

KETOHEXOKINASE (KHK) iRNA COMPOSITIONS AND METHODS OF USE THEREOF**RELATED APPLICATIONS**

This application claims the benefit of priority to U.S. Provisional Application No. 63/154,005, filed on February 26, 2021, U.S. Provisional Application No. 63/223,581, filed on July 20, 2021, and U.S. Provisional Application No. 63/280,668, filed on November 18, 2021. The entire contents of each of the foregoing applications are incorporated herein by reference.

SEQUENCE LISTING

The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on February 16, 2022, is named 121301_14720_SL.txt and is 572,214 bytes in size.

BACKGROUND OF THE INVENTION

Epidemiological studies have shown that a western diet is one of the leading causes of the modern obesity pandemic. Increase in fructose uptake, associated with the use of enriched soft drinks and processed food, is proposed to be a major contributing factor to the epidemic. High fructose corn sweeteners started gaining widespread use in the food industry by 1967. Although glucose and fructose have the same caloric value per molecule, the two sugars are metabolized differently and utilize different GLUT transporters. Fructose is almost exclusively metabolized in the liver, and unlike the glucose metabolism pathway, the fructose metabolism pathway is not regulated by feedback inhibition by the product (Khaitan Z *et al.*, (2013) *J. Nutr. Metab.* 2013, Article ID 682673, 1-12). While hexokinase and phosphofructokinase (PFK) regulate the production of glyceraldehyde-3-P from glucose, fructokinase or ketohexokinase (KHK), which is responsible for phosphorylation of fructose to fructose-1-phosphate in the liver, it is not down regulated by increasing concentrations of fructose-1-phosphate. As a result, all fructose entering the cell is rapidly phosphorylated. (Cirillo P. *et al.*, (2009) *J. Am. Soc. Nephrol.* 20: 545-553). Continued utilization of ATP to phosphorylate the fructose to fructose-1-phosphate results in intracellular phosphate depletion, ATP depletion, activation of AMP deaminase and formation of uric acid (Khaitan Z. *et al.*, (2013) *J. Nutr. Metab.* Article ID 682673, 1-12). Increased uric acid further stimulates the up-regulation of KHK (Lanaspa M.A. *et al.*, (2012) *PLOS ONE* 7(10): 1-11) and causes endothelial cell and adipocyte dysfunction. Fructose-1-phosphate is subsequently converted to glyceraldehyde by the action of aldolase B and is phosphorylated to glyceraldehyde-3-phosphate. The latter proceeds downstream to the glycolysis pathway to form pyruvate, which enters the citric acid cycle, wherefrom, under well-fed conditions, citrate is exported to the cytosol from the mitochondria, providing Acetyl Coenzyme A for lipogenesis (Figure 1).

The phosphorylation of fructose by KHK, and subsequent activation of lipogenesis leads to, for example, fatty liver, hypertriglyceridemia, dyslipidemia, and insulin resistance. Proinflammatory changes in renal proximal tubular cells have also been shown to be induced by

KHK activity (Cirillo P. *et al.*, (2009) *J. Am. Soc. Nephrol.* 20: 545-553). The phosphorylation of fructose by KHK is associated with diseases, disorders or conditions such as liver disease (*e.g.*, fatty liver, steatohepatitis), dyslipidemia (*e.g.*, hyperlipidemia, high LDL cholesterol, low HDL cholesterol, hypertriglyceridemia, postprandial hypertriglyceridemia), disorders of glycemic control (*e.g.*, insulin resistance, type 2 diabetes), cardiovascular disease (*e.g.*, hypertension, endothelial cell dysfunction), kidney disease (*e.g.*, acute kidney disorder, tubular dysfunction, proinflammatory changes to the proximal tubules, chronic kidney disease), metabolic syndrome, adipocyte dysfunction, visceral adipose deposition, obesity, hyperuricemia, gout, eating disorders, and excessive sugar craving. Accordingly, there is a need in the art for compositions and methods for treating diseases, disorders, and conditions associated with KHK activity.

SUMMARY OF THE INVENTION

The present invention provides iRNA compositions which affect the RNA-induced silencing complex (RISC)-mediated cleavage of RNA transcripts of a gene encoding ketohexokinase (KHK). The KHK gene may be within a cell, *e.g.*, a cell within a subject, such as a human subject.

In an aspect, the invention provides a double stranded ribonucleic acid (dsRNA) agent for inhibiting expression of ketohexokinase (KHK) in a cell, wherein the dsRNA agent comprises a sense strand and an antisense strand forming a double stranded region, wherein the sense strand comprises at least 15, *e.g.*, 15, 16, 17, 18, 19, 20, or 21, contiguous nucleotides differing by no more than 0, 1, 2, or 3 nucleotides from the nucleotide sequence of SEQ ID NO:1 and the antisense strand comprises at least 15, *e.g.*, 15, 16, 17, 18, 19, 20, 21, 22 or 23, contiguous nucleotides differing by no more than 1, 2, or 3 nucleotides from the nucleotide sequence of SEQ ID NO:2. In one embodiment, the dsRNA agent comprises at least one thermally destabilizing nucleotide modification, *e.g.*, an abasic modification; a mismatch with the opposing nucleotide in the duplex; and destabilizing sugar modification, a 2'-deoxy modification, an acyclic nucleotide, an unlocked nucleic acids (UNA), or a glycerol nucleic acid (GNA), *e.g.*, the antisense strand comprises at least one thermally destabilizing nucleotide modification.

In another aspect, the present invention provides a double stranded ribonucleic acid (dsRNA) for inhibiting expression of ketohexokinase (KHK) in a cell, wherein said dsRNA comprises a sense strand and an antisense strand forming a double stranded region, wherein the antisense strand comprises a region of complementarity to an mRNA encoding KHK, and wherein the region of complementarity comprises at least 15, *e.g.*, 15, 16, 17, 18, 19, 20, 21, 22 or 23, contiguous nucleotides differing by no more than 0, 1, 2, or 3 nucleotides from any one of the antisense nucleotide sequences in any one of Tables 2, 3, 5, 6, and 8-13.

In one embodiment, the dsRNA agent comprises a sense strand comprising a contiguous nucleotide sequence which has at least 85%, *e.g.*, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, nucleotide sequence identity over its entire length to any one of the nucleotide sequences of the sense strands in any one of Tables 2, 3, 5, 6 and 8-13 and an antisense strand

comprising a contiguous nucleotide sequence which has at least 85%, e.g., 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, nucleotide sequence identity over its entire length to any one of the nucleotide sequences of the antisense strands in any one of Tables 2, 3, 5, 6 and 8-13.

5 In one embodiment, the dsRNA agent comprises a sense strand comprising at least 15, e.g., 15, 16, 17, 18, 19, 20, or 21, contiguous nucleotides differing by no more than three nucleotides from any one of the nucleotide sequences of the sense strands in any one of Tables 2, 3, 5, 6 and 8-13 and an antisense strand comprising at least 15, e.g., 15, 16, 17, 18, 19, 20, 21, 22 or 23, contiguous
10 nucleotides differing by no more than three nucleotides from any one of the nucleotide sequences of the antisense strands in any one of Tables 2, 3, 5, 6 and 8-13.

In one embodiment, the dsRNA agent comprises a sense strand comprising at least 15, e.g., 15, 16, 17, 18, 19, 20, or 21, contiguous nucleotides differing by no more than two nucleotides from any one of the nucleotide sequences of the sense strands in any one of Tables 2, 3, 5, 6 and 8-13 and an antisense strand comprising at least 15, e.g., 15, 16, 17, 18, 19, 20, 21, 22 or 23, contiguous
15 nucleotides differing by no more than two nucleotides from any one of the nucleotide sequences of the antisense strands in any one of Tables 2, 3, 5, 6 and 8-13.

In one embodiment, the dsRNA agent comprises a sense strand comprising at least 15, e.g., 15, 16, 17, 18, 19, 20, or 21, contiguous nucleotides differing by no more than one nucleotide from any one of the nucleotide sequences of the sense strands in any one of Tables 2, 3, 5, 6 and 8-13 and an antisense strand comprising at least 15, e.g., 15, 16, 17, 18, 19, 20, 21, 22 or 23, contiguous
20 nucleotides differing by no more than one nucleotide from any one of the nucleotide sequences of the antisense strands in any one of Tables 2, 3, 5, 6 and 8-13.

In one embodiment, the dsRNA agent comprises a sense strand comprising or consisting of a nucleotide sequence selected from the group consisting of any one of the nucleotide sequences of the sense strands in any one of Tables 2, 3, 5, 6 and 8-13 and an antisense strand comprising or consisting
25 of a nucleotide sequence selected from the group consisting of any one of the nucleotide sequences of the antisense strands in any one of Tables 2, 3, 5, 6 and 8-13.

In one aspect, the present invention provides a double stranded ribonucleic acid (dsRNA) for inhibiting expression of ketohexokinase (KHK) in a cell, wherein said dsRNA comprises a sense
30 strand and an antisense strand forming a double stranded region, wherein the sense strand comprises at least 15, e.g., 15, 16, 17, 18, 19, 20, or 21, contiguous nucleotides differing by no more than 0, 1, 2, or 3 nucleotides from any one of the nucleotide sequence of nucleotides 120-162; 164-188; 181-207; 193-217; 209-231; 283-306; 508-546; 568-603; 596-632; 640-674; 746-806; 806-835; 917-942; 936-084; 1016-1041; 1100-1123; 1149-1175; 1160-1193; 1205-1229; 1252-1283; 1334-1356; 1407-1429;
35 1472-1497; 1506-1533; 1539-1561; 1704-1727; 1747-1787; 1850-1873; 1936-1964; 1960-1990; 2015-2048; 2060-2095; 2090-2118; 2124-2160; 2181-2200; 2221-2262 of SEQ ID NO: 1, and the antisense strand comprises at least 15, e.g., 15, 16, 17, 18, 19, 20, 21, 22 or 23, contiguous nucleotides

differing by no more than three, *e.g.*, 3, 2, 1, or 0, from the corresponding nucleotide sequence of SEQ ID NO:2.

In one aspect, the present invention provides a double stranded ribonucleic acid (dsRNA) for inhibiting expression of ketohexokinase (KHK) in a cell, wherein said dsRNA comprises a sense strand and an antisense strand forming a double stranded region, wherein the sense strand comprises at least 15, *e.g.*, 15, 16, 17, 18, 19, 20, or 21, contiguous nucleotides differing by no more than 0, 1, 2, or 3 nucleotides from any one of the nucleotide sequence of nucleotides 517-539; 521-543; 524-546; 517-546; 581-603; 610-632; 747-769; 749-771; 752-774; 755-777; 757-779; 758-780; 764-786; 776-798; 781-803; 747-803; 920-942; 941-963; 944-966; 950-972; 962-984; 920-984; 1149-1171; 1161-1183; 1165-1187; 1171-1193; 1149-1193; 1205-1227; 1206-1228; 1205-1228; 1334-1356; 1472-1494; 1475-1497; 1472-1497 of SEQ ID NO: 1, and the antisense strand comprises at least 15, *e.g.*, 15, 16, 17, 18, 19, 20, 21, 22 or 23, contiguous nucleotides differing by no more than three, *e.g.*, 3, 2, 1, or 0, from the corresponding nucleotide sequence of SEQ ID NO:2.

In one aspect, the present invention provides a double stranded ribonucleic acid (dsRNA) for inhibiting expression of ketohexokinase (KHK) in a cell, wherein said dsRNA comprises a sense strand and an antisense strand forming a double stranded region, wherein the sense strand comprises at least 15, *e.g.*, 15, 16, 17, 18, 19, 20, or 21, contiguous nucleotides differing by no more than 0, 1, 2, or 3 nucleotides from any one of the nucleotide sequence of nucleotides 517-539; 524-546; 517-546; 753-775; 757-779; 753-779; 764-786; 767-789; 768-790; 769-791; 764-791; 773-795; 781-803; 773-803; 753-803; 808-830; 937-959; 941-963; 944-966; 941-966; 948-970; 950-972; 948-972; 1160-1182; 1161-1183; 1160-1183; and 1207-1229 of SEQ ID NO: 1, and the antisense strand comprises at least 15, *e.g.*, 15, 16, 17, 18, 19, 20, 21, 22 or 23, contiguous nucleotides differing by no more than three, *e.g.*, 3, 2, 1, or 0, from the corresponding nucleotide sequence of SEQ ID NO:2.

In one embodiment, the antisense strand comprises at least 15, *e.g.*, 15, 16, 17, 18, 19, 20, 21, 22 or 23, contiguous nucleotides differing by no more than 0, 1, 2, or 3 nucleotides from any one of the antisense strand nucleotide sequences of a duplex selected from the group consisting of AD-1613400; AD-1613243; AD-1290757.3; AD-1290878.3; AD-1290969.3; AD-1423317.2; AD-1423327.2; AD-1423336.2; AD-1290599.3; AD-1523172.1; AD-1290837.3; AD-1523173.1; AD-1290884.3; AD-1523174.1; AD-1290959.3; AD-1523175.1; AD-1423311.2; AD-1423324.2; AD-1523176.1; AD-1423329.2; AD-1423333.2; AD-1423330.2; AD-1523177.1; AD-1290885.3; AD-1523178.1; AD-1423334.2; AD-1523179.1; AD-1523180.1; AD-1290539.3; and AD-1523181.1.

In another aspect, the present invention provides a double stranded ribonucleic acid (dsRNA) agent for inhibiting expression of ketohexokinase (KHK) in a cell, wherein said dsRNA comprises a sense strand and an antisense strand forming a double stranded region, wherein the sense strand comprises at least 15, *e.g.*, 15, 16, 17, 18, 19, 20, or 21, contiguous nucleotides differing by no more than three, *e.g.*, 3, 2, 1, or 0, nucleotides from any one of the nucleotide sequence of nucleotides 495-517, 492-517, 500-529, 514-551, 517-539, 524-546, 517-548, 614-643, 625-647, 625-660, 642-664, 642-672, 753-811, 754-780, 762-791, 764-786, 772-800, 781-803, 805-827, 808-830, 809-831, 792-

838, 931-982, 944-966, 947-969, 948-970, 948-982, 1011-1035, 1021-1043, 1019-1050, 1063-1091, 1150-1192, 1152-1176, 1160-1192, 1160-1182, 1162-1184, 1198-1230, 1198-1221, and 1202-1230 of SEQ ID NO: 1, and the antisense strand comprises at least 15, *e.g.*, 15, 16, 17, 18, 19, 20, 21, 22 or 23, contiguous nucleotides differing by no more than 3, *e.g.*, 3, 2, 1, or 0, nucleotides from the corresponding nucleotide sequence of SEQ ID NO:2.

In one aspect, the present invention provides a double stranded ribonucleic acid (dsRNA) agent for inhibiting expression of ketohexokinase (KHK) in a cell, wherein said dsRNA comprises a sense strand and an antisense strand forming a double stranded region, wherein the sense strand comprises at least 15, *e.g.*, 15, 16, 17, 18, 19, 20, or 21, contiguous nucleotides differing by no more than three, *e.g.*, 3, 2, 1, or 0, nucleotides from any one of the nucleotide sequence of nucleotides 513-556, 753-813, 936-981, 1155-1193, 1200-1229, 1704-1727, 1747-1787, 1850-1873, 1936-1964, 1960-1990, 1936-1990, 2015-2048, 2060-2095, 2090-2118, 2060-2118, 2124-2160, 2181-2220, 2221-2249, 2181-2249, 2240-2262, 2221-2262, and 2181-2262 of SEQ ID NO: 1, and the antisense strand comprises at least 15, *e.g.*, 15, 16, 17, 18, 19, 20, 21, 22 or 23, contiguous nucleotides differing by no more than 3, *e.g.*, 3, 2, 1, or 0, nucleotides from the corresponding nucleotide sequence of SEQ ID NO:2.

In one aspect, the present invention provides a double stranded ribonucleic acid (dsRNA) agent for inhibiting expression of ketohexokinase (KHK) in a cell, wherein said dsRNA comprises a sense strand and an antisense strand forming a double stranded region, wherein the sense strand comprises at least 15, *e.g.*, 15, 16, 17, 18, 19, 20, or 21, contiguous nucleotides differing by no more than 3, *e.g.*, 3, 2, 1, or 0, nucleotides from the nucleotide sequence of nucleotides 1207-1229 or 937-959 of SEQ ID NO: 1, and the antisense strand comprises at least 15, *e.g.*, 15, 16, 17, 18, 19, 20, 21, 22, or 23, contiguous nucleotides differing by no more than 3, *e.g.*, 3, 2, 1, or 0, from the corresponding nucleotide sequence of SEQ ID NO:2.

In one embodiment, the sense strand comprises at least 15, *e.g.*, 15, 16, 17, 18, 19, 20, or 21, contiguous nucleotides differing by no more than three, *e.g.*, 3, 2, 1, or 0, nucleotides from the nucleotide sequence of nucleotides 1207-1229 of SEQ ID NO: 1, and the antisense strand comprises at least 15, *e.g.*, 15, 16, 17, 18, 19, 20, 21, 22, or 23, contiguous nucleotides differing by no more than 3, *e.g.*, 3, 2, 1, or 0, from the corresponding nucleotide sequence of SEQ ID NO:2.

In one embodiment, the dsRNA agent comprises at least one modified nucleotide.

In one embodiment, substantially all of the nucleotides of the sense strand; substantially all of the nucleotides of the antisense strand comprise a modification; or substantially all of the nucleotides of the sense strand and substantially all of the nucleotides of the antisense strand comprise a modification.

In one embodiment, all of the nucleotides of the sense strand comprise a modification; all of the nucleotides of the antisense strand comprise a modification; or all of the nucleotides of the sense strand and all of the nucleotides of the antisense strand comprise a modification.

In one embodiment, at least one of the modified nucleotides is selected from the group consisting of a deoxy-nucleotide, a 3'-terminal deoxythymidine (dT) nucleotide, a 2'-O-methyl modified nucleotide, a 2'-fluoro modified nucleotide, a 2'-deoxy-modified nucleotide, a locked nucleotide, an unlocked nucleotide, a conformationally restricted nucleotide, a constrained ethyl nucleotide, an abasic nucleotide, a 2'-amino-modified nucleotide, a 2'-O-allyl-modified nucleotide, 2'-C-alkyl-modified nucleotide, 2'-hydroxyl-modified nucleotide, a 2'-methoxyethyl modified nucleotide, a 2'-O-alkyl-modified nucleotide, a morpholino nucleotide, a phosphoramidate, a non-natural base comprising nucleotide, a tetrahydropyran modified nucleotide, a 1,5-anhydrohexitol modified nucleotide, a cyclohexenyl modified nucleotide, a nucleotide comprising a phosphorothioate group, a nucleotide comprising a methylphosphonate group, a nucleotide comprising a 5'-phosphate, a nucleotide comprising a 5'-phosphate mimic, a thermally destabilizing nucleotide, a glycol modified nucleotide (GNA), a nucleotide comprising a 2' phosphate, and a 2-O-(N-methylacetamide) modified nucleotide; and combinations thereof.

In one embodiment, the modifications on the nucleotides are selected from the group consisting of LNA, HNA, CeNA, 2'-methoxyethyl, 2'-O-alkyl, 2'-O-allyl, 2'-C-allyl, 2'-fluoro, 2'-deoxy, 2'-hydroxyl, and glycol; and combinations thereof.

In one embodiment, at least one of the modified nucleotides is selected from the group consisting of a deoxy-nucleotide, a 2'-O-methyl modified nucleotide, a 2'-fluoro modified nucleotide, a 2'-deoxy-modified nucleotide, a glycol modified nucleotide (GNA), *e.g.*, Ggn, Cgn, Tgn, or Agn, a nucleotide comprising a 2' phosphate, *e.g.*, G2p, C2p, A2p, U2p, a vinyl-phosphonate nucleotide; and combinations thereof.

In another embodiment, at least one of the modifications on the nucleotides is a thermally destabilizing nucleotide modification.

In one embodiment, the thermally destabilizing nucleotide modification is selected from the group consisting of an abasic modification; a mismatch with the opposing nucleotide in the duplex; and destabilizing sugar modification, a 2'-deoxy modification, an acyclic nucleotide, an unlocked nucleic acids (UNA), and a glycerol nucleic acid (GNA).

In some embodiments, the modified nucleotide comprises a short sequence of 3'-terminal deoxythymidine nucleotides (dT).

In some embodiments, the modifications on the nucleotides are 2'-O-methyl, GNA and 2'-fluoro modifications.

In some embodiments, the dsRNA agent further comprises at least one phosphorothioate internucleotide linkage. In some embodiments, the dsRNA agent comprises 6-8 phosphorothioate internucleotide linkages. In one embodiment, the phosphorothioate or methylphosphonate internucleotide linkage is at the 3'-terminus of one strand. Optionally, the strand is the antisense strand. In another embodiment, the strand is the sense strand. In a related embodiment, the phosphorothioate or methylphosphonate internucleotide linkage is at the 5'-terminus of one strand. Optionally, the strand is the antisense strand. In another embodiment, the strand is the sense strand.

In another embodiment, the phosphorothioate or methylphosphonate internucleotide linkage is at the both the 5'- and 3'-terminus of one strand. Optionally, the strand is the antisense strand. In another embodiment, the strand is the sense strand.

The double stranded region may be 19-30 nucleotide pairs in length; 19-25 nucleotide pairs in length; 19-23 nucleotide pairs in length; 23-27 nucleotide pairs in length; or 21-23 nucleotide pairs in length.

In one embodiment, each strand is independently no more than 30 nucleotides in length.

In one embodiment, the sense strand is 21 nucleotides in length and the antisense strand is 23 nucleotides in length.

The region of complementarity may be at least 17 nucleotides in length; between 19 and 23 nucleotides in length; or 19 nucleotides in length.

In one embodiment, at least one strand comprises a 3' overhang of at least 1 nucleotide. In another embodiment, at least one strand comprises a 3' overhang of at least 2 nucleotides.

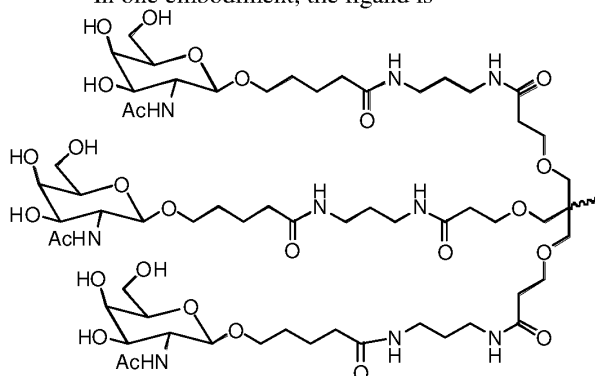
In one embodiment, the dsRNA agent further comprises a ligand.

In one embodiment, the ligand is conjugated to the 3' end of the sense strand of the dsRNA agent.

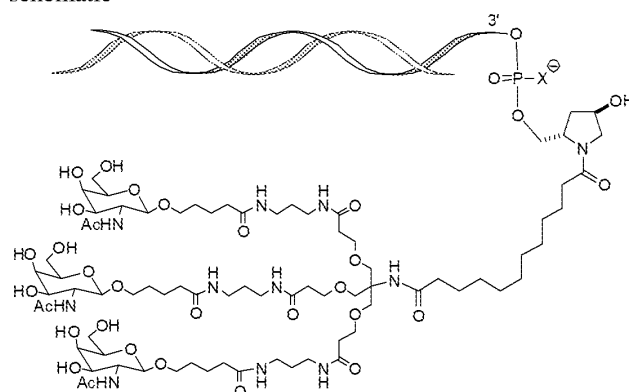
In one embodiment, the ligand is an N-acetylgalactosamine (GalNAc) derivative.

In one embodiment, the ligand is one or more GalNAc derivatives attached through a monovalent, bivalent, or trivalent branched linker.

In one embodiment, the ligand is



In one embodiment, the dsRNA agent is conjugated to the ligand as shown in the following schematic



and, wherein X is O or S.

5 In one embodiment, the X is O.

In one embodiment, the dsRNA agent further comprises at least one phosphorothioate or methylphosphonate internucleotide linkage.

In one embodiment, the phosphorothioate or methylphosphonate internucleotide linkage is at the 3'-terminus of one strand, *e.g.*, the antisense strand or the sense strand.

10 In another embodiment, the phosphorothioate or methylphosphonate internucleotide linkage is at the 5'-terminus of one strand, *e.g.*, the antisense strand or the sense strand.

In one embodiment, the phosphorothioate or methylphosphonate internucleotide linkage is at the both the 5'- and 3'-terminus of one strand. In one embodiment, the strand is the antisense strand.

In one embodiment, the base pair at the 1 position of the 5'-end of the antisense strand of the duplex is an AU base pair.

In one aspect, the present invention provides a double stranded ribonucleic acid (dsRNA) agent for inhibiting expression of ketohexokinase (KHK) in a cell, or a pharmaceutically acceptable salt thereof, comprising a sense strand and an antisense strand forming a double stranded region, wherein

20 a) the nucleotide sequence of the sense strand differs by no more than 4 bases from the nucleotide sequence 5'-gscsaggaagCfAfCfugagauucgu-3' and the nucleotide sequence of the antisense strand differs by no more than 4 bases from the nucleotide sequence 5'-asdCsgadAudCucagdTgCfuuccugcsasc-3', wherein a, g, c and u are 2'-O-methyl (2'-OMe) A, G, C, and U; Cf and Uf are 2'-deoxy-2'-fluoro (2'-F) C and U; dC, dA, and dT are 2'-deoxy C, A, and T; and s is a phosphorothioate linkage; or

25 b) the nucleotide sequence of the sense strand differs by no more than 4 bases from the nucleotide sequence 5'-csusacggagAfCfGfugguguuugu-3' and the nucleotide sequence of the antisense strand differs by no more than 4 bases from the nucleotide sequence 5'-asdCsaadAcdAccacdGuCfuceguagscsc-3', wherein a, g, c and u are 2'-O-methyl (2'-OMe) A, G, C,

and U; Cf and Uf are 2'-deoxy-2'-fluoro (2'-F) C and U; dC, dA, and dG are 2'-deoxy C, A, and G; and s is a phosphorothioate linkage.

In one embodiment,

- a) the nucleotide sequence of the sense strand differs by no more than 3 bases from the nucleotide sequence 5'-gscsaggaagCfAfCfugagauucgu-3' and the nucleotide sequence of the antisense strand differs by no more than 3 bases from the nucleotide sequence 5'-asdCsgadAudCucagdTgCfuuccugcsasc-3', wherein a, g, c and u are 2'-O-methyl (2'-OMe) A, G, C, and U; Cf and Uf are 2'-deoxy-2'-fluoro (2'-F) C and U; dC, dA, and dT are 2'-deoxy C, A, and T; and s is a phosphorothioate linkage; or
- b) the nucleotide sequence of the sense strand differs by no more than 3 bases from the nucleotide sequence 5'-csusacggagAfCfGfugguguuugu-3' and the nucleotide sequence of the antisense strand differs by no more than 3 bases from the nucleotide sequence 5'-asdCsaadAcdAccacdGuCfuccguagscsc-3', wherein a, g, c and u are 2'-O-methyl (2'-OMe) A, G, C, and U; Cf and Uf are 2'-deoxy-2'-fluoro (2'-F) C and U; dC, dA, and dG are 2'-deoxy C, A, and G; and s is a phosphorothioate linkage.

In one embodiment,

- a) the nucleotide sequence of the sense strand differs by no more than 2 bases from the nucleotide sequence 5'-gscsaggaagCfAfCfugagauucgu-3' and the nucleotide sequence of the antisense strand differs by no more than 2 bases from the nucleotide sequence 5'-asdCsgadAudCucagdTgCfuuccugcsasc-3', wherein a, g, c and u are 2'-O-methyl (2'-OMe) A, G, C, and U; Cf and Uf are 2'-deoxy-2'-fluoro (2'-F) C and U; dC, dA, and dT are 2'-deoxy C, A, and T; and s is a phosphorothioate linkage; or
- b) the nucleotide sequence of the sense strand differs by no more than 2 bases from the nucleotide sequence 5'-csusacggagAfCfGfugguguuugu-3' and the nucleotide sequence of the antisense strand differs by no more than 2 bases from the nucleotide sequence 5'-asdCsaadAcdAccacdGuCfuccguagscsc-3', wherein a, g, c and u are 2'-O-methyl (2'-OMe) A, G, C, and U; Cf and Uf are 2'-deoxy-2'-fluoro (2'-F) C and U; dC, dA, and dG are 2'-deoxy C, A, and G; and s is a phosphorothioate linkage.

In one embodiment,

- a) the nucleotide sequence of the sense strand differs by no more than 1 base from the nucleotide sequence 5'-gscsaggaagCfAfCfugagauucgu-3' and the nucleotide sequence of the antisense strand differs by no more than 1 base from the nucleotide sequence 5'-asdCsgadAudCucagdTgCfuuccugcsasc-3', wherein a, g, c and u are 2'-O-methyl (2'-OMe) A, G, C, and U; Cf and Uf are 2'-deoxy-2'-fluoro (2'-F) C and U; dC, dA, and dT are 2'-deoxy C, A, and T; and s is a phosphorothioate linkage; or
- b) the nucleotide sequence of the sense strand differs by no more than 1 base from the nucleotide sequence 5'-csusacggagAfCfGfugguguuugu-3' and the nucleotide sequence of the

antisense strand differs by no more than 1 base from the nucleotide sequence 5'-asdCsaadAcdAccacdGuCfuccguagscsc-3', wherein a, g, c and u are 2'-O-methyl (2'-OMe) A, G, C, and U; Cf and Uf are 2'-deoxy-2'-fluoro (2'-F) C and U; dC, dA, and dG are 2'-deoxy C, A, and G; and s is a phosphorothioate linkage.

5 In one embodiment,

a) the nucleotide sequence of the sense strand comprises the nucleotide sequence 5'-gscsaggaagCfAfCfugagauucgu-3' and the nucleotide sequence of the antisense strand comprises the nucleotide sequence 5'-asdCsgadAudCucagdTgCfuuccugcsasc-3', wherein a, g, c and u are 2'-O-methyl (2'-OMe) A, G, C, and U; Cf and Uf are 2'-deoxy-2'-fluoro (2'-F) C and U; dC, dA, and dT are 2'-deoxy C, A, and T; and s is a phosphorothioate linkage; or

b) the nucleotide sequence of the sense strand comprises the nucleotide sequence 5'-csusacggagAfCfGfugguguugu-3' and the nucleotide sequence of the antisense strand comprises the nucleotide sequence 5'-asdCsaadAcdAccacdGuCfuccguagscsc-3', wherein a, g, c and u are 2'-O-methyl (2'-OMe) A, G, C, and U; Cf and Uf are 2'-deoxy-2'-fluoro (2'-F) C and U; dC, dA, and dG are 2'-deoxy C, A, and G; and s is a phosphorothioate linkage.

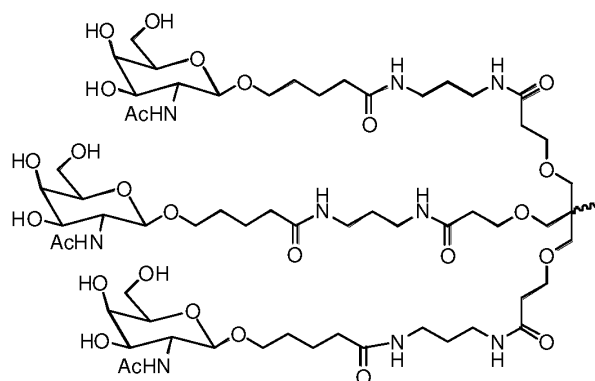
In one embodiment, the dsRNA agent further comprises a ligand.

In one embodiment, the ligand is conjugated to the 3' end of the sense strand of the dsRNA agent.

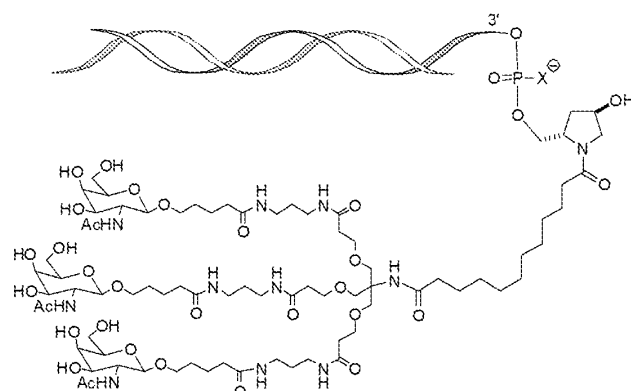
In one embodiment, the ligand is an N-acetylgalactosamine (GalNAc) derivative.

20 In one embodiment, the ligand is one or more GalNAc derivatives attached through a monovalent, bivalent, or trivalent branched linker.

In one embodiment, the ligand is



In one embodiment, the dsRNA agent is conjugated to the ligand as shown in the following schematic



and, wherein X is O or S.

5 In one embodiment, X is O.

The present invention also provides cells containing any of the dsRNA agents of the invention and pharmaceutical compositions comprising any of the dsRNA agents of the invention.

The pharmaceutical composition of the invention may include dsRNA agent in an unbuffered solution, *e.g.*, saline or water, or the pharmaceutical composition of the invention may include the dsRNA agent in a buffer solution, *e.g.*, a buffer solution comprising acetate, citrate, prolamine, carbonate, or phosphate or any combination thereof; or phosphate buffered saline (PBS).

In one aspect, the present invention provides a method of inhibiting expression of a ketohexokinase (KHK) gene in a cell. The method includes contacting the cell with any of the dsRNAs of the invention or any of the pharmaceutical compositions of the invention, thereby inhibiting expression of the KHK gene in the cell.

In one embodiment, the cell is within a subject, *e.g.*, a human subject, *e.g.*, a subject having a ketohexokinase (KHK)-associated disorder, such as a KHK-associated disorder selected from the group consisting of liver disease (*e.g.*, fatty liver, steatohepatitis, non-alcoholic steatohepatitis (NASH)), dyslipidemia (*e.g.*, hyperlipidemia, high LDL cholesterol, low HDL cholesterol, hypertriglyceridemia, postprandial hypertriglyceridemia), disorders of glycemic control (*e.g.*, insulin resistance, type 2 diabetes), cardiovascular disease (*e.g.*, hypertension, endothelial cell dysfunction), kidney disease (*e.g.*, acute kidney disorder, tubular dysfunction, proinflammatory changes to the proximal tubules, chronic kidney disease), metabolic syndrome, adipocyte dysfunction, visceral adipose deposition, obesity, hyperuricemia, gout, eating disorders, and excessive sugar craving.

In one embodiment, contacting the cell with the dsRNA agent inhibits the expression of KHK by at least 50%, 60%, 70%, 80%, 90%, or 95%.

In one embodiment, inhibiting expression of KHK decreases KHK protein level in serum of the subject by at least 50%, 60%, 70%, 80%, 90%, or 95%.

In one aspect, the present invention provides a method of treating a subject having a disorder that would benefit from reduction in ketohexokinase (KHK) expression. The method includes administering to the subject a therapeutically effective amount of any of the dsRNAs of the invention or any of the pharmaceutical compositions of the invention, thereby treating the subject having the disorder that would benefit from reduction in KHK expression.

In another aspect, the present invention provides a method of preventing at least one symptom in a subject having a disorder that would benefit from reduction in ketohexokinase (KHK) expression. The method includes administering to the subject a prophylactically effective amount of any of the dsRNAs of the invention or any of the pharmaceutical compositions of the invention, thereby preventing at least one symptom in the subject having the disorder that would benefit from reduction in KHK expression.

In certain embodiments, the KHK-associated disorder is a liver disease, *e.g.*, fatty liver disease such as NAFLD or NASH. In certain embodiments, the KHK-associated disorder is dyslipidemia, *e.g.*, elevated serum triglycerides, elevated serum LDL, elevated serum cholesterol, lowered serum HDL, postprandial hypertriglyceridemia. In another embodiment, the KHK-associated disorder is a disorder of glycemic control, *e.g.*, insulin resistance not resulting from an immune response against insulin, glucose resistance, type 2 diabetes. In certain embodiments, the KHK-associated disorder is a cardiovascular disease, *e.g.*, hypertension, endothelial cell dysfunction. In certain embodiments, the KHK-associated disorder is a kidney disease, *e.g.*, acute kidney disorder, tubular dysfunction, proinflammatory changes to the proximal tubules, chronic kidney disease. In certain embodiments, the disease is metabolic syndrome. In certain embodiments, the KHK-associated disorder is a disease of lipid deposition or dysfunction, *e.g.*, visceral adipose deposition, fatty liver, obesity. In certain embodiments, the KHK-associated disorder is a disease of elevated uric acid, *e.g.*, gout, hyperuricemia. In certain embodiments the KHK-associated disorder is an eating disorder such as excessive sugar craving.

In certain embodiments, the administration of the dsRNA to the subject causes a decrease in fructose metabolism. In certain embodiments, the administration of the dsRNA causes a decrease in the level of KHK in the subject, especially hepatic KHK, especially KHK-C in a subject with elevated KHK. In certain embodiments, the administration of the dsRNA causes a decrease in fructose metabolism in the subject. In certain embodiments, the administration of the dsRNA causes a decrease in the level of uric acid, *e.g.*, serum uric acid, in a subject with elevated serum uric acid, *e.g.*, elevated serum uric acid associated with gout. In certain embodiments, the administration of the dsRNA causes a normalization of serum lipids, *e.g.*, triglycerides including postprandial triglycerides, LDL, HDL, or cholesterol, in a subject with at least one abnormal serum lipid level. In certain embodiments, the administration of the dsRNA causes a normalization of lipid deposition, *e.g.*, a decrease of lipid deposition in the liver (*e.g.*, decrease of NAFLD or NASH), a decrease of visceral fat deposition, a decrease in body weight. In certain embodiments, the administration of the dsRNA causes a normalization of insulin or glucose response in a subject with abnormal insulin response not

related to an immune response to insulin, or abnormal glucose response. In certain embodiments, the administration of the dsRNA results in an improvement of kidney function, or a stoppage or reduction of the rate of loss of kidney function. In certain embodiments, the dsRNA causes a reduction of hypertension, *i.e.*, elevated blood pressure.

5 In certain embodiments, the invention further comprises administering an additional agent to a subject with a KHK-associated disease. In certain embodiments, treatments known in the art for the various KHK-associated diseases are used in combination with the RNAi agents of the invention. Such treatments are discussed below.

In one embodiment, the subject is human.

10 In one embodiment, the dsRNA agent is administered to the subject at a dose of about 0.01 mg/kg to about 50 mg/kg.

In one embodiment, the dsRNA agent is administered to the subject subcutaneously.

In one embodiment, the methods of the invention include further determining the level of KHK in a sample(s) from the subject.

15 In one embodiment, the level of KHK in the subject sample(s) is a KHK protein level in a blood or serum sample(s).

In one embodiment, the methods of the invention further comprise measuring the uric acid level, especially serum uric acid level, in the subject. In one embodiment, the methods of the invention further comprise measuring the urine fructose level in the subject. In one embodiment, the methods of the invention further comprise measuring a serum lipid level in a subject. In certain
20 embodiments, the methods of the invention further include measuring insulin or glucose sensitivity in a subject. In certain embodiments, a decrease in the levels of expression or activity of fructose metabolism indicates that the KHK-associated disease is being treated or prevented.

The present invention also provides kits comprising any of the dsRNAs of the invention or
25 any of the pharmaceutical compositions of the invention, and optionally, instructions for use.

The present invention further provides an RNA-induced silencing complex (RISC) comprising an antisense strand of any of the dsRNA agents of the invention.

In another embodiment, the RNAi agent is a pharmaceutically acceptable salt thereof. "Pharmaceutically acceptable salts" of each of RNAi agents herein include, but are not limited to, a
30 sodium salt, a calcium salt, a lithium salt, a potassium salt, an ammonium salt, a magnesium salt, an mixtures thereof. One skilled in the art will appreciate that the RNAi agent, when provided as a polycationic salt having one cation per free acid group of the optionally modified phosphodiester backbone and/or any other acidic modifications (e.g., 5'-terminal phosphonate groups). For example, an oligonucleotide of "n" nucleotides in length contains n-1 optionally modified phosphodiesters, so
35 that an oligonucleotide of 21 nt in length may be provided as a salt having up to 20 cations (e.g., 20 sodium cations). Similarly, an RNAi agent having a sense strand of 21 nt in length and an antisense strand of 23 nt in length may be provided as a salt having up to 42 cations (e.g., 42 sodium cations). In the preceding example, where the RNAi agent also includes a 5'-terminal phosphate or a 5'-

terminal vinylphosphonate group, the RNAi agent may be provided as a salt having up to 44 cations (e.g, 44 sodium cations).

The present invention is further illustrated by the following detailed description and drawings.

5

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 depicts the classic and alternative lipogenic pathways of fructose. In the classical pathway, triglycerides (TG) are a direct product of fructose metabolism by the action of multiple enzymes including aldolase B (Aldo B) and fatty acid synthase (FAS). In an alternative pathway, uric acid produced from the nucleotide turnover that occurs during the phosphorylation of fructose to fructose-1-phosphate (F-1-P) results in the generation of mitochondrial oxidative stress (mtROS), which causes a decrease in the activity of aconitase (ACO2) in the Krebs cycle. As a consequence, the ACO2 substrate, citrate, accumulates and is released to the cytosol where it acts as substrate for TG synthesis through the activation of ATP citrate lyase (ACL) and fatty acid synthase. AMPD2, AMP deaminase 2; IMP, inosine monophosphate; PO₄, phosphate (from Johnson *et al.* (2013) *Diabetes*. 62:3307-3315).

Figure 2 is a graph depicting the effect of administration of a single 3 mg/kg dose of the indicated duplexes on the level of KHK mRNA and KHK protein at Day 29 post-dose. The level of mRNA and protein are depicted as % remaining normalized to the pre-dose level of mRNA and protein.

Figure 3 is a graph depicting the effect of administration of a single 3 mg/kg dose of the indicated duplexes on the level of KHK mRNA at Day 50 post-dose. The level of mRNA is depicted as % remaining normalized to the pre-dose level of mRNA.

Figure 4 is a graph depicting the effect of administration of a single 3 mg/kg dose of the indicated duplexes on the level of KHK mRNA at Day 78 post-dose. The level of mRNA is depicted as % remaining normalized to the pre-dose level of mRNA.

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides iRNA compositions which effect the RNA-induced silencing complex (RISC)-mediated cleavage of RNA transcripts of a ketohexokinase (KHK) gene. The gene may be within a cell, *e.g.*, a cell within a subject, such as a human. The use of these iRNAs enables the targeted degradation of mRNAs of the corresponding gene (KHK gene) in mammals.

The iRNAs of the invention have been designed to target the human ketohexokinase (KHK) gene, including portions of the gene that are conserved in the ketohexokinase (KHK) orthologs of other mammalian species. Without intending to be limited by theory, it is believed that a combination or sub-combination of the foregoing properties and the specific target sites or the specific modifications in these iRNAs confer to the iRNAs of the invention improved efficacy, stability, potency, durability, and safety.

Accordingly, the present invention provides methods for treating and preventing a ketohexokinase (KHK)-associated disorder, *e.g.*, liver disease (*e.g.*, fatty liver, steatohepatitis, non-alcoholic steatohepatitis (NASH)), dyslipidemia (*e.g.*, hyperlipidemia, high LDL cholesterol, low HDL cholesterol, hypertriglyceridemia, postprandial hypertriglyceridemia), disorders of glycemic control (*e.g.*, insulin resistance, type 2 diabetes), cardiovascular disease (*e.g.*, hypertension, endothelial cell dysfunction), kidney disease (*e.g.*, acute kidney disorder, tubular dysfunction, proinflammatory changes to the proximal tubules, chronic kidney disease), metabolic syndrome, adipocyte dysfunction, visceral adipose deposition, obesity, hyperuricemia, gout, eating disorders, and excessive sugar craving, using iRNA compositions which effect the RNA-induced silencing complex (RISC)-mediated cleavage of RNA transcripts of a KHK gene.

The iRNAs of the invention include an RNA strand (the antisense strand) having a region which is up to about 30 nucleotides or less in length, *e.g.*, 19-30, 19-29, 19-28, 19-27, 19-26, 19-25, 19-24, 19-23, 19-22, 19-21, 19-20, 20-30, 20-29, 20-28, 20-27, 20-26, 20-25, 20-24, 20-23, 20-22, 20-21, 21-30, 21-29, 21-28, 21-27, 21-26, 21-25, 21-24, 21-23, or 21-22 nucleotides in length, which region is substantially complementary to at least part of an mRNA transcript of a KHK gene.

In certain embodiments, one or both of the strands of the double stranded RNAi agents of the invention is up to 66 nucleotides in length, *e.g.*, 36-66, 26-36, 25-36, 31-60, 22-43, 27-53 nucleotides in length, with a region of at least 19 contiguous nucleotides that is substantially complementary to at least a part of an mRNA transcript of a KHK gene. In some embodiments, such iRNA agents having longer length antisense strands can, for example, include a second RNA strand (the sense strand) of 20-60 nucleotides in length wherein the sense and antisense strands form a duplex of 18-30 contiguous nucleotides.

The use of iRNAs of the invention enables the targeted degradation of mRNAs of the corresponding gene (KHK gene) in mammals. Using *in vitro* assays, the present inventors have demonstrated that iRNAs targeting a KHK gene can potently mediate RNAi, resulting in significant inhibition of expression of a KHK gene. Thus, methods and compositions including these iRNAs are useful for treating a subject having a KHK-associated disorder, *e.g.*, liver disease (*e.g.*, fatty liver, steatohepatitis, non-alcoholic steatohepatitis (NASH)), dyslipidemia (*e.g.*, hyperlipidemia, high LDL cholesterol, low HDL cholesterol, hypertriglyceridemia, postprandial hypertriglyceridemia), disorders of glycemic control (*e.g.*, insulin resistance, type 2 diabetes), cardiovascular disease (*e.g.*, hypertension, endothelial cell dysfunction), kidney disease (*e.g.*, acute kidney disorder, tubular dysfunction, proinflammatory changes to the proximal tubules, chronic kidney disease), metabolic syndrome, adipocyte dysfunction, visceral adipose deposition, obesity, hyperuricemia, gout, eating disorders, and excessive sugar craving.

Accordingly, the present invention provides methods and combination therapies for treating a subject having a disorder that would benefit from inhibiting or reducing the expression of a KHK gene, *e.g.*, a KHK-associated disorder, such as liver disease (*e.g.*, fatty liver, steatohepatitis, non-alcoholic steatohepatitis (NASH)), dyslipidemia (*e.g.*, hyperlipidemia, high LDL cholesterol, low

HDL cholesterol, hypertriglyceridemia, postprandial hypertriglyceridemia), disorders of glycemic control (*e.g.*, insulin resistance, type 2 diabetes), cardiovascular disease (*e.g.*, hypertension, endothelial cell dysfunction), kidney disease (*e.g.*, acute kidney disorder, tubular dysfunction, proinflammatory changes to the proximal tubules, chronic kidney disease), metabolic syndrome, adipocyte dysfunction, visceral adipose deposition, obesity, hyperuricemia, gout, eating disorders, and excessive sugar craving, using iRNA compositions which effect the RNA-induced silencing complex (RISC)-mediated cleavage of RNA transcripts of a KHK gene.

The present invention also provides methods for preventing at least one symptom in a subject having a disorder that would benefit from inhibiting or reducing the expression of a KHK gene, *e.g.*, liver disease (*e.g.*, fatty liver, steatohepatitis, non-alcoholic steatohepatitis (NASH)), dyslipidemia (*e.g.*, hyperlipidemia, high LDL cholesterol, low HDL cholesterol, hypertriglyceridemia, postprandial hypertriglyceridemia), disorders of glycemic control (*e.g.*, insulin resistance, type 2 diabetes), cardiovascular disease (*e.g.*, hypertension, endothelial cell dysfunction), kidney disease (*e.g.*, acute kidney disorder, tubular dysfunction, proinflammatory changes to the proximal tubules, chronic kidney disease), metabolic syndrome, adipocyte dysfunction, visceral adipose deposition, obesity, hyperuricemia, gout, eating disorders, and excessive sugar craving.

The following detailed description discloses how to make and use compositions containing iRNAs to inhibit the expression of a KHK gene as well as compositions, uses, and methods for treating subjects that would benefit from inhibition and/or reduction of the expression of a KHK gene, *e.g.*, subjects susceptible to or diagnosed with a KHK-associated disorder.

I. Definitions

In order that the present invention may be more readily understood, certain terms are first defined. In addition, it should be noted that whenever a value or range of values of a parameter are recited, it is intended that values and ranges intermediate to the recited values are also intended to be part of this invention.

The articles “a” and “an” are used herein to refer to one or to more than one (*i.e.*, to at least one) of the grammatical object of the article. By way of example, “an element” means one element or more than one element, *e.g.*, a plurality of elements.

The term “including” is used herein to mean, and is used interchangeably with, the phrase “including but not limited to”.

The term “or” is used herein to mean, and is used interchangeably with, the term “and/or,” unless context clearly indicates otherwise. For example, “sense strand or antisense strand” is understood as “sense strand or antisense strand or sense strand and antisense strand.”

The term “about” is used herein to mean within the typical ranges of tolerances in the art. For example, “about” can be understood as about 2 standard deviations from the mean. In certain embodiments, about means $\pm 10\%$. In certain embodiments, about means $\pm 5\%$. When about is

present before a series of numbers or a range, it is understood that “about” can modify each of the numbers in the series or range.

The term “at least”, “no less than”, or “or more” prior to a number or series of numbers is understood to include the number adjacent to the term “at least”, and all subsequent numbers or integers that could logically be included, as clear from context. For example, the number of nucleotides in a nucleic acid molecule must be an integer. For example, “at least 19 nucleotides of a 21 nucleotide nucleic acid molecule” means that 19, 20, or 21 nucleotides have the indicated property. When at least is present before a series of numbers or a range, it is understood that “at least” can modify each of the numbers in the series or range.

As used herein, “no more than” or “or less” is understood as the value adjacent to the phrase and logical lower values or integers, as logical from context, to zero. For example, a duplex with an overhang of “no more than 2 nucleotides” has a 2, 1, or 0 nucleotide overhang. When “no more than” is present before a series of numbers or a range, it is understood that “no more than” can modify each of the numbers in the series or range. As used herein, ranges include both the upper and lower limit.

As used herein, methods of detection can include determination that the amount of analyte present is below the level of detection of the method.

In the event of a conflict between an indicated target site and the nucleotide sequence for a sense or antisense strand, the indicated sequence takes precedence.

In the event of a conflict between a sequence and its indicated site on a transcript or other sequence, the nucleotide sequence recited in the specification takes precedence.

As used herein, “ketohexokinase,” used interchangeably with the term “KHK,” refers to the naturally occurring gene that encodes an enzyme that catalyzes conversion of fructose to fructose-1-phosphate. The product of this gene is the first enzyme in the pathway that catabolizes dietary fructose. Alternatively spliced transcript variants encoding different isoforms have been identified.

The gene is also known as fructokinase.

Exemplary nucleotide and amino acid sequences of KHK can be found, for example, at GenBank Accession No. XM_017004061.1 (Homo sapiens KHK; SEQ ID NO:1; reverse complement, SEQ ID NO:2); NM_006488.3 (Homo sapiens KHK; SEQ ID NO:3; reverse complement, SEQ ID NO:4); NM_000221.3 (Homo sapiens KHK; SEQ ID NO:5; reverse complement, SEQ ID NO:6); GenBank Accession No. NM_001310524.1 (Mus musculus KHK; SEQ ID NO:7; reverse complement, SEQ ID NO:8); GenBank Accession No. NM_031855.3 (Rattus norvegicus KHK; SEQ ID NO:9; reverse complement, SEQ ID NO:10); GenBank Accession No. XM_005576322.2 (Macaca fascicularis KHK, SEQ ID NO:11; reverse complement, SEQ ID NO:12).

The KHK (Ketohexokinase) gene is located on chromosome 2p23 and encodes ketohexokinase, also known as fructokinase. KHK is a phosphotransferase enzyme with an alcohol as the phosphate acceptor. KHK belongs to the ribokinase family of carbohydrate kinases (Trinh *et al.*, *ACTA Cryst.*, D65: 201-211). Two isoforms of ketohexokinase have been identified, KHK-A and

KHK-C, that result from alternative splicing of the full length mRNA. These isoforms differ by inclusion of either exon 3a or 3c, and differ by 32 amino acids between positions 72 and 115. KHK-C mRNA is expressed at high levels, predominantly in the liver, kidney and small intestine. KHK-C has a much lower K_m for fructose binding than KHK-A, and as a result, is highly effective in phosphorylating dietary fructose. The sequence of a human KHK-C mRNA transcript may be found at, for example, GenBank Accession No. NM_006488.3 (Homo sapiens KHK; SEQ ID NO:3). The sequence of a human KHK-A mRNA transcript may be found at, for example GenBank Accession No. NM_000221.3; SEQ ID NO:5). The sequence of full-length human KHK mRNA is provided in GenBank Accession No. GI: XM_017004061.1 (SEQ ID NO:1).

10 The iRNA agents provided herein can be capable of silencing one or both KHK isoforms.

Additional examples of KHK mRNA sequences are readily available through publicly available databases, *e.g.*, GenBank, UniProt, OMIM, and the Macaca genome project web site.

Further information on KHK can be found, for example, at www.ncbi.nlm.nih.gov/gene/?term=khk.

15 The entire contents of each of the foregoing GenBank Accession numbers and the Gene database numbers are incorporated herein by reference as of the date of filing this application.

The term KHK, as used herein, also refers to variations of the KHK gene including variants provided in the SNP database. Numerous sequence variations within the KHK gene have been identified and may be found at, for example, NCBI dbSNP and UniProt (see, *e.g.*,

20 www.ncbi.nlm.nih.gov/snp/?term=KHK, the entire contents of which is incorporated herein by reference as of the date of filing this application.

As used herein, “target sequence” refers to a contiguous portion of the nucleotide sequence of an mRNA molecule formed during the transcription of a KHK gene, including mRNA that is a product of RNA processing of a primary transcription product. The target portion of the sequence will be at least long enough to serve as a substrate for iRNA-directed cleavage at or near that portion of the nucleotide sequence of an mRNA molecule formed during the transcription of a KHK gene. In one embodiment, the target sequence is within the protein coding region of KHK.

The target sequence may be from about 19-36 nucleotides in length, *e.g.*, about 19-30 nucleotides in length. For example, the target sequence can be about 19-30 nucleotides, 19-30, 19-29, 19-28, 19-27, 19-26, 19-25, 19-24, 19-23, 19-22, 19-21, 19-20, 20-30, 20-29, 20-28, 20-27, 20-26, 20-25, 20-24, 20-23, 20-22, 20-21, 21-30, 21-29, 21-28, 21-27, 21-26, 21-25, 21-24, 21-23, or 21-22 nucleotides in length. In certain embodiments, the target sequence is 19-23 nucleotides in length, optionally 21-23 nucleotides in length. Ranges and lengths intermediate to the above recited ranges and lengths are also contemplated to be part of the disclosure.

35 As used herein, the term “strand comprising a sequence” refers to an oligonucleotide comprising a chain of nucleotides that is described by the sequence referred to using the standard nucleotide nomenclature.

“G,” “C,” “A,” “T,” and “U” each generally stand for a nucleotide that contains guanine, cytosine, adenine, thymidine, and uracil as a base, respectively. However, it will be understood that the term “ribonucleotide” or “nucleotide” can also refer to a modified nucleotide, as further detailed below, or a surrogate replacement moiety (see, *e.g.*, Table 1). The skilled person is well aware that

5 guanine, cytosine, adenine, and uracil can be replaced by other moieties without substantially altering the base pairing properties of an oligonucleotide comprising a nucleotide bearing such replacement moiety. For example, without limitation, a nucleotide comprising inosine as its base can base pair with nucleotides containing adenine, cytosine, or uracil. Hence, nucleotides containing uracil, guanine, or adenine can be replaced in the nucleotide sequences of dsRNA featured in the invention

10 by a nucleotide containing, for example, inosine. In another example, adenine and cytosine anywhere in the oligonucleotide can be replaced with guanine and uracil, respectively to form G-U Wobble base pairing with the target mRNA. Sequences containing such replacement moieties are suitable for the compositions and methods featured in the invention.

The terms “iRNA”, “RNAi agent,” “iRNA agent,” “RNA interference agent” as used

15 interchangeably herein, refer to an agent that contains RNA as that term is defined herein, and which mediates the targeted cleavage of an RNA transcript *via* an RNA-induced silencing complex (RISC) pathway. iRNA directs the sequence-specific degradation of mRNA through a process known as RNA interference (RNAi). The iRNA modulates, *e.g.*, inhibits, the expression of a KHK gene in a cell, *e.g.*, a cell within a subject, such as a mammalian subject.

20 In one embodiment, an RNAi agent of the invention includes a single stranded RNA that interacts with a target RNA sequence, *e.g.*, a KHK target mRNA sequence, to direct the cleavage of the target RNA. Without wishing to be bound by theory it is believed that long double stranded RNA introduced into cells is broken down into siRNA by a Type III endonuclease known as Dicer (Sharp *et al.* (2001) *Genes Dev.* 15:485). Dicer, a ribonuclease-III-like enzyme, processes the dsRNA into 19-

25 23 base pair short interfering RNAs with characteristic two base 3' overhangs (Bernstein, *et al.*, (2001) *Nature* 409:363). The siRNAs are then incorporated into an RNA-induced silencing complex (RISC) where one or more helicases unwind the siRNA duplex, enabling the complementary antisense strand to guide target recognition (Nykanen, *et al.*, (2001) *Cell* 107:309). Upon binding to the appropriate target mRNA, one or more endonucleases within the RISC cleave the target to induce

30 silencing (Elbashir, *et al.*, (2001) *Genes Dev.* 15:188). Thus, in one aspect the invention relates to a single stranded RNA (siRNA) generated within a cell and which promotes the formation of a RISC complex to effect silencing of the target gene, *i.e.*, a KHK gene. Accordingly, the term “siRNA” is also used herein to refer to an iRNA as described above.

In certain embodiments, the RNAi agent may be a single-stranded siRNA (ssRNAi) that is

35 introduced into a cell or organism to inhibit a target mRNA. Single-stranded RNAi agents bind to the RISC endonuclease, Argonaute 2, which then cleaves the target mRNA. The single-stranded siRNAs are generally 15-30 nucleotides and are chemically modified. The design and testing of single-stranded siRNAs are described in U.S. Patent No. 8,101,348 and in Lima *et al.*, (2012) *Cell* 150:883-

894, the entire contents of each of which are hereby incorporated herein by reference. Any of the antisense nucleotide sequences described herein may be used as a single-stranded siRNA as described herein or as chemically modified by the methods described in Lima *et al.*, (2012) *Cell* 150:883-894.

In certain embodiments, an “iRNA” for use in the compositions, uses, and methods of the invention is a double stranded RNA and is referred to herein as a “double stranded RNA agent,” “double stranded RNA (dsRNA) molecule,” “dsRNA agent,” or “dsRNA”. The term “dsRNA”, refers to a complex of ribonucleic acid molecules, having a duplex structure comprising two anti-parallel and substantially complementary nucleic acid strands, referred to as having “sense” and “antisense” orientations with respect to a target RNA, *i.e.*, a KHK gene. In some embodiments of the invention, a double stranded RNA (dsRNA) triggers the degradation of a target RNA, *e.g.*, an mRNA, through a post-transcriptional gene-silencing mechanism referred to herein as RNA interference or RNAi.

In general, the majority of nucleotides of each strand of a dsRNA molecule are ribonucleotides, but as described in detail herein, each or both strands can also include one or more non-ribonucleotides, *e.g.*, a deoxyribonucleotide or a modified nucleotide. In addition, as used in this specification, an “iRNA” may include ribonucleotides with chemical modifications; an iRNA may include substantial modifications at multiple nucleotides. As used herein, the term “modified nucleotide” refers to a nucleotide having, independently, a modified sugar moiety, a modified internucleotide linkage, or modified nucleobase, or any combination thereof. Thus, the term modified nucleotide encompasses substitutions, additions or removal of, *e.g.*, a functional group or atom, to internucleoside linkages, sugar moieties, or nucleobases. The modifications suitable for use in the agents of the invention include all types of modifications disclosed herein or known in the art. Any such modifications, as used in a siRNA type molecule, are encompassed by “iRNA” or “RNAi agent” for the purposes of this specification and claims.

In certain embodiments of the instant disclosure, inclusion of a deoxy-nucleotide if present within an RNAi agent can be considered to constitute a modified nucleotide.

The duplex region may be of any length that permits specific degradation of a desired target RNA through a RISC pathway, and may range from about 19 to 36 base pairs in length, *e.g.*, about 19-30 base pairs in length, for example, about 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, or 36 base pairs in length, such as about 19-30, 19-29, 19-28, 19-27, 19-26, 19-25, 19-24, 19-23, 19-22, 19-21, 19-20, 20-30, 20-29, 20-28, 20-27, 20-26, 20-25, 20-24, 20-23, 20-22, 20-21, 21-30, 21-29, 21-28, 21-27, 21-26, 21-25, 21-24, 21-23, or 21-22 base pairs in length. In certain embodiments, the duplex region is 19-21 base pairs in length, *e.g.*, 21 base pairs in length. Ranges and lengths intermediate to the above recited ranges and lengths are also contemplated to be part of the disclosure.

The two strands forming the duplex structure may be different portions of one larger RNA molecule, or they may be separate RNA molecules. Where the two strands are part of one larger molecule, and therefore are connected by an uninterrupted chain of nucleotides between the 3'-end of one strand and the 5'-end of the respective other strand forming the duplex structure, the connecting

RNA chain is referred to as a “hairpin loop.” A hairpin loop can comprise at least one unpaired nucleotide. In some embodiments, the hairpin loop can comprise at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 23 or more unpaired nucleotides. In some embodiments, the hairpin loop can be 10 or fewer nucleotides. In some embodiments, the hairpin loop can be 8 or fewer unpaired nucleotides. In some
5 embodiments, the hairpin loop can be 4-10 unpaired nucleotides. In some embodiments, the hairpin loop can be 4-8 nucleotides.

Where the two substantially complementary strands of a dsRNA are comprised by separate RNA molecules, those molecules need not be, but can be covalently connected. Where the two strands are connected covalently by means other than an uninterrupted chain of nucleotides between
10 the 3'-end of one strand and the 5'-end of the respective other strand forming the duplex structure, the connecting structure is referred to as a “linker.” The RNA strands may have the same or a different number of nucleotides. The maximum number of base pairs is the number of nucleotides in the shortest strand of the dsRNA minus any overhangs that are present in the duplex. In addition to the duplex structure, an RNAi may comprise one or more nucleotide overhangs. In one embodiment of
15 the RNAi agent, at least one strand comprises a 3' overhang of at least 1 nucleotide. In another embodiment, at least one strand comprises a 3' overhang of at least 2 nucleotides, *e.g.*, 2, 3, 4, 5, 6, 7, 9, 10, 11, 12, 13, 14, or 15 nucleotides. In other embodiments, at least one strand of the RNAi agent comprises a 5' overhang of at least 1 nucleotide. In certain embodiments, at least one strand
20 comprises a 5' overhang of at least 2 nucleotides, *e.g.*, 2, 3, 4, 5, 6, 7, 9, 10, 11, 12, 13, 14, or 15 nucleotides. In still other embodiments, both the 3' and the 5' end of one strand of the RNAi agent comprise an overhang of at least 1 nucleotide.

In certain embodiments, an iRNA agent of the invention is a dsRNA, each strand of which comprises 19-23 nucleotides, that interacts with a target RNA sequence, *e.g.*, a KHK gene, to direct cleavage of the target RNA.

25 In some embodiments, an iRNA of the invention is a dsRNA of 24-30 nucleotides that interacts with a target RNA sequence, *e.g.*, a KHK target mRNA sequence, to direct the cleavage of the target RNA.

As used herein, the term “nucleotide overhang” refers to at least one unpaired nucleotide that protrudes from the duplex structure of a double stranded iRNA. For example, when a 3'-end of one
30 strand of a dsRNA extends beyond the 5'-end of the other strand, or *vice versa*, there is a nucleotide overhang. A dsRNA can comprise an overhang of at least one nucleotide; alternatively the overhang can comprise at least two nucleotides, at least three nucleotides, at least four nucleotides, at least five nucleotides or more. A nucleotide overhang can comprise or consist of a nucleotide/nucleoside analog, including a deoxynucleotide/nucleoside. The overhang(s) can be on the sense strand, the
35 antisense strand, or any combination thereof. Furthermore, the nucleotide(s) of an overhang can be present on the 5'-end, 3'-end, or both ends of either an antisense or sense strand of a dsRNA.

In one embodiment, the antisense strand of a dsRNA has a 1-10 nucleotide, *e.g.*, a 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 nucleotide, overhang at the 3'-end or the 5'-end. In one embodiment, the sense

strand of a dsRNA has a 1-10 nucleotide, *e.g.*, a 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 nucleotide, overhang at the 3'-end or the 5'-end. In another embodiment, one or more of the nucleotides in the overhang is replaced with a nucleoside thiophosphate.

In certain embodiments, the antisense strand of a dsRNA has a 1-10 nucleotide, *e.g.*, 0-3, 1-3, 2-4, 2-5, 4-10, 5-10, *e.g.*, a 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 nucleotide, overhang at the 3'-end or the 5'-end. In one embodiment, the sense strand of a dsRNA has a 1-10 nucleotide, *e.g.*, a 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 nucleotide, overhang at the 3'-end or the 5'-end. In another embodiment, one or more of the nucleotides in the overhang is replaced with a nucleoside thiophosphate.

In certain embodiments, the antisense strand of a dsRNA has a 1-10 nucleotides, *e.g.*, a 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 nucleotide, overhang at the 3'-end or the 5'-end. In certain embodiments, the overhang on the sense strand or the antisense strand, or both, can include extended lengths longer than 10 nucleotides, *e.g.*, 1-30 nucleotides, 2-30 nucleotides, 10-30 nucleotides, 10-25 nucleotides, 10-20 nucleotides, or 10-15 nucleotides in length. In certain embodiments, an extended overhang is on the sense strand of the duplex. In certain embodiments, an extended overhang is present on the 3' end of the sense strand of the duplex. In certain embodiments, an extended overhang is present on the 5' end of the sense strand of the duplex. In certain embodiments, an extended overhang is on the antisense strand of the duplex. In certain embodiments, an extended overhang is present on the 3' end of the antisense strand of the duplex. In certain embodiments, an extended overhang is present on the 5' end of the antisense strand of the duplex. In certain embodiments, one or more of the nucleotides in the extended overhang is replaced with a nucleoside thiophosphate. In certain embodiments, the overhang includes a self-complementary portion such that the overhang is capable of forming a hairpin structure that is stable under physiological conditions.

"Blunt" or "blunt end" means that there are no unpaired nucleotides at that end of the double stranded RNA agent, *i.e.*, no nucleotide overhang. A "blunt ended" double stranded RNA agent is double stranded over its entire length, *i.e.*, no nucleotide overhang at either end of the molecule. The RNAi agents of the invention include RNAi agents with no nucleotide overhang at one end (*i.e.*, agents with one overhang and one blunt end) or with no nucleotide overhangs at either end. Most often such a molecule will be double-stranded over its entire length.

The term "antisense strand" or "guide strand" refers to the strand of an iRNA, *e.g.*, a dsRNA, which includes a region that is substantially complementary to a target sequence, *e.g.*, a KHK mRNA.

As used herein, the term "region of complementarity" refers to the region on the antisense strand that is substantially complementary to a sequence, for example a target sequence, *e.g.*, a KHK nucleotide sequence, as defined herein. Where the region of complementarity is not fully complementary to the target sequence, the mismatches can be in the internal or terminal regions of the molecule. Generally, the most tolerated mismatches are in the terminal regions, *e.g.*, within 5, 4, or 3 nucleotides of the 5'- or 3'-end of the iRNA. In some embodiments, a double stranded RNA agent of the invention includes a nucleotide mismatch in the antisense strand. In some embodiments, the antisense strand of the double stranded RNA agent of the invention includes no more than 4

mismatches with the target mRNA, *e.g.*, the antisense strand includes 4, 3, 2, 1, or 0 mismatches with the target mRNA. In some embodiments, the antisense strand double stranded RNA agent of the invention includes no more than 4 mismatches with the sense strand, *e.g.*, the antisense strand includes 4, 3, 2, 1, or 0 mismatches with the sense strand. In some embodiments, a double stranded

5 RNA agent of the invention includes a nucleotide mismatch in the sense strand. In some embodiments, the sense strand of the double stranded RNA agent of the invention includes no more than 4 mismatches with the antisense strand, *e.g.*, the sense strand includes 4, 3, 2, 1, or 0 mismatches with the antisense strand. In some embodiments, the nucleotide mismatch is, for example, within 5, 4, 3 nucleotides from the 3'-end of the iRNA. In another embodiment, the nucleotide mismatch is, for

10 example, in the 3'-terminal nucleotide of the iRNA agent. In some embodiments, the mismatch(s) is not in the seed region.

Thus, an RNAi agent as described herein can contain one or more mismatches to the target sequence. In one embodiment, an RNAi agent as described herein contains no more than 3 mismatches (*i.e.*, 3, 2, 1, or 0 mismatches). In one embodiment, an RNAi agent as described herein

15 contains no more than 2 mismatches. In one embodiment, an RNAi agent as described herein contains no more than 1 mismatch. In one embodiment, an RNAi agent as described herein contains 0 mismatches. In certain embodiments, if the antisense strand of the RNAi agent contains mismatches to the target sequence, the mismatch can optionally be restricted to be within the last 5 nucleotides from either the 5'- or 3'-end of the region of complementarity. For example, in such embodiments, for

20 a 23 nucleotide RNAi agent, the strand which is complementary to a region of a KHK gene, generally does not contain any mismatch within the central 13 nucleotides. The methods described herein or methods known in the art can be used to determine whether an RNAi agent containing a mismatch to a target sequence is effective in inhibiting the expression of a KHK gene. Consideration of the efficacy of RNAi agents with mismatches in inhibiting expression of a KHK gene is important,

25 especially if the particular region of complementarity in a KHK gene is known to have polymorphic sequence variation within the population.

The term "sense strand" or "passenger strand" as used herein, refers to the strand of an iRNA that includes a region that is substantially complementary to a region of the antisense strand as that term is defined herein.

30 As used herein, "substantially all of the nucleotides are modified" are largely but not wholly modified and can include not more than 5, 4, 3, 2, or 1 unmodified nucleotides.

As used herein, the term "cleavage region" refers to a region that is located immediately adjacent to the cleavage site. The cleavage site is the site on the target at which cleavage occurs. In some embodiments, the cleavage region comprises three bases on either end of, and immediately

35 adjacent to, the cleavage site. In some embodiments, the cleavage region comprises two bases on either end of, and immediately adjacent to, the cleavage site. In some embodiments, the cleavage site specifically occurs at the site bound by nucleotides 10 and 11 of the antisense strand, and the cleavage region comprises nucleotides 11, 12 and 13.

As used herein, and unless otherwise indicated, the term “complementary,” when used to describe a first nucleotide sequence in relation to a second nucleotide sequence, refers to the ability of an oligonucleotide or polynucleotide comprising the first nucleotide sequence to hybridize and form a duplex structure under certain conditions with an oligonucleotide or polynucleotide comprising the second nucleotide sequence, as will be understood by the skilled person. Such conditions can, for example, be stringent conditions, where stringent conditions can include: 400 mM NaCl, 40 mM PIPES pH 6.4, 1 mM EDTA, 50°C or 70°C for 12-16 hours followed by washing (see, *e.g.*, “Molecular Cloning: A Laboratory Manual, Sambrook, *et al.* (1989) Cold Spring Harbor Laboratory Press). Such conditions can be, for example, “stringent conditions”, where stringent conditions can include: 400 mM NaCl, 40 mM PIPES pH 6.4, 1 mM EDTA, 50 oC or 70 oC for 12-16 hours followed by washing (see, *e.g.*, “Molecular Cloning: A Laboratory Manual, Sambrook, *et al.* (1989) Cold Spring Harbor Laboratory Press). Other conditions, such as physiologically relevant conditions as can be encountered inside an organism, can apply. The skilled person will be able to determine the set of conditions most appropriate for a test of complementarity of two sequences in accordance with the ultimate application of the hybridized nucleotides.

Complementary sequences within an iRNA, *e.g.*, within a dsRNA as described herein, include base-pairing of the oligonucleotide or polynucleotide comprising a first nucleotide sequence to an oligonucleotide or polynucleotide comprising a second nucleotide sequence over the entire length of one or both nucleotide sequences. Such sequences can be referred to as “fully complementary” with respect to each other herein. However, where a first sequence is referred to as “substantially complementary” with respect to a second sequence herein, the two sequences can be fully complementary, or they can form one or more, but generally not more than 5, 4, 3, or 2 mismatched base pairs upon hybridization for a duplex up to 30 base pairs, while retaining the ability to hybridize under the conditions most relevant to their ultimate application, *e.g.*, inhibition of gene expression, in vitro or in vivo. However, where two oligonucleotides are designed to form, upon hybridization, one or more single stranded overhangs, such overhangs shall not be regarded as mismatches with regard to the determination of complementarity. For example, a dsRNA comprising one oligonucleotide 21 nucleotides in length and another oligonucleotide 23 nucleotides in length, wherein the longer oligonucleotide comprises a sequence of 21 nucleotides that is fully complementary to the shorter oligonucleotide, can yet be referred to as “fully complementary” for the purposes described herein.

“Complementary” sequences, as used herein, can also include, or be formed entirely from, non-Watson-Crick base pairs or base pairs formed from non-natural and modified nucleotides, in so far as the above requirements with respect to their ability to hybridize are fulfilled. Such non-Watson-Crick base pairs include, but are not limited to, G:U Wobble or Hoogsteen base pairing.

The terms “complementary,” “fully complementary” and “substantially complementary” herein can be used with respect to the base matching between the sense strand and the antisense strand of a dsRNA, or between two oligonucleotides or polynucleotides, such as the antisense strand of a double stranded RNA agent and a target sequence, as will be understood from the context of their use.

As used herein, a polynucleotide that is “substantially complementary to at least part of” a messenger RNA (mRNA) refers to a polynucleotide that is substantially complementary to a contiguous portion of the mRNA of interest (*e.g.*, an mRNA encoding a KHK gene). For example, a polynucleotide is complementary to at least a part of a KHK mRNA if the sequence is substantially
5 complementary to a non-interrupted portion of an mRNA encoding a KHK gene.

Accordingly, in some embodiments, the antisense polynucleotides disclosed herein are fully complementary to the target KHK sequence. In other embodiments, the antisense polynucleotides disclosed herein are substantially complementary to the target KHK sequence and comprise a contiguous nucleotide sequence which is at least 80% complementary over its entire length to the
10 equivalent region of the nucleotide sequence of any one of SEQ ID NOs:1, 3, 5, 7, 9, or 11, or a fragment of any one of SEQ ID NOs:1, 3, 5, 7, 9, or 11, such as about 85%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, or about 99% complementary.

In some embodiments, the antisense polynucleotides disclosed herein are substantially
15 complementary to a fragment of a target KHK sequence and comprise a contiguous nucleotide sequence which is at least 80% complementary over its entire length to a fragment of SEQ ID NO: 1 selected from the group of nucleotides 120-162; 164-188; 181-207; 193-217; 209-231; 283-306; 508-546; 568-603; 596-632; 640-674; 746-806; 806-835; 917-942; 936-084; 1016-1041; 1100-1123; 1149-1175; 1160-1193; 1205-1229; 1252-1283; 1334-1356; 1407-1429; 1472-1497; 1506-1533;
20 1539-1561; 1704-1727; 1747-1787; 1850-1873; 1936-1964; 1960-1990; 2015-2048; 2060-2095; 2090-2118; 2124-2160; 2181-2200; 2221-2262 of SEQ ID NO: 1, such as about 85%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, or about 99% complementary.

In some embodiments, the antisense polynucleotides disclosed herein are substantially
25 complementary to a fragment of a target KHK sequence and comprise a contiguous nucleotide sequence which is at least 80% complementary over its entire length to a fragment of SEQ ID NO: 1 selected from the group of nucleotides 517-539; 521-543; 524-546; 517-546; 581-603; 610-632; 747-769; 749-771; 752-774; 755-777; 757-779; 758-780; 764-786; 776-798; 781-803; 747-803; 920-942; 941-963; 944-966; 950-972; 962-984; 920-984; 1149-1171; 1161-1183; 1165-1187; 1171-1193;
30 1149-1193; 1205-1227; 1206-1228; 1205-1228; 1334-1356; 1472-1494; 1475-1497; 1472-1497 of SEQ ID NO: 1, such as about 85%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, or about 99% complementary.

In some embodiments, the antisense polynucleotides disclosed herein are substantially
complementary to a fragment of a target KHK sequence and comprise a contiguous nucleotide
35 sequence which is at least 80% complementary over its entire length to a fragment of SEQ ID NO: 1 selected from the group of nucleotides 517-539; 524-546; 517-546; 753-775; 757-779; 753-779; 764-786; 767-789; 768-790; 769-791; 764-791; 773-795; 781-803; 773-803; 753-803; 808-830; 937-959; 941-963; 944-966; 941-966; 948-970; 950-972; 948-972; 1160-1182; 1161-1183; 1160-1183; and

1207-1229 of SEQ ID NO: 1, such as about 85%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, or about 99% complementary.

In some embodiments, the antisense polynucleotides disclosed herein are substantially complementary to a fragment of a target KHK sequence and comprise a contiguous nucleotide sequence which is at least 80% complementary over its entire length to a fragment of SEQ ID NO: 1 selected from the group of nucleotides 495-517, 492-517, 500-529, 514-551, 517-539, 524-546, 517-548, 614-643, 625-647, 625-660, 642-664, 642-672, 753-811, 754-780, 762-791, 764-786, 772-800, 781-803, 805-827, 808-830, 809-831, 792-838, 931-982, 944-966, 947-969, 948-970, 948-982, 1011-1035, 1021-1043, 1019-1050, 1063-1091, 1150-1192, 1152-1176, 1160-1192, 1160-1182, 1162-1184, 1198-1230, 1198-1221, and 1202-1230 of SEQ ID NO: 1, such as about 85%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, or about 99% complementary.

In some embodiments, the antisense polynucleotides disclosed herein are substantially complementary to a fragment of a target KHK sequence and comprise a contiguous nucleotide sequence which is at least 80% complementary over its entire length to a fragment of SEQ ID NO: 1 selected from the group of nucleotides 513-556, 753-813, 936-981, 1155-1193, 1200-1229, 1704-1727, 1747-1787, 1850-1873, 1936-1964, 1960-1990, 1936-1990, 2015-2048, 2060-2095, 2090-2118, 2060-2118, 2124-2160, 2181-2220, 2221-2249, 2181-2249, 2240-2262, 2221-2262, and 2181-2262 of SEQ ID NO: 1, such as about 85%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, or about 99% complementary.

In other embodiments, the antisense polynucleotides disclosed herein are substantially complementary to the target KHK sequence and comprise a contiguous nucleotide sequence which is at least about 80% complementary over its entire length to any one of the sense strand nucleotide sequences in any one of any one of Tables 2, 3, 5, 6, and 8-13, or a fragment of any one of the sense strand nucleotide sequences in any one of Tables 2, 3, 5, 6, and 8-13, such as about 85%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or 100% complementary.

In one embodiment, an RNAi agent of the disclosure includes a sense strand that is substantially complementary to an antisense polynucleotide which, in turn, is the same as a target KHK sequence, and wherein the sense strand polynucleotide comprises a contiguous nucleotide sequence which is at least about 80% complementary over its entire length to the equivalent region of the nucleotide sequence of SEQ ID NOs: 2, 4, 6, 8, 10, or 12, or a fragment of any one of SEQ ID NOs: 2, 4, 6, 8, 10, or 12, such as about 85%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or 100% complementary.

In some embodiments, an iRNA of the invention includes a sense strand that is substantially complementary to an antisense polynucleotide which, in turn, is complementary to a target KHK sequence, and wherein the sense strand polynucleotide comprises a contiguous nucleotide sequence which is at least about 80% complementary over its entire length to any one of the antisense strand

nucleotide sequences in any one of any one of Tables 2, 3, 5, 6, and 8-13, or a fragment of any one of the antisense strand nucleotide sequences in any one of Tables 2, 3, 5, 6, and 8-13, such as about 85%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or 100% complementary.

5 In certain embodiments, the sense and antisense strands are selected from any one of duplexes AD-1613400; AD-1613243; AD-1290757.3; AD-1290878.3; AD-1290969.3; AD-1423317.2; AD-1423327.2; AD-1423336.2; AD-1290599.3; AD-1523172.1; AD-1290837.3; AD-1523173.1; AD-1290884.3; AD-1523174.1; AD-1290959.3; AD-1523175.1; AD-1423311.2; AD-1423324.2; AD-1523176.1; AD-1423329.2; AD-1423333.2; AD-1423330.2; AD-1523177.1; AD-1290885.3; AD-1523178.1; AD-1423334.2; AD-1523179.1; AD-1523180.1; AD-1290539.3; and
10 AD-1523181.1.

In general, an “iRNA” includes ribonucleotides with chemical modifications. Such modifications may include all types of modifications disclosed herein or known in the art. Any such modifications, as used in a dsRNA molecule, are encompassed by “iRNA” for the purposes of this
15 specification and claims.

In certain embodiments of the instant disclosure, inclusion of a deoxy-nucleotide if present within an RNAi agent can be considered to constitute a modified nucleotide.

In an aspect of the invention, an agent for use in the methods and compositions of the invention is a single-stranded antisense oligonucleotide molecule that inhibits a target mRNA *via* an
20 antisense inhibition mechanism. The single-stranded antisense oligonucleotide molecule is complementary to a sequence within the target mRNA. The single-stranded antisense oligonucleotides can inhibit translation in a stoichiometric manner by base pairing to the mRNA and physically obstructing the translation machinery, see Dias, N. *et al.*, (2002) *Mol Cancer Ther* 1:347-355. The single-stranded antisense oligonucleotide molecule may be about 14 to about 30 nucleotides
25 in length and have a sequence that is complementary to a target sequence. For example, the single-stranded antisense oligonucleotide molecule may comprise a sequence that is at least about 14, 15, 16, 17, 18, 19, 20, or more contiguous nucleotides from any one of the antisense sequences described herein.

The phrase “contacting a cell with an iRNA,” such as a dsRNA, as used herein, includes
30 contacting a cell by any possible means. Contacting a cell with an iRNA includes contacting a cell *in vitro* with the iRNA or contacting a cell *in vivo* with the iRNA. The contacting may be done directly or indirectly. Thus, for example, the iRNA may be put into physical contact with the cell by the individual performing the method, or alternatively, the iRNA may be put into a situation that will permit or cause it to subsequently come into contact with the cell.

35 Contacting a cell *in vitro* may be done, for example, by incubating the cell with the iRNA. Contacting a cell *in vivo* may be done, for example, by injecting the iRNA into or near the tissue where the cell is located, or by injecting the iRNA into another area, *e.g.*, the bloodstream or the subcutaneous space, such that the agent will subsequently reach the tissue where the cell to be

contacted is located. For example, the iRNA may contain or be coupled to a ligand, *e.g.*, GalNAc, that directs the iRNA to a site of interest, *e.g.*, the liver. Combinations of *in vitro* and *in vivo* methods of contacting are also possible. For example, a cell may also be contacted *in vitro* with an iRNA and subsequently transplanted into a subject.

5 In certain embodiments, contacting a cell with an iRNA includes “introducing” or “delivering the iRNA into the cell” by facilitating or effecting uptake or absorption into the cell. Absorption or uptake of an iRNA can occur through unaided diffusion or active cellular processes, or by auxiliary agents or devices. Introducing an iRNA into a cell may be *in vitro* or *in vivo*. For example, for *in vivo* introduction, iRNA can be injected into a tissue site or administered systemically. *In vitro* introduction into a cell includes methods known in the art such as electroporation and lipofection. Further approaches are described herein below or are known in the art.

10 The term “lipid nanoparticle” or “LNP” is a vesicle comprising a lipid layer encapsulating a pharmaceutically active molecule, such as a nucleic acid molecule, *e.g.*, an iRNA or a plasmid from which an iRNA is transcribed. LNPs are described in, for example, U.S. Patent Nos. 6,858,225, 15 6,815,432, 8,158,601, and 8,058,069, the entire contents of which are hereby incorporated herein by reference.

 As used herein, a “subject” is an animal, such as a mammal, including a primate (such as a human, a non-human primate, *e.g.*, a monkey, and a chimpanzee), a non-primate (such as a cow, a pig, a horse, a goat, a rabbit, a sheep, a hamster, a guinea pig, a cat, a dog, a rat, or a mouse), or a bird 20 that expresses the target gene, either endogenously or heterologously. In an embodiment, the subject is a human, such as a human being treated or assessed for a disease or disorder that would benefit from reduction in KHK expression; a human at risk for a disease or disorder that would benefit from reduction in KHK expression; a human having a disease or disorder that would benefit from reduction in KHK expression; or human being treated for a disease or disorder that would benefit from 25 reduction in KHK expression as described herein. In some embodiments, the subject is a female human. In other embodiments, the subject is a male human. In one embodiment, the subject is an adult subject. In another embodiment, the subject is a pediatric subject.

 As used herein, the terms “treating” or “treatment” refer to a beneficial or desired result, such as reducing at least one sign or symptom of a KHK-associated disorder in a subject. Treatment also 30 includes a reduction of one or more sign or symptoms associated with unwanted KHK expression; diminishing the extent of unwanted KHK activation or stabilization; amelioration or palliation of unwanted KHK activation or stabilization. “Treatment” can also mean prolonging survival as compared to expected survival in the absence of treatment. The term “lower” in the context of the level of KHK in a subject or a disease marker or symptom refers to a statistically significant decrease in 35 such level. The decrease can be, for example, at least 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more. In certain embodiments, a decrease is at least 20%. In certain embodiments, the decrease is at least 50% in a disease marker, *e.g.*, protein or gene expression level. “Lower” in the context of the level of KHK in a subject is a

decrease to a level accepted as within the range of normal for an individual without such disorder. In certain embodiments, “lower” is the decrease in the difference between the level of a marker or symptom for a subject suffering from a disease and a level accepted within the range of normal for an individual, *e.g.*, the level of decrease in bodyweight between an obese individual and an individual

5 having a weight accepted within the range of normal.

As used herein, “prevention” or “preventing,” when used in reference to a disease, disorder or condition thereof, may be treated or ameliorated by a reduction in expression of a KHK gene, refers to a reduction in the likelihood that a subject will develop a symptom associated with such a disease, disorder, or condition, *e.g.*, a symptom of unwanted or excessive KHK expression and/or activity, *e.g.*, increased fructose metabolism, elevated uric acid and lipid levels. Without being bound by mechanism, it is known that fructose phosphorylation catalyzed by KHK to form fructose-1-phosphate is not regulated by feedback inhibition which can result in depletion of ATP and intracellular phosphate, and increased AMP levels, which results in the production of uric acid. Further, the fructose-1-phosphate is metabolized to glyceraldehyde which feeds into the citric acid cycle increasing the production of acetyl Co-A stimulating fatty acid synthesis. Diseases and conditions associated with elevated uric acid and fatty acid synthesis include, *e.g.*, liver disease (*e.g.*, fatty liver, steatohepatitis including non-alcoholic steatohepatitis (NASH)), dyslipidemia (*e.g.*, hyperlipidemia, high LDL cholesterol, low HDL cholesterol, hypertriglyceridemia, postprandial hypertriglyceridemia), disorders of glycemic control (*e.g.*, insulin resistance not related to immune response to insulin, type 2 diabetes), cardiovascular disease (*e.g.*, hypertension, endothelial cell dysfunction), kidney disease (*e.g.*, acute kidney disorder, tubular dysfunction, proinflammatory changes to the proximal tubules, chronic kidney disease), metabolic syndrome, disease of lipid deposition or dysfunction (*e.g.*, adipocyte dysfunction, visceral adipose deposition, obesity), disease of elevated uric acid (*e.g.*, hyperuricemia, gout), and eating disorders such as excessive sugar craving.

25 The failure to develop a disease, disorder or condition, or the reduction in the development of a symptom or comorbidity associated with such a disease, disorder or condition (*e.g.*, by at least about 10% on a clinically accepted scale for that disease or disorder), or the exhibition of delayed signs or symptoms or disease progression by days, weeks, months or years is considered effective prevention.

As used herein, the term “ketoheokinase (KHK)-associated disease” or “KHK-associated disorder,” is a disease or disorder that is caused by, or associated with KHK gene expression or KHK protein production. The term “KHK-associated disease” includes a disease, disorder or condition that would benefit from a decrease in KHK gene expression, replication, or protein activity. Non-limiting examples of KHK-associated diseases include, for example, liver disease (*e.g.*, fatty liver, steatohepatitis including non-alcoholic steatohepatitis (NASH)), dyslipidemia (*e.g.*, hyperlipidemia, high LDL cholesterol, low HDL cholesterol, hypertriglyceridemia, postprandial hypertriglyceridemia), disorders of glycemic control (*e.g.*, insulin resistance not related to immune response to insulin, type 2 diabetes), cardiovascular disease (*e.g.*, hypertension, endothelial cell dysfunction), kidney disease (*e.g.*, acute kidney disorder, tubular dysfunction, proinflammatory

changes to the proximal tubules, chronic kidney disease), metabolic syndrome, disease of lipid deposition or dysfunction (*e.g.*, adipocyte dysfunction, visceral adipose deposition, obesity), disease of elevated uric acid (*e.g.*, hyperuricemia, gout), and eating disorders such as excessive sugar craving.

In certain embodiments, a KHK-associated disease is associated with elevated uric acid (*e.g.* hyperuricemia, gout).

In certain embodiments, a KHK-associated disease is associated with elevated lipid levels (*e.g.*, fatty liver, steatohepatitis including non-alcoholic steatohepatitis (NASH), dyslipidemia).

"Therapeutically effective amount," as used herein, is intended to include the amount of an RNAi agent that, when administered to a subject having a KHK-associated disease, is sufficient to effect treatment of the disease (*e.g.*, by diminishing, ameliorating, or maintaining the existing disease or one or more symptoms of disease). The "therapeutically effective amount" may vary depending on the RNAi agent, how the agent is administered, the disease and its severity and the history, age, weight, family history, genetic makeup, the types of preceding or concomitant treatments, if any, and other individual characteristics of the subject to be treated.

"Prophylactically effective amount," as used herein, is intended to include the amount of an RNAi agent that, when administered to a subject having a KHK-associated disorder, is sufficient to prevent or ameliorate the disease or one or more symptoms of the disease. Ameliorating the disease includes slowing the course of the disease or reducing the severity of later-developing disease. The "prophylactically effective amount" may vary depending on the RNAi agent, how the agent is administered, the degree of risk of disease, and the history, age, weight, family history, genetic makeup, the types of preceding or concomitant treatments, if any, and other individual characteristics of the patient to be treated.

A "therapeutically-effective amount" or "prophylactically effective amount" also includes an amount of an RNAi agent that produces some desired effect at a reasonable benefit/risk ratio applicable to any treatment. The iRNA employed in the methods of the present invention may be administered in a sufficient amount to produce a reasonable benefit/risk ratio applicable to such treatment.

