequence comprising at least 8 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 3-3383. In certain embodiments, the compound comprises a modified oligonucleotide 16 to 80 linked nucleosides in length and having a nucleobase sequence comprising the nucleobase sequence of any one of SEQ ID NOs: 3-3383. In certain embodiments, the compound comprises a modified oligonucleotide consisting of the nucleobase sequence of any one of SEQ ID NOs: 3-3383. In certain embodiments, the compound comprises a modified oligonucleotide of 16 to 80 linked nucleosides in length having a nucleobase sequence comprising any one of SEQ ID NOs: 2021, 560, 559, 1330, 1540, or 3303. In certain embodiments, the compound comprises a modified oligonucleotide having a nucleobase sequence consisting of any one of SEQ ID NOs: 2021, 560, 559, 1330, 1540, or 3303. In any of the foregoing embodiments, the modified oligonucleotide can be 10 to 30 linked nucleosides in length. In certain embodiments, the compound is ION 690890, 935658, 935696, 935762, 935918, 935968, 882800, 1012795, 1014095, and 1014834. In any of the foregoing embodiments, the compound can be single-stranded or double-stranded. In any of the foregoing embodiments, the compound can be an antisense compound or oligomeric compound.

Certain embodiments are drawn to use of a compound comprising a IRF4 specific inhibitor for the manufacture or preparation of a medicament for reducing or inhibiting cancer cell proliferation, tumor growth, or metastasis in an individual having cancer. In certain embodiments, the cancer is a blood cancer, myeloma, multiple myeloma (MM), B cell malignancy, lymphoma, B cell lymphoma, T cell lymphoma, or leukemia.

Certain embodiments are drawn to use of a compound comprising a IRF4 specific inhibitor for the preparation of a medicament for reducing or inhibiting cancer cell proliferation, tumor growth, or metastasis in an individual having cancer. In certain embodiments, the cancer is a blood cancer, myeloma, multiple myeloma (MM), B cell malignancy, lymphoma, B cell lymphoma, T cell lymphoma, or leukemia. In certain
5 embodiments, the B-cell lymphoma is a non-Hodgkin's B-cell lymphoma. Examples of non-Hodgkin's B-cell lymphoma of certain embodiments include, but are not limited to, diffuse large B cell lymphoma (DLBCL), activated B-cell lymphoma (ABC-DLBCL), germinal center B-cell lymphoma (GCB DLBCL), follicular lymphoma, mucosa-associated lymphatic tissue lymphoma (MALT), small cell lymphocytic lymphoma, chronic lymphocytic leukemia, mantle cell lymphoma (MCL), Burkitt lymphoma, mediastinal large B cell
10 lymphoma, Waldenström macroglobulinemia, nodal marginal zone B cell lymphoma (NMZL), splenic marginal zone lymphoma (SMZL), intravascular large B-cell lymphoma, primary effusion lymphoma, and lymphomatoid granulomatosis. In certain embodiments, the T-cell lymphoma includes, but is not limited to, peripheral T-cell lymphoma, adult T cell leukemia/lymphoma (ATLL), and anaplastic large cell lymphoma (ALCL). In certain embodiments, the leukemia includes, but is not limited to, acute lymphocytic leukemia
15 (ALL). In certain embodiments, the compound comprises an antisense compound targeted to IRF4. In certain embodiments, the compound comprises an oligonucleotide targeted to IRF4. In certain embodiments, the compound comprises a modified oligonucleotide 8 to 80 linked nucleosides in length and having a nucleobase sequence comprising at least 8 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 3-3383. In certain embodiments, the compound comprises a modified oligonucleotide 16 to 80 linked nucleosides
20 in length and having a nucleobase sequence comprising the nucleobase sequence of any one of SEQ ID NOs: 3-3383. In certain embodiments, the compound comprises a modified oligonucleotide consisting of the nucleobase sequence of any one of SEQ ID NOs: 3-3383. In certain embodiments, the compound comprises a modified oligonucleotide of 16 to 80 linked nucleosides in length having a nucleobase sequence comprising any one of SEQ ID NOs: 2021, 560, 559, 1330, 1540, or 3303. In certain embodiments, the compound
25 comprises a modified oligonucleotide having a nucleobase sequence consisting of any one of SEQ ID NOs: 2021, 560, 559, 1330, 1540, or 3303. In any of the foregoing embodiments, the modified oligonucleotide can be 10 to 30 linked nucleosides in length. In certain embodiments, the compound is ION 690890, 935658, 935696, 935762, 935918, 935968, 882800, 1012795, 1014095, and 1014834. In any of the foregoing embodiments, the compound can be single-stranded or double-stranded. In any of the foregoing embodiments,
30 the compound can be an antisense compound or oligomeric compound.

In any of the foregoing methods or uses, the compound can be targeted to IRF4. In certain embodiments, the compound comprises or consists of a modified oligonucleotide, for example a modified oligonucleotide 8 to 80 linked nucleosides in length, 10 to 30 linked nucleosides in length, 12 to 30 linked nucleosides in length, or 20 linked nucleosides in length. In certain embodiments, the modified oligonucleotide
35 is at least 80%, 85%, 90%, 95% or 100% complementary to any of the nucleobase sequences recited in SEQ ID NOs: 1-2. In certain embodiments, the modified oligonucleotide comprises at least one modified

internucleoside linkage, at least one modified sugar and/or at least one modified nucleobase. In certain embodiments, the modified internucleoside linkage is a phosphorothioate internucleoside linkage, the modified sugar is a bicyclic sugar or a 2'-O-methoxyethyl, and the modified nucleobase is a 5-methylcytosine. In certain embodiments, the modified oligonucleotide comprises a gap segment consisting of linked deoxynucleosides; a 5' wing segment consisting of linked nucleosides; and a 3' wing segment consisting of linked nucleosides, wherein the gap segment is positioned immediately adjacent to and between the 5' wing segment and the 3' wing segment and wherein each nucleoside of each wing segment comprises a modified sugar.

In any of the foregoing embodiments, the modified oligonucleotide can be 12 to 30, 15 to 30, 15 to 25, 15 to 24, 16 to 24, 17 to 24, 18 to 24, 19 to 24, 20 to 24, 19 to 22, 20 to 22, 16 to 20, or 17 or 20 linked nucleosides in length. In certain embodiments, the modified oligonucleotide is at least 80%, 85%, 90%, 95% or 100% complementary to any of the nucleobase sequences recited in SEQ ID NOs: 1-2. In certain embodiments, the modified oligonucleotide comprises at least one modified internucleoside linkage, at least one modified sugar and/or at least one modified nucleobase. In certain embodiments, the modified internucleoside linkage is a phosphorothioate internucleoside linkage, the modified sugar is a bicyclic sugar or a 2'-O-methoxyethyl, and the modified nucleobase is a 5-methylcytosine. In certain embodiments, the modified oligonucleotide comprises a gap segment consisting of linked 2'-deoxynucleosides; a 5' wing segment consisting of linked nucleosides; and a 3' wing segment consisting of linked nucleosides, wherein the gap segment is positioned immediately adjacent to and between the 5' wing segment and the 3' wing segment and wherein each nucleoside of each wing segment comprises a modified sugar.

In any of the foregoing methods or uses, the compound can comprise or consist of a modified oligonucleotide 16 to 80 linked nucleosides in length and having a nucleobase sequence comprising any one of SEQ ID NOs: 3-3383, wherein the modified oligonucleotide comprises:

a gap segment consisting of linked 2'-deoxynucleosides;

a 5' wing segment consisting of linked nucleosides; and

a 3' wing segment consisting of linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment and wherein each nucleoside of each wing segment comprises a modified sugar. In certain embodiments, the modified oligonucleotide is 16-30 linked nucleosides in length. In certain embodiments, the modified oligonucleotide is 16 linked nucleosides in length.

In any of the foregoing methods or uses, the compound can comprise or consist of a modified oligonucleotide 16-80 linked nucleobases in length having a nucleobase sequence comprising the sequence recited in any one of SEQ ID NOs: 2021, 560, 559, 1330, 1540, or 3303, wherein the modified oligonucleotide comprises:

a gap segment consisting of linked deoxynucleosides;

a 5' wing segment consisting of linked nucleosides; and

a 3' wing segment consisting of linked nucleosides;

5 wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment and wherein each nucleoside of each wing segment comprises a modified sugar. In certain embodiments, the modified oligonucleotide is 16-30 linked nucleosides in length. In certain embodiments, the modified oligonucleotide is 16 linked nucleosides in length.

In any of the foregoing methods or uses, the compound can comprise or consist of a modified oligonucleotide 16-80 linked nucleobases in length having a nucleobase sequence comprising the sequence
10 recited in any one of SEQ ID NOs: 1330 or 3303, wherein the modified oligonucleotide comprises:

a gap segment consisting of ten linked deoxynucleosides;

a 5' wing segment consisting of three linked nucleosides; and

a 3' wing segment consisting of three linked nucleosides;

15 wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment; wherein each nucleoside of each wing segment comprises a cEt nucleoside; wherein each internucleoside linkage is a phosphorothioate linkage; and wherein each cytosine is a 5-methylcytosine. In certain embodiments, the modified oligonucleotide is 16-30 linked nucleosides in length. In certain embodiments, the modified oligonucleotide is 16 linked nucleosides in length.

In any of the foregoing methods or uses, the compound can comprise or consist of a modified oligonucleotide 16-80 linked nucleobases in length having a nucleobase sequence comprising the sequence
20 recited in any one of SEQ ID NOs: 559 or 560, wherein the modified oligonucleotide comprises:

a gap segment consisting of ten linked deoxynucleosides;

a 5' wing segment consisting of one linked nucleoside; and

a 3' wing segment consisting of five linked nucleosides;

25 wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment; wherein the 5' wing segment comprises a cEt nucleoside; wherein the 3' wing segment comprises a cEt nucleoside, a 2'-O-methoxyethyl nucleoside, a cEt nucleoside, a 2'-O-methoxyethyl nucleoside, and a cEt nucleoside in the 5' to 3' direction; wherein each internucleoside linkage is a phosphorothioate linkage; and wherein each cytosine is a 5-methylcytosine. In certain embodiments, the modified oligonucleotide is 16-30 linked
30 nucleosides in length. In certain embodiments, the modified oligonucleotide is 16 linked nucleosides in length.

In any of the foregoing methods or uses, the compound can comprise or consist of a modified oligonucleotide 16-80 linked nucleobases in length having a nucleobase sequence comprising the sequence recited in any one of SEQ ID NOs: 1330 or 2021, wherein the modified oligonucleotide comprises:

- a gap segment consisting of ten linked deoxynucleosides;
- 5 a 5' wing segment consisting of two linked nucleosides; and
- a 3' wing segment consisting of four linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment; wherein each nucleoside of the 5' wing segment comprises a cEt nucleoside; wherein the 3' wing segment comprises a cEt nucleoside, a 2'-O-methoxyethyl nucleoside, a cEt nucleoside, and a 2'-O-methoxyethyl nucleoside in the 5' to 3' direction; wherein each internucleoside linkage is a phosphorothioate linkage; and wherein each cytosine is a 5-methylcytosine. In certain embodiments, the modified oligonucleotide is 16-30 linked nucleosides in length. In certain embodiments, the modified oligonucleotide is 16 linked nucleosides in length.

In any of the foregoing methods or uses, the compound can comprise or consist of a modified oligonucleotide 16-80 linked nucleobases in length having a nucleobase sequence comprising the sequence recited in SEQ ID NO: 560, wherein the modified oligonucleotide comprises:

- a gap segment consisting of nine linked deoxynucleosides;
- a 5' wing segment consisting of two linked nucleosides; and
- a 3' wing segment consisting of five linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment; wherein each nucleoside of the 5' wing segment comprises a cEt nucleoside; wherein the 3' wing segment comprises a cEt nucleoside, a 2'-O-methoxyethyl nucleoside, a cEt nucleoside, a 2'-O-methoxyethyl nucleoside, and a cEt nucleoside in the 5' to 3' direction; wherein each internucleoside linkage is a phosphorothioate linkage; and wherein each cytosine is a 5-methylcytosine. In certain embodiments, the modified oligonucleotide is 16-30 linked nucleosides in length. In certain embodiments, the modified oligonucleotide is 16 linked nucleosides in length.

In any of the foregoing methods or uses, the compound can comprise or consist of a modified oligonucleotide 16-80 linked nucleobases in length having a nucleobase sequence comprising the sequence recited in SEQ ID NOs: 2021, wherein the modified oligonucleotide comprises:

- a gap segment consisting of nine linked deoxynucleosides;
- 30 a 5' wing segment consisting of two linked nucleosides; and
- a 3' wing segment consisting of five linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment; wherein each nucleoside of the 5' wing segment comprises a cEt nucleoside; wherein the 3' wing segment comprises a 2'-O-methoxyethyl nucleoside, a 2'-O-methoxyethyl nucleoside, a 2'-O-methoxyethyl nucleoside, a cEt nucleoside, and a cEt nucleoside in the 5' to 3' direction; wherein each internucleoside linkage is a phosphorothioate linkage; and wherein each cytosine is a 5-methylcytosine. In certain embodiments, the modified oligonucleotide is 16-30 linked nucleosides in length. In certain embodiments, the modified oligonucleotide is 16 linked nucleosides in length.

In any of the foregoing methods or uses, the compound can comprise or consist of a modified oligonucleotide 16-80 linked nucleobases in length having a nucleobase sequence comprising the sequence recited in SEQ ID NOs: 1540, wherein the modified oligonucleotide comprises:

a gap segment consisting of nine linked deoxynucleosides;

a 5' wing segment consisting of two linked nucleosides; and

a 3' wing segment consisting of five linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment; wherein each nucleoside of the 5' wing segment comprises a cEt nucleoside; wherein the 3' wing segment comprises a 2'-O-methoxyethyl nucleoside, a 2'-O-methoxyethyl nucleoside, a 2'-O-methoxyethyl nucleoside, a cEt nucleoside, and a cEt nucleoside in the 5' to 3' direction; wherein each internucleoside linkage is a phosphorothioate linkage; and wherein each cytosine is a 5-methylcytosine. In certain embodiments, the modified oligonucleotide is 16-30 linked nucleosides in length. In certain embodiments, the modified oligonucleotide is 16 linked nucleosides in length.

In any of the foregoing methods or uses, the compound can comprise or consist of a modified oligonucleotide 16-80 linked nucleobases in length having a nucleobase sequence comprising the sequence recited in SEQ ID NOs: 560, wherein the modified oligonucleotide comprises:

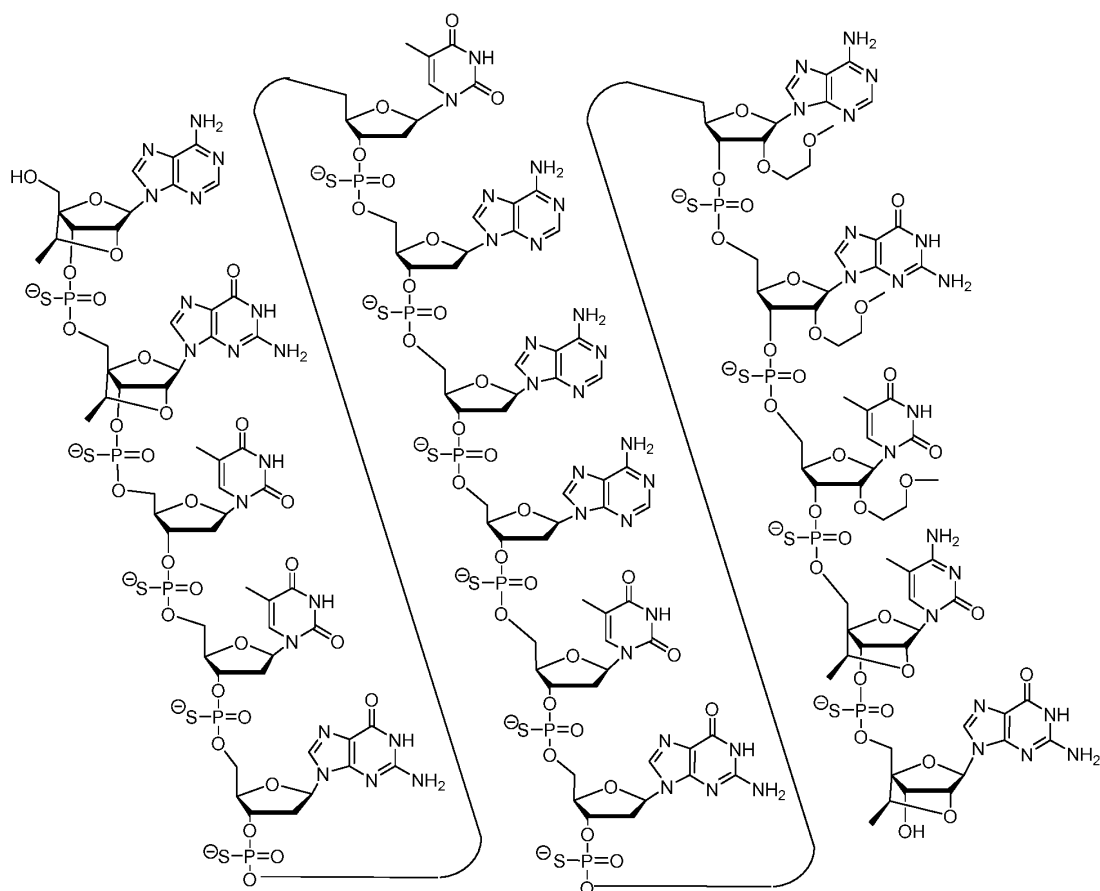
a gap segment consisting of nine linked deoxynucleosides;

a 5' wing segment consisting of two linked nucleosides; and

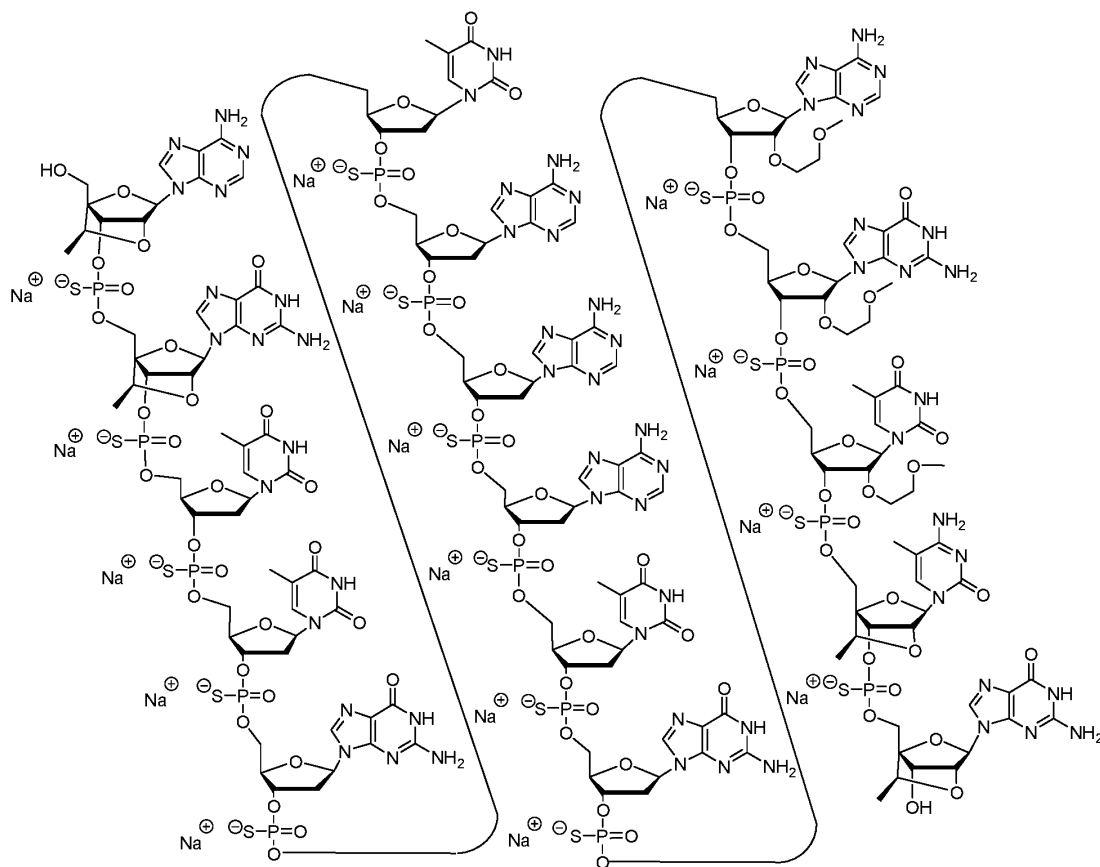
a 3' wing segment consisting of five linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment; wherein each nucleoside of the 5' wing segment comprises a cEt nucleoside; wherein the 3' wing segment comprises a 2'-O-methoxyethyl nucleoside, a cEt nucleoside, a 2'-O-methoxyethyl nucleoside, a cEt nucleoside, and a 2'-O-methoxyethyl nucleoside in the 5' to 3' direction; wherein each internucleoside linkage is a phosphorothioate linkage; and wherein each cytosine is a 5-methylcytosine. In certain embodiments, the modified oligonucleotide is 16-30 linked nucleosides in length. In certain embodiments, the modified oligonucleotide is 16 linked nucleosides in length.

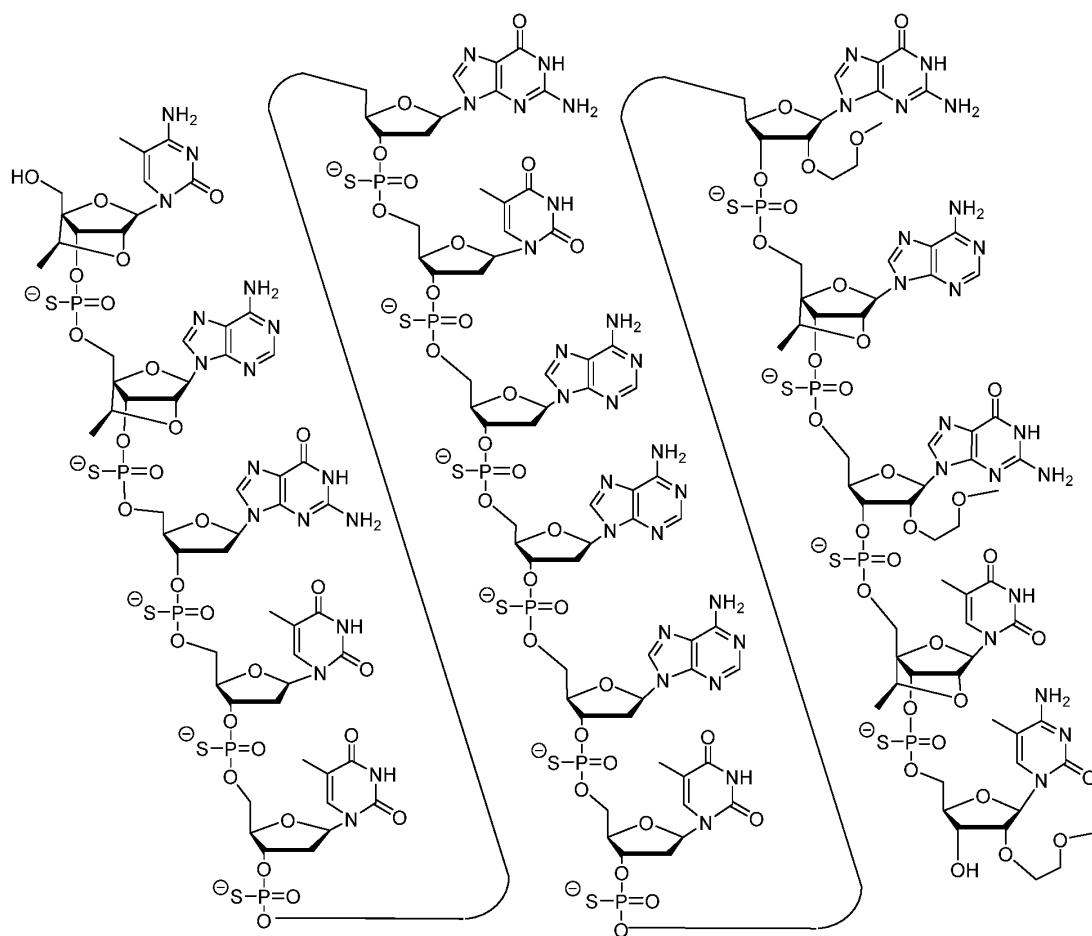
In any of the foregoing methods or uses, the compound can comprise or consist of ION 935918 or salt thereof, having the following chemical structure:



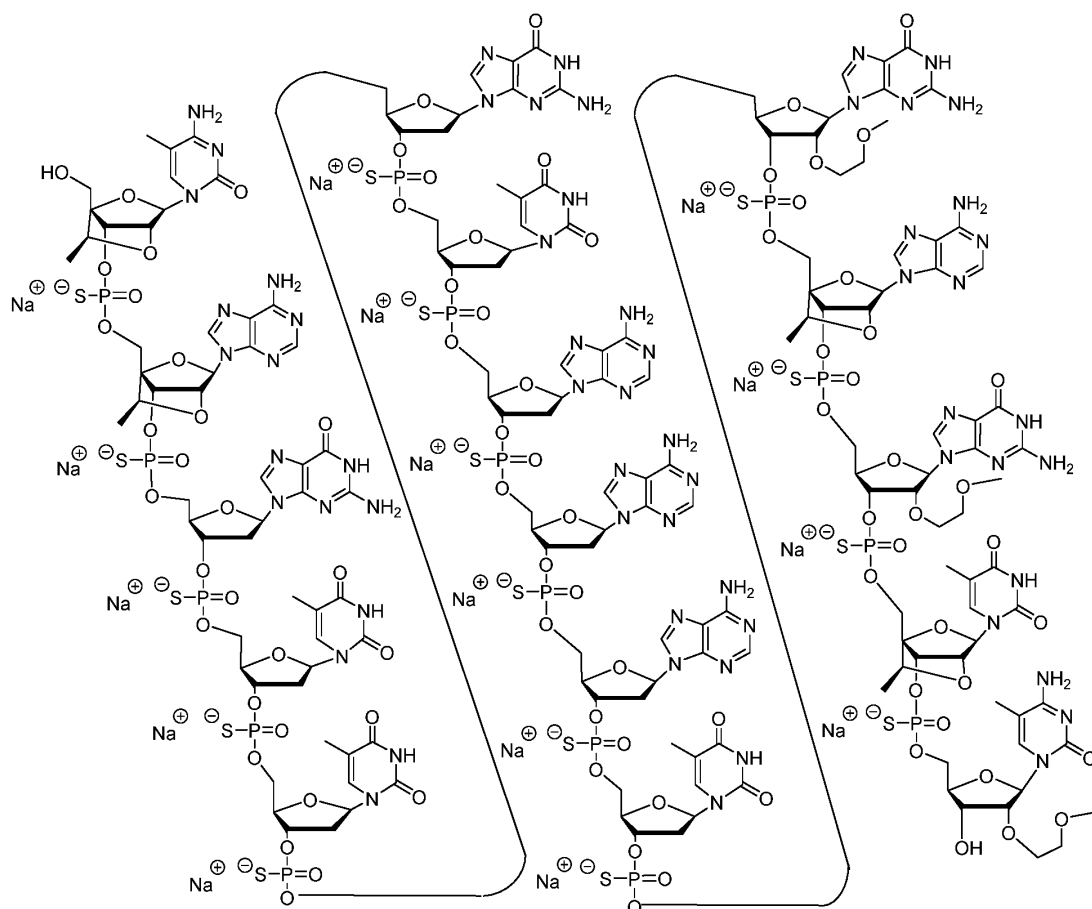
In any of the foregoing methods or uses, the compound can comprise or consist of the sodium salt of ION 935918, having the following chemical structure:



In any of the foregoing methods or uses, the compound can comprise or consist of ION 935968 or salt thereof, having the following chemical structure:



In any of the foregoing methods or uses, the compound can comprise or consist of the sodium salt of ION 935968, having the following chemical structure:



In any of the foregoing methods or uses, the compound can be administered parenterally. For example, in certain embodiments the compound can be administered through injection or infusion. Parenteral administration includes subcutaneous administration, intravenous administration, intramuscular administration, intraarterial administration, intraperitoneal administration, or intracranial administration, e.g. intrathecal or intracerebroventricular administration.

Certain Combinations and Combination Therapies

In certain embodiments, a first agent comprising a compound described herein is co-administered with one or more secondary agents. In certain embodiments, such second agents are designed to treat the same disease, disorder, or condition as the first agent described herein. In certain embodiments, such second agents are designed to treat a different disease, disorder, or condition as the first agent described herein. In certain embodiments, a first agent is designed to treat an undesired side effect of a second agent. In certain embodiments, second agents are co-administered with the first agent to treat an undesired effect of the first

agent. In certain embodiments, such second agents are designed to treat an undesired side effect of one or more pharmaceutical compositions as described herein. In certain embodiments, second agents are co-administered with the first agent to produce a combinational effect. In certain embodiments, second agents are co-administered with the first agent to produce a synergistic effect. In certain embodiments, the co-administration of the first and second agents permits use of lower dosages than would be required to achieve a therapeutic or prophylactic effect if the agents were administered as independent therapy.

In certain embodiments, one or more compounds or compositions provided herein are co-administered with one or more secondary agents. In certain embodiments, one or more compounds or compositions provided herein and one or more secondary agents, are administered at different times. In certain embodiments, one or more compounds or compositions provided herein and one or more secondary agents, are prepared together in a single formulation. In certain embodiments, one or more compounds or compositions provided herein and one or more secondary agents, are prepared separately. In certain embodiments, a secondary agent is selected from: proteasome inhibitors including but not limited to bortezomib, carfilzomib, and ixazomib; BTK inhibitors including but not limited to ibrutinib; IMiDs including but not limited to thalidomide, lenalidomide, and pomalidomide; BCL2 inhibitors including but not limited to venetoclax; HDAC inhibitors including but not limited to panobinostat; CDK inhibitors including but not limited to dinaciclib; XPO1 inhibitors including but not limited to selinexor; BET inhibitors including but not limited to CPI-0610; anti-CD38 antibodies including but not limited to daratumumab, isatuximab, and MOR202; anti-CD319 or anti-SLAMF7 antibodies including but not limited to elotuzumab; dexamethasone, cisplatin, doxorubicin, cyclophosphamide, and etoposide.

Certain embodiments are directed to the use of a compound targeted to IRF4 as described herein in combination with a secondary agent. In particular embodiments such use is in a method of treating a patient suffering from cancer including, but not limited to, blood cancer, myeloma, multiple myeloma (MM), B cell malignancies, lymphoma, B cell lymphoma, T cell lymphoma, or leukemia. In certain embodiments, such use is in the preparation or manufacture of a medicament for treating cancer including, but not limited to, blood cancer, myeloma, multiple myeloma (MM), B cell malignancies, lymphoma, B cell lymphoma, T cell lymphoma, or leukemia. In certain embodiments, the B-cell lymphoma is a non-Hodgkin's B-cell lymphoma. Examples of non-Hodgkin's B-cell lymphoma of certain embodiments that can be treated with compounds provided herein include, but are not limited to, diffuse large B cell lymphoma (DLBCL), activated B-cell lymphoma (ABC-DLBCL), germinal center B-cell lymphoma (GCB DLBCL), follicular lymphoma, mucosa-associated lymphatic tissue lymphoma (MALT), small cell lymphocytic lymphoma, chronic lymphocytic leukemia, mantle cell lymphoma (MCL), Burkitt lymphoma, mediastinal large B cell lymphoma, Waldenström macroglobulinemia, nodal marginal zone B cell lymphoma (NMZL), splenic marginal zone lymphoma (SMZL), intravascular large B-cell lymphoma, primary effusion lymphoma, and lymphomatoid granulomatosis. In certain embodiments, the T-cell lymphoma includes, but is not limited to, peripheral T-cell lymphoma, adult T cell leukemia/lymphoma (ATLL), and anaplastic large cell lymphoma (ALCL). In certain

embodiments, the leukemia includes, but is not limited to, acute lymphocytic leukemia (ALL). In certain embodiments, a secondary agent is selected from: proteasome inhibitors including but not limited to bortezomib, carfilzomib, and ixazomib; BTK inhibitors including but not limited to ibrutinib; IMiDs including but not limited to thalidomide, lenalidomide, and pomalidomide; BCL2 inhibitors including but not limited to venetoclax; HDAC inhibitors including but not limited to panobinostat; CDK inhibitors including but not limited to dinaciclib; XPO1 inhibitors including but not limited to selinexor; BET inhibitors including but not limited to CPI-0610; anti-CD38 antibodies including but not limited to daratumumab, isatuximab, and MOR202; anti-CD319 or anti-SLAMF7 antibodies including but not limited to elotuzumab; dexamethasone, cisplatin, doxorubicin, cyclophosphamide, and etoposide.

Certain embodiments are drawn to a combination of a compound targeted to IRF4 as described herein and a secondary agent, such as a secondary agent selected from: proteasome inhibitors including but not limited to bortezomib, carfilzomib, and ixazomib; BTK inhibitors including but not limited to ibrutinib; IMiDs including but not limited to thalidomide, lenalidomide, and pomalidomide; BCL2 inhibitors including but not limited to venetoclax; HDAC inhibitors including but not limited to panobinostat; CDK inhibitors including but not limited to dinaciclib; XPO1 inhibitors including but not limited to selinexor; BET inhibitors including but not limited to CPI-0610; dexamethasone, thalidomide, cisplatin, doxorubicin, cyclophosphamide, and etoposide. In certain embodiments, such a combination of a compound targeted to IRF4 as described herein and a secondary agent, such as a secondary agent selected from: proteasome inhibitors including but not limited to bortezomib, carfilzomib, and ixazomib; BTK inhibitors including but not limited to ibrutinib; IMiDs including but not limited to lenalidomide; BCL2 inhibitors including but not limited to venetoclax; HDAC inhibitors including but not limited to panobinostat; CDK inhibitors including but not limited to dinaciclib; XPO1 inhibitors including but not limited to selinexor; BET inhibitors including but not limited to CPI-0610; anti-CD38 antibodies including but not limited to daratumumab, isatuximab, and MOR202; anti-CD319 or anti-SLAMF7 antibodies including but not limited to elotuzumab; dexamethasone, cisplatin, doxorubicin, cyclophosphamide, and etoposide. Such combinations can be useful for reducing or inhibiting cancer cell proliferation, tumor growth, or metastasis and/or treating cancer including, but not limited to, blood cancer, myeloma, multiple myeloma (MM), B cell malignancies, lymphoma, B cell lymphoma, T cell lymphoma, or leukemia.

In certain embodiments the compound targeted to IRF4 as described herein and the secondary agent are used in combination treatment by administering the two agents simultaneously, separately or sequentially. In certain embodiments the two agents are formulated as a fixed dose combination product. In other embodiments the two agents are provided to the patient as separate units which can then either be taken simultaneously or serially (sequentially).

Certain Compounds

In certain embodiments, compounds described herein can be antisense compounds. In certain embodiments, the antisense compound comprises or consists of an oligomeric compound. In certain embodiments, the oligomeric compound comprises a modified oligonucleotide. In certain embodiments, the modified oligonucleotide has a nucleobase sequence complementary to that of a target nucleic acid.

5 In certain embodiments, a compound described herein comprises or consists of a modified oligonucleotide. In certain embodiments, the modified oligonucleotide has a nucleobase sequence complementary to that of a target nucleic acid.

In certain embodiments, a compound or antisense compound is single-stranded. Such a single-stranded compound or antisense compound comprises or consists of an oligomeric compound. In certain
10 embodiments, such an oligomeric compound comprises or consists of an oligonucleotide and optionally a conjugate group. In certain embodiments, the oligonucleotide is an antisense oligonucleotide. In certain embodiments, the oligonucleotide is modified. In certain embodiments, the oligonucleotide of a single-stranded antisense compound or oligomeric compound comprises a self-complementary nucleobase sequence.

In certain embodiments, compounds are double-stranded. Such double-stranded compounds comprise
15 a first modified oligonucleotide having a region complementary to a target nucleic acid and a second modified oligonucleotide having a region complementary to the first modified oligonucleotide. In certain embodiments, the modified oligonucleotide is an RNA oligonucleotide. In such embodiments, the thymine nucleobase in the modified oligonucleotide is replaced by a uracil nucleobase. In certain embodiments, compound comprises a conjugate group. In certain embodiments, one of the modified oligonucleotides is conjugated. In certain
20 embodiments, both the modified oligonucleotides are conjugated. In certain embodiments, the first modified oligonucleotide is conjugated. In certain embodiments, the second modified oligonucleotide is conjugated. In certain embodiments, the first modified oligonucleotide is 12-30 linked nucleosides in length and the second modified oligonucleotide is 12-30 linked nucleosides in length. In certain embodiments, one of the modified oligonucleotides has a nucleobase sequence comprising at least 8 contiguous nucleobases of any of SEQ ID
25 NOs: 3-3383.

In certain embodiments, antisense compounds are double-stranded. Such double-stranded antisense compounds comprise a first oligomeric compound having a region complementary to a target nucleic acid and a second oligomeric compound having a region complementary to the first oligomeric compound. The first oligomeric compound of such double stranded antisense compounds typically comprises or consists of a
30 modified oligonucleotide and optionally a conjugate group. The oligonucleotide of the second oligomeric compound of such double-stranded antisense compound may be modified or unmodified. Either or both oligomeric compounds of a double-stranded antisense compound may comprise a conjugate group. The oligomeric compounds of double-stranded antisense compounds may include non-complementary overhanging nucleosides.

Examples of single-stranded and double-stranded compounds include but are not limited to oligonucleotides, siRNAs, microRNA targeting oligonucleotides, and single-stranded RNAi compounds, such as small hairpin RNAs (shRNAs), single-stranded siRNAs (ssRNAs), and microRNA mimics.

5 In certain embodiments, a compound described herein has a nucleobase sequence that, when written in the 5' to 3' direction, comprises the reverse complement of the target segment of a target nucleic acid to which it is targeted.

In certain embodiments, a compound described herein comprises an oligonucleotide 10 to 30 linked subunits in length. In certain embodiments, a compound described herein comprises an oligonucleotide 12 to 30 linked subunits in length. In certain embodiments, a compound described herein comprises an oligonucleotide 12 to 22 linked subunits in length. In certain embodiments, compound described herein comprises an oligonucleotide 14 to 30 linked subunits in length. In certain embodiments, compound described herein comprises an oligonucleotide 14 to 20 linked subunits in length. In certain embodiments, a compound described herein comprises an oligonucleotide 15 to 30 linked subunits in length. In certain embodiments, a compound described herein comprises an oligonucleotide 15 to 20 linked subunits in length. In certain
15 embodiments, a compound described herein comprises an oligonucleotide 16 to 30 linked subunits in length. In certain embodiments, a compound described herein comprises an oligonucleotide 16 to 20 linked subunits in length. In certain embodiments, a compound described herein comprises an oligonucleotide 17 to 30 linked subunits in length. In certain embodiments, a compound described herein comprises an oligonucleotide 17 to 20 linked subunits in length. In certain embodiments, a compound described herein comprises an oligonucleotide 18 to 30 linked subunits in length. In certain embodiments, a compound described herein comprises an oligonucleotide 18 to 21 linked subunits in length. In certain embodiments, a compound described herein comprises an oligonucleotide 18 to 20 linked subunits in length. In certain embodiments, a compound described herein comprises an oligonucleotide 20 to 30 linked subunits in length. In other words, such oligonucleotides are 12 to 30 linked subunits, 14 to 30 linked subunits, 14 to 20 subunits, 15 to 30 subunits, 15 to 20 subunits, 16 to 30 subunits, 16 to 20 subunits, 17 to 30 subunits, 17 to 20 subunits, 18 to 30 subunits, 18 to 20 subunits, 18 to 21 subunits, 20 to 30 subunits, or 12 to 22 linked subunits in length, respectively. In certain
25 embodiments, a compound described herein comprises an oligonucleotide 14 linked subunits in length. In certain embodiments, a compound described herein comprises an oligonucleotide 16 linked subunits in length. In certain embodiments, a compound described herein comprises an oligonucleotide 17 linked subunits in length. In certain embodiments, compound described herein comprises an oligonucleotide 18 linked subunits in length. In certain embodiments, a compound described herein comprises an oligonucleotide 19 linked subunits in length. In certain embodiments, a compound described herein comprises an oligonucleotide 20 linked subunits in length. In other embodiments, a compound described herein comprises an oligonucleotide 8 to 80, 12 to 50, 13 to 30, 13 to 50, 14 to 30, 14 to 50, 15 to 30, 15 to 50, 16 to 30, 16 to 50, 17 to 30, 17 to 50, 18 to 22, 18 to 24, 18 to 30, 18 to 50, 19 to 22, 19 to 30, 19 to 50, or 20 to 30 linked subunits. In certain such
35 embodiments, the compound described herein comprises an oligonucleotide 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, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, or 80 linked subunits in length, or a range defined by any two of the above values. In some embodiments the linked subunits are nucleotides, nucleosides, or nucleobases.

5 In certain embodiments, the compound may further comprise additional features or elements, such as a conjugate group, that are attached to the oligonucleotide. In certain embodiments, such compounds are antisense compounds. In certain embodiments, such compounds are oligomeric compounds. In embodiments where a conjugate group comprises a nucleoside (*i.e.* a nucleoside that links the conjugate group to the oligonucleotide), the nucleoside of the conjugate group is not counted in the length of the oligonucleotide.

10 In certain embodiments, compounds may be shortened or truncated. For example, a single subunit may be deleted from the 5' end (5' truncation), or alternatively from the 3' end (3' truncation). A shortened or truncated compound targeted to an IRF4 nucleic acid may have two subunits deleted from the 5' end, or alternatively may have two subunits deleted from the 3' end, of the compound. Alternatively, the deleted nucleosides may be dispersed throughout the compound.

15 When a single additional subunit is present in a lengthened compound, the additional subunit may be located at the 5' or 3' end of the compound. When two or more additional subunits are present, the added subunits may be adjacent to each other, for example, in a compound having two subunits added to the 5' end (5' addition), or alternatively to the 3' end (3' addition), of the compound. Alternatively, the added subunits may be dispersed throughout the compound.

20 It is possible to increase or decrease the length of a compound, such as an oligonucleotide, and/or introduce mismatch bases without eliminating activity (Woolf et al. *Proc. Natl. Acad. Sci. USA* 1992, 89:7305-7309; Gautschi et al. *J. Natl. Cancer Inst.* March 2001, 93:463-471; Maher and Dolnick *Nuc. Acid. Res.* 1998, 16:3341-3358). However, seemingly small changes in oligonucleotide sequence, chemistry and motif can make large differences in one or more of the many properties required for clinical development (Seth et al. *J. Med. Chem.* 2009, 52, 10; Egli et al. *J. Am. Chem. Soc.* 2011, 133, 16642).

25 In certain embodiments, compounds described herein are interfering RNA compounds (RNAi), which include double-stranded RNA compounds (also referred to as short-interfering RNA or siRNA) and single-stranded RNAi compounds (or ssRNA). Such compounds work at least in part through the RISC pathway to degrade and/or sequester a target nucleic acid (thus, include microRNA/microRNA-mimic compounds). As used herein, the term siRNA is meant to be equivalent to other terms used to describe nucleic acid molecules that are capable of mediating sequence specific RNAi, for example short interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA), short hairpin RNA (shRNA), short interfering oligonucleotide, short interfering nucleic acid, short interfering modified oligonucleotide, chemically modified siRNA, post-transcriptional gene silencing RNA (ptgsRNA), and others. In addition, as used herein, the term "RNAi" is
30 meant to be equivalent to other terms used to describe sequence specific RNA interference, such as post transcriptional gene silencing, translational inhibition, or epigenetics.

In certain embodiments, a compound described herein can comprise any of the oligonucleotide sequences targeted to IRF4 described herein. In certain embodiments, the compound can be double-stranded. In certain embodiments, the compound comprises a first strand comprising at least an 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 contiguous nucleobase portion of any one of SEQ ID NOs: 3-3383 and a second strand.

5 In certain embodiments, the compound comprises a first strand comprising the nucleobase sequence of any one of SEQ ID NOs: 3-3383 and a second strand. In certain embodiments, the compound comprises ribonucleotides in which the first strand has uracil (U) in place of thymine (T) in any one of SEQ ID NOs: 3-3383. In certain embodiments, the compound comprises (i) a first strand comprising a nucleobase sequence complementary to the site on IRF4 to which any of SEQ ID NOs: 3-3383 is targeted, and (ii) a second strand. In certain

10 embodiments, the compound comprises one or more modified nucleotides in which the 2' position in the sugar contains a halogen (such as fluorine group; 2'-F) or contains an alkoxy group (such as a methoxy group; 2'-OMe). In certain embodiments, the compound comprises at least one 2'-F sugar modification and at least one 2'-OMe sugar modification. In certain embodiments, the at least one 2'-F sugar modification and at least one 2'-OMe sugar modification are arranged in an alternating pattern for at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13,

15 14, 15, 16, 17, 18, 19, or 20 contiguous nucleobases along a strand of the dsRNA compound. In certain embodiments, the compound comprises one or more linkages between adjacent nucleotides other than a naturally-occurring phosphodiester linkage. Examples of such linkages include phosphoramidate, phosphorothioate, and phosphorodithioate linkages. The compounds may also be chemically modified nucleic acid molecules as taught in U.S. Pat. No. 6,673,661. In other embodiments, the compound contains one or two

20 capped strands, as disclosed, for example, by WO 00/63364, filed Apr. 19, 2000.

In certain embodiments, the first strand of the compound is an siRNA guide strand and the second strand of the compound is an siRNA passenger strand. In certain embodiments, the second strand of the compound is complementary to the first strand. In certain embodiments, each strand of the compound is 16, 17, 18, 19, 20, 21, 22, or 23 linked nucleosides in length. In certain embodiments, the first or second strand of

25 the compound can comprise a conjugate group.

In certain embodiments, a compound described herein can comprise any of the oligonucleotide sequences targeted to IRF4 described herein. In certain embodiments, the compound is single stranded. In certain embodiments, such a compound is a single-stranded RNAi (ssRNAi) compound. In certain embodiments, the compound comprises at least an 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 contiguous

30 nucleobase portion of any one of SEQ ID NOs: 3-3383. In certain embodiments, the compound comprises the nucleobase sequence of any one of SEQ ID NOs: 3-3383. In certain embodiments, the compound comprises ribonucleotides in which uracil (U) is in place of thymine (T) in any one of SEQ ID NOs: 3-3383. In certain embodiments, the compound comprises a nucleobase sequence complementary to the site on IRF4 to which any of SEQ ID NOs: 3-3383 is targeted. In certain embodiments, the compound comprises one or more

35 modified nucleotides in which the 2' position in the sugar contains a halogen (such as fluorine group; 2'-F) or contains an alkoxy group (such as a methoxy group; 2'-OMe). In certain embodiments, the compound

comprises at least one 2'-F sugar modification and at least one 2'-OMe sugar modification. In certain embodiments, the at least one 2'-F sugar modification and at least one 2'-OMe sugar modification are arranged in an alternating pattern for at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 contiguous nucleobases along a strand of the compound. In certain embodiments, the compound comprises one or more linkages between adjacent nucleotides other than a naturally-occurring phosphodiester linkage. Examples of such linkages include phosphoramidate, phosphorothioate, and phosphorodithioate linkages. The compounds may also be chemically modified nucleic acid molecules as taught in U.S. Pat. No. 6,673,661. In other embodiments, the compound contains a capped strand, as disclosed, for example, by WO 00/63364, filed Apr. 19, 2000. In certain embodiments, the compound consists of 16, 17, 18, 19, 20, 21, 22, or 23 linked nucleosides. In certain embodiments, the compound can comprise a conjugate group.

In certain embodiments, compounds described herein comprise modified oligonucleotides. Certain 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. Included in the modified oligonucleotides provided herein are all such possible isomers, including their racemic and optically pure forms, unless specified otherwise. Likewise, all cis- and trans-isomers and tautomeric forms are also included.

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 compound that are beneficial for use as a therapeutic or research tool. In certain embodiments, radioactive isotopic substitutions may make the compound suitable for research or diagnostic purposes, such as an imaging assay.

Certain Mechanisms

In certain embodiments, compounds described herein comprise or consist of modified oligonucleotides. In certain embodiments, compounds described herein are antisense compounds. In certain embodiments, compounds comprise oligomeric compounds. In certain embodiments, compounds described herein are capable of hybridizing to a target nucleic acid, resulting in at least one antisense activity. In certain embodiments, compounds described herein selectively affect one or more target nucleic acid. Such 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 non-target nucleic acid or does not hybridize to one or more non-target nucleic acid in such a way that results in a significant undesired antisense activity.

In certain antisense activities, hybridization of a compound described herein to a target nucleic acid results in recruitment of a protein that cleaves the target nucleic acid. For example, certain compounds described herein result in RNase H mediated cleavage of the target nucleic acid. RNase H is a cellular endonuclease that 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, compounds described herein are sufficiently “DNA-like” to elicit RNase H activity. Further, in certain embodiments, one or more non-DNA-like nucleoside in the gap of a gapmer is tolerated.

In certain antisense activities, compounds described herein or a portion of the compound is loaded into an RNA-induced silencing complex (RISC), ultimately resulting in cleavage of the target nucleic acid. For example, certain compounds described herein result in cleavage of the target nucleic acid by Argonaute. 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 compounds described herein to a target nucleic acid does not result in recruitment of a protein that cleaves that target nucleic acid. In certain such embodiments, hybridization of the compound to the target nucleic acid results in alteration of splicing of the target nucleic acid. In certain embodiments, hybridization of the 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 such embodiments, hybridization of the 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 animal.

Target Nucleic Acids, Target Regions and Nucleotide Sequences

In certain embodiments, compounds described herein comprise or consist of an oligonucleotide comprising a region 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: an mRNA and a pre-mRNA, including intronic, exonic and untranslated regions. In certain embodiments, the target RNA is an 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.

Nucleotide sequences that encode IRF4 include, without limitation, the following: RefSEQ No. NM_002460.3 and NT_034880.3_TRUNC_328000_354000.

Hybridization

In some embodiments, hybridization occurs between a compound disclosed herein and a IRF4 nucleic acid. The most common mechanism of hybridization involves hydrogen bonding (e.g., Watson-Crick, Hoogsteen or reversed Hoogsteen hydrogen bonding) between complementary nucleobases of the nucleic acid molecules.

Hybridization can occur under varying conditions. Hybridization conditions are sequence-dependent and are determined by the nature and composition of the nucleic acid molecules to be hybridized.

Methods of determining whether a sequence is specifically hybridizable to a target nucleic acid are well known in the art. In certain embodiments, the compounds provided herein are specifically hybridizable with a IRF4 nucleic acid.

Complementarity

An oligonucleotide is said to be complementary to another nucleic acid when the nucleobase sequence of such oligonucleotide or one or more regions thereof matches the nucleobase sequence of another oligonucleotide or nucleic acid or one or more regions thereof when the two nucleobase sequences are aligned in opposing directions. Nucleobase matches or complementary nucleobases, as described herein, are limited to the following pairs: adenine (A) and thymine (T), adenine (A) and uracil (U), cytosine (C) and guanine (G), and 5-methyl cytosine (mC) and guanine (G) unless otherwise specified. Complementary oligonucleotides and/or nucleic acids need not have nucleobase complementarity at each nucleoside and may include one or more nucleobase mismatches. An oligonucleotide is fully complementary or 100% complementary when such oligonucleotides have nucleobase matches at each nucleoside without any nucleobase mismatches.

In certain embodiments, compounds described herein comprise or consist of modified oligonucleotides. In certain embodiments, compounds described herein are antisense compounds. In certain embodiments, compounds comprise oligomeric compounds. Non-complementary nucleobases between a compound and a IRF4 nucleic acid may be tolerated provided that the compound remains able to specifically hybridize to a target nucleic acid. Moreover, a compound may hybridize over one or more segments of a IRF4 nucleic acid such that intervening or adjacent segments are not involved in the hybridization event (e.g., a loop structure, mismatch or hairpin structure).

In certain embodiments, the compounds provided herein, or a specified portion thereof, are, are at least, or are up to 70%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% complementary to a IRF4 nucleic acid, a target region, target segment, or specified portion thereof. In certain embodiments, the compounds provided herein, or a specified portion thereof, are 70% to 75%, 75% to 80%, 80% to 85%, 85% to 90%, 90% to 95%, 95% to 100%, or any number in between these ranges, complementary to a IRF4 nucleic acid, a target region, target segment, or specified portion thereof. Percent complementarity of a compound with a target nucleic acid can be determined using routine methods.

For example, a compound in which 18 of 20 nucleobases of the compound are complementary to a target region, and would therefore specifically hybridize, would represent 90 percent complementarity. In this example, the remaining non-complementary nucleobases may be clustered or interspersed with complementary nucleobases and need not be contiguous to each other or to complementary nucleobases. As such, a compound which is 18 nucleobases in length having four non-complementary nucleobases which are flanked by two regions of complete complementarity with the target nucleic acid would have 77.8% overall complementarity with the target nucleic acid. Percent complementarity of a compound with a region of a target nucleic acid can be determined routinely using BLAST programs (basic local alignment search tools) and PowerBLAST programs known in the art (Altschul *et al.*, *J. Mol. Biol.*, 1990, 215, 403-410; Zhang and Madden, *Genome Res.*, 1997, 7, 649-656). Percent homology, sequence identity or complementarity, can be determined by, for example, the Gap program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, Madison Wis.), using default settings, which uses the algorithm of Smith and Waterman (*Adv. Appl. Math.*, 1981, 2, 482-489).

In certain embodiments, compounds described herein, or specified portions thereof, are fully complementary (i.e. 100% complementary) to a target nucleic acid, or specified portion thereof. For example, a compound may be fully complementary to a IRF4 nucleic acid, or a target region, or a target segment or target sequence thereof. As used herein, "fully complementary" means each nucleobase of a compound is complementary to the corresponding nucleobase of a target nucleic acid. For example, a 20 nucleobase compound is fully complementary to a target sequence that is 400 nucleobases long, so long as there is a corresponding 20 nucleobase portion of the target nucleic acid that is fully complementary to the compound. Fully complementary can also be used in reference to a specified portion of the first and /or the second nucleic acid. For example, a 20 nucleobase portion of a 30 nucleobase compound can be "fully complementary" to a target sequence that is 400 nucleobases long. The 20 nucleobase portion of the 30 nucleobase compound is fully complementary to the target sequence if the target sequence has a corresponding 20 nucleobase portion wherein each nucleobase is complementary to the 20 nucleobase portion of the compound. At the same time, the entire 30 nucleobase compound may or may not be fully complementary to the target sequence, depending on whether the remaining 10 nucleobases of the compound are also complementary to the target sequence.

In certain embodiments, compounds described herein comprise one or more mismatched nucleobases relative to the target nucleic acid. In certain such 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 such embodiments selectivity of the compound is improved. In certain embodiments, the mismatch is specifically positioned within an oligonucleotide having a gapmer motif. In certain such embodiments, the mismatch is at position 1, 2, 3, 4, 5, 6, 7, or 8 from the 5'-end of the gap region. In certain such 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 such embodiments, the mismatch is at position 1, 2, 3, or 4 from the 5'-end of the wing region. In certain such embodiments, the mismatch is at position 4, 3, 2, or 1 from the 3'-end of the wing region. In certain embodiments, the mismatch

is specifically positioned within an oligonucleotide not having a gapmer motif. In certain such embodiments, the mismatch is at position 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 from the 5'-end of the oligonucleotide. In certain such embodiments, the mismatch is at position , 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 from the 3'-end of the oligonucleotide.

5 The location of a non-complementary nucleobase may be at the 5' end or 3' end of the compound. Alternatively, the non-complementary nucleobase or nucleobases may be at an internal position of the compound. When two or more non-complementary nucleobases are present, they may be contiguous (i.e. linked) or non-contiguous. In one embodiment, a non-complementary nucleobase is located in the wing segment of a gapmer oligonucleotide.

10 In certain embodiments, compounds described herein that are, or are up to 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 nucleobases in length comprise no more than 4, no more than 3, no more than 2, or no more than 1 non-complementary nucleobase(s) relative to a target nucleic acid, such as a IRF4 nucleic acid, or specified portion thereof.

15 In certain embodiments, compounds described herein that are, or are up to 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 nucleobases in length comprise no more than 6, no more than 5, no more than 4, no more than 3, no more than 2, or no more than 1 non-complementary nucleobase(s) relative to a target nucleic acid, such as a IRF4 nucleic acid, or specified portion thereof.

20 In certain embodiments, compounds described herein also include those which are complementary to a portion of a target nucleic acid. As used herein, "portion" refers to a defined number of contiguous (i.e. linked) nucleobases within a region or segment of a target nucleic acid. A "portion" can also refer to a defined number of contiguous nucleobases of a compound. In certain embodiments, the—compounds, are complementary to at least an 8 nucleobase portion of a target segment. In certain embodiments, the compounds are complementary to at least a 9 nucleobase portion of a target segment. In certain embodiments, the compounds are complementary to at least a 10 nucleobase portion of a target segment. In certain embodiments, the compounds are complementary to at least an 11 nucleobase portion of a target segment. In certain
25 embodiments, the compounds are complementary to at least a 12 nucleobase portion of a target segment. In certain embodiments, the compounds are complementary to at least a 13 nucleobase portion of a target segment. In certain embodiments, the compounds are complementary to at least a 14 nucleobase portion of a target segment. In certain embodiments, the compounds are complementary to at least a 15 nucleobase portion of a
30 target segment. In certain embodiments, the compounds are complementary to at least a 16 nucleobase portion of a target segment. Also contemplated are compounds that are complementary to at least a 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more nucleobase portion of a target segment, or a range defined by any two of these values.

35 *Identity*

The compounds provided herein may also have a defined percent identity to a particular nucleotide sequence, SEQ ID NO, or compound represented by a specific ION number, or portion thereof. In certain embodiments, compounds described herein are antisense compounds or oligomeric compounds. In certain embodiments, compounds described herein are modified oligonucleotides. As used herein, a compound is identical to the sequence disclosed herein if it has the same nucleobase pairing ability. For example, a RNA which contains uracil in place of thymidine in a disclosed DNA sequence would be considered identical to the DNA sequence since both uracil and thymidine pair with adenine. Shortened and lengthened versions of the compounds described herein as well as compounds having non-identical bases relative to the compounds provided herein also are contemplated. The non-identical bases may be adjacent to each other or dispersed throughout the compound. Percent identity of an compound is calculated according to the number of bases that have identical base pairing relative to the sequence to which it is being compared.

In certain embodiments, compounds described herein, or portions thereof, are, or are at least, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to one or more of the compounds or SEQ ID NOs, or a portion thereof, disclosed herein. In certain embodiments, compounds described herein are about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical, or any percentage between such values, to a particular nucleotide sequence, SEQ ID NO, or compound represented by a specific ION number, or portion thereof, in which the compounds comprise an oligonucleotide having one or more mismatched nucleobases. In certain such embodiments, the mismatch is at position 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 from the 5'-end of the oligonucleotide. In certain such embodiments, the mismatch is at position , 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 from the 3'-end of the oligonucleotide.

In certain embodiments, compounds described herein comprise or consist of antisense compounds. In certain embodiments, a portion of the antisense compound is compared to an equal length portion of the target nucleic acid. In certain embodiments, an 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 nucleobase portion is compared to an equal length portion of the target nucleic acid.

In certain embodiments, compounds described herein comprise or consist of oligonucleotides. In certain embodiments, a portion of the oligonucleotide is compared to an equal length portion of the target nucleic acid. In certain embodiments, an 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 nucleobase portion is compared to an equal length portion of the target nucleic acid.

Certain Modified Compounds

In certain embodiments, compounds described herein comprise or consist of oligonucleotides consisting 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 (i.e., 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. Modified Nucleosides

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

1. Modified Sugar Moieties

In certain embodiments, 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 acyclic substituent, including but not limited to substituents at the 2', 4', and/or 5' positions. In certain embodiments one or more acyclic 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 linearly 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 sugars 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., US2010/190837 and Rajeev et al., US2013/0203836.

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

Nucleosides comprising modified sugar moieties, such as non-bicyclic modified sugar moieties, are referred to by the position(s) of the substitution(s) on the sugar moiety of the nucleoside. For example, nucleosides comprising 2'-substituted or 2'-modified sugar moieties are referred to as 2'-substituted nucleosides or 2'-modified nucleosides.

Certain modified sugar moieties comprise a bridging sugar substituent that forms 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” when in the *S* configuration), 4'-CH₂-
15 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).
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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)-;
25

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, C₁-C₁₂ alkyl, substituted C₁-C₁₂ alkyl, C₂-C₁₂ alkenyl, substituted C₂-C₁₂ alkenyl, C₂-C₁₂ alkynyl, substituted C₂-C₁₂ alkynyl, C₅-C₂₀ aryl, substituted C₅-C₂₀ aryl, heterocycle radical, substituted heterocycle radical, heteroaryl, substituted heteroaryl, C₅-C₇ alicyclic radical, substituted C₅-C₇ 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, C₁-C₁₂ alkyl, substituted C₁-C₁₂ alkyl, C₂-C₁₂ alkenyl, substituted C₂-C₁₂ alkenyl, C₂-C₁₂ alkynyl, substituted C₂-C₁₂ alkynyl, C₅-C₂₀ aryl, substituted C₅-C₂₀ aryl, acyl (C(=O)-H), substituted acyl, a heterocycle radical, a
35

substituted heterocycle radical, C₁-C₁₂ aminoalkyl, substituted C₁-C₁₂ 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; Wahlestedt *et al.*, *Proc. Natl. Acad. Sci. U. S. A.*, 2000, 97, 5633-5638; 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; Elayadi *et al.*, *Curr. Opinion Invens. Drugs*, 2001, 2, 558-561; Braasch *et al.*, *Chem. Biol.*, 2001, 8, 1-7; Orum *et al.*, *Curr. Opinion Mol. Ther.*, 2001, 3, 239-243; 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; and 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; 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) α -L-LNA (α -L-configuration)
 bridge = 4'-CH₂-O-2' bridge = 4'-CH₂-O-2'

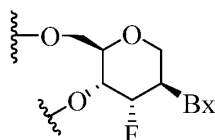
α -L-methyleneoxy (4'-CH₂-O-2') or α -L-LNA bicyclic nucleosides have been incorporated into oligonucleotides that showed antisense activity (Frieden *et al.*, *Nucleic Acids Research*, 2003, 31, 6365-6372). Herein, general descriptions of bicyclic nucleosides include both isomeric configurations. When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

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'-

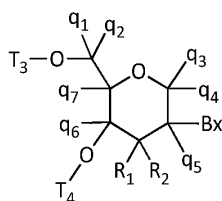
position (*see, e.g.*, Bhat et al., U.S. 7,875,733 and Bhat et al., U.S. 7,939,677) and/or the 5' position.

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 HNA:



F-HNA

("F-HNA", *see e.g.*, Swayze et al., U.S. 8,088,904; Swayze et al., U.S. 8,440,803; 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:



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

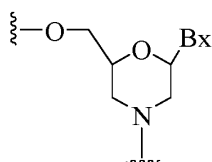
Bx is a nucleobase moiety;

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., US2013/130378.

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

2. Modified Nucleobases

Nucleobase (or base) modifications or substitutions are structurally distinguishable from, yet functionally interchangeable with, naturally occurring or synthetic unmodified nucleobases. Both natural and modified nucleobases are capable of participating in hydrogen bonding. Such nucleobase modifications can impart nuclease stability, binding affinity or some other beneficial biological property to antisense compounds.

In certain embodiments, compounds described herein comprise modified oligonucleotides. In certain embodiments, modified oligonucleotides comprise one or more nucleoside comprising an unmodified nucleobase. In certain embodiments, modified oligonucleotides comprise one or more nucleoside comprising a modified nucleobase. In certain embodiments, modified oligonucleotides comprise one or more nucleoside 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, 5-methylcytosine, 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.

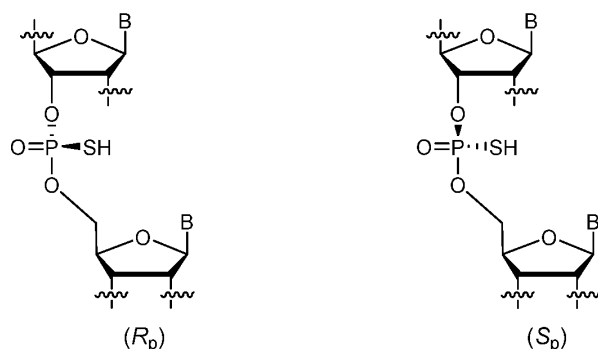
Publications that teach the preparation of certain of the above noted modified nucleobases as well as other modified nucleobases include without limitation, Manoharan et al., US2003/0158403, Manoharan et al., US2003/0175906; Dinh et al., U.S. 4,845,205; Spielvogel et al., U.S. 5,130,302; Rogers et al., 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., U.S. 6,166,199; and Matteucci et al., U.S. 6,005,096.

In certain embodiments, compounds targeted to a IRF4 nucleic acid comprise one or more modified nucleobases. In certain embodiments, the modified nucleobase is 5-methylcytosine. In certain embodiments, each cytosine is a 5-methylcytosine.

3. Modified Internucleoside Linkages

The naturally occurring internucleoside linkage of RNA and DNA is a 3' to 5' phosphodiester linkage. In certain embodiments, compounds described herein having one or more modified, i.e. non-naturally occurring, internucleoside linkages are often selected over compounds having naturally occurring internucleoside linkages because of desirable properties such as, for example, enhanced cellular uptake, enhanced affinity for target nucleic acids, and increased stability in the presence of nucleases.

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.

In certain embodiments, compounds targeted to an IRF4 nucleic acid comprise one or more modified internucleoside linkages. In certain embodiments, the modified internucleoside linkages are phosphorothioate linkages. In certain embodiments, each internucleoside linkage of an antisense compound is a phosphorothioate internucleoside linkage.

In certain embodiments, compounds described herein comprise oligonucleotides. Oligonucleotides having modified internucleoside linkages include internucleoside linkages that retain a phosphorus atom as well as internucleoside linkages that do not have a phosphorus atom. Representative phosphorus containing internucleoside linkages include, but are not limited to, phosphodiester, phosphotriesters, methylphosphonates, phosphoramidate, and phosphorothioates. Methods of preparation of phosphorous-containing and non-phosphorous-containing linkages are well known.

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 phosphates, which contain a phosphodiester bond ("P=O") (also referred to as unmodified or naturally occurring linkages), phosphotriesters, methylphosphonates, phosphoramidates, and phosphorothioates ("P=S"), and phosphorodithioates ("HS-P=S"). 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. Representative chiral internucleoside linkages include but are not limited to alkylphosphonates and phosphorothioates. Methods of preparation of phosphorous-containing and non-phosphorous-containing internucleoside linkages are well known to those skilled in the art.

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, 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.

In certain embodiments, oligonucleotides comprise modified internucleoside linkages arranged along the oligonucleotide or region thereof in a defined pattern or modified internucleoside linkage motif. In certain embodiments, internucleoside linkages are arranged in a gapped motif. In such embodiments, the

internucleoside linkages in each of two wing regions are different from the internucleoside linkages in the gap region. In certain embodiments the internucleoside linkages in the wings are phosphodiester and the internucleoside linkages in the gap are phosphorothioate. The nucleoside motif is independently selected, so such oligonucleotides having a gapped internucleoside linkage motif may or may not have a gapped nucleoside motif and if it does have a gapped nucleoside motif, the wing and gap lengths may or may not be the same.

In certain embodiments, oligonucleotides comprise a region having an alternating internucleoside linkage motif. In certain embodiments, oligonucleotides comprise a region of uniformly modified internucleoside linkages. In certain such embodiments, the oligonucleotide comprises a region that is uniformly linked by phosphorothioate internucleoside linkages. In certain embodiments, the oligonucleotide is uniformly linked by phosphorothioate. In certain embodiments, each internucleoside linkage of the oligonucleotide is selected from phosphodiester and phosphorothioate. In certain embodiments, each internucleoside linkage of the oligonucleotide is selected from phosphodiester and phosphorothioate and at least one internucleoside linkage is phosphorothioate.

In certain embodiments, the oligonucleotide comprises at least 6 phosphorothioate internucleoside linkages. In certain embodiments, the oligonucleotide comprises at least 8 phosphorothioate internucleoside linkages. In certain embodiments, the oligonucleotide comprises at least 10 phosphorothioate internucleoside linkages. In certain embodiments, the oligonucleotide comprises at least one block of at least 6 consecutive phosphorothioate internucleoside linkages. In certain embodiments, the oligonucleotide comprises at least one block of at least 8 consecutive phosphorothioate internucleoside linkages. In certain embodiments, the oligonucleotide comprises at least one block of at least 10 consecutive phosphorothioate internucleoside linkages. In certain embodiments, the oligonucleotide comprises at least one block of at least 12 consecutive phosphorothioate internucleoside linkages. In certain such embodiments, at least one such block is located at the 3' end of the oligonucleotide. In certain such embodiments, at least one such block is located within 3 nucleosides of the 3' end of the oligonucleotide.

In certain embodiments, oligonucleotides comprise one or more methylphosphonate linkages. In certain embodiments, oligonucleotides having a gapmer nucleoside motif comprise a linkage motif comprising all phosphorothioate linkages except for one or two methylphosphonate linkages. In certain embodiments, one methylphosphonate linkage is in the central gap of an oligonucleotide having a gapmer nucleoside motif.

In certain embodiments, it is desirable to arrange the number of phosphorothioate internucleoside linkages and phosphodiester internucleoside linkages to maintain nuclease resistance. In certain embodiments, it is desirable to arrange the number and position of phosphorothioate internucleoside linkages and the number and position of phosphodiester internucleoside linkages to maintain nuclease resistance. In certain embodiments, the number of phosphorothioate internucleoside linkages may be decreased and the number of phosphodiester internucleoside linkages may be increased. In certain embodiments, the number of phosphorothioate internucleoside linkages may be decreased and the number of phosphodiester internucleoside linkages may be increased while still maintaining nuclease resistance. In certain embodiments it is desirable to

decrease the number of phosphorothioate internucleoside linkages while retaining nuclease resistance. In certain embodiments it is desirable to increase the number of phosphodiester internucleoside linkages while retaining nuclease resistance.

5 *Certain Motifs*

In certain embodiments, compounds described herein comprise oligonucleotides. Oligonucleotides can have a motif, *e.g.* a pattern of unmodified and/or modified sugar moieties, nucleobases, and/or internucleoside linkages. In certain embodiments, modified oligonucleotides comprise one or more modified nucleoside comprising a modified sugar. In certain embodiments, modified oligonucleotides comprise one or more
10 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
15 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).

a. Certain Sugar Motifs

In certain embodiments, compounds described herein comprise oligonucleotides. In certain embodiments, oligonucleotides comprise one or more type of modified sugar and/or unmodified sugar moiety
20 arranged along the oligonucleotide or region 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 comprise or consist of a region having a gapmer motif, which comprises 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
25 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
30 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 1-5 nucleosides. In certain embodiments, the
35 wings of a gapmer comprise 2-5 nucleosides. In certain embodiments, the wings of a gapmer comprise 3-5

nucleosides. In certain embodiments, the nucleosides of a gapmer are all modified nucleosides.

In certain embodiments, the gap of a gapmer comprises 7-12 nucleosides. In certain embodiments, the gap of a gapmer comprises 7-10 nucleosides. In certain embodiments, the gap of a gapmer comprises 8-10 nucleosides. In certain embodiments, the gap of a gapmer comprises 10 nucleosides. In certain embodiment, each nucleoside of the gap of a gapmer is an unmodified 2'-deoxy nucleoside.

In certain embodiments, the gapmer is a deoxy gapmer. In such embodiments, the nucleosides on the gap side of each wing/gap junction are unmodified 2'-deoxy nucleosides and the nucleosides on the wing sides of each wing/gap junction are modified nucleosides. In certain such embodiments, each nucleoside of the gap is an unmodified 2'-deoxy nucleoside. In certain such embodiments, each nucleoside of each wing is a modified nucleoside.

In certain embodiments, a modified oligonucleotide has a fully modified sugar motif wherein each nucleoside of the modified oligonucleotide comprises a modified sugar moiety. In certain embodiments, modified oligonucleotides comprise or consist of a region having a fully modified sugar motif wherein each nucleoside of the region comprises a modified sugar moiety. In certain embodiments, modified oligonucleotides comprise or consist of a region having a fully modified sugar motif, wherein each nucleoside within the fully modified region 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.

In certain embodiments, a modified oligonucleotide can comprise a sugar motif described in Swayze et al., US2010/0197762; Freier et al., US2014/0107330; Freier et al., US2015/0184153; and Seth et al., US2015/0267195, each of which is incorporated by reference in its entirety herein.

Certain embodiments provided herein are directed to modified oligomeric compounds useful for inhibiting target nucleic acid expression, which can be useful for treating, preventing, ameliorating, or slowing progression of a disease associated with such a target nucleic acid. In certain embodiments, the modified oligomeric compounds comprise antisense oligonucleotides that are gapmers having certain sugar motifs. In certain embodiments, the gapmer sugar motifs provided herein can be combined with any nucleobase sequence and any internucleoside linkage motif to form potent antisense oligonucleotides.

In certain embodiments, a method comprises contacting a cell or administering to a subject a compound comprising a modified oligonucleotide 16 linked nucleosides in length having the motif: ekk-d9-kkee, wherein 'd' represents a 2'-deoxyribose sugar, 'k' represents a cEt nucleoside, and 'e' represents a 2'-MOE nucleoside. In certain embodiments, the cell is a cancer cell. In certain embodiments, the subject has cancer. In certain embodiments, administering the compound to the subject treats the subject's cancer.

In certain embodiments, a method comprises contacting a cell or administering to a subject a compound comprising a modified oligonucleotide 16 linked nucleosides in length having the motif: k-d9-kekeke, wherein 'd' represents a 2'-deoxyribose sugar, 'k' represents a cEt nucleoside, and 'e' represents a 2'-MOE nucleoside.

In certain embodiments, the cell is a cancer cell. In certain embodiments, the subject has cancer. In certain embodiments, administering the compound to the subject treats the subject's cancer.

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In certain embodiments, a method comprises contacting a cell or administering to a subject a compound comprising a modified oligonucleotide 16 linked nucleosides in length having the motif: kk-d9-kdkdk, wherein 'd' represents a 2'-deoxyribose sugar, 'k' represents a cEt nucleoside, and 'e' represents a 2'-MOE nucleoside. In certain embodiments, the cell is a cancer cell. In certain embodiments, the subject has cancer. In certain embodiments, administering the compound to the subject treats the subject's cancer.

In certain embodiments, a compound comprises a modified oligonucleotide 16 linked nucleosides in length having the motif: kk-d9-eeekk, wherein 'd' represents a 2'-deoxyribose sugar, 'k' represents a cEt nucleoside, and 'e' represents a 2'-MOE nucleoside. In certain embodiments, a method comprises contacting a cell or administering to a subject a compound comprising a modified oligonucleotide 16 linked nucleosides in length having the motif: kk-d9-eeekk, wherein 'd' represents a 2'-deoxyribose sugar, 'k' represents a cEt nucleoside, and 'e' represents a 2'-MOE nucleoside. In certain embodiments, the cell is a cancer cell. In certain embodiments, the subject has cancer. In certain embodiments, administering the compound to the subject treats the subject's cancer.

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b. Certain Nucleobase Motifs

In certain embodiments, compounds described herein comprise oligonucleotides. In certain embodiments, oligonucleotides comprise modified and/or unmodified nucleobases arranged along the oligonucleotide or region 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-methylcytosines.

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'-deoxyribosyl moiety. In certain embodiments, the modified nucleobase is selected from: a 2-thiopyrimidine and a 5-propynepyrimidine.

c. Certain Internucleoside Linkage Motifs

In certain embodiments, compounds described herein comprise oligonucleotides. In certain embodiments, oligonucleotides comprise modified and/or unmodified internucleoside linkages arranged along the oligonucleotide or region thereof in a defined pattern or motif. In certain embodiments, essentially each internucleoside linking group is a phosphate internucleoside linkage (P=O). In certain embodiments, each internucleoside linking group of a modified oligonucleotide is a phosphorothioate (P=S). In certain embodiments, each internucleoside linking group of a modified oligonucleotide is independently selected from a phosphorothioate and phosphate internucleoside linkage. 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 phosphate linkages. In certain embodiments, the terminal internucleoside linkages are modified.

4. Certain Modified Oligonucleotides

In certain embodiments, compounds described herein comprise 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 gapmer oligonucleotides may comprise one or more modified nucleobase independent of the gapmer pattern of the sugar modifications. Furthermore, in certain instances, an oligonucleotide is described by an overall length or range and by lengths or length ranges of two or more regions (e.g., a regions of nucleosides having specified sugar modifications), in such circumstances it may be possible to select numbers for each range that result in an oligonucleotide having an overall length falling outside the specified range. In such circumstances, both elements must be satisfied. For example, in certain embodiments, a modified oligonucleotide consists of 15-20 linked nucleosides and has a sugar motif consisting of three regions, A, B, and C, wherein region A consists of 2-6 linked nucleosides having a specified sugar motif, region B consists of 6-10 linked nucleosides having a specified sugar motif, and region C consists of 2-6 linked nucleosides having a specified sugar motif. Such embodiments do not include modified oligonucleotides where A and C each consist of 6 linked nucleosides and B consists of 10 linked nucleosides (even though those numbers of nucleosides are permitted within the requirements for A, B, and C) because the overall length of such oligonucleotide is 22, which exceeds the upper limit of the overall length of the modified oligonucleotide (20). Herein, if a description of an oligonucleotide is silent with respect to one or more parameter, such parameter is not limited. Thus, a modified oligonucleotide described only as having a gapmer sugar motif without further description may have any length, internucleoside linkage motif, and nucleobase motif. Unless otherwise indicated, all modifications are independent of nucleobase sequence.

Certain Conjugated Compounds

In certain embodiments, the compounds described herein comprise or 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 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.

In certain embodiments, the oligonucleotide is modified. In certain embodiments, the oligonucleotide of a compound has a nucleobase sequence that is complementary to a target nucleic acid. In certain embodiments, oligonucleotides are complementary to a messenger RNA (mRNA). In certain embodiments, oligonucleotides are complementary to a sense transcript.

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

A. Certain Conjugate Groups

5 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, 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
10 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., 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
15 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, 49-54), 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
20 polyethylene glycol chain (Manoharan et al., *Nucleosides & Nucleotides*, 1995, 14, 969-973), or adamantane acetic, a palmityl moiety (Mishra et al., *Biochim. Biophys. Acta*, 1995, 1264, 229-237), an octadecylamine or hexylamino-carbonyl-oxycholesterol moiety (Crooke et al., *J. Pharmacol. Exp. Ther.*, 1996, i, 923-937), a tocopherol group (Nishina et al., *Molecular Therapy Nucleic Acids*, 2015, 4, e220; doi:10.1038/mtna.2014.72 and Nishina et al., *Molecular Therapy*, 2008, 16, 734-740), or a GalNAc cluster (e.g., WO2014/179620).

25 1. Conjugate Moieties

Conjugate moieties include, without limitation, intercalators, reporter molecules, polyamines, polyamides, peptides, carbohydrates (e.g., GalNAc), 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
30 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 diazepam, indo-methicin, a barbiturate, a cephalosporin, a sulfa drug, an antidiabetic, an
35 antibacterial or an antibiotic.

2. Conjugate linkers

Conjugate moieties are attached to oligonucleotides through conjugate linkers. In certain compounds, a conjugate group is a single chemical bond (i.e. conjugate moiety is attached to an oligonucleotide via a conjugate linker 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 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 (AHX 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, 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-methylcytosine, 4-N-benzoyl-5-methylcytosine, adenine, 6-N-benzoyladenine, guanine and 2-N-isobutyrylguanine. It is typically desirable for linker-nucleosides to be cleaved from the compound after it reaches a target tissue. Accordingly, linker-

nucleosides are typically linked to one another and to the remainder of the 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 a 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 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, a 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 a compound is more than 30. Alternatively, an compound may comprise a modified oligonucleotide consisting of 8-30 nucleosides and no conjugate group. The total number of contiguous linked nucleosides in such a 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 compounds comprising a particular conjugate moiety are better taken up by a particular cell type, but once the compound has been taken up, it is desirable that the conjugate group be cleaved to release the unconjugated or parent oligonucleotide. Thus, certain conjugate may comprise one or more cleavable moieties, typically within the conjugate linker. 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, or 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 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, one or more linker-nucleosides are linked to one another and/or to the remainder of the compound through cleavable bonds. In certain embodiments, such cleavable bonds are unmodified phosphodiester bonds. In certain embodiments, a cleavable moiety is 2'-deoxy nucleoside that is attached to

either the 3' or 5'-terminal nucleoside of an oligonucleotide by a phosphate 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.

Compositions and Methods for Formulating Pharmaceutical Compositions

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

10 Certain embodiments provide pharmaceutical compositions comprising one or more compounds or a salt thereof. In certain embodiments, the compounds are antisense compounds or oligomeric compounds. In certain embodiments, the compounds comprise or consist of a modified oligonucleotide. In certain such embodiments, the pharmaceutical composition comprises a suitable pharmaceutically acceptable diluent or carrier. In certain embodiments, a pharmaceutical composition comprises a sterile saline solution and one or more compound. In certain embodiments, such pharmaceutical composition consists of a sterile saline solution
15 and one or more compound. In certain embodiments, the sterile saline is pharmaceutical grade saline. In certain embodiments, a pharmaceutical composition comprises one or more compound and sterile water. In certain embodiments, a pharmaceutical composition consists of one compound and sterile water. In certain embodiments, the sterile water is pharmaceutical grade water. In certain embodiments, a pharmaceutical composition comprises one or more compound and phosphate-buffered saline (PBS). In certain embodiments,
20 a pharmaceutical composition consists of one or more compound and sterile PBS. In certain embodiments, the sterile PBS is pharmaceutical grade PBS. Compositions and methods for the formulation of pharmaceutical compositions are dependent upon a number of criteria, including, but not limited to, route of administration, extent of disease, or dose to be administered.

25 A compound described herein targeted to IRF4 nucleic acid can be utilized in pharmaceutical compositions by combining the compound with a suitable pharmaceutically acceptable diluent or carrier. In certain embodiments, a pharmaceutically acceptable diluent is water, such as sterile water suitable for injection. Accordingly, in one embodiment, employed in the methods described herein is a pharmaceutical composition comprising a compound targeted to IRF4 nucleic acid and a pharmaceutically acceptable diluent. In certain
30 embodiments, the pharmaceutically acceptable diluent is water. In certain embodiments, the compound comprises or consists of a modified oligonucleotide provided herein.

35 Pharmaceutical compositions comprising compounds provided herein encompass any pharmaceutically acceptable salts, esters, or salts of such esters, or any other oligonucleotide which, upon administration to an animal, including a human, is capable of providing (directly or indirectly) the biologically active metabolite or residue thereof. In certain embodiments, the compounds are antisense compounds or oligomeric compounds. In certain embodiments, the compound comprises or consists of a modified

oligonucleotide. Accordingly, for example, the disclosure is also drawn to pharmaceutically acceptable salts of 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.

A prodrug can include the incorporation of additional nucleosides at one or both ends of a compound which are cleaved by endogenous nucleases within the body, to form the active compound. In certain embodiments, the compounds or compositions further comprise a pharmaceutically acceptable carrier or diluent.

EXAMPLES

The Examples below describe the screening process to identify lead compounds targeted to IRF4. Out of over 3,000 oligonucleotides that were screened, ION 690890, 935658, 935696, 935762, 935918, 935968, 882800, 1012795, 1014095, and 1014834 emerged as the top lead compounds. In particular, ION 935918 exhibited the best combination of properties in terms of potency and tolerability out of over 3,000 oligonucleotides.

Non-limiting disclosure and incorporation by reference

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 for the natural 2'-H of DNA) or as an RNA having a modified base (thymine (methylated uracil) for natural 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 oligonucleotide having the nucleobase sequence “ATCGATCG” encompasses any oligonucleotides 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 compounds having other modified nucleobases, such as “AT^mCGAUCG,” wherein ^mC indicates a cytosine base comprising a methyl group at the 5-position.

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 recited in the present application is incorporated herein by reference in its entirety.

Example 1: Effect of 5-10-5 MOE gapmers with phosphorothioate internucleoside linkages on human IRF4 *in vitro*, single dose

Modified oligonucleotides complementary to a human IRF4 nucleic acid were designed and tested for their effect on IRF4 mRNA *in vitro*.

Cultured SK-MEL-28 cells at a density of 60,000 cells per well were transfected using electroporation with 20,000 nM concentration of modified oligonucleotide or no modified oligonucleotide for untreated controls. After approximately 24 hours, RNA was isolated from the cells and IRF4 mRNA levels were measured by quantitative real-time PCR. Human primer probe set RTS3114 (forward sequence AAGCCTTGGCGTTCTCAGACT, designated herein as SEQ ID NO: 3386; reverse sequence TCAGCTCCTTCACGAGGATTTC, designated herein as SEQ ID NO: 3387; probe sequence CCGGCTGCACATCTGCCTGTACTACC, designated herein as SEQ ID: 3388) was used to measure mRNA levels. IRF4 mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented in the table below as percent control of the amount of IRF4 mRNA, relative to untreated control (UTC) cells.

The modified oligonucleotides in Table 1 are 5-10-5 MOE gapmers. The gapmers are 20 nucleobases in length, wherein the central gap segment comprises ten 2'-deoxynucleosides and is flanked by wing segments on both the 5' end and on the 3' end comprising five 2'-MOE nucleosides. The sugar motif for the gapmers is (from 5' to 3'): eeeeeeeeeeeeeee; wherein 'd' represents a 2'-deoxyribose sugar and 'e' represents a 2'-MOE modified sugar. Each internucleoside linkage is a phosphorothioate internucleoside linkage and each cytosine residue is a 5-methylcytosine. "Start Site" indicates the 5'-most nucleoside to which the gapmer is complementary in the human nucleic acid sequence. "Stop Site" indicates the 3'-most nucleoside to which the gapmer is complementary in the human nucleic acid sequence.

Each modified oligonucleotide listed in Table 1 below is complementary to human IRF4 nucleic acid sequences SEQ ID NO: 1 or SEQ ID NO: 2, as indicated. 'N/A' indicates that the modified oligonucleotide is not complementary to that particular nucleic acid sequence with 100% complementarity. As shown below, modified oligonucleotides complementary to human IRF4 reduced the amount of human IRF4 mRNA.

Table 1
Percent control of human IRF4 mRNA with 5-10-5 MOE gapmers
with phosphorothioate internucleoside linkages

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	IRF4 (% UTC)	SEQ ID NO
434887	164	183	5191	5210	GCAGCTCACCGCGCTCATGC	57	3

434888	175	194	5202	5221	TTCCCGTTGCCGCAGCTCAC	34	4
434889	190	209	5217	5236	AGCCACTGGCGGAGCTTCCC	43	5
434890	294	313	5321	5340	TGTAGTCCTGCTTGCCCGCG	51	6
434891	304	323	5331	5350	TCCTCGCGGTTGTAGTCCTG	53	7
434892	330	349	N/A	N/A	CCCAAGCCTTGAAGAGCGCG	44	8
434893	367	386	6846	6865	TTGTTCGATGCCTTCTCGGAA	47	9
434894	375	394	6854	6873	GGTCCGGCTTGTTCGATGCCT	40	10
434895	430	449	6909	6928	TCAAAGTCATTGCTCTTGTT	55	11
434896	436	455	6915	6934	AGTTCCTCAAAGTCATTGCT	42	12
434897	442	461	6921	6940	TCAACCAGTTCCTCAAAGTC	75	13
434898	447	466	6926	6945	TCCGCTCAACCAGTTCCTCA	32	14
434899	474	493	6953	6972	TGTACGGGTCTGAGATGTCC	44	15
434900	532	551	7850	7869	TCCAGGGTGAGCTGCTTGCG	43	16
434901	555	574	7873	7892	GGCTCATGGACATCTGCGGG	45	17
434902	675	694	9165	9184	TTCCCGGTGTGGCTGATCC	36	18
434903	690	709	9180	9199	GACATTGGTACGGGATTTCC	38	19
434904	732	751	9222	9241	CTGGGCCTTGCCAGTGGTGG	59	20
434905	739	758	9229	9248	TCACAAGCTGGGCCTTGCCA	30	21
434906	744	763	9234	9253	CATTTTCACAAGCTGGGCCT	37	22
434907	751	770	N/A	N/A	TGGCAACCATTTTCACAAGC	37	23
434908	758	777	N/A	N/A	TGTCACCTGGCAACCATTTT	49	24
434909	778	797	10843	10862	GCACAAGCATAAAAGGTTCC	26	25
434916	940	959	13493	13512	TGGGAGATCCGGCAGCCCTC	66	26
434917	1004	1023	13557	13576	GCCATTGTCTCTGGGTAGG	38	27
434918	1042	1061	13595	13614	TCCAGGTGGCTCAGCAGCTT	25	28
434919	1063	1082	13616	13635	ATCCAGAGGACCACGCCCTT	78	29
434920	1068	1087	13621	13640	GGGCCATCCAGAGGACCACG	36	30
434921	1119	1138	13672	13691	CGTCCCAGTAGATCCTGCTC	46	31
434922	1187	1206	13740	13759	GTCAAAGAGCTTGCAGGTCT	32	32
434923	1192	1211	13745	13764	TGTGTGTCAAAGAGCTTGCA	17	33
434924	1344	1363	19461	19480	GTGTCTGGCTAGCAGAGGT	33	34
434925	1364	1383	19481	19500	TTGTTGAGCAAAATAATATA	97	35
434926	1391	1410	19508	19527	GTAGCCCCTCAGGAAATGTC	15	36
434927	1420	1439	19537	19556	TCTGGATTGCTGATGTGTTT	46	37
434928	1430	1449	19547	19566	GTGGTAATCTTCTGGATTGC	42	38
434929	1450	1469	19567	19586	GAGGAATGGCGGATAGATCT	63	39
434930	1707	1726	19824	19843	CACTAAAGTCAAATATTTAC	88	40
434931	1712	1731	19829	19848	GCTTTCATAAAGTCAAATA	29	41
434932	1821	1840	19938	19957	CAGATGTCACTGATTTTCCA	41	42
434933	1826	1845	19943	19962	CCAATCAGATGTCACTGATT	44	43
434934	1838	1857	19955	19974	TAAGCTCATCTGCCAATCAG	71	44

434935	2196	2215	20313	20332	CCAAGGCTACAGGCACGGCT	29	45
434936	2234	2253	20351	20370	ACACCAGGAAACCGCTGGCA	37	46
434937	2293	2312	20410	20429	CTTCCAGGAAAGGCCAAGGA	23	47
434938	2356	2375	20473	20492	TGTCCCATCCAAGAGTAGCG	30	48
434939	2662	2681	20779	20798	CTTCCAGTGGTGGGTCCTGG	53	49
434940	2705	2724	20822	20841	AACAGCCCCTGAGTGTGCA	43	50
434941	2711	2730	20828	20847	AGCAGAAACAGCCCCTGAG	58	51
434942	3435	3454	21552	21571	CTGGGTACATGGCAGTGGAG	27	52
434943	3805	3824	21922	21941	GCATTTTCCAGAAAATTCAG	33	53
434944	4477	4496	22594	22613	CCCAGAGTTGTTCCACCCCT	21	54
434945	N/A	N/A	22826	22845	GCTGGCCACAGAGGACTTCG	21	55
434946	4737	4756	22854	22873	GCCTTCACGCACCATTGAGA	52	56
434947	4812	4831	22929	22948	CCACCTGCATCGAGATCAGT	31	57
434948	4818	4837	22935	22954	GGAGATCCACCTGCATCGAG	32	58
434949	5035	5054	23152	23171	GGAAGTGGACCCCATTCCT	17	59
434952	N/A	N/A	18834	18853	ATCTAAGGCAAGCTGAATGC	67	60
434953	N/A	N/A	18839	18858	ACAGCATCTAAGGCAAGCTG	38	61
434954	N/A	N/A	18845	18864	GAATTTACAGCATCTAAGGC	52	62
434955	N/A	N/A	18850	18869	TTCCTGAATTTACAGCATCT	21	63
434957	N/A	N/A	5359	5378	GCCGGAGACCTTGAAGAGCG	94	64
434958	N/A	N/A	7480	7499	ACTGGTCAGAATCTTGAAAA	94	65
434959	N/A	N/A	9101	9120	GTTGTGAACCTGCTAAAGGA	90	66
434960	N/A	N/A	10818	10837	CCTGGCAACCTGCATTGCA	43	67
434961	N/A	N/A	10823	10842	TGTCACCTGGCAACCTGCAT	45	68
434962	N/A	N/A	12030	12049	GGGCAGGTTTCATTTCAATT	33	69
434963	N/A	N/A	13414	13433	GCCGGCAGTCTGCAAACACA	58	70
434964	N/A	N/A	19448	19467	CAGAGGTTCTACCTTTAATA	50	71

Example 2: Effect of 3-10-3 cEt gapmers with phosphorothioate internucleoside linkages on human IRF4 *in vitro*, single dose

Modified oligonucleotides complementary to a human IRF4 nucleic acid were designed and tested for their effect on IRF4 mRNA *in vitro*.

Cultured SK-MEL-28 cells at a density of 20,000 cells per well were transfected using electroporation with 4,000 nM concentration of modified oligonucleotide or no modified oligonucleotide for untreated controls. After approximately 24 hours, RNA was isolated from the cells and IRF4 mRNA levels were measured by quantitative real-time PCR. Human primer probe set RTS3114 (described hereinabove in Example 1) was used to measure mRNA levels. IRF4 mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented in the table below as percent control of the amount of IRF4 mRNA, relative to untreated control (UTC) cells.

The modified oligonucleotides in Tables 2 and 3 are 3-10-3 cEt gapmers. The gapmers are 16 nucleobases in length, wherein the central gap segment comprises ten 2'-deoxynucleosides and is flanked by wing segments on both the 5' end and on the 3' end comprising three cEt nucleosides. The sugar motif for the gapmers is (from 5' to 3'): kkkddddd kkk; wherein 'd' represents a 2'-deoxyribose sugar and 'k' represents a cEt modified sugar. Each internucleoside linkage is a phosphorothioate internucleoside linkage and each cytosine residue is a 5-methylcytosine. "Start Site" indicates the 5'-most nucleoside to which the gapmer is complementary in the human nucleic acid sequence. "Stop Site" indicates the 3'-most nucleoside to which the gapmer is complementary in the human nucleic acid sequence.

Each modified oligonucleotide listed in Tables 2 and 3 below is complementary to human IRF4 nucleic acid sequences SEQ ID NO: 1 or SEQ ID NO: 2, as indicated. 'N/A' indicates that the modified oligonucleotide is not complementary to that particular nucleic acid sequence with 100% complementarity. As shown below, modified oligonucleotides complementary to human IRF4 reduced the amount of human IRF4 mRNA.

Table 2

Percent control of human IRF4 mRNA with 3-10-3 cEt gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609281	156	171	5183	5198	GCTCATGCCGA ACTCT	81	72
609282	213	228	5240	5255	GCTGTCGATCTGGTCG	91	73
609283	216	231	5243	5258	GCCGCTGTCGATCTGG	76	74
609284	219	234	5246	5261	CTTGCCGCTGTCGATC	75	75
609285	222	237	5249	5264	GTA CTTGCCGCTGTCG	73	76
609286	238	253	5265	5280	CCCACACCAGCCCGGG	106	77
609287	241	256	5268	5283	TCTCCACACCAGCCC	94	78
609288	244	259	5271	5286	CGTTCTCCCACACCAG	52	79
609289	294	309	5321	5336	GTCTGCTTGCCCGCG	69	80
609290	297	312	5324	5339	GTA GTCCTGCTTGCCC	56	81
609291	334	349	N/A	N/A	CCCAAGCCTTGAAGAG	94	82
609292	431	446	6910	6925	AAGTCATTGCTCTTGT	72	83
609293	434	449	6913	6928	TCAAAGTCATTGCTCT	79	84
609294	437	452	6916	6931	TCCTCAAAGTCATTGC	68	85
609295	496	511	6975	6990	GAACAATCCTGTACAC	105	86
609296	514	529	6993	7008	CTTTTTTGGCTCCCTC	64	87
609297	517	532	N/A	N/A	CTCCTTTTTTGGCTCC	81	88
609298	610	625	N/A	N/A	GAACCTGCTGGGCTGG	64	89

609299	730	745	9220	9235	CTTGCCAGTGGTGGCC	84	90
609300	733	748	9223	9238	GGCCTTGCCAGTGGTG	112	91
609301	752	767	N/A	N/A	CAACCATTTTCACAAG	83	92
609302	755	770	N/A	N/A	TGGCAACCATTTTCAC	93	93
609303	758	773	N/A	N/A	ACCTGGCAACCATTTT	96	94
609304	761	776	N/A	N/A	GTCACCTGGCAACCAT	59	95
609305	764	779	10829	10844	CCTGTCACCTGGCAAC	59	96
609306	767	782	10832	10847	GTTCTGTCACCTGGC	51	97
609307	770	785	10835	10850	AAGGTTCTGTCACCT	102	98
609308	773	788	10838	10853	TAAAAGGTTCTGTCA	94	99
609309	776	791	10841	10856	GCATAAAGGTTCTCTG	74	100
609310	780	795	10845	10860	ACAAGCATAAAAGGTT	96	101
609311	799	814	10864	10879	CCTGGGACTCAGGTGG	41	102
609312	802	817	10867	10882	GAGCCTGGGACTCAGG	51	103
609313	832	847	10897	10912	ACCTTATGCTTGGCTC	69	104
609314	835	850	10900	10915	CAGACCTTATGCTTGG	90	105
609317	943	958	13496	13511	GGGAGATCCGGCAGCC	110	106
609318	979	994	13532	13547	CCTGGTCCAGGTTGCT	74	107
609319	982	997	13535	13550	GGACCTGGTCCAGGTT	102	108
609320	985	1000	13538	13553	ACAGGACCTGGTCCAG	65	109
609321	1046	1061	13599	13614	TCCAGGTGGCTCAGCA	59	110
609322	1049	1064	13602	13617	CTCTCCAGGTGGCTCA	87	111
609323	1052	1067	13605	13620	CCCCTCTCCAGGTGGC	87	112
609324	1194	1209	13747	13762	TGTGTCAAAGAGCTTG	78	113
609325	1198	1213	13751	13766	GCTGTGTGTCAAAGAG	94	114
609326	1201	1216	13754	13769	ACTGCTGTGTGTCAAA	106	115
609327	1264	1279	17057	17072	GAGTCACCTGGAATCT	57	116
609328	1291	1306	17084	17099	GGTCTGGAAACTCCTC	48	117
609329	1294	1309	17087	17102	GAGGGTCTGGAAACTC	104	118
609330	1297	1312	17090	17105	TCTGAGGGTCTGGAAA	91	119
609331	1321	1336	17114	17129	GAGCTGTGATGAGCTT	90	120
609332	1342	1357	19459	19474	TGGCTAGCAGAGGTTT	44	121
609333	1345	1360	19462	19477	GTCTGGCTAGCAGAGG	34	122
609334	1348	1363	19465	19480	GTTGTCTGGCTAGCAG	41	123
609335	1389	1404	19506	19521	CCTCAGGAAATGTCCA	63	124
609336	1393	1408	19510	19525	AGCCCCCTCAGGAAATG	76	125
609337	2068	2083	20185	20200	CTTCCCTGAGAAATGG	50	126
609338	2071	2086	20188	20203	TTACTTCCCTGAGAAA	80	127
609339	2719	2734	20836	20851	AATAAGCAGAAACAGC	101	128
609340	3533	3548	21650	21665	ATCTATAAGATGTATA	101	129
609341	3536	3551	21653	21668	TGCATCTATAAGATGT	68	130

609342	3803	3818	21920	21935	TCCAGAAAATTCAGCT	52	131
609343	3809	3824	21926	21941	GCATTTTCCAGAAAAT	36	132
609344	N/A	N/A	6995	7010	ACCTTTTTTGGCTCCC	79	133
609345	N/A	N/A	7740	7755	ATTCTTAGAATGCATA	62	134
609346	N/A	N/A	8504	8519	CAAACCTCCTCAGGGAA	77	135
609347	N/A	N/A	9242	9257	TTACCATTTTCACAAG	92	136
609348	N/A	N/A	10796	10811	AATCAGATGATGTCTA	103	137
609349	N/A	N/A	10813	10828	CTGCATTTGCAAATAA	121	138
609350	N/A	N/A	10819	10834	GGCAACCTGCATTTGC	113	139
609351	N/A	N/A	10825	10840	TCACCTGGCAACCTGC	75	140
609352	N/A	N/A	11951	11966	CACCCACACAAGTCTT	91	141
609353	N/A	N/A	11972	11987	GTTTATTTCTACTCT	84	142
609354	N/A	N/A	11978	11993	ATAGCTGTTTATTTCC	38	143
609355	N/A	N/A	11985	12000	GATATAAATAGCTGTT	63	144
609356	N/A	N/A	12024	12039	CATTTCAATTAATGTC	67	145
609357	N/A	N/A	12031	12046	CAGGTTTCATTTCAAT	40	146
609358	N/A	N/A	13795	13810	CCTCCATTCTAACAGA	118	147

Table 3

Percent control of human IRF4 mRNA with 3-10-3 cEt gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609360	4711	4726	22828	22843	TGGCCACAGAGGACTT	67	148
609361	1	16	3740	3755	ACTGAGAGTGCGAGGT	120	149
609362	121	136	5148	5163	CCAGGTTTCATGCCCCG	46	150
609363	181	196	5208	5223	GCTTCCCGTTGCCGCA	82	151
609364	300	315	5327	5342	GTTGTAGTCCTGCTTG	78	152
609365	420	435	6899	6914	CTTGTTCAAAGCGCAC	68	153
609366	480	495	6959	6974	TTTGTACGGGTCTGAG	80	154
609367	672	687	9162	9177	GTGTGGCTGATCCGGG	73	155
609368	736	751	9226	9241	CTGGGCCCTTGCCAGTG	114	156
609369	810	825	10875	10890	GACTCCGGGAGCCTGG	35	157
609371	1004	1019	13557	13572	TTGTCCTCTGGGTAGG	70	158
609372	1124	1139	13677	13692	CCGTCCCAGTAGATCC	75	159
609373	1184	1199	13737	13752	AGCTTGCAGGTCTGGT	47	160
609374	1431	1446	19548	19563	GTAATCTTCTGGATTG	71	161
609375	1527	1542	19644	19659	TCCCCGTATCAAAAAA	112	162
609376	1682	1697	19799	19814	CACTTGTCTTGGGTGG	55	163
609377	1742	1757	19859	19874	AACAGTAAGAGGGCAG	37	164

609378	1866	1881	19983	19998	GCAAAGCCACCCTTCC	40	165
609379	1986	2001	20103	20118	TCTTCCAGCAAGACCT	72	166
609380	2111	2126	20228	20243	ATACATTTCTTTTACG	78	167
609381	2171	2186	20288	20303	GATTCATTTCTTCAC	51	168
609382	2231	2246	20348	20363	GAAACCGCTGGCAGGT	50	169
609383	2295	2310	20412	20427	TCCAGGAAAGGCCAAG	51	170
609384	2304	2319	20421	20436	TAAC TGGCTTCCAGGA	70	171
609385	2365	2380	20482	20497	AAAAATGTCCCATCCA	70	172
609386	2431	2446	20548	20563	GTCAAAAAGATGCAGA	50	173
609387	2494	2509	20611	20626	GATTTATGTTCTTAA	53	174
609388	2574	2589	20691	20706	AACAAACAGAGGAGCG	84	175
609389	2634	2649	20751	20766	GCCTGGGAGTCCCCGG	82	176
609390	2694	2709	20811	20826	GTGCAGTTCCGTAGTC	79	177
609391	2754	2769	20871	20886	ACTATAATTGGCACGA	31	178
609392	2816	2831	20933	20948	TCTTTGGGATTCTATA	40	179
609393	2936	2951	21053	21068	GGAGTAATAGTAAATA	64	180
609394	3081	3096	21198	21213	CTGCTCACTAAGCTTG	27	181
609395	3147	3162	21264	21279	GTATTAATATTCTGAC	37	182
609396	3216	3231	21333	21348	GGAGATCCTTTTTATT	68	183
609397	3336	3351	21453	21468	GACTCCATGAGGTTTT	30	184
609398	3437	3452	21554	21569	GGGTACATGGCAGTGG	32	185
609399	3591	3606	21708	21723	GCAGTTCTTAATATCA	40	186
609400	3657	3672	21774	21789	TGAAGTGCTGTGTGGG	43	187
609401	3717	3732	21834	21849	TCCGCTTGGAATAA	87	188
609402	3782	3797	21899	21914	GTAAAGCAGCATAAT	73	189
609403	3851	3866	21968	21983	AGATGTAAAGATAGGA	46	190
609404	3911	3926	22028	22043	AGTTCATTCCTAGGT	56	191
609405	3971	3986	22088	22103	GTTCCTTTTTCAGAGTC	28	192
609406	4031	4046	22148	22163	AGTACAACTAAATTC	76	193
609407	4166	4181	22283	22298	GAGGTTTTCTTAAATA	31	194
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	21	195
609409	4359	4374	22476	22491	CTGTAGGATTTTACAT	76	196
609410	4479	4494	22596	22611	CAGAGTTGTTCCACCC	38	197
609411	4599	4614	22716	22731	AATGAACGGAAGTTTA	67	198
609412	4665	4680	22782	22797	AACCAATCCCAACT	88	199
609413	4727	4742	22844	22859	TTCAGACAGATGCAGC	38	200
609414	4800	4815	22917	22932	CAGTCTCAAAAACGGG	49	201
609415	4862	4877	22979	22994	ACCTTTACTTCATTCC	36	202
609416	4987	5002	23104	23119	ACGGGAATTTCCATTG	33	203
609417	5037	5052	23154	23169	AAGTGGACCCCATTC	69	204
609418	5077	5092	23194	23209	TTCAGCAGAAAGTGGG	52	205

609419	5146	5161	23263	23278	CGCAGAGCCAGTAGGG	33	206
609420	N/A	N/A	2604	2619	AAAAGCCCAAATAGG	112	207
			2875	2890			
609421	N/A	N/A	8538	8553	CTGGCATTGAGACGGG	39	208
			8746	8761			
			8850	8865			
			8902	8917			
			9058	9073			
609422	N/A	N/A	8542	8557	AGCACTGGCATTGAGA	26	209
			8750	8765			
			8854	8869			
			8906	8921			
609423	N/A	N/A	9062	9077	TAAGAAGCACTGGCAT	74	210
			8547	8562			
			8703	8718			
			8807	8822			
			8963	8978			
609424	N/A	N/A	9067	9082	TGAGATAAGAAGCACT	80	211
			8552	8567			
			8708	8723			
			8812	8827			
			8968	8983			
609425	N/A	N/A	9072	9087	GGAGAGGCTGAGATAA	71	212
			8560	8575			
			8716	8731			
			8820	8835			
			8976	8991			
609426	N/A	N/A	9080	9095	AGGAGAGGCTGAGATA	79	213
			8561	8576			
			8613	8628			
			8665	8680			
			8717	8732			
			8769	8784			
			8821	8836			
			8873	8888			
			8925	8940			
			8977	8992			
609427	N/A	N/A	9029	9044	GTGCAGGAGAGGCTGA	68	214
			9081	9096			
			8565	8580			
			8617	8632			

			8669	8684			
			8721	8736			
			8773	8788			
			8825	8840			
			8877	8892			
			8929	8944			
			8981	8996			
			9033	9048			
			9085	9100			
609428	N/A	N/A	8567	8582	GAGTGCAGGAGAGGCT	69	215
			8619	8634			
			8671	8686			
			8723	8738			
			8775	8790			
			8827	8842			
			8879	8894			
			8931	8946			
			8983	8998			
			9035	9050			
			9087	9102			
609429	N/A	N/A	8568	8583	GGAGTGCAGGAGAGGC	84	216
			8620	8635			
			8672	8687			
			8724	8739			
			8776	8791			
			8828	8843			
			8880	8895			
			8932	8947			
			8984	8999			
			9036	9051			
			9088	9103			
609430	N/A	N/A	8572	8587	TAAAGGAGTGCAGGAG	107	217
			8624	8639			
			8676	8691			
			8728	8743			
			8780	8795			
			8832	8847			
			8884	8899			
			8936	8951			
			8988	9003			
			9040	9055			

			9092	9107			
609431	N/A	N/A	8573	8588	GTAAAGGAGTGCAGGA	91	218
			8625	8640			
			8677	8692			
			8729	8744			
			8833	8848			
			8885	8900			
			8937	8952			
			8989	9004			
			9041	9056			
609432	N/A	N/A	8575	8590	GGGTAAAGGAGTGCAG	81	219
			8627	8642			
			8679	8694			
			8731	8746			
			8835	8850			
			8887	8902			
			8939	8954			
			8991	9006			
			9043	9058			
609433	N/A	N/A	8590	8605	CTGGCATCGAGACGGG	53	220
			8642	8657			
			8694	8709			
			8798	8813			
			8954	8969			
			9006	9021			
609434	N/A	N/A	8593	8608	GCACTGGCATCGAGAC	43	221
			8645	8660			
			8697	8712			
			8801	8816			
			8957	8972			
			9009	9024			
609435	N/A	N/A	8596	8611	GAAGCACTGGCATCGA	56	222
			8648	8663			
			8700	8715			
			8804	8819			
			8960	8975			
			9012	9027			
609436	N/A	N/A	18852	18867	CCTGAATTTACAGCAT	60	223

Example 3: Effect of 4-8-4 cEt gapmers with phosphorothioate internucleoside linkages on human IRF4 *in vitro*, single dose

Modified oligonucleotides complementary to a human IRF4 nucleic acid were designed and tested for their effect on IRF4 mRNA *in vitro*.

5 Cultured SK-MEL-28 cells at a density of 20,000 cells per well were transfected using electroporation with 4,000 nM concentration of modified oligonucleotide or no modified oligonucleotide for untreated controls. After approximately 24 hours, RNA was isolated from the cells and IRF4 mRNA levels were measured by quantitative real-time PCR. Human primer probe set RTS3114 (described hereinabove in Example 1) was used to measure mRNA levels. IRF4 mRNA levels were adjusted according to total RNA
10 content, as measured by RIBOGREEN®. Results are presented in the table below as percent control of the amount of IRF4 mRNA, relative to untreated control (UTC) cells.

The modified oligonucleotides in Table 4 are 4-8-4 cEt gapmers. The gapmers are 16 nucleobases in length, wherein the central gap segment comprises eight 2'-deoxynucleosides and is flanked by wing segments on both the 5' end and on the 3' end comprising four cEt nucleosides. The sugar motif for the
15 gapmers is (from 5' to 3'): kkkkdddddskkkk; wherein 'd' represents a 2'-deoxyribose sugar and 'k' represents a cEt modified sugar. Each internucleoside linkage is a phosphorothioate internucleoside linkage and each cytosine residue is a 5-methylcytosine. "Start Site" indicates the 5'-most nucleoside to which the gapmer is complementary in the human nucleic acid sequence. "Stop Site" indicates the 3'-most nucleoside to which the gapmer is complementary in the human nucleic acid sequence.

20 Each modified oligonucleotide listed in Table 4 below is complementary to human IRF4 nucleic acid sequences SEQ ID NO: 1 or SEQ ID NO: 2, as indicated. 'N/A' indicates that the modified oligonucleotide is not complementary to that particular nucleic acid sequence with 100% complementarity. As shown below, modified oligonucleotides complementary to human IRF4 reduced the amount of human IRF4 mRNA.

25

Table 4

**Percent control of human IRF4 mRNA with 4-8-4 cEt gapmers
with phosphorothioate internucleoside linkages**

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609518	156	171	5183	5198	GCTCATGCCGAACCTCT	70	72
609519	213	228	5240	5255	GCTGTCGATCTGGTCG	94	73
609520	216	231	5243	5258	GCCGCTGTCGATCTGG	85	74
609521	219	234	5246	5261	CTTGCCGCTGTCGATC	58	75
609522	222	237	5249	5264	GTACTTGCCGCTGTCTG	64	76
609523	238	253	5265	5280	CCCACACCAGCCCGGG	106	77
609524	241	256	5268	5283	TCTCCCACACCAGCCC	75	78

609525	244	259	5271	5286	CGTTCTCCCACACCAG	101	79
609526	294	309	5321	5336	GTCCTGCTTGCCCGCG	86	80
609527	297	312	5324	5339	GTAGTCCTGCTTGCCC	89	81
609528	334	349	N/A	N/A	CCCAAGCCTTGAAGAG	78	82
609529	431	446	6910	6925	AAGTCATTGCTCTTGT	72	83
609530	434	449	6913	6928	TCAAAGTCATTGCTCT	43	84
609531	437	452	6916	6931	TCCTCAAAGTCATTGC	90	85
609532	496	511	6975	6990	GAACAATCCTGTACAC	100	86
609533	514	529	6993	7008	CTTTTTTGGCTCCCTC	54	87
609534	517	532	N/A	N/A	CTCCTTTTTTGGCTCC	93	88
609535	610	625	N/A	N/A	GAACCTGCTGGGCTGG	87	89
609536	730	745	9220	9235	CTTGCCAGTGGTGGCC	109	90
609537	733	748	9223	9238	GGCCTTGCCAGTGGTG	94	91
609538	752	767	N/A	N/A	CAACCATTTTCACAAG	95	92
609539	755	770	N/A	N/A	TGGCAACCATTTTCAC	93	93
609540	758	773	N/A	N/A	ACCTGGCAACCATTTT	81	94
609541	761	776	N/A	N/A	GTCACCTGGCAACCAT	59	95
609542	764	779	10829	10844	CCTGTCACCTGGCAAC	63	96
609543	767	782	10832	10847	GTTCTGTCACCTGGC	88	97
609544	770	785	10835	10850	AAGGTTCTGTCACCT	86	98
609545	773	788	10838	10853	TAAAAGGTTCTGTCA	57	99
609546	776	791	10841	10856	GCATAAAAGGTTCTCTG	53	100
609547	780	795	10845	10860	ACAAGCATAAAAGGTT	60	101
609548	799	814	10864	10879	CCTGGGACTCAGGTGG	93	102
609549	802	817	10867	10882	GAGCCTGGGACTCAGG	81	103
609550	832	847	10897	10912	ACCTTATGCTTGCTC	70	104
609551	835	850	10900	10915	CAGACCTTATGCTTGG	74	105
609554	943	958	13496	13511	GGGAGATCCGGCAGCC	113	106
609555	979	994	13532	13547	CCTGGTCCAGGTTGCT	66	107
609556	982	997	13535	13550	GGACCTGGTCCAGGTT	128	108
609557	985	1000	13538	13553	ACAGGACCTGGTCCAG	93	109
609558	1046	1061	13599	13614	TCCAGGTGGCTCAGCA	66	110
609559	1049	1064	13602	13617	CTCTCCAGGTGGCTCA	88	111
609560	1052	1067	13605	13620	CCCCTCTCCAGGTGGC	101	112
609561	1194	1209	13747	13762	TGTGTCAAAGAGCTTG	74	113
609562	1198	1213	13751	13766	GCTGTGTGTCAAAGAG	60	114
609563	1201	1216	13754	13769	ACTGCTGTGTGTCAAA	81	115
609564	1264	1279	17057	17072	GAGTCACCTGGAATCT	94	116
609565	1291	1306	17084	17099	GGTCTGGAAACTCCTC	69	117
609566	1294	1309	17087	17102	GAGGGTCTGGAAACTC	92	118
609567	1297	1312	17090	17105	TCTGAGGGTCTGGAAA	97	119

609568	1321	1336	17114	17129	GAGCTGTGATGAGCTT	95	120
609569	1342	1357	19459	19474	TGGCTAGCAGAGGTTC	91	121
609570	1345	1360	19462	19477	GTCTGGCTAGCAGAGG	91	122
609571	1348	1363	19465	19480	GTTGTCTGGCTAGCAG	48	123
609572	1389	1404	19506	19521	CCTCAGGAAATGTCCA	90	124
609574	2068	2083	20185	20200	CTTCCCTGAGAAATGG	64	126
609575	2071	2086	20188	20203	TTACTTCCCTGAGAAA	86	127
609576	2719	2734	20836	20851	AATAAGCAGAAACAGC	61	128
609577	3533	3548	21650	21665	ATCTATAAGATGTATA	64	129
609578	3536	3551	21653	21668	TGCATCTATAAGATGT	90	130
609579	3803	3818	21920	21935	TCCAGAAAATTCAGCT	74	131
609580	3809	3824	21926	21941	GCATTTTCCAGAAAAT	63	132
609581	N/A	N/A	6995	7010	ACCTTTTTTGGCTCCC	81	133
609582	N/A	N/A	7740	7755	ATTCTTAGAATGCATA	67	134
609583	N/A	N/A	8504	8519	CAAACCTCCTCAGGGAA	83	135
609584	N/A	N/A	9242	9257	TTACCATTTTCACAAG	93	136
609585	N/A	N/A	10796	10811	AATCAGATGATGTCTA	113	137
609586	N/A	N/A	10813	10828	CTGCATTGCAAATAA	108	138
609587	N/A	N/A	10819	10834	GGCAACCTGCATTTGC	112	139
609588	N/A	N/A	10825	10840	TCACCTGGCAACCTGC	72	140
609589	N/A	N/A	11951	11966	CACCCACACAAGTCTT	86	141
609590	N/A	N/A	11972	11987	GTTTATTTCTACTCT	56	142
609591	N/A	N/A	11978	11993	ATAGCTGTTTATTTC	41	143
609592	N/A	N/A	11985	12000	GATATAAATAGCTGTT	39	144
609593	N/A	N/A	12024	12039	CATTTTCATTTAATGTC	56	145
609594	N/A	N/A	12031	12046	CAGGTTTCATTTTCATT	46	146
609595	N/A	N/A	13795	13810	CCTCCATTCTAACAGA	122	147

Example 4: Effect of 3-10-3 cEt gapmers with phosphorothioate internucleoside linkages on human IRF4 *in vitro*, single dose

Modified oligonucleotides complementary to a human IRF4 nucleic acid were designed and tested for their effect on IRF4 mRNA *in vitro*.

Cultured SK-MEL-28 cells at a density of 20,000 cells per well were transfected using electroporation with 4,000 nM concentration of modified oligonucleotide or no modified oligonucleotide for untreated controls. After approximately 24 hours, RNA was isolated from the cells and IRF4 mRNA levels were measured by quantitative real-time PCR. Human primer probe set RTS3114 (described hereinabove in Example 1) was used to measure mRNA levels. IRF4 mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented in the table below as percent control of the amount of IRF4 mRNA, relative to untreated control (UTC) cells.

The modified oligonucleotides in Tables 5 through 12 are 3-10-3 cEt gapmers. The gapmers are 16 nucleobases in length, wherein the central gap segment comprises ten 2'-deoxynucleosides and is flanked by wing segments on both the 5' end and on the 3' end comprising three cEt nucleosides. The sugar motif for the gapmers is (from 5' to 3'): kkkddddd kkk; wherein 'd' represents a 2'-deoxyribose sugar and 'k' represents a cEt modified sugar. Each internucleoside linkage is a phosphorothioate internucleoside linkage and each cytosine residue is a 5-methylcytosine. "Start Site" indicates the 5'-most nucleoside to which the gapmer is complementary in the human nucleic acid sequence. "Stop Site" indicates the 3'-most nucleoside to which the gapmer is complementary in the human nucleic acid sequence.

Each modified oligonucleotide listed in Tables 5 through 12 below is complementary to human IRF4 nucleic acid sequences SEQ ID NO: 1 or SEQ ID NO: 2, as indicated. 'N/A' indicates that the modified oligonucleotide is not complementary to that particular nucleic acid sequence with 100% complementarity. As shown below, modified oligonucleotides complementary to human IRF4 reduced the amount of human IRF4 mRNA.

Table 5

Percent control of human IRF4 mRNA with 3-10-3 cEt gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	24	195
666225	5	20	3744	3759	TGAAACTGAGAGTGCG	81	224
666226	12	27	3751	3766	CGAGCGGTGAACTGA	67	225
666227	19	34	3758	3773	CCAAGATCGAGCGGTG	63	226
666228	26	41	3765	3780	GTGGGTCCCAAGATCG	60	227
666229	40	55	3779	3794	AGCTGAGGGCAGCGGT	107	228
666230	47	62	3786	3801	GACTCGGAGCTGAGGG	77	229
666231	54	69	3793	3808	CGCCCTGGACTCGGAG	64	230
666232	61	76	N/A	N/A	CTGCACTCGCCCTGGA	58	231
666233	68	83	N/A	N/A	CTCTGCTCTGCACTCG	59	232
666234	75	90	5102	5117	CCGCCCGCTCTGCTCT	46	233
666235	82	97	5109	5124	GGGTCTCCGCCCGCT	72	234
666236	101	116	5128	5143	CCGTCCGCGCCCGCGC	39	235
666237	129	144	5156	5171	GCCGCCCTCCAGGTTC	51	236
666238	136	151	5163	5178	CTCGGCCGCCGCCCTC	63	237
666239	143	158	5170	5185	TCTCCGCCTCGGCCGC	59	238
666240	150	165	5177	5192	GCCGAACTCTCCGCCT	49	239
666241	160	175	5187	5202	CCGCGCTCATGCCGAA	55	240

666242	167	182	5194	5209	CAGCTCACCGCGCTCA	58	241
666243	185	200	5212	5227	CGGAGCTTCCCGTTGC	65	242
666244	192	207	5219	5234	CCACTGGCGGAGCTTC	64	243
666245	304	319	5331	5346	CGCGGTTGTAGTCCTG	56	244
666246	311	326	5338	5353	TCCTCCTCGCGTTGT	41	245
666247	327	342	5354	5369	CTTGAAGAGCGCGGCG	79	246
666248	338	353	N/A	N/A	AGTGCCCAAGCCTTGA	52	247
666249	348	363	6827	6842	TCCTTTAAACAGTGCC	50	248
666250	356	371	6835	6850	CGGAACTTTCCTTTAA	63	249
666251	363	378	6842	6857	GCCTTCTCGGAACTTT	68	250
666252	370	385	6849	6864	TGTCGATGCCTTCTCG	72	251
666253	377	392	6856	6871	TCCGGCTTGTCGATGC	59	252
666254	396	411	6875	6890	CGTCTTCCAGGTGGGA	84	253
666256	425	440	6904	6919	TTGCTCTTGTTCAAAG	71	254
666257	449	464	6928	6943	CGCTCAACCAGTTCCT	72	255
666258	456	471	6935	6950	CTGGCTCCGCTCAACC	48	256
666259	463	478	6942	6957	TGTCCAGCTGGCTCCG	61	257
666260	470	485	6949	6964	TCTGAGATGTCCAGCT	55	258
666261	484	499	6963	6978	ACACTTTGTACGGGTC	44	259
666262	507	522	6986	7001	GGCTCCCTCAGGAACA	81	260
666263	521	536	N/A	N/A	TTGGCTCCTTTTTTGG	87	261
666264	528	543	7846	7861	GAGCTGCTTGGCTCCT	81	262
666265	535	550	7853	7868	CCAGGGTGAGCTGCTT	69	263
666266	546	561	7864	7879	CTGCGGGTCCTCCAGG	80	264
666267	553	568	7871	7886	TGGACATCTGCGGGTC	56	265
666268	560	575	7878	7893	TGGCTCATGGACATCT	68	266
666269	577	592	7895	7910	TTGTCATGGTGTAGGG	59	267
666270	593	608	7911	7926	AGCGAAGGGTAAGGCG	86	268
666271	621	636	9111	9126	CATGTAGTTGTGAACC	73	269
666272	628	643	9118	9133	GTGGCATCATGTAGTT	73	270
666273	644	659	9134	9149	CAGCTTCGGTCGAGGG	42	271
666274	651	666	9141	9156	GTCCCTCCAGCTTCGG	97	272
666275	676	691	9166	9181	CCGGGTGTGGCTGATC	84	273
666276	695	710	9185	9200	GGACATTGGTACGGGA	50	274
666277	702	717	9192	9207	CGTCATGGGACATTGG	44	275
666278	725	740	9215	9230	CAGTGGTGGCCGCGGG	73	276
666279	740	755	9230	9245	CAAGCTGGGCCTTGCC	66	277
666280	747	762	9237	9252	ATTTTCACAAGCTGGG	61	278
666281	771	786	10836	10851	AAAGGTTTCCTGTCACC	62	279
666282	775	790	10840	10855	CATAAAAGGTTCTGT	91	280
666283	777	792	10842	10857	AGCATAAAAGGTTCTCT	55	281

666284	779	794	10844	10859	CAAGCATAAAAGGTTC	71	282
666285	781	796	10846	10861	CACAAGCATAAAAGGT	74	283
666286	784	799	10849	10864	GGGCACAAGCATAAAA	80	284
666287	827	842	10892	10907	ATGCTTGGCTCTGTGG	24	285
666294	947	962	13500	13515	CCATGGGAGATCCGGC	46	286
666295	954	969	13507	13522	CGTATGTCCATGGGAG	12	287
666296	975	990	13528	13543	GTCCAGGTGCTGGCG	47	288
666297	989	1004	13542	13557	GGGAACAGGACCTGGT	45	289
666298	1008	1023	13561	13576	GCCATTGTCCTCTGGG	75	290
666299	1015	1030	13568	13583	TCCTCTGGCCATTGTC	59	291
666300	1033	1048	13586	13601	GCAGCTTCTCAATGTT	57	292
666301	1042	1057	13595	13610	GGTGGCTCAGCAGCTT	63	293

Table 6

Percent control of human IRF4 mRNA with 3-10-3 cEt gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	23	195
666302	1058	1073	13611	13626	ACCACGCCCTCTCCA	91	294
666303	1065	1080	13618	13633	CCAGAGGACCACGCCC	72	295
666306	1101	1116	13654	13669	GCACAGTCTTTTCGCA	80	296
666307	1109	1124	13662	13677	CTGCTCTGGCACAGTC	17	297
666308	1116	1131	13669	13684	GTAGATCCTGCTCTGG	55	298
666309	1128	1143	13681	13696	GGGCCCCGTCCAGTAG	80	299
666311	1167	1182	13720	13735	TCTCTCCAGTTTGTTG	86	300
666312	1188	1203	13741	13756	AAAGAGCTTGCAGGTC	63	301
666313	1205	1220	13758	13773	AAGAACTGCTGTGTGT	88	302
666314	1212	1227	N/A	N/A	CTCTGACAAGAACTGC	70	303
666315	1219	1234	N/A	N/A	CTTGCAGCTCTGACAA	91	304
666317	1241	1256	17034	17049	GAGCGGCCGTGGTGAG	59	305
666318	1248	1263	17041	17056	TGGCAGGGAGCGGCCG	89	306
666319	1255	1270	17048	17063	GGAATCTTGGCAGGGA	52	307
666321	1275	1290	17068	17083	TCCAAAGCATAGAGTC	47	308
666322	1287	1302	17080	17095	TGGAACTCCTCTCCA	84	309
666323	1311	1326	17104	17119	GAGCTTTCTTTGCCTC	87	310
666324	1338	1353	N/A	N/A	TAGCAGAGGTTCTACG	76	311
666326	1347	1362	19464	19479	TTGTCTGGCTAGCAGA	55	312
666327	1349	1364	19466	19481	AGTTGTCTGGCTAGCA	20	313
666328	1351	1366	19468	19483	ATAGTTGTCTGGCTAG	48	314

666329	1353	1368	19470	19485	ATATAGTTGTCTGGCT	59	315
666331	1381	1396	19498	19513	AATGTCCACTGTTTTG	53	316
666333	1417	1432	19534	19549	TGCTGATGTGTTCTGG	33	317
666335	1442	1457	19559	19574	ATAGATCTGTGGTAAT	62	318
666336	1449	1464	19566	19581	ATGGCGGATAGATCTG	43	319
666337	1456	1471	19573	19588	TAGAGGAATGGCGGAT	55	320
666338	1463	1478	19580	19595	TCTTGAATAGAGGAAT	58	321
666339	1485	1500	19602	19617	CACTCATCTTGACATT	64	322
666341	1538	1553	19655	19670	AAGACCCCGTATCCCC	58	323
666342	1686	1701	19803	19818	AAATCACTTGTCTTGG	51	324
666343	1715	1730	19832	19847	CTTTCATAAAGTCAA	49	325
666344	1730	1745	19847	19862	GCAGTCAATTGGACGC	23	326
666345	1737	1752	19854	19869	TAAGAGGGCAGTCAAT	83	327
666346	1762	1777	19879	19894	TCCACTTCTGAATTCC	81	328
666347	1775	1790	19892	19907	CTGAACTGAAATCTCC	36	329
666348	1782	1797	19899	19914	TCAACCGCTGAACTGA	65	330
666349	1789	1804	19906	19921	ATTCTCCTCAACCGCT	65	331
666351	1803	1818	19920	19935	CTTGTCTCGCCGCAAT	35	332
666352	1810	1825	19927	19942	TTCCATGCTTGTCTCG	38	333
666353	1826	1841	19943	19958	TCAGATGTCAGTATT	65	334
666354	1840	1855	19957	19972	AGCTCATCTGCCAATC	67	335
666355	1848	1863	19965	19980	TTGAAATAAGCTCATC	67	336
666356	1885	1900	20002	20017	TCTACAGAACACAAGA	108	337
666357	1892	1907	20009	20024	ATGGCAGTCTACAGAA	102	338
666358	1899	1914	20016	20031	ATCAATGATGGCAGTC	43	339
666359	1908	1923	20025	20040	ACAGTGATCATCAATG	44	340
666360	1915	1930	20032	20047	AATTTTCACAGTGATC	66	341
666361	1922	1937	20039	20054	CTTGGTCAATTTTCAC	47	342
666362	1929	1944	20046	20061	CACATCACTTGGTCAA	28	343
666363	1956	1971	20073	20088	TAAAGAGCGCATTTCA	59	344
666364	1963	1978	20080	20095	AACAAATTAAAGAGCG	77	345
666365	1972	1987	20089	20104	CTAATCTACAACAAAT	77	346
666366	2000	2015	20117	20132	GCAAGTTTTCTCTGTC	44	347
666368	2023	2038	20140	20155	CTAGTCAGTGTCATA	49	348
666369	2030	2045	20147	20162	CATCACTCTAGTCAGT	41	349
666370	2037	2052	20154	20169	AAGCAGTCATCACTCT	62	350
666371	2053	2068	20170	20185	GCACAGACATACCTAC	54	351
666373	2082	2097	20199	20214	CAATTTACATCTTACT	79	352
666374	2089	2104	20206	20221	GCTTCTTCAATTTACA	55	353
666375	2130	2145	20247	20262	GCAGCTCCTACATACA	47	354
666376	2138	2153	20255	20270	CAAGAACTGCAGCTCC	53	355

666377	2146	2161	20263	20278	GTCTTCCACAAGAACT	53	356
666378	2153	2168	20270	20285	AGCAAGTGTCTTCCAC	25	357

Table 7

Percent control of human IRF4 mRNA with 3-10-3 cEt gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	23	195
666379	2161	2176	20278	20293	CTTCACTCAGCAAGTG	57	358
666380	2179	2194	20296	20311	CAGTCAAAGATTCATT	60	359
666381	2193	2208	20310	20325	TACAGGCACGGCTTCA	42	360
666382	2200	2215	20317	20332	CCAAGGCTACAGGCAC	37	361
666383	2207	2222	20324	20339	GGCCTCCCCAAGGCTA	82	362
666384	2235	2250	20352	20367	CCAGGAAACCGCTGGC	62	363
666385	2243	2258	20360	20375	GACCCACACCAGGAAA	98	364
666386	2250	2265	20367	20382	GCAGAGGGACCCACAC	79	365
666387	2308	2323	20425	20440	TTACTAACTGGCTTCC	51	366
666388	2315	2330	20432	20447	AGGAAGTTTACTAACT	42	367
666389	2328	2343	20445	20460	GACTCAAGAAAATAGG	36	368
666390	2335	2350	20452	20467	GTTTTTTGACTCAAGA	33	369
666392	2355	2370	20472	20487	CATCCAAGAGTAGCGC	27	370
666393	2376	2391	20493	20508	GTAGGACAGACAAAAA	77	371
666394	2383	2398	20500	20515	CTAGATTGTAGGACAG	52	372
666395	2390	2405	20507	20522	GACATTACTAGATTGT	30	373
666396	2397	2412	20514	20529	TTACTTAGACATTACT	52	374
666397	2404	2419	20521	20536	TTAACCATTACTTAGA	55	375
666398	2435	2450	20552	20567	GAGGGTCAAAAAGATG	67	376
666399	2450	2465	20567	20582	GCATCTCTAAAGAATG	39	377
666400	2461	2476	20578	20593	GAAGAATTTTAGCATC	44	378
666401	2468	2483	20585	20600	TTTATGCGAAGAATTT	67	379
666402	2475	2490	20592	20607	CTTCTTCTTTATGCGA	34	380
666403	2498	2513	20615	20630	TTAAGATTTATGTTCC	36	381
666404	2514	2529	20631	20646	GGCAACAGTTCAAGTA	43	382
666405	2521	2536	20638	20653	ACAGAAGGGCAACAGT	57	383
666406	2528	2543	20645	20660	TACTTGACAGAAGGG	38	384
666407	2535	2550	20652	20667	AGTTAAGTACTTGGAC	58	385
666408	2542	2557	20659	20674	AACAGATAGTTAAGTA	81	386
666409	2578	2593	20695	20710	GCCAAACAAACAGAGG	78	387
666410	2585	2600	20702	20717	CTGGACAGCCAAACAA	79	388

666411	2592	2607	20709	20724	CTGATCGCTGGACAGC	80	389
666412	2599	2614	20716	20731	GCCATGGCTGATCGCT	70	390
666413	2606	2621	20723	20738	TAGTGTCGCCATGGCT	31	391
666414	2613	2628	20730	20745	CCTCCTTTAGTGTCGC	35	392
666415	2621	2636	20738	20753	CGGCTCCTCCTCCTTT	89	393
666416	2628	2643	20745	20760	GAGTCCCCGGCTCCTC	75	394
666417	2652	2667	20769	20784	TCCTGGCAGTGCTCTC	40	395
666418	2659	2674	20776	20791	TGGTGGGTCCTGGCAG	77	396
666420	2673	2688	20790	20805	CATCCTGCTTCCAGTG	70	397
666421	2681	2696	20798	20813	GTCAGCTCCATCCTGC	48	398
666422	2688	2703	20805	20820	TTCCGTAGTCAGCTCC	32	399
666423	2698	2713	20815	20830	GAGTGTGCAGTTCCGT	33	400
666424	2705	2720	20822	20837	GCCCACTGAGTGTGCA	90	401
666425	2714	2729	20831	20846	GCAGAAACAGCCCACT	59	402
666426	2737	2752	20854	20869	GAAGCATAGAACAGAT	49	403
666427	2744	2759	20861	20876	GCACGAGGAAGCATAG	42	404
666428	2749	2764	20866	20881	AATTGGCACGAGGAAG	72	405
666429	2751	2766	20868	20883	ATAATTGGCACGAGGA	33	406
666430	2753	2768	20870	20885	CTATAATTGGCACGAG	37	407
666431	2755	2770	20872	20887	AACTATAATTGGCACG	27	408
666432	2757	2772	20874	20889	CAAACCTATAATTGGCA	47	409
666433	2759	2774	20876	20891	GTCAAACCTATAATTGG	39	410
666434	2765	2780	20882	20897	GGCCCTGTCAAACCTAT	60	411
666435	2772	2787	20889	20904	ATTTTAAGGCCCTGTC	66	412
666436	2779	2794	20896	20911	CCAAGTAATTTTAAGG	66	413
666437	2793	2808	20910	20925	GCATTTGGAAAAAGCC	29	414
666438	2810	2825	20927	20942	GGATTCTATAAATAGA	75	415
666439	2820	2835	20937	20952	GAGGTCTTTGGGATTC	26	416
666440	2827	2842	20944	20959	GCAAGTGGAGGTCTTT	26	417
666441	2834	2849	20951	20966	TACTTAAGCAAGTGGA	25	418
666442	2841	2856	20958	20973	ATAGGTATACTTAAGC	20	419
666443	2848	2863	20965	20980	GTAAGTGATAGGTATA	24	420
666444	2872	2887	20989	21004	GTACTTTCTCAAAACC	30	421
666445	2879	2894	20996	21011	TACTGCTGTACTTTCT	57	422
666446	2886	2901	21003	21018	CCCAGTCTACTGCTGT	34	423
666447	2902	2917	21019	21034	GGCCTGGAGGTGACGC	59	424
666448	2909	2924	21026	21041	GAGAAACGGCCTGGAG	56	425
666449	2916	2931	21033	21048	GTAGTATGAGAAACGG	17	426
666450	2923	2938	21040	21055	ATATCCTGTAGTATGA	43	427
666451	2930	2945	21047	21062	ATAGTAAATATCCTGT	64	428
666452	2940	2955	21057	21072	CCTGGGAGTAATAGTA	47	429

666453	2947	2962	21064	21079	TGCTGATCCTGGGAGT	21	430
666454	2954	2969	21071	21086	AATCTTCTGCTGATCC	28	431
666455	2961	2976	21078	21093	GCTACGCAATCTTCTG	42	432

Table 8

Percent control of human IRF4 mRNA with 3-10-3 cEt gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	20	195
666457	2975	2990	21092	21107	ACACACATTTGAGAGC	34	433
666458	2992	3007	21109	21124	CCATTAGAAAAGCAGG	20	434
666459	3021	3036	21138	21153	TAGGTGCTTGTGAAT	50	435
666460	3031	3046	21148	21163	AGGCACTTACTAGGTG	46	436
666461	3039	3054	21156	21171	GATACAGCAGGCACTT	37	437
666462	3046	3061	21163	21178	ATGTAGGGATACAGCA	26	438
666463	3053	3068	21170	21185	CTGTGTAATGTAGGGA	58	439
666464	3060	3075	21177	21192	GGCTGAACTGTGTAAT	28	440
666465	3067	3082	21184	21199	TGATAAAGGCTGAACT	59	441
666466	3074	3089	21191	21206	CTAAGCTTGATAAAGG	46	442
666467	3085	3100	21202	21217	CTCACTGCTCACTAAG	36	443
666468	3092	3107	21209	21224	TTCAGTGCTCACTGCT	31	444
666469	3099	3114	21216	21231	ATAATGTTTCAGTGCT	24	445
666470	3136	3151	21253	21268	CTGACTTTAATATTAG	44	446
666471	3178	3193	21295	21310	GTCTTTTCTGTAGTTA	10	447
666472	3192	3207	21309	21324	GTTCTCTACTGTTTGT	32	448
666473	3239	3254	21356	21371	GGAGAATTTGGGCTGG	25	449
666474	3246	3261	21363	21378	TTAGAGAGGAGAATTT	65	450
666475	3253	3268	21370	21385	GACACTTTTAGAGAGG	13	451
666476	3260	3275	21377	21392	TCTTGTGGACACTTTT	35	452
666477	3267	3282	21384	21399	CACCCCTTCTGTGGA	60	453
666478	3274	3289	21391	21406	GAATAAACACCCCTTC	56	454
666479	3288	3303	21405	21420	GAAATGTGTTGGAAGA	32	455
666480	3335	3350	21452	21467	ACTCCATGAGGTTTTTC	27	456
666481	3337	3352	21454	21469	TGACTCCATGAGGTTT	35	457
666482	3339	3354	21456	21471	GATGACTCCATGAGGT	33	458
666483	3341	3356	21458	21473	AAGATGACTCCATGAG	36	459
666485	3355	3370	21472	21487	ATGAAAGTGTGTGCAA	36	460
666486	3362	3377	21479	21494	GCACTGCATGAAAGTG	60	461
666487	3371	3386	21488	21503	CTACAAAGAGCACTGC	47	462

666488	3378	3393	21495	21510	CTGTTAGCTACAAAGA	44	463
666489	3385	3400	21502	21517	ATCTTCACTGTTAGCT	26	464
666490	3392	3407	21509	21524	GAGGTAAATCTTCACT	30	465
666491	3399	3414	21516	21531	GCAGAACGAGGTAAAT	38	466
666492	3406	3421	21523	21538	CCTCTGAGCAGAACGA	24	467
666493	3413	3428	21530	21545	AGCAAGGCCTCTGAGC	45	468
666494	3420	3435	21537	21552	GCTCCACAGCAAGGCC	42	469
666495	3427	3442	21544	21559	CAGTGGAGCTCCACAG	59	470
666496	3432	3447	21549	21564	CATGGCAGTGGAGCTC	13	471
666497	3434	3449	21551	21566	TACATGGCAGTGGAGC	29	472
666498	3436	3451	21553	21568	GGTACATGGCAGTGGA	13	473
666499	3438	3453	21555	21570	TGGGTACATGGCAGTG	26	474
666500	3440	3455	21557	21572	ACTGGGTACATGGCAG	41	475
666501	3442	3457	21559	21574	CTACTGGGTACATGGC	16	476
666502	3448	3463	21565	21580	CAAACCCCTACTGGGTA	68	477
666503	3455	3470	21572	21587	GAAATGTCAAACCCTA	29	478
666504	3462	3477	21579	21594	GGCTAATGAAATGTCA	36	479
666505	3469	3484	21586	21601	GTTGCATGGCTAATGA	39	480
666506	3476	3491	21593	21608	TATCCATGTTGCATGG	39	481
666507	3491	3506	21608	21623	CTGCTGCCCAATACAT	53	482
666508	3498	3513	21615	21630	ACACAGTCTGCTGCCC	49	483
666509	3505	3520	21622	21637	TCACGAAACACAGTCT	32	484
666510	3512	3527	21629	21644	CTGCAGTTCACGAAAC	62	485
666511	3519	3534	21636	21651	TACATCACTGCAGTTC	32	486
666512	3526	3541	21643	21658	AGATGTATACATCACT	24	487
666513	3548	3563	21665	21680	CCCAAAATACTTTGCA	36	488
666514	3558	3573	21675	21690	GATAATATACCCCAAA	67	489
666515	3565	3580	21682	21697	CCCTTAGGATAATATA	51	490
666516	3572	3587	21689	21704	TTATCTTCCCTTAGGA	72	491
666517	3599	3614	21716	21731	GTGAAACAGCAGTTCT	38	492
666518	3606	3621	21723	21738	GGGCCCCGTGAAACAG	67	493
666519	3613	3628	21730	21745	CAGGTAAGGGCCCCGT	30	494
666520	3620	3635	21737	21752	AGGGTCACAGGTAAGG	32	495
666521	3627	3642	21744	21759	AGCAAAGAGGGTCACA	32	496
666522	3642	3657	21759	21774	GGTTAAATATTCTTCA	52	497
666523	3661	3676	21778	21793	TCTTTGAAGTGCTGTG	43	498
666524	3668	3683	21785	21800	GACAGCTTCTTTGAAG	64	499
666525	3675	3690	21792	21807	CTTCCAAGACAGCTTC	37	500
666526	3682	3697	21799	21814	AGACAGACTTCCAAGA	64	501
666527	3689	3704	21806	21821	GCTCCTGAGACAGACT	44	502
666528	3696	3711	21813	21828	ACAGGGTGCTCCTGAG	77	503

666529	3710	3725	21827	21842	GGAGAATTAAGAAGAC	68	504
666530	3721	3736	21838	21853	AGCATCCGCTTGGAGA	63	505
666531	3728	3743	21845	21860	GAAATGGAGCATCCGC	68	506
666532	3735	3750	21852	21867	AGCAATTGAAATGGAG	78	507

Table 9

Percent control of human IRF4 mRNA with 3-10-3 cEt gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	20	195
666533	3742	3757	21859	21874	GTCACAAAGCAATTGA	33	508
666534	3786	3801	21903	21918	CACTGTAAAGCAGCA	19	509
666535	3793	3808	21910	21925	TCAGCTCCACTGTAA	27	510
666537	3824	3839	21941	21956	GGCCCCAGCCAAGAAG	92	511
666538	3831	3846	21948	21963	AGGTAGTGGCCCCAGC	40	512
666539	3865	3880	21982	21997	GTCAACATACACATAG	42	513
666540	3886	3901	22003	22018	GATCACTCAGAATTTT	50	514
666541	3893	3908	22010	22025	TACCCTGGATCACTCA	35	515
666542	3900	3915	22017	22032	TAGGTCATACCCTGGA	28	516
666543	3907	3922	22024	22039	CATTCCCTAGGTCATA	46	517
666544	3915	3930	22032	22047	AGCTAGTTCATTCCCT	52	518
666545	3922	3937	22039	22054	ATTTTCATAGCTAGTTC	56	519
666546	3929	3944	22046	22061	CCTGAGTATTTTCATAG	58	520
666547	3936	3951	22053	22068	TCCTAACCCCTGAGTAT	73	521
666548	3950	3965	22067	22082	ACAAGTGCTAGGATTC	33	522
666549	3957	3972	22074	22089	TCCTGAGACAAGTGCT	45	523
666550	3964	3979	22081	22096	TTCAGAGTCCTGAGAC	54	524
666551	3968	3983	22085	22100	CCTTTTCAGAGTCCTG	42	525
666552	3972	3987	22089	22104	CGTTCCTTTTCAGAGT	70	526
666553	3974	3989	22091	22106	GCCGTTCCCTTTTCAGA	38	527
666554	3976	3991	22093	22108	AAGCCGTTCCCTTTTCA	71	528
666555	3982	3997	22099	22114	ATGAGGAAGCCGTTCC	42	529
666556	3996	4011	22113	22128	TATCAAGACAAGGAAT	93	530
666557	4003	4018	22120	22135	TCCACTTTATCAAGAC	35	531
666559	4017	4032	22134	22149	TCTAGTTTGCCAATTC	38	532
666560	4024	4039	22141	22156	ACTAAATTCTAGTTTG	100	533
666561	4035	4050	22152	22167	ACTGAGTACAACTAA	68	534
666562	4042	4057	22159	22174	ACTGTCCACTGAGTAC	39	535
666563	4049	4064	22166	22181	CAACAGCACTGTCCAC	57	536

666564	4056	4071	22173	22188	AAATCTTCAACAGCAC	55	537
666565	4063	4078	22180	22195	AGTCCTCAAATCTTCA	46	538
666566	4071	4086	22188	22203	CTTTAACAAGTCCTCA	48	539
666567	4078	4093	22195	22210	CAGTGCTCTTTAACAA	63	540
666568	4085	4100	22202	22217	TATGACCCAGTGCTCT	60	541
666569	4093	4108	22210	22225	TTTTTCCATATGACCC	25	542
666570	4107	4122	22224	22239	GGAGACACATACATTT	78	543
666571	4117	4132	22234	22249	AATGCACCTGGGAGAC	38	544
666572	4124	4139	22241	22256	ACCAAGAAATGCACCT	43	545
666573	4134	4149	22251	22266	CAAGACATAAACCAAG	49	546
666574	4169	4184	22286	22301	CTTGAGGTTTTCTTAA	60	547
666575	4171	4186	22288	22303	TGCTTGAGGTTTTCTT	20	548
666576	4177	4192	22294	22309	AATTACTGCTTGAGGT	42	549
666577	4185	4200	22302	22317	GAGATATTAATTACTG	37	550
666578	4192	4207	22309	22324	GTTCCAGGAGATATTA	48	551
666579	4199	4214	22316	22331	CTATAGTGTTCCAGGA	34	552
666580	4206	4221	22323	22338	TGGTTCTCTATAGTGT	29	553
666581	4213	4228	22330	22345	GGTCACTTGTTCTCT	21	554
666582	4220	4235	22337	22352	ATGAGTCGGTCACTTG	22	555
666583	4221	4236	22338	22353	AATGAGTCGGTCACTT	54	556
666584	4223	4238	22340	22355	TAAATGAGTCGGTCAC	24	557
666585	4225	4240	22342	22357	TGTAAATGAGTCGGTC	31	558
666586	4227	4242	22344	22359	GTTGTAAATGAGTCGG	13	559
666587	4229	4244	22346	22361	CAGTTGTAAATGAGTC	11	560
666588	4231	4246	22348	22363	TTCAGTTGTAAATGAG	44	561
666589	4237	4252	22354	22369	CTAGGTTTCAGTTGTA	46	562
666590	4244	4259	22361	22376	GGGCTTCCTAGGTTTC	61	563
666591	4272	4287	22389	22404	AACTCTCCTGTTTTTCG	58	564
666592	4279	4294	22396	22411	GGCGACTAACTCTCCT	37	565
666593	4286	4301	22403	22418	TCTGTAGGGCGACTAA	35	566
666594	4294	4309	22411	22426	CTGGGTTTTCTGTAGG	52	567
666595	4301	4316	22418	22433	AGTCTAGCTGGGTTTT	37	568
666596	4308	4323	22425	22440	ACCCAATAGTCTAGCT	75	569
666598	4322	4337	22439	22454	TCTTTTTAGTTCATAC	74	570
666599	4330	4345	22447	22462	GCACAGTCTCTTTTAA	64	571
666600	4337	4352	22454	22469	CACCATGGCACAGTCT	21	572
666601	4344	4359	22461	22476	TTTTTCTCACCATGGC	26	573
666602	4365	4380	22482	22497	ATTTCACTGTAGGATT	62	574
666603	4372	4387	22489	22504	GCTGCTCATTTCACTG	59	575
666604	4379	4394	22496	22511	TGTAAGGGCTGCTCAT	51	576
666605	4386	4401	22503	22518	ACAATACTGTAAGGGC	25	577

666607	4407	4422	22524	22539	ACCTACCTGCCCTTGG	72	578
666608	4414	4429	22531	22546	CACTAATACCTACCTG	94	579
666609	4425	4440	22542	22557	GCTTTTTCAAACACTA	32	580

Table 10

Percent control of human IRF4 mRNA with 3-10-3 cEt gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	25	195
666610	4434	4449	22551	22566	CAAAGACCAGCTTTTT	50	581
666611	4441	4456	22558	22573	CCTCGCTCAAAGACCA	50	582
666612	4448	4463	22565	22580	TTTATGCCCTCGCTCA	76	583
666613	4455	4470	22572	22587	AGCTGTATTTATGCC	42	584
666614	4474	4489	22591	22606	TTGTTCCACCCCTGGG	53	585
666615	4483	4498	22600	22615	CTCCCAGAGTTGTTCC	66	586
666616	4491	4506	22608	22623	ACCCAAGACTCCCAGA	55	587
666617	4498	4513	22615	22630	TGCGAGTACCCAAGAC	41	588
666618	4505	4520	22622	22637	CAAGAGGTGCGAGTAC	78	589
666619	4520	4535	22637	22652	GAGCATCAACAAAGCC	42	590
666620	4527	4542	22644	22659	CCTGGCGGAGCATCAA	58	591
666621	4534	4549	22651	22666	TGGCCTTCCTGGCGGA	91	592
666622	4541	4556	22658	22673	ACACAAGTGGCCTTCC	69	593
666623	4575	4590	22692	22707	CTGAATTGTTACTAAA	79	594
666624	4582	4597	22699	22714	ACTGGATCTGAATTGT	43	595
666625	4589	4604	22706	22721	AGTTTACACTGGATCT	26	596
666626	4603	4618	22720	22735	GAGCAATGAACGGAAG	28	597
666627	4612	4627	22729	22744	GTGACTGGAGAGCAAT	26	598
666628	4641	4656	22758	22773	AACCTTTCACCTGTGGG	50	599
666629	4669	4684	22786	22801	CCTTAACCAATCCCAA	57	600
666630	4676	4691	22793	22808	ATAAAGACCTTAACCA	73	601
666631	4686	4701	22803	22818	CGTAATACAAATAAAG	97	602
666632	4719	4734	22836	22851	GATGCAGCTGGCCACA	27	603
666633	4731	4746	22848	22863	ACCATTTCAGACAGATG	70	604
666634	4738	4753	22855	22870	TTCACGCACCATTTCAG	84	605
666635	4745	4760	22862	22877	GAGAGCCTTCACGCAC	77	606
666636	4752	4767	22869	22884	AAGGTCTGAGAGCCTT	83	607
666637	4759	4774	22876	22891	GGTGTGTAAGGTCTGA	59	608
666638	4766	4781	22883	22898	ACAAAATGGTGTGTAA	93	609
666639	4780	4795	22897	22912	GTAAACATAACTTAC	92	610

666640	4807	4822	22924	22939	TCGAGATCAGTCTCAA	18	611
666641	4814	4829	22931	22946	ACCTGCATCGAGATCA	47	612
666642	4825	4840	22942	22957	CAAGGAGATCCACCTG	121	613
666643	4836	4851	22953	22968	TATCAGGATCTCAAGG	94	614
666644	4843	4858	22960	22975	AACAGGCTATCAGGAT	83	615
666645	4850	4865	22967	22982	TTCCTGTAACAGGCTA	23	616
666646	4866	4881	22983	22998	ACTGACCTTTACTTCA	57	617
666647	4898	4913	23015	23030	CCTCAAAGCTGTGAAA	80	618
666648	4905	4920	23022	23037	GCATGTTCTCTCAAAGC	24	619
666649	4912	4927	23029	23044	TTCTTATGCATGTTCC	20	620
666650	4919	4934	23036	23051	GCTACATTTCTTATGC	80	621
666651	4927	4942	23044	23059	CTACTTCAGCTACATT	53	622
666652	4934	4949	23051	23066	GTCCCTCTACTTCAG	59	623
666653	4949	4964	23066	23081	TGGCCCTTCTCTCACG	89	624
666654	4956	4971	23073	23088	GCCGGCCTGGCCCTTC	114	625
666655	4963	4978	23080	23095	TTGGCCTGCCGGCCTG	96	626
666656	4970	4985	23087	23102	AGGAGGGTTGGCCTGC	96	627
666657	4977	4992	23094	23109	CCATTGGAGGAGGGTT	68	628
666658	4982	4997	23099	23114	AATTTCCATTGGAGGA	67	629
666659	4984	4999	23101	23116	GGAATTTCCATTGGAG	56	630
666660	4986	5001	23103	23118	CGGGAATTTCCATTGG	50	631
666661	4988	5003	23105	23120	CACGGGAATTTCCATT	29	632
666662	4990	5005	23107	23122	AACACGGGAATTTCCA	27	633
666663	4992	5007	23109	23124	GCAACACGGGAATTTTC	26	634
666664	5005	5020	23122	23137	GTCTCAGTTTGAAGCA	26	635
666665	5012	5027	23129	23144	CCCATCTGTCTCAGTT	34	636
666666	5019	5034	23136	23151	GTTAAGTCCCATCTGT	60	637
666667	5026	5041	23143	23158	ATTGCTGTTAAGTCC	27	638
666668	5086	5101	23203	23218	GGCAGTTCTTTCAGCA	63	639
666669	5093	5108	23210	23225	ACCTGCTGGCAGTTCT	39	640
666670	5100	5115	23217	23232	GGGTCTACCTGCTGG	64	641
666671	5124	5139	23241	23256	CAAGCTTTCATTTGGG	26	642
666672	5131	5146	23248	23263	GGAAATTCAAGCTTTC	36	643
666673	5147	5162	23264	23279	ACGCAGAGCCAGTAGG	50	644
666674	5149	5164	23266	23281	AAACGCAGAGCCAGTA	63	645
666675	5151	5166	23268	23283	CAAAACGCAGAGCCAG	42	646
666676	5171	5186	23288	23303	TCCTTTCCTACAGATC	67	647
666677	5179	5194	23296	23311	GTGAAGCATCCTTTCC	37	648
666678	5186	5201	23303	23318	TCAGTTTGTGAAGCAT	11	649
666679	5193	5208	23310	23325	ATCTACCTCAGTTTGT	58	650
666680	5200	5215	23317	23332	TAGCATTATCTACCTC	34	651

666681	5207	5222	23324	23339	GACAGCATAGCATTAT	23	652
666682	5214	5229	23331	23346	TACCAACGACAGCATA	39	653
666683	5221	5236	23338	23353	TGATGTATACCAACGA	13	654
666684	5246	5261	23363	23378	GCAGAGCAATTTACAT	34	655
666685	5253	5268	23370	23385	TTGCTTTGCAGAGCAA	72	656

Table 11

Percent control of human IRF4 mRNA with 3-10-3 cEt gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	15	195
666688	N/A	N/A	18773	18788	CTTAAGCTAAACTCCT	73	657
666689	N/A	N/A	18780	18795	ATGACGACTTAAGCTA	38	658
666690	N/A	N/A	18803	18818	ATATTAGAGACTGTAT	75	659
666691	N/A	N/A	18817	18832	CTCCATCAATCATGAT	67	660
666692	N/A	N/A	18824	18839	GAATGCTCTCCATCAA	55	661
666693	N/A	N/A	18831	18846	GCAAGCTGAATGCTCT	47	662
666694	N/A	N/A	18838	18853	ATCTAAGGCAAGCTGA	63	663
666695	N/A	N/A	18845	18860	TTACAGCATCTAAGGC	79	664
666696	N/A	N/A	18866	18881	AATGTTTCAGCTTTTCC	37	665
666697	N/A	N/A	18873	18888	ACGCCTTAATGTTTCAG	23	666
666699	N/A	N/A	22817	22832	GACTTCGGGAGATACG	86	667
666700	N/A	N/A	22824	22839	CACAGAGGACTTCGGG	51	668
666701	N/A	N/A	3917	3932	CCCTTCCCCTCCGAA	84	669
666702	N/A	N/A	4018	4033	AGGCTCGGGCAGAGCC	99	670
666703	N/A	N/A	4254	4269	GAGCACCGCGCCGGAG	93	671
666704	N/A	N/A	4288	4303	ATGTGGAGCTCCTCCT	80	672
666705	N/A	N/A	4546	4561	GCCCCGAATAGGACCC	79	673
666706	N/A	N/A	4593	4608	CCGGGTTCTCCACCC	91	674
666707	N/A	N/A	4653	4668	CCTGGCGGCCTCCACG	131	675
666709	N/A	N/A	4856	4871	AGGCTCCTACCCGCCT	94	676
666710	N/A	N/A	4965	4980	TGCCGTGTCAGGGTCG	89	677
666711	N/A	N/A	4993	5008	GAGTCTTTGAGGCTGC	66	678
666712	N/A	N/A	5759	5774	ACAGGCGCGGACGCAC	80	679
666713	N/A	N/A	5867	5882	CGAGAAGAGAGGCTGA	93	680
666714	N/A	N/A	6304	6319	GACACATTTTCTGGGT	36	681
666715	N/A	N/A	7071	7086	GATGCTCAGAATGAAG	57	682
666716	N/A	N/A	7190	7205	CTATGCTGAACCCAC	99	683
666717	N/A	N/A	7197	7212	AATTCTCCTATGCTGA	87	684

666718	N/A	N/A	7380	7395	AGTGATGAGATATTCC	41	685
666719	N/A	N/A	7519	7534	TCCAGATGCAGATTCC	54	686
666720	N/A	N/A	7536	7551	TCACCTGAAGGATTTG	75	687
666721	N/A	N/A	7731	7746	ATGCATAACACGGTGT	55	688
666722	N/A	N/A	7963	7978	ACACAGCCTCGCCCTC	80	689
666723	N/A	N/A	8094	8109	AGCACCGTGTGGAAAG	43	690
666724	N/A	N/A	8126	8141	ACCCTCCCCAACTTAA	90	691
666725	N/A	N/A	8336	8351	CTGGCACCAAAAGTAC	82	692
666726	N/A	N/A	8539	8554	ACTGGCATTGAGACGG	21	693
			8747	8762			
			8851	8866			
			8903	8918			
			9059	9074			
666727	N/A	N/A	8540	8555	CACTGGCATTGAGACG	24	694
			8748	8763			
			8852	8867			
			8904	8919			
			9060	9075			
666728	N/A	N/A	8541	8556	GCACTGGCATTGAGAC	27	695
			8749	8764			
			8853	8868			
			8905	8920			
			9061	9076			
666729	N/A	N/A	8543	8558	AAGCACTGGCATTGAG	58	696
			8751	8766			
			8855	8870			
			8907	8922			
			9063	9078			
666730	N/A	N/A	8544	8559	GAAGCACTGGCATTGA	45	697
			8752	8767			
			8856	8871			
			8908	8923			
			9064	9079			
666731	N/A	N/A	8545	8560	AGAAGCACTGGCATTG	55	698
			9065	9080			
666732	N/A	N/A	8548	8563	ATAAGAAGCACTGGCA	49	699
			8704	8719			
			8808	8823			
			8964	8979			
			9068	9083			
666733	N/A	N/A	8549	8564	GATAAGAAGCACTGGC	37	700

			8705	8720			
			8809	8824			
			8965	8980			
			9069	9084			
666734	N/A	N/A	8551	8566	GAGATAAGAAGCACTG	56	701
			8707	8722			
			8811	8826			
			8967	8982			
			9071	9086			
666735	N/A	N/A	8553	8568	CTGAGATAAGAAGCAC	63	702
			8709	8724			
			8813	8828			
			8969	8984			
			9073	9088			
666737	N/A	N/A	8574	8589	GGTAAAGGAGTGCAGG	54	703
			8626	8641			
			8678	8693			
			8730	8745			
			8834	8849			
			8886	8901			
			8938	8953			
			8990	9005			
			9042	9057			
666738	N/A	N/A	8591	8606	ACTGGCATCGAGACGG	21	704
			8643	8658			
			8695	8710			
			8799	8814			
			8955	8970			
			9007	9022			
666739	N/A	N/A	8592	8607	CACTGGCATCGAGACG	39	705
			8644	8659			
			8696	8711			
			8800	8815			
			8956	8971			
			9008	9023			
666740	N/A	N/A	8594	8609	AGCACTGGCATCGAGA	41	706
			8646	8661			
			8698	8713			
			8802	8817			
			8958	8973			
			9010	9025			

666741	N/A	N/A	8595	8610	AAGCACTGGCATCGAG	73	707
			8647	8662			
			8699	8714			
			8803	8818			
			8959	8974			
			9011	9026			
666742	N/A	N/A	8597	8612	GGAAGCACTGGCATCG	45	708
			8649	8664			
			9013	9028			
666743	N/A	N/A	8600	8615	ATAGGAAGCACTGGCA	58	709
			8652	8667			
			8756	8771			
			8860	8875			
			8912	8927			
			9016	9031			
666744	N/A	N/A	8601	8616	GATAGGAAGCACTGGC	38	710
			8653	8668			
			8757	8772			
			8861	8876			
			8913	8928			
			9017	9032			
666745	N/A	N/A	8602	8617	AGATAGGAAGCACTGG	54	711
			8654	8669			
			8758	8773			
			8862	8877			
			8914	8929			
			9018	9033			
666746	N/A	N/A	8603	8618	GAGATAGGAAGCACTG	52	712
			8655	8670			
			8759	8774			
			8863	8878			
			8915	8930			
			9019	9034			
666747	N/A	N/A	8604	8619	TGAGATAGGAAGCACT	62	713
			8656	8671			
			8760	8775			
			8864	8879			
			8916	8931			
			9020	9035			
666748	N/A	N/A	8605	8620	CTGAGATAGGAAGCAC	74	714
			8657	8672			

			8761	8776			
			8865	8880			
			8917	8932			
			9021	9036			
666749	N/A	N/A	9410	9425	GGATGCCACCATCCCA	105	715
666750	N/A	N/A	9490	9505	GGAGTGATCTCTGTGG	32	716
666751	N/A	N/A	9708	9723	GTAGGTAGGCACCTGT	25	717
666752	N/A	N/A	9796	9811	GAGGGAGCTCATTTTG	76	718
666753	N/A	N/A	9960	9975	AAAGGCCAAATTGCAA	48	719
666754	N/A	N/A	9997	10012	CTGCAGCCAAGGATAA	52	720
666818	N/A	N/A	3925	3940	GGCGCGCTCCCTTCCC	90	721
666819	N/A	N/A	4685	4700	CCCTTCCCCGCGACTC	81	722
666820	N/A	N/A	4717	4732	TTGCCTTCGCTCACTC	78	723
666821	N/A	N/A	5757	5772	AGGCGCGGACGCACGG	69	724
666822	N/A	N/A	6997	7012	CTACCTTTTTTGGCTC	83	725
666823	N/A	N/A	7585	7600	TGCCTTGTGACATAAA	55	726
666824	N/A	N/A	8151	8166	ATATTCCAACAGGCGG	47	727
666825	N/A	N/A	8437	8452	TGAACCCCTTCATCAGA	52	728
666826	N/A	N/A	9313	9328	AGACCAGGATTCGCCA	67	729

Table 12

Percent control of human IRF4 mRNA with 3-10-3 cEt gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	23	195
666755	N/A	N/A	10003	10018	CACTACCTGCAGCCAA	69	730
666756	N/A	N/A	10020	10035	AGAGTGGTACACCTCT	78	731
666757	N/A	N/A	10256	10271	GTCTCTACCTACTCCA	59	732
666758	N/A	N/A	10308	10323	AACACCTGATCTTGCT	110	733
666759	N/A	N/A	10366	10381	ACCATGTTCTGAAGA	56	734
666760	N/A	N/A	10660	10675	CTCTTGTGAGGCAAAG	52	735
666761	N/A	N/A	10712	10727	GCGCCCAATCACCTTC	97	736
666762	N/A	N/A	11002	11017	ATCGAATCTGCCCAA	74	737
666763	N/A	N/A	11010	11025	AAAGTCCCATCGAATC	87	738
666764	N/A	N/A	11024	11039	CAAAGCAAGTGTCTAA	77	739
666765	N/A	N/A	11070	11085	CTCACACACAGGATGT	82	740
666767	N/A	N/A	11344	11359	GAGGAGGAGGACTTAT	49	741
666768	N/A	N/A	11408	11423	TATTACTCTTAGGCAC	56	742
666769	N/A	N/A	11545	11560	GTGCCTTCTTTATAGT	51	743

666770	N/A	N/A	11551	11566	CTAGAGGTGCCTTCTT	74	744
666771	N/A	N/A	11682	11697	TGCCAGAGGGCAAGAT	98	745
666772	N/A	N/A	11975	11990	GCTGTTTATTTCTAC	34	746
666773	N/A	N/A	11988	12003	CGAGATATAAATAGCT	42	747
666774	N/A	N/A	11990	12005	GCCGAGATATAAATAG	60	748
666775	N/A	N/A	12032	12047	GCAGGTTTCATTTTCAT	56	749
666776	N/A	N/A	12034	12049	GGGCAGGTTTCATTTTC	68	750
666777	N/A	N/A	12067	12082	AGAGTGGGTGTTGGCC	75	751
666779	N/A	N/A	12274	12289	ATGGAACCCCAAATC	76	752
666780	N/A	N/A	12292	12307	GCTGCCACTGGTAACT	74	753
666781	N/A	N/A	12374	12389	TCGCCCATGAGTTGAA	61	754
666782	N/A	N/A	12516	12531	AGTTCATGTAAAGTCT	39	755
666783	N/A	N/A	12865	12880	TCGGTCCACATACCTG	61	756
666784	N/A	N/A	13199	13214	CTTGGAGAAGTCCCGT	61	757
666785	N/A	N/A	13330	13345	CCTGTGGTGGAACTCT	73	758
666786	N/A	N/A	14020	14035	AAGAGGCGACTGCTGA	65	759
666787	N/A	N/A	14028	14043	ACTGTTTTAAGAGGCG	30	760
666788	N/A	N/A	14046	14061	ATAGTGCAATGAAATG	64	761
666789	N/A	N/A	14094	14109	GGGAACCTGAAAAGAG	79	762
666790	N/A	N/A	14338	14353	GAGGTTCGCTGAATTG	70	763
666791	N/A	N/A	14687	14702	ATCTGGATGAGCTTAC	62	764
666792	N/A	N/A	14732	14747	AGCTTAGTTATCTGGG	41	765
666793	N/A	N/A	15213	15228	GAACACCATGCCCAAC	93	766
666794	N/A	N/A	15304	15319	GAGCTCTTCCAGATCC	95	767
666795	N/A	N/A	15596	15611	TAGTCGCGCAAGTCTA	108	768
666796	N/A	N/A	15777	15792	ATCCTTAATTATGCAG	61	769
666797	N/A	N/A	15790	15805	GTGTTTGGTGGGAATC	54	770
666798	N/A	N/A	15985	16000	CTAACTTACAGGACTA	69	771
666799	N/A	N/A	16059	16074	TAGTGCTGTGCAGACC	68	772
666800	N/A	N/A	16069	16084	GGGCTGTCCCTAGTGC	109	773
666801	N/A	N/A	16171	16186	AATGTACGCCCCGCAA	81	774
666802	N/A	N/A	16340	16355	GGCCTCCCGCTTGTGG	118	775
666803	N/A	N/A	16383	16398	GAACAGTAACTTGACT	96	776
666804	N/A	N/A	16419	16434	AACTCTGAGTAGACTT	72	777
666805	N/A	N/A	16471	16486	GAGCACCAGCCATCGG	77	778
666806	N/A	N/A	16649	16664	GACCAATTTATGCCAT	62	779
666807	N/A	N/A	16664	16679	CACGCAATGGCAAAG	81	780
666808	N/A	N/A	16824	16839	TCCTTTGGGTGCTTTC	68	781
666809	N/A	N/A	16888	16903	CTCTTACTCCGCTGAG	105	782
666810	N/A	N/A	16953	16968	ACACACCAGGTAAAC	88	783
666811	N/A	N/A	17135	17150	AGTGTAAGTGGAGT	107	784

666812	N/A	N/A	17740	17755	TGTTACTTGCCACAGT	61	785
666813	N/A	N/A	17916	17931	ATGCAAGCCCGTTAAT	96	786
666814	N/A	N/A	17966	17981	ATGAGAACTTTGATGT	85	787
666815	N/A	N/A	18136	18151	AAGTCAATCACTGGAG	39	788
666816	N/A	N/A	18196	18211	TTAGCAATTCCTGTTG	80	789
666817	N/A	N/A	18938	18953	GCTAACTGGCCTCAAA	91	790
666827	N/A	N/A	10288	10303	CTTCATTTACTGTTAC	69	791
666828	N/A	N/A	10484	10499	CAACAGAGCTGAGAGT	80	792
666829	N/A	N/A	11844	11859	CTCACGAGCACCTCAG	58	793
666830	N/A	N/A	13244	13259	CTTGTCTCCCCCAGAG	97	794
666831	N/A	N/A	13798	13813	CCACCTCCATTCTAAC	115	795
666832	N/A	N/A	14081	14096	GAGCCGCCACATCAGC	77	796
666833	N/A	N/A	14193	14208	CCACCCTCCGTCTCAC	67	797
666834	N/A	N/A	14242	14257	TATAGCACTCTCCTAT	98	798
666836	N/A	N/A	16203	16218	CAAGACAAATCTTCTG	87	799
666837	N/A	N/A	16641	16656	TATGCCATGGACAAGT	81	800
666838	N/A	N/A	16948	16963	CCAGGTTAAACAGGAA	94	801
666839	N/A	N/A	19232	19247	GACTTAATTCTGGGTT	65	802
666840	N/A	N/A	19412	19427	ACTGAGATATCCTGCA	81	803

Example 5: Effect of 3-10-3 cEt gapmers with phosphorothioate internucleoside linkages on human IRF4 *in vitro*, single dose

Modified oligonucleotides complementary to a human IRF4 nucleic acid were designed and tested for their effect on IRF4 mRNA *in vitro*.