The phrase "pharmaceutically acceptable" is employed herein to refer to those compounds (including salts), materials, compositions, or dosage forms which are, within the scope of sound medical judgment, suitable for use in contact with the tissues of human subjects and animal subjects without excessive toxicity, irritation, allergic response, or other problem or complication, commensurate with a reasonable benefit/risk ratio.

The phrase "pharmaceutically-acceptable carrier" as used herein means a pharmaceutically-acceptable material, composition, or vehicle, such as a liquid or solid filler, diluent, excipient, manufacturing aid (*e.g.*, lubricant, talc magnesium, calcium or zinc stearate, or steric acid), or solvent encapsulating material, involved in carrying or transporting the subject compound from one organ, or portion of the body, to another organ, or portion of the body. Each carrier must be "acceptable" in the sense of being compatible with the other ingredients of the formulation and not injurious to the

subject being treated. Such carriers are known in the art. Pharmaceutically acceptable carriers include carriers for administration by injection.

The term “lower” in the context of the level of KHK gene expression or KHK protein production in a subject, or a disease marker or symptom refers to a statistically significant decrease in such level. The decrease can be, for example, at least 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, or 95%, or below the level of detection for the detection method. In certain embodiments, the expression of the target is normalized, *i.e.*, decreased towards or to a level accepted as within the range of normal for an individual without such disorder, *e.g.*, normalization of body weight, blood pressure, or a serum lipid level. As used here, “lower” in a subject can refer to lowering of gene expression or protein production in a cell in a subject does not require lowering of expression in all cells or tissues of a subject. For example, as used herein, lowering in a subject can include lowering of gene expression or protein production in the liver of a subject.

The term “lower” can also be used in association with normalizing a symptom of a disease or condition, *i.e.* decreasing the difference between a level in a subject suffering from a KHK-associated disease towards or to a level in a normal subject not suffering from a KHK-associated disease. For example, if a subject with a normal weight of 70 kg weighs 90 kg prior to treatment (20 kg overweight) and 80 kg after treatment (10 kg overweight), the subject’s weight is lowered towards a normal weight by 50% ($10/20 \times 100\%$). Similarly, if the HDL level of a woman is increased from 50 mg/dL (poor) to 57 mg/dL, with a normal level being 60 mg/dL, the difference between the prior level of the subject and the normal level is decreased by 70% (difference of 10 mg/dL between subject level and normal is decreased by 7 mg/dL, $7/10 \times 100\%$). As used herein, if a disease is associated with an elevated value for a symptom, “normal” is considered to be the upper limit of normal. If a disease is associated with a decreased value for a symptom, “normal” is considered to be the lower limit of normal.

The term “sample,” as used herein, includes a collection of similar fluids, cells, or tissues isolated from a subject, as well as fluids, cells, or tissues present within a subject. Examples of biological fluids include blood, serum and serosal fluids, plasma, cerebrospinal fluid, ocular fluids, lymph, urine, saliva, and the like. Tissue samples may include samples from tissues, organs, or localized regions. For example, samples may be derived from particular organs, parts of organs, or fluids or cells within those organs. In certain embodiments, samples may be derived from the liver (*e.g.*, whole liver or certain segments of liver or certain types of cells in the liver, such as, *e.g.*, hepatocytes). In some embodiments, a “sample derived from a subject” refers to urine obtained from the subject. A “sample derived from a subject” can refer to blood (which can be readily converted to plasma or serum) drawn from the subject.

II. iRNAs of the Invention

The present invention provides iRNAs which inhibit the expression of a KHK gene. In certain embodiments, the iRNA includes double stranded ribonucleic acid (dsRNA) molecules for inhibiting the expression of a KHK gene in a cell, such as a cell within a subject, *e.g.*, a mammal, such as a human having or susceptible to developing a KHK-associated disease. The dsRNAi agent includes an antisense strand having a region of complementarity which is complementary to at least a part of an mRNA formed in the expression of a KHK gene. The region of complementarity is about 30 nucleotides or less in length (*e.g.*, about 30, 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, or 18 nucleotides or less in length). Upon contact with a cell expressing the KHK gene, the iRNA inhibits the expression of the KHK gene (*e.g.*, a human, a primate, a non-primate, or a rat KHK gene) by at least about 50% as assayed by, for example, a PCR or branched DNA (bDNA)-based method, or by a protein-based method, such as by immunofluorescence analysis, using, for example, western blotting or flow cytometric techniques. In certain embodiments, inhibition of expression is determined by the qPCR method provided in the examples herein with the siRNA at, *e.g.*, a 10 nM concentration, in an appropriate organism cell line provided therein. In certain embodiments, inhibition of expression in vivo is determined by knockdown of the human gene in a rodent expressing the human gene, *e.g.*, a mouse or an AAV-infected mouse expressing the human target gene, *e.g.*, when administered as single dose, *e.g.*, at 3 mg/kg at the nadir of RNA expression.

A dsRNA includes two RNA strands that are complementary and hybridize to form a duplex structure under conditions in which the dsRNA will be used. One strand of a dsRNA (the antisense strand) includes a region of complementarity that is substantially complementary, and generally fully complementary, to a target sequence. The target sequence can be derived from the sequence of an mRNA formed during the expression of a KHK gene. The other strand (the sense strand) includes a region that is complementary to the antisense strand, such that the two strands hybridize and form a duplex structure when combined under suitable conditions. As described elsewhere herein and as known in the art, the complementary sequences of a dsRNA can also be contained as self-complementary regions of a single nucleic acid molecule, as opposed to being on separate oligonucleotides.

Generally, the duplex structure is 15 to 30 base pairs in length, *e.g.*, 15-29, 15-28, 15-27, 15-26, 15-25, 15-24, 15-23, 15-22, 15-21, 15-20, 15-19, 15-18, 15-17, 18-30, 18-29, 18-28, 18-27, 18-26, 18-25, 18-24, 18-23, 18-22, 18-21, 18-20, 19-30, 19-29, 19-28, 19-27, 19-26, 19-25, 19-24, 19-23, 19-22, 19-21, 19-20, 20-30, 20-29, 20-28, 20-27, 20-26, 20-25, 20-24, 20-23, 20-22, 20-21, 21-30, 21-29, 21-28, 21-27, 21-26, 21-25, 21-24, 21-23, or 21-22 base pairs in length. In certain embodiments, the duplex structure is 18 to 25 base pairs in length, *e.g.*, 18-25, 18-24, 18-23, 18-22, 18-21, 18-20, 19-25, 19-24, 19-23, 19-22, 19-21, 19-20, 20-25, 20-24, 20-23, 20-22, 20-21, 21-25, 21-24, 21-23, 21-22, 22-25, 22-24, 22-23, 23-25, 23-24 or 24-25 base pairs in length, for example, 19-21 basepairs in length. Ranges and lengths intermediate to the above recited ranges and lengths are also contemplated to be part of the disclosure.

Similarly, the region of complementarity to the target sequence is 15 to 30 nucleotides in length, *e.g.*, 15-29, 15-28, 15-27, 15-26, 15-25, 15-24, 15-23, 15-22, 15-21, 15-20, 15-19, 15-18, 15-17, 18-30, 18-29, 18-28, 18-27, 18-26, 18-25, 18-24, 18-23, 18-22, 18-21, 18-20, 19-30, 19-29, 19-28, 19-27, 19-26, 19-25, 19-24, 19-23, 19-22, 19-21, 19-20, 20-30, 20-29, 20-28, 20-27, 20-26, 20-25, 20-24, 20-23, 20-22, 20-21, 21-30, 21-29, 21-28, 21-27, 21-26, 21-25, 21-24, 21-23, or 21-22 nucleotides in length, for example 19-23 nucleotides in length or 21-23 nucleotides in length. Ranges and lengths intermediate to the above recited ranges and lengths are also contemplated to be part of the disclosure. In some embodiments, the duplex structure is 19 to 30 base pairs in length. Similarly, the region of complementarity to the target sequence is 19 to 30 nucleotides in length.

In some embodiments, the dsRNA is about 19 to about 23 nucleotides in length, or about 25 to about 30 nucleotides in length. In general, the dsRNA is long enough to serve as a substrate for the Dicer enzyme. For example, it is well-known in the art that dsRNAs longer than about 21-23 nucleotides in length may serve as substrates for Dicer. As the ordinarily skilled person will also recognize, the region of an RNA targeted for cleavage will most often be part of a larger RNA molecule, often an mRNA molecule. Where relevant, a “part” of an mRNA target is a contiguous sequence of an mRNA target of sufficient length to allow it to be a substrate for RNAi-directed cleavage (*i.e.*, cleavage through a RISC pathway).

One of skill in the art will also recognize that the duplex region is a primary functional portion of a dsRNA, *e.g.*, a duplex region of about 19 to about 30 base pairs, *e.g.*, about 19-30, 19-29, 19-28, 19-27, 19-26, 19-25, 19-24, 19-23, 19-22, 19-21, 19-20, 20-30, 20-29, 20-28, 20-27, 20-26, 20-25, 20-24, 20-23, 20-22, 20-21, 21-30, 21-29, 21-28, 21-27, 21-26, 21-25, 21-24, 21-23, or 21-22 base pairs. Thus, in one embodiment, to the extent that it becomes processed to a functional duplex, of *e.g.*, 15-30 base pairs, that targets a desired RNA for cleavage, an RNA molecule or complex of RNA molecules having a duplex region greater than 30 base pairs is a dsRNA. Thus, an ordinarily skilled artisan will recognize that in one embodiment, a miRNA is a dsRNA. In another embodiment, a dsRNA is not a naturally occurring miRNA. In another embodiment, an iRNA agent useful to target KHK gene expression is not generated in the target cell by cleavage of a larger dsRNA.

A dsRNA as described herein can further include one or more single-stranded nucleotide overhangs *e.g.*, 1-4, 2-4, 1-3, 2-3, 1, 2, 3, or 4 nucleotides. dsRNAs having at least one nucleotide overhang can have superior inhibitory properties relative to their blunt-ended counterparts. A nucleotide overhang can comprise or consist of a nucleotide/nucleoside analog, including a deoxynucleotide/nucleoside. The overhang(s) can be on the sense strand, the antisense strand, or any combination thereof. Furthermore, the nucleotide(s) of an overhang can be present on the 5'-end, 3'-end, or both ends of an antisense or sense strand of a dsRNA.

A dsRNA can be synthesized by standard methods known in the art. Double stranded RNAi compounds of the invention may be prepared using a two-step procedure. First, the individual strands of the double stranded RNA molecule are prepared separately. Then, the component strands are annealed. The individual strands of the siRNA compound can be prepared using solution-phase or

solid-phase organic synthesis or both. Organic synthesis offers the advantage that the oligonucleotide strands comprising unnatural or modified nucleotides can be easily prepared. Similarly, single-stranded oligonucleotides of the invention can be prepared using solution-phase or solid-phase organic synthesis or both.

5 In an aspect, a dsRNA of the invention includes at least two nucleotide sequences, a sense sequence and an anti-sense sequence. The sense strand is selected from the group of sequences provided in any one of Tables 2, 3, 5, 6, and 8-13, and the corresponding antisense strand of the sense strand is selected from the group of sequences of any one of Tables 2, 3, 5, 6, and 8-13. In this aspect, one of the two sequences is complementary to the other of the two sequences, with one of the
10 sequences being substantially complementary to a sequence of an mRNA generated in the expression of a KHK gene. As such, in this aspect, a dsRNA will include two oligonucleotides, where one oligonucleotide is described as the sense strand in any one of Tables 2, 3, 5, 6, and 8-13, and the second oligonucleotide is described as the corresponding antisense strand of the sense strand in any one of Tables 2, 3, 5, 6, and 8-13.

15 In certain embodiments, the substantially complementary sequences of the dsRNA are contained on separate oligonucleotides. In other embodiments, the substantially complementary sequences of the dsRNA are contained on a single oligonucleotide.

In certain embodiments, the sense or antisense strand is selected from the sense or antisense strand of any one of duplexes AD-517197.2; AD-517258.2; AD-516748.2; AD-516851.2; AD-
20 519351.2; AD-519754.2; AD-519828.2; AD-520018.2; AD-520035.2; AD-520062.2; AD-520064.2; AD-520065.2; AD-520067.2; AD-75289.2; AD-520069.2; AD-520099.2; AD-67575.7; AD-520101.2; AD-1193323.1; AD-1193344.1; AD-1193350.1; AD-1193365.1; AD-1193379.1; AD-1193407.1; AD-1193421.1; AD-1193422.1; AD-1193429.1; AD-1193437.1; AD-1193443.1; AD-1193471.1; AD-1193481.1 or AD-67605.7.

25 In some embodiments, the sense or antisense strand is selected from the sense or antisense strand of any one of duplexes AD-519345.1, AD-519346.1, AD-519347.1, AD-67554.7, AD-519752.3, AD-1010731.1, AD-1010732.1, AD-519343.1, AD-519344.1, AD-519349.1, AD-519350.1, AD-519753.2, AD-519932.1, AD-519935.2, AD-520018.6, AD-517837.2, AD-805635.2, AD-519329.2, AD-520063.2, AD-519757.2, AD-805631.2, AD-516917.2, AD-516828.2, AD-
30 518983.2, AD-805636.2, AD-519754.7, AD-520062.2, AD-67575.9, AD-518923.3, AD-520053.4, AD-519667.2, AD-519773.2, AD-519354.2, AD-520060.4, AD-520061.4, AD-1010733.2, AD-1010735.2, AD-1193323.1; AD-1193344.1; AD-1193350.1; AD-1193365.1; AD-1193379.1; AD-1193407.1; AD-1193421.1; AD-1193422.1; AD-1193429.1; AD-1193437.1; AD-1193443.1; AD-1193471.1; or AD-1193481.1.

35 In some embodiments, the sense or antisense strand is selected from the sense or antisense strand of duplex AD-519351.

It will be understood that, although the sequences in, for example, Tables 2, 5, 8 and 10 are not described as modified or conjugated sequences, the RNA of the iRNA of the invention *e.g.*, a

dsRNA of the invention, may comprise any one of the sequences set forth in any one of Tables 2, 3, 5, 6, and 8-13 that is un-modified, un-conjugated, or modified or conjugated differently than described therein. In other words, the invention encompasses dsRNA of Tables 2, 3, 5, 6, and 8-13 which are un-modified, un-conjugated, modified, or conjugated, as described herein.

5 The skilled person is well aware that dsRNAs having a duplex structure of about 20 to 23 base pairs, *e.g.*, 21, base pairs have been hailed as particularly effective in inducing RNA interference (Elbashir *et al.*, EMBO 2001, 20:6877-6888). However, others have found that shorter or longer RNA duplex structures can also be effective (Chu and Rana (2007) RNA 14:1714-1719; Kim *et al.* (2005) Nat Biotech 23:222-226). In the embodiments described above, by virtue of the nature of the
10 oligonucleotide sequences provided in any one of Tables 2, 3, 5, 6, and 8-13. dsRNAs described herein can include at least one strand of a length of minimally 21 nucleotides. It can be reasonably expected that shorter duplexes having any one of the sequences in any one of Tables 2, 3, 5, 6, and 8-13 minus only a few nucleotides on one or both ends can be similarly effective as compared to the dsRNAs described above. Hence, dsRNAs having a sequence of at least 19, 20, 21, 22, 23 or more
15 contiguous nucleotides derived from any one of the sequences of any one of Tables 2, 3, 5, 6, and 8-13, and differing in their ability to inhibit the expression of a KHK gene by not more than about 5, 10, 15, 20, 25, or 30 % inhibition from a dsRNA comprising the full sequence, are contemplated to be within the scope of the present invention.

 In addition, the RNAs provided in Tables 2, 3, 5, 6, and 8-13 identify a site(s) in a KHK
20 transcript that is susceptible to RISC-mediated cleavage. As such, the present invention further features iRNAs that target within one of these sites. As used herein, an iRNA is said to target within a particular site of an RNA transcript if the iRNA promotes cleavage of the transcript anywhere within that particular site. Such an iRNA will generally include at least about 19 contiguous nucleotides from any one of the sequences provided in any one of Tables 2, 3, 5, 6, and 8-13 coupled to additional
25 nucleotide sequences taken from the region contiguous to the selected sequence in a KHK gene.

III. Modified iRNAs of the Invention

 In certain embodiments, the RNA of the iRNA of the invention *e.g.*, a dsRNA, is un-modified, and does not comprise, *e.g.*, chemical modifications or conjugations known in the art and
30 described herein. In other embodiments, the RNA of an iRNA of the invention, *e.g.*, a dsRNA, is chemically modified to enhance stability or other beneficial characteristics. In certain embodiments of the invention, substantially all of the nucleotides of an iRNA of the invention are modified. In other embodiments of the invention, all of the nucleotides of an iRNA or substantially all of the nucleotides of an iRNA are modified, *i.e.*, not more than 5, 4, 3, 2, or 1 unmodified nucleotides are present in a
35 strand of the iRNA.

 The nucleic acids featured in the invention can be synthesized or modified by methods well established in the art, such as those described in "Current protocols in nucleic acid chemistry," Beaucage, S.L. *et al.* (Edrs.), John Wiley & Sons, Inc., New York, NY, USA, which is hereby

incorporated herein by reference. Modifications include, for example, end modifications, *e.g.*, 5'-end modifications (phosphorylation, conjugation, inverted linkages) or 3'-end modifications (conjugation, DNA nucleotides, inverted linkages, *etc.*); base modifications, *e.g.*, replacement with stabilizing bases, destabilizing bases, or bases that base pair with an expanded repertoire of partners, removal of
5 bases (abasic nucleotides), or conjugated bases; sugar modifications (*e.g.*, at the 2'-position or 4'-position) or replacement of the sugar; or backbone modifications, including modification or replacement of the phosphodiester linkages. Specific examples of iRNA compounds useful in the embodiments described herein include, but are not limited to RNAs containing modified backbones or no natural internucleoside linkages. RNAs having modified backbones include, among others, those
10 that do not have a phosphorus atom in the backbone. For the purposes of this specification, and as sometimes referenced in the art, modified RNAs that do not have a phosphorus atom in their internucleoside backbone can also be considered to be oligonucleosides. In some embodiments, a modified iRNA will have a phosphorus atom in its internucleoside backbone.

Modified RNA backbones include, for example, phosphorothioates, chiral phosphorothioates,
15 phosphorodithioates, phosphotriesters, aminoalkylphosphotriesters, methyl and other alkyl phosphonates including 3'-alkylene phosphonates and chiral phosphonates, phosphinates, phosphoramidates including 3'-amino phosphoramidate and aminoalkylphosphoramidates, thionophosphoramidates, thionoalkylphosphonates, thionoalkylphosphotriesters, and boranophosphates having normal 3'-5' linkages, 2'-5'-linked analogs of these, and those having
20 inverted polarity wherein the adjacent pairs of nucleoside units are linked 3'-5' to 5'-3' or 2'-5' to 5'-2'. Various salts, mixed salts and free acid forms are also included. In some embodiments of the invention, the dsRNA agents of the invention are in a free acid form. In other embodiments of the invention, the dsRNA agents of the invention are in a salt form. In one embodiment, the dsRNA agents of the invention are in a sodium salt form. In certain embodiments, when the dsRNA agents of
25 the invention are in the sodium salt form, sodium ions are present in the agent as counterions for substantially all of the phosphodiester and/or phosphorothioate groups present in the agent. Agents in which substantially all of the phosphodiester and/or phosphorothioate linkages have a sodium counterion include not more than 5, 4, 3, 2, or 1 phosphodiester and/or phosphorothioate linkages without a sodium counterion. In some embodiments, when the dsRNA agents of the invention are in
30 the sodium salt form, sodium ions are present in the agent as counterions for all of the phosphodiester and/or phosphorothioate groups present in the agent.

Representative U.S. Patents that teach the preparation of the above phosphorus-containing linkages include, but are not limited to, U.S. Patent Nos. 3,687,808; 4,469,863; 4,476,301; 5,023,243; 5,177,195; 5,188,897; 5,264,423; 5,276,019; 5,278,302; 5,286,717; 5,321,131; 5,399,676; 5,405,939;
35 5,453,496; 5,455,233; 5,466,677; 5,476,925; 5,519,126; 5,536,821; 5,541,316; 5,550,111; 5,563,253; 5,571,799; 5,587,361; 5,625,050; 6,028,188; 6,124,445; 6,160,109; 6,169,170; 6,172,209; 6,239,265; 6,277,603; 6,326,199; 6,346,614; 6,444,423; 6,531,590; 6,534,639; 6,608,035; 6,683,167; 6,858,715;

6,867,294; 6,878,805; 7,015,315; 7,041,816; 7,273,933; 7,321,029; and U.S. Pat RE39464, the entire contents of each of which are hereby incorporated herein by reference.

Modified RNA backbones that do not include a phosphorus atom therein have backbones that are formed by short chain alkyl or cycloalkyl internucleoside linkages, mixed heteroatoms and alkyl
 5 or cycloalkyl internucleoside linkages, or one or more short chain heteroatomic or heterocyclic internucleoside linkages. These include those having morpholino linkages (formed in part from the sugar portion of a nucleoside); siloxane backbones; sulfide, sulfoxide and sulfone backbones; formacetyl and thioformacetyl backbones; methylene formacetyl and thioformacetyl backbones; alkene containing backbones; sulfamate backbones; methyleneimino and methylenehydrazino
 10 backbones; sulfonate and sulfonamide backbones; amide backbones; and others having mixed N, O, S, and CH₂ component parts.

Representative U.S. Patents that teach the preparation of the above oligonucleosides include, but are not limited to, U.S. Patent Nos. 5,034,506; 5,166,315; 5,185,444; 5,214,134; 5,216,141; 5,235,033; 5,64,562; 5,264,564; 5,405,938; 5,434,257; 5,466,677; 5,470,967; 5,489,677; 5,541,307;
 15 5,561,225; 5,596,086; 5,602,240; 5,608,046; 5,610,289; 5,618,704; 5,623,070; 5,663,312; 5,633,360; 5,677,437; and 5,677,439, the entire contents of each of which are hereby incorporated herein by reference.

Suitable RNA mimetics are contemplated for use in iRNAs provided herein, in which both the sugar and the internucleoside linkage, *i.e.*, the backbone, of the nucleotide units are replaced with
 20 novel groups. The base units are maintained for hybridization with an appropriate nucleic acid target compound. One such oligomeric compound in which an RNA mimetic that has been shown to have excellent hybridization properties is referred to as a peptide nucleic acid (PNA). In PNA compounds, the sugar backbone of an RNA is replaced with an amide containing backbone, in particular an aminoethylglycine backbone. The nucleobases are retained and are bound directly or indirectly to aza
 25 nitrogen atoms of the amide portion of the backbone. Representative US patents that teach the preparation of PNA compounds include, but are not limited to, U.S. Patent Nos. 5,539,082; 5,714,331; and 5,719,262, the entire contents of each of which are hereby incorporated herein by reference. Additional PNA compounds suitable for use in the iRNAs of the invention are described in, for example, in Nielsen *et al.*, *Science*, 1991, 254, 1497-1500.

Some embodiments featured in the invention include RNAs with phosphorothioate backbones and oligonucleosides with heteroatom backbones, and in particular --CH₂--NH--CH₂--, --CH₂--N(CH₃)--O--CH₂--[known as a methylene (methylimino) or MMI backbone], --CH₂--O--N(CH₃)--CH₂--, --CH₂--N(CH₃)--N(CH₃)--CH₂-- and --N(CH₃)--CH₂--CH₂-- of the above-referenced U.S. Patent No. 5,489,677, and the amide backbones of the above-referenced U.S. Patent No. 5,602,240. In
 35 some embodiments, the RNAs featured herein have morpholino backbone structures of the above-referenced U.S. Patent No. 5,034,506. The native phosphodiester backbone can be represented as O-P(O)(OH)-OCH₂-.

Modified RNAs can also contain one or more substituted sugar moieties. The iRNAs, *e.g.*, dsRNAs, featured herein can include one of the following at the 2'-position: OH; F; O-, S-, or N-alkyl; O-, S-, or N-alkenyl; O-, S- or N-alkynyl; or O-alkyl-O-alkyl, wherein the alkyl, alkenyl and alkynyl can be substituted or unsubstituted C₁ to C₁₀ alkyl or C₂ to C₁₀ alkenyl and alkynyl. Exemplary

5 suitable modifications include O[(CH₂)_nO]_mCH₃, O(CH₂)_nOCH₃, O(CH₂)_nNH₂, O(CH₂)_nCH₃, O(CH₂)_nONH₂, and O(CH₂)_nON[(CH₂)_nCH₃]₂, where n and m are from 1 to about 10. In other embodiments, dsRNAs include one of the following at the 2' position: C₁ to C₁₀ lower alkyl, substituted lower alkyl, alkaryl, aralkyl, O-alkaryl or O-aralkyl, SH, SCH₃, OCN, Cl, Br, CN, CF₃, OCF₃, SOCH₃, SO₂CH₃, ONO₂, NO₂, N₃, NH₂, heterocycloalkyl, heterocycloalkaryl,

10 aminoalkylamino, polyalkylamino, substituted silyl, an RNA cleaving group, a reporter group, an intercalator, a group for improving the pharmacokinetic properties of an iRNA, or a group for improving the pharmacodynamic properties of an iRNA, and other substituents having similar properties. In some embodiments, the modification includes a 2'-methoxyethoxy (2'-O--CH₂CH₂OCH₃, also known as 2'-O-(2-methoxyethyl) or 2'-MOE) (Martin *et al.*, *Helv. Chim. Acta*,

15 1995, 78:486-504) *i.e.*, an alkoxy-alkoxy group. Another exemplary modification is 2'-dimethylaminoethoxy, *i.e.*, a O(CH₂)₂ON(CH₃)₂ group, also known as 2'-DMAOE, as described in examples herein below, and 2'-dimethylaminoethoxyethoxy (also known in the art as 2'-O-dimethylaminoethoxyethyl or 2'-DMAEOE), *i.e.*, 2'-O--CH₂--O--CH₂--N(CH₃)₂. Further exemplary modifications include : 5'-Me-2'-F nucleotides, 5'-Me-2'-OMe nucleotides, 5'-Me-2'-

20 deoxynucleotides, (both R and S isomers in these three families); 2'-alkoxyalkyl; and 2'-NMA (N-methylacetamide).

Other modifications include 2'-methoxy (2'-OCH₃), 2'-aminopropoxy (2'-OCH₂CH₂CH₂NH₂) and 2'-fluoro (2'-F). Similar modifications can also be made at other positions on the RNA of an iRNA, particularly the 3' position of the sugar on the 3' terminal nucleotide or in 2'-5' linked dsRNAs

25 and the 5' position of 5' terminal nucleotide. iRNAs can also have sugar mimetics such as cyclobutyl moieties in place of the pentofuranosyl sugar. Representative US patents that teach the preparation of such modified sugar structures include, but are not limited to, U.S. Patent Nos. 4,981,957; 5,118,800; 5,319,080; 5,359,044; 5,393,878; 5,446,137; 5,466,786; 5,514,785; 5,519,134; 5,567,811; 5,576,427; 5,591,722; 5,597,909; 5,610,300; 5,627,053; 5,639,873; 5,646,265; 5,658,873; 5,670,633; and

30 5,700,920, certain of which are commonly owned with the instant application,. The entire contents of each of the foregoing are hereby incorporated herein by reference.

An iRNA can also include nucleobase (often referred to in the art simply as "base") modifications or substitutions. As used herein, "unmodified" or "natural" nucleobases include the purine bases adenine (A) and guanine (G), and the pyrimidine bases thymine (T), cytosine (C), and

35 uracil (U). Modified nucleobases include other synthetic and natural nucleobases such as deoxythymidine (dT), 5-methylcytosine (5-me-C), 5-hydroxymethyl cytosine, xanthine, hypoxanthine, 2-aminoadenine, 6-methyl and other alkyl derivatives of adenine and guanine, 2-propyl and other alkyl derivatives of adenine and guanine, 2-thiouracil, 2-thiothymine and 2-thiocytosine, 5-halouracil

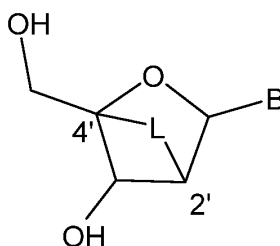
and cytosine, 5-propynyl uracil and cytosine, 6-azo uracil, cytosine and thymine, 5-uracil (pseudouracil), 4-thiouracil, 8-halo, 8-amino, 8-thiol, 8-thioalkyl, 8-hydroxyl and other 8-substituted adenines and guanines, 5-halo, particularly 5-bromo, 5-trifluoromethyl and other 5-substituted uracils and cytosines, 7-methylguanine and 7-methyladenine, 8-azaguanine and 8-azaadenine, 7-deazaguanine and 7-daazaadenine and 3-deazaguanine and 3-deazaadenine. Further nucleobases include those disclosed in U.S. Pat. No. 3,687,808, those disclosed in *Modified Nucleosides in Biochemistry, Biotechnology and Medicine*, Herdewijn, P. ed. Wiley-VCH, 2008; those disclosed in *The Concise Encyclopedia Of Polymer Science And Engineering*, pages 858-859, Kroschwitz, J. L., ed. John Wiley & Sons, 1990, those disclosed by Englisch *et al.*, *Angewandte Chemie*, International Edition, 1991, 30, 613, and those disclosed by Sanghvi, Y. S., Chapter 15, *dsRNA Research and Applications*, pages 289-302, Crooke, S. T. and Lebleu, B., Ed., CRC Press, 1993. Certain of these nucleobases are particularly useful for increasing the binding affinity of the oligomeric compounds featured in the invention. These include 5-substituted pyrimidines, 6-azapyrimidines and N-2, N-6 and 0-6 substituted purines, including 2-aminopropyladenine, 5-propynyluracil and 5-propynylcytosine. 5-methylcytosine substitutions have been shown to increase nucleic acid duplex stability by 0.6-1.2°C (Sanghvi, Y. S., Crooke, S. T. and Lebleu, B., Eds., *dsRNA Research and Applications*, CRC Press, Boca Raton, 1993, pp. 276-278) and are exemplary base substitutions, even more particularly when combined with 2'-O-methoxyethyl sugar modifications.

Representative U.S. Patents that teach the preparation of certain of the above noted modified nucleobases as well as other modified nucleobases include, but are not limited to, the above noted U.S. Patent Nos. 3,687,808, 4,845,205; 5,130,30; 5,134,066; 5,175,273; 5,367,066; 5,432,272; 5,457,187; 5,459,255; 5,484,908; 5,502,177; 5,525,711; 5,552,540; 5,587,469; 5,594,121, 5,596,091; 5,614,617; 5,681,941; 5,750,692; 6,015,886; 6,147,200; 6,166,197; 6,222,025; 6,235,887; 6,380,368; 6,528,640; 6,639,062; 6,617,438; 7,045,610; 7,427,672; and 7,495,088, the entire contents of each of which are hereby incorporated herein by reference.

An iRNA agent of the disclosure can also be modified to include one or more bicyclic sugar moieties. A "bicyclic sugar" is a furanosyl ring modified by a ring formed by the bridging of two carbons, whether adjacent or non-adjacent. A "bicyclic nucleoside" ("BNA") is a nucleoside having a sugar moiety comprising a ring formed by bridging two carbons, whether adjacent or non-adjacent, of the sugar ring, thereby forming a bicyclic ring system. In certain embodiments, the bridge connects the 4'-carbon and the 2'-carbon of the sugar ring, optionally, via the 2'-acyclic oxygen atom. Thus, in some embodiments an agent of the invention may include one or more locked nucleic acids (LNA). A locked nucleic acid is a nucleotide having a modified ribose moiety in which the ribose moiety comprises an extra bridge connecting the 2' and 4' carbons. In other words, an LNA is a nucleotide comprising a bicyclic sugar moiety comprising a 4'-CH₂-O-2' bridge. This structure effectively "locks" the ribose in the 3'-endo structural conformation. The addition of locked nucleic acids to siRNAs has been shown to increase siRNA stability in serum, and to reduce off-target effects (Elmen, J. *et al.*, (2005) *Nucleic Acids Research* 33(1):439-447; Mook, OR. *et al.*, (2007) *Mol Canc Ther*

6(3):833-843; Grunweller, A. *et al.*, (2003) *Nucleic Acids Research* 31(12):3185-3193). Examples of bicyclic nucleosides for use in the polynucleotides of the invention include without limitation nucleosides comprising a bridge between the 4' and the 2' ribosyl ring atoms. In certain embodiments, the antisense polynucleotide agents of the invention include one or more bicyclic nucleosides comprising a 4' to 2' bridge.

A locked nucleoside can be represented by the structure (omitting stereochemistry),



wherein B is a nucleobase or modified nucleobase and L is the linking group that joins the 2'-carbon to the 4'-carbon of the ribose ring. Examples of such 4' to 2' bridged bicyclic nucleosides, include but are not limited to 4'-(CH₂)—O-2' (LNA); 4'-(CH₂)—S-2'; 4'-(CH₂)₂—O-2' (ENA); 4'-CH(CH₃)—O-2' (also referred to as "constrained ethyl" or "cEt") and 4'-CH(CH₂OCH₃)—O-2' (and analogs thereof; see, *e.g.*, U.S. Patent No. 7,399,845); 4'-C(CH₃)(CH₃)—O-2' (and analogs thereof; see *e.g.*, U.S. Patent No. 8,278,283); 4'-CH₂—N(OCH₃)-2' (and analogs thereof; see *e.g.*, U.S. Patent No. 8,278,425); 4'-CH₂—O—N(CH₃)-2' (see, *e.g.*, U.S. Patent Publication No. 2004/0171570); 4'-CH₂—N(R)—O-2', wherein R is H, C1-C12 alkyl, or a nitrogen protecting group (see, *e.g.*, U.S. Patent No. 7,427,672); 4'-CH₂—C(H)(CH₃)-2' (see, *e.g.*, Chattopadhyaya *et al.*, *J. Org. Chem.*, 2009, 74, 118-134); and 4'-CH₂—C(=CH₂)-2' (and analogs thereof; see, *e.g.*, U.S. Patent No. 8,278,426). The entire contents of each of the foregoing are hereby incorporated herein by reference.

Additional representative U.S. Patents and U.S. Patent Publications that teach the preparation of locked nucleic acid nucleotides include, but are not limited to, the following: U.S. Patent Nos. 6,268,490; 6,525,191; 6,670,461; 6,770,748; 6,794,499; 6,998,484; 7,053,207; 7,034,133; 7,084,125; 7,399,845; 7,427,672; 7,569,686; 7,741,457; 8,022,193; 8,030,467; 8,278,425; 8,278,426; 8,278,283; US 2008/0039618; and US 2009/0012281, the entire contents of each of which are hereby incorporated herein by reference.

Any of the foregoing bicyclic nucleosides can be prepared having one or more stereochemical sugar configurations including for example α -L-ribofuranose and β -D-ribofuranose (see WO 99/14226).

The RNA of an iRNA can also be modified to include one or more constrained ethyl nucleotides. As used herein, a "constrained ethyl nucleotide" or "cEt" is a locked nucleic acid comprising a bicyclic sugar moiety comprising a 4'-CH(CH₃)-O-2' bridge (*i.e.*, L in the preceding structure). In one embodiment, a constrained ethyl nucleotide is in the S conformation referred to herein as "S-cEt."

An iRNA of the invention may also include one or more “conformationally restricted nucleotides” (“CRN”). CRN are nucleotide analogs with a linker connecting the C2' and C4' carbons of ribose or the C3 and -C5' carbons of ribose. CRN lock the ribose ring into a stable conformation and increase the hybridization affinity to mRNA. The linker is of sufficient length to place the oxygen in an optimal position for stability and affinity resulting in less ribose ring puckering.

Representative publications that teach the preparation of certain of the above noted CRN include, but are not limited to, U.S. Patent Publication No. 2013/0190383; and PCT publication WO 2013/036868, the entire contents of each of which are hereby incorporated herein by reference.

In some embodiments, an iRNA of the invention comprises one or more monomers that are UNA (unlocked nucleic acid) nucleotides. UNA is unlocked acyclic nucleic acid, wherein any of the bonds of the sugar has been removed, forming an unlocked “sugar” residue. In one example, UNA also encompasses monomer with bonds between C1'-C4' have been removed (*i.e.* the covalent carbon-oxygen-carbon bond between the C1' and C4' carbons). In another example, the C2'-C3' bond (*i.e.* the covalent carbon-carbon bond between the C2' and C3' carbons) of the sugar has been removed (see *Nuc. Acids Symp. Series*, 52, 133-134 (2008) and Fluiter *et al.*, *Mol. Biosyst.*, 2009, 10, 1039 hereby incorporated by reference).

Representative U.S. publications that teach the preparation of UNA include, but are not limited to, U.S. Patent No. 8,314,227; and U.S. Patent Publication Nos. 2013/0096289; 2013/0011922; and 2011/0313020, the entire contents of each of which are hereby incorporated herein by reference.

Potentially stabilizing modifications to the ends of RNA molecules can include N-(acetylaminocaproyl)-4-hydroxyprolinol (Hyp-C6-NHAc), N-(caproyl-4-hydroxyprolinol (Hyp-C6), N-(acetyl-4-hydroxyprolinol (Hyp-NHAc), thymidine-2'-O-deoxythymidine (ether), N-(aminocaproyl)-4-hydroxyprolinol (Hyp-C6-amino), 2-docosanoyl-uridine-3'-phosphate, inverted 2'-deoxy-modified ribonucleotide, such as inverted dT(idT), inverted dA (idA), and inverted abasic 2'-deoxyribonucleotide (iAb) and others. Disclosure of this modification can be found in WO 2011/005861.

In one example, the 3' or 5' terminal end of an oligonucleotide is linked to an inverted 2'-deoxy-modified ribonucleotide, such as inverted dT(idT), inverted dA (idA), or an inverted abasic 2'-deoxyribonucleotide (iAb). In one particular example, the inverted 2'-deoxy-modified ribonucleotide is linked to the 3'-end of an oligonucleotide, such as the 3'-end of a sense strand described herein, where the linking is via a 3'-3' phosphodiester linkage or a 3'-3'-phosphorothioate linkage.

In another example, the 3'-end of a sense strand is linked via a 3'-3'-phosphorothioate linkage to an inverted abasic ribonucleotide (iAb). In another example, the 3'-end of a sense strand is linked via a 3'-3'-phosphorothioate linkage to an inverted dA (idA).

In one particular example, the inverted 2'-deoxy-modified ribonucleotide is linked to the 3'-end of an oligonucleotide, such as the 3'-end of a sense strand described herein, where the linking is via a 3'-3' phosphodiester linkage or a 3'-3'-phosphorothioate linkage.

In another example, the 3'-terminal nucleotides of a sense strand is an inverted dA (idA) and is linked to the preceding nucleotide via a 3'-3' linkage (e.g., 3'-3'-phosphorothioate linkage).

Other modifications of the nucleotides of an iRNA of the invention include a 5' phosphate or 5' phosphate mimic, e.g., a 5'-terminal phosphate or phosphate mimic on the antisense strand of an
5 iRNA. Suitable phosphate mimics are disclosed in, for example U.S. Patent Publication No. 2012/0157511, the entire contents of which are incorporated herein by reference.

A. Modified iRNAs Comprising Motifs of the Invention

In certain aspects of the invention, the double stranded RNA agents of the invention include
10 agents with chemical modifications as disclosed, for example, in WO2013/075035, the entire contents of each of which are incorporated herein by reference. As shown herein and in WO2013/075035, one or more motifs of three identical modifications on three consecutive nucleotides may be introduced into a sense strand or antisense strand of a dsRNAi agent, particularly at or near the cleavage site. In some embodiments, the sense strand and antisense strand of the dsRNAi agent may otherwise be
15 completely modified. The introduction of these motifs interrupts the modification pattern, if present, of the sense or antisense strand. The dsRNAi agent may be optionally conjugated with a GalNAc derivative ligand, for instance on the sense strand.

More specifically, when the sense strand and antisense strand of the double stranded RNA agent are completely modified to have one or more motifs of three identical modifications on three
20 consecutive nucleotides at or near the cleavage site of at least one strand of a dsRNAi agent, the gene silencing activity of the dsRNAi agent was observed.

Accordingly, the invention provides double stranded RNA agents capable of inhibiting the expression of a target gene (i.e., KHK gene) *in vivo*. The RNAi agent comprises a sense strand and an antisense strand. Each strand of the RNAi agent may be, for example, 17-30 nucleotides in length,
25 25-30 nucleotides in length, 27-30 nucleotides in length, 19-25 nucleotides in length, 19-23 nucleotides in length, 19-21 nucleotides in length, 21-25 nucleotides in length, or 21-23 nucleotides in length.

The sense strand and antisense strand typically form a duplex double stranded RNA ("dsRNA"), also referred to herein as "dsRNAi agent." The duplex region of a dsRNAi agent may be,
30 for example, the duplex region can be 27-30 nucleotide pairs in length, 19-25 nucleotide pairs in length, 19-23 nucleotide pairs in length, 19-21 nucleotide pairs in length, 21-25 nucleotide pairs in length, or 21-23 nucleotide pairs in length. In another example, the duplex region is selected from 19, 20, 21, 22, 23, 24, 25, 26, and 27 nucleotides in length.

In certain embodiments, the dsRNAi agent may contain one or more overhang regions or
35 capping groups at the 3'-end, 5'-end, or both ends of one or both strands. The overhang can be, independently, 1-6 nucleotides in length, for instance 2-6 nucleotides in length, 1-5 nucleotides in length, 2-5 nucleotides in length, 1-4 nucleotides in length, 2-4 nucleotides in length, 1-3 nucleotides in length, 2-3 nucleotides in length, or 1-2 nucleotides in length. In certain embodiments, the

overhang regions can include extended overhang regions as provided above. The overhangs can be the result of one strand being longer than the other, or the result of two strands of the same length being staggered. The overhang can form a mismatch with the target mRNA or it can be complementary to the gene sequences being targeted or can be another sequence. The first and second strands can also be joined, *e.g.*, by additional bases to form a hairpin, or by other non-base linkers.

In certain embodiments, the nucleotides in the overhang region of the dsRNAi agent can each independently be a modified or unmodified nucleotide including, but not limited to 2'-sugar modified, such as, 2'-F, 2'-O-methyl, thymidine (T), 2'-O-methoxyethyl-5-methyluridine (Teo), 2'-O-methoxyethyladenosine (Aeo), 2'-O-methoxyethyl-5-methylcytidine (m5Ceo), and any combinations thereof.

For example, TT can be an overhang sequence for either end on either strand. The overhang can form a mismatch with the target mRNA or it can be complementary to the gene sequences being targeted or can be another sequence.

The 5'- or 3'- overhangs at the sense strand, antisense strand, or both strands of the dsRNAi agent may be phosphorylated. In some embodiments, the overhang region(s) contains two nucleotides having a phosphorothioate between the two nucleotides, where the two nucleotides can be the same or different. In some embodiments, the overhang is present at the 3'-end of the sense strand, antisense strand, or both strands. In some embodiments, this 3'-overhang is present in the antisense strand. In some embodiments, this 3'-overhang is present in the sense strand.

The dsRNAi agent may contain only a single overhang, which can strengthen the interference activity of the RNAi, without affecting its overall stability. For example, the single-stranded overhang may be located at the 3'-end of the sense strand or, alternatively, at the 3'-end of the antisense strand. The RNAi may also have a blunt end, located at the 5'-end of the antisense strand (or the 3'-end of the sense strand) or *vice versa*. Generally, the antisense strand of the dsRNAi agent has a nucleotide overhang at the 3'-end, and the 5'-end is blunt. While not wishing to be bound by theory, the asymmetric blunt end at the 5'-end of the antisense strand and 3'-end overhang of the antisense strand favor the guide strand loading into RISC process.

In certain embodiments, the dsRNAi agent is a double blunt-ended of 19 nucleotides in length, wherein the sense strand contains at least one motif of three 2'-F modifications on three consecutive nucleotides at positions 7, 8, and 9 from the 5'-end. The antisense strand contains at least one motif of three 2'-O-methyl modifications on three consecutive nucleotides at positions 11, 12, and 13 from the 5'-end.

In other embodiments, the dsRNAi agent is a double blunt-ended of 20 nucleotides in length, wherein the sense strand contains at least one motif of three 2'-F modifications on three consecutive nucleotides at positions 8, 9, and 10 from the 5'-end. The antisense strand contains at least one motif of three 2'-O-methyl modifications on three consecutive nucleotides at positions 11, 12, and 13 from the 5'-end.

In yet other embodiments, the dsRNAi agent is a double blunt-ended of 21 nucleotides in length, wherein the sense strand contains at least one motif of three 2'-F modifications on three consecutive nucleotides at positions 9, 10, and 11 from the 5' end. The antisense strand contains at least one motif of three 2'-O-methyl modifications on three consecutive nucleotides at positions 11, 12, and 13 from the 5' end.

In certain embodiments, the dsRNAi agent comprises a 21 nucleotide sense strand and a 23 nucleotide antisense strand, wherein the sense strand contains at least one motif of three 2'-F modifications on three consecutive nucleotides at positions 9, 10, and 11 from the 5' end; the antisense strand contains at least one motif of three 2'-O-methyl modifications on three consecutive nucleotides at positions 11, 12, and 13 from the 5' end, wherein one end of the RNAi agent is blunt, while the other end comprises a two nucleotide overhang. In some embodiments, the two nucleotide overhang is at the 3'-end of the antisense strand.

When the two nucleotide overhang is at the 3'-end of the antisense strand, there may be two phosphorothioate internucleotide linkages between the terminal three nucleotides, wherein two of the three nucleotides are the overhang nucleotides, and the third nucleotide is a paired nucleotide next to the overhang nucleotide. In one embodiment, the RNAi agent additionally has two phosphorothioate internucleotide linkages between the terminal three nucleotides at both the 5'-end of the sense strand and at the 5'-end of the antisense strand. In certain embodiments, every nucleotide in the sense strand and the antisense strand of the dsRNAi agent, including the nucleotides that are part of the motifs are modified nucleotides. In certain embodiments each residue is independently modified with a 2'-O-methyl or 2'-fluoro, *e.g.*, in an alternating motif. Optionally, the dsRNAi agent further comprises a ligand (such as, GalNAc₃).

In certain embodiments, the dsRNAi agent comprises a sense and an antisense strand, wherein the sense strand is 25-30 nucleotide residues in length, wherein starting from the 5' terminal nucleotide (position 1) positions 1 to 23 of the first strand comprise at least 8 ribonucleotides; the antisense strand is 36-66 nucleotide residues in length and, starting from the 3' terminal nucleotide, comprises at least 8 ribonucleotides in the positions paired with positions 1-23 of sense strand to form a duplex; wherein at least the 3' terminal nucleotide of antisense strand is unpaired with sense strand, and up to 6 consecutive 3' terminal nucleotides are unpaired with sense strand, thereby forming a 3' single stranded overhang of 1-6 nucleotides; wherein the 5' terminus of antisense strand comprises from 10-30 consecutive nucleotides which are unpaired with sense strand, thereby forming a 10-30 nucleotide single stranded 5' overhang; wherein at least the sense strand 5' terminal and 3' terminal nucleotides are base paired with nucleotides of antisense strand when sense and antisense strands are aligned for maximum complementarity, thereby forming a substantially duplexed region between sense and antisense strands; and antisense strand is sufficiently complementary to a target RNA along at least 19 ribonucleotides of antisense strand length to reduce target gene expression when the double stranded nucleic acid is introduced into a mammalian cell; and wherein the sense strand contains at least one motif of three 2'-F modifications on three consecutive nucleotides, where at least one of the

motifs occurs at or near the cleavage site. The antisense strand contains at least one motif of three 2'-O-methyl modifications on three consecutive nucleotides at or near the cleavage site.

In certain embodiments, the dsRNAi agent comprises sense and antisense strands, wherein the dsRNAi agent comprises a first strand having a length which is at least 25 and at most 29 nucleotides and a second strand having a length which is at most 30 nucleotides with at least one motif of three 2'-O-methyl modifications on three consecutive nucleotides at position 11, 12, 13 from the 5' end; wherein the 3' end of the first strand and the 5' end of the second strand form a blunt end and the second strand is 1-4 nucleotides longer at its 3' end than the first strand, wherein the duplex region which is at least 25 nucleotides in length, and the second strand is sufficiently complementary to a target mRNA along at least 19 nucleotide of the second strand length to reduce target gene expression when the RNAi agent is introduced into a mammalian cell, and wherein Dicer cleavage of the dsRNAi agent results in an siRNA comprising the 3'-end of the second strand, thereby reducing expression of the target gene in the mammal. Optionally, the dsRNAi agent further comprises a ligand.

In certain embodiments, the sense strand of the dsRNAi agent contains at least one motif of three identical modifications on three consecutive nucleotides, where one of the motifs occurs at the cleavage site in the sense strand.

In certain embodiments, the antisense strand of the dsRNAi agent can also contain at least one motif of three identical modifications on three consecutive nucleotides, where one of the motifs occurs at or near the cleavage site in the antisense strand.

For a dsRNAi agent having a duplex region of 19-23 nucleotides in length, the cleavage site of the antisense strand is typically around the 10, 11, and 12 positions from the 5'-end. Thus the motifs of three identical modifications may occur at the 9, 10, and 11 positions; the 10, 11, and 12 positions; the 11, 12, and 13 positions; the 12, 13, and 14 positions; or the 13, 14, and 15 positions of the antisense strand, the count starting from the first nucleotide from the 5'-end of the antisense strand, or, the count starting from the first paired nucleotide within the duplex region from the 5'-end of the antisense strand. The cleavage site in the antisense strand may also change according to the length of the duplex region of the dsRNAi agent from the 5'-end.

The sense strand of the dsRNAi agent may contain at least one motif of three identical modifications on three consecutive nucleotides at the cleavage site of the strand; and the antisense strand may have at least one motif of three identical modifications on three consecutive nucleotides at or near the cleavage site of the strand. When the sense strand and the antisense strand form a dsRNA duplex, the sense strand and the antisense strand can be so aligned that one motif of the three nucleotides on the sense strand and one motif of the three nucleotides on the antisense strand have at least one nucleotide overlap, *i.e.*, at least one of the three nucleotides of the motif in the sense strand forms a base pair with at least one of the three nucleotides of the motif in the antisense strand. Alternatively, at least two nucleotides may overlap, or all three nucleotides may overlap.

In some embodiments, the sense strand of the dsRNAi agent may contain more than one motif of three identical modifications on three consecutive nucleotides. The first motif may occur at or near

the cleavage site of the strand and the other motifs may be a wing modification. The term “wing modification” herein refers to a motif occurring at another portion of the strand that is separated from the motif at or near the cleavage site of the same strand. The wing modification is either adjacent to the first motif or is separated by at least one or more nucleotides. When the motifs are immediately adjacent to each other then the chemistries of the motifs are distinct from each other, and when the motifs are separated by one or more nucleotide than the chemistries can be the same or different. Two or more wing modifications may be present. For instance, when two wing modifications are present, each wing modification may occur at one end relative to the first motif which is at or near cleavage site or on either side of the lead motif.

Like the sense strand, the antisense strand of the dsRNAi agent may contain more than one motif of three identical modifications on three consecutive nucleotides, with at least one of the motifs occurring at or near the cleavage site of the strand. This antisense strand may also contain one or more wing modifications in an alignment similar to the wing modifications that may be present on the sense strand.

In some embodiments, the wing modification on the sense strand or antisense strand of the dsRNAi agent typically does not include the first one or two terminal nucleotides at the 3'-end, 5'-end, or both ends of the strand.

In other embodiments, the wing modification on the sense strand or antisense strand of the dsRNAi agent typically does not include the first one or two paired nucleotides within the duplex region at the 3'-end, 5'-end, or both ends of the strand.

When the sense strand and the antisense strand of the dsRNAi agent each contain at least one wing modification, the wing modifications may fall on the same end of the duplex region, and have an overlap of one, two, or three nucleotides.

When the sense strand and the antisense strand of the dsRNAi agent each contain at least two wing modifications, the sense strand and the antisense strand can be so aligned that two modifications each from one strand fall on one end of the duplex region, having an overlap of one, two, or three nucleotides; two modifications each from one strand fall on the other end of the duplex region, having an overlap of one, two or three nucleotides; two modifications one strand fall on each side of the lead motif, having an overlap of one, two or three nucleotides in the duplex region.

In some embodiments, every nucleotide in the sense strand and antisense strand of the dsRNAi agent, including the nucleotides that are part of the motifs, may be modified. Each nucleotide may be modified with the same or different modification which can include one or more alteration of one or both of the non-linking phosphate oxygens or of one or more of the linking phosphate oxygens; alteration of a constituent of the ribose sugar, *e.g.*, of the 2'-hydroxyl on the ribose sugar; wholesale replacement of the phosphate moiety with “dephospho” linkers; modification or replacement of a naturally occurring base; and replacement or modification of the ribose-phosphate backbone.

As nucleic acids are polymers of subunits, many of the modifications occur at a position which is repeated within a nucleic acid, *e.g.*, a modification of a base, or a phosphate moiety, or a non-linking O of a phosphate moiety. In some cases the modification will occur at all of the subject positions in the nucleic acid but in many cases it will not. By way of example, a modification may
 5 only occur at a 3'- or 5' terminal position, may only occur in a terminal region, *e.g.*, at a position on a terminal nucleotide or in the last 2, 3, 4, 5, or 10 nucleotides of a strand. A modification may occur in a double strand region, a single strand region, or in both. A modification may occur only in the double strand region of an RNA or may only occur in a single strand region of a RNA. For example, a phosphorothioate modification at a non-linking O position may only occur at one or both termini, may
 10 only occur in a terminal region, *e.g.*, at a position on a terminal nucleotide or in the last 2, 3, 4, 5, or 10 nucleotides of a strand, or may occur in double strand and single strand regions, particularly at termini. The 5'-end or ends can be phosphorylated.

It may be possible, *e.g.*, to enhance stability, to include particular bases in overhangs, or to include modified nucleotides or nucleotide surrogates, in single strand overhangs, *e.g.*, in a 5'- or 3'-
 15 overhang, or in both. For example, it can be desirable to include purine nucleotides in overhangs. In some embodiments all or some of the bases in a 3'- or 5'-overhang may be modified, *e.g.*, with a modification described herein. Modifications can include, *e.g.*, the use of modifications at the 2' position of the ribose sugar with modifications that are known in the art, *e.g.*, the use of deoxyribonucleotides, 2'-deoxy-2'-fluoro (2'-F) or 2'-O-methyl modified instead of the ribosugar of
 20 the nucleobase, and modifications in the phosphate group, *e.g.*, phosphorothioate modifications. Overhangs need not be homologous with the target sequence.

In some embodiments, each residue of the sense strand and antisense strand is independently modified with LNA, CRN, cET, UNA, HNA, CeNA, 2'-methoxyethyl, 2'-O-methyl, 2'-O-allyl, 2'-C-allyl, 2'-deoxy, 2'-hydroxyl, or 2'-fluoro. The strands can contain more than one modification. In
 25 one embodiment, each residue of the sense strand and antisense strand is independently modified with 2'-O-methyl or 2'-fluoro.

At least two different modifications are typically present on the sense strand and antisense strand. Those two modifications may be the 2'-O-methyl or 2'-fluoro modifications, or others.

In certain embodiments, the N_a or N_b comprise modifications of an alternating pattern. The
 30 term "alternating motif" as used herein refers to a motif having one or more modifications, each modification occurring on alternating nucleotides of one strand. The alternating nucleotide may refer to one per every other nucleotide or one per every three nucleotides, or a similar pattern. For example, if A, B and C each represent one type of modification to the nucleotide, the alternating motif can be "ABABABABABAB...", "AABBAABBAABB...", "AABAABAABAAB...",
 35 "AAABAAABAAAB...", "AAABBBAAABBB...", or "ABCABCABCABC...", *etc.*

The type of modifications contained in the alternating motif may be the same or different. For example, if A, B, C, D each represent one type of modification on the nucleotide, the alternating pattern, *i.e.*, modifications on every other nucleotide, may be the same, but each of the sense strand or

antisense strand can be selected from several possibilities of modifications within the alternating motif such as “ABABAB...”, “ACACAC...”, “BDBDBD...” or “CDCDCD...,” *etc.*

In some embodiments, the dsRNAi agent of the invention comprises the modification pattern for the alternating motif on the sense strand relative to the modification pattern for the alternating motif on the antisense strand is shifted. The shift may be such that the modified group of nucleotides of the sense strand corresponds to a differently modified group of nucleotides of the antisense strand and *vice versa*. For example, the sense strand when paired with the antisense strand in the dsRNA duplex, the alternating motif in the sense strand may start with “ABABAB” from 5’ to 3’ of the strand and the alternating motif in the antisense strand may start with “BABABA” from 5’ to 3’ of the strand within the duplex region. As another example, the alternating motif in the sense strand may start with “AABBAABB” from 5’ to 3’ of the strand and the alternating motif in the antisense strand may start with “BBAABBAA” from 5’ to 3’ of the strand within the duplex region, so that there is a complete or partial shift of the modification patterns between the sense strand and the antisense strand.

In one particular example, the alternating motif in the sense strand is “ABABAB” from 5’ to 3’ of the strand, where each A is an unmodified ribonucleotide and each B is a 2’-O-methyl modified nucleotide.

In one particular example, the alternating motif in the sense strand is “ABABAB” from 5’ to 3’ of the strand, where each A is a 2’-deoxy-2’-fluoro modified nucleotide and each B is a 2’-O-methyl modified nucleotide.

In another particular example, the alternating motif in the antisense strand is “BABABA” from 3’-5’ of the strand, where each A is a 2’-deoxy-2’-fluoro modified nucleotide and each B is a 2’-O-methyl modified nucleotide.

In one particular example, the alternating motif in the sense strand is “ABABAB” from 5’ to 3’ of the strand and the alternating motif in the antisense strand is “BABABA” from 3’-5’ of the strand, where each A is an unmodified ribonucleotide and each B is a 2’-O-methyl modified nucleotide.

In one particular example, the alternating motif in the sense strand is “ABABAB” from 5’ to 3’ of the strand and the alternating motif in the antisense strand is “BABABA” from 3’-5’ of the strand, where each A is a 2’-deoxy-2’-fluoro modified nucleotide and each B is a 2’-O-methyl modified nucleotide.

In some embodiments, the dsRNAi agent comprises the pattern of the alternating motif of 2’-O-methyl modification and 2’-F modification on the sense strand initially has a shift relative to the pattern of the alternating motif of 2’-O-methyl modification and 2’-F modification on the antisense strand initially, *i.e.*, the 2’-O-methyl modified nucleotide on the sense strand base pairs with a 2’-F modified nucleotide on the antisense strand and *vice versa*. The 1 position of the sense strand may start with the 2’-F modification, and the 1 position of the antisense strand may start with the 2’-O-methyl modification.

The introduction of one or more motifs of three identical modifications on three consecutive nucleotides to the sense strand or antisense strand interrupts the initial modification pattern present in

the sense strand or antisense strand. This interruption of the modification pattern of the sense or antisense strand by introducing one or more motifs of three identical modifications on three consecutive nucleotides to the sense or antisense strand may enhance the gene silencing activity against the target gene.

5 In some embodiments, when the motif of three identical modifications on three consecutive nucleotides is introduced to any of the strands, the modification of the nucleotide next to the motif is a different modification than the modification of the motif. For example, the portion of the sequence containing the motif is "...N_aYYYN_b...", where "Y" represents the modification of the motif of three identical modifications on three consecutive nucleotide, and "N_a" and "N_b" represent a modification to
10 the nucleotide next to the motif "YYY" that is different than the modification of Y, and where N_a and N_b can be the same or different modifications. Alternatively, N_a or N_b may be present or absent when there is a wing modification present.

The iRNA may further comprise at least one phosphorothioate or methylphosphonate internucleotide linkage. The phosphorothioate or methylphosphonate internucleotide linkage
15 modification may occur on any nucleotide of the sense strand, antisense strand, or both strands in any position of the strand. For instance, the internucleotide linkage modification may occur on every nucleotide on the sense strand or antisense strand; each internucleotide linkage modification may occur in an alternating pattern on the sense strand or antisense strand; or the sense strand or antisense strand may contain both internucleotide linkage modifications in an alternating pattern. The
20 alternating pattern of the internucleotide linkage modification on the sense strand may be the same or different from the antisense strand, and the alternating pattern of the internucleotide linkage modification on the sense strand may have a shift relative to the alternating pattern of the internucleotide linkage modification on the antisense strand. In one embodiment, a double-stranded RNAi agent comprises 6-8 phosphorothioate internucleotide linkages. In some embodiments, the
25 antisense strand comprises two phosphorothioate internucleotide linkages at the 5'-end and two phosphorothioate internucleotide linkages at the 3'-end, and the sense strand comprises at least two phosphorothioate internucleotide linkages at either the 5'-end or the 3'-end.

In some embodiments, the dsRNAi agent comprises a phosphorothioate or methylphosphonate internucleotide linkage modification in the overhang region. For example, the
30 overhang region may contain two nucleotides having a phosphorothioate or methylphosphonate internucleotide linkage between the two nucleotides. Internucleotide linkage modifications also may be made to link the overhang nucleotides with the terminal paired nucleotides within the duplex region. For example, at least 2, 3, 4, or all the overhang nucleotides may be linked through phosphorothioate or methylphosphonate internucleotide linkage, and optionally, there may be
35 additional phosphorothioate or methylphosphonate internucleotide linkages linking the overhang nucleotide with a paired nucleotide that is next to the overhang nucleotide. For instance, there may be at least two phosphorothioate internucleotide linkages between the terminal three nucleotides, in which two of the three nucleotides are overhang nucleotides, and the third is a paired nucleotide next

to the overhang nucleotide. These terminal three nucleotides may be at the 3'-end of the antisense strand, the 3'-end of the sense strand, the 5'-end of the antisense strand, or the 5'-end of the antisense strand.

In some embodiments, the 2-nucleotide overhang is at the 3'-end of the antisense strand, and there are two phosphorothioate internucleotide linkages between the terminal three nucleotides, wherein two of the three nucleotides are the overhang nucleotides, and the third nucleotide is a paired nucleotide next to the overhang nucleotide. Optionally, the dsRNAi agent may additionally have two phosphorothioate internucleotide linkages between the terminal three nucleotides at both the 5'-end of the sense strand and at the 5'-end of the antisense strand.

In one embodiment, the dsRNAi agent comprises mismatch(es) with the target, within the duplex, or combinations thereof. The mismatch may occur in the overhang region or the duplex region. The base pair may be ranked on the basis of their propensity to promote dissociation or melting (*e.g.*, on the free energy of association or dissociation of a particular pairing, the simplest approach is to examine the pairs on an individual pair basis, though next neighbor or similar analysis can also be used). In terms of promoting dissociation: A:U is preferred over G:C; G:U is preferred over G:C; and I:C is preferred over G:C (I=inosine). Mismatches, *e.g.*, non-canonical or other than canonical pairings (as described elsewhere herein) are preferred over canonical (A:T, A:U, G:C) pairings; and pairings which include a universal base are preferred over canonical pairings.

In certain embodiments, the dsRNAi agent comprises at least one of the first 1, 2, 3, 4, or 5 base pairs within the duplex regions from the 5'-end of the antisense strand independently selected from the group of: A:U, G:U, I:C, and mismatched pairs, *e.g.*, non-canonical or other than canonical pairings or pairings which include a universal base, to promote the dissociation of the antisense strand at the 5'-end of the duplex.

In certain embodiments, the nucleotide at the 1 position within the duplex region from the 5'-end in the antisense strand is selected from A, dA, dU, U, and dT. Alternatively, at least one of the first 1, 2, or 3 base pair within the duplex region from the 5'-end of the antisense strand is an AU base pair. For example, the first base pair within the duplex region from the 5'-end of the antisense strand is an AU base pair.

In other embodiments, the nucleotide at the 3'-end of the sense strand is deoxythymidine (dT) or the nucleotide at the 3'-end of the antisense strand is deoxythymidine (dT). For example, there is a short sequence of deoxythymidine nucleotides, for example, two dT nucleotides on the 3'-end of the sense, antisense strand, or both strands.

In certain embodiments, the sense strand sequence may be represented by formula (I):



wherein:

i and j are each independently 0 or 1;

p and q are each independently 0-6;

each N_a independently represents an oligonucleotide sequence comprising 0-25 modified nucleotides, each sequence comprising at least two differently modified nucleotides;

each N_b independently represents an oligonucleotide sequence comprising 0-10 modified nucleotides;

5 each n_p and n_q independently represent an overhang nucleotide;

wherein N_b and Y do not have the same modification; and

XXX , YYY , and ZZZ each independently represent one motif of three identical modifications on three consecutive nucleotides. In some embodiments, YYY is all 2'-F modified nucleotides.

In some embodiments, the N_a or N_b comprises modifications of alternating pattern.

10 In some embodiments, the YYY motif occurs at or near the cleavage site of the sense strand. For example, when the dsRNAi agent has a duplex region of 17-23 nucleotides in length, the YYY motif can occur at or the vicinity of the cleavage site (*e.g.*: can occur at positions 6, 7, 8; 7, 8, 9; 8, 9, 10; 9, 10, 11; 10, 11, 12; or 11, 12, 13) of the sense strand, the count starting from the first nucleotide, from the 5'-end; or optionally, the count starting at the first paired nucleotide within the duplex

15 region, from the 5'-end.

In one embodiment, i is 1 and j is 0, or i is 0 and j is 1, or both i and j are 1. The sense strand can therefore be represented by the following formulas:

5' n_p - N_a - YYY - N_b - ZZZ - N_a - n_q 3' (Ib);

5' n_p - N_a - XXX - N_b - YYY - N_a - n_q 3' (Ic); or

20 5' n_p - N_a - XXX - N_b - YYY - N_b - ZZZ - N_a - n_q 3' (Id).

When the sense strand is represented by formula (Ib), N_b represents an oligonucleotide sequence comprising 0-10, 0-7, 0-5, 0-4, 0-2, or 0 modified nucleotides. Each N_a independently can represent an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides.

25 When the sense strand is represented as formula (Ic), N_b represents an oligonucleotide sequence comprising 0-10, 0-7, 0-10, 0-7, 0-5, 0-4, 0-2, or 0 modified nucleotides. Each N_a can independently represent an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides.

30 When the sense strand is represented as formula (Id), each N_b independently represents an oligonucleotide sequence comprising 0-10, 0-7, 0-5, 0-4, 0-2, or 0 modified nucleotides. In some embodiments, N_b is 0, 1, 2, 3, 4, 5, or 6. Each N_a can independently represent an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides.

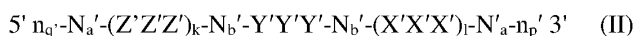
Each of X , Y and Z may be the same or different from each other.

In other embodiments, i is 0 and j is 0, and the sense strand may be represented by the formula:

35 5' n_p - N_a - YYY - N_a - n_q 3' (Ia).

When the sense strand is represented by formula (Ia), each N_a independently can represent an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides.

In one embodiment, the antisense strand sequence of the RNAi may be represented by formula (II):



wherein:

5 k and l are each independently 0 or 1;

p' and q' are each independently 0-6;

each N_a' independently represents an oligonucleotide sequence comprising 0-25 modified nucleotides, each sequence comprising at least two differently modified nucleotides;

10 each N_b' independently represents an oligonucleotide sequence comprising 0-10 modified nucleotides;

each n_p' and n_q' independently represent an overhang nucleotide;

wherein N_b' and Y' do not have the same modification; and

X'X'X', Y'Y'Y', and Z'Z'Z' each independently represent one motif of three identical modifications on three consecutive nucleotides.

15 In some embodiments, the N_a' or N_b' comprises modifications of alternating pattern.

The Y'Y'Y' motif occurs at or near the cleavage site of the antisense strand. For example, when the dsRNAi agent has a duplex region of 17-23 nucleotides in length, the Y'Y'Y' motif can occur at positions 9, 10, 11; 10, 11, 12; 11, 12, 13; 12, 13, 14; or 13, 14, 15 of the antisense strand, with the count starting from the first nucleotide, from the 5'-end; or optionally, the count starting at 20 the first paired nucleotide within the duplex region, from the 5'-end. In some embodiments, the Y'Y'Y' motif occurs at positions 11, 12, 13.

In certain embodiments, Y'Y'Y' motif is all 2'-OMe modified nucleotides.

In certain embodiments, k is 1 and l is 0, or k is 0 and l is 1, or both k and l are 1.

The antisense strand can therefore be represented by the following formulas:

25 5' n_q'-N_a'-Z'Z'Z'-N_b'-Y'Y'Y'-N_a'-n_p' 3' (IIb);

5' n_q'-N_a'-Y'Y'Y'-N_b'-X'X'X'-n_p' 3' (IIc); or

5' n_q'-N_a'-Z'Z'Z'-N_b'-Y'Y'Y'-N_b'-X'X'X'-N_a'-n_p' 3' (IId).

When the antisense strand is represented by formula (IIb), N_b' represents an oligonucleotide sequence comprising 0-10, 0-7, 0-10, 0-7, 0-5, 0-4, 0-2, or 0 modified nucleotides. Each N_a' 30 independently represents an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides.

When the antisense strand is represented as formula (IIc), N_b' represents an oligonucleotide sequence comprising 0-10, 0-7, 0-10, 0-7, 0-5, 0-4, 0-2, or 0 modified nucleotides. Each N_a' 35 independently represents an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides.

When the antisense strand is represented as formula (IId), each N_b' independently represents an oligonucleotide sequence comprising 0-10, 0-7, 0-10, 0-7, 0-5, 0-4, 0-2, or 0 modified nucleotides.

Each N_a' independently represents an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides. In some embodiments, N_b is 0, 1, 2, 3, 4, 5, or 6.

In other embodiments, k is 0 and l is 0 and the antisense strand may be represented by the formula:

5 $5' n_p'-N_a'-Y'Y'Y'-N_a'-n_q' 3' \text{ (Ia)}.$

When the antisense strand is represented as formula (IIa), each N_a' independently represents an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides.

Each of X' , Y' and Z' may be the same or different from each other.

Each nucleotide of the sense strand and antisense strand may be independently modified with
10 LNA, CRN, UNA, cEt, HNA, CeNA, 2'-methoxyethyl, 2'-O-methyl, 2'-O-allyl, 2'-C- allyl, 2'-hydroxyl, or 2'-fluoro. For example, each nucleotide of the sense strand and antisense strand is independently modified with 2'-O-methyl or 2'-fluoro. Each X , Y , Z , X' , Y' , and Z' , in particular, may represent a 2'-O-methyl modification or a 2'-fluoro modification.

In some embodiments, the sense strand of the dsRNAi agent may contain YYY motif
15 occurring at 9, 10, and 11 positions of the strand when the duplex region is 21 nt, the count starting from the first nucleotide from the 5'-end, or optionally, the count starting at the first paired nucleotide within the duplex region, from the 5'- end; and Y represents 2'-F modification. The sense strand may additionally contain XXX motif or ZZZ motifs as wing modifications at the opposite end of the duplex region; and XXX and ZZZ each independently represents a 2'-OMe modification or 2'-F
20 modification.

In some embodiments the antisense strand may contain $Y'Y'Y'$ motif occurring at positions
11, 12, 13 of the strand, the count starting from the first nucleotide from the 5'-end, or optionally, the count starting at the first paired nucleotide within the duplex region, from the 5'- end; and Y' represents 2'-O-methyl modification. The antisense strand may additionally contain $X'X'X'$ motif or
25 $Z'Z'Z'$ motifs as wing modifications at the opposite end of the duplex region; and $X'X'X'$ and $Z'Z'Z'$ each independently represents a 2'-OMe modification or 2'-F modification.

The sense strand represented by any one of the above formulas (Ia), (Ib), (Ic), and (Id) forms a duplex with an antisense strand being represented by any one of formulas (IIa), (IIb), (IIc), and (IId), respectively.

30 Accordingly, the dsRNAi agents for use in the methods of the invention may comprise a sense strand and an antisense strand, each strand having 14 to 30 nucleotides, the iRNA duplex represented by formula (III):

sense: $5' n_p'-N_a'-(X X X)_i-N_b'-Y Y Y-N_b'-(Z Z Z)_j-N_a'-n_q' 3'$

antisense: $3' n_p'-N_a'-(X'X'X')_k-N_b'-Y'Y'Y'-N_b'-(Z'Z'Z')_l-N_a'-n_q' 5'$

35 (III)

wherein:

i, j, k , and l are each independently 0 or 1;

p, p', q , and q' are each independently 0-6;

each N_a and N_a' independently represents an oligonucleotide sequence comprising 0-25 modified nucleotides, each sequence comprising at least two differently modified nucleotides;

each N_b and N_b' independently represents an oligonucleotide sequence comprising 0-10 modified nucleotides;

5 wherein each n_p' , n_p , n_q' , and n_q , each of which may or may not be present, independently represents an overhang nucleotide; and

XXX, YYY, ZZZ, X'X'X', Y'Y'Y', and Z'Z'Z' each independently represent one motif of three identical modifications on three consecutive nucleotides.

10 In one embodiment, i is 0 and j is 0; or i is 1 and j is 0; or i is 0 and j is 1; or both i and j are 0; or both i and j are 1. In another embodiment, k is 0 and l is 0; or k is 1 and l is 0; k is 0 and l is 1; or both k and l are 0; or both k and l are 1.

Exemplary combinations of the sense strand and antisense strand forming an iRNA duplex include the formulas below:

15
$$\begin{array}{l} 5' n_p - N_a - Y Y Y - N_a - n_q 3' \\ 3' n_p' - N_a' - Y'Y'Y' - N_a' n_q' 5' \end{array}$$
 (IIIa)

$$\begin{array}{l} 5' n_p - N_a - Y Y Y - N_b - Z Z Z - N_a - n_q 3' \\ 3' n_p' - N_a' - Y'Y'Y' - N_b' - Z'Z'Z' - N_a' n_q' 5' \end{array}$$
 (IIIb)

20
$$\begin{array}{l} 5' n_p - N_a - X X X - N_b - Y Y Y - N_a - n_q 3' \\ 3' n_p' - N_a' - X'X'X' - N_b' - Y'Y'Y' - N_a' - n_q' 5' \end{array}$$
 (IIIc)

25
$$\begin{array}{l} 5' n_p - N_a - X X X - N_b - Y Y Y - N_b - Z Z Z - N_a - n_q 3' \\ 3' n_p' - N_a' - X'X'X' - N_b' - Y'Y'Y' - N_b' - Z'Z'Z' - N_a' n_q' 5' \end{array}$$
 (IIId)

When the dsRNAi agent is represented by formula (IIIa), each N_a independently represents an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides.

30 When the dsRNAi agent is represented by formula (IIIb), each N_b independently represents an oligonucleotide sequence comprising 1-10, 1-7, 1-5, or 1-4 modified nucleotides. Each N_a independently represents an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides.

When the dsRNAi agent is represented as formula (IIIc), each N_b , N_b' independently represents an oligonucleotide sequence comprising 0-10, 0-7, 0-10, 0-7, 0-5, 0-4, 0-2, or 0 modified nucleotides. Each N_a independently represents an oligonucleotide sequence comprising 2-20, 2-15, or 35 2-10 modified nucleotides.

When the dsRNAi agent is represented as formula (IIId), each N_b , N_b' independently represents an oligonucleotide sequence comprising 0-10, 0-7, 0-10, 0-7, 0-5, 0-4, 0-2, or 0 modified nucleotides. Each N_a , N_a' independently represents an oligonucleotide sequence comprising 2-20, 2-

15, or 2-10 modified nucleotides. Each of N_a , N_a' , N_b , and N_b' independently comprises modifications of alternating pattern.

Each of X, Y, and Z in formulas (III), (IIIa), (IIIb), (IIIc), and (IIId) may be the same or different from each other.

5 When the dsRNAi agent is represented by formula (III), (IIIa), (IIIb), (IIIc), and (IIId), at least one of the Y nucleotides may form a base pair with one of the Y' nucleotides. Alternatively, at least two of the Y nucleotides form base pairs with the corresponding Y' nucleotides; or all three of the Y nucleotides all form base pairs with the corresponding Y' nucleotides.

10 When the dsRNAi agent is represented by formula (IIIb) or (IIId), at least one of the Z nucleotides may form a base pair with one of the Z' nucleotides. Alternatively, at least two of the Z nucleotides form base pairs with the corresponding Z' nucleotides; or all three of the Z nucleotides all form base pairs with the corresponding Z' nucleotides.

When the dsRNAi agent is represented as formula (IIIc) or (IIId), at least one of the X nucleotides may form a base pair with one of the X' nucleotides. Alternatively, at least two of the X nucleotides form base pairs with the corresponding X' nucleotides; or all three of the X nucleotides all form base pairs with the corresponding X' nucleotides.

20 In certain embodiments, the modification on the Y nucleotide is different than the modification on the Y' nucleotide, the modification on the Z nucleotide is different than the modification on the Z' nucleotide, or the modification on the X nucleotide is different than the modification on the X' nucleotide.

In certain embodiments, when the dsRNAi agent is represented by formula (IIId), the N_a modifications are 2'-O-methyl or 2'-fluoro modifications. In other embodiments, when the RNAi agent is represented by formula (IIId), the N_a modifications are 2'-O-methyl or 2'-fluoro modifications and $n_p' > 0$ and at least one n_p' is linked to a neighboring nucleotide *via* phosphorothioate linkage. In yet other embodiments, when the RNAi agent is represented by formula (IIId), the N_a modifications are 2'-O-methyl or 2'-fluoro modifications, $n_p' > 0$ and at least one n_p' is linked to a neighboring nucleotide *via* phosphorothioate linkage, and the sense strand is conjugated to one or more GalNAc derivatives attached through a bivalent or trivalent branched linker (described below). In other embodiments, when the RNAi agent is represented by formula (IIId), the N_a modifications are 2'-O-methyl or 2'-fluoro modifications, $n_p' > 0$ and at least one n_p' is linked to a neighboring nucleotide *via* phosphorothioate linkage, the sense strand comprises at least one phosphorothioate linkage, and the sense strand is conjugated to one or more GalNAc derivatives attached through a bivalent or trivalent branched linker.

35 In some embodiments, when the dsRNAi agent is represented by formula (IIIa), the N_a modifications are 2'-O-methyl or 2'-fluoro modifications, $n_p' > 0$ and at least one n_p' is linked to a neighboring nucleotide *via* phosphorothioate linkage, the sense strand comprises at least one phosphorothioate linkage, and the sense strand is conjugated to one or more GalNAc derivatives attached through a bivalent or trivalent branched linker.

In some embodiments, the dsRNAi agent is a multimer containing at least two duplexes represented by formula (III), (IIIa), (IIIb), (IIIc), and (IIId), wherein the duplexes are connected by a linker. The linker can be cleavable or non-cleavable. Optionally, the multimer further comprises a ligand. Each of the duplexes can target the same gene or two different genes; or each of the duplexes can target same gene at two different target sites.

In some embodiments, the dsRNAi agent is a multimer containing three, four, five, six, or more duplexes represented by formula (III), (IIIa), (IIIb), (IIIc), and (IIId), wherein the duplexes are connected by a linker. The linker can be cleavable or non-cleavable. Optionally, the multimer further comprises a ligand. Each of the duplexes can target the same gene or two different genes; or each of the duplexes can target same gene at two different target sites.

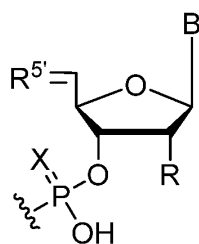
In one embodiment, two dsRNAi agents represented by at least one of formulas (III), (IIIa), (IIIb), (IIIc), and (IIId) are linked to each other at the 5' end, and one or both of the 3' ends, and are optionally conjugated to a ligand. Each of the agents can target the same gene or two different genes; or each of the agents can target same gene at two different target sites.

In certain embodiments, an RNAi agent of the invention may contain a low number of nucleotides containing a 2'-fluoro modification, *e.g.*, 10 or fewer nucleotides with 2'-fluoro modification. For example, the RNAi agent may contain 10, 9, 8, 7, 6, 5, 4, 3, 2, 1 or 0 nucleotides with a 2'-fluoro modification. In a specific embodiment, the RNAi agent of the invention contains 10 nucleotides with a 2'-fluoro modification, *e.g.*, 4 nucleotides with a 2'-fluoro modification in the sense strand and 6 nucleotides with a 2'-fluoro modification in the antisense strand. In another specific embodiment, the RNAi agent of the invention contains 6 nucleotides with a 2'-fluoro modification, *e.g.*, 4 nucleotides with a 2'-fluoro modification in the sense strand and 2 nucleotides with a 2'-fluoro modification in the antisense strand.

In other embodiments, an RNAi agent of the invention may contain an ultra low number of nucleotides containing a 2'-fluoro modification, *e.g.*, 2 or fewer nucleotides containing a 2'-fluoro modification. For example, the RNAi agent may contain 2, 1 or 0 nucleotides with a 2'-fluoro modification. In a specific embodiment, the RNAi agent may contain 2 nucleotides with a 2'-fluoro modification, *e.g.*, 0 nucleotides with a 2-fluoro modification in the sense strand and 2 nucleotides with a 2'-fluoro modification in the antisense strand.

Various publications describe multimeric iRNAs that can be used in the methods of the invention. Such publications include WO2007/091269, U.S. Patent No. 7,858,769, WO2010/141511, WO2007/117686, WO2009/014887, and WO2011/031520 the entire contents of each of which are hereby incorporated herein by reference.

In certain embodiments, the compositions and methods of the disclosure include a vinyl phosphonate (VP) modification of an RNAi agent as described herein. In exemplary embodiments, a 5'-vinyl phosphonate modified nucleotide of the disclosure has the structure:



wherein X is O or S;

R is hydrogen, hydroxy, fluoro, or C₁₋₂₀alkoxy (*e.g.*, methoxy or n-hexadecyloxy);

R^{5'} is =C(H)-P(O)(OH)₂ and the double bond between the C5' carbon and R^{5'} is in the *E* or *Z* orientation (*e.g.*, *E* orientation); and

B is a nucleobase or a modified nucleobase, optionally where B is adenine, guanine, cytosine, thymine, or uracil.

A vinyl phosphonate of the instant disclosure may be attached to either the antisense or the sense strand of a dsRNA of the disclosure. In certain embodiments, a vinyl phosphonate of the instant disclosure is attached to the antisense strand of a dsRNA, optionally at the 5' end of the antisense strand of the dsRNA.

Vinyl phosphonate modifications are also contemplated for the compositions and methods of the instant disclosure. An exemplary vinyl phosphonate structure includes the preceding structure, where R^{5'} is =C(H)-OP(O)(OH)₂ and the double bond between the C5' carbon and R^{5'} is in the *E* or *Z* orientation (*e.g.*, *E* orientation).

As described in more detail below, the iRNA that contains conjugations of one or more carbohydrate moieties to an iRNA can optimize one or more properties of the iRNA. In many cases, the carbohydrate moiety will be attached to a modified subunit of the iRNA. For example, the ribose sugar of one or more ribonucleotide subunits of a iRNA can be replaced with another moiety, *e.g.*, a non-carbohydrate (such as, cyclic) carrier to which is attached a carbohydrate ligand. A ribonucleotide subunit in which the ribose sugar of the subunit has been so replaced is referred to herein as a ribose replacement modification subunit (RRMS). A cyclic carrier may be a carbocyclic ring system, *i.e.*, all ring atoms are carbon atoms, or a heterocyclic ring system, *i.e.*, one or more ring atoms may be a heteroatom, *e.g.*, nitrogen, oxygen, sulfur. The cyclic carrier may be a monocyclic ring system, or may contain two or more rings, *e.g.* fused rings. The cyclic carrier may be a fully saturated ring system, or it may contain one or more double bonds.

The ligand may be attached to the polynucleotide *via* a carrier. The carriers include (i) at least one “backbone attachment point,” such as, two “backbone attachment points” and (ii) at least one “tethering attachment point.” A “backbone attachment point” as used herein refers to a functional group, *e.g.* a hydroxyl group, or generally, a bond available for, and that is suitable for incorporation of the carrier into the backbone, *e.g.*, the phosphate, or modified phosphate, *e.g.*, sulfur containing, backbone, of a ribonucleic acid. A “tethering attachment point” (TAP) in some embodiments refers to a constituent ring atom of the cyclic carrier, *e.g.*, a carbon atom or a heteroatom (distinct from an atom

which provides a backbone attachment point), that connects a selected moiety. The moiety can be, *e.g.*, a carbohydrate, *e.g.* monosaccharide, disaccharide, trisaccharide, tetrasaccharide, oligosaccharide, or polysaccharide. Optionally, the selected moiety is connected by an intervening tether to the cyclic carrier. Thus, the cyclic carrier will often include a functional group, *e.g.*, an amino group, or generally, provide a bond, that is suitable for incorporation or tethering of another chemical entity, *e.g.*, a ligand to the constituent ring.

The iRNA may be conjugated to a ligand *via* a carrier, wherein the carrier can be cyclic group or acyclic group. In some embodiments, the cyclic group is selected from pyrrolidinyl, pyrazolinyl, pyrazolidinyl, imidazolinyl, imidazolidinyl, piperidinyl, piperazinyl, [1,3]dioxolane, oxazolidinyl, isoxazolidinyl, morpholinyl, thiazolidinyl, isothiazolidinyl, quinoxalinyl, pyridazinonyl, tetrahydrofuryl, and decalin. In some embodiments, the acyclic group is a serinol backbone or diethanolamine backbone.

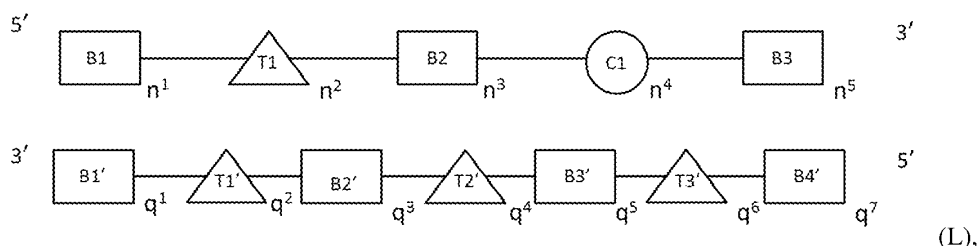
i. Thermally Destabilizing Modifications

In certain embodiments, a dsRNA molecule can be optimized for RNA interference by incorporating thermally destabilizing modifications in the seed region of the antisense strand. As used herein “seed region” means at positions 2-9 of the 5'-end of the referenced strand or at positions 2-8 of the 5'-end of the referenced strand. For example, thermally destabilizing modifications can be incorporated in the seed region of the antisense strand to reduce or inhibit off-target gene silencing.

The term “thermally destabilizing modification(s)” includes modification(s) that would result with a dsRNA with a lower overall melting temperature (T_m) than the T_m of the dsRNA without having such modification(s). For example, the thermally destabilizing modification(s) can decrease the T_m of the dsRNA by 1 – 4 °C, such as one, two, three or four degrees Celcius. And, the term “thermally destabilizing nucleotide” refers to a nucleotide containing one or more thermally destabilizing modifications.

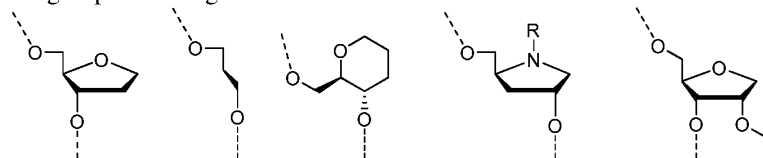
It has been discovered that dsRNAs with an antisense strand comprising at least one thermally destabilizing modification of the duplex within the first 9 nucleotide positions, counting from the 5' end, of the antisense strand have reduced off-target gene silencing activity. Accordingly, in some embodiments, the antisense strand comprises at least one (*e.g.*, one, two, three, four, five or more) thermally destabilizing modification of the duplex within the first 9 nucleotide positions of the 5' region of the antisense strand. In some embodiments, one or more thermally destabilizing modification(s) of the duplex is/are located in positions 2-9, such as, positions 4-8, from the 5'-end of the antisense strand. In some further embodiments, the thermally destabilizing modification(s) of the duplex is/are located at position 6, 7 or 8 from the 5'-end of the antisense strand. In still some further embodiments, the thermally destabilizing modification of the duplex is located at position 7 from the 5'-end of the antisense strand. In some embodiments, the thermally destabilizing modification of the duplex is located at position 2, 3, 4, 5 or 9 from the 5'-end of the antisense strand.

An iRNA agent comprises a sense strand and an antisense strand, each strand having 14 to 40 nucleotides. The RNAi agent may be represented by formula (L):

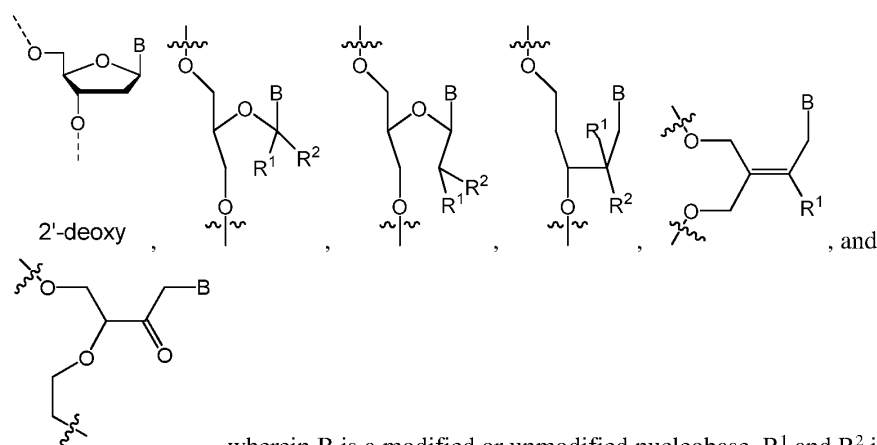


In formula (L), B1, B2, B3, B1', B2', B3', and B4' each are independently a nucleotide containing a modification selected from the group consisting of 2'-O-alkyl, 2'-substituted alkoxy, 2'-substituted alkyl, 2'-halo, ENA, and BNA/LNA. In one embodiment, B1, B2, B3, B1', B2', B3', and B4' each contain 2'-OMe modifications. In one embodiment, B1, B2, B3, B1', B2', B3', and B4' each contain 2'-OMe or 2'-F modifications. In one embodiment, at least one of B1, B2, B3, B1', B2', B3', and B4' contain 2'-O-N-methylacetamido (2'-O-NMA, , 2'-O-CH₂C(O)N(Me)H) modification.

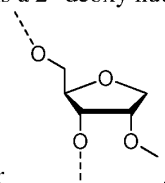
C1 is a thermally destabilizing nucleotide placed at a site opposite to the seed region of the antisense strand (*i.e.*, at positions 2-8 of the 5'-end of the antisense strand or at positions 2-9 of the 5'-end of the referenced strand). For example, C1 is at a position of the sense strand that pairs with a nucleotide at positions 2-8 of the 5'-end of the antisense strand. In one example, C1 is at position 15 from the 5'-end of the sense strand. C1 nucleotide bears the thermally destabilizing modification which can include abasic modification; mismatch with the opposing nucleotide in the duplex; and sugar modification such as 2'-deoxy modification or acyclic nucleotide *e.g.*, unlocked nucleic acids (UNA) or glycerol nucleic acid (GNA); and 2'-5'-linked ribonucleotides ("3'-RNA"). In one embodiment, C1 has thermally destabilizing modification selected from the group consisting of: i) mismatch with the opposing nucleotide in the antisense strand; ii) abasic modification selected from the group consisting of:



; and iii) sugar modification selected from the group consisting of:



- 5 , wherein B is a modified or unmodified nucleobase, R¹ and R² independently are H, halogen, OR₃, or alkyl; and R₃ is H, alkyl, cycloalkyl, aryl, aralkyl, heteroaryl or sugar. In one embodiment, the thermally destabilizing modification in C1 is a mismatch selected from the group consisting of G:G, G:A, G:U, G:T, A:A, A:C, C:C, C:U, C:T, U:U, T:T, and U:T; and optionally, at least one nucleobase in the mismatch pair is a 2'-deoxy nucleobase. In one example, the thermally



- destabilizing modification in C1 is GNA or T1, T1', T2', and T3' each independently represent a nucleotide comprising a modification providing the nucleotide a steric bulk that is less or equal to the steric bulk of a 2'-OMe modification. A steric bulk refers to the sum of steric effects of a modification. Methods for determining steric effects of a modification of a nucleotide are known to one skilled in the art. The modification can be at the 2' position of a ribose sugar of the nucleotide, or a modification to a non-ribose nucleotide, acyclic nucleotide, or the backbone of the nucleotide that is similar or equivalent to the 2' position of the ribose sugar, and provides the nucleotide a steric bulk that is less than or equal to the steric bulk of a 2'-OMe modification. For example, T1, T1', T2', and T3' are each independently selected from DNA, RNA, LNA, 2'-F, and 2'-F-5'-methyl. In one embodiment, T1 is DNA. In one embodiment, T1' is DNA, RNA or LNA. In one embodiment, T2' is DNA or RNA. In one embodiment, T3' is DNA or RNA.

- n¹, n³, and q¹ are independently 4 to 15 nucleotides in length.
 20 n⁵, q³, and q⁷ are independently 1-6 nucleotide(s) in length.
 n⁴, q², and q⁶ are independently 1-3 nucleotide(s) in length; alternatively, n⁴ is 0.
 q⁵ is independently 0-10 nucleotide(s) in length.
 n² and q⁴ are independently 0-3 nucleotide(s) in length.

Alternatively, n⁴ is 0-3 nucleotide(s) in length.

- 25 In one embodiment, n⁴ can be 0. In one example, n⁴ is 0, and q² and q⁶ are 1. In another example, n⁴ is 0, and q² and q⁶ are 1, with two phosphorothioate internucleotide linkage modifications

within position 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand).

5 In one embodiment, n^4 , q^2 , and q^6 are each 1.

In one embodiment, n^2 , n^4 , q^2 , q^4 , and q^6 are each 1.

In one embodiment, C1 is at position 14-17 of the 5'-end of the sense strand, when the sense strand is 19-22 nucleotides in length, and n^4 is 1. In one embodiment, C1 is at position 15 of the 5'-end of the sense strand

10 In one embodiment, T3' starts at position 2 from the 5' end of the antisense strand. In one example, T3' is at position 2 from the 5' end of the antisense strand and q^6 is equal to 1.

In one embodiment, T1' starts at position 14 from the 5' end of the antisense strand. In one example, T1' is at position 14 from the 5' end of the antisense strand and q^2 is equal to 1.

In an exemplary embodiment, T3' starts from position 2 from the 5' end of the antisense strand and T1' starts from position 14 from the 5' end of the antisense strand. In one example, T3' starts from position 2 from the 5' end of the antisense strand and q^6 is equal to 1 and T1' starts from position 14 from the 5' end of the antisense strand and q^2 is equal to 1.

In one embodiment, T1' and T3' are separated by 11 nucleotides in length (*i.e.* not counting the T1' and T3' nucleotides).

20 In one embodiment, T1' is at position 14 from the 5' end of the antisense strand. In one example, T1' is at position 14 from the 5' end of the antisense strand and q^2 is equal to 1, and the modification at the 2' position or positions in a non-ribose, acyclic or backbone that provide less steric bulk than a 2'-OMe ribose.

In one embodiment, T3' is at position 2 from the 5' end of the antisense strand. In one example, T3' is at position 2 from the 5' end of the antisense strand and q^6 is equal to 1, and the modification at the 2' position or positions in a non-ribose, acyclic or backbone that provide less than or equal to steric bulk than a 2'-OMe ribose.

In one embodiment, T1 is at the cleavage site of the sense strand. In one example, T1 is at position 11 from the 5' end of the sense strand, when the sense strand is 19-22 nucleotides in length, and n^2 is 1. In an exemplary embodiment, T1 is at the cleavage site of the sense strand at position 11 from the 5' end of the sense strand, when the sense strand is 19-22 nucleotides in length, and n^2 is 1,

In one embodiment, T2' starts at position 6 from the 5' end of the antisense strand. In one example, T2' is at positions 6-10 from the 5' end of the antisense strand, and q^4 is 1.

In an exemplary embodiment, T1 is at the cleavage site of the sense strand, for instance, at position 11 from the 5' end of the sense strand, when the sense strand is 19-22 nucleotides in length, and n^2 is 1; T1' is at position 14 from the 5' end of the antisense strand, and q^2 is equal to 1, and the modification to T1' is at the 2' position of a ribose sugar or at positions in a non-ribose, acyclic or backbone that provide less steric bulk than a 2'-OMe ribose; T2' is at positions 6-10 from the 5' end

of the antisense strand, and q^4 is 1; and T3' is at position 2 from the 5' end of the antisense strand, and q^6 is equal to 1, and the modification to T3' is at the 2' position or at positions in a non-ribose, acyclic or backbone that provide less than or equal to steric bulk than a 2'-OMe ribose.

In one embodiment, T2' starts at position 8 from the 5' end of the antisense strand. In one example,

5 T2' starts at position 8 from the 5' end of the antisense strand, and q^4 is 2.

In one embodiment, T2' starts at position 9 from the 5' end of the antisense strand. In one example, T2' is at position 9 from the 5' end of the antisense strand, and q^4 is 1.

In one embodiment, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, T2' is 2'-F, q^4 is 1, B3' is 2'-OMe or 2'-F, q^5 is 6, T3' is 2'-F, q^6 is 1, B4' is 2'-OMe, and q^7 is 1; with two phosphorothioate internucleotide linkage modifications within positions 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand).

15 In one embodiment, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, T2' is 2'-F, q^4 is 1, B3' is 2'-OMe or 2'-F, q^5 is 6, T3' is 2'-F, q^6 is 1, B4' is 2'-OMe, and q^7 is 1; with two phosphorothioate internucleotide linkage modifications within positions 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand).

20 In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, T2' is 2'-F, q^4 is 2, B3' is 2'-OMe or 2'-F, q^5 is 5, T3' is 2'-F, q^6 is 1, B4' is 2'-OMe, and q^7 is 1.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, T2' is 2'-F, q^4 is 2, B3' is 2'-OMe or 2'-F, q^5 is 5, T3' is 2'-F, q^6 is 1, B4' is 2'-OMe, and q^7 is 1; with two phosphorothioate internucleotide linkage modifications within positions 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand).

25 In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 6, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 7, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, T2' is 2'-F, q^4 is 2, B3' is 2'-OMe or 2'-F, q^5 is 5, T3' is 2'-F, q^6 is 1, B4' is 2'-OMe, and q^7 is 1.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 6, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 7, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4,

T2' is 2'-F, q^4 is 2, B3' is 2'-OMe or 2'-F, q^5 is 5, T3' is 2'-F, q^6 is 1, B4' is 2'-OMe, and q^7 is 1; with two phosphorothioate internucleotide linkage modifications within positions 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand).

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, T2' is 2'-F, q^4 is 1, B3' is 2'-OMe or 2'-F, q^5 is 6, T3' is 2'-F, q^6 is 1, B4' is 2'-OMe, and q^7 is 1.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, T2' is 2'-F, q^4 is 1, B3' is 2'-OMe or 2'-F, q^5 is 6, T3' is 2'-F, q^6 is 1, B4' is 2'-OMe, and q^7 is 1; with two phosphorothioate internucleotide linkage modifications within positions 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand).

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 5, T2' is 2'-F, q^4 is 1, B3' is 2'-OMe or 2'-F, q^5 is 5, T3' is 2'-F, q^6 is 1, B4' is 2'-OMe, and q^7 is 1; optionally with at least 2 additional TT at the 3'-end of the antisense strand.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 5, T2' is 2'-F, q^4 is 1, B3' is 2'-OMe or 2'-F, q^5 is 5, T3' is 2'-F, q^6 is 1, B4' is 2'-OMe, and q^7 is 1;

optionally with at least 2 additional TT at the 3'-end of the antisense strand; with two phosphorothioate internucleotide linkage modifications within positions 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand).

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, q^4 is 0, B3' is 2'-OMe or 2'-F, q^5 is 7, T3' is 2'-F, q^6 is 1, B4' is 2'-OMe, and q^7 is 1.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4,

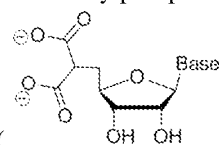
q^4 is 0, B3' is 2'-OMe or 2'-F, q^5 is 7, T3' is 2'-F, q^6 is 1, B4' is 2'-OMe, and q^7 is 1; with two phosphorothioate internucleotide linkage modifications within positions 1-5 of the sense strand (counting from the 5'-end), and two phosphorothioate internucleotide linkage modifications at

positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end).

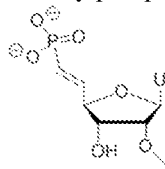
In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, T2' is 2'-F, q^4 is 2, B3' is 2'-OMe or 2'-F, q^5 is 5, T3' is 2'-F, q^6 is 1, B4' is 2'-F, and q^7 is 1. In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, T2' is 2'-F, q^4 is 2, B3' is 2'-OMe or 2'-F, q^5 is 5, T3' is 2'-F, q^6 is 1, B4' is 2'-F, and q^7 is 1; with two phosphorothioate internucleotide linkage modifications within positions 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand).

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, q^4 is 0, B3' is 2'-OMe or 2'-F, q^5 is 7, T3' is 2'-F, q^6 is 1, B4' is 2'-F, and q^7 is 1. In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, q^4 is 0, B3' is 2'-OMe or 2'-F, q^5 is 7, T3' is 2'-F, q^6 is 1, B4' is 2'-F, and q^7 is 1; with two phosphorothioate internucleotide linkage modifications within positions 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand).

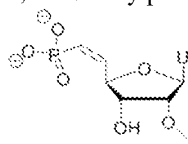
The RNAi agent can comprise a phosphorus-containing group at the 5'-end of the sense strand or antisense strand. The 5'-end phosphorus-containing group can be 5'-end phosphate (5'-P), 5'-end phosphorothioate (5'-PS), 5'-end phosphorodithioate (5'-PS₂), 5'-end vinylphosphonate (5'-



VP), 5'-end methylphosphonate (MePhos), or 5'-deoxy-5'-C-malonyl (). When the 5'-end phosphorus-containing group is 5'-end vinylphosphonate (5'-VP), the 5'-VP can be either



5'-E-VP isomer (i.e., *trans*-vinylphosphonate,



vinylphosphonate, or mixtures thereof.

In one embodiment, the RNAi agent comprises a phosphorus-containing group at the 5'-end of the sense strand. In one embodiment, the RNAi agent comprises a phosphorus-containing group at the 5'-end of the antisense strand.

In one embodiment, the RNAi agent comprises a 5'-P. In one embodiment, the RNAi agent comprises a 5'-P in the antisense strand.

In one embodiment, the RNAi agent comprises a 5'-PS. In one embodiment, the RNAi agent comprises a 5'-PS in the antisense strand.

In one embodiment, the RNAi agent comprises a 5'-VP. In one embodiment, the RNAi agent comprises a 5'-VP in the antisense strand. In one embodiment, the RNAi agent comprises a 5'-E-VP in the antisense strand. In one embodiment, the RNAi agent comprises a 5'-Z-VP in the antisense strand.

In one embodiment, the RNAi agent comprises a 5'-PS₂. In one embodiment, the RNAi agent comprises a 5'-PS₂ in the antisense strand.

In one embodiment, the RNAi agent comprises a 5'-PS₂. In one embodiment, the RNAi agent comprises a 5'-deoxy-5'-C-malonyl in the antisense strand.

In one embodiment, B1 is 2'-OMe or 2'-F, n¹ is 8, T1 is 2'-F, n² is 3, B2 is 2'-OMe, n³ is 7, n⁴ is 0, B3 is 2'-OMe, n⁵ is 3, B1' is 2'-OMe or 2'-F, q¹ is 9, T1' is 2'-F, q² is 1, B2' is 2'-OMe or 2'-F, q³ is 4, T2' is 2'-F, q⁴ is 2, B3' is 2'-OMe or 2'-F, q⁵ is 5, T3' is 2'-F, q⁶ is 1, B4' is 2'-OMe, and q⁷ is 1. The RNAi agent also comprises a 5'-PS.

In one embodiment, B1 is 2'-OMe or 2'-F, n¹ is 8, T1 is 2'-F, n² is 3, B2 is 2'-OMe, n³ is 7, n⁴ is 0, B3 is 2'-OMe, n⁵ is 3, B1' is 2'-OMe or 2'-F, q¹ is 9, T1' is 2'-F, q² is 1, B2' is 2'-OMe or 2'-F, q³ is 4, T2' is 2'-F, q⁴ is 2, B3' is 2'-OMe or 2'-F, q⁵ is 5, T3' is 2'-F, q⁶ is 1, B4' is 2'-OMe, and q⁷ is 1. The RNAi agent also comprises a 5'-P.

In one embodiment, B1 is 2'-OMe or 2'-F, n¹ is 8, T1 is 2'-F, n² is 3, B2 is 2'-OMe, n³ is 7, n⁴ is 0, B3 is 2'-OMe, n⁵ is 3, B1' is 2'-OMe or 2'-F, q¹ is 9, T1' is 2'-F, q² is 1, B2' is 2'-OMe or 2'-F, q³ is 4, T2' is 2'-F, q⁴ is 2, B3' is 2'-OMe or 2'-F, q⁵ is 5, T3' is 2'-F, q⁶ is 1, B4' is 2'-OMe, and q⁷ is 1. The RNAi agent also comprises a 5'-VP. The 5'-VP may be 5'-E-VP, 5'-Z-VP, or combination thereof.

In one embodiment, B1 is 2'-OMe or 2'-F, n¹ is 8, T1 is 2'-F, n² is 3, B2 is 2'-OMe, n³ is 7, n⁴ is 0, B3 is 2'-OMe, n⁵ is 3, B1' is 2'-OMe or 2'-F, q¹ is 9, T1' is 2'-F, q² is 1, B2' is 2'-OMe or 2'-F, q³ is 4, T2' is 2'-F, q⁴ is 2, B3' is 2'-OMe or 2'-F, q⁵ is 5, T3' is 2'-F, q⁶ is 1, B4' is 2'-OMe, and q⁷ is 1. The RNAi agent also comprises a 5'-PS₂.

In one embodiment, B1 is 2'-OMe or 2'-F, n¹ is 8, T1 is 2'-F, n² is 3, B2 is 2'-OMe, n³ is 7, n⁴ is 0, B3 is 2'-OMe, n⁵ is 3, B1' is 2'-OMe or 2'-F, q¹ is 9, T1' is 2'-F, q² is 1, B2' is 2'-OMe or 2'-F, q³ is 4, T2' is 2'-F, q⁴ is 2, B3' is 2'-OMe or 2'-F, q⁵ is 5, T3' is 2'-F, q⁶ is 1, B4' is 2'-OMe, and q⁷ is 1. The RNAi agent also comprises a 5'-deoxy-5'-C-malonyl.

In one embodiment, B1 is 2'-OMe or 2'-F, n¹ is 8, T1 is 2'-F, n² is 3, B2 is 2'-OMe, n³ is 7, n⁴ is 0, B3 is 2'-OMe, n⁵ is 3, B1' is 2'-OMe or 2'-F, q¹ is 9, T1' is 2'-F, q² is 1, B2' is 2'-OMe or 2'-F,

q³ is 4, T2' is 2'-F, q⁴ is 2, B3' is 2'-OMe or 2'-F, q⁵ is 5, T3' is 2'-F, q⁶ is 1, B4' is 2'-OMe, and q⁷ is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand). The RNAi agent also comprises a 5'-P.

In one embodiment, B1 is 2'-OMe or 2'-F, n¹ is 8, T1 is 2'-F, n² is 3, B2 is 2'-OMe, n³ is 7, n⁴ is 0, B3 is 2'-OMe, n⁵ is 3, B1' is 2'-OMe or 2'-F, q¹ is 9, T1' is 2'-F, q² is 1, B2' is 2'-OMe or 2'-F, q³ is 4, T2' is 2'-F, q⁴ is 2, B3' is 2'-OMe or 2'-F, q⁵ is 5, T3' is 2'-F, q⁶ is 1, B4' is 2'-OMe, and q⁷ is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand). The RNAi agent also comprises a 5'-PS.

In one embodiment, B1 is 2'-OMe or 2'-F, n¹ is 8, T1 is 2'-F, n² is 3, B2 is 2'-OMe, n³ is 7, n⁴ is 0, B3 is 2'-OMe, n⁵ is 3, B1' is 2'-OMe or 2'-F, q¹ is 9, T1' is 2'-F, q² is 1, B2' is 2'-OMe or 2'-F, q³ is 4, T2' is 2'-F, q⁴ is 2, B3' is 2'-OMe or 2'-F, q⁵ is 5, T3' is 2'-F, q⁶ is 1, B4' is 2'-OMe, and q⁷ is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand). The RNAi agent also comprises a 5'-VP. The 5'-VP may be 5'-E-VP, 5'-Z-VP, or combination thereof.

In one embodiment, B1 is 2'-OMe or 2'-F, n¹ is 8, T1 is 2'-F, n² is 3, B2 is 2'-OMe, n³ is 7, n⁴ is 0, B3 is 2'-OMe, n⁵ is 3, B1' is 2'-OMe or 2'-F, q¹ is 9, T1' is 2'-F, q² is 1, B2' is 2'-OMe or 2'-F, q³ is 4, T2' is 2'-F, q⁴ is 2, B3' is 2'-OMe or 2'-F, q⁵ is 5, T3' is 2'-F, q⁶ is 1, B4' is 2'-OMe, and q⁷ is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand). The RNAi agent also comprises a 5'-PS₂.

In one embodiment, B1 is 2'-OMe or 2'-F, n¹ is 8, T1 is 2'-F, n² is 3, B2 is 2'-OMe, n³ is 7, n⁴ is 0, B3 is 2'-OMe, n⁵ is 3, B1' is 2'-OMe or 2'-F, q¹ is 9, T1' is 2'-F, q² is 1, B2' is 2'-OMe or 2'-F, q³ is 4, T2' is 2'-F, q⁴ is 2, B3' is 2'-OMe or 2'-F, q⁵ is 5, T3' is 2'-F, q⁶ is 1, B4' is 2'-OMe, and q⁷ is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand).

strand). The RNAi agent also comprises a 5'-deoxy-5'-C-malonyl.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, q^4 is 0, B3' is 2'-OMe or 2'-F, q^5 is 7, T3' is 2'-F, q^6 is 1, B4' is 2'-OMe, and q^7 is 1. The

5 RNAi agent also comprises a 5'-P.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, q^4 is 0, B3' is 2'-OMe or 2'-F, q^5 is 7, T3' is 2'-F, q^6 is 1, B4' is 2'-OMe, and q^7 is 1. The dsRNA agent also comprises a 5'-PS.

10 In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, q^4 is 0, B3' is 2'-OMe or 2'-F, q^5 is 7, T3' is 2'-F, q^6 is 1, B4' is 2'-OMe, and q^7 is 1. The RNAi agent also comprises a 5'-VP. The 5'-VP may be 5'-E-VP, 5'-Z-VP, or combination thereof.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, q^4 is 0, B3' is 2'-OMe or 2'-F, q^5 is 7, T3' is 2'-F, q^6 is 1, B4' is 2'-OMe, and q^7 is 1. The RNAi agent also comprises a 5'-PS₂.

20 In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, q^4 is 0, B3' is 2'-OMe or 2'-F, q^5 is 7, T3' is 2'-F, q^6 is 1, B4' is 2'-OMe, and q^7 is 1. The RNAi agent also comprises a 5'-deoxy-5'-C-malonyl.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, q^4 is 0, B3' is 2'-OMe or 2'-F, q^5 is 7, T3' is 2'-F, q^6 is 1, B4' is 2'-OMe, and q^7 is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end). The RNAi agent also comprises a 5'-P.

25 In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, q^4 is 0, B3' is 2'-OMe or 2'-F, q^5 is 7, T3' is 2'-F, q^6 is 1, B4' is 2'-OMe, and q^7 is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end). The RNAi agent also comprises a 5'-PS.

30 In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, q^4 is 0, B3' is 2'-OMe or 2'-F, q^5 is 7, T3' is 2'-F, q^6 is 1, B4' is 2'-OMe, and q^7 is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end). The RNAi agent also comprises a 5'-PS.

phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end). The RNAi agent also comprises a 5'-VP. The

5 5'-VP may be 5'-E-VP, 5'-Z-VP, or combination thereof.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, q^4 is 0, B3' is 2'-OMe or 2'-F, q^5 is 7, T3' is 2'-F, q^6 is 1, B4' is 2'-OMe, and q^7 is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end). The RNAi agent also comprises a 5'-PS₂.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, q^4 is 0, B3' is 2'-OMe or 2'-F, q^5 is 7, T3' is 2'-F, q^6 is 1, B4' is 2'-OMe, and q^7 is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end). The RNAi agent also comprises a 5'-deoxy-5'-C-malonyl.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, T2' is 2'-F, q^4 is 2, B3' is 2'-OMe or 2'-F, q^5 is 5, T3' is 2'-F, q^6 is 1, B4' is 2'-F, and q^7 is 1. The RNAi agent also comprises a 5'-P.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, T2' is 2'-F, q^4 is 2, B3' is 2'-OMe or 2'-F, q^5 is 5, T3' is 2'-F, q^6 is 1, B4' is 2'-F, and q^7 is 1. The RNAi agent also comprises a 5'-PS.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, T2' is 2'-F, q^4 is 2, B3' is 2'-OMe or 2'-F, q^5 is 5, T3' is 2'-F, q^6 is 1, B4' is 2'-F, and q^7 is 1. The RNAi agent also comprises a 5'-VP. The 5'-VP may be 5'-E-VP, 5'-Z-VP, or combination thereof.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, T2' is 2'-F, q^4 is 2, B3' is 2'-OMe or 2'-F, q^5 is 5, T3' is 2'-F, q^6 is 1, B4' is 2'-F, and q^7 is 1. The dsRNAi RNA agent also comprises a 5'-PS₂.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, T2' is 2'-F, q^4 is 2, B3' is 2'-OMe or 2'-F, q^5 is 5, T3' is 2'-F, q^6 is 1, B4' is 2'-F, and q^7 is 1. The RNAi agent also comprises a 5'-deoxy-5'-C-malonyl.

- 5 In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, T2' is 2'-F, q^4 is 2, B3' is 2'-OMe or 2'-F, q^5 is 5, T3' is 2'-F, q^6 is 1, B4' is 2'-F, and q^7 is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand). The RNAi agent also comprises a 5'-P.

- 10 In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, T2' is 2'-F, q^4 is 2, B3' is 2'-OMe or 2'-F, q^5 is 5, T3' is 2'-F, q^6 is 1, B4' is 2'-F, and q^7 is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand). The RNAi agent also comprises a 5'-PS.

- 15 In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, T2' is 2'-F, q^4 is 2, B3' is 2'-OMe or 2'-F, q^5 is 5, T3' is 2'-F, q^6 is 1, B4' is 2'-F, and q^7 is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand). The RNAi agent also comprises a 5'-VP. The 5'-VP may be 5'-E-VP, 5'-Z-VP, or combination thereof.

- 20 In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, T2' is 2'-F, q^4 is 2, B3' is 2'-OMe or 2'-F, q^5 is 5, T3' is 2'-F, q^6 is 1, B4' is 2'-F, and q^7 is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand). The RNAi agent also comprises a 5'-PS₂.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, T2' is 2'-F, q^4 is 2, B3' is 2'-OMe or 2'-F, q^5 is 5, T3' is 2'-F, q^6 is 1, B4' is 2'-F, and q^7 is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand). The RNAi agent also comprises a 5'-deoxy-5'-C-malonyl.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, q^4 is 0, B3' is 2'-OMe or 2'-F, q^5 is 7, T3' is 2'-F, q^6 is 1, B4' is 2'-F, and q^7 is 1. The RNAi agent also comprises a 5'-P.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, q^4 is 0, B3' is 2'-OMe or 2'-F, q^5 is 7, T3' is 2'-F, q^6 is 1, B4' is 2'-F, and q^7 is 1. The RNAi agent also comprises a 5'-PS.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, q^4 is 0, B3' is 2'-OMe or 2'-F, q^5 is 7, T3' is 2'-F, q^6 is 1, B4' is 2'-F, and q^7 is 1. The RNAi agent also comprises a 5'-VP. The 5'-VP may be 5'-E-VP, 5'-Z-VP, or combination thereof.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, q^4 is 0, B3' is 2'-OMe or 2'-F, q^5 is 7, T3' is 2'-F, q^6 is 1, B4' is 2'-F, and q^7 is 1. The RNAi agent also comprises a 5'-PS₂.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, q^4 is 0, B3' is 2'-OMe or 2'-F, q^5 is 7, T3' is 2'-F, q^6 is 1, B4' is 2'-F, and q^7 is 1. The RNAi agent also comprises a 5'-deoxy-5'-C-malonyl.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, q^4 is 0, B3' is 2'-OMe or 2'-F, q^5 is 7, T3' is 2'-F, q^6 is 1, B4' is 2'-F, and q^7 is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand). The RNAi agent also comprises a 5'-P.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F,

q³ is 4, q⁴ is 0, B3' is 2'-OMe or 2'-F, q⁵ is 7, T3' is 2'-F, q⁶ is 1, B4' is 2'-F, and q⁷ is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand). The RNAi agent also comprises a 5'-PS.

In one embodiment, B1 is 2'-OMe or 2'-F, n¹ is 8, T1 is 2'-F, n² is 3, B2 is 2'-OMe, n³ is 7, n⁴ is 0, B3 is 2'-OMe, n⁵ is 3, B1' is 2'-OMe or 2'-F, q¹ is 9, T1' is 2'-F, q² is 1, B2' is 2'-OMe or 2'-F, q³ is 4, q⁴ is 0, B3' is 2'-OMe or 2'-F, q⁵ is 7, T3' is 2'-F, q⁶ is 1, B4' is 2'-F, and q⁷ is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand). The RNAi agent also comprises a 5'-VP. The 5'-VP may be 5'-E-VP, 5'-Z-VP, or combination thereof.

In one embodiment, B1 is 2'-OMe or 2'-F, n¹ is 8, T1 is 2'-F, n² is 3, B2 is 2'-OMe, n³ is 7, n⁴ is 0, B3 is 2'-OMe, n⁵ is 3, B1' is 2'-OMe or 2'-F, q¹ is 9, T1' is 2'-F, q² is 1, B2' is 2'-OMe or 2'-F, q³ is 4, q⁴ is 0, B3' is 2'-OMe or 2'-F, q⁵ is 7, T3' is 2'-F, q⁶ is 1, B4' is 2'-F, and q⁷ is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand). The RNAi agent also comprises a 5'-PS₂.

In one embodiment, B1 is 2'-OMe or 2'-F, n¹ is 8, T1 is 2'-F, n² is 3, B2 is 2'-OMe, n³ is 7, n⁴ is 0, B3 is 2'-OMe, n⁵ is 3, B1' is 2'-OMe or 2'-F, q¹ is 9, T1' is 2'-F, q² is 1, B2' is 2'-OMe or 2'-F, q³ is 4, q⁴ is 0, B3' is 2'-OMe or 2'-F, q⁵ is 7, T3' is 2'-F, q⁶ is 1, B4' is 2'-F, and q⁷ is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand). The RNAi agent also comprises a 5'-deoxy-5'-C-malonyl.

In one embodiment, B1 is 2'-OMe or 2'-F, n¹ is 8, T1 is 2'-F, n² is 3, B2 is 2'-OMe, n³ is 7, n⁴ is 0, B3 is 2'-OMe, n⁵ is 3, B1' is 2'-OMe or 2'-F, q¹ is 9, T1' is 2'-F, q² is 1, B2' is 2'-OMe or 2'-F, q³ is 4, T2' is 2'-F, q⁴ is 2, B3' is 2'-OMe or 2'-F, q⁵ is 5, T3' is 2'-F, q⁶ is 1, B4' is 2'-OMe, and q⁷ is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand).

strand). The RNAi agent also comprises a 5'-P and a targeting ligand. In one embodiment, the 5'-P is at the 5'-end of the antisense strand, and the targeting ligand is at the 3'-end of the sense strand.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, T2' is 2'-F, q^4 is 2, B3' is 2'-OMe or 2'-F, q^5 is 5, T3' is 2'-F, q^6 is 1, B4' is 2'-OMe, and q^7 is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand). The RNAi agent also comprises a 5'-PS and a targeting ligand. In one embodiment, the 5'-PS is at the 5'-end of the antisense strand, and the targeting ligand is at the 3'-end of the sense strand.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, T2' is 2'-F, q^4 is 2, B3' is 2'-OMe or 2'-F, q^5 is 5, T3' is 2'-F, q^6 is 1, B4' is 2'-OMe, and q^7 is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand). The RNAi agent also comprises a 5'-VP (e.g., a 5'-E-VP, 5'-Z-VP, or combination thereof), and a targeting ligand.

In one embodiment, the 5'-VP is at the 5'-end of the antisense strand, and the targeting ligand is at the 3'-end of the sense strand.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, T2' is 2'-F, q^4 is 2, B3' is 2'-OMe or 2'-F, q^5 is 5, T3' is 2'-F, q^6 is 1, B4' is 2'-OMe, and q^7 is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand). The RNAi agent also comprises a 5'-PS₂ and a targeting ligand. In one embodiment, the 5'-PS₂ is at the 5'-end of the antisense strand, and the targeting ligand is at the 3'-end of the sense strand.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, T2' is 2'-F, q^4 is 2, B3' is 2'-OMe or 2'-F, q^5 is 5, T3' is 2'-F, q^6 is 1, B4' is 2'-OMe, and q^7 is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand).

strand). The RNAi agent also comprises a 5'-deoxy-5'-C-malonyl and a targeting ligand. In one embodiment, the 5'-deoxy-5'-C-malonyl is at the 5'-end of the antisense strand, and the targeting ligand is at the 3'-end of the sense strand.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, q^4 is 0, B3' is 2'-OMe or 2'-F, q^5 is 7, T3' is 2'-F, q^6 is 1, B4' is 2'-OMe, and q^7 is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end). The RNAi agent also comprises a 5'-P and a targeting ligand. In one embodiment, the 5'-P is at the 5'-end of the antisense strand, and the targeting ligand is at the 3'-end of the sense strand.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, q^4 is 0, B3' is 2'-OMe or 2'-F, q^5 is 7, T3' is 2'-F, q^6 is 1, B4' is 2'-OMe, and q^7 is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end). The RNAi agent also comprises a 5'-PS and a targeting ligand. In one embodiment, the 5'-PS is at the 5'-end of the antisense strand, and the targeting ligand is at the 3'-end of the sense strand.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, q^4 is 0, B3' is 2'-OMe or 2'-F, q^5 is 7, T3' is 2'-F, q^6 is 1, B4' is 2'-OMe, and q^7 is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end). The RNAi agent also comprises a 5'-VP (*e.g.*, a 5'-E-VP, 5'-Z-VP, or combination thereof) and a targeting ligand. In one embodiment, the 5'-VP is at the 5'-end of the antisense strand, and the targeting ligand is at the 3'-end of the sense strand.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, q^4 is 0, B3' is 2'-OMe or 2'-F, q^5 is 7, T3' is 2'-F, q^6 is 1, B4' is 2'-OMe, and q^7 is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end). The RNAi agent also comprises a 5'-PS₂ and a

targeting ligand. In one embodiment, the 5'-PS₂ is at the 5'-end of the antisense strand, and the targeting ligand is at the 3'-end of the sense strand.

In one embodiment, B1 is 2'-OMe or 2'-F, n¹ is 8, T1 is 2'-F, n² is 3, B2 is 2'-OMe, n³ is 7, n⁴ is 0, B3 is 2'-OMe, n⁵ is 3, B1' is 2'-OMe or 2'-F, q¹ is 9, T1' is 2'-F, q² is 1, B2' is 2'-OMe or 2'-F, q³ is 4, q⁴ is 0, B3' is 2'-OMe or 2'-F, q⁵ is 7, T3' is 2'-F, q⁶ is 1, B4' is 2'-OMe, and q⁷ is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end). The RNAi agent also comprises a 5'-deoxy-5'-C-malonyl and a targeting ligand. In one embodiment, the 5'-deoxy-5'-C-malonyl is at the 5'-end of the antisense strand, and the targeting ligand is at the 3'-end of the sense strand.

In one embodiment, B1 is 2'-OMe or 2'-F, n¹ is 8, T1 is 2'-F, n² is 3, B2 is 2'-OMe, n³ is 7, n⁴ is 0, B3 is 2'-OMe, n⁵ is 3, B1' is 2'-OMe or 2'-F, q¹ is 9, T1' is 2'-F, q² is 1, B2' is 2'-OMe or 2'-F, q³ is 4, T2' is 2'-F, q⁴ is 2, B3' is 2'-OMe or 2'-F, q⁵ is 5, T3' is 2'-F, q⁶ is 1, B4' is 2'-F, and q⁷ is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand). The RNAi agent also comprises a 5'-P and a targeting ligand. In one embodiment, the 5'-P is at the 5'-end of the antisense strand, and the targeting ligand is at the 3'-end of the sense strand.

In one embodiment, B1 is 2'-OMe or 2'-F, n¹ is 8, T1 is 2'-F, n² is 3, B2 is 2'-OMe, n³ is 7, n⁴ is 0, B3 is 2'-OMe, n⁵ is 3, B1' is 2'-OMe or 2'-F, q¹ is 9, T1' is 2'-F, q² is 1, B2' is 2'-OMe or 2'-F, q³ is 4, T2' is 2'-F, q⁴ is 2, B3' is 2'-OMe or 2'-F, q⁵ is 5, T3' is 2'-F, q⁶ is 1, B4' is 2'-F, and q⁷ is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand). The RNAi agent also comprises a 5'-PS and a targeting ligand. In one embodiment, the 5'-PS is at the 5'-end of the antisense strand, and the targeting ligand is at the 3'-end of the sense strand.

In one embodiment, B1 is 2'-OMe or 2'-F, n¹ is 8, T1 is 2'-F, n² is 3, B2 is 2'-OMe, n³ is 7, n⁴ is 0, B3 is 2'-OMe, n⁵ is 3, B1' is 2'-OMe or 2'-F, q¹ is 9, T1' is 2'-F, q² is 1, B2' is 2'-OMe or 2'-F, q³ is 4, T2' is 2'-F, q⁴ is 2, B3' is 2'-OMe or 2'-F, q⁵ is 5, T3' is 2'-F, q⁶ is 1, B4' is 2'-F, and q⁷ is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand). The RNAi agent also comprises a 5'-VP (e.g., a 5'-E-VP, 5'-Z-VP, or combination thereof).

and a targeting ligand. In one embodiment, the 5'-VP is at the 5'-end of the antisense strand, and the targeting ligand is at the 3'-end of the sense strand.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, T2' is 2'-F, q^4 is 2, B3' is 2'-OMe or 2'-F, q^5 is 5, T3' is 2'-F, q^6 is 1, B4' is 2'-F, and q^7 is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand). The RNAi agent also comprises a 5'-PS₂ and a targeting ligand. In one embodiment, the 5'-PS₂ is at the 5'-end of the antisense strand, and the targeting ligand is at the 3'-end of the sense strand.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, T2' is 2'-F, q^4 is 2, B3' is 2'-OMe or 2'-F, q^5 is 5, T3' is 2'-F, q^6 is 1, B4' is 2'-F, and q^7 is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand). The RNAi agent also comprises a 5'-deoxy-5'-C-malonyl and a targeting ligand. In one embodiment, the 5'-deoxy-5'-C-malonyl is at the 5'-end of the antisense strand, and the targeting ligand is at the 3'-end of the sense strand.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, q^4 is 0, B3' is 2'-OMe or 2'-F, q^5 is 7, T3' is 2'-F, q^6 is 1, B4' is 2'-F, and q^7 is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand). The RNAi agent also comprises a 5'-P and a targeting ligand. In one embodiment, the 5'-P is at the 5'-end of the antisense strand, and the targeting ligand is at the 3'-end of the sense strand.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, q^4 is 0, B3' is 2'-OMe or 2'-F, q^5 is 7, T3' is 2'-F, q^6 is 1, B4' is 2'-F, and q^7 is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand). The

RNAi agent also comprises a 5'-PS and a targeting ligand. In one embodiment, the 5'-PS is at the 5'-end of the antisense strand, and the targeting ligand is at the 3'-end of the sense strand.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, q^4 is 0, B3' is 2'-OMe or 2'-F, q^5 is 7, T3' is 2'-F, q^6 is 1, B4' is 2'-F, and q^7 is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand). The RNAi agent also comprises a 5'-VP (*e.g.*, a 5'-E-VP, 5'-Z-VP, or combination thereof) and a targeting ligand. In one embodiment, the 5'-VP is at the 5'-end of the antisense strand, and the targeting ligand is at the 3'-end of the sense strand.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, q^4 is 0, B3' is 2'-OMe or 2'-F, q^5 is 7, T3' is 2'-F, q^6 is 1, B4' is 2'-F, and q^7 is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand). The RNAi agent also comprises a 5'-PS₂ and a targeting ligand. In one embodiment, the 5'-PS₂ is at the 5'-end of the antisense strand, and the targeting ligand is at the 3'-end of the sense strand.

In one embodiment, B1 is 2'-OMe or 2'-F, n^1 is 8, T1 is 2'-F, n^2 is 3, B2 is 2'-OMe, n^3 is 7, n^4 is 0, B3 is 2'-OMe, n^5 is 3, B1' is 2'-OMe or 2'-F, q^1 is 9, T1' is 2'-F, q^2 is 1, B2' is 2'-OMe or 2'-F, q^3 is 4, q^4 is 0, B3' is 2'-OMe or 2'-F, q^5 is 7, T3' is 2'-F, q^6 is 1, B4' is 2'-F, and q^7 is 1; with two phosphorothioate internucleotide linkage modifications within position 1-5 of the sense strand (counting from the 5'-end of the sense strand), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end of the antisense strand). The RNAi agent also comprises a 5'-deoxy-5'-C-malonyl and a targeting ligand. In one embodiment, the 5'-deoxy-5'-C-malonyl is at the 5'-end of the antisense strand, and the targeting ligand is at the 3'-end of the sense strand.

In a particular embodiment, an RNAi agent of the present invention comprises:

- (a) a sense strand having:
 - (i) a length of 21 nucleotides;
 - (ii) an ASGPR ligand attached to the 3'-end, wherein said ASGPR ligand comprises three GalNAc derivatives attached through a trivalent branched linker; and
 - (iii) 2'-F modifications at positions 1, 3, 5, 7, 9 to 11, 13, 17, 19, and 21, and 2'-OMe modifications at positions 2, 4, 6, 8, 12, 14 to 16, 18, and 20 (counting from the 5' end);

and

(b) an antisense strand having:

(i) a length of 23 nucleotides;

(ii) 2'-OMe modifications at positions 1, 3, 5, 9, 11 to 13, 15, 17, 19, 21, and 23, and 2'F modifications at positions 2, 4, 6 to 8, 10, 14, 16, 18, 20, and 22 (counting from the 5' end); and

(iii) phosphorothioate internucleotide linkages between nucleotide positions 21 and 22, and between nucleotide positions 22 and 23 (counting from the 5' end);

wherein the dsRNA agents have a two nucleotide overhang at the 3'-end of the antisense strand, and a blunt end at the 5'-end of the antisense strand.

In another particular embodiment, an RNAi agent of the present invention comprises:

(a) a sense strand having:

(i) a length of 21 nucleotides;

(ii) an ASGPR ligand attached to the 3'-end, wherein said ASGPR ligand comprises three GalNAc derivatives attached through a trivalent branched linker;

(iii) 2'-F modifications at positions 1, 3, 5, 7, 9 to 11, 13, 15, 17, 19, and 21, and 2'-OMe modifications at positions 2, 4, 6, 8, 12, 14, 16, 18, and 20 (counting from the 5' end); and

(iv) phosphorothioate internucleotide linkages between nucleotide positions 1 and 2, and between nucleotide positions 2 and 3 (counting from the 5' end);

and

(b) an antisense strand having:

(i) a length of 23 nucleotides;

(ii) 2'-OMe modifications at positions 1, 3, 5, 7, 9, 11 to 13, 15, 17, 19, and 21 to 23, and 2'F modifications at positions 2, 4, 6, 8, 10, 14, 16, 18, and 20 (counting from the 5' end); and

(iii) phosphorothioate internucleotide linkages between nucleotide positions 1 and 2, between nucleotide positions 2 and 3, between nucleotide positions 21 and 22, and between nucleotide positions 22 and 23 (counting from the 5' end);

wherein the RNAi agents have a two nucleotide overhang at the 3'-end of the antisense strand, and a blunt end at the 5'-end of the antisense strand.

In another particular embodiment, a RNAi agent of the present invention comprises:

(a) a sense strand having:

(i) a length of 21 nucleotides;

(ii) an ASGPR ligand attached to the 3'-end, wherein said ASGPR ligand comprises three GalNAc derivatives attached through a trivalent branched linker;

(iii) 2'-OMe modifications at positions 1 to 6, 8, 10, and 12 to 21, 2'-F modifications at positions 7, and 9, and a deoxy-nucleotide (*e.g.* dT) at position 11 (counting from the 5' end); and

(iv) phosphorothioate internucleotide linkages between nucleotide positions 1 and 2, and between nucleotide positions 2 and 3 (counting from the 5' end);

and

(b) an antisense strand having:

(i) a length of 23 nucleotides;

(ii) 2'-OMe modifications at positions 1, 3, 7, 9, 11, 13, 15, 17, and 19 to 23, and 2'-F modifications at positions 2, 4 to 6, 8, 10, 12, 14, 16, and 18 (counting from the 5' end); and

(iii) phosphorothioate internucleotide linkages between nucleotide positions 1 and 2, between nucleotide positions 2 and 3, between nucleotide positions 21 and 22, and between nucleotide positions 22 and 23 (counting from the 5' end);

wherein the RNAi agents have a two nucleotide overhang at the 3'-end of the antisense strand, and a blunt end at the 5'-end of the antisense strand.

In another particular embodiment, a RNAi agent of the present invention comprises:

(a) a sense strand having:

(i) a length of 21 nucleotides;

(ii) an ASGPR ligand attached to the 3'-end, wherein said ASGPR ligand comprises three GalNAc derivatives attached through a trivalent branched linker;

(iii) 2'-OMe modifications at positions 1 to 6, 8, 10, 12, 14, and 16 to 21, and 2'-F modifications at positions 7, 9, 11, 13, and 15; and

(iv) phosphorothioate internucleotide linkages between nucleotide positions 1 and 2, and between nucleotide positions 2 and 3 (counting from the 5' end);

and

(b) an antisense strand having:

(i) a length of 23 nucleotides;

(ii) 2'-OMe modifications at positions 1, 5, 7, 9, 11, 13, 15, 17, 19, and 21 to 23, and 2'-F modifications at positions 2 to 4, 6, 8, 10, 12, 14, 16, 18, and 20 (counting from the 5' end); and

(iii) phosphorothioate internucleotide linkages between nucleotide positions 1 and 2, between nucleotide positions 2 and 3, between nucleotide positions 21 and 22, and between nucleotide positions 22 and 23 (counting from the 5' end);

wherein the RNAi agents have a two nucleotide overhang at the 3'-end of the antisense strand, and a blunt end at the 5'-end of the antisense strand.

In another particular embodiment, a RNAi agent of the present invention comprises:

- (a) a sense strand having:
- (i) a length of 21 nucleotides;
 - (ii) an ASGPR ligand attached to the 3'-end, wherein said ASGPR ligand comprises three GalNAc derivatives attached through a trivalent branched linker;
 - (iii) 2'-OMe modifications at positions 1 to 9, and 12 to 21, and 2'-F modifications at positions 10, and 11; and
 - (iv) phosphorothioate internucleotide linkages between nucleotide positions 1 and 2, and between nucleotide positions 2 and 3 (counting from the 5' end);

10 and

- (b) an antisense strand having:
- (i) a length of 23 nucleotides;
 - (ii) 2'-OMe modifications at positions 1, 3, 5, 7, 9, 11 to 13, 15, 17, 19, and 21 to 23, and 2'-F modifications at positions 2, 4, 6, 8, 10, 14, 16, 18, and 20 (counting from the 5' end); and
 - (iii) phosphorothioate internucleotide linkages between nucleotide positions 1 and 2, between nucleotide positions 2 and 3, between nucleotide positions 21 and 22, and between nucleotide positions 22 and 23 (counting from the 5' end);

15

20 wherein the RNAi agents have a two nucleotide overhang at the 3'-end of the antisense strand, and a blunt end at the 5'-end of the antisense strand.

In another particular embodiment, a RNAi agent of the present invention comprises:

- (a) a sense strand having:
- (i) a length of 21 nucleotides;
 - (ii) an ASGPR ligand attached to the 3'-end, wherein said ASGPR ligand comprises three GalNAc derivatives attached through a trivalent branched linker;
 - (iii) 2'-F modifications at positions 1, 3, 5, 7, 9 to 11, and 13, and 2'-OMe modifications at positions 2, 4, 6, 8, 12, and 14 to 21; and
 - (iv) phosphorothioate internucleotide linkages between nucleotide positions 1 and 2, and between nucleotide positions 2 and 3 (counting from the 5' end);

25

30 and

- (b) an antisense strand having:
- (i) a length of 23 nucleotides;
 - (ii) 2'-OMe modifications at positions 1, 3, 5 to 7, 9, 11 to 13, 15, 17 to 19, and 21 to 23, and 2'-F modifications at positions 2, 4, 8, 10, 14, 16, and 20 (counting from the 5' end); and
 - (iii) phosphorothioate internucleotide linkages between nucleotide positions 1 and 2, between nucleotide positions 2 and 3, between nucleotide positions 21 and 22, and between nucleotide positions 22 and 23 (counting from the 5' end);

35

wherein the RNAi agents have a two nucleotide overhang at the 3'-end of the antisense strand, and a blunt end at the 5'-end of the antisense strand.

In another particular embodiment, a RNAi agent of the present invention comprises:

- (a) a sense strand having:
 - 5 (i) a length of 21 nucleotides;
 - (ii) an ASGPR ligand attached to the 3'-end, wherein said ASGPR ligand comprises three GalNAc derivatives attached through a trivalent branched linker;
 - (iii) 2'-OMe modifications at positions 1, 2, 4, 6, 8, 12, 14, 15, 17, and 19 to 21, and 2'-F modifications at positions 3, 5, 7, 9 to 11, 13, 16, and 18; and
 - 10 (iv) phosphorothioate internucleotide linkages between nucleotide positions 1 and 2, and between nucleotide positions 2 and 3 (counting from the 5' end);
- and
- (b) an antisense strand having:
 - 15 (i) a length of 25 nucleotides;
 - (ii) 2'-OMe modifications at positions 1, 4, 6, 7, 9, 11 to 13, 15, 17, and 19 to 23, 2'-F modifications at positions 2, 3, 5, 8, 10, 14, 16, and 18, and desoxy-nucleotides (*e.g.* dT) at positions 24 and 25 (counting from the 5' end); and
 - (iii) phosphorothioate internucleotide linkages between nucleotide positions 1 and 2, between nucleotide positions 2 and 3, between nucleotide positions 21 and 22, and
 - 20 between nucleotide positions 22 and 23 (counting from the 5' end);

wherein the RNAi agents have a four nucleotide overhang at the 3'-end of the antisense strand, and a blunt end at the 5'-end of the antisense strand.

In another particular embodiment, a RNAi agent of the present invention comprises:

- (a) a sense strand having:
 - 25 (i) a length of 21 nucleotides;
 - (ii) an ASGPR ligand attached to the 3'-end, wherein said ASGPR ligand comprises three GalNAc derivatives attached through a trivalent branched linker;
 - (iii) 2'-OMe modifications at positions 1 to 6, 8, and 12 to 21, and 2'-F modifications at positions 7, and 9 to 11; and
 - 30 (iv) phosphorothioate internucleotide linkages between nucleotide positions 1 and 2, and between nucleotide positions 2 and 3 (counting from the 5' end);
- and
- (b) an antisense strand having:
 - (i) a length of 23 nucleotides;
 - 35 (ii) 2'-OMe modifications at positions 1, 3 to 5, 7, 8, 10 to 13, 15, and 17 to 23, and 2'-F modifications at positions 2, 6, 9, 14, and 16 (counting from the 5' end); and

(iii) phosphorothioate internucleotide linkages between nucleotide positions 1 and 2, between nucleotide positions 2 and 3, between nucleotide positions 21 and 22, and between nucleotide positions 22 and 23 (counting from the 5' end);

wherein the RNAi agents have a two nucleotide overhang at the 3'-end of the antisense strand, and a blunt end at the 5'-end of the antisense strand.

In another particular embodiment, a RNAi agent of the present invention comprises:

(a) a sense strand having:

(i) a length of 21 nucleotides;

(ii) an ASGPR ligand attached to the 3'-end, wherein said ASGPR ligand comprises three GalNAc derivatives attached through a trivalent branched linker;

(iii) 2'-OMe modifications at positions 1 to 6, 8, and 12 to 21, and 2'-F modifications at positions 7, and 9 to 11; and

(iv) phosphorothioate internucleotide linkages between nucleotide positions 1 and 2, and between nucleotide positions 2 and 3 (counting from the 5' end);

and

(b) an antisense strand having:

(i) a length of 23 nucleotides;

(ii) 2'-OMe modifications at positions 1, 3 to 5, 7, 10 to 13, 15, and 17 to 23, and 2'-F modifications at positions 2, 6, 8, 9, 14, and 16 (counting from the 5' end); and

(iii) phosphorothioate internucleotide linkages between nucleotide positions 1 and 2, between nucleotide positions 2 and 3, between nucleotide positions 21 and 22, and between nucleotide positions 22 and 23 (counting from the 5' end);

wherein the RNAi agents have a two nucleotide overhang at the 3'-end of the antisense strand, and a blunt end at the 5'-end of the antisense strand.

In another particular embodiment, a RNAi agent of the present invention comprises:

(a) a sense strand having:

(i) a length of 19 nucleotides;

(ii) an ASGPR ligand attached to the 3'-end, wherein said ASGPR ligand comprises three GalNAc derivatives attached through a trivalent branched linker;

(iii) 2'-OMe modifications at positions 1 to 4, 6, and 10 to 19, and 2'-F modifications at positions 5, and 7 to 9; and

(iv) phosphorothioate internucleotide linkages between nucleotide positions 1 and 2, and between nucleotide positions 2 and 3 (counting from the 5' end);

and

(b) an antisense strand having:

(i) a length of 21 nucleotides;

(ii) 2'-OMe modifications at positions 1, 3 to 5, 7, 10 to 13, 15, and 17 to 21, and 2'-F modifications at positions 2, 6, 8, 9, 14, and 16 (counting from the 5' end); and

- (iii) phosphorothioate internucleotide linkages between nucleotide positions 1 and 2, between nucleotide positions 2 and 3, between nucleotide positions 19 and 20, and between nucleotide positions 20 and 21 (counting from the 5' end);

wherein the RNAi agents have a two nucleotide overhang at the 3'-end of the antisense strand, and a blunt end at the 5'-end of the antisense strand.

In certain embodiments, the iRNA for use in the methods of the invention is an agent selected from agents listed in any one of Tables 2, 3, 5, 6, and 8-13. These agents may further comprise a ligand.

IV. iRNAs Conjugated to Ligands

Another modification of the RNA of an iRNA of the invention involves chemically linking to the iRNA one or more ligands, moieties or conjugates that enhance the activity, cellular distribution, or cellular uptake of the iRNA *e.g.*, into a cell. Such moieties include but are not limited to lipid moieties such as a cholesterol moiety (Letsinger *et al.*, *Proc. Natl. Acad. Sci. USA*, 1989, 86: 6553-6556). In other embodiments, the ligand is cholic acid (Manoharan *et al.*, *Biorg. Med. Chem. Lett.*, 1994, 4:1053-1060), a thioether, *e.g.*, beryl-S-tritylthiol (Manoharan *et al.*, *Ann. N.Y. Acad. Sci.*, 1992, 660:306-309; Manoharan *et al.*, *Biorg. Med. Chem. Lett.*, 1993, 3:2765-2770), a thiocholesterol (Oberhauser *et al.*, *Nucl. Acids Res.*, 1992, 20:533-538), an aliphatic chain, *e.g.*, dodecandiol 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-phosphonate (Manoharan *et al.*, *Tetrahedron Lett.*, 1995, 36:3651-3654; Shea *et al.*, *Nucl. Acids Res.*, 1990, 18:3777-3783), a polyamine or a polyethylene glycol chain (Manoharan *et al.*, *Nucleosides & Nucleotides*, 1995, 14:969-973), or adamantane acetic acid (Manoharan *et al.*, *Tetrahedron Lett.*, 1995, 36:3651-3654), a palmityl moiety (Mishra *et al.*, *Biochim. Biophys. Acta*, 1995, 1264:229-237), or an octadecylamine or hexylamino-carbonyloxycholesterol moiety (Crooke *et al.*, *J. Pharmacol. Exp. Ther.*, 1996, 277:923-937).

In certain embodiments, a ligand alters the distribution, targeting, or lifetime of an iRNA agent into which it is incorporated. In some embodiments a ligand provides an enhanced affinity for a selected target, *e.g.*, molecule, cell or cell type, compartment, *e.g.*, a cellular or organ compartment, tissue, organ or region of the body, as, *e.g.*, compared to a species absent such a ligand. In some embodiments, ligands do not take part in duplex pairing in a duplexed nucleic acid.

Ligands can include a naturally occurring substance, such as a protein (*e.g.*, human serum albumin (HSA), low-density lipoprotein (LDL), or globulin); carbohydrate (*e.g.*, a dextran, pullulan, chitin, chitosan, inulin, cyclodextrin, N-acetylglucosamine, N-acetylgalactosamine, or hyaluronic acid); or a lipid. The ligand can also be a recombinant or synthetic molecule, such as a synthetic polymer, *e.g.*, a synthetic polyamino acid. Examples of polyamino acids include polyamino acid is a polylysine (PLL), poly L-aspartic acid, poly L-glutamic acid, styrene-maleic acid anhydride

copolymer, poly(L-lactide-co-glycolide) copolymer, divinyl ether-maleic anhydride copolymer, N-(2-hydroxypropyl)methacrylamide copolymer (HMPA), polyethylene glycol (PEG), polyvinyl alcohol (PVA), polyurethane, poly(2-ethylacrylic acid), N-isopropylacrylamide polymers, or polyphosphazine. Example of polyamines include: polyethylenimine, polylysine (PLL), spermine, spermidine, polyamine, pseudopeptide-polyamine, peptidomimetic polyamine, dendrimer polyamine, arginine, amidine, protamine, cationic lipid, cationic porphyrin, quaternary salt of a polyamine, or an alpha helical peptide.

Ligands can also include targeting groups, *e.g.*, a cell or tissue targeting agent, *e.g.*, a lectin, glycoprotein, lipid or protein, *e.g.*, an antibody, that binds to a specified cell type such as a kidney cell. A targeting group can be a thyrotropin, melanotropin, lectin, glycoprotein, surfactant protein A, Mucin carbohydrate, multivalent lactose, multivalent galactose, N-acetyl-galactosamine, N-acetyl-glucosamine multivalent mannose, multivalent fucose, glycosylated polyaminoacids, multivalent galactose, transferrin, bisphosphonate, polyglutamate, polyaspartate, a lipid, cholesterol, a steroid, bile acid, folate, vitamin B12, vitamin A, biotin, or an RGD peptide or RGD peptide mimetic. In certain embodiments, the ligand is a multivalent galactose, *e.g.*, an N-acetyl-galactosamine.

Other examples of ligands include dyes, intercalating agents (*e.g.* acridines), cross-linkers (*e.g.* psoralene, mitomycin C), porphyrins (TPPC4, texaphyrin, Sapphyrin), polycyclic aromatic hydrocarbons (*e.g.*, phenazine, dihydrophenazine), artificial endonucleases (*e.g.* EDTA), lipophilic molecules, *e.g.*, cholesterol, cholic acid, adamantane acetic acid, 1-pyrene butyric acid, dihydrotestosterone, 1,3-Bis-O(hexadecyl)glycerol, geranyloxyhexyl group, hexadecylglycerol, borneol, menthol, 1,3-propanediol, heptadecyl group, palmitic acid, myristic acid, O3-(oleoyl)lithocholic acid, O3-(oleoyl)cholenic acid, dimethoxytrityl, or phenoxazine) and peptide conjugates (*e.g.*, antennapedia peptide, Tat peptide), alkylating agents, phosphate, amino, mercapto, PEG (*e.g.*, PEG-40K), MPEG, [MPEG]₂, polyamino, alkyl, substituted alkyl, radiolabeled markers, enzymes, haptens (*e.g.* biotin), transport/absorption facilitators (*e.g.*, aspirin, vitamin E, folic acid), synthetic ribonucleases (*e.g.*, imidazole, bisimidazole, histamine, imidazole clusters, acridine-imidazole conjugates, Eu³⁺ complexes of tetraazamacrocycles), dinitrophenyl, HRP, or AP.

Ligands can be proteins, *e.g.*, glycoproteins, or peptides, *e.g.*, molecules having a specific affinity for a co-ligand, or antibodies *e.g.*, an antibody, that binds to a specified cell type such as a hepatic cell. Ligands can also include hormones and hormone receptors. They can also include non-peptidic species, such as lipids, lectins, carbohydrates, vitamins, cofactors, multivalent lactose, multivalent galactose, N-acetyl-galactosamine, N-acetyl-glucosamine multivalent mannose, or multivalent fucose. The ligand can be, for example, a lipopolysaccharide, an activator of p38 MAP kinase, or an activator of NF- κ B.

The ligand can be a substance, *e.g.*, a drug, which can increase the uptake of the iRNA agent into the cell, for example, by disrupting the cell's cytoskeleton, *e.g.*, by disrupting the cell's microtubules, microfilaments, or intermediate filaments. The drug can be, for example, taxol,

vincristine, vinblastine, cytochalasin, nocodazole, japlakinolide, latrunculin A, phalloidin, swinholide A, indanocine, or myoservin.

In some embodiments, a ligand attached to an iRNA as described herein acts as a pharmacokinetic modulator (PK modulator). PK modulators include lipophiles, bile acids, steroids, phospholipid analogues, peptides, protein binding agents, PEG, vitamins, *etc.* Exemplary PK modulators include, but are not limited to, cholesterol, fatty acids, cholic acid, lithocholic acid, dialkylglycerides, diacylglyceride, phospholipids, sphingolipids, naproxen, ibuprofen, vitamin E, biotin. Oligonucleotides that comprise a number of phosphorothioate linkages are also known to bind to serum protein, thus short oligonucleotides, *e.g.*, oligonucleotides of about 5 bases, 10 bases, 15 bases, or 20 bases, comprising multiple of phosphorothioate linkages in the backbone are also amenable to the present invention as ligands (*e.g.* as PK modulating ligands). In addition, aptamers that bind serum components (*e.g.* serum proteins) are also suitable for use as PK modulating ligands in the embodiments described herein.

Ligand-conjugated iRNAs of the invention may be synthesized by the use of an oligonucleotide that bears a pendant reactive functionality, such as that derived from the attachment of a linking molecule onto the oligonucleotide (described below). This reactive oligonucleotide may be reacted directly with commercially-available ligands, ligands that are synthesized bearing any of a variety of protecting groups, or ligands that have a linking moiety attached thereto.

The oligonucleotides used in the conjugates of the present invention may be conveniently and routinely made through the well-known technique of solid-phase synthesis. Equipment for such synthesis is sold by several vendors including, for example, Applied Biosystems® (Foster City, Calif.). Any other methods for such synthesis known in the art may additionally or alternatively be employed. It is also known to use similar techniques to prepare other oligonucleotides, such as the phosphorothioates and alkylated derivatives.

In the ligand-conjugated iRNAs and ligand-molecule bearing sequence-specific linked nucleosides of the present invention, the oligonucleotides and oligonucleosides may be assembled on a suitable DNA synthesizer utilizing standard nucleotide or nucleoside precursors, or nucleotide or nucleoside conjugate precursors that already bear the linking moiety, ligand-nucleotide or nucleoside-conjugate precursors that already bear the ligand molecule, or non-nucleoside ligand-bearing building blocks.

When using nucleotide-conjugate precursors that already bear a linking moiety, the synthesis of the sequence-specific linked nucleosides is typically completed, and the ligand molecule is then reacted with the linking moiety to form the ligand-conjugated oligonucleotide. In some embodiments, the oligonucleotides or linked nucleosides of the present invention are synthesized by an automated synthesizer using phosphoramidites derived from ligand-nucleoside conjugates in addition to the standard phosphoramidites and non-standard phosphoramidites that are commercially available and routinely used in oligonucleotide synthesis.

A. Lipid Conjugates

In certain embodiments, the ligand or conjugate is a lipid or lipid-based molecule. Such a lipid or lipid-based molecule may bind a serum protein, *e.g.*, human serum albumin (HSA). An HSA binding ligand allows for distribution of the conjugate to a target tissue, *e.g.*, a non-kidney target
5 tissue of the body. For example, the target tissue can be the liver, including parenchymal cells of the liver. Other molecules that can bind HSA can also be used as ligands. For example, naproxen or aspirin can be used. A lipid or lipid-based ligand can (a) increase resistance to degradation of the conjugate, (b) increase targeting or transport into a target cell or cell membrane, or (c) can be used to adjust binding to a serum protein, *e.g.*, HSA.

10 A lipid based ligand can be used to inhibit, *e.g.*, control the binding of the conjugate to a target tissue. For example, a lipid or lipid-based ligand that binds to HSA more strongly will be less likely to be targeted to the kidney and therefore less likely to be cleared from the body. A lipid or lipid-based ligand that binds to HSA less strongly can be used to target the conjugate to the kidney.

In certain embodiments, the lipid based ligand binds HSA. In some embodiments, it binds
15 HSA with a sufficient affinity such that the conjugate will be distributed to a non-kidney tissue. However, it is preferred that the affinity not be so strong that the HSA-ligand binding cannot be reversed.

In other embodiments, the lipid based ligand binds HSA weakly or not at all, such that the conjugate will be distributed to the kidney. Other moieties that target to kidney cells can also be used
20 in place of, or in addition to, the lipid based ligand.

In another aspect, the ligand is a moiety, *e.g.*, a vitamin, which is taken up by a target cell, *e.g.*, a proliferating cell. These are particularly useful for treating disorders characterized by unwanted cell proliferation, *e.g.*, of the malignant or non-malignant type, *e.g.*, cancer cells. Exemplary vitamins include vitamin A, E, and K. Other exemplary vitamins include are B vitamin,
25 *e.g.*, folic acid, B12, riboflavin, biotin, pyridoxal or other vitamins or nutrients taken up by target cells such as liver cells. Also included are HSA and low density lipoprotein (LDL).

B. Cell Permeation Agents

In another aspect, the ligand is a cell-permeation agent, such as, a helical cell-permeation
30 agent. In some embodiments, the agent is amphipathic. An exemplary agent is a peptide such as tat or antennopodia. If the agent is a peptide, it can be modified, including a peptidylmimetic, invertomers, non-peptide or pseudo-peptide linkages, and use of D-amino acids. In some embodiments, the helical agent is an alpha-helical agent, which has a lipophilic and a lipophobic phase.

35 The ligand can be a peptide or peptidomimetic. A peptidomimetic (also referred to herein as an oligopeptidomimetic) is a molecule capable of folding into a defined three-dimensional structure similar to a natural peptide. The attachment of peptide and peptidomimetics to iRNA agents can affect pharmacokinetic distribution of the iRNA, such as by enhancing cellular recognition and

absorption. The peptide or peptidomimetic moiety can be about 5-50 amino acids long, *e.g.*, about 5, 10, 15, 20, 25, 30, 35, 40, 45, or 50 amino acids long.

A peptide or peptidomimetic can be, for example, a cell permeation peptide, cationic peptide, amphipathic peptide, or hydrophobic peptide (*e.g.*, consisting primarily of Tyr, Trp, or Phe). The peptide moiety can be a dendrimer peptide, constrained peptide or crosslinked peptide. In another alternative, the peptide moiety can include a hydrophobic membrane translocation sequence (MTS). An exemplary hydrophobic MTS-containing peptide is RFGF having the amino acid sequence AAVALLPAVLLALLAP (SEQ ID NO: 14). An RFGF analogue (*e.g.*, amino acid sequence AALLPVLLAAP (SEQ ID NO:15) containing a hydrophobic MTS can also be a targeting moiety.

The peptide moiety can be a “delivery” peptide, which can carry large polar molecules including peptides, oligonucleotides, and protein across cell membranes. For example, sequences from the HIV Tat protein (GRKKRRQRRRPPQ (SEQ ID NO:16) and the Drosophila Antennapedia protein (RQIKIWFQNRRMKWKK (SEQ ID NO:17) have been found to be capable of functioning as delivery peptides. A peptide or peptidomimetic can be encoded by a random sequence of DNA, such as a peptide identified from a phage-display library, or one-bead-one-compound (OBOC) combinatorial library (Lam *et al.*, Nature, 354:82-84, 1991). Examples of a peptide or peptidomimetic tethered to a dsRNA agent *via* an incorporated monomer unit for cell targeting purposes is an arginine-glycine-aspartic acid (RGD)-peptide, or RGD mimic. A peptide moiety can range in length from about 5 amino acids to about 40 amino acids. The peptide moieties can have a structural modification, such as to increase stability or direct conformational properties. Any of the structural modifications described below can be utilized.

An RGD peptide for use in the compositions and methods of the invention may be linear or cyclic, and may be modified, *e.g.*, glycosylated or methylated, to facilitate targeting to a specific tissue(s). RGD-containing peptides and peptidomimetics may include D-amino acids, as well as synthetic RGD mimics. In addition to RGD, one can use other moieties that target the integrin ligand, *e.g.*, PECAM-1 or VEGF.

A “cell permeation peptide” is capable of permeating a cell, *e.g.*, a microbial cell, such as a bacterial or fungal cell, or a mammalian cell, such as a human cell. A microbial cell-permeating peptide can be, for example, an α -helical linear peptide (*e.g.*, LL-37 or Ceropin P1), a disulfide bond-containing peptide (*e.g.*, α -defensin, β -defensin or bactenecin), or a peptide containing only one or two dominating amino acids (*e.g.*, PR-39 or indolicidin). A cell permeation peptide can also include a nuclear localization signal (NLS). For example, a cell permeation peptide can be a bipartite amphipathic peptide, such as MPG, which is derived from the fusion peptide domain of HIV-1 gp41 and the NLS of SV40 large T antigen (Simeoni *et al.*, Nucl. Acids Res. 31:2717-2724, 2003).

C. Carbohydrate Conjugates

In some embodiments of the compositions and methods of the invention, an iRNA further comprises a carbohydrate. The carbohydrate conjugated iRNA is advantageous for the *in vivo*

delivery of nucleic acids, as well as compositions suitable for *in vivo* therapeutic use, as described herein. As used herein, "carbohydrate" refers to a compound which is either a carbohydrate *per se* made up of one or more monosaccharide units having at least 6 carbon atoms (which can be linear, branched or cyclic) with an oxygen, nitrogen or sulfur atom bonded to each carbon atom; or a
5 compound having as a part thereof a carbohydrate moiety made up of one or more monosaccharide units each having at least six carbon atoms (which can be linear, branched or cyclic), with an oxygen, nitrogen or sulfur atom bonded to each carbon atom. Representative carbohydrates include the sugars (mono-, di-, tri-, and oligosaccharides containing from about 4, 5, 6, 7, 8, or 9 monosaccharide units), and polysaccharides such as starches, glycogen, cellulose and polysaccharide gums. Specific
10 monosaccharides include C5 and above (*e.g.*, C5, C6, C7, or C8) sugars; di- and trisaccharides include sugars having two or three monosaccharide units (*e.g.*, C5, C6, C7, or C8).

In certain embodiments, a carbohydrate conjugate for use in the compositions and methods of the invention is a monosaccharide.

In certain embodiments, the monosaccharide is an N-acetylgalactosamine (GalNAc). GalNAc
15 conjugates, which comprise one or more N-acetylgalactosamine (GalNAc) derivatives, are described, for example, in US 8,106,022, the entire content of which is hereby incorporated herein by reference. In some embodiments, the GalNAc conjugate serves as a ligand that targets the iRNA to particular cells. In some embodiments, the GalNAc conjugate targets the iRNA to liver cells, *e.g.*, by serving as a ligand for the asialoglycoprotein receptor of liver cells (*e.g.*, hepatocytes).

20 In some embodiments, the carbohydrate conjugate comprises one or more GalNAc derivatives. The GalNAc derivatives may be attached *via* a linker, *e.g.*, a bivalent or trivalent branched linker. In some embodiments the GalNAc conjugate is conjugated to the 3' end of the sense strand. In some embodiments, the GalNAc conjugate is conjugated to the iRNA agent (*e.g.*, to the 3' end of the sense strand) *via* a linker, *e.g.*, a linker as described herein. In some embodiments the
25 GalNAc conjugate is conjugated to the 5' end of the sense strand. In some embodiments, the GalNAc conjugate is conjugated to the iRNA agent (*e.g.*, to the 5' end of the sense strand) *via* a linker, *e.g.*, a linker as described herein.

In certain embodiments of the invention, the GalNAc or GalNAc derivative is attached to an iRNA agent of the invention *via* a monovalent linker. In some embodiments, the GalNAc or GalNAc
30 derivative is attached to an iRNA agent of the invention *via* a bivalent linker. In yet other embodiments of the invention, the GalNAc or GalNAc derivative is attached to an iRNA agent of the invention *via* a trivalent linker. In other embodiments of the invention, the GalNAc or GalNAc derivative is attached to an iRNA agent of the invention *via* a tetravalent linker.

In certain embodiments, the double stranded RNAi agents of the invention comprise one
35 GalNAc or GalNAc derivative attached to the iRNA agent. In certain embodiments, the double stranded RNAi agents of the invention comprise a plurality (*e.g.*, 2, 3, 4, 5, or 6) GalNAc or GalNAc derivatives, each independently attached to a plurality of nucleotides of the double stranded RNAi agent through a plurality of monovalent linkers.

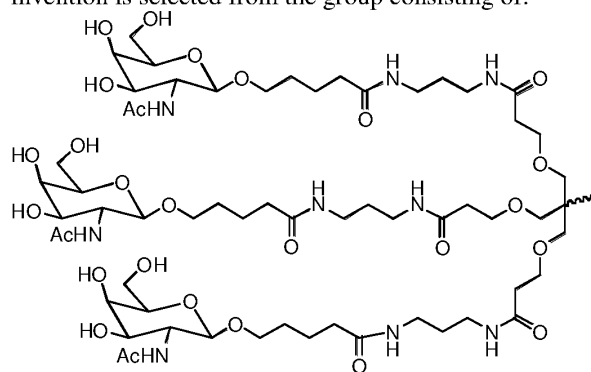
In some embodiments, for example, when the two strands of an iRNA agent of the invention are part of one larger molecule connected by an uninterrupted chain of nucleotides between the 3'-end of one strand and the 5'-end of the respective other strand forming a hairpin loop comprising, a plurality of unpaired nucleotides, each unpaired nucleotide within the hairpin loop may independently

5 comprise a GalNAc or GalNAc derivative attached *via* a monovalent linker. The hairpin loop may also be formed by an extended overhang in one strand of the duplex.

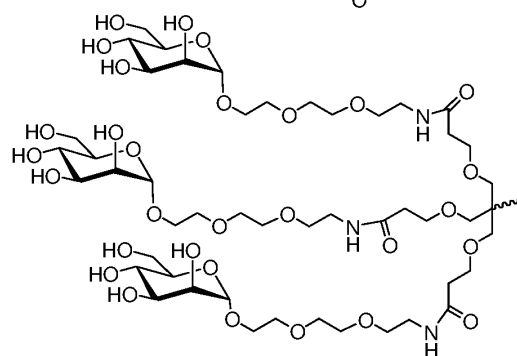
In some embodiments, for example, when the two strands of an iRNA agent of the invention are part of one larger molecule connected by an uninterrupted chain of nucleotides between the 3'-end of one strand and the 5'-end of the respective other strand forming a hairpin loop comprising, a

10 plurality of unpaired nucleotides, each unpaired nucleotide within the hairpin loop may independently comprise a GalNAc or GalNAc derivative attached *via* a monovalent linker. The hairpin loop may also be formed by an extended overhang in one strand of the duplex.

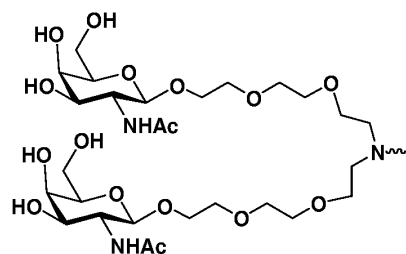
In one embodiment, a carbohydrate conjugate for use in the compositions and methods of the invention is selected from the group consisting of:



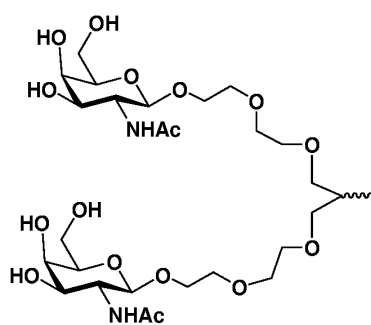
Formula II,



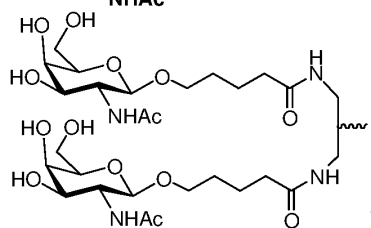
Formula III,



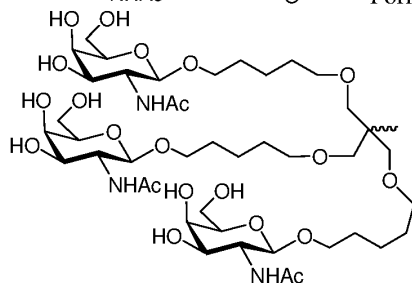
Formula IV,



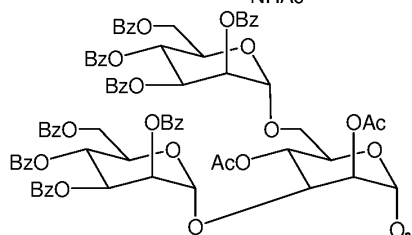
Formula V,



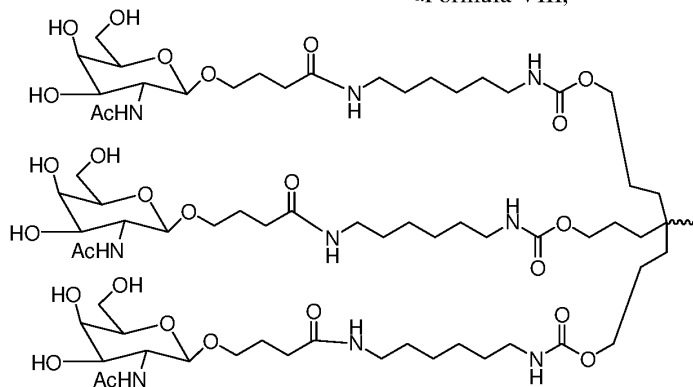
Formula VI,



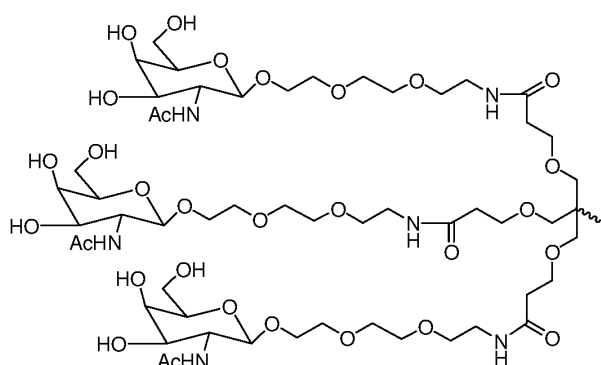
Formula VII,



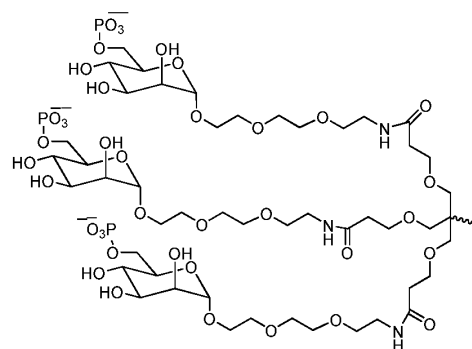
Formula VIII,



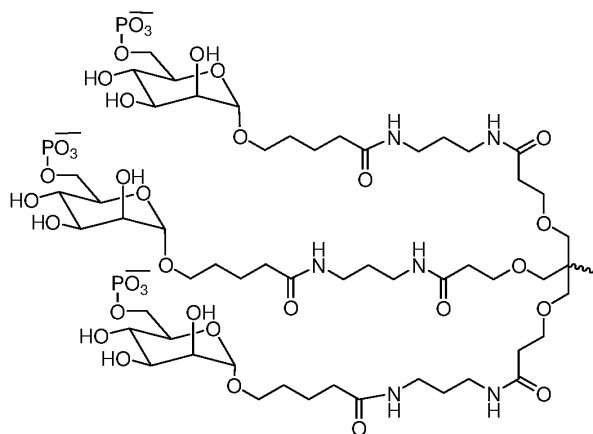
Formula IX,



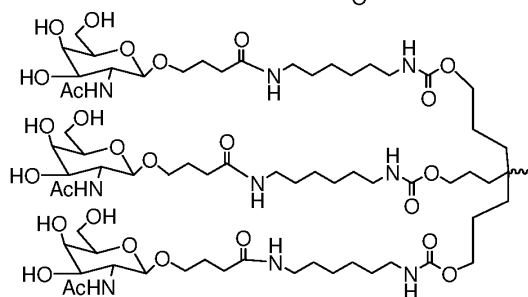
Formula X,



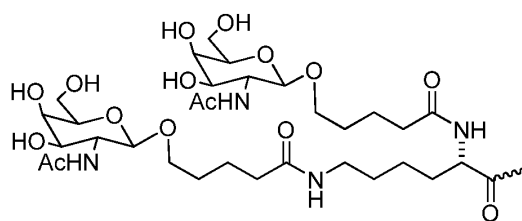
Formula XI,



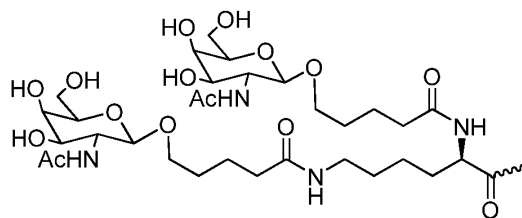
Formula XII,



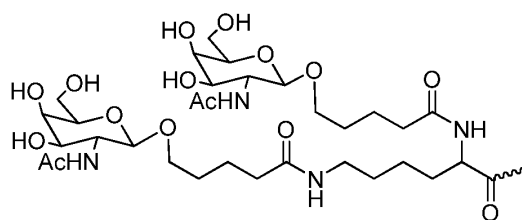
Formula XIII,



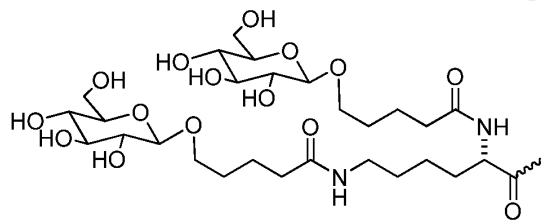
Formula XIV,



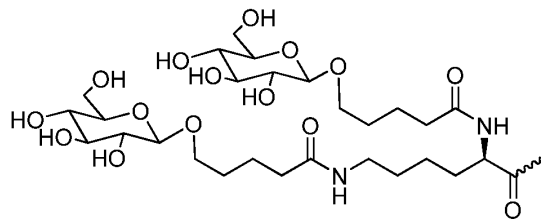
Formula XV,



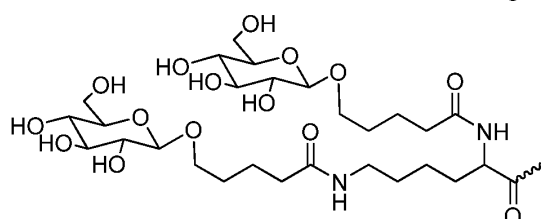
Formula XVI,



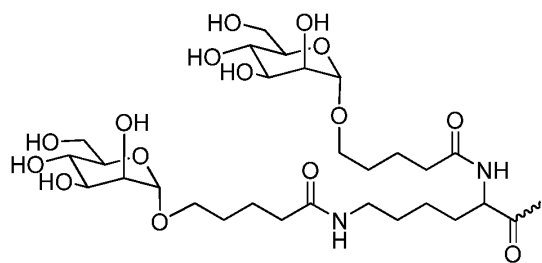
Formula XVII,



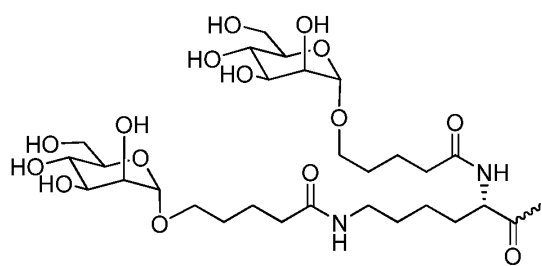
Formula XVIII,



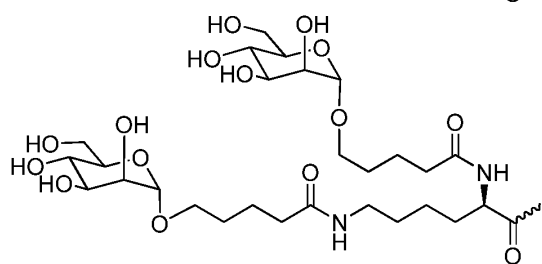
Formula XIX,



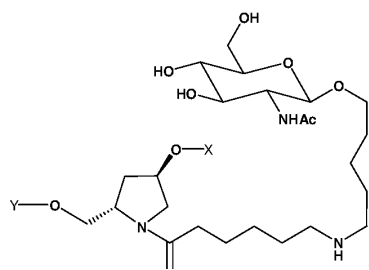
Formula XX,



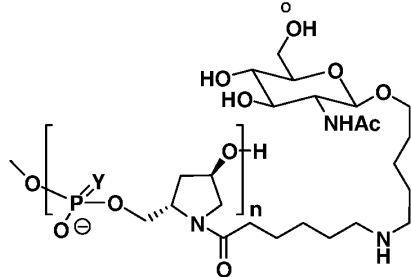
Formula XXI,



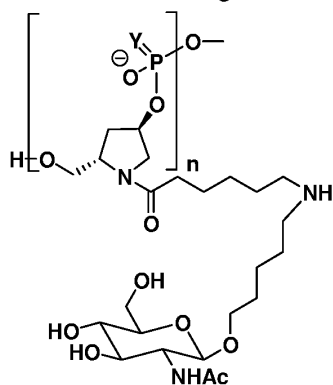
Formula XXII,



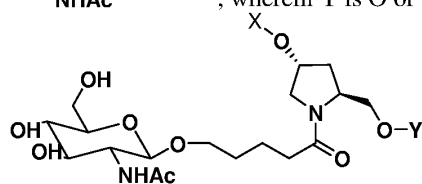
Formula XXIII;



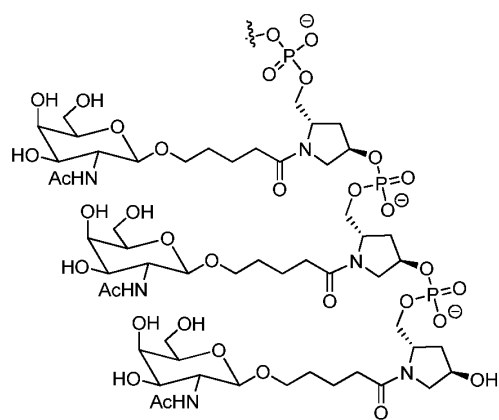
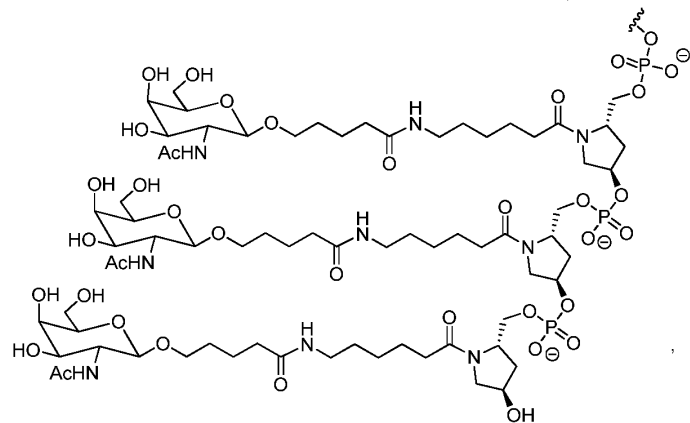
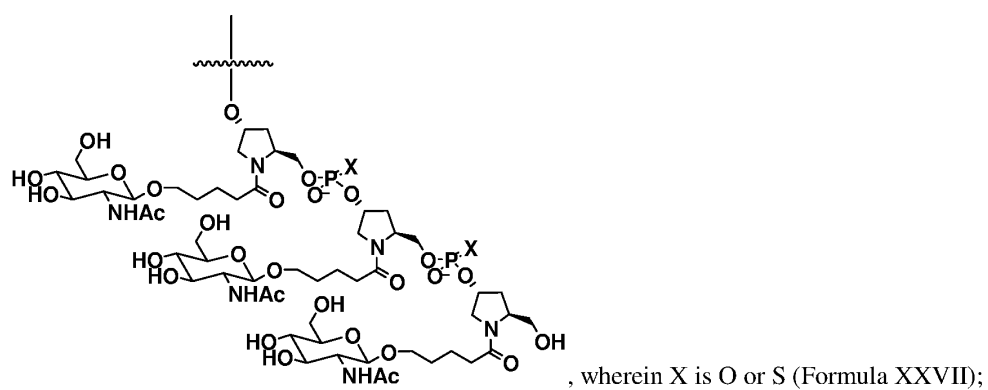
, wherein Y is O or S and n is 3 -6 (Formula XXIV);



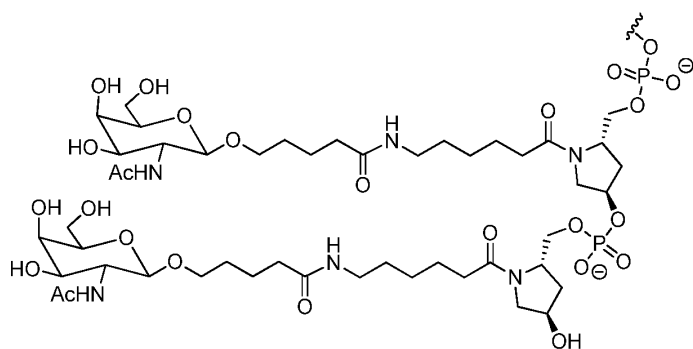
, wherein Y is O or S and n is 3-6 (Formula XXV);



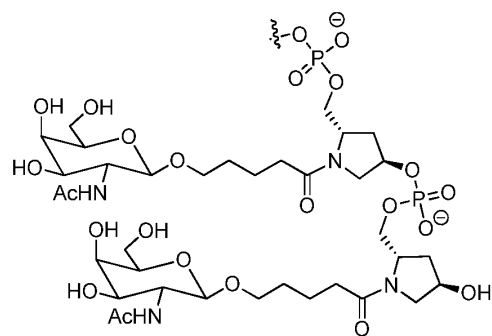
Formula XXVI;



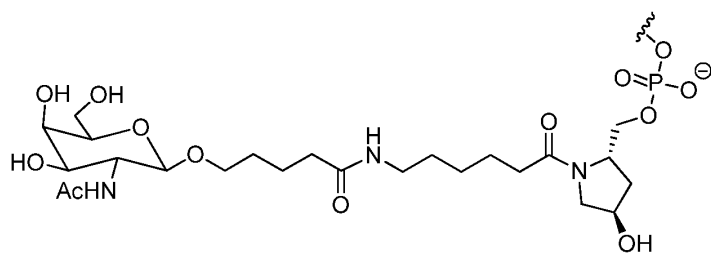
Formula XXVII; Formula XXIX;



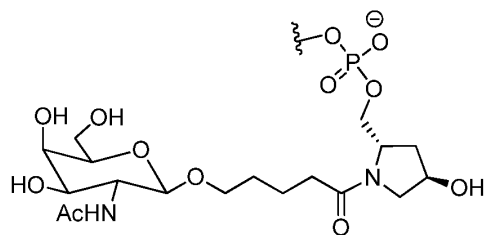
Formula XXXI;



Formula XXX;

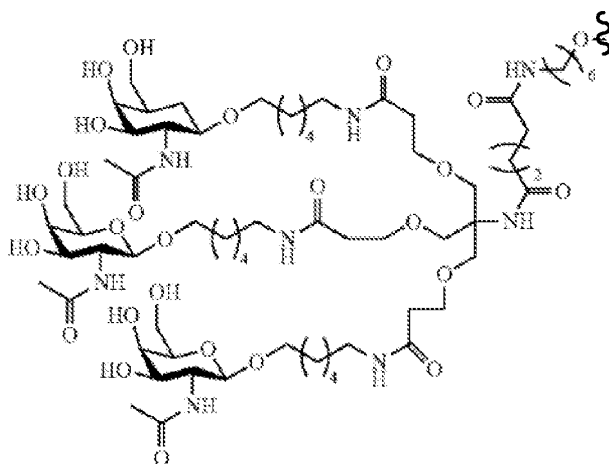


, and



Formula XXXII;

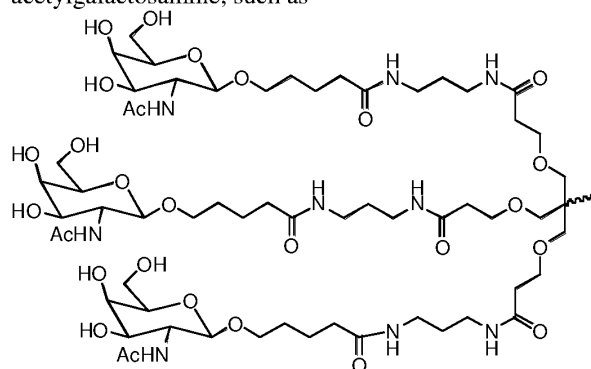
5 Formula XXXIII.