Cultured SK-MEL-28 cells at a density of 20,000 cells per well were transfected using electroporation with 4,000 nM concentration of modified oligonucleotide or no modified oligonucleotide for untreated controls. After approximately 24 hours, RNA was isolated from the cells and IRF4 mRNA levels were measured by quantitative real-time PCR. Human primer probe set RTS3114 (described hereinabove in Example 1) was used to measure mRNA levels. IRF4 mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented in the table below as percent control of the amount of IRF4 mRNA, relative to untreated control (UTC) cells.

The modified oligonucleotides in Tables 13 through 24 are 3-10-3 cEt gapmers. The gapmers are 16 nucleobases in length, wherein the central gap segment comprises ten 2'-deoxynucleosides and is flanked by wing segments on both the 5' end and on the 3' end comprising three cEt nucleosides. The sugar motif for the gapmers is (from 5' to 3'): kkkddddd kkk; wherein 'd' represents a 2'-deoxyribose sugar and 'k' represents a cEt modified sugar. Each internucleoside linkage is a phosphorothioate internucleoside linkage and each cytosine residue is a 5-methylcytosine. "Start Site" indicates the 5'-most nucleoside to which the gapmer is complementary in the human nucleic acid sequence. "Stop Site" indicates the 3'-most nucleoside to which the gapmer is complementary in the human nucleic acid sequence.

Each modified oligonucleotide listed in Tables 13 through 24 below is complementary to human IRF4 nucleic acid sequences SEQ ID NO: 1 or SEQ ID NO: 2, as indicated. 'N/A' indicates that the modified oligonucleotide is not complementary to that particular nucleic acid sequence with 100% complementarity.

As shown below, modified oligonucleotides complementary to human IRF4 reduced the amount of human IRF4 mRNA.

5

Table 13
Percent control of human IRF4 mRNA with 3-10-3 cEt gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	24	195
881075	2	17	3741	3756	AACTGAGAGTGCGAGG	99	804
881099	342	357	6821	6836	AAACAGTGCCCAAGCC	75	805
881122	624	639	9114	9129	CATCATGTAGTTGTGA	59	806
881169	1192	1207	13745	13760	TGTCAAAGAGCTTGCA	89	807
881193	1416	1431	19533	19548	GCTGATGTGTTCTGGT	21	808
881217	1740	1755	19857	19872	CAGTAAGAGGGCAGTC	50	809
881241	1927	1942	20044	20059	CATCACTTGGTCAATT	71	810
881265	2042	2057	20159	20174	CCTACAAGCAGTCATC	46	811
881289	2194	2209	20311	20326	CTACAGGCACGGCTTC	48	812
881313	2385	2400	20502	20517	TACTAGATTGTAGGAC	73	813
881337	2512	2527	20629	20644	CAACAGTTCAAGTATT	65	814
881361	2665	2680	20782	20797	TTCCAGTGGTGGGTCC	71	815
881385	2826	2841	20943	20958	CAAGTGGAGGTCTTTG	33	816
881409	2911	2926	21028	21043	ATGAGAAACGGCCTGG	36	817
881433	3047	3062	21164	21179	AATGTAGGGATACAGC	38	818
881457	3273	3288	21390	21405	AATAAACACCCCTTCT	79	819
881481	3419	3434	21536	21551	CTCCACAGCAAGGCCT	49	820
881505	3507	3522	21624	21639	GTTCACGAAACACAGT	37	821
881528	3625	3640	21742	21757	CAAAGAGGGTCACAGG	37	822
881552	3903	3918	22020	22035	CCCTAGGTCATACCCT	43	823
881576	4052	4067	22169	22184	CTTCAACAGCACTGTC	44	824
881595	4285	4300	22402	22417	CTGTAGGGCGACTAAC	51	825
881619	4412	4427	22529	22544	CTAATACCTACCTGCC	53	826
881643	4545	4560	22662	22677	GCACACACAAGTGCC	36	827
881667	4602	4617	22719	22734	AGCAATGAACGGAAGT	20	828
881691	4839	4854	22956	22971	GGCTATCAGGATCTCA	55	829
881715	5030	5045	23147	23162	CCCCATTGCCTGTAA	80	830

881739	5206	5221	23323	23338	ACAGCATAGCATTATC	36	831
881763	N/A	N/A	18778	18793	GACGACTTAAGCTAAA	38	832
881787	N/A	N/A	18847	18862	ATTTACAGCATCTAAG	53	833
881809	N/A	N/A	4075	4090	GCTCATCCCGTCCAGC	85	834
881832	N/A	N/A	4402	4417	GGAGAGCGGAGGCGGG	79	835
881855	N/A	N/A	4644	4659	CTCCACGCGCGGAGGA	101	836
881879	N/A	N/A	5038	5053	GGGCACCCCGCCCCGA	99	837
881903	N/A	N/A	5660	5675	GCACGGACGAACGCGC	77	838
881925	N/A	N/A	5777	5792	ACGAAAACAGCCGCCG	86	839
881947	N/A	N/A	6136	6151	GAGCAAATTGAGACCA	45	840
881971	N/A	N/A	6415	6430	GCGCATAGGTCCTTCA	37	841
881993	N/A	N/A	7155	7170	CCACATAACTCAGGCA	30	842
882017	N/A	N/A	7376	7391	ATGAGATATTCCTCTC	68	843
882041	N/A	N/A	7696	7711	CAGCAACTCCCTTGGG	77	844
882065	N/A	N/A	8145	8160	CAACAGGCGGACACGC	58	845
882088	N/A	N/A	8385	8400	ATGGAGATACTTGATC	38	846
882112	N/A	N/A	8554	8569	GCTGAGATAAGAAGCA	68	847
			8710	8725			
			8814	8829			
			8970	8985			
			9074	9089			
882135	N/A	N/A	9362	9377	GCACACGCAGCCTCTA	95	848
882158	N/A	N/A	9606	9621	CCACTATTCGAGAGAA	43	849
882182	N/A	N/A	9981	9996	CCTGAACATGACTGGG	62	850
882205	N/A	N/A	10162	10177	GAATTTTCAGGAGCTAG	39	851
882229	N/A	N/A	10314	10329	GCACAGAACACCTGAT	44	852
882253	N/A	N/A	10616	10631	AGCTGATGGAGAAACG	90	853
882277	N/A	N/A	11088	11103	CTAAATCACCCCTGGTC	53	854
882301	N/A	N/A	11366	11381	GAACATAATGTCCCCAG	39	855
882325	N/A	N/A	11666	11681	GAGAATTCCAAACCTT	24	856
882349	N/A	N/A	11940	11955	GTCTTAGGTGTTCAAG	44	857
882373	N/A	N/A	12157	12172	CAGCAGGTTTTGAGAC	80	858
882397	N/A	N/A	12512	12527	CATGTAAAGTCTGCTG	42	859
882420	N/A	N/A	12893	12908	ATATAACGGTGTTTCA	42	860
882443	N/A	N/A	13175	13190	ACCCATTTAATCTGTC	43	861
882465	N/A	N/A	13791	13806	CATTCTAACAGATAAC	102	862
882487	N/A	N/A	14150	14165	ACACACCTGACAACCA	64	863
882510	N/A	N/A	14374	14389	GCATGACAGGGCGAGG	57	864
882533	N/A	N/A	14708	14723	TGCTTTGGGCACCAAA	48	865
882557	N/A	N/A	15460	15475	GCCCAGCAAGAGGCAC	93	866
882580	N/A	N/A	15804	15819	TAGATAACATGAGAGT	50	867

882603	N/A	N/A	15925	15940	CAAATGACTTAGTCAG	45	868
882627	N/A	N/A	16168	16183	GTCACGCCCGCAAAAG	61	869
882650	N/A	N/A	16388	16403	GGATGGAACAGTAACT	48	870
882674	N/A	N/A	16667	16682	AGTCACGCAATGGCAA	50	871
882698	N/A	N/A	16900	16915	GAGGAATGAGCACTCT	74	872
882722	N/A	N/A	17238	17253	GGTTACGCTTATTTTT	36	873
882746	N/A	N/A	17493	17508	GCTAGATAGCATTCTT	44	874
882770	N/A	N/A	17733	17748	TGCCACAGTTGAACCC	50	875
882794	N/A	N/A	17987	18002	TAGCATCAGAGCTAGA	51	876
882817	N/A	N/A	18582	18597	CTGGATTGATGTGATA	57	877
882841	N/A	N/A	18961	18976	ACTACTATTGTGGAAA	82	878
882864	N/A	N/A	19234	19249	GTGACTTAATTCTGGG	49	879

Table 14

Percent control of human IRF4 mRNA with 3-10-3 cEt gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	14	195
881076	6	21	3745	3760	GTGAAACTGAGAGTGC	120	880
881100	343	358	6822	6837	TAAACAGTGCCCAAGC	59	881
881123	682	697	9172	9187	GGATTTCCGGGTGTGG	39	882
881170	1206	1221	13759	13774	CAAGAACTGCTGTGTG	105	883
881194	1432	1447	19549	19564	GGTAATCTTCTGGATT	70	884
881218	1741	1756	19858	19873	ACAGTAAGAGGGCAGT	16	885
881242	1930	1945	20047	20062	ACACATCACTTGGTCA	22	886
881266	2043	2058	20160	20175	ACCTACAAGCAGTCAT	54	887
881290	2195	2210	20312	20327	GCTACAGGCACGGCTT	16	888
881314	2387	2402	20504	20519	ATTACTAGATTGTAGG	50	889
881338	2515	2530	20632	20647	GGGCAACAGTTCAAGT	64	890
881362	2686	2701	20803	20818	CCGTAGTCAGCTCCAT	27	891
881386	2828	2843	20945	20960	AGCAAGTGGAGGTCTT	37	892
881410	2912	2927	21029	21044	TATGAGAAACGGCCTG	55	893
881434	3048	3063	21165	21180	TAATGTAGGGATACAG	22	894
881458	3275	3290	21392	21407	AGAATAAACACCCCTT	26	895
881482	3429	3444	21546	21561	GGCAGTGGAGCTCCAC	27	896
881506	3510	3525	21627	21642	GCAGTTCACGAAACAC	20	897
881529	3628	3643	21745	21760	CAGCAAAGAGGGTCAC	39	898
881553	3904	3919	22021	22036	TCCCTAGGTCATACCC	42	899
881577	4058	4073	22175	22190	TCAAATCTTCAACAGC	24	900

881596	4300	4315	22417	22432	GTCTAGCTGGGTTTTTC	37	901
881620	4413	4428	22530	22545	ACTAATACCTACCTGC	52	902
881644	4547	4562	22664	22679	ACGCACACACAAGTGG	41	903
881668	4608	4623	22725	22740	CTGGAGAGCAATGAAC	33	904
881692	4844	4859	22961	22976	TAACAGGCTATCAGGA	74	905
881716	5040	5055	23157	23172	GGGAAGTGGACCCCAT	91	906
881740	5208	5223	23325	23340	CGACAGCATAGCATT	25	907
881764	N/A	N/A	18782	18797	ATATGACGACTTAAGC	62	908
881788	N/A	N/A	18849	18864	GAATTTACAGCATCTA	24	909
881810	N/A	N/A	4084	4099	GTCCGGTTAGCTCATC	55	910
881833	N/A	N/A	4403	4418	GGGAGAGCGGAGGCGG	78	911
881856	N/A	N/A	4703	4718	TCCCAACCCGCTTCTC	86	912
881880	N/A	N/A	5056	5071	CACGAGGCACCGCACT	113	913
881904	N/A	N/A	5664	5679	GAACGCACGGACGAAC	82	914
881926	N/A	N/A	5778	5793	GACGAAAACAGCCGCC	38	915
881948	N/A	N/A	6141	6156	TCTGAGAGCAAATTGA	71	916
881994	N/A	N/A	7157	7172	ACCCACATAACTCAGG	69	917
882018	N/A	N/A	7384	7399	GCATAGTGATGAGATA	41	918
882042	N/A	N/A	7717	7732	GTTGACAAATAAGGTA	40	919
882066	N/A	N/A	8146	8161	CCAACAGGCGGACACG	17	920
882089	N/A	N/A	8391	8406	AGGACAATGGAGATAC	28	921
882113	N/A	N/A	8566	8581	AGTGCAGGAGAGGCTG	64	922
			8618	8633			
			8670	8685			
			8722	8737			
			8774	8789			
			8826	8841			
			8878	8893			
			8930	8945			
			8982	8997			
			9034	9049			
			9086	9101			
882136	N/A	N/A	9386	9401	AGAAAACCCCCCTCTC	77	923
882159	N/A	N/A	9608	9623	CACCACTATTCGAGAG	52	924
882183	N/A	N/A	9986	10001	GATAACCTGAACATGA	83	925
882206	N/A	N/A	10172	10187	ACGCAAGTCTGAATTT	35	926
882230	N/A	N/A	10352	10367	GACAATGTTGTATGAA	28	927
882254	N/A	N/A	10634	10649	GACCAACTGGAAAACC	44	928
882278	N/A	N/A	11089	11104	CCTAAATCACCCCTGGT	73	929
882302	N/A	N/A	11368	11383	CAGAACTAATGTCCCC	31	930
882326	N/A	N/A	11669	11684	GATGAGAATTCCAAAC	16	931

882350	N/A	N/A	11950	11965	ACCCACACAAGTCTTA	104	932
882374	N/A	N/A	12161	12176	TCAACAGCAGGTTTTG	59	933
882398	N/A	N/A	12515	12530	GTTCATGTAAAGTCTG	14	934
882421	N/A	N/A	12896	12911	AAAATATAACGGTGTT	69	935
882444	N/A	N/A	13196	13211	GGAGAAGTCCCGTGGGA	41	936
882466	N/A	N/A	13881	13896	CGCCGAAGTCAACAGG	56	937
882488	N/A	N/A	14160	14175	CATGAGGGTGACACAC	53	938
882511	N/A	N/A	14376	14391	CAGCATGACAGGGCGA	44	939
882534	N/A	N/A	14716	14731	GACATATTTGCTTTGG	42	940
882558	N/A	N/A	15497	15512	AGCTTAGTCACCACGG	33	941
882581	N/A	N/A	15805	15820	CTAGATAACATGAGAG	47	942
882604	N/A	N/A	15926	15941	CCAAATGACTTAGTCA	49	943
882628	N/A	N/A	16177	16192	CAATAAAATGTCACGC	53	944
882651	N/A	N/A	16390	16405	AGGGATGGAACAGTAA	53	945
882675	N/A	N/A	16691	16706	CGGGAGATAAAGAACA	69	946
882699	N/A	N/A	16905	16920	TGCAAGAGGAATGAGC	16	947
882723	N/A	N/A	17239	17254	GGGTTACGCTTATTTT	35	948
882747	N/A	N/A	17508	17523	AATGAAGATCCACTAG	39	949
882771	N/A	N/A	17746	17761	TTTTAGTGTTACTTGC	68	950
882795	N/A	N/A	17990	18005	AAATAGCATCAGAGCT	87	951
882818	N/A	N/A	18584	18599	AACTGGATTGATGTGA	23	952
882842	N/A	N/A	18964	18979	AAAATACTATTGTGG	86	953
882865	N/A	N/A	19240	19255	GCCAAAGTGACTTAAT	30	954
882898	N/A	N/A	6422	6437	AAGAATGGCGCATAGG	19	955

Table 15

Percent control of human IRF4 mRNA with 3-10-3 cEt gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	45	195
881077	7	22	3746	3761	GGTGAAACTGAGAGTG	92	956
881101	344	359	6823	6838	TTAAACAGTGCCCAAG	79	957
881124	689	704	9179	9194	TGGTACGGGATTTC CG	63	958
881171	1207	1222	13760	13775	ACAAGAACTGCTGTGT	93	959
881195	1433	1448	19550	19565	TGGTAATCTTCTGGAT	76	960
881219	1744	1759	19861	19876	AAAACAGTAAGAGGGC	61	961
881243	1934	1949	20051	20066	GTAAACACATCACTTG	49	962
881267	2044	2059	20161	20176	TACCTACAAGCAGTCA	44	963
881291	2196	2211	20313	20328	GGCTACAGGCACGGCT	58	964

881315	2388	2403	20505	20520	CATTACTAGATTGTAG	91	965
881339	2520	2535	20637	20652	CAGAAGGGCAACAGTT	62	966
881363	2701	2716	20818	20833	ACTGAGTGTGCAGTTC	64	967
881387	2829	2844	20946	20961	AAGCAAGTGGAGGTCT	49	968
881411	2913	2928	21030	21045	GTATGAGAAACGGCCT	41	969
881435	3049	3064	21166	21181	GTAATGTAGGGATACA	52	970
881459	3277	3292	21394	21409	GAAGAATAAACACCCC	48	971
881483	3430	3445	21547	21562	TGGCAGTGGAGCTCCA	54	972
881507	3517	3532	21634	21649	CATCACTGCAGTTCAC	53	973
881530	3631	3646	21748	21763	CTTCAGCAAAGAGGGT	41	974
881554	3918	3933	22035	22050	CATAGCTAGTTCATTC	65	975
881578	4089	4104	22206	22221	TCCATATGACCCAGTG	34	976
881597	4305	4320	22422	22437	CAATAGTCTAGCTGGG	37	977
881621	4418	4433	22535	22550	CAAACACTAATACCTA	69	978
881645	4556	4571	22673	22688	GTAAGTACACGCACA	49	979
881669	4618	4633	22735	22750	GGGCATGTGACTGGAG	50	980
881693	4845	4860	22962	22977	GTAACAGGCTATCAGG	55	981
881717	5152	5167	23269	23284	GCAAAACGCAGAGCCA	43	982
881741	5209	5224	23326	23341	ACGACAGCATAGCATT	33	983
881765	N/A	N/A	18783	18798	TATATGACGACTTAAG	70	984
881789	N/A	N/A	18853	18868	TCCTGAATTTACAGCA	52	985
881834	N/A	N/A	4404	4419	CGGGAGAGCGGAGGCG	100	986
881857	N/A	N/A	4740	4755	CCGCACTCACTCGCAG	92	987
881881	N/A	N/A	5057	5072	CCACGAGGCACCGCAC	119	988
881905	N/A	N/A	5668	5683	ACGAGAACGCACGGAC	60	989
881927	N/A	N/A	5779	5794	AGACGAAAACAGCCGC	75	990
881949	N/A	N/A	6209	6224	ACTAAGGACAGCTGTG	85	991
881972	N/A	N/A	6424	6439	GAAAGAATGGCGCATA	51	992
881995	N/A	N/A	7168	7183	TTCAACTTGTGACCCA	51	993
882019	N/A	N/A	7385	7400	TGCATAGTGATGAGAT	63	994
882043	N/A	N/A	7726	7741	TAACACGGTGTGACA	65	995
882067	N/A	N/A	8147	8162	TCCAACAGGCGGACAC	71	996
882090	N/A	N/A	8399	8414	GATCATAAAGGACAAT	70	997
882114	N/A	N/A	8570	8585	AAGGAGTGCAGGAGAG	87	998
			8622	8637			
			8674	8689			
			8726	8741			
			8778	8793			
			8830	8845			
			8882	8897			
			8934	8949			

			8986	9001			
			9038	9053			
			9090	9105			
882137	N/A	N/A	9387	9402	GAGAAAACCCCCCTCT	83	999
882160	N/A	N/A	9611	9626	ACACACCACTATTCGA	65	1000
882184	N/A	N/A	9990	10005	CAAGGATAACCTGAAC	74	1001
882207	N/A	N/A	10179	10194	GCAGTAAACGCAAGTC	46	1002
882231	N/A	N/A	10357	10372	CTGAAGACAATGTTGT	45	1003
882255	N/A	N/A	10672	10687	TAGCAGGGCACGCTCT	69	1004
882279	N/A	N/A	11090	11105	TCCTAAATCACCCCTGG	79	1005
882303	N/A	N/A	11370	11385	ACCAGAACTAATGTCC	68	1006
882327	N/A	N/A	11674	11689	GGCAAGATGAGAATTC	75	1007
882351	N/A	N/A	11987	12002	GAGATATAAATAGCTG	49	1008
882375	N/A	N/A	12175	12190	AACTATCTTATTCCTC	70	1009
882422	N/A	N/A	12897	12912	AAAAATATAACGGTGT	76	1010
882445	N/A	N/A	13203	13218	AACACTTGGAGAAGTC	57	1011
882467	N/A	N/A	13904	13919	AGTCAAGCCCCAAGCC	87	1012
882489	N/A	N/A	14161	14176	GCATGAGGGTGACACA	58	1013
882512	N/A	N/A	14432	14447	TCCCACGCGGGAGGCT	99	1014
882535	N/A	N/A	14717	14732	GGACATATTTGCTTTG	68	1015
882559	N/A	N/A	15501	15516	TTCCAGCTTAGTCACC	63	1016
882582	N/A	N/A	15806	15821	CCTAGATAACATGAGA	74	1017
882605	N/A	N/A	15927	15942	CCCAAATGACTTAGTC	68	1018
882629	N/A	N/A	16178	16193	ACAATAAAATGTCACG	71	1019
882652	N/A	N/A	16394	16409	CTCCAGGGATGGAACA	81	1020
882676	N/A	N/A	16705	16720	GACCACAGTGAAGTCG	86	1021
882700	N/A	N/A	16926	16941	GCTTACTGTGATTCTG	66	1022
882724	N/A	N/A	17241	17256	AAGGGTTACGCTTATT	48	1023
882748	N/A	N/A	17545	17560	ATGGATAGTTTCTCAT	75	1024
882772	N/A	N/A	17760	17775	TCCTAACCCTACCCTT	70	1025
882796	N/A	N/A	17991	18006	GAAATAGCATCAGAGC	55	1026
882819	N/A	N/A	18601	18616	ATCCATGTCAACTTTA	41	1027
882843	N/A	N/A	18965	18980	CAAACTACTATTGTG	77	1028
882866	N/A	N/A	19241	19256	AGCCAAAGTGACTTAA	42	1029
882892	N/A	N/A	4089	4104	CGACAGTCCGGTTAGC	89	1030
882904	N/A	N/A	12597	12612	TTCCACACTGGATATG	59	1031

Table 16
Percent control of human IRF4 mRNA with 3-10-3 cEt gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	39	195
881078	14	29	3753	3768	ATCGAGCGGTGAACT	71	1032
881102	357	372	6836	6851	TCGGAACTTTCCTTTA	67	1033
881125	692	707	9182	9197	CATTGGTACGGGATTT	84	1034
881172	1208	1223	13761	13776	GACAAGAAGTGTCTGTG	85	1035
881196	1444	1459	19561	19576	GGATAGATCTGTGGTA	51	1036
881220	1745	1760	19862	19877	CAAAACAGTAAGAGGG	69	1037
881244	1950	1965	20067	20082	GCGCATTTTCAGTAAAT	67	1038
881268	2046	2061	20163	20178	CATACCTACAAGCAGT	57	1039
881292	2199	2214	20316	20331	CAAGGCTACAGGCACG	49	1040
881316	2389	2404	20506	20521	ACATTACTAGATTGTA	59	1041
881340	2525	2540	20642	20657	TTGGACAGAAGGGCAA	71	1042
881364	2710	2725	20827	20842	AAACAGCCCACTGAGT	89	1043
881388	2830	2845	20947	20962	TAAGCAAGTGGAGGTC	53	1044
881412	2914	2929	21031	21046	AGTATGAGAAACGGCC	38	1045
881436	3050	3065	21167	21182	TGTAATGTAGGGATAC	47	1046
881460	3343	3358	21460	21475	GCAAGATGACTCCATG	37	1047
881484	3431	3446	21548	21563	ATGGCAGTGGAGCTCC	44	1048
881508	3520	3535	21637	21652	ATACATCACTGCAGTT	64	1049
881531	3643	3658	21760	21775	GGGTAAATATTCTTC	48	1050
881555	3919	3934	22036	22051	TCATAGCTAGTTCATT	48	1051
881579	4125	4140	22242	22257	AACCAAGAAATGCACC	67	1052
881598	4306	4321	22423	22438	CCAATAGTCTAGCTGG	81	1053
881622	4419	4434	22536	22551	TCAAACACTAATACCT	75	1054
881646	4557	4572	22674	22689	AGTAACTGACACGCAC	49	1055
881670	4667	4682	22784	22799	TTAACCAATCCCAACA	70	1056
881694	4846	4861	22963	22978	TGTAACAGGCTATCAG	69	1057
881718	5153	5168	23270	23285	AGCAAAACGCAGAGCC	39	1058
881742	5210	5225	23327	23342	AACGACAGCATAGCAT	26	1059
881766	N/A	N/A	18784	18799	ATATATGACGACTTAA	94	1060
881790	N/A	N/A	18871	18886	GCCTTAATGTTCAGCT	51	1061
881811	N/A	N/A	4126	4141	GCCTTGGACGGCCCCG	77	1062
881835	N/A	N/A	4416	4431	CCGGAGCAGGCCCGGG	113	1063
881858	N/A	N/A	4806	4821	CCGACACGCGCCGCTC	70	1064
881882	N/A	N/A	5059	5074	AGCCACGAGGCACCGC	88	1065

881906	N/A	N/A	5672	5687	GGAAACGAGAACGCAC	70	1066
881928	N/A	N/A	5783	5798	TGAGAGACGAAAACAG	109	1067
881950	N/A	N/A	6216	6231	GCCTAGGACTAAGGAC	67	1068
881973	N/A	N/A	6426	6441	AAGAAAGAATGGCGCA	37	1069
881996	N/A	N/A	7187	7202	TGCTGAACCCACAGG	67	1070
882020	N/A	N/A	7386	7401	ATGCATAGTGATGAGA	55	1071
882044	N/A	N/A	7728	7743	CATAACACGGTGTTGA	64	1072
882068	N/A	N/A	8148	8163	TTCCAACAGGCGGACA	57	1073
882091	N/A	N/A	8406	8421	CATGGAGGATCATAAA	78	1074
882115	N/A	N/A	8598	8613	AGGAAGCACTGGCATC	43	1075
			8650	8665			
			9014	9029			
882138	N/A	N/A	9424	9439	TAAACTTGGCTGTGGG	73	1076
882161	N/A	N/A	9632	9647	TTCCAACAATAGCAAC	54	1077
882208	N/A	N/A	10181	10196	GAGCAGTAAACGCAAG	46	1078
882232	N/A	N/A	10367	10382	AACCATGTTCTGAAG	59	1079
882256	N/A	N/A	10674	10689	ACTAGCAGGGCACGCT	62	1080
882280	N/A	N/A	11101	11116	TCTAATGGTGCTCCTA	49	1081
882304	N/A	N/A	11378	11393	GATGAGGGACCAGAAC	80	1082
882328	N/A	N/A	11675	11690	GGGCAAGATGAGAATT	100	1083
882352	N/A	N/A	11989	12004	CCGAGATATAAATAGC	39	1084
882376	N/A	N/A	12206	12221	TATCATGCATACCAAA	42	1085
882399	N/A	N/A	12654	12669	TGGTAGAATGTGATAT	57	1086
882423	N/A	N/A	12900	12915	GCAAAAAATATAACGG	53	1087
882446	N/A	N/A	13275	13290	CGTCAAGGAGGCCTGG	57	1088
882468	N/A	N/A	13913	13928	CTCTACTGGAGTCAAG	75	1089
882490	N/A	N/A	14162	14177	TGCATGAGGGTGACAC	55	1090
882513	N/A	N/A	14458	14473	GGCGAGTGGCGGGTAG	92	1091
882536	N/A	N/A	14736	14751	CTGAAGCTTAGTTATC	62	1092
882560	N/A	N/A	15515	15530	ACTCAATGTGCACCTT	71	1093
882583	N/A	N/A	15807	15822	CCCTAGATAACATGAG	83	1094
882606	N/A	N/A	15982	15997	ACTTACAGGACTATTT	84	1095
882630	N/A	N/A	16200	16215	GACAAATCTTCTGCCT	74	1096
882653	N/A	N/A	16422	16437	TGTAACCTCTGAGTAGA	57	1097
882677	N/A	N/A	16708	16723	GTAGACCACAGTGAAG	71	1098
882701	N/A	N/A	16934	16949	AAGCAAGAGCTTACTG	86	1099
882725	N/A	N/A	17246	17261	AGTTTAAGGGTTACGC	37	1100
882749	N/A	N/A	17546	17561	AATGGATAGTTTCTCA	37	1101
882773	N/A	N/A	17771	17786	TCTAACCTAATCCTA	95	1102
882797	N/A	N/A	18030	18045	GTTCAAGATTAAACCA	29	1103
882820	N/A	N/A	18605	18620	TTGCATCCATGTCAAC	53	1104

882844	N/A	N/A	19017	19032	GTATAGTTCTCAACCA	53	1105
882867	N/A	N/A	19266	19281	TCCATAGATCAACATG	55	1106
882903	N/A	N/A	9991	10006	CCAAGGATAACCTGAA	56	1107

Table 17

Percent control of human IRF4 mRNA with 3-10-3 cEt gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	37	195
881079	15	30	3754	3769	GATCGAGCGGTGAAAC	77	1108
881103	412	427	6891	6906	AAGCGCACCGCAGGCG	96	1109
881126	694	709	9184	9199	GACATTGGTACGGGAT	64	1110
881173	1209	1224	13762	13777	TGACAAGAACTGCTGT	82	1111
881197	1446	1461	19563	19578	GCGGATAGATCTGTGG	45	1112
881221	1777	1792	19894	19909	CGCTGAACTGAAATCT	63	1113
881245	1955	1970	20072	20087	AAAGAGCGCATTTTCAG	94	1114
881269	2047	2062	20164	20179	ACATACCTACAAGCAG	55	1115
881293	2202	2217	20319	20334	CCCCAAGGCTACAGGC	75	1116
881317	2391	2406	20508	20523	AGACATTACTAGATTG	34	1117
881341	2530	2545	20647	20662	AGTACTTGACAGAAG	57	1118
881365	2740	2755	20857	20872	GAGGAAGCATAGAACA	82	1119
881389	2832	2847	20949	20964	CTTAAGCAAGTGGAGG	30	1120
881413	2915	2930	21032	21047	TAGTATGAGAAACGGC	22	1121
881437	3051	3066	21168	21183	GTGTAATGTAGGGATA	36	1122
881461	3344	3359	21461	21476	TGCAAGATGACTCCAT	43	1123
881485	3433	3448	21550	21565	ACATGGCAGTGGAGCT	36	1124
881509	3522	3537	21639	21654	GTATACATCACTGCAG	56	1125
881532	3660	3675	21777	21792	CTTTGAAGTGCTGTGT	84	1126
881556	3920	3935	22037	22052	TTCATAGCTAGTTCAT	56	1127
881580	4168	4183	22285	22300	TTGAGGTTTTCTAAA	71	1128
881599	4307	4322	22424	22439	CCCAATAGTCTAGCTG	44	1129
881623	4430	4445	22547	22562	GACCAGCTTTTTCAAA	62	1130
881647	4558	4573	22675	22690	AAGTAACTGACACGCA	77	1131
881671	4670	4685	22787	22802	ACCTTAACCAATCCCA	29	1132
881695	4847	4862	22964	22979	CTGTAACAGGCTATCA	56	1133
881719	5154	5169	23271	23286	CAGCAAAACGCAGAGC	46	1134
881743	5212	5227	23329	23344	CCAACGACAGCATAGC	24	1135
881767	N/A	N/A	18785	18800	TATATATGACGACTTA	80	1136
881791	N/A	N/A	18872	18887	CGCCTTAATGTTTCAGC	34	1137

881812	N/A	N/A	4152	4167	AGGCAGTTGTGCCGTC	162	1138
881836	N/A	N/A	4423	4438	CCGGACCCCGGAGCAG	124	1139
881859	N/A	N/A	4807	4822	CCCGACACGCGCCGCT	88	1140
881883	N/A	N/A	5062	5077	TTCAGCCACGAGGCAC	95	1141
881907	N/A	N/A	5674	5689	GTGGAAACGAGAACGC	97	1142
881929	N/A	N/A	5794	5809	CAGAGACGCGGTGAGA	161	1143
881951	N/A	N/A	6217	6232	TGCCTAGGACTAAGGA	74	1144
881974	N/A	N/A	6479	6494	GCTAAACCCAAAATAC	96	1145
881997	N/A	N/A	7192	7207	TCCTATGCTGAACCCC	64	1146
882021	N/A	N/A	7390	7405	TACCATGCATAGTGAT	56	1147
882045	N/A	N/A	7730	7745	TGCATAACACGGTGTT	62	1148
882069	N/A	N/A	8153	8168	GCATATTCCAACAGGC	34	1149
882092	N/A	N/A	8409	8424	ACTCATGGAGGATCAT	81	1150
882116	N/A	N/A	8599	8614	TAGGAAGCACTGGCAT	72	1151
			8651	8666			
			8755	8770			
			8859	8874			
			8911	8926			
			9015	9030			
882139	N/A	N/A	9425	9440	GTAAACTTGGCTGTGG	82	1152
882162	N/A	N/A	9669	9684	TGGTATTTTCCGTTT	31	1153
882185	N/A	N/A	9992	10007	GCCAAGGATAACCTGA	31	1154
882209	N/A	N/A	10186	10201	AGCCAGAGCAGTAAAC	85	1155
882233	N/A	N/A	10371	10386	ACTGAACCATGTTCTT	49	1156
882257	N/A	N/A	10676	10691	CAACTAGCAGGGCACG	62	1157
882281	N/A	N/A	11102	11117	TTCTAATGGTGCTCCT	93	1158
882305	N/A	N/A	11396	11411	GCACATCAATGTTTTA	33	1159
882329	N/A	N/A	11687	11702	AAAGATGCCAGAGGGC	77	1160
882353	N/A	N/A	11991	12006	TGCCGAGATATAAATA	77	1161
882377	N/A	N/A	12207	12222	GTATCATGCATACCAA	35	1162
882400	N/A	N/A	12675	12690	GCCTTAATGGTGATTT	74	1163
882447	N/A	N/A	13289	13304	ACAAAAGGTTCCCGCG	97	1164
882469	N/A	N/A	13921	13936	CAGAAGATCTCTACTG	88	1165
882491	N/A	N/A	14163	14178	CTGCATGAGGGTGACA	81	1166
882514	N/A	N/A	14477	14492	GAAGAGTTGGCGGTGG	85	1167
882537	N/A	N/A	14737	14752	CCTGAAGCTTAGTTAT	65	1168
882561	N/A	N/A	15531	15546	ACGCAGTGACCTGTG	107	1169
882584	N/A	N/A	15813	15828	CTCCAACCCTAGATAA	98	1170
882607	N/A	N/A	15983	15998	AACTTACAGGACTATT	87	1171
882631	N/A	N/A	16201	16216	AGACAAATCTTCTGCC	104	1172
882654	N/A	N/A	16430	16445	CTGAAGTGTGTAAGTC	72	1173

882678	N/A	N/A	16710	16725	TAGTAGACCACAGTGA	91	1174
882702	N/A	N/A	16950	16965	CACCAGGTTAAACAGG	108	1175
882726	N/A	N/A	17247	17262	TAGTTTAAGGGTTACG	51	1176
882750	N/A	N/A	17554	17569	CTCCAGGGAATGGATA	73	1177
882774	N/A	N/A	17777	17792	GAAAACTCTAACCCTA	91	1178
882798	N/A	N/A	18087	18102	TTATATACTGGTTGGT	51	1179
882821	N/A	N/A	18620	18635	TTAGAGGACAGTGACT	82	1180
882845	N/A	N/A	19018	19033	TGTATAGTTCTCAACC	57	1181
882868	N/A	N/A	19267	19282	TTCCATAGATCAACAT	56	1182
882905	N/A	N/A	12921	12936	CCCTAAGTTTAATTTA	103	1183

Table 18

Percent control of human IRF4 mRNA with 3-10-3 cEt gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	38	195
881080	16	31	3755	3770	AGATCGAGCGGTGAAA	76	1184
881104	415	430	6894	6909	TCAAAGCGCACCGCAG	57	1185
881127	697	712	9187	9202	TGGGACATTGGTACGG	31	1186
881174	1210	1225	13763	13778	CTGACAAGAACTGCTG	79	1187
881198	1447	1462	19564	19579	GGCGGATAGATCTGTG	49	1188
881222	1780	1795	19897	19912	AACCGCTGAACTGAAA	87	1189
881246	1957	1972	20074	20089	TTAAAGAGCGCATTTTC	59	1190
881270	2048	2063	20165	20180	GACATACCTACAAGCA	50	1191
881294	2229	2244	20346	20361	AACCGCTGGCAGGTGG	60	1192
881318	2393	2408	20510	20525	TTAGACATTACTAGAT	55	1193
881342	2531	2546	20648	20663	AAGTACTTGGACAGAA	46	1194
881366	2743	2758	20860	20875	CACGAGGAAGCATAGA	44	1195
881390	2833	2848	20950	20965	ACTTAAGCAAGTGGAG	37	1196
881414	2917	2932	21034	21049	TGTAGTATGAGAAACG	31	1197
881438	3059	3074	21176	21191	GCTGAACTGTGTAATG	42	1198
881462	3345	3360	21462	21477	GTGCAAGATGACTCCA	44	1199
881486	3435	3450	21552	21567	GTACATGGCAGTGGAG	44	1200
881510	3523	3538	21640	21655	TGTATACATCACTGCA	37	1201
881533	3665	3680	21782	21797	AGCTTCTTTGAAGTGC	38	1202
881557	3921	3936	22038	22053	TTTCATAGCTAGTTCA	44	1203
881581	4170	4185	22287	22302	GCTTGAGGTTTTCTTA	23	1204
881600	4312	4327	22429	22444	TCATACCCAATAGTCT	48	1205
881624	4438	4453	22555	22570	CGCTCAAAGACCAGCT	44	1206

881648	4559	4574	22676	22691	AAAGTAACTGACACGC	33	1207
881672	4671	4686	22788	22803	GACCTTAACCAATCCC	36	1208
881696	4863	4878	22980	22995	GACCTTTACTTCATTC	48	1209
881720	5157	5172	23274	23289	TCTCAGCAAAACGCAG	73	1210
881744	5213	5228	23330	23345	ACCAACGACAGCATAG	33	1211
881768	N/A	N/A	18786	18801	TTATATATGACGACTT	65	1212
881813	N/A	N/A	4156	4171	TCGCAGGCAGTTGTGC	120	1213
881837	N/A	N/A	4425	4440	CGCCGGACCCCGGAGC	91	1214
881860	N/A	N/A	4816	4831	CCAAAGGCTCCCGACA	71	1215
881884	N/A	N/A	5065	5080	CCCTTCAGCCACGAGG	92	1216
881908	N/A	N/A	5675	5690	CGTGGAACGAGAACG	71	1217
881952	N/A	N/A	6229	6244	TCTGAGTGAGCTTGCC	51	1218
881975	N/A	N/A	6541	6556	TGCATAGGCATCCTTC	32	1219
881998	N/A	N/A	7200	7215	ATTAATTCTCCTATGC	85	1220
882022	N/A	N/A	7393	7408	TATTACCATGCATAGT	70	1221
882046	N/A	N/A	7732	7747	AATGCATAACACGGTG	51	1222
882070	N/A	N/A	8154	8169	AGCATATTCCAACAGG	31	1223
882093	N/A	N/A	8417	8432	GTGAAAACACTCATGG	40	1224
882117	N/A	N/A	8606	8621	GCTGAGATAGGAAGCA	81	1225
			8658	8673			
			8762	8777			
			8866	8881			
			8918	8933			
			9022	9037			
882140	N/A	N/A	9426	9441	AGTAAACTTGGCTGTG	62	1226
882163	N/A	N/A	9710	9725	TGGTAGGTAGGCACCT	65	1227
882186	N/A	N/A	10006	10021	CTTCACTACCTGCAGC	78	1228
882210	N/A	N/A	10190	10205	ATAGAGCCAGAGCAGT	34	1229
882234	N/A	N/A	10372	10387	CACTGAACCATGTTCC	39	1230
882258	N/A	N/A	10677	10692	GCAACTAGCAGGGCAC	47	1231
882282	N/A	N/A	11116	11131	AGTGATGTCAGGTTTT	28	1232
882306	N/A	N/A	11398	11413	AGGCACATCAATGTTT	49	1233
882330	N/A	N/A	11688	11703	TAAAGATGCCAGAGGG	61	1234
882354	N/A	N/A	11999	12014	CACGAGGTTGCCGAGA	36	1235
882378	N/A	N/A	12209	12224	CTGTATCATGCATACC	39	1236
882401	N/A	N/A	12682	12697	CACTGAGGCCTTAATG	66	1237
882424	N/A	N/A	12927	12942	AATGAACCCTAAGTTT	97	1238
882448	N/A	N/A	13290	13305	AACAAAAGGTTCCCGC	60	1239
882470	N/A	N/A	13922	13937	ACAGAAAGATCTCTACT	68	1240
882492	N/A	N/A	14205	14220	GTACAGTCCACTCCAC	90	1241
882515	N/A	N/A	14550	14565	GGCACATGAGAAATCA	67	1242

882538	N/A	N/A	14993	15008	AACTGCAGCACCGTGG	55	1243
882562	N/A	N/A	15533	15548	TCACGCAGTGCACCTG	54	1244
882585	N/A	N/A	15826	15841	TGAGAAAGCATGGCTC	60	1245
882608	N/A	N/A	15987	16002	AGCTAACTTACAGGAC	104	1246
882632	N/A	N/A	16208	16223	GTACACAAGACAAATC	79	1247
882655	N/A	N/A	16433	16448	TGCCTGAACTGTGTAA	65	1248
882679	N/A	N/A	16713	16728	AGGTAGTAGACCACAG	41	1249
882703	N/A	N/A	16955	16970	GAACACACCAGGTTAA	102	1250
882727	N/A	N/A	17248	17263	CTAGTTTAAGGGTTAC	73	1251
882751	N/A	N/A	17565	17580	CTACAAAATGCCTCCA	58	1252
882775	N/A	N/A	17778	17793	AGAAAACCTCTAACCT	75	1253
882799	N/A	N/A	18089	18104	GATTATATACTGGTTG	41	1254
882822	N/A	N/A	18623	18638	GACTTAGAGGACAGTG	52	1255
882846	N/A	N/A	19019	19034	CTGTATAGTTCTCAAC	48	1256
882869	N/A	N/A	19283	19298	ATTTTTTGGTTAGTCC	47	1257
882896	N/A	N/A	5796	5811	AACAGAGACGCGGTGA	90	1258

Table 19

Percent control of human IRF4 mRNA with 3-10-3 cEt gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	38	195
881081	18	33	3757	3772	CAAGATCGAGCGGTGA	62	1259
881105	416	431	6895	6910	TTCAAAGCGCACCGCA	51	1260
881128	728	743	9218	9233	TGCCAGTGGTGGCCGC	70	1261
881175	1211	1226	N/A	N/A	TCTGACAAGAAGTCT	88	1262
881199	1448	1463	19565	19580	TGGCGGATAGATCTGT	66	1263
881223	1784	1799	19901	19916	CCTCAACCGCTGAACT	70	1264
881247	1958	1973	20075	20090	ATTAAAGAGCGCATTT	87	1265
881271	2049	2064	20166	20181	AGACATACCTACAAGC	50	1266
881295	2233	2248	20350	20365	AGGAAACCGCTGGCAG	44	1267
881319	2395	2410	20512	20527	ACTTAGACATTACTAG	80	1268
881343	2534	2549	20651	20666	GTAAAGTACTTGGACA	68	1269
881367	2745	2760	20862	20877	GGCACGAGGAAGCATA	38	1270
881391	2835	2850	20952	20967	ATACTTAAGCAAGTGG	24	1271
881415	2918	2933	21035	21050	CTGTAGTATGAGAAAC	55	1272
881439	3066	3081	21183	21198	GATAAAGGCTGAACTG	33	1273
881463	3359	3374	21476	21491	CTGCATGAAAGTGTGT	44	1274
881487	3443	3458	21560	21575	CCTACTGGGTACATGG	37	1275

881511	3524	3539	21641	21656	ATGTATACATCACTGC	33	1276
881534	3686	3701	21803	21818	CCTGAGACAGACTTCC	45	1277
881558	3924	3939	22041	22056	GTATTTTCATAGCTAGT	31	1278
881582	4172	4187	22289	22304	CTGCTTGAGGTTTTCC	26	1279
881601	4314	4329	22431	22446	GTTCATACCCAATAGT	34	1280
881625	4449	4464	22566	22581	ATTTATGCCCTCGCTC	74	1281
881649	4560	4575	22677	22692	AAAAGTAACTGACACG	39	1282
881673	4675	4690	22792	22807	TAAAGACCTTAACCAA	70	1283
881697	4909	4924	23026	23041	TTATGCATGTTCTCA	43	1284
881721	5164	5179	23281	23296	CTACAGATCTCAGCAA	82	1285
881745	5216	5231	23333	23348	TATACCAACGACAGCA	51	1286
881769	N/A	N/A	18787	18802	TTTATATATGACGACT	61	1287
881793	N/A	N/A	19455	19470	TAGCAGAGGTTCTACC	74	1288
881814	N/A	N/A	4215	4230	AGGAACGAAGAGCAGG	57	1289
881838	N/A	N/A	4447	4462	GGGATTCCGCGCGCAG	86	1290
881861	N/A	N/A	4818	4833	GCCCAAAGGCTCCCGA	89	1291
881885	N/A	N/A	5362	5377	CCGGAGACCTTGAAGA	91	1292
881930	N/A	N/A	5797	5812	AAACAGAGACGCGGTG	82	1293
881953	N/A	N/A	6241	6256	ACCCACCCAGTGTCTG	82	1294
881976	N/A	N/A	6542	6557	TTGCATAGGCATCCTT	53	1295
881999	N/A	N/A	7203	7218	GTGATTAATTCTCCTA	30	1296
882023	N/A	N/A	7414	7429	CACTTTAAAAGTTGAC	72	1297
882047	N/A	N/A	7733	7748	GAATGCATAACACGGT	39	1298
882071	N/A	N/A	8158	8173	GAGAAGCATATTCCAA	43	1299
882094	N/A	N/A	8431	8446	CTTCATCAGACTAAGT	69	1300
882118	N/A	N/A	8607	8622	GGCTGAGATAGGAAGC	64	1301
			8659	8674			
			8763	8778			
			8867	8882			
			8919	8934			
			9023	9038			
882141	N/A	N/A	9427	9442	GAGTAAACTTGGCTGT	62	1302
882164	N/A	N/A	9716	9731	ACCCAGTGGTAGGTAG	70	1303
882187	N/A	N/A	10014	10029	GTACACCTCTTCACTA	93	1304
882211	N/A	N/A	10191	10206	CATAGAGCCAGAGCAG	40	1305
882235	N/A	N/A	10448	10463	GCCAAAGAGCCCAATT	67	1306
882259	N/A	N/A	10772	10787	GTCCGACGCACCGCGG	82	1307
882283	N/A	N/A	11122	11137	ACAAGCAGTGATGTCA	27	1308
882307	N/A	N/A	11403	11418	CTCTTAGGCACATCAA	39	1309
882331	N/A	N/A	11689	11704	TTAAAGATGCCAGAGG	72	1310
882355	N/A	N/A	12000	12015	TCACGAGGTTGCCGAG	38	1311

882379	N/A	N/A	12221	12236	CTGATAATTAATCTGT	37	1312
882402	N/A	N/A	12689	12704	GGGTAAGCACTGAGGC	39	1313
882425	N/A	N/A	12990	13005	TTTAAGTCATGTGTCA	50	1314
882449	N/A	N/A	13291	13306	GAACAAAAGGTTCCCG	82	1315
882471	N/A	N/A	13923	13938	GACAGAAGATCTCTAC	83	1316
882493	N/A	N/A	14210	14225	AACCAGTACAGTCCAC	65	1317
882516	N/A	N/A	14551	14566	AGGCACATGAGAAATC	77	1318
882539	N/A	N/A	15020	15035	GGCAATGGAGTCTCGC	50	1319
882563	N/A	N/A	15535	15550	TCTCACGCAGTGCACC	56	1320
882586	N/A	N/A	15837	15852	GCACAATTCTCTGAGA	66	1321
882609	N/A	N/A	16031	16046	TATCAAAGATCTCCAC	75	1322
882633	N/A	N/A	16231	16246	CTTTAGCCCATGCTCC	80	1323
882656	N/A	N/A	16438	16453	CACTATGCCTGAACTG	90	1324
882680	N/A	N/A	16718	16733	TCAAAAGGTAGTAGAC	71	1325
882704	N/A	N/A	16959	16974	CACCGAACACACCAGG	80	1326
882728	N/A	N/A	17287	17302	TCAGACTGTGCTGCTC	64	1327
882752	N/A	N/A	17566	17581	CCTACAAAATGCCTCC	53	1328
882776	N/A	N/A	17808	17823	GTTATCTATGGAAACC	58	1329
882800	N/A	N/A	18090	18105	GGATTATATACTGGTT	23	1330
882823	N/A	N/A	18682	18697	ATGGACCACGCAGCCT	61	1331
882847	N/A	N/A	19026	19041	AGGTAATCTGTATAGT	38	1332
882870	N/A	N/A	19311	19326	TTCATATTTGGAGCCA	34	1333
882894	N/A	N/A	5700	5715	GCCCGGAGGAAGGGCG	106	1334

Table 20

Percent control of human IRF4 mRNA with 3-10-3 cEt gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	26	195
881082	20	35	3759	3774	CCCAAGATCGAGCGGT	72	1335
881106	417	432	6896	6911	GTTCAAAGCGCACC GC	35	1336
881129	741	756	9231	9246	ACAAGCTGGGCCTTGC	73	1337
881152	942	957	13495	13510	GGAGATCCGGCAGCCC	77	1338
881176	1222	1237	N/A	N/A	ACGCTTGCAGCTCTGA	52	1339
881200	1452	1467	19569	19584	GGAATGGCGGATAGAT	67	1340
881224	1785	1800	19902	19917	TCCTCAACCGCTGAAC	63	1341
881248	1959	1974	20076	20091	AATTAAAGAGCGCATT	83	1342
881272	2050	2065	20167	20182	CAGACATACCTACAAG	56	1343
881296	2234	2249	20351	20366	CAGGAAACCGCTGGCA	26	1344

881320	2396	2411	20513	20528	TACTTAGACATTACTA	61	1345
881344	2536	2551	20653	20668	TAGTTAAGTACTTGGA	44	1346
881368	2746	2761	20863	20878	TGGCACGAGGAAGCAT	54	1347
881392	2836	2851	20953	20968	TATACTTAAGCAAGTG	53	1348
881416	2919	2934	21036	21051	CCTGTAGTATGAGAAA	43	1349
881440	3068	3083	21185	21200	TTGATAAAGGCTGAAC	33	1350
881464	3364	3379	21481	21496	GAGCACTGCATGAAAG	49	1351
881488	3444	3459	21561	21576	CCCTACTGGGTACATG	63	1352
881512	3525	3540	21642	21657	GATGTATACATCACTG	30	1353
881535	3722	3737	21839	21854	GAGCATCCGCTTGAG	69	1354
881559	3926	3941	22043	22058	GAGTATTTTCATAGCTA	29	1355
881583	4173	4188	22290	22305	ACTGCTTGAGGTTTTTC	42	1356
881602	4319	4334	22436	22451	TTTTAGTTCATACCCA	48	1357
881626	4450	4465	22567	22582	TATTTATGCCCTCGCT	74	1358
881650	4576	4591	22693	22708	TCTGAATTGTTACTAA	65	1359
881674	4677	4692	22794	22809	AATAAAGACCTTAACC	89	1360
881698	4911	4926	23028	23043	TCTTATGCATGTTTCCT	38	1361
881722	5176	5191	23293	23308	AAGCATCCTTTCCTAC	65	1362
881746	5217	5232	23334	23349	GTATACCAACGACAGC	22	1363
881770	N/A	N/A	18788	18803	TTTTATATATGACGAC	66	1364
881794	N/A	N/A	22820	22835	GAGGACTTCGGGAGAT	77	1365
881815	N/A	N/A	4217	4232	TTAGGAACGAAGAGCA	68	1366
881839	N/A	N/A	4487	4502	GACAAGTGGCGCAGAC	89	1367
881862	N/A	N/A	4853	4868	CTCCTACCCGCCTGCT	85	1368
881886	N/A	N/A	5364	5379	GGCCGGAGACCTTGAA	97	1369
881909	N/A	N/A	5712	5727	CGGCAGACGGGAGCCC	88	1370
881931	N/A	N/A	5798	5813	GAAACAGAGACGCGGT	99	1371
881954	N/A	N/A	6265	6280	GCGGAGGTTTCCTTGAG	56	1372
882000	N/A	N/A	7211	7226	CATACAGTGTGATTAA	47	1373
882024	N/A	N/A	7424	7439	GACCATGTTACACTTT	50	1374
882048	N/A	N/A	7736	7751	TTAGAATGCATAACAC	56	1375
882072	N/A	N/A	8159	8174	TGAGAAGCATATTCCA	28	1376
882095	N/A	N/A	8443	8458	CTGGAGTGAACCCTTC	44	1377
882119	N/A	N/A	8701	8716	AGAAGCACTGGCATCG	63	1378
			8805	8820			
			8961	8976			
882142	N/A	N/A	9430	9445	TGAGAGTAAACTTGGC	35	1379
882165	N/A	N/A	9742	9757	ATCCACAATCAGCAAG	49	1380
882188	N/A	N/A	10016	10031	TGGTACACCTCTTCAC	68	1381
882212	N/A	N/A	10192	10207	CCATAGAGCCAGAGCA	36	1382
882236	N/A	N/A	10464	10479	GTCTACTTGAGTCTGT	49	1383

882260	N/A	N/A	10780	10795	GACAGAGAGTCCGACG	101	1384
882284	N/A	N/A	11123	11138	CACAAGCAGTGATGTC	40	1385
882308	N/A	N/A	11405	11420	TACTCTTAGGCACATC	41	1386
882332	N/A	N/A	11723	11738	TCAGAATTTAGTTAGT	67	1387
882356	N/A	N/A	12001	12016	ATCACGAGGTTGCCGA	40	1388
882380	N/A	N/A	12223	12238	GGCTGATAATTAATCT	53	1389
882403	N/A	N/A	12695	12710	ATTAAAGGGTAAGCAC	68	1390
882426	N/A	N/A	13007	13022	TGATAGTGGTGATGTC	46	1391
882450	N/A	N/A	13292	13307	GGAACAAAAGGTTCCC	88	1392
882472	N/A	N/A	13956	13971	TCTGATCCGGACTCTC	59	1393
882494	N/A	N/A	14213	14228	CAAAACCAAGTACAGTC	51	1394
882517	N/A	N/A	14622	14637	CCAGAGCACACAGACG	64	1395
882540	N/A	N/A	15021	15036	GGGCAATGGAGTCTCG	76	1396
882564	N/A	N/A	15538	15553	GTCTCTCACGCAGTGC	50	1397
882587	N/A	N/A	15838	15853	GGCACAATTCTCTGAG	57	1398
882610	N/A	N/A	16033	16048	GATATCAAAGATCTCC	43	1399
882634	N/A	N/A	16254	16269	AAAGACAAGTGCCCAT	76	1400
882657	N/A	N/A	16441	16456	TGTCATATGCCTGAA	73	1401
882681	N/A	N/A	16726	16741	ACGAAGATTCAAAGG	64	1402
882705	N/A	N/A	16962	16977	CATCACCGAACACACC	76	1403
882729	N/A	N/A	17289	17304	CCTCAGACTGTGCTGC	70	1404
882753	N/A	N/A	17567	17582	ACCTACAAAATGCCTC	58	1405
882777	N/A	N/A	17826	17841	GGCAAAATTAATGCTTC	24	1406
882801	N/A	N/A	18096	18111	TCTATGGGATTATATA	74	1407
882824	N/A	N/A	18684	18699	TTATGGACCACGCAGC	69	1408
882848	N/A	N/A	19030	19045	TTCTAGGTAATCTGTA	62	1409
882871	N/A	N/A	19312	19327	TTTCATATTTGGAGCC	25	1410
882899	N/A	N/A	6633	6648	AGTAGCTGGGCCCTCG	38	1411

Table 21

Percent control of human IRF4 mRNA with 3-10-3 cEt gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	31	195
668815	436	451	6915	6930	CCTCAAAGTCATTGCT	79	1412
881083	21	36	3760	3775	TCCCAAGATCGAGCGG	84	1413
881130	743	758	9233	9248	TCACAAGCTGGGCCTT	70	1414
881153	946	961	13499	13514	CATGGGAGATCCGGCA	59	1415
881177	1235	1250	17028	17043	CCGTGGTGAGCAAACG	68	1416

881201	1453	1468	19570	19585	AGGAATGGCGGATAGA	62	1417
881225	1793	1808	19910	19925	CGCAATTCTCCTCAAC	62	1418
881249	1960	1975	20077	20092	AAATTAAAGAGCGCAT	87	1419
881273	2054	2069	20171	20186	GGCACAGACATACCTA	52	1420
881297	2237	2252	20354	20369	CACCAGGAAACCGCTG	85	1421
881321	2399	2414	20516	20531	CATTACTTAGACATTA	81	1422
881345	2537	2552	20654	20669	ATAGTTAAGTACTTGG	52	1423
881369	2752	2767	20869	20884	TATAATTGGCACGAGG	59	1424
881393	2837	2852	20954	20969	GTATACTTAAGCAAGT	58	1425
881417	2921	2936	21038	21053	ATCCTGTAGTATGAGA	55	1426
881441	3069	3084	21186	21201	CTTGATAAAGGCTGAA	40	1427
881465	3372	3387	21489	21504	GCTACAAAGAGCACTG	37	1428
881489	3449	3464	21566	21581	TCAAACCCTACTGGGT	92	1429
881513	3532	3547	21649	21664	TCTATAAGATGTATAC	74	1430
881536	3726	3741	21843	21858	AATGGAGCATCCGCTT	107	1431
881560	3945	3960	22062	22077	TGCTAGGATTCCTAAC	74	1432
881584	4174	4189	22291	22306	TACTGCTTGAGGTTTT	50	1433
881603	4320	4335	22437	22452	TTTTTAGTTCATACCC	59	1434
881627	4451	4466	22568	22583	GTATTTATGCCCTCGC	47	1435
881651	4577	4592	22694	22709	ATCTGAATTGTTACTA	88	1436
881675	4732	4747	22849	22864	CACCATTCAGACAGAT	167	1437
881699	4918	4933	23035	23050	CTACATTTCTTATGCA	61	1438
881723	5180	5195	23297	23312	TGTGAAGCATCCTTTC	55	1439
881747	5218	5233	23335	23350	TGTATACCAACGACAG	42	1440
881771	N/A	N/A	18804	18819	GATATTAGAGACTGTA	49	1441
881795	N/A	N/A	22823	22838	ACAGAGGACTTCGGGA	136	1442
881816	N/A	N/A	4218	4233	CTTAGGAACGAAGAGC	93	1443
881840	N/A	N/A	4491	4506	AAACGACAAGTGGCGC	79	1444
881863	N/A	N/A	4860	4875	GCGAAGGCTCCTACCC	115	1445
881887	N/A	N/A	5369	5384	CCCGAGGCCGGAGACC	94	1446
881910	N/A	N/A	5720	5735	GACGGAGGCGGCAGAC	143	1447
881932	N/A	N/A	5815	5830	GAAAAGCAGCGAAAAG	98	1448
881955	N/A	N/A	6278	6293	GGTAGAGTGAGATGCG	42	1449
881977	N/A	N/A	6663	6678	GTTCTAGGGTCCTCCT	50	1450
882001	N/A	N/A	7213	7228	GGCATAAGTGTGATT	75	1451
882025	N/A	N/A	7428	7443	AGCTGACCATGTTACA	119	1452
882049	N/A	N/A	7737	7752	CTTAGAATGCATAACA	74	1453
882073	N/A	N/A	8213	8228	GGCACTACTTCCAAAA	69	1454
882096	N/A	N/A	8452	8467	CCGAAAAGACTGGAGT	43	1455
882120	N/A	N/A	8702	8717	AAGAAGCACTGGCATC	77	1456
			8806	8821			

			8962	8977			
882143	N/A	N/A	9432	9447	CCTGAGAGTAAACTTG	82	1457
882166	N/A	N/A	9745	9760	CTAATCCACAATCAGC	55	1458
882189	N/A	N/A	10024	10039	TTAAAGAGTGGTACAC	94	1459
882213	N/A	N/A	10194	10209	TTCCATAGAGCCAGAG	63	1460
882237	N/A	N/A	10497	10512	CAAAGCGGGTTCACAA	84	1461
882261	N/A	N/A	10781	10796	AGACAGAGAGTCCGAC	93	1462
882285	N/A	N/A	11126	11141	AACCACAAGCAGTGAT	83	1463
882309	N/A	N/A	11409	11424	GTATTACTCTTAGGCA	36	1464
882333	N/A	N/A	11750	11765	GCCACAACCTCTCGCT	75	1465
882357	N/A	N/A	12004	12019	GAAATCACGAGGTTGC	38	1466
882381	N/A	N/A	12241	12256	TCTAATAAATGTGCTC	56	1467
882404	N/A	N/A	12698	12713	CACATTAAAGGGTAAG	101	1468
882427	N/A	N/A	13049	13064	ACTATTAAGAACTTGC	79	1469
882451	N/A	N/A	13293	13308	GGGAACAAAAGGTTCC	111	1470
882473	N/A	N/A	13957	13972	ATCTGATCCGGACTCT	91	1471
882495	N/A	N/A	14214	14229	GCAAAACCAGTACAGT	42	1472
882518	N/A	N/A	14630	14645	CAACAGTGCCAGAGCA	89	1473
882541	N/A	N/A	15070	15085	TCCTATGGTCAGCCTC	52	1474
882565	N/A	N/A	15590	15605	CGCAAGTCTACAGCCC	41	1475
882588	N/A	N/A	15839	15854	TGGCACAATTCTCTGA	87	1476
882611	N/A	N/A	16042	16057	GAATAGGAAGATATCA	94	1477
882635	N/A	N/A	16256	16271	GGAAAGACAAGTGCCC	46	1478
882658	N/A	N/A	16447	16462	TCCCACTGTCACTATG	85	1479
882682	N/A	N/A	16727	16742	CACGAAGATTCAAAAG	90	1480
882706	N/A	N/A	16971	16986	AGAAACCCCTCATCACC	105	1481
882730	N/A	N/A	17330	17345	CTTTGATGAGCAGATC	88	1482
882754	N/A	N/A	17570	17585	GAGACCTACAAAATGC	89	1483
882778	N/A	N/A	17856	17871	GTCTTAAGGGTTCAAG	51	1484
882802	N/A	N/A	18097	18112	GTCTATGGGATTATAT	79	1485
882825	N/A	N/A	18685	18700	TTTATGGACCACGCAG	62	1486
882849	N/A	N/A	19033	19048	GATTTCTAGGTAATCT	69	1487
882872	N/A	N/A	19337	19352	TTACATCCTAGAACAC	97	1488

Table 22

Percent control of human IRF4 mRNA with 3-10-3 cEt gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	35	195

669124	3537	3552	21654	21669	TTGCATCTATAAGATG	69	1489
881084	44	59	3783	3798	TCGGAGCTGAGGGCAG	82	1490
881107	448	463	6927	6942	GCTCAACCAGTTCCTC	62	1491
881131	754	769	N/A	N/A	GGCAACCATTTTCACA	117	1492
881154	949	964	13502	13517	GTCCATGGGAGATCCG	48	1493
881178	1245	1260	17038	17053	CAGGGAGCGGCCGTGG	83	1494
881202	1454	1469	19571	19586	GAGGAATGGCGGATAG	69	1495
881226	1794	1809	19911	19926	CCGCAATTCTCCTCAA	80	1496
881250	1961	1976	20078	20093	CAAATTAAAGAGCGCA	43	1497
881274	2055	2070	20172	20187	TGGCACAGACATACCT	62	1498
881298	2240	2255	20357	20372	CCACACCAGGAAACCG	86	1499
881322	2400	2415	20517	20532	CCATTACTTAGACATT	36	1500
881346	2538	2553	20655	20670	GATAGTTAAGTACTTG	51	1501
881370	2756	2771	20873	20888	AAACTATAATTGGCAC	70	1502
881394	2838	2853	20955	20970	GGTATACTTAAGCAAG	32	1503
881418	2927	2942	21044	21059	GTAAATATCCTGTAGT	67	1504
881442	3070	3085	21187	21202	GCTTGATAAAGGCTGA	27	1505
881466	3373	3388	21490	21505	AGCTACAAAGAGCACT	67	1506
881490	3450	3465	21567	21582	GTCAAACCCTACTGGG	69	1507
881537	3729	3744	21846	21861	TGAAATGGAGCATCCG	91	1508
881561	3951	3966	22068	22083	GACAAGTGCTAGGATT	39	1509
881585	4176	4191	22293	22308	ATTACTGCTTGAGGTT	38	1510
881604	4321	4336	22438	22453	CTTTTTAGTTCATACC	63	1511
881628	4452	4467	22569	22584	TGTATTTATGCCCTCG	56	1512
881652	4580	4595	22697	22712	TGGATCTGAATTGTTA	45	1513
881676	4735	4750	22852	22867	ACGCACCATTCAGACA	102	1514
881700	4972	4987	23089	23104	GGAGGAGGGTTGGCCT	99	1515
881724	5181	5196	23298	23313	TTGTGAAGCATCCTTT	37	1516
881748	5219	5234	23336	23351	ATGTATACCAACGACA	37	1517
881772	N/A	N/A	18805	18820	TGATATTAGAGACTGT	40	1518
881796	N/A	N/A	22825	22840	CCACAGAGGACTTCGG	73	1519
881817	N/A	N/A	4220	4235	CCCTTAGGAACGAAGA	106	1520
881841	N/A	N/A	4494	4509	TGCAAACGACAAGTGG	79	1521
881864	N/A	N/A	4861	4876	CGCGAAGGCTCCTACC	141	1522
881888	N/A	N/A	5370	5385	TCCCGAGGCCGAGAC	127	1523
881911	N/A	N/A	5723	5738	ACGGACGGAGGCGGCA	89	1524
881956	N/A	N/A	6279	6294	CGGTAGAGTGAGATGC	46	1525
881978	N/A	N/A	6677	6692	CATCGAACTCCTGAGT	69	1526
882002	N/A	N/A	7218	7233	ATTGAGGCATACAGTG	70	1527
882026	N/A	N/A	7437	7452	AAACACCTCAGCTGAC	84	1528
882050	N/A	N/A	7784	7799	GACCTAACTAAATGTC	118	1529

882074	N/A	N/A	8218	8233	GATAAGGCACTACTTC	53	1530
882097	N/A	N/A	8463	8478	CATTTTATCATCCGAA	45	1531
882121	N/A	N/A	8753	8768	GGAAGCACTGGCATTG	51	1532
			8857	8872			
			8909	8924			
882144	N/A	N/A	9442	9457	TAGCATGGATCCTGAG	100	1533
882167	N/A	N/A	9746	9761	TCTAATCCACAATCAG	59	1534
882190	N/A	N/A	10025	10040	ATTAAAGAGTGGTACA	107	1535
882214	N/A	N/A	10198	10213	CTAATTCCATAGAGCC	20	1536
882238	N/A	N/A	10500	10515	TCACAAAGCGGGTTCA	77	1537
882262	N/A	N/A	10785	10800	GTCTAGACAGAGAGTC	98	1538
882286	N/A	N/A	11151	11166	AGCCAGTGGCTGAAAC	79	1539
882310	N/A	N/A	11411	11426	GTGTATTACTCTTAGG	14	1540
882334	N/A	N/A	11751	11766	TGCCACAACCTCTCGCC	69	1541
882358	N/A	N/A	12005	12020	AGAAATCACGAGGTTG	36	1542
882382	N/A	N/A	12260	12275	TCAATGGGAATCACAG	60	1543
882405	N/A	N/A	12699	12714	ACACATTAAAGGGTAA	89	1544
882428	N/A	N/A	13050	13065	CACTATTAAGAACTTG	67	1545
882452	N/A	N/A	13309	13324	CCCACATGTCCCGTGG	95	1546
882474	N/A	N/A	13995	14010	TTGCAAGAGAACAGCC	61	1547
882496	N/A	N/A	14215	14230	TGCAAAACCAGTACAG	72	1548
882519	N/A	N/A	14639	14654	AGCACATGTCAACAGT	69	1549
882542	N/A	N/A	15091	15106	AACCAGCACAGTTCTC	118	1550
882566	N/A	N/A	15591	15606	GCGCAAGTCTACAGCC	120	1551
882589	N/A	N/A	15854	15869	ATCAGAATGGCGAGTT	53	1552
882612	N/A	N/A	16046	16061	ACCTGAATAGGAAGAT	69	1553
882636	N/A	N/A	16258	16273	TTGGAAAGACAAGTGC	85	1554
882659	N/A	N/A	16464	16479	AGCCATCGGCAGCTGA	86	1555
882683	N/A	N/A	16733	16748	TGGAACCCACGAAGATT	62	1556
882707	N/A	N/A	16972	16987	CAGAAACCCTCATCAC	96	1557
882731	N/A	N/A	17367	17382	AAAGAGGCACCCTCCT	138	1558
882755	N/A	N/A	17588	17603	TGCTAGGACACAGCTG	57	1559
882779	N/A	N/A	17862	17877	TCAAAAGTCTTAAGGG	93	1560
882803	N/A	N/A	18111	18126	GAGAAAACCTCCTGAGT	95	1561
882826	N/A	N/A	18686	18701	TTTTATGGACCACGCA	69	1562
882850	N/A	N/A	19079	19094	CACAACTGCAGTTTGA	86	1563
882873	N/A	N/A	19343	19358	CCAAAGTTACATCCTA	61	1564
882897	N/A	N/A	5887	5902	CCGCAGAGAGCTAGCA	106	1565

Table 23
Percent control of human IRF4 mRNA with 3-10-3 cEt gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	48	195
881085	49	64	3788	3803	TGGAATCGGAGCTGAG	76	1566
881108	462	477	6941	6956	GTCCAGCTGGCTCCGC	47	1567
881132	762	777	N/A	N/A	TGTCACCTGGCAACCA	91	1568
881155	987	1002	13540	13555	GAACAGGACCTGGTCC	75	1569
881203	1455	1470	19572	19587	AGAGGAATGGCGGATA	58	1570
881251	1962	1977	20079	20094	ACAAATTAAGAGCGC	36	1571
881275	2078	2093	20195	20210	TTACATCTTACTTCCC	58	1572
881299	2306	2321	20423	20438	ACTAACTGGCTTCCAG	69	1573
881323	2401	2416	20518	20533	ACCATTACTTAGACAT	35	1574
881347	2539	2554	20656	20671	AGATAGTTAAGTACTT	89	1575
881371	2758	2773	20875	20890	TCAAACCTATAATTGGC	26	1576
881395	2839	2854	20956	20971	AGGTATACTTAAGCAA	32	1577
881419	2929	2944	21046	21061	TAGTAAATATCCTGTA	58	1578
881443	3071	3086	21188	21203	AGCTTGATAAAGGCTG	64	1579
881467	3376	3391	21493	21508	GTTAGCTACAAAGAGC	59	1580
881491	3451	3466	21568	21583	TGTCAAACCCCTACTGG	77	1581
881514	3549	3564	21666	21681	CCCCAAAATACTTTGC	0	1582
881538	3730	3745	21847	21862	TTGAAATGGAGCATCC	78	1583
881562	3952	3967	22069	22084	AGACAAGTGCTAGGAT	44	1584
881586	4186	4201	22303	22318	GGAGATATTAATTACT	50	1585
881605	4369	4384	22486	22501	GCTCATTTCACTGTAG	36	1586
881629	4453	4468	22570	22585	CTGTATTTATGCCCTC	40	1587
881653	4584	4599	22701	22716	AACTGGATCTGAATT	54	1588
881677	4742	4757	22859	22874	AGCCTTCACGCACCAT	70	1589
881701	4976	4991	23093	23108	CATTGGAGGAGGGTTG	102	1590
881725	5183	5198	23300	23315	GTTTGTGAAGCATCCT	35	1591
881749	5220	5235	23337	23352	GATGTATACCAACGAC	32	1592
881773	N/A	N/A	18806	18821	ATGATATTAGAGACTG	26	1593
881797	N/A	N/A	3804	3819	AGCCCTTACCTCGCCC	75	1594
881818	N/A	N/A	4239	4254	GGCCGCCGTGAGCTTG	97	1595
881865	N/A	N/A	4862	4877	CCGCGAAGGCTCCTAC	86	1596
881912	N/A	N/A	5724	5739	CACGGACGGAGGCGGC	82	1597
881933	N/A	N/A	5894	5909	GGAGTACCCGCAGAGA	75	1598
881957	N/A	N/A	6282	6297	AACCGGTAGAGTGAGA	94	1599

881979	N/A	N/A	6682	6697	CGCAGCATCGAACTCC	67	1600
882003	N/A	N/A	7219	7234	CATTGAGGCATACAGT	45	1601
882027	N/A	N/A	7439	7454	ATAAACACCTCAGCTG	79	1602
882051	N/A	N/A	7791	7806	AGGAACTGACCTAACT	69	1603
882075	N/A	N/A	8219	8234	TGATAAGGCACTACTT	65	1604
882098	N/A	N/A	8464	8479	GCATTTTATCATCCGA	37	1605
882122	N/A	N/A	8754	8769	AGGAAGCACTGGCATT	41	1606
			8858	8873			
			8910	8925			
882145	N/A	N/A	9458	9473	CACGAAGGGCAGTGCC	83	1607
882168	N/A	N/A	9747	9762	ATCTAATCCACAATCA	70	1608
882191	N/A	N/A	10026	10041	CATTAAAGAGTGGTAC	103	1609
882215	N/A	N/A	10199	10214	ACTAATTCCATAGAGC	21	1610
882239	N/A	N/A	10519	10534	TGACATGCTTTGTCCT	41	1611
882263	N/A	N/A	10795	10810	ATCAGATGATGTCTAG	103	1612
882287	N/A	N/A	11160	11175	CTCCATTCAAGCCAGT	42	1613
882311	N/A	N/A	11446	11461	GCAAGCTATATTAAAG	29	1614
882335	N/A	N/A	11757	11772	CAAAAGTGCCACAACCT	90	1615
882359	N/A	N/A	12008	12023	ATCAGAAATCACGAGG	29	1616
882383	N/A	N/A	12261	12276	ATCAATGGGAATCACA	10	1617
882406	N/A	N/A	12701	12716	ACACACATTAAAGGGT	57	1618
882429	N/A	N/A	13055	13070	AGCATCACTATTAAGA	28	1619
882453	N/A	N/A	13323	13338	TGGAACCTAGTGTCC	98	1620
882475	N/A	N/A	14002	14017	ACCAGAATTGCAAGAG	40	1621
882497	N/A	N/A	14216	14231	GTGCAAAACCAGTACA	67	1622
882520	N/A	N/A	14640	14655	GAGCACATGTCAACAG	60	1623
882543	N/A	N/A	15112	15127	TCACTTGCCGCCGCCT	51	1624
882567	N/A	N/A	15600	15615	GTTCTAGTCGCGCAAG	73	1625
882590	N/A	N/A	15855	15870	AATCAGAATGGCGAGT	61	1626
882613	N/A	N/A	16052	16067	GTGCAGACCTGAATAG	86	1627
882637	N/A	N/A	16269	16284	CTGGAACATTGTTGGA	54	1628
882660	N/A	N/A	16501	16516	CAGAAAATATGTAACG	78	1629
882684	N/A	N/A	16736	16751	CATTGGACCCACGAAG	72	1630
882708	N/A	N/A	16975	16990	GTTCAGAAACCCTCAT	87	1631
882732	N/A	N/A	17368	17383	GAAAGAGGCACCCTCC	81	1632
882756	N/A	N/A	17597	17612	TAAAAGAGGTGCTAGG	73	1633
882780	N/A	N/A	17889	17904	GTATGTAGCAATGTGA	79	1634
882804	N/A	N/A	18126	18141	CTGGAGAGAACTCATG	62	1635
882827	N/A	N/A	18687	18702	ATTTTATGGACCACGC	51	1636
882851	N/A	N/A	19080	19095	CCACAACCTGCAGTTTG	77	1637
882874	N/A	N/A	19346	19361	AGCCCAAAGTTACATC	58	1638

882893	N/A	N/A	4508	4523	CACTAAGTGGGCTCTG	59	1639
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Table 24

Percent control of human IRF4 mRNA with 3-10-3 cEt gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	23	195
881086	149	164	5176	5191	CCGAATCTCCGCCTC	64	1640
881133	774	789	10839	10854	ATAAAAAGGTTCTGTC	16	1641
881180	1256	1271	17049	17064	TGGAATCTTGGCAGGG	60	1642
881204	1457	1472	19574	19589	ATAGAGGAATGGCGGA	35	1643
881228	1828	1843	19945	19960	AATCAGATGTCCTGA	97	1644
881252	1973	1988	20090	20105	CCTAATCTACAACAAA	85	1645
881276	2124	2139	20241	20256	CCTACATACATTAATA	107	1646
881300	2307	2322	20424	20439	TACTAACTGGCTTCCA	72	1647
881324	2402	2417	20519	20534	AACCATTACTTAGACA	55	1648
881348	2540	2555	20657	20672	CAGATAGTTAAGTACT	56	1649
881372	2760	2775	20877	20892	TGTCAAATATAATTG	85	1650
881396	2840	2855	20957	20972	TAGGTATACTTAAGCA	21	1651
881420	2933	2948	21050	21065	GTAATAGTAAATATCC	39	1652
881444	3076	3091	21193	21208	CACTAAGCTTGATAAA	111	1653
881468	3377	3392	21494	21509	TGTTAGCTACAAAGAG	53	1654
881492	3456	3471	21573	21588	TGAAATGTCAAACCT	46	1655
881515	3559	3574	21676	21691	GGATAATATACCCCAA	36	1656
881539	3731	3746	21848	21863	ATTGAAATGGAGCATC	101	1657
881587	4187	4202	22304	22319	AGGAGATATTAATTAC	43	1658
881606	4378	4393	22495	22510	GTAAGGGCTGCTCATT	48	1659
881630	4459	4474	22576	22591	GGCTAGCTGTATTTAT	63	1660
881654	4586	4601	22703	22718	TTACACTGGATCTGAA	62	1661
881678	4755	4770	22872	22887	TGTAAGGTCTGAGAGC	75	1662
881702	4978	4993	23095	23110	TCCATTGGAGGAGGGT	67	1663
881726	5184	5199	23301	23316	AGTTTGTGAAGCATCC	31	1664
881750	5222	5237	23339	23354	ATGATGTATACCAACG	14	1665
881774	N/A	N/A	18807	18822	CATGATATTAGAGACT	44	1666
881798	N/A	N/A	3865	3880	CTGGTTCGCGCTCCGG	93	1667
881819	N/A	N/A	4244	4259	CCGGAGGCCGCCGTGA	87	1668
881842	N/A	N/A	4510	4525	CGCACTAAGTGGGCTC	86	1669
881866	N/A	N/A	4892	4907	GCACAGCCGTCCGCCT	84	1670
881890	N/A	N/A	5492	5507	CGCCACCTGATGCCTC	70	1671

881913	N/A	N/A	5726	5741	CCCACGGACGGAGGCG	109	1672
881934	N/A	N/A	5896	5911	TGGGAGTACCCGCAGA	74	1673
881958	N/A	N/A	6284	6299	ATAACCGGTAGAGTGA	50	1674
881980	N/A	N/A	6683	6698	CCGCAGCATCGAACTC	58	1675
882028	N/A	N/A	7481	7496	GGTCAGAATCTTGAAA	91	1676
882052	N/A	N/A	7795	7810	AAACAGGAACTGACCT	80	1677
882076	N/A	N/A	8220	8235	ATGATAAGGCACTACT	87	1678
882099	N/A	N/A	8465	8480	AGCATTTTATCATCCG	19	1679
882123	N/A	N/A	8781	8796	TTAAAGGAGTGCAGGA	84	1680
882146	N/A	N/A	9460	9475	CCCACGAAGGGCAGTG	65	1681
882169	N/A	N/A	9751	9766	CCACATCTAATCCACA	33	1682
882192	N/A	N/A	10049	10064	GTGAACATGCCACTCA	38	1683
882216	N/A	N/A	10200	10215	TACTAATTCCATAGAG	74	1684
882240	N/A	N/A	10520	10535	ATGACATGCTTTGTCC	54	1685
882264	N/A	N/A	10939	10954	AGCAAACCCTGCACTC	92	1686
882288	N/A	N/A	11215	11230	GGTAAAGGCACATTCC	53	1687
882312	N/A	N/A	11448	11463	TTGCAAGCTATATTAA	66	1688
882336	N/A	N/A	11790	11805	TGGTAGGTCAAACCTCC	113	1689
882360	N/A	N/A	12009	12024	CATCAGAAATCACGAG	45	1690
882384	N/A	N/A	12283	12298	GGTAACTGTATGGAAC	24	1691
882407	N/A	N/A	12757	12772	GAATTAGGTGCTTAAT	41	1692
882430	N/A	N/A	13060	13075	TATAGAGCATCACTAT	59	1693
882454	N/A	N/A	13324	13339	GTGGAACCTAGTGTC	88	1694
882476	N/A	N/A	14021	14036	TAAGAGGCGACTGCTG	145	1695
882498	N/A	N/A	14233	14248	CTCCTATAACTTCTCC	67	1696
882521	N/A	N/A	14643	14658	TACGAGCACATGTCAA	64	1697
882544	N/A	N/A	15146	15161	TAGAATGAGAGGTGTC	71	1698
882568	N/A	N/A	15609	15624	TAATAGTAAGTTCTAG	100	1699
882591	N/A	N/A	15860	15875	AGGCTAATCAGAATGG	58	1700
882614	N/A	N/A	16099	16114	TCAGATACACACCCTC	63	1701
882638	N/A	N/A	16276	16291	AAACGGACTGGAACAT	93	1702
882661	N/A	N/A	16516	16531	GTAACCTCAGGCACCAC	53	1703
882685	N/A	N/A	16758	16773	GCTAAAGAACACTGCT	97	1704
882709	N/A	N/A	16981	16996	GACCATGTTTCAGAAAC	4	1705
882733	N/A	N/A	17369	17384	GGAAAGAGGCACCCTC	72	1706
882757	N/A	N/A	17640	17655	TATCATATGCCCAATA	68	1707
882781	N/A	N/A	17894	17909	TGCAAGTATGTAGCAA	97	1708
882805	N/A	N/A	18131	18146	AATCACTGGAGAGAAC	71	1709
882828	N/A	N/A	18688	18703	CATTTTATGGACCACG	38	1710
882852	N/A	N/A	19099	19114	GGCCAATGATTTTGTT	94	1711
882875	N/A	N/A	19350	19365	GTAAAGCCCAAAGTTA	73	1712

Example 6: Effect of 3-10-3 cEt gapmers with phosphorothioate internucleoside linkages on human IRF4 *in vitro*, single dose

Modified oligonucleotides complementary to a human IRF4 nucleic acid were designed and tested for their effect on IRF4 mRNA *in vitro*.

Cultured SK-MEL-28 cells at a density of 20,000 cells per well were transfected using electroporation with 4,000 nM concentration of modified oligonucleotide or no modified oligonucleotide for untreated controls. After approximately 24 hours, RNA was isolated from the cells and IRF4 mRNA levels were measured by quantitative real-time PCR. Human primer probe set RTS3114 (described hereinabove in Example 1) was used to measure mRNA levels. IRF4 mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented in the table below as percent control of the amount of IRF4 mRNA, relative to untreated control (UTC) cells.

The modified oligonucleotides in Tables 25 through 36 are 3-10-3 cEt gapmers. The gapmers are 16 nucleobases in length, wherein the central gap segment comprises ten 2'-deoxynucleosides and is flanked by wing segments on both the 5' end and on the 3' end comprising three cEt nucleosides. The sugar motif for the gapmers is (from 5' to 3'): kkkddddd kkk; wherein 'd' represents a 2'-deoxyribose sugar and 'k' represents a cEt modified sugar. Each internucleoside linkage is a phosphorothioate internucleoside linkage and each cytosine residue is a 5-methylcytosine. "Start Site" indicates the 5'-most nucleoside to which the gapmer is complementary in the human nucleic acid sequence. "Stop Site" indicates the 3'-most nucleoside to which the gapmer is complementary in the human nucleic acid sequence.

Each modified oligonucleotide listed in Tables 25 through 36 below is complementary to human IRF4 nucleic acid sequences SEQ ID NO: 1 or SEQ ID NO: 2, as indicated. 'N/A' indicates that the modified oligonucleotide is not complementary to that particular nucleic acid sequence with 100% complementarity. As shown below, modified oligonucleotides complementary to human IRF4 reduced the amount of human IRF4 mRNA.

Table 25
Percent control of human IRF4 mRNA with 3-10-3 cEt gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	44	195
881087	151	166	5178	5193	TGCCGAACCTCTCCGCC	57	1713
881110	482	497	6961	6976	ACTTTGTACGGGTCTG	61	1714
881134	778	793	10843	10858	AAGCATAAAAGGTTCC	72	1715

881157	1059	1074	13612	13627	GACCACGCCCCCTCTCC	45	1716
881181	1263	1278	17056	17071	AGTCACCTGGAATCTT	53	1717
881205	1458	1473	19575	19590	AATAGAGGAATGGCGG	47	1718
881229	1831	1846	19948	19963	GCCAATCAGATGTCAC	54	1719
881253	1974	1989	20091	20106	ACCTAATCTACAACAA	83	1720
881277	2128	2143	20245	20260	AGCTCCTACATACATT	56	1721
881301	2309	2324	20426	20441	TTTACTAACTGGCTTC	55	1722
881325	2432	2447	20549	20564	GGTCAAAAAGATGCAG	49	1723
881349	2541	2556	20658	20673	ACAGATAGTTAAGTAC	65	1724
881373	2770	2785	20887	20902	TTTAAGGCCCTGTCAA	117	1725
881397	2842	2857	20959	20974	GATAGGTATACTTAAG	49	1726
881421	2938	2953	21055	21070	TGGGAGTAATAGTAAA	84	1727
881445	3077	3092	21194	21209	TCTACTAAGCTTGATAA	63	1728
881469	3383	3398	21500	21515	CTTCACTGTTAGCTAC	49	1729
881493	3468	3483	21585	21600	TTGCATGGCTAATGAA	58	1730
881516	3560	3575	21677	21692	AGGATAATATACCCCA	26	1731
881540	3733	3748	21850	21865	CAATTGAAATGGAGCA	74	1732
881564	3956	3971	22073	22088	CCTGAGACAAGTGCTA	57	1733
881588	4200	4215	22317	22332	TCTATAGTGTTCAGG	20	1734
881607	4380	4395	22497	22512	CTGTAAGGGCTGCTCA	44	1735
881631	4482	4497	22599	22614	TCCCAGAGTTGTTCCA	74	1736
881655	4587	4602	22704	22719	TTTACACTGGATCTGA	75	1737
881679	4756	4771	22873	22888	GTGTAAGGTCTGAGAG	84	1738
881703	4979	4994	23096	23111	TTCCATTGGAGGAGGG	72	1739
881727	5185	5200	23302	23317	CAGTTTGTGAAGCATC	22	1740
881751	5223	5238	23340	23355	CATGATGTATACCAAC	49	1741
881775	N/A	N/A	18808	18823	TCATGATATTAGAGAC	65	1742
881799	N/A	N/A	3874	3889	GTCGAACCTCTGGTTC	110	1743
881820	N/A	N/A	4246	4261	CGCCGGAGGCCGCCGT	97	1744
881843	N/A	N/A	4511	4526	GCGCACTAAGTGGGCT	110	1745
881867	N/A	N/A	4893	4908	GGCACAGCCGTCCGCC	89	1746
881891	N/A	N/A	5535	5550	CTGAGAGCCGAGGCCT	117	1747
881914	N/A	N/A	5727	5742	ACCCACGGACGGAGGC	109	1748
881935	N/A	N/A	5903	5918	ACAGAGGTGGGAGTAC	174	1749
881959	N/A	N/A	6285	6300	TATAACCGGTAGAGTG	79	1750
881981	N/A	N/A	6697	6712	ACGATGATAGCTCACC	92	1751
882005	N/A	N/A	7221	7236	TACATTGAGGCATACA	59	1752
882029	N/A	N/A	7547	7562	CCCAAGTGAGGTCACC	80	1753
882053	N/A	N/A	7837	7852	GGCTCCTACATGTTTG	146	1754
882077	N/A	N/A	8222	8237	ACATGATAAGGCACTA	39	1755
882100	N/A	N/A	8470	8485	GCCGAAGCATTTTATC	71	1756

882124	N/A	N/A	8782	8797	GTAAAGGAGTGCAGG	114	1757
882147	N/A	N/A	9461	9476	TCCCACGAAGGGCAGT	94	1758
882170	N/A	N/A	9788	9803	TCATTTTGATGTCTGG	37	1759
882193	N/A	N/A	10078	10093	GCCAATGCAACTGAAT	64	1760
882217	N/A	N/A	10202	10217	GTTACTAATTCCATAG	51	1761
882241	N/A	N/A	10525	10540	GACAGATGACATGCTT	91	1762
882265	N/A	N/A	10940	10955	GAGCAAACCCTGCACT	116	1763
882289	N/A	N/A	11216	11231	AGGTAAAGGCACATTC	81	1764
882313	N/A	N/A	11469	11484	TCAGATTGAATCCATA	36	1765
882337	N/A	N/A	11793	11808	AGCTGGTAGGTCAAAC	105	1766
882361	N/A	N/A	12050	12065	TTCGAGGTGATTCTCG	95	1767
882385	N/A	N/A	12284	12299	TGGTAACTGTATGGAA	52	1768
882408	N/A	N/A	12758	12773	AGAATTAGGTGCTTAA	39	1769
882431	N/A	N/A	13064	13079	CTATTATAGAGCATCA	45	1770
882455	N/A	N/A	13356	13371	GGCCAACGACTCCACA	77	1771
882477	N/A	N/A	14022	14037	TTAAGAGGCGACTGCT	88	1772
882499	N/A	N/A	14244	14259	CTTATAGCACTCTCCT	67	1773
882522	N/A	N/A	14645	14660	AGTACGAGCACATGTC	66	1774
882545	N/A	N/A	15191	15206	AAGGATGGGACCGCCC	61	1775
882569	N/A	N/A	15613	15628	AGATTAATAGTAAGTT	96	1776
882592	N/A	N/A	15864	15879	ACACAGGCTAATCAGA	93	1777
882615	N/A	N/A	16100	16115	ATCAGATACACACCCT	108	1778
882639	N/A	N/A	16278	16293	CAAAACGGACTGGAAC	84	1779
882662	N/A	N/A	16517	16532	CGTAACTCAGGCACCA	70	1780
882686	N/A	N/A	16762	16777	GACAGCTAAAGAACAC	81	1781
882710	N/A	N/A	16993	17008	CCACAAGAAAGAGACC	109	1782
882734	N/A	N/A	17400	17415	CGACAACCTTCCTGAA	79	1783
882758	N/A	N/A	17644	17659	CAAATATCATATGCC	31	1784
882782	N/A	N/A	17904	17919	TAATAATGCTTGCAAG	88	1785
882806	N/A	N/A	18135	18150	AGTCAATCACTGGAGA	40	1786
882829	N/A	N/A	18691	18706	ATTCATTTTATGGACC	58	1787
882853	N/A	N/A	19108	19123	GGTAATTTAGGCCAAT	65	1788
882876	N/A	N/A	19366	19381	CTAAGGAGACAGTAAC	71	1789

Table 26

Percent control of human IRF4 mRNA with 3-10-3 cEt gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	42	195

881088	157	172	5184	5199	CGCTCATGCCGAACTC	89	1790
881111	485	500	6964	6979	TACACTTTGTACGGGT	72	1791
881135	782	797	10847	10862	GCACAAGCATAAAAGG	84	1792
881158	1062	1077	13615	13630	GAGGACCACGCCCCCTC	103	1793
881182	1269	1284	17062	17077	GCATAGAGTCACCTGG	61	1794
881206	1459	1474	19576	19591	GAATAGAGGAATGGCG	61	1795
881230	1832	1847	19949	19964	TGCCAATCAGATGTCA	78	1796
881254	1975	1990	20092	20107	GACCTAATCTACAACA	67	1797
881278	2150	2165	20267	20282	AAGTGTCTTCCACAAG	46	1798
881302	2310	2325	20427	20442	GTTTACTAACTGGCTT	73	1799
881326	2443	2458	20560	20575	TAAAGAATGAGGGTCA	55	1800
881350	2543	2558	20660	20675	GAACAGATAGTTAAGT	83	1801
881374	2771	2786	20888	20903	TTTTAAGGCCCTGTCA	82	1802
881398	2843	2858	20960	20975	TGATAGGTATACTTAA	72	1803
881422	2957	2972	21074	21089	CGCAATCTTCTGCTGA	36	1804
881446	3079	3094	21196	21211	GCTCACTAAGCTTGAT	44	1805
881470	3390	3405	21507	21522	GGTAAATCTTCACTGT	35	1806
881494	3475	3490	21592	21607	ATCCATGTTGCATGGC	39	1807
881517	3561	3576	21678	21693	TAGGATAATATACCCC	26	1808
881541	3734	3749	21851	21866	GCAATTGAAATGGAGC	76	1809
881565	3979	3994	22096	22111	AGGAAGCCGTTCTTT	58	1810
881589	4201	4216	22318	22333	CTCTATAGTGTCCAG	34	1811
881608	4381	4396	22498	22513	ACTGTAAGGGCTGCTC	31	1812
881632	4495	4510	22612	22627	GAGTACCCAAGACTCC	75	1813
881656	4588	4603	22705	22720	GTTTACACTGGATCTG	39	1814
881680	4765	4780	22882	22897	CAAAATGGTGTGTAAG	75	1815
881704	4983	4998	23100	23115	GAATTTCCATTGGAGG	57	1816
881728	5187	5202	23304	23319	CTCAGTTTGTGAAGCA	15	1817
881752	5224	5239	23341	23356	TCATGATGTATACCAA	35	1818
881776	N/A	N/A	18810	18825	AATCATGATATTAGAG	69	1819
881800	N/A	N/A	3880	3895	CTGGAGGTCGAACCTC	98	1820
881821	N/A	N/A	4257	4272	GGTGAGCACCGCGCCG	108	1821
881844	N/A	N/A	4522	4537	GCCCAGCTAGCGCGCA	71	1822
881868	N/A	N/A	4909	4924	GCGCATCCCCCTGGGCG	104	1823
881892	N/A	N/A	5538	5553	CCGCTGAGAGCCGAGG	104	1824
881915	N/A	N/A	5730	5745	GGGACCCACGGACGGA	91	1825
881936	N/A	N/A	5972	5987	CTCTAGACAGAGGCC	80	1826
881960	N/A	N/A	6286	6301	TTATAACCGGTAGAGT	62	1827
881982	N/A	N/A	6761	6776	GGTTTATTAGCTTTCT	101	1828
882006	N/A	N/A	7226	7241	CCATATACATTGAGGC	56	1829
882030	N/A	N/A	7574	7589	ATAAAGGACCCCGCCA	82	1830

882054	N/A	N/A	8019	8034	GGCAAGTTCTGCTGTC	42	1831
882078	N/A	N/A	8226	8241	TTTCACATGATAAGGC	57	1832
882101	N/A	N/A	8471	8486	AGCCGAAGCATTITAT	56	1833
882125	N/A	N/A	9093	9108	CTAAAGGAGTGCAGGA	94	1834
882148	N/A	N/A	9467	9482	ATAAGATCCCACGAAG	142	1835
882171	N/A	N/A	9816	9831	AGCTAATGAGAGCTTC	83	1836
882194	N/A	N/A	10086	10101	CTTGAAAAGCCAATGC	42	1837
882218	N/A	N/A	10203	10218	GGTTACTAATTCCATA	44	1838
882242	N/A	N/A	10526	10541	AGACAGATGACATGCT	50	1839
882266	N/A	N/A	11013	11028	TCTAAAGTCCCATCGA	69	1840
882290	N/A	N/A	11220	11235	GTAAAGGTAAAGGCAC	58	1841
882314	N/A	N/A	11528	11543	GGTAAGATCTCCATGG	55	1842
882338	N/A	N/A	11798	11813	GAAAGAGCTGGTAGGT	100	1843
882362	N/A	N/A	12054	12069	GCCATTCGAGGTGATT	44	1844
882386	N/A	N/A	12355	12370	ACCAAGCTGGGTTTGC	47	1845
882409	N/A	N/A	12760	12775	ATAGAATTAGGTGCTT	36	1846
882432	N/A	N/A	13065	13080	CCTATTATAGAGCATC	32	1847
882456	N/A	N/A	13361	13376	CTCGAGGCCAACGACT	99	1848
882478	N/A	N/A	14025	14040	GTTTTAAGAGGCGACT	67	1849
882500	N/A	N/A	14246	14261	AACTTATAGCACTCTC	72	1850
882523	N/A	N/A	14648	14663	AGAAGTACGAGCACAT	56	1851
882546	N/A	N/A	15192	15207	GAAGGATGGGACCGCC	59	1852
882570	N/A	N/A	15617	15632	TCACAGATTAAAGTA	77	1853
882593	N/A	N/A	15867	15882	CCTACACAGGCTAATC	87	1854
882616	N/A	N/A	16101	16116	TATCAGATACACCCC	81	1855
882640	N/A	N/A	16279	16294	ACAAAACGGACTGGAA	86	1856
882663	N/A	N/A	16535	16550	TGCTACTGCGGACATC	57	1857
882687	N/A	N/A	16763	16778	CGACAGCTAAAGAACA	63	1858
882711	N/A	N/A	17000	17015	TAGAAGCCCACAAGAA	99	1859
882735	N/A	N/A	17402	17417	TACGACAACCTTTCCTG	59	1860
882759	N/A	N/A	17662	17677	GAAAGATTCAGCCTCT	55	1861
882783	N/A	N/A	17906	17921	GTTAATAATGCTTGCA	98	1862
882807	N/A	N/A	18141	18156	TTATTAAGTCAATCAC	101	1863
882830	N/A	N/A	18714	18729	CTCATAGGTGTACACG	41	1864
882854	N/A	N/A	19114	19129	CTGCAGGGTAATTTAG	66	1865
882877	N/A	N/A	19379	19394	CAGCACTCAGATTCTA	88	1866

Table 27

Percent control of human IRF4 mRNA with 3-10-3 cEt gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	41	195
668855	783	798	10848	10863	GGCACAAGCATAAAAG	99	1867
690520	4222	4237	22339	22354	AAATGAGTCGGTCACT	45	1868
881089	165	180	5192	5207	GCTCACCGCGCTCATG	52	1869
881112	486	501	6965	6980	GTACACTTTGTACGGG	36	1870
881159	1067	1082	13620	13635	ATCCAGAGGACCACGC	81	1871
881183	1270	1285	17063	17078	AGCATAGAGTCACCTG	37	1872
881207	1460	1475	19577	19592	TGAATAGAGGAATGGC	79	1873
881231	1844	1859	19961	19976	AATAAGCTCATCTGCC	64	1874
881255	1978	1993	20095	20110	CAAGACCTAATCTACA	88	1875
881279	2151	2166	20268	20283	CAAGTGTCTTCCACAA	35	1876
881303	2311	2326	20428	20443	AGTTTACTAACTGGCT	37	1877
881327	2444	2459	20561	20576	CTAAAGAATGAGGGTC	38	1878
881351	2545	2560	20662	20677	GGGAACAGATAGTTAA	74	1879
881375	2773	2788	20890	20905	AATTTTAAGGCCCTGT	76	1880
881399	2844	2859	20961	20976	GTGATAGGTATACTTA	35	1881
881423	2958	2973	21075	21090	ACGCAATCTTCTGCTG	48	1882
881447	3086	3101	21203	21218	GCTCACTGCTCACTAA	67	1883
881471	3391	3406	21508	21523	AGGTAAATCTTCACTG	46	1884
881495	3479	3494	21596	21611	ACATATCCATGTTGCA	21	1885
881518	3562	3577	21679	21694	TTAGGATAATATACCC	48	1886
881542	3785	3800	21902	21917	ACTGTTAAAGCAGCAT	29	1887
881566	3980	3995	22097	22112	GAGGAAGCCGTTTCCTT	49	1888
881609	4383	4398	22500	22515	ATACTGTAAGGGCTGC	46	1889
881633	4504	4519	22621	22636	AAGAGGTGCGAGTACC	66	1890
881657	4590	4605	22707	22722	AAGTTTACACTGGATC	42	1891
881681	4786	4801	22903	22918	GGGCATGTAAACATA	77	1892
881705	4985	5000	23102	23117	GGGAATTTCCATTGGA	56	1893
881729	5188	5203	23305	23320	CCTCAGTTTGTGAAGC	31	1894
881753	5226	5241	23343	23358	ATTCATGATGTATACC	38	1895
881777	N/A	N/A	18811	18826	CAATCATGATATTAGA	62	1896
881801	N/A	N/A	3897	3912	GGGTACCCTGCGCTGC	56	1897
881822	N/A	N/A	4292	4307	CCAAATGTGGAGCTCC	77	1898
881845	N/A	N/A	4542	4557	CGAATAGGACCCCTAT	91	1899
881869	N/A	N/A	4916	4931	GGCCCGGGCGCATCCC	95	1900

881893	N/A	N/A	5548	5563	CCCCGCGGTCCCGCTG	59	1901
881916	N/A	N/A	5749	5764	ACGCACGGAGAGGGCG	99	1902
881937	N/A	N/A	5974	5989	AGCTCTAGACAGAGGC	65	1903
881961	N/A	N/A	6287	6302	TTTATAACCGGTAGAG	46	1904
881983	N/A	N/A	6783	6798	CGAAAAGTCAAAATAC	100	1905
882007	N/A	N/A	7228	7243	CCCCATATACATTGAG	63	1906
882031	N/A	N/A	7576	7591	ACATAAAGGACCCCGC	72	1907
882055	N/A	N/A	8027	8042	TAGCAAATGGCAAGTT	83	1908
882079	N/A	N/A	8248	8263	GAAGAGATCAGCTGCC	58	1909
882102	N/A	N/A	8475	8490	TGACAGCCGAAGCATT	62	1910
882126	N/A	N/A	9094	9109	GCTAAAGGAGTGCAGG	93	1911
882149	N/A	N/A	9468	9483	AATAAGATCCCACGAA	85	1912
882172	N/A	N/A	9820	9835	ACCCAGCTAATGAGAG	65	1913
882195	N/A	N/A	10098	10113	CTGCAAATCCCTCTTG	133	1914
882219	N/A	N/A	10230	10245	CAGTTCTAAGCATTGC	67	1915
882243	N/A	N/A	10551	10566	GACTAACAGGGAGACT	109	1916
882267	N/A	N/A	11014	11029	GTCTAAAGTCCCATCG	60	1917
882291	N/A	N/A	11251	11266	CGTGAGAATGTTGGCT	51	1918
882315	N/A	N/A	11533	11548	TAGTAGGTAAGATCTC	77	1919
882339	N/A	N/A	11799	11814	AGAAAGAGCTGGTAGG	64	1920
882363	N/A	N/A	12074	12089	CCCAAAGAGAGTGGGT	100	1921
882387	N/A	N/A	12364	12379	GTTGAAAGAACCAAGC	89	1922
882410	N/A	N/A	12761	12776	TATAGAATTAGGTGCT	60	1923
882433	N/A	N/A	13112	13127	GGAACAAGTGTATCTT	24	1924
882457	N/A	N/A	13367	13382	CACCACCTCGAGGCCA	76	1925
882479	N/A	N/A	14027	14042	CTGTTTTAAGAGGCCA	42	1926
882501	N/A	N/A	14250	14265	AGCCAACTTATAGCAC	46	1927
882524	N/A	N/A	14649	14664	CAGAAGTACGAGCACA	53	1928
882547	N/A	N/A	15195	15210	CAAGAAGGATGGGACC	75	1929
882571	N/A	N/A	15619	15634	GCTCACAGATTAATAG	84	1930
882594	N/A	N/A	15871	15886	TACACCTACACAGGCT	81	1931
882617	N/A	N/A	16121	16136	CTGCAGAACAGACGCG	89	1932
882641	N/A	N/A	16280	16295	TACAAAACGGACTGGA	62	1933
882664	N/A	N/A	16551	16566	CATAATCCAGTATCTG	82	1934
882688	N/A	N/A	16767	16782	TAGTCGACAGCTAAAG	54	1935
882712	N/A	N/A	17001	17016	GTAGAAGCCCACAAGA	104	1936
882736	N/A	N/A	17404	17419	AATACGACAACTTTCC	50	1937
882760	N/A	N/A	17664	17679	TTGAAAGATTGAGCCT	97	1938
882784	N/A	N/A	17918	17933	GCATGCAAGCCCGTTA	101	1939
882808	N/A	N/A	18183	18198	TTGTTAACAATGTATC	53	1940
882831	N/A	N/A	18715	18730	ACTCATAGGTGTACAC	55	1941

882855	N/A	N/A	19126	19141	GTCTGAGGGAATCTGC	51	1942
882878	N/A	N/A	19384	19399	TTAAACAGCACTCAGA	67	1943

Table 28

Percent control of human IRF4 mRNA with 3-10-3 cEt gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	20	195
690521	4224	4239	22341	22356	GTAAATGAGTCGGTCA	21	1944
881090	170	185	5197	5212	CCGCAGCTCACC GCGC	64	1945
881113	488	503	6967	6982	CTGTACACTTTGTACG	66	1946
881136	837	852	10902	10917	GGCAGACCTTATGCTT	79	1947
881160	1071	1086	13624	13639	GGCCATCCAGAGGACC	75	1948
881184	1271	1286	17064	17079	AAGCATAGAGTCACCT	64	1949
881208	1461	1476	19578	19593	TTGAATAGAGGAATGG	58	1950
881232	1886	1901	20003	20018	GTCTACAGAACACAAG	76	1951
881256	1984	1999	20101	20116	TTCCAGCAAGACCTAA	73	1952
881280	2152	2167	20269	20284	GCAAGTGTCTTCCACA	23	1953
881304	2312	2327	20429	20444	AAGTTTACTAACTGGC	37	1954
881328	2462	2477	20579	20594	CGAAGAATTTTAGCAT	42	1955
881352	2546	2561	20663	20678	AGGGAACAGATAGTTA	66	1956
881376	2774	2789	20891	20906	TAATTTTAAGGCCCTG	61	1957
881400	2845	2860	20962	20977	AGTGATAGGTATACTT	61	1958
881424	2962	2977	21079	21094	AGCTACGCAATCTTCT	53	1959
881448	3250	3265	21367	21382	ACTTTTAGAGAGGAGA	36	1960
881472	3394	3409	21511	21526	ACGAGGTAAATCTTCA	39	1961
881496	3480	3495	21597	21612	TACATATCCATGTTGC	26	1962
881519	3564	3579	21681	21696	CCTTAGGATAATATAC	77	1963
881543	3787	3802	21904	21919	CCACTGTTAAAGCAGC	34	1964
881567	3983	3998	22100	22115	AATGAGGAAGCCGTTT	53	1965
881610	4384	4399	22501	22516	AATACTGTAAGGGCTG	36	1966
881634	4506	4521	22623	22638	CCAAGAGGTGCGAGTA	67	1967
881658	4591	4606	22708	22723	GAAGTTTACACTGGAT	35	1968
881682	4802	4817	22919	22934	ATCAGTCTCAAAAACG	59	1969
881706	4989	5004	23106	23121	ACACGGGAATTTCCAT	44	1970
881730	5189	5204	23306	23321	ACCTCAGTTTGTGAAG	61	1971
881754	5248	5263	23365	23380	TTGCAGAGCAATTTAC	50	1972
881778	N/A	N/A	18814	18829	CATCAATCATGATATT	75	1973
881823	N/A	N/A	4304	4319	GCTCGGAGCGACCCAA	92	1974

881846	N/A	N/A	4543	4558	CCGAATAGGACCCCTA	68	1975
881870	N/A	N/A	4920	4935	GGCCGGCCCGGGCGCA	99	1976
881894	N/A	N/A	5566	5581	CAGGACCCGGCTCCCG	86	1977
881917	N/A	N/A	5752	5767	CGGACGCACGGAGAGG	72	1978
881938	N/A	N/A	5982	5997	AGGGAGACAGCTCTAG	75	1979
881962	N/A	N/A	6290	6305	GTATTTATAACCGGTA	33	1980
881984	N/A	N/A	7014	7029	CAAATTCAGGAGAGCC	81	1981
882008	N/A	N/A	7247	7262	ACATATTCAATGCACC	53	1982
882032	N/A	N/A	7578	7593	TGACATAAAGGACCCC	52	1983
882056	N/A	N/A	8032	8047	AGCCATAGCAAATGGC	95	1984
882080	N/A	N/A	8302	8317	CTTTTACCCACCAAAG	82	1985
882103	N/A	N/A	8481	8496	TTAGACTGACAGCCGA	47	1986
882127	N/A	N/A	9278	9293	CAATTAGCTCTTCTAT	86	1987
882150	N/A	N/A	9471	9486	TTAAATAAGATCCCAC	77	1988
882173	N/A	N/A	9835	9850	CTAGATTCTCCCTGCA	66	1989
882196	N/A	N/A	10110	10125	AACCAGCCCTTGCTGC	79	1990
882220	N/A	N/A	10237	10252	CTTTACACAGTTCTAA	113	1991
882244	N/A	N/A	10554	10569	ACTGACTAACAGGGAG	51	1992
882268	N/A	N/A	11021	11036	AGCAAGTGCTAAAGT	38	1993
882292	N/A	N/A	11271	11286	TCCAAGCAATTATTCC	88	1994
882316	N/A	N/A	11534	11549	ATAGTAGGTAAGATCT	113	1995
882340	N/A	N/A	11800	11815	TAGAAAGAGCTGGTAG	91	1996
882364	N/A	N/A	12075	12090	CCCCAAAGAGAGTGGG	111	1997
882388	N/A	N/A	12372	12387	GCCCATGAGTTGAAAG	68	1998
882411	N/A	N/A	12762	12777	ATATAGAATTAGGTGC	84	1999
882434	N/A	N/A	13113	13128	AGGAACAAGTGTATCT	54	2000
882502	N/A	N/A	14254	14269	ACAGAGCCAACTTATA	94	2001
882525	N/A	N/A	14652	14667	ACCCAGAAGTACGAGC	79	2002
882548	N/A	N/A	15218	15233	CCCATGAACACCATGC	68	2003
882572	N/A	N/A	15635	15650	GCCAAGACCAGCTCTT	70	2004
882595	N/A	N/A	15872	15887	CTACACCTACACAGGC	84	2005
882618	N/A	N/A	16132	16147	CGCTACAGCTTCTGCA	80	2006
882642	N/A	N/A	16281	16296	ATACAAAACGGACTGG	85	2007
882665	N/A	N/A	16553	16568	CACATAATCCAGTATC	57	2008
882689	N/A	N/A	16773	16788	AGGAACTAGTCGACAG	60	2009
882713	N/A	N/A	17133	17148	TGTAAGTGAAGACTCA	102	2010
882737	N/A	N/A	17405	17420	AAATACGACAACCTTTC	79	2011
882761	N/A	N/A	17676	17691	TGCTTGAATTCCTTGA	33	2012
882785	N/A	N/A	17923	17938	GCTCAGCATGCAAGCC	100	2013
882809	N/A	N/A	18225	18240	GCTTATCAATGCCAAG	60	2014
882832	N/A	N/A	18716	18731	AACTCATAGGTGTACA	39	2015

882856	N/A	N/A	19154	19169	TCAAGTAAAGTGATCA	52	2016
882879	N/A	N/A	19387	19402	CTATTAAACAGCACTC	82	2017
882890	N/A	N/A	3949	3964	GTGGGAGTCGGAGCTC	83	2018
882906	N/A	N/A	13375	13390	GCCAAGGACACCACCT	102	2019
882908	N/A	N/A	14061	14076	GTATTTGTCGAGATCA	41	2020

Table 29

Percent control of human IRF4 mRNA with 3-10-3 cEt gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	33	195
690522	4228	4243	22345	22360	AGTTGTAAATGAGTCG	15	2021
881091	186	201	5213	5228	GCGGAGCTTCCCGTTG	67	2022
881114	495	510	6974	6989	AACAATCCTGTACACT	78	2023
881161	1088	1103	13641	13656	GCATAGAGCCCGTCGG	50	2024
881185	1272	1287	17065	17080	AAAGCATAGAGTCACC	66	2025
881209	1532	1547	19649	19664	CCGTATCCCCGTATCA	65	2026
881233	1891	1906	20008	20023	TGGCAGTCTACAGAAC	122	2027
881257	2001	2016	20118	20133	GGCAAGTTTTCTCTGT	64	2028
881281	2154	2169	20271	20286	CAGCAAGTGTCTTCCA	36	2029
881305	2313	2328	20430	20445	GAAGTTTACTAACTGG	43	2030
881329	2463	2478	20580	20595	GCGAAGAATTTTAGCA	88	2031
881353	2547	2562	20664	20679	AAGGGAACAGATAGTT	80	2032
881377	2775	2790	20892	20907	GTAATTTTAAGGCCCT	45	2033
881401	2846	2861	20963	20978	AAGTGATAGGTATACT	50	2034
881425	2965	2980	21082	21097	GAGAGCTACGCAATCT	43	2035
881449	3251	3266	21368	21383	CACTTTTAGAGAGGAG	38	2036
881473	3395	3410	21512	21527	AACGAGGTAAATCTTC	49	2037
881497	3484	3499	21601	21616	CCAATACATATCCATG	40	2038
881520	3566	3581	21683	21698	TCCCTTAGGATAATAT	52	2039
881544	3788	3803	21905	21920	TCCACTGTAAAGCAG	45	2040
881568	3984	3999	22101	22116	GAATGAGGAAGCCGTT	61	2041
881611	4385	4400	22502	22517	CAATACTGTAAGGGCT	44	2042
881635	4507	4522	22624	22639	GCCAAGAGGTGCGAGT	65	2043
881659	4592	4607	22709	22724	GGAAGTTTACACTGGA	15	2044
881683	4808	4823	22925	22940	ATCGAGATCAGTCTCA	24	2045
881707	4991	5006	23108	23123	CAACACGGAATTTCC	45	2046
881731	5191	5206	23308	23323	CTACCTCAGTTTGTGA	59	2047
881755	N/A	N/A	18767	18782	CTAAACTCCTAAGTAC	86	2048

881779	N/A	N/A	18827	18842	GCTGAATGCTCTCCAT	48	2049
881802	N/A	N/A	3965	3980	GCTCAGCGCAGATGGG	102	2050
881824	N/A	N/A	4310	4325	CGCAAGGCTCGGAGCG	90	2051
881847	N/A	N/A	4544	4559	CCCGAATAGGACCCCT	60	2052
881871	N/A	N/A	4932	4947	AGGCACCTTCGCGGCC	82	2053
881918	N/A	N/A	5754	5769	CGCGGACGCACGGAGA	81	2054
881939	N/A	N/A	5995	6010	CGCGCAAAGGGCAAGG	66	2055
881963	N/A	N/A	6292	6307	GGGTATTTATAACCGG	41	2056
881985	N/A	N/A	7032	7047	TGCCTCTGTTAGGTGA	66	2057
882009	N/A	N/A	7268	7283	TTGAAAGACTAACTGG	80	2058
882033	N/A	N/A	7580	7595	TGTGACATAAAGGACC	73	2059
882057	N/A	N/A	8040	8055	GTTGGAGCAGCCATAG	69	2060
882081	N/A	N/A	8329	8344	CAAAAGTACCACAGGG	60	2061
882104	N/A	N/A	8484	8499	TTATTAGACTGACAGC	63	2062
882128	N/A	N/A	9279	9294	GCAATTAGCTCTTCTA	79	2063
882151	N/A	N/A	9525	9540	CTATATAAAAAGTGGG	84	2064
882174	N/A	N/A	9837	9852	TGCTAGATTCTCCCTG	67	2065
882197	N/A	N/A	10114	10129	TGGAAACCAGCCCTTG	52	2066
882221	N/A	N/A	10250	10265	ACCTACTCCATCACTT	103	2067
882245	N/A	N/A	10559	10574	CTGTAAGTACTGACTAACA	77	2068
882269	N/A	N/A	11022	11037	AAGCAAGTGTCTAAAG	71	2069
882293	N/A	N/A	11278	11293	CTACACTTCCAAGCAA	105	2070
882317	N/A	N/A	11535	11550	TATAGTAGGTAAGATC	87	2071
882341	N/A	N/A	11801	11816	CTAGAAAGAGCTGGTA	85	2072
882365	N/A	N/A	12087	12102	TCAGACAGTGC GCCC	74	2073
882389	N/A	N/A	12379	12394	AAATATCGCCCATGAG	61	2074
882412	N/A	N/A	12763	12778	TATATAGAATTAGGTG	116	2075
882435	N/A	N/A	13115	13130	TAAGGAACAAGTGTAT	82	2076
882458	N/A	N/A	13393	13408	CCGGAGTCAGTGCTGG	107	2077
882480	N/A	N/A	14062	14077	CGTATTTGTCGAGATC	50	2078
882503	N/A	N/A	14256	14271	TCACAGAGCCAACTTA	112	2079
882526	N/A	N/A	14656	14671	TTACACCCAGAAGTAC	95	2080
882549	N/A	N/A	15312	15327	GCCCATGTGAGCTCTT	50	2081
882573	N/A	N/A	15704	15719	GAACACTTTGAGGTGA	86	2082
882596	N/A	N/A	15874	15889	GACTACACCTACACAG	68	2083
882619	N/A	N/A	16135	16150	AGCCGCTACAGCTTCT	108	2084
882643	N/A	N/A	16282	16297	GATACAAAACG GACTG	56	2085
882666	N/A	N/A	16556	16571	GCCACATAATCCAGT	78	2086
882690	N/A	N/A	16774	16789	GAGGAACTAGTCGACA	61	2087
882714	N/A	N/A	17139	17154	TAGGAGTGTAAGT GAG	63	2088
882738	N/A	N/A	17406	17421	GAAATACGACA ACTTT	78	2089

882762	N/A	N/A	17693	17708	TACGAGAGGGTCTGAT	100	2090
882786	N/A	N/A	17936	17951	TTTACCTGGTATTGCT	62	2091
882810	N/A	N/A	18226	18241	TGCTTATCAATGCCAA	30	2092
882833	N/A	N/A	18717	18732	GAAGTCATAGGTGTAC	33	2093
882880	N/A	N/A	19389	19404	CACTATTAAACAGCAC	81	2094
882916	N/A	N/A	19155	19170	ATCAAGTAAAGTGATC	71	2095

Table 30

Percent control of human IRF4 mRNA with 3-10-3 cEt gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	29	195
690523	4230	4245	22347	22362	TCAGTTGTAAATGAGT	28	2096
881092	187	202	5214	5229	GGCGGAGCTTCCCGTT	74	2097
881115	498	513	6977	6992	AGGAACAATCCTGTAC	84	2098
881162	1089	1104	13642	13657	CGCATAGAGCCCGTCG	47	2099
881186	1273	1288	17066	17081	CAAAGCATAGAGTCAC	64	2100
881210	1534	1549	19651	19666	CCCCGTATCCCCGTAT	55	2101
881234	1896	1911	20013	20028	AATGATGGCAGTCTAC	67	2102
881258	2014	2029	20131	20146	GTCAATACTGAAAGGC	34	2103
881282	2155	2170	20272	20287	TCAGCAAGTGTCTTCC	34	2104
881306	2316	2331	20433	20448	TAGGAAGTTTACTAAC	64	2105
881330	2464	2479	20581	20596	TGCGAAGAATTTTAGC	59	2106
881354	2548	2563	20665	20680	GAAGGGAACAGATAGT	83	2107
881378	2776	2791	20893	20908	AGTAATTTTAAGGCC	40	2108
881402	2847	2862	20964	20979	TAAGTGATAGGTATAC	40	2109
881426	2972	2987	21089	21104	CACATTTGAGAGCTAC	26	2110
881450	3252	3267	21369	21384	ACACTTTTAGAGAGGA	37	2111
881474	3396	3411	21513	21528	GAACGAGGTAAATCTT	44	2112
881498	3485	3500	21602	21617	CCCAATACATATCCAT	26	2113
881521	3600	3615	21717	21732	CGTGAAACAGCAGTTC	60	2114
881545	3789	3804	21906	21921	CTCCACTGTTAAAGCA	48	2115
881569	3986	4001	22103	22118	AGGAATGAGGAAGCCG	44	2116
881612	4387	4402	22504	22519	AACAATACTGTAAGGG	49	2117
881636	4508	4523	22625	22640	AGCCAAGAGGTGCGAG	62	2118
881660	4593	4608	22710	22725	CGGAAGTTTACACTGG	15	2119
881684	4809	4824	22926	22941	CATCGAGATCAGTCTC	35	2120
881708	4993	5008	23110	23125	AGCAACACGGGAATTT	43	2121
881732	5197	5212	23314	23329	CATTATCTACCTCAGT	65	2122

881756	N/A	N/A	18768	18783	GCTAAACTCCTAAGTA	70	2123
881780	N/A	N/A	18828	18843	AGCTGAATGCTCTCCA	22	2124
881803	N/A	N/A	3993	4008	GGCCTTGGAGCCCAA	80	2125
881825	N/A	N/A	4311	4326	ACGCAAGGCTCGGAGC	79	2126
881848	N/A	N/A	4545	4560	CCCCGAATAGGACCCC	44	2127
881872	N/A	N/A	4937	4952	GAAGAAGGCACCTTCG	75	2128
881896	N/A	N/A	5646	5661	GCAAAACCCCTCAAGC	80	2129
881919	N/A	N/A	5755	5770	GCGCGGACGCACGGAG	98	2130
881940	N/A	N/A	6001	6016	TGCACTCGCGCAAAGG	72	2131
881964	N/A	N/A	6315	6330	GCCAAGTTGAAGACAC	43	2132
881986	N/A	N/A	7057	7072	AGTTAAGGTGCCTCAA	101	2133
882010	N/A	N/A	7304	7319	TAACAAGTTATCCAGT	88	2134
882034	N/A	N/A	7593	7608	TGCGAATGTGCCTTGT	57	2135
882058	N/A	N/A	8095	8110	CAGCACCGTGTGGAAA	49	2136
882082	N/A	N/A	8335	8350	TGGCACCAAAAGTACC	66	2137
882105	N/A	N/A	8485	8500	CTTATTAGACTGACAG	59	2138
882129	N/A	N/A	9287	9302	CCACATTAGCAATTAG	81	2139
882152	N/A	N/A	9550	9565	TTTATGAGCTTCCACA	46	2140
882175	N/A	N/A	9843	9858	CCGCATTGCTAGATTC	28	2141
882198	N/A	N/A	10115	10130	TTGGAAACCAGCCCTT	61	2142
882222	N/A	N/A	10253	10268	TCTACCTACTCCATCA	53	2143
882246	N/A	N/A	10580	10595	AGGAAACTTGGAGCGC	23	2144
882270	N/A	N/A	11025	11040	GCAAAGCAAGTGTCTA	57	2145
882294	N/A	N/A	11313	11328	GAAGGATGATCAGCTT	74	2146
882318	N/A	N/A	11536	11551	TTATAGTAGGTAAGAT	98	2147
882342	N/A	N/A	11819	11834	TGCAAGCCTCATTCAC	58	2148
882366	N/A	N/A	12089	12104	AGTCAGACAGTGCGCC	90	2149
882390	N/A	N/A	12380	12395	AAAATATCGCCCATGA	59	2150
882413	N/A	N/A	12827	12842	TGACATCATTTAGGTA	46	2151
882436	N/A	N/A	13133	13148	GGCCACCGACTCTTTT	87	2152
882459	N/A	N/A	13780	13795	ATAACGAGGTGCCTTA	87	2153
882481	N/A	N/A	14077	14092	CGCCACATCAGCAGAC	88	2154
882527	N/A	N/A	14658	14673	ACTTACACCCAGAAGT	110	2155
882550	N/A	N/A	15328	15343	GGCCTTAGCCTTCCTG	83	2156
882574	N/A	N/A	15765	15780	GCAGAAGCTGGTTGGC	42	2157
882597	N/A	N/A	15877	15892	TGAGACTACACCTACA	81	2158
882620	N/A	N/A	16140	16155	ACAGGAGCCGCTACAG	69	2159
882644	N/A	N/A	16284	16299	AAGATACAAAACGGAC	61	2160
882667	N/A	N/A	16568	16583	CCTCACTACAGAGCCC	76	2161
882691	N/A	N/A	16778	16793	TCAAGAGGAACTAGTC	76	2162
882715	N/A	N/A	17140	17155	GTAGGAGTGTAAGTGA	59	2163

882739	N/A	N/A	17407	17422	GGAAATACGACAACTT	37	2164
882763	N/A	N/A	17694	17709	TTACGAGAGGGTCTGA	49	2165
882787	N/A	N/A	17937	17952	TTTTACCTGGTATTGC	102	2166
882811	N/A	N/A	18247	18262	GATCATCAACTTCTTA	53	2167
882834	N/A	N/A	18719	18734	TGGAACATCATAGGTGT	38	2168
882857	N/A	N/A	19164	19179	CTGCATCAAATCAAGT	53	2169
882881	N/A	N/A	19390	19405	TCACTATTAAACAGCA	84	2170
882910	N/A	N/A	14263	14278	GTTCATATCACAGAGC	55	2171

Table 31

Percent control of human IRF4 mRNA with 3-10-3 cEt gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	23	195
690526	4234	4249	22351	22366	GGTTTCAGTTGTAAAT	42	2172
881093	193	208	5220	5235	GCCACTGGCGGAGCTT	77	2173
881116	554	569	7872	7887	ATGGACATCTGCGGGT	50	2174
881163	1090	1105	13643	13658	TCGCATAGAGCCCGTC	43	2175
881187	1274	1289	17067	17082	CCAAAGCATAGAGTCA	42	2176
881211	1539	1554	19656	19671	CAAGACCCCGTATCCC	56	2177
881235	1897	1912	20014	20029	CAATGATGGCAGTCTA	60	2178
881259	2015	2030	20132	20147	TGTCAATACTGAAAGG	64	2179
881283	2156	2171	20273	20288	CTCAGCAAGTGTCTTC	55	2180
881307	2317	2332	20434	20449	ATAGGAAGTTTACTAA	87	2181
881331	2465	2480	20582	20597	ATGCGAAGAATTTTATAG	79	2182
881355	2583	2598	20700	20715	GGACAGCCAAACAAAC	93	2183
881379	2778	2793	20895	20910	CAAGTAATTTTAAGGC	59	2184
881403	2849	2864	20966	20981	TGTAAGTGATAGGTAT	47	2185
881427	2973	2988	21090	21105	ACACATTTGAGAGCTA	31	2186
881451	3254	3269	21371	21386	GGACACTTTTAGAGAG	38	2187
881475	3397	3412	21514	21529	AGAACGAGGTAAATCT	60	2188
881499	3486	3501	21603	21618	GCCCAATACATATCCA	42	2189
881522	3601	3616	21718	21733	CCGTGAAACAGCAGTT	44	2190
881546	3791	3806	21908	21923	AGCTCCACTGTTAAAG	56	2191
881570	3999	4014	22116	22131	CTTTATCAAGACAAGG	44	2192
881613	4388	4403	22505	22520	TAACAATACTGTAAGG	55	2193
881637	4523	4538	22640	22655	GCGGAGCATCAACAAA	70	2194
881661	4594	4609	22711	22726	ACGGAAGTTTACTACTG	23	2195
881685	4810	4825	22927	22942	GCATCGAGATCAGTCT	43	2196

881709	4994	5009	23111	23126	AAGCAACACGGGAATT	78	2197
881733	5198	5213	23315	23330	GCATTATCTACCTCAG	31	2198
881757	N/A	N/A	18769	18784	AGCTAAACTCCTAAGT	85	2199
881781	N/A	N/A	18832	18847	GGCAAGCTGAATGCTC	71	2200
881804	N/A	N/A	4002	4017	AAGGAGGCGGGCCTTG	98	2201
881826	N/A	N/A	4315	4330	CCGCACGCAAGGCTCG	84	2202
881849	N/A	N/A	4563	4578	TCGCATCCAGACCCTT	72	2203
881873	N/A	N/A	4939	4954	CGGAAGAAGGCACCTT	112	2204
881897	N/A	N/A	5647	5662	CGCAAAACCCCTCAAG	81	2205
881920	N/A	N/A	5760	5775	CACAGGCGCGGACGCA	86	2206
881941	N/A	N/A	6021	6036	GTAACAACGACACACG	41	2207
881965	N/A	N/A	6325	6340	CCCTATCACTGCCAAG	62	2208
881987	N/A	N/A	7065	7080	CAGAATGAAGTTAAGG	50	2209
882011	N/A	N/A	7325	7340	GACTATTAGATAAGTA	71	2210
882035	N/A	N/A	7602	7617	CAGATGGCATGCGAAT	65	2211
882059	N/A	N/A	8097	8112	GGCAGCACCGTGTGGA	47	2212
882083	N/A	N/A	8344	8359	GGCTAAACCTGGCACC	60	2213
882106	N/A	N/A	8486	8501	CCTTATTAGACTGACA	52	2214
882130	N/A	N/A	9288	9303	GCCACATTAGCAATTA	92	2215
882153	N/A	N/A	9557	9572	CTTATTATTTATGAGC	63	2216
882176	N/A	N/A	9845	9860	TACCGCATTGCTAGAT	77	2217
882199	N/A	N/A	10119	10134	CATATTGGAAACCAGC	27	2218
882223	N/A	N/A	10264	10279	CAAGACAGGTCTCTAC	66	2219
882247	N/A	N/A	10581	10596	AAGGAACTTGGAGCG	41	2220
882271	N/A	N/A	11026	11041	AGCAAAGCAAGTGTCT	42	2221
882295	N/A	N/A	11321	11336	TCAACCTGGAAGGATG	70	2222
882319	N/A	N/A	11537	11552	TTTATAGTAGGTAAGA	94	2223
882343	N/A	N/A	11827	11842	AAAAAAGGTGCAAGCC	93	2224
882367	N/A	N/A	12093	12108	AGCGAGTCAGACAGTG	84	2225
882391	N/A	N/A	12382	12397	TTAAATATCGCCCAT	68	2226
882414	N/A	N/A	12871	12886	AGCAAGTCGGTCCACA	46	2227
882437	N/A	N/A	13154	13169	CAGCATATTACAAACG	42	2228
882460	N/A	N/A	13781	13796	GATAACGAGGTGCCTT	82	2229
882504	N/A	N/A	14295	14310	ACTCACTGGTTCTGAA	86	2230
882528	N/A	N/A	14661	14676	GTCACCTACACCCAGA	48	2231
882551	N/A	N/A	15359	15374	GTCCAGAGTCTTCAGA	94	2232
882575	N/A	N/A	15772	15787	TAATTATGCAGAAGCT	103	2233
882598	N/A	N/A	15879	15894	TCTGAGACTACACCTA	73	2234
882621	N/A	N/A	16146	16161	GTTGACACAGGAGCCG	47	2235
882645	N/A	N/A	16285	16300	AAAGATACAAAACGGA	62	2236
882668	N/A	N/A	16581	16596	TAAAACCTCATCCCCT	126	2237

882692	N/A	N/A	16779	16794	TTCAAGAGGAACTAGT	94	2238
882716	N/A	N/A	17146	17161	ACTATGGTAGGAGTGT	75	2239
882740	N/A	N/A	17409	17424	ATGGAAATACGACAAC	65	2240
882764	N/A	N/A	17696	17711	CATTACGAGAGGGTCT	56	2241
882788	N/A	N/A	17940	17955	AACTTTTACCTGGTAT	72	2242
882812	N/A	N/A	18251	18266	GGCCGATCATCAACTT	93	2243
882835	N/A	N/A	18720	18735	GTGGAACATCATAGGTG	47	2244
882858	N/A	N/A	19173	19188	TAACTAAACTGCATC	90	2245
882882	N/A	N/A	19391	19406	CTCACTATTAAACAGC	76	2246
882909	N/A	N/A	14080	14095	AGCCGCCACATCAGCA	79	2247

Table 32

Percent control of human IRF4 mRNA with 3-10-3 cEt gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	26	195
881094	194	209	5221	5236	AGCCACTGGCGGAGCT	62	2248
881117	558	573	7876	7891	GCTCATGGACATCTGC	61	2249
881164	1097	1112	13650	13665	AGTCTTTTCGCATAGA	55	2250
881188	1276	1291	17069	17084	CTCCAAAGCATAGAGT	77	2251
881212	1685	1700	19802	19817	AATCACTTGTCTTGGG	40	2252
881236	1898	1913	20015	20030	TCAATGATGGCAGTCT	46	2253
881260	2021	2036	20138	20153	AGTCAGTGTCAATACT	53	2254
881284	2157	2172	20274	20289	ACTCAGCAAGTGTCTT	53	2255
881308	2341	2356	20458	20473	GCTCATGTTTTTTGAC	44	2256
881332	2469	2484	20586	20601	CTTTATGCGAAGAATT	70	2257
881356	2587	2602	20704	20719	CGCTGGACAGCCAAAC	59	2258
881380	2780	2795	20897	20912	GCCAAGTAATTTTAAG	65	2259
881404	2850	2865	20967	20982	ATGTAAGTGATAGGTA	30	2260
881428	2995	3010	21112	21127	TATCCATTAGAAAAGC	37	2261
881452	3255	3270	21372	21387	TGGACACTTTTAGAGA	28	2262
881476	3398	3413	21515	21530	CAGAACGAGGTAAATC	41	2263
881500	3487	3502	21604	21619	TGCCCAATACATATCC	41	2264
881523	3611	3626	21728	21743	GGTAAGGGCCCCGTGA	67	2265
881547	3835	3850	21952	21967	AAGGAGGTAGTGGCCC	53	2266
881571	4009	4024	22126	22141	GCCAATTCCACTTTAT	36	2267
881590	4239	4254	22356	22371	TCCTAGGTTTCAGTTG	52	2268
881614	4389	4404	22506	22521	GTAACAATACTGTAAG	45	2269
881638	4524	4539	22641	22656	GGCGGAGCATCAACAA	40	2270

881662	4595	4610	22712	22727	AACGGAAGTTTACACT	41	2271
881686	4812	4827	22929	22944	CTGCATCGAGATCAGT	48	2272
881710	4996	5011	23113	23128	TGAAGCAACACGGGAA	40	2273
881734	5199	5214	23316	23331	AGCATTATCTACCTCA	22	2274
881758	N/A	N/A	18770	18785	AAGCTAAACTCCTAAG	85	2275
881782	N/A	N/A	18837	18852	TCTAAGGCAAGCTGAA	79	2276
881805	N/A	N/A	4003	4018	CAAGGAGGCGGGCCTT	102	2277
881827	N/A	N/A	4325	4340	GGCTAGGCCACCGCAC	72	2278
881850	N/A	N/A	4633	4648	GAGGACCTCGCCTGCG	102	2279
881874	N/A	N/A	4940	4955	CCGGAAGAAGGCACCT	83	2280
881898	N/A	N/A	5648	5663	GCGCAAAACCCCTCAA	78	2281
881921	N/A	N/A	5763	5778	CGGCACAGGCGCGGAC	96	2282
881942	N/A	N/A	6047	6062	GTAAACTGCCTTAGGG	56	2283
881966	N/A	N/A	6369	6384	AAAGACCCAGCTATG	77	2284
881988	N/A	N/A	7068	7083	GCTCAGAATGAAGTTA	52	2285
882012	N/A	N/A	7327	7342	AAGACTATTAGATAAG	78	2286
882036	N/A	N/A	7629	7644	GTACAGGACAGGTAAA	75	2287
882060	N/A	N/A	8103	8118	ACCAATGGCAGCACCG	39	2288
882084	N/A	N/A	8347	8362	TATGGCTAAACCTGGC	57	2289
882107	N/A	N/A	8487	8502	CCCTTATTAGACTGAC	33	2290
882131	N/A	N/A	9312	9327	GACCAGGATTCGCCAT	77	2291
882177	N/A	N/A	9850	9865	TGAGTTACCGCATTGC	20	2292
882200	N/A	N/A	10121	10136	ACCATATTGGAAACCA	26	2293
882224	N/A	N/A	10278	10293	TGTTACCGATGCTTCA	51	2294
882248	N/A	N/A	10606	10621	GAAACGAGCCAGTGCA	48	2295
882272	N/A	N/A	11027	11042	GAGCAAAGCAAGTGTC	58	2296
882296	N/A	N/A	11323	11338	GCTCAACCTGGAAGGA	75	2297
882320	N/A	N/A	11541	11556	CTTCTTTATAGTAGGT	80	2298
882344	N/A	N/A	11843	11858	TCACGAGCACCTCAGA	64	2299
882368	N/A	N/A	12111	12126	TTCAACACACTGTCTG	131	2300
882392	N/A	N/A	12386	12401	CTCTTTAAATATCGC	44	2301
882415	N/A	N/A	12872	12887	AAGCAAGTCGGTCCAC	68	2302
882438	N/A	N/A	13161	13176	TCTAAACCAGCATATT	67	2303
882482	N/A	N/A	14085	14100	AAAAGAGCCGCCACAT	84	2304
882505	N/A	N/A	14321	14336	CATGAAATCCAAGGTA	51	2305
882529	N/A	N/A	14671	14686	AAAAACTTGGGTCCT	119	2306
882552	N/A	N/A	15366	15381	CACCAAGGTCCAGAGT	80	2307
882599	N/A	N/A	15893	15908	TCACACTGCCGTGATC	78	2308
882622	N/A	N/A	16151	16166	AACGAGTTGACACAGG	45	2309
882646	N/A	N/A	16314	16329	GTACATCCTGAAGCCA	74	2310
882669	N/A	N/A	16612	16627	ATCAGAATGTTTCGAC	54	2311

882693	N/A	N/A	16807	16822	CCCCAGGGCCCTCGGT	82	2312
882717	N/A	N/A	17147	17162	CACTATGGTAGGAGTG	112	2313
882741	N/A	N/A	17448	17463	GGGCAACTTTAACCAT	92	2314
882765	N/A	N/A	17699	17714	GAACATTACGAGAGGG	30	2315
882789	N/A	N/A	17945	17960	GGTGTAACTTTTACCT	89	2316
882813	N/A	N/A	18558	18573	GATCATCAACTTCTTT	57	2317
882836	N/A	N/A	18760	18775	CCTAAGTACCTGAAAT	89	2318
882859	N/A	N/A	19203	19218	TCAAATCGACTGCCAC	46	2319
882883	N/A	N/A	19392	19407	GCTCACTATTAAACAG	112	2320
882902	N/A	N/A	9579	9594	CAATAATCTCCCAGCA	63	2321
882907	N/A	N/A	13782	13797	AGATAACGAGGTGCCT	77	2322
882912	N/A	N/A	15773	15788	TTAATTATGCAGAAGC	87	2323

Table 33

Percent control of human IRF4 mRNA with 3-10-3 cEt gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	26	195
881095	217	232	5244	5259	TGCCGCTGTCGATCTG	68	2324
881118	559	574	7877	7892	GGCTCATGGACATCTG	64	2325
881165	1103	1118	13656	13671	TGGCACAGTCTTTTCG	72	2326
881189	1341	1356	19458	19473	GGCTAGCAGAGGTTCT	49	2327
881213	1717	1732	19834	19849	CGCTTTCACTAAAGTC	29	2328
881237	1900	1915	20017	20032	CATCAATGATGGCAGT	50	2329
881261	2025	2040	20142	20157	CTCTAGTCAGTGTCAA	41	2330
881285	2158	2173	20275	20290	CACTCAGCAAGTGTCT	50	2331
881309	2358	2373	20475	20490	TCCCATCCAAGAGTAG	67	2332
881333	2470	2485	20587	20602	TCTTTATGCGAAGAAT	58	2333
881357	2600	2615	20717	20732	CGCCATGGCTGATCGC	47	2334
881381	2817	2832	20934	20949	GTCTTTGGGATTCTAT	35	2335
881405	2851	2866	20968	20983	AATGTAAGTGATAGGT	20	2336
881429	3024	3039	21141	21156	TACTAGGTGCTTGTTG	51	2337
881453	3256	3271	21373	21388	GTGGACACTTTTAGAG	48	2338
881477	3400	3415	21517	21532	AGCAGAACGAGGTAAA	30	2339
881501	3500	3515	21617	21632	AAACACAGTCTGCTGC	65	2340
881524	3612	3627	21729	21744	AGGTAAGGGCCCCGTG	53	2341
881548	3836	3851	21953	21968	AAAGGAGGTAGTGGCC	79	2342
881572	4022	4037	22139	22154	TAAATTCTAGTTTGCC	32	2343
881591	4258	4273	22375	22390	CGCTCAGGACTCAGGG	45	2344

881615	4390	4405	22507	22522	GGTAACAATACTGTAA	41	2345
881639	4525	4540	22642	22657	TGGCGGAGCATCAACA	63	2346
881663	4596	4611	22713	22728	GAACGGAAGTTTACAC	33	2347
881687	4817	4832	22934	22949	TCCACCTGCATCGAGA	53	2348
881711	4997	5012	23114	23129	TTGAAGCAACACGGGA	39	2349
881735	5202	5217	23319	23334	CATAGCATTATCTACC	57	2350
881759	N/A	N/A	18772	18787	TTAAGCTAAACTCCTA	90	2351
881783	N/A	N/A	18840	18855	GCATCTAAGGCAAGCT	66	2352
881806	N/A	N/A	4006	4021	AGCCAAGGAGGCGGGC	101	2353
881828	N/A	N/A	4334	4349	CGCCAGGCCGGCTAGG	90	2354
881851	N/A	N/A	4636	4651	GCGGAGGACCTCGCCT	92	2355
881875	N/A	N/A	4942	4957	CCCCGGAAGAAGGCAC	64	2356
881899	N/A	N/A	5654	5669	ACGAACGCGCAAAACC	94	2357
881922	N/A	N/A	5769	5784	AGCCGCCGGCACAGGC	99	2358
881943	N/A	N/A	6048	6063	GGTAAACTGCCTTAGG	75	2359
881967	N/A	N/A	6371	6386	TGAAAGACCCCAGCTA	96	2360
881989	N/A	N/A	7080	7095	CTAGAAAGTGATGCTC	61	2361
882013	N/A	N/A	7332	7347	CACTAAAGACTATTAG	95	2362
882037	N/A	N/A	7631	7646	TTGTACAGGACAGGTA	72	2363
882061	N/A	N/A	8109	8124	ATCCACACCAATGGCA	66	2364
882108	N/A	N/A	8494	8509	AGGGAATCCCTTATTA	94	2365
882132	N/A	N/A	9317	9332	GGACAGACCAGGATTC	75	2366
882154	N/A	N/A	9580	9595	TCAATAATCTCCCAGC	45	2367
882178	N/A	N/A	9853	9868	GCCTGAGTTACCGCAT	30	2368
882201	N/A	N/A	10122	10137	TACCATATTGGAACCC	52	2369
882225	N/A	N/A	10283	10298	TTTACTGTTACCGATG	52	2370
882249	N/A	N/A	10608	10623	GAGAAACGAGCCAGTG	61	2371
882273	N/A	N/A	11048	11063	ATCTACTCCAGACCCC	73	2372
882297	N/A	N/A	11324	11339	GGCTCAACCTGGAAGG	71	2373
882321	N/A	N/A	11552	11567	CCTAGAGGTGCCTTCT	59	2374
882345	N/A	N/A	11846	11861	TACTCACGAGCACCTC	59	2375
882369	N/A	N/A	12114	12129	TGCTTCAACACACTGT	97	2376
882393	N/A	N/A	12432	12447	TAAACAAGATGAATCC	56	2377
882416	N/A	N/A	12875	12890	AAGAAGCAAGTCGGTC	45	2378
882439	N/A	N/A	13162	13177	GTCTAAACCAGCATAT	81	2379
882461	N/A	N/A	13783	13798	CAGATAACGAGGTGCC	70	2380
882483	N/A	N/A	14086	14101	GAAAAGAGCCGCCACA	93	2381
882506	N/A	N/A	14331	14346	GCTGAATTGTCATGAA	64	2382
882553	N/A	N/A	15369	15384	TGGCACCAAGGTCCAG	99	2383
882576	N/A	N/A	15776	15791	TCCTTAATTATGCAGA	56	2384
882600	N/A	N/A	15895	15910	ATTCACTGCCGTGA	66	2385

882623	N/A	N/A	16152	16167	AAACGAGTTGACACAG	80	2386
882670	N/A	N/A	16646	16661	CAATTTATGCCATGGA	38	2387
882694	N/A	N/A	16838	16853	TAGCATGTATGCATTC	48	2388
882718	N/A	N/A	17150	17165	AGCCACTATGGTAGGA	57	2389
882742	N/A	N/A	17471	17486	ATCTTAACCTGGAGAA	72	2390
882766	N/A	N/A	17703	17718	TAGAGAACATTACGAG	40	2391
882790	N/A	N/A	17976	17991	CTAGAACATGATGAGA	71	2392
882837	N/A	N/A	18921	18936	TTATACTGTCTGGTTA	56	2393
882860	N/A	N/A	19205	19220	TTTCAAATCGACTGCC	69	2394
882884	N/A	N/A	19400	19415	TGCAACTGGCTCACTA	83	2395
882900	N/A	N/A	8350	8365	TCATATGGCTAAACCT	51	2396
882911	N/A	N/A	14672	14687	CAAAAACCTGGGTCAC	80	2397
882914	N/A	N/A	16378	16393	GTAACCTTGACTTGAGA	51	2398
882915	N/A	N/A	18567	18582	AGCTGAGCTGATCATC	44	2399

Table 34

Percent control of human IRF4 mRNA with 3-10-3 cEt gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	24	195
881096	328	343	5355	5370	CCTTGAAGAGCGCGGC	76	2400
881119	594	609	7912	7927	GAGCGAAGGGTAAGGC	62	2401
881166	1121	1136	13674	13689	TCCCAGTAGATCCTGC	60	2402
881190	1354	1369	19471	19486	AATATAGTTGTCTGGC	50	2403
881214	1732	1747	19849	19864	GGGCAGTCAATTGGAC	75	2404
881238	1903	1918	20020	20035	GATCATCAATGATGGC	37	2405
881262	2033	2048	20150	20165	AGTCATCACTCTAGTC	47	2406
881286	2189	2204	20306	20321	GGCACGGCTTCAGTCA	25	2407
881310	2366	2381	20483	20498	CAAAAATGTCCCATCC	81	2408
881334	2471	2486	20588	20603	TTCTTTATGCGAAGAA	91	2409
881358	2609	2624	20726	20741	CTTTAGTGTGCGCCATG	71	2410
881382	2822	2837	20939	20954	TGGAGGTCTTTGGGAT	42	2411
881406	2882	2897	20999	21014	GTCTACTGCTGTACTT	48	2412
881430	3025	3040	21142	21157	TTACTAGGTGCTTGTT	50	2413
881454	3258	3273	21375	21390	TTGTGGACACTTTTAG	51	2414
881478	3401	3416	21518	21533	GAGCAGAACGAGGTAA	45	2415
881502	3502	3517	21619	21634	CGAAACACAGTCTGCT	47	2416
881525	3616	3631	21733	21748	TCACAGGTAAGGGCCC	53	2417
881549	3837	3852	21954	21969	GAAAGGAGGTAGTGGC	77	2418

881573	4023	4038	22140	22155	CTAAATTCTAGTTTGC	79	2419
881592	4276	4291	22393	22408	GACTAACTCTCCTGTT	83	2420
881616	4391	4406	22508	22523	TGGTAACAATACTGTA	35	2421
881640	4533	4548	22650	22665	GGCCTTCCTGGCGGAG	78	2422
881664	4598	4613	22715	22730	ATGAACGGAAGTTTAC	46	2423
881688	4828	4843	22945	22960	TCTCAAGGAGATCCAC	99	2424
881712	4998	5013	23115	23130	TTTGAAGCAACACGGG	53	2425
881736	5203	5218	23320	23335	GCATAGCATTATCTAC	49	2426
881760	N/A	N/A	18774	18789	ACTTAAGCTAAACTCC	79	2427
881784	N/A	N/A	18841	18856	AGCATCTAAGGCAAGC	43	2428
881807	N/A	N/A	4042	4057	CAGGAGCGCGGAGGGC	89	2429
881829	N/A	N/A	4367	4382	ACGACAGCTGCGGAGC	73	2430
881852	N/A	N/A	4638	4653	GCGCGGAGGACCTCGC	90	2431
881876	N/A	N/A	5008	5023	GACCACGAGGCCCCGG	69	2432
881900	N/A	N/A	5656	5671	GGACGAACGCGCAAAA	65	2433
881923	N/A	N/A	5773	5788	AAACAGCCGCCGGCAC	89	2434
881944	N/A	N/A	6117	6132	TCCCGGAGGAAGTCCC	70	2435
881968	N/A	N/A	6377	6392	GTAAACTGAAAGACCC	65	2436
881990	N/A	N/A	7152	7167	CATAACTCAGGCAAGG	64	2437
882014	N/A	N/A	7335	7350	ACTCACTAAAGACTAT	82	2438
882038	N/A	N/A	7645	7660	CTACAAGGTCTGAGTT	83	2439
882062	N/A	N/A	8116	8131	ACTTAAATCCACACC	93	2440
882085	N/A	N/A	8366	8381	TTTATGTAAAGCTTCG	25	2441
882109	N/A	N/A	8498	8513	CCTCAGGGAATCCCTT	70	2442
882133	N/A	N/A	9340	9355	GGAAAGAGCTTTGGTG	88	2443
882155	N/A	N/A	9581	9596	CTCAATAATCTCCCAG	47	2444
882179	N/A	N/A	9877	9892	GTAATAACTCAAAAG	101	2445
882202	N/A	N/A	10125	10140	CACTACCATATTGGAA	78	2446
882226	N/A	N/A	10284	10299	ATTTACTGTTACCGAT	71	2447
882250	N/A	N/A	10609	10624	GGAGAAACGAGCCAGT	53	2448
882274	N/A	N/A	11052	11067	CTACATCTACTCCAGA	78	2449
882298	N/A	N/A	11332	11347	TTATTTGTGGCTCAAC	82	2450
882322	N/A	N/A	11554	11569	AGCCTAGAGGTGCCTT	59	2451
882346	N/A	N/A	11859	11874	GGGCATCCTCAGTTAC	67	2452
882370	N/A	N/A	12138	12153	ACCCACATCACTGTCT	85	2453
882394	N/A	N/A	12456	12471	CTAAAACTGCGCTCTC	76	2454
882417	N/A	N/A	12878	12893	AGAAAGAAGCAAGTCG	63	2455
882440	N/A	N/A	13169	13184	TTAATCTGTCTAAACC	84	2456
882462	N/A	N/A	13784	13799	ACAGATAACGAGGTGC	70	2457
882484	N/A	N/A	14116	14131	TTCCAACCTTTATGAT	93	2458
882507	N/A	N/A	14335	14350	GTTCGCTGAATTGTCA	63	2459

882530	N/A	N/A	14674	14689	TACAAAAACTTGGGTC	91	2460
882554	N/A	N/A	15406	15421	TAGAAAGCCCTCACCT	95	2461
882577	N/A	N/A	15781	15796	GGGAATCCTTAATTAT	88	2462
882601	N/A	N/A	15898	15913	TACATTACACTGCCG	42	2463
882624	N/A	N/A	16154	16169	AGAAACGAGTTGACAC	85	2464
882647	N/A	N/A	16380	16395	CAGTAACTTGACTTGA	61	2465
882671	N/A	N/A	16647	16662	CCAATTTATGCCATGG	88	2466
882695	N/A	N/A	16857	16872	GAACATCTCAGATACA	58	2467
882719	N/A	N/A	17158	17173	GAACAGGAAGCCACTA	77	2468
882743	N/A	N/A	17481	17496	TCTTACAGCAATCTTA	68	2469
882767	N/A	N/A	17709	17724	CTATGCTAGAGAACAT	77	2470
882791	N/A	N/A	17977	17992	GCTAGAACATGATGAG	86	2471
882814	N/A	N/A	18570	18585	GATAGCTGAGCTGATC	68	2472
882838	N/A	N/A	18923	18938	ATTTATACTGTCTGGT	51	2473
882861	N/A	N/A	19211	19226	TGTTACTTTCAAATCG	52	2474
882885	N/A	N/A	19401	19416	CTGCAACTGGCTCACT	90	2475

Table 35

Percent control of human IRF4 mRNA with 3-10-3 cEt gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	12	195
881097	329	344	N/A	N/A	GCCTTGAAGAGCGCGG	91	2476
881120	613	628	N/A	N/A	TGTGAACCTGCTGGGC	98	2477
881167	1189	1204	13742	13757	CAAAGAGCTTGCAGGT	96	2478
881191	1355	1370	19472	19487	TAATATAGTTGTCTGG	60	2479
881215	1738	1753	19855	19870	GTAAGAGGGCAGTCAA	56	2480
881239	1910	1925	20027	20042	TCACAGTGATCATCAA	57	2481
881263	2040	2055	20157	20172	TACAAGCAGTCATCAC	71	2482
881287	2190	2205	20307	20322	AGGCACGGCTTCAGTC	51	2483
881311	2382	2397	20499	20514	TAGATTGTAGGACAGA	72	2484
881335	2472	2487	20589	20604	CTTCTTTATGCGAAGA	105	2485
881359	2610	2625	20727	20742	CCTTTAGTGTGCCAT	42	2486
881383	2824	2839	20941	20956	AGTGGAGGTCTTTGGG	45	2487
881407	2887	2902	21004	21019	CCCCAGTCTACTGCTG	53	2488
881431	3026	3041	21143	21158	CTTACTAGGTGCTTGT	62	2489
881455	3270	3285	21387	21402	AAACACCCCTTCTTGT	113	2490
881479	3404	3419	21521	21536	TCTGAGCAGAACGAGG	53	2491
881503	3503	3518	21620	21635	ACGAAACACAGTCTGC	48	2492

881526	3618	3633	21735	21750	GGTCACAGGTAAGGGC	75	2493
881550	3896	3911	22013	22028	TCATACCCTGGATCAC	57	2494
881574	4039	4054	22156	22171	GTCCACTGAGTACAAA	87	2495
881593	4278	4293	22395	22410	GCGACTAACTCTCCTG	30	2496
881617	4410	4425	22527	22542	AATACCTACCTGCCCT	85	2497
881641	4540	4555	22657	22672	CACAAGTGGCCTTCCT	55	2498
881665	4600	4615	22717	22732	CAATGAACGGAAGTTT	67	2499
881689	4837	4852	22954	22969	CTATCAGGATCTCAAG	91	2500
881713	5020	5035	23137	23152	TGTTAAGTCCCATCTG	75	2501
881737	5204	5219	23321	23336	AGCATAGCATTATCTA	66	2502
881761	N/A	N/A	18775	18790	GACTTAAGCTAAACTC	42	2503
881785	N/A	N/A	18842	18857	CAGCATCTAAGGCAAG	46	2504
881830	N/A	N/A	4368	4383	GACGACAGCTGCGGAG	55	2505
881853	N/A	N/A	4640	4655	ACGCGCGGAGGACCTC	87	2506
881877	N/A	N/A	5011	5026	AGTGACCACGAGGCCC	85	2507
881901	N/A	N/A	5657	5672	CGGACGAACGCGCAAA	61	2508
881924	N/A	N/A	5775	5790	GAAAACAGCCGCCGGC	74	2509
881945	N/A	N/A	6122	6137	CAAATTCCCGGAGGAA	95	2510
881969	N/A	N/A	6378	6393	CGTAAACTGAAAGACC	52	2511
881991	N/A	N/A	7153	7168	ACATAACTCAGGCAAG	99	2512
882015	N/A	N/A	7345	7360	CAAAATAGTCACTCAC	103	2513
882039	N/A	N/A	7646	7661	TCTACAAGGTCTGAGT	43	2514
882063	N/A	N/A	8119	8134	CCAACTTAAAATCCAC	91	2515
882086	N/A	N/A	8380	8395	GATACTTGTA CTGTTT	22	2516
882110	N/A	N/A	8546	8561	AAGAAGCACTGGCATT	78	2517
			9066	9081			
882134	N/A	N/A	9341	9356	GGGAAAGAGCTTTGGT	95	2518
882156	N/A	N/A	9592	9607	AAATATACCAGCTCAA	75	2519
882180	N/A	N/A	9921	9936	CCAAAGGGTTCAGTGT	74	2520
882203	N/A	N/A	10128	10143	CTCCACTACCATATTG	99	2521
882227	N/A	N/A	10285	10300	CATTTACTGTIACCGA	21	2522
882251	N/A	N/A	10610	10625	TGGAGAAACGAGCCAG	62	2523
882275	N/A	N/A	11054	11069	GTCTACATCTACTCCA	62	2524
882299	N/A	N/A	11333	11348	CTTATTTGTGGCTCAA	45	2525
882323	N/A	N/A	11655	11670	ACCTTAAGCTATTTGG	39	2526
882347	N/A	N/A	11865	11880	CCCAAAGGGCATCCTC	59	2527
882371	N/A	N/A	12143	12158	ACTTAACCCACATCAC	122	2528
882395	N/A	N/A	12484	12499	GGCTTTGTGTTTAAGT	77	2529
882418	N/A	N/A	12890	12905	TAACGGTGTTTCAGAA	74	2530
882441	N/A	N/A	13173	13188	CCATTTAATCTGTCTA	72	2531
882463	N/A	N/A	13785	13800	AACAGATAACGAGGTG	104	2532

882485	N/A	N/A	14124	14139	CAATATGCTTCCAACC	115	2533
882508	N/A	N/A	14343	14358	AGCCAGAGGTTTCGCTG	75	2534
882531	N/A	N/A	14677	14692	GCTTACAAAACTTGG	74	2535
882555	N/A	N/A	15407	15422	TTAGAAAGCCCTCACC	116	2536
882578	N/A	N/A	15782	15797	TGGGAATCCTTAATTA	88	2537
882625	N/A	N/A	16155	16170	AAGAAACGAGTTGACA	78	2538
882648	N/A	N/A	16385	16400	TGGAACAGTAACTTGA	88	2539
882672	N/A	N/A	16648	16663	ACCAATTTATGCCATG	83	2540
882696	N/A	N/A	16860	16875	TGTGAACATCTCAGAT	88	2541
882720	N/A	N/A	17170	17185	GGCCTTTACAAAGAAC	119	2542
882744	N/A	N/A	17487	17502	TAGCATTCTTACAGCA	43	2543
882768	N/A	N/A	17726	17741	GTTGAACCCATCTTGA	84	2544
882792	N/A	N/A	17978	17993	AGCTAGAACATGATGA	95	2545
882815	N/A	N/A	18571	18586	TGATAGCTGAGCTGAT	63	2546
882839	N/A	N/A	18939	18954	AGCTAACTGGCCTCAA	77	2547
882862	N/A	N/A	19221	19236	GGGTTAAAGATGTTAC	50	2548
882886	N/A	N/A	19408	19423	AGATATCCTGCAACTG	109	2549
882891	N/A	N/A	4045	4060	TCGCAGGAGCGCGGAG	137	2550
882913	N/A	N/A	15899	15914	ATACATTCACTGACC	55	2551

Table 36

Percent control of human IRF4 mRNA with 3-10-3 cEt gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	26	195
881098	335	350	N/A	N/A	GCCCAAGCCTTGAAGA	85	2552
881121	620	635	9110	9125	ATGTAGTTGTGAACCT	61	2553
881168	1191	1206	13744	13759	GTCAAAGAGCTTGCAG	56	2554
881192	1356	1371	19473	19488	ATAATATAGTTGTCTG	65	2555
881216	1739	1754	19856	19871	AGTAAGAGGGCAGTCA	50	2556
881240	1919	1934	20036	20051	GGTCAATTTTCACAGT	36	2557
881264	2041	2056	20158	20173	CTACAAGCAGTCATCA	56	2558
881288	2192	2207	20309	20324	ACAGGCACGGCTTCAG	36	2559
881312	2384	2399	20501	20516	ACTAGATTGTAGGACA	109	2560
881336	2507	2522	20624	20639	GTTCAAGTATTAAGAT	71	2561
881360	2611	2626	20728	20743	TCCTTTAGTGTCCCA	24	2562
881384	2825	2840	20942	20957	AAGTGGAGGTCTTTGG	34	2563
881432	3043	3058	21160	21175	TAGGGATACAGCAGGC	27	2564
881456	3272	3287	21389	21404	ATAAACACCCCTTCTT	70	2565

881480	3408	3423	21525	21540	GGCCTCTGAGCAGAAC	73	2566
881504	3504	3519	21621	21636	CACGAAACACAGTCTG	48	2567
881527	3624	3639	21741	21756	AAAGAGGGTCACAGGT	66	2568
881551	3898	3913	22015	22030	GGTCATACCCCTGGATC	51	2569
881575	4051	4066	22168	22183	TTCAACAGCACTGTCC	35	2570
881594	4284	4299	22401	22416	TGTAGGGCGACTAACT	79	2571
881618	4411	4426	22528	22543	TAATACCTACCTGCCC	96	2572
881642	4543	4558	22660	22675	ACACACAAGTGGCCTT	56	2573
881666	4601	4616	22718	22733	GCAATGAACGGAAGTT	55	2574
881690	4838	4853	22955	22970	GCTATCAGGATCTCAA	62	2575
881714	5021	5036	23138	23153	CTGTTAAGTCCCATCT	46	2576
881738	5205	5220	23322	23337	CAGCATAGCATTATCT	151	2577
881762	N/A	N/A	18777	18792	ACGACTTAAGCTAAAC	42	2578
881786	N/A	N/A	18846	18861	TTTACAGCATCTAAGG	66	2579
881808	N/A	N/A	4055	4070	GGCGACCCCGTCGCAG	70	2580
881831	N/A	N/A	4372	4387	GGGCGACGACAGCTGC	68	2581
881854	N/A	N/A	4642	4657	CCACGCGCGGAGGACC	81	2582
881878	N/A	N/A	5015	5030	CGCCAGTGACCACGAG	58	2583
881902	N/A	N/A	5659	5674	CACGGACGAACGCGCA	102	2584
881946	N/A	N/A	6124	6139	ACCAAATTCCTGGAGG	93	2585
881970	N/A	N/A	6413	6428	GCATAGGTCCTTCAGA	69	2586
881992	N/A	N/A	7154	7169	CACATAACTCAGGCAA	63	2587
882016	N/A	N/A	7347	7362	TGCAAAATAGTCACTC	52	2588
882040	N/A	N/A	7647	7662	TTCTACAAGGTCTGAG	53	2589
882064	N/A	N/A	8139	8154	GCGGACACGCCCCGACC	85	2590
882087	N/A	N/A	8383	8398	GGAGATACTTGTACTG	34	2591
882111	N/A	N/A	8550	8565	AGATAAGAAGCACTGG	75	2592
			8706	8721			
			8810	8825			
			8966	8981			
			9070	9085			
882157	N/A	N/A	9593	9608	GAAATATACCAGCTCA	39	2593
882181	N/A	N/A	9957	9972	GGCCAAATTGCAAAGG	52	2594
882204	N/A	N/A	10149	10164	TAGTTTTATGTTAGCC	25	2595
882228	N/A	N/A	10287	10302	TTCATTTACTGTTACC	29	2596
882252	N/A	N/A	10615	10630	GCTGATGGAGAAACGA	93	2597
882276	N/A	N/A	11087	11102	TAAATCACCTGGTCA	78	2598
882300	N/A	N/A	11347	11362	GTAGAGGAGGAGGACT	84	2599
882324	N/A	N/A	11660	11675	TCCAAACCTTAAGCTA	63	2600
882348	N/A	N/A	11891	11906	AGCCTTCCTGCTCAGA	45	2601
882372	N/A	N/A	12144	12159	GACTTAACCCACATCA	266	2602

882396	N/A	N/A	12492	12507	TCCCACTGGGCTTTGT	68	2603
882419	N/A	N/A	12891	12906	ATAACGGTGTTCAGA	53	2604
882442	N/A	N/A	13174	13189	CCCATTTAATCTGTCT	67	2605
882464	N/A	N/A	13787	13802	CTAACAGATAACGAGG	77	2606
882486	N/A	N/A	14129	14144	GTTAACAATATGCTTC	75	2607
882509	N/A	N/A	14347	14362	AGCCAGCCAGAGGTTTC	70	2608
882532	N/A	N/A	14691	14706	GAAAATCTGGATGAGC	36	2609
882556	N/A	N/A	15437	15452	AGCCAGTGCCAGTTCC	61	2610
882579	N/A	N/A	15803	15818	AGATAACATGAGAGTG	59	2611
882602	N/A	N/A	15923	15938	AATGACTTAGTCAGAA	73	2612
882626	N/A	N/A	16159	16174	GCAAAAGAAACGAGTT	92	2613
882649	N/A	N/A	16387	16402	GATGGAACAGTAACTT	49	2614
882673	N/A	N/A	16663	16678	ACGCAATGGCAAAAGA	89	2615
882697	N/A	N/A	16887	16902	TCTTACTCCGCTGAGT	65	2616
882721	N/A	N/A	17224	17239	TTCCAGGTCATTGAC	34	2617
882745	N/A	N/A	17492	17507	CTAGATAGCATTCTTA	61	2618
882769	N/A	N/A	17731	17746	CCACAGTTGAACCCAT	64	2619
882793	N/A	N/A	17982	17997	TCAGAGCTAGAACATG	62	2620
882816	N/A	N/A	18579	18594	GATTGATGTGATAGCT	44	2621
882840	N/A	N/A	18960	18975	CTACTATTGTGGAAAA	97	2622
882863	N/A	N/A	19230	19245	CTTAATTCTGGGTAA	47	2623
882887	N/A	N/A	19417	19432	ACATTACTGAGATATC	84	2624
882895	N/A	N/A	5776	5791	CGAAAACAGCCGCCGG	85	2625
882901	N/A	N/A	9358	9373	ACGCAGCCTCTAAGAA	75	2626

Example 7: Effect of mixed MOE and cEt gapmers with phosphorothioate internucleoside linkages on human IRF4 *in vitro*, single dose

Modified oligonucleotides complementary to a human IRF4 nucleic acid were designed and tested for their effect on IRF4 mRNA *in vitro*.

Cultured MM.1R cells at a density of 5,000 cells per well were transfected by free uptake with 1,000 nM concentration of modified oligonucleotide or no modified oligonucleotide for untreated controls. After approximately 24 hours, RNA was isolated from the cells and IRF4 mRNA levels were measured by quantitative real-time PCR. Human primer probe set hIRF4_LTS34726 (forward sequence GGCAAAGAAAGCTCATCACAG, designated herein as SEQ ID NO: 3389; reverse sequence GGATTGCTGATGTGTTCTGGTA designated herein as SEQ ID NO: 3390; probe sequence TAGCCCCTCAGGAAATGTCCACTG, designated herein as SEQ ID: 3391) was used to measure mRNA levels. IRF4 mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented in the table below as percent control of the amount of IRF4 mRNA, relative to untreated control (UTC) cells.

The modified oligonucleotides in Table 37 are cEt and/or MOE containing gapmers. The modified oligonucleotides have a central gap segment comprising 2'-deoxynucleosides which is flanked by wing segments on the 5' direction and the 3' direction. At least one nucleoside in the 5' wing segment and/or one nucleoside in the 3' wing segment has a MOE and/or cEt sugar modification. The "Motif" column describes the sugar modifications of each oligonucleotide. "k" indicates a cEt sugar modification; "d" indicates deoxyribose; and "e" indicates a MOE modification. Each internucleoside linkage is a phosphorothioate internucleoside linkage and each cytosine residue is a 5-methylcytosine. "Start Site" indicates the 5'-most nucleoside to which the gapmer is complementary in the human nucleic acid sequence. "Stop Site" indicates the 3'-most nucleoside to which the gapmer is complementary in the human nucleic acid sequence.