Formula XXXIV.

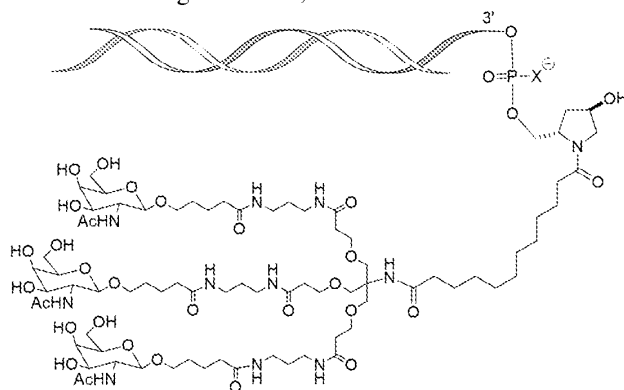
In another embodiment, a carbohydrate conjugate for use in the compositions and methods of the invention is a monosaccharide. In one embodiment, the monosaccharide is an N-

5 acetylgalactosamine, such as

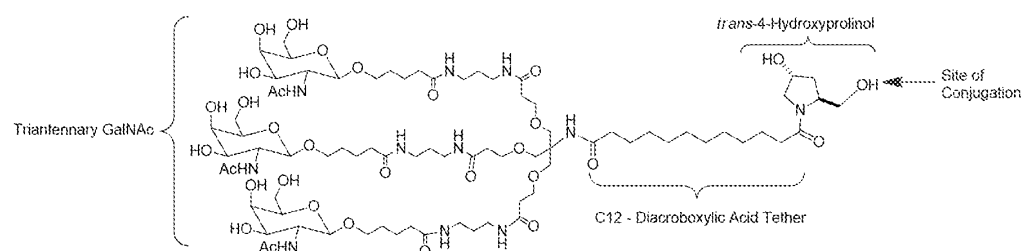


Formula II.

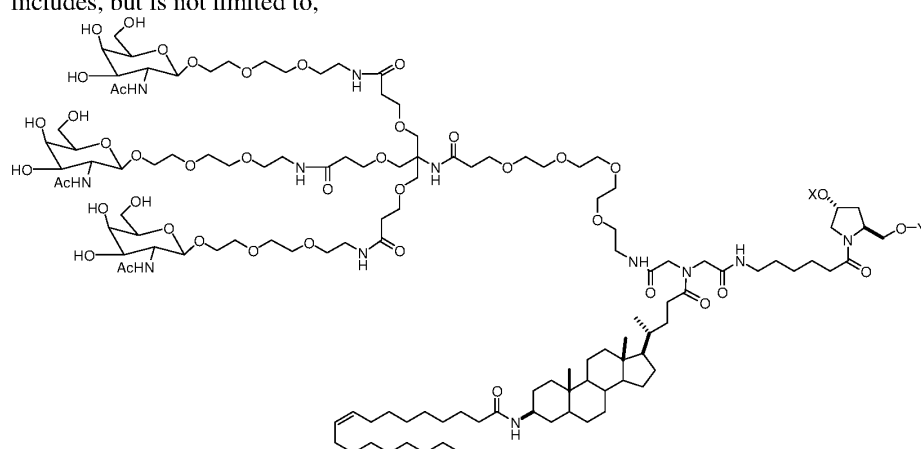
In some embodiments, the RNAi agent is attached to the carbohydrate conjugate *via* a linker as shown in the following schematic, wherein X is O or S



In some embodiments, the RNAi agent is conjugated to L96 as defined in Table 1 and shown below:



Another representative carbohydrate conjugate for use in the embodiments described herein includes, but is not limited to,

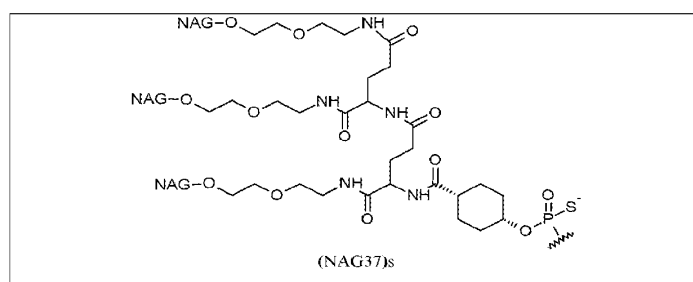


(Formula XXXVI), when one of X or Y is an oligonucleotide, the other is a hydrogen.

In some embodiments, a suitable ligand is a ligand disclosed in WO 2019/055633, the entire contents of which are incorporated herein by reference. In one embodiment the ligand comprises the structure below:

15

20



In certain embodiments of the invention, the GalNAc or GalNAc derivative is attached to an iRNA agent of the invention *via* a monovalent linker. In some embodiments, the GalNAc or GalNAc

derivative is attached to an iRNA agent of the invention *via* a bivalent linker. In yet other embodiments of the invention, the GalNAc or GalNAc derivative is attached to an iRNA agent of the invention *via* a trivalent linker.

In one embodiment, the double stranded RNAi agents of the invention comprise one or more GalNAc or GalNAc derivative attached to the iRNA agent. The GalNAc may be attached to any nucleotide *via* a linker on the sense strand or antisense strand. The GalNAc may be attached to the 5'-end of the sense strand, the 3' end of the sense strand, the 5'-end of the antisense strand, or the 3' – end of the antisense strand. In one embodiment, the GalNAc is attached to the 3' end of the sense strand, *e.g.*, *via* a trivalent linker.

In other embodiments, the double stranded RNAi agents of the invention comprise a plurality (*e.g.*, 2, 3, 4, 5, or 6) GalNAc or GalNAc derivatives, each independently attached to a plurality of nucleotides of the double stranded RNAi agent through a plurality of linkers, *e.g.*, monovalent linkers.

In some embodiments, for example, when the two strands of an iRNA agent of the invention is part of one larger molecule connected by an uninterrupted chain of nucleotides between the 3'-end of one strand and the 5'-end of the respective other strand forming a hairpin loop comprising, a plurality of unpaired nucleotides, each unpaired nucleotide within the hairpin loop may independently comprise a GalNAc or GalNAc derivative attached *via* a monovalent linker.

In some embodiments, the carbohydrate conjugate further comprises one or more additional ligands as described above, such as, but not limited to, a PK modulator or a cell permeation peptide.

Additional carbohydrate conjugates and linkers suitable for use in the present invention include those described in PCT Publication Nos. WO 2014/179620 and WO 2014/179627, the entire contents of each of which are incorporated herein by reference.

D. Linkers

In some embodiments, the conjugate or ligand described herein can be attached to an iRNA oligonucleotide with various linkers that can be cleavable or non-cleavable.

The term "linker" or "linking group" means an organic moiety that connects two parts of a compound, *e.g.*, covalently attaches two parts of a compound. Linkers typically comprise a direct bond or an atom such as oxygen or sulfur, a unit such as NR₂, C(O), C(O)NH, SO, SO₂, SO₂NH or a chain of atoms, such as, but not limited to, substituted or unsubstituted alkyl, substituted or unsubstituted alkenyl, substituted or unsubstituted alkynyl, arylalkyl, arylalkenyl, arylalkynyl, heteroarylalkyl, heteroarylalkenyl, heteroarylalkynyl, heterocyclalkyl, heterocyclalkenyl, heterocyclalkynyl, aryl, heteroaryl, heterocycl, cycloalkyl, cycloalkenyl, alkylarylalkyl, alkylarylalkenyl, alkylarylalkynyl, alkenylarylalkyl, alkenylarylalkenyl, alkenylarylalkynyl, alkynylarylalkyl, alkynylarylalkenyl, alkynylarylalkynyl, alkylheteroarylalkyl, alkylheteroarylalkenyl, alkylheteroarylalkynyl, alkenylheteroarylalkyl, alkenylheteroarylalkenyl, alkenylheteroarylalkynyl, alkynylheteroarylalkyl, alkynylheteroarylalkenyl, alkynylheteroarylalkynyl, alkylheterocyclalkyl, alkylheterocyclalkenyl, alkylheterocyclalkynyl, alkenylheterocyclalkyl,

alkenylheterocyclalkenyl, alkenylheterocyclalkynyl, alkynylheterocyclalkyl, alkynylheterocyclalkenyl, alkynylheterocyclalkynyl, alkylaryl, alkenylaryl, alkynylaryl, alkylheteroaryl, alkenylheteroaryl, alkynylheteroaryl, which one or more methylenes can be interrupted or terminated by O, S, S(O), SO₂, N(R₈), C(O), substituted or unsubstituted aryl, substituted or unsubstituted heteroaryl, or substituted or unsubstituted heterocyclic; where R₈ is hydrogen, acyl, aliphatic, or substituted aliphatic. In one embodiment, the linker is about 1-24 atoms, 2-24, 3-24, 4-24, 5-24, 6-24, 6-18, 7-18, 8-18, 7-17, 8-17, 6-16, 7-17, or 8-16 atoms.

A cleavable linking group is one which is sufficiently stable outside the cell, but which upon entry into a target cell is cleaved to release the two parts the linker is holding together. In one embodiment, the cleavable linking group is cleaved at least about 10 times, 20, times, 30 times, 40 times, 50 times, 60 times, 70 times, 80 times, 90 times, or more, or at least 100 times faster in a target cell or under a first reference condition (which can, *e.g.*, be selected to mimic or represent intracellular conditions) than in the blood of a subject, or under a second reference condition (which can, *e.g.*, be selected to mimic or represent conditions found in the blood or serum).

Cleavable linking groups are susceptible to cleavage agents, *e.g.*, pH, redox potential, or the presence of degradative molecules. Generally, cleavage agents are more prevalent or found at higher levels or activities inside cells than in serum or blood. Examples of such degradative agents include: redox agents which are selected for particular substrates or which have no substrate specificity, including, *e.g.*, oxidative or reductive enzymes or reductive agents such as mercaptans, present in cells, that can degrade a redox cleavable linking group by reduction; esterases; endosomes or agents that can create an acidic environment, *e.g.*, those that result in a pH of five or lower; enzymes that can hydrolyze or degrade an acid cleavable linking group by acting as a general acid, peptidases (which can be substrate specific), and phosphatases.

A cleavable linkage group, such as a disulfide bond can be susceptible to pH. The pH of human serum is 7.4, while the average intracellular pH is slightly lower, ranging from about 7.1-7.3. Endosomes have a more acidic pH, in the range of 5.5-6.0, and lysosomes have an even more acidic pH at around 5.0. Some linkers will have a cleavable linking group that is cleaved at a selected pH, thereby releasing a cationic lipid from the ligand inside the cell, or into the desired compartment of the cell.

A linker can include a cleavable linking group that is cleavable by a particular enzyme. The type of cleavable linking group incorporated into a linker can depend on the cell to be targeted. For example, a liver-targeting ligand can be linked to a cationic lipid through a linker that includes an ester group. Liver cells are rich in esterases, and therefore the linker will be cleaved more efficiently in liver cells than in cell types that are not esterase-rich. Other cell-types rich in esterases include cells of the lung, renal cortex, and testis.

Linkers that contain peptide bonds can be used when targeting cell types rich in peptidases, such as liver cells and synoviocytes.

In general, the suitability of a candidate cleavable linking group can be evaluated by testing the ability of a degradative agent (or condition) to cleave the candidate linking group. It will also be desirable to also test the candidate cleavable linking group for the ability to resist cleavage in the blood or when in contact with other non-target tissue. Thus, one can determine the relative

5 susceptibility to cleavage between a first and a second condition, where the first is selected to be indicative of cleavage in a target cell and the second is selected to be indicative of cleavage in other tissues or biological fluids, *e.g.*, blood or serum. The evaluations can be carried out in cell free systems, in cells, in cell culture, in organ or tissue culture, or in whole animals. It can be useful to make initial evaluations in cell-free or culture conditions and to confirm by further evaluations in

10 whole animals. In some embodiments, useful candidate compounds are cleaved at least about 2, 4, 10, 20, 30, 40, 50, 60, 70, 80, 90, or 100 times faster in the cell (or under *in vitro* conditions selected to mimic intracellular conditions) as compared to blood or serum (or under *in vitro* conditions selected to mimic extracellular conditions).

15 *i. Redox cleavable linking groups*

In certain embodiments, a cleavable linking group is a redox cleavable linking group that is cleaved upon reduction or oxidation. An example of reductively cleavable linking group is a disulphide linking group (-S-S-). To determine if a candidate cleavable linking group is a suitable

20 “reductively cleavable linking group,” or for example is suitable for use with a particular iRNA moiety and particular targeting agent one can look to methods described herein. For example, a candidate can be evaluated by incubation with dithiothreitol (DTT), or other reducing agent using reagents known in the art, which mimic the rate of cleavage which would be observed in a cell, *e.g.*, a target cell. The candidates can also be evaluated under conditions which are selected to mimic blood or serum conditions. In one, candidate compounds are cleaved by at most about 10% in the blood. In

25 other embodiments, useful candidate compounds are degraded at least about 2, 4, 10, 20, 30, 40, 50, 60, 70, 80, 90, or about 100 times faster in the cell (or under *in vitro* conditions selected to mimic intracellular conditions) as compared to blood (or under *in vitro* conditions selected to mimic extracellular conditions). The rate of cleavage of candidate compounds can be determined using standard enzyme kinetics assays under conditions chosen to mimic intracellular media and compared

30 to conditions chosen to mimic extracellular media.

ii. Phosphate-based cleavable linking groups

In other embodiments, a cleavable linker comprises a phosphate-based cleavable linking group. A phosphate-based cleavable linking group is cleaved by agents that degrade or hydrolyze the

35 phosphate group. An example of an agent that cleaves phosphate groups in cells are enzymes such as phosphatases in cells. Examples of phosphate-based linking groups are -O-P(O)(ORk)-O-, -O-P(S)(ORk)-O-, -O-P(S)(SRk)-O-, -S-P(O)(ORk)-O-, -O-P(O)(ORk)-S-, -S-P(O)(ORk)-S-, -O-P(S)(ORk)-S-, -S-P(S)(ORk)-O-, -O-P(O)(Rk)-O-, -O-P(S)(Rk)-O-, -S-P(O)(Rk)-O-, -S-P(S)(Rk)-O-,

-S-P(O)(Rk)-S-, -O-P(S)(Rk)-S-, wherein Rk at each occurrence can be, independently, C1-C20 alkyl, C1-C20 haloalkyl, C6-C10 aryl, or C7-C12 aralkyl. Exemplary embodiments include -O-P(O)(OH)-O-, -O-P(S)(OH)-O-, -O-P(S)(SH)-O-, -S-P(O)(OH)-O-, -O-P(O)(OH)-S-, -S-P(O)(OH)-S-, -O-P(S)(OH)-S-, -S-P(S)(OH)-O-, -O-P(O)(H)-O-, -O-P(S)(H)-O-, -S-P(O)(H)-O-, -S-P(S)(H)-O-, -S-P(O)(H)-S-, and -O-P(S)(H)-S-. In certain embodiments, a phosphate-based linking group is -O-P(O)(OH)-O-. These candidates can be evaluated using methods analogous to those described above.

iii. Acid cleavable linking groups

In other embodiments, a cleavable linker comprises an acid cleavable linking group. An acid cleavable linking group is a linking group that is cleaved under acidic conditions. In some embodiments acid cleavable linking groups are cleaved in an acidic environment with a pH of about 6.5 or lower (*e.g.*, about 6.0, 5.5, 5.0, or lower), or by agents such as enzymes that can act as a general acid. In a cell, specific low pH organelles, such as endosomes and lysosomes can provide a cleaving environment for acid cleavable linking groups. Examples of acid cleavable linking groups include but are not limited to hydrazones, esters, and esters of amino acids. Acid cleavable groups can have the general formula -C=NN-, C(O)O, or -OC(O). An exemplary embodiment is when the carbon attached to the oxygen of the ester (the alkoxy group) is an aryl group, substituted alkyl group, or tertiary alkyl group such as dimethyl pentyl or t-butyl. These candidates can be evaluated using methods analogous to those described above.

iv. Ester-based linking groups

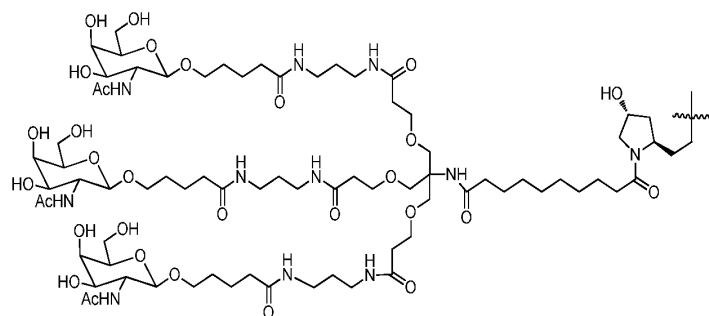
In other embodiments, a cleavable linker comprises an ester-based cleavable linking group. An ester-based cleavable linking group is cleaved by enzymes such as esterases and amidases in cells. Examples of ester-based cleavable linking groups include, but are not limited to, esters of alkylene, alkenylene and alkynylene groups. Ester cleavable linking groups have the general formula -C(O)O-, or -OC(O)-. These candidates can be evaluated using methods analogous to those described above.

v. Peptide-based cleaving groups

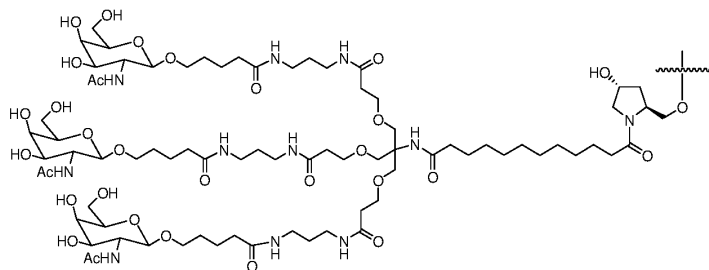
In yet other embodiments, a cleavable linker comprises a peptide-based cleavable linking group. A peptide-based cleavable linking group is cleaved by enzymes such as peptidases and proteases in cells. Peptide-based cleavable linking groups are peptide bonds formed between amino acids to yield oligopeptides (*e.g.*, dipeptides, tripeptides *etc.*) and polypeptides. Peptide-based cleavable groups do not include the amide group (-C(O)NH-). The amide group can be formed between any alkylene, alkenylene or alkynylene. A peptide bond is a special type of amide bond formed between amino acids to yield peptides and proteins. The peptide based cleavage group is generally limited to the peptide bond (*i.e.*, the amide bond) formed between amino acids yielding peptides and proteins and does not include the entire amide functional group. Peptide-based cleavable linking groups have the general formula -NHCHRAC(O)NHCHRBC(O)-, where RA and RB are the

R groups of the two adjacent amino acids. These candidates can be evaluated using methods analogous to those described above.

In some embodiments, an iRNA of the invention is conjugated to a carbohydrate through a linker. Non-limiting examples of iRNA carbohydrate conjugates with linkers of the compositions and methods of the invention include, but are not limited to,

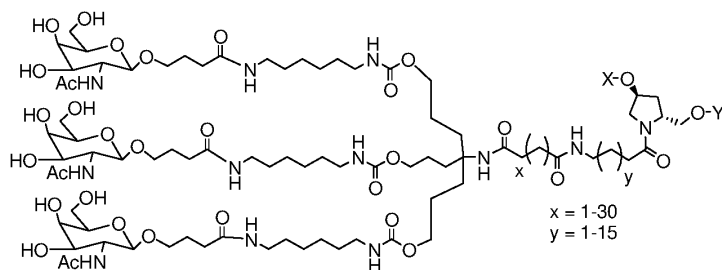


(Formula XXXVII),

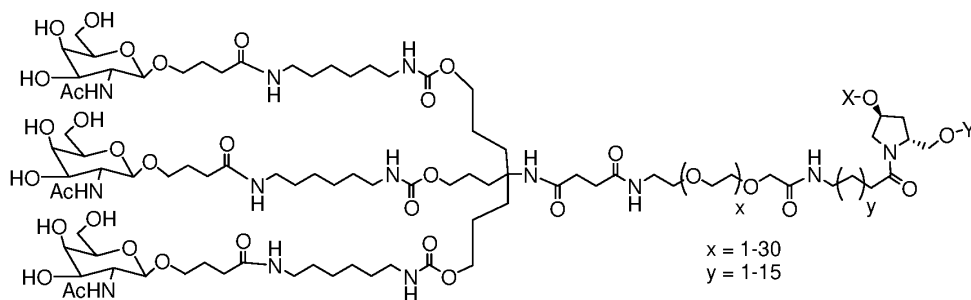


(Formula XXXVIII),

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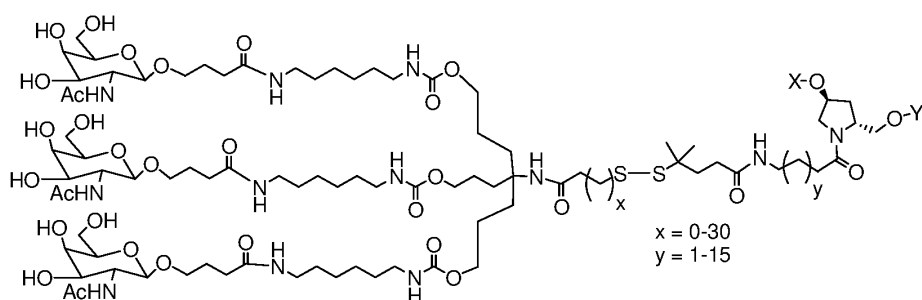


(Formula XXXIX),

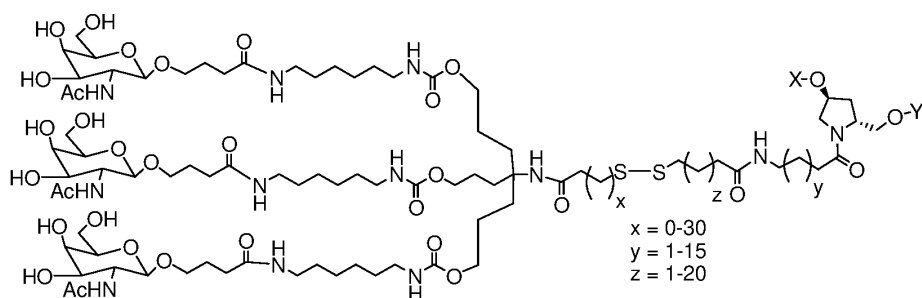


(Formula XL),

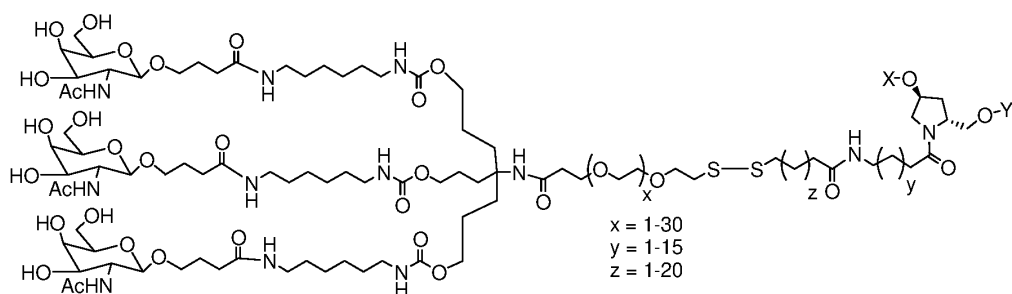
15



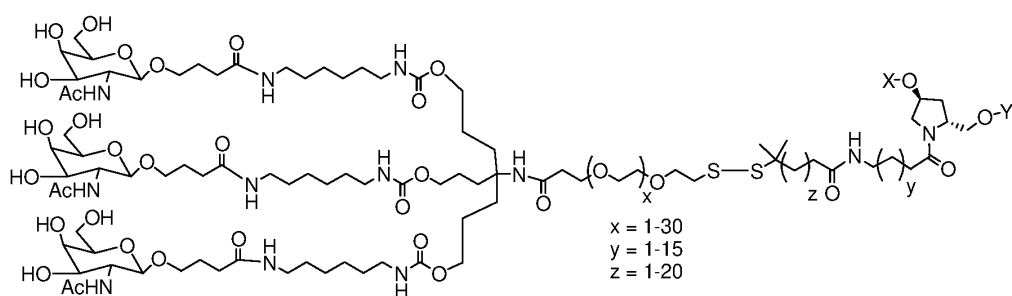
(Formula XLI),



5 (Formula XLII),



(Formula XLIII), and



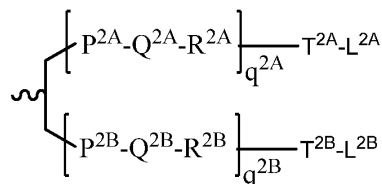
10

(Formula XLIV), when one of X or Y is an oligonucleotide, the other is a hydrogen.

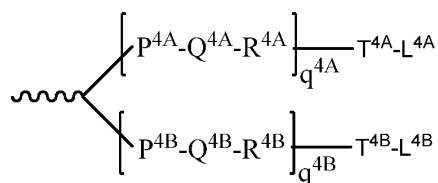
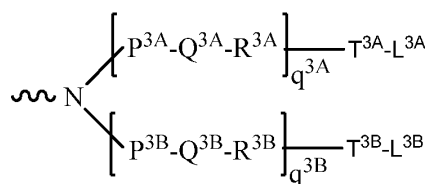
In certain embodiments of the compositions and methods of the invention, a ligand is one or more “GalNAc” (N-acetylgalactosamine) derivatives attached through a bivalent or trivalent branched linker.

In one embodiment, a dsRNA of the invention is conjugated to a bivalent or trivalent branched linker selected from the group of structures shown in any of formula (XLV) – (XLVI):

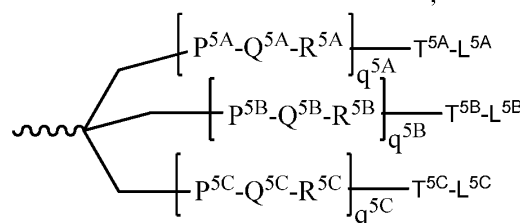
Formula XXXXV



Formula XLVI



Formula (VII)



Formula (VIII)

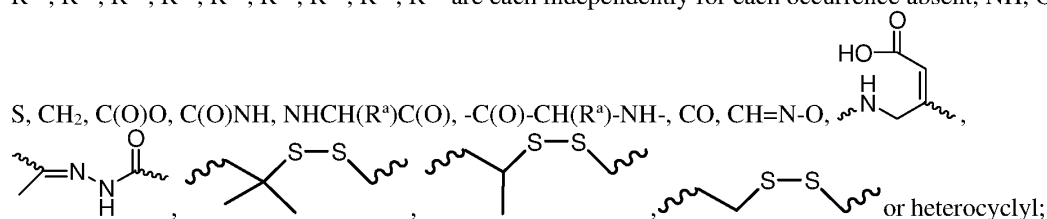
5

Formula XLVII

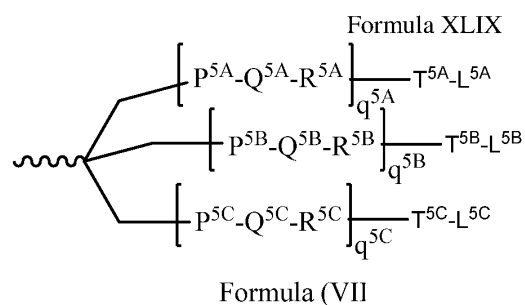
Formula XLVIII

wherein:

- q^{2A}, q^{2B}, q^{3A}, q^{3B}, q^{4A}, q^{4B}, q^{5A}, q^{5B} and q^{5C} represent independently for each occurrence 0-20 and wherein the repeating unit can be the same or different;
- 10 p^{2A}, p^{2B}, p^{3A}, p^{3B}, p^{4A}, p^{4B}, p^{5A}, p^{5B}, p^{5C}, T^{2A}, T^{2B}, T^{3A}, T^{3B}, T^{4A}, T^{4B}, T^{5A}, T^{5B}, T^{5C} are each independently for each occurrence absent, CO, NH, O, S, OC(O), NHC(O), CH₂, CH₂NH or CH₂O; Q^{2A}, Q^{2B}, Q^{3A}, Q^{3B}, Q^{4A}, Q^{4B}, Q^{5A}, Q^{5B}, Q^{5C} are independently for each occurrence absent, alkylene, substituted alkylene wherein one or more methylenes can be interrupted or terminated by one or more of O, S, S(O), SO₂, N(R^N), C(R')=C(R''), C≡C or C(O);
- 15 R^{2A}, R^{2B}, R^{3A}, R^{3B}, R^{4A}, R^{4B}, R^{5A}, R^{5B}, R^{5C} are each independently for each occurrence absent, NH, O,



- L^{2A}, L^{2B}, L^{3A}, L^{3B}, L^{4A}, L^{4B}, L^{5A}, L^{5B} and L^{5C} represent the ligand; *i.e.* each independently for each occurrence a monosaccharide (such as GalNAc), disaccharide, trisaccharide, tetrasaccharide, oligosaccharide, or polysaccharide; and R^a is H or amino acid side chain. Trivalent conjugating GalNAc derivatives are particularly useful for use with RNAi agents for inhibiting the expression of a target gene, such as those of formula (XLIX):
- 20



wherein L^{5A}, L^{5B} and L^{5C} represent a monosaccharide, such as GalNAc derivative.

Examples of suitable bivalent and trivalent branched linker groups conjugating GalNAc derivatives include, but are not limited to, the structures recited above as formulas II, VII, XI, X, and XIII.

Representative U.S. Patents that teach the preparation of RNA conjugates include, but are not limited to, U.S. Patent Nos. 4,828,979; 4,948,882; 5,218,105; 5,525,465; 5,541,313; 5,545,730; 5,552,538; 5,578,717; 5,580,731; 5,591,584; 5,109,124; 5,118,802; 5,138,045; 5,414,077; 5,486,603; 5,512,439; 5,578,718; 5,608,046; 4,587,044; 4,605,735; 4,667,025; 4,762,779; 4,789,737; 4,824,941; 4,835,263; 4,876,335; 4,904,582; 4,958,013; 5,082,830; 5,112,963; 5,214,136; 5,082,830; 5,112,963; 5,214,136; 5,245,022; 5,254,469; 5,258,506; 5,262,536; 5,272,250; 5,292,873; 5,317,098; 5,371,241; 5,391,723; 5,416,203; 5,451,463; 5,510,475; 5,512,667; 5,514,785; 5,565,552; 5,567,810; 5,574,142; 5,585,481; 5,587,371; 5,595,726; 5,597,696; 5,599,923; 5,599,928; 5,688,941; 6,294,664; 6,320,017; 6,576,752; 6,783,931; 6,900,297; 7,037,646; and 8,106,022, the entire contents of each of which are hereby incorporated herein by reference.

It is not necessary for all positions in a given compound to be uniformly modified, and in fact more than one of the aforementioned modifications can be incorporated in a single compound or even at a single nucleoside within an iRNA. The present invention also includes iRNA compounds that are chimeric compounds.

“Chimeric” iRNA compounds or “chimeras,” in the context of this invention, are iRNA compounds, such as, dsRNAi agents, that contain two or more chemically distinct regions, each made up of at least one monomer unit, *i.e.*, a nucleotide in the case of a dsRNA compound. These iRNAs typically contain at least one region wherein the RNA is modified so as to confer upon the iRNA increased resistance to nuclease degradation, increased cellular uptake, or increased binding affinity for the target nucleic acid. An additional region of the iRNA can serve as a substrate for enzymes capable of cleaving RNA:DNA or RNA:RNA hybrids. By way of example, RNase H is a cellular endonuclease which cleaves the RNA strand of an RNA:DNA duplex. Activation of RNase H, therefore, results in cleavage of the RNA target, thereby greatly enhancing the efficiency of iRNA inhibition of gene expression. Consequently, comparable results can often be obtained with shorter iRNAs when chimeric dsRNAs are used, compared to phosphorothioate deoxy dsRNAs hybridizing to the same target region. Cleavage of the RNA target can be routinely detected by gel electrophoresis and, if necessary, associated nucleic acid hybridization techniques known in the art.

In certain instances, the RNA of an iRNA can be modified by a non-ligand group. A number of non-ligand molecules have been conjugated to iRNAs in order to enhance the activity, cellular distribution or cellular uptake of the iRNA, and procedures for performing such conjugations are available in the scientific literature. Such non-ligand moieties have included lipid moieties, such as cholesterol (Kubo, T. *et al.*, *Biochem. Biophys. Res. Comm.*, 2007, 365(1):54-61; Letsinger *et al.*, *Proc. Natl. Acad. Sci. USA*, 1989, 86:6553), cholic acid (Manoharan *et al.*, *Bioorg. Med. Chem. Lett.*, 1994, 4:1053), a thioether, *e.g.*, hexyl-S-tritylthiol (Manoharan *et al.*, *Ann. N.Y. Acad. Sci.*, 1992, 660:306; Manoharan *et al.*, *Bioorg. Med. Chem. Lett.*, 1993, 3:2765), a thiocholesterol (Oberhauser *et al.*, *Nucl. Acids Res.*, 1992, 20:533), an aliphatic chain, *e.g.*, dodecandiol or undecyl residues (Saison-Behmoaras *et al.*, *EMBO J.*, 1991, 10:111; Kabanov *et al.*, *FEBS Lett.*, 1990, 259:327; Svinarchuk *et al.*, *Biochimie*, 1993, 75:49), a phospholipid, *e.g.*, di-hexadecyl-rac-glycerol or triethylammonium 1,2-di-O-hexadecyl-rac-glycero-3-H-phosphonate (Manoharan *et al.*, *Tetrahedron Lett.*, 1995, 36:3651; Shea *et al.*, *Nucl. Acids Res.*, 1990, 18:3777), a polyamine or a polyethylene glycol chain (Manoharan *et al.*, *Nucleosides & Nucleotides*, 1995, 14:969), or adamantane acetic acid (Manoharan *et al.*, *Tetrahedron Lett.*, 1995, 36:3651), a palmityl moiety (Mishra *et al.*, *Biochim. Biophys. Acta*, 1995, 1264:229), or an octadecylamine or hexylamino-carbonyl-oxycholesterol moiety (Crooke *et al.*, *J. Pharmacol. Exp. Ther.*, 1996, 277:923). Representative United States patents that teach the preparation of such RNA conjugates have been listed above. Typical conjugation protocols involve the synthesis of RNAs bearing an aminolinker at one or more positions of the sequence. The amino group is then reacted with the molecule being conjugated using appropriate coupling or activating reagents. The conjugation reaction can be performed either with the RNA still bound to the solid support or following cleavage of the RNA, in solution phase. Purification of the RNA conjugate by HPLC typically affords the pure conjugate.

25 V. Delivery of an iRNA of the Invention

The delivery of an iRNA of the invention to a cell *e.g.*, a cell within a subject, such as a human subject (*e.g.*, a subject in need thereof, such as a subject susceptible to or diagnosed with a KHK-associated disorder, as described herein) can be achieved in a number of different ways. For example, delivery may be performed by contacting a cell with an iRNA of the invention either *in vitro* or *in vivo*. *In vivo* delivery may also be performed directly by administering a composition comprising an iRNA, *e.g.*, a dsRNA, to a subject. Alternatively, *in vivo* delivery may be performed indirectly by administering one or more vectors that encode and direct the expression of the iRNA. These alternatives are discussed further below.

In general, any method of delivering a nucleic acid molecule (*in vitro* or *in vivo*) can be adapted for use with an iRNA of the invention (see *e.g.*, Akhtar S. and Julian RL. (1992) *Trends Cell. Biol.* 2(5):139-144 and WO94/02595, which are incorporated herein by reference in their entireties). For *in vivo* delivery, factors to consider in order to deliver an iRNA molecule include, for example, biological stability of the delivered molecule, prevention of non-specific effects, and accumulation of

the delivered molecule in the target tissue. RNA interference has also shown success with local delivery to the CNS by direct injection (Dorn, G., *et al.* (2004) *Nucleic Acids* 32:e49; Tan, PH., *et al.* (2005) *Gene Ther.* 12:59-66; Makimura, H., *et al.* (2002) *BMC Neurosci.* 3:18; Shishkina, GT., *et al.* (2004) *Neuroscience* 129:521-528; Thakker, ER., *et al.* (2004) *Proc. Natl. Acad. Sci. U.S.A.* 101:17270-17275; Akaneya, Y., *et al.* (2005) *J. Neurophysiol.* 93:594-602). Modification of the RNA or the pharmaceutical carrier can also permit targeting of the iRNA to the target tissue and avoid undesirable off-target effects. iRNA molecules can be modified by chemical conjugation to lipophilic groups such as cholesterol to enhance cellular uptake and prevent degradation. For example, an iRNA directed against ApoB conjugated to a lipophilic cholesterol moiety was injected systemically into mice and resulted in knockdown of apoB mRNA in both the liver and jejunum (Soutschek, J., *et al.* (2004) *Nature* 432:173-178).

In an alternative embodiment, the iRNA can be delivered using drug delivery systems such as a nanoparticle, a dendrimer, a polymer, liposomes, or a cationic delivery system. Positively charged cationic delivery systems facilitate binding of an iRNA molecule (negatively charged) and also enhance interactions at the negatively charged cell membrane to permit efficient uptake of an iRNA by the cell. Cationic lipids, dendrimers, or polymers can either be bound to an iRNA, or induced to form a vesicle or micelle (see *e.g.*, Kim SH, *et al.* (2008) *Journal of Controlled Release* 129(2):107-116) that encases an iRNA. The formation of vesicles or micelles further prevents degradation of the iRNA when administered systemically. Methods for making and administering cationic- iRNA complexes are well within the abilities of one skilled in the art (see *e.g.*, Sorensen, DR, *et al.* (2003) *J. Mol. Biol* 327:761-766; Verma, UN, *et al.* (2003) *Clin. Cancer Res.* 9:1291-1300; Arnold, AS *et al.* (2007) *J. Hypertens.* 25:197-205, which are incorporated herein by reference in their entirety). Some non-limiting examples of drug delivery systems useful for systemic delivery of iRNAs include DOTAP (Sorensen, DR., *et al.* (2003), *supra*; Verma, UN, *et al.* (2003), *supra*), "solid nucleic acid lipid particles" (Zimmermann, TS, *et al.* (2006) *Nature* 441:111-114), cardiolipin (Chien, PY, *et al.* (2005) *Cancer Gene Ther.* 12:321-328; Pal, A, *et al.* (2005) *Int J. Oncol.* 26:1087-1091), polyethyleneimine (Bonnet ME, *et al.* (2008) *Pharm. Res.* Aug 16 Epub ahead of print; Aigner, A. (2006) *J. Biomed. Biotechnol.* 71659), Arg-Gly-Asp (RGD) peptides (Liu, S. (2006) *Mol. Pharm.* 3:472-487), and polyamidoamines (Tomalia, DA, *et al.* (2007) *Biochem. Soc. Trans.* 35:61-67; Yoo, H., *et al.* (1999) *Pharm. Res.* 16:1799-1804). In some embodiments, an iRNA forms a complex with cyclodextrin for systemic administration. Methods for administration and pharmaceutical compositions of iRNAs and cyclodextrins can be found in U.S. Patent No. 7,427,605, which is herein incorporated by reference in its entirety.

35 A. Vector encoded iRNAs of the Invention

iRNA targeting the KHK gene can be expressed from transcription units inserted into DNA or RNA vectors (see, *e.g.*, Couture, A, *et al.*, *TIG.* (1996), 12:5-10; Skillern, A, *et al.*, International PCT Publication No. WO 00/22113, Conrad, International PCT Publication No. WO 00/22114, and

Conrad, U.S. Patent No. 6,054,299). Expression can be transient (on the order of hours to weeks) or sustained (weeks to months or longer), depending upon the specific construct used and the target tissue or cell type. These transgenes can be introduced as a linear construct, a circular plasmid, or a viral vector, which can be an integrating or non-integrating vector. The transgene can also be
5 constructed to permit it to be inherited as an extrachromosomal plasmid (Gassmann, *et al.*, *Proc. Natl. Acad. Sci. USA* (1995) 92:1292).

Viral vector systems which can be utilized with the methods and compositions described herein include, but are not limited to, (a) adenovirus vectors; (b) retrovirus vectors, including but not limited to lentiviral vectors, moloney murine leukemia virus, *etc.*; (c) adeno- associated virus vectors;
10 (d) herpes simplex virus vectors; (e) SV 40 vectors; (f) polyoma virus vectors; (g) papilloma virus vectors; (h) picornavirus vectors; (i) pox virus vectors such as an orthopox, *e.g.*, vaccinia virus vectors or avipox, *e.g.* canary pox or fowl pox; and (j) a helper-dependent or gutless adenovirus. Replication-defective viruses can also be advantageous. Different vectors will or will not become incorporated into the cells' genome. The constructs can include viral sequences for transfection, if desired.

15 Alternatively, the construct can be incorporated into vectors capable of episomal replication, *e.g.* EPV and EBV vectors. Constructs for the recombinant expression of an iRNA will generally require regulatory elements, *e.g.*, promoters, enhancers, *etc.*, to ensure the expression of the iRNA in target cells. Other aspects to consider for vectors and constructs are known in the art.

20 VI. Pharmaceutical Compositions of the Invention

The present invention also includes pharmaceutical compositions and formulations which include the iRNAs of the invention. In one embodiment, provided herein are pharmaceutical compositions containing an iRNA, as described herein, and a pharmaceutically acceptable carrier. The pharmaceutical compositions containing the iRNA are useful for treating a disease or disorder
25 associated with the expression or activity of a KHK gene. Such pharmaceutical compositions are formulated based on the mode of delivery. One example is compositions that are formulated for systemic administration via parenteral delivery, *e.g.*, by subcutaneous (SC) or intravenous (IV) delivery. The pharmaceutical compositions of the invention may be administered in dosages sufficient to inhibit expression of a KHK gene.

30 In some embodiments, the pharmaceutical compositions of the invention are sterile. In another embodiment, the pharmaceutical compositions of the invention are pyrogen free.

The pharmaceutical compositions of the invention may be administered in dosages sufficient to inhibit expression of a KHK gene. In general, a suitable dose of an iRNA of the invention will be in the range of about 0.001 to about 200.0 milligrams per kilogram body weight of the recipient per
35 day, generally in the range of about 1 to 50 mg per kilogram body weight per day. Typically, a suitable dose of an iRNA of the invention will be in the range of about 0.1 mg/kg to about 5.0 mg/kg, about 0.3 mg/kg and about 3.0 mg/kg. A repeat-dose regimen may include administration of a therapeutic amount of iRNA on a regular basis, such as every month, once every 3-6 months, or once

a year. In certain embodiments, the iRNA is administered about once per month to about once per six months.

After an initial treatment regimen, the treatments can be administered on a less frequent basis. Duration of treatment can be determined based on the severity of disease.

5 In other embodiments, a single dose of the pharmaceutical compositions can be long lasting, such that doses are administered at not more than 1, 2, 3, or 4 month intervals. In some embodiments of the invention, a single dose of the pharmaceutical compositions of the invention is administered about once per month. In other embodiments of the invention, a single dose of the pharmaceutical compositions of the invention is administered quarterly (*i.e.*, about every three months). In other
10 embodiments of the invention, a single dose of the pharmaceutical compositions of the invention is administered twice per year (*i.e.*, about once every six months).

The skilled artisan will appreciate that certain factors can influence the dosage and timing required to effectively treat a subject, including but not limited to mutations present in the subject, previous treatments, the general health or age of the subject, and other diseases present. Moreover,
15 treatment of a subject with a prophylactically or therapeutically effective amount, as appropriate, of a composition can include a single treatment or a series of treatments.

The iRNA can be delivered in a manner to target a particular tissue (*e.g.*, hepatocytes).

Pharmaceutical compositions of the present invention include, but are not limited to, solutions, emulsions, and liposome-containing formulations. These compositions can be generated
20 from a variety of components that include, but are not limited to, preformed liquids, self-emulsifying solids, and self-emulsifying semisolids. Formulations include those that target the liver.

The pharmaceutical formulations of the present invention, which can conveniently be presented in unit dosage form, can be prepared according to conventional techniques well known in the pharmaceutical industry. Such techniques include the step of bringing into association the active
25 ingredients with the pharmaceutical carrier(s) or excipient(s). In general, the formulations are prepared by uniformly and intimately bringing into association the active ingredients with liquid carriers.

A. Additional Formulations

30 i. Emulsions

The compositions of the present invention can be prepared and formulated as emulsions. Emulsions are typically heterogeneous systems of one liquid dispersed in another in the form of droplets usually exceeding 0.1 μm in diameter (see *e.g.*, Ansel's Pharmaceutical Dosage Forms and Drug Delivery Systems, Allen, LV., Popovich NG., and Ansel HC., 2004, Lippincott Williams &
35 Wilkins (8th ed.), New York, NY; Idson, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 199; Rosoff, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., Volume 1, p. 245; Block in Pharmaceutical Dosage Forms, Lieberman, Rieger and

Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 2, p. 335; Higuchi *et al.*, in Remington's Pharmaceutical Sciences, Mack Publishing Co., Easton, Pa., 1985, p. 301). Emulsions are often biphasic systems comprising two immiscible liquid phases intimately mixed and dispersed with each other. In general, emulsions can be of either the water-in-oil (w/o) or the oil-in-water (o/w) variety. When an aqueous phase is finely divided into and dispersed as minute droplets into a bulk oily phase, the resulting composition is called a water-in-oil (w/o) emulsion. Alternatively, when an oily phase is finely divided into and dispersed as minute droplets into a bulk aqueous phase, the resulting composition is called an oil-in-water (o/w) emulsion. Emulsions can contain additional components in addition to the dispersed phases, and the active drug which can be present as a solution either in the aqueous phase, oily phase or itself as a separate phase. Pharmaceutical excipients such as emulsifiers, stabilizers, dyes, and anti-oxidants can also be present in emulsions as needed. Pharmaceutical emulsions can also be multiple emulsions that are comprised of more than two phases such as, for example, in the case of oil-in-water-in-oil (o/w/o) and water-in-oil-in-water (w/o/w) emulsions. Such complex formulations often provide certain advantages that simple binary emulsions do not. Multiple emulsions in which individual oil droplets of an o/w emulsion enclose small water droplets constitute a w/o/w emulsion. Likewise a system of oil droplets enclosed in globules of water stabilized in an oily continuous phase provides an o/w/o emulsion.

Emulsions are characterized by little or no thermodynamic stability. Often, the dispersed or discontinuous phase of the emulsion is well dispersed into the external or continuous phase and maintained in this form through the means of emulsifiers or the viscosity of the formulation. Other means of stabilizing emulsions entail the use of emulsifiers that can be incorporated into either phase of the emulsion. Emulsifiers can broadly be classified into four categories: synthetic surfactants, naturally occurring emulsifiers, absorption bases, and finely dispersed solids (see *e.g.*, Ansel's Pharmaceutical Dosage Forms and Drug Delivery Systems, Allen, LV., Popovich NG., and Ansel HC., 2004, Lippincott Williams & Wilkins (8th ed.), New York, NY; Idson, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 199).

Synthetic surfactants, also known as surface active agents, have found wide applicability in the formulation of emulsions and have been reviewed in the literature (see *e.g.*, Ansel's Pharmaceutical Dosage Forms and Drug Delivery Systems, Allen, LV., Popovich NG., and Ansel HC., 2004, Lippincott Williams & Wilkins (8th ed.), New York, NY; Rieger, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 285; Idson, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), Marcel Dekker, Inc., New York, N.Y., 1988, volume 1, p. 199). Surfactants are typically amphiphilic and comprise a hydrophilic and a hydrophobic portion. The ratio of the hydrophilic to the hydrophobic nature of the surfactant has been termed the hydrophile/lipophile balance (HLB) and is a valuable tool in categorizing and selecting surfactants in the preparation of formulations. Surfactants can be classified into different classes based on the nature of the hydrophilic group: nonionic, anionic,

cationic, and amphoteric (see *e.g.*, Ansel's Pharmaceutical Dosage Forms and Drug Delivery Systems, Allen, LV., Popovich NG., and Ansel HC., 2004, Lippincott Williams & Wilkins (8th ed.), New York, NY Rieger, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 285).

5 A large variety of non-emulsifying materials are also included in emulsion formulations and contribute to the properties of emulsions. These include fats, oils, waxes, fatty acids, fatty alcohols, fatty esters, humectants, hydrophilic colloids, preservatives, and antioxidants (Block, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 335; Idson, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 199).

10 The application of emulsion formulations *via* dermatological, oral, and parenteral routes, and methods for their manufacture have been reviewed in the literature (see *e.g.*, Ansel's Pharmaceutical Dosage Forms and Drug Delivery Systems, Allen, LV., Popovich NG., and Ansel HC., 2004, Lippincott Williams & Wilkins (8th ed.), New York, NY; Idson, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 199).

ii. Microemulsions

In one embodiment of the present invention, the compositions of iRNAs and nucleic acids are formulated as microemulsions. A microemulsion can be defined as a system of water, oil, and amphiphile which is a single optically isotropic and thermodynamically stable liquid solution (see *e.g.*, Ansel's Pharmaceutical Dosage Forms and Drug Delivery Systems, Allen, LV., Popovich NG., and Ansel HC., 2004, Lippincott Williams & Wilkins (8th ed.), New York, NY; Rosoff, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 245). Typically microemulsions are systems that are prepared by first dispersing an oil in an aqueous surfactant solution and then adding a sufficient amount of a fourth component, generally an intermediate chain-length alcohol to form a transparent system. Therefore, microemulsions have also been described as thermodynamically stable, isotropically clear dispersions of two immiscible liquids that are stabilized by interfacial films of surface-active molecules (Leung and Shah, in: Controlled Release of Drugs: Polymers and Aggregate Systems, Rosoff, M., Ed., 1989, VCH Publishers, New York, pages 185-215).

iii. Microparticles

An iRNA of the invention may be incorporated into a particle, *e.g.*, a microparticle. Microparticles can be produced by spray-drying, but may also be produced by other methods including lyophilization, evaporation, fluid bed drying, vacuum drying, or a combination of these techniques.

iv. Penetration Enhancers

In one embodiment, the present invention employs various penetration enhancers to effect the efficient delivery of nucleic acids, particularly iRNAs, to the skin of animals. Most drugs are present in solution in both ionized and nonionized forms. However, usually only lipid soluble or lipophilic drugs readily cross cell membranes. It has been discovered that even non-lipophilic drugs can cross cell membranes if the membrane to be crossed is treated with a penetration enhancer. In addition to aiding the diffusion of non-lipophilic drugs across cell membranes, penetration enhancers also enhance the permeability of lipophilic drugs.

Penetration enhancers can be classified as belonging to one of five broad categories, *i.e.*, surfactants, fatty acids, bile salts, chelating agents, and non-chelating non-surfactants (see *e.g.*, Malmsten, M. Surfactants and polymers in drug delivery, Informa Health Care, New York, NY, 2002; Lee *et al.*, Critical Reviews in Therapeutic Drug Carrier Systems, 1991, p.92). Each of the above mentioned classes of penetration enhancers and their use in manufacture of pharmaceutical compositions and delivery of pharmaceutical agents are well known in the art.

v. Excipients

In contrast to a carrier compound, a “pharmaceutical carrier” or “excipient” is a pharmaceutically acceptable solvent, suspending agent, or any other pharmacologically inert vehicle for delivering one or more nucleic acids to an animal. The excipient can be liquid or solid and is selected, with the planned manner of administration in mind, so as to provide for the desired bulk, consistency, etc., when combined with a nucleic acid and the other components of a given pharmaceutical composition. Such agent are well known in the art.

vi. Other Components

The compositions of the present invention can additionally contain other adjunct components conventionally found in pharmaceutical compositions, at their art-established usage levels. Thus, for example, the compositions can contain additional, compatible, pharmaceutically-active materials such as, for example, antipruritics, astringents, local anesthetics or anti-inflammatory agents, or can contain additional materials useful in physically formulating various dosage forms of the compositions of the present invention, such as dyes, flavoring agents, preservatives, antioxidants, opacifiers, thickening agents and stabilizers. However, such materials, when added, should not unduly interfere with the biological activities of the components of the compositions of the present invention. The formulations can be sterilized and, if desired, mixed with auxiliary agents, *e.g.*, lubricants, preservatives, stabilizers, wetting agents, emulsifiers, salts for influencing osmotic pressure, buffers, colorings, flavorings, or aromatic substances, and the like which do not deleteriously interact with the nucleic acid(s) of the formulation.

Aqueous suspensions can contain substances which increase the viscosity of the suspension including, for example, sodium carboxymethylcellulose, sorbitol, or dextran. The suspension can also contain stabilizers.

In some embodiments, pharmaceutical compositions featured in the invention include (a) one or more iRNA and (b) one or more agents which function by a non-iRNA mechanism and which are useful in treating a KHK-associated disorder, *e.g.*, liver disease (*e.g.*, fatty liver, steatohepatitis, non-alcoholic steatohepatitis (NASH)), dyslipidemia (*e.g.*, hyperlipidemia, high LDL cholesterol, low HDL cholesterol, hypertriglyceridemia, postprandial hypertriglyceridemia), disorders of glycemic control (*e.g.*, insulin resistance, type 2 diabetes), cardiovascular disease (*e.g.*, hypertension, endothelial cell dysfunction), kidney disease (*e.g.*, acute kidney disorder, tubular dysfunction, proinflammatory changes to the proximal tubules, chronic kidney disease), metabolic syndrome, adipocyte dysfunction, visceral adipose deposition, obesity, hyperuricemia, gout, eating disorders, and excessive sugar craving.

Toxicity and prophylactic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, *e.g.*, for determining the LD50 (the dose lethal to 50% of the population) and the ED50 (the dose prophylactically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD50/ED50. Compounds that exhibit high therapeutic indices are preferred.

The data obtained from cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of compositions featured herein in the invention lies generally within a range of circulating concentrations that include the ED50, such as, an ED80 or ED90, with little or no toxicity. The dosage can vary within this range depending upon the dosage form employed and the route of administration utilized. For any compound used in the methods featured in the invention, the prophylactically effective dose can be estimated initially from cell culture assays. A dose can be formulated in animal models to achieve a circulating plasma concentration range of the compound or, when appropriate, of the polypeptide product of a target sequence (*e.g.*, achieving a decreased concentration of the polypeptide) that includes the IC50 (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of symptoms) or higher levels of inhibition as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma can be measured, for example, by high performance liquid chromatography.

In addition to their administration, as discussed above, the iRNAs featured in the invention can be administered in combination with other known agents used for the prevention or treatment of a KHK-associated disorder, *e.g.*, liver disease (*e.g.*, fatty liver, steatohepatitis, non-alcoholic steatohepatitis (NASH)), dyslipidemia (*e.g.*, hyperlipidemia, high LDL cholesterol, low HDL cholesterol, hypertriglyceridemia, postprandial hypertriglyceridemia), disorders of glycemic control (*e.g.*, insulin resistance, type 2 diabetes), cardiovascular disease (*e.g.*, hypertension, endothelial cell

dysfunction), kidney disease (*e.g.*, acute kidney disorder, tubular dysfunction, proinflammatory changes to the proximal tubules, chronic kidney disease), metabolic syndrome, adipocyte dysfunction, visceral adipose deposition, obesity, hyperuricemia, gout, eating disorders, and excessive sugar craving. In any event, the administering physician can adjust the amount and timing of iRNA administration on the basis of results observed using standard measures of efficacy known in the art or described herein.

VII. Methods For Inhibiting KHK Expression

The present invention also provides methods of inhibiting expression of a KHK gene in a cell. The methods include contacting a cell with an RNAi agent, *e.g.*, double stranded RNAi agent, in an amount effective to inhibit expression of KHK in the cell, thereby inhibiting expression of KHK in the cell.

Contacting of a cell with an iRNA, *e.g.*, a double stranded RNA agent, may be done *in vitro* or *in vivo*. Contacting a cell *in vivo* with the iRNA includes contacting a cell or group of cells within a subject, *e.g.*, a human subject, with the iRNA. Combinations of *in vitro* and *in vivo* methods of contacting a cell are also possible. Contacting a cell may be direct or indirect, as discussed above. Furthermore, contacting a cell may be accomplished *via* a targeting ligand, including any ligand described herein or known in the art. In some embodiments, the targeting ligand is a carbohydrate moiety, *e.g.*, a GalNAc₃ ligand, or any other ligand that directs the RNAi agent to a site of interest.

The term “inhibiting,” as used herein, is used interchangeably with “reducing,” “silencing,” “downregulating,” “suppressing,” and other similar terms, and includes any level of inhibition.

The phrase “inhibiting expression of a KHK” is intended to refer to inhibition of expression of any KHK gene (such as, *e.g.*, a mouse KHK 3 gene, a rat KHK gene, a monkey KHK gene, or a human KHK gene) as well as variants or mutants of a KHK gene. Thus, the KHK gene may be a wild-type KHK gene, a mutant KHK gene, or a transgenic KHK gene in the context of a genetically manipulated cell, group of cells, or organism.

“Inhibiting expression of a KHK gene” includes any level of inhibition of a KHK gene, *e.g.*, at least partial suppression of the expression of a KHK gene. The expression of the KHK gene may be assessed based on the level, or the change in the level, of any variable associated with KHK gene expression, *e.g.*, KHK mRNA level or KHK protein level. This level may be assessed in an individual cell or in a group of cells, including, for example, a sample derived from a subject.

Inhibition may be assessed by a decrease in an absolute or relative level of one or more variables that are associated with KHK expression compared with a control level. The control level may be any type of control level that is utilized in the art, *e.g.*, a pre-dose baseline level, or a level determined from a similar subject, cell, or sample that is untreated or treated with a control (such as, *e.g.*, buffer only control or inactive agent control).

It is understood that the degree and duration of elevation of a sign of a KHK-associated disease will vary depending upon the sign. For example, lipid signs, *e.g.*, fasting lipid levels,

NAFLD, NASH, obesity; signs of liver and kidney function, and glucose or insulin response, are durable signs that will not vary in a clinically significant manner within a day or even within a week. Other markers, *e.g.*, serum uric acid and glucose levels, and urine fructose levels, will vary within and likely between days. Blood pressure can be elevated transiently and durably in response to fructose.

- 5 As fructose likely results in weight gain at least in part by reducing satiety, fructose consumption in conjunction with caloric limitation may not result in weight gain.

Further, depending on the disease state in the subject, as many as one third of adults and two thirds of children malabsorb fructose (Johnson *et al.* (2013) Diabetes. 62:3307-3315), *e.g.*, due to variations in expression of the GLUT5 transporter in the gut. However, repeated exposure to fructose can increase fructose absorption. Fructose metabolism has demonstrated to be different depending on the source of fructose, *e.g.*, in high fructose corn syrup vs. in natural fruit, and at high concentrations, such as those provided by soft drinks, glucose can be converted to fructose by the polyol pathway. However, fructose will have more metabolic effects than glucose. Body composition, *e.g.*, lean body mass, has also been demonstrated to affect fructose metabolism. Therefore, both the timing of testing and controls must be carefully selected.

In some embodiments of the methods of the invention, expression of a KHK gene is inhibited by at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, or 95%, or to below the level of detection of the assay. In some embodiments, expression of a KHK gene is inhibited by at least 70%. In some embodiments, expression level is determined using the assay method provided in Example 2 with a 10 nM siRNA concentration in the appropriate species matched cell line.

In certain embodiments, inhibition of expression *in vivo* is determined by knockdown of the human gene in a rodent expressing the human gene, *e.g.*, an AAV-infected mouse expressing the human target gene (*i.e.*, KHK), *e.g.*, when administered as a single dose, *e.g.*, at 3 mg/kg at the nadir of RNA expression. Knockdown of expression of an endogenous gene in a model animal system can also be determined, *e.g.*, after administration of a single dose at, *e.g.*, 3 mg/kg at the nadir of RNA expression. Such systems are useful when the nucleic acid sequence of the human gene and the model animal gene are sufficiently close such that the human iRNA provides effective knockdown of the model animal gene. RNA expression in liver is determined using the PCR methods provided in Example 2.

Inhibition of the expression of a KHK gene may be manifested by a reduction of the amount of mRNA expressed by a first cell or group of cells (such cells may be present, for example, in a sample derived from a subject) in which a KHK gene is transcribed and which has or have been treated (*e.g.*, by contacting the cell or cells with an iRNA of the invention, or by administering an iRNA of the invention to a subject in which the cells are or were present) such that the expression of a KHK gene is inhibited, as compared to a second cell or group of cells substantially identical to the first cell or group of cells but which has not or have not been so treated (control cell(s) not treated with an iRNA or not treated with an iRNA targeted to the gene of interest). In some embodiments, the inhibition is assessed by the method provided in Example 2 using a 10nM siRNA concentration in

the species matched cell line and expressing the level of mRNA in treated cells as a percentage of the level of mRNA in control cells, using the following formula:

$$\frac{(\text{mRNA in control cells}) - (\text{mRNA in treated cells})}{(\text{mRNA in control cells})} \bullet 100\%$$

In other embodiments, inhibition of the expression of a KHK gene may be assessed in terms of a reduction of a parameter that is functionally linked to KHK gene expression, *e.g.*, KHK protein level in blood or serum from a subject. KHK gene silencing may be determined in any cell expressing KHK, either endogenous or heterologous from an expression construct, and by any assay known in the art.

Inhibition of the expression of a KHK protein may be manifested by a reduction in the level of the KHK protein that is expressed by a cell or group of cells or in a subject sample (*e.g.*, the level of protein in a blood sample derived from a subject). As explained above, for the assessment of mRNA suppression, the inhibition of protein expression levels in a treated cell or group of cells may similarly be expressed as a percentage of the level of protein in a control cell or group of cells, or the change in the level of protein in a subject sample, *e.g.*, blood or serum derived therefrom.

A control cell, a group of cells, or subject sample that may be used to assess the inhibition of the expression of a KHK gene includes a cell, group of cells, or subject sample that has not yet been contacted with an RNAi agent of the invention. For example, the control cell, group of cells, or subject sample may be derived from an individual subject (*e.g.*, a human or animal subject) prior to treatment of the subject with an RNAi agent or an appropriately matched population control.

The level of KHK mRNA that is expressed by a cell or group of cells may be determined using any method known in the art for assessing mRNA expression. In one embodiment, the level of expression of KHK in a sample is determined by detecting a transcribed polynucleotide, or portion thereof, *e.g.*, mRNA of the KHK gene. RNA may be extracted from cells using RNA extraction techniques including, for example, using acid phenol/guanidine isothiocyanate extraction (RNAzol B; Biogenesis), RNeasyTM RNA preparation kits (Qiagen®) or PAXgeneTM (PreAnalytixTM, Switzerland). Typical assay formats utilizing ribonucleic acid hybridization include nuclear run-on assays, RT-PCR, RNase protection assays, northern blotting, *in situ* hybridization, and microarray analysis.

In some embodiments, the level of expression of KHK is determined using a nucleic acid probe. The term “probe”, as used herein, refers to any molecule that is capable of selectively binding to a specific KHK. Probes can be synthesized by one of skill in the art, or derived from appropriate biological preparations. Probes may be specifically designed to be labeled. Examples of molecules that can be utilized as probes include, but are not limited to, RNA, DNA, proteins, antibodies, and organic molecules.

Isolated mRNA can be used in hybridization or amplification assays that include, but are not limited to, Southern or northern analyses, polymerase chain reaction (PCR) analyses and probe arrays. One method for the determination of mRNA levels involves contacting the isolated mRNA with a

nucleic acid molecule (probe) that can hybridize to KHK mRNA. In one embodiment, the mRNA is immobilized on a solid surface and contacted with a probe, for example by running the isolated mRNA on an agarose gel and transferring the mRNA from the gel to a membrane, such as nitrocellulose. In an alternative embodiment, the probe(s) are immobilized on a solid surface and the mRNA is contacted with the probe(s), for example, in an Affymetrix® gene chip array. A skilled artisan can readily adapt known mRNA detection methods for use in determining the level of KHK mRNA.

An alternative method for determining the level of expression of KHK in a sample involves the process of nucleic acid amplification or reverse transcriptase (to prepare cDNA) of for example mRNA in the sample, *e.g.*, by RT-PCR (the experimental embodiment set forth in Mullis, 1987, U.S. Patent No. 4,683,202), ligase chain reaction (Barany (1991) *Proc. Natl. Acad. Sci. USA* 88:189-193), self sustained sequence replication (Guatelli *et al.* (1990) *Proc. Natl. Acad. Sci. USA* 87:1874-1878), transcriptional amplification system (Kwoh *et al.* (1989) *Proc. Natl. Acad. Sci. USA* 86:1173-1177), Q-Beta Replicase (Lizardi *et al.* (1988) *Bio/Technology* 6:1197), rolling circle replication (Lizardi *et al.*, U.S. Patent No. 5,854,033) or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers. In particular aspects of the invention, the level of expression of KHK is determined by quantitative fluorogenic RT-PCR (*i.e.*, the TaqMan™ System). In some embodiments, expression level is determined by the method provided in Example 2 using, *e.g.*, a 10nM siRNA concentration, in the species matched cell line.

The expression levels of KHK mRNA may be monitored using a membrane blot (such as used in hybridization analysis such as northern, Southern, dot, and the like), or microwells, sample tubes, gels, beads or fibers (or any solid support comprising bound nucleic acids). See U.S. Patent Nos. 5,770,722, 5,874,219, 5,744,305, 5,677,195 and 5,445,934, which are incorporated herein by reference. The determination of KHK expression level may also comprise using nucleic acid probes in solution.

In some embodiments, the level of mRNA expression is assessed using branched DNA (bDNA) assays or real time PCR (qPCR). The use of these methods is described and exemplified in the Examples presented herein. In some embodiments, expression level is determined by the method provided in Example 2 using a 10nM siRNA concentration in the species matched cell line.

The level of KHK protein expression may be determined using any method known in the art for the measurement of protein levels. Such methods include, for example, electrophoresis, capillary electrophoresis, high performance liquid chromatography (HPLC), thin layer chromatography (TLC), hyperdiffusion chromatography, fluid or gel precipitin reactions, absorption spectroscopy, a colorimetric assays, spectrophotometric assays, flow cytometry, immunodiffusion (single or double), immunoelectrophoresis, western blotting, radioimmunoassay (RIA), enzyme-linked immunosorbent assays (ELISAs), immunofluorescent assays, electrochemiluminescence assays, and the like.

In some embodiments, the efficacy of the methods of the invention are assessed by a decrease in KHK mRNA or protein level (*e.g.*, in a liver biopsy).

In some embodiments of the methods of the invention, the iRNA is administered to a subject such that the iRNA is delivered to a specific site within the subject. The inhibition of expression of KHK may be assessed using measurements of the level or change in the level of KHK mRNA or KHK protein in a sample derived from fluid or tissue from the specific site within the subject (*e.g.*, liver or blood).

As used herein, the terms detecting or determining a level of an analyte are understood to mean performing the steps to determine if a material, *e.g.*, protein, RNA, is present. As used herein, methods of detecting or determining include detection or determination of an analyte level that is below the level of detection for the method used.

VIII. Prophylactic and Treatment Methods of the Invention

The present invention also provides methods of using an iRNA of the invention or a composition containing an iRNA of the invention to inhibit expression of KHK, thereby preventing or treating an KHK-associated disorder, *e.g.*, liver disease (*e.g.*, fatty liver, steatohepatitis, non-alcoholic steatohepatitis (NASH)), dyslipidemia (*e.g.*, hyperlipidemia, high LDL cholesterol, low HDL cholesterol, hypertriglyceridemia, postprandial hypertriglyceridemia), disorders of glycemic control (*e.g.*, insulin resistance, type 2 diabetes), cardiovascular disease (*e.g.*, hypertension, endothelial cell dysfunction), kidney disease (*e.g.*, acute kidney disorder, tubular dysfunction, proinflammatory changes to the proximal tubules, chronic kidney disease), metabolic syndrome, adipocyte dysfunction, visceral adipose deposition, obesity, hyperuricemia, gout, eating disorders, and excessive sugar craving. In the methods of the invention the cell may be contacted with the siRNA *in vitro* or *in vivo*, *i.e.*, the cell may be within a subject.

A cell suitable for treatment using the methods of the invention may be any cell that expresses a KHK gene, *e.g.*, a liver cell. A cell suitable for use in the methods of the invention may be a mammalian cell, *e.g.*, a primate cell (such as a human cell, including human cell in a chimeric non-human animal, or a non-human primate cell, *e.g.*, a monkey cell or a chimpanzee cell), or a non-primate cell. In certain embodiments, the cell is a human cell, *e.g.*, a human liver cell. In the methods of the invention, KHK expression is inhibited in the cell by at least 50, 55, 60, 65, 70, 75, 80, 85, 90, or 95, or to a level below the level of detection of the assay.

The *in vivo* methods of the invention may include administering to a subject a composition containing an iRNA, where the iRNA includes a nucleotide sequence that is complementary to at least a part of an RNA transcript of the KHK gene of the mammal to which the RNAi agent is to be administered. The composition can be administered by any means known in the art including, but not limited to oral, intraperitoneal, or parenteral routes, including intracranial (*e.g.*, intraventricular, intraparenchymal, and intrathecal), intravenous, intramuscular, subcutaneous, transdermal, airway (aerosol), nasal, rectal, and topical (including buccal and sublingual) administration. In certain

embodiments, the compositions are administered by intravenous infusion or injection. In certain embodiments, the compositions are administered by subcutaneous injection. In certain embodiments, the compositions are administered by intramuscular injection.

In one aspect, the present invention also provides methods for inhibiting the expression of an KHK gene in a mammal. The methods include administering to the mammal a composition comprising a dsRNA that targets a KHK gene in a cell of the mammal and maintaining the mammal for a time sufficient to obtain degradation of the mRNA transcript of the KHK gene, thereby inhibiting expression of the KHK gene in the cell. Reduction in gene expression can be assessed by any methods known in the art and by methods, *e.g.* qRT-PCR, described herein, *e.g.*, in Example 2. Reduction in protein production can be assessed by any methods known in the art, *e.g.* ELISA. In certain embodiments, a puncture liver biopsy sample serves as the tissue material for monitoring the reduction in the KHK gene or protein expression. In other embodiments, a blood sample serves as the subject sample for monitoring the reduction in the KHK protein expression. A reduction in the expression of KHK may also be assessed indirectly by measuring a decrease in fructose metabolism by detecting one or more indicators of fructose metabolism, *e.g.*, the presence of fructose in the urine indicating lack of fructose metabolism.

The present invention further provides methods of treatment in a subject in need thereof, *e.g.*, a subject diagnosed with a KHK-associated disorder, such as, liver disease (*e.g.*, fatty liver, steatohepatitis, non-alcoholic steatohepatitis (NASH)), dyslipidemia (*e.g.*, hyperlipidemia, high LDL cholesterol, low HDL cholesterol, hypertriglyceridemia, postprandial hypertriglyceridemia), disorders of glycemic control (*e.g.*, insulin resistance, type 2 diabetes), cardiovascular disease (*e.g.*, hypertension, endothelial cell dysfunction), kidney disease (*e.g.*, acute kidney disorder, tubular dysfunction, proinflammatory changes to the proximal tubules, chronic kidney disease), metabolic syndrome, adipocyte dysfunction, visceral adipose deposition, obesity, hyperuricemia, gout, eating disorders, and excessive sugar craving.

The present invention further provides methods of prophylaxis in a subject in need thereof. The treatment methods of the invention include administering an iRNA of the invention to a subject, *e.g.*, a subject that would benefit from a reduction of KHK expression, in a prophylactically effective amount of an iRNA targeting a KHK gene or a pharmaceutical composition comprising an iRNA targeting a KHK gene.

In one aspect, the present invention provides methods of treating a subject having a disorder that would benefit from reduction in KHK expression, *e.g.*, a KHK-associated disease, such as liver disease (*e.g.*, fatty liver, steatohepatitis, non-alcoholic steatohepatitis (NASH)), dyslipidemia (*e.g.*, hyperlipidemia, high LDL cholesterol, low HDL cholesterol, hypertriglyceridemia, postprandial hypertriglyceridemia), disorders of glycemic control (*e.g.*, insulin resistance, type 2 diabetes), cardiovascular disease (*e.g.*, hypertension, endothelial cell dysfunction), kidney disease (*e.g.*, acute kidney disorder, tubular dysfunction, proinflammatory changes to the proximal tubules, chronic kidney disease), metabolic

syndrome, adipocyte dysfunction, visceral adipose deposition, obesity, hyperuricemia, gout, eating disorders, and excessive sugar craving.

In certain embodiments, the KHK-associated disorder is a liver disease, *e.g.*, fatty liver disease such as NAFLD or NASH. In certain embodiments, the KHK-associated disorder is
 5 dyslipidemia, *e.g.*, elevated serum triglycerides, elevated serum LDL, elevated serum cholesterol, lowered serum HDL, postprandial hypertriglyceridemia. In another embodiment, the KHK-associated disorder is a disorder of glycemic control, *e.g.*, insulin resistance not resulting from an immune response against insulin, glucose resistance, type 2 diabetes. In certain embodiments, the KHK-associated disorder is a cardiovascular disease, *e.g.*, hypertension, endothelial cell dysfunction. In
 10 certain embodiments, the KHK-associated disorder is a kidney disease, *e.g.*, acute kidney disorder, tubular dysfunction, proinflammatory changes to the proximal tubules, chronic kidney disease. In certain embodiments, the disease is metabolic syndrome. In certain embodiments, the KHK-associated disorder is a disease of lipid deposition or dysfunction, *e.g.*, visceral adipose deposition, fatty liver, obesity. In certain embodiments, the KHK-associated disorder is a disease of elevated uric
 15 acid, *e.g.*, gout, hyperuricemia. In certain embodiments the KHK-associated disorder is an eating disorder such as excessive sugar craving.

An iRNA of the invention may be administered as a “free iRNA.” A free iRNA is administered in the absence of a pharmaceutical composition. The naked iRNA may be in a suitable buffer solution. The buffer solution may comprise acetate, citrate, prolamine, carbonate, or
 20 phosphate, or any combination thereof. In one embodiment, the buffer solution is phosphate buffered saline (PBS). The pH and osmolarity of the buffer solution containing the iRNA can be adjusted such that it is suitable for administering to a subject.

Alternatively, an iRNA of the invention may be administered as a pharmaceutical composition, such as a dsRNA liposomal formulation.

25 Subjects that would benefit from an inhibition of KHK gene expression are subjects susceptible to or diagnosed with an KHK-associated disorder, such as liver disease (*e.g.*, fatty liver, steatohepatitis, non-alcoholic steatohepatitis (NASH)), dyslipidemia (*e.g.*, hyperlipidemia, high LDL cholesterol, low HDL cholesterol, hypertriglyceridemia, postprandial hypertriglyceridemia), disorders of glycemic control (*e.g.*, insulin resistance, type 2 diabetes), cardiovascular disease (*e.g.*,
 30 hypertension, endothelial cell dysfunction), kidney disease (*e.g.*, acute kidney disorder, tubular dysfunction, proinflammatory changes to the proximal tubules, chronic kidney disease), metabolic syndrome, adipocyte dysfunction, visceral adipose deposition, obesity, hyperuricemia, gout, eating disorders, and excessive sugar craving.

In an embodiment, the method includes administering a composition featured herein such that
 35 expression of the target a KHK gene is decreased, such as for about 1, 2, 3, 4, 5, 6, 1-6, 1-3, or 3-6 months per dose. In certain embodiments, the composition is administered once every 3-6 months.

In some embodiments, the iRNAs useful for the methods and compositions featured herein specifically target RNAs (primary or processed) of the target a KHK gene. Compositions and

methods for inhibiting the expression of these genes using iRNAs can be prepared and performed as described herein.

Administration of the iRNA according to the methods of the invention may result prevention or treatment of a KHK-associated disorder, *e.g.*, liver disease (*e.g.*, fatty liver, steatohepatitis, non-alcoholic steatohepatitis (NASH)), dyslipidemia (*e.g.*, hyperlipidemia, high LDL cholesterol, low HDL cholesterol, hypertriglyceridemia, postprandial hypertriglyceridemia), disorders of glycemic control (*e.g.*, insulin resistance, type 2 diabetes), cardiovascular disease (*e.g.*, hypertension, endothelial cell dysfunction), kidney disease (*e.g.*, acute kidney disorder, tubular dysfunction, proinflammatory changes to the proximal tubules, chronic kidney disease), metabolic syndrome, adipocyte dysfunction, visceral adipose deposition, obesity, hyperuricemia, gout, eating disorders, and excessive sugar craving.

Subjects can be administered a therapeutic amount of iRNA, such as about 0.01 mg/kg to about 200 mg/kg.

In some embodiments, the iRNA is administered subcutaneously, *i.e.*, by subcutaneous injection. One or more injections may be used to deliver the desired dose of iRNA to a subject. The injections may be repeated over a period of time.

The administration may be repeated on a regular basis. In certain embodiments, after an initial treatment regimen, the treatments can be administered on a less frequent basis. A repeat-dose regimen may include administration of a therapeutic amount of iRNA on a regular basis, such as once per month to once a year. In certain embodiments, the iRNA is administered about once per month to about once every three months, or about once every three months to about once every six months.

The invention further provides methods and uses of an iRNA agent or a pharmaceutical composition thereof for treating a subject that would benefit from reduction and/or inhibition of KHK gene expression, *e.g.*, a subject having an KHK-associated disease, in combination with other pharmaceuticals and/or other therapeutic methods, *e.g.*, with known pharmaceuticals and/or known therapeutic methods, such as, for example, those which are currently employed for treating these disorders.

Accordingly, in some aspects of the invention, the methods which include either a single iRNA agent of the invention, further include administering to the subject one or more additional therapeutic agents.

The iRNA agent and an additional therapeutic agent and/or treatment may be administered at the same time and/or in the same combination, *e.g.*, parenterally, or the additional therapeutic agent can be administered as part of a separate composition or at separate times and/or by another method known in the art or described herein.

IX. Diagnostic Criteria and Treatment for KHK-Associated diseases

Diagnostic criteria, therapeutic agents, and considerations for treatment for various KHK-associated diseases are provided below.

A. Hyperuricemia

Serum uric acid levels are not routinely obtained as clinical lab values. However, hyperuricemia (elevated uric acid) is associated with a number of diseases and conditions including gout, NAFLD, NASH, metabolic disorder, insulin resistance (not resulting from an immune response to insulin), cardiovascular disease, hypertension, and type 2 diabetes. It is expected that decreasing KHK expression can be useful in the prevention or treatment of one or more conditions associated with elevated serum uric acid levels. Further, it is expected that a subject would derive clinical benefit from normalization of serum uric acid levels towards or to a normal serum uric acid level, *e.g.*, no more than 6.8 mg/dl, such as, no more than 6 mg/dl, even in the absence of overt signs or symptoms of one or more conditions associated with elevated uric acid.

Animal models of hyperuricemia include, for example, high fructose diet, *e.g.*, in rats and mice, which can induce one or more of fat accumulation including fatty liver, insulin resistance, type 2 diabetes, obesity including visceral obesity, metabolic syndrome, decreased adiponectin secretion, reduced renal function, and inflammation (see, *e.g.*, Johnson *et al.* (2013) *Diabetes*. 62:3307-3315). Administration of oxonic acid, a uricase inhibitor, can also be used to induce hyperuricemia (see, *e.g.*, Mazalli *et al.* (2001) *Hypertens.* 38:1101-1106). Genetic models of hyperuricemia include the B6;129S7-Uox^{tm1Bay}/J mouse available from Jackson Laboratory ([/jaxmice.jax.org/strain/002223.html](http://jaxmice.jax.org/strain/002223.html)) which develops hyperuricemia, with 10-fold higher levels of serum uric acid levels.

Various treatments for hyperuricemia are known in the art. However, some of the agents can only be used in limited populations. For example, allopurinol is a xanthine oxidase inhibitor that is used to reduce serum uric acid levels for the treatment of a number of conditions, *e.g.*, gout, cardiovascular disease including ischemia-reperfusion injury, hypertension, atherosclerosis, and stroke, and inflammatory diseases (Pacher *et al.*, (2006) *Pharma. Rev.* 58:87-114). However, the use of allopurinol is contraindicated in subjects with impaired renal function, *e.g.*, chronic kidney disease, hypothyroidism, hyperinsulinemia, or insulin resistance; or in subjects predisposed to kidney disease or impaired renal function, *e.g.*, subjects with hypertension, metabolic disorder, diabetes, and the elderly. Further, allopurinol should not be taken by subjects taking oral coagulants or probenecid as well as subjects taking diuretics, especially thiazide diuretics or other drugs that can reduce kidney function or have potential kidney toxicity.

In certain embodiments, the compositions and methods of the invention are used in combination with other compositions and methods to treat hyperuricemia, *e.g.*, allopurinol, oxypurinol, febuxostat. In certain embodiments, the compositions and methods of the invention are used for treatment of subjects with reduced kidney function or susceptible to reduced kidney function, *e.g.*, due to age, comorbidities, or drug interactions.

B. Gout

Gout affects approximately 1 in 40 adults, most commonly men between 30-60 years of age. Gout less commonly affects women. Gout is one of a few types of arthritis where future damage to

joints can be avoided by treatment. Gout is characterized by recurrent attacks of acute inflammatory arthritis caused by an inflammatory reaction to uric acid crystals in the joint due to hyperuricemia resulting from insufficient renal clearance of uric acid or excessive uric acid production. Fructose associated gout is sometimes associated with variants of transporters expressed in the kidney,
 5 intestine, and liver. Gout is characterized by the formation and deposition of tophi, monosodium urate (MSU) crystals, in the joints and subcutaneously. Pain associated with gout is not related to the size of the tophi, but is a result of an immune response against the MSU crystals. There is a linear inverse relation between serum uric acid and the rate of decrease in tophus size. For example, in one study of 18 patients with non-tophaceous gout, serum uric acid declined to 2.7–5.4 mg/dL (0.16–0.32
 10 mM) in all subjects within 3 months of starting urate lowering therapy (Pascual and Sivera (2007) Ann. Rheum. Dis. 66:1056-1058). However, it took 12 months with normalized serum uric acid for MSU crystals to disappear from asymptomatic knee or first MTP joints in patients who had gout for less than 10 years, vs. 18 months in those with gout for more than 10 years. Therefore, effective treatment of gout does not require complete clearance of tophi or resolution of all symptoms, *e.g.*,
 15 joint pain and swelling, inflammation, but simply a reduction in at least one sign or symptom of gout, *e.g.*, reduction in severity or frequency of gout attacks, in conjunction with a reduction in serum urate levels.

Animal models of gout include oxonic acid- induced hyperuricemia (see, *e.g.*, Jang *et al.* (2014) Mycobiology. 42:296-300).

20 Currently available treatments for gout are contraindicated or ineffective in a number of subjects. Allopurinol, a common first line treatment to reduce uric acid levels in subjects with gout, is contraindicated in a number of populations, especially those with compromised renal function, as discussed above. Further, a number of subjects fail treatment with allopurinol, *e.g.*, subjects who suffer gout flares despite treatment, or subjects who suffer from rashes or hypersensitivity reactions
 25 associated with allopurinol.

In certain embodiments, the compositions and methods of the invention are used in combination with other agents to reduce serum uric acid. In certain embodiments, the compositions and methods of the invention are used in combination with agents for treatment of symptoms of gout, *e.g.*, analgesic or anti-inflammatory agents, *e.g.*, NSAIDS. In certain embodiments, the compositions
 30 and methods of the invention are used for treatment of subjects with reduced kidney function or susceptible to reduced kidney function, *e.g.*, due to age, comorbidities, or drug interactions.

C. Liver disease

NAFLD is associated with hyperuricemia (Xu *et al.* (2015) J. Hepatol. 62:1412-1419) which,
 35 in turn, is associated with elevated fructose metabolism. The definition of nonalcoholic fatty liver disease (NAFLD) requires that (a) there is evidence of hepatic steatosis, either by imaging or by histology and (b) there are no causes for secondary hepatic fat accumulation such as significant alcohol consumption, use of steatogenic medication or hereditary disorders. In the majority of

patients, NAFLD is associated with metabolic risk factors such as obesity, diabetes mellitus, and dyslipidemia. NAFLD is histologically further categorized into nonalcoholic fatty liver (NAFL) and nonalcoholic steatohepatitis (NASH). NAFL is defined as the presence of hepatic steatosis with no evidence of hepatocellular injury in the form of ballooning of the hepatocytes. NASH is defined as the presence of hepatic steatosis and inflammation with hepatocyte injury (ballooning) with or without fibrosis (Chalasani *et al.* (2012) *Hepatology*. 55:2005-2023). It is generally agreed that patients with simple steatosis have very slow, if any, histological progression, while patients with NASH can exhibit histological progression to cirrhotic-stage disease. The long term outcomes of patients with NAFLD and NASH have been reported in several studies. Their findings can be summarized as follows; (a) patients with NAFLD have increased overall mortality compared to matched control populations, (b) the most common cause of death in patients with NAFLD, NAFL, and NASH is cardiovascular disease, and (c) patients with NASH (but not NAFL) have an increased liver-related mortality rate.

Animal models of NAFLD include various high fat- or high fructose-fed animal models. Genetic models of NAFLD include the B6.129S7-Ldlr^{tm1Her}/J and the B6.129S4-Pten^{tm1Hwu}/J mice available from The Jackson Laboratory.

Treatment of NAFLD is typically to manage the conditions that resulted in development of NAFLD. For example, patients with dyslipidemia are treated with agents to normalize cholesterol or triglycerides, as needed, to treat or prevent further progression of NAFLD. Patients with type 2 diabetes are treated with agents to normalize glucose or insulin sensitivity. Lifestyle changes, *e.g.*, changes in diet and exercise, are also used to treat NAFLD. In a mouse model of NAFLD, treatment with allopurinol both prevented the development of hepatic steatosis, but also significantly ameliorated established hepatic steatosis in mice (Xu *et al.*, *J. Hepatology*. 62:1412-1419, 2015).

In certain embodiments, the compositions and methods of the invention are used in combination with other agents to reduce serum uric acid. In certain embodiments, the compositions and methods of the invention are used in combination with agents for treatment of symptoms of NAFLD. In certain embodiments, the compositions and methods of the invention are used for treatment of subjects with reduced kidney function or susceptible to reduced kidney function, *e.g.*, due to age, comorbidities, or drug interactions.

30

D. Dyslipidemia, disorders of glycemic control, metabolic syndrome, and obesity

Dyslipidemia (*e.g.*, hyperlipidemia, high LDL cholesterol, low HDL cholesterol, hypertriglyceridemia, postprandial hypertriglyceridemia), disorders of glycemic control (*e.g.*, insulin resistance, type 2 diabetes), metabolic syndrome, adipocyte dysfunction, visceral adipose deposition, obesity, and excessive sugar craving are associated with elevated fructose metabolism. Characteristics or diagnostic criteria for the conditions are provided below. Animal models of metabolic disorder and the component features include various high fat- or high fructose-fed animal

models. Genetic models include leptin deficient B6.Cg-*Lep^{ob}/J*, commonly known as *ob* or *ob/ob* mice, which are available from The Jackson Laboratory.

Normal and abnormal fasting levels of the lipids are provided in the table below.

Lipid	Value	Interpretation
Total cholesterol	Below 200 mg/dL	Desirable
	200-239 mg/dL	Borderline high
	240 mg/dL and above	High
LDL cholesterol	Below 70 mg/dL	Best for people who have heart disease or diabetes.
	Below 100 mg/dL	Optimal for people at risk of heart disease.
	100-129 mg/dL	Near optimal if there is no heart disease. High if there is heart disease.
	130-159 mg/dL	Borderline high if there is no heart disease. High if there is heart disease.
	160-189 mg/dL	High if there is no heart disease. Very high if there is heart disease.
	190 mg/dL and above	Very high
HDL cholesterol	Below 40 mg/dL (men) Below 50 mg/dL (women)	Poor
	50-59 mg/dL	Moderate
	60 mg/dL and above	Normal
Triglycerides	Below 150 mg/dL	Desirable
	150-199 mg/dL	Borderline high
	200-499 mg/dL	High
	500 mg/dL and above	Very High

- 5 Postprandial hypertriglyceridemia is principally initiated by overproduction or decreased catabolism of triglyceride-rich lipoproteins (TRLs) and is a consequence of predisposing genetic variations and medical conditions such as obesity and insulin resistance.

Insulin resistance is characterized by the presence of at least one of:

1. A fasting blood glucose level of 100-125 mg/dL taken at two different times; or
 2. An oral glucose tolerance test with a result of a glucose level of 140-199 mg/dL at 2 hours
- 10 after glucose consumption.

As used herein, insulin resistance does not include a lack of response to insulin as a result of an immune response to administered insulin as often occurs in late stages of insulin dependent diabetes, especially type 1 diabetes.

Type 2 diabetes is characterized by at least one of:

- 15 1. A fasting blood glucose level $\geq$ 126 mg/dL taken at two different times;

2. A hemoglobin A1c (A1C) test with a result of $\geq 6.5\%$ or higher; or
3. An oral glucose tolerance test with a result of a glucose level ≥ 200 mg/dL at 2 hours after glucose consumption.

Pharmacological treatments for type 2 diabetes and insulin resistance include treatment with
 5 agents to normalize blood sugar such as metformin (*e.g.*, glucophage, glumetza), sulfonylureas (*e.g.*, glyburide, glipizide, glimepiride), meglitinides (*e.g.*, repaglinide, nateglinide), thiazolidinediones (rosiglitazone, pioglitazone), DPP-4 inhibitors (sitagliptin, saxagliptin, linagliptin), GLP-1 receptor antagonists (exenatide, liraglutide), and SGLT2 inhibitors (*e.g.*, canagliflozin, dapagliflozin).

Obesity is characterized as disease of excess body fat. Body mass index (BMI), which is
 10 calculated by dividing body weight in kilograms (kg) by height in meters (m) squared, provides a reasonable estimate of body fat for most, but not all, people. Generally, a BMI below 18.5 is characterized as underweight, 18.5 to 24.9 is normal, 25.0-29.9 is overweight, 30.0-34.9 is obese (class I), 35-39.9 is obese (class II), and 40.0 and higher is extremely obese (class III).

Methods for assessment of subcutaneous vs. visceral fat are provided, for example, in
 15 Wajchenberg (2000) Subcutaneous and visceral adipose tissue: their relation to the metabolic syndrome, *Endocr Rev.* 21:697-738, which is incorporated herein by reference.

Metabolic syndrome is characterized by a cluster of conditions defined as at least three of the five following metabolic risk factors:

1. Large waistline (≥ 35 inches for women or ≥ 40 inches for men);
- 20 2. High triglyceride level (≥ 150 mg/dl);
3. Low HDL cholesterol (≤ 50 mg/dl for women or ≤ 40 mg/dl for men);
4. Elevated blood pressure ($\geq 130/85$) or on medicine to treat high blood pressure; and
5. High fasting blood sugar (≥ 100 mg/dl) or being in medicine to treat high blood sugar.

As with NAFLD, the agents for treatment of metabolic syndrome depend on the specific risk
 25 factors present, *e.g.*, normalize lipids when lipids are abnormal, normalize glucose or insulin sensitivity when they are abnormal.