Each modified oligonucleotide listed in Table 37 below is complementary to human IRF4 nucleic acid sequences SEQ ID NO: 1 or SEQ ID NO: 2, as indicated. 'N/A' indicates that the modified oligonucleotide is not complementary to that particular nucleic acid sequence with 100% complementarity. As shown below, modified oligonucleotides complementary to human IRF4 reduced the amount of human IRF4 mRNA.

Table 37

Percent control of human IRF4 mRNA with gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	Motif	IRF4 (% UTC)	SEQ ID NO
881450	3252	3267	21369	21384	ACACTTTTAGAGAGGA	kkk-d10-kkk	47	2111
881659	4592	4607	22709	22724	GGAAAGTTTACACTGGA	kkk-d10-kkk	15	2044
935895	4200	4215	22317	22332	TCTATAGTGTTCAGG	kk-d9-eeekk	50	1734
935896	3070	3085	21187	21202	GCTTGATAAAGGCTGA	kk-d9-eeekk	72	1505
935897	3251	3266	21368	21383	CACTTTTAGAGAGGAG	kk-d9-eeekk	67	2036
935898	4227	4242	22344	22359	GTTGTAAATGAGTCGG	kk-d9-eeekk	18	559
935899	4591	4606	22708	22723	GAAGTTTACACTGGAT	kk-d9-eeekk	72	1968
935900	N/A	N/A	8464	8479	GCATTTTATCATCCGA	kk-d9-eeekk	62	1605
935901	N/A	N/A	11115	11130	GTGATGTCAGGTTTTC	kk-d9-eeekk	62	2627
935902	5186	5201	23303	23318	TCAGTTTGTGAAGCAT	kk-d9-eeekk	61	649
935903	4171	4186	22288	22303	TGCTTGAGGTTTTCCT	kk-d9-eeekk	68	548
935904	2914	2929	21031	21046	AGTATGAGAAACGGCC	kk-d9-eeekk	84	1045
935905	4199	4214	22316	22331	CTATAGTGTTCAGGA	kk-d9-eeekk	66	552
935906	3069	3084	21186	21201	CTTGATAAAGGCTGAA	kk-d9-eeekk	90	1427
935907	3250	3265	21367	21382	ACTTTTAGAGAGGAGA	kk-d9-eeekk	64	1960
935908	4226	4241	22343	22358	TTGTAAATGAGTCGGT	kk-d9-eeekk	52	195
935909	4593	4608	22710	22725	CGGAAGTTTACACTGG	kk-d9-eeekk	66	2119

935910	N/A	N/A	8466	8481	AAGCATTTTATCATCC	kk-d9-eeekk	79	2628
935911	N/A	N/A	11117	11132	CAGTGATGTCAGGTTT	kk-d9-eeekk	44	2629
935912	5188	5203	23305	23320	CCTCAGTTTGTGAAGC	kk-d9-eeekk	67	1894
935913	4173	4188	22290	22305	ACTGCTTGAGGTTTTC	kk-d9-eeekk	55	1356
935914	2916	2931	21033	21048	GTAGTATGAGAAACGG	kk-d9-eeekk	49	426
935915	4201	4216	22318	22333	CTCTATAGTGTTCAG	kk-d9-eeekk	52	1811
935916	3071	3086	21188	21203	AGCTTGATAAAGGCTG	kk-d9-eeekk	97	1579
935917	3252	3267	21369	21384	ACACTTTTAGAGAGGA	kk-d9-eeekk	79	2111
935918	4228	4243	22345	22360	AGTTGTAAATGAGTCG	kk-d9-eeekk	34	2021
935919	4594	4609	22711	22726	ACGGAAGTTTACACTG	kk-d9-eeekk	85	2195
935920	N/A	N/A	8467	8482	GAAGCATTTTATCATC	kk-d9-eeekk	91	2630
935921	N/A	N/A	11118	11133	GCAGTGATGTCAGGTT	kk-d9-eeekk	19	2631
935922	5189	5204	23306	23321	ACCTCAGTTTGTGAAG	kk-d9-eeekk	96	1971
935923	4174	4189	22291	22306	TACTGCTTGAGGTTTT	kk-d9-eeekk	90	1433
935924	2917	2932	21034	21049	TGTAGTATGAGAAACG	kk-d9-eeekk	93	1197
935925	4202	4217	22319	22334	TCTCTATAGTGTTCAC	kk-d9-eeekk	43	2632
935926	3072	3087	21189	21204	AAGCTTGATAAAGGCT	kk-d9-eeekk	47	2633
935927	3253	3268	21370	21385	GACACTTTTAGAGAGG	kk-d9-eeekk	75	451
935928	4229	4244	22346	22361	CAGTTGTAAATGAGTC	kk-d9-eeekk	38	560
935929	4592	4607	22709	22724	GGAAGTTTACACTGGA	kk-d9-ekeke	36	2044
935930	N/A	N/A	8465	8480	AGCATTTTATCATCCG	kk-d9-ekeke	54	1679
935931	N/A	N/A	11116	11131	AGTGATGTCAGGTTTT	kk-d9-ekeke	67	1232
935932	5187	5202	23304	23319	CTCAGTTTGTGAAGCA	kk-d9-ekeke	72	1817
935933	4172	4187	22289	22304	CTGCTTGAGGTTTTCC	kk-d9-ekeke	51	1279
935934	2915	2930	21032	21047	TAGTATGAGAAACGGC	kk-d9-ekeke	50	1121
935935	4200	4215	22317	22332	TCTATAGTGTTCAGG	kk-d9-ekeke	44	1734
935936	3070	3085	21187	21202	GCTTGATAAAGGCTGA	kk-d9-ekeke	61	1505
935937	3251	3266	21368	21383	CACTTTTAGAGAGGAG	kk-d9-ekeke	74	2036
935938	4227	4242	22344	22359	GTTGTAAATGAGTCGG	kk-d9-ekeke	52	559
935939	4591	4606	22708	22723	GAAGTTTACACTGGAT	kk-d9-ekeke	42	1968
935940	N/A	N/A	8464	8479	GCATTTTATCATCCGA	kk-d9-ekeke	56	1605
935941	N/A	N/A	11115	11130	GTGATGTCAGGTTTTC	kk-d9-ekeke	42	2627
935942	5186	5201	23303	23318	TCAGTTTGTGAAGCAT	kk-d9-ekeke	55	649
935943	4171	4186	22288	22303	TGCTTGAGGTTTTCCT	kk-d9-ekeke	55	548
935944	2914	2929	21031	21046	AGTATGAGAAACGGCC	kk-d9-ekeke	89	1045
935945	4199	4214	22316	22331	CTATAGTGTTCAGGA	kk-d9-ekeke	52	552
935946	3069	3084	21186	21201	CTTGATAAAGGCTGAA	kk-d9-ekeke	81	1427
935947	3250	3265	21367	21382	ACTTTTAGAGAGGAGA	kk-d9-ekeke	48	1960
935948	4226	4241	22343	22358	TTGTAAATGAGTCGGT	kk-d9-ekeke	43	195
935949	4593	4608	22710	22725	CGGAAGTTTACACTGG	kk-d9-ekeke	67	2119
935950	N/A	N/A	8466	8481	AAGCATTTTATCATCC	kk-d9-ekeke	75	2628

935951	N/A	N/A	11117	11132	CAGTGATGTCAGGTTT	kk-d9-ekeke	53	2629
935952	5188	5203	23305	23320	CCTCAGTTTGTGAAGC	kk-d9-ekeke	79	1894
935953	4173	4188	22290	22305	ACTGCTTGAGGTTTTC	kk-d9-ekeke	60	1356
935954	2916	2931	21033	21048	GTAGTATGAGAAACGG	kk-d9-ekeke	65	426
935955	4201	4216	22318	22333	CTCTATAGTGTTCAG	kk-d9-ekeke	57	1811
935956	3071	3086	21188	21203	AGCTTGATAAAGGCTG	kk-d9-ekeke	82	1579
935957	3252	3267	21369	21384	ACACTTTTAGAGAGGA	kk-d9-ekeke	59	2111
935958	4228	4243	22345	22360	AGTTGTAAATGAGTCG	kk-d9-ekeke	27	2021
935959	4594	4609	22711	22726	ACGGAAGTTTACACTG	kk-d9-ekeke	92	2195
935960	N/A	N/A	8467	8482	GAAGCATTTTATCATC	kk-d9-ekeke	94	2630
935961	N/A	N/A	11118	11133	GCAGTGATGTCAGGTT	kk-d9-ekeke	20	2631
935962	5189	5204	23306	23321	ACCTCAGTTTGTGAAG	kk-d9-ekeke	87	1971
935963	4174	4189	22291	22306	TACTGCTTGAGGTTT	kk-d9-ekeke	82	1433
935964	2917	2932	21034	21049	TGTAGTATGAGAAACG	kk-d9-ekeke	87	1197
935965	4202	4217	22319	22334	TCTCTATAGTGTTC	kk-d9-ekeke	61	2632
935966	3072	3087	21189	21204	AAGCTTGATAAAGGCT	kk-d9-ekeke	62	2633
935967	3253	3268	21370	21385	GACACTTTTAGAGAGG	kk-d9-ekeke	78	451
935968	4229	4244	22346	22361	CAGTTGTAAATGAGTC	kk-d9-ekeke	28	560
935969	4592	4607	22709	22724	GGAAGTTTACACTGGA	k-d9-kekeke	68	2044
935970	N/A	N/A	8465	8480	AGCATTTTATCATCCG	k-d9-kekeke	76	1679

Example 8: Effect of mixed MOE and cEt gapmers with phosphorothioate internucleoside linkages on human IRF4 *in vitro*, single dose

Modified oligonucleotides complementary to a human IRF4 nucleic acid were designed and tested for their effect on IRF4 mRNA *in vitro*.

Cultured MM.1R cells at a density of 5,000 cells per well were transfected by free uptake with 1,000 nM concentration of modified oligonucleotide or no modified oligonucleotide for untreated controls. After approximately 24 hours, RNA was isolated from the cells and IRF4 mRNA levels were measured by quantitative real-time PCR. Human primer probe set hIRF4_LTS34726 (described hereinabove in Example 7) was used to measure mRNA levels. IRF4 mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented in the table below as percent control of the amount of IRF4 mRNA, relative to untreated control (UTC) cells.

The modified oligonucleotides in Tables 38 through 42 are cEt and/or MOE containing gapmers. The modified oligonucleotides have a central gap segment comprising 2'-deoxynucleosides which is flanked by wing segments on the 5' direction and the 3' direction. At least one nucleoside in the 5' wing segment and/or one nucleoside in the 3' wing segment has a MOE and/or cEt sugar modification. The "Motif" column describes the sugar modifications of each oligonucleotide. "k" indicates a cEt sugar modification; "d" indicates deoxyribose; and "e" indicates a MOE modification. Each internucleoside linkage is a

phosphorothioate internucleoside linkage and each cytosine residue is a 5-methylcytosine. “Start Site” indicates the 5’-most nucleoside to which the gapmer is complementary in the human nucleic acid sequence. “Stop Site” indicates the 3’-most nucleoside to which the gapmer is complementary in the human nucleic acid sequence.

- 5 Each modified oligonucleotide listed in Tables 38 through 42 below is complementary to human IRF4 nucleic acid sequences SEQ ID NO: 1 or SEQ ID NO: 2, as indicated. ‘N/A’ indicates that the modified oligonucleotide is not complementary to that particular nucleic acid sequence with 100% complementarity. As shown below, modified oligonucleotides complementary to human IRF4 reduced the amount of human IRF4 mRNA.

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Table 38
Percent control of human IRF4 mRNA with gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	Motif	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	kkk-d10-kkk	37	195
881450	3252	3267	21369	21384	ACACTTTTAGAGAGGA	kkk-d10-kkk	53	2111
881659	4592	4607	22709	22724	GGAAGTTTACACTGGA	kkk-d10-kkk	14	2044
935570	N/A	N/A	8455	8470	CATCCGAAAAGACTGG	kkk-d10-kkk	86	2634
935571	N/A	N/A	8456	8471	TCATCCGAAAAGACTG	kkk-d10-kkk	84	2635
935572	N/A	N/A	8457	8472	ATCATCCGAAAAGACT	kkk-d10-kkk	96	2636
935573	N/A	N/A	8458	8473	TATCATCCGAAAAGAC	kkk-d10-kkk	97	2637
935574	N/A	N/A	8459	8474	TTATCATCCGAAAAGA	kkk-d10-kkk	96	2638
935575	N/A	N/A	8460	8475	TTTATCATCCGAAAAG	kkk-d10-kkk	93	2639
935576	N/A	N/A	8472	8487	CAGCCGAAGCATTTTA	kkk-d10-kkk	100	2640
935577	N/A	N/A	8473	8488	ACAGCCGAAGCATTTT	kkk-d10-kkk	92	2641
935578	N/A	N/A	8474	8489	GACAGCCGAAGCATTT	kkk-d10-kkk	94	2642
935580	N/A	N/A	11115	11130	GTGATGTCAGGTTTTTC	kkk-d10-kkk	34	2627
935581	N/A	N/A	11117	11132	CAGTGATGTCAGGTTT	kkk-d10-kkk	38	2629
935582	N/A	N/A	11118	11133	GCAGTGATGTCAGGTT	kkk-d10-kkk	61	2631
935584	N/A	N/A	11124	11139	CCACAAGCAGTGATGT	kkk-d10-kkk	84	2643
935585	N/A	N/A	11125	11140	ACCACAAGCAGTGATG	kkk-d10-kkk	99	2644
935586	2905	2920	21022	21037	AACGGCCTGGAGGTGA	kkk-d10-kkk	99	2645
935587	2906	2921	21023	21038	AAACGGCCTGGAGGTG	kkk-d10-kkk	89	2646
935588	2907	2922	21024	21039	GAAACGGCCTGGAGGT	kkk-d10-kkk	83	2647
935590	2920	2935	21037	21052	TCCTGTAGTATGAGAA	kkk-d10-kkk	78	2648
935591	2922	2937	21039	21054	TATCTGTAGTATGAG	kkk-d10-kkk	58	2649
935593	3072	3087	21189	21204	AAGCTTGATAAAGGCT	kkk-d10-kkk	97	2633

935597	3080	3095	21197	21212	TGCTCACTAAGCTTGA	kkk-d10-kkk	88	2650
935603	4178	4193	22295	22310	TAATTACTGCTTGAGG	kkk-d10-kkk	38	2651
935606	4194	4209	22311	22326	GTGTTCCAGGAGATAT	kkk-d10-kkk	70	2652
935608	4196	4211	22313	22328	TAGTGTTCCAGGAGAT	kkk-d10-kkk	47	2653
935611	4208	4223	22325	22340	CTTGTTCTCTATAGT	kkk-d10-kkk	73	2654
935614	4597	4612	22714	22729	TGAACGGAAGTTTACA	kkk-d10-kkk	86	2655
935616	5190	5205	23307	23322	TACCTCAGTTTGTGAA	kkk-d10-kkk	89	2656
935618	N/A	N/A	8466	8481	AAGCATTTTATCATCC	kkk-d10-kkk	75	2628
935619	N/A	N/A	8467	8482	GAAGCATTTTATCATC	kkk-d10-kkk	96	2630
935620	4202	4217	22319	22334	TCTCTATAGTGTTCCA	kkk-d10-kkk	30	2632
935621	4592	4607	22709	22724	GGAAGTTTACACTGGA	k-d10-kekek	67	2044
935622	N/A	N/A	8465	8480	AGCATTTTATCATCCG	k-d10-kekek	64	1679
935623	N/A	N/A	11116	11131	AGTGATGTCAGGTTTT	k-d10-kekek	75	1232
935624	5187	5202	23304	23319	CTCAGTTTGTGAAGCA	k-d10-kekek	76	1817
935625	4172	4187	22289	22304	CTGCTTGAGGTTTCC	k-d10-kekek	92	1279
935626	2915	2930	21032	21047	TAGTATGAGAAACGGC	k-d10-kekek	76	1121
935627	4200	4215	22317	22332	TCTATAGTGTTCCAGG	k-d10-kekek	84	1734
935628	3070	3085	21187	21202	GCTTGATAAAGGCTGA	k-d10-kekek	83	1505
935629	3251	3266	21368	21383	CACTTTTAGAGAGGAG	k-d10-kekek	81	2036
935630	4591	4606	22708	22723	GAAGTTTACACTGGAT	k-d10-kekek	73	1968
935631	N/A	N/A	8464	8479	GCATTTTATCATCCGA	k-d10-kekek	79	1605
935632	N/A	N/A	11115	11130	GTGATGTCAGGTTTTTC	k-d10-kekek	78	2627
935633	5186	5201	23303	23318	TCAGTTTGTGAAGCAT	k-d10-kekek	79	649
935634	4171	4186	22288	22303	TGCTTGAGGTTTTCCT	k-d10-kekek	64	548
935635	2914	2929	21031	21046	AGTATGAGAAACGGCC	k-d10-kekek	90	1045
935636	4199	4214	22316	22331	CTATAGTGTTCCAGGA	k-d10-kekek	66	552
935637	3069	3084	21186	21201	CTTGATAAAGGCTGAA	k-d10-kekek	83	1427
935638	3250	3265	21367	21382	ACTTTTAGAGAGGAGA	k-d10-kekek	68	1960
935639	4593	4608	22710	22725	CGGAAGTTTACACTGG	k-d10-kekek	90	2119
935640	N/A	N/A	8466	8481	AAGCATTTTATCATCC	k-d10-kekek	86	2628
935641	N/A	N/A	11117	11132	CAGTGATGTCAGGTTT	k-d10-kekek	54	2629
935642	5188	5203	23305	23320	CCTCAGTTTGTGAAGC	k-d10-kekek	74	1894
935643	4173	4188	22290	22305	ACTGCTTGAGGTTTTTC	k-d10-kekek	78	1356
935644	2916	2931	21033	21048	GTAGTATGAGAAACGG	k-d10-kekek	54	426
935645	4201	4216	22318	22333	CTCTATAGTGTTCCAG	k-d10-kekek	76	1811
935646	3071	3086	21188	21203	AGCTTGATAAAGGCTG	k-d10-kekek	99	1579
935647	3252	3267	21369	21384	ACACTTTTAGAGAGGA	k-d10-kekek	106	2111
935648	4228	4243	22345	22360	AGTTGTAAATGAGTCG	k-d10-kekek	56	2021
935649	4594	4609	22711	22726	ACGGAAGTTTACACTG	k-d10-kekek	93	2195
935650	N/A	N/A	8467	8482	GAAGCATTTTATCATC	k-d10-kekek	112	2630
935651	N/A	N/A	11118	11133	GCAGTGATGTCAGGTT	k-d10-kekek	64	2631

935652	5189	5204	23306	23321	ACCTCAGTTTGTGAAG	k-d10-kekek	82	1971
935653	4174	4189	22291	22306	TACTGCTTGAGGTTTT	k-d10-kekek	76	1433
935654	2917	2932	21034	21049	TGTAGTATGAGAAACG	k-d10-kekek	93	1197
935655	4202	4217	22319	22334	TCTCTATAGTGTTCCA	k-d10-kekek	39	2632
935656	3072	3087	21189	21204	AAGCTTGATAAAGGCT	k-d10-kekek	97	2633
935657	3253	3268	21370	21385	GACACTTTTAGAGAGG	k-d10-kekek	77	451
935658	4229	4244	22346	22361	CAGTTGTAAATGAGTC	k-d10-kekek	35	560
935659	4592	4607	22709	22724	GGAAGTTTACACTGGA	kk-d9-kekek	53	2044
935660	N/A	N/A	8465	8480	AGCATTTTATCATCCG	kk-d9-kekek	61	1679
935661	N/A	N/A	11116	11131	AGTGATGTCAGGTTTT	kk-d9-kekek	61	1232
935662	5187	5202	23304	23319	CTCAGTTTGTGAAGCA	kk-d9-kekek	78	1817
935663	4172	4187	22289	22304	CTGCTTGAGGTTTTCC	kk-d9-kekek	70	1279
935664	2915	2930	21032	21047	TAGTATGAGAAACGGC	kk-d9-kekek	73	1121
935665	4200	4215	22317	22332	TCTATAGTGTTCCAGG	kk-d9-kekek	72	1734
935666	3070	3085	21187	21202	GCTTGATAAAGGCTGA	kk-d9-kekek	93	1505

Table 39

Percent control of human IRF4 mRNA with gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	Motif	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	kkk-d10-kkk	37	195
881450	3252	3267	21369	21384	ACACTTTTAGAGAGGA	kkk-d10-kkk	49	2111
881659	4592	4607	22709	22724	GGAAGTTTACACTGGA	kkk-d10-kkk	15	2044
935667	3251	3266	21368	21383	CACTTTTAGAGAGGAG	kk-d9-kekek	83	2036
935668	4591	4606	22708	22723	GAAGTTTACACTGGAT	kk-d9-kekek	45	1968
935669	N/A	N/A	8464	8479	GCATTTTATCATCCGA	kk-d9-kekek	52	1605
935670	N/A	N/A	11115	11130	GTGATGTCAGGTTTTTC	kk-d9-kekek	60	2627
935671	5186	5201	23303	23318	TCAGTTTGTGAAGCAT	kk-d9-kekek	42	649
935672	4171	4186	22288	22303	TGCTTGAGGTTTTCCT	kk-d9-kekek	64	548
935673	2914	2929	21031	21046	AGTATGAGAAACGGCC	kk-d9-kekek	97	1045
935674	4199	4214	22316	22331	CTATAGTGTTCCAGGA	kk-d9-kekek	57	552
935675	3069	3084	21186	21201	CTTGATAAAGGCTGAA	kk-d9-kekek	88	1427
935676	3250	3265	21367	21382	ACTTTTAGAGAGGAGA	kk-d9-kekek	60	1960
935677	4593	4608	22710	22725	CGGAAGTTTACACTGG	kk-d9-kekek	80	2119
935678	N/A	N/A	8466	8481	AAGCATTTTATCATCC	kk-d9-kekek	82	2628
935679	N/A	N/A	11117	11132	CAGTGATGTCAGGTTT	kk-d9-kekek	36	2629
935680	5188	5203	23305	23320	CCTCAGTTTGTGAAGC	kk-d9-kekek	85	1894
935681	4173	4188	22290	22305	ACTGCTTGAGGTTTTTC	kk-d9-kekek	76	1356
935682	2916	2931	21033	21048	GTAGTATGAGAAACGG	kk-d9-kekek	50	426

935683	4201	4216	22318	22333	CTCTATAGTGTTCAG	kk-d9-kekek	78	1811
935684	3071	3086	21188	21203	AGCTTGATAAAGGCTG	kk-d9-kekek	84	1579
935685	3252	3267	21369	21384	ACACTTTTAGAGAGGA	kk-d9-kekek	73	2111
935686	4228	4243	22345	22360	AGTTGTAAATGAGTCG	kk-d9-kekek	44	2021
935687	4594	4609	22711	22726	ACGGAAGTTTACACTG	kk-d9-kekek	79	2195
935688	N/A	N/A	8467	8482	GAAGCATTTTATCATC	kk-d9-kekek	120	2630
935689	N/A	N/A	11118	11133	GCAGTGATGTCAGGTT	kk-d9-kekek	31	2631
935690	5189	5204	23306	23321	ACCTCAGTTTGTGAAG	kk-d9-kekek	87	1971
935691	4174	4189	22291	22306	TACTGCTTGAGGTTTT	kk-d9-kekek	78	1433
935692	2917	2932	21034	21049	TGTAGTATGAGAAACG	kk-d9-kekek	88	1197
935693	4202	4217	22319	22334	TCTCTATAGTGTTC	kk-d9-kekek	72	2632
935694	3072	3087	21189	21204	AAGCTTGATAAAGGCT	kk-d9-kekek	119	2633
935695	3253	3268	21370	21385	GACACTTTTAGAGAGG	kk-d9-kekek	83	451
935696	4229	4244	22346	22361	CAGTTGTAAATGAGTC	kk-d9-kekek	19	560
935697	4592	4607	22709	22724	GGAAGTTTACACTGGA	kkk-d9-kkke	22	2044
935698	N/A	N/A	8465	8480	AGCATTTTATCATCCG	kkk-d9-kkke	34	1679
935699	N/A	N/A	11116	11131	AGTGATGTCAGGTTTT	kkk-d9-kkke	35	1232
935700	5187	5202	23304	23319	CTCAGTTTGTGAAGCA	kkk-d9-kkke	31	1817
935701	4172	4187	22289	22304	CTGCTTGAGGTTTCC	kkk-d9-kkke	35	1279
935702	2915	2930	21032	21047	TAGTATGAGAAACGGC	kkk-d9-kkke	52	1121
935703	4200	4215	22317	22332	TCTATAGTGTTCAGG	kkk-d9-kkke	48	1734
935704	3070	3085	21187	21202	GCTTGATAAAGGCTGA	kkk-d9-kkke	77	1505
935705	3251	3266	21368	21383	CACTTTTAGAGAGGAG	kkk-d9-kkke	60	2036
935706	4591	4606	22708	22723	GAAGTTTACACTGGAT	kkk-d9-kkke	55	1968
935707	N/A	N/A	8464	8479	GCATTTTATCATCCGA	kkk-d9-kkke	38	1605
935708	N/A	N/A	11115	11130	GTGATGTCAGGTTTT	kkk-d9-kkke	29	2627
935709	5186	5201	23303	23318	TCAGTTTGTGAAGCAT	kkk-d9-kkke	42	649
935710	4171	4186	22288	22303	TGCTTGAGGTTTTCT	kkk-d9-kkke	54	548
935711	2914	2929	21031	21046	AGTATGAGAAACGGCC	kkk-d9-kkke	93	1045
935712	4199	4214	22316	22331	CTATAGTGTTCAGGA	kkk-d9-kkke	69	552
935713	3069	3084	21186	21201	CTTGATAAAGGCTGAA	kkk-d9-kkke	64	1427
935714	3250	3265	21367	21382	ACTTTTAGAGAGGAGA	kkk-d9-kkke	64	1960
935715	4593	4608	22710	22725	CGGAAGTTTACACTGG	kkk-d9-kkke	75	2119
935716	N/A	N/A	8466	8481	AAGCATTTTATCATCC	kkk-d9-kkke	67	2628
935717	N/A	N/A	11117	11132	CAGTGATGTCAGGTTT	kkk-d9-kkke	51	2629
935718	5188	5203	23305	23320	CCTCAGTTTGTGAAGC	kkk-d9-kkke	98	1894
935719	4173	4188	22290	22305	ACTGCTTGAGGTTTT	kkk-d9-kkke	48	1356
935720	2916	2931	21033	21048	GTAGTATGAGAAACGG	kkk-d9-kkke	60	426
935721	4201	4216	22318	22333	CTCTATAGTGTTCAG	kkk-d9-kkke	35	1811
935722	3071	3086	21188	21203	AGCTTGATAAAGGCTG	kkk-d9-kkke	98	1579
935723	3252	3267	21369	21384	ACACTTTTAGAGAGGA	kkk-d9-kkke	71	2111

935724	4228	4243	22345	22360	AGTTGTAAATGAGTCG	kkk-d9-kkke	13	2021
935725	4594	4609	22711	22726	ACGGAAGTTTACACTG	kkk-d9-kkke	71	2195
935726	N/A	N/A	8467	8482	GAAGCATTTTATCATC	kkk-d9-kkke	99	2630
935727	N/A	N/A	11118	11133	GCAGTGATGTCAGGTT	kkk-d9-kkke	38	2631
935728	5189	5204	23306	23321	ACCTCAGTTTGTGAAG	kkk-d9-kkke	90	1971
935729	4174	4189	22291	22306	TACTGCTTGAGGTTTT	kkk-d9-kkke	87	1433
935730	2917	2932	21034	21049	TGTAGTATGAGAAACG	kkk-d9-kkke	67	1197
935731	4202	4217	22319	22334	TCTCTATAGTGTCCA	kkk-d9-kkke	44	2632
935732	3072	3087	21189	21204	AAGCTTGATAAAGGCT	kkk-d9-kkke	95	2633
935733	3253	3268	21370	21385	GACACTTTTAGAGAGG	kkk-d9-kkke	76	451
935734	4229	4244	22346	22361	CAGTTGTAAATGAGTC	kkk-d9-kkke	32	560
935735	4592	4607	22709	22724	GGAAGTTTACACTGGA	kk-d10-keke	54	2044
935736	N/A	N/A	8465	8480	AGCATTTTATCATCCG	kk-d10-keke	67	1679
935737	N/A	N/A	11116	11131	AGTGATGTCAGGTTTT	kk-d10-keke	68	1232
935738	5187	5202	23304	23319	CTCAGTTTGTGAAGCA	kk-d10-keke	70	1817
935739	4172	4187	22289	22304	CTGCTTGAGGTTTTCC	kk-d10-keke	56	1279
935740	2915	2930	21032	21047	TAGTATGAGAAACGGC	kk-d10-keke	54	1121
935741	4200	4215	22317	22332	TCTATAGTGTCCAGG	kk-d10-keke	34	1734
935742	3070	3085	21187	21202	GCTTGATAAAGGCTGA	kk-d10-keke	69	1505

Table 40

Percent control of human IRF4 mRNA with gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	Motif	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	kkk-d10-kkk	37	195
881450	3252	3267	21369	21384	ACACTTTTAGAGAGGA	kkk-d10-kkk	53	2111
881659	4592	4607	22709	22724	GGAAGTTTACACTGGA	kkk-d10-kkk	20	2044
935743	3251	3266	21368	21383	CACTTTTAGAGAGGAG	kk-d10-keke	73	2036
935744	4591	4606	22708	22723	GAAGTTTACACTGGAT	kk-d10-keke	54	1968
935745	N/A	N/A	8464	8479	GCATTTTATCATCCGA	kk-d10-keke	61	1605
935746	N/A	N/A	11115	11130	GTGATGTCAGGTTTTTC	kk-d10-keke	82	2627
935747	5186	5201	23303	23318	TCAGTTTGTGAAGCAT	kk-d10-keke	67	649
935748	4171	4186	22288	22303	TGCTTGAGGTTTTCCT	kk-d10-keke	67	548
935749	2914	2929	21031	21046	AGTATGAGAAACGGCC	kk-d10-keke	91	1045
935750	4199	4214	22316	22331	CTATAGTGTTCAGGA	kk-d10-keke	64	552
935751	3069	3084	21186	21201	CTTGATAAAGGCTGAA	kk-d10-keke	96	1427
935752	3250	3265	21367	21382	ACTTTTAGAGAGGAGA	kk-d10-keke	77	1960
935753	4593	4608	22710	22725	CGGAAGTTTACACTGG	kk-d10-keke	67	2119
935754	N/A	N/A	8466	8481	AAGCATTTTATCATCC	kk-d10-keke	80	2628

935755	N/A	N/A	11117	11132	CAGTGATGTCAGGTTT	kk-d10-keke	59	2629
935756	5188	5203	23305	23320	CCTCAGTTTGTGAAGC	kk-d10-keke	84	1894
935757	4173	4188	22290	22305	ACTGCTTGAGGTTTTC	kk-d10-keke	79	1356
935758	2916	2931	21033	21048	GTAGTATGAGAAACGG	kk-d10-keke	72	426
935759	4201	4216	22318	22333	CTCTATAGTGTTCAG	kk-d10-keke	73	1811
935760	3071	3086	21188	21203	AGCTTGATAAAGGCTG	kk-d10-keke	99	1579
935761	3252	3267	21369	21384	ACACTTTTAGAGAGGA	kk-d10-keke	86	2111
935762	4228	4243	22345	22360	AGTTGTAAATGAGTCG	kk-d10-keke	41	2021
935763	4594	4609	22711	22726	ACGGAAGTTTACACTG	kk-d10-keke	87	2195
935764	N/A	N/A	8467	8482	GAAGCATTTTATCATC	kk-d10-keke	107	2630
935765	N/A	N/A	11118	11133	GCAGTGATGTCAGGTT	kk-d10-keke	33	2631
935766	5189	5204	23306	23321	ACCTCAGTTTGTGAAG	kk-d10-keke	112	1971
935767	4174	4189	22291	22306	TACTGCTTGAGGTTTT	kk-d10-keke	89	1433
935768	2917	2932	21034	21049	TGTAGTATGAGAAACG	kk-d10-keke	90	1197
935769	4202	4217	22319	22334	TCTCTATAGTGTCCA	kk-d10-keke	73	2632
935770	3072	3087	21189	21204	AAGCTTGATAAAGGCT	kk-d10-keke	118	2633
935771	3253	3268	21370	21385	GACACTTTTAGAGAGG	kk-d10-keke	91	451
935772	4229	4244	22346	22361	CAGTTGTAAATGAGTC	kk-d10-keke	41	560
935773	4592	4607	22709	22724	GGAAGTTTACACTGGA	kk-d9-kdkdk	76	2044
935774	N/A	N/A	8465	8480	AGCATTTTATCATCCG	kk-d9-kdkdk	89	1679
935775	N/A	N/A	11116	11131	AGTGATGTCAGGTTTT	kk-d9-kdkdk	69	1232
935776	5187	5202	23304	23319	CTCAGTTTGTGAAGCA	kk-d9-kdkdk	101	1817
935777	4172	4187	22289	22304	CTGCTTGAGGTTTTCC	kk-d9-kdkdk	64	1279
935778	2915	2930	21032	21047	TAGTATGAGAAACGGC	kk-d9-kdkdk	61	1121
935779	4200	4215	22317	22332	TCTATAGTGTTCAGG	kk-d9-kdkdk	50	1734
935780	3070	3085	21187	21202	GCTTGATAAAGGCTGA	kk-d9-kdkdk	96	1505
935781	3251	3266	21368	21383	CACTTTTAGAGAGGAG	kk-d9-kdkdk	84	2036
935782	4227	4242	22344	22359	GTTGTAAATGAGTCGG	kk-d9-kdkdk	42	559
935783	4591	4606	22708	22723	GAAGTTTACACTGGAT	kk-d9-kdkdk	77	1968
935784	N/A	N/A	8464	8479	GCATTTTATCATCCGA	kk-d9-kdkdk	84	1605
935785	N/A	N/A	11115	11130	GTGATGTCAGGTTTTC	kk-d9-kdkdk	73	2627
935786	5186	5201	23303	23318	TCAGTTTGTGAAGCAT	kk-d9-kdkdk	75	649
935787	4171	4186	22288	22303	TGCTTGAGGTTTTCCCT	kk-d9-kdkdk	55	548
935788	2914	2929	21031	21046	AGTATGAGAAACGGCC	kk-d9-kdkdk	94	1045
935789	4199	4214	22316	22331	CTATAGTGTTCAGGA	kk-d9-kdkdk	51	552
935790	3069	3084	21186	21201	CTTGATAAAGGCTGAA	kk-d9-kdkdk	99	1427
935791	3250	3265	21367	21382	ACTTTTAGAGAGGAGA	kk-d9-kdkdk	66	1960
935792	4226	4241	22343	22358	TTGTAAATGAGTCGGT	kk-d9-kdkdk	57	195
935793	4593	4608	22710	22725	CGGAAGTTTACACTGG	kk-d9-kdkdk	87	2119
935794	N/A	N/A	8466	8481	AAGCATTTTATCATCC	kk-d9-kdkdk	97	2628
935795	N/A	N/A	11117	11132	CAGTGATGTCAGGTTT	kk-d9-kdkdk	53	2629

935796	5188	5203	23305	23320	CCTCAGTTTGTGAAGC	kk-d9-kdkdk	92	1894
935797	4173	4188	22290	22305	ACTGCTTGAGGTTTTC	kk-d9-kdkdk	81	1356
935798	2916	2931	21033	21048	GTAGTATGAGAAACGG	kk-d9-kdkdk	68	426
935799	4201	4216	22318	22333	CTCTATAGTGTTCAG	kk-d9-kdkdk	69	1811
935800	3071	3086	21188	21203	AGCTTGATAAAGGCTG	kk-d9-kdkdk	103	1579
935801	3252	3267	21369	21384	ACACTTTTAGAGAGGA	kk-d9-kdkdk	97	2111
935802	4228	4243	22345	22360	AGTTGTAAATGAGTCG	kk-d9-kdkdk	61	2021
935803	4594	4609	22711	22726	ACGGAAGTTTACACTG	kk-d9-kdkdk	102	2195
935804	N/A	N/A	8467	8482	GAAGCATTTTATCATC	kk-d9-kdkdk	99	2630
935805	N/A	N/A	11118	11133	GCAGTGATGTCAGGTT	kk-d9-kdkdk	47	2631
935806	5189	5204	23306	23321	ACCTCAGTTTGTGAAG	kk-d9-kdkdk	103	1971
935807	4174	4189	22291	22306	TACTGCTTGAGGTTTT	kk-d9-kdkdk	85	1433
935808	2917	2932	21034	21049	TGTAGTATGAGAAACG	kk-d9-kdkdk	106	1197
935809	4202	4217	22319	22334	TCTCTATAGTGTCCA	kk-d9-kdkdk	62	2632
935810	3072	3087	21189	21204	AAGCTTGATAAAGGCT	kk-d9-kdkdk	102	2633
935811	3253	3268	21370	21385	GACACTTTTAGAGAGG	kk-d9-kdkdk	86	451
935812	4229	4244	22346	22361	CAGTTGTAAATGAGTC	kk-d9-kdkdk	54	560
935813	4592	4607	22709	22724	GGAAGTTTACACTGGA	kkk-d8-kekek	57	2044
935814	N/A	N/A	8465	8480	AGCATTTTATCATCCG	kkk-d8-kekek	78	1679
935815	N/A	N/A	11116	11131	AGTGATGTCAGGTTTT	kkk-d8-kekek	63	1232
935816	5187	5202	23304	23319	CTCAGTTTGTGAAGCA	kkk-d8-kekek	63	1817
935817	4172	4187	22289	22304	CTGCTTGAGGTTTTCC	kkk-d8-kekek	74	1279
935818	2915	2930	21032	21047	TAGTATGAGAAACGGC	kkk-d8-kekek	70	1121

Table 41

Percent control of human IRF4 mRNA with gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	Motif	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	kkk-d10-kkk	34	195
881450	3252	3267	21369	21384	ACACTTTTAGAGAGGA	kkk-d10-kkk	63	2111
881659	4592	4607	22709	22724	GGAAGTTTACACTGGA	kkk-d10-kkk	17	2044
935819	4200	4215	22317	22332	TCTATAGTGTTCAGG	kkk-d8-kekek	87	1734
935820	3070	3085	21187	21202	GCTTGATAAAGGCTGA	kkk-d8-kekek	99	1505
935821	3251	3266	21368	21383	CACTTTTAGAGAGGAG	kkk-d8-kekek	93	2036
935822	4591	4606	22708	22723	GAAGTTTACACTGGAT	kkk-d8-kekek	48	1968
935823	N/A	N/A	8464	8479	GCATTTTATCATCCGA	kkk-d8-kekek	55	1605
935824	N/A	N/A	11115	11130	GTGATGTCAGGTTTTC	kkk-d8-kekek	43	2627
935825	5186	5201	23303	23318	TCAGTTTGTGAAGCAT	kkk-d8-kekek	59	649
935826	4171	4186	22288	22303	TGCTTGAGGTTTTCT	kkk-d8-kekek	73	548

935827	2914	2929	21031	21046	AGTATGAGAAACGGCC	kkk-d8-kekek	90	1045
935828	4199	4214	22316	22331	CTATAGTGTTCAGGA	kkk-d8-kekek	77	552
935829	3069	3084	21186	21201	CTTGATAAAGGCTGAA	kkk-d8-kekek	88	1427
935830	3250	3265	21367	21382	ACTTTTAGAGAGGAGA	kkk-d8-kekek	79	1960
935831	4593	4608	22710	22725	CGGAAGTTTACACTGG	kkk-d8-kekek	82	2119
935832	N/A	N/A	8466	8481	AAGCATTTTATCATCC	kkk-d8-kekek	90	2628
935833	N/A	N/A	11117	11132	CAGTGATGTCAGGTTT	kkk-d8-kekek	44	2629
935834	5188	5203	23305	23320	CCTCAGTTTGTGAAGC	kkk-d8-kekek	97	1894
935835	4173	4188	22290	22305	ACTGCTTGAGGTTTTTC	kkk-d8-kekek	68	1356
935836	2916	2931	21033	21048	GTAGTATGAGAAACGG	kkk-d8-kekek	57	426
935837	4201	4216	22318	22333	CTCTATAGTGTTCAG	kkk-d8-kekek	85	1811
935838	3071	3086	21188	21203	AGCTTGATAAAGGCTG	kkk-d8-kekek	108	1579
935839	3252	3267	21369	21384	ACACTTTTAGAGAGGA	kkk-d8-kekek	85	2111
935840	4228	4243	22345	22360	AGTTGTAAATGAGTCG	kkk-d8-kekek	39	2021
935841	4594	4609	22711	22726	ACGGAAGTTTACACTG	kkk-d8-kekek	86	2195
935842	N/A	N/A	8467	8482	GAAGCATTTTATCATC	kkk-d8-kekek	105	2630
935843	N/A	N/A	11118	11133	GCAGTGATGTCAGGTT	kkk-d8-kekek	64	2631
935844	5189	5204	23306	23321	ACCTCAGTTTGTGAAG	kkk-d8-kekek	103	1971
935845	4174	4189	22291	22306	TACTGCTTGAGGTTTT	kkk-d8-kekek	108	1433
935846	2917	2932	21034	21049	TGTAGTATGAGAAACG	kkk-d8-kekek	77	1197
935847	4202	4217	22319	22334	TCTCTATAGTGTTC	kkk-d8-kekek	92	2632
935848	3072	3087	21189	21204	AAGCTTGATAAAGGCT	kkk-d8-kekek	104	2633
935849	3253	3268	21370	21385	GACACTTTTAGAGAGG	kkk-d8-kekek	108	451
935850	4229	4244	22346	22361	CAGTTGTAAATGAGTC	kkk-d8-kekek	24	560
935851	4592	4607	22709	22724	GGAAGTTTACACTGGA	kkk-d9-keke	22	2044
935852	N/A	N/A	8465	8480	AGCATTTTATCATCCG	kkk-d9-keke	58	1679
935853	N/A	N/A	11116	11131	AGTGATGTCAGGTTTT	kkk-d9-keke	41	1232
935854	5187	5202	23304	23319	CTCAGTTTGTGAAGCA	kkk-d9-keke	36	1817
935855	4172	4187	22289	22304	CTGCTTGAGGTTTTCC	kkk-d9-keke	50	1279
935856	2915	2930	21032	21047	TAGTATGAGAAACGGC	kkk-d9-keke	38	1121
935857	4200	4215	22317	22332	TCTATAGTGTTCAGG	kkk-d9-keke	32	1734
935858	3070	3085	21187	21202	GCTTGATAAAGGCTGA	kkk-d9-keke	76	1505
935859	3251	3266	21368	21383	CACTTTTAGAGAGGAG	kkk-d9-keke	43	2036
935860	4591	4606	22708	22723	GAAGTTTACACTGGAT	kkk-d9-keke	51	1968
935861	N/A	N/A	8464	8479	GCATTTTATCATCCGA	kkk-d9-keke	68	1605
935862	N/A	N/A	11115	11130	GTGATGTCAGGTTTTTC	kkk-d9-keke	66	2627
935863	5186	5201	23303	23318	TCAGTTTGTGAAGCAT	kkk-d9-keke	47	649
935864	4171	4186	22288	22303	TGCTTGAGGTTTTCTT	kkk-d9-keke	65	548
935865	2914	2929	21031	21046	AGTATGAGAAACGGCC	kkk-d9-keke	84	1045
935866	4199	4214	22316	22331	CTATAGTGTTCAGGA	kkk-d9-keke	78	552
935867	3069	3084	21186	21201	CTTGATAAAGGCTGAA	kkk-d9-keke	76	1427

935868	3250	3265	21367	21382	ACTTTTAGAGAGGAGA	kkk-d9-keke	59	1960
935869	4593	4608	22710	22725	CGGAAGTTTACACTGG	kkk-d9-keke	58	2119
935870	N/A	N/A	8466	8481	AAGCATTTTATCATCC	kkk-d9-keke	79	2628
935871	N/A	N/A	11117	11132	CAGTGATGTCAGGTTT	kkk-d9-keke	66	2629
935872	5188	5203	23305	23320	CCTCAGTTTGTGAAGC	kkk-d9-keke	92	1894
935873	4173	4188	22290	22305	ACTGCTTGAGGTTTTC	kkk-d9-keke	62	1356
935874	2916	2931	21033	21048	GTAGTATGAGAAACGG	kkk-d9-keke	85	426
935875	4201	4216	22318	22333	CTCTATAGTGTTCCAG	kkk-d9-keke	51	1811
935876	3071	3086	21188	21203	AGCTTGATAAAGGCTG	kkk-d9-keke	108	1579
935877	3252	3267	21369	21384	ACACTTTTAGAGAGGA	kkk-d9-keke	63	2111
935878	4228	4243	22345	22360	AGTTGTAAATGAGTCG	kkk-d9-keke	23	2021
935879	4594	4609	22711	22726	ACGGAAGTTTACACTG	kkk-d9-keke	87	2195
935880	N/A	N/A	8467	8482	GAAGCATTTTATCATC	kkk-d9-keke	92	2630
935881	N/A	N/A	11118	11133	GCAGTGATGTCAGGTT	kkk-d9-keke	44	2631
935882	5189	5204	23306	23321	ACCTCAGTTTGTGAAG	kkk-d9-keke	92	1971
935883	4174	4189	22291	22306	TACTGCTTGAGGTTTT	kkk-d9-keke	93	1433
935884	2917	2932	21034	21049	TGTAGTATGAGAAACG	kkk-d9-keke	71	1197
935885	4202	4217	22319	22334	TCTCTATAGTGTTCCA	kkk-d9-keke	67	2632
935886	3072	3087	21189	21204	AAGCTTGATAAAGGCT	kkk-d9-keke	118	2633
935887	3253	3268	21370	21385	GACACTTTTAGAGAGG	kkk-d9-keke	76	451
935888	4229	4244	22346	22361	CAGTTGTAAATGAGTC	kkk-d9-keke	42	560
935889	4592	4607	22709	22724	GGAAGTTTACACTGGA	kk-d9-eeekk	53	2044
935890	N/A	N/A	8465	8480	AGCATTTTATCATCCG	kk-d9-eeekk	72	1679
935891	N/A	N/A	11116	11131	AGTGATGTCAGGTTTT	kk-d9-eeekk	75	1232
935892	5187	5202	23304	23319	CTCAGTTTGTGAAGCA	kk-d9-eeekk	82	1817
935893	4172	4187	22289	22304	CTGCTTGAGGTTTTCC	kk-d9-eeekk	69	1279
935894	2915	2930	21032	21047	TAGTATGAGAAACGGC	kk-d9-eeekk	63	1121

Table 42

Percent control of human IRF4 mRNA with gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	Motif	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	kkk-d10-kkk	31	195
881450	3252	3267	21369	21384	ACACTTTTAGAGAGGA	kkk-d10-kkk	54	2111
881659	4592	4607	22709	22724	GGAAGTTTACACTGGA	kkk-d10-kkk	15	2044
935971	N/A	N/A	11116	11131	AGTGATGTCAGGTTTT	k-d9-kekeke	60	1232
935972	5187	5202	23304	23319	CTCAGTTTGTGAAGCA	k-d9-kekeke	81	1817
935973	4172	4187	22289	22304	CTGCTTGAGGTTTTCC	k-d9-kekeke	80	1279
935974	2915	2930	21032	21047	TAGTATGAGAAACGGC	k-d9-kekeke	68	1121

935975	4200	4215	22317	22332	TCTATAGTGTTCAGG	k-d9-kekeke	88	1734
935976	3070	3085	21187	21202	GCTTGATAAAGGCTGA	k-d9-kekeke	101	1505
935977	3251	3266	21368	21383	CACTTTTAGAGAGGAG	k-d9-kekeke	91	2036
935978	4591	4606	22708	22723	GAAGTTTACACTGGAT	k-d9-kekeke	89	1968
935979	N/A	N/A	8464	8479	GCATTTTATCATCCGA	k-d9-kekeke	77	1605
935980	N/A	N/A	11115	11130	GTGATGTCAGGTTTTTC	k-d9-kekeke	70	2627
935981	5186	5201	23303	23318	TCAGTTTGTGAAGCAT	k-d9-kekeke	91	649
935982	4171	4186	22288	22303	TGCTTGAGGTTTTTCCT	k-d9-kekeke	91	548
935983	2914	2929	21031	21046	AGTATGAGAAACGGCC	k-d9-kekeke	96	1045
935984	4199	4214	22316	22331	CTATAGTGTTCAGGA	k-d9-kekeke	88	552
935985	3069	3084	21186	21201	CTTGATAAAGGCTGAA	k-d9-kekeke	95	1427
935986	3250	3265	21367	21382	ACTTTTAGAGAGGAGA	k-d9-kekeke	83	1960
935987	4593	4608	22710	22725	CGGAAGTTTACACTGG	k-d9-kekeke	83	2119
935988	N/A	N/A	8466	8481	AAGCATTTTATCATCC	k-d9-kekeke	94	2628
935989	N/A	N/A	11117	11132	CAGTGATGTCAGGTTT	k-d9-kekeke	52	2629
935990	5188	5203	23305	23320	CCTCAGTTTGTGAAGC	k-d9-kekeke	89	1894
935991	4173	4188	22290	22305	ACTGCTTGAGGTTTTTC	k-d9-kekeke	79	1356
935992	2916	2931	21033	21048	GTAGTATGAGAAACGG	k-d9-kekeke	72	426
935993	4201	4216	22318	22333	CTCTATAGTGTTCAG	k-d9-kekeke	89	1811
935994	3071	3086	21188	21203	AGCTTGATAAAGGCTG	k-d9-kekeke	98	1579
935995	3252	3267	21369	21384	ACACTTTTAGAGAGGA	k-d9-kekeke	94	2111
935996	4228	4243	22345	22360	AGTTGTAAATGAGTCG	k-d9-kekeke	53	2021
935997	4594	4609	22711	22726	ACGGAAGTTTACACTG	k-d9-kekeke	98	2195
935998	N/A	N/A	8467	8482	GAAGCATTTTATCATC	k-d9-kekeke	96	2630
935999	N/A	N/A	11118	11133	GCAGTGATGTCAGGTT	k-d9-kekeke	67	2631
936000	5189	5204	23306	23321	ACCTCAGTTTGTGAAG	k-d9-kekeke	84	1971
936001	4174	4189	22291	22306	TACTGCTTGAGGTTTT	k-d9-kekeke	86	1433
936002	2917	2932	21034	21049	TGTAGTATGAGAAACG	k-d9-kekeke	86	1197
936003	4202	4217	22319	22334	TCTCTATAGTGTTCGA	k-d9-kekeke	82	2632
936004	3072	3087	21189	21204	AAGCTTGATAAAGGCT	k-d9-kekeke	98	2633
936005	3253	3268	21370	21385	GACACTTTTAGAGAGG	k-d9-kekeke	91	451
936006	4229	4244	22346	22361	CAGTTGTAAATGAGTC	k-d9-kekeke	38	560
936007	4592	4607	22709	22724	GGAAGTTTACACTGGA	ekk-d9-kkee	45	2044
936008	N/A	N/A	8465	8480	AGCATTTTATCATCCG	ekk-d9-kkee	57	1679
936009	N/A	N/A	11116	11131	AGTGATGTCAGGTTTT	ekk-d9-kkee	61	1232
936010	5187	5202	23304	23319	CTCAGTTTGTGAAGCA	ekk-d9-kkee	55	1817
936011	4172	4187	22289	22304	CTGCTTGAGGTTTTCC	ekk-d9-kkee	48	1279
936012	2915	2930	21032	21047	TAGTATGAGAAACGGC	ekk-d9-kkee	62	1121
936013	4200	4215	22317	22332	TCTATAGTGTTCAGG	ekk-d9-kkee	42	1734
936014	3070	3085	21187	21202	GCTTGATAAAGGCTGA	ekk-d9-kkee	65	1505
936015	3251	3266	21368	21383	CACTTTTAGAGAGGAG	ekk-d9-kkee	59	2036

936016	4227	4242	22344	22359	GTTGTAAATGAGTCGG	ekk-d9-kkee	31	559
936017	4591	4606	22708	22723	GAAGTTTACACTGGAT	ekk-d9-kkee	52	1968
936018	N/A	N/A	8464	8479	GCATTTTATCATCCGA	ekk-d9-kkee	39	1605
936019	N/A	N/A	11115	11130	GTGATGTCAGGTTTTTC	ekk-d9-kkee	52	2627
936020	5186	5201	23303	23318	TCAGTTTGTGAAGCAT	ekk-d9-kkee	53	649
936021	4171	4186	22288	22303	TGCTTGAGGTTTTTCCT	ekk-d9-kkee	65	548
936022	2914	2929	21031	21046	AGTATGAGAAACGGCC	ekk-d9-kkee	88	1045
936023	4199	4214	22316	22331	CTATAGTGTTCAGGA	ekk-d9-kkee	92	552
936024	3069	3084	21186	21201	CTTGATAAAGGCTGAA	ekk-d9-kkee	83	1427
936025	3250	3265	21367	21382	ACTTTTAGAGAGGAGA	ekk-d9-kkee	72	1960
936026	4226	4241	22343	22358	TTGTAAATGAGTCGGT	ekk-d9-kkee	49	195
936027	4593	4608	22710	22725	CGGAAGTTTACACTGG	ekk-d9-kkee	76	2119
936028	N/A	N/A	8466	8481	AAGCATTTTATCATCC	ekk-d9-kkee	86	2628
936029	N/A	N/A	11117	11132	CAGTGATGTCAGGTTT	ekk-d9-kkee	80	2629
936030	5188	5203	23305	23320	CCTCAGTTTGTGAAGC	ekk-d9-kkee	89	1894
936031	4173	4188	22290	22305	ACTGCTTGAGGTTTTTC	ekk-d9-kkee	54	1356
936032	2916	2931	21033	21048	GTAGTATGAGAAACGG	ekk-d9-kkee	71	426
936033	4201	4216	22318	22333	CTCTATAGTGTTCAG	ekk-d9-kkee	41	1811
936034	3071	3086	21188	21203	AGCTTGATAAAGGCTG	ekk-d9-kkee	99	1579
936035	3252	3267	21369	21384	ACACTTTTAGAGAGGA	ekk-d9-kkee	71	2111
936036	4228	4243	22345	22360	AGTTGTAAATGAGTCG	ekk-d9-kkee	51	2021
936037	4594	4609	22711	22726	ACGGAAGTTTACACTG	ekk-d9-kkee	83	2195
936038	N/A	N/A	8467	8482	GAAGCATTTTATCATC	ekk-d9-kkee	99	2630
936039	N/A	N/A	11118	11133	GCAGTGATGTCAGGTT	ekk-d9-kkee	44	2631
936040	5189	5204	23306	23321	ACCTCAGTTTGTGAAG	ekk-d9-kkee	98	1971
936041	4174	4189	22291	22306	TACTGCTTGAGGTTTT	ekk-d9-kkee	94	1433
936042	2917	2932	21034	21049	TGTAGTATGAGAAACG	ekk-d9-kkee	94	1197
936043	4202	4217	22319	22334	TCTCTATAGTGTCCA	ekk-d9-kkee	61	2632
936044	3072	3087	21189	21204	AAGCTTGATAAAGGCT	ekk-d9-kkee	101	2633
936045	3253	3268	21370	21385	GACACTTTTAGAGAGG	ekk-d9-kkee	76	451
936046	4229	4244	22346	22361	CAGTTGTAAATGAGTC	ekk-d9-kkee	45	560

Example 9: Effect of 3-10-3 cEt gapmers with phosphorothioate internucleoside linkages on human IRF4 *in vitro*, single dose

Modified oligonucleotides complementary to a human IRF4 nucleic acid were designed and tested
5 for their effect on IRF4 mRNA *in vitro*.

Cultured MM.1R cells at a density of 5,000 cells per well were transfected by free uptake with 1,000 nM concentration of modified oligonucleotide or no modified oligonucleotide for untreated controls. After approximately 24 hours, RNA was isolated from the cells and IRF4 mRNA levels were measured by quantitative real-time PCR. Human primer probe set hIRF4_LTS34726 (described hereinabove in Example 7)

was used to measure mRNA levels. IRF4 mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented in the table below as percent control of the amount of IRF4 mRNA, relative to untreated control (UTC) cells.

The modified oligonucleotides in Tables 43 through 52 are 3-10-3 cEt gapmers. The gapmers are 16 nucleobases in length, wherein the central gap segment comprises ten 2'-deoxynucleosides and is flanked by wing segments on both the 5' end and on the 3' end comprising three cEt nucleosides. The sugar motif for the gapmers is (from 5' to 3'): kkkddddd kkk; wherein 'd' represents a 2'-deoxyribose sugar and 'k' represents a cEt modified sugar. Each internucleoside linkage is a phosphorothioate internucleoside linkage and each cytosine residue is a 5-methylcytosine. "Start Site" indicates the 5'-most nucleoside to which the gapmer is complementary in the human nucleic acid sequence. "Stop Site" indicates the 3'-most nucleoside to which the gapmer is complementary in the human nucleic acid sequence.

Each modified oligonucleotide listed in Tables 43 through 52 below is complementary to human IRF4 nucleic acid sequences SEQ ID NO: 1 or SEQ ID NO: 2, as indicated. 'N/A' indicates that the modified oligonucleotide is not complementary to that particular nucleic acid sequence with 100% complementarity. As shown below, modified oligonucleotides complementary to human IRF4 reduced the amount of human IRF4 mRNA.

Table 43
Percent control of human IRF4 mRNA with gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	37	195
969844	N/A	N/A	3801	3816	CCTTACCTCGCCCTGG	131	2657
969854	N/A	N/A	4265	4280	CGCCAGCGGGTGAGCA	81	2658
969864	N/A	N/A	4371	4386	GGCGACGACAGCTGCG	115	2659
969874	N/A	N/A	4518	4533	AGCTAGCGCGCACTAA	108	2660
969884	N/A	N/A	4836	4851	TCCTGTAACGCACCCG	113	2661
969894	N/A	N/A	5487	5502	CCTGATGCCTCCGCCG	94	2662
969904	N/A	N/A	5667	5682	CGAGAACGCACGGACG	111	2663
969914	N/A	N/A	5761	5776	GCACAGGCGCGGACGC	106	2664
969924	N/A	N/A	6002	6017	GTGCACTCGCGCAAAG	105	2665
969934	N/A	N/A	6266	6281	TGCGGAGGTTCTTGA	88	2666
969944	N/A	N/A	6317	6332	CTGCCAAGTTGAAGAC	67	2667
969954	N/A	N/A	6407	6422	GTCTTCAGATTTACA	117	2668
969964	N/A	N/A	6771	6786	ATACATGTCTGGTTTA	96	2669
969974	511	526	6990	7005	TTTTGGCTCCCTCAGG	103	2670

969984	N/A	N/A	7169	7184	TTTCAACTTGTGACCC	99	2671
969994	N/A	N/A	7222	7237	ATACATTGAGGCATAC	98	2672
970004	N/A	N/A	7577	7592	GACATAAAGGACCCCG	92	2673
970014	N/A	N/A	7639	7654	GGTCTGAGTTGTACAG	80	2674
970024	N/A	N/A	8104	8119	CACCAATGGCAGCACC	84	2675
970034	N/A	N/A	8221	8236	CATGATAAGGCACTAC	106	2676
970044	N/A	N/A	8384	8399	TGGAGATACTTGTACT	58	2677
970054	N/A	N/A	8489	8504	ATCCCTTATTAGACTG	107	2678
970064	645	660	9135	9150	CCAGCTTCGGTCGAGG	105	2679
970074	701	716	9191	9206	GTCATGGGACATTGGT	74	2680
970084	N/A	N/A	9431	9446	CTGAGAGTAACTTGG	101	2681
970094	N/A	N/A	9582	9597	GCTCAATAATCTCCCA	100	2682
970104	N/A	N/A	9679	9694	GTGTTTGCCATGGTAT	43	2683
970114	N/A	N/A	9842	9857	CGCATTGCTAGATTCT	63	2684
970124	N/A	N/A	9987	10002	GGATAACCTGAACATG	91	2685
970134	N/A	N/A	10120	10135	CCATATTGGAAACCAG	90	2686
970144	N/A	N/A	10178	10193	CAGTAAACGCAAGTCT	114	2687
970154	N/A	N/A	10262	10277	AGACAGGTCTCTACCT	112	2688
970164	N/A	N/A	10449	10464	TGCCAAAGAGCCCAAT	119	2689
970174	N/A	N/A	10675	10690	AACTAGCAGGGCACGC	98	2690
970184	811	826	10876	10891	GGACTCCGGGAGCCTG	108	2691
970194	N/A	N/A	11103	11118	TTTCTAATGGTGCTCC	96	2692
970203	N/A	N/A	11365	11380	AACTAATGTCCCCAGG	112	2693
970213	N/A	N/A	11452	11467	TTGTTTGCAAGCTATA	64	2694
970223	N/A	N/A	11540	11555	TTCTTTATAGTAGGTA	85	2695
970233	N/A	N/A	11664	11679	GAATTCCAAACCTTAA	96	2696
970243	N/A	N/A	11946	11961	ACACAAGTCTTAGGTG	253	2697
970253	N/A	N/A	12007	12022	TCAGAAATCACGAGGT	57	2698
970263	N/A	N/A	12213	12228	TAATCTGTATCATGCA	78	2699
970273	N/A	N/A	12293	12308	AGCTGCCACTGGTAAC	100	2700
970283	N/A	N/A	12676	12691	GGCCTTAATGGTGATT	116	2701
970293	N/A	N/A	12929	12944	GAAATGAACCCTAAGT	105	2702
970303	N/A	N/A	13129	13144	ACCGACTCTTTTTTTA	102	2703
970313	N/A	N/A	13400	13415	CAGAGCTCCGGAGTCA	106	2704
970323	N/A	N/A	14015	14030	GCGACTGCTGAAAACC	104	2705
970333	N/A	N/A	14206	14221	AGTACAGTCCACTCCA	93	2706
970343	N/A	N/A	14248	14263	CCAACCTTATAGCACTC	86	2707
970353	N/A	N/A	14673	14688	ACAAAAACTTGGGTCA	113	2708
970363	N/A	N/A	15188	15203	GATGGGACCGCCCTGG	113	2709
970373	N/A	N/A	15597	15612	CTAGTCGCGCAAGTCT	104	2710
970383	N/A	N/A	15852	15867	CAGAAATGGCGAGTTGG	69	2711

970393	N/A	N/A	15918	15933	CTTAGTCAGAATCTGT	99	2712
970403	N/A	N/A	16174	16189	TAAAATGTCACGCCCCG	100	2713
970413	N/A	N/A	16468	16483	CACCAGCCATCGGCAG	119	2714
970423	N/A	N/A	16699	16714	AGTGAAGTCGGGAGAT	92	2715
970433	N/A	N/A	16869	16884	GGCTCTTGATGTGAAC	112	2716
970443	N/A	N/A	16961	16976	ATCACCGAACACACCA	112	2717

Table 44

Percent control of human IRF4 mRNA with gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	26	195
935583	N/A	N/A	11119	11134	AGCAGTGATGTCAGGT	16	2718
969845	N/A	N/A	4005	4020	GCCAAGGAGGCGGGCC	102	2719
969855	N/A	N/A	4294	4309	ACCCAAATGTGGAGCT	97	2720
969865	N/A	N/A	4377	4392	GGAGAGGGCGACGACA	101	2721
969875	N/A	N/A	4541	4556	GAATAGGACCCCTATC	103	2722
969885	N/A	N/A	4876	4891	TCCGAGCTCGGCCCCC	110	2723
969895	N/A	N/A	5506	5521	TGCGGCTCCGGCGACG	120	2724
969905	N/A	N/A	5670	5685	AAACGAGAACGCACGG	91	2725
969915	N/A	N/A	5766	5781	CGCCGGCACAGGCGCG	86	2726
969925	N/A	N/A	6006	6021	GTGTGTGCACTCGCGC	81	2727
969935	N/A	N/A	6269	6284	AGATGCGGAGGTTCTT	68	2728
969945	N/A	N/A	6324	6339	CCTATCACTGCCAAGT	103	2729
969955	N/A	N/A	6412	6427	CATAGGTCCTTCAGAT	105	2730
969965	414	429	6893	6908	CAAAGCGCACCGCAGG	104	2731
969975	N/A	N/A	6999	7014	CCCTACCTTTTTTGGC	107	2732
969985	N/A	N/A	7186	7201	GCTGAACCCACAGGA	100	2733
969995	N/A	N/A	7223	7238	TATACATTGAGGCATA	93	2734
970005	N/A	N/A	7579	7594	GTGACATAAAGGACCC	90	2735
970015	N/A	N/A	7641	7656	AAGGTCTGAGTTGTAC	80	2736
970025	N/A	N/A	8130	8145	CCCGACCCTCCCCAAC	135	2737
970035	N/A	N/A	8223	8238	CACATGATAAGGCACT	79	2738
970045	N/A	N/A	8387	8402	CAATGGAGATACTTGT	116	2739
970055	N/A	N/A	8493	8508	GGGAATCCCTTATTAG	100	2740
970065	647	662	9137	9152	CTCCAGCTTCGGTCTGA	91	2741
970075	N/A	N/A	9280	9295	AGCAATTAGCTCTTCT	89	2742
970085	N/A	N/A	9435	9450	GATCCTGAGAGTAAAC	94	2743

970095	N/A	N/A	9583	9598	AGCTCAATAATCTCCC	94	2744
970105	N/A	N/A	9740	9755	CCACAATCAGCAAGTC	100	2745
970115	N/A	N/A	9844	9859	ACCGCATTGCTAGATT	73	2746
970125	N/A	N/A	9995	10010	GCAGCCAAGGATAACC	94	2747
970135	N/A	N/A	10127	10142	TCCACTACCATATTGG	129	2748
970145	N/A	N/A	10180	10195	AGCAGTAAACGCAAGT	73	2749
970155	N/A	N/A	10268	10283	GCTTCAAGACAGGTCT	71	2750
970165	N/A	N/A	10477	10492	GCTGAGAGTTCAGGTC	93	2751
970175	N/A	N/A	10678	10693	AGCAACTAGCAGGGCA	102	2752
970185	N/A	N/A	11001	11016	TCGAATCTGCCCAAAG	77	2753
970204	N/A	N/A	11369	11384	CCAGAATAATGTCCC	94	2754
970214	N/A	N/A	11455	11470	TATTTGTTTGCAAGCT	70	2755
970224	N/A	N/A	11549	11564	AGAGGTGCCTTCTTTA	82	2756
970234	N/A	N/A	11749	11764	CCACAATACTCGCCTC	109	2757
970244	N/A	N/A	11948	11963	CCACACAAGTCTTAGG	85	2758
970254	N/A	N/A	12048	12063	CGAGGTGATTCTCGGG	85	2759
970264	N/A	N/A	12222	12237	GCTGATAATTAATCTG	109	2760
970274	N/A	N/A	12373	12388	CGCCCATGAGTTGAAA	87	2761
970284	N/A	N/A	12692	12707	AAAGGGTAAGCACTGA	81	2762
970294	N/A	N/A	12991	13006	ATTTAAGTCATGTGTC	83	2763
970304	N/A	N/A	13132	13147	GCCACCGACTCTTTTT	105	2764
970314	N/A	N/A	13416	13431	CGGCAGTCTGCAAACA	76	2765
970324	N/A	N/A	14016	14031	GGCGACTGCTGAAAAC	110	2766
970334	N/A	N/A	14207	14222	CAGTACAGTCCACTCC	95	2767
970344	N/A	N/A	14249	14264	GCCAACTTATAGCACT	62	2768
970354	N/A	N/A	14686	14701	TCTGGATGAGCTTACA	86	2769
970364	N/A	N/A	15375	15390	ATCCACTGGCACCAAG	95	2770
970374	N/A	N/A	15599	15614	TTCTAGTCGCGCAAGT	107	2771
970384	N/A	N/A	15866	15881	CTACACAGGCTAATCA	96	2772
970394	N/A	N/A	15920	15935	GACTTAGTCAGAATCT	90	2773
970404	N/A	N/A	16176	16191	AATAAAATGTCACGCC	80	2774
970414	N/A	N/A	16610	16625	CAGAATGTTTCGACAT	86	2775
970424	N/A	N/A	16703	16718	CCACAGTGAAGTCGGG	94	2776
970434	N/A	N/A	16885	16900	TTACTCCGCTGAGTGG	104	2777
970444	N/A	N/A	16964	16979	CTCATCACCGAACACA	92	2778

Table 45
Percent control of human IRF4 mRNA with gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	33	195
969846	N/A	N/A	4037	4052	GCGCGGAGGGCAGGCG	132	2779
969856	N/A	N/A	4298	4313	AGCGACCCAAATGTGG	102	2780
969866	N/A	N/A	4407	4422	GCCCGGGAGAGCGGAG	132	2781
969876	N/A	N/A	4637	4652	CGCGGAGGACCTCGCC	107	2782
969886	N/A	N/A	4896	4911	GCGGGCACAGCCGTCC	121	2783
969896	N/A	N/A	5530	5545	AGCCGAGGCCTCCTTT	128	2784
969906	N/A	N/A	5673	5688	TGGAACGAGAACGCA	107	2785
969916	N/A	N/A	5774	5789	AAAACAGCCGCCGCA	109	2786
969926	N/A	N/A	6022	6037	CGTAACAACGACACAC	135	2787
969936	N/A	N/A	6272	6287	GTGAGATGCGGAGGTT	61	2788
969946	N/A	N/A	6360	6375	AGCTATGCTCTAGGAA	89	2789
969956	N/A	N/A	6414	6429	CGCATAGGTCCTTCAG	94	2790
969966	429	444	6908	6923	GTCATTGCTCTTGTTT	82	2791
969976	N/A	N/A	7004	7019	AGAGCCCCTACCTTTT	107	2792
969986	N/A	N/A	7188	7203	ATGCTGAACCCACAG	84	2793
969996	N/A	N/A	7224	7239	ATATACATTGAGGCAT	131	2794
970006	N/A	N/A	7592	7607	GCGAATGTGCCTTGTTG	88	2795
970016	N/A	N/A	7644	7659	TACAAGGTCTGAGTTG	106	2796
970026	N/A	N/A	8132	8147	CGCCCGACCCTCCCCA	124	2797
970036	N/A	N/A	8224	8239	TCACATGATAAGGCAC	81	2798
970046	N/A	N/A	8390	8405	GGACAATGGAGATACT	97	2799
970056	N/A	N/A	8496	8511	TCAGGGAATCCCTTAT	96	2800
970066	650	665	9140	9155	TCCCTCCAGCTTCGGT	121	2801
970076	N/A	N/A	9284	9299	CATTAGCAATTAGCTC	137	2802
970086	N/A	N/A	9437	9452	TGGATCCTGAGAGTAA	100	2803
970096	N/A	N/A	9587	9602	TACCAGCTCAATAATC	127	2804
970106	N/A	N/A	9744	9759	TAATCCACAATCAGCA	127	2805
970116	N/A	N/A	9847	9862	GTTACCGCATTGCTAG	84	2806
970126	N/A	N/A	10002	10017	ACTACCTGCAGCCAAG	96	2807
970136	N/A	N/A	10130	10145	TCCTCCACTACCATAT	113	2808
970146	N/A	N/A	10184	10199	CCAGAGCAGTAAACGC	89	2809
970156	N/A	N/A	10273	10288	CCGATGCTTCAAGACA	87	2810
970166	N/A	N/A	10489	10504	GTTCAACAACAGAGCTG	116	2811
970176	N/A	N/A	10711	10726	CGCCCAATCACCTTCC	119	2812

970186	N/A	N/A	11005	11020	CCCATCGAATCTGCCC	124	2813
970195	N/A	N/A	11127	11142	GAACCACAAGCAGTGA	132	2814
970205	N/A	N/A	11371	11386	GACCAGAACTAATGTC	127	2815
970215	N/A	N/A	11468	11483	CAGATTGAATCCATAT	80	2816
970225	N/A	N/A	11553	11568	GCCTAGAGGTGCCTTC	87	2817
970235	N/A	N/A	11797	11812	AAAGAGCTGGTAGGTC	135	2818
970245	N/A	N/A	11960	11975	CTCTTCAGGCACCCAC	87	2819
970255	N/A	N/A	12052	12067	CATTCGAGGTGATTCT	89	2820
970265	N/A	N/A	12224	12239	TGGCTGATAATTAATC	105	2821
970275	N/A	N/A	12383	12398	TTTAAAATATCGCCCA	101	2822
970285	N/A	N/A	12694	12709	TTAAAGGGTAAGCACT	118	2823
970295	N/A	N/A	13039	13054	ACTTGCTAAGTCTTAT	87	2824
970305	N/A	N/A	13197	13212	TGGAGAAGTCCCGTGG	109	2825
970315	N/A	N/A	13769	13784	CCTTACCTGACAAGAA	111	2826
970325	N/A	N/A	14019	14034	AGAGGCGACTGCTGAA	119	2827
970335	N/A	N/A	14208	14223	CCAGTACAGTCCACTC	106	2828
970345	N/A	N/A	14332	14347	CGCTGAATTGTCATGA	101	2829
970355	N/A	N/A	14688	14703	AATCTGGATGAGCTTA	96	2830
970365	N/A	N/A	15410	15425	TCATTAGAAAGCCCTC	119	2831
970375	N/A	N/A	15602	15617	AAGTTCTAGTCGCGCA	89	2832
970385	N/A	N/A	15868	15883	ACCTACACAGGCTAAT	104	2833
970395	N/A	N/A	15986	16001	GCTAACTTACAGGACT	108	2834
970405	N/A	N/A	16252	16267	AGACAAGTGCCCATCC	99	2835
970415	N/A	N/A	16611	16626	TCAGAATGTTTCGACA	94	2836
970425	N/A	N/A	16712	16727	GGTAGTAGACCACAGT	77	2837
970435	N/A	N/A	16890	16905	CACTCTTACTCCGCTG	112	2838
970445	N/A	N/A	16966	16981	CCCTCATCACCGAACA	125	2839

Table 46

Percent control of human IRF4 mRNA with gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	33	195
969847	N/A	N/A	4044	4059	CGCAGGAGCGCGGAGG	128	2840
969857	N/A	N/A	4302	4317	TCGGAGCGACCCAAAT	88	2841
969867	N/A	N/A	4444	4459	ATTCCGCGCGCAGAGC	121	2842
969877	N/A	N/A	4643	4658	TCCACGCGCGGAGGAC	143	2843
969887	N/A	N/A	4928	4943	ACCTTCGCGGCCGCGCC	142	2844

969897	N/A	N/A	5570	5585	CGCCCAGGACCCGGCT	101	2845
969907	N/A	N/A	5705	5720	CGGGAGCCCGGAGGAA	103	2846
969917	N/A	N/A	5782	5797	GAGAGACGAAAACAGC	95	2847
969927	N/A	N/A	6112	6127	GAGGAAGTCCCCTTCC	96	2848
969937	N/A	N/A	6274	6289	GAGTGAGATGCGGAGG	45	2849
969947	N/A	N/A	6364	6379	CCCCAGCTATGCTCTA	130	2850
969957	N/A	N/A	6416	6431	GGCGCATAGGTCCCTTC	107	2851
969967	446	461	6925	6940	TCAACCAGTTCCTCAA	123	2852
969977	N/A	N/A	7008	7023	CAGGAGAGCCCCCTACC	108	2853
969987	N/A	N/A	7191	7206	CCTATGCTGAACCCCA	112	2854
969997	N/A	N/A	7225	7240	CATATACATTGAGGCA	80	2855
970007	N/A	N/A	7598	7613	TGGCATGCGAATGTGC	121	2856
970017	N/A	N/A	7648	7663	TTTCTACAAGGTCTGA	97	2857
970027	N/A	N/A	8135	8150	ACACGCCCCGACCCTCC	96	2858
970037	N/A	N/A	8231	8246	TGTGGTTTCACATGAT	79	2859
970047	N/A	N/A	8403	8418	GGAGGATCATAAAGGA	68	2860
970057	N/A	N/A	8520	8535	GTGCTCTTACAGCCTC	115	2861
970067	655	670	9145	9160	CGTAGTCCCTCCAGCT	73	2862
970077	N/A	N/A	9289	9304	GGCCACATTAGCAATT	100	2863
970087	N/A	N/A	9440	9455	GCATGGATCCTGAGAG	89	2864
970097	N/A	N/A	9600	9615	TTCGAGAGAAATATAC	78	2865
970107	N/A	N/A	9748	9763	CATCTAATCCACAATC	119	2866
970117	N/A	N/A	9849	9864	GAGTTACCGCATIGCT	53	2867
970127	N/A	N/A	10004	10019	TCACTACCTGCAGCCA	94	2868
970137	N/A	N/A	10133	10148	AATTCCTCCACTACCA	141	2869
970147	N/A	N/A	10187	10202	GAGCCAGAGCAGTAAA	102	2870
970157	N/A	N/A	10275	10290	TACCGATGCTTCAAGA	103	2871
970167	N/A	N/A	10499	10514	CACAAAGCGGGTTCAC	112	2872
970177	N/A	N/A	10777	10792	AGAGAGTCCGACGCAC	118	2873
970187	N/A	N/A	11006	11021	TCCCATCGAATCTGCC	105	2874
970196	N/A	N/A	11136	11151	CGGTCAGCAGAACCAC	108	2875
970206	N/A	N/A	11377	11392	ATGAGGGACCAGAACT	94	2876
970216	N/A	N/A	11470	11485	ATCAGATTGAATCCAT	77	2877
970226	N/A	N/A	11555	11570	AAGCCTAGAGGTGCCT	71	2878
970236	N/A	N/A	11813	11828	CCTCATTCACAACCTAG	95	2879
970246	N/A	N/A	11963	11978	CTACTCTTCAGGCACC	82	2880
970256	N/A	N/A	12055	12070	GGCCATTGAGGTGAT	99	2881
970266	N/A	N/A	12229	12244	GCTCATGGCTGATAAT	117	2882
970276	N/A	N/A	12385	12400	TCTTTAAAATATCGCC	145	2883
970286	N/A	N/A	12697	12712	ACATTAAAGGGTAAGC	123	2884
970296	N/A	N/A	13042	13057	AGAACTTGCTAAGTCT	134	2885

970306	N/A	N/A	13207	13222	GGTCAACACTTGGAGA	123	2886
970316	N/A	N/A	13771	13786	TGCCTTACCTGACAAG	96	2887
970326	N/A	N/A	14023	14038	TTTAAGAGGCGACTGC	200	2888
970336	N/A	N/A	14211	14226	AAACCAGTACAGTCCA	123	2889
970346	N/A	N/A	14431	14446	CCCACGCGGGAGGCTC	123	2890
970356	N/A	N/A	14706	14721	CTTTGGGCACCAAAAG	133	2891
970366	N/A	N/A	15411	15426	TTCATTAGAAAGCCCT	122	2892
970376	N/A	N/A	15606	15621	TAGTAAGTTCTAGTCG	113	2893
970386	N/A	N/A	15878	15893	CTGAGACTACACCTAC	140	2894
970396	N/A	N/A	15991	16006	TTCTAGCTAAGTTACA	118	2895
970406	N/A	N/A	16271	16286	GACTGGAACATTGTTG	141	2896
970416	N/A	N/A	16639	16654	TGCCATGGACAAGTTT	118	2897
970426	N/A	N/A	16717	16732	CAAAAGGTAGTAGACC	89	2898
970436	N/A	N/A	16891	16906	GCACTCTTACTCCGCT	98	2899
970446	N/A	N/A	16970	16985	GAAACCCTCATCACCG	138	2900

Table 47

Percent control of human IRF4 mRNA with gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	23	195
969848	N/A	N/A	4047	4062	CGTCGCAGGAGCGCGG	99	2901
969858	N/A	N/A	4313	4328	GCACGCAAGGCTCGGA	93	2902
969868	N/A	N/A	4446	4461	GGATTCCGCGCGCAGA	79	2903
969878	N/A	N/A	4677	4692	CGCGACTCTGTCAATT	92	2904
969888	N/A	N/A	4981	4996	CTGCGAAGCGCGCGCG	106	2905
969898	N/A	N/A	5600	5615	GCCTTCAGCGGTTTCC	96	2906
969908	N/A	N/A	5719	5734	ACGGAGGCGGCAGACG	109	2907
969918	N/A	N/A	5785	5800	GGTGAGAGACGAAAAC	116	2908
969928	N/A	N/A	6115	6130	CCGGAGGAAGTCCCCT	100	2909
969938	N/A	N/A	6277	6292	GTAGAGTGAGATGCGG	49	2910
969948	N/A	N/A	6397	6412	TTTACACCGTTGCTCA	97	2911
969958	N/A	N/A	6418	6433	ATGGCGCATAGGTCCT	105	2912
969968	450	465	6929	6944	CCGCTCAACCAGTTCC	112	2913
969978	N/A	N/A	7011	7026	ATTCAGGAGAGCCCCT	115	2914
969988	N/A	N/A	7193	7208	CTCCTATGCTGAACCC	91	2915
969998	N/A	N/A	7227	7242	CCCATATACATTGAGG	84	2916
970008	N/A	N/A	7603	7618	ACAGATGGCATGCGAA	81	2917

970018	N/A	N/A	7666	7681	TGCTATTAAACTGATT	103	2918
970028	N/A	N/A	8138	8153	CGGACACGCCCCGACCC	93	2919
970038	N/A	N/A	8331	8346	ACCAAAAAGTACCACAG	108	2920
970048	N/A	N/A	8445	8460	GACTGGAGTGAACCCT	62	2921
970058	N/A	N/A	8522	8537	GGGTGCTCTTACAGCC	102	2922
970068	677	692	9167	9182	TCCGGGTGTGGCTGAT	74	2923
970078	N/A	N/A	9310	9325	CCAGGATTCGCCATGG	87	2924
970088	N/A	N/A	9445	9460	GCCTAGCATGGATCCT	104	2925
970098	N/A	N/A	9605	9620	CACTATTCGAGAGAAA	70	2926
970108	N/A	N/A	9754	9769	GGACCACATCTAATCC	112	2927
970118	N/A	N/A	9852	9867	CCTGAGTTACCGCATT	76	2928
970128	N/A	N/A	10011	10026	CACCTCTTCACTACCT	100	2929
970138	N/A	N/A	10138	10153	TAGCCAATTCCTCCAC	99	2930
970148	N/A	N/A	10193	10208	TCCATAGAGCCAGAGC	80	2931
970158	N/A	N/A	10277	10292	GTTACCGATGCTTCAA	54	2932
970168	N/A	N/A	10550	10565	ACTAACAGGGAGACTG	119	2933
970178	N/A	N/A	10779	10794	ACAGAGAGTCCGACGC	108	2934
970188	N/A	N/A	11012	11027	CTAAAGTCCCATCGAA	102	2935
970197	N/A	N/A	11142	11157	CTGAAACGGTCAGCAG	97	2936
970207	N/A	N/A	11399	11414	TAGGCACATCAATGTT	88	2937
970217	N/A	N/A	11525	11540	AAGATCTCCATGGTGC	61	2938
970227	N/A	N/A	11557	11572	CCAAGCCTAGAGGTGC	79	2939
970237	N/A	N/A	11820	11835	GTGCAAGCCTCATICA	81	2940
970247	N/A	N/A	11993	12008	GTTGCCGAGATATAAA	87	2941
970257	N/A	N/A	12085	12100	AGACAGTGCGCCCCAA	117	2942
970267	N/A	N/A	12231	12246	GTGCTCATGGCTGATA	76	2943
970277	N/A	N/A	12455	12470	TAAAACTGCGCTCTCT	114	2944
970287	N/A	N/A	12860	12875	CCACATACCTGAAACG	109	2945
970297	N/A	N/A	13056	13071	GAGCATCACTATTAAG	86	2946
970307	N/A	N/A	13216	13231	CATGAGCTCGGTCAAC	101	2947
970317	N/A	N/A	13779	13794	TAACGAGGTGCCTTAC	87	2948
970327	N/A	N/A	14026	14041	TGTTTTAAGAGGCGAC	97	2949
970337	N/A	N/A	14217	14232	TGTGCAAAACCAGTAC	120	2950
970347	N/A	N/A	14448	14463	GGGTAGAGCAGCTCCC	116	2951
970357	N/A	N/A	14710	14725	TTTGCTTTGGGCACCA	76	2952
970367	N/A	N/A	15431	15446	TGCCAGTTCCTTGTGA	102	2953
970377	N/A	N/A	15607	15622	ATAGTAAGTTCTAGTC	89	2954
970387	N/A	N/A	15880	15895	ATCTGAGACTACACCT	108	2955
970397	N/A	N/A	16095	16110	ATACACACCCTCGGGC	110	2956
970407	N/A	N/A	16274	16289	ACGGACTGGAACATTG	62	2957
970417	N/A	N/A	16640	16655	ATGCCATGGACAAGTT	82	2958

970427	N/A	N/A	16728	16743	CCACGAAGATTCAAAA	107	2959
970437	N/A	N/A	16894	16909	TGAGCACTCTTACTCC	106	2960
970447	N/A	N/A	16976	16991	TGTTTCAGAAACCCTCA	115	2961

Table 48

Percent control of human IRF4 mRNA with gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	27	195
969849	N/A	N/A	4081	4096	CGGTTAGCTCATCCCG	95	2962
969859	N/A	N/A	4320	4335	GGCCACCGCACGCAAG	124	2963
969869	N/A	N/A	4488	4503	CGACAAGTGGCGCAGA	98	2964
969879	N/A	N/A	4805	4820	CGACACGCGCCGCTCG	62	2965
969889	N/A	N/A	4989	5004	CTTTGAGGCTGCGAAG	98	2966
969899	N/A	N/A	5610	5625	GCCCGGCCGGGCCTTC	104	2967
969909	N/A	N/A	5725	5740	CCACGGACGGAGGCGG	106	2968
969919	N/A	N/A	5793	5808	AGAGACGCGGTGAGAG	120	2969
969929	N/A	N/A	6123	6138	CCAAATTCCCGGAGGA	125	2970
969939	N/A	N/A	6280	6295	CCGGTAGAGTGAGATG	103	2971
969949	N/A	N/A	6398	6413	ATTTACACCGTTGCTC	87	2972
969959	N/A	N/A	6420	6435	GAATGGCGCATAGGTC	74	2973
969969	454	469	6933	6948	GGCTCCGCTCAACCAG	91	2974
969979	N/A	N/A	7026	7041	TGTTAGGTGACCCAAA	98	2975
969989	N/A	N/A	7198	7213	TAATTCTCCTATGCTG	97	2976
969999	N/A	N/A	7243	7258	ATTCAATGCACCCCCC	98	2977
970009	N/A	N/A	7604	7619	GACAGATGGCATGCGA	84	2978
970019	N/A	N/A	7727	7742	ATAACACGGTGTTGAC	79	2979
970029	N/A	N/A	8140	8155	GGCGGACACGCCCGAC	93	2980
970039	N/A	N/A	8343	8358	GCTAAACCTGGCACCA	93	2981
970049	N/A	N/A	8451	8466	CGAAAAGACTGGAGTG	74	2982
970059	N/A	N/A	8784	8799	GGGTTAAAGGAGTGCA	100	2983
970069	681	696	9171	9186	GATTTCCGGGTGTGGC	25	2984
970079	N/A	N/A	9371	9386	CCCCGAGCTGCACACG	105	2985
970089	N/A	N/A	9457	9472	ACGAAGGGCAGTGCCT	105	2986
970099	N/A	N/A	9613	9628	GAACACACCACTATTC	120	2987
970109	N/A	N/A	9772	9787	GGAACCTCCCGAGGGCA	87	2988
970119	N/A	N/A	9854	9869	GGCCTGAGTTACCGCA	92	2989
970129	N/A	N/A	10013	10028	TACACCTCTTCACTAC	118	2990

970139	N/A	N/A	10143	10158	TATGTTAGCCAATTCC	59	2991
970149	N/A	N/A	10196	10211	AATTCCATAGAGCCAG	82	2992
970159	N/A	N/A	10279	10294	CTGTTACCGATGCTTC	44	2993
970169	N/A	N/A	10558	10573	TGTAAGTACTAACAG	131	2994
970179	N/A	N/A	10783	10798	CTAGACAGAGAGTCCG	95	2995
970189	N/A	N/A	11017	11032	AGTGTCTAAAGTCCCA	58	2996
970198	N/A	N/A	11143	11158	GCTGAAACGGTCAGCA	92	2997
970208	N/A	N/A	11401	11416	CTTAGGCACATCAATG	92	2998
970218	N/A	N/A	11527	11542	GTAAGATCTCCATGGT	83	2999
970228	N/A	N/A	11566	11581	GTGTGCTTGCCAAGCC	34	3000
970238	N/A	N/A	11826	11841	AAAAAGGTGCAAGCCT	94	3001
970248	N/A	N/A	11996	12011	GAGGTTGCCGAGATAT	71	3002
970258	N/A	N/A	12094	12109	AAGCGAGTCAGACAGT	122	3003
970268	N/A	N/A	12278	12293	CTGTATGGAACCCCAA	97	3004
970278	N/A	N/A	12511	12526	ATGTAAAGTCTGCTGA	80	3005
970288	N/A	N/A	12862	12877	GTCCACATACCTGAAA	92	3006
970298	N/A	N/A	13059	13074	ATAGAGCATCACTATT	100	3007
970308	N/A	N/A	13219	13234	CAGCATGAGCTCGGTC	78	3008
970318	N/A	N/A	13786	13801	TAACAGATAACGAGGT	88	3009
970328	N/A	N/A	14054	14069	TCGAGATCATAGTGCA	71	3010
970338	N/A	N/A	14219	14234	CCTGTGCAAAACCAAGT	110	3011
970348	N/A	N/A	14459	14474	TGGCGAGTGGCGGGTA	118	3012
970358	N/A	N/A	14733	14748	AAGCTTAGTTATCTGG	65	3013
970368	N/A	N/A	15573	15588	AGGACACTCACAGGCG	92	3014
970378	N/A	N/A	15614	15629	CAGATTAATAGTAAAGT	112	3015
970388	N/A	N/A	15885	15900	CCGTGATCTGAGACTA	55	3016
970398	N/A	N/A	16144	16159	TGACACAGGAGCCGCT	85	3017
970408	N/A	N/A	16283	16298	AGATACAAAACGGACT	115	3018
970418	N/A	N/A	16642	16657	TTATGCCATGGACAAG	81	3019
970428	N/A	N/A	16730	16745	ACCCACGAAGATTCAA	117	3020
970438	N/A	N/A	16899	16914	AGGAATGAGCACTCTT	93	3021
970448	N/A	N/A	16984	16999	AGAGACCATGTTCAGA	88	3022
970608	1440	1455	19557	19572	AGATCTGTGGTAATCT	103	3023

Table 49
Percent control of human IRF4 mRNA with gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	19	195
969850	N/A	N/A	4151	4166	GGCAGTTGTGCCGTCT	117	3024
969860	N/A	N/A	4342	4357	AGGGACCGCGCCAGGC	100	3025
969870	N/A	N/A	4490	4505	AACGACAAGTGGCGCA	88	3026
969880	N/A	N/A	4808	4823	TCCCGACACGCGCCGC	112	3027
969890	N/A	N/A	5006	5021	CCACGAGGCCCGGAG	96	3028
969900	N/A	N/A	5655	5670	GACGAACGCGCAAAAC	85	3029
969910	N/A	N/A	5747	5762	GCACGGAGAGGGCGAG	96	3030
969920	N/A	N/A	5795	5810	ACAGAGACGCGGTGAG	86	3031
969930	N/A	N/A	6211	6226	GGACTAAGGACAGCTG	87	3032
969940	N/A	N/A	6283	6298	TAACCGGTAGAGTGAG	73	3033
969950	N/A	N/A	6400	6415	AGATTTACACCGTTGC	70	3034
969960	N/A	N/A	6423	6438	AAAGAATGGCGCATAG	90	3035
969970	471	486	6950	6965	GTCTGAGATGTCCAGC	93	3036
969980	N/A	N/A	7156	7171	CCCACATAACTCAGGC	116	3037
969990	N/A	N/A	7201	7216	GATTAATTCTCCTATG	119	3038
970000	N/A	N/A	7375	7390	TGAGATATTCCTCTCA	82	3039
970010	N/A	N/A	7628	7643	TACAGGACAGGTAAAG	129	3040
970020	N/A	N/A	7735	7750	TAGAATGCATAACACG	92	3041
970030	N/A	N/A	8142	8157	CAGGCGGACACGCCCCG	105	3042
970040	N/A	N/A	8346	8361	ATGGCTAAACCTGGCA	78	3043
970050	N/A	N/A	8453	8468	TCCGAAAAGACTGGAG	107	3044
970060	N/A	N/A	9095	9110	TGCTAAAGGAGTGCAG	117	3045
970070	688	703	9178	9193	GGTACGGGATTTCCGG	88	3046
970080	N/A	N/A	9390	9405	AGTGAGAAAACCCCCC	92	3047
970090	N/A	N/A	9459	9474	CCACGAAGGGCAGTGC	100	3048
970100	N/A	N/A	9649	9664	TTTAGTATCACCTCTA	70	3049
970110	N/A	N/A	9795	9810	AGGGAGCTCATTTTGA	108	3050
970120	N/A	N/A	9857	9872	GAAGGCCTGAGTTACC	71	3051
970130	N/A	N/A	10022	10037	AAAGAGTGGTACACCT	90	3052
970140	N/A	N/A	10154	10169	GGAGCTAGTTTTATGT	128	3053
970150	N/A	N/A	10201	10216	TTACTAATTCCATAGA	97	3054
970160	N/A	N/A	10280	10295	ACTGTTACCGATGCTT	57	3055
970170	N/A	N/A	10561	10576	CTCTGTAAGTACTAA	84	3056
970180	N/A	N/A	10827	10842	TGTCACCTGGCAACCT	104	3057

970190	N/A	N/A	11019	11034	CAAGTGTCTAAAGTCC	97	3058
970199	N/A	N/A	11144	11159	GGCTGAAACGGTCAGC	127	3059
970209	N/A	N/A	11404	11419	ACTCTTAGGCACATCA	73	3060
970219	N/A	N/A	11529	11544	AGGTAAGATCTCCATG	68	3061
970229	N/A	N/A	11654	11669	CCTTAAGCTATTTGGT	886	3062
970239	N/A	N/A	11848	11863	GTTACTCACGAGCACC	117	3063
970249	N/A	N/A	11998	12013	ACGAGGTTGCCGAGAT	38	3064
970259	N/A	N/A	12098	12113	CTGAAAGCGAGTCAGA	94	3065
970269	N/A	N/A	12279	12294	ACTGTATGGAACCCCA	70	3066
970279	N/A	N/A	12513	12528	TCATGTAAAGTCTGCT	79	3067
970289	N/A	N/A	12876	12891	AAAGAAGCAAGTCGGT	102	3068
970299	N/A	N/A	13062	13077	ATTATAGAGCATCACT	106	3069
970309	N/A	N/A	13308	13323	CCACATGTCCCGTGGG	128	3070
970319	N/A	N/A	13788	13803	TCTAACAGATAACGAG	103	3071
970329	N/A	N/A	14089	14104	CCTGAAAAGAGCCGCC	103	3072
970339	N/A	N/A	14227	14242	TAACTTCTCCTGTGCA	85	3073
970349	N/A	N/A	14644	14659	GTACGAGCACATGTCA	100	3074
970359	N/A	N/A	14741	14756	CTGGCCTGAAGCTTAG	75	3075
970369	N/A	N/A	15587	15602	AAGTCTACAGCCCCAG	105	3076
970379	N/A	N/A	15668	15683	GCACAGCCCTTGTTA	97	3077
970389	N/A	N/A	15890	15905	CACTGCCGTGATCTGA	91	3078
970399	N/A	N/A	16153	16168	GAAACGAGTTGACACA	100	3079
970409	N/A	N/A	16333	16348	CGCTIGTGGATATACA	100	3080
970419	N/A	N/A	16650	16665	AGACCAATTTATGCCA	93	3081
970429	N/A	N/A	16739	16754	CAGCATTGGACCCACG	96	3082
970439	N/A	N/A	16901	16916	AGAGGAATGAGCACTC	95	3083
970449	N/A	N/A	17002	17017	TGTAGAAGCCCACAAG	107	3084
970609	1443	1458	19560	19575	GATAGATCTGTGGTAA	78	3085

Table 50

Percent control of human IRF4 mRNA with gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	21	195
969851	N/A	N/A	4214	4229	GGAACGAAGAGCAGGG	88	3086
969861	N/A	N/A	4344	4359	GCAGGGACCGCGCCAG	90	3087
969871	N/A	N/A	4493	4508	GCAAACGACAAGTGGC	115	3088
969881	N/A	N/A	4823	4838	CCGACGCCCAAAGGCT	96	3089

969891	N/A	N/A	5046	5061	CGCACTCCGGGCACCC	89	3090
969901	N/A	N/A	5658	5673	ACGGACGAACGCGCAA	107	3091
969911	N/A	N/A	5751	5766	GGACGCACGGAGAGGG	85	3092
969921	N/A	N/A	5799	5814	AGAAACAGAGACGCGG	89	3093
969931	N/A	N/A	6213	6228	TAGGACTAAGGACAGC	105	3094
969941	N/A	N/A	6288	6303	ATTTATAACCGGTAGA	72	3095
969951	N/A	N/A	6401	6416	CAGATTTACACCGTTG	85	3096
969961	N/A	N/A	6540	6555	GCATAGGCATCCTTCC	92	3097
969971	474	489	6953	6968	CGGGTCTGAGATGTCC	102	3098
969981	N/A	N/A	7160	7175	GTGACCCACATAACTC	93	3099
969991	N/A	N/A	7205	7220	GTGTGATTAATTCTCC	36	3100
970001	N/A	N/A	7377	7392	GATGAGATATTCCTCT	124	3101
970011	N/A	N/A	7630	7645	TGTACAGGACAGGTAA	92	3102
970021	N/A	N/A	7783	7798	ACCTAACTAAATGTCA	124	3103
970031	N/A	N/A	8149	8164	ATTCCAACAGGCGGAC	98	3104
970041	N/A	N/A	8348	8363	ATATGGCTAAACCTGG	82	3105
970051	N/A	N/A	8454	8469	ATCCGAAAAGACTGGA	120	3106
970061	N/A	N/A	9103	9118	TGTGAACCTGCTAAAG	110	3107
970071	690	705	9180	9195	TTGGTACGGGATTTCC	66	3108
970081	N/A	N/A	9412	9427	TGGGATGCCACCATCC	102	3109
970091	N/A	N/A	9466	9481	TAAGATCCCACGAAGG	91	3110
970101	N/A	N/A	9659	9674	CCGTTCCCTTTTTTAGT	103	3111
970111	N/A	N/A	9834	9849	TAGATTCTCCCTGCAC	82	3112
970121	N/A	N/A	9914	9929	GTTCAAGTGTGTTGACC	70	3113
970131	N/A	N/A	10100	10115	TGCTGCAAATCCCTCT	79	3114
970141	N/A	N/A	10159	10174	TTTCAGGAGCTAGTTT	92	3115
970151	N/A	N/A	10206	10221	CATGGTTACTAATTCC	75	3116
970161	N/A	N/A	10281	10296	TACTGTTACCGATGCT	63	3117
970171	N/A	N/A	10568	10583	GCGCTCTCTCTGTAAC	107	3118
970181	763	778	10828	10843	CTGTCACCTGGCAACC	89	3119
970191	N/A	N/A	11085	11100	AATCACCCCTGGTCACC	99	3120
970200	N/A	N/A	11334	11349	ACTTATTTGTGGCTCA	64	3121
970210	N/A	N/A	11407	11422	ATTACTCTTAGGCACA	70	3122
970220	N/A	N/A	11531	11546	GTAAGTAAGATCTCCA	78	3123
970230	N/A	N/A	11656	11671	AACCTTAAGCTATTTG	49	3124
970240	N/A	N/A	11851	11866	TCAGTTACTCACGAGC	103	3125
970250	N/A	N/A	12002	12017	AATCACGAGGTTGCCG	106	3126
970260	N/A	N/A	12149	12164	TTTGAGACTTAACCCA	69	3127
970270	N/A	N/A	12281	12296	TAAGTGTATGGAACCC	72	3128
970280	N/A	N/A	12590	12605	CTGGATATGTGGTGTT	70	3129
970290	N/A	N/A	12892	12907	TATAACGGTGTTTCAG	64	3130

970300	N/A	N/A	13066	13081	TCCTATTATAGAGCAT	97	3131
970310	N/A	N/A	13352	13367	AACGACTCCACAGAGC	96	3132
970320	N/A	N/A	13880	13895	GCCGAAGTCAACAGGA	117	3133
970330	N/A	N/A	14115	14130	TCCAACCTTTATGATT	103	3134
970340	N/A	N/A	14229	14244	TATAACTTCTCCTGTG	93	3135
970350	N/A	N/A	14647	14662	GAAGTACGAGCACATG	82	3136
970360	N/A	N/A	14988	15003	CAGCACCGTGGTGCGA	127	3137
970370	N/A	N/A	15589	15604	GCAAGTCTACAGCCCC	51	3138
970380	N/A	N/A	15801	15816	ATAACATGAGAGTGTT	117	3139
970390	N/A	N/A	15892	15907	CACACTGCCGTGATCT	80	3140
970400	N/A	N/A	16156	16171	AAAGAAACGAGTTGAC	86	3141
970410	N/A	N/A	16379	16394	AGTAACTTGACTTGAG	103	3142
970420	N/A	N/A	16658	16673	ATGGCAAAAGACCAAT	105	3143
970430	N/A	N/A	16746	16761	TGCTTTGCAGCATTGG	70	3144
970440	N/A	N/A	16927	16942	AGCTTACTGTGATICT	87	3145
970450	1250	1265	17043	17058	CTTGGCAGGGAGCGGC	75	3146
970610	1445	1460	19562	19577	CGGATAGATCTGTGGT	54	3147

Table 51

Percent control of human IRF4 mRNA with gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	28	195
969852	N/A	N/A	4219	4234	CCTTAGGAACGAAGAG	106	3148
969862	N/A	N/A	4346	4361	AGGCAGGGACCGCGCC	111	3149
969872	N/A	N/A	4495	4510	CTGCAAAACGACAAGTG	118	3150
969882	N/A	N/A	4829	4844	ACGCACCCGCAGCCCA	110	3151
969892	N/A	N/A	5052	5067	AGGCACCGCACTCCGG	113	3152
969902	N/A	N/A	5661	5676	CGCACGGACGAACGCG	117	3153
969912	N/A	N/A	5753	5768	GCGGACGCACGGAGAG	109	3154
969922	N/A	N/A	5878	5893	GCTAGCAGGAGCGAGA	105	3155
969932	N/A	N/A	6215	6230	CCTAGGACTAAGGACA	103	3156
969942	N/A	N/A	6291	6306	GGTATTTATAACCGGT	90	3157
969952	N/A	N/A	6402	6417	TCAGATTTACACCGTT	86	3158
969962	N/A	N/A	6543	6558	GTTGCATAGGCATCCT	73	3159
969972	483	498	6962	6977	CACTTTGTACGGGTCT	89	3160
969982	N/A	N/A	7164	7179	ACTTGTGACCCACATA	104	3161
969992	N/A	N/A	7207	7222	CAGTGTGATTAATTCT	83	3162

970002	N/A	N/A	7563	7578	CGCCAGCCAGATGTTT	115	3163
970012	N/A	N/A	7632	7647	GTTGTACAGGACAGGT	67	3164
970022	N/A	N/A	7792	7807	CAGGAAGTACCTAAC	107	3165
970032	N/A	N/A	8152	8167	CATATTCCAACAGGCG	101	3166
970042	N/A	N/A	8351	8366	GTCATATGGCTAAACC	77	3167
970052	N/A	N/A	8478	8493	GACTGACAGCCGAAGC	73	3168
970062	626	641	9116	9131	GGCATCATGTAGTTGT	101	3169
970072	693	708	9183	9198	ACATTGGTACGGGATT	98	3170
970082	N/A	N/A	9420	9435	CTTGGCTGTGGGATGC	79	3171
970092	N/A	N/A	9469	9484	AAATAAGATCCCACGA	107	3172
970102	N/A	N/A	9668	9683	GGTATTTTTCCGTTCC	70	3173
970112	N/A	N/A	9836	9851	GCTAGATTCTCCCTGC	113	3174
970122	N/A	N/A	9922	9937	TCCAAAGGGTTCAGTG	93	3175
970132	N/A	N/A	10104	10119	CCCTTGCTGCAAATCC	104	3176
970142	N/A	N/A	10173	10188	AACGCAAGTCTGAATT	97	3177
970152	N/A	N/A	10209	10224	TCCCATGGTTACTAAT	110	3178
970162	N/A	N/A	10286	10301	TCATTTACTGTTACCG	44	3179
970172	769	784	10604	10619	AACGAGCCAGTGCACA	101	3180
970182	N/A	N/A	10834	10849	AGGTCCTGTCACCTG	107	3181
970192	N/A	N/A	11095	11110	GGTGCTCCTAAATCAC	101	3182
970201	N/A	N/A	11335	11350	GACTTATTTGTGGCTC	80	3183
970211	N/A	N/A	11410	11425	TGTATTACTCTTAGGC	35	3184
970221	N/A	N/A	11538	11553	CTTTATAGTAGGTAAG	101	3185
970231	N/A	N/A	11658	11673	CAAACCTTAAGCTATT	66	3186
970241	N/A	N/A	11928	11943	CAAGACAAGGGTTTGA	103	3187
970251	N/A	N/A	12003	12018	AAATCACGAGGTTGCC	79	3188
970261	N/A	N/A	12208	12223	TGTATCATGCATACCA	97	3189
970271	N/A	N/A	12285	12300	CTGGTAACTGTATGGA	83	3190
970281	N/A	N/A	12591	12606	ACTGGATATGTGGTGT	90	3191
970291	N/A	N/A	12894	12909	AATATAACGGTGTTTC	92	3192
970301	N/A	N/A	13111	13126	GAACAAGTGTATCTTT	95	3193
970311	N/A	N/A	13370	13385	GGACACCACCTCGAGG	99	3194
970321	N/A	N/A	13912	13927	TCTACTGGAGTCAAGC	70	3195
970331	N/A	N/A	14194	14209	TCCACCCTCCGTCTCA	109	3196
970341	N/A	N/A	14231	14246	CCTATAACTTCTCCTG	107	3197
970351	N/A	N/A	14650	14665	CCAGAAGTACGAGCAC	103	3198
970361	N/A	N/A	14990	15005	TGCAGCACCGTGGTGC	101	3199
970371	N/A	N/A	15592	15607	CGCGCAAGTCTACAGC	87	3200
970381	N/A	N/A	15812	15827	TCCAACCCTAGATAAC	105	3201
970391	N/A	N/A	15894	15909	TTCACACTGCCGTGAT	112	3202
970401	N/A	N/A	16161	16176	CCGCAAAAGAAACGAG	107	3203

970411	N/A	N/A	16386	16401	ATGGAACAGTAACTTG	97	3204
970421	N/A	N/A	16666	16681	GTCACGCAATGGCAAA	102	3205
970431	N/A	N/A	16770	16785	AACTAGTCGACAGCTA	107	3206
970441	N/A	N/A	16933	16948	AGCAAGAGCTTACTGT	106	3207
970451	1254	1269	17047	17062	GAATCTTGGCAGGGAG	100	3208
970611	1451	1466	19568	19583	GAATGGCGGATAGATC	103	3209

Table 52

Percent control of human IRF4 mRNA with gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	27	195
969853	N/A	N/A	4221	4236	CCCCTTAGGAACGAAG	106	3210
969863	N/A	N/A	4362	4377	AGCTGCGGAGCCTGGG	69	3211
969873	N/A	N/A	4499	4514	GGCTCTGCAAACGACA	100	3212
969883	N/A	N/A	4833	4848	TGTAACGCACCCGCAG	104	3213
969893	N/A	N/A	5464	5479	GTCCGCCCCGCGCGGT	97	3214
969903	N/A	N/A	5665	5680	AGAACGCACGGACGAA	99	3215
969913	N/A	N/A	5756	5771	GGCGCGGACGCACGGA	90	3216
969923	N/A	N/A	5996	6011	TCGCGCAAAGGGCAAG	104	3217
969933	N/A	N/A	6264	6279	CGGAGGTTCTTGAGG	58	3218
969943	N/A	N/A	6293	6308	TGGGTATTTATAACCG	96	3219
969953	N/A	N/A	6405	6420	CCTTCAGATTTACACC	109	3220
969963	N/A	N/A	6545	6560	ATGTTGCATAGGCATC	90	3221
969973	489	504	6968	6983	CCTGTACACTTTGTAC	102	3222
969983	N/A	N/A	7167	7182	TCAACTTGTGACCCAC	86	3223
969993	N/A	N/A	7216	7231	TGAGGCATACAGTGTG	82	3224
970003	N/A	N/A	7575	7590	CATAAAGGACCCCGCC	105	3225
970013	N/A	N/A	7636	7651	CTGAGTTGTACAGGAC	45	3226
970023	N/A	N/A	8100	8115	AATGGCAGCACCGTGT	100	3227
970033	N/A	N/A	8216	8231	TAAGGCACTACTTCCA	90	3228
970043	N/A	N/A	8382	8397	GAGATACTTGTACTGT	51	3229
970053	N/A	N/A	8480	8495	TAGACTGACAGCCGAA	97	3230
970063	630	645	9120	9135	GGGTGGCATCATGTAG	73	3231
970073	699	714	9189	9204	CATGGGACATTGGTAC	82	3232
970083	N/A	N/A	9429	9444	GAGAGTAACTTGGCT	88	3233
970093	N/A	N/A	9552	9567	TATTTATGAGCTTCCA	79	3234
970103	N/A	N/A	9671	9686	CATGGTATTTTCCGT	62	3235

970113	N/A	N/A	9838	9853	TTGCTAGATTCTCCCT	84	3236
970123	N/A	N/A	9927	9942	AAACATCCAAAGGGTT	101	3237
970133	N/A	N/A	10106	10121	AGCCCTTGCTGCAAAT	111	3238
970143	N/A	N/A	10176	10191	GTAAACGCAAGTCTGA	86	3239
970153	N/A	N/A	10212	10227	CTTCCCATGGTTACT	92	3240
970163	N/A	N/A	10306	10321	CACCTGATCTTGCTGC	88	3241
970173	N/A	N/A	10613	10628	TGATGGAGAAACGAGC	102	3242
970183	772	787	10837	10852	AAAAGGTTCTGTAC	105	3243
970193	N/A	N/A	11100	11115	CTAATGGTGCTCCTAA	96	3244
970202	N/A	N/A	11338	11353	GAGGACTTATTTGTGG	78	3245
970212	N/A	N/A	11412	11427	TGTGTATTACTCTTAG	25	3246
970222	N/A	N/A	11539	11554	TCTTTATAGTAGGTAA	86	3247
970232	N/A	N/A	11662	11677	ATTCCAAACCTTAAGC	101	3248
970242	N/A	N/A	11931	11946	GTTCAAGACAAGGGTT	85	3249
970252	N/A	N/A	12006	12021	CAGAAATCACGAGGTT	75	3250
970262	N/A	N/A	12211	12226	ATCTGTATCATGCATA	76	3251
970272	N/A	N/A	12291	12306	CTGCCACTGGTAACTG	79	3252
970282	N/A	N/A	12657	12672	GGGTGGTAGAATGTGA	67	3253
970292	N/A	N/A	12926	12941	ATGAACCCTAAGTTTA	104	3254
970302	N/A	N/A	13114	13129	AAGGAACAAGTGTATC	87	3255
970312	N/A	N/A	13395	13410	CTCCGGAGTCAGTGCT	99	3256
970322	N/A	N/A	13961	13976	GACCATCTGATCCGGA	98	3257
970332	N/A	N/A	14203	14218	ACAGTCCACTCCACCC	86	3258
970342	N/A	N/A	14245	14260	ACTTATAGCACTCTCC	99	3259
970352	N/A	N/A	14669	14684	AAACTTGGGTCACTTA	95	3260
970362	N/A	N/A	15148	15163	CTTAGAATGAGAGGTG	99	3261
970372	N/A	N/A	15595	15610	AGTCGCGCAAGTCTAC	100	3262
970382	N/A	N/A	15846	15861	GGCGAGTTGGCACAAAT	51	3263
970392	N/A	N/A	15896	15911	CATTCACTGCCGTG	94	3264
970402	N/A	N/A	16163	16178	GCCCGCAAAAGAAACG	98	3265
970412	N/A	N/A	16416	16431	TCTGAGTAGACTTCTT	86	3266
970422	N/A	N/A	16670	16685	CGTAGTCACGCAATGG	85	3267
970432	N/A	N/A	16772	16787	GGAAGTAGTCGACAGC	82	3268
970442	N/A	N/A	16958	16973	ACCGAACACACCAGGT	114	3269
970452	1277	1292	17070	17085	TCTCAAAGCATAGAG	108	3270
970612	1465	1480	19582	19597	ATTCTTGAATAGAGGA	84	3271

Example 10: Effect of mixed MOE and cEt gapmers with phosphorothioate internucleoside linkages on human IRF4 *in vitro*, single dose

Modified oligonucleotides complementary to a human IRF4 nucleic acid were designed and tested
5 for their effect on IRF4 mRNA *in vitro*.

Cultured MM.1R cells at a density of 5,000 cells per well were transfected by free uptake with 1,000 nM concentration of modified oligonucleotide or no modified oligonucleotide for untreated controls. After approximately 24 hours, RNA was isolated from the cells and IRF4 mRNA levels were measured by quantitative real-time PCR. Human primer probe set hIRF4_LTS34726 (described hereinabove in Example 7) was used to measure mRNA levels. IRF4 mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented in the tables below as percent control of the amount of IRF4 mRNA, relative to untreated control (UTC) cells.

The modified oligonucleotides in Tables 53 through 58 are cEt and/or MOE containing gapmers. The modified oligonucleotides have a central gap segment comprising 2'-deoxynucleosides which is flanked by wing segments on the 5' direction and the 3' direction. At least one nucleoside in the 5' wing segment and/or one nucleoside in the 3' wing segment has a MOE and/or cEt sugar modification. The "Motif" column describes the sugar modifications of each oligonucleotide. "k" indicates a cEt sugar modification; "d" indicates deoxyribose; and "e" indicates a MOE modification. Each internucleoside linkage is a phosphorothioate internucleoside linkage and each cytosine residue is a 5-methylcytosine. "Start Site" indicates the 5'-most nucleoside to which the gapmer is complementary in the human nucleic acid sequence. "Stop Site" indicates the 3'-most nucleoside to which the gapmer is complementary in the human nucleic acid sequence.

Each modified oligonucleotide listed in Tables 53 through 58 below is complementary to human IRF4 nucleic acid sequences SEQ ID NO: 1 or SEQ ID NO: 2, as indicated. 'N/A' indicates that the modified oligonucleotide is not complementary to that particular nucleic acid sequence with 100% complementarity. As shown below, modified oligonucleotides complementary to human IRF4 reduced the amount of human IRF4 mRNA.

Table 53

Percent control of human IRF4 mRNA with gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	Motif	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	kkk-d10-kkk	13	195
881450	3252	3267	21369	21384	ACACTTTTAGAGAGGA	kkk-d10-kkk	27	2111
881659	4592	4607	22709	22724	GGAAGTTTACACTGGA	kkk-d10-kkk	4	2044
1013023	N/A	N/A	10142	10157	ATGTTAGCCAATTCCT	k-d10-kekek	100	3272
1013024	N/A	N/A	10143	10158	TATGTTAGCCAATTCC	k-d10-kekek	99	2991
1013025	N/A	N/A	10144	10159	TTATGTTAGCCAATTC	k-d10-kekek	98	3273
1013026	N/A	N/A	10145	10160	TTTATGTTAGCCAATT	k-d10-kekek	100	3274
1013032	N/A	N/A	10278	10293	TGTTACCGATGCTTCA	k-d10-kekek	74	2294

1013033	N/A	N/A	10279	10294	CTGTTACCGATGCTTC	k-d10-kekek	64	2993
1013034	N/A	N/A	10280	10295	ACTGTTACCGATGCTT	k-d10-kekek	80	3055
1013035	N/A	N/A	10281	10296	TACTGTTACCGATGCT	k-d10-kekek	90	3117
1013046	N/A	N/A	11016	11031	GTGTCTAAAGTCCCAT	k-d10-kekek	66	3275
1013047	N/A	N/A	11017	11032	AGTGTCTAAAGTCCCA	k-d10-kekek	101	2996
1013048	N/A	N/A	11018	11033	AAGTGTCTAAAGTCCC	k-d10-kekek	101	3276
1013049	N/A	N/A	11019	11034	CAAGTGTCTAAAGTCC	k-d10-kekek	93	3058
1013053	N/A	N/A	11119	11134	AGCAGTGATGTCAGGT	k-d10-kekek	23	2718
1013054	N/A	N/A	11120	11135	AAGCAGTGATGTCAGG	k-d10-kekek	72	3277
1013055	N/A	N/A	11121	11136	CAAGCAGTGATGTCAG	k-d10-kekek	65	3278
1013060	N/A	N/A	11395	11410	CACATCAATGTTTTAG	k-d10-kekek	55	3279
1013061	N/A	N/A	11396	11411	GCACATCAATGTTTTA	k-d10-kekek	87	1159
1013062	N/A	N/A	11397	11412	GGCACATCAATGTTTT	k-d10-kekek	72	3280
1013063	N/A	N/A	11398	11413	AGGCACATCAATGTTT	k-d10-kekek	95	1233
1013074	N/A	N/A	11411	11426	GTGTATTACTCTTAGG	k-d10-kekek	16	1540
1013075	N/A	N/A	11412	11427	TGTGTATTACTCTTAG	k-d10-kekek	42	3246
1013076	N/A	N/A	11413	11428	ATGTGTATTACTCTTA	k-d10-kekek	83	3281
1013077	N/A	N/A	11414	11429	AATGTGTATTACTCTT	k-d10-kekek	76	3282
1013090	N/A	N/A	11565	11580	TGTGCTTGCCAAGCCT	k-d10-kekek	101	3283
1013091	N/A	N/A	11566	11581	GTGTGCTTGCCAAGCC	k-d10-kekek	60	3000
1013092	N/A	N/A	11567	11582	CGTGTGCTTGCCAAGC	k-d10-kekek	70	3284
1013093	N/A	N/A	11568	11583	ACGTGTGCTTGCCAAG	k-d10-kekek	53	3285
1013125	N/A	N/A	12514	12529	TTCATGTAAAGTCTGC	k-d10-kekek	98	3286
1013126	N/A	N/A	12515	12530	GTTTCATGTAAAGTCTG	k-d10-kekek	55	934
1013127	N/A	N/A	12516	12531	AGTTCATGTAAAGTCT	k-d10-kekek	75	755
1013128	N/A	N/A	12517	12532	AAGTTCATGTAAAGTC	k-d10-kekek	86	3287
1013462	N/A	N/A	10142	10157	ATGTTAGCCAATTCCT	kk-d9-kekek	72	3272
1013463	N/A	N/A	10143	10158	TATGTTAGCCAATTCC	kk-d9-kekek	92	2991
1013464	N/A	N/A	10144	10159	TTATGTTAGCCAATTC	kk-d9-kekek	89	3273
1013465	N/A	N/A	10145	10160	TTTATGTTAGCCAATT	kk-d9-kekek	91	3274
1013471	N/A	N/A	10278	10293	TGTTACCGATGCTTCA	kk-d9-kekek	72	2294
1013472	N/A	N/A	10279	10294	CTGTTACCGATGCTTC	kk-d9-kekek	48	2993
1013473	N/A	N/A	10280	10295	ACTGTTACCGATGCTT	kk-d9-kekek	70	3055
1013474	N/A	N/A	10281	10296	TACTGTTACCGATGCT	kk-d9-kekek	91	3117
1013485	N/A	N/A	11016	11031	GTGTCTAAAGTCCCAT	kk-d9-kekek	87	3275
1013486	N/A	N/A	11017	11032	AGTGTCTAAAGTCCCA	kk-d9-kekek	74	2996
1013487	N/A	N/A	11018	11033	AAGTGTCTAAAGTCCC	kk-d9-kekek	88	3276
1013488	N/A	N/A	11019	11034	CAAGTGTCTAAAGTCC	kk-d9-kekek	85	3058
1013492	N/A	N/A	11119	11134	AGCAGTGATGTCAGGT	kk-d9-kekek	34	2718
1013493	N/A	N/A	11120	11135	AAGCAGTGATGTCAGG	kk-d9-kekek	57	3277
1013494	N/A	N/A	11121	11136	CAAGCAGTGATGTCAG	kk-d9-kekek	49	3278

1013499	N/A	N/A	11395	11410	CACATCAATGTTTTAG	kk-d9-kekek	81	3279
1013500	N/A	N/A	11396	11411	GCACATCAATGTTTTA	kk-d9-kekek	82	1159
1013501	N/A	N/A	11397	11412	GGCACATCAATGTTTT	kk-d9-kekek	77	3280
1013502	N/A	N/A	11398	11413	AGGCACATCAATGTTT	kk-d9-kekek	84	1233
1013513	N/A	N/A	11411	11426	GTGTATTACTCTTAGG	kk-d9-kekek	14	1540
1013514	N/A	N/A	11412	11427	TGTGTATTACTCTTAG	kk-d9-kekek	13	3246
1013515	N/A	N/A	11413	11428	ATGTGTATTACTCTTA	kk-d9-kekek	46	3281
1013516	N/A	N/A	11414	11429	AATGTGTATTACTCTT	kk-d9-kekek	48	3282
1013529	N/A	N/A	11565	11580	TGTGCTTGCCAAGCCT	kk-d9-kekek	98	3283

Table 54

Percent control of human IRF4 mRNA with gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	Motif	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	kkk-d10-kkk	11	195
881450	3252	3267	21369	21384	ACACTTTTAGAGAGGA	kkk-d10-kkk	27	2111
881659	4592	4607	22709	22724	GGAAGTTTACACTGGA	kkk-d10-kkk	3	2044
1013530	N/A	N/A	11566	11581	GTGTGCTTGCCAAGCC	kk-d9-kekek	59	3000
1013531	N/A	N/A	11567	11582	CGTGTGCTTGCCAAGC	kk-d9-kekek	51	3284
1013532	N/A	N/A	11568	11583	ACGTGTGCTTGCCAAG	kk-d9-kekek	51	3285
1013564	N/A	N/A	12514	12529	TTCATGTAAAGTCTGC	kk-d9-kekek	90	3286
1013565	N/A	N/A	12515	12530	GTTTCATGTAAAGTCTG	kk-d9-kekek	58	934
1013566	N/A	N/A	12516	12531	AGTTCATGTAAAGTCT	kk-d9-kekek	58	755
1013567	N/A	N/A	12517	12532	AAGTTCATGTAAAGTC	kk-d9-kekek	66	3287
1013902	N/A	N/A	10142	10157	ATGTTAGCCAATTCCT	kk-d10-keke	80	3272
1013903	N/A	N/A	10143	10158	TATGTTAGCCAATTCC	kk-d10-keke	92	2991
1013904	N/A	N/A	10144	10159	TTATGTTAGCCAATTC	kk-d10-keke	89	3273
1013905	N/A	N/A	10145	10160	TTTATGTTAGCCAATT	kk-d10-keke	89	3274
1013911	N/A	N/A	10278	10293	TGTTACCGATGCTTCA	kk-d10-keke	75	2294
1013912	N/A	N/A	10279	10294	CTGTTACCGATGCTTC	kk-d10-keke	57	2993
1013913	N/A	N/A	10280	10295	ACTGTTACCGATGCTT	kk-d10-keke	70	3055
1013914	N/A	N/A	10281	10296	TACTGTTACCGATGCT	kk-d10-keke	76	3117
1013925	N/A	N/A	11016	11031	GTGTCTAAAGTCCCAT	kk-d10-keke	91	3275
1013926	N/A	N/A	11017	11032	AGTGTCTAAAGTCCCA	kk-d10-keke	68	2996
1013927	N/A	N/A	11018	11033	AAGTGTCTAAAGTCCC	kk-d10-keke	90	3276
1013928	N/A	N/A	11019	11034	CAAGTGTCTAAAGTCC	kk-d10-keke	84	3058
1013932	N/A	N/A	11119	11134	AGCAGTGATGTCAGGT	kk-d10-keke	33	2718
1013933	N/A	N/A	11120	11135	AAGCAGTGATGTCAGG	kk-d10-keke	26	3277
1013934	N/A	N/A	11121	11136	CAAGCAGTGATGTCAG	kk-d10-keke	80	3278

1013939	N/A	N/A	11395	11410	CACATCAATGTTTTAG	kk-d10-keke	75	3279
1013940	N/A	N/A	11396	11411	GCACATCAATGTTTTA	kk-d10-keke	51	1159
1013941	N/A	N/A	11397	11412	GGCACATCAATGTTTT	kk-d10-keke	91	3280
1013942	N/A	N/A	11398	11413	AGGCACATCAATGTTT	kk-d10-keke	84	1233
1013953	N/A	N/A	11411	11426	GTGTATTACTCTTAGG	kk-d10-keke	22	1540
1013954	N/A	N/A	11412	11427	TGTGTATTACTCTTAG	kk-d10-keke	49	3246
1013955	N/A	N/A	11413	11428	ATGTGTATTACTCTTA	kk-d10-keke	53	3281
1013956	N/A	N/A	11414	11429	AATGTGTATTACTCTT	kk-d10-keke	92	3282
1013969	N/A	N/A	11565	11580	TGTGCTTGCCAAGCCT	kk-d10-keke	74	3283
1013970	N/A	N/A	11566	11581	GTGTGCTTGCCAAGCC	kk-d10-keke	63	3000
1013971	N/A	N/A	11567	11582	CGTGTGCTTGCCAAGC	kk-d10-keke	45	3284
1013972	N/A	N/A	11568	11583	ACGTGTGCTTGCCAAG	kk-d10-keke	94	3285
1014004	N/A	N/A	12514	12529	TTCATGTAAAGTCTGC	kk-d10-keke	51	3286
1014005	N/A	N/A	12515	12530	GTTCATGTAAAGTCTG	kk-d10-keke	69	934
1014006	N/A	N/A	12516	12531	AGTTCATGTAAAGTCT	kk-d10-keke	55	755
1014007	N/A	N/A	12517	12532	AAGTTCATGTAAAGTC	kk-d10-keke	72	3287

Table 55

Percent control of human IRF4 mRNA with gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID 2: Stop Site	Sequence	Motif	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	kkk-d10-kkk	9	195
881450	3252	3267	21369	21384	ACACTTTTAGAGAGGA	kkk-d10-kkk	17	2111
881659	4592	4607	22709	22724	GGAAGTTTACACTGGA	kkk-d10-kkk	2	2044
1014342	N/A	N/A	10142	10157	ATGTTAGCCAATTCCT	kk-d9-kdkdk	70	3272
1014343	N/A	N/A	10143	10158	TATGTTAGCCAATTCC	kk-d9-kdkdk	98	2991
1014344	N/A	N/A	10144	10159	TTATGTTAGCCAATTC	kk-d9-kdkdk	83	3273
1014345	N/A	N/A	10145	10160	TTTATGTTAGCCAATT	kk-d9-kdkdk	89	3274
1014351	N/A	N/A	10278	10293	TGTTACCGATGCTTCA	kk-d9-kdkdk	65	2294
1014352	N/A	N/A	10279	10294	CTGTTACCGATGCTTC	kk-d9-kdkdk	42	2993
1014353	N/A	N/A	10280	10295	ACTGTTACCGATGCTT	kk-d9-kdkdk	78	3055
1014354	N/A	N/A	10281	10296	TACTGTTACCGATGCT	kk-d9-kdkdk	93	3117
1014365	N/A	N/A	11016	11031	GTGTCTAAAGTCCCAT	kk-d9-kdkdk	80	3275
1014366	N/A	N/A	11017	11032	AGTGTCTAAAGTCCCA	kk-d9-kdkdk	86	2996
1014367	N/A	N/A	11018	11033	AAGTGTCTAAAGTCCC	kk-d9-kdkdk	87	3276
1014368	N/A	N/A	11019	11034	CAAGTGTCTAAAGTCC	kk-d9-kdkdk	97	3058
1014372	N/A	N/A	11119	11134	AGCAGTGATGTCAGGT	kk-d9-kdkdk	45	2718
1014373	N/A	N/A	11120	11135	AAGCAGTGATGTCAGG	kk-d9-kdkdk	40	3277
1014374	N/A	N/A	11121	11136	CAAGCAGTGATGTCAG	kk-d9-kdkdk	54	3278

1014379	N/A	N/A	11395	11410	CACATCAATGTTTTAG	kk-d9-kdkdk	72	3279
1014380	N/A	N/A	11396	11411	GCACATCAATGTTTTA	kk-d9-kdkdk	89	1159
1014381	N/A	N/A	11397	11412	GGCACATCAATGTTTT	kk-d9-kdkdk	74	3280
1014382	N/A	N/A	11398	11413	AGGCACATCAATGTTT	kk-d9-kdkdk	96	1233
1014393	N/A	N/A	11411	11426	GTGTATTACTCTTAGG	kk-d9-kdkdk	11	1540
1014394	N/A	N/A	11412	11427	TGTGTATTACTCTTAG	kk-d9-kdkdk	19	3246
1014395	N/A	N/A	11413	11428	ATGTGTATTACTCTTA	kk-d9-kdkdk	56	3281
1014396	N/A	N/A	11414	11429	AATGTGTATTACTCTT	kk-d9-kdkdk	90	3282
1014409	N/A	N/A	11565	11580	TGTGCTTGCCAAGCCT	kk-d9-kdkdk	77	3283
1014410	N/A	N/A	11566	11581	GTGTGCTTGCCAAGCC	kk-d9-kdkdk	41	3000
1014411	N/A	N/A	11567	11582	CGTGTGCTTGCCAAGC	kk-d9-kdkdk	33	3284
1014412	N/A	N/A	11568	11583	ACGTGTGCTTGCCAAG	kk-d9-kdkdk	25	3285
1014444	N/A	N/A	12514	12529	TTCATGTAAAGTCTGC	kk-d9-kdkdk	86	3286
1014445	N/A	N/A	12515	12530	GTTCATGTAAAGTCTG	kk-d9-kdkdk	66	934
1014446	N/A	N/A	12516	12531	AGTTCATGTAAAGTCT	kk-d9-kdkdk	68	755
1014447	N/A	N/A	12517	12532	AAGTTCATGTAAAGTC	kk-d9-kdkdk	68	3287
1014783	N/A	N/A	10142	10157	ATGTTAGCCAATTCCCT	kk-d9-eeekk	83	3272
1014784	N/A	N/A	10143	10158	TATGTTAGCCAATTCC	kk-d9-eeekk	92	2991
1014785	N/A	N/A	10144	10159	TTATGTTAGCCAATTC	kk-d9-eeekk	86	3273
1014786	N/A	N/A	10145	10160	TTTATGTTAGCCAATT	kk-d9-eeekk	97	3274
1014792	N/A	N/A	10278	10293	TGTTACCGATGCTTCA	kk-d9-eeekk	69	2294
1014793	N/A	N/A	10279	10294	CTGTTACCGATGCTTC	kk-d9-eeekk	36	2993
1014794	N/A	N/A	10280	10295	ACTGTTACCGATGCTT	kk-d9-eeekk	73	3055
1014795	N/A	N/A	10281	10296	TACTGTTACCGATGCT	kk-d9-eeekk	71	3117
1014806	N/A	N/A	11016	11031	GTGTCTAAAGTCCCAT	kk-d9-eeekk	77	3275
1014807	N/A	N/A	11017	11032	AGTGTCTAAAGTCCCA	kk-d9-eeekk	74	2996
1014808	N/A	N/A	11018	11033	AAGTGTCTAAAGTCCC	kk-d9-eeekk	79	3276
1014809	N/A	N/A	11019	11034	CAAGTGTCTAAAGTCC	kk-d9-eeekk	78	3058
1014813	N/A	N/A	11119	11134	AGCAGTGATGTCAGGT	kk-d9-eeekk	31	2718
1014814	N/A	N/A	11120	11135	AAGCAGTGATGTCAGG	kk-d9-eeekk	38	3277
1014815	N/A	N/A	11121	11136	CAAGCAGTGATGTCAG	kk-d9-eeekk	85	3278
1014820	N/A	N/A	11395	11410	CACATCAATGTTTTAG	kk-d9-eeekk	88	3279
1014821	N/A	N/A	11396	11411	GCACATCAATGTTTTA	kk-d9-eeekk	80	1159
1014822	N/A	N/A	11397	11412	GGCACATCAATGTTTT	kk-d9-eeekk	78	3280
1014823	N/A	N/A	11398	11413	AGGCACATCAATGTTT	kk-d9-eeekk	64	1233
1014834	N/A	N/A	11411	11426	GTGTATTACTCTTAGG	kk-d9-eeekk	12	1540

Table 56
Percent control of human IRF4 mRNA with gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	Motif	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	kkk-d10-kkk	14	195
881450	3252	3267	21369	21384	ACACTTTTAGAGAGGA	kkk-d10-kkk	24	2111
881659	4592	4607	22709	22724	GGAAGTTTACACTGGA	kkk-d10-kkk	2	2044
1014835	N/A	N/A	11412	11427	TGTGTATTACTCTTAG	kk-d9-eeekk	59	3246
1014836	N/A	N/A	11413	11428	ATGTGTATTACTCTTA	kk-d9-eeekk	60	3281
1014837	N/A	N/A	11414	11429	AATGTGTATTACTCTT	kk-d9-eeekk	85	3282
1014850	N/A	N/A	11565	11580	TGTGCTTGCCAAGCCT	kk-d9-eeekk	55	3283
1014851	N/A	N/A	11566	11581	GTGTGCTTGCCAAGCC	kk-d9-eeekk	25	3000
1014852	N/A	N/A	11567	11582	CGTGTGCTTGCCAAGC	kk-d9-eeekk	40	3284
1014853	N/A	N/A	11568	11583	ACGTGTGCTTGCCAAG	kk-d9-eeekk	56	3285
1014885	N/A	N/A	12514	12529	TTCATGTAAAGTCTGC	kk-d9-eeekk	73	3286
1014886	N/A	N/A	12515	12530	GTTCATGTAAAGTCTG	kk-d9-eeekk	71	934
1014887	N/A	N/A	12516	12531	AGTTCATGTAAAGTCT	kk-d9-eeekk	59	755
1014888	N/A	N/A	12517	12532	AAGTTCATGTAAAGTC	kk-d9-eeekk	79	3287
1015224	N/A	N/A	10142	10157	ATGTTAGCCAATTCCT	kk-d9-ekeke	73	3272
1015225	N/A	N/A	10143	10158	TATGTTAGCCAATTCC	kk-d9-ekeke	98	2991
1015226	N/A	N/A	10144	10159	TTATGTTAGCCAATTC	kk-d9-ekeke	91	3273
1015227	N/A	N/A	10145	10160	TTTATGTTAGCCAATT	kk-d9-ekeke	88	3274
1015233	N/A	N/A	10278	10293	TGTTACCGATGCTTCA	kk-d9-ekeke	65	2294
1015234	N/A	N/A	10279	10294	CTGTTACCGATGCTTC	kk-d9-ekeke	50	2993
1015235	N/A	N/A	10280	10295	ACTGTTACCGATGCTT	kk-d9-ekeke	77	3055
1015236	N/A	N/A	10281	10296	TACTGTTACCGATGCT	kk-d9-ekeke	78	3117
1015247	N/A	N/A	11016	11031	GTGTCTAAAGTCCCAT	kk-d9-ekeke	68	3275
1015248	N/A	N/A	11017	11032	AGTGTCTAAAGTCCCA	kk-d9-ekeke	82	2996
1015249	N/A	N/A	11018	11033	AAGTGTCTAAAGTCCC	kk-d9-ekeke	87	3276
1015250	N/A	N/A	11019	11034	CAAGTGTCTAAAGTCC	kk-d9-ekeke	77	3058
1015254	N/A	N/A	11119	11134	AGCAGTGATGTCAGGT	kk-d9-ekeke	28	2718
1015255	N/A	N/A	11120	11135	AAGCAGTGATGTCAGG	kk-d9-ekeke	35	3277
1015256	N/A	N/A	11121	11136	CAAGCAGTGATGTCAG	kk-d9-ekeke	74	3278
1015261	N/A	N/A	11395	11410	CACATCAATGTTTTAG	kk-d9-ekeke	72	3279
1015262	N/A	N/A	11396	11411	GCACATCAATGTTTTA	kk-d9-ekeke	90	1159
1015263	N/A	N/A	11397	11412	GGCACATCAATGTTTT	kk-d9-ekeke	78	3280
1015264	N/A	N/A	11398	11413	AGGCACATCAATGTTT	kk-d9-ekeke	58	1233
1015275	N/A	N/A	11411	11426	GTGTATTACTCTTAGG	kk-d9-ekeke	11	1540
1015276	N/A	N/A	11412	11427	TGTGTATTACTCTTAG	kk-d9-ekeke	46	3246

1015277	N/A	N/A	11413	11428	ATGTGTATTACTCTTA	kk-d9-ekeke	40	3281
1015278	N/A	N/A	11414	11429	AATGTGTATTACTCTT	kk-d9-ekeke	76	3282
1015291	N/A	N/A	11565	11580	TGTGCTTGCCAAGCCT	kk-d9-ekeke	79	3283
1015292	N/A	N/A	11566	11581	GTGTGCTTGCCAAGCC	kk-d9-ekeke	83	3000
1015293	N/A	N/A	11567	11582	CGTGTGCTTGCCAAGC	kk-d9-ekeke	53	3284
1015294	N/A	N/A	11568	11583	ACGTGTGCTTGCCAAG	kk-d9-ekeke	41	3285
1015326	N/A	N/A	12514	12529	TTCATGTAAAGTCTGC	kk-d9-ekeke	68	3286
1015327	N/A	N/A	12515	12530	GTTCATGTAAAGTCTG	kk-d9-ekeke	64	934
1015328	N/A	N/A	12516	12531	AGTTCATGTAAAGTCT	kk-d9-ekeke	49	755
1015329	N/A	N/A	12517	12532	AAGTTCATGTAAAGTC	kk-d9-ekeke	66	3287

Table 57

Percent control of human IRF4 mRNA with gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID 2: Stop Site	Sequence	Motif	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	kkk-d10-kkk	18	195
881450	3252	3267	21369	21384	ACACTTTTAGAGAGGA	kkk-d10-kkk	28	2111
881659	4592	4607	22709	22724	GGAAGTTTACACTGGA	kkk-d10-kkk	4	2044
1012810	N/A	N/A	10142	10157	ATGTTAGCCAATTCCT	kkk-d10-kkk	70	3272
1012811	N/A	N/A	10144	10159	TTATGTTAGCCAATTC	kkk-d10-kkk	91	3273
1012812	N/A	N/A	10145	10160	TTTATGTTAGCCAATT	kkk-d10-kkk	75	3274
1012816	N/A	N/A	11016	11031	GTGTCTAAAGTCCCAT	kkk-d10-kkk	82	3275
1012817	N/A	N/A	11018	11033	AAGTGTCTAAAGTCCC	kkk-d10-kkk	50	3276
1012819	N/A	N/A	11120	11135	AAGCAGTGATGTCAGG	kkk-d10-kkk	34	3277
1012820	N/A	N/A	11121	11136	CAAGCAGTGATGTCAG	kkk-d10-kkk	40	3278
1012821	N/A	N/A	11395	11410	CACATCAATGTTTTAG	kkk-d10-kkk	34	3279
1012822	N/A	N/A	11397	11412	GGCACATCAATGTTTT	kkk-d10-kkk	82	3280
1012826	N/A	N/A	11413	11428	ATGTGTATTACTCTTA	kkk-d10-kkk	48	3281
1012827	N/A	N/A	11414	11429	AATGTGTATTACTCTT	kkk-d10-kkk	47	3282
1012835	N/A	N/A	11565	11580	TGTGCTTGCCAAGCCT	kkk-d10-kkk	62	3283
1012836	N/A	N/A	11567	11582	CGTGTGCTTGCCAAGC	kkk-d10-kkk	33	3284
1012837	N/A	N/A	11568	11583	ACGTGTGCTTGCCAAG	kkk-d10-kkk	46	3285
1012845	N/A	N/A	12514	12529	TTCATGTAAAGTCTGC	kkk-d10-kkk	43	3286
1012846	N/A	N/A	12517	12532	AAGTTCATGTAAAGTC	kkk-d10-kkk	57	3287
1015665	N/A	N/A	10142	10157	ATGTTAGCCAATTCCT	k-d9-kekeke	100	3272
1015666	N/A	N/A	10143	10158	TATGTTAGCCAATTCC	k-d9-kekeke	90	2991
1015667	N/A	N/A	10144	10159	TTATGTTAGCCAATTC	k-d9-kekeke	91	3273
1015668	N/A	N/A	10145	10160	TTTATGTTAGCCAATT	k-d9-kekeke	95	3274
1015674	N/A	N/A	10278	10293	TGTTACCGATGCTTCA	k-d9-kekeke	90	2294

1015675	N/A	N/A	10279	10294	CTGTTACCGATGCTTC	k-d9-kekeke	98	2993
1015676	N/A	N/A	10280	10295	ACTGTTACCGATGCTT	k-d9-kekeke	102	3055
1015677	N/A	N/A	10281	10296	TACTGTTACCGATGCT	k-d9-kekeke	82	3117
1015688	N/A	N/A	11016	11031	GTGTCTAAAGTCCCAT	k-d9-kekeke	95	3275
1015689	N/A	N/A	11017	11032	AGTGTCTAAAGTCCCA	k-d9-kekeke	112	2996
1015690	N/A	N/A	11018	11033	AAGTGTCTAAAGTCCC	k-d9-kekeke	96	3276
1015691	N/A	N/A	11019	11034	CAAGTGTCTAAAGTCC	k-d9-kekeke	89	3058
1015695	N/A	N/A	11119	11134	AGCAGTGATGTCAGGT	k-d9-kekeke	74	2718
1015696	N/A	N/A	11120	11135	AAGCAGTGATGTCAGG	k-d9-kekeke	66	3277
1015697	N/A	N/A	11121	11136	CAAGCAGTGATGTCAG	k-d9-kekeke	90	3278
1015702	N/A	N/A	11395	11410	CACATCAATGTTTTAG	k-d9-kekeke	102	3279
1015703	N/A	N/A	11396	11411	GCACATCAATGTTTTA	k-d9-kekeke	83	1159
1015704	N/A	N/A	11397	11412	GGCACATCAATGTTTT	k-d9-kekeke	91	3280
1015705	N/A	N/A	11398	11413	AGGCACATCAATGTTT	k-d9-kekeke	109	1233
1015716	N/A	N/A	11411	11426	GTGTATTACTCTTAGG	k-d9-kekeke	16	1540
1015717	N/A	N/A	11412	11427	TGTGTATTACTCTTAG	k-d9-kekeke	68	3246
1015718	N/A	N/A	11413	11428	ATGTGTATTACTCTTA	k-d9-kekeke	64	3281
1015719	N/A	N/A	11414	11429	AATGTGTATTACTCTT	k-d9-kekeke	88	3282
1015732	N/A	N/A	11565	11580	TGTGCTTGCCAAGCCT	k-d9-kekeke	103	3283
1015733	N/A	N/A	11566	11581	GTGTGCTTGCCAAGCC	k-d9-kekeke	94	3000
1015734	N/A	N/A	11567	11582	CGTGTGCTTGCCAAGC	k-d9-kekeke	76	3284
1015735	N/A	N/A	11568	11583	ACGTGTGCTTGCCAAG	k-d9-kekeke	60	3285
1015767	N/A	N/A	12514	12529	TTCATGTAAAGTCTGC	k-d9-kekeke	91	3286
1015768	N/A	N/A	12515	12530	GTTTCATGTAAAGTCTG	k-d9-kekeke	76	934
1015769	N/A	N/A	12516	12531	AGTTCATGTAAAGTCT	k-d9-kekeke	71	755
1015770	N/A	N/A	12517	12532	AAGTTCATGTAAAGTC	k-d9-kekeke	86	3287

Table 58

Percent control of human IRF4 mRNA with gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID 2: Stop Site	Sequence	Motif	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	kkk-d10-kkk	11	195
881450	3252	3267	21369	21384	ACACTTTTAGAGAGGA	kkk-d10-kkk	29	2111
881659	4592	4607	22709	22724	GGAAGTTTACACTGGA	kkk-d10-kkk	4	2044
935595	3075	3090	21192	21207	ACTAAGCTTGATAAAG	kkk-d10-kkk	86	3288
935607	4195	4210	22312	22327	AGTGTTCAGGAGATA	kkk-d10-kkk	20	3289
1012769	N/A	N/A	4810	4825	GCTCCCGACACGCGCC	kkk-d10-kkk	97	3290
1012772	N/A	N/A	6267	6282	ATGCGGAGGTTCCCTG	kkk-d10-kkk	53	3291
1012774	N/A	N/A	6271	6286	TGAGATGCGGAGGTTC	kkk-d10-kkk	67	3292

1012775	N/A	N/A	6273	6288	AGTGAGATGCGGAGGT	kkk-d10-kkk	35	3293
1012776	N/A	N/A	6275	6290	AGAGTGAGATGCGGAG	kkk-d10-kkk	35	3294
1012778	N/A	N/A	6281	6296	ACCGGTAGAGTGAGAT	kkk-d10-kkk	84	3295
1012782	N/A	N/A	7634	7649	GAGTTGTACAGGACAG	kkk-d10-kkk	49	3296
1012785	N/A	N/A	7638	7653	GTCTGAGTTGTACAGG	kkk-d10-kkk	48	3297
1012786	N/A	N/A	7640	7655	AGGTCTGAGTTGTACA	kkk-d10-kkk	45	3298
1012788	N/A	N/A	8386	8401	AATGGAGATACTTGTA	kkk-d10-kkk	74	3299
1012790	N/A	N/A	8389	8404	GACAATGGAGATACTT	kkk-d10-kkk	67	3300
1012791	678	693	9168	9183	TTCCGGGTGTGGCTGA	kkk-d10-kkk	75	3301
1012793	680	695	9170	9185	ATTTCCGGGTGTGGCT	kkk-d10-kkk	93	3302
1012795	N/A	N/A	9667	9682	GTATTTTTCCTTCCT	kkk-d10-kkk	16	3303
1012796	N/A	N/A	9670	9685	ATGGTATTTTTCCTT	kkk-d10-kkk	68	3304
1012799	N/A	N/A	9677	9692	GTTTGCCATGGTATTT	kkk-d10-kkk	59	3305
1012804	N/A	N/A	9840	9855	CATTGCTAGATTCTCC	kkk-d10-kkk	82	3306
1012806	N/A	N/A	9846	9861	TTACCGCATTGCTAGA	kkk-d10-kkk	87	3307
1012808	N/A	N/A	9851	9866	CTGAGTTACCGCATTG	kkk-d10-kkk	51	3308
1012809	N/A	N/A	10139	10154	TTAGCCAATTCCTCCA	kkk-d10-kkk	64	3309
1012813	N/A	N/A	10274	10289	ACCGATGCTTCAAGAC	kkk-d10-kkk	69	3310
1012814	N/A	N/A	10276	10291	TTACCGATGCTTCAAG	kkk-d10-kkk	84	3311
1012815	N/A	N/A	10282	10297	TTACTGTTACCGATGC	kkk-d10-kkk	74	3312
1012818	N/A	N/A	11020	11035	GCAAGTGTCTAAAGTC	kkk-d10-kkk	51	3313
1012823	N/A	N/A	11400	11415	TTAGGCACATCAATGT	kkk-d10-kkk	88	3314
1012825	N/A	N/A	11406	11421	TTACTCTTAGGCACAT	kkk-d10-kkk	56	3315
1012828	N/A	N/A	11523	11538	GATCTCCATGGTGCAG	kkk-d10-kkk	78	3316
1012831	N/A	N/A	11530	11545	TAGGTAAGATCTCCAT	kkk-d10-kkk	65	3317
1012834	N/A	N/A	11564	11579	GTGCTTGCCAAGCCTA	kkk-d10-kkk	73	3318
1012840	N/A	N/A	11659	11674	CCAAACCTTAAGCTAT	kkk-d10-kkk	82	3319
1012841	N/A	N/A	11663	11678	AATTCCAAACCTTAAG	kkk-d10-kkk	102	3320
1012843	N/A	N/A	11995	12010	AGGTTGCCGAGATATA	kkk-d10-kkk	46	3321
1012844	N/A	N/A	11997	12012	CGAGGTTGCCGAGATA	kkk-d10-kkk	34	3322
1012848	N/A	N/A	14251	14266	GAGCCAACCTTAGCA	kkk-d10-kkk	89	3323
1012850	N/A	N/A	14253	14268	CAGAGCCAACCTTAGAG	kkk-d10-kkk	70	3324
1012852	N/A	N/A	14734	14749	GAAGCTTAGTTATCTG	kkk-d10-kkk	55	3325
1012855	N/A	N/A	14739	14754	GGCCTGAAGCTTAGTT	kkk-d10-kkk	105	3326
1012859	N/A	N/A	15594	15609	GTCGCGCAAGTCTACA	kkk-d10-kkk	96	3327
1012860	N/A	N/A	15841	15856	GTTGGCACAATTCTCT	kkk-d10-kkk	78	3328
1012864	N/A	N/A	15845	15860	GCGAGTTGCACAATT	kkk-d10-kkk	73	3329
1012866	N/A	N/A	15848	15863	ATGGCGAGTTGGCACA	kkk-d10-kkk	51	3330
1012867	N/A	N/A	15850	15865	GAATGGCGAGTTGGCA	kkk-d10-kkk	61	3331
1012869	N/A	N/A	15884	15899	CGTGATCTGAGACTAC	kkk-d10-kkk	75	3332
1012872	N/A	N/A	15889	15904	ACTGCCGTGATCTGAG	kkk-d10-kkk	66	3333

1012920	1441	1456	19558	19573	TAGATCTGTGGTAATC	kkk-d10-kkk	80	3334
1012921	1450	1465	19567	19582	AATGGCGGATAGATCT	kkk-d10-kkk	90	3335

Example 11: Effect of mixed MOE and cEt gapmers with phosphorothioate internucleoside linkages on human IRF4 *in vitro*, single dose

Modified oligonucleotides complementary to a human IRF4 nucleic acid were designed and tested for their effect on IRF4 mRNA *in vitro*.

Cultured MM.1R cells at a density of 5,000 cells per well were transfected by free uptake with 1,000 nM concentration of modified oligonucleotide or no modified oligonucleotide for untreated controls. After approximately 24 hours, RNA was isolated from the cells and IRF4 mRNA levels were measured by quantitative real-time PCR. Human primer probe set RTS4522 (forward sequence CGGAAATCCCGTACCAATGT, designated herein as SEQ ID NO: 3392; reverse sequence TGGCAACCATTTTCACAAGCT designated herein as SEQ ID NO: 3393; probe sequence TTTGGACCCCGCGGCCAC, designated herein as SEQ ID: 3394) was used to measure mRNA levels. IRF4 mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented in the tables below as percent control of the amount of IRF4 mRNA, relative to untreated control (UTC) cells.

The modified oligonucleotides in Tables 59 through 64 are cEt and/or MOE containing gapmers. The modified oligonucleotides have a central gap segment comprising 2'-deoxynucleosides which is flanked by wing segments on the 5' direction and the 3' direction. At least one nucleoside in the 5' wing segment and/or one nucleoside in the 3' wing segment has a MOE and/or cEt sugar modification. The "Motif" column describes the sugar modifications of each oligonucleotide. "k" indicates a cEt sugar modification; "d" indicates deoxyribose; and "e" indicates a MOE modification. Each internucleoside linkage is a phosphorothioate internucleoside linkage and each cytosine residue is a 5-methylcytosine. "Start Site" indicates the 5'-most nucleoside to which the gapmer is complementary in the human nucleic acid sequence. "Stop Site" indicates the 3'-most nucleoside to which the gapmer is complementary in the human nucleic acid sequence.

Each modified oligonucleotide listed in Table 59 through 64 below is complementary to human IRF4 nucleic acid sequences SEQ ID NO: 1 or SEQ ID NO: 2, as indicated. 'N/A' indicates that the modified oligonucleotide is not complementary to that particular nucleic acid sequence with 100% complementarity. As shown below, modified oligonucleotides complementary to human IRF4 reduced the amount of human IRF4 mRNA.

Table 59
Percent control of human IRF4 mRNA with gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID: 2 Stop Site	Sequence	Motif	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	kkk-d10-kkk	24	195
881450	3252	3267	21369	21384	ACACTTTTAGAGAGGA	kkk-d10-kkk	29	2111
881659	4592	4607	22709	22724	GGAAGTTTACACTGGA	kkk-d10-kkk	14	2044
1013023	N/A	N/A	10142	10157	ATGTTAGCCAATTCCT	k-d10-kekek	93	3272
1013024	N/A	N/A	10143	10158	TATGTTAGCCAATTCC	k-d10-kekek	99	2991
1013025	N/A	N/A	10144	10159	TTATGTTAGCCAATTC	k-d10-kekek	94	3273
1013026	N/A	N/A	10145	10160	TTTATGTTAGCCAATT	k-d10-kekek	112	3274
1013032	N/A	N/A	10278	10293	TGTTACCGATGCTTCA	k-d10-kekek	82	2294
1013033	N/A	N/A	10279	10294	CTGTTACCGATGCTTC	k-d10-kekek	74	2993
1013034	N/A	N/A	10280	10295	ACTGTTACCGATGCTT	k-d10-kekek	80	3055
1013035	N/A	N/A	10281	10296	TACTGTTACCGATGCT	k-d10-kekek	98	3117
1013046	N/A	N/A	11016	11031	GTGTCTAAAGTCCCAT	k-d10-kekek	77	3275
1013047	N/A	N/A	11017	11032	AGTGTCTAAAGTCCCA	k-d10-kekek	97	2996
1013048	N/A	N/A	11018	11033	AAGTGTCTAAAGTCCC	k-d10-kekek	101	3276
1013049	N/A	N/A	11019	11034	CAAGTGTCTAAAGTCC	k-d10-kekek	88	3058
1013053	N/A	N/A	11119	11134	AGCAGTGATGTCAGGT	k-d10-kekek	33	2718
1013054	N/A	N/A	11120	11135	AAGCAGTGATGTCAGG	k-d10-kekek	61	3277
1013055	N/A	N/A	11121	11136	CAAGCAGTGATGTCAG	k-d10-kekek	57	3278
1013060	N/A	N/A	11395	11410	CACATCAATGTTTTAG	k-d10-kekek	81	3279
1013061	N/A	N/A	11396	11411	GCACATCAATGTTTTA	k-d10-kekek	100	1159
1013062	N/A	N/A	11397	11412	GGCACATCAATGTTTT	k-d10-kekek	75	3280
1013063	N/A	N/A	11398	11413	AGGCACATCAATGTTT	k-d10-kekek	95	1233
1013074	N/A	N/A	11411	11426	GTGTATTACTCTTAGG	k-d10-kekek	20	1540
1013075	N/A	N/A	11412	11427	TGTGTATTACTCTTAG	k-d10-kekek	44	3246
1013076	N/A	N/A	11413	11428	ATGTGTATTACTCTTA	k-d10-kekek	96	3281
1013077	N/A	N/A	11414	11429	AATGTGTATTACTCTT	k-d10-kekek	71	3282
1013090	N/A	N/A	11565	11580	TGTGCTTGCCAAGCCT	k-d10-kekek	97	3283
1013091	N/A	N/A	11566	11581	GTGTGCTTGCCAAGCC	k-d10-kekek	77	3000
1013092	N/A	N/A	11567	11582	CGTGTGCTTGCCAAGC	k-d10-kekek	68	3284
1013093	N/A	N/A	11568	11583	ACGTGTGCTTGCCAAG	k-d10-kekek	63	3285
1013125	N/A	N/A	12514	12529	TTCATGTAAAGTCTGC	k-d10-kekek	118	3286
1013126	N/A	N/A	12515	12530	GTTCATGTAAAGTCTG	k-d10-kekek	78	934
1013127	N/A	N/A	12516	12531	AGTTCATGTAAAGTCT	k-d10-kekek	78	755
1013128	N/A	N/A	12517	12532	AAGTTCATGTAAAGTC	k-d10-kekek	94	3287
1013207	N/A	N/A	18073	18088	GTTGGCTGGTCTTTGT	k-d10-kekek	77	3336

1013208	N/A	N/A	18074	18089	GGTTGGCTGGTCTTTG	k-d10-kekek	53	3337
1013209	N/A	N/A	18075	18090	TGGTTGGCTGGTCTTT	k-d10-kekek	91	3338
1013210	N/A	N/A	18076	18091	TTGGTTGGCTGGTCTT	k-d10-kekek	66	3339
1013213	N/A	N/A	18087	18102	TTATATACTGGTTGGT	k-d10-kekek	78	1179
1013214	N/A	N/A	18088	18103	ATTATATACTGGTTGG	k-d10-kekek	78	3340
1013215	N/A	N/A	18089	18104	GATTATATACTGGTTG	k-d10-kekek	52	1254
1013216	N/A	N/A	18090	18105	GGATTATATACTGGTT	k-d10-kekek	65	1330
1013217	N/A	N/A	18091	18106	GGGATTATATACTGGT	k-d10-kekek	66	3341
1013218	N/A	N/A	18092	18107	TGGGATTATATACTGG	k-d10-kekek	57	3342
1013232	N/A	N/A	18571	18586	TGATAGCTGAGCTGAT	k-d10-kekek	78	2546
1013233	N/A	N/A	18572	18587	GTGATAGCTGAGCTGA	k-d10-kekek	71	3343
1013234	N/A	N/A	18573	18588	TGTGATAGCTGAGCTG	k-d10-kekek	102	3344
1013235	N/A	N/A	18574	18589	ATGTGATAGCTGAGCT	k-d10-kekek	103	3345
1013236	N/A	N/A	18575	18590	GATGTGATAGCTGAGC	k-d10-kekek	50	3346
1013237	N/A	N/A	18576	18591	TGATGTGATAGCTGAG	k-d10-kekek	82	3347
1013238	N/A	N/A	18577	18592	TTGATGTGATAGCTGA	k-d10-kekek	88	3348
1013252	N/A	N/A	18611	18626	AGTGACTTGCATCCAT	k-d10-kekek	98	3349
1013253	N/A	N/A	18612	18627	CAGTGACTTGCATCCA	k-d10-kekek	71	3350
1013254	N/A	N/A	18613	18628	ACAGTGACTTGCATCC	k-d10-kekek	105	3351
1013255	N/A	N/A	18614	18629	GACAGTGACTTGCATC	k-d10-kekek	92	3352
1013462	N/A	N/A	10142	10157	ATGTTAGCCAATTCCT	kk-d9-kekek	56	3272
1013463	N/A	N/A	10143	10158	TATGTTAGCCAATTCC	kk-d9-kekek	97	2991
1013464	N/A	N/A	10144	10159	TTATGTTAGCCAATTC	kk-d9-kekek	81	3273
1013465	N/A	N/A	10145	10160	TTTATGTTAGCCAATT	kk-d9-kekek	85	3274
1013471	N/A	N/A	10278	10293	TGTTACCGATGCTTCA	kk-d9-kekek	79	2294
1013472	N/A	N/A	10279	10294	CTGTTACCGATGCTTC	kk-d9-kekek	56	2993
1013473	N/A	N/A	10280	10295	ACTGTTACCGATGCTT	kk-d9-kekek	82	3055
1013474	N/A	N/A	10281	10296	TACTGTTACCGATGCT	kk-d9-kekek	73	3117
1013485	N/A	N/A	11016	11031	GTGTCTAAAGTCCCAT	kk-d9-kekek	61	3275
1013486	N/A	N/A	11017	11032	AGTGCTAAAGTCCCA	kk-d9-kekek	91	2996
1013487	N/A	N/A	11018	11033	AAGTGTCTAAAGTCCC	kk-d9-kekek	78	3276
1013488	N/A	N/A	11019	11034	CAAGTGTCTAAAGTCC	kk-d9-kekek	94	3058
1013492	N/A	N/A	11119	11134	AGCAGTGATGTCAGGT	kk-d9-kekek	33	2718
1013493	N/A	N/A	11120	11135	AAGCAGTGATGTCAGG	kk-d9-kekek	56	3277
1013494	N/A	N/A	11121	11136	CAAGCAGTGATGTCAG	kk-d9-kekek	48	3278
1013499	N/A	N/A	11395	11410	CACATCAATGTTTTAG	kk-d9-kekek	66	3279
1013500	N/A	N/A	11396	11411	GCACATCAATGTTTTA	kk-d9-kekek	85	1159
1013501	N/A	N/A	11397	11412	GGCACATCAATGTTTT	kk-d9-kekek	81	3280
1013502	N/A	N/A	11398	11413	AGGCACATCAATGTTT	kk-d9-kekek	81	1233
1013513	N/A	N/A	11411	11426	GTGTATTACTCTTAGG	kk-d9-kekek	22	1540
1013514	N/A	N/A	11412	11427	TGTGTATTACTCTTAG	kk-d9-kekek	21	3246

1013515	N/A	N/A	11413	11428	ATGTGTATTACTCTTA	kk-d9-kekek	51	3281
1013516	N/A	N/A	11414	11429	AATGTGTATTACTCTT	kk-d9-kekek	59	3282
1013529	N/A	N/A	11565	11580	TGTGCTTGCCAAGCCT	kk-d9-kekek	82	3283

Table 60

Percent control of human IRF4 mRNA with gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID 2: Stop Site	Sequence	Motif	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	kkk-d10-kkk	18	195
881450	3252	3267	21369	21384	ACACTTTTAGAGAGGA	kkk-d10-kkk	36	2111
881659	4592	4607	22709	22724	GGAAGTTTACACTGGA	kkk-d10-kkk	10	2044
1013530	N/A	N/A	11566	11581	GTGTGCTTGCCAAGCC	kk-d9-kekek	61	3000
1013531	N/A	N/A	11567	11582	CGTGTGCTTGCCAAGC	kk-d9-kekek	57	3284
1013532	N/A	N/A	11568	11583	ACGTGTGCTTGCCAAG	kk-d9-kekek	56	3285
1013564	N/A	N/A	12514	12529	TTCATGTAAAGTCTGC	kk-d9-kekek	88	3286
1013565	N/A	N/A	12515	12530	GTTTCATGTAAAGTCTG	kk-d9-kekek	66	934
1013566	N/A	N/A	12516	12531	AGTTCATGTAAAGTCT	kk-d9-kekek	69	755
1013567	N/A	N/A	12517	12532	AAGTTCATGTAAAGTC	kk-d9-kekek	73	3287
1013646	N/A	N/A	18073	18088	GTTGGCTGGTCTTTGT	kk-d9-kekek	38	3336
1013647	N/A	N/A	18074	18089	GGTTGGCTGGTCTTTG	kk-d9-kekek	33	3337
1013648	N/A	N/A	18075	18090	TGGTTGGCTGGTCTTT	kk-d9-kekek	56	3338
1013649	N/A	N/A	18076	18091	TTGGTTGGCTGGTCTT	kk-d9-kekek	35	3339
1013652	N/A	N/A	18087	18102	TTATATACTGGTTGGT	kk-d9-kekek	50	1179
1013653	N/A	N/A	18088	18103	ATTATATACTGGTTGG	kk-d9-kekek	48	3340
1013654	N/A	N/A	18089	18104	GATTATATACTGGTTG	kk-d9-kekek	55	1254
1013655	N/A	N/A	18090	18105	GGATTATATACTGGTT	kk-d9-kekek	35	1330
1013656	N/A	N/A	18091	18106	GGGATTATATACTGGT	kk-d9-kekek	60	3341
1013657	N/A	N/A	18092	18107	TGGGATTATATACTGG	kk-d9-kekek	58	3342
1013672	N/A	N/A	18572	18587	GTGATAGCTGAGCTGA	kk-d9-kekek	61	3343
1013673	N/A	N/A	18573	18588	TGTGATAGCTGAGCTG	kk-d9-kekek	83	3344
1013674	N/A	N/A	18574	18589	ATGTGATAGCTGAGCT	kk-d9-kekek	76	3345
1013675	N/A	N/A	18575	18590	GATGTGATAGCTGAGC	kk-d9-kekek	69	3346
1013676	N/A	N/A	18576	18591	TGATGTGATAGCTGAG	kk-d9-kekek	102	3347
1013677	N/A	N/A	18577	18592	TTGATGTGATAGCTGA	kk-d9-kekek	76	3348
1013691	N/A	N/A	18611	18626	AGTGACTTGCATCCAT	kk-d9-kekek	73	3349
1013692	N/A	N/A	18612	18627	CAGTGACTTGCATCCA	kk-d9-kekek	74	3350
1013693	N/A	N/A	18613	18628	ACAGTGACTTGCATCC	kk-d9-kekek	68	3351
1013694	N/A	N/A	18614	18629	GACAGTGACTTGCATC	kk-d9-kekek	95	3352
1013902	N/A	N/A	10142	10157	ATGTTAGCCAATTCCT	kk-d10-keke	85	3272

1013903	N/A	N/A	10143	10158	TATGTTAGCCAATTCC	kk-d10-keke	75	2991
1013904	N/A	N/A	10144	10159	TTATGTTAGCCAATTC	kk-d10-keke	84	3273
1013905	N/A	N/A	10145	10160	TTTATGTTAGCCAATT	kk-d10-keke	105	3274
1013911	N/A	N/A	10278	10293	TGTTACCGATGCTTCA	kk-d10-keke	58	2294
1013912	N/A	N/A	10279	10294	CTGTTACCGATGCTTC	kk-d10-keke	63	2993
1013913	N/A	N/A	10280	10295	ACTGTTACCGATGCTT	kk-d10-keke	52	3055
1013914	N/A	N/A	10281	10296	TACTGTTACCGATGCT	kk-d10-keke	83	3117
1013925	N/A	N/A	11016	11031	GTGTCTAAAGTCCCAT	kk-d10-keke	94	3275
1013926	N/A	N/A	11017	11032	AGTGTCTAAAGTCCCA	kk-d10-keke	61	2996
1013927	N/A	N/A	11018	11033	AAGTGTCTAAAGTCCC	kk-d10-keke	88	3276
1013928	N/A	N/A	11019	11034	CAAGTGTCTAAAGTCC	kk-d10-keke	83	3058
1013932	N/A	N/A	11119	11134	AGCAGTGATGTCAGGT	kk-d10-keke	36	2718
1013933	N/A	N/A	11120	11135	AAGCAGTGATGTCAGG	kk-d10-keke	24	3277
1013934	N/A	N/A	11121	11136	CAAGCAGTGATGTCAG	kk-d10-keke	74	3278
1013939	N/A	N/A	11395	11410	CACATCAATGTTTTAG	kk-d10-keke	61	3279
1013940	N/A	N/A	11396	11411	GCACATCAATGTTTTA	kk-d10-keke	50	1159
1013941	N/A	N/A	11397	11412	GGCACATCAATGTTTT	kk-d10-keke	91	3280
1013942	N/A	N/A	11398	11413	AGGCACATCAATGTTT	kk-d10-keke	86	1233
1013953	N/A	N/A	11411	11426	GTGTATTACTCTTAGG	kk-d10-keke	28	1540
1013954	N/A	N/A	11412	11427	TGTGTATTACTCTTAG	kk-d10-keke	61	3246
1013955	N/A	N/A	11413	11428	ATGTGTATTACTCTTA	kk-d10-keke	52	3281
1013956	N/A	N/A	11414	11429	AATGTGTATTACTCTT	kk-d10-keke	78	3282
1013969	N/A	N/A	11565	11580	TGTGCTTGCCAAGCCT	kk-d10-keke	70	3283
1013970	N/A	N/A	11566	11581	GTGTGCTTGCCAAGCC	kk-d10-keke	53	3000
1013971	N/A	N/A	11567	11582	CGTGTGCTTGCCAAGC	kk-d10-keke	55	3284
1013972	N/A	N/A	11568	11583	ACGTGTGCTTGCCAAG	kk-d10-keke	74	3285
1014004	N/A	N/A	12514	12529	TTCATGTAAAGTCTGC	kk-d10-keke	72	3286
1014005	N/A	N/A	12515	12530	GTTTCATGTAAAGTCTG	kk-d10-keke	58	934
1014006	N/A	N/A	12516	12531	AGTTCATGTAAAGTCT	kk-d10-keke	51	755
1014007	N/A	N/A	12517	12532	AAGTTCATGTAAAGTC	kk-d10-keke	80	3287
1014086	N/A	N/A	18073	18088	GTTGGCTGGTCTTTGT	kk-d10-keke	75	3336
1014087	N/A	N/A	18074	18089	GGTTGGCTGGTCTTTG	kk-d10-keke	24	3337
1014088	N/A	N/A	18075	18090	TGGTTGGCTGGTCTTT	kk-d10-keke	20	3338
1014089	N/A	N/A	18076	18091	TTGGTTGGCTGGTCTT	kk-d10-keke	73	3339
1014092	N/A	N/A	18087	18102	TTATATACTGGTTGGT	kk-d10-keke	53	1179
1014093	N/A	N/A	18088	18103	ATTATATACTGGTTGG	kk-d10-keke	68	3340
1014094	N/A	N/A	18089	18104	GATTATATACTGGTTG	kk-d10-keke	55	1254
1014095	N/A	N/A	18090	18105	GGATTATATACTGGTT	kk-d10-keke	22	1330
1014096	N/A	N/A	18091	18106	GGGATTATATACTGGT	kk-d10-keke	54	3341
1014097	N/A	N/A	18092	18107	TGGGATTATATACTGG	kk-d10-keke	32	3342
1014111	N/A	N/A	18571	18586	TGATAGCTGAGCTGAT	kk-d10-keke	117	2546