Metabolic syndrome, insulin resistance, and type 2 diabetes are often associated with decreased renal function or the potential for decreased renal function.

In certain embodiments, the compositions and methods of the invention are for use in
 30 treatment of subjects with dyslipidemia, disorders of glycemic control, metabolic syndrome, and obesity. For example, in certain embodiments, the compositions and methods of the invention are for use in subjects with metabolic syndrome, insulin resistance, or type 2 diabetes and chronic kidney disease. In certain embodiments, the compositions and methods are for use in subjects with metabolic syndrome, insulin resistance, or type 2 diabetes who are suffering from one or more of cardiovascular
 35 disease, hypothyroidism, or inflammatory disease; or elderly subjects (*e.g.*, over 65). In certain embodiments, the compositions and methods are for use in subjects with metabolic syndrome, insulin resistance, or type 2 diabetes who are also taking a drug that can reduce kidney function as demonstrated by the drug label. For example, in certain embodiments the compositions and methods

of the invention are for use in subjects with metabolic syndrome, insulin resistance, or type 2 diabetes who are being treated with oral coagulants or probenecid. For example, in certain embodiments the compositions and methods of the invention are for use in subjects with metabolic syndrome, insulin resistance, or type 2 diabetes who are being treated with diuretics, especially thiazide diuretics.

5 In certain embodiments, the compositions and methods of the invention are used in combination with other agents to reduce serum uric acid. In certain embodiments, the compositions and methods of the invention are used in combination with agents for treatment of symptoms of metabolic syndrome, insulin resistance, or type 2 diabetes. In certain embodiments, subjects are treated with *e.g.*, agents to decrease blood pressure, *e.g.*, diuretics, beta-blockers, ACE inhibitors, 10 angiotensin II receptor blockers, calcium channel blockers, alpha blockers, alpha-2 receptor antagonists, combined alpha- and beta-blockers, central agonists, peripheral adrenergic inhibitors, and blood vessel dilators; agents to decrease cholesterol, *e.g.*, statins, selective cholesterol absorption inhibitors, resins, or lipid lowering therapies; or agents to normalize blood sugar, *e.g.*, metformin, sulfonylureas, meglitinides, thiazolidinediones, DPP-4 inhibitors, GLP-1 receptor antagonists, and 15 SGLT2 inhibitors.

In certain embodiments, the compositions and methods of the invention are used for treatment of subjects with reduced kidney function or susceptible to reduced kidney function, *e.g.*, due to age, comorbidities, or drug interactions.

20 The iRNA and additional therapeutic agents may be administered at the same time or in the same combination, *e.g.*, parenterally, or the additional therapeutic agent can be administered as part of a separate composition or at separate times or by another method known in the art or described herein.

E. Cardiovascular disease

In certain embodiments, the compositions and methods of the invention are for use in 25 treatment of subjects with cardiovascular disease. For example, in certain embodiments, the compositions and methods of the invention are for use in subjects with cardiovascular disease and chronic kidney disease. In certain embodiments, the compositions and methods are for use in subjects with cardiovascular disease who are suffering from one or more of metabolic disorder, insulin resistance, hyperinsulinemia, diabetes, hypothyroidism, or inflammatory disease. In certain 30 embodiments, the compositions and methods are for use in subjects with cardiovascular disease who are also taking a drug that can reduce kidney function as demonstrated by the drug label. For example, in certain embodiments the compositions and methods of the invention are for use in subjects with cardiovascular disease who are being treated with oral coagulants or probenecid. For example, in certain embodiments the compositions and methods of the invention are for use in 35 subjects with cardiovascular disease who are being treated with diuretics, especially thiazide diuretics. For example, in certain embodiments the compositions and methods of the invention are for use in subjects with cardiovascular disease who have failed treatment with allopurinol.

In certain embodiments, the compositions and methods of the invention are used in combination with other agents to reduce serum uric acid. In certain embodiments, the compositions and methods of the invention are used in combination with agents for treatment of symptoms of cardiovascular disease, *e.g.*, agents to decrease blood pressure, *e.g.*, diuretics, beta-blockers, ACE inhibitors, angiotensin II receptor blockers, calcium channel blockers, alpha blockers, alpha-2 receptor antagonists, combined alpha- and beta-blockers, central agonists, peripheral adrenergic inhibitors, and blood vessel dilators; or agents to decrease cholesterol, *e.g.*, statins, selective cholesterol absorption inhibitors, resins, or lipid lowering therapies.

10 F. Kidney disease

Kidney disease includes, for example, acute kidney disorder, tubular dysfunction, proinflammatory changes to the proximal tubules, and chronic kidney disease.

Acute kidney (renal) failure occurs when the kidneys suddenly become unable to filter waste products from the blood resulting in accumulation of dangerous levels of wastes in serum and systemic chemical imbalance. Acute kidney failure can develop rapidly over a few hours or a few days, and is most common in individuals who are already hospitalized, particularly in critically ill individuals who need intensive care. Acute kidney failure can be fatal and requires intensive treatment. However, acute kidney failure may be reversible. If you're otherwise in good health, you may recover normal or nearly normal kidney function.

Chronic kidney disease, also called chronic kidney failure, describes the gradual loss of kidney function. When chronic kidney disease reaches an advanced stage, dangerous levels of fluid, electrolytes and wastes can accumulate in the body. Signs and symptoms of kidney disease may include nausea, vomiting, loss of appetite, fatigue and weakness, sleep problems, changes in urine output, decreased mental sharpness, muscle twitches and cramps, hiccups, swelling of feet and ankles, persistent itching, chest pain, if fluid builds up around the lining of the heart, shortness of breath, if fluid builds up in the lungs, high blood pressure (hypertension) that's difficult to control. Signs and symptoms of chronic kidney disease are often nonspecific and can develop slowly, and may not appear until irreversible damage has occurred.

Kidney disease is treated by removing the damaging agent or condition that is causing kidney damage, *e.g.* normalize blood pressure to improve kidney function, end treatment with agents that can induce kidney damage, reduce inflammation that is causing kidney damage, or by providing renal support (*e.g.*, renal dialysis) to assist kidney function.

Renal function is typically determined using one or more routine laboratory tests, BUN (blood urea nitrogen), creatinine (blood), creatinine (urine), or creatinine clearance (see, *e.g.*, www.nlm.nih.gov/medlineplus/ency/article/003435.htm). The tests may also be diagnostic of conditions in other organs.

Generally, a BUN level of 6 to 20 mg/dL is considered normal, although normal values may vary among different laboratories. Elevated BUN level can be indicative of kidney disease, including glomerulonephritis, pyelonephritis, and acute tubular necrosis, or kidney failure.

A normal result for blood creatinine is 0.7 to 1.3 mg/dL for men and 0.6 to 1.1 mg/dL for women. Elevated blood creatinine can be indicative of compromised kidney function due to kidney damage or failure, infection, or reduced blood flow.

Urine creatinine (24-hour sample) values can range from 500 to 2000 mg/day. Results depend on age and amount of lean body mass. Normal results are 14 to 26 mg per kg of body mass per day for men and 11 to 20 mg per kg of body mass per day for women. Abnormal results can be indicative of kidney damage, such as damage to the tubule cells, kidney failure, decreased blood flow to the kidneys, or kidney infection (pyelonephritis).

The creatinine clearance test helps provide information regarding kidney function by comparing the creatinine level in urine with the creatinine level in blood. Clearance is often measured as milliliters per minute (ml/min). Normal values are 97 to 137 ml/min. for men and 88 to 128 ml/min. for women. Lower than normal creatinine clearance can be indicative of kidney damage, such as damage to the tubule cells, kidney failure, decreased blood flow to the kidneys, or reduced glomerular filtration in the kidneys.

In certain embodiments, the compositions and methods of the invention can be used for the treatment of kidney disease. It is expected that such agents would not cause damage to the kidney.

X. Kits

In certain aspects, the instant disclosure provides kits that include a suitable container containing a pharmaceutical formulation of a siRNA compound, *e.g.*, a double-stranded siRNA compound, or siRNA compound, (*e.g.*, a precursor, *e.g.*, a larger siRNA compound which can be processed into a siRNA compound, or a DNA which encodes an siRNA compound, *e.g.*, a double-stranded siRNA compound, or ssiRNA compound, or precursor thereof).

Such kits include one or more dsRNA agent(s) and instructions for use, *e.g.*, instructions for administering a prophylactically or therapeutically effective amount of a dsRNA agent(s). The dsRNA agent may be in a vial or a pre-filled syringe. The kits may optionally further comprise means for administering the dsRNA agent (*e.g.*, an injection device, such as a pre-filled syringe), or means for measuring the inhibition of KHK (*e.g.*, means for measuring the inhibition of KHK mRNA, KHK protein, and/or KHK activity). Such means for measuring the inhibition of KHK may comprise a means for obtaining a sample from a subject, such as, *e.g.*, a plasma sample. The kits of the invention may optionally further comprise means for determining the therapeutically effective or prophylactically effective amount.

In certain embodiments the individual components of the pharmaceutical formulation may be provided in one container, *e.g.*, a vial or a pre-filled syringe. Alternatively, it may be desirable to provide the components of the pharmaceutical formulation separately in two or more containers, *e.g.*,

one container for a siRNA compound preparation, and at least another for a carrier compound. The kit may be packaged in a number of different configurations such as one or more containers in a single box. The different components can be combined, *e.g.*, according to instructions provided with the kit. The components can be combined according to a method described herein, *e.g.*, to prepare and
5 administer a pharmaceutical composition. The kit can also include a delivery device.

This invention is further illustrated by the following examples which should not be construed as limiting. The entire contents of all references, patents and published patent applications cited
10 throughout this application, as well as the informal Sequence Listing, are hereby incorporated herein by reference.

EXAMPLES

Example 1. iRNA Synthesis

15 Source of reagents

Where the source of a reagent is not specifically given herein, such reagent can be obtained from any supplier of reagents for molecular biology at a quality/purity standard for application in molecular biology.

20 siRNA Design

siRNAs targeting the human KHK (human NCBI refseqID: XM_017004061.1; NCBI GeneID: 3795) were designed using custom R and Python scripts. The human KHK REFSEQ mRNA has a length of 2283 bases.

Detailed lists of the unmodified KHK sense and antisense strand nucleotide sequences are
25 shown in Tables 2, 5 and 8. Detailed lists of the modified KHK sense and antisense strand nucleotide sequences are shown in Tables 3, 6 and 9.

It is to be understood that, throughout the application, a duplex name without a decimal is equivalent to a duplex name with a decimal which merely references the batch number of the duplex. For example, AD-959917 is equivalent to AD-959917.1.

30

siRNA Synthesis

siRNAs were designed, synthesized, and prepared using methods known in the art.

Briefly, siRNA sequences were synthesized on a 1 μ mol scale using a Mermade 192 synthesizer (BioAutomation) with phosphoramidite chemistry on solid supports. The solid support
35 was controlled pore glass (500-1000 Å) loaded with a custom GalNAc ligand (3'-GalNAc conjugates), universal solid support (AM Chemicals), or the first nucleotide of interest. Ancillary synthesis reagents and standard 2-cyanoethyl phosphoramidite monomers (2'-deoxy-2'-fluoro, 2'-O-methyl, RNA, DNA) were obtained from Thermo-Fisher (Milwaukee, WI), Hongene (China), or

Chemgenes (Wilmington, MA, USA). Additional phosphoramidite monomers were procured from commercial suppliers, prepared in-house, or procured using custom synthesis from various CMOs. Phosphoramidites were prepared at a concentration of 100 mM in either acetonitrile or 9:1 acetonitrile:DMF and were coupled using 5-Ethylthio-1H-tetrazole (ETT, 0.25 M in acetonitrile) with a reaction time of 400 s. Phosphorothioate linkages were generated using a 100 mM solution of 3-((Dimethylamino-methylidene) amino)-3H-1,2,4-dithiazole-3-thione (DDTT, obtained from Chemgenes (Wilmington, MA, USA)) in anhydrous acetonitrile/pyridine (9:1 v/v). Oxidation time was 5 minutes. All sequences were synthesized with final removal of the DMT group ("DMT-Off").

Upon completion of the solid phase synthesis, solid-supported oligoribonucleotides were treated with 300 μ L of Methylamine (40% aqueous) at room temperature in 96 well plates for approximately 2 hours to afford cleavage from the solid support and subsequent removal of all additional base-labile protecting groups. For sequences containing any natural ribonucleotide linkages (2'-OH) protected with a tert-butyl dimethyl silyl (TBDMS) group, a second deprotection step was performed using TEA.3HF (triethylamine trihydrofluoride). To each oligonucleotide solution in aqueous methylamine was added 200 μ L of dimethyl sulfoxide (DMSO) and 300 μ L TEA.3HF and the solution was incubated for approximately 30 mins at 60 °C. After incubation, the plate was allowed to come to room temperature and crude oligonucleotides were precipitated by the addition of 1 mL of 9:1 acetonitrile:ethanol or 1:1 ethanol:isopropanol. The plates were then centrifuged at 4 °C for 45 mins and the supernatant carefully decanted with the aid of a multichannel pipette. The oligonucleotide pellet was resuspended in 20 mM NaOAc and subsequently desalted using a HiTrap size exclusion column (5 mL, GE Healthcare) on an Agilent LC system equipped with an autosampler, UV detector, conductivity meter, and fraction collector. Desalted samples were collected in 96 well plates and then analyzed by LC-MS and UV spectrometry to confirm identity and quantify the amount of material, respectively.

Duplexing of single strands was performed on a Tecan liquid handling robot. Sense and antisense single strands were combined in an equimolar ratio to a final concentration of 10 μ M in 1x PBS in 96 well plates, the plate sealed, incubated at 100 °C for 10 minutes, and subsequently allowed to return slowly to room temperature over a period of 2-3 hours. The concentration and identity of each duplex was confirmed and then subsequently utilized for in vitro screening assays.

Example 2. In vitro screening methods

HepG2 Cell culture and 96-well transfections

HepG2 cells were grown to near confluence at 37°C in an atmosphere of 5% CO₂ in Eagle's Minimum Essential Medium (Gibco) supplemented with 10% FBS (ATCC) before being released from the plate by trypsinization. Transfection was carried out by adding 18.5 μ L of Opti-MEM plus 0.25 μ L of Lipofectamine RNAiMax per well (Invitrogen, Carlsbad CA. cat # 13778-150) to 5 μ L of each siRNA duplex to an individual well in a 96-well plate. The mixture was then incubated at room temperature for 15 minutes. Eighty μ L of complete growth media without antibiotic containing ~2

$\times 10^4$ HepG2 cells were then added to the siRNA mixture. Cells were incubated for 24 hours prior to RNA purification. Dose experiments were performed at 10 nM, 1 nM and 0.1 nM final duplex concentration.

5 *Total RNA isolation using DYNABEADS mRNA Isolation Kit (Invitrogen™, part #: 610-12)*

Cells were lysed in 75 μ L of Lysis/Binding Buffer containing 3 μ L of beads per well and mixed for 10 minutes on an electrostatic shaker. The washing steps were automated on a Biotek EL406, using a magnetic plate support. Beads were washed (in 90 μ L) once in Buffer A, once in Buffer B, and twice in Buffer E, with aspiration steps in between. Following a final aspiration,
10 complete 10 μ L RT mixture was added to each well, as described below.

cDNA synthesis using ABI High capacity cDNA reverse transcription kit (Applied Biosystems, Foster City, CA, Cat #4368813)

A master mix of 1 μ L 10X Buffer, 0.4 μ L 25X dNTPs, 1 μ L Random primers, 0.5 μ L Reverse
15 Transcriptase, 0.5 μ L RNase inhibitor and 6.6 μ L of H₂O per reaction were added per well. Plates were sealed, agitated for 10 minutes on an electrostatic shaker, and then incubated at 37 degrees C for 2 hours. Following this, the plates were agitated at 80 degrees C for 8 minutes.

Real time PCR

20 Two microlitre (μ L) of cDNA were added to a master mix containing 0.5 μ L of human GAPDH TaqMan Probe (4326317E), 0.5 μ L human KHK, 2 μ L nuclease-free water and 5 μ L Lightcycler 480 probe master mix (Roche Cat # 04887301001) per well in a 384 well plates (Roche cat # 04887301001). Real time PCR was done in a LightCycler480 Real Time PCR system (Roche).

To calculate relative fold change, data were analyzed using the $\Delta\Delta$ Ct method and normalized
25 to assays performed with cells transfected with 10nM AD-1955, or mock transfected cells. IC50s were calculated using a 4 parameter fit model using XLFit and normalized to cells transfected with AD-1955 or mock-transfected. The sense and antisense sequences of AD-1955 are: sense: cuuAcGcuGAGuAcuucGAdTsdT (SEQ ID NO: 18) and antisense UCGAAGuACUcAGCGuAAGdTsdT (SEQ ID NO: 19).

30

The results of the transfection assays of the dsRNA agents listed in Tables 2 and 3 in HepG2 cells are shown in Table 4.

Table 1. Abbreviations of nucleotide monomers used in nucleic acid sequence representation. It will
35 be understood that these monomers, when present in an oligonucleotide, are mutually linked by 5'-3'-phosphodiester bonds; and it is understood that when the nucleotide contains a 2'-fluoro modification,

then the fluoro replaces the hydroxy at that position in the parent nucleotide (*i.e.*, it is a 2'-deoxy-2'-fluoronucleotide).

Abbreviation	Nucleotide(s)
A	Adenosine-3'-phosphate
Ab	beta-L-adenosine-3'-phosphate
Abs	beta-L-adenosine-3'-phosphorothioate
Af	2'-fluoroadenosine-3'-phosphate
Afs	2'-fluoroadenosine-3'-phosphorothioate
As	adenosine-3'-phosphorothioate
C	cytidine-3'-phosphate
Cb	beta-L-cytidine-3'-phosphate
Cbs	beta-L-cytidine-3'-phosphorothioate
Cf	2'-fluorocytidine-3'-phosphate
Cfs	2'-fluorocytidine-3'-phosphorothioate
Cs	cytidine-3'-phosphorothioate
G	guanosine-3'-phosphate
Gb	beta-L-guanosine-3'-phosphate
Gbs	beta-L-guanosine-3'-phosphorothioate
Gf	2'-fluoroguanosine-3'-phosphate
Gfs	2'-fluoroguanosine-3'-phosphorothioate
Gs	guanosine-3'-phosphorothioate
T	5'-methyluridine-3'-phosphate
Tf	2'-fluoro-5-methyluridine-3'-phosphate
Tfs	2'-fluoro-5-methyluridine-3'-phosphorothioate
Ts	5-methyluridine-3'-phosphorothioate
U	Uridine-3'-phosphate
Uf	2'-fluorouridine-3'-phosphate
Ufs	2'-fluorouridine-3'-phosphorothioate
Us	uridine-3'-phosphorothioate
N	any nucleotide, modified or unmodified
a	2'-O-methyladenosine-3'-phosphate
as	2'-O-methyladenosine-3'-phosphorothioate
c	2'-O-methylcytidine-3'-phosphate
cs	2'-O-methylcytidine-3'-phosphorothioate
g	2'-O-methylguanosine-3'-phosphate
gs	2'-O-methylguanosine-3'-phosphorothioate
t	2'-O-methyl-5-methyluridine-3'-phosphate
ts	2'-O-methyl-5-methyluridine-3'-phosphorothioate
u	2'-O-methyluridine-3'-phosphate
us	2'-O-methyluridine-3'-phosphorothioate
s	phosphorothioate linkage
L10	N-(cholesterylcarboxamidocaproyl)-4-hydroxyprolinol (Hyp-C6-Chol)

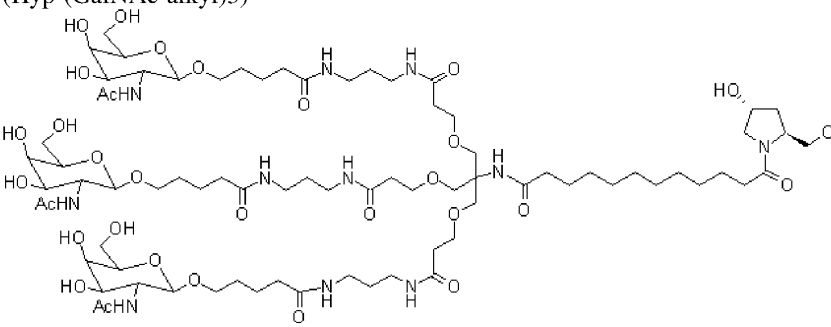
Abbreviation	Nucleotide(s)
L96	N-[tris(GalNAc-alkyl)-amidodecanoyl]-4-hydroxyprolinol (Hyp-(GalNAc-alkyl)₃) 
Y34	2-hydroxymethyl-tetrahydrofuran-4-methoxy-3-phosphate (abasic 2'-OMe furanose)
Y44	inverted abasic DNA (2-hydroxymethyl-tetrahydrofuran-5-phosphate)
(Agn)	Adenosine-glycol nucleic acid (GNA) S-Isomer
(Cgn)	Cytidine-glycol nucleic acid (GNA) S-Isomer
(Ggn)	Guanosine-glycol nucleic acid (GNA) S-Isomer
(Tgn)	Thymidine-glycol nucleic acid (GNA) S-Isomer
P	Phosphate
VP	Vinyl-phosphonate
dA	2'-deoxyadenosine-3'-phosphate
dAs	2'-deoxyadenosine-3'-phosphorothioate
dC	2'-deoxycytidine-3'-phosphate
dCs	2'-deoxycytidine-3'-phosphorothioate
dG	2'-deoxyguanosine-3'-phosphate
dGs	2'-deoxyguanosine-3'-phosphorothioate
dT	2'-deoxythymidine-3'-phosphate
dTs	2'-deoxythymidine-3'-phosphorothioate
dU	2'-deoxyuridine
dUs	2'-deoxyuridine-3'-phosphorothioate
(C2p)	cytidine-2'-phosphate
(G2p)	guanosine-2'-phosphate
(U2p)	uridine-2'-phosphate
(A2p)	adenosine-2'-phosphate
(Chd)	2'-O-hexadecyl-cytidine-3'-phosphate
(Ahd)	2'-O-hexadecyl-adenosine-3'-phosphate
(Ghd)	2'-O-hexadecyl-guanosine-3'-phosphate
(Uhd)	2'-O-hexadecyl-uridine-3'-phosphate
s	phosphorothioate

Table 2. Unmodified Sense and Antisense Strand Sequences of KHK dsRNAs

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Range in XM_017004061.1	Antisense sequence 5' to 3'	SEQ ID NO:	Range in XM_017004061.1
AD-1290652	GUGGUGUUUUGCAGCAAGAU	20	810-830	AUCUUUGCUGACAAACACCACGU	244	808-830
AD-1290731	ACGUGGUGUUUGCAGCAAAU	21	808-828	AUUUGCUGACAAACACCACGUCU	245	806-828
AD-1290560	UCAGAGCAAAUAAAUUCUCCU	22	1336-1356	AGGAAGAUUUAUUUGCUCUGAGG	246	1334-1356
AD-1290854	CAGUUCAGUGGAUCCACAUU	23	642-662	AAUGUGGAUCCACUUGAACUGGG	247	640-662
AD-1290629	AGUAGCGCAUUUCUCUUUGU	24	122-142	ACAAAGAGAAAUUGCGUACUUG	248	120-142
AD-1290517	GCGCAUUUUCUCUUUGCAUUU	25	126-146	AAAUGCAAAAGAGAAAUUGCGCUA	249	124-146
AD-1290526	CGCAUUUUCUCUUUGCAUUU	26	127-147	AGAAUGCAAAAGAGAAAUUGCGCU	250	125-147
AD-1290559	GCAUUUUCUCUUUGCAUUU	27	128-148	AAGAAUGCAAAAGAGAAAUUGCGC	251	126-148
AD-1290548	CAUUUUCUCUUUGCAUUUCUCU	28	129-149	AGAGAAUGCAAAAGAGAAAUUGCG	252	127-149
AD-1290569	UUUUCUCUUUGCAUUUCGUAU	29	131-151	AUCGAGAAUGCAAAAGAGAAAUUG	253	129-151
AD-1290547	UUUCUUUUGCAUUUCGAGAU	30	133-153	AUCUCGAGAAUGCAAAAGAGAAAA	254	131-153
AD-1290544	UCUCUUUGCAUUUCGAGAUU	31	134-154	AAUCUGAGAAUGCAAAAGAGAAA	255	132-154
AD-1290667	CUCUUUGCAUUUCGAGAUUCU	32	135-155	AGAUCUCGAGAAUGCAAAAGAGAA	256	133-155
AD-1290685	UCUUUGCAUUUCGAGAUUCGU	33	136-156	ACGAUCUCGAGAAUGCAAAAGAGA	257	134-156
AD-1290695	UUUGCAUUUCGAGAUUCGCUU	34	138-158	AAGCAUCUCGAGAAUGCAAAAGA	258	136-158
AD-1290653	UGCAUUUCGAGAUUCGCUUAU	35	140-160	AUAAAGCGAUUCUCGAGAAUGCAAA	259	138-160
AD-1290853	GCAUUCUCGAGAUUCGCUUAGU	36	141-161	ACUAAAGCGAUUCUCGAGAAUGCAA	260	139-161
AD-1290990	CAUUCUCGAGAUUCGCUUAGCU	37	142-162	AGCUAAGCGAUUCUCGAGAAUGCA	261	140-162
AD-1290540	CUUUAAAAAGGUUUGCAUCAU	38	166-186	AUGAUGCAAAACCUUUUUAAAAGCG	262	164-186
AD-1290580	UUUAAAAAGGUUUGCAUCAU	39	167-187	ACUGAUGCAAAACCUUUUUAAAAGC	263	165-187
AD-1290664	UUAAAAAGGUUUGCAUCAUCU	40	168-188	AGCUGAUGCAAAACCUUUUUAAAAG	264	166-188
AD-1290916	UCAGCUGUGAGUCCAUUCUGAU	41	183-203	AUCAGAUGGACUCACAGCUGAUG	265	181-203
AD-1290938	GCUGUGAGUCCAUUCUGACAAU	42	186-206	AUUUGCAGAUUGGACUCACAGCUG	266	184-206
AD-1290896	CUGUGAGUCCAUUCUGACAAU	43	187-207	ACUUGUCAGAUUGGACUCACAGCU	267	185-207
AD-1290914	CCAUCUGACAAGCGAGGAAU	44	195-215	AUUUCCUCGCUUGUCAGAUUGGAC	268	193-215
AD-1290982	CAUCUGACAAGCGAGGAAACU	45	196-216	AGUUUCCUCGCUUGUCAGAUUGGA	269	194-216

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Range in XM_017004061.1	Antisense sequence 5' to 3'	SEQ ID NO:	Range in XM_017004061.1
AD-1290708	GGAAACUAAAGGCUAGAGAAAGUU	46	210-230	AACUUCUCAGCCUUAGUUUCCUC	270	208-230
AD-1290693	GAAACUAAAGGCUAGAGAAAGUU	47	211-231	ACACUUCUCAGCCUUAGUUUCCU	271	209-231
AD-1290942	AGACCUCUGGGUUGGCUUUUCU	48	286-306	AGAAAGCCAACCCAGAGGUCUUG	272	284-306
AD-1290807	AGUAGCCUCUAGGAAAGAGAAU	49	514-534	AUUCUCUCCAUAGAGGCUACUCC	273	512-534
AD-1290881	CCUCAUGGAAGAGAAAGCAGAU	50	519-539	AUCUGCUUCUCUCCAUAGAGGCU	274	517-539
AD-1290745	CUCAUGGAAGAGAAAGCAGAUU	51	520-540	AAUCUGCUUCUCUCCAUAGAGGC	275	518-540
AD-1290814	AUGGAAGAGAAAGCAGAUCCUU	52	523-543	AAGGAUCUGCUUCUCUCCAUAGA	276	521-543
AD-1290900	GGAAGAGAAAGCAGAUCCUGUU	53	525-545	AACAGGAUCUGCUUCUCUCCAU	277	523-545
AD-1290964	GAAGAGAAAGCAGAUCCUGUGU	54	526-546	ACACAGGAUCUGCUUCUCUCCAU	278	524-546
AD-1290802	AUCAGCCUGGUGGACAAAGUUAU	55	571-591	AUACUUGUCCACCAGGCUGAUGA	279	569-591
AD-1290816	GUGGACAAAGUACCCUAAAGGAU	56	580-600	AUCCUUAAGGUACUUGUCCACCA	280	578-600
AD-1290821	GACAAAGUACCCUAAAGGAGGAU	57	583-603	AUCCUCCUUAAGGUACUUGUCCA	281	581-603
AD-1290870	GAGGACUCGGAGAUAAAGGUGU	58	598-618	ACACCUUAUCUCCGAGUCCUCCU	282	596-618
AD-1290984	UAAGGUGUUUUGUCCAGAGAU	59	611-631	AUCUCUGGGACAAACACCUUAUC	283	609-631
AD-1290682	AAGGUGUUUUGUCCAGAGAUU	60	612-632	AAUCUCUGGGACAAACACCUUAU	284	610-632
AD-1290872	CAACUCCUGCACCGUUCUCUU	61	654-674	AAGAGAACGGUUGCAGGAGUUGGA	285	652-674
AD-1290663	UCUGCUACAGACUUUGAGAAU	62	748-768	AUUCUCAAAAGUCUGUAGCAGACA	286	746-768
AD-1290627	CUGCUACAGACUUUGAGAAAGU	63	749-769	ACUUCUCAAAAGUCUGUAGCAGAC	287	747-769
AD-1290730	UGCUACAGACUUUGAGAAAGGU	64	750-770	ACCUUCUCAAAAGUCUGUAGCAGA	288	748-770
AD-1290692	GCUACAGACUUUGAGAAAGGUU	65	751-771	AACCUUCUCAAAAGUCUGUAGCAG	289	749-771
AD-1290579	CUACAGACUUUGAGAAAGGUUU	66	752-772	AAACCUUCUCAAAAGUCUGUAGCA	290	750-772
AD-1290591	ACAGACUUUUGAGAAAGGUUGAU	67	754-774	AUCAACCUUCUCAAAAGUCUGUAG	291	752-774
AD-1290539	CAGACUUUUGAGAAAGGUUGAUU	68	755-775	AAUCAACCUUCUCAAAAGUCUGUA	292	753-775
AD-1290611	AGACUUUUGAGAAAGGUUGAUCU	69	756-776	AGAUAACCUUCUCAAAAGUCUGU	293	754-776
AD-1290530	GACUUUGAGAAAGGUUGAUCUU	70	757-777	AAGAUAACCUUCUCAAAAGUCUG	294	755-777
AD-1290576	CUUUGAGAAAGGUUGAUCUGAU	71	759-779	AUCAGAUCAACCUUCUCAAAAGUC	295	757-779
AD-1290546	UUUGAGAAAGGUUGAUCUGACU	72	760-780	AGUCAGAUCAACCUUCUCAAAAGU	296	758-780

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Range in XM_017004061.1	Antisense sequence 5' to 3'	SEQ ID NO:	Range in XM_017004061.1
AD-1290823	AAGGUUGAUCUGACCCAGUUU	73	766-786	AAACUGGGUCAGAUCAACCUUCU	297	764-786
AD-1290757	GUUGAUCUGACCCAGUUCAAU	74	769-789	AUUGAACUGGGUCAGAUCAACCU	298	767-789
AD-1290959	UUGAUCUGACCCAGUUCAGU	75	770-790	ACUUGAACUGGGUCAGAUCAACC	299	768-790
AD-1290837	UGAUCUGACCCAGUUCAGUU	76	771-791	AACUUGAACUGGGUCAGAUCAAC	300	769-791
AD-1290861	GAUCUGACCCAGUUCAGUGU	77	772-792	ACACUUGAACUGGGUCAGAUCAA	301	770-792
AD-1290885	CUGACCCAGUUCAGUGGAUU	78	775-795	AAUCCACUUGAACUGGGUCAGAU	302	773-795
AD-1290970	ACCCAGUUCAGUGGAUCCAU	79	778-798	AUGGAUCCACUUGAACUGGGUCA	303	776-798
AD-1290962	CCAGUUCAGUGGAUCCACAU	80	780-800	AUGUGGAUCCACUUGAACUGGGU	304	778-800
AD-1290759	AGUUCAGUGGAUCCACAUUU	81	782-802	AAAUUGGAUCCACUUGAACUGG	305	780-802
AD-1290736	UUCAAGUGGAUCCACAUUGAU	82	784-804	AUCAAGUGGAUCCACAUUGAACU	306	782-804
AD-1290739	UCAAGUGGAUCCACAUUGAGU	83	785-805	ACUCAAGUGGAUCCACAUUGAAC	307	783-805
AD-1290828	CAAGUGGAUCCACAUUGAGGU	84	786-806	ACCUCAAGUGGAUCCACAUUGAA	308	784-806
AD-1291001	GCAUCGGAGCAGGUGAAGAUU	85	814-834	AAUCUUCACCUUGCUCCGAGCGU	309	812-834
AD-1290933	CAUCGGAGCAGGUGAAGAUU	86	815-835	ACAUCUUCACCUUGCUCCGAGCG	310	813-835
AD-1290988	GAGCUCUUCACGUGUUUGGU	87	919-939	ACCAAAACAGCUGGAAAGAGCUCCU	311	917-939
AD-1290955	CUCUUCACGUGUUUGGCUAU	88	922-942	AUAGCCAAACAGCUGGAAAGAGCU	312	920-942
AD-1290810	CUACGGAGACGUGGUGUUUGU	89	939-959	ACAAACACACGUCUCCGUAAGCC	313	937-959
AD-1290740	UACGGAGACGUGGUGUUUGUU	90	940-960	AACAAACACACGUCUCCGUAAGC	314	938-960
AD-1290752	CGGAGACGUGGUGUUUGUCAU	91	942-962	AUGACAAACACACGUCUCCGUA	315	940-962
AD-1290878	GGAGACGUGGUGUUUGUCAU	92	943-963	ACUGACAAACACACGUCUCCGUA	316	941-963
AD-1290599	UGGUGUUUGUCAGCAAAAGAUU	93	950-970	AAUCUUUGCUGACAAACACACG	317	948-970
AD-1290632	GGUGUUUGUCAGCAAAAGAUU	94	951-971	ACAUCUUUGCUGACAAACACACAC	318	949-971
AD-1290584	GUGUUUGUCAGCAAAAGAUU	95	952-972	AACAUCUUUGCUGACAAACACCA	319	950-972
AD-1290734	UGUUUGUCAGCAAAAGAUUGU	96	953-973	ACACAUCUUUGCUGACAAACACC	320	951-973
AD-1290882	GUUUGUCAGCAAAAGAUUGGU	97	954-974	ACCACAUCUUUGCUGACAAACAC	321	952-974
AD-1290987	UUUGUCAGCAAAAGAUUGGCU	98	955-975	AGCCACAUCUUUGCUGACAAACA	322	953-975
AD-1290963	AAAGAUGUGGCCCAAGCACUUU	99	964-984	AAAGUCUUGGCCCAACAUUUUGC	323	962-984

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Range in XM_017004061.1	Antisense sequence 5' to 3'	SEQ ID NO:	Range in XM_017004061.1
AD-1290710	UGUAUGGUCGUGUGAGGAAA	100	1019-1039	AUUUCCUCACACGACC'CAUACAAG	324	1017-1039
AD-1290656	GUUUGGUCGUGUGAGGAAAGU	101	1020-1040	ACUUUCCUCACACGACCAUACAA	325	1018-1040
AD-1290890	UAUGGUCGUGUGAGGAAAAGGU	102	1021-1041	ACUUUCCUCACACGACCAUACA	326	1019-1041
AD-1290887	UGCUCACUGGGAUGCUUUCU	103	1103-1123	AGAAAGCAUCCGAGUGGAGCAAU	327	1101-1123
AD-1290923	GAGCUGGAGACACCUUCAAUU	104	1151-1171	AAUUGAAGGUGUCUCAGCUC	328	1149-1171
AD-1290904	AGCUGGAGACACCUUCAAUGU	105	1152-1172	ACAUUGAAGGUGUCUCCAGCUC	329	1150-1172
AD-1290980	CUGGAGACACCUUCAAUGCCU	106	1154-1174	AGCAUUGAAGGUGUCUCCAGCU	330	1152-1174
AD-1290860	UGGAGACACCUUCAAUGCCUU	107	1155-1175	AAGCAUUGAAGGUGUCUCCAGC	331	1153-1175
AD-1290969	ACCUUCAAUGCCUCCGUCAUU	108	1162-1182	AAUGACGGAGGCAUUGAAAGGUGU	332	1160-1182
AD-1290811	CCUUCAAUGCCUCCGUCAUUCU	109	1163-1183	AGAUACGGAGGCAUUGAAAGGUG	333	1161-1183
AD-1290886	UUCAAUGCCUCCGUCAUUCUU	110	1165-1185	AAAGAUGACGGAGGCAUUGAAAGG	334	1163-1185
AD-1290668	CAAUGCCUCCGUCAUUCUUAU	111	1167-1187	AUGAAGAUGACGGAGGCAUUGAA	335	1165-1187
AD-1290852	AAUGCCUCCGUCAUUCUUAU	112	1168-1188	ACUGAAGAUGACGGAGGCAUUGA	336	1166-1188
AD-1290915	CUCCGUCAUUCUAGCCUUAU	113	1173-1193	AAGAGGUGAAGAUGACGGAGGC	337	1171-1193
AD-1290874	GUGCAGGAAGCACUGAGAUUU	114	1207-1227	AAAUCUCAGUGCUUCCUGCACGC	338	1205-1227
AD-1290818	UGCAGGAAGCACUGAGAUUCU	115	1208-1228	AGAAUCUCAGUGCUUCCUGCACG	339	1206-1228
AD-1290884	GCAGGAAGCACUGAGAUUCGU	116	1209-1229	ACGAAUCUCAGUGCUUCCUGCAC	340	1207-1229
AD-1290977	UGGCCUGCAGGGCUUUGAUGU	117	1254-1274	ACAUCAAAGCCUUGCAGGCCACA	341	1252-1274
AD-1290961	CUGCAGGGCUUUGAUGGCAUU	118	1258-1278	AAUGCCAUCAAAAGCCUUGCAGGC	342	1256-1278
AD-1290834	CAGGGCUUUGAUGGCAUCGUU	119	1261-1281	AACGAUGCCAUCAAAAGCCUUGCA	343	1259-1281
AD-1290867	GGGCUUUGAUGGCAUCGUGUU	120	1263-1283	AACACGAUGCCAUCAAAAGCCUUG	344	1261-1283
AD-1290879	CUCUGCCUGUGUCCUGUGUUU	121	1409-1429	AAACACAGGACACAGGCAGAGUC	345	1407-1429
AD-1290549	CUCAGAGCAAAUAAUUCUUCU	122	1474-1494	AGAAGAUUUUAUUUGCUCUGAGGC	346	1472-1494
AD-1290525	CAGAGCAAAUAAUUCUUCUUCU	123	1476-1496	AAGGAAGAUUUUAUUUGCUCUGAG	347	1474-1496
AD-1290622	CUCCUCUCAAUGUCUGAACUU	124	1508-1528	AAGUUCAGACAUUUGAGAGGAGAA	348	1506-1528
AD-1290638	UCCUCUCAAUUGUCUGAACUGU	125	1509-1529	ACAGUUCAGACAUUUGAGAGGAGA	349	1507-1529
AD-1290921	CCUCUCAUUGUCUGAACUGCU	126	1510-1530	AGCAUUCAGACAUUUGAGAGGAG	350	1508-1530

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Range in XM_017004061.1	Antisense sequence 5' to 3'	SEQ ID NO:	Range in XM_017004061.1
AD-1290621	CUCUCAUUGUCUGAACUCUCUU	127	1511-1531	AAGCAGUUCAGACAUUGAGAGGA	351	1509-1531
AD-1290775	CUCAUUGUCUGAACUCUCUU	128	1513-1533	AAGAGCAGUUCAGACAUUGAGAG	352	1511-1533
AD-1290748	AUUCUGAGGUCUCUGACUCUU	129	1541-1561	AAGAGUCAGAGCCUCAGGAAUGC	353	1539-1561
AD-1290865	CUGCGUUGGCAGACUCUAUU	130	1749-1769	AAUAGAGUCUGCACAAGCAGGG	354	1747-1769
AD-1290897	UGCGUUGUGCAGACUCUAUUU	131	1750-1770	AAAUAGAGUCUGCACAACGCAGG	355	1748-1770
AD-1290989	GCGUUGUGCAGACUCUAUUU	132	1751-1771	AGAAUAGAGUCUGCACAACGCAG	356	1749-1771
AD-1290983	CGUUGGCAGACUCUAUUCCU	133	1752-1772	AGGAAUAGAGUCUGCACAACGCA	357	1750-1772
AD-1290909	UUUGCAGACUCUAUUCCAU	134	1754-1774	AUGGGAUAGAGUCUGCACAACG	358	1752-1774
AD-1290993	UAUUCACAGCUCAGAAAGCU	135	1766-1786	AGCUUCUGAGCUGUGGGAUAGA	359	1764-1786
AD-1290841	AUUCACAGCUCAGAAAGCUU	136	1767-1787	AAGCUUCUGAGCUGUGGGAUAG	360	1765-1787
AD-1290880	CUUGGAGCCACCUUGGAAUU	137	1938-1958	AAUCCAAGGUGGGCUCCAAAGG	361	1936-1958
AD-1290747	GGAGCCACCUUGGAAUUAUU	138	1941-1961	AUUAUUCCAAGGUGGGCUCCAA	362	1939-1961
AD-1290842	GAGCCACCUUGGAAUUAAGU	139	1942-1962	ACUUAUUCCAAGGUGGGCUCUA	363	1940-1962
AD-1290911	AGCCACCUUGGAAUUAAGGU	140	1943-1963	ACCUUAUUCCAAGGUGGGCUCU	364	1941-1963
AD-1290926	GCCACCUUGGAAUUAAGGGU	141	1944-1964	ACCCUUAUUCCAAGGUGGGCUC	365	1942-1964
AD-1291003	GGCGUGCCUCAGCCACAAUU	142	1962-1982	AAUUUGGGCUGAGGCACGCCCU	366	1960-1982
AD-1290931	UCAGCCACAAUUGACCCAU	143	1970-1990	AUGGGUCACAUUUUGGGCUGAGG	367	1968-1990
AD-1290764	GGUCCGAUCUGGAACACAUU	144	2018-2038	AUAUGUGUCCAGAUCCGACCUC	368	2016-2038
AD-1290763	GUCCGAUCUGGAACACAUUU	145	2019-2039	AAUAUGUGUCCAGAUCCGACCUC	369	2017-2039
AD-1290670	UCCGAUCUGGAACACAUUUU	146	2020-2040	AAAUAUGUGUCCAGAUCCGACC	370	2018-2040
AD-1290712	CCGAUCUGGAACACAUUUUGU	147	2021-2041	ACAAUUGUGUCCAGAUCCGAC	371	2019-2041
AD-1290612	AUCUGGAACACAUUUUGGAU	148	2024-2044	AUCCAAUAUGUGUCCAGAUCCG	372	2022-2044
AD-1290522	UCUGGAACACAUUUUGGAUU	149	2025-2045	AAUCCAAUAUGUGUCCAGAUCC	373	2023-2045
AD-1290528	CUGGAACACAUUUUGGAUUU	150	2026-2046	AAAUCCAAUAUGUGUCCAGAU	374	2024-2046
AD-1290543	UGGAACACAUUUUGGAUUUGU	151	2027-2047	ACAAUCCAAUAUGUGUCCAG	375	2025-2047
AD-1290589	GGAAACACAUUUUGGAUUUGGU	152	2028-2048	ACCAAUCCAAUAUGUGUCCAG	376	2026-2048
AD-1290800	GGGUGGGUAAGGCCUUUAUU	153	2064-2084	AUUUAAGGCCUUUACCCACCCUA	377	2062-2084

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Range in XM_017004061.1	Antisense sequence 5' to 3'	SEQ ID NO:	Range in XM_017004061.1
AD-1290755	GGUGGUAAAGGCCUUUAUAAU	154	2065-2085	AAUUAUAAAGGCCUUUACCCACCCU	378	2063-2085
AD-1290742	GU'GGGU'AGGGCCUUUAAU'GU	155	2066-2086	ACA'UU'AU'AAAGGCCUU'ACCCACCC	379	2064-2086
AD-1290563	GUAAAGGCCUUUAUAAUGUAAAU	156	2070-2090	AUUUACA'UU'AAAGGCCUU'ACCC	380	2068-2090
AD-1290570	AAGGCCUUUAUAAUGUAAAGAU	157	2072-2092	AUCUUACA'UU'AAAGGCCUU'AC	381	2070-2092
AD-1290515	AGGCCUUUAUAAUGUAAAGAGU	158	2073-2093	ACUCUUACA'UU'AAAGGCCUU'AA	382	2071-2093
AD-1290556	GCCUUUAUAAUGUAAAGAGCAU	159	2075-2095	AUGCUCUUACA'UU'AAAGGCCU	383	2073-2095
AD-1290661	GCAUUAUAAUGUAAAGGCCUUU	160	2092-2112	AAAGCCUUUACA'UU'AAUAGCUC	384	2090-2112
AD-1290555	AUAUAUAAUGUAAAGGCCUUUAU	161	2094-2114	AUAAAGCCUUUACA'UU'AAUAGC	385	2092-2114
AD-1290554	AUAUAUAAAGGGCUUUUAGAU	162	2096-2116	AUCUAAAGCCUUUACA'UU'AAU	386	2094-2116
AD-1290639	UAUAUAAAGGGCUUUUAGAGU	163	2097-2117	ACUCUAAAGCCUUUACA'UU'AAU	387	2095-2117
AD-1290618	AAUGUAAAGGGCUUUUAGAGUU	164	2098-2118	AACUCUAAAGCCUUUACA'UU'AAU	388	2096-2118
AD-1290660	CCUGGAUUAAAAUCUGCCA'UU	165	2126-2146	AAUGGCAGAUUUUAAUCCAGGUC	389	2124-2146
AD-1290551	CUGGAUUAAAAUCUGCCA'UUU	166	2127-2147	AAAUGGCAGAUUUUAAUCCAGGU	390	2125-2147
AD-1290509	GAUUAUAAUCUGCCA'UUUAAU	167	2130-2150	AUUAAUUGGCAGAUUUUAAUCCA	391	2128-2150
AD-1290597	AUUAAAAUCUGCCA'UUUAAU	168	2131-2151	AAUAAAAUUGGCAGAUUUUAAUCC	392	2129-2151
AD-1290533	AAAU'CGCC'AUUUAAU'AAU'AGCU	169	2135-2155	AGCUAAU'U'AAU'GGCAGAUUU'U'AA	393	2133-2155
AD-1290535	AAUCUGCCA'UUUAAU'U'AGCUU	170	2136-2156	AAGCUAAU'U'AAU'GGCAGAUUU'U	394	2134-2156
AD-1290604	AUCUGCCA'UUUAAU'U'AGCUGU	171	2137-2157	ACAGCUAAU'U'AAU'GGCAGAUUU	395	2135-2157
AD-1290633	CUGCCA'UUUAAU'U'AGCUGCAU	172	2139-2159	AUGCAGCUAAU'U'AAU'GGCAGAU	396	2137-2159
AD-1290741	ACGCAAU'CGCC'UCAAU'U'UCU	173	2183-2203	AGAAAU'UGAGGCAGAU'U'UGCGUUA	397	2181-2203
AD-1290650	CGCAAU'CGCC'UCAAU'U'UCU	174	2184-2204	AAGAAU'UGAGGCAGAU'U'UGCGUU	398	2182-2204
AD-1290672	GCAAU'CGCC'UCAAU'U'UCUU	175	2185-2205	AAAGAAU'UGAGGCAGAU'U'UGCGU	399	2183-2205
AD-1290605	AAUCUGCCUCAAU'U'U'UCU'CAU	176	2187-2207	AUGAAAGAAU'UGAGGCAGAU'U'GC	400	2185-2207
AD-1290573	AUCUGCCUCAAU'U'U'UCU'CAU	177	2188-2208	AAUGAAGAAU'UGAGGCAGAU'U'G	401	2186-2208
AD-1290615	UCUGCCUCAAU'U'U'UCU'CAUCU	178	2189-2209	AGAUGAAGAAU'UGAGGCAGAU'U	402	2187-2209
AD-1290531	CUGCCUCAAU'U'U'UCU'CAUCU	179	2190-2210	AAGAUGAAGAAU'UGAGGCAGAU	403	2188-2210
AD-1290602	UGCCUCAAU'U'U'UCU'CAUCUGU	180	2191-2211	ACAGAUGAAGAAU'UGAGGCAGAU	404	2189-2211

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Range in XM_017004061.1	Antisense sequence 5' to 3'	SEQ ID NO:	Range in XM_017004061.1
AD-1290523	GCCUCAUUUCUUAUCUGUU	181	2192-2212	AACAGAUAGAGAAUUUGAGGCAG	405	2190-2212
AD-1290514	CAAUUCUUCUUAUCUGUCAAU	182	2196-2216	AUUUGACAGAUAGAGAAUUUGAG	406	2194-2216
AD-1290510	AAUUUCUUAUCUGUCAAUU	183	2197-2217	AAUUUGACAGAUAGAGAAUUUGA	407	2195-2217
AD-1290524	AUUUCUUAUCUGUCAAUUGU	184	2198-2218	ACAUUUGACAGAUAGAGAAUUUG	408	2196-2218
AD-1290836	AAUUCUGCUUGGCUACAGAAU	185	2223-2243	AUUCUGUAGCCAAAGCAGAAUUGG	409	2221-2243
AD-1290719	AUUCUGCUUGGCUACAGAAUU	186	2224-2244	AAUUCUGUAGCCAAAGCAGAAUUG	410	2222-2244
AD-1290722	UCUGCUUGGCUACAGAAUUU	187	2226-2246	AUAAUUCUGUAGCCAAAGCAGAAU	411	2224-2246
AD-1290687	CUGCUUGGCUACAGAAUUU	188	2227-2247	AAUAAUUCUGUAGCCAAAGCAGAA	412	2225-2247
AD-1290643	UGCUUGGCUACAGAAUUU	189	2228-2248	AAAUAAUUCUGUAGCCAAAGCAG	413	2226-2248
AD-1290600	GCUUGGCUACAGAAUUUUGU	190	2229-2249	ACAAUAAUUCUGUAGCCAAAGCAG	414	2227-2249
AD-1290507	UUCUUAUCUGUCAAUUGGAU	191	2200-2220	AUCCAUUUGACAGAUAGAGAAAU	415	2198-2220
AD-1290516	GGAUUAAAUCUGGCAUUU	192	2129-2149	AUAAAUGGCAGAUUUUAAUCCAG	416	2127-2149
AD-1290527	UGGAUUAAAUCUGGCAUUUU	193	2128-2148	AAAAUGGCAGAUUUUAAUCCAGG	417	2126-2148
AD-1290542	UCAUUUCUUAUCUGUCAAU	194	2195-2215	AUUGACAGAUAGAGAAUUUGAGG	418	2193-2215
AD-1290552	UUUCUUAUCUGUCAAAUUGGU	195	2199-2219	ACCAUUUGACAGAUAGAGAAAUU	419	2197-2219
AD-1290557	GGCCUUAAUAAUGUAAAGAGCU	196	2074-2094	AGCUCUUUACAUAUAAAGGCCUU	420	2072-2094
AD-1290558	UAUAAUGUAAAGGCCUUUAGU	197	2095-2115	ACUAAAGCCUUUACAUUAUUG	421	2093-2115
AD-1290561	AUUUCUUAUUGCAUUCUCGU	198	130-150	ACGAGAAUGCAAAAGAGAAAUGC	422	128-150
AD-1290564	CCUCAUUUUCUUAUCUGUCU	199	2193-2213	AGACAGAUAGAGAAUUUGAGGCA	423	2191-2213
AD-1290565	CUCAUUUUCUUAUCUGUCAU	200	2194-2214	AUGACAGAUAGAGAAUUUGAGGC	424	2192-2214
AD-1290574	UAAGGCCUUUAUAAUGUAAAGU	201	2071-2091	ACUUUACAUAUAAAGCCUUUACC	425	2069-2091
AD-1290592	CAUAUAAUGUAAAGGCCUUUU	202	2093-2113	AAAAGCCUUUACAUAUUAUUGCU	426	2091-2113
AD-1290609	UGCCAUUUAAUUAAGCUGCAU	203	2140-2160	AAUGCAGCUAAUUAUAAUUGCAGA	427	2138-2160
AD-1290624	AUUUUUGUGAGGAUAAAUCU	204	2242-2262	AGAUUUUUAUCCUCACAAUAAUUC	428	2240-2262
AD-1290626	GGUAAGGCCUUUAUAAUGUAAU	205	2069-2089	AUUACAUAUAUAAAGCCUUUACCCA	429	2067-2089
AD-1290635	UUCUGCUUUGGCUACAGAAUU	206	2225-2245	AAAUCUCUGUAGCCAAAGCAGAAU	430	2223-2245
AD-1290651	GUUCAAGUGGAUCCACAUUGU	207	783-803	ACAAUGUGGAUCCACUUUGAACUG	431	781-803

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Range in XM_017004061.1	Antisense sequence 5' to 3'	SEQ ID NO:	Range in XM_017004061.1
AD-1290654	GGGUAAGGCCUUUAUAAUUGUAU	208	2068-2088	AUACAUUAUAAAGGCCUUAC'CCAC	432	2066-2088
AD-1290655	GAUCUGGAACACAUAUUGGAU	209	2023-2043	AU'CCAAUAUGUGUUCAGAU'CGG	433	2021-2043
AD-1290657	UUUCUCUUUGCAUUCUCGAGU	210	132-152	ACUCGAGAAUGCAAAGAGAAAAU	434	130-152
AD-1290659	CAAUCGCCUCAAUUUCUUCU	211	2186-2206	AGAAGAAUUGAGGCAGAUUGCG	435	2184-2206
AD-1290665	AGAGCAAAUAAAUCUUCUCU	212	1477-1497	AGAGGAAGAUUUUUUUGCUCUGA	436	1475-1497
AD-1290666	ACUUUGAGAAAGGUUGAUCUGU	213	758-778	ACAGAUCAACCUUCUCAAAGUCU	437	756-778
AD-1290680	UACAGACUUUGAGAAAGGUUGU	214	753-773	ACAACCUUCUCAAAGUCUGUAGC	438	751-773
AD-1290681	UGGGUAAGGCCUUUAUAAU'GUU	215	2067-2087	AACAUUAUAAAGGCCUUAC'CCACC	439	2065-2087
AD-1290683	UU'GCAUUCUCGAGAU'CGCUUU	216	139-159	AAAAGCAUCUCGAGAAU'GCAAAG	440	137-159
AD-1290684	CGAUCUGGAACACAUUUGGU	217	2022-2042	ACCAAUAUGUGUUC'CCAGAU'CGGA	441	2020-2042
AD-1290702	UCUGCCAUUUAAU'UAGCUGCU	218	2138-2158	AGCAGCUAAUUAU'UAGGCAGAUU	442	2136-2158
AD-1290718	CGUGGUGUUUGUCAGCAAAAGU	219	948-968	ACUUUGCUGACAAACAC'CCACGUC	443	946-968
AD-1290746	UU'GUAU'GGUCUGUGAGGAAU	220	1018-1038	AU'UCCUCACACGACCAU'ACAAGC	444	1016-1038
AD-1290750	CCCAGUGAACCGU'GCCAAAGAU	221	1706-1726	AUCUUUGGCAGGUUCACUGGGUG	445	1704-1726
AD-1290765	GACGUGGUGUUUGUCAGCAAU	222	946-966	AU'UGCUGACAAACAC'CCACGUCUC	446	944-966
AD-1290778	UCAAU'GCCUCCGUAUCUUCU	223	1166-1186	AGAAAGAU'GACGGAGGCAU'UGAAG	447	1164-1186
AD-1290795	UU'GCUCCACUCGGAU'GCUUUU	224	1102-1122	AAAAGCAU'CCGAGUGGAGCAAUU	448	1100-1122
AD-1290796	UU'GGAGCCCA'CCU'UGGAAUUU	225	1939-1959	AAAU'CCAAGGUGGGCUC'CAAGG	449	1937-1959
AD-1290803	AUCUGACAAGCGAGGAAACUU	226	197-217	AAGUU'UCCUCGCUUGUCAGAU'GG	450	195-217
AD-1290805	UGGAGCCCA'CCU'UGGAAUUU	227	1940-1960	AU'AAU'UCCAAGGUGGGCUC'CAAG	451	1938-1960
AD-1290835	GCUCU'UCCAGCUGUUU'GGCUU	228	921-941	AAGCCAAACAGCUGGAAAGAGCUC	452	919-941
AD-1290857	UGCCCA'CCAGCCUGUGAUUUU	229	1852-1872	AAAAUCACAGGCUUGGUGGGCAGG	453	1850-1872
AD-1290863	AAGACCUCUGGGUU'GGCUUUU	230	285-305	AAAAAGCCAA'CCCAAGAGGU'CUUGG	454	283-305
AD-1290875	GCCCA'CCAGCCUGUGAUUUUGU	231	1853-1873	ACAAAU'CACAGGCUUGGUGGGCAG	455	1851-1873
AD-1290891	ACGGAGACGUGGUGUUU'UGUCU	232	941-961	AGACAAACAC'CCAGCUC'UCCGUAG	456	939-961
AD-1290894	AGGU'CCGAUCUGGAAACACAUU	233	2017-2037	AAU'GUGU'UCCAGAU'CGGAC'CUCC	457	2015-2037
AD-1290903	GAGUAGCCCUCAUGGAAAGAGAU	234	513-533	AUCUCU'UCCAUGAGGCUACU'CCC	458	511-533

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Range in XM_017004061.1	Antisense sequence 5' to 3'	SEQ ID NO:	Range in XM_017004061.1
AD-1290908	CCAGUGAACCUGCCAAGAAU	235	1707-1727	AUUCUUUGCAGGUACUGGGU	459	1705-1727
AD-1290910	UAGGGUGGGUUAAGGCCUUAAU	236	2062-2082	AAUAAAGGCCUUACCCACCCUAUA	460	2060-2082
AD-1290924	UGGGAGUAGCCUCAUGGAAU	237	510-530	ACUCCAUGAGGCUACUCCACA	461	508-530
AD-1290939	AGGGUGGGUAAAGCCUUAAU	238	2063-2083	AUAUAAAGCCUUACCCACCCUAU	462	2061-2083
AD-1290946	GGUUGAUCUGACCCAGUUAU	239	768-788	AUGAACUUGGGUCAGAUCAACCUU	463	766-788
AD-1290950	CAUCAGCCUGGUGGACAAAGU	240	570-590	AACUUUGUCCACCAAGGUCUGAGAC	464	568-590
AD-1290956	AGCUGUGAGUCCAUCUGACAU	241	185-205	AUGUCAGAUGGACUCACAGCUGA	465	183-205
AD-1290971	GCUACGGAGACGUGGUGUUUU	242	938-958	AAAACACCAAGUCUCCGUAGCCA	466	936-958
AD-1290973	GUUUGGCAGACUCUAUUCUU	243	1753-1773	AGGGAUAUAGUCUCGACAAACGC	467	1751-1773

Table 3. Modified Sense and Antisense Strand Sequences of KHK dsRNAs

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:	mRNA target sequence	SEQ ID NO:
AD-1290652	gtsugggUfUfUGfUfcagcaagaauL96	1187	asUfscuuUfjcgugaaaCfaCaccacsgu	692	ACGUGGUUUUCAGCACGAAGAAGAU	916
AD-1290731	ascsguggUfgUfUTUfUfgnucagaaauL96	469	asUfiscngChugacaaaCfaCccaguscus	693	AGACGUGGUUUUGUCAGCAAAAG	917
AD-1290560	uscsagaggCfaAfAUfUaaauuccuuL96	470	asGfsngaGflaanuaauUfjGfctucagsgg	694	CCUCAGACAAAUAUUUUUUUUUU	918
AD-1290854	csasgmueAfaGfUfUfgfnucaccauuL96	471	asAfisngUfjgauncacUfhGfiaucjsgsg	695	CCCAGUUC AAGUGGAUCCACAUIU	919
AD-1290629	asgsuagcGfcAfUfUfnnucunnguL96	472	asCfsaaaGlagaanaUfjcGfuacuusug	696	CAGU AGCGAUUUUUUUUUUUUGC	920
AD-1290517	gscsgcaanUfuUfCUfUfnnucnnaauL96	473	asAfisangCfaaagagaAfaAfugecgcsusa	697	UAGCGCAUUUUUUUUUUUUUGCAUUC	921
AD-1290526	csgscaannUfhCFUfUfnnucnnaauL96	474	asGfsaanGfcaaaagAfaAfagecgscsu	698	AGCGAUUUUUUUUUUUUUUGCAUUCU	922
AD-1290559	gscsaanuUfcUfCTUfUfnnucauuuL96	475	asAfisgaalUfjgcaaaagaGfaAfaaugcsgsc	699	GC CGCAUUUUUUUUUUUUUGCAUUCUC	923
AD-1290548	csasnuuuChfCTUfUfnnucauuuL96	476	asGfsigaAfhugcaaaAgfAfaaungscsg	700	CGCAUUUUUUUUUUUUUGCAUUCUCG	924
AD-1290569	ususmuuCfUfUfUfGfcauucgaauiL96	477	asUfiscgaGlaaungcaaAfgAfgaanaasug	701	CAUUUUUUUUUUUUUUUGCAUUCUCGAG	925
AD-1290547	ususuenuChfUfUfUfGfcauucgaauiL96	478	asUfiscuGfagaauugCfaAfafagaasasa	702	UUUUUUUUUUUUUUUGCAUUCUGAGAU	926
AD-1290544	ususcenuUfGfCAFUfUfncugagaauiL96	479	asAfiscuClfagaaugCfaAfafagaasasa	703	UUUCUUUUUGCAUUCUCUGAGAUUC	927
AD-1290667	csuscuuuGfcAfUfUfUfncugagaauiL96	480	asGfsaucUfjcgagaauGfcAfaagagsasa	704	UUCUUUUUGCAUUCUCUGAGAUUCG	928
AD-1290685	uscsnuuGfUfUfUfUfUfncugagaauiL96	481	asCfsigaUfUfUfUfUfncugagaauiL96	705	UCUUUUUGCAUUCUCUGAGAUUCGC	929
AD-1290695	usussugaUfhCTUfUfUfUfUfncugagaauiL96	482	asAfisggAfuhcugagAgfAfaaugsasa	706	UUUUUGCAUUCUCUGAGAUUCGCUU	930
AD-1290653	usgscauuCfbCfGfAfgauncgaauiL96	483	asUfisaagCfjgauncgAfgAfangaasasa	707	UUUGCAUUCUCUGAGAUUCGCUUAG	931
AD-1290853	gscsaunuUfcGfAFgfAfgauncgaauiL96	484	asCfsuaaGfjgauncGfAfgaungcsasa	708	UUGCAUUCUCUGAGAUUCGCUUAGC	932
AD-1290990	csasnuuChfGfAfgahucgnagaauiL96	485	asGfsicuaAfjcgaaucCfGfAfgaungcsa	709	UGCAUUCUCUGAGAUUCGCUUAGCC	933
AD-1290540	csusuaaaAfaAfGHgfnnucnnaauL96	486	asUfiscuaGfcaaacuUfhUfuaaagscg	710	CGCUUU AAAAAGGUUUUGCAUCAG	934
AD-1290580	ususuuaaAfaAfGFUfUfnnucauuiL96	487	asCfsingaUfjcaaacUfhUfumaagscg	711	GCUUU AAAAAGGUUUUGCAUCAGC	935
AD-1290664	ususaanaAfGfUfUfUfnnucauuiL96	488	asGfiscngAfhgcaaacChfUfumaagscg	712	CUUUAAAAAGGUUUUGCAUCAGCU	936

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:	mRNA target sequence	SEQ ID NO:
AD-1290916	uscsagcuGhuGfAfGhccaugcauL.96	489	asUfscagAfugacucAfcAfGcugasug	713	CAUCAGCUGUGAGUCCAUCUGAC	937
AD-1290938	gscsugugAfgUfcCfCfancugacaauL.96	490	asUfscugCfagauggaCfuCfagcagsug	714	CAGCUGUGAGUCCAUCUGACAAG	938
AD-1290986	csusnguaGhuCfCfAfCfancugacaauL.96	491	asCfscugUfcagauagAfcUfcagcagsu	715	AGCUGUGAGUCCAUCUGACAAGC	939
AD-1290914	cscauauGfAfCfAfCfagaggaauL.96	492	asUfscuuCfucgucUfcAfGfagugasc	716	GUCCAUCUGAC AAGCAGGAAAC	940
AD-1290982	csasucugAfcAfAfGfagaggaauL.96	493	asGfscuuCfucgucUfcAfGfagugasc	717	UCCAUCUGACA AAGCAGGAAACU	941
AD-1290708	gsgsaacUfAfAfGfGfugagagauL.96	494	asAfscuuCfucagcuUfcAfGfscucsc	718	GAGGAAACU AAGGUGAGAAAGUG	942
AD-1290693	gsasaacuAfAfGfGfCfugagagauL.96	495	asCfscuuCfucagcuUfcAfGfscucsc	719	AGGAAACU AAGGUGAGAAAGUGG	943
AD-1290942	asgsaacuCfuGfGfGfugagagauL.96	496	asGfscuuCfucagcuUfcAfGfscucsc	720	CAAGACCUUGGUGGUGGCUUUC	944
AD-1290807	asgsaagCfuGfGfGfugagagauL.96	497	asUfscuuCfucagcuUfcAfGfscucsc	721	GGAGUAGCCUUGGUGGUGGCUUUC	945
AD-1290881	cscauauGfAfAfGfagagagauL.96	498	asUfscuuCfucagcuUfcAfGfscucsc	722	AGCCUAGGUGGUGGUGGCUUUC	946
AD-1290745	csuscaugGfAfAfGfAfGfagagagauL.96	499	asAfscuuCfucagcuUfcAfGfscucsc	723	GCCUAGGUGGUGGUGGCUUUC	947
AD-1290814	asusggaaGfAfAfGfAfGfagagagauL.96	500	asAfscuuCfucagcuUfcAfGfscucsc	724	UCAUGGAGAGAGAGAGAGAGAG	948
AD-1290900	ggsaagaGfAfAfGfAfGfagagagauL.96	501	asAfscuuCfucagcuUfcAfGfscucsc	725	AUGGAGAGAGAGAGAGAGAGAG	949
AD-1290964	gsasagagAfAfGfAfGfAfGfagagauL.96	502	asCfscuuCfucagcuUfcAfGfscucsc	726	UGGAGAGAGAGAGAGAGAGAG	950
AD-1290802	asusagagCfuGfGfGfUfgagagauL.96	503	asUfscuuCfucagcuUfcAfGfscucsc	727	UCAUAGCCUUGGUGGUGGCUUUC	951
AD-1290816	gsusggagAfAfGfAfGfAfGfagagauL.96	504	asUfscuuCfucagcuUfcAfGfscucsc	728	UGGUGGAGAGAGAGAGAGAGAG	952
AD-1290821	gsasagagUfAfGfGfGfUfgagagauL.96	505	asUfscuuCfucagcuUfcAfGfscucsc	729	UGGAGAGAGAGAGAGAGAGAG	953
AD-1290870	gsasagagUfAfGfGfGfUfgagagauL.96	506	asCfscuuCfucagcuUfcAfGfscucsc	730	AGGAGAGAGAGAGAGAGAGAG	954
AD-1290984	usasagagUfAfGfGfGfUfgagagauL.96	507	asUfscuuCfucagcuUfcAfGfscucsc	731	GAUAGGUGGUGGUGGUGGCUUUC	955
AD-1290682	asasggugUfAfGfGfGfUfgagagauL.96	508	asAfscuuCfucagcuUfcAfGfscucsc	732	AUAAGGUGGUGGUGGUGGCUUUC	956
AD-1290872	csasacucCfuGfGfGfUfgagagauL.96	509	asAfscuuCfucagcuUfcAfGfscucsc	733	UCCAUCUUGGUGGUGGUGGCUUUC	957
AD-1290663	uscsugcuAfcAfGfAfGfGfUfgagagauL.96	510	asUfscuuCfucagcuUfcAfGfscucsc	734	UGUCUACAGAGAGAGAGAGAGAG	958
AD-1290627	csusgcuAfAfGfAfGfGfUfgagagauL.96	511	asCfscuuCfucagcuUfcAfGfscucsc	735	GUCUCUACAGAGAGAGAGAGAGAG	959
AD-1290730	usgsuacAfAfGfAfGfGfUfgagagauL.96	512	asCfscuuCfucagcuUfcAfGfscucsc	736	UCUGUACAGAGAGAGAGAGAGAG	960
AD-1290692	gscsuacaGfAfGfAfGfGfUfgagagauL.96	513	asAfscuuCfucagcuUfcAfGfscucsc	737	CUGCUACAGAGAGAGAGAGAGAG	961
AD-1290579	csusacagAfAfGfAfGfGfUfgagagauL.96	514	asAfscuuCfucagcuUfcAfGfscucsc	738	UGCUACAGAGAGAGAGAGAGAG	962
AD-1290591	ascagacuUfAfGfAfGfGfUfgagagauL.96	515	asUfscuuCfucagcuUfcAfGfscucsc	739	CUACAGAGAGAGAGAGAGAGAG	963
AD-1290539	csasagacuUfAfGfAfGfGfUfgagagauL.96	516	asAfscuuCfucagcuUfcAfGfscucsc	740	UACAGAGAGAGAGAGAGAGAG	964
AD-1290611	asgsacuUfAfGfAfGfGfUfgagagauL.96	517	asGfscuuCfucagcuUfcAfGfscucsc	741	ACAGAGAGAGAGAGAGAGAGAG	965
AD-1290530	gsasacuGfAfGfAfGfGfUfgagagauL.96	518	asAfscuuCfucagcuUfcAfGfscucsc	742	CAGAGAGAGAGAGAGAGAGAG	966
AD-1290576	csusungAfAfGfAfGfGfUfgagagauL.96	519	asUfscuuCfucagcuUfcAfGfscucsc	743	GACUUGAGAGAGAGAGAGAGAG	967
AD-1290546	usussagAfAfGfAfGfGfUfgagagauL.96	520	asGfscuuCfucagcuUfcAfGfscucsc	744	ACUUGAGAGAGAGAGAGAGAG	968
AD-1290823	asasugcuGfAfGfAfGfGfUfgagagauL.96	521	asAfscuuCfucagcuUfcAfGfscucsc	745	AGAGAGAGAGAGAGAGAGAG	969
AD-1290757	gsusgcuCfuGfAfGfGfGfUfgagagauL.96	522	asUfscuuCfucagcuUfcAfGfscucsc	746	AGGUGAGAGAGAGAGAGAGAG	970
AD-1290959	usussagUfAfGfAfGfGfUfgagagauL.96	523	asCfscuuCfucagcuUfcAfGfscucsc	747	GGUUGAGAGAGAGAGAGAGAG	971
AD-1290837	usgsacuGfAfGfAfGfGfUfgagagauL.96	524	asAfscuuCfucagcuUfcAfGfscucsc	748	GUUGAGAGAGAGAGAGAGAG	972
AD-1290861	gsasucugAfAfGfAfGfGfUfgagagauL.96	525	asCfscuuCfucagcuUfcAfGfscucsc	749	UUUGAGAGAGAGAGAGAGAG	973
AD-1290885	csusgaccCfuGfAfGfGfGfUfgagagauL.96	526	asAfscuuCfucagcuUfcAfGfscucsc	750	AUCUAGAGAGAGAGAGAGAG	974
AD-1290970	ascscagUfAfGfAfGfGfUfgagagauL.96	527	asUfscuuCfucagcuUfcAfGfscucsc	751	UGAGAGAGAGAGAGAGAGAG	975

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:	mRNA target sequence	SEQ ID NO:
AD-1290962	cscsaunCfAaAfGfUfGfGfAaUcCaaU.L96	528	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	752	ACCCAGUUC AAGUGGAUCCACAU	976
AD-1290759	asgsaunCfAaAfGfUfGfGfAaUcCaaU.L96	529	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	753	CCAGUUC AAGUGGAUCCACAU	977
AD-1290736	uscsaagUfGfGfAaUcCaaU.L96	530	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	754	GUUCAAAGUGGAUCCACAU	978
AD-1290739	uscsaagUfGfGfAaUcCaaU.L96	531	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	755	GUUCAAAGUGGAUCCACAU	979
AD-1290828	csasagUfGfAaUcCaaU.L96	532	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	756	UUC AAGUGGAUCCACAU	980
AD-1291001	gscsaunCfAaAfGfUfGfGfAaUcCaaU.L96	533	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	757	ACGAUCGGAGC AGGUGAAGAU	981
AD-1290933	csasagUfGfAaUcCaaU.L96	534	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	758	CGAUCGGAGC AGGUGAAGAU	982
AD-1290988	gscsaunCfAaAfGfUfGfGfAaUcCaaU.L96	535	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	759	AGGACUCUCCAGCUUUGG	983
AD-1290955	csasagUfGfAaUcCaaU.L96	536	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	760	AGCUCUCCAGCUUUGG	984
AD-1290810	csasagUfGfAaUcCaaU.L96	537	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	761	GGUACGGAGC AGGUGAAGAU	985
AD-1290740	uscsaagUfGfGfAaUcCaaU.L96	538	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	762	GUUCAAAGUGGAUCCACAU	986
AD-1290752	csasagUfGfAaUcCaaU.L96	539	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	763	UACGGAGC AGGUGAAGAU	987
AD-1290878	gscsaunCfAaAfGfUfGfGfAaUcCaaU.L96	540	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	764	ACGGAGC AGGUGAAGAU	988
AD-1290599	uscsaagUfGfGfAaUcCaaU.L96	541	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	765	CGUGGUUUGUCAGCAAAGAU	989
AD-1290632	gscsaunCfAaAfGfUfGfGfAaUcCaaU.L96	542	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	766	GUUCAAAGUGGAUCCACAU	990
AD-1290584	uscsaagUfGfGfAaUcCaaU.L96	543	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	767	GUUCAAAGUGGAUCCACAU	991
AD-1290734	uscsaagUfGfGfAaUcCaaU.L96	544	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	768	GUUCAAAGUGGAUCCACAU	992
AD-1290882	gscsaunCfAaAfGfUfGfGfAaUcCaaU.L96	545	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	769	GUUCAAAGUGGAUCCACAU	993
AD-1290987	uscsaagUfGfGfAaUcCaaU.L96	546	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	770	GUUCAAAGUGGAUCCACAU	994
AD-1290963	asasagUfGfAaUcCaaU.L96	547	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	771	GC AAGUGGAGC ACCUUAU	995
AD-1290710	uscsaagUfGfGfAaUcCaaU.L96	548	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	772	GUUCAAAGUGGAUCCACAU	996
AD-1290656	uscsaagUfGfGfAaUcCaaU.L96	549	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	773	GUUCAAAGUGGAUCCACAU	997
AD-1290890	uscsaagUfGfGfAaUcCaaU.L96	550	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	774	GUUCAAAGUGGAUCCACAU	998
AD-1290887	uscsaagUfGfGfAaUcCaaU.L96	551	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	775	AUUGUCCACUGGAGUCCU	999
AD-1290923	gscsaunCfAaAfGfUfGfGfAaUcCaaU.L96	552	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	776	GGGAGUGGAGC ACCUUAU	1000
AD-1290904	uscsaagUfGfGfAaUcCaaU.L96	553	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	777	GGGAGUGGAGC ACCUUAU	1001
AD-1290980	uscsaagUfGfGfAaUcCaaU.L96	554	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	778	AGCUGGAGC ACCUUAU	1002
AD-1290860	uscsaagUfGfGfAaUcCaaU.L96	555	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	779	GCUGGAGC ACCUUAU	1003
AD-1290969	uscsaagUfGfGfAaUcCaaU.L96	556	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	780	ACACCUUAUUGCCUGCAUC	1004
AD-1290811	uscsaagUfGfGfAaUcCaaU.L96	557	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	781	CACCUUAUUGCCUGCAUCU	1005
AD-1290886	uscsaagUfGfGfAaUcCaaU.L96	558	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	782	CCUUAUUGCCUGCAUCU	1006
AD-1290668	uscsaagUfGfGfAaUcCaaU.L96	559	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	783	UUAUUGCCUGCAUCU	1007
AD-1290852	uscsaagUfGfGfAaUcCaaU.L96	560	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	784	UUAUUGCCUGCAUCU	1008
AD-1290915	uscsaagUfGfGfAaUcCaaU.L96	561	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	785	GCUCUGCAUCU	1009
AD-1290874	uscsaagUfGfGfAaUcCaaU.L96	562	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	786	GCUCUGCAUCU	1010
AD-1290818	uscsaagUfGfGfAaUcCaaU.L96	563	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	787	CGUGCAGGAGC ACUGAGAU	1011
AD-1290884	uscsaagUfGfGfAaUcCaaU.L96	564	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	788	GUGCAGGAGC ACUGAGAU	1012
AD-1290977	uscsaagUfGfGfAaUcCaaU.L96	565	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	789	UGUGCCUGCAGGCGUUGG	1013
AD-1290961	uscsaagUfGfGfAaUcCaaU.L96	566	asUfsguGfAaUcCaaUfUfGfAaUcGfsgsu	790	GCCUGCAGGCGUUGG	1014

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:	mRNA target sequence	SEQ ID NO:
AD-1290834	csasggagcUfUfGfAfugcaucgumL96	567	asAfiscgUfjggcaucaAfAfGccugscsa	791	UGCAGGGUUUGAUGGCAUCGUG	1015
AD-1290867	gsgsgcunUfUfUfGfUfGfucagugumL96	568	asAfiscacGfagagccanUfAfAfagccesusc	792	CAGGGUUUUGAUGGCAUCGUGUG	1016
AD-1290879	csusugccUfUfGfUfGfucagugumL96	569	asAfisacaGfagagcacAfGfGfagagsgsc	793	GACUCUGCCUGAUGGCUUGUGUUC	1017
AD-1290549	csuscgagGfCfAfAfAfuaaagacumL96	570	asGfisaagAfuaaunuuGfCfUfcugagsgsc	794	GCCUCAGAGCAAAUAAAUCUCC	1018
AD-1290525	csasgagcAfAfAfUfAfuaucunumL96	571	asAfisgagAfuaunuuUfUfGfucugsgag	795	CUCAGAGCAAAUAAAUCUCCUC	1019
AD-1290622	csusccucUfcAfAfUfUfugugaacumL96	572	asAfisgnUfagacaunUfAfGfagaggsasa	796	UUCUCUCUCAUUGUCUGAACUG	1020
AD-1290638	csesccunCfAfAfUfUfGfucagucumL96	573	asGfiscagUfucagacUfUfAfGfaggsasa	797	UUCUCUCUCAUUGUCUGAACUGC	1021
AD-1290921	csesccucAfAfUfUfUfGfucagucumL96	574	asGfiscagUfucagacaUfUfGfagaggsag	798	CUCCUCUCAUUGUCUGAACUGCUC	1022
AD-1290621	csusccucaAfUfUfUfGfucagucumL96	575	asAfisgcaGfucagacAfUfUfagaggsasa	799	UUCUCUCAUUGUCUGAACUGCUC	1023
AD-1290775	csuseaanGfUfUfGfUfGfuaucugumL96	576	asAfisgagCfagumcagAfCfAfuaugsgag	800	CUCUAAUGUCUGAACUGCUCUG	1024
AD-1290748	asusuccuGfAfGfGfUfagagucumL96	577	asAfisgagUfcagagccUfcAfGfuaugsgc	801	GC AUUCUGAGGCUCUGACUCUU	1025
AD-1290865	csusgcuUfUfUGfGfUfagacumL96	578	asAfisuaGfagucgaCfAfAfagcgsgag	802	CCUGCGUUGUGCAGACUCUAUU	1026
AD-1290877	usgsccuGfUfUfGfUfGfUfagacumL96	579	asAfisuaGfagucgcAfCfAfagcgsgag	803	CCUGCGUUGUGCAGACUCUAUUC	1027
AD-1290989	gsgsguugUfGfCfAfGfUfagacumL96	580	asGfisaauAfagucugCfAfCfagcgsgag	804	CUGCGUUGUGCAGACUCUAUCC	1028
AD-1290983	csgsuugUfGfCfAfGfAfucunumL96	581	asGfisaauUfagagucUfGfAfagcgscsa	805	UGCGUUGUGCAGACUCUAUCC	1029
AD-1290909	usugugcAfGfCfUfUfUfuaucumL96	582	asUfisggAfuaagagUfUfGfagcgscg	806	CGUUGUGCAGACUCUAUCCAC	1030
AD-1290993	usasunccCfAfCfAfGfUfcagagumL96	583	asGfiscunUfugagucUfUfGfuaugsga	807	UCUAUCCCAACAGCUCAGAAAGU	1031
AD-1290841	asusuccAfCfAfGfUfagagumL96	584	asAfiscunUfcugagucUfUfGfuaugsg	808	CUAUUCCCAACAGCUCAGAAAGU	1032
AD-1290880	csusuggaGfCfCfAfUfcuugagumL96	585	asAfiscunUfcagugugGfCfUfcagsgag	809	CCUUGGAGCCCAUUGGAAU	1033
AD-1290747	gsgsagccCfAfCfUfUfugagaumL96	586	asUfisaauUfuccagUfUfGfucgscsa	810	UUGGAGCCCAUUGGAAUUAAG	1034
AD-1290842	gsasgccAfCfCfUfUfUfagumL96	587	asCfsmuaUfuccaagGfUfGfucgscsa	811	UGGAGCCCAUUGGAAUUAAGG	1035
AD-1290911	asgscccaCfCfUfUfGfagumL96	588	asCfiscunAfuaucuaGfGfUfGfucgscsc	812	GGAGCCCAUUGGAAUUAAGG	1036
AD-1290926	gsgscacCfUfUfGfUfagumL96	589	asCfiscunUfuaucuaAfGfUfGfucgscsc	813	GAGCCCAUUGGAAUUAAGG	1037
AD-1291003	gsgsgcgcUfcUfCfAfUfagcaumL96	590	asAfiscunUfugugagGfGfCfagcgscsu	814	AGGGCGUCCUCAGCCCAAAUG	1038
AD-1290931	uscsagccAfCfAfAfUfugagacumL96	591	asUfisggUfcacuumUfUfGfucgagsgg	815	CCUCAGCCCAAAUGAGCCAG	1039
AD-1290764	gsgsucgAfUfCfUfUfGfagacumL96	592	asUfisaugUfugucagAfUfUfagcgscsc	816	GAGGUCCGAUUGGAAACACAUAU	1040
AD-1290763	uscsccgUfcUfGfGfagacumL96	593	asAfisaauUfugumcgaGfUfUfagcgscsu	817	AGGUCCGAUUGGAAACACAUAU	1041
AD-1290670	uscsagauCfUfGfGfAfacacumL96	594	asAfisaauUfugumccAfGfUfUfagcgsc	818	GUCCGACUUGGAAACACAUAUUG	1042
AD-1290712	cscsgaauUfGfAfAfUfagcaumL96	595	asCfisaauUfugumccAfGfUfUfagcgsc	819	GUCGACUUGGAAACACAUAUUG	1043
AD-1290612	asusuccGfAfCfAfUfuaucumL96	596	asUfiscucAfuaugugUfUfCfagagsgag	820	CGAUCUGGAACACAUAUUGGAAU	1044
AD-1290522	uscsuggaAfCfAfCfUfuaucumL96	597	asAfiscucUfuaaunUfUfUfagcgscsc	821	GAUCUGGAACACAUAUUGGAAU	1045
AD-1290528	csusggacCfAfCfUfuaucumL96	598	asAfisaauUfuaaunUfUfUfagcgscsu	822	AUCUGGAACACAUAUUGGAAUUG	1046
AD-1290543	usgsaacAfCfAfUfuaucumL96	599	asCfisaauUfuaaunUfUfUfagcgsgsa	823	UCUGGAACACAUAUUGGAAUUGG	1047
AD-1290589	gsgsaacAfUfAfUfuaucumL96	600	asCfiscacUfuaaunUfUfUfagcgsgag	824	CUGGAACACAUAUUGGAAUUGGG	1048
AD-1290800	gsgsgugGfUfAfAfGfagcaumL96	601	asUfisaauUfagggcUfUfCfagcgscsa	825	UAGGUGGGUAAGGCCUUAUAU	1049
AD-1290755	gsgsuggUfAfAfGfagcaumL96	602	asAfisuaUfagggcUfUfCfagcgscsu	826	AGGGUGGGUAAGGCCUUAUAUG	1050
AD-1290742	gsgsgggUfAfGfGfUfuaucumL96	603	asCfisaauUfuaagggUfUfAfagcgscsc	827	GGGUAGGCCUUAUAUUG	1051
AD-1290563	gssuagggCfUfUfUfuaucumL96	604	asUfisaauUfuaaunUfUfUfagcgscsc	828	GGUAAGGCCUUAUAUUGAAG	1052
AD-1290570	asuscccUfUfUfUfuaucumL96	605	asUfiscunUfuaaunUfUfUfagcgscsc	829	GUUAGGCCUUAUAUUGAAGAG	1053

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:	mRNA target sequence	SEQ ID NO:
AD-1290515	asgsgccuUfaUfAfAfuGuaaagagcuL96	606	asCfscnuUfuacanuUfaAfuGccususa	830	UAAAGCCUUUAUAAUGUAAAAGAGC	1054
AD-1290556	gscscnuUfaUfAfGfuAaagagcuL96	607	asUfsgcuCfuuacuUfuAfuAagccsu	831	AGGCCUUUAUAAUGUAAAAGAGC	1055
AD-1290661	gscsauauAfaUfGfUfaaagagcuL96	608	asAfsagCfcccnuUfaUfuauagcsc	832	GAGCAUUAUAAUGUAAAAGGCUU	1056
AD-1290555	asusauaaUfgUfAfAfuagccuauL96	609	asUfsaaUfcccnuUfaUfuauagcsc	833	GCAUUAUAAUGUAAAAGGCUUAG	1057
AD-1290554	asusaugUfaUfAfGfGccuuaugcuL96	610	asUfsuaAfagcccuUfaCfuaauusua	834	AUAUAUGUAAAAGGCUUUAAGAG	1058
AD-1290639	usasaugUfaUfAfGfGccuuaugcuL96	611	asCfscnuAfaagcccuUfuAfuauusua	835	UAUAUUAUAAAGGCUUUAAGAGU	1059
AD-1290618	asasuguaAfaGfGfGccuuaugcuL96	612	asAfsnuCfagcccuUfuUfuaauusua	836	AUAUUAUAAAGGCUUUAAGAGUG	1060
AD-1290660	cscsuggaUfuUfAfAfauugccauL96	613	asAfsnuCfagcccuUfuUfuaauusua	837	GACCGGAUUAUAAUUCGCCAUU	1061
AD-1290551	cscsuggaUfuUfAfAfauugccauL96	614	asAfsnuCfagcccuUfuUfuaauusua	838	ACCGGAUUAUAAUUCGCCAUU	1062
AD-1290509	gsasuaaAfaUfCfUfGccuuaauL96	615	asUfsuaAfagcccuUfuUfuaauusua	839	UGGAUUAUAAUUCGCCAUUUAU	1063
AD-1290597	asusuaaAfuCfUfGfGccuuaauL96	616	asAfsuaAfagcccuUfuUfuaauusua	840	GGAUUAUAAUUCGCCAUUUAU	1064
AD-1290533	asasaucGfCfAfUfuaauuagcuL96	617	asGfscuaAfuuaaagGfCfuaauusua	841	UAAAAUCUGCCAUUUAUUAAGCU	1065
AD-1290535	asascugCfCfAfUfuaauuagcuL96	618	asAfsnuAfuuaaagGfCfuaauusua	842	AAAAUCUGCCAUUUAUUAAGCU	1066
AD-1290604	asuscugCfCfAfUfuaauuagcuL96	619	asCfsagCfuaaauUfgGfuaauusua	843	AAAAUCUGCCAUUUAUUAAGCU	1067
AD-1290633	cscsugcaUfuUfAfAfuaugcguL96	620	asUfsgaCfuaaauUfgGfuaauusua	844	AUCUGCCAUUUAUUAAGCUGCAU	1068
AD-1290741	ascsgcaaUfcUfGfCfuaauuagcuL96	621	asGfscuaAfuuaaagGfCfuaauusua	845	UAACGCAUUCUGCCAUUUAUUAU	1069
AD-1290650	csgscuauCfCfGfCfuaauuagcuL96	622	asAfsuaAfuuaaagGfCfuaauusua	846	AACGCAUUCUGCCAUUUAUUAU	1070
AD-1290672	gscsaucUfgCfCfUfuaauuagcuL96	623	asAfsuaAfuuaaagGfCfuaauusua	847	ACGCAUUCUGCCAUUUAUUAU	1071
AD-1290605	asascugCfCfUfCfAfuuaucuuL96	624	asUfsgaCfuaaauUfgGfuaauusua	848	GCAUUCUGCCAUUUAUUAUUAU	1072
AD-1290573	asuscugCfCfAfAfAfuuaucuuL96	625	asAfsuaAfuuaaagGfCfuaauusua	849	CAUUCUGCCAUUUAUUAUUAU	1073
AD-1290615	uscsgccUfcAfAfUfuaucuuL96	626	asGfscuaAfuuaaagGfCfuaauusua	850	AAUUCUGCCAUUUAUUAUUAU	1074
AD-1290531	cscsugcuCfAfAfUfuaucuuL96	627	asAfsuaAfuuaaagGfCfuaauusua	851	AUCUGCCAUUUAUUAUUAUUAU	1075
AD-1290602	uscsgccUfcAfAfUfuaucuuL96	628	asCfsagUfuaaauUfgGfuaauusua	852	UCUGCCAUUUAUUAUUAUUAU	1076
AD-1290523	gscscuaAfuUfUfCfuaucuuL96	629	asAfsuaAfuuaaagGfCfuaauusua	853	CUGCCAUUUAUUAUUAUUAU	1077
AD-1290514	csasaauUfCfAfAfAfuuaucuuL96	630	asUfsgaCfuaaauUfgGfuaauusua	854	CUCAUUAUUAUUAUUAUUAU	1078
AD-1290510	asasnuCfCfAfAfUfuaucuuL96	631	asAfsuaAfuuaaagGfCfuaauusua	855	UCAUUAUUAUUAUUAUUAU	1079
AD-1290524	asusnuCfCfAfAfUfuaucuuL96	632	asCfsagUfuaaauUfgGfuaauusua	856	CAUUAUUAUUAUUAUUAUUAU	1080
AD-1290836	asasnuCfCfUfUfGfuaucuuL96	633	asUfsgaCfuaaauUfgGfuaauusua	857	CCAAUUCUGCCAUUUAUUAUUAU	1081
AD-1290719	asusnuCfCfUfUfGfuaucuuL96	634	asAfsuaAfuuaaagGfCfuaauusua	858	CAUUAUUAUUAUUAUUAUUAU	1082
AD-1290722	uscsgcuUfgGfCfUfuaucuuL96	635	asUfsgaCfuaaauUfgGfuaauusua	859	AUUCUGCCAUUUAUUAUUAUUAU	1083
AD-1290687	cscsugcuGfCfUfAfuuaucuuL96	636	asAfsuaAfuuaaagGfCfuaauusua	860	UUCUGCCAUUUAUUAUUAUUAU	1084
AD-1290643	uscsgcuGfCfUfAfuuaucuuL96	637	asAfsuaAfuuaaagGfCfuaauusua	861	UCUGCCAUUUAUUAUUAUUAU	1085
AD-1290600	gscsugcuGfCfUfAfuuaucuuL96	638	asCfsagUfuaaauUfgGfuaauusua	862	CUGCCAUUUAUUAUUAUUAUUAU	1086
AD-1290507	ususcuaAfuUfUfGfuaucuuL96	639	asUfsgaCfuaaauUfgGfuaauusua	863	AUUAUUAUUAUUAUUAUUAU	1087
AD-1290516	gscsaauAfaUfCfGfuaucuuL96	640	asUfsgaCfuaaauUfgGfuaauusua	864	CUGGAUUAUUAUUAUUAUUAU	1088
AD-1290527	uscsgauAfaUfUfGfuaucuuL96	641	asAfsuaAfuuaaagGfCfuaauusua	865	CCUGGAUUAUUAUUAUUAUUAU	1089
AD-1290542	uscsgauUfcUfUfGfuaucuuL96	642	asUfsgaCfuaaauUfgGfuaauusua	866	CCUGGAUUAUUAUUAUUAUUAU	1090
AD-1290552	ususcuaAfuUfUfGfuaucuuL96	643	asCfsagUfuaaauUfgGfuaauusua	867	AAUUAUUAUUAUUAUUAUUAU	1091
AD-1290557	gscscuAfuUfUfGfuaucuuL96	644	asGfscuaAfuuaaagGfCfuaauusua	868	AAGCCUUUAUAAUGUAAAAGAGC	1092