1014112	N/A	N/A	18572	18587	GTGATAGCTGAGCTGA	kk-d10-keke	65	3343
1014113	N/A	N/A	18573	18588	TGTGATAGCTGAGCTG	kk-d10-keke	84	3344
1014114	N/A	N/A	18574	18589	ATGTGATAGCTGAGCT	kk-d10-keke	96	3345
1014115	N/A	N/A	18575	18590	GATGTGATAGCTGAGC	kk-d10-keke	36	3346
1014116	N/A	N/A	18576	18591	TGATGTGATAGCTGAG	kk-d10-keke	46	3347
1014117	N/A	N/A	18577	18592	TTGATGTGATAGCTGA	kk-d10-keke	89	3348

Table 61

Percent control of human IRF4 mRNA with gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID 2: Stop Site	Sequence	Motif	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	kkk-d10-kkk	24	195
881450	3252	3267	21369	21384	ACACTTTTAGAGAGGA	kkk-d10-kkk	32	2111
881659	4592	4607	22709	22724	GGAAGTTTACACTGGA	kkk-d10-kkk	11	2044
1014131	N/A	N/A	18611	18626	AGTGACTTGCATCCAT	kk-d10-keke	50	3349
1014132	N/A	N/A	18612	18627	CAGTGACTTGCATCCA	kk-d10-keke	67	3350
1014133	N/A	N/A	18613	18628	ACAGTGACTTGCATCC	kk-d10-keke	70	3351
1014134	N/A	N/A	18614	18629	GACAGTGACTTGCATC	kk-d10-keke	75	3352
1014342	N/A	N/A	10142	10157	ATGTTAGCCAATTCCCT	kk-d9-kdkdk	97	3272
1014343	N/A	N/A	10143	10158	TATGTTAGCCAATTCC	kk-d9-kdkdk	66	2991
1014344	N/A	N/A	10144	10159	TTATGTTAGCCAATTC	kk-d9-kdkdk	74	3273
1014345	N/A	N/A	10145	10160	TTTATGTTAGCCAATT	kk-d9-kdkdk	66	3274
1014351	N/A	N/A	10278	10293	TGTTACCGATGCTTCA	kk-d9-kdkdk	74	2294
1014352	N/A	N/A	10279	10294	CTGTTACCGATGCTTC	kk-d9-kdkdk	48	2993
1014353	N/A	N/A	10280	10295	ACTGTTACCGATGCTT	kk-d9-kdkdk	69	3055
1014354	N/A	N/A	10281	10296	TACTGTTACCGATGCT	kk-d9-kdkdk	82	3117
1014365	N/A	N/A	11016	11031	GTGTCTAAAGTCCCAT	kk-d9-kdkdk	95	3275
1014366	N/A	N/A	11017	11032	AGTGTCTAAAGTCCCA	kk-d9-kdkdk	105	2996
1014367	N/A	N/A	11018	11033	AAGTGTCTAAAGTCCC	kk-d9-kdkdk	79	3276
1014368	N/A	N/A	11019	11034	CAAGTGTCTAAAGTCC	kk-d9-kdkdk	71	3058
1014372	N/A	N/A	11119	11134	AGCAGTGATGTCAGGT	kk-d9-kdkdk	52	2718
1014373	N/A	N/A	11120	11135	AAGCAGTGATGTCAGG	kk-d9-kdkdk	39	3277
1014374	N/A	N/A	11121	11136	CAAGCAGTGATGTCAG	kk-d9-kdkdk	51	3278
1014379	N/A	N/A	11395	11410	CACATCAATGTTTTAG	kk-d9-kdkdk	63	3279
1014380	N/A	N/A	11396	11411	GCACATCAATGTTTTA	kk-d9-kdkdk	93	1159
1014381	N/A	N/A	11397	11412	GGCACATCAATGTTTT	kk-d9-kdkdk	84	3280
1014382	N/A	N/A	11398	11413	AGGCACATCAATGTTT	kk-d9-kdkdk	81	1233
1014393	N/A	N/A	11411	11426	GTGTATTACTCTTAGG	kk-d9-kdkdk	17	1540
1014394	N/A	N/A	11412	11427	TGTGTATTACTCTTAG	kk-d9-kdkdk	29	3246

1014395	N/A	N/A	11413	11428	ATGTGTATTACTCTTA	kk-d9-kdkdk	68	3281
1014396	N/A	N/A	11414	11429	AATGTGTATTACTCTT	kk-d9-kdkdk	85	3282
1014409	N/A	N/A	11565	11580	TGTGCTTGCCAAGCCT	kk-d9-kdkdk	79	3283
1014410	N/A	N/A	11566	11581	GTGTGCTTGCCAAGCC	kk-d9-kdkdk	41	3000
1014411	N/A	N/A	11567	11582	CGTGTGCTTGCCAAGC	kk-d9-kdkdk	47	3284
1014412	N/A	N/A	11568	11583	ACGTGTGCTTGCCAAG	kk-d9-kdkdk	34	3285
1014444	N/A	N/A	12514	12529	TTCATGTAAAGTCTGC	kk-d9-kdkdk	65	3286
1014445	N/A	N/A	12515	12530	GTTCATGTAAAGTCTG	kk-d9-kdkdk	64	934
1014446	N/A	N/A	12516	12531	AGTTCATGTAAAGTCT	kk-d9-kdkdk	53	755
1014447	N/A	N/A	12517	12532	AAGTTCATGTAAAGTC	kk-d9-kdkdk	66	3287
1014526	N/A	N/A	18073	18088	GTTGGCTGGTCTTTGT	kk-d9-kdkdk	44	3336
1014527	N/A	N/A	18074	18089	GGTTGGCTGGTCTTTG	kk-d9-kdkdk	36	3337
1014528	N/A	N/A	18075	18090	TGGTTGGCTGGTCTTT	kk-d9-kdkdk	49	3338
1014529	N/A	N/A	18076	18091	TTGGTTGGCTGGTCTT	kk-d9-kdkdk	45	3339
1014532	N/A	N/A	18087	18102	TTATATACTGGTTGGT	kk-d9-kdkdk	82	1179
1014533	N/A	N/A	18088	18103	ATTATATACTGGTTGG	kk-d9-kdkdk	72	3340
1014534	N/A	N/A	18089	18104	GATTATATACTGGTTG	kk-d9-kdkdk	65	1254
1014535	N/A	N/A	18090	18105	GGATTATATACTGGTT	kk-d9-kdkdk	41	1330
1014536	N/A	N/A	18091	18106	GGGATTATATACTGGT	kk-d9-kdkdk	59	3341
1014537	N/A	N/A	18092	18107	TGGGATTATATACTGG	kk-d9-kdkdk	75	3342
1014551	N/A	N/A	18571	18586	TGATAGCTGAGCTGAT	kk-d9-kdkdk	122	2546
1014552	N/A	N/A	18572	18587	GTGATAGCTGAGCTGA	kk-d9-kdkdk	66	3343
1014553	N/A	N/A	18573	18588	TGTGATAGCTGAGCTG	kk-d9-kdkdk	53	3344
1014554	N/A	N/A	18574	18589	ATGTGATAGCTGAGCT	kk-d9-kdkdk	73	3345
1014555	N/A	N/A	18575	18590	GATGTGATAGCTGAGC	kk-d9-kdkdk	66	3346
1014556	N/A	N/A	18576	18591	TGATGTGATAGCTGAG	kk-d9-kdkdk	86	3347
1014557	N/A	N/A	18577	18592	TTGATGTGATAGCTGA	kk-d9-kdkdk	64	3348
1014571	N/A	N/A	18611	18626	AGTGACTTGCATCCAT	kk-d9-kdkdk	78	3349
1014572	N/A	N/A	18612	18627	CAGTGACTTGCATCCA	kk-d9-kdkdk	64	3350
1014573	N/A	N/A	18613	18628	ACAGTGACTTGCATCC	kk-d9-kdkdk	82	3351
1014574	N/A	N/A	18614	18629	GACAGTGACTTGCATC	kk-d9-kdkdk	107	3352
1014783	N/A	N/A	10142	10157	ATGTTAGCCAATTCC	kk-d9-eeekk	94	3272
1014784	N/A	N/A	10143	10158	TATGTTAGCCAATTCC	kk-d9-eeekk	73	2991
1014785	N/A	N/A	10144	10159	TTATGTTAGCCAATT	kk-d9-eeekk	91	3273
1014786	N/A	N/A	10145	10160	TTTATGTTAGCCAATT	kk-d9-eeekk	79	3274
1014792	N/A	N/A	10278	10293	TGTTACCGATGCTTCA	kk-d9-eeekk	61	2294
1014793	N/A	N/A	10279	10294	CTGTTACCGATGCTTC	kk-d9-eeekk	44	2993
1014794	N/A	N/A	10280	10295	ACTGTTACCGATGCTT	kk-d9-eeekk	66	3055
1014795	N/A	N/A	10281	10296	TACTGTTACCGATGCT	kk-d9-eeekk	92	3117
1014806	N/A	N/A	11016	11031	GTGTCTAAAGTCCCAT	kk-d9-eeekk	123	3275
1014807	N/A	N/A	11017	11032	AGTGTCTAAAGTCCCA	kk-d9-eeekk	88	2996

1014808	N/A	N/A	11018	11033	AAGTGTCTAAAGTCCC	kk-d9-eeekk	54	3276
1014809	N/A	N/A	11019	11034	CAAGTGTCTAAAGTCC	kk-d9-eeekk	69	3058
1014813	N/A	N/A	11119	11134	AGCAGTGATGTCAGGT	kk-d9-eeekk	44	2718
1014814	N/A	N/A	11120	11135	AAGCAGTGATGTCAGG	kk-d9-eeekk	49	3277
1014815	N/A	N/A	11121	11136	CAAGCAGTGATGTCAG	kk-d9-eeekk	92	3278
1014820	N/A	N/A	11395	11410	CACATCAATGTTTTAG	kk-d9-eeekk	89	3279
1014821	N/A	N/A	11396	11411	GCACATCAATGTTTTA	kk-d9-eeekk	80	1159
1014822	N/A	N/A	11397	11412	GGCACATCAATGTTTT	kk-d9-eeekk	64	3280
1014823	N/A	N/A	11398	11413	AGGCACATCAATGTTT	kk-d9-eeekk	57	1233
1014834	N/A	N/A	11411	11426	GTGTATTACTCTTAGG	kk-d9-eeekk	25	1540

Table 62

Percent control of human IRF4 mRNA with gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID 2: Stop Site	Sequence	Motif	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	kkk-d10-kkk	26	195
881450	3252	3267	21369	21384	ACACTTTTAGAGAGGA	kkk-d10-kkk	39	2111
881659	4592	4607	22709	22724	GGAAGTTTACACTGGA	kkk-d10-kkk	9	2044
1014835	N/A	N/A	11412	11427	TGTGTATTACTCTTAG	kk-d9-eeekk	76	3246
1014836	N/A	N/A	11413	11428	ATGTGTATTACTCTTA	kk-d9-eeekk	56	3281
1014837	N/A	N/A	11414	11429	AATGTGTATTACTCTT	kk-d9-eeekk	83	3282
1014850	N/A	N/A	11565	11580	TGTGCTTGCCAAGCCT	kk-d9-eeekk	60	3283
1014851	N/A	N/A	11566	11581	GTGTGCTTGCCAAGCC	kk-d9-eeekk	38	3000
1014852	N/A	N/A	11567	11582	CGTGTGCTTGCCAAGC	kk-d9-eeekk	34	3284
1014853	N/A	N/A	11568	11583	ACGTGTGCTTGCCAAG	kk-d9-eeekk	57	3285
1014885	N/A	N/A	12514	12529	TTCATGTAAAGTCTGC	kk-d9-eeekk	65	3286
1014886	N/A	N/A	12515	12530	GTTTCATGTAAAGTCTG	kk-d9-eeekk	76	934
1014887	N/A	N/A	12516	12531	AGTTCATGTAAAGTCT	kk-d9-eeekk	70	755
1014888	N/A	N/A	12517	12532	AAGTTCATGTAAAGTC	kk-d9-eeekk	97	3287
1014967	N/A	N/A	18073	18088	GTTGGCTGGTCTTTGT	kk-d9-eeekk	76	3336
1014968	N/A	N/A	18074	18089	GGTTGGCTGGTCTTTG	kk-d9-eeekk	31	3337
1014969	N/A	N/A	18075	18090	TGGTTGGCTGGTCTTT	kk-d9-eeekk	60	3338
1014970	N/A	N/A	18076	18091	TTGGTTGGCTGGTCTT	kk-d9-eeekk	50	3339
1014973	N/A	N/A	18087	18102	TTATATACTGGTTGGT	kk-d9-eeekk	60	1179
1014974	N/A	N/A	18088	18103	ATTATATACTGGTTGG	kk-d9-eeekk	63	3340
1014975	N/A	N/A	18089	18104	GATTATATACTGGTTG	kk-d9-eeekk	58	1254
1014976	N/A	N/A	18090	18105	GGATTATATACTGGTT	kk-d9-eeekk	22	1330
1014977	N/A	N/A	18091	18106	GGGATTATATACTGGT	kk-d9-eeekk	65	3341
1014978	N/A	N/A	18092	18107	TGGGATTATATACTGG	kk-d9-eeekk	46	3342

1014992	N/A	N/A	18571	18586	TGATAGCTGAGCTGAT	kk-d9-eeekk	102	2546
1014993	N/A	N/A	18572	18587	GTGATAGCTGAGCTGA	kk-d9-eeekk	87	3343
1014994	N/A	N/A	18573	18588	TGTGATAGCTGAGCTG	kk-d9-eeekk	88	3344
1014995	N/A	N/A	18574	18589	ATGTGATAGCTGAGCT	kk-d9-eeekk	100	3345
1014996	N/A	N/A	18575	18590	GATGTGATAGCTGAGC	kk-d9-eeekk	48	3346
1014997	N/A	N/A	18576	18591	TGATGTGATAGCTGAG	kk-d9-eeekk	53	3347
1014998	N/A	N/A	18577	18592	TTGATGTGATAGCTGA	kk-d9-eeekk	83	3348
1015012	N/A	N/A	18611	18626	AGTGACTTGCATCCAT	kk-d9-eeekk	48	3349
1015013	N/A	N/A	18612	18627	CAGTGACTTGCATCCA	kk-d9-eeekk	72	3350
1015014	N/A	N/A	18613	18628	ACAGTGACTTGCATCC	kk-d9-eeekk	73	3351
1015015	N/A	N/A	18614	18629	GACAGTGACTTGCATC	kk-d9-eeekk	76	3352
1015224	N/A	N/A	10142	10157	ATGTTAGCCAATTCCCT	kk-d9-ekeke	70	3272
1015225	N/A	N/A	10143	10158	TATGTTAGCCAATTCC	kk-d9-ekeke	110	2991
1015226	N/A	N/A	10144	10159	TTATGTTAGCCAATTC	kk-d9-ekeke	92	3273
1015227	N/A	N/A	10145	10160	TTTATGTTAGCCAATT	kk-d9-ekeke	113	3274
1015233	N/A	N/A	10278	10293	TGTTACCGATGCTTCA	kk-d9-ekeke	51	2294
1015234	N/A	N/A	10279	10294	CTGTTACCGATGCTTC	kk-d9-ekeke	40	2993
1015235	N/A	N/A	10280	10295	ACTGTTACCGATGCTT	kk-d9-ekeke	63	3055
1015236	N/A	N/A	10281	10296	TACTGTTACCGATGCT	kk-d9-ekeke	86	3117
1015247	N/A	N/A	11016	11031	GTGTCTAAAGTCCCAT	kk-d9-ekeke	77	3275
1015248	N/A	N/A	11017	11032	AGTGTCTAAAGTCCCA	kk-d9-ekeke	81	2996
1015249	N/A	N/A	11018	11033	AAGTGTCTAAAGTCCC	kk-d9-ekeke	101	3276
1015250	N/A	N/A	11019	11034	CAAGTGTCTAAAGTCC	kk-d9-ekeke	75	3058
1015254	N/A	N/A	11119	11134	AGCAGTGATGTCAGGT	kk-d9-ekeke	30	2718
1015255	N/A	N/A	11120	11135	AAGCAGTGATGTCAGG	kk-d9-ekeke	35	3277
1015256	N/A	N/A	11121	11136	CAAGCAGTGATGTCAG	kk-d9-ekeke	66	3278
1015261	N/A	N/A	11395	11410	CACATCAATGTTTTAG	kk-d9-ekeke	73	3279
1015262	N/A	N/A	11396	11411	GCACATCAATGTTTTA	kk-d9-ekeke	88	1159
1015263	N/A	N/A	11397	11412	GGCACATCAATGTTTT	kk-d9-ekeke	74	3280
1015264	N/A	N/A	11398	11413	AGGCACATCAATGTTT	kk-d9-ekeke	65	1233
1015275	N/A	N/A	11411	11426	GTGTATTACTCTTAGG	kk-d9-ekeke	16	1540
1015276	N/A	N/A	11412	11427	TGTGTATTACTCTTAG	kk-d9-ekeke	34	3246
1015277	N/A	N/A	11413	11428	ATGTGTATTACTCTTA	kk-d9-ekeke	39	3281
1015278	N/A	N/A	11414	11429	AATGTGTATTACTCTT	kk-d9-ekeke	70	3282
1015291	N/A	N/A	11565	11580	TGTGCTTGCCAAGCCT	kk-d9-ekeke	99	3283
1015292	N/A	N/A	11566	11581	GTGTGCTTGCCAAGCC	kk-d9-ekeke	81	3000
1015293	N/A	N/A	11567	11582	CGTGTGCTTGCCAAGC	kk-d9-ekeke	64	3284
1015294	N/A	N/A	11568	11583	ACGTGTGCTTGCCAAG	kk-d9-ekeke	39	3285
1015326	N/A	N/A	12514	12529	TTCATGTAAAGTCTGC	kk-d9-ekeke	61	3286
1015327	N/A	N/A	12515	12530	GTTCATGTAAAGTCTG	kk-d9-ekeke	68	934
1015328	N/A	N/A	12516	12531	AGTTCATGTAAAGTCT	kk-d9-ekeke	51	755

1015329	N/A	N/A	12517	12532	AAGTTCATGTAAAGTC	kk-d9-ekeke	71	3287
1015408	N/A	N/A	18073	18088	GTTGGCTGGTCTTTGT	kk-d9-ekeke	77	3336
1015409	N/A	N/A	18074	18089	GGTGGCTGGTCTTTG	kk-d9-ekeke	27	3337
1015410	N/A	N/A	18075	18090	TGGTTGGCTGGTCTTT	kk-d9-ekeke	40	3338
1015411	N/A	N/A	18076	18091	TTGGTTGGCTGGTCTT	kk-d9-ekeke	66	3339
1015414	N/A	N/A	18087	18102	TTATATACTGGTTGGT	kk-d9-ekeke	36	1179
1015415	N/A	N/A	18088	18103	ATTATATACTGGTTGG	kk-d9-ekeke	57	3340
1015416	N/A	N/A	18089	18104	GATTATATACTGGTTG	kk-d9-ekeke	54	1254
1015417	N/A	N/A	18090	18105	GGATTATATACTGGTT	kk-d9-ekeke	21	1330
1015418	N/A	N/A	18091	18106	GGGATTATATACTGGT	kk-d9-ekeke	66	3341
1015419	N/A	N/A	18092	18107	TGGGATTATATACTGG	kk-d9-ekeke	37	3342
1015433	N/A	N/A	18571	18586	TGATAGCTGAGCTGAT	kk-d9-ekeke	85	2546
1015434	N/A	N/A	18572	18587	GTGATAGCTGAGCTGA	kk-d9-ekeke	76	3343
1015435	N/A	N/A	18573	18588	TGTGATAGCTGAGCTG	kk-d9-ekeke	59	3344

Table 63

Percent control of human IRF4 mRNA with gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID 2: Stop Site	Sequence	Motif	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	kkk-d10-kkk	33	195
881450	3252	3267	21369	21384	ACACTTTTAGAGAGGA	kkk-d10-kkk	30	2111
881659	4592	4607	22709	22724	GGAAGTTTACACTGGA	kkk-d10-kkk	13	2044
1012810	N/A	N/A	10142	10157	ATGTTAGCCAATTCCT	kkk-d10-kkk	67	3272
1012811	N/A	N/A	10144	10159	TTATGTTAGCCAATTC	kkk-d10-kkk	78	3273
1012812	N/A	N/A	10145	10160	TTTATGTTAGCCAATT	kkk-d10-kkk	87	3274
1012816	N/A	N/A	11016	11031	GTGTCTAAAGTCCCAT	kkk-d10-kkk	72	3275
1012817	N/A	N/A	11018	11033	AAGTGTCTAAAGTCCC	kkk-d10-kkk	59	3276
1012819	N/A	N/A	11120	11135	AAGCAGTGATGTCAGG	kkk-d10-kkk	34	3277
1012820	N/A	N/A	11121	11136	CAAGCAGTGATGTCAG	kkk-d10-kkk	49	3278
1012821	N/A	N/A	11395	11410	CACATCAATGTTTATAG	kkk-d10-kkk	25	3279
1012822	N/A	N/A	11397	11412	GGCACATCAATGTTTT	kkk-d10-kkk	86	3280
1012826	N/A	N/A	11413	11428	ATGTGTATTACTCTTA	kkk-d10-kkk	51	3281
1012827	N/A	N/A	11414	11429	AATGTGTATTACTCTT	kkk-d10-kkk	59	3282
1012835	N/A	N/A	11565	11580	TGTGCTTGCCAAGCCT	kkk-d10-kkk	51	3283
1012836	N/A	N/A	11567	11582	CGTGTGCTTGCCAAGC	kkk-d10-kkk	34	3284
1012837	N/A	N/A	11568	11583	ACGTGTGCTTGCCAAG	kkk-d10-kkk	45	3285
1012845	N/A	N/A	12514	12529	TTCATGTAAAGTCTGC	kkk-d10-kkk	45	3286
1012846	N/A	N/A	12517	12532	AAGTTCATGTAAAGTC	kkk-d10-kkk	59	3287
1015436	N/A	N/A	18574	18589	ATGTGATAGCTGAGCT	kk-d9-ekeke	98	3345

1015437	N/A	N/A	18575	18590	GATGTGATAGCTGAGC	kk-d9-ekeke	47	3346
1015438	N/A	N/A	18576	18591	TGATGTGATAGCTGAG	kk-d9-ekeke	40	3347
1015439	N/A	N/A	18577	18592	TTGATGTGATAGCTGA	kk-d9-ekeke	72	3348
1015453	N/A	N/A	18611	18626	AGTGACTTGCATCCAT	kk-d9-ekeke	66	3349
1015454	N/A	N/A	18612	18627	CAGTGACTTGCATCCA	kk-d9-ekeke	66	3350
1015455	N/A	N/A	18613	18628	ACAGTGACTTGCATCC	kk-d9-ekeke	91	3351
1015456	N/A	N/A	18614	18629	GACAGTGACTTGCATC	kk-d9-ekeke	70	3352
1015665	N/A	N/A	10142	10157	ATGTTAGCCAATTCCT	k-d9-kekeke	95	3272
1015666	N/A	N/A	10143	10158	TATGTTAGCCAATTCC	k-d9-kekeke	86	2991
1015667	N/A	N/A	10144	10159	TTATGTTAGCCAATTC	k-d9-kekeke	98	3273
1015668	N/A	N/A	10145	10160	TTTATGTTAGCCAATT	k-d9-kekeke	86	3274
1015674	N/A	N/A	10278	10293	TGTTACCGATGCTTCA	k-d9-kekeke	87	2294
1015675	N/A	N/A	10279	10294	CTGTTACCGATGCTTC	k-d9-kekeke	76	2993
1015676	N/A	N/A	10280	10295	ACTGTTACCGATGCTT	k-d9-kekeke	83	3055
1015677	N/A	N/A	10281	10296	TACTGTTACCGATGCT	k-d9-kekeke	82	3117
1015688	N/A	N/A	11016	11031	GTGTCTAAAGTCCCAT	k-d9-kekeke	95	3275
1015689	N/A	N/A	11017	11032	AGTGTCTAAAGTCCCA	k-d9-kekeke	88	2996
1015690	N/A	N/A	11018	11033	AAGTGTCTAAAGTCCC	k-d9-kekeke	95	3276
1015691	N/A	N/A	11019	11034	CAAGTGTCTAAAGTCC	k-d9-kekeke	90	3058
1015695	N/A	N/A	11119	11134	AGCAGTGATGTCAGGT	k-d9-kekeke	64	2718
1015696	N/A	N/A	11120	11135	AAGCAGTGATGTCAGG	k-d9-kekeke	65	3277
1015697	N/A	N/A	11121	11136	CAAGCAGTGATGTCAG	k-d9-kekeke	88	3278
1015702	N/A	N/A	11395	11410	CACATCAATGTTTTAG	k-d9-kekeke	82	3279
1015703	N/A	N/A	11396	11411	GCACATCAATGTTTTA	k-d9-kekeke	85	1159
1015704	N/A	N/A	11397	11412	GGCACATCAATGTTTT	k-d9-kekeke	94	3280
1015705	N/A	N/A	11398	11413	AGGCACATCAATGTTT	k-d9-kekeke	97	1233
1015716	N/A	N/A	11411	11426	GTGTATTACTCTTAGG	k-d9-kekeke	23	1540
1015717	N/A	N/A	11412	11427	TGTGTATTACTCTTAG	k-d9-kekeke	48	3246
1015718	N/A	N/A	11413	11428	ATGTGTATTACTCTTA	k-d9-kekeke	51	3281
1015719	N/A	N/A	11414	11429	AATGTGTATTACTCTT	k-d9-kekeke	85	3282
1015732	N/A	N/A	11565	11580	TGTGCTTGCCAAGCCT	k-d9-kekeke	84	3283
1015733	N/A	N/A	11566	11581	GTGTGCTTGCCAAGCC	k-d9-kekeke	78	3000
1015734	N/A	N/A	11567	11582	CGTGTGCTTGCCAAGC	k-d9-kekeke	89	3284
1015735	N/A	N/A	11568	11583	ACGTGTGCTTGCCAAG	k-d9-kekeke	65	3285
1015767	N/A	N/A	12514	12529	TTCATGTAAAGTCTGC	k-d9-kekeke	97	3286
1015768	N/A	N/A	12515	12530	GTTTCATGTAAAGTCTG	k-d9-kekeke	90	934
1015769	N/A	N/A	12516	12531	AGTTCATGTAAAGTCT	k-d9-kekeke	90	755
1015770	N/A	N/A	12517	12532	AAGTTCATGTAAAGTC	k-d9-kekeke	79	3287
1015849	N/A	N/A	18073	18088	GTTGGCTGGTCTTTGT	k-d9-kekeke	82	3336
1015850	N/A	N/A	18074	18089	GGTTGGCTGGTCTTTG	k-d9-kekeke	74	3337
1015851	N/A	N/A	18075	18090	TGTTGGCTGGTCTTT	k-d9-kekeke	69	3338

1015852	N/A	N/A	18076	18091	TTGGTTGGCTGGTCTT	k-d9-kekeke	107	3339
1015855	N/A	N/A	18087	18102	TTATATACTGGTTGGT	k-d9-kekeke	80	1179
1015856	N/A	N/A	18088	18103	ATTATATACTGGTTGG	k-d9-kekeke	73	3340
1015857	N/A	N/A	18089	18104	GATTATATACTGGTTG	k-d9-kekeke	88	1254
1015858	N/A	N/A	18090	18105	GGATTATATACTGGTT	k-d9-kekeke	90	1330
1015859	N/A	N/A	18091	18106	GGGATTATATACTGGT	k-d9-kekeke	71	3341
1015860	N/A	N/A	18092	18107	TGGGATTATATACTGG	k-d9-kekeke	60	3342
1015874	N/A	N/A	18571	18586	TGATAGCTGAGCTGAT	k-d9-kekeke	83	2546
1015875	N/A	N/A	18572	18587	GTGATAGCTGAGCTGA	k-d9-kekeke	84	3343
1015876	N/A	N/A	18573	18588	TGTGATAGCTGAGCTG	k-d9-kekeke	82	3344
1015877	N/A	N/A	18574	18589	ATGTGATAGCTGAGCT	k-d9-kekeke	85	3345
1015878	N/A	N/A	18575	18590	GATGTGATAGCTGAGC	k-d9-kekeke	82	3346
1015879	N/A	N/A	18576	18591	TGATGTGATAGCTGAG	k-d9-kekeke	53	3347
1015880	N/A	N/A	18577	18592	TTGATGTGATAGCTGA	k-d9-kekeke	66	3348
1015894	N/A	N/A	18611	18626	AGTGACTTGCATCCAT	k-d9-kekeke	92	3349
1015895	N/A	N/A	18612	18627	CAGTGACTTGCATCCA	k-d9-kekeke	81	3350
1015896	N/A	N/A	18613	18628	ACAGTGACTTGCATCC	k-d9-kekeke	94	3351
1015897	N/A	N/A	18614	18629	GACAGTGACTTGCATC	k-d9-kekeke	100	3352

Table 64

Percent control of human IRF4 mRNA with gapmers
with phosphorothioate internucleoside linkages

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	SEQ ID: 2 Start Site	SEQ ID 2: Stop Site	Sequence	Motif	IRF4 (% UTC)	SEQ ID NO
609408	4226	4241	22343	22358	TTGTAAATGAGTCGGT	kkk-d10-kkk	23	195
881450	3252	3267	21369	21384	ACACTTTTAGAGAGGA	kkk-d10-kkk	35	2111
881659	4592	4607	22709	22724	GGAAGTTTACACTGGA	kkk-d10-kkk	9	2044
935595	3075	3090	21192	21207	ACTAAGCTTGATAAAG	kkk-d10-kkk	95	3288
935607	4195	4210	22312	22327	AGTGTTCAGGAGATA	kkk-d10-kkk	28	3289
1012769	N/A	N/A	4810	4825	GCTCCCGACACGCGCC	kkk-d10-kkk	81	3290
1012772	N/A	N/A	6267	6282	ATGCGGAGGTTTCCTTG	kkk-d10-kkk	48	3291
1012774	N/A	N/A	6271	6286	TGAGATGCGGAGGTTC	kkk-d10-kkk	73	3292
1012775	N/A	N/A	6273	6288	AGTGAGATGCGGAGGT	kkk-d10-kkk	35	3293
1012776	N/A	N/A	6275	6290	AGAGTGAGATGCGGAG	kkk-d10-kkk	37	3294
1012778	N/A	N/A	6281	6296	ACCGGTAGAGTGAGAT	kkk-d10-kkk	98	3295
1012782	N/A	N/A	7634	7649	GAGTTGTACAGGACAG	kkk-d10-kkk	48	3296
1012785	N/A	N/A	7638	7653	GTCTGAGTTGTACAGG	kkk-d10-kkk	43	3297
1012786	N/A	N/A	7640	7655	AGGTCTGAGTTGTACA	kkk-d10-kkk	55	3298
1012788	N/A	N/A	8386	8401	AATGGAGATACTTGTA	kkk-d10-kkk	74	3299
1012790	N/A	N/A	8389	8404	GACAATGGAGATACTT	kkk-d10-kkk	63	3300

1012795	N/A	N/A	9667	9682	GTATTTTCCGTTTCCT	kkk-d10-kkk	16	3303
1012796	N/A	N/A	9670	9685	ATGGTATTTTCCGTT	kkk-d10-kkk	57	3304
1012799	N/A	N/A	9677	9692	GTTTGCCATGGTATTT	kkk-d10-kkk	50	3305
1012804	N/A	N/A	9840	9855	CATTGCTAGATTCTCC	kkk-d10-kkk	70	3306
1012806	N/A	N/A	9846	9861	TTACCGCATTGCTAGA	kkk-d10-kkk	74	3307
1012808	N/A	N/A	9851	9866	CTGAGTTACCGCATTG	kkk-d10-kkk	46	3308
1012809	N/A	N/A	10139	10154	TTAGCCAATTCCTCCA	kkk-d10-kkk	53	3309
1012813	N/A	N/A	10274	10289	ACCGATGCTTCAAGAC	kkk-d10-kkk	44	3310
1012814	N/A	N/A	10276	10291	TTACCGATGCTTCAAG	kkk-d10-kkk	81	3311
1012815	N/A	N/A	10282	10297	TTACTGTTACCGATGC	kkk-d10-kkk	65	3312
1012818	N/A	N/A	11020	11035	GCAAGTGTCTAAAGTC	kkk-d10-kkk	47	3313
1012823	N/A	N/A	11400	11415	TTAGGCACATCAATGT	kkk-d10-kkk	83	3314
1012825	N/A	N/A	11406	11421	TTACTCTTAGGCACAT	kkk-d10-kkk	55	3315
1012828	N/A	N/A	11523	11538	GATCTCCATGGTGCAG	kkk-d10-kkk	88	3316
1012831	N/A	N/A	11530	11545	TAGGTAAGATCTCCAT	kkk-d10-kkk	67	3317
1012834	N/A	N/A	11564	11579	GTGCTTGCCAAGCCTA	kkk-d10-kkk	64	3318
1012840	N/A	N/A	11659	11674	CCAAACCTTAAGCTAT	kkk-d10-kkk	66	3319
1012841	N/A	N/A	11663	11678	AATTCCAAACCTTAAG	kkk-d10-kkk	74	3320
1012843	N/A	N/A	11995	12010	AGGTTGCCGAGATATA	kkk-d10-kkk	33	3321
1012844	N/A	N/A	11997	12012	CGAGGTTGCCGAGATA	kkk-d10-kkk	40	3322
1012848	N/A	N/A	14251	14266	GAGCCAACTTATAGCA	kkk-d10-kkk	92	3323
1012850	N/A	N/A	14253	14268	CAGAGCCAACTTATAG	kkk-d10-kkk	57	3324
1012852	N/A	N/A	14734	14749	GAAGCTTAGTTATCTG	kkk-d10-kkk	61	3325
1012855	N/A	N/A	14739	14754	GGCCTGAAGCTTAGTT	kkk-d10-kkk	94	3326
1012859	N/A	N/A	15594	15609	GTCGCGCAAGTCTACA	kkk-d10-kkk	84	3327
1012860	N/A	N/A	15841	15856	GTTGGCACAATTCTCT	kkk-d10-kkk	84	3328
1012864	N/A	N/A	15845	15860	GCGAGTTGGCACAATT	kkk-d10-kkk	63	3329
1012866	N/A	N/A	15848	15863	ATGGCGAGTTGGCACA	kkk-d10-kkk	52	3330
1012867	N/A	N/A	15850	15865	GAATGGCGAGTTGGCA	kkk-d10-kkk	60	3331
1012869	N/A	N/A	15884	15899	CGTGATCTGAGACTAC	kkk-d10-kkk	64	3332
1012872	N/A	N/A	15889	15904	ACTGCCGTGATCTGAG	kkk-d10-kkk	71	3333
1012875	N/A	N/A	17236	17251	TTACGCTTATTTTCC	kkk-d10-kkk	61	3353
1012879	N/A	N/A	17473	17488	CAATCTTAACCTGGAG	kkk-d10-kkk	60	3354
1012881	N/A	N/A	18073	18088	GTTGGCTGGTCTTTGT	kkk-d10-kkk	37	3336
1012882	N/A	N/A	18075	18090	TGGTTGGCTGGTCTTT	kkk-d10-kkk	12	3338
1012883	N/A	N/A	18076	18091	TTGGTTGGCTGGTCTT	kkk-d10-kkk	24	3339
1012884	N/A	N/A	18083	18098	ATACTGGTTGGTTGGC	kkk-d10-kkk	31	3355
1012885	N/A	N/A	18250	18265	GCCGATCATCAACTTC	kkk-d10-kkk	74	3356
1012888	N/A	N/A	18254	18269	CCCGGCCGATCATCAA	kkk-d10-kkk	77	3357
1012889	N/A	N/A	18569	18584	ATAGCTGAGCTGATCA	kkk-d10-kkk	70	3358
1012890	N/A	N/A	18573	18588	TGTGATAGCTGAGCTG	kkk-d10-kkk	53	3344

1012891	N/A	N/A	18574	18589	ATGTGATAGCTGAGCT	kkk-d10-kkk	74	3345
1012892	N/A	N/A	18576	18591	TGATGTGATAGCTGAG	kkk-d10-kkk	41	3347
1012893	N/A	N/A	18577	18592	TTGATGTGATAGCTGA	kkk-d10-kkk	45	3348
1012895	N/A	N/A	18581	18596	TGGATTGATGTGATAG	kkk-d10-kkk	52	3359
1012897	N/A	N/A	18607	18622	ACTTGCATCCATGTCA	kkk-d10-kkk	65	3360
1012899	N/A	N/A	18610	18625	GTGACTTGCATCCATG	kkk-d10-kkk	38	3361
1012900	N/A	N/A	18611	18626	AGTGA CTTCATCCAT	kkk-d10-kkk	33	3349
1012901	N/A	N/A	18613	18628	ACAGTGA CTTCATCC	kkk-d10-kkk	66	3351
1012902	N/A	N/A	18614	18629	GACAGTGA CTTCATC	kkk-d10-kkk	76	3352
1012903	N/A	N/A	18722	18737	AAGTGGA ACTCATAGG	kkk-d10-kkk	75	3362
1012904	N/A	N/A	19021	19036	ATCTGTATAGTTCTCA	kkk-d10-kkk	45	3363
1012906	N/A	N/A	19023	19038	TAATCTGTATAGTTCT	kkk-d10-kkk	58	3364
1012907	1344	1359	19461	19476	TCTGGCTAGCAGAGGT	kkk-d10-kkk	74	3365
1012911	1412	1427	19529	19544	ATGTGTTCTGGTAAAT	kkk-d10-kkk	66	3366
1012914	1422	1437	19539	19554	TGGATTGCTGATGTGT	kkk-d10-kkk	29	3367
1012915	1424	1439	19541	19556	TCTGGATTGCTGATGT	kkk-d10-kkk	64	3368
1012918	1427	1442	19544	19559	TCTTCTGGATTGCTGA	kkk-d10-kkk	80	3369
1012919	1429	1444	19546	19561	AATCTTCTGGATTGCT	kkk-d10-kkk	86	3370
1012920	1441	1456	19558	19573	TAGATCTGTGGTAATC	kkk-d10-kkk	94	3334
1012921	1450	1465	19567	19582	AATGGCGGATAGATCT	kkk-d10-kkk	75	3335

Example 12: Effect of modified oligonucleotides on human IRF4 *in vitro*, multiple doses

Modified oligonucleotides selected from the examples above were tested at various doses in SK-MEL-28 cells. Cells were plated at a density of 20,000 cells per well and transfected using electroporation with 185 nM, 555 nM, 1,666 nM, 5,000 nM, and 15,000 nM concentrations of modified oligonucleotide, as specified in the tables below. After a treatment period of approximately 24 hours, RNA was isolated from the cells and IRF4 mRNA levels were measured by RT-qPCR. Human IRF4 primer probe set RTS3114 (described hereinabove in Example 1) was used to measure mRNA levels. IRF4 mRNA levels were adjusted according to total RNA content, as measured by RiboGreen. Results are presented as the percent level of IRF4 mRNA transcript, relative to that of untreated control (UTC) cells. As illustrated in the tables below, IRF4 mRNA levels were reduced in a dose-dependent manner in cells treated with modified oligonucleotides.

Table 65

Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides

Compound Number	IRF4 expression (% UTC)				
	185 nM	555 nM	1,666 nM	5,000 nM	15,000 nM
609311	91	79	68	36	9
609312	93	91	78	42	13

609328	99	73	57	37	14
609332	99	92	62	38	15
609333	90	82	59	32	11
609334	80	71	50	30	11
609337	84	81	57	40	15
609343	87	80	56	26	11
609354	87	79	46	25	10
609357	85	80	50	29	9
609391	94	82	53	28	10
609398	81	77	39	24	8
609407	80	71	40	25	11
609408	102	73	49	19	12

Table 66

Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides

Compound Number	IRF4 expression (% UTC)				
	185 nM	555 nM	1,666 nM	5,000 nM	15,000 nM
609394	94	82	59	52	22
609397	86	77	57	42	24
609405	84	86	75	40	36
609408	100	92	62	33	27
609416	89	80	54	43	17
609419	84	75	66	44	19
609422	104	87	69	50	14
609530	96	99	78	71	49
609533	96	91	80	55	37
609546	96	107	84	66	25
609571	94	86	78	58	38
609591	102	95	94	50	19
609592	98	89	67	43	31
609594	86	73	68	43	26

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Table 67

Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides

Compound Number	IRF4 expression (% UTC)				
	185 nM	555 nM	1,666 nM	5,000 nM	15,000 nM
609394	95	76	60	52	20
609397	90	74	59	45	22
609405	96	82	77	46	37
609408	99	84	62	39	27

609416	95	76	51	39	21
609419	96	73	71	41	18
609422	90	83	82	48	17
609530	104	99	81	74	45
609533	91	97	79	58	32
609546	91	88	85	63	28
609571	96	95	78	56	35
609591	110	83	76	49	21
609592	94	88	73	43	38
609594	87	84	68	45	28

Table 68

Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides

Compound Number	IRF4 expression (% UTC)				
	185 nM	555 nM	1,666 nM	5,000 nM	15,000 nM
609394	101	94	61	25	6
609397	99	75	46	23	13
609405	97	80	53	17	4
609408	87	88	39	15	5
609416	99	83	47	18	6
609419	88	84	54	23	9
609422	111	92	66	17	2
609530	100	92	63	37	17
609533	92	84	65	38	19
609546	83	97	72	50	11
609571	94	90	72	47	17
609591	103	88	53	24	9
609592	90	90	55	24	8
609594	82	75	52	33	28

5 Example 13: Effect of modified oligonucleotides on human IRF4 *in vitro*, multiple doses

Modified oligonucleotides selected from the examples above were tested at various doses in SK-MEL-28 cells. Cells were plated at a density of 20,000 cells per well and transfected using electroporation with 500 nM, 1,000 nM, 2,000 nM, 4,000 nM, and 8,000 nM concentrations of modified oligonucleotide, as specified in the tables below. After a treatment period of approximately 24 hours, RNA was isolated from the cells and IRF4 mRNA levels were measured by RT-qPCR. Human IRF4 primer probe set RTS3114 (described hereinabove in Example 1) was used to measure mRNA levels. IRF4 mRNA levels were adjusted according to total RNA content, as measured by RiboGreen. Results are presented as the percent level of IRF4 mRNA transcript, relative to that of untreated control (UTC) cells. As illustrated in the tables below, IRF4 mRNA levels were reduced in a dose-dependent manner in cells treated with modified oligonucleotides.

Table 69

Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides

Compound Number	IRF4 expression (% UTC)				
	500 nM	1,000 nM	2,000 nM	4,000 nM	8,000 nM
609408	70	52	46	26	29
666273	85	97	76	53	27
666333	77	78	64	42	24
666347	80	74	56	37	19
666351	79	68	59	53	24
666378	71	57	43	28	20
666392	77	64	42	37	34
666431	85	69	47	41	24
666440	69	55	38	21	27
666441	79	60	47	29	26
666442	62	50	35	21	19
666443	71	62	46	32	13
666449	53	47	31	20	19
666458	69	52	41	22	25
666471	57	50	23	23	11

5

Table 70

Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides

Compound Number	IRF4 expression (% UTC)				
	500 nM	1,000 nM	2,000 nM	4,000 nM	8,000 nM
609408	71	58	47	37	19
666475	54	42	26	22	32
666496	54	45	30	18	13
666512	76	70	49	29	36
666534	64	55	33	19	9
666575	71	53	31	24	34
666582	80	58	45	28	30
666584	88	63	58	35	21
666586	49	28	29	19	21
666587	61	44	26	14	19
666605	68	55	38	32	18
666625	71	63	45	30	17
666640	73	59	39	42	18
666645	83	64	55	37	34

666649	80	55	48	35	21
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Table 71

Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides

Compound Number	IRF4 expression (% UTC)				
	500 nM	1,000 nM	2,000 nM	4,000 nM	8,000 nM
609408	74	57	65	47	23
666663	78	78	43	34	67
666664	77	64	43	31	62
666678	57	42	23	25	59
666681	74	59	47	28	60
666683	64	47	35	38	55
666714	81	77	54	47	75
666726	75	60	33	28	56
666727	83	65	42	31	72
666769	98	94	94	87	71
666773	83	81	71	47	36
666782	78	79	49	44	23
666787	75	66	44	32	26
666792	84	75	61	46	32
666815	81	80	47	50	32

5 Example 14: Effect of modified oligonucleotides on human IRF4 *in vitro*, multiple doses

Modified oligonucleotides selected from the examples above were tested at various doses in SK-MEL-28 cells. Cells were plated at a density of 20,000 cells per well and transfected using electroporation with 296 nM, 888 nM, 2,666 nM, and 8,000 nM concentrations of modified oligonucleotide, as specified in the tables below. After a treatment period of approximately 24 hours, RNA was isolated from the cells and IRF4 mRNA levels were measured by RT-qPCR. Human IRF4 primer probe set RTS3114 (described hereinabove in Example 1) was used to measure mRNA levels. IRF4 mRNA levels were adjusted according to total RNA content, as measured by RiboGreen. Results are presented as the percent level of IRF4 mRNA transcript, relative to that of untreated control (UTC) cells. As illustrated in the tables below, IRF4 mRNA levels were reduced in a dose-dependent manner in cells treated with modified oligonucleotides.

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Table 72

Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides

Compound Number	IRF4 expression (% UTC)				IC ₅₀ (μM)
	296 nM	888 nM	2,666 nM	8,000 nM	
609408	96	53	25	9	1.3
881193	90	72	54	23	2.5
881218	86	70	44	38	2.9
881242	106	65	38	27	2.2
881290	77	56	44	27	1.6
881385	99	106	84	54	> 8.0
881409	91	82	51	28	2.9
881434	78	59	29	14	1.2
881506	61	37	15	11	0.5
881667	80	63	41	16	1.5
881993	94	101	73	43	> 8.0
882066	99	72	53	25	2.7
882325	76	55	36	31	1.5
882326	79	73	42	31	2.3
882398	83	56	32	16	1.3
882699	88	81	65	50	> 8.0
882722	97	102	84	58	> 8.0
882818	134	94	75	31	4.8
882898	80	66	48	26	2.1

Table 73

Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides

Compound Number	IRF4 expression (% UTC)				IC ₅₀ (μM)
	296 nM	888 nM	2,666 nM	8,000 nM	
609408	85	50	22	11	1.1
881411	101	70	45	22	2.3
881412	105	74	33	21	2.1
881460	71	50	26	17	0.9
881530	83	57	34	20	1.4
881577	89	71	39	20	1.9
881578	67	48	32	18	0.8
881597	83	69	49	30	2.4
881717	70	46	20	15	0.8
881718	91	62	31	20	1.6
881741	73	49	24	16	0.9

881742	64	42	22	14	0.6
881973	79	58	43	35	2.0
882352	112	59	36	16	1.9
882725	90	68	43	20	2.0
882749	94	83	49	23	2.7
882797	69	52	27	16	0.9
882819	97	82	61	28	3.5
882866	136	119	65	28	4.5

Table 74**Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides**

Compound Number	IRF4 expression (% UTC)				IC ₅₀ (μM)
	296 nM	888 nM	2,666 nM	8,000 nM	
609408	96	45	25	15	1.3
881127	100	72	44	21	2.3
881317	74	48	33	18	1.0
881389	79	67	42	23	1.8
881413	59	43	35	20	0.6
881414	97	79	37	20	2.2
881437	91	67	36	21	1.8
881581	62	43	27	21	0.6
881671	80	66	47	41	3.1
881743	68	55	30	24	1.0
881791	81	61	34	13	1.3
882069	74	60	39	30	1.6
882070	81	60	42	33	2.0
882162	79	67	42	17	1.6
882185	73	50	24	22	1.0
882282	65	38	22	14	0.6
882305	62	43	15	19	0.5
882376	97	88	61	33	4.1
882377	82	46	22	13	1.0

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Table 75**Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides**

Compound Number	IRF4 expression (% UTC)				IC ₅₀ (μM)
	296 nM	888 nM	2,666 nM	8,000 nM	
609408	69	41	21	11	0.7
881391	100	67	36	21	2.0

881439	76	48	32	19	1.1
881511	82	73	36	26	2.0
881558	70	49	29	14	0.9
881582	61	42	21	15	0.5
881601	92	76	47	18	2.2
881648	78	68	36	21	1.6
881672	66	51	30	18	0.8
881744	95	78	43	19	2.2
881746	69	41	26	15	0.7
881975	101	91	63	51	> 8.0
881999	71	53	31	26	1.1
882210	91	78	50	22	2.5
882283	79	55	29	17	1.2
882354	81	57	34	20	1.4
882379	108	86	60	25	3.4
882800	77	55	28	15	1.1
882870	69	42	23	12	0.7

Table 76

Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides

Compound Number	IRF4 expression (% UTC)				IC ₅₀ (μM)
	296 nM	888 nM	2,666 nM	8,000 nM	
609408	81	47	29	18	1.1
881296	84	60	57	38	3.2
881440	75	74	46	26	2.2
881441	93	68	34	26	2.0
881465	85	63	38	29	1.9
881512	82	60	38	27	1.7
881559	84	62	47	31	2.2
881747	80	57	37	26	1.5
881955	73	66	35	30	1.6
882072	82	73	51	32	2.8
882142	85	68	48	31	2.5
882214	77	46	30	13	1.0
882309	74	54	51	24	1.6
882310	81	35	31	14	0.9
882357	74	58	35	31	1.5
882495	93	76	52	33	3.2
882565	90	77	55	33	3.3
882777	96	75	35	33	2.5
882871	67	49	44	21	1.1

Table 77

Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides

Compound Number	IRF4 expression (% UTC)				IC ₅₀ (μM)
	296 nM	888 nM	2,666 nM	8,000 nM	
609408	83	48	25	15	1.1
881322	98	71	42	17	2.0
881371	91	70	37	22	1.9
881394	77	47	27	14	1.0
881395	77	49	26	15	1.0
881442	51	36	22	9	0.3
881514	88	75	46	21	2.2
881561	92	62	38	18	1.7
881585	76	52	34	23	1.2
881724	100	72	39	22	2.2
881748	81	61	34	20	1.5
881749	70	46	27	12	0.8
881773	88	59	33	20	1.5
882215	83	60	50	26	2.0
882311	82	63	36	21	1.6
882358	80	52	32	17	1.2
882359	91	57	34	11	1.4
882383	92	86	64	37	4.8
882429	74	52	32	11	1.0

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Table 78

Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides

Compound Number	IRF4 expression (% UTC)				IC ₅₀ (μM)
	296 nM	888 nM	2,666 nM	8,000 nM	
609408	85	53	36	14	1.3
881133	101	88	76	63	> 8.0
881204	92	79	50	26	2.7
881396	71	46	29	16	0.9
881515	90	67	44	21	2.0
881516	81	49	35	17	1.2
881588	69	52	26	18	0.9
881726	73	42	44	8	1.0
881727	66	50	35	19	0.9
881750	73	49	19	17	0.9

882077	93	78	54	37	3.7
882099	61	46	18	23	0.6
882169	101	84	51	18	2.6
882170	92	76	39	25	2.2
882313	87	60	32	18	1.5
882384	93	68	40	18	1.9
882408	84	61	41	19	1.6
882709	104	106	108	98	> 8.0
882758	82	53	36	17	1.3

Table 79

Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides

Compound Number	IRF4 expression (% UTC)				IC ₅₀ (μM)
	296 nM	888 nM	2,666 nM	8,000 nM	
609408	83	49	25	10	1.1
881279	87	73	43	22	2.1
881399	79	49	23	24	1.1
881422	85	63	44	29	2.1
881470	109	92	54	19	3.0
881494	68	50	33	20	0.9
881495	68	46	24	17	0.8
881517	75	41	14	12	0.7
881542	76	55	31	13	1.1
881589	80	48	26	10	1.0
881607	90	64	32	19	1.6
881608	73	45	22	21	0.8
881728	58	32	17	11	0.4
881729	94	75	40	29	2.4
881752	75	47	28	14	0.9
882409	86	66	42	20	1.8
882432	101	67	34	12	1.7
882433	72	38	25	16	0.7
882806	92	35	45	34	1.7

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Table 80

Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides

Compound Number	IRF4 expression (% UTC)				IC ₅₀ (μM)
	296 nM	888 nM	2,666 nM	8,000 nM	
609408	99	55	43	12	1.7

690521	88	58	36	21	1.6
881112	133	107	73	56	> 8.0
881183	109	93	58	31	3.9
881280	94	61	40	23	1.9
881303	90	79	55	28	3.0
881304	94	86	86	37	7.9
881327	125	115	71	44	6.9
881448	82	58	36	21	1.5
881496	72	55	34	21	1.2
881543	86	67	37	24	1.8
881610	71	49	22	13	0.8
881657	83	61	46	29	2.0
881658	77	53	29	13	1.1
881753	81	70	48	20	2.0
881962	87	67	49	29	2.5
882268	110	72	50	31	3.0
882479	96	81	45	42	3.7
882761	76	67	37	25	1.6

Table 81

Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides

Compound Number	IRF4 expression (% UTC)				IC ₅₀ (μM)
	296 nM	888 nM	2,666 nM	8,000 nM	
609408	87	48	28	15	1.2
690522	63	32	13	11	0.4
690523	90	61	37	19	1.7
881281	95	69	49	32	2.8
881305	76	60	42	23	1.6
881425	71	53	34	21	1.1
881426	73	45	29	19	0.9
881449	65	50	28	16	0.8
881497	129	95	57	19	3.3
881498	98	71	34	16	1.9
881659	53	25	13	9	< 0.3
881660	65	32	17	10	0.5
881683	74	60	37	22	1.4
881780	82	54	34	17	1.3
881963	91	66	39	33	2.3
882175	79	43	24	12	0.9
882246	69	44	29	11	0.8
882810	100	66	45	25	2.3

882833	101	86	57	23	3.1
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Table 82**Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides**

Compound Number	IRF4 expression (% UTC)				IC ₅₀ (μM)
	296 nM	888 nM	2,666 nM	8,000 nM	
609408	87	51	28	14	1.2
881258	115	91	60	31	3.9
881282	104	89	42	32	3.1
881404	89	81	43	27	2.5
881427	87	65	48	19	1.9
881450	63	42	26	12	0.6
881451	100	77	49	30	2.9
881452	77	67	49	27	2.2
881499	84	74	44	35	2.7
881661	122	92	51	23	3.2
881684	106	89	55	33	3.8
881733	82	63	32	29	1.7
881734	72	49	34	23	1.0
881941	94	86	60	41	5.2
882177	94	62	35	30	2.0
882199	90	81	38	16	2.0
882200	89	60	36	22	1.7
882247	79	60	47	33	2.2
882765	101	82	57	30	3.5

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Table 83**Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides**

Compound Number	IRF4 expression (% UTC)				IC ₅₀ (μM)
	296 nM	888 nM	2,666 nM	8,000 nM	
609408	87	49	30	11	1.2
881213	85	67	50	20	2.1
881238	83	58	33	19	1.4
881286	64	51	35	22	0.9
881381	77	55	34	26	1.3
881382	83	71	49	37	3.0
881405	86	58	42	16	1.6
881477	80	62	56	28	2.4
881478	102	69	47	30	2.7

881571	109	90	47	27	3.1
881572	87	67	39	25	1.9
881616	104	76	47	36	3.3
881663	130	108	63	32	4.6
881784	117	87	50	35	3.7
882085	82	66	46	27	2.1
882107	109	83	74	37	5.5
882178	114	69	36	16	2.1
882601	123	99	64	26	4.0
882670	91	85	66	34	4.7

Table 84

Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides

Compound Number	IRF4 expression (% UTC)				IC ₅₀ (μM)
	296 nM	888 nM	2,666 nM	8,000 nM	
609408	101	60	32	14	1.6
881240	103	79	47	23	2.6
881359	124	89	57	35	4.1
881360	83	58	40	22	1.6
881384	85	72	42	39	2.8
881432	73	62	49	29	2.0
881575	92	67	52	40	3.4
881593	84	71	57	31	3.1
881761	94	93	72	56	> 8.0
882039	95	79	68	50	> 8.0
882086	96	79	50	25	2.7
882087	72	55	36	32	1.4
882204	67	77	38	30	1.9
882227	111	90	54	47	5.2
882228	96	75	52	40	3.8
882323	106	87	62	34	4.3
882532	114	85	54	33	3.7
882721	98	78	69	45	6.6
882744	84	79	50	31	2.9

5 Example 15: Effect of modified oligonucleotides on human IRF4 *in vitro*, multiple doses

Modified oligonucleotides selected from the examples above were tested at various doses in MM.1R cells. Cells were plated at a density of 5,000 cells per well and transfected by free uptake with 74 nM, 222 nM, 666 nM, and 2,000 nM concentrations of modified oligonucleotide, as specified in the tables below. After a treatment period of approximately 24 hours, RNA was isolated from the cells and IRF4 mRNA levels

were measured by RT-qPCR. Human IRF4 primer probe set hIRF4_LTS34726 (described hereinabove in Example 7) was used to measure mRNA levels. IRF4 mRNA levels were adjusted according to total RNA content, as measured by RiboGreen. Results are presented as the percent level of IRF4 mRNA transcript, relative to that of untreated control (UTC) cells. As illustrated in the tables below, IRF4 mRNA levels were reduced in a dose-dependent manner in cells treated with modified oligonucleotides.

Table 85

Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides

Compound Number	IRF4 expression (% UTC)				IC ₅₀ (μM)
	74 nM	222 nM	666 nM	2,000 nM	
609408	86	66	43	17	0.4
935580	89	62	34	10	0.4
935603	91	69	46	23	0.5
935620	84	64	37	15	0.4
935658	82	56	37	15	0.3
935898	74	47	24	7	0.2
935911	100	88	66	43	1.5
935918	90	75	45	23	0.6
935921	80	52	27	9	0.3
935925	98	67	62	36	0.9
935928	90	72	48	23	0.6
935929	96	85	60	36	1.1
935935	95	83	63	32	1.0
935939	86	74	50	41	0.9
935941	86	84	70	41	1.7
935948	86	62	45	24	0.5
935958	83	56	33	14	0.3
935961	78	51	27	8	0.3
935968	88	61	35	12	0.4

Table 86

Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides

Compound Number	IRF4 expression (% UTC)				IC ₅₀ (μM)
	74 nM	222 nM	666 nM	2,000 nM	
609408	79	59	37	14	0.3
935581	78	61	38	15	0.4
935608	85	71	48	20	0.5
935655	93	88	70	46	> 2.0

935679	92	72	47	23	0.6
935689	86	63	40	19	0.4
935696	72	45	22	9	0.2
935697	80	55	23	9	0.3
935698	83	68	39	17	0.4
935699	87	60	36	14	0.4
935700	72	59	26	7	0.3
935701	82	64	40	18	0.4
935707	84	68	49	23	0.5
935708	84	59	34	15	0.4
935721	86	70	46	24	0.5
935724	73	39	20	5	0.2
935727	85	67	49	27	0.6
935734	74	58	35	16	0.3
935741	85	68	42	17	0.4

Table 87

Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides

Compound Number	IRF4 expression (% UTC)				IC ₅₀ (μM)
	74 nM	222 nM	666 nM	2,000 nM	
609408	77	60	41	16	0.4
935668	94	78	51	25	0.7
935671	91	73	54	27	0.7
935686	90	69	53	34	0.8
935709	72	78	57	36	0.9
935731	80	66	52	36	0.7
935762	72	56	35	19	0.3
935765	75	55	37	15	0.3
935772	81	65	51	27	0.6
935779	78	72	55	28	0.7
935782	66	55	36	15	0.2
935789	81	77	58	32	0.9
935795	95	77	60	33	0.9
935805	85	68	42	21	0.5
935850	74	48	25	12	0.2
935851	78	54	26	9	0.3
935854	79	64	35	14	0.3
935857	78	66	44	19	0.4
935878	71	42	24	10	0.2

Table 88

Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides

Compound Number	IRF4 expression (% UTC)				IC ₅₀ (μM)
	74 nM	222 nM	666 nM	2,000 nM	
609408	79	62	39	15	0.4
881450	100	75	56	28	0.8
881659	76	45	21	5	0.2
935824	86	65	46	23	0.5
935833	81	60	44	26	0.5
935840	82	54	51	27	0.5
935853	85	64	45	21	0.5
935856	92	71	50	29	0.7
935859	90	81	63	36	1.1
935888	79	72	43	20	0.5
936006	80	64	41	21	0.4
936007	87	65	34	13	0.4
936011	94	79	62	40	1.2
936013	78	67	48	26	0.5
936016	83	62	43	21	0.4
936018	82	66	43	17	0.4
936033	80	63	47	25	0.5
936039	85	67	48	25	0.5
936046	88	66	49	30	0.6

Example 16: Effect of modified oligonucleotides on human IRF4 *in vitro*, multiple doses

5 Modified oligonucleotides selected from the examples above were tested at various doses in MM.1R cells. Cells were plated at a density of 5,000 cells per well and transfected by free uptake with 74 nM, 222 nM, 666 nM, and 2,000 nM concentrations of modified oligonucleotide, as specified in the tables below. After a treatment period of approximately 24 hours, RNA was isolated from the cells and IRF4 mRNA levels were measured by RT-qPCR. Human IRF4 primer probe set hIRF4_LTS34726 (described hereinabove in

10 Example 7) was used to measure mRNA levels. IRF4 mRNA levels were adjusted according to total RNA content, as measured by RiboGreen. Results are presented as the percent level of IRF4 mRNA transcript, relative to that of untreated control (UTC) cells. As illustrated in the tables below, IRF4 mRNA levels were reduced in a dose-dependent manner in cells treated with modified oligonucleotides.

Table 89

Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides

Compound Number	IRF4 expression (% UTC)			
	74 nM	222 nM	666 nM	2,000 nM
609311	94	106	100	87
609312	97	96	103	93
609328	87	86	88	83
609337	94	98	99	96
609354	93	88	76	50
609357	101	87	90	61
609408	83	57	35	11
609422	96	100	90	76
609530	103	94	94	87
609533	103	103	91	75
609546	100	103	107	97
609591	93	94	89	68
609592	95	94	88	76

Table 90

Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides

Compound Number	IRF4 expression (% UTC)			
	74 nM	222 nM	666 nM	2,000 nM
609408	93	61	37	12
609592	97	85	88	81
609594	98	97	81	85
881127	96	98	87	66
881183	93	89	75	55
881193	25	21	17	13
881204	97	82	49	26
881955	97	73	44	16
881962	119	96	93	67
881963	104	119	104	91
881973	99	95	89	74
881999	98	91	80	46
882066	108	103	104	94
882069	109	99	91	65
882070	108	106	81	68
882072	112	104	94	72
882077	107	122	101	102

882085	96	85	71	37
882086	90	77	50	17

Table 91**Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides**

Compound Number	IRF4 expression (% UTC)			
	74 nM	222 nM	666 nM	2,000 nM
609408	84	68	36	12
882087	84	75	52	23
882142	95	99	82	68
882162	87	94	76	49
882169	97	79	59	41
882170	86	77	60	28
882175	98	101	72	46
882177	94	96	80	60
882178	103	105	109	95
882185	100	95	87	63
882199	98	105	98	85
882200	111	118	101	87
882204	101	96	78	61
882214	113	106	96	80
882215	112	113	110	104
882227	114	100	109	90
882228	101	92	85	63
882247	114	105	104	102
882268	108	94	89	67

5

Table 92**Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides**

Compound Number	IRF4 expression (% UTC)			
	74 nM	222 nM	666 nM	2,000 nM
609408	81	69	39	9
882283	98	94	86	54
882309	85	93	79	49
882310	91	94	85	92
882311	83	74	59	18
882313	87	73	57	25
882323	92	95	81	50
882325	99	87	62	31

882326	100	98	100	68
882352	93	91	78	62
882354	96	93	78	66
882357	103	84	78	48
882358	90	74	42	13
882359	109	112	104	91
882376	104	107	97	86
882377	98	94	89	64
882379	101	101	108	101
882383	106	112	104	104
882384	101	98	80	62

Table 93**Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides**

Compound Number	IRF4 expression (% UTC)			
	74 nM	222 nM	666 nM	2,000 nM
609408	74	64	38	13
882398	81	74	63	28
882408	88	77	64	37
882409	101	67	89	92
882429	98	90	90	89
882432	88	93	91	83
882479	86	91	89	56
882495	83	100	96	87
882532	89	101	126	N/A
882565	107	109	109	92
882601	103	98	85	91
882670	104	95	91	60
882721	98	97	91	73
882725	93	92	80	72
882744	100	66	73	48
882749	89	92	77	55
882758	88	79	72	56
882761	87	88	77	61
882765	89	103	94	98

Table 94

Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides

Compound Number	IRF4 expression (% UTC)			
	74 nM	222 nM	666 nM	2,000 nM
609408	54	34	41	N/A
881450	65	59	29	11
881659	45	19	6	2
882777	109	133	93	105
882797	113	106	93	63
882800	112	83	56	22
882806	100	115	107	91
882810	88	88	84	50

Example 17: Design of 3-10-3 cEt gapmers with phosphorothioate internucleoside linkages

5 Modified oligonucleotides complementary to a human IRF4 nucleic acid were designed. The modified oligonucleotides in Table 95 are 3-10-3 cEt gapmers. The gapmers are 16 nucleobases in length, wherein the central gap segment comprises ten 2'-deoxynucleosides and is flanked by wing segments on both the 5' end and on the 3' end comprising three cEt nucleosides. The sugar motif for the gapmers is (from 5' to 3'): kkkddddd kkk; wherein 'd' represents a 2'-deoxyribose sugar and 'k' represents a cEt modified sugar. Each internucleoside linkage is a phosphorothioate internucleoside linkage and each cytosine residue is a 5-methylcytosine. "Start Site" indicates the 5'-most nucleoside to which the gapmer is complementary in the human nucleic acid sequence. "Stop Site" indicates the 3'-most nucleoside to which the gapmer is complementary in the human nucleic acid sequence.

Each modified oligonucleotide listed in Table 95 below is complementary to human IRF4 nucleic acid sequences SEQ ID NO: 1 or SEQ ID NO: 2, as indicated. 'N/A' indicates that the modified oligonucleotide is not complementary to that particular nucleic acid sequence with 100% complementarity.

Table 95

Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides

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	SEQ ID NO
970454	N/A	N/A	17700	17715	AGAACATTACGAGAGG	3371
970466	N/A	N/A	18074	18089	GGTTGGCTGGTCTTTG	3337
970500	N/A	N/A	18088	18103	ATTATATACTGGTTGG	3340
970524	N/A	N/A	18248	18263	CGATCATCAACTTCTT	3372
970527	N/A	N/A	18572	18587	GTGATAGCTGAGCTGA	3343

970539	N/A	N/A	18583	18598	ACTGGATTGATGTGAT	3373
970545	N/A	N/A	18718	18733	GGAAGTCATAGGTGTA	3374
970546	1415	1430	19532	19547	CTGATGTGTTCTGGTA	3375
970547	N/A	N/A	17235	17250	TACGCTTATTTTCCA	3376
970548	N/A	N/A	17474	17489	GCAATCTTAACCTGGA	3377
970552	N/A	N/A	18580	18595	GGATTGATGTGATAGC	3378
970554	N/A	N/A	19020	19035	TCTGTATAGTTCTCAA	3379
970574	1350	1365	19467	19482	TAGTTGTCTGGCTAGC	3380
970597	N/A	N/A	18575	18590	GATGTGATAGCTGAGC	3346
970598	N/A	N/A	18612	18627	CAGTGACTTGCAATCCA	3350
970600	1346	1361	19463	19478	TGTCTGGCTAGCAGAG	3381
970602	1396	1411	19513	19528	CGTAGCCCCTCAGGAA	3382
970603	1423	1438	19540	19555	CTGGATTGCTGATGTG	3383

Example 18: Effect of modified oligonucleotides on human IRF4 *in vitro*, multiple doses

Modified oligonucleotides selected from the examples above were tested at various doses in MM.1R cells. Cells were plated at a density of 5,000 cells per well and transfected by free uptake with 62.5 nM, 250 nM, 1,000 nM, and 4,000 nM concentrations of modified oligonucleotide, as specified in the tables below. After a treatment period of approximately 24 hours, RNA was isolated from the cells and IRF4 mRNA levels were measured by RT-qPCR. Human IRF4 primer probe set hIRF4_LTS34726 (described hereinabove in Example 7) was used to measure mRNA levels. IRF4 mRNA levels were adjusted according to total RNA content, as measured by RiboGreen. Results are presented as the percent level of IRF4 mRNA transcript, relative to that of untreated control (UTC) cells. As illustrated in the tables below, IRF4 mRNA levels were reduced in a dose-dependent manner in cells treated with modified oligonucleotides.

Table 96

Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides

Compound Number	IRF4 expression (% UTC)			
	62.5 nM	250 nM	1,000 nM	4,000 nM
609408	84	55	28	7
935583	99	77	32	8
969936	86	88	61	34
969937	94	100	75	33
969938	104	84	60	30
970044	115	107	79	42
970069	86	111	97	67
970104	101	87	60	30

970114	109	96	73	45
970117	109	84	48	19
970139	78	60	44	24
970158	101	102	81	46
970159	82	64	45	18
970189	85	66	42	25
970217	96	90	71	44
970228	65	77	37	13
970253	111	105	100	63
970344	83	117	124	92
970388	100	87	70	29

Table 97

Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides

Compound Number	IRF4 expression (% UTC)			
	62.5 nM	250 nM	1,000 nM	4,000 nM
609408	92	55	28	8
969879	106	110	107	113
969933	94	71	48	36
969991	115	92	56	13
970013	96	78	48	19
970043	102	82	43	16
970103	96	64	52	34
970160	111	96	75	35
970161	106	104	82	62
970162	94	82	60	18
970211	93	79	59	32
970212	97	80	38	7
970230	110	105	84	52
970231	113	105	114	94
970249	116	93	59	22
970358	113	110	87	55
970370	107	93	77	32
970382	113	97	70	40
970610	125	103	88	50

Table 98

Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides

Compound Number	IRF4 expression (% UTC)			
	62.5 nM	250 nM	1,000 nM	4,000 nM
609408	84	56	30	7
970454	98	84	59	35
970466	102	84	51	34
970500	97	85	61	23
970524	76	50	28	8
970527	87	62	30	11
970539	98	94	75	35
970545	89	74	47	25
970546	86	73	55	31
970547	99	71	49	35
970548	103	92	63	30
970552	93	76	41	12
970554	102	84	58	31
970574	96	84	68	32
970597	38	21	15	8
970598	60	57	47	25
970600	49	35	29	21
970602	41	39	32	19
970603	55	47	44	17

5 Example 19: Effect of modified oligonucleotides on human IRF4 *in vitro*, multiple doses

Modified oligonucleotides selected from the examples above were tested at various doses in MM.1R cells. Cells were plated at a density of 5,000 cells per well and transfected by free uptake with 62.5 nM, 250 nM, 1,000 nM, and 4,000 nM concentrations of modified oligonucleotide, as specified in the tables below. After a treatment period of approximately 24 hours, RNA was isolated from the cells and IRF4 mRNA levels were measured by RT-qPCR. Human IRF4 primer probe set RTS4523 (forward sequence AAGCCTTGCGTTCTCAGACT, designated herein as SEQ ID NO: 3386; reverse sequence TCAGCTCCTTCACGAGGATTTC, designated herein as SEQ ID NO: 3387; probe sequence CCGGCTGCACATCTGCCTGTACTACC, designated herein as SEQ ID: 3388), was used to measure mRNA levels. IRF4 mRNA levels were adjusted according to total RNA content, as measured by RiboGreen.

Results are presented as the percent level of IRF4 mRNA transcript, relative to that of untreated control (UTC) cells. As illustrated in the table below, IRF4 mRNA levels were reduced in a dose-dependent manner in cells treated with modified oligonucleotides.

Table 99

Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides

Compound Number	IRF4 expression (% UTC)			
	62.5 nM	250 nM	1,000 nM	4,000 nM
609408	75	51	31	10
970454	88	80	49	34
970466	85	80	65	30
970500	91	75	43	26
970524	77	50	25	7
970527	83	53	25	12
970539	91	80	61	31
970545	68	58	35	20
970546	64	59	47	30
970547	88	56	44	23
970548	97	92	62	29
970552	76	80	40	12
970554	100	74	60	29
970574	93	76	67	32
970597	93	99	78	51
970598	80	76	62	39
970600	82	87	80	63
970602	85	80	66	41
970603	83	77	64	29

5 Example 20: Effect of modified oligonucleotides on human IRF4 *in vitro*, multiple doses

Modified oligonucleotides selected from the examples above were tested at various doses in MM.1R cells. Cells were plated at a density of 5,000 cells per well and transfected by free uptake with 62.5 nM, 250 nM, 1,000 nM, and 4,000 nM concentrations of modified oligonucleotide, as specified in the tables below. After a treatment period of approximately 24 hours, RNA was isolated from the cells and IRF4 mRNA levels were measured by RT-qPCR. Human IRF4 primer probe set hIRF4_LTS34726 (described hereinabove in Example 7) was used to measure mRNA levels. IRF4 mRNA levels were adjusted according to total RNA content, as measured by RiboGreen. Results are presented as the percent level of IRF4 mRNA transcript, relative to that of untreated control (UTC) cells. As illustrated in the tables below, IRF4 mRNA levels were reduced in a dose-dependent manner in cells treated with modified oligonucleotides.

15

Table 100**Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides**

Compound Number	IRF4 expression (% UTC)			
	62.5 nM	250 nM	1,000 nM	4,000 nM
609408	72	43	19	4
881955	89	69	40	10
881962	107	92	66	23
881963	116	116	99	88
881973	109	101	86	59
881999	117	98	72	32
882066	110	114	107	105
882069	100	95	75	43
882070	101	94	82	42
882072	95	98	83	59
882077	101	96	90	68
882085	96	71	49	13
882086	92	68	37	8
882087	98	74	45	13
882142	103	89	80	56
882162	94	80	61	27
882169	102	93	93	77
882170	99	84	71	35
882175	89	75	45	21

Table 101**Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides**

Compound Number	IRF4 expression (% UTC)			
	62.5 nM	250 nM	1,000 nM	4,000 nM
609408	73	43	19	4
882177	83	66	38	11
882178	101	100	87	59
882185	99	90	73	41
882199	108	111	96	82
882200	112	106	97	66
882204	96	82	55	22
882214	98	92	53	12
882215	118	112	117	106
882228	89	75	46	15
882246	101	98	85	58

882247	97	101	92	74
882268	101	88	78	49
882283	104	95	86	48
882309	87	76	59	31
882310	96	103	105	107
882311	99	99	119	99
882313	98	82	61	31
882323	89	89	81	68

Table 102**Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides**

Compound Number	IRF4 expression (% UTC)			
	62.5 nM	250 nM	1,000 nM	4,000 nM
609408	74	49	23	5
882325	94	95	85	45
882326	101	98	86	64
882352	97	88	75	48
882354	103	91	52	38
882357	106	91	68	36
882358	96	92	74	37
882359	98	99	94	64
882377	104	99	82	43
882384	96	82	67	39
882398	85	63	36	10
882408	91	68	41	11
882409	105	94	75	44
882429	105	99	90	74
882432	101	102	102	103
882479	98	99	94	83
882495	97	94	89	74
882532	93	92	78	41
882565	100	99	94	88

5

Table 103**Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides**

Compound Number	IRF4 expression (% UTC)			
	62.5 nM	250 nM	1,000 nM	4,000 nM
609408	77	50	23	6
881955	92	75	43	11

881962	96	91	64	26
881963	95	100	93	76
882725	102	102	96	78
882744	104	107	93	74
882749	102	94	79	55
882758	108	94	76	44
882761	106	99	77	47
882765	99	89	61	34
882777	105	111	108	90
882797	107	96	78	44
882800	89	68	36	9
882806	99	96	84	60
882810	94	93	65	31
882833	101	102	83	67
882870	98	88	69	34
882871	103	90	75	55
882898	101	88	72	45

Example 21: Effect of modified oligonucleotides on human IRF4 *in vitro*, multiple doses

Modified oligonucleotides selected from the examples above were tested at various doses in MM.1R cells. Cells were plated at a density of 5,000 cells per well and transfected by free uptake with 62.5 nM, 250 nM, 1,000 nM, and 4,000 nM concentrations of modified oligonucleotide, as specified in the tables below. After a treatment period of approximately 24 hours, RNA was isolated from the cells and IRF4 mRNA levels were measured by RT-qPCR. Human IRF4 primer probe set RTS4523 (described hereinabove in Example 19) was used to measure mRNA levels. IRF4 mRNA levels were adjusted according to total RNA content, as measured by RiboGreen. Results are presented as the percent level of IRF4 mRNA transcript, relative to that of untreated control (UTC) cells. As illustrated in the table below, IRF4 mRNA levels were reduced in a dose-dependent manner in cells treated with modified oligonucleotides.

Table 104

Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides

Compound Number	IRF4 expression (% UTC)			
	62.5 nM	250 nM	1,000 nM	4,000 nM
609408	84	47	22	5
881955	82	64	33	8
881962	109	79	63	25
881963	99	78	74	66
882725	85	72	76	60
882744	85	104	80	60

882749	114	95	64	50
882758	111	98	67	37
882761	114	108	75	32
882765	85	75	52	27
882777	83	95	79	63
882797	80	72	59	40
882800	53	60	28	7
882806	108	95	78	55
882810	128	119	69	34
882833	94	91	75	69
882870	114	97	71	31
882871	79	82	55	40
882898	81	73	58	34

Example 22: Effect of modified oligonucleotides on human IRF4 *in vitro*, multiple doses

Modified oligonucleotides selected from the examples above were tested at various doses in MM.1R cells. Cells were plated at a density of 5,000 cells per well and transfected by free uptake with 62.5 nM, 250 nM, 1,000 nM, and 4,000 nM concentrations of modified oligonucleotide, as specified in the tables below. After a treatment period of approximately 24 hours, RNA was isolated from the cells and IRF4 mRNA levels were measured by RT-qPCR. Human IRF4 primer probe set RTS4522 (described hereinabove in Example 11) was used to measure mRNA levels. IRF4 mRNA levels were adjusted according to total RNA content, as measured by RiboGreen. Results are presented as the percent level of IRF4 mRNA transcript, relative to that of untreated control (UTC) cells. As illustrated in the tables below, IRF4 mRNA levels were reduced in a dose-dependent manner in cells treated with modified oligonucleotides.

Table 105

Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides

Compound Number	IRF4 expression (% UTC)				IC ₅₀ (μM)
	62.5 nM	250 nM	1,000 nM	4,000 nM	
609408	61	41	26	12	0.1
881450	68	59	41	26	0.4
881659	59	34	16	9	0.1
1013053	63	50	32	16	0.2
1013074	89	71	49	14	0.7
1013492	66	46	36	21	0.2
1013513	72	64	37	21	0.4
1013514	81	68	41	15	0.5
1013647	66	56	37	18	0.3
1013933	92	78	44	13	0.7

1013953	97	62	40	13	0.6
1014087	82	67	40	28	0.7
1014088	59	44	32	15	0.2
1014095	42	35	24	12	< 0.1
1014097	79	57	40	17	0.4
1014393	60	49	26	9	0.2
1014394	46	38	28	9	< 0.1
1014412	85	57	44	23	0.6
1014834	50	40	22	9	< 0.1

Table 106

Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides

Compound Number	IRF4 expression (% UTC)				IC ₅₀ (μM)
	62.5 nM	250 nM	1,000 nM	4,000 nM	
609408	63	46	28	15	0.2
881659	58	32	16	9	0.1
935607	57	41	28	16	0.1
1012795	66	43	26	7	0.2
1012819	92	75	35	25	0.7
1012821	52	38	28	11	0.1
1012836	103	69	44	19	0.8
1012882	94	60	31	11	0.5
1012883	60	42	28	11	0.1
1012884	49	39	25	14	< 0.1
1012900	90	72	42	22	0.7
1012914	55	42	25	10	0.1
1014968	56	48	35	16	0.2
1014976	76	43	37	14	0.3
1015254	68	46	31	14	0.2
1015275	86	61	24	12	0.4
1015409	66	53	34	16	0.3
1015417	76	56	37	16	0.4
1015716	59	46	24	10	0.1

5

Example 23: Effect of modified oligonucleotides on human IRF4 *in vitro*, multiple doses

Modified oligonucleotides selected from the examples above were tested at various doses in KMS11 cells for their effects on target knockdown and on cell line proliferation.

Target knockdown

10

KMS11 cells were plated at a density of 10,000 cells per well and transfected by free uptake with 8 nM, 40 nM, 200 nM, and 1,000 nM concentrations of modified oligonucleotide, as specified in the tables

below. After a treatment period of approximately 48 hours, RNA was isolated from the cells and IRF4 mRNA levels were measured by RT-qPCR. Human IRF4 primer probe set RTS4522 (described hereinabove in Example 11) was used to measure mRNA levels. IRF4 mRNA levels were adjusted according to total RNA content, as measured by RiboGreen. Results are presented as the percent level of IRF4 mRNA transcript, relative to that of untreated control (UTC) cells. As illustrated in the tables below, IRF4 mRNA levels were reduced in a dose-dependent manner in cells treated with modified oligonucleotides.

Table 107**Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides**

Compound Number	IRF4 expression (% UTC)			
	8 nM	40 nM	200 nM	1,000 nM
609408	79	67	38	14
935762	79	41	17	10
935918	71	35	14	10
936007	81	67	25	14
970527	90	53	23	15
882085	86	56	24	11
882408	74	70	37	17

Table 108**Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides**

Compound Number	IRF4 expression (% UTC)			
	8 nM	40 nM	200 nM	1,000 nM
609408	92	69	30	13
882800	78	52	24	10
969933	96	88	72	61
1012795	70	41	18	9
1012821	84	53	39	20
1012884	85	51	26	17
1014095	82	41	19	10

Table 109**Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides**

Compound Number	IRF4 expression (% UTC)			
	8 nM	40 nM	200 nM	1,000 nM
609408	89	67	30	14
1014393	80	50	22	12

1014394	86	74	38	19
1014834	86	51	17	9
1015716	95	78	43	17
881413	92	64	35	13
881449	94	85	48	22

Table 110**Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides**

Compound Number	IRF4 expression (% UTC)			
	8 nM	40 nM	200 nM	1,000 nM
609408	98	78	33	15
935658	87	61	23	13
935696	90	48	17	11
935898	103	81	50	31
935928	92	48	17	11
935968	95	52	17	11
936006	99	81	38	19

5

Proliferation

KMS11 cells were plated at a density of 2,000 cells per well and transfected by free uptake with 8 nM, 40 nM, 200 nM, and 1,000 nM concentrations of modified oligonucleotide, as specified in the tables below.

After seven days, CellTiterGlo-2.0 (Promega) was added and luminescence was measured on Glomax

10 (Promega).

Table 111**Dose-dependent reduction of KMS11 proliferation by modified oligonucleotides**

Compound Number	IRF4 proliferation (% UTC)			
	8 nM	40 nM	200 nM	1,000 nM
690890	93	79	22	7
935762	89	34	9	6
935918	85	28	8	7
936007	93	66	20	8
970527	92	50	11	5
882085	97	55	11	6
882408	95	68	25	10

Table 112

Dose-dependent reduction of KMS11 proliferation by modified oligonucleotides

Compound Number	IRF4 proliferation (% UTC)			
	8 nM	40 nM	200 nM	1,000 nM
690890	98	82	26	9
882800	87	48	16	9
969933	93	86	79	78
1012795	89	25	4	1
1012821	98	47	22	5
1012884	104	61	24	12
1014095	95	35	15	13

Table 113

Dose-dependent reduction of KMS11 proliferation by modified oligonucleotides

Compound Number	IRF4 proliferation (% UTC)			
	8 nM	40 nM	200 nM	1,000 nM
690890	91	67	21	7
1014393	89	45	15	9
1014394	91	70	26	11
1014834	86	43	12	6
1015716	92	78	32	12
881413	98	67	15	11
881449	97	81	39	21

Table 114

Dose-dependent reduction of KMS11 proliferation by modified oligonucleotides

Compound Number	IRF4 proliferation (% UTC)			
	8 nM	40 nM	200 nM	1,000 nM
690890	90	77	22	8
935658	91	51	11	7
935696	86	29	7	6
935898	96	82	56	38
935928	94	45	9	7
935968	94	49	10	5
936006	97	80	26	12

Example 24: Effect of modified oligonucleotides on human IRF4 *in vitro*, multiple doses

Modified oligonucleotides selected from the examples above were tested at various doses in H929 cells for their effects on target knockdown and on cell line proliferation.

Target knockdown

5 H929 cells were plated at a density of 10,000 cells per well and transfected by free uptake with 8 nM, 40 nM, 200 nM, and 1,000 nM concentrations of modified oligonucleotide or 0.67 nM, 2 nM, 6.67 nM or 20 nM concentrations of modified oligonucleotide, as specified in the tables below. After a treatment period of approximately 48 hours, RNA was isolated from the cells and IRF4 mRNA levels were measured by RT-qPCR. Human IRF4 primer probe set RTS4522 (described hereinabove in Example 11) was used to measure
 10 mRNA levels. IRF4 mRNA levels were adjusted according to total RNA content, as measured by RiboGreen. Results are presented as the percent level of IRF4 mRNA transcript, relative to that of untreated control (UTC) cells. As illustrated in the tables below, IRF4 mRNA levels were reduced in a dose-dependent manner in cells treated with modified oligonucleotides.

Table 115

15 **Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides**

Compound Number	IRF4 expression (% UTC)			
	8 nM	40 nM	200 nM	1,000 nM
609408	88	66	39	34
935762	76	47	29	31
935918	70	43	34	24
936007	85	62	39	32
970527	83	49	41	24
882085	107	70	48	16
882408	99	88	59	42

Table 116

Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides

Compound Number	IRF4 expression (% UTC)			
	8 nM	40 nM	200 nM	1,000 nM
609408	69	53	35	30
882800	63	62	38	28
969933	112	95	87	83
1012795	72	67	45	31
1012821	69	86	47	35
1012884	82	88	51	32
1014095	71	68	31	21

Table 117

Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides

Compound Number	IRF4 expression (% UTC)			
	8 nM	40 nM	200 nM	1,000 nM
609408	88	57	31	37
1014393	70	43	38	24
1014394	83	60	43	32
1014834	84	45	33	23
1015716	88	75	46	17
881413	86	67	46	24
881449	109	90	63	51

Table 118

Dose-dependent reduction of human IRF4 mRNA by modified oligonucleotides

Compound Number	IRF4 expression (% UTC)			
	0.67 nM	2 nM	6.67 nM	20 nM
609408	74	53	26	37
935658	84	75	48	32
935696	78	59	33	26
935898	94	79	55	43
935928	74	54	36	28
935968	99	73	55	40
936006	91	74	61	52

Proliferation

H929 cells were plated at a density of 2,000 cells per well and transfected by free uptake with 8 nM, 40 nM, 200 nM, and 1,000 nM concentrations of modified oligonucleotide, as specified in the tables below. After seven days, CellTiterGlo-2.0 (Promega) was added and luminescence was measured on Glomax (Promega).

Table 119

Dose-dependent reduction of H929 proliferation by modified oligonucleotides

Compound Number	IRF4 proliferation (% UTC)			
	8 nM	40 nM	200 nM	1,000 nM
690890	94	69	32	12
935762	71	27	16	3
935918	87	58	26	2

936007	89	64	26	3
970527	95	58	15	1
882085	96	65	24	1
882408	88	65	45	9

Table 120**Dose-dependent reduction of H929 proliferation by modified oligonucleotides**

Compound Number	IRF4 proliferation (% UTC)			
	8 nM	40 nM	200 nM	1,000 nM
690890	73	75	21	6
882800	89	87	30	4
969933	92	90	77	77
1012795	89	86	36	4
1012821	95	86	41	13
1012884	68	62	9	2
1014095	78	63	22	5

5

Table 121**Dose-dependent reduction of H929 proliferation by modified oligonucleotides**

Compound Number	IRF4 proliferation (% UTC)			
	8 nM	40 nM	200 nM	1,000 nM
690890	86	74	48	30
1014393	95	65	30	2
1014394	77	53	35	6
1014834	89	61	34	2
1015716	99	74	31	2
881413	85	53	33	4
881449	94	76	54	25

Table 122**Dose-dependent reduction of H929 proliferation by modified oligonucleotides**

Compound Number	IRF4 proliferation (% UTC)			
	8 nM	40 nM	200 nM	1,000 nM
690890	92	79	52	30
935658	95	62	23	7
935696	84	60	32	3
935898	101	87	62	26

935928	75	50	25	6
935968	96	66	40	10
936006	98	73	38	9

Example 25: Effect of modified oligonucleotides on human IRF4 *in vitro*, multiple doses

Modified oligonucleotides selected from the examples above were tested at various doses in ABC-DLBCL lines U2932 and TMD8 for their effects on target knockdown and on cell line proliferation.

5 *Target knockdown*

Cells were plated at a density of 10,000 cells per well and transfected by free uptake with 50 nM, 200 nM, 1,000 nM, or 5,000 nM concentrations of modified oligonucleotide, as specified in the tables below. Control oligonucleotide ION 792169, a 3-10-3 cEt gapmer with the sequence CGCCGATAAGGTACAC (SEQ ID NO: 3384), was also included. After a treatment period of approximately 48 hours, RNA was isolated from the cells and IRF4 mRNA levels were measured by RT-qPCR. Human IRF4 primer probe set RTS4522 (described hereinabove in Example 11) was used to measure mRNA levels. IRF4 mRNA levels were adjusted according to total RNA content, as measured by RiboGreen. Results are presented as the percent level of IRF4 mRNA transcript, relative to untreated control (UTC) cells. As illustrated in the tables below, IRF4 mRNA levels were reduced in a dose-dependent manner in cells treated with modified oligonucleotides.

Table 123

Dose-dependent reduction of IRF4 expression by modified oligonucleotides in U2932 cells

Compound Number	IRF4 expression (% UTC)			
	50 nM	200 nM	1,000 nM	5,000 nM
792169	98	102	102	99
690890	84	64	55	38
882800	85	63	51	38
695696	71	62	54	49
695968	84	70	55	43
695918	83	64	47	33

Table 124

Dose-dependent reduction of IRF4 expression by modified oligonucleotides in TMD8 cells

Compound Number	IRF4 expression (% UTC)			
	50 nM	200 nM	1,000 nM	5,000 nM
792169	115	99	99	91
690890	97	75	53	26
882800	97	64	38	19

695696	94	68	45	29
695968	95	63	46	25
695918	105	65	44	24

Proliferation

Cells were plated at a density of 2,000 cells per well and transfected by free uptake with 50 nM, 200 nM, 1,000 nM, or 5,000 nM concentrations of modified oligonucleotide, as specified in the tables below. After seven days, CellTiterGlo-2.0 (Promega) was added and luminescence was measured on Glomax (Promega).

Table 125

Dose-dependent reduction of proliferation of U2932 cells by modified oligonucleotides

Compound Number	IRF4 proliferation (% UTC)			
	50 nM	200 nM	1,000 nM	5,000 nM
792169	99	115	111	75
690890	111	109	63	2
882800	113	103	40	2
695696	107	111	77	17
695968	102	101	74	24
695918	89	100	70	7

Table 126

Dose-dependent reduction of proliferation of TMD8 cells by modified oligonucleotides

Compound Number	IRF4 proliferation (% UTC)			
	50 nM	200 nM	1,000 nM	5,000 nM
792169	93	108	102	98
690890	110	120	118	17
882800	132	149	108	27
695696	125	143	94	5
695968	85	131	131	10
695918	139	130	122	4

Example 26: Effect of modified oligonucleotides on human IRF4 *in vitro*, multiple doses

Modified oligonucleotides selected from the examples above were tested at various doses in ALCL cell lines for their effects on target knockdown and on cell line proliferation.

Target knockdown

Cells were plated at a density of 10,000 cells per well and transfected by free uptake with 16 nM, 80 nM, or 400 nM concentrations of modified oligonucleotide, or 40 nM, 200 nM, 1,000 nM, or 5,000 nM concentrations of modified oligonucleotide, as specified in the tables below. After a treatment period of approximately 48 hours, RNA was isolated from the cells and IRF4 mRNA levels were measured by RT-qPCR. Human IRF4 primer probe set RTS4522 (described hereinabove in Example 11) was used to measure mRNA levels. IRF4 mRNA levels were adjusted according to total RNA content, as measured by RiboGreen. Results are presented as the percent level of IRF4 mRNA transcript, relative to untreated control (UTC) cells. Control oligonucleotide 549148, a 3-10-3 cEt gapmer with the sequence GGCTACTACGCCGTCA (SEQ ID NO: 3385), was also included. As illustrated in the tables below, IRF4 mRNA levels were reduced in a dose-dependent manner in cells treated with modified oligonucleotides.

Table 127

Dose-dependent reduction of IRF4 expression by modified oligonucleotides in Karpas299 cells

Compound Number	IRF4 expression (% UTC)			
	16 nM	80 nM	400 nM	2,000 nM
549148	92	85	86	83
609408	85	65	39	23
609416	82	75	66	53

Table 128

Dose-dependent reduction of IRF4 expression by modified oligonucleotides in SupM2 cells

Compound Number	IRF4 expression (% UTC)			
	40 nM	200 nM	1,000 nM	5,000 nM
549148	109	100	118	117
609408	83	91	32	10
609416	93	85	48	21

Proliferation

Cells were plated at a density of 2,000 cells per well and transfected by free uptake with 50 nM, 200 nM, 1,000 nM, or 5,000 nM concentrations of modified oligonucleotide, as specified in the tables below. After seven days, CellTiterGlo-2.0 (Promega) was added and luminescence was measured on Glomax (Promega).

Table 129

Dose-dependent reduction of proliferation of Karpas299 cells by modified oligonucleotides

Compound Number	IRF4 proliferation (% UTC)			
	50 nM	200 nM	1,000 nM	5,000 nM
549148	99	106	106	89
609408	105	91	31	22
609416	104	119	72	59

Table 130

Dose-dependent reduction of proliferation of SupM2 cells by modified oligonucleotides

Compound Number	IRF4 proliferation (% UTC)			
	16 nM	80 nM	400 nM	2,000 nM
549148	93	97	94	85
609408	93	96	55	3
609416	93	98	49	15

Example 27: Effect of modified oligonucleotides on human IRF4 *in vitro*, multiple doses

Modified oligonucleotides selected from the examples above were tested at various doses in mantle cell lymphoma (MCL) lines MAVER1, JVM2, Granta519, Mino, and Z138 for their effects on target knockdown and on cell line proliferation.

Target knockdown

Cells were plated at a density of 10,000 cells per well and transfected by free uptake with 40 nM, 200 nM, 1,000 nM, or 5,000 nM concentrations of modified oligonucleotide, as specified in the tables below. Control oligonucleotide 549148, a 3-10-3 cEt gapmer with the sequence GGCTACTACGCCGTCA (SEQ ID NO: 3385), was also included. After a treatment period of approximately 48 hours, RNA was isolated from the cells and IRF4 mRNA levels were measured by RT-qPCR. Human IRF4 primer probe set RTS4522 (described hereinabove in Example 11) was used to measure mRNA levels. IRF4 mRNA levels were adjusted according to total RNA content, as measured by RiboGreen. Results are presented as the percent level of IRF4 mRNA transcript, relative to untreated control (UTC) cells. As illustrated in the tables below, IRF4 mRNA levels were reduced in a dose-dependent manner in cells treated with modified oligonucleotides.

Table 131

Dose-dependent reduction of IRF4 expression by modified oligonucleotides in MAVER1 cells

Compound Number	IRF4 expression (% UTC)			
	40 nM	200 nM	1,000 nM	5,000 nM
549148	115	103	96	99
609408	121	102	80	35
609416	108	109	87	65

Table 132

5 Dose-dependent reduction of IRF4 expression by modified oligonucleotides in JVM2 cells

Compound Number	IRF4 expression (% UTC)			
	40 nM	200 nM	1,000 nM	5,000 nM
549148	108	114	108	100
609408	90	72	66	39
609416	101	82	74	93

Table 133

Dose-dependent reduction of IRF4 expression by modified oligonucleotides in Granta519 cells

Compound Number	IRF4 expression (% UTC)			
	40 nM	200 nM	1,000 nM	5,000 nM
549148	106	95	95	65
609408	176	165	134	122
609416	119	168	130	97
690890	161	160	143	102

Table 134

10

Dose-dependent reduction of IRF4 expression by modified oligonucleotides in Mino cells

Compound Number	IRF4 expression (% UTC)			
	40 nM	200 nM	1,000 nM	5,000 nM
549148	123	116	112	78
609408	124	109	67	31
609416	123	119	113	92
690890	122	116	103	42

Table 135

Dose-dependent reduction of IRF4 expression by modified oligonucleotides in Z138 cells

Compound Number	IRF4 expression (% UTC)			
	40 nM	200 nM	1,000 nM	5,000 nM
549148	68	72	78	19
609408	67	69	78	59
609416	76	69	89	72
690890	69	67	78	28

Proliferation

- 5 Cells were plated at a density of 2,000 cells per well and transfected by free uptake with 50 nM, 200 nM, 1,000 nM, or 5,000 nM concentrations of modified oligonucleotide, as specified in the tables below. After seven days, CellTiterGlo-2.0 (Promega) was added and luminescence was measured on Glomax (Promega).

Table 136

10 Dose-dependent reduction of proliferation of MAVER1 cells by modified oligonucleotides

Compound Number	IRF4 proliferation (% UTC)			
	80 nM	400 nM	2,000 nM	10,000 nM
549148	108	103	104	102
609408	104	102	83	40
609416	106	100	94	60

Table 137

Dose-dependent reduction of proliferation of JVM2 cells by modified oligonucleotides

Compound Number	IRF4 proliferation (% UTC)			
	80 nM	400 nM	2,000 nM	10,000 nM
549148	108	114	108	100
609408	117	95	66	37
609416	114	101	97	86

Table 138

Dose-dependent reduction of proliferation of Granta519 cells by modified oligonucleotides

Compound Number	IRF4 proliferation (% UTC)			
	80 nM	400 nM	2,000 nM	10,000 nM
549148	110	99	95	106
609408	34	10	4	2
609416	85	44	19	9
690890	58	24	12	7

Table 139

Dose-dependent reduction of proliferation of Mino cells by modified oligonucleotides

Compound Number	IRF4 proliferation (% UTC)			
	80 nM	400 nM	2,000 nM	10,000 nM
549148	90	103	106	101
609408	93	82	54	22
609416	94	84	68	56
690890	88	77	68	49

Table 140

Dose-dependent reduction of proliferation of Z138 cells by modified oligonucleotides

Compound Number	IRF4 proliferation (% UTC)			
	80 nM	400 nM	2,000 nM	10,000 nM
549148	91	88	89	82
609408	98	83	70	46
609416	91	82	74	56
690890	95	84	74	50

Example 28: *In Vivo* Activity in MM1.R Xenograft Model

A xenograft MM1.R model was used to evaluate activity of modified oligonucleotides targeted to human IRF4. Female NOD/SCID mice (JAX) at 4-6 weeks of age were given a subcutaneous injection of 6 million MM1.R cells to form a xenograft tumor. Two weeks later, groups of 3 mice were administered 25, 50, or 100 mg/kg/dose modified oligonucleotide once a day for three days by subcutaneous injection. One group of mice received subcutaneous injections of PBS once a day for three days. The saline-injected group served as the control group to which oligonucleotide-treated groups were compared. Mice were sacrificed 48 hours after the final dose and tumors were collected for further analysis.

RNA Analysis

RNA was extracted from tumor tissue for RT-PCR analysis, which was performed as described above. Data were analyzed with primer probe set 34726, described above in Example 7 or primer probe set 35624 (forward sequence TCCCGTGTGCTTCAAAC, designated herein as SEQ ID NO: 3395; reverse sequence TACCTGCTGGCAGTTCTTTC, designated herein as SEQ ID NO: 3396; probe sequence ACAGATGGGACTTAACAGGCAATGGG, designated herein as SEQ ID: 3397), which specifically detect human IRF4, as indicated in the tables below. Results are presented as percent change of mRNA, relative to PBS control, normalized with human B-Actin levels from the human tumor cells and mouse stromal cells using human specific primer probe set 5002 (forward sequence CGGACTATGACTTAGTTGCGTTAC; designated herein as SEQ ID NO: 3398; reverse sequence GCCATGCCAATCTCATCTTGT, designated herein as SEQ ID NO: 3399; probe sequence CCTTTCTTGACAAAACCTAACTTGCGCAGA, designated herein as SEQ ID NO: 3400).

Table 141**Activity of modified oligonucleotides in MM1.R xenograft model**

Compound ID	Dose	PPset	IRF4 mRNA (% PBS)
PBS	n/a	34726	100
690890	25	34726	59
	50	34726	53
	100	34726	24
882800	50	34726	43
	100	34726	18
935658	50	34726	52
	100	34726	22
935918	50	34726	39
	100	34726	18
935968	50	34726	52
	100	34726	22
1012795	50	34726	45
	100	34726	26
1014095	50	34726	71
	100	34726	34
1014834	50	34726	56
	100	34726	32
935762	50	34726	31
	100	34726	27

Table 142
Activity of modified oligonucleotides in MM1.R xenograft model

PBS	n/a	34726	100
935696	50	34726	28
	100	34726	13

Table 143
Activity of modified oligonucleotides in MM1.R xenograft model

Compound ID	Dose	Ppset	IRF4 mRNA (% PBS)
PBS	n/a	35624	100
690890	50	35624	55
	100	35624	33
882800	50	35624	51
	100	35624	31
935658	50	35624	56
	100	35624	27
935918	50	35624	39
	100	35624	9.9
935968	50	35624	26
	100	35624	9.1
1012795	50	35624	18
	100	35624	21
1014095	50	35624	28
	100	35624	27
1014834	50	35624	33
	100	35624	15
935762	50	35624	37
	100	35624	22
935696	50	35624	19
	100	35624	15

Protein Analysis

Levels of hIRF4 protein were measured in the xenograft tumors by a human-specific IRF4 antibody (abcam EP5699) on the WES system (ProteinSimple).

- 10 Levels of Ig λ , a clinically-relevant biomarker for MM, were also measured on the WES system. Reductions of hIRF4 and Ig λ were observed.

Table 144
Protein Levels in MM1.R Xenografts

Compound ID	Dose (mg/kg/day)	IRF4 Protein (% PBS)	Igλ Protein (% PBS)
PBS	n/a	100	100
690890	50	53	83
	100	28	64
882800	50	67	88
	100	27	68
935918	50	41	103
	100	17	57
935968	50	36	91
	100	15	52
1012795	50	32	105
	100	14	60
1014095	50	35	78
	100	15	56
1014834	50	57	83
	100	31	69
935762	50	46	69
	100	22	54
935696	50	26	40
	100	15	37
935658	50	45	102
	100	24	80

Example 29: Anti-Tumor Activity of modified oligonucleotides in a MM1.R Xenograft Model

5 A xenograft MM1.R model was used to evaluate activity of modified oligonucleotides targeted to human IRF4. Female NOD-SCID mice at 5-6 weeks of age were given a subcutaneous injection of 3 million MM1.R cells to form a xenograft tumor. 23 days later, groups of 8 mice were administered 50 mg/kg/dose modified oligonucleotide five times a week by subcutaneous injection for 3.5 weeks. One group of mice received subcutaneous injections of PBS five times a week. The saline-injected group served as the control group to which oligonucleotide-treated groups were compared. Tumor volume was estimated by caliper measurement. Mice were sacrificed 24 hours after the last dose and tissue was collected for RNA and protein analysis.

10

*Tumor Volume***Table 145****Tumor volume (mm³)**

Compound ID	Days after MM1.R Cell Injection						
	23	27	30	34	37	41	44
PBS	215	374	590	936	1597	1877*	2530*
792169	228	400	615	1194	1451	1669*	2394*
1014834	225	319	451	606	931	1202	1733
1014095	222	291	504	554	886	795*	932*
1012795	221	355	459	472	610*	n.d.	n.d.
935968	210	313	463	587	771	447*	585*
935918	219	346	569	705	899	746*	1024*
935696	219	357	422	422	379	364	426
935658	269	340	557	619	856	983	1299
935762	220	290	397	488*	593*	770*	949*
882800	218	394	520	735	1075	907*	1279*
690890	216	307	419	498	643	830	1191

5 *Values represent the average of 3-7 mice

Body Weight

Body weights were measured throughout the study as a measure of tolerability.

10

Table 146**Body Weight (% of Day 23)**

Compound ID	Days after MM1.R Cell Injection						
	23	27	30	34	37	41	44
PBS	100	101	101	106	104*	111*	115*
792169	100	106	106	116	121*	121*	126*
1014834	100	102	101	103	107	107	108
1014095	100	100	98	98	98*	98*	95*
1012795	100	101	97	82	n.d.	n.d.	n.d.
935968	100	102	101	103	102*	102*	101*
935918	100	101	101	102	100*	100*	98*
935762	100	102	99	103	104	104	100
935696	100	104	103	105	101	101	97
935658	100	100	100	100	98	98	95
882800	100	102	101	106	103*	103*	98*
690890	100	100	97	96	93	93	94

*Values represent the average of 3-7 animals

Liver function

To evaluate the effect of modified oligonucleotides on hepatic function, plasma levels of transaminases were measured using an automated clinical chemistry analyzer (Hitachi Olympus AU400e, Melville, NY). Plasma levels of ALT (alanine transaminase) were measured and the results are presented in the table below expressed in IU/L.

Table 147**Liver Transaminases**

Compound ID	ALT (IU/L)
PBS	24
792169	45
1014834	894
1014095	1601
1012795	1915
935968	289
935918	192
935762	1016
935696	1334
935658	91
882800	5219
690890	496

10 *RNA and Protein Analysis*

IRF4 mRNA in tumor samples was measured by RT-PCR using PPset RTS34726, described above. IRF4 protein in tumor samples was determined by western blot as described in Example 28 above.

Table 148**IRF4 Protein and mRNA Levels**

	hIRF4 mRNA Level	hIRF4 Protein Level
PBS	98	100
792169	159	110
1014834	53	39
1014095	58	43
1012795	37	n.d.
935968	41	35
935918	28	31
935762	47	34

935696	39	27
935658	51	43
882800	57	32
690890	49	46

Example 30: Efficacy of modified oligonucleotides targeted to hIRF4 in a Systemically Disseminated MM1.R Model with Bone Marrow Involvement

5 A systemically disseminated MM1.R model was used to evaluate activity of modified oligonucleotides targeted to human IRF4. Female nod-scid IL2R γ^{null} mice at 4-6 weeks of age were first administered 50 mg/kg cyclophosphamide on day 0, and on day 1 were administered 10 million MM1.R cells via an intravenous injection. On day 14, plasma human Ig λ was tested by ELISA and mice were randomized to groups based on these results. Starting on day 21, groups of 4 mice were administered 50 mg/kg/day modified oligonucleotide once a day for three days, and sacrificed 48 hours after the last dose. Levels of hIRF4 mRNA were measured in bone marrow. The tumor burden was measured by measuring levels of hActin mRNA. Results are presented as percent change of mRNA, relative to PBS control treated mice.

15

Table 149

Bone marrow IRF4 mRNA and Tumor Burden.

Compound ID	IRF4 mRNA in bone marrow (% PBS)	Tumor Burden
PBS	100	4276
792169	70	830
882800	24	33
935918	36*	118
935696	38*	559
935968	34*	18

*Values represent the average of 1-3 mice, excluding mice with undetectable hIRF mRNA levels in bone marrow.

20 **Example 31: Efficacy of modified oligonucleotides targeted to hIRF4 in a Systemically Disseminated MM1.R Model with Bone Marrow Involvement**

A systemically disseminated MM1.R model was used to evaluate activity of modified oligonucleotides targeted to human IRF4. Female NOD-SCID IL2R γ^{null} mice at 4-6 weeks of age were first administered 50 mg/kg cyclophosphamide on day 0, and on day 1 were administered 10 million MM1.R cells via an intravenous injection. On day 14, serum human Ig λ was tested by ELISA and mice were randomized to groups based on these results. Starting on day 15, groups of ten mice were administered modified oligonucleotide with a loading dose of 50mg/kg/day for 1 week, and then 3 doses a week at 50mg/kg/day continuing until animal death, bodyweight drop of <20% or paralysis. One group of ten mice was administered PBS as a control, and another group was administered the control oligonucleotide 792169.

Table 150
Survival Percentage

Treatment Day	Compound ID					
	PBS	792169	882800	935918	935696	935968
0	100	100	100	100	100	100
40	90	60	100	100	100	100
42	90	60	90	100	90	100
43	60	60	90	100	90	100
44	40	20	90	100	90	100
45	20	0	90	100	80	100
46	0	0	90	100	80	100
49	0	0	70	90	80	100
51	0	0	70	90	80	100

Example 32: Activity of Modified oligonucleotides Targeting hIRF4 in a TMD8 human ABC-DLBCL tumor model

A xenograft tumor model was used to evaluate activity of modified oligonucleotides targeted to human IRF4. 4 million ABC-DLBCL TMD8 cells were implanted into the flanks of 5 week old female NOD/SCID mice. When tumors reached an average volume of 100 mm³, approximately two weeks post-implantation, groups of eight mice were administered 50mg/kg/day modified oligonucleotide for two weeks. Mice were sacrificed after the last dose and tumors were collected for mRNA analysis.

Tumor volume was estimated with caliper measurement. Levels of hIRF4 mRNA were measured in tumor tissue and normalized to control animals.

Table 151
Tumor volume (mm³)

Days post-implantation	15	19	22	25	27	29	32
Compound ID	Tumor Volume (mm ³)						
PBS	112	276	602	872	1162	1365	2012
792169	112	232	488	797	1044	1359	1850

690890	114	206	392	481	589	675	777
882800	113	227	417	603	712	729	860
935696	113	225	448	570	676	761	729

Table 152**hIRF4 mRNA levels**

	hIRF4 mRNA Level
PBS	100
792169	127
690890	84
882800	72
935696	58

5 Example 33: Tolerability of Modified Oligonucleotides Targeting hIRF4 in Balb/c mice

Balb/c mice are frequently utilized for safety and efficacy testing. The mice were treated with antisense oligonucleotides selected from studies described above and evaluated for changes in the levels of various plasma chemistry markers.

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Treatment

Groups of 4-6 week old male Balb/c mice were injected subcutaneously twice a week for four weeks with 50 mg/kg of modified oligonucleotides (100 mg/kg/week dose). One group of male Balb/c mice was injected subcutaneously twice a week for 4 weeks with PBS. Mice were euthanized 48 hours after the last dose, and

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Plasma chemistry markers

To evaluate the effect of modified oligonucleotides on liver and kidney function, plasma levels of transaminases, bilirubin, and BUN were measured using an automated clinical chemistry analyzer (Hitachi Olympus AU400e, 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.

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Table 153**Plasma chemistry markers in Balb/c mouse plasma at week 4**

Compound ID	ALT (U/L)	AST (U/L)	BUN (mg/dL)	T.Bil (mg/dL)
PBS	37	84	22.9	0.25
609296	n.d.	n.d.	n.d.	n.d.

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609343	n.d.	n.d.	n.d.	n.d.
609354	n.d.	n.d.	n.d.	n.d.
609357	n.d.	n.d.	n.d.	n.d.
609391	1799	1362	16.7	0.31
609408	859	507	18.4	0.28
609416	93	114	21.1	0.23
609296	n.d.	n.d.	n.d.	n.d.
609547	982	802	27.3	0.34
609592	53	170	21.2	0.25

Table 154**Plasma chemistry markers in Balb/c mouse plasma at week 4**

Compound ID	ALT (U/L)	AST (U/L)	BUN (mg/dL)	T.Bil (mg/dL)
PBS	35.8	53	21.1	0.25
666431	85.5	120	21.1	0.29
666440	8173	3432	26.2	3.84
666449	150	124	24.9	0.18
666471	n.d.	n.d.	n.d.	n.d.
666475	1989	1607	25.0	0.23
666496	2926	2423	22.4	0.30
666569	3427	3288	23.8	0.23
666575	525	385	24.5	0.21
666582	3543	2893	20.0	0.44
666584	43.3	57	25.4	0.21
666586	2970	2051	23.8	0.26
666587	1057	964	28.1	0.16
666649	4662	3970	23.8	10.99
666683	1363	1657	21.3	0.19

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Table 155**Plasma chemistry markers in Balb/c mouse plasma at week 4**

Compound ID	ALT (U/L)	AST (U/L)	BUN (mg/dL)	T.Bil (mg/dL)
PBS	32	89	24.1	0.29
609555	737	238	25.9	0.15
666772	n.d.	n.d.	n.d.	n.d.
666775	n.d.	n.d.	n.d.	n.d.
668818	n.d.	n.d.	n.d.	n.d.
668849	105	131	24.7	0.12
668850	547	394	27.8	0.11

668902	53	103	21.5	0.18
668934	n.d.	n.d.	n.d.	n.d.
668936	2260	3211	24.8	0.13
668937	39	89	23.2	0.14
668947	n.d.	n.d.	n.d.	n.d.
668998	102	101	21.7	0.14
668999	625	404	28.9	0.21
669018	198	157	28.1	0.17
669022	33	60	19.9	0.19
669040	176	170	23.2	0.11
669066	589	300	23.8	0.27
669067	n.d.	n.d.	n.d.	n.d.
669068	95	137	20.0	0.16
669075	647	400	19.4	0.15

Table 156**Plasma chemistry markers in Balb/c mouse plasma at week 4**

Compound ID	ALT (U/L)	AST (U/L)	BUN (mg/dL)	T.Bil (mg/dL)
PBS	21	77	22.8	0.16
690508	n.d.	n.d.	n.d.	n.d.
690509	n.d.	n.d.	n.d.	n.d.
690510	n.d.	n.d.	n.d.	n.d.
690511	n.d.	n.d.	n.d.	n.d.
690512	n.d.	n.d.	n.d.	n.d.
690514	595	440	19.3	0.15
690515	n.d.	n.d.	n.d.	n.d.
690522	2440	1878	26.6	0.23
690527	n.d.	n.d.	n.d.	n.d.
690861	933	752	12.2	0.19
690863	889	798	17.0	0.56
690865	n.d.	n.d.	n.d.	n.d.
690873	1844	1160	16.6	0.28
690875	887	770	16.3	0.16
690877	n.d.	n.d.	n.d.	n.d.
690879	887	652	22.2	0.21
690881	442	320	23.0	0.12
690883	1505	901	38.9	0.34
690890	76	64	25.6	0.14
690892	56	126	23.9	0.17
690898	47	120	27.4	0.11

691028	n.d.	n.d.	n.d.	n.d.
691032	588	216	216	0.16
691033	709	451	31.4	0.13

Organ weights

- 5 Liver, kidney, and spleen weights were measured at the end of the study, and are presented as the percent change compared to PBS-treated animals 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.

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Table 157
Organ Weights (g)

Compound ID	Liver	Kidney	Spleen
PBS	1.25	0.39	0.11
609296	n.d.	n.d.	n.d.
609343	n.d.	n.d.	n.d.
609354	n.d.	n.d.	n.d.
609357	n.d.	n.d.	n.d.
609391	1.29	0.32	0.23
609408	1.48	0.37	0.14
609416	1.57	0.38	0.14
609296	n.d.	n.d.	n.d.
609547	2.56	0.35	0.55
609592	1.41	0.37	0.13

Table 158
Organ Weights (g)

Compound ID	Liver	Kidney	Spleen
PBS	1.30	0.40	0.10
666431	1.21	0.38	0.15
666440	2.38	0.37	0.10
666449	1.39	0.40	0.11
666471	n.d.	n.d.	n.d.
666475	1.49	0.40	0.10
666496	1.66	0.44	0.12
666569	1.09	0.34	0.13
666575	1.33	0.37	0.10
666582	2.03	0.42	0.13

666584	1.34	0.40	0.11
666586	1.36	0.29	0.12
666587	1.77	0.38	0.11
666649	0.81	0.30	0.07
666683	2.05	0.38	0.12

Table 159**Organ weights (g)**

Compound ID	Liver (g)	Kidney (g)	Spleen (g)
PBS	1.49	0.43	0.12
609555	1.50	0.36	0.17
666772	n.d.	n.d.	n.d.
666775	n.d.	n.d.	n.d.
668818	n.d.	n.d.	n.d.
668849	1.75	0.41	0.22
668850	1.96	0.41	0.16
668902	1.50	0.39	0.12
668934	n.d.	n.d.	n.d.
668936	1.97	0.33	0.13
668937	1.58	0.41	0.14
668947	n.d.	n.d.	n.d.
668998	1.53	0.38	0.16
668999	1.64	0.38	0.13
669018	1.92	0.41	0.14
669022	1.47	0.41	0.12
669040	1.66	0.44	0.11
669066	1.64	0.39	0.15
669067	1.52	0.38	0.13
669068	n.d.	n.d.	n.d.
669075	1.43	0.36	0.17

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Table 160**Organ weights (g)**

Compound ID	Liver (g)	Kidney (g)	Spleen (g)
PBS	0.86	0.29	0.10
690508	n.d.	n.d.	n.d.
690509	n.d.	n.d.	n.d.
690510	n.d.	n.d.	n.d.
690511	n.d.	n.d.	n.d.

690512	n.d.	n.d.	n.d.
690514	1.68	0.28	0.19
690515	n.d.	n.d.	n.d.
690522	1.40	0.26	0.11
690527	n.d.	n.d.	n.d.
690861	1.29	0.27	0.12
690863	1.27	0.27	0.15
690865	n.d.	n.d.	n.d.
690873	1.17	0.28	0.14
690875	1.36	0.28	0.17
690877	n.d.	n.d.	n.d.
690879	1.04	0.26	0.14
690881	1.19	0.28	0.13
690883	1.59	0.30	0.10
690890	0.97	0.27	0.13
690892	1.08	0.30	0.17
690898	1.08	0.30	0.15
691028	n.d.	n.d.	n.d.
691032	1.33	0.29	0.1525
691033	1.625	0.3175	0.125

Example 34: Tolerability of Modified Oligonucleotides Targeting hIRF4 in CD1 mice

CD1® mice (Charles River, MA) are frequently utilized for safety and efficacy testing. The mice were treated with antisense oligonucleotides selected from studies described above and evaluated for changes in the levels of various plasma chemistry markers.

Treatment

Groups of 4-6 week old male CD1 mice were injected subcutaneously twice a week for four weeks with 50 mg/kg of modified oligonucleotides (100 mg/kg/week dose). One group of male CD1 mice was injected subcutaneously twice a week for 4 weeks with PBS. Mice were euthanized 48 hours after the last dose, and organs and plasma were harvested for further analysis.

Plasma chemistry markers

To evaluate the effect of modified oligonucleotides on liver and kidney function, plasma levels of transaminases, bilirubin, and BUN were measured using an automated clinical chemistry analyzer (Hitachi Olympus AU400e, 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.

Table 161**Plasma chemistry markers in CD1 mouse plasma at week 4**

Compound ID	ALT (U/L)	AST (U/L)	BUN (mg/dL)	T.Bil (mg/dL)
PBS	27	65	19.7	0.19
881413	43	78	19.3	0.18
881442	594	484	23.1	0.24
881449	36	52	19.9	0.24
881450	100	146	20.8	0.18
881506	683	417	8.7	0.18
881517	121	103	22.1	0.16
881581	501	413	23.7	0.27
881610	44	79	18.5	0.19
881658	39	66	16.0	0.17
881659	4924	3485	15.3	5.48
881660	267	176	19.7	0.16
881728	644	389	21.1	0.23
881742	780	443	17.6	0.23
882099	3607	1971	23.1	0.28
882282	n.d.	n.d.	n.d.	n.d.
882305	2688	1379	24.9	0.31
882433	2683	1944	19.5	0.42

Table 162**Plasma chemistry markers in CD1 mouse plasma at week 4**

Compound ID	ALT (U/L)	AST (U/L)	BUN (mg/dL)	T.Bil (mg/dL)
PBS	23	69	17.0	0.19
881449	34	65	19.2	0.23
881582	206	211	18.6	0.15
881588	902	829	15.2	0.32
881658	334	226	14.0	0.18
881727	1120	748	16.8	0.40
792169	23	43	18.0	0.21

Table 163**Plasma chemistry markers in CD1 mouse plasma at week 4**

Compound ID	ALT (U/L)	AST (U/L)	BUN (mg/dL)	T.Bil (mg/dL)
PBS	25	41	22.2	0.17
935765	n.d.	n.d.	n.d.	n.d.
935580	n.d.	n.d.	n.d.	n.d.

935805	n.d.	n.d.	n.d.	n.d.
935853	n.d.	n.d.	n.d.	n.d.
935824	n.d.	n.d.	n.d.	n.d.
935581	n.d.	n.d.	n.d.	n.d.
935689	n.d.	n.d.	n.d.	n.d.
935698	1462	1523	17.5	0.19
935699	n.d.	n.d.	n.d.	n.d.
935707	1334	703	17.3	0.21
935679	n.d.	n.d.	n.d.	n.d.
935727	n.d.	n.d.	n.d.	n.d.
935795	n.d.	n.d.	n.d.	n.d.
935898	101	129	20.3	0.18
935782	680	278	19.0	0.20
935878	1805	1128	19.1	0.21
935850	661	492	21.2	0.08
935724	1630	1341	19.9	0.25
935658	53	65	19.5	0.24
935762	106	132	18.0	0.18
935851	513	300	18.0	0.13

Table 164

Plasma chemistry markers in CD1 mouse plasma at week 4

Compound ID	ALT (U/L)	AST (U/L)	BUN (mg/dL)	T.Bil (mg/dL)
PBS	19	34	18.6	0.17
935921	708	372	15.5	0.19
935961	1068	754	14.8	0.28
936018	609	358	17.9	0.14
936039	n.d.	n.d.	n.d.	n.d.
935708	n.d.	n.d.	n.d.	n.d.
935958	97	117	17.5	0.10
935854	304	205	18.6	0.14
935968	53	70	18.9	0.12
935620	1883	2950	17.2	1.17
935697	1504	763	16.9	0.22
935700	722	480	18.8	0.18
935734	1253	500	17.9	0.17
935857	1270	1233	17.7	0.29
936016	731	571	22.7	0.15
936006	38	47	16.9	0.13
936007	131	152	18.1	0.10

935948	192	183	19.5	0.15
935603	193	260	17.0	0.19
935701	426	277	18.0	0.06
935928	69	84	17.4	0.10

Table 165**Plasma chemistry markers in CD1 mouse plasma at week 4**

Compound ID	ALT (U/L)	AST (U/L)	BUN (mg/dL)	T.Bil (mg/dL)
PBS	23	44	22.5	0.20
969991	n.d.	n.d.	n.d.	n.d.
970013	n.d.	n.d.	n.d.	n.d.
970043	636	610	19.6	0.33
970103	786	512	20.1	0.17
970117	1786	877	22.5	0.29
970139	1011	1244	21.0	1.69
970159	1772	3821	15.7	2.68
970162	470	422	18.0	0.15
970189	353	377	21.0	0.19
970212	1714	1062	22.7	1.00
970524	n.d.	n.d.	n.d.	n.d.
970527	182	181	18.1	0.12

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Table 166**Plasma chemistry markers in CD1 mouse plasma at week 4**

Compound ID	ALT (U/L)	AST (U/L)	BUN (mg/dL)	T.Bil (mg/dL)
PBS	24	99	20.1	0.21
881955	4127	3743	45.7	2.61
882085	53	73	22.3	0.18
882086	2522	2002	25.5	0.43
882087	377	276	23.1	0.15
882175	575	554	9.4	0.68
882177	2666	3030	26.6	4.87
882228	893	1659	19.3	0.22
882398	980	1070	22.1	7.91
882408	46	69	17.9	0.17
882800	70	84	23.4	0.20
969933	383	272	21.7	0.15
969936	n.d.	n.d.	n.d.	n.d.
969938	1142	1009	18.1	0.76
970211	301	224	20.1	0.15

970249	1724	2104	20.0	6.21
970545	836	1049	24.8	0.34
970546	1248	1334	23.8	0.31
970547	878	665	18.4	0.53
970548	1607	3352	17.7	4.86
970552	n.d.	n.d.	n.d.	n.d.

Table 167**Plasma chemistry markers in CD1 mouse plasma at week 4**

Compound ID	ALT (U/L)	AST (U/L)	BUN (mg/dL)	T.Bil (mg/dL)
PBS	23	44	19.7	0.22
1012795	143	235	20.9	0.16
1012821	1189	1434	24.6	0.22
1012884	1523	1939	27.0	0.69
1014095	63	71	19.4	0.18
1014393	666	627	19.3	0.25
1014394	117	129	17.8	0.16
1014834	301	190	19.7	0.21
1015716	230	205	18.4	0.17

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Table 168**Plasma chemistry markers in CD1 mice plasma at week 4**

Compound ID	ALT (U/L)	AST (U/L)	T.Bil (mg/dL)	BUN (mg/dL)	Albumin
PBS	21	45	0.190	21.8	2.54
935918	87	91	0.118	18.8	2.07
935696	71	108	0.143	21.7	2.22

Organ weights

- 10 Liver, kidney, and spleen weights were measured at the end of the study, and are presented as the percent change compared to PBS-treated animals 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.

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Table 169**Organ Weights (g)**

Compound ID	Liver	Kidney	Spleen
PBS	2.1	0.56	0.141

881413	2.2	0.57	0.217
881442	2.7	0.52	0.186
881449	2.1	0.47	0.169
881450	2.2	0.50	0.151
881506	2.9	0.62	0.191
881517	2.4	0.48	0.180
881581	2.2	0.51	0.192
881610	1.9	0.53	0.165
881658	2.0	0.54	0.158
881659	1.7	0.43	0.153
881660	1.9	0.52	0.175
881728	2.3	0.48	0.161
881742	1.9	0.48	0.127
882099	2.2	0.47	0.193
882282	n.d.	n.d.	n.d.
882305	2.1	0.52	0.181
882433	2.0	0.54	0.155

Table 170
Organ weights (g)

Compound ID	Liver	Kidney	Spleen
PBS	1.8	0.54	0.111
881449	2.1	0.54	0.146
881582	2.0	0.48	0.177
881588	1.9	0.39	0.171
881658	2.2	0.58	0.188
881727	2.1	0.51	0.201
792169	1.9	0.55	0.128
UTC	2.0	0.69	0.144

5

Table 171
Organ weights (g)

Compound ID	Liver	Kidney	Spleen
PBS	2.0	0.50	0.109
935765	n.d.	n.d.	n.d.
935580	n.d.	n.d.	n.d.
935805	n.d.	n.d.	n.d.
935853	n.d.	n.d.	n.d.
935824	n.d.	n.d.	n.d.
935581	n.d.	n.d.	n.d.

935689	n.d.	n.d.	n.d.
935698	2.4	0.55	0.213
935699	n.d.	n.d.	n.d.
935707	2.3	0.54	0.199
935679	n.d.	n.d.	n.d.
935727	n.d.	n.d.	n.d.
935795	n.d.	n.d.	n.d.
935898	2.2	0.58	0.245
935782	2.9	0.56	0.279
935878	2.7	0.56	0.192
935850	2.8	0.70	0.203
935724	2.6	0.45	0.110
935658	2.0	0.71	0.205
935762	2.3	0.57	0.197
935851	2.4	0.60	0.176

Table 172

Organ weights (g)

Compound ID	Liver	Kidney	Spleen
PBS	1.9	0.52	0.117
935921	2.3	0.51	0.219
935961	2.1	0.53	0.190
936018	2.2	0.41	0.200
936039	n.d.	n.d.	n.d.
935708	n.d.	n.d.	n.d.
935958	2.2	0.47	0.219
935854	2.0	0.44	0.102
935968	2.4	0.58	0.157
935620	3.2	0.57	0.243
935697	2.9	0.56	0.208
935700	2.0	0.49	0.121
935734	2.7	0.55	0.162
935857	1.5	0.34	0.110
936016	2.8	0.57	0.416
936006	2.3	0.48	0.136
936007	2.3	0.55	0.149
935948	1.9	0.54	0.166
935603	1.6	0.49	0.125
935701	1.9	0.43	0.144
935928	2.3	0.53	0.155

Table 173
Organ weights (g)

Compound ID	Liver	Kidney	Spleen
PBS	1.8	0.51	0.133
969991	n.d.	n.d.	n.d.
970013	n.d.	n.d.	n.d.
970043	2.3	0.48	0.238
970103	2.2	0.54	0.175
970117	3.2	0.48	0.255
970139	2.7	0.56	0.210
970159	2.7	0.62	0.183
970162	2.2	0.54	0.215
970189	3.1	0.45	0.135
970212	2.3	0.45	0.218
970524	n.d.	n.d.	n.d.
970527	2.4	0.60	0.178

Table 174
Organ weights (g)

Compound ID	Liver	Kidney	Spleen
PBS	1.7	0.42	0.095
881955	1.8	0.32	0.110
882085	2.0	0.45	0.110
882086	4.9	0.41	0.258
882087	2.4	0.47	0.130
882175	1.4	0.46	0.098
882177	3.6	0.43	0.185
882228	2.8	0.49	0.193
882398	1.7	0.44	0.113
882408	2.0	0.51	0.135
882800	1.9	0.41	0.128
969933	2.2	0.50	0.145
969936	n.d.	n.d.	n.d.
969938	1.8	0.45	0.150
970211	2.1	0.40	0.143
970249	3.3	0.65	0.190
970545	2.5	0.44	0.133
970546	0.9	0.28	0.060
970547	2.1	0.50	0.243
970548	2.8	0.52	0.260

970552	n.d.	n.d.	n.d.
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Table 175**Organ weights (g)**

Compound	Liver	Kidney	Spleen
PBS	1.78	0.56	0.115
935918	2.44	0.62	0.167
935696	2.20	0.61	0.352

5 Example 35: Tolerability of modified oligonucleotides targeting hIRF4 in Sprague-Dawley rats

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

Treatment

10 Male Sprague-Dawley rats were maintained on a 12-hour light/dark cycle and fed ad libitum with Purina normal rat chow, diet 5001. Groups of 4 Sprague-Dawley rats each were injected subcutaneously once a week for 6 weeks with 50 mg/kg of ISIS oligonucleotide (50 mg/kg weekly dose). Forty eight hours after the last dose, rats were euthanized and organs and plasma were harvested for further analysis.

Liver and Kidney function

15 To evaluate the effect of modified oligonucleotides on hepatic function, plasma levels of transaminases were measured using an automated clinical chemistry analyzer (Hitachi Olympus AU400e, Melville, NY). Plasma levels of ALT (alanine transaminase), AST (aspartate transaminase), blood urea nitrogen (BUN), and T. bilirubin were measured and the results are presented in the table below. Plasma levels of bilirubin were also measured using the same clinical chemistry analyzer and the results are also
20 presented in the table below. Values represent the % change normalized to PBS-treated animals. Modified oligonucleotides that caused changes in the levels of any markers of liver function outside the expected range for antisense oligonucleotides were excluded in further studies.

Table 176**Liver function markers in Sprague-Dawley rats**

Compound ID	ALT (IU/L)	AST (IU/L)	T.Bil (mg/dL)	BUN (mg/dL)	Albumin (g/dL)
PBS	47	67	0.14	16.4	3.92
690898	41	73	0.17	20.7	3.19
881413	42	61	0.18	18.1	3.66
881449	47	67	0.26	19.7	3.77
935658	47	55	0.16	17.4	3.80
935696	41	70	0.18	16.9	3.55

935898	72	81	0.19	18.0	4.23
935928	189	188	0.19	19.7	3.59
935968	39	85	0.21	17.2	3.61
936006	40	55	0.14	14.3	3.97

Table 177

Liver function markers in Sprague-Dawley rats

Compound ID	ALT (IU/L)	AST (IU/L)	T.Bil (mg/dL)	BUN (mg/dL)	Albumin (g/dL)
PBS	34	58	0.09	15.7	2.20
690890	32	70	0.16	20.1	2.39
690892	42	77	0.15	18.5	1.82
882085	68	73	0.09	47.1	1.36
882800	40	100	0.16	20.2	2.30
970527	45	80	0.12	19.8	2.09

5

Table 178

Liver function markers in Sprague-Dawley rats

Compound ID	ALT (IU/L)	AST (IU/L)	T.Bil (mg/dL)	BUN (mg/dL)	Albumin (g/dL)
PBS	41	70	0.14	14.4	3.60
882408	38	68	0.15	17.0	2.80
1012795	25	70	0.09	22.3	2.47
1014095	37	101	0.12	20.3	2.41
1014393	41	70	0.09	20.3	2.28
1014394	32	74	0.08	21.1	2.53
1014834	34	68	0.10	14.2	3.04

Table 179

Liver function markers in Sprague-Dawley rats

Compound ID	ALT (IU/L)	AST (IU/L)	T.Bil (mg/dL)	BUN (mg/dL)	Albumin (g/dL)
PBS	55	51	0.15	17.1	3.04
935762	35	53	0.14	18.7	2.63
935918	31	55	0.15	19.7	2.60

10

Hematology assays

Blood obtained from all rat groups were sent to Antech Diagnostics for hematocrit (HCT) measurements and analysis, as well as measurements of the various blood cells, such as WBC, RBC, and total hemoglobin content. The results are presented in the table below. Modified oligonucleotides that caused changes in the levels of any of the hematology markers outside the expected range for antisense oligonucleotides were excluded in further studies.

15

Table 180**Hematology markers in Sprague-Dawley rats**

Compound ID	WBC (K/ μ L)	RBC (M/ μ L)	HGB (g/dL)	HCT (%)	LYM (/ μ L)	MON (/ μ L)	EOS (/ μ L)	BAS (/ μ L)	PLT (K/ μ L)	Retic (K/ μ L)
PBS	10.38	8.15	14.80	43.9	8711	357	68.3	12.3	868	252
690898	17.83	6.46	12.27	37.1	15745	1109	75.0	145.0	214	201
881413	7.08	6.71	12.55	36.6	6342	286	44.3	15.3	523	152
881449	6.68	7.53	13.60	39.8	5414	396	153.0	27.5	583	133
935658	9.73	7.97	14.53	42.4	8250	777	19.7	70.0	685	138
935696	7.80	7.33	13.10	38.6	6354	645	48.8	23.0	480	97
935898	7.75	8.64	15.20	43.3	6248	529	29.3	26.8	712	114
935928	13.15	7.36	13.23	40.1	7231	1177	8.5	90.3	476	160
935968	6.15	6.17	11.28	33.7	5292	436	8.0	68.8	462	178
936006	7.28	8.07	14.45	42.7	5875	729	20.3	57.3	621	220

Table 181**Hematology markers in Sprague-Dawley rats**

Compound ID	WBC (K/ μ L)	RBC (M/ μ L)	HGB (g/dL)	HCT (%)	LYM (/ μ L)	MON (/ μ L)	EOS (/ μ L)	BAS (/ μ L)	PLT (K/ μ L)	Retic (K/ μ L)
PBS	4.35	5.18	9.68	29.4	3546	116	102.8	10.5	292	136
690890	4.75	4.84	8.98	27.4	3844	325	25.3	55.0	190	113
690892	4.70	5.46	10.65	31.4	3917	276	42.3	34.5	184	120
882085	7.18	5.18	9.43	29.2	5159	758	73.0	24.5	352	122
882800	5.10	5.08	9.13	27.9	4190	479	46.0	40.3	165	157
970527	9.60	6.10	10.88	32.4	7990	846	28.3	50.8	249	123

Table 182**Hematology markers in Sprague-Dawley rats**

Compound ID	WBC (K/ μ L)	RBC (M/ μ L)	HGB (g/dL)	HCT (%)	LYM (/ μ L)	MON (/ μ L)	EOS (/ μ L)	BAS (/ μ L)	PLT (K/ μ L)	Retic (K/ μ L)
PBS	9.35	7.81	14.28	46.6	7820	330	208.3	11.3	344	214
882408	13.25	9.46	16.73	52.0	8387	1020	35.3	29.3	407	163
1012795	15.20	4.86	10.03	33.6	11767	1996	28.5	12.8	149	304
1014095	18.55	6.93	12.35	41.4	11958	1500	95.0	22.3	727	281
1014393	21.90	7.25	13.08	41.8	17709	2038	50.5	156.3	491	123
1014394	23.55	7.21	13.58	43.3	19656	2121	31.8	67.5	270	207
1014834	14.43	7.97	14.65	45.9	12543	1009	42.3	180.0	395	182

Table 183**Hematology markers in Sprague-Dawley rats**

Compound ID	WBC (K/ μ L)	RBC (M/ μ L)	HGB (g/dL)	HCT (%)	LYM (/ μ L)	MON (/ μ L)	EOS (/ μ L)	BAS (/ μ L)	PLT (K/ μ L)	Retic (K/ μ L)
PBS	11.13	9.45	16.70	52.8	9156	686	103	8.0	82	238
935762	14.53	7.72	13.43	42.4	13586	510	0	29.3	92	232
935918	9.25	7.08	12.50	40.5	8509	456	51	5.0	92	286

Organ weights

- 5 Liver, heart, spleen and kidney 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 antisense oligonucleotides were excluded from further studies.

Table 184
Organ weights (g)

10

Compound ID	Liver (g)	Kidney (g)	Spleen (g)
PBS	15.8	2.91	0.90
690898	16.9	3.18	3.65
881413	15.0	2.83	1.32
881449	15.4	3.07	1.19
935658	13.8	2.40	1.33
935696	12.6	2.60	1.22
935898	12.0	2.44	1.07
935928	16.8	3.23	1.94
935968	14.9	2.85	1.56
936006	14.2	2.75	1.59

Table 185
Organ weights (g)

Compound ID	Liver (g)	Kidney (g)	Spleen (g)
PBS	15.2	3.38	0.72
690890	15.8	3.17	1.62
690892	15.2	3.27	1.72
882085	12.5	3.78	1.41
882800	17.0	3.46	3.24
970527	14.0	3.72	1.94

15

Table 186
Organ weights (g)

Compound ID	Liver (g)	Kidney (g)	Spleen (g)
PBS	18.6	3.70	0.92
882408	15.1	3.60	1.51

1012795	18.9	3.70	4.06
1014095	18.2	3.63	3.05
1014393	15.9	3.98	2.30
1014394	18.3	4.41	2.79
1014834	14.4	3.35	5.01

Table 187

Organ weights (g)

Compound ID	Liver (g)	Kidney (g)	Spleen (g)
PBS	14.6	3.20	0.88
935762	16.1	3.43	1.73
935918	18.7	3.89	2.01

5 **Example 36: Tolerability of modified oligonucleotides in Non-human Primates**

Modified oligonucleotides described above were further evaluated for potency in non-human primates.

Treatment

10 Male cynomolgus monkeys were divided into groups of 4 non-human primates (NHP) each. Groups received a dose of 40mg/kg of modified oligonucleotide by subcutaneous injection on day 1, 3, 5, and 7, and then once/week for six weeks. One group of NHP received doses of PBS. The PBS-injected group served as the control group to which oligonucleotide-treated groups were compared. After six weeks, NHP were sacrificed and tissues were collected for analysis.

15 *Tolerability*

To evaluate the effect of these antisense oligonucleotides on liver and kidney function, samples of blood, plasma, serum and urine were collected from all study groups on day 44. The blood samples were collected via femoral venipuncture, 48 hrs post-dosing. The monkeys were fasted overnight prior to blood collection. Approximately 1.5 mL of blood was collected from each animal into tubes without anticoagulant for serum separation. Levels of the various markers were measured using an automated clinical chemistry analyzer (Hitachi Olympus AU400e, Melville, NY). Total urine protein and urine creatinine levels were measured, and the ratio of total urine protein to creatinine (P/C Ratio) was determined.

20 To evaluate the effect of the antisense oligonucleotides on hepatic function, plasma concentrations of transaminases (ALT, AST), Albumin (Alb) and total bilirubin ("T. Bil") were measured. To evaluate the effect of the antisense oligonucleotides on kidney function, plasma concentrations of blood urea nitrogen (BUN) and creatinine (Cre) were measured. Urine levels of albumin (Alb), creatinine (Cre) and total urine protein (Micro Total Protein (MTP)) were measured, and the ratio of total urine protein to creatinine (P/C ratio) was determined.

25 To evaluate any inflammatory effect of the ISIS oligonucleotides in cynomolgus monkeys, C-reactive protein (CRP), which is synthesized in the liver and which serves as a marker of inflammation, was measured

on day 44. For this, blood samples were taken from fasted monkeys, the tubes were kept at room temperature for a minimum of 90 min., and centrifuged at 3,000 rpm for 10 min at room temperature to obtain serum. The results are presented in the Tables below and indicate that most of the antisense oligonucleotides targeting human IRF4 were well tolerated in cynomolgus monkeys. ION 935918 and 935968 were well tolerated.

5

Table 188
Serum and urine clinical chemistry

ISIS No.	Serum (day 44)								Urine (day 42)		
	C3 mg/dL	ALT U/L	AST U/L	Alb g/dL	BUN mg/dL	CRP mg/L	Cre mg/dL	T.bil mg/dL	Alb g/dL	Cre mg/dL	P/C ratio
PBS	120.73	48.00	69.10	4.35	25.60	1.66	0.858	0.29	0.35	55.0	0.00
690890	71.20	50.18	75.20	3.66	26.10	9.52	0.988	0.23	0.53	56.2	0.04
935658	95.90	42.33	81.85	3.99	21.70	4.53	0.808	0.29	0.68	39.0	0.12
935696	88.58	48.32	62.78	4.03	26.06	6.55	0.780	0.26	0.18	36.6	0.04
935762	100.10	47.58	52.63	3.91	24.98	6.88	0.76	0.25	0.03	37.9	0.01
935918	94.45	49.45	79.20	4.05	29.85	4.65	0.90	0.24	0.12	60.2	0.01
935968	108.83	54.45	83.33	4.10	28.68	6.65	0.813	0.23	0.10	38.8	0.07
882800	100.83	46.55	61.80	4.00	24.10	2.53	0.818	0.22	0.36	34.9	0.14
1012795	82.05	37.08	51.40	3.05	27.45	21.28	0.763	0.20	0.50	55.0	0.10
1014095	85.83	38.15	46.85	2.81	15.10	11.16	0.593	0.15	0.03	43.9	0.07
1014834	89.13	54.73	75.28	3.88	23.65	7.03	0.978	0.25	0.14	75.9	0.05

Table 189
Body Weight

10

Compound ID	Body Weight (g) day 1	Body weight (g) day 42
PBS	2521	2594
690890	2508	2514
935658	2499	2557
935696	2412	2511
935762	2473	2653
935918	2483	2657
935968	2605	2798
882800	2577	2676
1012795	2623	2577
1014095	2567	2719
1014834	2556	2685

RNA analysis

RNA was extracted from various tissues for real-time PCR analysis of mRNA expression of IRF4 as in previous examples. Results are presented as percent change of mRNA, relative to PBS control, normalized with NHP Cyclophilin A. As shown in the table below, treatment with modified oligonucleotides resulted in reduction of IRF4 mRNA in comparison to the PBS control with some of the treatment groups.

5

Table 190**% Inhibition of cynomolgus IRF4**

Compound ID	Bone marrow	PBMC	Spleen
PBS	100	100	100
690890*	98	119	205
935658*	174	170	200
935696*	71	80	125
935762*	112	90	129
935918*	98	41	192
935968*	129	49	131
882800***	107	75	133
1012795*	97	95	151
1014095***	80	80	188
1014834*	139	180	192

*Compounds have one mismatch to cynomolgus monkey IRF4; *** compounds have three mismatches to cynomolgus monkey IRF4.

10

Example 37: Viscosity

Viscosity of modified oligonucleotide solutions was measured. The viscosity of 935918 is compatible with weekly subcutaneous injection, and the viscosities of both 935918 and 935968 are compatible with IV dosing.

15

Table 191**Viscosity**

Compound ID	Dose (mg/mL) by weight	Viscosity (cP)
690890	300	16.14
935658	300	48.79
935696	300	120.2
935762	300	11.39
935918	100	2.12
935968	300	53.76
882800	100	3.4

WHAT IS CLAIMED:

1. A compound comprising a modified oligonucleotide 8 to 80 linked nucleosides in length having a nucleobase sequence comprising at least 8 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 3-3383.
2. A compound comprising a modified oligonucleotide 9 to 80 linked nucleosides in length having a nucleobase sequence comprising at least 9 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 3-3383.
3. A compound comprising a modified oligonucleotide 10 to 80 linked nucleosides in length having a nucleobase sequence comprising at least 10 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 3-3383.
4. A compound comprising a modified oligonucleotide 11 to 80 linked nucleosides in length having a nucleobase sequence comprising at least 11 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 3-3383.
5. A compound comprising a modified oligonucleotide 12 to 80 linked nucleosides in length having a nucleobase sequence comprising at least 12 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 3-3383.
6. A compound comprising a modified oligonucleotide 16 to 80 linked nucleosides in length having a nucleobase sequence comprising the nucleobase sequence of any one of SEQ ID NOs: 3-3383.
7. A compound comprising a modified oligonucleotide having a nucleobase sequence consisting of any one of SEQ ID NOs: 3-3383.
8. A compound comprising a modified oligonucleotide 8 to 80 linked nucleosides in length complementary within nucleotides 4227-4244, 4227-4242, 4228-4243, or 4229-4244 of SEQ ID NO: 1 or within nucleotides 9667-9682, 11411-11426, or 18090-18105 of SEQ ID NO: 2.
9. A compound comprising a modified oligonucleotide 8 to 80 linked nucleosides in length having a nucleobase sequence comprising any one of SEQ ID NOs: 2021, 560, 559, 1330, 1540, or 3303.
10. A compound comprising a modified oligonucleotide having a nucleobase sequence consisting of any one of SEQ ID NOs: 2021, 560, 559, 1330, 1540, or 3303.
11. The compound of any one of claims 1-10, wherein the modified oligonucleotide comprises at least one modified internucleoside linkage, at least one modified sugar, or at least one modified nucleobase.
12. The compound of claim 11, wherein the modified internucleoside linkage is a phosphorothioate internucleoside linkage.

13. The compound of claim 11 or 12, wherein the modified sugar is a bicyclic sugar.
14. The compound of claim 13, wherein the bicyclic sugar is selected from the group consisting of: 4'-(CH₂)-O-2' (LNA); 4'-(CH₂)₂-O-2' (ENA); and 4'-CH(CH₃)-O-2' (cEt).
15. The compound of claim 11 or 12, wherein the modified sugar is 2'-O-methoxyethyl.
16. The compound of any one of claims 11-15, wherein the modified nucleobase is a 5-methylcytosine.
17. The compound of any one of claims 1-16, wherein the modified oligonucleotide comprises:
a gap segment consisting of linked deoxynucleosides;
a 5' wing segment consisting of linked nucleosides; and
a 3' wing segment consisting of linked nucleosides;
wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment and wherein each nucleoside of each wing segment comprises a modified sugar.
18. A compound comprising a modified oligonucleotide 16 to 80 linked nucleosides in length having a nucleobase sequence comprising any one of SEQ ID NOs: 2021, 560, 559, 1330, 1540, or 3303, wherein the modified oligonucleotide comprises:
a gap segment consisting of linked deoxynucleosides;
a 5' wing segment consisting of linked nucleosides; and
a 3' wing segment consisting of linked nucleosides;
wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment and wherein each nucleoside of each wing segment comprises a modified sugar.
19. A compound comprising a modified oligonucleotide 16-80 linked nucleobases in length having a nucleobase sequence comprising the sequence recited in any one of SEQ ID NOs: 1330 or 3303, wherein the modified oligonucleotide comprises:
a gap segment consisting of ten linked deoxynucleosides;
a 5' wing segment consisting of three linked nucleosides; and
a 3' wing segment consisting of three linked nucleosides;
wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment; wherein each nucleoside of each wing segment comprises a cEt nucleoside; wherein each internucleoside linkage is a phosphorothioate linkage; and wherein each cytosine is a 5-methylcytosine.

20. A compound comprising a modified oligonucleotide 16-80 linked nucleobases in length having a nucleobase sequence comprising the sequence recited in any one of SEQ ID NOs: 559 or 560, wherein the modified oligonucleotide comprises:

- a gap segment consisting of ten linked deoxynucleosides;
- a 5' wing segment consisting of one linked nucleoside; and
- a 3' wing segment consisting of five linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment; wherein the 5' wing segment comprises a cEt nucleoside; wherein the 3' wing segment comprises a cEt nucleoside, a 2'-O-methoxyethyl nucleoside, a cEt nucleoside, a 2'-O-methoxyethyl nucleoside, and a cEt nucleoside in the 5' to 3' direction; wherein each internucleoside linkage is a phosphorothioate linkage; and wherein each cytosine is a 5-methylcytosine.

21. A compound comprising a modified oligonucleotide 16-80 linked nucleobases in length having a nucleobase sequence comprising the sequence recited in any one of SEQ ID NOs: 1330 or 2021, wherein the modified oligonucleotide comprises:

- a gap segment consisting of ten linked deoxynucleosides;
- a 5' wing segment consisting of two linked nucleosides; and
- a 3' wing segment consisting of four linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment; wherein each nucleoside of the 5' wing segment comprises a cEt nucleoside; wherein the 3' wing segment comprises a cEt nucleoside, a 2'-O-methoxyethyl nucleoside, a cEt nucleoside, and a 2'-O-methoxyethyl nucleoside in the 5' to 3' direction; wherein each internucleoside linkage is a phosphorothioate linkage; and wherein each cytosine is a 5-methylcytosine.

22. A compound comprising a modified oligonucleotide 16-80 linked nucleobases in length having a nucleobase sequence comprising the sequence recited in SEQ ID NO: 560, wherein the modified oligonucleotide comprises:

- a gap segment consisting of nine linked deoxynucleosides;
- a 5' wing segment consisting of two linked nucleosides; and
- a 3' wing segment consisting of five linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment; wherein each nucleoside of the 5' wing segment comprises a cEt nucleoside; wherein the 3' wing segment comprises a cEt nucleoside, a 2'-O-methoxyethyl nucleoside, a cEt nucleoside, a 2'-O-methoxyethyl nucleoside, and a cEt

nucleoside in the 5' to 3' direction; wherein each internucleoside linkage is a phosphorothioate linkage; and wherein each cytosine is a 5-methylcytosine.

23. A compound comprising a modified oligonucleotide 16-80 linked nucleobases in length having a nucleobase sequence comprising the sequence recited in SEQ ID NOs: 2021, wherein the modified oligonucleotide comprises:

a gap segment consisting of nine linked deoxynucleosides;

a 5' wing segment consisting of two linked nucleosides; and

a 3' wing segment consisting of five linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment; wherein each nucleoside of the 5' wing segment comprises a cEt nucleoside; wherein the 3' wing segment comprises a 2'-O-methoxyethyl nucleoside, a 2'-O-methoxyethyl nucleoside, a 2'-O-methoxyethyl nucleoside, a cEt nucleoside, and a cEt nucleoside in the 5' to 3' direction; wherein each internucleoside linkage is a phosphorothioate linkage; and wherein each cytosine is a 5-methylcytosine.

24. A compound comprising a modified oligonucleotide 16-80 linked nucleobases in length having a nucleobase sequence comprising the sequence recited in SEQ ID NOs: 1540, wherein the modified oligonucleotide comprises:

a gap segment consisting of nine linked deoxynucleosides;

a 5' wing segment consisting of two linked nucleosides; and

a 3' wing segment consisting of five linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment; wherein each nucleoside of the 5' wing segment comprises a cEt nucleoside; wherein the 3' wing segment comprises a 2'-O-methoxyethyl nucleoside, a 2'-O-methoxyethyl nucleoside, a 2'-O-methoxyethyl nucleoside, a cEt nucleoside, and a cEt nucleoside in the 5' to 3' direction; wherein each internucleoside linkage is a phosphorothioate linkage; and wherein each cytosine is a 5-methylcytosine.

25. A compound comprising a modified oligonucleotide 16-80 linked nucleobases in length having a nucleobase sequence comprising the sequence recited in SEQ ID NOs: 560, wherein the modified oligonucleotide comprises:

a gap segment consisting of nine linked deoxynucleosides;

a 5' wing segment consisting of two linked nucleosides; and

a 3' wing segment consisting of five linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment; wherein each nucleoside of the 5' wing segment comprises a cEt nucleoside; wherein the 3' wing segment comprises a

2'-O-methoxyethyl nucleoside, a cEt nucleoside, a 2'-O-methoxyethyl nucleoside, a cEt nucleoside, and a 2'-O-methoxyethyl nucleoside in the 5' to 3' direction; wherein each internucleoside linkage is a phosphorothioate linkage; and wherein each cytosine is a 5-methylcytosine.

26. The compound of any one of claims 1-25, wherein the oligonucleotide is at least 80%, 85%, 90%, 95% or 100% complementary to SEQ ID NO: 1 or 2.

27. The compound of any one of claims 1-26, wherein the compound is single-stranded.

28. The compound of any one of claims 1-26, wherein the compound is double-stranded.

29. The compound of any one of claims 1-28, wherein the compound comprises ribonucleotides.

30. The compound of any one of claims 1-28, wherein the compound comprises deoxyribonucleotides.

31. The compound of any one of claims 1-30, wherein the modified oligonucleotide consists of 16 to 30 linked nucleosides.

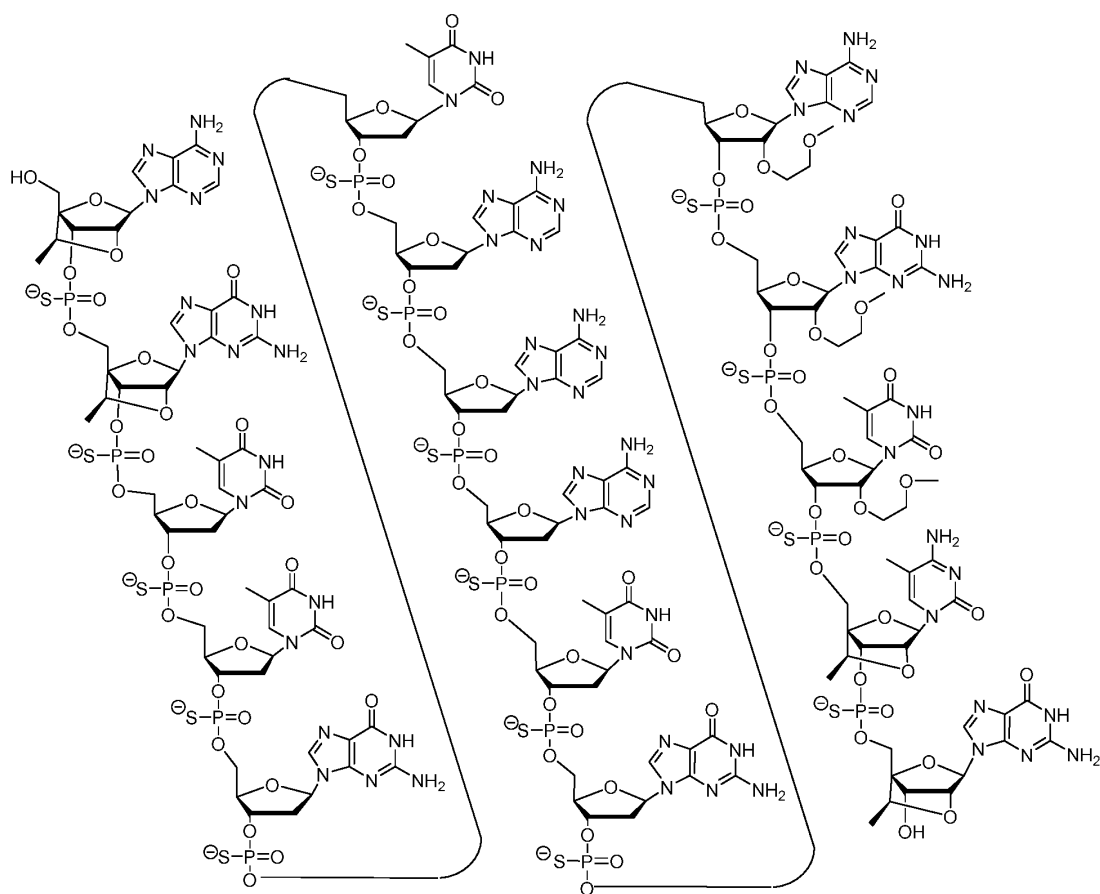
32. The compound of any preceding claim, wherein the compound consists of the modified oligonucleotide.

33. A compound consisting of a pharmaceutically acceptable salt of any of the compounds of claims 1-32.

34. The compound of claim 33, wherein the pharmaceutically acceptable salt is a sodium salt.

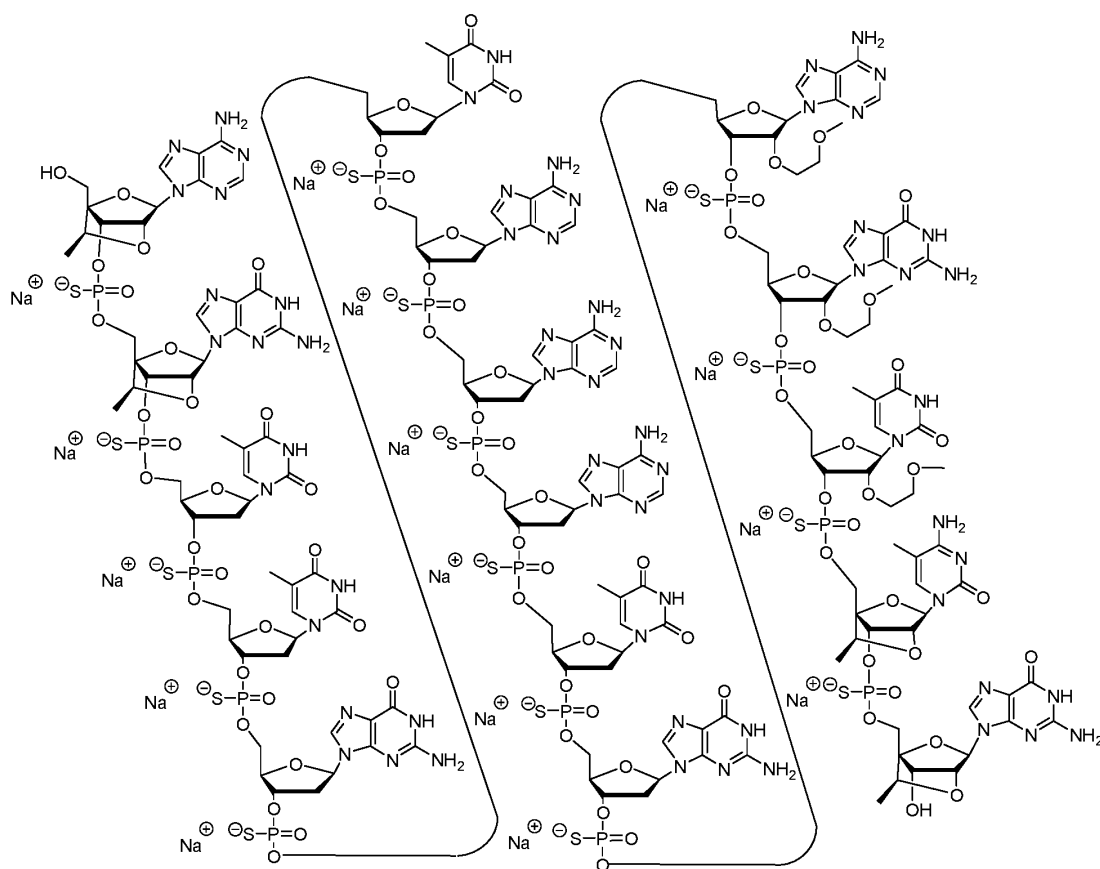
35. The compound of claim 33, wherein the pharmaceutically acceptable salt is a potassium salt.

36. A compound having the formula:

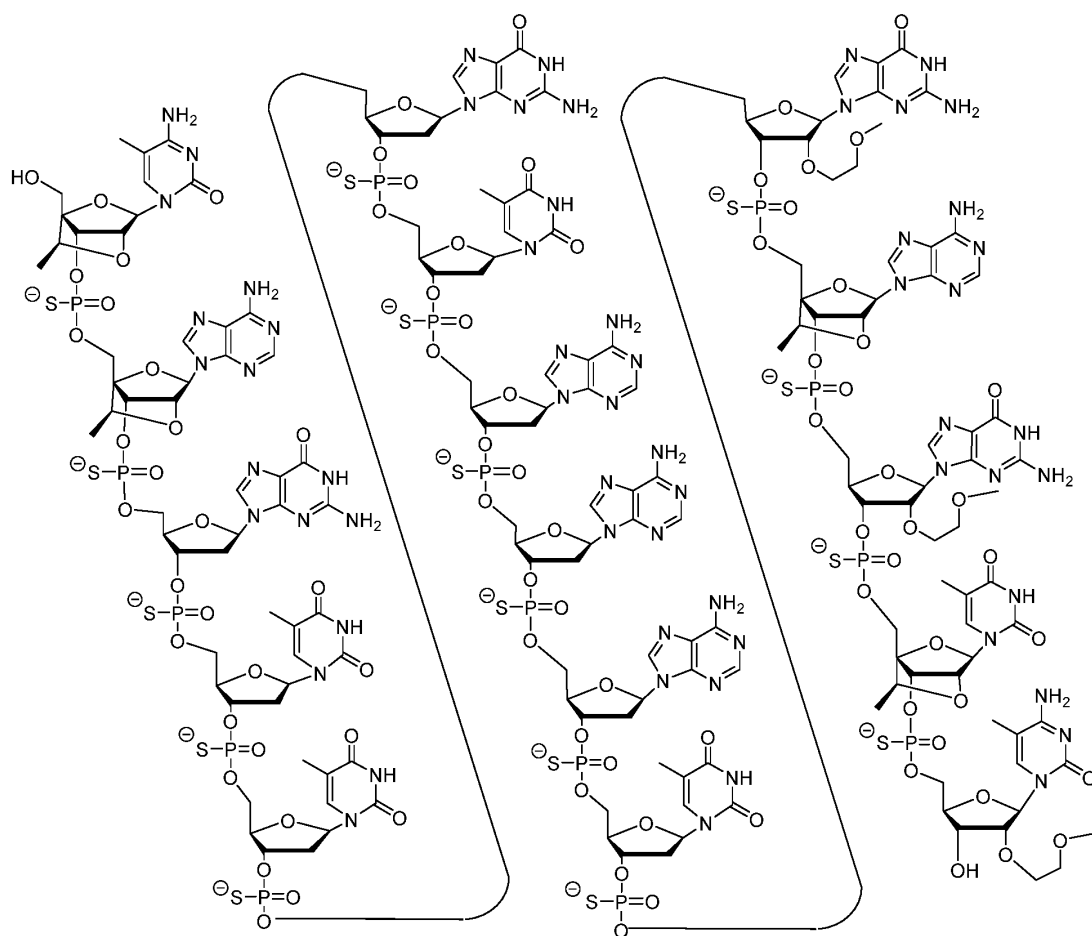


, or a salt thereof.

37. A compound having the formula:

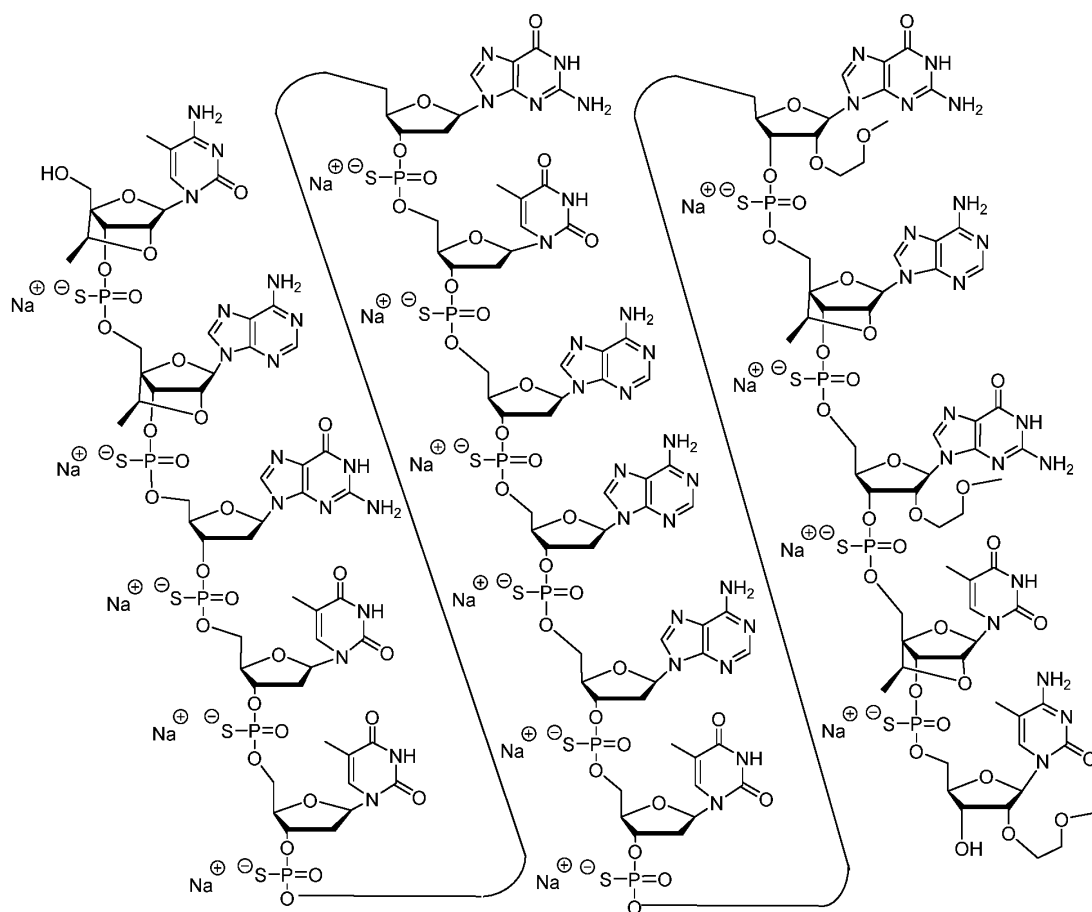


38. A compound having the formula:



, or a salt thereof.

39. A compound having the formula:



40. A composition comprising the compound of any one of claims 1-39 and a pharmaceutically acceptable carrier.
41. A composition comprising a compound or modified oligonucleotide of any preceding claim, for use in therapy.
42. A method of treating or ameliorating cancer in an individual comprising administering to the individual a compound targeted to IRF4, thereby treating or ameliorating the cancer.
43. The method of claim 42, wherein the compound is an antisense compound targeted to IRF4.
44. The method of claim 42 or 43, wherein the cancer is a blood cancer, myeloma, multiple myeloma (MM), B cell malignancy, lymphoma, B cell lymphoma, T cell lymphoma, or leukemia.
45. The method of any of claims 42-44, wherein administering the compound inhibits or reduces cancer cell proliferation, tumor growth, or metastasis.

46. A method of inhibiting expression of IRF4 in a cell comprising contacting the cell with a compound targeted to IRF4, thereby inhibiting expression of IRF4 in the cell.
47. The method of claim 48, wherein the cell is a cancer cell.
48. The method of claim 47, wherein the individual has a blood cancer, myeloma, multiple myeloma (MM), B cell malignancy, lymphoma, B cell lymphoma, T cell lymphoma, or leukemia.
49. A method of reducing or inhibiting cancer cell proliferation, tumor growth, or metastasis in an individual having cancer comprising administering a compound targeted to IRF4 to the individual, thereby reducing or inhibiting cancer cell proliferation, tumor growth, or metastasis in the individual.
50. The method of claim 49, wherein the individual has a blood cancer, myeloma, multiple myeloma (MM), B cell malignancy, lymphoma, B cell lymphoma, T cell lymphoma, or leukemia.
51. The method of any one of claims 46-50, wherein the compound is an antisense compound targeted to IRF4.
52. The method of any one of claims 46-51, wherein the compound is the compound of any one of claims 1-39 or composition of claim 40 or 41.
53. The method of any of claims 42-52, wherein the compound is administered parenterally.
54. Use of a compound targeted to IRF4 for treating, preventing, or ameliorating a cancer associated with IRF4.
55. The use of claim 54, wherein the cancer is a blood cancer, myeloma, multiple myeloma (MM), B cell malignancy, lymphoma, B cell lymphoma, T cell lymphoma, or leukemia.
56. The use of claim 54 or 55, wherein the compound is an antisense compound targeted to IRF4.
57. The use of any one of claims 54-56, wherein the compound is the compound of any one of claims 1-39 or composition of claim 40 or 41.
58. Use of a compound targeted to IRF4 in the manufacture of a medicament for treating or ameliorating a cancer associated with IRF4.
59. The use of claim 58, wherein the cancer is a blood cancer, myeloma, multiple myeloma (MM), B cell malignancy, lymphoma, B cell lymphoma, T cell lymphoma, or leukemia.
60. The use of claim 58 or 59, wherein the compound is an antisense compound targeted to IRF4.
61. The use of any one of claims 58-60, wherein the compound is the compound of any one of claims 1-39 or composition of claim 40 or 41.
62. Use of a compound targeted to IRF4 in the preparation of a medicament for treating or ameliorating a cancer associated with IRF4.
63. The use of claim 62, wherein the cancer is a blood cancer, myeloma, multiple myeloma (MM), B cell malignancy, lymphoma, B cell lymphoma, T cell lymphoma, or leukemia.
64. The use of claim 62 or 63, wherein the compound is an antisense compound targeted to IRF4.
65. The use of any one of claims 62-64, wherein the compound is the compound of any one of claims 1-39 or composition of claim 40 or 41.