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:	mRNA target sequence	SEQ ID NO:
AD-1290558	usasuauGfuAfAfAfgggcunuaugL96	645	asCfsuuaAfgccunuaAfcAfuaauasug	869	CAUUAUUAUUAAGGGCUUUUAGA	1093
AD-1290561	asusuuucUfcUfUfUfgcauucugul96	646	asCfsagAfaugcaaaGfaGfaaauagsc	870	GCAUUUUCUUCUUUGCAUUCUCGA	1094
AD-1290564	cscsucaaUfuUfUfUfcauucugul96	647	asCfsacaGfaugaagaAfaUfugaagcsa	871	UGCCUCAUUUUCUUAUCUCUGCAA	1095
AD-1290565	cscsucaaUfuUfUfUfcauucugul96	648	asUfsagAfaugaagAfaUfugaagsc	872	GGCCUAAUUUUCUUAUCUCUGCAA	1096
AD-1290574	usasagccCfuUfAfUfUfauguaaagL96	649	asCfsuuuAfaumuaaAfgGfcuuausc	873	GGUAAGGCCUUUAUAUUAAGAA	1097
AD-1290592	csasuuaaAfuGfuUfAfaagggcunuaL96	650	asAfsaagCfcuunuaAfuUfaugscsu	874	AGCAUUAUUAUUAAGGGCUUUUA	1098
AD-1290609	usgsccauUfuUfAfUfUfaugcugcaul96	651	asAfsuagAfgcuuaaAfaUfugaagcsa	875	UGGCCAUUUUAUUAGCUGCAUA	1099
AD-1290624	asusauuGfuGfAfGfagaauaauL96	652	asAfsauUfuaucucAfcAfuaauusc	876	GAAUUAUUUGAGGAAUAAAUA	1100
AD-1290626	gsgsuagGfcCfuUfUfaaauaauL96	653	asUfsuacAfuuaaagGfcCfuuaacscsa	877	UGGUAAAGGCCUUUAUUAUUA	1101
AD-1290635	ususcgcUfuGfGfCfuacagaauL96	654	asAfsauUfugaagGfcAfgaauasusu	878	AAUUCUGCUUGGCUACAGAAUA	1102
AD-1290651	gsuucuaGfuGfAfAfuacauugul96	655	asCfsauUfugaagGfcUfugaagscsu	879	CAGUUAAGUGGUAUCCACAUUA	1103
AD-1290654	gsgsguaaGfGfCfUfuaaauaauL96	656	asUfsacaUfuaaagGfcUfuaagcsa	880	GUGGUUAAGGCCUUUAUUAUUA	1104
AD-1290655	gsasucgGfaAfcAfAfaauuagauL96	657	asUfsacaUfuaaagGfcUfuaagcsa	881	CCGUAUGGAAACACAUUAUUA	1105
AD-1290657	ususcucUfuUfGfCfuauucugul96	658	asCfsuagAfgaagGfcUfuaaasusu	882	AUUUCUCUUUGCAUUCUGGAGA	1106
AD-1290659	csasauuGfcCfuUfCfuauuucunuaL96	659	asGfsaagAfaauagGfcAfgaauagscsu	883	CGCAUUCUGCCUAAUUAUUA	1107
AD-1290665	asgsagcaAfaUfAfAfaucucucul96	660	asGfsaagAfaaauuaUfuUfucucusa	884	UCAGAGCAAAUUAUUAUUAUUA	1108
AD-1290666	ascsuuugAfgAfAfGfuaugcugul96	661	asCfsagaUfaaauuaUfuUfucucusa	885	AGACUUUGAGAAAGGUUAUUA	1109
AD-1290680	usascagaCfuUfUfGfagaagcugul96	662	asCfsaagCfuuaaauaAfuUfugaagscsu	886	GCUACAGACUUUGGAAAGGUUA	1110
AD-1290681	usgsuguaAfgGfCfuaaauaauL96	663	asAfsauUfuaaagGfcUfuaaagcsa	887	GGUGGUUAAGGCCUUUAUUAUUA	1111
AD-1290683	usugscuuUfcUfCfGfagaucugul96	664	asAfsagGfuaucuaGfaAfgaauasusu	888	CUUUGCAUUCUGAGAAUUAUUA	1112
AD-1290684	csgsaucUgGfAfAfCfacaauugul96	665	asCfsaaUfuaaagGfcAfgaagcsa	889	UCCGAUCUGGAAACAAUUAUUA	1113
AD-1290702	uscsugccAfuUfUfAfaaagcugul96	666	asCfsagCfuuaaauaAfuUfugaagscsu	890	AAUCUGCAUUUAUUAUUAUUA	1114
AD-1290718	csgsuugGfuUfUfGfagaagcugul96	667	asCfsuugGfuaaauaAfuUfugaagscsu	891	GACUGGUGUUUGGAAAGGUUA	1115
AD-1290746	usugsuauGfGfUfCfGfugaagcugul96	668	asUfsuagGfuaaauaAfuUfugaagscsu	892	GUUUGUAUGGUGGUAUUAUUA	1116
AD-1290750	cscsagaGfaAfcCfCfugcaaaagul96	669	asUfsuagGfuaaauaAfuUfugaagscsu	893	CACCAAGUAAACCGCAAAAGAA	1117
AD-1290765	gsasagGfuGfUfUfugcagcaul96	670	asUfsuagGfuaaauaAfuUfugaagscsu	894	GAGACUGGUGUUUGGAAAGGUUA	1118
AD-1290778	uscsaagGfcUfCfCfugcaaaagul96	671	asUfsuagGfuaaauaAfuUfugaagscsu	895	CUUUGGAGCCACCGCAUUAUUA	1119
AD-1290795	usugcucCfaCfUfCfugaagcunuaL96	672	asAfsaagCfuaaauaAfuUfugaagscsu	896	AAUUGCUCACUGGAAAGGUUA	1120
AD-1290796	usugsgagCfcCfAfCfugaagcunuaL96	673	asAfsaagCfuaaauaAfuUfugaagscsu	897	CCUUGGAGCCACCGCAUUAUUA	1121
AD-1290803	asuscgaCfaAfcCfCfugaagcunuaL96	674	asAfsaagCfuaaauaAfuUfugaagscsu	898	CCAUCUGACAAAGGAAAGGUUA	1122
AD-1290805	usgsagCfcCfAfCfugaagcunuaL96	675	asUfsaagCfuaaauaAfuUfugaagscsu	899	CUUUGGAGCCACCGCAUUAUUA	1123
AD-1290835	gsasucuuCfcAfcCfugaagcunuaL96	676	asAfsaagCfuaaauaAfuUfugaagscsu	900	GAGCUUUCACCGCAUUAUUA	1124
AD-1290857	usgscccaCfcAfcCfugaagcunuaL96	677	asAfsaagCfuaaauaAfuUfugaagscsu	901	CCUUGGAGCCACCGCAUUAUUA	1125
AD-1290863	asasagCfcUfGfGfugaagcunuaL96	678	asAfsaagCfuaaauaAfuUfugaagscsu	902	CCAAGACCCUGGUAUUAUUA	1126
AD-1290875	gscccaCfaGfCfCfugaagcunuaL96	679	asCfsaagCfuaaauaAfuUfugaagscsu	903	CUGCCACACCGCAUUAUUA	1127
AD-1290891	ascsgagAfcGfUfGfugaagcunuaL96	680	asCfsaagCfuaaauaAfuUfugaagscsu	904	CUACGAGACCGCAUUAUUA	1128
AD-1290894	asgsuagCfaUfCfUfugaagcunuaL96	681	asAfsuagCfuaaauaAfuUfugaagscsu	905	GGAGUCCGACCGCAUUAUUA	1129
AD-1290903	gsasagGfCfcUfCfUfugaagcunuaL96	682	asUfsuagCfuaaauaAfuUfugaagscsu	906	GAGAGUCCGACCGCAUUAUUA	1130
AD-1290908	cscsagGfAfcCfCfUfugaagcunuaL96	683	asUfsuagCfuaaauaAfuUfugaagscsu	907	ACCCAGUAGCCGCAUUAUUA	1131

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:	mRNA target sequence	SEQ ID NO:
AD-1290910	usagggguGfgGfUfAfagccuuaunL96	684	asAfsnaaGfgccuuaCfcAfccuusa	908	UAUAGGGUGGGU/AGGCCUUUAUA	1132
AD-1290924	usggggagUfaGfCfCfcauggaagnL96	685	asCfsuncCfaugaggcUfaCfucccsaga	909	UCUGGGAGU/AGCCUC/UGGAAGA	1133
AD-1290939	asgggugGfgUfAfAfagccuuaunL96	686	asUfsanaAfagccuuaCfcCfaccusasu	910	AUAGGGUGGGU/AGGCCUUUAUA	1134
AD-1290946	gsgsuugaUfcUfGfAfccaguucaunL96	687	asUfsgaaCfugggucaGfaUfcaaccsuu	911	AAGGUUGAUCUG/ACCCAGUUCAA	1135
AD-1290950	csatucagCfcUfGfGfHgagacaagnL96	688	asAfseuuGfuccaccaGfgChugaugsase	912	GUC/UCAGCCUGGUGGAC/AGUA	1136
AD-1290956	asgscuguGfaGfUfCfcaucugacauL96	689	asUfsgucAfgauggaCfCfcaucugsga	913	UCAGCUGUGAGUCC/UCUGACAA	1137
AD-1290971	gscsuacgGfaGfAfCfHguguguuunL96	690	asAfsaacAfccacgucUfcCfignagcsca	914	UGGCU/ACGGAGAC/CGUGGUGUUUG	1138
AD-1290973	gsusungCfaGfAfCfcauaucccuL96	691	asGfsggaAfuaagucUfgCfacaacsesc	915	GCGUUGUGCAGACUCUAU/CCCCA	1139

Table 4. KHK Dose Screen in HepG2 cells

Duplex Name	KHK/gapdh					
	10 nM		1 nM		0.1 nM	
	mean	SD	mean	SD	mean	SD
AD-1290887.1	0.404	0.066	0.946	0.145	1.155	0.187
AD-1290629.1	0.613	0.010	1.098	0.229	1.020	0.166
AD-1290807.1	0.247	0.007	0.663	0.138	1.226	0.074
AD-1290681.1	0.990	0.171	1.179	0.170	1.183	0.178
AD-1290639.1	0.927	0.044	1.302	0.254	1.104	0.178
AD-1290597.1	0.904	0.040	1.425	0.206	1.156	0.123
AD-1290775.1	0.870	0.026	1.498	0.159	1.210	0.162
AD-1290795.1	0.182	0.023	0.526	0.119	1.005	0.106
AD-1291003.1	0.835	0.113	1.353	0.222	1.296	0.081
AD-1290903.1	0.419	0.021	1.151	0.233	0.887	0.055
AD-1290896.1	0.807	0.065	1.389	0.334	0.970	0.054
AD-1290605.1	0.675	0.077	1.474	0.345	0.989	0.083
AD-1290742.1	0.991	0.143	1.355	0.379	1.054	0.145
AD-1290554.1	0.924	0.069	1.578	0.256	1.118	0.082
AD-1290509.1	0.865	0.048	1.256	0.129	1.118	0.165
AD-1290938.1	0.482	0.044	0.772	0.164	0.990	0.327
AD-1290750.1	0.990	0.051	1.077	0.059	1.058	0.116
AD-1290659.1	0.690	0.031	0.937	0.194	0.971	0.100
AD-1290755.1	0.916	0.058	1.122	0.098	1.100	0.119
AD-1290558.1	0.888	0.034	1.064	0.214	0.850	0.035
AD-1290516.1	0.777	0.044	1.046	0.236	0.864	0.132
AD-1290621.1	0.893	0.039	0.990	0.210	0.910	0.148
AD-1290956.1	0.498	0.040	0.582	0.063	0.762	0.089
AD-1290672.1	0.814	0.034	0.828	0.073	0.826	0.210
AD-1290800.1	0.859	0.116	0.898	0.082	0.764	0.096
AD-1290555.1	0.781	0.061	0.843	0.036	0.805	0.143
AD-1290527.1	0.912	0.114	0.908	0.056	0.664	0.037
AD-1290921.1	0.920	0.045	0.896	0.102	0.741	0.082
AD-1290664.1	0.693	0.071	0.956	0.095	0.806	0.035
AD-1290924.1	0.282	0.025	0.576	0.045	0.630	0.011
AD-1290650.1	0.756	0.035	0.914	0.130	0.830	0.081
AD-1290939.1	0.829	0.027	0.873	0.030	0.804	0.128
AD-1290592.1	0.784	0.055	0.894	0.136	0.775	0.069
AD-1290551.1	0.724	0.024	0.891	0.189	0.687	0.009
AD-1290638.1	0.921	0.052	0.976	0.230	0.758	0.071
AD-1290580.1	0.410	0.017	0.702	0.116	0.741	0.112
AD-1290916.1	0.552	0.026	0.694	0.024	0.723	0.105
AD-1290741.1	0.799	0.057	0.864	0.034	0.731	0.075
AD-1290910.1	0.945	0.078	0.948	0.020	0.665	0.030
AD-1290661.1	0.985	0.065	0.937	0.064	0.665	0.011

Duplex Name	KHK/gapdh					
	10 nM		1 nM		0.1 nM	
	mean	SD	mean	SD	mean	SD
AD-1290660.1	0.901	0.159	0.936	0.022	0.912	0.032
AD-1290622.1	1.020	0.207	0.940	0.040	0.932	0.174
AD-1290540.1	0.474	0.033	0.698	0.062	0.978	0.109
AD-1290618.1	1.075	0.102	0.930	0.116	0.786	0.032
AD-1290600.1	1.072	0.213	0.901	0.055	0.953	0.133
AD-1290908.1	0.812	0.052	0.810	0.019	0.802	0.172
AD-1290665.1	0.191	0.030	0.216	0.116	0.656	0.117
AD-1290870.1	0.831	0.092	0.916	0.071	0.731	0.047
AD-1290990.1	0.698	0.020	0.687	0.036	0.785	0.075
AD-1290989.1	0.829	0.167	0.862	0.101	0.607	0.241
AD-1290987.1	0.376	0.042	0.581	0.024	0.985	0.177
AD-1290983.1	0.987	0.249	0.993	0.176	0.883	0.125
AD-1290982.1	0.949	0.138	0.846	0.054	0.866	0.052
AD-1290973.1	0.884	0.229	0.954	0.070	0.813	0.127
AD-1290971.1	0.135	0.043	0.289	0.029	0.699	0.071
AD-1290970.1	0.153	0.039	0.207	0.011	0.660	0.127
AD-1290969.1	0.140	0.034	0.221	0.017	0.608	0.113
AD-1290964.1	0.265	0.038	0.360	0.026	0.709	0.100
AD-1290963.1	0.158	0.045	0.311	0.063	0.739	0.176
AD-1290962.1	0.317	0.114	0.436	0.042	0.730	0.095
AD-1290959.1	0.157	0.044	0.295	0.014	0.835	0.044
AD-1290950.1	0.282	0.044	0.624	0.049	0.896	0.080
AD-1290946.1	0.656	0.156	0.866	0.031	0.883	0.042
AD-1290915.1	0.117	0.040	0.396	0.024	0.882	0.121
AD-1290914.1	0.676	0.046	0.689	0.038	0.862	0.102
AD-1290911.1	1.052	0.136	0.914	0.028	0.930	0.143
AD-1290900.1	0.230	0.034	0.512	0.013	0.805	0.026
AD-1290897.1	1.054	0.014	0.957	0.027	0.867	0.065
AD-1290891.1	0.534	0.134	0.675	0.016	0.853	0.068
AD-1290890.1	1.094	0.160	0.905	0.025	0.945	0.138
AD-1290886.1	0.626	0.146	0.764	0.044	0.953	0.112
AD-1290885.1	0.115	0.017	0.217	0.066	0.770	0.030
AD-1290884.1	0.133	0.025	0.264	0.014	0.783	0.120
AD-1290882.1	0.265	0.032	0.659	0.013	0.897	0.032
AD-1290881.1	0.156	0.052	0.393	0.024	0.952	0.137
AD-1290878.1	0.156	0.026	0.381	0.011	0.933	0.201
AD-1290874.1	0.135	0.006	0.371	0.010	0.827	0.127
AD-1290872.1	0.269	0.055	0.256	0.013	0.606	0.098
AD-1290865.1	0.680	0.264	0.838	0.020	0.895	0.202
AD-1290861.1	0.814	0.323	0.885	0.022	0.961	0.088
AD-1290860.1	0.169	0.022	0.641	0.031	0.957	0.032

Duplex Name	KHK/gapdh					
	10 nM		1 nM		0.1 nM	
	mean	SD	mean	SD	mean	SD
AD-1290857.1	0.656	0.179	0.921	0.068	0.990	0.068
AD-1290854.1	0.532	0.083	0.644	0.032	0.994	0.041
AD-1290853.1	0.550	0.135	0.732	0.018	0.966	0.051
AD-1290852.1	0.750	0.108	0.762	0.161	1.074	0.156
AD-1290842.1	0.887	0.182	0.748	0.049	0.982	0.039
AD-1290837.1	0.409	0.365	0.260	0.016	0.919	0.135
AD-1290828.1	0.370	0.070	0.565	0.059	0.904	0.028
AD-1290823.1	0.213	0.072	0.329	0.034	0.916	0.051
AD-1290821.1	0.198	0.043	0.363	0.012	1.036	0.111
AD-1290818.1	0.053	0.009	0.162	0.011	0.699	0.039
AD-1290816.1	0.208	0.040	0.472	0.026	0.916	0.037
AD-1290814.1	0.116	0.037	0.221	0.012	0.625	0.025
AD-1290811.1	0.120	0.031	0.291	0.023	0.830	0.034
AD-1290810.1	0.194	0.025	0.572	0.033	0.949	0.018
AD-1290802.1	0.332	0.110	0.511	0.004	0.983	0.032
AD-1290778.1	0.146	0.019	0.440	0.037	0.961	0.045
AD-1290765.1	0.086	0.017	0.141	0.010	0.647	0.020
AD-1290759.1	0.262	0.082	0.432	0.008	0.948	0.065
AD-1290757.1	0.136	0.041	0.242	0.011	0.838	0.035
AD-1290752.1	0.155	0.018	0.423	0.074	0.893	0.042
AD-1290746.1	0.123	0.013	0.598	0.099	0.970	0.125
AD-1290745.1	0.199	0.018	0.614	0.068	0.964	0.081
AD-1290740.1	0.138	0.016	0.620	0.120	0.985	0.031
AD-1290739.1	0.379	0.035	1.002	0.121	0.992	0.049
AD-1290736.1	0.525	0.046	1.239	0.176	1.017	0.173
AD-1290734.1	0.512	0.029	1.320	0.191	1.066	0.083
AD-1290731.1	0.154	0.004	0.536	0.100	1.089	0.077
AD-1290718.1	0.128	0.051	0.699	0.158	1.227	0.081
AD-1290710.1	0.237	0.082	0.841	0.138	1.133	0.125
AD-1290702.1	0.771	0.024	1.217	0.214	1.069	0.019
AD-1290695.1	0.379	0.050	0.758	0.127	0.997	0.026
AD-1290685.1	0.373	0.009	0.887	0.154	1.003	0.045
AD-1290683.1	0.363	0.013	0.741	0.104	1.030	0.056
AD-1290668.1	0.096	0.008	0.285	0.042	0.874	0.040
AD-1290667.1	0.549	0.036	0.987	0.122	1.200	0.067
AD-1290657.1	0.459	0.045	1.116	0.220	1.181	0.044
AD-1290656.1	0.591	0.104	1.197	0.190	1.231	0.021
AD-1290653.1	0.325	0.008	0.636	0.092	1.087	0.022
AD-1290652.1	0.106	0.008	0.382	0.063	1.143	0.023
AD-1290651.1	0.232	0.008	0.415	0.053	0.983	0.091
AD-1290633.1	0.943	0.033	0.882	0.084	0.898	0.126

Duplex Name	KHK/gapdh					
	10 nM		1 nM		0.1 nM	
	mean	SD	mean	SD	mean	SD
AD-1290632.1	0.406	0.154	0.773	0.099	0.866	0.099
AD-1290604.1	1.000	0.035	0.737	0.043	0.934	0.078
AD-1290599.1	0.128	0.003	0.200	0.016	0.749	0.027
AD-1290589.1	0.992	0.050	0.731	0.038	0.839	0.047
AD-1290584.1	0.222	0.012	0.362	0.031	0.830	0.037
AD-1290576.1	0.140	0.009	0.218	0.020	0.846	0.118
AD-1290569.1	0.531	0.139	0.575	0.056	0.814	0.192
AD-1290565.1	1.031	0.070	0.703	0.049	0.911	0.086
AD-1290561.1	0.400	0.039	0.640	0.106	1.109	0.180
AD-1290559.1	0.429	0.037	0.573	0.086	1.094	0.053
AD-1290557.1	0.861	0.121	0.917	0.251	1.148	0.214
AD-1290552.1	0.866	0.110	0.759	0.128	0.739	0.317
AD-1290548.1	0.427	0.040	0.436	0.041	0.854	0.037
AD-1290547.1	0.534	0.102	0.569	0.065	1.079	0.218
AD-1290546.1	0.081	0.017	0.127	0.070	0.689	0.115
AD-1290544.1	0.420	0.176	0.533	0.047	0.964	0.045
AD-1290543.1	0.798	0.127	0.855	0.085	0.973	0.049
AD-1290542.1	0.807	0.059	0.730	0.024	0.901	0.187
AD-1290528.1	0.638	0.045	0.777	0.049	1.080	0.063
AD-1290526.1	0.496	0.040	0.680	0.045	1.027	0.164
AD-1290524.1	0.886	0.029	1.005	0.038	0.998	0.132
AD-1290522.1	0.825	0.036	0.937	0.042	0.863	0.034
AD-1290515.1	0.925	0.061	0.886	0.060	0.802	0.049
AD-1290514.1	1.056	0.046	1.130	0.080	0.899	0.030
AD-1290510.1	0.794	0.058	0.921	0.052	0.869	0.073
AD-1290980.1	0.309	0.016	0.756	0.022	0.804	0.042
AD-1290933.1	0.444	0.029	0.747	0.039	0.862	0.125
AD-1290834.1	0.296	0.017	0.611	0.064	0.904	0.119
AD-1290747.1	0.839	0.068	0.831	0.135	1.002	0.093
AD-1290666.1	0.265	0.003	0.457	0.036	0.988	0.117
AD-1290612.1	0.776	0.084	0.811	0.050	0.828	0.027
AD-1290570.1	0.811	0.035	0.909	0.096	0.844	0.016
AD-1290564.1	0.956	0.026	0.910	0.053	1.112	0.182
AD-1290535.1	0.916	0.048	0.820	0.086	0.772	0.175
AD-1290517.1	0.443	0.038	0.508	0.035	0.908	0.157
AD-1291001.1	0.214	0.024	0.423	0.052	0.874	0.134
AD-1290805.1	0.927	0.033	0.863	0.094	0.948	0.152
AD-1290655.1	0.926	0.058	0.999	0.085	0.902	0.068
AD-1290574.1	0.978	0.105	0.874	0.046	0.826	0.069
AD-1290533.1	0.937	0.105	0.788	0.035	0.885	0.090
AD-1290530.1	0.127	0.007	0.230	0.022	0.731	0.057

Duplex Name	KHK/gapdh					
	10 nM		1 nM		0.1 nM	
	mean	SD	mean	SD	mean	SD
AD-1290523.1	0.997	0.162	0.713	0.015	0.937	0.168
AD-1290904.1	0.465	0.035	0.660	0.132	0.973	0.114
AD-1290796.1	0.944	0.075	0.734	0.131	0.936	0.147
AD-1290684.1	1.012	0.060	0.678	0.064	0.957	0.197
AD-1290611.1	0.201	0.009	0.224	0.023	0.781	0.084
AD-1290602.1	0.927	0.141	0.648	0.089	1.032	0.068
AD-1290563.1	0.839	0.111	0.650	0.045	1.135	0.189
AD-1290961.1	0.289	0.029	0.473	0.028	0.923	0.133
AD-1290923.1	0.137	0.005	0.280	0.038	0.771	0.071
AD-1290880.1	0.913	0.055	0.859	0.098	0.855	0.084
AD-1290712.1	0.942	0.014	0.729	0.038	0.935	0.078
AD-1290626.1	0.730	0.044	0.705	0.068	0.991	0.097
AD-1290539.1	0.121	0.012	0.166	0.041	0.609	0.026
AD-1290531.1	0.909	0.182	0.781	0.132	1.007	0.135
AD-1290670.1	0.973	0.038	0.790	0.179	1.075	0.159
AD-1290654.1	0.921	0.046	0.798	0.151	1.175	0.185
AD-1290615.1	0.918	0.026	0.772	0.081	1.243	0.213
AD-1290591.1	0.096	0.006	0.163	0.012	0.767	0.159
AD-1290879.1	0.209	0.012	0.478	0.021	0.920	0.147
AD-1290763.1	0.665	0.047	0.752	0.030	0.810	0.057
AD-1290680.1	0.092	0.013	0.198	0.018	0.759	0.050
AD-1290643.1	0.708	0.049	0.770	0.033	0.873	0.029
AD-1290573.1	0.585	0.040	0.744	0.034	0.909	0.065
AD-1290764.1	0.607	0.049	0.788	0.031	1.020	0.087
AD-1290687.1	0.646	0.032	0.894	0.092	1.038	0.155
AD-1290579.1	0.118	0.007	0.456	0.015	1.022	0.022
AD-1290977.1	0.688	0.059	0.950	0.061	1.176	0.120
AD-1290955.1	0.172	0.011	0.269	0.025	0.963	0.125
AD-1290894.1	0.864	0.038	0.804	0.051	0.997	0.068
AD-1290722.1	0.822	0.068	0.839	0.044	0.907	0.040
AD-1290692.1	0.106	0.011	0.192	0.022	0.840	0.025
AD-1290835.1	0.384	0.030	0.692	0.019	0.975	0.135
AD-1290730.1	0.246	0.020	0.491	0.022	0.990	0.131
AD-1290693.1	0.553	0.051	0.740	0.120	1.105	0.191
AD-1290682.1	0.250	0.020	0.348	0.036	0.884	0.105
AD-1290635.1	0.765	0.068	0.800	0.075	1.070	0.110
AD-1290525.1	0.128	0.019	0.203	0.019	0.958	0.069
AD-1290984.1	0.411	0.044	0.685	0.045	0.754	0.043
AD-1290942.1	0.474	0.024	0.586	0.037	0.673	0.103
AD-1290841.1	0.995	0.059	0.960	0.049	0.767	0.029
AD-1290719.1	0.887	0.047	0.789	0.043	0.913	0.113

Duplex Name	KHK/gapdh					
	10 nM		1 nM		0.1 nM	
	mean	SD	mean	SD	mean	SD
AD-1290708.1	0.751	0.032	0.794	0.046	0.980	0.136
AD-1290627.1	0.222	0.018	0.309	0.132	0.986	0.113
AD-1290624.1	0.828	0.027	0.737	0.053	0.899	0.140
AD-1290560.1	0.145	0.005	0.213	0.021	0.854	0.151
AD-1290993.1	1.013	0.140	0.825	0.053	1.298	0.137
AD-1290988.1	0.433	0.023	0.650	0.031	1.274	0.288
AD-1290863.1	0.856	0.088	0.914	0.050	0.916	0.041
AD-1290836.1	0.818	0.080	0.906	0.072	0.922	0.124
AD-1290663.1	0.247	0.019	0.496	0.025	1.019	0.180
AD-1290549.1	0.126	0.009	0.263	0.019	0.885	0.056
AD-1290931.1	1.106	0.034	0.850	0.043	1.057	0.104
AD-1290926.1	1.096	0.033	0.849	0.016	0.934	0.044
AD-1290909.1	1.023	0.042	0.776	0.065	0.935	0.089
AD-1290875.1	0.982	0.074	0.704	0.047	0.943	0.096
AD-1290867.1	1.168	0.044	0.798	0.033	1.048	0.189
AD-1290803.1	0.646	0.007	0.569	0.021	0.852	0.263
AD-1290748.1	0.830	0.098	0.901	0.126	1.229	0.126
AD-1290609.1	0.822	0.087	0.808	0.259	1.227	0.116
AD-1290556.1	0.915	0.043	0.826	0.240	1.251	0.124
AD-1290507.1	0.927	0.080	0.691	0.130	1.342	0.077
Neg ctrl	1.130	0.343	0.981	0.222	0.863	0.237
Neg ctrl	0.897	0.088	1.089	0.141	1.102	0.113
Pos ctrl	0.091	0.013	0.101	0.008	0.196	0.037

Example 3. Design, Synthesis and *In Vitro* Screening of Additional dsRNA Duplexes

Additional siRNAs were designed, synthesized, and prepared using methods known in the art and described above in Example 1.

Detailed lists of the additional unmodified KHK sense and antisense strand nucleotide sequences are shown in Table 5. Detailed lists of the modified KHK sense and antisense strand nucleotide sequences are shown in Table 6.

For transfections, Hep3b cells (ATCC, Manassas, VA) were grown to near confluence at 37°C in an atmosphere of 5% CO₂ in Eagle's Minimum Essential Medium (Gibco) supplemented with 10% FBS (ATCC) before being released from the plate by trypsinization. Transfection was carried out by adding 7.5 µl of Opti-MEM plus 0.1 µl of Lipofectamine RNAiMax per well (Invitrogen, Carlsbad CA, cat # 13778-150) to 2.5 µl of each siRNA duplex to an individual well in a 384-well plate. The mixture was then incubated at room temperature for 15 minutes. Forty µl of complete growth media without antibiotic containing ~1.5 x10⁴ Hep3b cells were then added to the siRNA

mixture. Cells were incubated for 24 hours prior to RNA purification. Single dose experiments were performed at 10 nM final duplex concentration.

Total RNA isolation was performed using DYNABEADS. Briefly, cells were lysed in 10µl of Lysis/Binding Buffer containing 3 µL of beads per well and mixed for 10 minutes on an electrostatic shaker. The washing steps were automated on a Biotek EL406, using a magnetic plate support. Beads were washed (in 3µL) once in Buffer A, once in Buffer B, and twice in Buffer E, with aspiration steps in between. Following a final aspiration, complete 12µL RT mixture was added to each well, as described below.

For cDNA synthesis, a master mix of 1.5µl 10X Buffer, 0.6µl 10X dNTPs, 1.5µl Random primers, 0.75µl Reverse Transcriptase, 0.75µl RNase inhibitor and 9.9µl of H₂O per reaction were added per well. Plates were sealed, agitated for 10 minutes on an electrostatic shaker, and then incubated at 37 degrees C for 2 hours. Following this, the plates were agitated at 80 degrees C for 8 minutes.

RT-qPCR was performed as described above and relative fold change was calculated as described above.

The results of the transfection assays of the dsRNA agents listed in Tables 5 and 6 in Hep3b cells are shown in Table 7.

Table 8 provides a list of the unmodified KHK sense and antisense strand nucleotide sequences of selected dsRNA agents. Table 9 provides a list of the modified KHK sense and antisense strand nucleotide sequences of selected dsRNA agents.

Table 5. Unmodified Sense and Antisense Strand Sequences of KHK dsRNAs

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO	Range in XM_017004061.1	Antisense Sequence 5' to 3'	SEQ ID NO	Range in XM_017004061.1
AD-1423310.1	UUUGAGAAAGGUUGAUCUGACU	1140	760-780	AGUCAGAUCAACCUUCUCAAAGU	296	758-780
AD-1423311.1	GACGUGGUGUUUGUCAGCAAU	222	946-966	AUUGCUGACAAAACACACGUCUC	446	944-966
AD-1423312.1	UGCAGGAAGCACUGAGAUUCU	115	1208-1228	AGAATCTCAGUGCUUCCUGCAG	1141	1206-1228
AD-1423313.1	ACAGACUUUGAGAAAGGUUGAU	67	754-774	AUCAACCUUCUCAAGUCUUGAG	291	752-774
AD-1423314.1	GCUACAGACUUUGAGAAGGUU	65	751-771	AACCTUCUCAAAAGUCUGUAGCAG	1142	749-771
AD-1423315.1	ACCCAGUUCAAGUGGAUCCAU	79	778-798	AUGGAUCCACUUGAACUGGGUCA	303	776-798
AD-1423316.1	UCAGAGCAAUAUAUCUUCU	22	1336-1356	AGGAAGAUUUAUUUGCUCUGAGG	246	1334-1356
AD-1290665.2	AGAGCAAUAUAUCUUCUUCU	212	1477-1497	AGAGGAAGAUAUUUUUGCUCUGA	436	1475-1497
AD-1423317.1	CUUUGAGAAAGGUUGAUCUGAU	71	759-779	AUCAGATCAACCUUCUCAAAAGUC	1143	757-779
AD-1423318.1	AUGGAAGAGAAAGCAGAUCCUU	52	523-543	AAGGAUCUGCUUCUUCUCCAUUA	276	521-543
AD-1423319.1	GACUUUGAGAAAGGUUGAUCUU	70	757-777	AAGATCAACCUUCUCAAAAGUCUG	1144	755-777
AD-1423320.1	CUCAGAGCAAUAUAUCUUCU	122	1474-1494	AGAAGATUUAUUUGCUCUGAGGC	1145	1472-1494
AD-1423321.1	CUCUUCCAGCUGUUUGGCUAU	88	922-942	AUAGCCAAACAGCUGGAAGAGCU	312	920-942
AD-1423322.1	GAGCUGGAGACACCUUCAAUU	104	1151-1171	AAUUGAAGGUGUCUCCAGCUCUCC	328	1149-1171
AD-1423323.1	CAAUGCCUCCGUCUACUUCU	111	1167-1187	AUGAAGAUACGAGGAGGCAUUGAA	335	1165-1187
AD-1423324.1	CCUUCAAUGCCUCCGUCUACU	109	1163-1183	AGAUGACGGAGGCAUUGAAGGUG	333	1161-1183
AD-1423325.1	CUGCUACAGACUUUGAGAAAGU	63	749-769	ACUUCUCAAAAGUCUGUAGCAGAC	287	747-769
AD-1423326.1	AAAGAUUGGGCCAAAGCACUUU	99	964-984	AAAGTGCUUGGGCCACAUUUUUGC	1146	962-984
AD-1423327.1	AAGGUUGAUCUGACCCAGUUU	73	766-786	AAACTGGGUCAGAUCAACCUUCU	1147	764-786
AD-1423328.1	AAGGUGUUUGUCCAGAGAUU	60	612-632	AAUCTCTGGGACAAACACCUUAU	1148	610-632
AD-1423329.1	GAAGAGAAGCAGAUCCUGUGU	54	526-546	ACACAGGAUCUGCUUUCUCCUCCA	278	524-546
AD-1423330.1	GUGUUUGUCAGCAAAAGAUUGU	95	952-972	AACATCTUUGCUGACAAAACACCA	1149	950-972
AD-1423331.1	GACAAAGUACCCUAAGGAGGAU	57	583-603	AUCCCTCCUUAGGGUACUUGUCCA	1150	581-603
AD-1423332.1	GUGCAGGAAGCACUGAGAUUU	114	1207-1227	AAAUUCAGUGCUUCCUGCACGC	338	1205-1227
AD-1290878.2	GGAGACGUGGUGUUUGUCAGU	92	943-963	ACUGACAAACACACGUCUCCGU	316	941-963
AD-1423334.1	CCUCAUGGAAGAGAAAGCAGAU	50	519-539	AUCUGCTUCUCUCCAUAGAGGCU	1151	517-539

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO	Range in XM_017004061.1	Antisense Sequence 5' to 3'	SEQ ID NO	Range in XM_017004061.1
AD-1423335.1	CUCCGUAUCUUCAGCCUCUU	113	1173-1193	AAGAGGCUAGAGAACGGAGGC	337	1171-1193
AD-1423336.1	GUUCAAGUGGAUCCACAUUGU	207	783-803	ACAATGTGGAUCCACUUGAACUG	1152	781-803

Table 6. Modified Sense and Antisense Strand Sequences of KHK dsRNAs

Duplex Name	Sense sequence 5' to 3'	SEQ ID NO:	Antisense sequence 5' to 3'	SEQ ID NO:	mRNA target sequence	SEQ ID NO:
AD-1423310.1	ususugagAfaGfGfUfugaucugacuL9 6	1153	asGfsuadAg(Agn)ucaaccUfuCfuaaaagsu	1154	ACUUUGAGAAAGGUUGAUCUGAC C	968
AD-1423311.1	gsasegugGfuGfUfufugueageacuL9 6	670	asUfsugdCu(G2p)acaaccAfcCfagguetsuc	1155	GAGACGUGGUUUUGUCAGCAA A	1118
AD-1423312.1	usgscaggAfaGfCfAfcugagaauL9 6	563	asGfsaadTc(Tgn)cagugeUfuCfcugcascsg	1156	CGUGCAGGAAGCACUGAGAUUC G	1011
AD-1423313.1	ascagacUfuUfGfAfgaagguL9 6	515	asUfscadAc(C2p)uueucaAfaGfucugusag	1157	CUACAGACUUUGAGAAAGGUUGA U	963
AD-1423314.1	gscsuacaGfaCfuUfufugagaagguL9 6	513	asAfscedTu(C2p)ucaaaagUfcUfguagcsag	1158	CUGCUACAGACUUUGAGAAAGGU U	961
AD-1423315.1	ascscagUfuCfAfAfguggaucL9 6	527	asUfsggdAu(C2p)cacungAfaCfuggguL9 6	1159	UGACCCAGUUCAAAGUGGAUCCA C	975
AD-1423316.1	uscsagagCfaAfaUfaaaucuuL9 6	470	asGfsagadAg(Agn)uuuuuuUfgCfucugags	1160	CCUCAGAGCAAUAUAAAUUUUCC U	918
AD-1290665.2	asgsagcaAfaUfAfAfaucuuL9 6	660	asGfsaggAfaaaauuUfuUfgcucugsa	884	UCAGAGCAAUAUAAAUUUUCCUC A	1108
AD-1423317.1	csusuugaGfaAfgGfGfugaucugauL9 6	519	asUfscadGa(Tgn)caaccuUfcUfcaaaagsuc	1161	GACUUUGAGAAAGGUUGAUCUGA C	967
AD-1423318.1	asusggaaGfaGfAfAfgcagaucL9 6	500	asAfsaggAu(C2p)ugcuucUfcUfuccausgsa	1162	UCAUGGAAGAGAAAGCAGAUCCU G	948
AD-1423319.1	gsascuunGfaGfAfAfgguugauL9 96	518	asAfsagdTc(Agn)accuucUfcAfaaguetug	1163	CAGACUUUGAGAAAGGUUGAUCU G	966
AD-1423320.1	csuscagaGfcAfAfAfuaaaucuuL9 6	570	asGfsaadGa(Tgn)uuuuuuGfcUfcugagsgsc	1164	GCCUCAGAGCAAUAUAAAUUUUCC C	1018
AD-1423321.1	csuscuucCfaGfCfUfguuugcuL9 6	536	asUfsagdTc(Agn)aacagcUfgGfaagagscu	1165	AGCUCUUUCCAGCUGUUUUGGCUA C	984
AD-1423322.1	gsasgcugGfaGfAfCfaccuucL9 6	552	asAfsuadGa(Agn)ggugucUfcCfagcucsc	1166	GGGAGCUGGAGACACCUUUAU C	1000

Duplex Name	Sense sequence 5' to 3'	SEQ ID NO:	Antisense sequence 5' to 3'	SEQ ID NO:	mRNA target sequence	SEQ ID NO:
AD-1423323.1	6 csasaugeCfuCfCfGfuaucucuaL9	559	asUfsgadAg(Agn)uagcggAfgGfcauugsas a	1167	G UUCAAUUGCCUCCGUAUCUUA	1007
AD-1423324.1	6 cscsucaAfuGfCfCfuecguaucL9	557	asGfsaudGfa(C2p)ggagcAfuUfgaaggsus g	1168	U CACCUCAAUGCCUCCGUAUC	1005
AD-1423325.1	6 csusgcuACfaGfAfCfuuuagagaL9	511	asCfsuudCu(C2p)aaagucUfgUfagcagsase	1169	G GUCUGCUACAGACUUAUGAGAAG	959
AD-1423326.1	6 asasagauGfuGfGfCfcaagcagauL9	547	asAfsagdTg(C2p)uuaggccAfcAfucuuusgsc	1170	G GCAAAGAUUGGGCCAAAGCACUU	995
AD-1423327.1	6 asasgguuGfaUfCfUfagaccagauL9	521	asAfsaedTg(G2p)guacagaUfcAfaccuuuscsu	1171	C AGAAGGUUGAUCUGACCCAGUU	969
AD-1423328.1	6 gsasagagAfaGfCfAfgaucucugauL9	508	asAfsuedTc(Tgn)ggggacaAfaCfaccuuasasu	1172	G AUAAAGGUUGUUGUCCCCAGAGAU	956
AD-1423329.1	6 gsusguuuGfuCfAfGfcaagauL9	502	asCfsaedAg(G2p)auucigeUfuCfucuuuscsa	1173	C UGGAAGAGAAAGCAGAUCCUGUG	950
AD-1423330.1	6 gsascaagUfaCfCfCfuaaggaggauL9	543	asAfsaedTc(Tgn)uuugcugAfcAfaacacscsa	1174	G UGGUGUUUGUCAGCAAAAGAUGU	991
AD-1423331.1	6 gsusgcagGfaAfGfCfagagagauL9	505	asUfscedTc(C2p)uuagggUfaCfuuugucscsa	1175	C UGGACAAAGUACCCUAAAGGAGGA	953
AD-1423332.1	6 gsusgcagGfaAfGfCfagagagauL9	562	asAfsaudCu(C2p)agugcuUfcCfugcacsagsc	1176	C GCGUGCAGGAAGCACUGAGAUU	1010
AD-1290878.2	96 gsusgcagGfuGfGfUfguuuugueagL	540	asCfsugaCfaaacaccAfcGfucuecsesu	764	C ACGGAGACGUGGUGUUUUGUCAG	988
AD-1423334.1	6 cscsucuuGfGfAfAfGfagagagagauL9	498	asUfscudGc(Tgn)ucucuuCfcAfugaggscsu	1177	U AGCCUCAUGGAAGAGAAAGCAGA	946
AD-1423335.1	6 csusecguCfaUfCfUfucagccuL9	561	asAfsagdGg(C2p)uugaagaUfgAfcggagsgsc	1178	C GCCUCCGUAUCUUCAGCCUCU	1009
AD-1423336.1	6 gsusucuuGfuGfGfAfuccacauL9	655	asCfsaadTg(Tgn)ggauccAfcUfugaacsusg	1179	A CAGUUCAAAGUGGAUCCACAUUG	1103

Table 7. KHK Single Dose Screen in Hep3b cells

Duplex Name	% Message Remaining (qPCR)
AD-1423317	9.38
AD-1423327	7.75
AD-1423336	7.70
AD-1423311	6.06
AD-1423320	21.59
AD-1423324	10.44
AD-1423329	12.28
AD-1423333	9.09
AD-1423330	8.78
AD-1423310	6.66
AD-1423314	8.66
AD-1423316	10.59
AD-1423322	18.97
AD-1423325	16.15
AD-1423334	10.71
AD-1423312	12.77
AD-1423313	9.33
AD-1423315	7.66
AD-1423318	13.43
AD-1423319	8.34
AD-1423321	11.82
AD-1423323	9.65
AD-1423326	5.15
AD-1423328	22.84
AD-1423331	13.21
AD-1423332	10.54
AD-1423335	8.60

Table 8. Unmodified Sense and Antisense Strand Sequences of KHK dsRNAs

Duplex Name	Sense sequence 5' to 3'	SEQ ID NO:	Source Name	Range in GenBank Source Name	Antisense sequence 5' to 3'	SEQ ID NO:	Range in GenBank Source Name
AD-1290757.3	GUUGAUCUGACCCAGUUCAAU	1180	XM_017004061.1_769-789_G21U_s	769-789	AUUGAACUGGGUCAGAUCAACCU	298	767-789
AD-1290878.3	GGAGACGUGGUGUUUUGUCAGU	92	XM_017004061.1_943-963_C21U_s	943-963	ACUGACAAACACCCACGUCUCCGU	316	941-963
AD-1290969.3	ACCUCAAUAGCCUCCGCAU	108	XM_017004061.1_1162-1182_C21U_s	1162-1182	AAUGACGGAGGCAUUGAAGGUGU	332	1160-1182
AD-1423317.2	CUUUGAGAAAGGUUGAUCUGAU	71	XM_017004061.1_759-779_C21U_s	759-779	AUCAGATCAACCUUCUCAAAGUC	1143	757-779
AD-1423327.2	AAGGUUGAUCUGACCCAGUUU	73	XM_017004061.1_766-786_C21U_s	766-786	AAACTGGGUCAGAUCAACCUUCU	1147	764-786
AD-1423336.2	GUUCAAGUGGAUCCACAUUGU	207	XM_017004061.1_950-970_G21U_s	783-803	ACAAATGTGGAUCCACUUGAACUG	1152	781-803
AD-1290599.3	UGGUGUUUGUCAGCAAAAGAUU	93	XM_017004061.1_950-970_G21U_s	950-970	AAUCUUUGCUGACAAACACACG	317	948-970
AD-1523172.1	UGGUGUUUGUCAGCAAAAGAUU	93	XM_017004061.1_950-970_G21U_s	950-970	AAUCTUUGCUGACAAACACACG	1182	948-970
AD-1290837.3	UGAUCUGACCCAGUUCAAAGUU	76	XM_017004061.1_771-791_G21U_s	771-791	AACUUGAACUGGGUCAGAUCAAC	300	769-791
AD-1523173.1	UGAUCUGACCCAGUUCAAAGUU	76	XM_017004061.1_771-791_G21U_s	771-791	AACUTGAACUGGGUCAGAUCAAC	1183	769-791
AD-1290884.3	GCAGGAAGCACUGAGAUUCGU	116	XM_017004061.1_1209-1229_G21U_s	1209-1229	ACGAAUCUCAGUGCUUCCUGCAC	340	1207-1229
AD-1523174.1	GCAGGAAGCACUGAGAUUCGU	116	XM_017004061.1_1209-1229_G21U_s	1209-1229	ACGAAUCUCAGUGCUUCCUGCAC	340	1207-1229
AD-1290959.3	UUGAUCUGACCCAGUUCAAAGU	75	XM_017004061.1_770-790_s	770-790	ACUUGAACUGGGUCAGAUCAACC	299	768-790
AD-1523175.1	UUGAUCUGACCCAGUUCAAAGU	75	XM_017004061.1_770-790_s	770-790	ACUUGAACUGGGUCAGAUCAACC	299	768-790
AD-1423311.2	GACGUGGUGUUUGUCAGCAAU	222		946-966	AUUGCUGACAAACACACGUCUC	446	944-966
AD-1423324.2	CCUUCAAUGCCUCCGCAUCU	109	XM_017004061.1_1163-1183_s	1163-1183	AGAUGACGGAGGCAUUGAAGGUG	333	1161-1183
AD-1523176.1	CCUUCAAUGCCUCCGCAUCU	109	XM_017004061.1_1163-1183_s	1163-1183	AGAUGACGGAGGCAUUGAAGGUG	333	1161-1183

Duplex Name	Sense sequence 5' to 3'	SEQ ID NO:	Source Name	Range in GenBank Source Name	Antisense sequence 5' to 3'	SEQ ID NO:	Range in GenBank Source Name
AD-1423329.2	GAAGAGAAAGCAGAUCCUGUGU	54	XM_017004061.1_526-546_C21U_s	526-546	ACACAGGAUCUGCUUCUUCUCCA	278	524-546
AD-1423333.2	GUGGUGUUUGUCAGCAAGAAU	1181	XM_005264298.1_812-830_s	810-830	AUCUTUGCUGACAAAACACACGU	1184	808-830
AD-1423330.2	GUGUUUGUCAGCAAGAAU	95	XM_017004061.1_952-972_G21U_s	952-972	AACATCTUUGCUGACAAAACACCA	1149	950-972
AD-1523177.1	GUGUUUGUCAGCAAGAAU	95	XM_017004061.1_952-972_G21U_s	952-972	AACATCTUUGCUGACAAAACACCA	1185	950-972
AD-1290885.3	CUGACCCAGUUCAGGUAU	78	XM_017004061.1_775-795_C21U_s	775-795	AAUCCACUUGAACUGGGGUCAGAU	302	773-795
AD-1523178.1	CUGACCCAGUUCAGGUAU	78	XM_017004061.1_775-795_C21U_s	775-795	AAUCCACUUGAACUGGGGUCAGAU	302	773-795
AD-1423334.2	CCUCAUGGAAGAGAGCAGAU	50	XM_017004061.1_519-539_s	519-539	AUCUGCTUCUCUCCAUAGAGGCU	1151	517-539
AD-1523179.1	CCUCAUGGAAGAGAGCAGAU	50	XM_017004061.1_519-539_s	519-539	AUCUGCTUCUCUCCAUAGAGGCU	274	517-539
AD-1523180.1	CCUCAUGGAAGAGAGCAGAU	50	XM_017004061.1_519-539_s	519-539	AUCUGCTUCUCUCCAUAGAGGCU	1151	517-539
AD-1290539.3	CAGACUUUGAGAGGUUGAU	68	XM_017004061.1_755-775_C21U_s	755-775	AAUCAAACCUUCUCAAAAGUCUGUA	292	753-775
AD-1523181.1	CAGACUUUGAGAGGUUGAU	68	XM_017004061.1_755-775_C21U_s	755-775	AAUCAAACCUUCUCAAAAGUCUGUA	292	753-775

Table 9. Modified Sense and Antisense Strand Sequences of KHK dsRNAs

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:	mRNA Target Sequence	SEQ ID NO:
AD-1290757.3	gsusugauCfuGfAfCfccaguucauL9 6	1186	asUfsugaAfcugggucAfgAfucaacsu	746	AGGUUGAUCUGACCCAGUUCAG	970
AD-1290878.3	gsgsagacGfuGfGfUfguuugucaguL9 6	540	asCfsugaCfaaacaceAfcGfucuccgsu	764	ACGGAGACGUGGUGUUUGUCAGC	988
AD-1290969.3	ascsuucAfaUfGfCfcuccgucuuL9 6	556	asAfsugaCfaggagcaUfuGfaaggugsu	780	ACACCUUCAAUGCCUCCGUCUAC	1004
AD-1423317.2	csusuugaGfaAfGfGfUfguugaucuL9 6	519	asUfscadGa(Tgm)caaccuUfeUfcaags usc	1161	GACUUUGAGAGGUUGAUCUGAC	967
AD-1423327.2	asasgguuGfaUfCfUfgaccaguuL9 6	521	asAfsacdTg(G2p)guccagaUfcAfaccuu scsu	1171	AGAAAGGUUGAUCUGACCCAGUUC	969

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:	mRNA Target Sequence	SEQ ID NO:
AD-1423336.2	gsusuaaGfuGfAfuccaauuuL9 6	655	asCfsaadTg(Tgn)ggaucAfcUfugaac susg	1179	CAGUUC AAGUGGAUCCACAUUGA	1103
AD-1290599.3	usgsuguuUfuGfUfCfagcaagaauL9 6	541	asAfsuauUfugucgacAfaAfacacascg asAfsuadTu(U2p)gcugacAfaAfacca scsg	765 1188	CGUGGUGUUUGUCAGCAAAAGAUG CGUGGUGUUUGUCAGCAAAAGAUG	989 989
AD-1290837.3	usgsauauGfaCfCfCfaguucaaguL9 6	524	asAfsuauGfaucugggUfcAfgaucasac asAfsuadTg(A2p)acugggUfcAfgauca sasc	748 1189	GUUGAUCUGACCCAGUUC AAGUG GUUGAUCUGACCCAGUUC AAGUG	972 972
AD-1290884.3	gscsaggaAfgCfAfCfugagaauuL9 6	564	asCfsgaaUfucagugCfuUfcucgcsac asCfsgadAu(C2p)ucagugCfuUfcucgc sasc	788 1190	GUGCAGGAAGCACUGAGAUUCGG GUGCAGGAAGCACUGAGAUUCGG	1012 1012
AD-1290959.3	usgsauauUfgAfCfCfCfaguucaaguL9 6	523	asCfsuugAfacuggguCfaGfaucasac asCfsuudGa(A2p)cuggguCfaGfaucac sasc	747 1191	GGUUGAUCUGACCCAGUUC AAGU GGUUGAUCUGACCCAGUUC AAGU	971 971
AD-1423311.2	gsascgugGfuGfUfUfugucagcauuL9 6	670	asUfsgudCu(G2p)acaaacAfcCfaguc susc	1155	GAGACGUGGUGUUUGUCAGCAAA	1118
AD-1423324.2	csesuuaAfuGfCfCfuccgucacuuL9 6	557	asGfsaudGa(C2p)ggaggcAfuUfgaag gsusg	1168	CACCUUCA AUGCCUCCGUC AUCU	1005
AD-1523176.1	gsasagagAfaGfCfAfgauccuguuL9 6	557	asGfsaudGa(Cgn)ggaggcAfuUfgaag gsusg	1192	CACCUUCA AUGCCUCCGUC AUCU	1005
AD-1423329.2	gsusggugUfuUfGfUfCfagcaagaauL9 6	502	asCfsaadAg(G2p)aucugcUfuCfucuc scsa	1173	UGGAAGAGAAAGCAGAUCCUGUC	950
AD-1423333.2	gsusggugUfuUfGfUfCfagcaagaauL9 6	468	asUfscudTu(G2p)cugacaAfaCfaccac sgsu	1193	ACGUGGUGUUUGUCAGCAAAAGAU	916
AD-1423330.2	gsusggugUfuUfGfUfCfagcaagaauL9 6	543	asAfsuadTc(Tgn)uugcugAfaAfaacac scsa	1174	UGGUGUUUGUCAGCAAAAGAUGUG	991
AD-1523177.1	gsusggugUfuUfGfUfCfagcaagaauL9 6	543	asAfsuadTc(U2p)uugcugAfaAfaacac scsa	1194	UGGUGUUUGUCAGCAAAAGAUGUG	991
AD-1290885.3	csusgaccCfaGfUfUfcaaguggauL9 6	526	asAfsuacAfeuagacUfgGfugcagsu asAfsuadCa(C2p)uugaacUfgGfugcag	750 1195	AUCUGACCCAGUUC AAGUGGAUC AUCUGACCCAGUUC AAGUGGAUC	974 974

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:	mRNA Target Sequence	SEQ ID NO:
	6		sasu			
AD-1423334.2	csesucuuGfgAfAfGfagaagcagauL9 6	498	asUfscudGc(Tgn)ucucuuCfcAfugagg scsu	1177	AGCCUCAUGGAAGAGAAAGCAGAU	946
AD-1523179.1	csesucuuGfgAfAfGfagaagcagauL9 6	498	asUfscudGc(U2p)ucucuuCfcAfugag gscsu	1196	AGCCUCAUGGAAGAGAAAGCAGAU	946
AD-1523180.1	csesucuuGfgAfAfGfagaagcagauL9 6	498	asUfscudGcdTucucuuCfcAfugaggsc su	1197	AGCCUCAUGGAAGAGAAAGCAGAU	946
AD-1290539.3	csasgacuUfuGfAfGfaagguuL9 6	516	asAfsucaAfcuucucAfaAfgucugsusa asAfsucdAa(C2p)cucucAfaAfgucug	740	UACAGACUUUUGAGAAAGGUUGAUC	964
AD-1523181.1	csasgacuUfuGfAfGfaagguuL9 6	516	susa	1198	UACAGACUUUUGAGAAAGGUUGAUC	964

Example 4. Design, Synthesis and In Vitro Screening of Additional dsRNA Duplexes

Additional siRNAs were designed, synthesized, and prepared using the methods described above in Example 1.

Detailed lists of the additional unmodified KHK sense and antisense strand nucleotide sequences are shown in Table 10. Detailed lists of the modified KHK sense and antisense strand nucleotide sequences are shown in Table 11.

Table 10. Unmodified Sense and Antisense Strand Sequences of KHK dsRNA

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Range in XM_017004061.1	Antisense Sequence 5' to 3'	SEQ ID NO:	Range in XM_017004061.1
AD-1290969	ACCUCAAUUGCCUCCGUCAUU	1199	1162-1182	AAUGACGGAGGCAUUGAAAGGUGU	332	1160-1182
AD-1423310	UUUGAGAAAGGUUGAUCUGACU	72	760-780	AGUCAGAUCAACCUUCUCAAAAGU	296	758-780
AD-1423311	GACGUGGUGUUUGUCAGCAAU	222	946-966	AUUGCUGACAAACACACACGUCUC	446	944-966
AD-1423312	UGCAGGAAGCACUCUGAGAUUCU	115	1208-1228	AGAATCTCAGUGCUUCCUGCACG	1141	1206-1228
AD-1423317	CUUUGAGAAAGGUUGAUCUGAU	71	759-779	AUCAGATCAACCUUCUCAAAAGUC	1143	757-779
AD-1423319	GACUUUGAGAAAGGUUGAUCUU	70	757-777	AAGATCAACCUUCUCAAAAGUCUG	1144	755-777
AD-1423323	CAUUGCCUCCGUCAUUCUUAU	111	1167-1187	AUGAAGAUGACGGAGGCAUUGAA	335	1165-1187
AD-1423327	AAGGUUGAUCUGACCCAGUUU	73	766-786	AAACTGGGUCAGAUCAACCUUCU	1147	764-786
AD-1423329	GAAGAGAAAGCAGAUCCUGUGU	54	526-546	ACACAGGAUCUGCUUCUCUUCCA	278	524-546
AD-1423330	GUGUUUGUCAGCAAAAGAUUU	95	952-972	AACATCTUUGCUGACAAACACCCA	1149	950-972
AD-1423333	GUGGUGUUUUGUCAGCAAAAGAU	20	949-969	AUCUTUGCUGACAAACACACCGU	1184	947-969
AD-1423334	CCUCAUGGAAAGAGAAAGCAGAU	50	519-539	AUCUGCTUCUCUUCCAUGAGGCU	1151	517-539
AD-1423336	GUUCAAGUGGAUCCACAUUUGU	207	783-803	ACAATGTGGAUCCACUUGAACUG	1152	781-803
AD-1523180	CCUCAUGGAAAGAGAAAGCAGAU	50	519-539	AUCUGCTUCUCUUCCAUGAGGCU	1151	517-539
AD-1548743	UGGUGUUUUGUCAGCAAAAGAUU	93	950-970	AAUCTUTGCUGACAAACACCCACG	1269	948-970
AD-	GCCUCAUGGAAAGAGAAAGCAGU	1200	518-538	ACUGCUTCUCUTCCAUGAGGGCUA	1270	516-538

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Range in XM_017004061.1	Antisense Sequence 5' to 3'	SEQ ID NO:	Range in XM_017004061.1
1612957						
AD- 1612958	CCUCAUGGAAGAGAGCAGAU	50	519-539	ATCUGCTUCUCTUCCAUGAGGCU	1271	517-539
AD- 1612963	UGGAAGAGAAAGCAGAUCCUGU	1201	524-544	ACAGGATCUGCTUCUCUCCCAUG	1272	522-544
AD- 1612967	AGAGAAAGCAGAUCCUGUGCGU	1202	528-548	ACGCACAGGAUCUGCUUCUCUUC	1273	526-548
AD- 1612969	AGAAAGCAGAUCCUGUGCGUGU	1203	530-550	ACACGCACAGGAUCUGCUUCUCU	1274	528-550
AD- 1612970	GAAGCAGAUCCUGUGCGUGGU	1204	531-551	ACCACGCACAGGAUCUGCUUCUC	1275	529-551
AD- 1613059	CAGACUUUGAGAAAGGUUGAUU	68	755-775	AAUCAACCUUUCTCAAAGUCUGUA	1276	753-775
AD- 1613060	AGACUUUGAGAAAGGUUGAUUCU	69	756-776	AGAUAACCUUUCUCAAAGUCUGU	293	754-776
AD- 1613062	ACUUUGAGAAAGGUUGAUUCUGU	213	758-778	ACAGAUCAACCTTUCUCAAAGUCU	1277	756-778
AD- 1613070	AAGGUUGAUUCUGACCCAGUUU	73	766-786	AAACTGGGUCAGAUCAACCUUCU	1147	764-786
AD- 1613073	GUUGAUCUGACCCAGUUCAAU	74	769-789	ATUGAACUGGGTCAAGAUCAACCU	1278	767-789
AD- 1613074	UUGAUCUGACCCAGUUCAAAGU	75	770-790	ACUUGAACUGGGUCAGAUCAACC	299	768-790
AD- 1613075	UGAUCUGACCCAGUUCAAAGUU	76	771-791	AACUTGAACUGGGUCAGAUCAAC	1183	769-791
AD- 1613076	GAUCUGACCCAGUUCAAAGUGU	77	772-792	ACACTUGAACUGGGUCAGAUCAA	1279	770-792
AD- 1613077	AUCUGACCCAGUUCAAAGUGGU	1205	773-793	ACCACUTGAACCTGGGUCAGAUCA	1280	771-793
AD- 1613079	CUGACCCAGUUCAAAGUGGAUU	78	775-795	AAUCCACUUGAACUGGGUCAGAU	302	773-795
AD- 1613088	UUCAAGUGGAUCCACAUUGAU	82	784-804	ATCAAUGUGGATCCACUUGAACU	1281	782-804
AD- 1613089	UCAAGUGGAUCCACAUUGAGU	83	785-805	ACUCAATGUGGAUCCACUUGAAC	1282	783-805

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Range in XM_017004061.1	Antisense Sequence 5' to 3'	SEQ ID NO:	Range in XM_017004061.1
1613089						
AD- 1613090	CAAGUGGAUCCACAUUGAGGU	84	786-806	ACCUCAAUGUGGAUCCACUUGAA	308	784-806
AD- 1613091	AAGUGGAUCCACAUUGAGGGU	1206	787-807	ACCCCTCAAUUGUGGAUCCACUUGA	1283	785-807
AD- 1613094	UGGAUCCACAUUGAGGGCCGU	1207	790-810	ACGGCCCUCAATGUGGAUCCACU	1284	788-810
AD- 1613095	GGAUCCACAUUGAGGGCCGU	1208	791-811	ACGGGCCCUCAAUUGUGGAUCCAC	1285	789-811
AD- 1613237	GUUUGGCUACGGAGACGUGGU	1209	933-953	ACCACGTCUCCGUAGCCAAACAG	1286	931-953
AD- 1613238	UUUGGCUACGGAGACGUGGU	1210	934-954	AACCACGUCUCCGUAGCCAAACA	1287	932-954
AD- 1613239	UUGGCUACGGAGACGUGGU	1211	935-955	ACACCACGUCUCCGUAGCCAAAC	1288	933-955
AD- 1613240	UGGCUACGGAGACGUGGU	1212	936-956	AACACCACGUCTCCGUAGCCAAA	1289	934-956
AD- 1613241	GGCUACGGAGACGUGGU	1213	937-957	AAACACCACGUCUCCGUAGCCAA	1290	935-957
AD- 1613242	GCUACGGAGACGUGGUUUU	242	938-958	AAACACCACGTCUCCGUAGCCA	1291	936-958
AD- 1613243	CUACGGAGACGUGGUUUUGU	89	939-959	ACAAACACCACGUCUCCGUAGCC	313	937-959
AD- 1613244	UACGGAGACGUGGUUUUGU	90	940-960	AACAAACACCACGUCUCCGUAGC	314	938-960
AD- 1613245	ACGGAGACGUGGUUUUGUCU	232	941-961	AGACAAACACCACGUCUCCGUAG	456	939-961
AD- 1613246	CGGAGACGUGGUUUUGUCAU	91	942-962	ATGACAAACACCACGUCUCCGUA	1292	940-962
AD- 1613247	GGAGACGUGGUUUUGUCAGU	92	943-963	ACUGACAAACACCACGUCUCCGU	316	941-963
AD- 1613254	UGGUGUUUUGUCAGCAAAAGAU	93	950-970	AAUCTUTGCUGACAAACACCACG	1269	948-970
AD-	GGUGUUUUGUCAGCAAAAGAU	94	951-971	ACAUCUTUGCUGACAAACACCAC	1293	949-971

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Range in XM_017004061.1	Antisense Sequence 5' to 3'	SEQ ID NO:	Range in XM_017004061.1
1613255						
AD-1613256	GUGUUUGUCAGCAAAAGAUGUU	95	952-972	AACATCTUUGCTGACAAACACCA	1294	950-972
AD-1613257	UGUUUGUCAGCAAAAGAUGUGU	96	953-973	ACACAUCUUUGCUGACAAACACC	320	951-973
AD-1613258	GUUUUGUCAGCAAAAGAUGUGGU	97	954-974	ACCACATCUUUGCUGACAAACAC	1295	952-974
AD-1613259	UUUGUCAGCAAAAGAUGUGGCU	98	955-975	AGCCACAUCUUTGCUGACAAACA	1296	953-975
AD-1613361	AGCUGGAGACACCCUUCAAUGU	105	1152-1172	ACAUTGAAGGUGUCUCCAGCUCC	1297	1150-1172
AD-1613362	GCUGGAGACACCUUCAAUGCU	1214	1153-1173	AGCATUGAAAGGTGUCUCCAGCUC	1298	1151-1173
AD-1613363	CUGGAGACACCUUCAAUGCCU	106	1154-1174	AGGCAUTGAAGGUGUCUCCAGCU	1299	1152-1174
AD-1613369	ACACCUUCAAUUGCCUCCGUCU	1215	1160-1180	AGACGGAGGCATUGAAGGUGUCU	1300	1158-1180
AD-1613370	CACCUUCAAUUGCCUCCGUCAU	1216	1161-1181	ATGACGGAGGCAUUGAAGGUGUC	1301	1159-1181
AD-1613371	ACCUUCAAUUGCCUCCGUCAUU	108	1162-1182	AAUGACGGAGGCAUUGAAGGUGU	332	1160-1182
AD-1613374	UUCAAUGCCUCCGUCUUCUUCU	110	1165-1185	AAAGAUGACGGAGGCAUUGAAGG	334	1163-1185
AD-1613377	AAUGCCUCCGUCUUCUUCAGU	112	1168-1188	ACUGAAGAUGACGGAGGCAUUGA	336	1166-1188
AD-1613378	AUGCCUCCGUCUUCUUCAGCU	1217	1169-1189	AGCUGAAGAUGACGGAGGCAUUG	1302	1167-1189
AD-1613395	AGCGUGCAGGAAGCACUCAGU	1218	1204-1224	ACUCAGTGUUCCUGCACGCUC	1303	1202-1224
AD-1613400	GCAGGAAGCACUGAGAUUCGU	116	1209-1229	ACGAAUCUCAGTGUUCCUGCAC	1304	1207-1229
AD-1613401	CAGGAAGCACUGAGAUUCGGU	1219	1210-1230	ACCGAATCUCAGUGCUUCCUGCA	1305	1208-1230
AD-	UAGCCUCAUGGAAGAGAGAGCU	1220	516-536	AGCUTCTCUUCCAUAGAGGCUACU	1306	514-536

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Range in XM_017004061.1	Antisense Sequence 5' to 3'	SEQ ID NO:	Range in XM_017004061.1
1634353						
AD- 1634354	GCCUCAUGGAAGAGAGCAGU	1200	518-538	ACUGCUTCUCUCCAUAGAGGCUA	1307	516-538
AD- 1634355	CAUGGAAGAGAGCAGAUCCU	1221	522-542	AGGATCTGCUUCUCUCCAUAGAG	1308	520-542
AD- 1634356	GGAAGAGAGAGCAGAUCCUGUU	53	525-545	AACAGGAUCUGCUUCUCUCCAU	277	523-545
AD- 1634357	AGAGAGCAGAUCCUGUGCGU	1202	528-548	ACGCACAGGAUCUGCUUCUCUUC	1273	526-548
AD- 1634358	AGACUUUGAGAGAGGUUGAUCU	69	756-776	AGAUCAAACCUUCUCAAAGUCUGU	293	754-776
AD- 1634359	UGAGAGGUUGAUCUGAGCCCU	1222	762-782	AGGGTCAGAUCAACCUUCUCAAA	1309	760-782
AD- 1634360	AGAGGUUGAUCUGAGCCAGU	1223	764-784	ACUGGGTCAGAUCAACCUUCUCA	1310	762-784
AD- 1634361	GGUUGAUCUGAGCCAGUUCU	239	768-788	AUGAACTGGGUCAGAUCAACCUU	1311	766-788
AD- 1634362	UGAUCUGAGCCAGUUCAGUU	76	771-791	AACUTGAACUGGGUCAGAUCAAC	1183	769-791
AD- 1634363	UCUGAGCCAGUUCAGUGGAGU	1224	774-794	AUCCACTUGAACUGGGUCAGAU	1312	772-794
AD- 1634364	UGAGCCAGUUCAGUGGAGU	1225	776-796	AGAUCACUUUGAACUGGGUCAGA	1313	774-796
AD- 1634365	CCCAGUUCAGUGGAGUCCACU	1226	779-799	AGUGGATCCACUUUGAACUGGGUC	1314	777-799
AD- 1634366	CCAGUUCAGUGGAGUCCACAU	80	780-800	AUGUGGAUCCACUUUGAACUGGGU	304	778-800
AD- 1634367	GUGGAUCCACAUUGAGGGCCU	1227	789-809	AGGCCCTCAAUGUGGAUCCACUU	1315	787-809
AD- 1634368	AGACGUGGUGUUUGUCAGCAU	1228	945-965	AUGCTGACAAACACACCGUCUCC	1316	943-965
AD- 1634369	ACGUGGUGUUUGUCAGCAAU	21	947-967	AUUUGCTGACAAACACCGUCUCU	1317	945-967
AD- 1634370	UUUGUCAGCAAGAUUGUGGCU	98	955-975	AGCCACAUCUUUGUCAGCAACA	322	953-975

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Range in XM_017004061.1	Antisense Sequence 5' to 3'	SEQ ID NO:	Range in XM_017004061.1
1634370						
AD- 1634371	UGUCAGCAAAAGAUUGGGCCAU	1229	957-977	AUGGCCACAUCUUUGCUGACAAA	1318	955-977
AD- 1634372	GCAAAGAUGUGGCCAAGCACU	1230	962-982	AGUGCUTGGCCACAUCUUUGCUG	1319	960-982
AD- 1634373	CUGGAGACACCUUCA AUGCCU	106	1154-1174	AGGCAUTGAAAGGUGUCUCCAGCU	1299	1152-1174
AD- 1634374	UGGAGACACCUUCA AUGCCUU	107	1155-1175	AAGGCATUGAAGGUGUCUCCAGC	1320	1153-1175
AD- 1634375	GGAGACACCUUCA AUGCCUCU	1231	1156-1176	AGAGGCAUUGAAGGUGUCUCCAG	1321	1154-1176
AD- 1634376	ACACCUUCA AUGCCUCCGUCU	1215	1160-1180	AGACGGAGGCAUUGAAGGUGUCU	1322	1158-1180
AD- 1634377	CUUCA AUGCCUCCGUCU CAUCUU	1232	1164-1184	AAGATGACGGAGGCAUUGAAGGU	1323	1162-1184
AD- 1634378	UCAAUGCCUCCGUCU CAUCUU	223	1166-1186	AGAAGATGACGGAGGCAUUGAAG	1324	1164-1186
AD- 1634379	AUGCCUCCGUCU CAUCUUCAGCU	1217	1169-1189	AGCUGAAGAUGACGGAGGCAUUG	1302	1167-1189
AD- 1634380	UGCCUCCGUCU CAUCUUCAGCCU	1233	1170-1190	AGGCTGAAGAUGACGGAGGCAU	1325	1168-1190
AD- 1634381	CCUCCGUCU CAUCUUCAGCCUCU	1234	1172-1192	AGAGGCTGAAGAUGACGGAGGCA	1326	1170-1192
AD- 1634382	GAGGAGCGUGCAGGAAGCACU	1235	1200-1220	AGUGCUTCCUGCAGCUCUCCUCCC	1327	1198-1220
AD- 1634383	AGGAGCGUGCAGGAAGCACUU	1236	1201-1221	AAGUGCTUCCUGCAGCUCUCCUCC	1328	1199-1221
AD- 1634384	AGCGUGCAGGAAGCACUCUGAGU	1218	1204-1224	ACUCAGTGUUCCUGCAGCUCUCC	1303	1202-1224
AD- 1634385	CGUGCAGGAAGCACUCUGAGAUU	1237	1206-1226	AAUCTCAGUGCUUCCUGCAGCUCU	1329	1204-1226
AD- 1634386	CUUCA AUGCCUCCGUCU CAU	1238	1164-1182	AAUGACGGAGGCAUUGAAGGU	1330	1162-1182
AD- 1634387	ACCUACA AUGCCUCCGUCU CAU	1239	1162-1182	AAUGACGGAGGCAUUGAAGGU	1331	1160-1182

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Range in XM_017004061.1	Antisense Sequence 5' to 3'	SEQ ID NO:	Range in XM_017004061.1
1634387						
AD- 1634388	ACCAUCAAUGCCUCCGUGAUU	1240	1162-1182	AAUGACGGAGGCAUUGAUGGUGU	1332	1160-1182
AD- 1634389	ACGUUCAAUGCCUCCGUGAUU	1241	1162-1182	AAUGACGGAGGCAUUGAAGCGUGU	1333	1160-1182
AD- 1634390	ACAUUCAAUGCCUCCGUGAUU	1242	1162-1182	AAUGACGGAGGCAUUGAAUUGUGU	1334	1160-1182
AD- 1634391	CUUCAAUGCCUCCGUGAUU	1238	1164-1182	AAUGACGGAGGCAUUGAAAGGU	1330	1162-1182
AD- 1634392	ACCUACAAUGCCUCCGUGAUU	1239	1162-1182	AAUGACGGAGGCAUUGAAGGUGU	1331	1160-1182
AD- 1634393	ACCAUCAAUGCCUCCGUGAUU	1240	1162-1182	AAUGACGGAGGCAUUGAUGGUGU	1332	1160-1182
AD- 1634394	ACGUUCAAUGCCUCCGUGAUU	1241	1162-1182	AAUGACGGAGGCAUUGAAGCGUGU	1333	1160-1182
AD- 1634395	ACAUUCAAUGCCUCCGUGAUU	1242	1162-1182	AAUGACGGAGGCAUUGAAUUGUGU	1334	1160-1182
AD- 1634396	GUUCAAGUGGAUCCACAUUGU	207	783-803	ACAATGTGGAUCCACUUGAACUG	1152	781-803
AD- 1634397	GUUCAAGUGGAUCCACAUUGU	207	783-803	ACAATGTGGAUCCACUUGAACUG	1152	781-803
AD- 1634398	GUUCUAGUGGAUCCACAUUGU	1243	783-803	ACAATGTGGAUCCACUAGAACUG	1335	781-803
AD- 1634399	GUUGAAGUGGAUCCACAUUGU	1244	783-803	ACAATGTGGAUCCACUUCACACUG	1336	781-803
AD- 1634400	GUUAAAGUGGAUCCACAUUGU	1245	783-803	ACAATGTGGAUCCACUUAACUG	1337	781-803
AD- 1634401	GUACAAGUGGAUCCACAUUGU	1246	783-803	ACAATGTGGAUCCACUUGUACUG	1338	781-803
AD- 1634402	AAGGUUGAUCUGACCUAGUUU	1247	766-786	AAACTAGGUCAGAUCAACCUUCU	1339	764-786
AD- 1634403	AAGGUUGAUCUGACUCAGUUU	1248	766-786	AAACTGAGUCAGAUCAACCUUCU	1340	764-786
AD- 1634404	AAGUUUGAUCUGACCUAGUUU	1249	766-786	AAACTAGGUCAGAUCAACCUUCU	1341	764-786

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Range in XM_017004061.1	Antisense Sequence 5' to 3'	SEQ ID NO:	Range in XM_017004061.1
1634404						
AD-1634405	AAUGUUGAUCUGACCUAGUUU	1250	766-786	AAACTAGGUCAGAUCAACAUUCU	1342	764-786
AD-1634406	AAGUUUGAUCUGACUCAGUUU	1251	766-786	AAACTGAGUCAGAUCAACAUUCU	1343	764-786
AD-1634407	AAUGUUGAUCUGACUCAGUUU	1252	766-786	AAACTGAGUCAGAUCAACAUUCU	1344	764-786
AD-1634408	UGGUUUUUUGUCAGCAAAAGAUU	1253	950-970	AAUCTUTGCUGACAAAAACCACG	1345	948-970
AD-1634409	UGGUCUUUUGUCAGCAAAAGAUU	1254	950-970	AAUCTUTGCUGACAAAGACCACG	1346	948-970
AD-1634410	UGGAGUUUUGUCAGCAAAAGAUU	1255	950-970	AAUCTUTGCUGACAAACUCCACG	1347	948-970
AD-1634411	UGUUGUUUUGUCAGCAAAAGAUU	1256	950-970	AAUCTUTGCUGACAAACAACACG	1348	948-970
AD-1634412	UGCUGUUUUGUCAGCAAAAGAUU	1257	950-970	AAUCTUTGCUGACAAACAGCACG	1349	948-970
AD-1634413	UGGUGUUUUGUCAGCAAAAGAUU	93	950-970	AAUCTUTGCUGACAAACACCACU	1350	948-970
AD-1634414	UGGUGUUUUGUCAGCAAAAGAUU	93	950-970	AAUCTUTGCUGACAAACACCACG	1269	948-970
AD-1634415	CCUCAUGGAAAGAGAAUCAGAU	1258	519-539	ATCUGATUCUCTUCCAUGAGGCU	1351	517-539
AD-1634416	CCUCUUGGAAAGAGAAUCAGAU	1259	519-539	ATCUGATUCUCTUCCAAGAGGCU	1352	517-539
AD-1634417	CCUGAUGGAAAGAGAAUCAGAU	1260	519-539	ATCUGATUCUCTUCCAUCAGGCU	1353	517-539
AD-1634418	CCUAAUGGAAAGAGAAUCAGAU	1261	519-539	ATCUGATUCUCTUCCAUAAGGCU	1354	517-539
AD-1634419	CCACAUGGAAAGAGAAUCAGAU	1262	519-539	ATCUGATUCUCTUCCAUGUGGCU	1355	517-539
AD-1634420	GACGUGGUGUUUGUCAGCAAU	222	946-966	AUUGCUGACAAACACCACGUCUC	446	944-966
AD-	GACGUGGUGUUUGUCAGCAAU	222	946-966	AUUGCTGACAAACACCACGUCUC	1356	944-966

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Range in XM_017004061.1	Antisense Sequence 5' to 3'	SEQ ID NO:	Range in XM_017004061.1
1634421						
AD-1634422	GACGUGGUGUUUGUCAGCAAU	222	946-966	AUUGCTGACAAAACACCCACGUCUC	1356	944-966
AD-1634423	GUGGUGUUUGUCAGCAAAAGAU	20	949-969	AUCUTUGCUGACAAACACCCACGU	1184	947-969
AD-1634424	GUGGUGUUUGUCAGUAAAAGAU	1263	949-969	AUCUTUACUGACAAACACCCACGU	1357	947-969
AD-1634425	GUGGUGUUUGUCAGCAAAAGAU	20	949-969	AUCTUTGCUGACAAACACCCACGU	1358	947-969
AD-1634426	GUGGAGUUUGUCAGUAAAAGAU	1264	949-969	AUCUTUACUGACAAACUCCACGU	1359	947-969
AD-1634427	GUGCUGUUUGUCAGUAAAAGAU	1265	949-969	AUCUTUACUGACAAACAGCACGU	1360	947-969
AD-1634428	GUGUUGUUUGUCAGUAAAAGAU	1266	949-969	AUCUTUACUGACAAACACACGU	1361	947-969
AD-1634429	GUCGUGUUUGUCAGUAAAAGAU	1267	949-969	AUCUTUACUGACAAACACGACGU	1362	947-969
AD-1634430	GUUGUGUUUGUCAGUAAAAGAU	1268	949-969	AUCUTUACUGACAAACACACGU	1363	947-969
AD-1634431	GUGGAGUUUGUCAGUAAAAGAU	1264	949-969	AUCTUTGCUGACAAACUCCACGU	1364	947-969
AD-1634432	GUGCUGUUUGUCAGUAAAAGAU	1265	949-969	AUCTUTGCUGACAAACAGCACGU	1365	947-969
AD-1634433	GUGUUGUUUGUCAGUAAAAGAU	1266	949-969	AUCTUTGCUGACAAACACACGU	1366	947-969
AD-1634434	GUCGUGUUUGUCAGUAAAAGAU	1267	949-969	AUCTUTGCUGACAAACACGACGU	1367	947-969
AD-1634435	GUUGUGUUUGUCAGUAAAAGAU	1268	949-969	AUCTUTGCUGACAAACACACGU	1368	947-969
AD-1634436	GAAGAGAAAGCAGAUCCUGUGU	54	526-546	ACACAGGAUCUGCUUCUCUCCU	1369	524-546
AD-1634437	GAAGAGAAAGCAGAUCCUGUGU	54	526-546	ACACAGGAUCUGCUUCUCUCCU	1369	524-546

Table 11. Modified Sense and Antisense Strand Sequences of KHK dsRNA

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:	mRNA Target Sequence	SEQ ID NO:
AD-1290969	ascsuucAfaUfGfCfuccgucanuL96	1370	asAfsuacCfaggagcaUfuGfaaggsu	780	ACACCUUCAAUGCCUCCGUCAU	1004
AD-1423310	ususugagAfaGfGfUfugaucugauL96	1153	asGfsuadAg(Agn)ucaaccUfuCfucaasgs	1154	ACUUUGAGAAGGUUGAUCUGAC	968
AD-1423311	gsascgugGfuGfUfufugucagcauL96	670	asUfsuadCu(G2p)acaacAfcCfagucsuc	1155	GAGACGUGGUGUUUGUCAGCAA	1118
AD-1423312	usgscaggAfaGfCfAfcugagauuL96	563	asGfsaadTc(Tgn)caugcUfuCfugcascsg	1156	CGUGCAGGAAGCACUCUGAGAUUC	1011
AD-1423317	csusuugaGfaAfgGfugaucugauL96	519	asUfscadGa(Tgn)caacuUfcUfcaagsuc	1161	GACUUUGAGAAGGUUGAUCUGA	967
AD-1423319	gsasuuuGfaGfAfgguigaucuuL96	518	asAfsuadTc(Agn)accuucUfcAfaagucsu	1163	CAGACUUUGAGAAGGUUGAUCU	966
AD-1423323	csasaugcCfuCfCfGfucuaucuuL96	559	asUfsgadAg(Agn)ugacggAfgGfcauugsas	1167	UUCAAUGCCUCCGUCUUCUUA	1007
AD-1423327	asasgguuGfaUfCfUfagaccaguuL96	521	asAfsuadTg(G2p)gucagaUfcAfaacuucsu	1171	AGAAGGUUGAUCUCUGACCCAGUU	969
AD-1423329	gsasagagAfaGfCfAfgauccuguuL96	502	asCfsuadAg(G2p)aucuucUfuCfucucsu	1173	UGGAAGAGAAGCAGAUCCUGUG	950
AD-1423330	gsusguuuGfuCfAfgfcaagauuuL96	543	asAfsuadTc(Tgn)uugcuAfcAfaacacsa	1174	UGGUGUUUGUCAGCAAAAGAUGU	991
AD-1423333	gsusggugUfuUfGfUfcagcaagauL96	468	asUfscudTu(G2p)ucgacaAfaCfaccacgsu	1193	ACGUGGUGUUUGUCAGCAAAAGA	916
AD-1423334	csesucuuGfgAfaGfagagagauL96	498	asUfscudGc(Tgn)ucucuuCfcAfuaggsu	1177	AGCCUCAUGGAAGAGAAAGCAGA	946
AD-1423336	gsusucuuGfuGfGfAfucauauuuL96	655	asCfsuadTg(Tgn)ggaucAfcUfugaucsu	1179	CAGUUCAAUGGGAUCCACAUUG	1103
AD-1523180	csesucuuGfgAfaGfagagagauL96	498	asUfscudGedTucuuCfcAfuaggsu	1197	AGCCUCAUGGAAGAGAAAGCAGA	946
AD-1548743	usgsguguUfuGfUfCfagcaagauL96	541	asAfsuadTu(Tgn)gcuacAfaAfcaccacsg	1482	CGUGGUGUUUGUCAGCAAAAGA	989
AD-1612957	gsesucuuGfAfaGfagagagauL96	1371	asCsuadCudTucudTcCfagaggsu	1483	UAGCCUCAUGGAAGAGAAAGCAG	1619

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:	mRNA Target Sequence	SEQ ID NO:
AD-1612958	csesucuauggAfAfGfagaagcagaulL96	1372	asdTscudGcdTucudTtuCfcaugaggscsu	1484	AGCCUCAUGGAAGAGAGCAGA U	946
AD-1612963	usgsaagagAfAfGfagaucucugulL96	1373	asdCsagdGadTcugcdTtuCfucuccasug	1485	CAUGGAAGAGAGCAGAUCCUG	1620
AD-1612967	asgsagaagcAfGfAfuccugugcgulL96	1374	asdCsagdAcdAggaudCuGfucucucusc	1486	GAAAGAGAGCAGAUCCUGGCG U	1621
AD-1612969	asgsaagcagAfUfCfcugugcgugulL96	1375	asdCsacdGcdAcagadAuCfugcucucscu	1487	AGAGAAGCAGAUCCUGUGCGUG G	1622
AD-1612970	gsasagcagaUfCfCfugugcgugulL96	1376	asdCsacdCgdCacagdGaUfucgucucusc	1488	GAGAAGCAGAUCCUGUGCGUG G	1623
AD-1613059	csasgacuuuGfAfGfagaagguagaunL96	1377	asdAsucdAadCcuudTcAfaagucugsusa	1489	UACAGACUUUGAGAGAGGUUGAU C	964
AD-1613060	asgsacuuugAfGfAfagguuagauculL96	1378	asdGsaudCadAccuudCuCfaagucucsgsu	1490	ACAGACUUUGAGAGAGGUUGAU U	965
AD-1613062	ascsuuuugAfAfGfagaagguagaunL96	1379	asdCsagdAudCaacdTtuCfcaaaagucsu	1491	AGACUUUGAGAGAGGUUGAU A	1109
AD-1613070	asasgguugaUfCfUfagaccaguuulL96	1380	asdAsacdTgdGgugcadGaUfcaacucucsu	1492	AGAAGGUUGAUCUGAGCCCAGUU C	969
AD-1613073	gsusugaucuGfAfCfcaaguucaaulL96	1381	asdTsugdAadCugggdTcAfgauncaacsu	1493	AGGUUGAUCUGAGCCCAGUUCAA G	970
AD-1613074	ususgaucugAfCfCfcaaguucaagulL96	1382	asdCsundGadAcuggdGuCfagauncaasc	1494	GGUUGAUCUGAGCCCAGUUCAA U	971
AD-1613075	usgsaucugaCfCfCfaguucaaguuulL96	1383	asdAscudTgdAacugdGgUfcaucaucasac	1495	GUUGAUCUGAGCCCAGUUCAAAG G	972
AD-1613076	gsasucugacCfCfAfguucaagugulL96	1384	asdCsacdTudGaacudGgGfucagaucsa	1496	UUGAUCUGAGCCCAGUUCAAAGUG G	973
AD-1613077	asusucugaccCfAfGfuucaagugulL96	1385	asdCsacdCudTgaacdTgGfugagaucsa	1497	UGAUCUGAGCCCAGUUCAAAGUG A	1624
AD-1613079	csusgacccaGfUfUfcaaguggaunL96	1386	asdAsucdCadCuugadAcUfggucagucsa	1498	AUCUGAGCCCAGUUCAAAGUGGAU C	974
AD-1613088	ususcaagugGfAfUfcaacuuagaulL96	1387	asdTscadAudGuggadTcCfacuugaucsu	1499	AGUUCAAAGUGGAUCCACAUUGA G	978
AD-1613089	uscsaagugGfAfUfcaacuuagagulL96	1388	asdCsucdAadTuggadAuCfcaucugasac	1500	GUUCAAGUGGAUCCACAUUGAG G	979
AD-	csasaguggaUfCfCfcaacuuagagulL96	1389	asdCsucdCadAugugdGaUfccacuuagsa	1501	UUCAAGUGGAUCCACAUUGAGG	980

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:	mRNA Target Sequence	SEQ ID NO:
1613090					G	
AD-1613091	asasugugauCfCfAfcuugagggul96	1390	asdCscddTcdAaugndGgAfuccacumgsa	1502	UCAAGUGGAUCCACAUAUGAGGG	1625
AD-1613094	usgsauecaCfAfUfugagggccgul96	1391	asdCsggdCcdCucadTgUfggauecascu	1503	AGUGGAUCCACAUAUGAGGGCCG	1626
AD-1613095	gsesauecaAfUfUfgagggccggul96	1392	asdCsggdGcdCucadAuGfuggauecasc	1504	GUGGAUCCACAUAUGAGGGCCGG	1627
AD-1613237	gsusuuugcuAfCfGfagagggugul96	1393	asdCscddCgdTfuecdGuAfgecaaacasg	1505	CUGUUGGCUACGGAGACGUGG	1628
AD-1613238	usuuugcuafCfGfagagggugul96	1394	asdAscddAcddGucudCgUfagccaaascsa	1506	UGUUGGCUACGGAGACGUGGU	1629
AD-1613239	usuuugcuafCfGfagagggugul96	1395	asdCsaddCadCgucudCcGfuaagccaaascsa	1507	GUUUGGCUACGGAGACGUGGUG	1630
AD-1613240	usuuugcuafCfGfagagggugul96	1396	asdAscddCcdAcgucdTcCfuaagccaaascsa	1508	UUUGGCUACGGAGACGUGGUGU	1631
AD-1613241	gsesuacggAfGfAfegugggugul96	1397	asdAsaddAcddCagudCuCfeguaagccaaascsa	1509	UUGGCUACGGAGACGUGGUGUU	1632
AD-1613242	gsesuacggAfGfAfegugggugul96	1398	asdAsaddCadCagudTcUfeguaagccaaascsa	1510	UGGCUACGGAGACGUGGUGUUU	1138
AD-1613243	csuuacggAfGfAfegugggugul96	1399	asdCsaddAcddAcgudCuCfuecuaagccaaascsa	1511	GGCUACGGAGACGUGGUGUUUG	985
AD-1613244	usuuacggAfGfAfegugggugul96	1400	asdAscddAadCagudCgUfuecuaagccaaascsa	1512	GCUACGGAGACGUGGUGUUUGU	986
AD-1613245	ascsuacggAfGfAfegugggugul96	1401	asdGscddAadAcgudAcgudAcGfuecuaagccaaascsa	1513	CUACGGAGACGUGGUGUUUGUC	1128
AD-1613246	csuuacggAfGfAfegugggugul96	1402	asdTsgddCadAacddCaCfuecuaagccaaascsa	1514	UACGGAGACGUGGUGUUUGUCA	987
AD-1613247	gsesuacggAfGfAfegugggugul96	1403	asdCsuddAcddAacddCcAfcuecuaagccaaascsa	1515	ACGGAGACGUGGUGUUUGUCAG	988
AD-1613254	usgsuuguuGfUfCfagaaagauul96	1404	asdAsuddTudTgucudAcAfaaacaccascg	1516	CGUGGUGUUUGUCAGCAAAAGAU	989
AD-1613255	gsesuuguuGfUfCfAfagaaagauul96	1405	asdCsuddCudTgucudGaCfaaacaccasc	1517	GUGGUGUUUGUCAGCAAAAGAU	990
AD-1613256	gsusuuguuGfUfCfAfagaaagauul96	1406	asdAscddTcdTgucudTgAfaaacaccasc	1518	UGGUGUUUGUCAGCAAAAGAU	991

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:	mRNA Target Sequence	SEQ ID NO:
AD-1613257	usgsuuugucAfGfCfaaagaugugul96	1407	asdCsacdAudCuuugdCuGfacaacasc	1519	GGUUUUGUCAGCAAAAGAUGUG	992
AD-1613258	gsuuugucaGfCfAfaagaugugul96	1408	asdCscadCadTcuundGeUfgacaacsasc	1520	GUGUUUGUCAGCAAAAGAUGUGG	993
AD-1613259	usuuugucagCfAfAfaagaugugul96	1409	asdGscadAcdAucundTgCfugacaacsca	1521	UGUUUUGUCAGCAAAAGAUGUGGC	994
AD-1613361	asgsuugagAfCfAfcuucacugul96	1410	asdCsaudTgdAaggudGuCfuccagcusc	1522	GGAGCUGGAGACACCUUCAAAUG	1001
AD-1613362	gsesuggagAfCfCfcuucacugul96	1411	asdGscadTudGaaagdTgUfuccagcusc	1523	GAGCUGGAGACACCUUCAAAUGC	1633
AD-1613363	csusggagacAfCfCfcuucacugul96	1412	asdGsgcdAudTgaagdGuGfuccagcsu	1524	AGCUGGAGACACCUUCAAAUGCC	1002
AD-1613369	asesaccuucAfAfUfgcuucgucul96	1413	asdGscadGgdAaggdTuGfaaggugucsu	1525	AGACACCUUCAAAUGCCUCCGUC	1634
AD-1613370	csasccuucAfUfGfcuucgucul96	1414	asdTsgadCgdGaggdAuUfgaaggugusc	1526	GACACCUUCAAAUGCCUCCGUC	1635
AD-1613371	asescuucAaUfGfCfcuucgucul96	1415	asdAsugdAcdGaggdCaUfugaaggugsu	1527	ACACCUUCAAAUGCCUCCGUC	1004
AD-1613374	usuuuagcCfUfCfcuucacucul96	1416	asdAsagdAudGaggdAgGfcauugaasgs	1528	CCUCAAUGCCUCCGUCUUCU	1006
AD-1613377	asasugcuucCfGfUfcauucacul96	1417	asdCsugdAadGaugdCgGfagcauugsa	1529	UCAAUGCCUCCGUCUUCUUCAG	1008
AD-1613378	asusgccuccGfUfCfcauucacul96	1418	asdGscudGadAgaugdAcGfagcauugsa	1530	CAAUGCCUCCGUCUUCUUCAGC	1636
AD-1613395	asgsuugcGfGfAfaagacugul96	1419	asdCsudAgdTgcundCeUfgcagcusc	1531	GGAGCUGGAGCAAGCACACUGAG	1637
AD-1613400	gsesaggagCfAfCfugagacugul96	1420	asdCsgadAudCucagdTgCfuccagcsac	1532	GUGCAGGAAGCACUGAGAUUCG	1012
AD-1613401	csasggagcAfCfUfagacugul96	1421	asdCscgdAadTcucadGuGfuccuugcsa	1533	UGCAGGAAGCACUGAGAUUCGG	1638
AD-1634353	usasgccuCfAfUfGfGfaagagacul96	1422	asGfscudTc(Tgn)cuucaUfgAfgcuascu	1534	AGUAGCCUCAUGGAAGAGAAAGC	1639
AD-1634354	gsesucaUfgGfAfafagagacul96	1423	asCfsugdCu(Tgn)cuucCfAfUfgagcsus	1535	UAGCCUCAUGGAAGAGAAAGCAG	1619
AD-	csasuggaAfGfAfagcagacul96	1424	asGfsgadTc(Tgn)gcuuCfUfcaugsasg	1536	CUCAUGGAAGAGAAAGCAGAUCC	1640

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:	mRNA Target Sequence	SEQ ID NO:
1634355					U	
AD-1634356	gsgsaagaGfaAfGfCfagauccuguuL96	501	asAfscadGg(Agn)ueguenUfeUfucucsas u	1537	AUGGAAGAGAAAGCAGAUCCUGU G	949
AD-1634357	asgsaagaGfcAfGfAfucucugcgulL96	1425	asCfsgcdAc(Agn)ggauucGfcUfucucusus c	1538	GAAGAGAAGCAGAUCCUGUGCG U	1621
AD-1634358	asgsacuuUfgAfGfAfagguugauL96	517	asGfsaudCa(Agn)ccuucUcfaAfagucugs u	1539	ACAGACUUUGAGAAGGUUGAUC U	965
AD-1634359	usgsaagaGfgUfUfGfaucugaccuL96	1426	asGfsggdTc(Agn)gaucacCfcUfucucasasa	1540	UUUGAGAAGGUUGAUCUGAGCCC A	1641
AD-1634360	asgsaaggUfuGfAfUfucugaccaguuL96	1427	asCfsugdGg(Tgn)cagaucAfaCfcuucucsa a	1541	UGAGAAGGUUGAUCUGAGCCCAG U	1642
AD-1634361	gsgsuugaUfcUfGfAfceaguuL96	687	asUfsgadAc(Tgn)gggucaGfaUfcaacsus u	1542	AAGGUUGAUCUGAGCCCAGUUCA A	1135
AD-1634362	usgsaucuGfaCfCfCfaguucaaguL96	524	asAfscudTg(Agn)acuggUfcAfagucasas c	1543	GUUGAUCUGAGCCCAGUUCAAGU G	972
AD-1634363	uscsugacCfcAfGfUfucaguggauL96	1428	asUfscddAc(Tgn)ugaauCfGfGfucagusus c	1544	GAUCUGAGCCCAGUUCAAGUGGA U	1643
AD-1634364	usgsacccAfgUfUfCfaaguggauL96	1429	asGfsaudCc(Agn)cuugaaCfuGfGfucasgs a	1545	UCUGAGCCCAGUUCAAGUGGAUC C	1644
AD-1634365	csescaguUfcAfAfGfugauccauL96	1430	asGfsugdGa(Tgn)ccauuGfaAfecuggsus c	1546	GAGCCAGUUCAAGUGGAUCCAC A	1645
AD-1634366	csesaguuCfaAfGfUfugauccacuL96	528	asUfsgudGg(Agn)uccauUfgAfucugsgs u	1547	AGCCAGUUCAAGUGGAUCCACA U	976
AD-1634367	gsusggauCfcAfCfAfugaggccuL96	1431	asGfsgcdCc(Tgn)caauuGfgAfuccasus u	1548	AAGUGGAUCCACAUGAGGGGCC G	1646
AD-1634368	asgsacguGfgUfGfUfugucagcuL96	1432	asUfsgcdTg(Agn)caacaCfcAfecucuscsc	1549	GGAGACGUGGUGUUGUUGUCAGCA A	1647
AD-1634369	asesguggUfgUfUfugucagcaauL96	469	asUfsuudGc(Tgn)gacaaCfaCfcaucucusu	1550	AGACGUGGUGUUGUUGUCAGCAAA G	917
AD-1634370	ususugucAfgCfAfAfagauuggcuL96	546	asGfscddAc(Agn)ucuuuGfuGfacaascs a	1551	UGUUUGUCAGCAAAAGAUUGUGGC C	994
AD-1634371	usgsucagCfaAfAfGfauugggccuL96	1433	asUfsggdCc(Agn)cauuuUfgCfugacusas a	1552	UUUGUCAGCAAAAGAUUGUGGGCCA A	1648
AD-1634372	gscsaagAfuGfUfGfgccagcacuL96	1434	asGfsugdCu(Tgn)ggccacAfuCfuucgusus g	1553	CAGCAAAAGAUUGUGGGCCAAGCAC U	1649

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:	mRNA Target Sequence	SEQ ID NO:
AD-1634373	csusggagAfcAfCfcfucaaaagccuL96	554	asGfsacdAu(Tgn)gaagguGfuCfuccagcs	1554	AGCUGGAGACACCUUCAAUGGCC	1002
AD-1634374	usgsagagaCfaCfCfucaaaagccuL96	555	asAfsagCdCa(Tgn)ugaaggUfgUfuccagcs	1555	GCUGGAGACACCUUCAAUGCCU	1003
AD-1634375	gsgsagagAfcCfCfucaaaagccuL96	1435	asGfsagCdGc(Agn)ugaaggGfuGfuccagcs	1556	CUGGAGACACCUUCAAUGCCU	1650
AD-1634376	asesaccuUfcAfAfUfuccuagccuL96	1436	asGfsacdGg(Agn)ggcauuGfaAfggugcs	1557	AGACACCUUCAAUGCCUCCGUC	1634
AD-1634377	csusucaaUfgCfCfUfuccuagccuL96	1437	asAfsagdTg(Agn)cgaggGfUfugaagcs	1558	ACCUUCAAUGCCUCCGUCUUCU	1651
AD-1634378	uscsaagCfcUfCfCfuccuagccuL96	671	asGfsaadGa(Tgn)gacggaGfgCfaugagcs	1559	CUUCAAUGCCUCCGUCUUCUUC	1119
AD-1634379	asusgccuCfcGfUfCfaucucagcuL96	1438	asGfsacdGa(Agn)gaagacGfgAfggcaus	1560	CAAUGCCUCCGUCUUCUUCAGC	1636
AD-1634380	usgsccuCfcUfCfAfucaagccuL96	1439	asGfsagdTg(Agn)agaagaCfGfgagagcs	1561	AAUGCCUCCGUCUUCUUCAGCC	1652
AD-1634381	csesuagUfcAfUfCfucaagccuL96	1440	asGfsagCdGc(Tgn)gaagauGfaCfaggagcs	1562	UGCCUCCGUCUUCUUCAGCCU	1653
AD-1634382	gsasggagCfcUfGfCfaggagccuL96	1441	asGfsagCdCu(Tgn)ccugcaCfGfuccuagcs	1563	GGGAGGAGCGUGCAGGAAGCAC	1654
AD-1634383	asgsagagCfcUfGfCfaggagccuL96	1442	asAfsagCdGc(Tgn)uccugcAfcGfuccuagcs	1564	GGAGGAGCGUGCAGGAAGCACU	1655
AD-1634384	asgsagagCfcUfGfCfaggagccuL96	1443	asCfsagCdAg(Tgn)gcuuagUfgCfaggagcs	1565	GGAGCGUGCAGGAAGCACUAG	1637
AD-1634385	csusgcaGfgAfAfGfcaugagcuL96	1444	asAfsagCdTc(Agn)gugcuuCfcUfaggagcs	1566	AGCGUGCAGGAAGCACUAGAGAU	1656
AD-1634386	csusucaaUfgCfCfuccuagccuL96	1445	asAfsagCdAcGgagCdCaUfugaagcs	1567	ACCUUCAAUGCCUCCGUCUUC	1657
AD-1634387	asesucaaUfgCfCfuccuagccuL96	1446	asAfsagCdAcGgagCdCaUfugaagcs	1568	ACACCUUCAAUGCCUCCGUCUUC	1004
AD-1634388	asesucaaUfgCfCfuccuagccuL96	1447	asAfsagCdAcGgagCdCaUfugaagcs	1569	ACACCUUCAAUGCCUCCGUCUUC	1004
AD-1634389	asesucaaUfgCfCfuccuagccuL96	1448	asAfsagCdAcGgagCdCaUfugaagcs	1570	ACACCUUCAAUGCCUCCGUCUUC	1004
AD-1634390	asesucaaUfgCfCfuccuagccuL96	1449	asAfsagCdAcGgagCdCaUfugaagcs	1571	ACACCUUCAAUGCCUCCGUCUUC	1004

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:	mRNA Target Sequence	SEQ ID NO:
1634390					C	
AD-1634391	csusucAfaUfGfCfcuccgucanuL96	1450	asAfsugaCfaggaggaUfuGfaagsgsu	1572	ACCUUCAUAGCCUCCGUCAC	1657
AD-1634392	ascsuacAfaUfGfCfcuccgucanuL96	1451	asAfsugaCfaggaggaUfuGfaagsgsu	1573	ACACCUUCAUAGCCUCCGUCAC	1004
AD-1634393	ascsaucAfaUfGfCfcuccgucanuL96	1452	asAfsugaCfaggaggaUfuGfaagsgsu	1574	ACACCUUCAUAGCCUCCGUCAC	1004
AD-1634394	ascsuucAfaUfGfCfcuccgucanuL96	1453	asAfsugaCfaggaggaUfuGfaagsgsu	1575	ACACCUUCAUAGCCUCCGUCAC	1004
AD-1634395	ascsauucAfaUfGfCfcuccgucanuL96	1454	asAfsugaCfaggaggaUfuGfaagsgsu	1576	ACACCUUCAUAGCCUCCGUCAC	1004
AD-1634396	gsusucaaguGfGfAfuccacauuL96	1455	asdCsaadTg(Tgn)ggauCCcAfcuugaacsusg	1577	CAGUUCAAGUGGAUCCACAUUG	1103
AD-1634397	gsusucaaguGfGfAfuccacauuL96	1455	asdCsaadTg(Tgn)ggauCCcAfcUfugaacsusg	1578	CAGUUCAAGUGGAUCCACAUUG	1103
AD-1634398	gsusucuaGfuGfGfAfuccacauuL96	1456	asCfsaadTg(Tgn)ggauccAfcUfagaacsusg	1579	CAGUUCAAGUGGAUCCACAUUG	1103
AD-1634399	gsusugaaGfuGfGfAfuccacauuL96	1457	asCfsaadTg(Tgn)ggauccAfcUfugaacsusg	1580	CAGUUCAAGUGGAUCCACAUUG	1103
AD-1634400	gsusuaaaGfuGfGfAfuccacauuL96	1458	asCfsaadTg(Tgn)ggauccAfcUfugaacsusg	1581	CAGUUCAAGUGGAUCCACAUUG	1103
AD-1634401	gsusacaaGfuGfGfAfuccacauuL96	1459	asCfsaadTg(Tgn)ggauccAfcUfugaacsusg	1582	CAGUUCAAGUGGAUCCACAUUG	1103
AD-1634402	asasguugaUfCfUfgaccuaguuuL96	1460	asdAsaadTadGgucadGaUfcaacuunscsu	1583	AGAAGGUUGAUCUGACCCAGUU	969
AD-1634403	asasguugaUfCfUfgaccuaguuuL96	1461	asdAsaadTgdAgucadGaUfcaacuunscsu	1584	AGAAGGUUGAUCUGACCCAGUU	969
AD-1634404	asasguugaUfCfUfgaccuaguuuL96	1462	asdAsaadTadGgucadGaUfcaacuunscsu	1585	AGAAGGUUGAUCUGACCCAGUU	969
AD-1634405	asasguugaUfCfUfgaccuaguuuL96	1463	asdAsaadTadGgucadGaUfcaacuunscsu	1586	AGAAGGUUGAUCUGACCCAGUU	969
AD-1634406	asasguugaUfCfUfgaccuaguuuL96	1464	asdAsaadTgdAgucadGaUfcaacuunscsu	1587	AGAAGGUUGAUCUGACCCAGUU	969
AD-1634407	asasguugaUfCfUfgaccuaguuuL96	1465	asdAsaadTgdAgucadGaUfcaacuunscsu	1588	AGAAGGUUGAUCUGACCCAGUU	969

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:	mRNA Target Sequence	SEQ ID NO:
AD-1634408	usgsuuuUfuGfUfCfagcaagaauL96	1466	asAfsudTu(Tgn)gcugacAfaAfaaccascsg	1589	CGUGGUGUUUGUCAGCAAAAGAU G	989
AD-1634409	usgsuuuUfuGfUfCfagcaagaauL96	1467	asAfsudTu(Tgn)gcugacAfaAfaaccascsg	1590	CGUGGUGUUUGUCAGCAAAAGAU G	989
AD-1634410	usgsuuuUfuGfUfCfagcaagaauL96	1468	asAfsudTu(Tgn)gcugacAfaAfaaccascsg	1591	CGUGGUGUUUGUCAGCAAAAGAU G	989
AD-1634411	usgsuuuUfuGfUfCfagcaagaauL96	1469	asAfsudTu(Tgn)gcugacAfaAfaaccascsg	1592	CGUGGUGUUUGUCAGCAAAAGAU G	989
AD-1634412	usgsuuuUfuGfUfCfagcaagaauL96	1470	asAfsudTu(Tgn)gcugacAfaAfaaccascsg	1593	CGUGGUGUUUGUCAGCAAAAGAU G	989
AD-1634413	usgsuuuUfuGfUfCfagcaagaauL96	541	asAfsudTu(Tgn)gcugacAfaAfaaccascsg	1594	CGUGGUGUUUGUCAGCAAAAGAU G	989
AD-1634414	usgsuuuUfuGfUfCfagcaagaauL96	1404	asAfsudTu(Tgn)gcugacAfaAfaaccascsg	1595	CGUGGUGUUUGUCAGCAAAAGAU G	989
AD-1634415	csesucaaggAfAfGfagaaucauL96	1471	asdTscudGadTucudTuCfcauagagsgcsu	1596	AGCCUCAUGGAAGAGAAAGCAGA U	946
AD-1634416	csesucaaggAfAfGfagaaucauL96	1472	asdTscudGadTucudTuCfcauagagsgcsu	1597	AGCCUCAUGGAAGAGAAAGCAGA U	946
AD-1634417	csesucaaggAfAfGfagaaucauL96	1473	asdTscudGadTucudTuCfcauagagsgcsu	1598	AGCCUCAUGGAAGAGAAAGCAGA U	946
AD-1634418	csesucaaggAfAfGfagaaucauL96	1474	asdTscudGadTucudTuCfcauagagsgcsu	1599	AGCCUCAUGGAAGAGAAAGCAGA U	946
AD-1634419	csesucaaggAfAfGfagaaucauL96	1475	asdTscudGadTucudTuCfcauagagsgcsu	1600	AGCCUCAUGGAAGAGAAAGCAGA U	946
AD-1634420	gsasegugGfuGfUfUfugcagaauL96	670	asUfsudGadTucudTuCfcauagagsgcsu	1601	GAGACGUGGUGUUUGUCAGCAA A	1118
AD-1634421	gsasegugGfuGfUfUfugcagaauL96	670	asUfsudGc(Tgn)gacaacAfcCfagcucsuc	1602	GAGACGUGGUGUUUGUCAGCAA A	1118
AD-1634422	gsasegugGfuGfUfUfugcagaauL96	670	asUfsudGc(Tg)gacaacAfcCfagcucsuc	1603	GAGACGUGGUGUUUGUCAGCAA A	1118
AD-1634423	gsusggugUfuUfGfUfagcaagaauL96	468	asUfscudTudGcugacaAfaCfaccacsgsu	1604	ACGUGGUGUUUGUCAGCAAAAGA U	916
AD-1634424	gsusggugUfuUfGfUfagcaagaauL96	1476	asUfscudTudAcugacaAfaCfaccacsgsu	1605	ACGUGGUGUUUGUCAGCAAAAGA U	916
AD-	gsusggugUfuUfGfUfagcaagaauL96	468	asUfscudTu(Tgn)gcugacaAfaCfaccacsgsu	1606	ACGUGGUGUUUGUCAGCAAAAGA U	916

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:	mRNA Target Sequence	SEQ ID NO:
1634425					U	
AD-1634426	gsusggagUfuUfGfUfcaguaaagaulL96	1477	asUfscudTudAcugacaAfaCfuaacsgsu	1607	ACGUGGUGUUUGUCAGCAAAAGA	916
AD-1634427	gsusgcugUfuUfGfUfcaguaaagaulL96	1478	asUfscudTudAcugacaAfaCfuaacsgsu	1608	ACGUGGUGUUUGUCAGCAAAAGA	916
AD-1634428	gsusguugUfuUfGfUfcaguaaagaulL96	1479	asUfscudTudAcugacaAfaCfuaacsgsu	1609	ACGUGGUGUUUGUCAGCAAAAGA	916
AD-1634429	gsuscgugUfuUfGfUfcaguaaagaulL96	1480	asUfscudTudAcugacaAfaCfuaacsgsu	1610	ACGUGGUGUUUGUCAGCAAAAGA	916
AD-1634430	gsusugugUfuUfGfUfcaguaaagaulL96	1481	asUfscudTudAcugacaAfaCfuaacsgsu	1611	ACGUGGUGUUUGUCAGCAAAAGA	916
AD-1634431	gsusggagUfuUfGfUfcaguaaagaulL96	1477	asUfscdTu(Tgn)gcugacaAfaCfuaacsgsu	1612	ACGUGGUGUUUGUCAGCAAAAGA	916
AD-1634432	gsusgcugUfuUfGfUfcaguaaagaulL96	1478	asUfscdTu(Tgn)gcugacaAfaCfuaacsgsu	1613	ACGUGGUGUUUGUCAGCAAAAGA	916
AD-1634433	gsusguugUfuUfGfUfcaguaaagaulL96	1479	asUfscdTu(Tgn)gcugacaAfaCfuaacsgsu	1614	ACGUGGUGUUUGUCAGCAAAAGA	916
AD-1634434	gsuscgugUfuUfGfUfcaguaaagaulL96	1480	asUfscdTu(Tgn)gcugacaAfaCfuaacsgsu	1615	ACGUGGUGUUUGUCAGCAAAAGA	916
AD-1634435	gsusugugUfuUfGfUfcaguaaagaulL96	1481	asUfscdTu(Tgn)gcugacaAfaCfuaacsgsu	1616	ACGUGGUGUUUGUCAGCAAAAGA	916
AD-1634436	gsasagagAfaGfCfAfgauccugugulL96	502	asdCsacdAgdGaucudGcUfucucucscsu	1617	UGGAAGAGAAGCAGAUCCUGUG	950
AD-1634437	gsasagagAfaGfCfAfgauccugugulL96	502	asCfsacadGg(Agn)ucugcUfuCfucucscs	1618	UGGAAGAGAAGCAGAUCCUGUG	950

Example 5. Design, Synthesis and In Vitro Screening of Additional dsRNA Duplexes

Based on the *in vitro* analyses, structure-active relationship (SAR) analyses were performed. In particular, additional duplexes were designed, synthesized, and assayed.

siRNAs were designed, synthesized, and prepared using the methods described above. *In vitro* screening assays in Hep3B and PCH cells with these siRNAs were performed as described above.

Detailed lists of the unmodified KHK sense and antisense strand nucleotide sequences are shown in Table 12. Detailed lists of the modified KHK sense and antisense strand nucleotide sequences are shown in Table 13.

For transfections, cells (ATCC, Manassas, VA) were grown to near confluence at 37°C in an atmosphere of 5% CO₂ in Eagle's Minimum Essential Medium (Gibco) supplemented with 10% FBS (ATCC) before being released from the plate by trypsinization. Transfection was carried out by adding 7.5 µl of Opti-MEM plus 0.1 µl of Lipofectamine RNAiMax per well (Invitrogen, Carlsbad CA, cat # 13778-150) to 2.5 µl of each siRNA duplex to an individual well in a 384-well plate. The mixture was then incubated at room temperature for 15 minutes. Forty µl of complete growth media without antibiotic containing $\sim 1.5 \times 10^4$ cells were then added to the siRNA mixture. Cells were incubated for 24 hours prior to RNA purification. Single dose experiments were performed at 10, 1 and 0.1 nM final duplex concentration.

Total RNA isolation was performed using DYNABEADS. Briefly, cells were lysed in 10µl of Lysis/Binding Buffer containing 3 µL of beads per well and mixed for 10 minutes on an electrostatic shaker. The washing steps were automated on a Biotek EL406, using a magnetic plate support. Beads were washed (in 3µL) once in Buffer A, once in Buffer B, and twice in Buffer E, with aspiration steps in between. Following a final aspiration, complete 12µL RT mixture was added to each well, as described below.

For cDNA synthesis, a master mix of 1.5µl 10X Buffer, 0.6µl 10X dNTPs, 1.5µl Random primers, 0.75µl Reverse Transcriptase, 0.75µl RNase inhibitor and 9.9µl of H₂O per reaction were added per well. Plates were sealed, agitated for 10 minutes on an electrostatic shaker, and then incubated at 37 degrees C for 2 hours. Following this, the plates were agitated at 80 degrees C for 8 minutes.

RT-qPCR was performed as described above and relative fold change was calculated as described above. The results of the transfection assays of the dsRNA agents listed in Tables 12 and 13 in Hep3B cells are shown in Table 14. The results of the transfection assays of the dsRNA agents listed in Tables 12 and 13 in primary cynomolgus hepatocytes (PCH) are shown in Table 15.

For Dual-Glo® Luciferase assay, cells (ATCC, Manassas, VA) were grown to near confluence at 37°C in an atmosphere of 5% CO₂ in Eagle's Minimum Essential Medium (Gibco) supplemented with 10% FBS (ATCC) before being released from the plate by trypsinization. Dual-Glo® Luciferase constructs were generated in the psiCHECK2 plasmid containing the human KHK genomic sequence. Each dual-luciferase plasmid was co-transfected with siRNA (Tables 12 and 13)

into approximately 2×10^4 cells using Lipofectamine 2000 (Invitrogen, Carlsbad CA. cat # 11668-019). For each well of a 96 well plate, 0.5 μ l of Lipofectamine was added to 100 ng of plasmid vector and a single siRNA (Tables 12 and 13) in 14.8 μ l of Opti-MEM and allowed to complex at room temperature for 15 minutes. The mixture was then added to the cells which were resuspended in 80 μ l of fresh complete media. Cells were incubated for 24 hours before luciferase was measured. Single dose experiments were performed at 10, 1 and 0.1 nM final duplex concentration.

Forty-eight hours after the siRNAs were transfected, Firefly (transfection control) and Renilla (fused to KHK target sequence) luciferase were measured. First, media was removed from cells. Then Firefly luciferase activity was measured by adding 75 μ l of Dual-Glo® Luciferase Reagent equal to the culture medium volume to each well and mix. The mixture was incubated at room temperature for 30 minutes before luminescence (500 nm) was measured on a Spectramax (Molecular Devices) to detect the Firefly luciferase signal. Renilla luciferase activity was measured by adding 75 μ l of room temperature Dual-Glo® Stop & Glo® Reagent to each well and the plates were incubated for 10-15 minutes before luminescence was again measured to determine the Renilla luciferase signal. The Dual-Glo® Stop & Glo® Reagent, quenches the firefly luciferase signal and sustains luminescence for the Renilla luciferase reaction. siRNA activity was determined by normalizing the Renilla (KHK) signal to the Firefly (control) signal within each well. The magnitude of siRNA activity was then assessed relative to cells that were transfected with the same vector but were not treated with siRNA or were treated with a non-targeting siRNA. All transfections were done in quadruplicates.

Table 16 shows the Dual-Glo® Luciferase assay results of a single dose screen in cells transfected with the indicated agents in Tables 12 and 13.

Table 12. Unmodified Sense and Antisense Strand Sequences of KHK dsRNA

Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO.	Range in XM_017004061.1	Antisense Strand Sequence 5' to 3'	SEQ ID NO.	Range in XM_017004061.1
AD-1290507.2	UUCUUCACUCUGUCAAUUGGAU	1658	2200-2220	AUCCAUUUUGACAGAGAAGAAAU	415	2198-2220
AD-1290509.2	GAUUAUUUUGGCUUUUAAU	167	2130-2150	AUUAAAUGGCAGAUUUUAAUCCA	391	2128-2150
AD-1290510.2	AAUUCUUCAUCUGUCAAUUU	183	2197-2217	AAUUUGACAGAGAAGAAAUUUA	407	2195-2217
AD-1290514.2	CAAUUUUUUUAUCUGUCAAUU	182	2196-2216	AUUUGACAGAGAAGAAAUUUGAG	406	2194-2216
AD-1290515.2	AGGCCUUUAUUAUGUAAAGAGU	158	2073-2093	ACUCUUUACAUUAUAAAGGCCUUA	382	2071-2093
AD-1290516.2	GGAUUAAAAUUCUGCCAUUUU	192	2129-2149	AUAAAUGGCAGAUUUUAAAUCCAG	416	2127-2149
AD-1290522.2	UCUGGAACACAUUUUGGAUUU	149	2025-2045	AAUCCAAUUAUGUGUUUCCAGAU	373	2023-2045
AD-1290523.2	GCCUCAUUUUUUAUCUUGUUU	181	2192-2212	AACAGAUAGAAGAAAUUUGAGGCAG	405	2190-2212
AD-1290524.2	AUUUCUUCAUCUGUCAAUUGU	184	2198-2218	ACAUUUGACAGAGAAGAAAUUUG	408	2196-2218
AD-1290527.2	UGGAUUAAAAUUCUGCCAUUUU	193	2128-2148	AAAAUGGCAGAUUUUAAAUCCAGG	417	2126-2148
AD-1290528.2	CUGGAACACAUUUUGGAUUUU	150	2026-2046	AAAUUCCAAUUAUGUGUUUCCAGAU	374	2024-2046
AD-1290531.2	CUGCCUCAUUUUUUAUCUUAU	179	2190-2210	AAGAUAGAAGAAAUUUGAGGCAGAU	403	2188-2210
AD-1290533.2	AAAUUCGCCAUUUAAUUAAGCU	169	2135-2155	AGCUAAUAAAUGGCAGAUUUUA	393	2133-2155
AD-1290535.2	AAUCUGCCAUUUAAUUAAGCUU	170	2136-2156	AAGCUAAUAAAUGGCAGAUUUU	394	2134-2156
AD-1290539.5	CAGACUUUUGAGAGGUUGAUU	68	755-775	AAUAAACCUUCUCAAAGUCUGUA	292	753-775
AD-1290542.2	UCAAUUUUUUAUCUUGUCAAU	194	2195-2215	AUUGACAGAGAAGAAAUUUGAGG	418	2193-2215
AD-1290543.2	UGGAACACAUUAUUGGAUUUGU	151	2027-2047	ACAAUCCAAUUAUGUGUUUCCAGA	375	2025-2047
AD-1290551.2	CUGGAUUAAAAUUCUGCCAUUU	166	2127-2147	AAAUUGGCAGAUUUUAAAUCCAGGU	390	2125-2147
AD-1290552.2	UUUCUUCAUCUGUCAAUUGGU	195	2199-2219	ACCAUUUGACAGAGAAGAAAUUU	419	2197-2219
AD-1290554.2	AUAAUGUAAAAGGGCUUUUAGAU	162	2096-2116	AUCUAAAAGCCCUUUAACAUUAUUAU	386	2094-2116
AD-1290555.2	AUAUAAUGUAAAAGGGCUUUUAU	161	2094-2114	AUAAAAGCCCUUUAACAUUAUUAUGC	385	2092-2114
AD-1290556.2	GCCUUUAUUAUGUAAAGAGCAU	159	2075-2095	AUGCUCUUUAACAUUAUUAAGGCCU	383	2073-2095
AD-1290557.2	GGCCUUUAUUAUGUAAAAGAGCU	196	2074-2094	AGCUCUUUAACAUUAUUAAGGCCUU	420	2072-2094
AD-1290558.2	UAUAAUGUAAAAGGGCUUUUAGU	197	2095-2115	ACUAAAAGCCCUUUAACAUUAUUAUG	421	2093-2115
AD-1290563.2	GUAAGGCCUUUAUUAUGUAAAU	156	2070-2090	AUUUACAUUAUUAAGGCCUUACCC	380	2068-2090
AD-1290564.2	CCUCAUUUUUAUCUUAUCUGUCU	199	2193-2213	AGACAGAUAGAAGAAAUUUGAGGCA	423	2191-2213

Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO.	Range in XM_017004061.1	Antisense Strand Sequence 5' to 3'	SEQ ID NO.	Range in XM_017004061.1
AD-1290565.2	CUCAUUUUCUUCUUCUUCAU	200	2194-2214	AUGACAGAUAGAAUUAUUGAGGC	424	2192-2214
AD-1290570.2	AAGGCCUUAUAAUGUAAAGAU	157	2072-2092	AUCUUUACAUUAUAAAGGCCUUAAC	381	2070-2092
AD-1290573.2	AUCUGCCCUCAUUUUCUUCAUU	177	2188-2208	AAUGAAGAAUUAUUGAGGCAGAUUG	401	2186-2208
AD-1290574.2	UAAGGCCUUUAUAUGUAAAGU	201	2071-2091	ACUUUACAUUAUAAAGGCCUUUACC	425	2069-2091
AD-1290584.2	GUGUUUGUCAGCAAAAGAUUU	95	952-972	AACAUUUUGCUGACAAAACACCA	319	950-972
AD-1290589.2	GGAACACAUUUUGGAUUUGGU	152	2028-2048	ACCAAUUCCAAUAUGUGUUCACG	376	2026-2048
AD-1290592.2	CAUAUAAUGUAAAGGCCUUUU	202	2093-2113	AAAAGCCUUUACAUUAUAUUGCU	426	2091-2113
AD-1290597.2	AUUAAAACUGCCCAUUUAAUU	168	2131-2151	AAUUAAAUGGCAGAUUUUAAUCC	392	2129-2151
AD-1290599.7	UGGUGUUUGUCAGCAAAAGAUU	93	950-970	AAUCUUUGCUGACAAAACACCACG	317	948-970
AD-1290600.2	GCUUGGCUACAGAAUUAUUGU	190	2229-2249	ACAUAUAUUCUGUAGCCAAAGCAG	414	2227-2249
AD-1290602.2	UGCCUCAAUUUUCUUCACUCUGU	180	2191-2211	ACAGAUAGAAGAAUUAUUGAGGCAGA	404	2189-2211
AD-1290604.2	AUCUGCCAUUUAAUUAAGCUGU	171	2137-2157	ACAGCUAAUUAUUAUUGGCAGAUUU	395	2135-2157
AD-1290605.2	AAUCUGCCCUCAUUUUCUUCAU	176	2187-2207	AUGAAGAAUUAUUGAGGCAGAUUGC	400	2185-2207
AD-1290609.2	UGCCAUUUAAUUAAGCUGCAUU	203	2140-2160	AAUGCAGCUAAUUAUUAUUGGCAGA	427	2138-2160
AD-1290611.3	AGACUUUGAGAAAGGUUGAUCU	69	756-776	AGAUCAAACCUUCUCAAAAGUCUGU	293	754-776
AD-1290612.2	AUCUGGAACACAUUAUUGGAU	148	2024-2044	AUUCCAAUAUGUGUUCACAGAUUCG	372	2022-2044
AD-1290615.2	UCUGCCCUCAUUUUCUUCUUCU	178	2189-2209	AGAUAGAAGAAUUAUUGAGGCAGAUU	402	2187-2209
AD-1290618.2	AAUGUAAAAGGGCUUUUAGAGUU	164	2098-2118	AACUCUAAAAGCCCUUUUACAUUAU	388	2096-2118
AD-1290624.2	AUUUUUGUGAGGAUAAAACUCU	204	2242-2262	AGAUUUUAUCCUCACAAUAAAUUC	428	2240-2262
AD-1290626.2	GGUAAAGGCCUUUAUUAUGUAAU	205	2069-2089	AUUACAUUAUAAAGGCCUUUACCCA	429	2067-2089
AD-1290633.2	CUGCCAUUUAAUUAAGCUGCAU	172	2139-2159	AUGCAGCUAAUUAUUAUUGGCAGAU	396	2137-2159
AD-1290635.2	UUCUGCUUGGCUACAGAAUUU	206	2225-2245	AAAUUCUGUAGCCAAAGCAGAAUU	430	2223-2245
AD-1290639.2	UAAUGUAAAAGGCCUUUAAGAGU	163	2097-2117	ACUCUAAAAGCCCUUUACAUUAUA	387	2095-2117
AD-1290643.2	UGCUGGCCUACAGAAUUAUUU	189	2228-2248	AAAUAAUUCUGUAGCCAAAGCAGA	413	2226-2248
AD-1290650.2	CGCAAUCUGCCCUCAAUUUCUU	174	2184-2204	AAGAAAUAUUGAGGCAGAUUUGCGUU	398	2182-2204
AD-1290651.2	GUUCAAGUGGAUCCACAUUGU	207	783-803	ACAAUUGUGGAUCCACUUGAACUG	431	781-803
AD-1290654.2	GGGUAAAGGCCUUUAUUAUGUAU	208	2068-2088	AUACAUUAUAAAGGCCUUUACCCAC	432	2066-2088

Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO.	Range in XM_017004061.1	Antisense Strand Sequence 5' to 3'	SEQ ID NO.	Range in XM_017004061.1
AD-1290655.2	GAUCUGGAAACACAUUUUGGAU	209	2023-2043	AUCCAAUAUGUGUUCCAGAUUCGG	433	2021-2043
AD-1290659.2	CAAUUCUGCCCAAAUUCUUCU	211	2186-2206	AGAAGAAAUAUAGGCAGAUUUGCG	435	2184-2206
AD-1290660.2	CCUGGAUUAAAAUCUGCCAUAU	165	2126-2146	AAUGGCAGAUUUUAUCCAGGUC	389	2124-2146
AD-1290661.2	GCAUAUAUUGUAAAGGGCUUU	160	2092-2112	AAAGCCUUUAACAUUAUAUGCUC	384	2090-2112
AD-1290666.2	ACUUUGAGAAAGGUUGAUCUGU	213	758-778	ACAGAUCAACCUUCUCAAAGUCU	437	756-778
AD-1290670.2	UCCGAUCUGGAAACACAUUUU	146	2020-2040	AAAUUGUGUUCUCCAGAUCCGACC	370	2018-2040
AD-1290672.2	GCAAUUCUGCCUCAAUUCUUAU	175	2185-2205	AAAGAAAUUGAGGCAGAUUUGCGU	399	2183-2205
AD-1290681.2	UGGGUAAAGGCCUUUAUAUGUU	215	2067-2087	AACAUUAUAAGGCCUUUACCCACC	439	2065-2087
AD-1290684.2	CGAUCUGGAAACACAUUUUGGU	217	2022-2042	ACCAAU AUGUGUUCUCCAGAUCCGA	441	2020-2042
AD-1290687.2	CUGCUUGGCCUACAGAAUUAU	188	2227-2247	AAUAUUCUGUAGCCAAAGCAGAA	412	2225-2247
AD-1290702.2	UCUGCCAUUUAAUUAAGCUGCU	218	2138-2158	AGCAGCUAAUUAUAAUGGCAGAUU	442	2136-2158
AD-1290712.2	CCGAUCUGGAAACACAUUUUGU	147	2021-2041	ACAAUAUGUGUUCUCCAGAUCCGAC	371	2019-2041
AD-1290719.2	AUUCUGCUUUGGCUACAGAAU	186	2224-2244	AAUUCUGUAGCCAAAGCAGAAUUG	410	2222-2244
AD-1290722.2	UCUGCUUGGCCUACAGAAUUAU	187	2226-2246	AUAUUCUGUAGCCAAAGCAGAAU	411	2224-2246
AD-1290741.2	ACGCAAUUCUGCCUCAAUUCU	173	2183-2203	AGAAAUUGAGGCAGAUUUGCGUUA	397	2181-2203
AD-1290742.2	GUGGUAAAGGCCUUUAUAUGU	155	2066-2086	ACAUUAUAAGGCCUUUACCCACCC	379	2064-2086
AD-1290747.2	GGAGCCCACCUUGGAAUUAU	138	1941-1961	AUUAUUAUCCAAAGGUGGGCUCCAA	362	1939-1961
AD-1290750.2	CCCAGUAAACCUUGCCAAAGAU	221	1706-1726	AUCUUUGGCAGGUUCACUGGGUG	445	1704-1726
AD-1290755.2	GGUGGGUAAAGGCCUUUAUAU	154	2065-2085	AAUUAUAAGGCCUUUACCCACCCU	378	2063-2085
AD-1290763.2	GUCCGAUCUGGAAACACAUUAU	145	2019-2039	AAUAUGUGUUCUCCAGAUCCGACCU	369	2017-2039
AD-1290764.2	GGUCCGAUCUGGAAACACAUUAU	144	2018-2038	AUAUGUGUUCUCCAGAUCCGACCU	368	2016-2038
AD-1290796.2	UUGGAGCCCACCUUGGAAUUAU	225	1939-1959	AAAUUCCAAAGGUGGGCUCCAAAGG	449	1937-1959
AD-1290800.2	GGGUGGGUAAAGGCCUUUAUAU	153	2064-2084	AUUAUAAGGCCUUUACCCACCCUA	377	2062-2084
AD-1290805.2	UGGAGCCCACCUUGGAAUUAU	227	1940-1960	AUAUAUCCAAAGGUGGGCUCCAAAG	451	1938-1960
AD-1290836.2	AAUUCUGCUUGGCCUACAGAAU	185	2223-2243	AUUCUGUAGCCAAAGCAGAAUUGG	409	2221-2243
AD-1290837.5	UGAUCUGAGCCACAGUUCAGUU	76	771-791	AACUUGAACUCUGGGUCAGAUCAAC	300	769-791
AD-1290841.2	AUCCCCACAGCUCAGAAAGCUU	136	1767-1787	AAGCUUCUGAGCUCUGGGAAUAG	360	1765-1787

Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO.	Range in XM_017004061.1	Antisense Strand Sequence 5' to 3'	SEQ ID NO.	Range in XM_017004061.1
AD-1290842.2	GAGCCACCCUUGGAAUUAAGU	139	1942-1962	ACUUAUUUCCAAAGGUGGGCUCCA	363	1940-1962
AD-1290857.2	UGCCACACAGCCUGUGAUUUU	229	1852-1872	AAAAUCACAGGCUUGGUGGCAGG	453	1850-1872
AD-1290865.2	CUGCGUUGUGCAGACUCUAUU	130	1749-1769	AAUAGAGUCUGCACAACGCAGGG	354	1747-1769
AD-1290875.2	GCCACACAGCCUGUGAUUUUGU	231	1853-1873	ACAAUUCACAGGCUUGGUGGCAG	455	1851-1873
AD-1290880.2	CUUGGAGCCACCCUUGGAAUU	137	1938-1958	AAUCCAAAGGUGGGCUCCAAAGGG	361	1936-1958
AD-1290884.5	GCAGGAAGCACUGAGAUUCGU	116	1209-1229	ACGAAUCUCAGUGCUUCCUGCAC	340	1207-1229
AD-1290885.5	CUGACCCAGUUCAGUGGAUU	78	775-795	AAUCCACUUGAACUUGGGUCAGAU	302	773-795
AD-1290894.2	AGGUCCGAUUCUGGAACACAUU	233	2017-2037	AAUGUUAUCCAGAUCCGACCUC	457	2015-2037
AD-1290897.2	UGCGUUGUGCAGACUCUAUUU	131	1750-1770	AAAUAGAGUCUGCACAACGCAGG	355	1748-1770
AD-1290908.2	CCAGUGAACCCUGCCAAAGAAU	235	1707-1727	AUUCUUUGGCAGGUUCACUGGGU	459	1705-1727
AD-1290909.2	UUGUGCAGACUCUAUUCUCAU	134	1754-1774	AUGGGAUAAGAGUCUGCACAACG	358	1752-1774
AD-1290910.2	UAGGGUGGGUAAGGCCUUAUU	236	2062-2082	AAUAAAGGCCUUAACCCACCCUAUA	460	2060-2082
AD-1290911.2	AGCCCACCUUGGAAUUAAGGU	140	1943-1963	ACCUAAUUAUCCAAAGGUGGGCUCC	364	1941-1963
AD-1290926.2	GCCCACCUUGGAAUUAAGGGU	141	1944-1964	ACCUUAAUUAUCCAAAGGUGGGCUC	365	1942-1964
AD-1290931.2	UCAGCCACAAAUUGUGACCCAU	143	1970-1990	AUGGGUCACAUUUUGUGGCUGAGG	367	1968-1990
AD-1290939.2	AGGGUGGGUAAAGGCCUUAUAU	238	2063-2083	AUAUAAAGGCCUUAACCCACCCUAU	462	2061-2083
AD-1290969.7	ACCUUCAUUGCCUCCGUCAUU	108	1162-1182	AUAGACGGAGGCAUUGAAGGUGU	332	1160-1182
AD-1290971.3	GCUACGGAGACGUGGUGUUAU	242	938-958	AAACACACCGUCUCCGUAGCCA	466	936-958
AD-1290973.2	GUUGGCAGACUCUAUUCCCU	243	1753-1773	AGGAAUAAGAGUCUCGACAAACGC	467	1751-1773
AD-1290983.2	CGUUGUGCAGACUCUAUUCU	133	1752-1772	AGGAAUAGAGUCUCGACAAACGCA	357	1750-1772
AD-1290989.2	GCGUUGUGCAGACUCUAUUCU	132	1751-1771	AGAAUAGAGUCUCGACAAACGCAG	356	1749-1771
AD-1290993.2	UAUUCACACAGCUCAGAAAGCU	135	1766-1786	AGCUUCUGAGCUGUGGGAAUAGA	359	1764-1786
AD-1291003.2	GGCGUGCCUCAGCCACAAAUU	142	1962-1982	AAUUUGUGGCUGAGGCACGCCCU	366	1960-1982
AD-1423312.3	UGCAGGAAGCAGUGAGAUUCU	115	1208-1228	AGAATCTCAGUGCUUCCUGCACG	1141	1206-1228
AD-1423319.3	GACUUUGAGAAAGGUUGAUUCU	70	757-777	AAGATCAACCUUCUCAAAGUCUG	1144	755-777
AD-1423336.7	GUUCAAGUGGAUCCACAUUGU	207	783-803	ACAATGTGGAUCCACAUUGAACUG	1152	781-803
AD-1548743.7	UGGUGUUUGUCAGCAAAAGAUU	93	950-970	AAUCTUTGCUGACAAACACCACG	1269	948-970

Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO.	Range in XM_017004061.1	Antisense Strand Sequence 5' to 3'	SEQ ID NO.	Range in XM_017004061.1
AD-1612957.2	GCCUCAUGGAAGAGAAAGCAGU	1200	518-538	ACUGCUTCUCUTCCAUAGAGGCUA	1270	516-538
AD-1612963.2	UGGAAGAGAAAGCAGAUCCUGU	1201	524-544	ACAGGATCUGCTUCUCUCCAUUG	1272	522-544
AD-1612969.2	AGAAAGCAGAUCCUGGCGUGU	1203	530-550	ACACGCACAGGAUCUGCUUCUCU	1274	528-550
AD-1613059.2	CAGACUUUGAGAAAGGUUGAUU	68	755-775	AAUCAACCUUUCTCAAAGUCUGUA	1276	753-775
AD-1613060.2	AGACUUUGAGAAAGGUUGAUCU	69	756-776	AGAUCAAACCUUCUCAAAGUCUGU	293	754-776
AD-1613061.1	GACUUUGAGAAAGGUUGAUCUU	70	757-777	AAGATCAACCCUTCUCAAAGUCUG	1696	755-777
AD-1613062.2	ACUUUGAGAAAGGUUGAUCUGU	213	758-778	ACAGAUCAAACCTUCUCAAAAGUCU	1277	756-778
AD-1613072.1	GGUUGAUCUGACCCAGUUCAU	239	768-788	ATGAACTGGGUCAGAUCAACCUU	1697	766-788
AD-1613075.2	UGAUCUGACCCAGUUCAAAGUU	76	771-791	AACUTGAACUCUGGGUCAGAUCAAC	1183	769-791
AD-1613079.2	CUGACCCAGUUCAAAGUGGAUU	78	775-795	AAUCCACUUGAACUGGGUCAGAU	302	773-795
AD-1613087.1	GUUCAAGUGGAUCCACAUUGU	207	783-803	ACAATGTGGAUCCACAUUGAACUG	1152	781-803
AD-1613094.2	UGGAUCCACAUUGAGGGCCGU	1207	790-810	ACGGCCUCAATGUGGAUCCACU	1284	788-810
AD-1613242.2	GCUACGGAGACGUGGUGUUUU	242	938-958	AAAACACCCACGTCUCCGUAGCCA	1291	936-958
AD-1613254.2	UGGUGUUUGUCAGCAAAAGAUU	93	950-970	AAUCTUTGCUGACAAACACCCACG	1269	948-970
AD-1613256.2	GUGUUUGUCAGCAAAAGAUUU	95	952-972	AACATCTUUGCTGACAAACACCA	1294	950-972
AD-1613371.3	ACCUUCAAUGCCUCCGUCAUU	108	1162-1182	AAUGACGGAGGCAUUGAAGGUGU	332	1160-1182
AD-1613400.2	GCAGGAAGCACUGAGAUUCGU	116	1209-1229	ACGAUUCACAGTGCUUCCUGCAC	1304	1207-1229
AD-1684592.1	GUAGCCUCAUGGAAGAGAAAGU	1659	515-535	ACUUCUCUCCAUAGAGGCUACUC	1698	513-535
AD-1684593.1	AGCCUCAUGGAAGAGAAAGCAU	1660	517-537	AUGCTUCUCUCCAUAGAGGCUAC	1699	515-537
AD-1684594.1	CUCAUGGAAGAGAAAGCAGAUU	51	520-540	AAUCTGCUUCUCUCCAUAGAGGC	1700	518-540
AD-1684595.1	UCAUGGAAGAGAAAGCAGAUUCU	1661	521-541	AGAUUGCUUUCUCCAUAGAGG	1701	519-541
AD-1684596.1	AUGGAAGAGAAAGCAGAUCCUU	52	523-543	AAGGAUCUGCUUCUCUCCAUAGA	276	521-543
AD-1684597.1	AAGAGAAAGCAGAUCCUGUGCU	1662	527-547	AGCACAGGAUCUGCUUCUCUCC	1702	525-547
AD-1684598.1	GAGAAAGCAGAUCCUGUGCGUU	1663	529-549	AAGCACAGGAUCUGCUUCUCUU	1703	527-549
AD-1684599.1	AAGCAGAUCCUGUGCGUGGGU	1664	532-552	ACCCACGCACAGGAUCUGCUUCU	1704	530-552
AD-1684600.1	AAGCAGAUCCUGUGCGUGGGU	1664	532-552	ACCCACGCACAGGAUCUGCUUCU	1704	530-552
AD-1684601.1	AGCAGAUCCUGUGCGUGGGGU	1665	533-553	ACCCACGCACAGGAUCUGCUUC	1705	531-553

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AD-1684602.1	AGCAGAUCCUGUGCGUGGGGU	1665	533-553	ACCCACGCACAGGAUCUGCUUC	1705	531-553
AD-1684603.1	GCAGAUCCUGUGCGUGGGGU	1666	534-554	AGCCCCACGCACAGGAUCUGCUU	1706	532-554
AD-1684604.1	CAGAUCCUGUGCGUGGGGU	1667	535-555	AAGCCCCACGCACAGGAUCUGCU	1707	533-555
AD-1684605.1	AGAUCCUGUGCGUGGGGU	1668	536-556	AUAGCCCCACGCACAGGAUCUGC	1708	534-556
AD-1684606.1	CAGACUUUGAGAAAGGUUGAUU	68	755-775	AAUCAACCUUUCTCAAAAGUCUGUG	1709	753-775
AD-1684607.1	CAGACUUUGAGAAAGGUUGAUU	68	755-775	AAUCAACCUUUCTCAAAAGUCUGCU	1710	753-775
AD-1684608.1	CAGACUUUGAGAAAGGUUGAUU	1669	755-775	UAUCAACCUUUCTCAAAAGUCUGCU	1711	753-775
AD-1684609.1	GACUUUGAGAAAGGUUGAUU	1670	757-775	AAUCAACCUUUCTCAAAAGUCUG	1712	755-775
AD-1684610.1	GACUUUGAGAAAGGUUGAUU	70	757-777	AAGATCAACCUUUCTCAAAAGUCUG	1696	755-777
AD-1684611.1	UUUGAGAAAGGUUGAUCUGU	1671	760-778	ACAGAUCAACCTUCUCACAAAGU	1713	758-778
AD-1684612.1	ACUUUAGAAAGGUUGAUCUGU	1672	758-778	ACAGAUCAACCTUCUUUAAAGUCU	1714	756-778
AD-1684613.1	UUGAGAAAGGUUGAUCUGACCU	1673	761-781	AGGUCAGAUCAACCUUUCUCAAAG	1715	759-781
AD-1684614.1	GAGAAAGGUUGAUCUGACCCAU	1674	763-783	AUGGGUCAGAUCAACCUUCUCAA	1716	761-783
AD-1684615.1	GAAGGUUGAUCUGACCCAGUU	1675	765-785	AACUGGGUCAGAUCAACCUUCUC	1717	763-785
AD-1684616.1	AGGUUGAUCUGACCCAGUUUCU	1676	767-787	AGAACUGGGUCAGAUCAACCUUC	1718	765-787
AD-1684617.1	UGAUCUGACCCAGUUUCAAGUU	76	771-791	AACUTGAACUGGGUCAGAUACAGC	1719	769-791
AD-1684618.1	UGAUCUGACCCAGUUUCAAGUU	76	771-791	AACUTGAACUGGGUCAGAUACACU	1720	769-791
AD-1684619.1	UGAUCUGACCCAGUUUCAAGUA	1677	771-791	UACUTGAACUGGGUCAGAUACACU	1721	769-791
AD-1684620.1	AUCUGACCCAGUUUCAAGUU	1678	773-791	AACUTGAACUGGGUCAGAUACG	1722	771-791
AD-1684621.1	GACCCAGUUUCAAGUGGAUCCU	1679	777-797	AGGATCCACUUUGAACUGGGUCAG	1723	775-797
AD-1684622.1	ACCCAGUUUCAAGUGGAUCCAU	79	778-798	AUGGAUCCACUUUGAACUGGGUCA	303	776-798
AD-1684623.1	CAGUUCAGUGGAUCCACAUU	23	781-801	AAUGTGGAUCCACUUUGAACUGGG	1724	779-801
AD-1684624.1	AGUUCAGUGGAUCCACAUUU	81	782-802	AAAUGUGGAUCCACUUUGAACUGG	305	780-802
AD-1684625.1	AGUGGAUCCACAUUGAGGGGU	1680	788-808	AGCCCUCAUUGUGGAUCCACUUG	1725	786-808
AD-1684626.1	UGGAUCCACAUUGAGGGCCGU	1207	790-810	ACGGCCCUCAUUGUGGAUCCACU	1726	788-810
AD-1684627.1	GAUCCACAUUGAGGGCCCGAU	1681	792-812	AUCCGGCCCUCAUUGUGGAUCCA	1727	790-812
AD-1684628.1	AUCCACAUUGAGGGCCCGAAU	1682	793-813	AUUCGGCCCUCAUUGUGGAUCC	1728	791-813

Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO.	Range in XM_017004061.1	Antisense Strand Sequence 5' to 3'	SEQ ID NO.	Range in XM_017004061.1
AD-1684629.1	GAGACGUGUGUUUUGUCAGCU	1683	944-964	AGCUGACAAACACCCACGUCUCCG	1729	942-964
AD-1684630.1	CGUGGUGUUUGUCAGCAAAGU	219	948-968	ACUUTGCUGACAAACACACGUC	1730	946-968
AD-1684631.1	UUUGACGAAAGAUUGGGCCU	1684	956-976	AGGCCACAUUUUGCUGACAAAC	1731	954-976
AD-1684632.1	GUCAGCAAAGAUUGGGCCAU	1685	958-978	AUUGGCCACAUUUUGCUGACAA	1732	956-978
AD-1684633.1	UCAGCAAAGAUUGGGCCAAAGU	1686	959-979	ACUUGGCCACAUUUUGCUGACA	1733	957-979
AD-1684634.1	CAGCAAAGAUUGGGCCAAAGCU	1687	960-980	AGCUTGGCCACAUUUUGCUGAC	1734	958-980
AD-1684635.1	AGCAAAGAUUGGGCCAAAGCAU	1688	961-981	AUGCTUGGCCACAUUUUGCUGA	1735	959-981
AD-1684636.1	GAGACACCUUCAAUGCCUCCU	1689	1157-1177	AGGAGCAUUUGAAGGUGUCUCCA	1736	1155-1177
AD-1684637.1	AGACACCUUCAAUGCCUCCGU	1690	1158-1178	ACGGAGGCAUUUGAAGGUGUCUCC	1737	1156-1178
AD-1684638.1	GACACCUUCAAUGCCUCCGUU	1691	1159-1179	AACGGAGGCAUUUGAAGGUGUCUC	1738	1157-1179
AD-1684639.1	CCUUCAAUGCCUCCGUCACUCU	109	1163-1183	AGAUGACGGAGGCAUUUGAAGGUG	333	1161-1183
AD-1684640.1	GCCUCCGUCACUUCUACAGCCU	1692	1171-1191	AAGGCUGAAGAUACGGAGGCAU	1739	1169-1191
AD-1684641.1	CUCCGUCACUUCUACAGCCUUCU	113	1173-1193	AAGAGGCUGAAGAUACGGAGGCG	337	1171-1193
AD-1684642.1	GGAGCGUUGCAGGAAGCACUGU	1693	1202-1222	ACAGTGUUCCUGCAGGUCCUCC	1740	1200-1222
AD-1684643.1	GAGCGUGCAGGAAGCACUGAU	1694	1203-1223	AUCAGUGCUUCCUGCAGGUCCU	1741	1201-1223
AD-1684644.1	GCGUGCAGGAAGCACUGAGAU	1695	1205-1225	AUCUCAGUGCUUCCUGCAGGUCC	1742	1203-1225
AD-1684645.1	GUGCAGGAAGCACUGAGAUUU	114	1207-1227	AAAUUCAGUGCUUCCUGCAGCGC	338	1205-1227
AD-1684646.1	CCCAGUGAACCUUGCCAAAGAU	221	1706-1726	ATCUTUGGCAGGUUACUGGGGUG	1743	1704-1726
AD-1684647.1	CCAGUGAACCUUGCCAAAGAAU	235	1707-1727	ATUCUTUGGCAGGUUACUGGGU	1744	1705-1727
AD-1684648.1	CUGCGUUUGCAGACUCUAUU	130	1749-1769	AAUAGAGUUCUGCACAAACGAGG	354	1747-1769
AD-1684649.1	UGCGUUUGCAGACUCUAUUU	131	1750-1770	AAAUAGAGUUCUGCACAAACGAGG	355	1748-1770
AD-1684650.1	GCGUUUGCAGACUCUAUUUCU	132	1751-1771	AGAATAGAGUUCTGCACAAACGCG	1745	1749-1771
AD-1684651.1	CGUUUGCAGACUCUAUUCCU	133	1752-1772	AGGAAUAGAGUCUGCACAAACGCA	357	1750-1772
AD-1684652.1	GUUGUGCAGACUCUAUUCCCU	243	1753-1773	AGGGAATAGAGTCUGCACAAACGC	1746	1751-1773
AD-1684653.1	UUUGCAGACUCUAUUCCCCAU	134	1754-1774	ATGGGAAUAGAGUCUGCACAAACG	1747	1752-1774
AD-1684654.1	UAUUCCCACAGCUCAGAAAGCU	135	1766-1786	AGCUTCTGAGCTGUGGGAAUAGA	1748	1764-1786
AD-1684655.1	AUUCCCACAGCUCAGAAAGCUU	136	1767-1787	AAGTUCUGAGCUGUGGGAAUAG	1749	1765-1787

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AD-1684656.1	UGCCCAACAGCCUGUGAUUUU	229	1852-1872	AAATATCACAGGUGGUGGCAGG	1750	1850-1872
AD-1684657.1	GCCCAACAGCCUGUGAUUUU	231	1853-1873	ACAAAUACACAGGUGGUGGCAG	455	1851-1873
AD-1684658.1	CUUGGAGCCACCUUGGAAUU	137	1938-1958	AAUCCAAAGGUGGUGGCACAGG	361	1936-1958
AD-1684659.1	UUGGAGCCACCUUGGAAUUU	225	1939-1959	AAATCCAAAGTGGGCUCCAAAG	1751	1937-1959
AD-1684660.1	UGGAGCCACCUUGGAAUUU	227	1940-1960	ATAATUCCAAAGGUGGUGGCAG	1752	1938-1960
AD-1684661.1	GGAGCCACCUUGGAAUUU	138	1941-1961	ATUAAUTCCAAAGGUGGUGGCAG	1753	1939-1961
AD-1684662.1	GAGCCACCUUGGAAUUU	139	1942-1962	ACUUAATUCCAAAGGUGGUGGCAG	1754	1940-1962
AD-1684663.1	AGCCACCUUGGAAUUU	140	1943-1963	ACCUTAAUCCAAAGGUGGUGGCAG	1755	1941-1963
AD-1684664.1	GCCACCUUGGAAUUU	141	1944-1964	ACCCUAAUCCAAAGGUGGUGGCAG	1756	1942-1964
AD-1684665.1	GGCGUGCCUCAGCCACAAUU	142	1962-1982	AAUUTGTGGCUGAGGCACGCCCU	1757	1960-1982
AD-1684666.1	UCAGCCACAAUUGUACCCAU	143	1970-1990	ATGGGUCACAUTUGUGGCUGAGG	1758	1968-1990
AD-1684667.1	AGGUCCGAUCUGGAAACACAUU	233	2017-2037	AAUUTGTUCCAGAUCCGACCCU	1759	2015-2037
AD-1684668.1	GGUCCGAUCUGGAAACACAUU	144	2018-2038	ATAUGUGUCCAGAUCCGACCCU	1760	2016-2038
AD-1684669.1	GUCCGAUCUGGAAACACAUU	145	2019-2039	AAUATGTUCCAGAUCCGACCCU	1761	2017-2039
AD-1684670.1	UCCGAUCUGGAAACACAUU	146	2020-2040	AAAUUGUGUCCAGAUCCGACCC	370	2018-2040
AD-1684671.1	CCGAUCUGGAAACACAUU	147	2021-2041	ACAATATGUGUTCCAGAUCCGAC	1762	2019-2041
AD-1684672.1	CGAUCUGGAAACACAUU	217	2022-2042	ACCAAUUGUGTUCAGAUCCGGA	1763	2020-2042
AD-1684673.1	GAUCUGGAAACACAUU	209	2023-2043	ATCCAATUGUGUCCAGAUCCG	1764	2021-2043
AD-1684674.1	AUCUGGAAACACAUU	148	2024-2044	ATUCCAAUUGTGUCCAGAUCCG	1765	2022-2044
AD-1684675.1	UCUGGAAACACAUU	149	2025-2045	AAUCCAAUUGUGUCCAGAUCC	373	2023-2045
AD-1684676.1	CUGGAAACACAUU	150	2026-2046	AAAUTCCAUAUTGUUCCAGAU	1766	2024-2046
AD-1684677.1	UGGAAACACAUU	151	2027-2047	ACAATUCCAAUAUGUGUCCAG	1767	2025-2047
AD-1684678.1	GGAACACAUU	152	2028-2048	ACCAAUTCCAUAUTGUUCCAG	1768	2026-2048
AD-1684679.1	UAGGGUGGUAAGGCCCUU	236	2062-2082	AAUAAGGCCUUAACCCACCCUA	460	2060-2082
AD-1684680.1	AGGGUGGUAAGGCCCUU	238	2063-2083	ATAUAAGGCCUTACCCACCCUA	1769	2061-2083
AD-1684681.1	GGGUGGGUAAGGCCCUU	153	2064-2084	ATUATAAGGCCUUAACCCACCCUA	1770	2062-2084
AD-1684682.1	GGUGGGUAAGGCCCUU	154	2065-2085	AAUUAUAGGCCCUUAACCCACCCU	378	2063-2085

Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO.	Range in XM_017004061.1	Antisense Strand Sequence 5' to 3'	SEQ ID NO.	Range in XM_017004061.1
AD-1684683.1	GUGGGUAAAGGCCUUUAUAAUGU	155	2066-2086	ACAUTATAAGGCCUUUACCCACCC	1771	2064-2086
AD-1684684.1	UGGGUAAAGGCCUUUAUAAUGUU	215	2067-2087	AACATUAUAAAGGCCUUUACCCACC	1772	2065-2087
AD-1684685.1	GGUAAAGGCCUUUAUAAUGUAU	208	2068-2088	ATACAUTAAAGGCCUUUACCCAC	1773	2066-2088
AD-1684686.1	GGUAAAGGCCUUUAUAAUGUAAU	205	2069-2089	ATUACATUAUAAAGGCCUUUACCCA	1774	2067-2089
AD-1684687.1	GUAAGGCCUUUAUAAUGUAAAU	156	2070-2090	ATUACAUUAAUAAAGGCCUUUACCC	1775	2068-2090
AD-1684688.1	UAAGGCCUUUAUAAUGUAAAGU	201	2071-2091	ACUUTACAUUATAAGGCCUUUACC	1776	2069-2091
AD-1684689.1	AAGGCCUUUAUAAUGUAAAGAU	157	2072-2092	ATCUTUACAUUAAUAAAGGCCUUAC	1777	2070-2092
AD-1684690.1	AGGCCUUUAUAAUGUAAAGAGU	158	2073-2093	ACUCTUTACAUTAAUAAAGGCCUUUA	1778	2071-2093
AD-1684691.1	GGCCUUUAUAAUGUAAAGAGCU	196	2074-2094	AGCUCUTUACATUAUAAAGGCCUU	1779	2072-2094
AD-1684692.1	GCCUUUAUAAUGUAAAGAGCAU	159	2075-2095	ATGCTCTUUAUAAUAAAGGCCUU	1780	2073-2095
AD-1684693.1	GCAUUAUAAUGUAAAGGGCUUU	160	2092-2112	AAAGCCUUUACAUUAAUUAUGCUC	384	2090-2112
AD-1684694.1	CAUUAUAAUGUAAAGGGCUUUU	202	2093-2113	AAAAGCCUUUACAUUAAUUAUGCU	426	2091-2113
AD-1684695.1	AUAUAAUGUAAAGGGCUUUUAU	161	2094-2114	ATAAAGCCUUUACAUUAAUUAUGC	1781	2092-2114
AD-1684696.1	UAUAAUGUAAAGGGCUUUUAGU	197	2095-2115	ACUAAAGCCCUUACAUUAAUUAUG	1782	2093-2115
AD-1684697.1	AUAUAAUGUAAAGGGCUUUUAGAU	162	2096-2116	ATCUAAAGCCCTUUACAUUAAUUAU	1783	2094-2116
AD-1684698.1	UAUAAUGUAAAGGGCUUUUAGAGU	163	2097-2117	ACUCTAAAGCCCUUUACAUUAAUUA	1784	2095-2117
AD-1684699.1	AUUAUAAAGGGCUUUUAGAGUU	164	2098-2118	AACUCUAAAGCCCUUUACAUUAAU	388	2096-2118
AD-1684700.1	CCUGGAUUAAAUUUGCCAUU	165	2126-2146	AUUGGCAGAUUUUAAUCCAGGUC	1785	2124-2146
AD-1684701.1	CUGGAUUAAAUUUGCCAUUUU	166	2127-2147	AAAUGGCAGAUUUUAAUCCAGGU	1786	2125-2147
AD-1684702.1	UGGAUUAAAUUUGCCAUUUU	193	2128-2148	AAAATGGCAGAUUUUAAUCCAGG	1787	2126-2148
AD-1684703.1	GGAUUAAAUUUGCCAUUUU	192	2129-2149	ATAAUGGCAGAUUUUAAUCCAG	1788	2127-2149
AD-1684704.1	GAUUAUAAAUUUGCCAUUUU	167	2130-2150	ATUAAATGGCAGAUUUUAAUCCCA	1789	2128-2150
AD-1684705.1	AUUAAAUUUGCCAUUUUAAU	168	2131-2151	AAUUAUAAUUGGCAGAUUUUAAUCC	392	2129-2151
AD-1684706.1	AAUUCUGCCAUUUUAAUUAAGCU	169	2135-2155	AGCUAATUAAATGGCAGAUUUUA	1790	2133-2155
AD-1684707.1	AAUCUGCCAUUUUAAUUAAGCUU	170	2136-2156	AAGCTAAUUAUAAUUGGCAGAUUUU	1791	2134-2156
AD-1684708.1	AUCUGCCAUUUUAAUUAAGCUGU	171	2137-2157	ACAGCUAAUUAUAAUUGGCAGAUUU	395	2135-2157
AD-1684709.1	UCUGCCAUUUUAAUUAAGCUGCU	218	2138-2158	AGCAGCTAAUUAUAAUUGGCAGAUU	1792	2136-2158

Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO.	Range in XM_017004061.1	Antisense Strand Sequence 5' to 3'	SEQ ID NO.	Range in XM_017004061.1
AD-1684710.1	CUGCCAUUUAAUUAAGCUGCAU	172	2139-2159	ATGCAGCUAAUAAAUGGCAGAU	1793	2137-2159
AD-1684711.1	UGCCAUUUAAUUAAGCUGCAU	203	2140-2160	AAUGCAGCUAATUAAAUGGCAGA	1794	2138-2160
AD-1684712.1	ACGCAAUUCUGCCUCAAUUUCU	173	2183-2203	AGAAUUTGAGGCAGAUUGCGUUA	1795	2181-2203
AD-1684713.1	CGCAAUUCUGCCUCAAUUUCU	174	2184-2204	AAGAAAUTGAGGCAGAUUGCGUU	1796	2182-2204
AD-1684714.1	GCAAUUCUGCCUCAAUUUCU	175	2185-2205	AAAGAAAUUGAGGCAGAUUGCGU	399	2183-2205
AD-1684715.1	CAAUCUGCCUCAAUUUCU	211	2186-2206	AGAAGAAAUUGAGGCAGAUUGCG	435	2184-2206
AD-1684716.1	AUUCUGCCUCAAUUUCU	176	2187-2207	ATGAAGAAAUUGAGGCAGAUUGC	1797	2185-2207
AD-1684717.1	AUCUGCCUCAAUUUCU	177	2188-2208	AAUGAAGAAAUTGAGGCAGAUUG	1798	2186-2208
AD-1684718.1	UCUGCCUCAAUUUCU	178	2189-2209	AGAUGAAGAAAATUGAGGCAGAUU	1799	2187-2209
AD-1684719.1	CUGCCUCAAUUUCU	179	2190-2210	AAGATGAAGAAAUUGAGGCAGAU	1800	2188-2210
AD-1684720.1	UGCCUCAAUUUCU	180	2191-2211	ACAGAUGAAGAAAUUGAGGCAGA	404	2189-2211
AD-1684721.1	GCCUCAAUUUCU	181	2192-2212	AACAGATGAAGAAAUUGAGGCAG	1801	2190-2212
AD-1684722.1	CCUCAAUUUCU	199	2193-2213	AGACAGAUGAAGAAAUUGAGGCA	423	2191-2213
AD-1684723.1	CUCAUUUCU	200	2194-2214	ATGACAGAUGAAGAAAUUGAGGC	1802	2192-2214
AD-1684724.1	UCAUUUCU	194	2195-2215	ATUGACAGAUGAAGAAAUUGAGG	1803	2193-2215
AD-1684725.1	CAAUUCU	182	2196-2216	ATUUGACAGAUGAAGAAAUUGAG	1804	2194-2216
AD-1684726.1	AUUUCU	183	2197-2217	AAUUTGACAGATGAAGAAAUUGA	1805	2195-2217
AD-1684727.1	AUUUCU	184	2198-2218	ACAUTUGACAGAUGAAGAAAUUG	1806	2196-2218
AD-1684728.1	UUUCU	195	2199-2219	ACCATUTGACAGAUGAAGAAAUUG	1807	2197-2219
AD-1684729.1	UUUCU	191	2200-2220	ATCCAUTUGACAGAUGAAGAAAUUG	1808	2198-2220
AD-1684730.1	AUUUCU	185	2223-2243	ATUCTGTAGCCCAAGCAGAAUUGG	1809	2221-2243
AD-1684731.1	AUUCUGCU	186	2224-2244	AAUUCUGUAGCCCAAGCAGAAUUG	410	2222-2244
AD-1684732.1	UUUCUGCU	206	2225-2245	AAAUUTCTGUAGCCCAAGCAGAAUUG	1810	2223-2245
AD-1684733.1	UCUGCU	187	2226-2246	ATAATUCUGUAGCCCAAGCAGAAUUG	1811	2224-2246
AD-1684734.1	CUGCU	188	2227-2247	AAUAAUTCUGUAGCCCAAGCAGAAUUG	1812	2225-2247
AD-1684735.1	UGCU	189	2228-2248	AAAUAAATUCUGUAGCCCAAGCAGAAUUG	1813	2226-2248
AD-1684736.1	GCU	190	2229-2249	ACAATAAUUCUGUAGCCCAAGCAGAAUUG	1814	2227-2249

Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO.	Range in XM_017004061.1	Antisense Strand Sequence 5' to 3'	SEQ ID NO.	Range in XM_017004061.1
AD-1684737.1	AUUAAUUGUGAGGAUAAAAUCU	204	2242-2262	AGAUTUTAUCCCTCACAAUAUUC	1815	2240-2262

Table 13. Modified Sense and Antisense Strand Sequences of KHK dsRNA

Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO.	Antisense Strand Sequence 5' to 3'	SEQ ID NO.	mRNA target sequence	SEQ ID NO.
AD-1290507.2	ususcucAfUcUfGfucaauuggaunL96	1816	asUfsccaUfuugacagAfuGfaagaasasu	863	AUUUCUUAUCUGUCAAAUUGGAA	1087
AD-1290509.2	gsasuuuaAfaUfcUfUfgccauuuauL96	615	asUfsuaaAfuugcgagaUfuUfuuaucscsa	839	UGGAUUAAAAUUCUGCCAUUUAA	1063
AD-1290510.2	asasuuucUfuCfaFUfcugucaaaunL96	631	asAfsuuuGfacagaugAfaGfaaanugsas	855	UCAAUUUCUUAUCUGUCAAAAUG	1079
AD-1290514.2	csasaunuCUfUfcFAfucuguccaaunL96	630	asUfsuugAfcagaugaAfgAFfaanugsasg	854	CUCAUUUCUUAUCUGUCAAAU	1078
AD-1290515.2	asgsgccuUfaUfaFAfufuguaaagagnL96	606	asCfsucuUfiuacaunaUfaAfggccususa	830	UAAGGCCUUUAAAUGUAAAGAG	1054
AD-1290516.2	ggsaaaAfaAFUcFugccauuuauL96	640	asUfsaaaUfggcgaganUfuUfaauccsasg	864	CUGGAUUAAAAUCUGCCAUUUAA	1088
AD-1290522.2	uscsluggaAfcAFcfAfuaauuggaunL96	597	asAfsuncCFaauaanguGfuUfccagausc	821	GAUCUGGAACACAUAUUGGAAU	1045
AD-1290523.2	gscscucaAfUfUfCfCucaucugnL96	629	asAfscegAfugaagaaAfuUfgagccsasg	853	CUGCCUCAUUUCUUAUCUUAUCUGUC	1077
AD-1290524.2	asusuucUfcAFUcFugucaaaugnL96	632	asCfsanuUfgcacagauGfaAfgaaanusg	856	CAAUUUCUUAUCUGUCAAAUUGG	1080
AD-1290527.2	usgsgauAfaFAfAFUfcugecauuunL96	641	asAfsaauGfgcagannUfuUfauecasgsg	865	CCUGGAUUAAAAUCUGCCAUUUA	1089
AD-1290528.2	csusggaaCfaCfaFAfUfaunggaunL96	598	asAfsanuCFcaauaugUfgUfuuccagsasu	822	AUCUGGAACACAUAUUGGAAUU	1046
AD-1290531.2	csusgccuCFaAFUfUfucuucaunL96	627	asAfsgauGfaagaaauUfgAfggcagsasu	851	AUCUGCCUCAUUUCUUAUCUUAUCUG	1075
AD-1290533.2	asasaucGfcCFAfUfuaauagcuL96	617	asGfsceuaAfuaaaaugGfcAfgaaunuusa	841	UAAAAUCUGCCAUUUAAUUAAGCU	1065
AD-1290535.2	asascucCfcAFUfUfuaauagcuL96	618	asAfsgeuAfamaaauGfgCfagaunusu	842	AAAAUCUGCCAUUUAAUUAAGCUG	1066
AD-1290539.5	csasgacuUfuGFaFAfGaagguaunL96	516	asAfsucaAfcuucucAfaAfgucugsusa	740	UACAGACUUUGAGAAGGUUGAU	964
AD-1290542.2	uscsaauUfcUFUfCfCauevguaanL96	642	asUfsugaCFagaugaaGfaAfaunigsgsg	866	CCUCAUUUCUUAUCUGUCAAA	1090
AD-1290543.2	usgsaacAfcAFUfAFuuggaungnL96	599	asCfsaauUfccaaunGfuGfuuccagsas	823	UCUGGAACACAUAUUGGAAUUG	1047
AD-1290551.2	csusggauUfaFAFAfucugccaaunL96	614	asAfsaugGfcagaunUfaAfuuccagsgu	838	ACCUGGAUUAAAAUCUGCCAUUU	1062
AD-1290552.2	ususucuuCfaUFCUfUfgucaaaugnL96	643	asCfscauUfugacagaUfgAfagaasasu	867	AUUUCUUAUCUGUCAAAUUGGA	1091
AD-1290554.2	asusaauUfFaFAFAFGfcocmuiaeanL96	610	asUfsceaAfaocccmUfFaCFamuanasan	834	AUAUAAGUAAAGGGCUUUAGA	1058

Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO.	Antisense Strand Sequence 5' to 3'	SEQ ID NO.	mRNA target sequence	SEQ ID NO.
AD-1290555.2	asusauaaUfgUfAfAfagggcuuuauL96	609	asUfsaaGfcccuuuaCfaUfuauaugsc	833	GCAUAUAUGUAAAAGGGCUUUA G	1057
AD-1290556.2	gscscuuUfaAfUfGfuaaagagcauL96	607	asUfsgcuCfuuaacauUfaUfaaggcscsu	831	AGGCCUUAUAUGUAAAAGAGCA U	1055
AD-1290557.2	gsgscuuAfuaAfAfUfGfuaaagagcauL96	644	asGfscueUfuuaacauAfuaAfaggcscsu	868	AAGGCCUUAUAUGUAAAAGAGC A	1092
AD-1290558.2	usasuaauGfuAfAfAfagggcuuuauL96	645	asCfsuaaAfggccuuuAfCfAfuuausug	869	CAUAUAUGUAAAAGGGCUUUAUAG A	1093
AD-1290563.2	gsusaaggCfcUfUfAfuaaanguaaauL96	604	asUfsuaaCfuaaauaaGfgCfcuuacscsc	828	GGUAAGGCCUUAUAUGUAAA G	1052
AD-1290564.2	cscsuaaUfuUfCfUfuaucuguculL96	647	asGfsacaGfaugaagaAfaUfugaggsca	871	UGCCUCAUUUCUUCUUCUUGUCA A	1095
AD-1290565.2	csuscauUfuCfUfcaucuguculL96	648	asUfsgacAfgaugaagAfaAfuugagsgsc	872	GCCUCAUUUCUUCUUCUUGUCA A	1096
AD-1290570.2	asasggccUfuAfUfAfuaaanguaaauL96	605	asUfscuuUfacaauuAfaGfgccuusasc	829	GUAAGGCCUUAUAUGUAAAAGA G	1053
AD-1290573.2	asuscugCfcUfAfAfuaucuucauL96	625	asAfsugaAfgaauugAfgGfcagausus g	849	CAUCUGCCUCAUUUCUUCUUC A	1073
AD-1290574.2	usasaggeCfuUfAfUfuaaanguaaauL96	649	asCfsuuAfcauuaaAfgGfccuuascsc	873	GGUAAGGCCUUAUAUGUAAA A	1097
AD-1290584.2	gsusguuuGfuCfAfGfcaaaagauuuL96	543	asAfscauChuuugcugAfcAfaacacscsa	767	UGGUGUUUGUCAGCAAAAGAUGU G	991
AD-1290589.2	gsgsaacaCfaUfAfUfuggaauugguL96	600	asCfscaaUfuaaauUfgUfguuccsag	824	CUGGAACACAUUUGGAAUUGG G	1048
AD-1290592.2	csasuaaAfuaGfuUfAfagggcuuuuL96	650	asAfsaaGfccuuuacAfuaUfaauugscsu	874	AGCAUAUAUGUAAAAGGGCUUU A	1098
AD-1290597.2	asusuaaaAfuaCfUfGfccaauuuauuL96	616	asAfsuaaAfuaaggcagAfuUfuuaauesc	840	GGAUUAUAUCUGCCAUAUUAAU U	1064
AD-1290599.7	usgsuguuUfuGfuUfCfagcaaaagauL96	541	asAfsueuUfugcugacAfaAfcaccascsg	765	CGUGGUGUUUGUCAGCAAAAGAU G	989
AD-1290600.2	gscsuuggCfuAfCfAfgaauuauuuL96	638	asCfsaaAfauucuguAfgCfcaagcsag	862	CUGCUUGGCUACAGAAUAUUUGU G	1086
AD-1290602.2	usgsccueAfuaUfUfUfcaucucugulL96	628	asCfsagaUfagaagaaUfuGfaggcagsga	852	UCUGCCUCAUUUCUUCUUCUUGU G	1076
AD-1290604.2	asuscugCfaUfUfUfuaaageugulL96	619	asCfsageUfaauuaaaUfgGfcagausus	843	AAUCUGCCAUUUAAUAGCUGC G	1067
AD-1290605.2	asascugCfcUfCfAfaauucuucauL96	624	asUfsgaaGfaaauugaGfgCfagaauugsc	848	GCAUCUGCCUCAUUUCUUCUUCU A	1072
AD-1290609.2	usgsccauUfuAfAfUfuaagcugcauL96	651	asAfsugcAfcauuaaAfaAfuugcagsga	875	UCUGCCAUUUAAUAGCUGCAUA A	1099
AD-1290611.3	asgsacuuUfgAfGfAfagguuagcauL96	517	asGfsaucAfaccuuuUfAfaagucugsu	741	ACAGACUUUGAGAAAGGUUGAUC U	965

Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO.	Antisense Strand Sequence 5' to 3'	SEQ ID NO.	mRNA target sequence	SEQ ID NO.
AD-1290612.2	asuscuugAfAfcAfCfaauuggaauL96	596	asUfsuccAfauaugUfUfcfcauacsug	820	CGAUCUGGAACACAUAUUGGAAU	1044
AD-1290615.2	uscsugccUfcAfAfUfuuucuecauL96	626	asGfsaugAfagaaauGfAfGfgeagasu	850	AUUCUGCCUCAAUUUCUUCAUU	1074
AD-1290618.2	asasuguaAfAfGfGfGfcuuuagauL96	612	asAfscucUfaaagcccUfuUfacaunasu	836	AUAAUGUAAAGGGCUUUAGAGU	1060
AD-1290624.2	asusuaauGfuGfAfGfauaaaaauL96	652	asGfsauuUfuauccucAfCfAuaaauusc	876	GAAUUAUUGUGAGGAUAAAAUC	1100
AD-1290626.2	gsgsuaagGfcCfUfUfauaauguaauL96	653	asUfsuacAfuaaagGfcCfuaaccsca	877	UGGGUAAAGGCCUUUAUAAUGUAA	1101
AD-1290633.2	csusgccAUfuUfAfAfauagcugauL96	620	asUfsgcaGfcuaauuaAfAfUfgcaggsa	844	AUCUGCCAUUUAUUUAGCUGCAU	1068
AD-1290635.2	ususcugeUfuUfGfGfCfuacagaaauL96	654	asAfsauUcfuugagccAfAfGfcagaasuu	878	AUUCUGCUUGGCUACAGAAUUA	1102
AD-1290639.2	usasauguAfAfAfGfGfcuuuagauL96	611	asCfsucuAfaaagcccuUfuAfcauuasusa	835	UAUAAUGUAAAGGGCUUUAGAG	1059
AD-1290643.2	usgscuugGfcUfAfCfagaauuaauL96	637	asAfsauaAfuuucuguaGfcCfagaacsuga	861	UCUGCUUGGCUACAGAAUUAUUG	1085
AD-1290650.2	csugscaaUfUfGfCfCfuaauuuuuL96	622	asAfsagaaAfuuagagccAfIgAfuuagcgsuu	846	AACGCAAUUCUGCCUCAAUUUCUU	1070
AD-1290651.2	gsusucaaGfuUfGfAfuccaauuL96	655	asCfsauuGfuggauccAfCfUfugaacsug	879	CAGUUCAAAGUGGAUCCACAUUGA	1103
AD-1290654.2	gsgsguaaGfGfCfCfUfuaauuagauL96	656	asUfsacaUfuaaagGfcUfuaccsasc	880	GUGGGUAAGGCCUUUAUAAUGUA	1104
AD-1290655.2	gsasucugGfAfAfCfAfaauugauL96	657	asUfsccaAfuaugugUfCfagaucsgsg	881	CCGAUCUGGAACACAUAUUGGAA	1105
AD-1290659.2	csasaucUfGfCfUfCfaauuucuuL96	659	asGfsaagAfauugagGfcAfgaauugscsg	883	CGCAAUCUGCCUCAAUUUCUUA	1107
AD-1290660.2	cscsuggaUfuAfAfAfaucugccaauL96	613	asAfsugGfagaauuuAfAfUfccaggsusc	837	GACUUGGAUUAAAUCUGCCAUU	1061
AD-1290661.2	gscsaauAfAfUfGfUfaaaggccuuL96	608	asAfsagcCfcuuuacaUfuAfuaugcsusc	832	GAGCAUUAUUGUAAAGGGCUU	1056
AD-1290666.2	ascsuuugAfGfAfGfuuuagauL96	661	asCfsagaUfcaacuuUfuCfaaagusesu	885	AGACUUUGAGAAGGUUGAUCUG	1109
AD-1290670.2	uscscgaUfUfGfGfAfacaauuuL96	594	asAfsauaUfuguuuUfAfUfugagcscc	818	GGUCCGAUCUGGAACACAUAUUG	1042
AD-1290672.2	gscsaauUfGfCfCfUfcaauuucuuL96	623	asAfsagaAfauugaggCfAfGfaauugcgsu	847	ACGCAUCUGCCUCAAUUUCUUC	1071
AD-1290681.2	usgsguaaAfGfGfCfCfuuaauuL96	663	asAfscauUfaaagagccUfuUfaccasesc	887	GGUGGUAAGGCCUUUAUAAUGU	1111
AD-1290684.2	csgsaauGfGfAfAfCfacaauugauL96	665	asCfscaaUfauuguuUfCfAfgaucsgsga	889	UCCGAUCUGGAACACAUAUUGGA	1113
AD-1290687.2	csuscuuGfGfUfAfCfagaauuuL96	636	asAfsuaaUfucuguaGfCfAfgcagsasa	860	UUCUGCUUGGCUACAGAAUUAU	1084
AD-1290702.2	uscsugccAfUfUfAfAfauiagauL96	666	asGfscagCfuaauuaAfAfGfgeagasu	890	AUCUGCCAUUUAUUUAGCUGCA	1114
AD-1290712.2	cscsgaueUfGfAfAfCfacaauuL96	595	asCfsaauAfuguuUfCfAfuaucggsasc	819	GUCCCAUCUGGAACACAUAUUG	1043
AD-1290719.2	asusucugCfuUfGfGfcaacagaauL96	634	asAfsuucUfuaagccAfAfCfagaasug	858	CAAUUCUGCUUGGCUACAGAAU	1082
AD-1290722.2	uscscuecuUfGfGfUfacaauuuL96	635	asUfsaauUfcuguaGfCfAfcaagasu	859	AUUCUGCUUGGCUACAGAAUUA	1083

Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO.	Antisense Strand Sequence 5' to 3'	SEQ ID NO.	mRNA target sequence	SEQ ID NO.
AD-1290741.2	ascsgcaUfcUfGfCfcuacuuuL96	621	asGfsaaaUfugaggcaGfaUfugegusasa	845	UACGCAAUUCUGCCCAUUUUCU	1069
AD-1290742.2	gsusggguAfaGfGfCfcuuuaauuL96	603	asCfsauuAfuuaaggeUfuAfcceacscsc	827	GGGUGGGUAAGGCCUUUAUAUG	1051
AD-1290747.2	gsgsagccCfaCfCfUfuggaunaaL96	586	asUfsuaaUfuuccaagUfgGfgeuccsasa	810	UUGGAGCCCACCUUGGAAUAAG	1034
AD-1290750.2	cscscaguGfaAfCfCfugeccaagaL96	669	asUfscuuUfggcagguUfcAfcugggsusg	893	CACCCAGUGAACCCUGCCAAAGAA	1117
AD-1290755.2	gsgsuggUfaAfGfGfccuuuaauL96	602	asAfsuaaUfaagccuUfaCfcaccscsu	826	AGGGUGGUAAGCCUUUAUAU	1050
AD-1290763.2	gsuseccgUfcUfGfGfGaacaauuL96	593	asAfsuaaUfguinuccaGfaUfcgacscsu	817	AGGUCCGAUCUGGAACACAUAU	1041
AD-1290764.2	gsgsucggAfuCfUfGfGaacaauuL96	592	asUfsauaUfguuccagAfuCfggaccsuc	816	GAGGUCCGAUCUGGAACACAUAU	1040
AD-1290796.2	usugggagCfcCfAfCfcuuggaauuL96	673	asAfsauaUfcaaggugGfgCfucaasgsg	897	CCUUGGAGCCCACCUUGGAUAUA	1121
AD-1290800.2	gsgsuggGfuAfAfGfGfcuuuaauL96	601	asUfsuaaUfaggecuAfcCfcaccsusa	825	UAGGUGGGUAAGGCCUUUAUA	1049
AD-1290805.2	usgsagccCfcAfCfCfuggaauuL96	675	asUfsaaUfccaagguGfgGfuccasasg	899	CUUGGAGCCCACCUUGGAUAUA	1123
AD-1290836.2	asasuucGfcUfUfGfGfcuacagaL96	633	asUfsucuGfuagccaaGfcAfgaauusgsg	857	CCAUAUCUGCUUGGCUACAGAAU	1081
AD-1290837.5	usgsauuGfaCfCfCfagucaaguL96	524	asAfsuuGfcaucuggUfcAfgaucasasc	748	GUUGAUCUGACCCAGUUAAGUG	972
AD-1290841.2	asusuccAfCfAfGfCfucagaagcuL96	584	asAfsgeuUfciugagcuGfuGfggausasa	808	CUAUUCCCCACAGCUCAGAAAGCUG	1032
AD-1290842.2	gsasgcccAfCfUfUfGfgaunaaL96	587	asCfsuaaAfuuccaagGfuGfggcucscsa	811	UGGAGCCCACCUUGGAUAUAAGG	1035
AD-1290857.2	usgscccaCfcAfGfCfcuugauuuL96	677	asAfsaaUfCacaggeUfGfUfgggcasgsg	901	CCUGCCCACCAAGCCUGAGAUUUG	1125
AD-1290865.2	csusgguUfgUfGfGfCfagacuaauL96	578	asAfsuaaUfguugcaCfaAfcgcagsgsg	802	CCUUGCUUGUCAGACUCUAUU	1026
AD-1290875.2	gscscacCfaGfCfCfuguaunuuL96	679	asCfsaaaUfcaagccUfGfUfgggcsasg	903	CUGCCCACCAAGCCUGAGUAUUUA	1127
AD-1290880.2	csusuggaGfcCfCfAfCfcuuggaauL96	585	asAfsuucCfcaaguggGfcUfccaaagsgsg	809	CCUUGGAGCCCCACCUUGGAUU	1033
AD-1290884.5	gscsaggaAfGfCfAfCfugaauuL96	564	asCfsgaaUfuccagugCfuUfccugcsasc	788	GUGCAGGAAGCACUGAGAUUCGG	1012
AD-1290885.5	csusgaccCfaGfUfUfcaagugaauL96	526	asAfsuccAfuungaaeUfgGfgeucgsasu	750	AUCUGACCCAGUUCUAAGUUGAU	974
AD-1290894.2	asgsuguccGfaUfCfUfGfgaacaauL96	681	asAfsuugCfmuuccagaUfcGfaccucscsc	905	GGAGGUCCGAUCUUGGAACACAUA	1129
AD-1290897.2	usgsccguGfuGfCfAfGacuaauuL96	579	asAfsuaaUfgauncugAfcAfaccagsgsg	803	CCUUGCUUGUGCAGACUCUAUUC	1027
AD-1290908.2	cscsagugAfaCfCfUfGfccaagaL96	683	asUfsucuUfuggcaggUfuCfacuggsusg	907	ACCCAGUGAACCCUGCCAAAGAA	1131
AD-1290909.2	usugugccAfGfAfCfUfcauuccaL96	582	asUfsgggAfauaagguCfuGfcaacaasg	806	CGUUGUGCAGACUCUAUUCAC	1030
AD-1290910.2	usasggguGfgGfUfAfaggecuauuL96	684	asAfsuaaUfggeuucCfcAfcceuasusa	908	UAUAGGGUGGGUAAGGCCUUUAU	1132
AD-1290911.2	asgscccaCfcUfUfGfGfaunaaL96	588	asCfsuuAfaunccaaGfgUfgggcscsc	812	GGAGCCCACCUUGGAUAUAAGG	1036
AD-1290926.2	cscscacCfuUfGfGfGfaunaaL96	589	asCfsuuUfaunccaaGfGfugeccscsc	813	GAGCCCACCUUGGUAUAAGGCG	1037

Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO.	Antisense Strand Sequence 5' to 3'	SEQ ID NO.	mRNA target sequence	SEQ ID NO.
AD-1290931.2	uscsagccAfcAfAfAfugugacccauL96	591	asUfsgggUfcacauuuGfuGfcugasgs	815	CCUCAGCCACAAUUGUGACCCAG	1039
AD-1290939.2	asgsaggugGfgUfAfAfAggcccuaauL96	686	asUfsauAfagccuuaCfcCfaccucasu	910	AUAGGGUGGGUAAAGGCCUUUAUA	1134
AD-1290969.7	ascsuucAfaUfGfCfcuccgucuuL96	556	asAfsugaCfaggagcaUfuGfaagugs	780	ACACCUCAAUAGCCUCCGUCAUUC	1004
AD-1290971.3	gscsuacgGfaGfAfCfuguguuuuL96	690	asAfsaacAfccacagucUfcCfuaagcsca	914	UGGCUACGGAGACGUGGUGUUU	1138
AD-1290973.2	gsusugugCfaGfAfCfucuaucuuL96	691	asGfsggaAfuagagucUfgCfacaacgsc	915	GCGUUGUGCAGACUCUAUUCCCA	1139
AD-1290983.2	csgsuugGfcAfGfAfucuaucuuL96	581	asGfsgaaUfagagucUfcAfaacgscsa	805	UGCGUUGUGCAGACUCUAUCC	1029
AD-1290989.2	gscsguugUfgCfAfGfucuaucuuL96	580	asGfssauAfagagucUfcAfaacgscsag	804	CUGCGUUGUGCAGACUCUAUCC	1028
AD-1290993.2	usasuuccCfaCfAfGfucuaaguuL96	583	asGfscuuCfugagucUfgGfgaauasgsa	807	UCUAUUCCCCACAGCUCAGAAAGCU	1031
AD-1291003.2	gsgscgugCfcUfCfAfGccacaaauL96	590	asAfsuunGfuggucugaGfgCfacgcsesu	814	AGGGCGUGCCUCAGCCACAAUUG	1038
AD-1423312.3	usgscaggAfaGfCfAfcugagaauuL96	563	asGfssadTc(Tgn)CagugeUfuCfugca	1156	CGUGCAGGAAGCACUGAGAUUCG	1011
AD-1423319.3	gsascuuuGfaGfAfAfuguuuauuL96	518	asAfsgadTc(Agn)accuueUfcAfaugu	1163	CAGACUUUGAGAAGGUUGAUUCU	966
AD-1423336.7	gsusucaaGfuGfGfAfucacauuuL96	655	asCfssadTg(Tgn)ggauceAfcUfugaac	1179	CAGUUCAAAGUGGAUCCACAUUGA	1103
AD-1548743.7	usgsguguUfuGfUfCfagcaagaauL96	541	asAfsuedTu(Tgn)gcugacAfaAfaacca	1482	CGUGGUGUUUGUCAGCAAAAGAU	989
AD-1612957.2	gscscucaugGfAfAfagagaagcaguL96	1371	asdCsugdCudTcucudTcCfaugaggcs	1483	UAGCCUCAUGGAAGAGAAAGCAGA	1619
AD-1612963.2	usgsaaagagAfaGfCfagaucuuL96	1373	asdCsagdGadTcugedTuCfucuuccasu	1485	CAUGGAAGAGAAAGCAGAUCCUGU	1620
AD-1612969.2	asgsaaagcagAfUfCfugugcguguL96	1375	asdCsacdGadAcaggdAuCfugcuucis	1487	AGAGAAAGCAGAUCCUGUGCGUGG	1622
AD-1613059.2	csasgacuuuGfAfGfagguuauuL96	1377	asdAsucdAadCcuucdTcAfaagucgs	1489	UACAGACUUUGAGAAGGUUGAU	964
AD-1613060.2	asgsacuuuugAfGfAfagguuauuL96	1378	asdGsaudCadAacuuuCuCfaaagucis	1490	ACAGACUUUGAGAAGGUUGAUUC	965
AD-1613061.1	gsascuuuugaGfAfAfagguuauuL96	1817	asdAsgadTcdAaccudTcUfcaagucsu	1859	CAGACUUUGAGAAGGUUGAUUCU	966
AD-1613062.2	ascsuuuugagAfaGfGfuuuauuL96	1379	asdCsagdAudCaaccdTcUfcaaaagusc	1491	AGACUUUGAGAAGGUUGAUUCUG	1109

Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO.	Antisense Strand Sequence 5' to 3'	SEQ ID NO.	mRNA target sequence	SEQ ID NO.
AD-1613072.1	gsguugaucUfGfAfcccaaguuL96	1818	asdTsgadAcdTggudCaGfaucacsu su	1860	AAGGUUGAUCUGACCCAGUUCAA	1135
AD-1613075.2	usgsaucugaCfCfCfaguucaaguuL96	1383	asdAascdTgdAacugdGgUfagaucaas asc	1495	GUUGAUCUGACCCAGUUCAAAGUG	972
AD-1613079.2	csusgacccaGfUfUfcaaguggauuL96	1386	asdAsucdCadCuugadAcUfggucags asu	1498	AUCUGACCCAGUUCAAAGUGGAUC	974
AD-1613087.1	gsusucaaguGfGfAfucccaauuuL96	1455	asdCsaadTgdTggandCcAfcuugaacsu sg	1861	CAGUUCAAAGUGGAUCCACAUUGA	1103
AD-1613094.2	usgsauccaCfAfUfugaggccguL96	1391	asdCsggdCcdCucaadTgUfggauccasc su	1503	AGUGGAUCCACAUUGAGGGCCGG	1626
AD-1613242.2	gsusuaaggaGfAfCfuggguguuuuL96	1398	asdAasaadCadCcaagdTcUfecnagasc sa	1510	UGGCUACGGAGACGUGGUGUUU	1138
AD-1613254.2	usgsuguuuuGfUfCfagcaaaaguuL96	1404	asdAsucdTudTgcugdAcAfaacaccasc sg	1516	CGUGGUGUUUGUCAGCAAAAGAU	989
AD-1613256.2	gsusuuuuuGfAfGfcaaaaguuuuL96	1406	asdAseadTcdTuugedTgAfcuaaacasc sa	1518	UGGUGUUUGUCAGCAAAAGAU	991
AD-1613371.3	ascscuucaaUfGfCfencegucauuL96	1415	asdAsugdAcdTggagdCaUfugaaguss gsu	1527	ACACCUUCAUUGCCUCCGUCUAC	1004
AD-1613400.2	gscaaggaagCfAfCfugagaauuuL96	1420	asdCsgadAndCucaagdTgCfuuceuages asc	1532	GUGCAGGAAGCACUGAGAUUCGG	1012
AD-1684592.1	gsusagccUfcAfUfGfagaagagaaguuL96	1819	asCfsuudCudCuuccauGfaGfgcuacsu sc	1862	GAGUAGCCUCUAGGAAGAGAAAGC	2008
AD-1684593.1	asgscucAfUfGfAfagagaagcauuL96	1820	asUfsgdTudCuueucAfUfGfaggeusa sc	1863	GUAGCCUCUAGGAAGAGAAAGCAG	2009
AD-1684594.1	csusaugGfaAfGfAfgaagcagaauL96	499	asAfsucdTgdCuucucuUfcCfaugagsg sc	1864	GCCUCAUGGAAGAGAAAGCAGAU	947
AD-1684595.1	uscsaugGfAfGfAfgaagcagaauL96	1821	asGfsaudCudGcuuucUfuCfcaugagsg sg	1865	CCUCAUGGAAGAGAAAGCAGAUCC	2010
AD-1684596.1	asusggaGfAfGfAfagcagaauuuL96	500	asAfsaggdAndCugcuucUfcUfucaaus gsa	1866	UCAUGGAAGAGAAAGCAGAUCCUG	948
AD-1684597.1	asasgagaAfGfAfGfauccuguguuL96	1822	asGfsacdCadGgaucugCfuUfucuuisc sc	1867	GGAAGAGAAAGCAGAUCCUGGCG	2011
AD-1684598.1	gsasgaagCfAfAfUfucugugcguuL96	1823	asAfsagdCadCaggauucUfgCfuucucsu su	1868	AAGAGAAGCAGAUCCUGUGCGUG	2012
AD-1684599.1	asasgcagauCfCfUfugcuguggguuL96	1824	asdCscddAcdTGeacadGfAfucugcuus asd	1869	AGAAGCAGAUCCUGUGCGUGGGG	2013

Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO.	Antisense Strand Sequence 5' to 3'	SEQ ID NO.	mRNA target sequence	SEQ ID NO.
AD-1684600.1	asasgcagAfuCfUfGfGcGgGgguL96	1825	csu asCfscacCfGcacaggAfuCfGcGgGgguL96	1870	AGAACGAGAUCCUGUGCGUGGGG	2013
AD-1684601.1	asgscagaCfUfGfGcGgGgguL96	1826	usc asdCscddCadCgcacdAgGfGcGgGgguL96	1871	GAAGCAGAUCCUGUGCGUGGGG	2014
AD-1684602.1	asgscagaUfcCfUfGfGcGgGgguL96	1827	usc asCfscacAfGcacagGfUfGcGgGgguL96	1872	GAAGCAGAUCCUGUGCGUGGGG	2014
AD-1684603.1	gscsagauCfcUfGfUfGcGgGgguL96	1828	csu asGfscddCc(Agn)GgcacaGfGfUfGcGgGgguL96	1873	AAGCAGAUCCUGUGCGUGGGG	2015
AD-1684604.1	csasgaucCfuGfUfGfGcGgGgguL96	1829	su asAfsGcdCcdCacgcacAfGfGcGgGgguL96	1874	AGCAGAUCCUGUGCGUGGGGCUA	2016
AD-1684605.1	asgsaueCfUfGfGcGgGgguL96	1830	sc asUfsagdCcdCcacgcaCfGfGcGgGgguL96	1875	GCAGAUCCUGUGCGUGGGGCUAG	2017
AD-1684606.1	csasgaucuuGfAfGfGcGgGgguL96	1377	usc asdAsucdAadCcuucdTcAfaagucg	1876	UACAGACUUUGAGAGGUGUAGU	964
AD-1684607.1	csasgaucuuGfAfGfGcGgGgguL96	1377	csu asdAsucdAadCcuucdTcAfaagucg	1877	UACAGACUUUGAGAGGUGUAGU	964
AD-1684608.1	csasgaucuuGfAfGfGcGgGgguL96	1831	csu usdAsucdAadCcuucdTcAfaagucg	1878	UACAGACUUUGAGAGGUGUAGU	964
AD-1684609.1	gsascuuuGfAfGfGcGgGgguL96	1832	g asdAsucdAadCcuucdTcAfaagucg	1879	CAGACUUUGAGAGGUGUAGU	2018
AD-1684610.1	gsascuuuGfAfGfGcGgGgguL96	1817	usc asdAsgadTc(Agn)accudTcUfcAfaag	1880	CAGACUUUGAGAGGUGUAGU	966
AD-1684611.1	usugagAfAfGfGcGgGgguL96	1833	usc asdCsagdAadCcaacdTuCfuaaaguc	1881	ACUUUGAGAGGUGUAGU	2019
AD-1684612.1	ascsuuuagAfAfGfGcGgGgguL96	1834	su asdCsagdAadCcaacdTuCfuaaaguc	1882	AGACUUUGAGAGGUGUAGU	1109
AD-1684613.1	ususgagAfGfUfUfGcGgGgguL96	1835	sg asGfsgudCadGaucacCfuUfcuaca	1883	CUUUGAGAGGUGUAGU	2020
AD-1684614.1	gsasgaagGfuUfGfAfGcGgGgguL96	1836	sa asUfsggdGudCagaucAfCfhuucsa	1884	UUGAGAGGUGUAGU	2021
AD-1684615.1	gsasagguUfGfAfUfGcGgGgguL96	1837	sc asAfsudGgdGucagauCfAfCfhuucsu	1885	GAGAGGUGUAGU	2022
AD-1684616.1	asgsuuuGfAfUfGfGcGgGgguL96	1838	sc asGfSaadCudGgucagAfuCfhuucsu	1886	GAAGGUGUAGU	2023
AD-1684617.1	usgsaucugaCfCfGfGcGgGgguL96	1383	gsc asdAscudTgdAacugdGgUfcagauca	1887	GUUGAUCUGACCCAGUUAAGUG	972
AD-1684618.1	usgsaucugaCfCfGfGcGgGgguL96	1383	gsc asdAscudTgdAacugdGgUfcagauca	1888	GUUGAUCUGACCCAGUUAAGUG	972

Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO.	Antisense Strand Sequence 5' to 3'	SEQ ID NO.	mRNA target sequence	SEQ ID NO.
AD-1684619.1	usgsaucugaCfCfCfaguucaagualL96	1839	csu usdAscudTgdAacugdGgUfcagaucas	1889	GUUGAUCUGACCCAGUUAAGUG	972
AD-1684620.1	asuscugaCfCfCfaguucaagunL96	1840	csu asdAscudTgdAacugdGgUfcagauses	1890	UGAUCUGACCCAGUUAAGUG	2024
AD-1684621.1	gsascccaGfuUfCfAfaguggaueculL96	1841	g asGfsgadTcdCacuugaAfcUfggguuca	1891	CUGACCCAGUUAAGUGGAUCCA	2025
AD-1684622.1	ascscagUfuUfCfAfaguggaueculL96	527	csa asUfsggdAudCcaungAfaCfugggus	1892	UGACCCAGUUAAGUGGAUCCA	975
AD-1684623.1	csasguucAfaGfUfGfaguccaauL96	471	sg asAfsugdTgdGauccacUfuGfaacugsg	1893	CCCAGUUAAGUGGAUCCAUAU	919
AD-1684624.1	asgsuicaAfgUfGfGfauccaauL96	529	sg asAfsaudGudGauccaCfuUfgaacugsg	1894	CCAGUUAAGUGGAUCCAUAU	977
AD-1684625.1	asgsuggaUfcCfAfCfauggagggcuL96	1842	sg asGfscddCudCaungugGfaUfecaustu	1895	CAAGUGGAUCCAUAUAGGGGCC	2026
AD-1684626.1	usgsaucCfaCfAfUfugagggccuL96	1843	sa asCfsggcCfcauauUfgGfauccascu	1896	AGUGGAUCCAUAUAGGGCCGG	1626
AD-1684627.1	gsasuccaCfaUfUfGfagggccggauL96	1844	sa asUfscddGgdCccucaaUfgUfgaucsc	1897	UGGAUCCAUAUAGGGGCCGGA	2027
AD-1684628.1	asusccacAfuUfGfAfggggccgaauL96	1845	sc asUfsuedCgdGccucaaAfuGfuggaunc	1898	GGAUCCAUAUAGGGGCCGAAC	2028
AD-1684629.1	gsasgacgUfgGfUfGfuuugueagcuL96	1846	g asGfscudGadCaacacCfaCfugucscs	1899	CGGAGACGUGGUGUUAUUGUCAGCA	2029
AD-1684630.1	csgsugguGfuUfUfGfucagcaagcuL96	667	sc asCfssudTgdCugacaaAfcAfcacgsu	1900	GACGUGGUGUUAUUGUCAGCAAAG	1115
AD-1684631.1	ususgucaGfcAfaAfAfgaugggccuL96	1847	sc asGfsgcdCadCauuuuGfcUfgacaasa	1901	GUUUGUCAGCAAAGAUGUGGCCA	2030
AD-1684632.1	gsuscagcAfaAfGfAfugggccaauL96	1848	sa asUfsugdGedCacaucUfuGfuegacsa	1902	UUGUCAGCAAAGAUGUGGCCAAG	2031
AD-1684633.1	uscsageaAfaGfAfUfugggccaagcuL96	1849	sa asCfssudGgdCcaucUfuUfuegasc	1903	UGUCAGCAAAGAUGUGGCCAAGC	2032
AD-1684634.1	csasgcaaAfgAfuUfGfugggccaagcuL96	1850	sc asGfscudTgdGccaauCfuUfuegusa	1904	GUCAGCAAAGAUGUGGCCAAGCA	2033
AD-1684635.1	asgscaaaGfaUfGfUfugggccaagcuL96	1851	sa asUfsgcdTudGgecacaUfcUfuuegusc	1905	UCAGCAAAGAUGUGGCCAAGCAC	2034
AD-1684636.1	gsasgacaCfcUfUfCfaugccuL96	1852	sa asGfsgadGgdCaungaaGfgUfgucuse	1906	UGGAGACACCUUAAGCCUCCG	2035

Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO.	Antisense Strand Sequence 5' to 3'	SEQ ID NO.	mRNA target sequence	SEQ ID NO.
AD-1684637.1	asgsaacCfuUfCfAfauGCCUCCGUL96	1853	asCfsggdAgdGcaungAfgGfugucus	1907	GGAGACACCUUCAAUGCCUCCGUC	2036
AD-1684638.1	gsasaccUfuCfAfAfugCCUCCGUL96	1854	asAfscgdGadGcaungAfaGfugucus	1908	GAGACACCUUCAAUGCCUCCGUC	2037
AD-1684639.1	cscsuucaAfuGfCfCfuecguauL96	557	asGfsaudGadCggaggcAfuUfgaags	1909	CACCUUCAUUGCCUCCGUCUUCU	1005
AD-1684640.1	gscscuccGfuCfAfUfucucagccuL96	1855	asAfsggdCudGaagangAfcGfaggcsa	1910	AUGCCUCCGUCUUCUUCAGCCUC	2038
AD-1684641.1	csusceguCfaUfCfUfucagccuL96	561	asAfsgadGgdCugaagaUfgAfcggags	1911	GCCUCCGUCUUCUUCAGCCUCUC	1009
AD-1684642.1	gsgsagcgUfgCfAfGfagagcacuL96	1856	asCfsagdTgdCuucugCfaCfucucsu	1912	GAGGAGCGUGCAGGAAGCACUGA	2039
AD-1684643.1	gsasgeguGfcAfGfGfagagcacuL96	1857	asUfscadGudGcuucUgfcAfcgucsc	1913	AGGAGCGUGCAGGAAGCACUGAG	2040
AD-1684644.1	gscsgugcAfgGfAfAfagcacagauL96	1858	asUfscudCadGugcucCfuGfagcscu	1914	GAGCGUGCAGGAAGCACUGAGAU	2041
AD-1684645.1	gsusgcagGfaAfGfCfagagagauL96	562	asAfsaudCudCagugeUfcCfugcacsg	1915	GCGUGCAGGAAGCACUGAGAUUC	1010
AD-1684646.1	cscscaguGfaAfCfCfugccaaagauL96	669	asdTscudTudGgcagdGuUfcaucgggs	1916	CACCCAGUGAACCUGCCAAAGAA	1117
AD-1684647.1	cscsagugAfaCfCfUfGCCAAAGAU96	683	asdTscudTudTggcadGgUfucacuggs	1917	ACCCAGUGAACCUGCCAAAGAAA	1131
AD-1684648.1	csusgcguUfgUfGfCfagacucuaL96	578	asdAsuadGadGucugdCaCfaacgcags	1918	CCUUGCGUUGUGCAGACUCUAUUC	1026
AD-1684649.1	usgscguuGfuGfCfAfagacucuaL96	579	asdAsaudAgdAgueudGcAfaacgcas	1919	CCUUGCGUUGUGCAGACUCUAUUC	1027
AD-1684650.1	gscsguugUfgCfAfGfagacucuaL96	580	asdGsaudTadGaguedTgCfacaacgsa	1920	CUGCGUUGUGCAGACUCUAUUC	1028
AD-1684651.1	csgsuugUgfcAfGfAfucuaucuuL96	581	asdGsgadAudAgagudCuGfacaacgs	1921	UGCGUUGUGCAGACUCUAUUC	1029
AD-1684652.1	gsusugugCfaGfAfCfucuaucuuL96	691	asdGsggdAadTagagdTcUfgcacaacsg	1922	GCGUUGUGCAGACUCUAUUC	1139
AD-1684653.1	usugugcAfgAfcUfucuaucuuL96	582	asdTsggdGadAuagadGuCfugcacaas	1923	CGUUGUGCAGACUCUAUUC	1030

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Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO.	Antisense Strand Sequence 5' to 3'	SEQ ID NO.	mRNA target sequence	SEQ ID NO.
AD-1684654.1	usasuuccCfaCfAfGfcuagagcuL96	583	asdGscudTcdTgagcdTgUfgggaauas gsa	1924	UCUAUUCCCCACAGCUCAGAAAGCU	1031
AD-1684655.1	asusuccAfcAfGfcuagagcuL96	584	asdAsgcdTudCugagdCuGfugggaauas asg	1925	CUAUUCCCCACAGCUCAGAAAGCUG	1032
AD-1684656.1	usgscccaCfcAfGfcuagagcuL96	677	asdAsaadTcdAcaggdCuGfuggggcas gsg	1926	CCUGCCCCACCAGCCUGUGAUUUUG	1125
AD-1684657.1	gsccscacCfaGfCfCfugaguuuL96	679	asdCsaadAudCacagdGcUfgggggcas asg	1927	CUGCCCCACCAGCCUGUGAUUUUGA	1127
AD-1684658.1	csusuggaGfcCfCfAfcuaggaaL96	585	asdAsuudCcdAaggudGgGfcuccaags gsg	1928	CCUUGGAGCCCCACCUCUUGGAAUUA	1033
AD-1684659.1	usugggagCfcCfAfCfcuaggaaL96	673	asdAsaudTcdCaaggdTgGfgcuccaasg sg	1929	CCUUGGAGCCCCACCUCUUGGAAUUA	1121
AD-1684660.1	usggagcCfcAfCfCfugaguuuL96	675	asdTsaadTudCcaagdGuGfgcuccasa sg	1930	CUUGGAGCCCCACCUCUUGGAAUUA	1123
AD-1684661.1	gsagaccCfaCfCfUfuggaauuL96	586	asdTsuadAudTccaadGgUfgggcuces asa	1931	UUGGAGCCCCACCUCUUGGAAUUAAG	1034
AD-1684662.1	gsasgccAfcCfUfUfggaauuL96	587	asdCsuudAadTuccadAgGfugggcucs csa	1932	UGGAGCCCCACCUCUUGGAAUUAAGG	1035
AD-1684663.1	asgscccaCfcUfUfGfgaauuL96	588	asdCscudTadAuuuccAaGfugggcucs csc	1933	GGAGCCCCACCUCUUGGAAUUAAGGG	1036
AD-1684664.1	gsccscacCfuUfGfGfaauuL96	589	asdCscddTudAuuuccCaAfgggggcas usc	1934	GAGCCCCACCUCUUGGAAUUAAGGGC	1037
AD-1684665.1	gsccgugCfcUfCfAfGCCaauuL96	590	asdAsuudTgdTggcudGaGfgcagcccs csu	1935	AGGGCGUGCCUCAGCCACAAUUG	1038
AD-1684666.1	uscsagccAfcAfAfAfugagcccaL96	591	asdTsggdGudCacaudTuGfuggcugcas gsg	1936	CCUCAGCCCCACAAUUGAGACCCAG	1039
AD-1684667.1	asgsuccGfaUfCfUfGgaacaaL96	681	asdAsugdTgdTuccadGaUfaggaccus csc	1937	GGAGGUCCGAUCUGGAAACACAUUA	1129
AD-1684668.1	gsusuccAfuCfUfGfgaacacaaL96	592	asdTsaudGudGuuuccAgAfcaggaccs usc	1938	GAGGUCCGAUCUGGAAACACAUUA	1040
AD-1684669.1	gsusccgaUfcUfGfGfaacacaaL96	593	asdAsuadTgdTguuccCaGfaucggcas csu	1939	AGGUCCGAUCUGGAAACACAUUAU	1041
AD-1684670.1	uscscauCfuGfGfAfacaauuL96	594	asdAsaudAudGuguudCcAfgaucggas csc	1940	GGUCCGAUCUGGAAACACAUUAUUG	1042
AD-1684671.1	csccgaucUfgGfAfAfacaauuL96	595	asdCsaadTadTguudTcCfagaucggsa csc	1941	GUCCGAUCUGGAAACACAUUAUUGG	1043

Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO.	Antisense Strand Sequence 5' to 3'	SEQ ID NO.	mRNA target sequence	SEQ ID NO.
AD-1684672.1	csgsaucuGfgAfAfCfAcacauuugguL96	665	sc asdCscadAudAugudTgUfcagauacs gsa	1942	UCCGAUCUGGAAACACAUAUUGGA	1113
AD-1684673.1	gsasucugGfaAfCfAfcacauugguL96	657	gsd asdTscadAadTaugudGuUfcagauacs gsd	1943	CCGAUCUGGAAACACAUAUUGGAA	1105
AD-1684674.1	asuscuggAfaCfAfCfauuuuggaauL96	596	csd asdTsudCadAuaudTgUfuccagaus csd	1944	CGAUCUGGAAACACAUAUUGGAAU	1044
AD-1684675.1	uscsuggAfcAfCfAfuauuggaauL96	597	usc asdAsuudCcdAuaudGuGfuuccagaus usc	1945	GAUCUGGAAACACAUAUUGGAAU U	1045
AD-1684676.1	csusggaaCfaCfAfUfauuggaauuL96	598	su asdAsaudTcdCaauadTgUfguuccagaus su	1946	AUCUGGAAACACAUAUUGGAAUU G	1046
AD-1684677.1	usgsaacAfCfAfUfAuuggaauuL96	599	gsa asdCsaadTudCaauadAuGfuuccagaus gsa	1947	UCUGGAAACACAUAUUGGAAUUG G	1047
AD-1684678.1	gsgsaacaCfaUfAfUfUfggaauuL96	600	sg asdCscadAudTccadTaUfguuccagaus sg	1948	CUGGAAACACAUAUUGGAAUUGG G	1048
AD-1684679.1	usasggguGfgGfuAfAfGfgccuuauL96	684	usa asdAsuadAgdGccuudAcCfaccuacs usa	1949	UAUAGGGUGGGUAAGGCCUUUAU A	1132
AD-1684680.1	asgsuggGfgUfAfAfGfgccuuauL96	686	su asdTsaudAadGgeudTaCfaccuacs su	1950	AUAGGGUGGGUAAGGCCUUUAU A	1134
AD-1684681.1	gsdggugGfuAfAfGfgccuuauL96	601	sa asdTsuadTadAggedTuAfccaccuacs sa	1951	UAGGGUGGGUAAGGCCUUUAUAA U	1049
AD-1684682.1	gsdggugUfaAfGfGfgccuuauuL96	602	csu asdAsuudAudAagcdCuUfaccaccs csu	1952	AGGGUGGGUAAGGCCUUUAUAAU G	1050
AD-1684683.1	gsdggguAfaGfGfCfCfuuaauuL96	603	sc asdCsaudTadTaagcdCcUfaccaccs sc	1953	GGGUGGGUAAGGCCUUUAUAAUG U	1051
AD-1684684.1	usgsuggAfgGfCfCfuuaauuL96	663	sc asdAcsadTudAuaagdGcCfuaccaccs sc	1954	GGUGGGUAAGGCCUUUAUAAUGU A	1111
AD-1684685.1	gsdgguaaGfgCfCfUfuaauuL96	656	sc asdTsacdAudTuaadGgCfuaccaccs sc	1955	GUGGGUAAGGCCUUUAUAAUGUA A	1104
AD-1684686.1	gsdguagGfcCfUfUfuaauuL96	653	sa asdTsudCadTuaadAgGfuccuaccs sa	1956	UGGGUAAGGCCUUUAUAAUGUAA A	1101
AD-1684687.1	gsusaagCfcUfUfAfuauuL96	604	csc asdTsudAcadAuaudAaGfgccuacs csc	1957	GGGUAAGGCCUUUAUAAUGUAAA G	1052
AD-1684688.1	usasaggCfuUfAfUfuaauuL96	649	sc asdCsudTadCaauadTaAfgccuacs sc	1958	GGUAAGGCCUUUAUAAUGUAAAG A	1097

Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO.	Antisense Strand Sequence 5' to 3'	SEQ ID NO.	mRNA target sequence	SEQ ID NO.
AD-1684689.1	asasggccUfuAfUfAfauGuaaagauL96	605	asdTscudTudAcauudAuAfaagccuus asc	1959	GUAAAGGCCUUUAAAUGUAAAAGA G	1053
AD-1684690.1	asgsgecuUfaUfAfAfuguaaagaguL96	606	asdCstcdTudTaaudTaUfaagccuu sa	1960	UAAGGCCUUUAAAUGUAAAAGAG C	1054
AD-1684691.1	gsgscuuAfuAfAfUfguaaagagcuL96	644	asdGscudCudTuaudTuAfaagccs usu	1961	AAGGCCUUUAAAUGUAAAAGAGC A	1092
AD-1684692.1	gscscuuAfuAfUfGfuuaagagcuL96	607	asdTsgcdTcdTuaudAuUfaaagccs su	1962	AGGCCUUUAAAUGUAAAAGAGCA U	1055
AD-1684693.1	gscsauuAfaUfGfUfaaaggccuuuL96	608	asdAsagdCcdCuuaudCaUfuaaugs usc	1963	GAGCAUAAAUGUAAAAGGGCUU U	1056
AD-1684694.1	csasuuaAfuGfUfAfaaggccuuuL96	650	asdAsaadGcdCeuudAcAfuuaaugs csu	1964	AGCAUAAAUGUAAAAGGGCUUU A	1098
AD-1684695.1	asusauuUfgUfAfAfaggccuuuauL96	609	asdTsaadAgdCccudTaCfauaaugs sc	1965	GCAUAAAUGUAAAAGGGCUUUA G	1057
AD-1684696.1	usasauuGfuAfAfAfgggccuuuagL96	645	asdCsuadAadGccudTuAfaaanaas usg	1966	CAUAAAUGUAAAAGGGCUUUAG A	1093
AD-1684697.1	asusaugUfaAfAfGfggcuuagauL96	610	asdTscudAadAgecdTuUfaaanaas su	1967	AUAUAAAUGUAAAAGGGCUUUAG G	1058
AD-1684698.1	usasauuAfaAfGfGfgcuuagaguL96	611	asdCstcdTadAagcdCuUfuaanaas usa	1968	UAUAAAUGUAAAAGGGCUUUAGAG U	1059
AD-1684699.1	asasuguaAfaGfGfgfuuuagaguL96	612	asdAscudCudAagcdCcUfuaanaas asu	1969	AUAUAAAUGUAAAAGGGCUUUAGAGU G	1060
AD-1684700.1	cscsuggaUfuAfAfAfaucccauuL96	613	asdAsugdGcdAgaudTuAfaucagg usc	1970	GACCUGGAUUAAAUCUGCCAUIU U	1061
AD-1684701.1	csusggauUfaAfAfAfucugccauuL96	614	asdAsaudGgdCgaudTuUfaucagg gsu	1971	ACCUGGAUUAAAUCUGCCAUIUU U	1062
AD-1684702.1	usgsauuAfaAfAfUfcugccauuL96	641	asdAsaadTgdGeagadTuUfaaauccag sg	1972	CCUGGAUUAAAUCUGCCAUIUUA U	1089
AD-1684703.1	gsgsauuAfaAfUfCfugccauuauL96	640	asdTsaadAudGgcagAuUfuaauccs asg	1973	CUGGAUUAAAUCUGCCAUIUUA U	1088
AD-1684704.1	gsasuuuAfaUfCfUfgccauuauL96	615	asdTsuadAadTggcadGaUfuaauacs csa	1974	UGGAUUAAAUCUGCCAUIUUA U	1063
AD-1684705.1	asusuaaAfuCfUfGfcauuuauL96	616	asdAsuudAadAugcdAgAfuuaau sesc	1975	GGAUUAAAUCUGCCAUIUUA U	1064
AD-1684706.1	asasaucGfcCfAfUfuaauagcuL96	617	asdGscudAadTuaadTgGfcagaau asd	1976	UAAAUCUGCCAUIUUAUAGCU U	1065

Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO.	Antisense Strand Sequence 5' to 3'	SEQ ID NO.	mRNA target sequence	SEQ ID NO.
AD-1684707.1	asasueugCfcAfUfUfuaauuagcuuL96	618	usa asdAsgcdTadAuuadAuGfcgagauus			
AD-1684708.1	asuscugcCfaUfUfUfaauuagcuguL96	619	usu asdCsagdCudAauuadAaUfggcagaus	1977	AAAAUCUGCCCAUUUAAUUAGCUG	1066
AD-1684709.1	uscugcccAfuUfUfAfaauuagcuguL96	666	usu asdGscadGcdTaaudAaAfuggcgagas	1978	AAAUUCUGCCAUUUAAUUAGCUGC	1067
AD-1684710.1	csusgccuUfuUfAfAfuuagcuguL96	620	asu asdTsgcdAgdCuauadTaAfauggcags	1979	AAUCUGCCCAUUUAAUUAGCUGCA	1114
AD-1684711.1	usgscuuUfuUfAfUfUfaugcuguL96	651	gsa asdAsugdCadGcuadTuAfauggcas	1980	AUCUGCCAUUUAAUUAGCUGCAU	1068
AD-1684712.1	ascsgcaaUfcUfGfCfcucaaauuL96	621	usa asdGsaadAudTgagagdCaGfaungcgus	1981	UCUGCCAUUUAAUUAGCUGCAUA	1099
AD-1684713.1	csgscaauCfuGfCfcucaaauuL96	622	usu asdAsgadAadTugagdGcAfgauugcgs	1982	UAACGCAAUUCUGCCCUCAAUUUUCU	1069
AD-1684714.1	gscsaauCfugCfCfUfcaauuL96	623	gsu asdAsagdAadAungadGgCfagaungcs	1983	AACGCAAUUCUGCCCUCAAUUUUCU	1070
AD-1684715.1	csasaucUfCfUfCfUfcaauuL96	659	esg asdGsaadGadAauugdAgGfcagauugs	1984	ACGCAAUUCUGCCCUCAAUUUUCU	1071
AD-1684716.1	asasueugCfcUfCfAfaauuL96	624	gsc asdTsgadAgdAaaudGaGfcgagauus	1985	CGCAAUUCUGCCCUCAAUUUUCU	1107
AD-1684717.1	asuscugcCfuCfAfAfuuuL96	625	usg asdAsugdAadGaaudTgAfggcagaus	1986	GCAAUUCUGCCCUCAAUUUUCU	1072
AD-1684718.1	uscugcccUfcAfUfUfuuuL96	626	usu asdGsaadGadAgaadTuGfaggcgagas	1987	CAAUCUGCCCUCAAUUUUCU	1073
AD-1684719.1	csusgccuCfaUfUfUfuuuL96	627	asu asdAsgadTgdAgaadAuUfgaggcags	1988	AAUCUGCCCUCAAUUUUCU	1074
AD-1684720.1	usgscuuAfaUfUfUfuuuL96	628	gsa asdCsagdAudGaagadAaUfaggcgas	1989	AUCUGCCCUCAAUUUUCU	1075
AD-1684721.1	gscscucaAfuUfUfCfucauL96	629	asg asdAseadGadTgaagdAaAfuugagcgs	1990	UCUGCCCUCAAUUUUCU	1076
AD-1684722.1	csesucaUfuUfCfUfuuuL96	647	csa asdGsacdAgdAugadGaAfaungaggs	1991	CUGCCCUCAAUUUUCU	1077
AD-1684723.1	csuscaauUfuUfUfuuuL96	648	gsc asdTsgadCadGaugadAgAfaungaggs	1992	UGCCCUCAAUUUUCU	1095
				1993	GCCUCAAUUUUCU	1096

Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO.	Antisense Strand Sequence 5' to 3'	SEQ ID NO.	mRNA target sequence	SEQ ID NO.
AD-1684724.1	uscsaaauUfcUfUfCfaucuguaauL96	642	asdTsuagAcdaAgaugdAaGfaaaauasgsg	1994	CCUCAAUUUCUUCACUCUGUCAAA	1090
AD-1684725.1	csasaauuCfuUfCfAfucugucaauL96	630	asdTsuudGadCagandGaAfgaauuags	1995	CUCAAUUUCUUCACUCUGUCAAAU	1078
AD-1684726.1	asasuueUfuCfAfUfcuguaauuL96	631	asdAsuudTgdAcagadTgAfagaauusgsa	1996	UCAAUUUCUUCACUCUGUCAAAUG	1079
AD-1684727.1	asusuueUfcAfUfCfuguaaaugL96	632	asdCsaudTudGacagdAuGfaagaaus	1997	CAAUUUCUUCACUCUGUCAAAUGG	1080
AD-1684728.1	ususuueCfuUfCfUfuguaaaugL96	643	asdCscadTudTgacadGaUfgaagaaasu	1998	AUUUCUUCACUCUGUCAAAUGGA	1091
AD-1684729.1	ususuueAfUfCfUfGfuaaaugauL96	639	asdTtsedAudTugacdAgAfugaagaasu	1999	AUUUCUUCACUCUGUCAAAUGGAA	1087
AD-1684730.1	asasuueGfcUfUfGfGfcuaagaauL96	633	asdTsuedTgdTgaccdAaGfcagaauusg	2000	CCAAUUCUGCUUGGCUACAGAAU	1081
AD-1684731.1	asusucugCfuUfGfGfcuaacagaauL96	634	asdAsuudCudGuaagdCaAfgcagaasu	2001	CAAUUCUGCUUGGCUACAGAAU	1082
AD-1684732.1	ususuueUfuGfGfCfuacagaauuL96	654	asdAsaudTcdTguagdCcAfagcagaasu	2002	AAUUCUGCUUGGCUACAGAAUUA	1102
AD-1684733.1	uscsugcuUfgGfCfUfacagaauuuL96	635	asdTtsaadTudCugnadGcCfaagcagasa	2003	AUUCUGCUUGGCUACAGAAUUAU	1083
AD-1684734.1	csuscuuGfgCfUfAfcaagaauuuL96	636	asdAsuadAudTevugdAgCfcaagcags	2004	UUCUGCUUGGCUACAGAAUUAU	1084
AD-1684735.1	usgscuugGfcUfAfCfagaauuuuL96	637	asdAsaudAadTucugdTaGfccagcags	2005	UCUGCUUGGCUACAGAAUUAUUG	1085
AD-1684736.1	gscsuuugCfuAfCfAfgaauuuuL96	638	asdCsaadTadAuueudGuAfgccaaags	2006	CUGCUUGGCUACAGAAUUAUUGU	1086
AD-1684737.1	asusuaunGfuGfAfGfgaauuuuL96	652	asdGsaudTudTaucddTcAfcaauaasu	2007	GAAUUAUUGUGAGGAUAAAAUC	1100

Table 14. KHK Single Dose Screen in Hep3b Cells

	10 nM		1 nM		0.1 nM	
Duplex ID	Average % message remaining	STDEV	Average % message remaining	STDEV	Average % message remaining	STDEV
AD-1290635.2	98.30	12.80	109.90	0.00	133.00	0.00
AD-1684641.1	25.30	0.00	51.50	14.40	18.60	10.60
AD-1684620.1	7.20	2.70	11.30	0.70	10.10	2.10
AD-1684619.1	6.60	1.50	13.70	3.60	17.90	2.90
AD-1684610.1	7.60	1.60	15.40	3.70	25.00	7.40
AD-1684617.1	7.60	1.40	13.30	5.40	12.50	4.00
AD-1613079.2	9.70	2.20	36.70	8.80	33.60	5.70
AD-1684618.1	5.60	0.70	13.00	4.60	9.50	1.60
AD-1684622.1	8.30	2.50	14.00	2.30	17.60	4.50
AD-1684607.1	8.30	0.90	14.40	2.70	12.10	2.10
AD-1684614.1	7.80	1.50	22.00	7.60	23.30	7.70
AD-1613059.2	8.50	0.50	11.70	1.40	11.80	1.50
AD-1613075.2	6.90	0.70	16.00	4.90	19.60	6.80
AD-1613061.1	5.90	2.20	8.00	2.50	10.50	6.10
AD-1684608.1	10.20	2.80	19.20	3.00	18.80	6.80
AD-1684624.1	16.50	3.50	31.80	5.70	50.70	12.80
AD-1423319.3	9.20	0.70	14.40	2.10	14.90	1.60
AD-1684606.1	8.10	2.00	12.40	2.20	14.10	4.40
AD-1684609.1	8.40	1.20	17.00	2.90	14.00	4.00
AD-1684616.1	15.20	2.90	29.70	8.40	31.50	3.00
AD-1613060.2	13.60	1.70	27.00	1.90	29.80	9.50
AD-1613087.1	16.80	2.90	35.50	6.30	39.80	10.40
AD-1290539.5	12.30	2.80	18.30	2.90	21.70	2.50
AD-1290885.5	17.50	5.90	41.70	7.50	63.60	1.40
AD-1613062.2	12.10	2.10	24.10	4.90	28.60	9.00
AD-1684611.1	14.70	3.70	22.30	2.40	26.50	6.10
AD-1684623.1	18.60	3.60	31.90	3.00	59.60	13.80
AD-1612969.2	15.40	4.00	30.40	10.90	52.70	6.80
AD-1613256.2	8.30	1.20	23.60	6.70	33.40	3.80
AD-1423312.3	5.70	2.30	20.50	5.50	16.00	5.80
AD-1548743.7	14.60	2.40	24.20	2.30	34.60	8.10
AD-1684596.1	21.40	8.00	20.40	0.70	24.30	6.00
AD-1423336.7	10.90	1.50	32.80	3.40	36.60	5.80
AD-1612963.2	12.30	4.10	26.50	5.90	28.70	7.10
AD-1290611.3	15.60	3.80	32.40	7.40	54.20	10.00
AD-1613254.2	11.60	2.20	20.70	4.50	24.00	2.80
AD-1684612.1	11.70	1.00	19.50	2.70	31.70	9.10
AD-1684645.1	14.90	2.80	28.80	6.70	35.70	4.70
AD-1684621.1	21.20	6.50	59.50	12.40	42.00	9.10

	10 nM		1 nM		0.1 nM	
Duplex ID	Average % message remaining	STDEV	Average % message remaining	STDEV	Average % message remaining	STDEV
AD-1290837.5	17.70	6.20	49.70	7.60	69.90	15.10
AD-1684598.1	37.30	9.50	67.00	19.00	66.40	10.90
AD-1684638.1	23.00	6.60	47.50	13.90	40.40	7.20
AD-1290599.7	11.00	1.20	18.60	3.30	40.00	5.00
AD-1613400.2	7.80	1.70	19.10	7.80	23.00	2.20
AD-1684615.1	17.50	3.20	41.00	2.90	52.70	6.40
AD-1684630.1	14.20	1.30	45.40	10.30	51.20	10.00
AD-1613072.1	43.70	14.40	72.70	6.50	86.70	11.40
AD-1684632.1	17.50	5.60	36.80	7.70	53.40	3.40
AD-1613242.2	11.60	2.60	28.40	9.80	35.20	8.90
AD-1684605.1	53.80	6.00	72.00	8.60	102.80	17.40
AD-1684594.1	16.70	3.90	27.10	4.20	35.80	9.10
AD-1612957.2	14.90	5.10	29.60	7.40	25.90	6.30
AD-1290971.3	13.60	2.40	37.60	9.50	36.90	12.60
AD-1684595.1	29.60	9.90	49.80	12.20	52.40	9.80
AD-1613371.3	14.20	4.40	27.70	5.80	32.10	2.80
AD-1684593.1	20.10	5.10	32.70	10.70	39.60	13.90
AD-1684639.1	13.50	4.50	35.10	6.50	39.90	2.30
AD-1613094.2	16.80	5.20	38.70	4.90	58.50	17.50
AD-1684597.1	30.30	3.00	61.00	14.40	48.90	4.70
AD-1290563.2	50.40	7.90	92.60	14.00	95.40	26.70
AD-1684599.1	41.60	13.60	66.40	17.20	66.80	14.50
AD-1684640.1	17.80	3.60	50.90	10.60	62.70	11.10
AD-1290584.2	32.10	9.80	70.00	11.80	76.10	20.40
AD-1684627.1	20.10	10.50	54.00	12.10	71.60	11.20
AD-1290969.7	18.50	5.40	31.80	7.00	34.30	5.10
AD-1290651.2	51.80	11.50	100.80	20.90	117.60	24.10
AD-1684628.1	17.40	7.00	26.80	5.30	34.10	6.40
AD-1290884.5	20.80	7.20	37.60	7.60	39.00	5.00
AD-1684633.1	25.60	5.90	52.30	3.50	77.80	17.00
AD-1684637.1	31.90	10.90	55.00	9.20	68.60	17.60
AD-1684629.1	38.00	5.90	86.00	13.60	91.70	16.40
AD-1684635.1	32.60	4.30	87.20	14.10	45.90	4.10
AD-1684613.1	43.20	9.20	84.20	23.20	75.90	26.30
AD-1684604.1	47.30	8.80	78.10	15.50	83.00	11.40
AD-1290666.2	28.30	8.10	62.20	16.50	74.10	11.60
AD-1684634.1	39.90	11.00	76.80	9.60	86.20	17.40
AD-1684600.1	70.30	11.40	101.80	5.30	63.80	22.40
AD-1684644.1	68.00	19.10	159.30	17.60	131.10	15.50
AD-1684643.1	96.80	16.70	130.10	23.00	140.40	19.50

Duplex ID	10 nM		1 nM		0.1 nM	
	Average % message remaining	STDEV	Average % message remaining	STDEV	Average % message remaining	STDEV
AD-1684601.1	92.10	22.20	136.00	33.00	115.30	33.70
AD-1684626.1	35.10	7.20	65.30	10.50	66.90	5.70
AD-1684642.1	72.30	18.80	116.80	22.20	124.30	8.60
AD-1684592.1	68.50	13.90	120.10	23.20	85.70	6.80
AD-1684636.1	52.00	18.10	88.40	34.10	87.30	10.60
AD-1684603.1	133.70	13.10	143.80	21.30	128.00	22.60
AD-1684631.1	114.50	35.20	163.20	10.70	162.80	24.90
AD-1684625.1	74.60	12.90	121.80	25.30	105.40	20.30
AD-1290523.2	38.30	4.50	44.10	3.20	49.20	15.10
AD-1684602.1	91.40	21.30	151.40	24.60	110.60	24.70
AD-1290570.2	113.50	16.00	137.90	22.90	94.90	11.30
AD-1684666.1	116.20	5.80	109.50	14.40	143.90	23.60
AD-1290865.2	58.40	13.50	64.50	10.30	77.90	7.80
AD-1290589.2	92.60	17.80	108.80	5.90	113.00	7.50
AD-1684681.1	111.40	18.20	129.40	13.10	131.70	21.70
AD-1684689.1	148.40	36.10	91.30	3.00	122.40	27.70
AD-1684708.1	51.20	10.40	83.10	17.60	93.00	21.90
AD-1290557.2	118.30	12.80	76.90	5.70	125.20	33.40
AD-1290515.2	106.60	14.40	116.50	20.20	98.10	9.30
AD-1290741.2	109.20	9.20	119.20	28.90	144.10	20.80
AD-1684713.1	91.70	14.60	84.70	7.90	116.30	17.60
AD-1290650.2	89.60	6.80	75.90	10.30	123.80	18.30
AD-1290897.2	54.80	10.60	81.70	22.90	75.20	24.00
AD-1290556.2	123.30	14.80	92.50	13.30	115.10	12.00
AD-1290750.2	93.70	13.30	95.10	14.20	100.10	12.50
AD-1684714.1	98.00	6.20	136.70	24.30	118.10	12.60
AD-1290654.2	102.80	15.70	119.50	14.80	134.00	32.20
AD-1290909.2	91.20	10.30	108.90	34.40	81.90	22.00
AD-1684674.1	96.60	21.20	118.40	19.30	112.90	27.70
AD-1684712.1	46.90	8.60	88.20	13.40	75.30	13.50
AD-1290796.2	111.90	12.00	119.70	14.30	171.60	18.40
AD-1290612.2	65.20	11.20	94.10	16.20	87.40	11.00
AD-1290633.2	106.60	11.10	94.20	9.50	97.00	23.00
AD-1684691.1	142.10	25.10	112.20	13.20	129.20	9.80
AD-1290659.2	79.40	14.80	103.40	10.30	120.70	13.50
AD-1684686.1	107.60	17.70	129.20	33.80	108.30	23.50
AD-1290604.2	60.90	12.20	64.30	15.40	76.30	16.10
AD-1290574.2	121.10	5.80	122.10	15.40	128.60	12.90
AD-1290609.2	87.60	13.30	111.90	17.40	91.70	17.20
AD-1290911.2	134.00	15.60	65.80	14.70	82.30	16.50

Duplex ID	10 nM		1 nM		0.1 nM	
	Average % message remaining	STDEV	Average % message remaining	STDEV	Average % message remaining	STDEV
AD-1290615.2	110.30	11.00	127.90	11.60	158.20	13.00
AD-1684710.1	95.20	12.40	103.60	33.60	117.10	10.50
AD-1684709.1	89.50	19.50	81.20	18.80	92.00	6.10
AD-1290533.2	91.20	19.70	104.90	13.90	99.00	13.30
AD-1684671.1	78.00	7.50	102.80	18.70	98.50	11.20
AD-1684650.1	108.50	3.10	127.80	12.40	118.90	14.50
AD-1684711.1	109.10	20.40	116.90	21.40	106.80	24.30
AD-1684670.1	73.90	14.70	104.70	17.20	127.80	8.90
AD-1684692.1	96.10	16.30	113.50	17.10	103.70	8.30
AD-1290939.2	112.00	10.60	108.90	18.70	101.00	11.20
AD-1684662.1	113.70	21.40	115.40	20.80	117.00	19.60
AD-1684700.1	97.00	21.20	99.20	20.90	65.60	13.10
AD-1290742.2	120.00	18.60	140.80	26.00	97.10	12.40
AD-1684715.1	85.70	18.20	72.70	18.50	120.60	8.70
AD-1290894.2	102.60	11.70	125.50	28.90	149.60	44.30
AD-1684718.1	112.50	13.00	122.40	22.90	136.80	18.20
AD-1290702.2	112.80	29.70	73.50	8.90	80.50	18.40
AD-1684688.1	106.50	25.50	124.40	36.40	123.10	16.60
AD-1684690.1	110.50	5.50	94.50	13.40	106.60	11.50
AD-1684672.1	94.00	12.20	91.00	4.70	98.10	9.30
AD-1684684.1	124.60	21.80	134.40	17.30	121.20	11.40
AD-1684723.1	122.90	4.90	137.70	20.30	142.70	35.90
AD-1684651.1	121.50	44.40	94.60	19.10	107.00	15.50
AD-1684683.1	86.10	5.00	122.80	16.60	91.60	12.10
AD-1290973.2	135.00	19.60	121.30	17.90	129.00	27.10
AD-1290857.2	106.00	12.00	105.00	22.10	89.90	13.10
AD-1684649.1	61.80	9.50	90.40	9.30	67.00	31.50
AD-1290516.2	106.50	19.40	84.40	15.50	70.60	6.80
AD-1290554.2	71.60	21.20	72.80	12.90	71.10	20.50
AD-1290509.2	115.50	16.80	112.90	19.60	92.90	15.10
AD-1290660.2	132.60	30.90	135.00	21.70	98.20	28.10
AD-1684698.1	116.30	8.30	111.20	6.20	90.70	25.00
AD-1290670.2	122.20	6.90	135.80	24.50	150.90	20.40
AD-1684673.1	101.80	11.20	103.80	5.00	105.40	30.20
AD-1684646.1	148.30	19.10	159.50	17.50	128.30	21.40
AD-1290597.2	109.30	23.60	97.80	15.50	109.10	34.10
AD-1290573.2	71.20	7.50	88.60	4.80	93.50	6.40
AD-1684707.1	88.20	7.50	94.50	13.40	91.10	19.00
AD-1684722.1	102.60	11.40	147.30	34.10	162.60	1.40
AD-1290639.2	88.00	11.40	74.20	8.40	83.20	11.10

Duplex ID	10 nM		1 nM		0.1 nM	
	Average % message remaining	STDEV	Average % message remaining	STDEV	Average % message remaining	STDEV
AD-1290551.2	100.60	27.30	74.50	19.50	105.80	31.00
AD-1684655.1	146.00	14.60	127.60	21.40	109.60	18.60
AD-1684678.1	148.20	38.60	144.00	24.60	160.70	11.20
AD-1290800.2	129.20	17.20	141.00	10.40	119.30	16.10
AD-1684726.1	83.90	6.80	95.10	21.20	153.80	21.30
AD-1290764.2	85.70	9.50	100.30	16.60	89.50	14.40
AD-1290672.2	90.20	14.50	108.20	6.50	122.60	29.80
AD-1684685.1	158.00	23.20	147.70	27.30	131.50	17.80
AD-1290528.2	17.30	2.30	26.80	4.40	35.90	7.40
AD-1684696.1	83.80	15.70	87.80	20.90	56.60	13.20
AD-1290836.2	120.80	24.10	138.00	20.80	153.80	22.50
AD-1684682.1	99.50	7.40	121.50	22.20	102.10	19.30
AD-1684659.1	61.20	13.60	89.50	3.40	102.00	18.30
AD-1684669.1	101.90	15.80	114.60	19.50	112.10	24.30
AD-1684704.1	115.60	9.50	143.60	36.20	111.10	34.60
AD-1684716.1	83.10	11.60	87.30	7.90	106.30	22.40
AD-1684699.1	106.50	14.40	111.70	29.80	64.20	17.80
AD-1290510.2	112.30	18.30	137.60	27.30	155.40	21.70
AD-1290531.2	87.20	9.20	113.60	33.80	125.10	21.60
AD-1684703.1	101.00	14.00	104.40	15.90	81.80	17.40
AD-1290910.2	96.60	6.80	96.30	35.70	123.50	13.10
AD-1684705.1	98.30	15.30	108.60	32.30	96.40	21.30
AD-1290618.2	109.80	9.20	117.20	13.60	72.30	17.00
AD-1684668.1	95.50	5.80	105.80	16.30	103.00	8.00
AD-1684701.1	61.40	12.80	59.40	11.60	81.70	15.50
AD-1290542.2	110.40	18.30	120.10	23.60	110.00	3.90
AD-1290626.2	92.50	9.90	95.20	10.10	105.00	8.60
AD-1684724.1	98.40	8.20	106.50	12.10	144.80	26.30
AD-1290535.2	131.60	18.00	137.80	13.30	127.70	33.60
AD-1290558.2	129.70	41.60	107.30	30.00	61.90	12.50
AD-1684647.1	118.10	43.70	124.50	25.80	94.60	17.50
AD-1290763.2	91.60	6.90	121.20	18.40	105.70	16.10
AD-1684677.1	94.50	18.30	97.10	22.20	103.50	4.00
AD-1684658.1	115.10	25.50	108.90	16.00	126.20	12.60
AD-1684687.1	92.20	17.60	107.40	15.70	104.80	11.50
AD-1684719.1	97.00	5.10	121.20	5.20	106.00	10.70
AD-1290681.2	130.40	12.30	120.30	17.30	113.50	18.10
AD-1684653.1	133.20	34.50	112.90	7.20	94.80	25.20
AD-1290841.2	166.20	35.70	140.10	1.50	147.10	15.70
AD-1290687.2	83.90	6.80	140.00	15.70	138.80	12.90

Duplex ID	10 nM		1 nM		0.1 nM	
	Average % message remaining	STDEV	Average % message remaining	STDEV	Average % message remaining	STDEV
AD-1290592.2	75.50	4.00	63.30	22.80	53.40	4.00
AD-1290522.2	86.40	5.50	102.50	18.10	95.70	11.40
AD-1290880.2	125.50	24.70	94.30	11.10	126.00	12.60
AD-1684693.1	56.90	19.40	53.80	7.10	46.50	6.60
AD-1684679.1	96.50	11.30	111.50	11.40	115.70	21.40
AD-1290555.2	102.60	12.20	59.80	6.50	74.00	33.30
AD-1684648.1	64.70	25.60	86.20	8.10	69.90	28.10
AD-1684725.1	97.40	10.30	109.20	10.50	143.70	21.00
AD-1684706.1	37.50	4.70	46.80	16.60	55.10	14.90
AD-1684663.1	111.70	15.50	118.30	30.30	86.10	35.10
AD-1684702.1	100.20	11.00	79.80	12.00	81.80	10.10
AD-1291003.2	110.40	24.90	108.30	14.50	122.30	20.40
AD-1684664.1	110.20	5.00	117.70	22.00	98.80	7.20
AD-1684697.1	58.70	13.20	66.60	14.80	62.10	15.80
AD-1290514.2	89.80	6.40	108.60	7.20	151.30	18.10
AD-1290989.2	93.40	7.70	101.00	18.70	110.30	13.70
AD-1684657.1	90.30	11.70	98.80	16.00	99.70	29.30
AD-1684654.1	128.30	24.50	109.50	22.10	105.60	33.40
AD-1684695.1	106.60	19.70	91.90	14.50	58.70	7.60
AD-1290712.2	78.60	8.50	126.00	31.80	96.20	13.60
AD-1290931.2	144.80	16.70	127.50	23.50	120.60	18.50
AD-1684729.1	117.20	9.80	134.20	14.70	138.70	25.30
AD-1290805.2	87.90	18.00	94.50	33.50	102.90	20.50
AD-1290755.2	117.00	13.30	124.90	28.50	125.00	29.10
AD-1290527.2	124.10	2.80	76.20	21.60	92.30	31.20
AD-1684652.1	102.00	14.00	96.20	28.30	72.30	18.50
AD-1290507.2	107.20	18.20	118.90	22.10	145.70	41.10
AD-1290747.2	119.20	36.80	103.60	5.30	102.40	14.10
AD-1290926.2	104.90	20.70	105.00	24.10	85.60	16.00
AD-1290983.2	93.70	26.10	136.80	26.50	117.40	15.60
AD-1684680.1	119.70	9.90	115.70	20.40	112.70	18.00
AD-1290605.2	82.10	14.20	96.30	22.40	90.80	9.80
AD-1290842.2	147.60	23.00	145.10	24.30	151.50	27.20
AD-1290565.2	90.90	12.90	107.40	14.80	162.30	28.00
AD-1290661.2	81.70	18.70	82.70	7.80	73.00	24.20
AD-1684667.1	41.60	3.10	54.00	5.90	61.80	5.20
AD-1290684.2	85.00	8.00	92.90	11.80	101.60	7.90
AD-1290524.2	114.60	17.20	143.40	15.60	139.30	26.90
AD-1290655.2	142.20	24.00	128.40	16.50	136.10	21.10
AD-1684660.1	110.20	18.10	134.30	16.20	122.60	20.30

	10 nM		1 nM		0.1 nM	
Duplex ID	Average % message remaining	STDEV	Average % message remaining	STDEV	Average % message remaining	STDEV
AD-1684656.1	87.70	37.40	75.00	26.10	76.20	25.20
AD-1684676.1	37.60	2.80	58.60	12.60	72.40	5.00
AD-1684727.1	104.30	31.00	110.10	20.50	117.50	12.10
AD-1684665.1	115.00	28.50	115.70	16.40	105.90	4.90
AD-1290993.2	126.50	14.30	107.50	12.10	98.50	26.30
AD-1684721.1	84.80	4.40	115.10	9.00	144.20	10.10
AD-1290543.2	41.90	8.40	52.50	9.70	54.00	10.30
AD-1290719.2	102.80	11.70	107.60	10.40	136.50	13.40
AD-1290602.2	97.50	7.70	111.60	23.90	116.30	21.10
AD-1290564.2	51.40	1.80	55.70	6.00	75.50	15.00
AD-1684737.1	96.80	16.70	111.80	9.20	105.40	18.20
AD-1684694.1	63.70	21.10	65.10	20.50	72.20	15.80
AD-1290875.2	116.90	11.10	123.80	27.30	72.10	27.80
AD-1684732.1	99.40	14.40	91.50	17.70	138.80	7.00
AD-1684717.1	49.00	11.30	101.40	15.10	104.80	3.30
AD-1290908.2	118.70	7.20	117.70	15.60	97.80	14.70
AD-1684720.1	86.00	2.70	90.20	15.90	112.10	6.60
AD-1290552.2	98.50	16.80	121.20	17.10	137.80	29.70
AD-1684728.1	101.60	25.20	113.60	20.10	136.80	29.60
AD-1684731.1	137.20	10.40	126.20	11.10	142.60	2.40
AD-1290722.2	137.00	19.70	166.40	13.80	170.50	18.70
AD-1684730.1	130.20	30.50	117.60	15.60	117.80	9.00
AD-1684736.1	128.90	12.90	137.40	13.70	135.60	30.10
AD-1684733.1	169.30	14.60	170.60	26.10	178.70	11.10
AD-1684661.1	31.60	6.40	41.70	8.40	48.80	15.50
AD-1684734.1	80.20	13.20	65.20	20.10	85.00	20.90
AD-1684735.1	114.70	26.20	94.40	18.00	119.80	18.20
AD-1290600.2	120.90	18.80	101.00	13.30	118.60	9.70
AD-1290624.2	130.50	13.50	141.60	27.20	115.50	17.40
AD-1290643.2	111.40	14.00	62.10	21.50	114.00	21.40
AD-1684675.1	94.00	21.20	89.60	10.90	84.00	7.70

Table 15. KHK Single Dose Screen in PCH Cells

	10 nM		1 nM		0.1 nM	
Duplex ID	Average % message remaining	STDEV	Average % message remaining	STDEV	Average % message remaining	STDEV
AD-1290635.2	23.50	10.50	0.00	0.00	21.60	5.20
AD-1684641.1	0.00	0.00	0.00	0.00	6.00	0.20
AD-1684620.1	1.00	0.10	1.70	0.50	3.20	0.30

Duplex ID	10 nM		1 nM		0.1 nM	
	Average % message remaining	STDEV	Average % message remaining	STDEV	Average % message remaining	STDEV
AD-1684619.1	1.30	0.10	2.00	0.10	2.80	0.30
AD-1684610.1	2.00	0.60	2.10	0.20	4.20	0.50
AD-1684617.1	1.70	0.10	2.10	0.40	3.00	0.50
AD-1613079.2	1.40	0.40	2.30	0.20	3.90	1.00
AD-1684618.1	1.00	0.30	2.30	0.30	3.40	0.60
AD-1684622.1	1.80	0.20	2.40	0.20	4.20	0.80
AD-1684607.1	1.60	0.10	2.50	0.40	5.60	0.80
AD-1684614.1	2.10	0.70	2.60	0.30	4.30	0.30
AD-1613059.2	1.90	0.40	2.70	0.40	5.10	0.20
AD-1613075.2	1.10	0.30	2.70	0.30	3.50	0.20
AD-1613061.1	1.90	0.70	2.80	0.30	5.00	0.80
AD-1684608.1	2.10	0.30	2.80	0.20	6.10	1.10
AD-1684624.1	1.70	0.20	2.80	1.00	7.00	1.30
AD-1423319.3	1.90	0.40	2.90	0.80	4.90	0.70
AD-1684606.1	2.00	0.30	3.10	0.20	5.80	0.80
AD-1684609.1	2.00	0.30	3.10	0.30	5.50	0.60
AD-1684616.1	2.20	0.50	3.10	0.80	5.20	1.40
AD-1613060.2	2.00	0.70	3.30	0.20	6.30	1.40
AD-1613087.1	1.50	0.20	3.30	0.10	5.30	0.70
AD-1290539.5	2.50	0.10	3.80	0.10	6.20	0.70
AD-1290885.5	2.00	0.40	3.90	0.60	6.30	0.90
AD-1613062.2	2.80	0.40	3.90	0.10	6.90	0.80
AD-1684611.1	2.00	0.20	4.00	0.80	7.70	0.80
AD-1684623.1	3.10	0.30	4.00	0.80	7.90	1.80
AD-1612969.2	3.90	0.40	4.70	0.60	11.30	1.20
AD-1613256.2	3.60	0.40	4.70	1.10	7.20	1.00
AD-1423312.3	3.60	1.70	4.80	0.90	7.60	2.20
AD-1548743.7	4.40	1.30	4.90	0.30	9.30	1.90
AD-1684596.1	4.40	0.60	4.90	0.70	13.40	3.90
AD-1423336.7	2.40	0.70	5.00	1.30	8.00	2.30
AD-1612963.2	4.40	0.70	5.00	0.30	12.50	1.60
AD-1290611.3	2.60	0.70	5.20	1.10	12.60	3.50
AD-1613254.2	3.50	1.00	5.20	1.40	9.80	2.60
AD-1684612.1	3.40	1.00	5.30	0.90	9.60	0.40
AD-1684645.1	3.00	0.60	5.50	1.20	6.20	0.40
AD-1684621.1	3.10	0.40	5.80	0.10	12.10	3.10
AD-1290837.5	2.50	0.60	5.90	0.80	13.90	1.50
AD-1684598.1	4.60	1.10	6.00	0.70	14.80	2.90
AD-1684638.1	4.00	1.30	6.30	1.10	8.60	1.80
AD-1290599.7	3.70	1.00	6.50	1.10	11.80	1.80
AD-1613400.2	4.50	1.30	6.60	1.40	10.30	2.40

Duplex ID	10 nM		1 nM		0.1 nM	
	Average % message remaining	STDEV	Average % message remaining	STDEV	Average % message remaining	STDEV
AD-1684615.1	2.70	0.80	6.60	1.10	13.00	1.90
AD-1684630.1	4.00	1.70	6.70	1.30	9.60	1.70
AD-1613072.1	3.30	1.00	6.90	0.70	12.30	1.80
AD-1684632.1	4.10	1.50	7.00	1.30	8.00	1.10
AD-1613242.2	5.10	2.20	7.10	1.20	9.20	2.30
AD-1684605.1	7.30	1.30	7.60	0.90	17.10	1.90
AD-1684594.1	6.70	1.00	7.70	1.20	15.60	2.10
AD-1612957.2	5.00	0.80	7.80	1.80	14.00	1.10
AD-1290971.3	6.20	1.90	8.10	1.50	12.80	2.00
AD-1684595.1	5.90	0.70	8.20	2.20	18.90	1.30
AD-1613371.3	4.40	1.10	8.80	1.00	9.60	1.10
AD-1684593.1	6.30	0.80	8.80	1.10	12.00	2.50
AD-1684639.1	5.70	1.90	8.80	1.70	19.10	5.30
AD-1613094.2	6.90	1.20	9.70	0.90	19.90	4.60
AD-1684597.1	5.70	1.00	9.70	1.60	22.40	2.80
AD-1290563.2	17.60	5.00	9.80	0.00	27.40	8.90
AD-1684599.1	4.90	1.80	9.90	1.80	19.80	2.70
AD-1684640.1	6.40	2.70	10.10	1.50	18.20	4.00
AD-1290584.2	5.50	2.50	10.40	1.30	15.80	3.80
AD-1684627.1	5.90	1.70	12.30	1.00	21.60	3.70
AD-1290969.7	6.70	2.40	12.60	4.00	16.80	5.60
AD-1290651.2	3.90	1.10	13.30	1.50	24.70	4.10
AD-1684628.1	9.10	2.40	13.30	0.20	18.50	2.20
AD-1290884.5	5.40	1.60	13.60	1.70	22.20	5.90
AD-1684633.1	8.20	3.80	14.20	0.90	27.10	5.90
AD-1684637.1	7.80	3.50	15.10	2.00	23.00	2.60
AD-1684629.1	5.80	1.90	16.90	3.20	24.00	1.40
AD-1684635.1	12.10	2.70	17.10	1.20	27.50	7.70
AD-1684613.1	7.10	2.10	18.20	3.80	35.50	5.20
AD-1684604.1	11.80	0.40	19.90	0.60	41.60	2.50
AD-1290666.2	10.00	3.00	20.80	4.80	37.00	2.30
AD-1684634.1	10.00	4.00	22.70	4.00	37.30	6.30
AD-1684600.1	11.60	1.90	27.90	0.80	53.10	5.40
AD-1684644.1	15.60	4.80	28.80	3.10	55.40	19.80
AD-1684643.1	12.20	4.20	30.20	2.80	41.90	4.30
AD-1684601.1	16.00	2.10	31.20	3.80	60.10	6.00
AD-1684626.1	21.50	6.40	31.60	5.10	60.50	16.20
AD-1684642.1	13.50	4.60	35.50	5.20	56.50	8.40
AD-1684592.1	21.80	1.90	35.70	5.00	59.70	6.20
AD-1684636.1	11.30	4.50	38.10	6.60	59.60	14.00
AD-1684603.1	22.70	4.00	51.50	2.10	77.80	11.40

Duplex ID	10 nM		1 nM		0.1 nM	
	Average % message remaining	STDEV	Average % message remaining	STDEV	Average % message remaining	STDEV
AD-1684631.1	21.40	7.60	53.80	9.50	68.00	7.30
AD-1684625.1	12.80	4.50	54.20	7.70	67.50	14.20
AD-1290523.2	68.70	17.50	67.80	25.20	105.40	19.60
AD-1684602.1	37.60	3.30	69.00	5.10	99.90	5.60
AD-1290570.2	113.90	17.40	74.40	15.30	118.80	10.50
AD-1684666.1	114.80	4.60	75.40	12.40	99.60	7.20
AD-1290865.2	90.60	6.20	76.50	35.10	107.90	14.00
AD-1290589.2	133.30	30.50	77.30	8.40	120.40	23.60
AD-1684681.1	118.30	35.00	80.70	18.10	115.30	14.10
AD-1684689.1	145.00	30.40	82.20	13.40	100.00	21.80
AD-1684708.1	85.20	12.90	83.50	7.60	89.10	5.30
AD-1290557.2	143.10	27.50	85.40	13.60	142.40	27.30
AD-1290515.2	146.90	30.00	85.90	15.30	152.80	28.10
AD-1290741.2	77.20	17.70	86.30	19.50	88.50	16.50
AD-1684713.1	81.30	21.10	86.80	14.00	89.80	15.00
AD-1290650.2	70.10	15.20	87.00	13.50	93.80	15.50
AD-1290897.2	84.50	12.20	88.50	35.40	98.20	8.90
AD-1290556.2	130.10	24.90	88.60	21.40	149.90	29.90
AD-1290750.2	41.60	15.10	89.20	24.30	131.10	34.80
AD-1684714.1	84.20	10.00	89.20	7.70	80.10	8.10
AD-1290654.2	117.30	18.70	89.50	16.40	107.40	13.50
AD-1290909.2	79.50	5.30	89.50	12.00	87.40	12.00
AD-1684674.1	109.80	18.20	89.60	26.20	94.20	6.20
AD-1684712.1	75.20	12.40	89.70	6.10	87.70	10.50
AD-1290796.2	94.60	12.30	90.70	8.80	104.30	13.60
AD-1290612.2	141.60	32.40	90.80	5.60	116.90	22.40
AD-1290633.2	92.10	16.50	90.80	4.20	91.90	11.20
AD-1684691.1	130.90	21.50	90.80	10.80	147.30	22.50
AD-1290659.2	77.40	11.60	91.50	10.90	83.40	8.80
AD-1684686.1	115.30	23.00	91.80	23.80	132.80	20.30
AD-1290604.2	102.20	21.70	92.60	11.90	91.50	11.60
AD-1290574.2	118.10	16.60	93.80	4.40	138.30	11.10
AD-1290609.2	76.10	7.50	93.90	12.10	79.40	4.90
AD-1290911.2	83.20	10.90	94.10	22.60	85.00	20.70
AD-1290615.2	83.40	11.20	94.90	16.30	87.60	9.90
AD-1684710.1	83.80	5.80	95.20	11.00	89.50	7.60
AD-1684709.1	74.10	5.00	95.40	15.30	91.70	6.20
AD-1290533.2	60.80	2.90	96.00	21.40	98.10	5.80
AD-1684671.1	109.90	24.30	96.10	27.80	114.60	15.80
AD-1684650.1	88.00	6.10	96.50	24.20	100.70	11.50
AD-1684711.1	74.10	6.90	97.00	3.80	91.30	7.20

Duplex ID	10 nM		1 nM		0.1 nM	
	Average % message remaining	STDEV	Average % message remaining	STDEV	Average % message remaining	STDEV
AD-1684670.1	87.20	10.00	97.30	28.90	90.90	5.20
AD-1684692.1	141.10	33.00	97.50	14.20	136.30	32.50
AD-1290939.2	122.30	10.60	98.30	11.70	128.50	6.70
AD-1684662.1	99.20	17.30	98.60	8.40	100.00	20.40
AD-1684700.1	99.30	9.10	98.60	9.60	106.60	10.90
AD-1290742.2	129.20	16.80	98.90	12.20	128.20	17.60
AD-1684715.1	93.70	10.90	98.90	10.10	100.70	9.00
AD-1290894.2	68.90	12.30	99.60	29.10	80.80	16.30
AD-1684718.1	83.00	3.60	99.60	5.80	96.10	14.40
AD-1290702.2	82.00	17.20	100.60	20.70	90.80	15.10
AD-1684688.1	126.60	29.80	100.60	9.30	144.00	31.80
AD-1684690.1	156.10	29.90	101.30	11.40	156.50	25.20
AD-1684672.1	119.50	27.80	101.40	23.10	125.10	34.20
AD-1684684.1	109.90	17.40	102.00	9.20	116.50	8.10
AD-1684723.1	89.40	12.20	102.40	7.90	107.30	6.20
AD-1684651.1	77.60	7.90	102.50	16.10	86.80	14.20
AD-1684683.1	122.10	20.10	102.50	12.50	135.40	19.70
AD-1290973.2	66.80	15.60	103.80	13.80	93.70	11.40
AD-1290857.2	92.30	5.20	103.90	6.10	105.60	6.90
AD-1684649.1	78.90	6.80	103.90	27.90	103.80	11.00
AD-1290516.2	89.30	12.20	105.20	7.00	107.80	12.00
AD-1290554.2	101.40	2.80	105.20	10.30	102.20	6.50
AD-1290509.2	93.00	10.80	105.40	4.20	113.40	8.80
AD-1290660.2	101.60	7.50	105.40	4.70	98.80	6.00
AD-1684698.1	105.40	4.50	105.60	11.70	110.20	7.20
AD-1290670.2	88.70	6.50	106.10	15.30	94.50	10.60
AD-1684673.1	88.30	5.20	106.10	2.50	94.50	11.50
AD-1684646.1	68.80	21.90	106.60	19.00	127.30	25.00
AD-1290597.2	105.80	10.00	107.40	3.40	110.00	12.20
AD-1290573.2	97.40	12.60	107.90	15.20	92.20	10.80
AD-1684707.1	86.40	2.60	108.00	4.80	98.50	11.00
AD-1684722.1	96.60	11.70	108.00	12.10	96.90	8.80
AD-1290639.2	106.10	7.10	108.40	8.50	103.50	6.20
AD-1290551.2	111.70	7.50	109.50	7.80	104.80	7.70
AD-1684655.1	91.50	9.00	109.50	7.40	94.60	5.10
AD-1684678.1	91.10	9.20	109.50	5.60	88.50	3.60
AD-1290800.2	107.10	7.30	109.60	10.90	93.70	8.50
AD-1684726.1	104.90	16.30	109.60	14.60	114.50	8.20
AD-1290764.2	77.50	7.80	110.10	17.00	93.00	12.00
AD-1290672.2	99.10	10.80	110.70	9.90	104.30	13.40
AD-1684685.1	133.70	29.90	110.70	29.30	128.50	32.50

Duplex ID	10 nM		1 nM		0.1 nM	
	Average % message remaining	STDEV	Average % message remaining	STDEV	Average % message remaining	STDEV
AD-1290528.2	45.40	4.40	110.80	15.30	84.60	13.70
AD-1684696.1	114.00	11.70	111.00	5.70	120.50	6.60
AD-1290836.2	118.10	8.10	111.70	12.30	123.80	4.70
AD-1684682.1	111.90	18.40	111.80	9.50	124.20	10.20
AD-1684659.1	97.90	4.90	111.90	8.60	99.50	10.20
AD-1684669.1	64.50	9.70	111.90	15.10	81.40	7.10
AD-1684704.1	108.80	8.60	112.00	6.30	97.30	6.70
AD-1684716.1	102.80	16.80	112.00	22.40	98.40	12.60
AD-1684699.1	103.80	5.50	112.40	6.40	105.30	13.70
AD-1290510.2	99.80	10.70	112.70	7.50	115.90	10.10
AD-1290531.2	113.00	19.70	113.00	27.70	118.50	20.40
AD-1684703.1	85.30	9.20	113.40	14.70	107.50	6.00
AD-1290910.2	109.50	15.50	113.50	20.80	133.70	28.50
AD-1684705.1	94.20	4.80	113.50	8.20	113.00	5.90
AD-1290618.2	113.70	12.60	114.20	7.30	103.40	5.70
AD-1684668.1	74.50	13.50	114.20	6.00	84.80	9.70
AD-1684701.1	92.50	14.90	114.30	10.30	105.10	6.80
AD-1290542.2	104.10	14.20	114.40	10.00	123.10	10.40
AD-1290626.2	119.70	13.70	114.40	15.00	144.90	14.70
AD-1684724.1	107.40	11.70	114.40	19.80	121.90	13.70
AD-1290535.2	90.80	4.90	114.60	14.70	101.60	7.00
AD-1290558.2	109.40	6.40	114.90	15.30	115.40	12.00
AD-1684647.1	99.40	27.50	114.90	19.80	136.90	32.80
AD-1290763.2	75.90	7.30	115.50	16.90	111.20	14.60
AD-1684677.1	91.30	8.80	115.50	15.40	95.80	18.60
AD-1684658.1	92.50	14.90	116.50	15.90	109.20	12.60
AD-1684687.1	114.50	18.10	116.90	13.90	132.30	10.30
AD-1684719.1	102.40	6.30	117.20	11.70	96.70	8.20
AD-1290681.2	107.00	9.00	117.60	11.00	117.40	4.40
AD-1684653.1	80.70	3.20	117.70	17.10	81.80	9.30
AD-1290841.2	75.10	4.00	118.00	11.00	85.70	4.70
AD-1290687.2	107.70	12.90	118.20	6.40	124.20	4.50
AD-1290592.2	119.00	9.20	118.30	4.30	120.60	11.50
AD-1290522.2	118.50	37.70	118.50	20.40	136.80	37.60
AD-1290880.2	96.70	19.90	118.70	21.80	110.10	20.90
AD-1684693.1	114.30	7.70	118.70	10.70	116.50	13.10
AD-1684679.1	117.20	20.30	118.80	6.80	126.50	13.80
AD-1290555.2	125.00	8.30	118.90	4.70	113.50	16.10
AD-1684648.1	81.50	12.40	119.10	21.00	95.30	6.60
AD-1684725.1	114.50	12.10	119.50	17.20	127.60	7.20
AD-1684706.1	89.90	9.20	119.60	27.40	124.10	22.90

Duplex ID	10 nM		1 nM		0.1 nM	
	Average % message remaining	STDEV	Average % message remaining	STDEV	Average % message remaining	STDEV
AD-1684663.1	82.10	7.70	120.20	13.70	84.40	10.90
AD-1684702.1	98.10	2.80	120.40	5.00	107.50	3.20
AD-1291003.2	85.70	8.50	120.50	8.30	95.90	9.20
AD-1684664.1	87.30	9.50	120.70	17.50	98.60	17.10
AD-1684697.1	86.40	5.20	121.00	8.60	109.80	7.60
AD-1290514.2	110.00	18.00	121.20	8.80	125.50	8.40
AD-1290989.2	88.80	3.60	121.60	11.60	110.00	12.50
AD-1684657.1	82.50	2.60	121.60	14.20	104.60	5.40
AD-1684654.1	81.10	4.50	121.80	15.10	101.60	2.30
AD-1684695.1	103.90	12.30	122.10	6.90	105.10	10.90
AD-1290712.2	122.10	28.40	122.40	10.60	114.50	28.30
AD-1290931.2	82.00	3.10	122.40	14.10	89.10	11.20
AD-1684729.1	104.60	9.20	123.10	7.70	123.50	12.60
AD-1290805.2	101.60	3.30	123.20	9.40	100.50	5.90
AD-1290755.2	120.80	13.20	123.60	3.30	110.50	19.00
AD-1290527.2	105.70	3.50	123.80	6.20	116.20	6.30
AD-1684652.1	81.80	9.60	123.80	14.40	91.50	12.50
AD-1290507.2	119.00	5.80	124.40	10.90	119.80	5.30
AD-1290747.2	91.90	6.10	124.50	3.30	102.50	17.60
AD-1290926.2	74.50	8.60	125.30	8.90	92.90	15.90
AD-1290983.2	88.30	10.80	125.70	4.10	96.00	6.30
AD-1684680.1	105.10	11.90	125.90	2.90	126.30	18.10
AD-1290605.2	99.20	7.80	126.50	19.90	107.40	14.50
AD-1290842.2	100.80	20.90	127.20	11.10	105.20	14.70
AD-1290565.2	104.90	15.40	127.30	19.20	120.90	17.40
AD-1290661.2	115.40	2.60	127.70	5.70	116.60	9.50
AD-1684667.1	79.60	10.90	129.10	19.10	93.80	5.00
AD-1290684.2	100.20	19.10	129.20	10.90	111.00	9.40
AD-1290524.2	114.10	8.60	129.40	21.20	134.10	19.90
AD-1290655.2	84.20	4.60	129.90	7.20	91.70	2.40
AD-1684660.1	106.80	17.30	130.10	13.70	119.80	14.80
AD-1684656.1	94.10	9.30	130.40	15.20	90.80	14.70
AD-1684676.1	125.80	31.60	130.70	10.10	141.50	42.50
AD-1684727.1	112.30	11.80	130.80	15.60	134.10	10.20
AD-1684665.1	82.50	19.00	131.30	9.90	103.40	6.40
AD-1290993.2	81.50	10.60	132.90	17.10	96.40	5.80
AD-1684721.1	118.30	29.70	133.40	22.80	129.60	16.70
AD-1290543.2	117.30	33.60	133.80	5.80	134.30	21.30
AD-1290719.2	125.50	4.70	134.50	18.60	135.30	13.50
AD-1290602.2	122.90	13.50	135.30	23.70	117.30	12.20
AD-1290564.2	105.80	15.20	136.20	13.00	109.20	11.40

Duplex ID	10 nM		1 nM		0.1 nM	
	Average % message remaining	STDEV	Average % message remaining	STDEV	Average % message remaining	STDEV
AD-1684737.1	139.10	33.20	136.40	12.50	142.70	28.20
AD-1684694.1	113.60	7.10	136.60	11.80	118.50	7.50
AD-1290875.2	100.10	5.10	138.20	5.60	104.20	4.30
AD-1684732.1	115.40	13.50	139.80	6.40	131.10	6.80
AD-1684717.1	119.30	16.20	140.00	30.80	120.10	24.90
AD-1290908.2	96.80	28.00	140.10	27.80	147.20	37.70
AD-1684720.1	124.30	14.00	140.50	23.90	120.80	14.90
AD-1290552.2	123.10	4.70	142.50	18.90	137.50	12.20
AD-1684728.1	128.40	15.80	143.40	23.80	139.10	18.30
AD-1684731.1	131.10	12.90	147.20	5.60	148.60	29.20
AD-1290722.2	121.90	13.20	147.80	22.40	124.10	19.20
AD-1684730.1	144.30	31.10	150.10	41.90	121.70	5.50
AD-1684736.1	132.70	21.70	151.10	19.90	144.20	15.80
AD-1684733.1	130.50	19.30	151.20	22.00	141.30	22.00
AD-1684661.1	117.60	34.20	151.80	0.00	134.50	29.30
AD-1684734.1	140.80	29.20	153.70	37.90	150.30	28.10
AD-1684735.1	147.10	29.80	154.10	1.60	159.80	22.20
AD-1290600.2	130.70	35.00	160.60	27.90	150.40	19.70
AD-1290624.2	150.80	32.00	161.90	26.00	151.90	33.80
AD-1290643.2	139.30	26.20	163.80	27.20	160.60	26.00
AD-1684675.1	116.00	28.80	NA	0.00	130.20	26.80

Table 16. KHK Single Dose Screen (Dual-Luciferase Assay)

Duplex Name	RLuc/FLuc		RLuc/FLuc		RLuc/FLuc	
	10 nM		1 nM		0.1 nM	
	Avg (%)	SD (%)	Avg (%)	SD (%)	Avg (%)	SD (%)
AD-1290635.2	27.55	4.72	75.07	12.04	82.87	2.65
AD-1684641.1	110.35	9.02	108.94	4.27	110.57	4.47
AD-1684620.1	49.87	8.22	58.56	6.05	70.53	11.50
AD-1684619.1	52.62	8.75	75.71	10.40	80.49	2.91
AD-1684610.1	37.56	5.38	67.47	3.80	80.31	4.72
AD-1684617.1	55.49	13.45	70.80	1.77	75.55	1.72
AD-1613079.2	53.10	14.44	59.41	4.50	81.54	6.24
AD-1684618.1	55.17	9.77	69.69	5.23	72.30	5.02
AD-1684622.1	63.23	13.55	78.66	4.27	89.31	3.28
AD-1684607.1	58.97	7.60	72.73	7.51	76.63	5.82
AD-1684614.1	64.70	10.39	80.88	8.02	79.18	5.68
AD-1613059.2	51.21	4.83	77.16	7.06	74.45	6.20
AD-1613075.2	60.08	8.05	77.04	7.40	83.17	6.93
AD-1613061.1	33.86	3.11	66.45	5.22	75.37	1.85
AD-1684608.1	57.25	9.23	78.62	6.26	78.71	3.21
AD-1684624.1	79.54	24.34	87.68	11.58	90.36	3.70
AD-1423319.3	36.18	4.92	71.09	4.29	81.57	7.77
AD-1684606.1	54.06	6.46	69.09	8.66	81.86	3.98
AD-1684609.1	50.63	11.26	69.42	5.35	75.07	4.46
AD-1684616.1	68.70	8.45	83.79	6.71	90.02	5.65
AD-1613060.2	66.82	13.96	88.93	7.79	85.14	3.13
AD-1613087.1	74.02	4.74	88.43	10.42	86.90	7.15
AD-1290539.5	54.13	8.10	76.99	5.02	77.45	2.84
AD-1290885.5	61.23	8.10	86.40	22.40	86.33	2.17
AD-1613062.2	41.02	9.84	61.06	10.45	78.05	7.96
AD-1684611.1	28.66	7.54	68.17	4.16	73.93	11.62
AD-1684623.1	70.49	21.68	78.20	8.68	93.68	4.29
AD-1612969.2	82.38	14.04	98.61	3.54	88.83	5.84
AD-1613256.2	63.57	23.77	80.73	3.90	85.86	7.48
AD-1423312.3	78.78	18.49	89.56	6.87	93.64	11.24
AD-1548743.7	60.42	7.72	80.40	4.82	87.16	5.21
AD-1684596.1	66.99	3.42	89.91	18.17	93.12	9.16
AD-1423336.7	55.41	10.18	75.06	10.07	81.43	5.09
AD-1612963.2	68.21	8.77	90.00	8.17	89.11	10.05
AD-1290611.3	72.79	17.88	87.65	5.54	89.02	6.88
AD-1613254.2	60.32	9.01	93.11	8.72	91.19	7.21
AD-1684612.1	57.05	5.54	68.77	6.05	77.64	4.46
AD-1684645.1	94.74	17.21	100.78	3.85	97.29	4.48
AD-1684621.1	70.57	13.92	96.48	4.17	102.25	8.16
AD-1290837.5	75.64	11.34	87.27	7.07	89.95	5.79

Duplex Name	RLuc/FLuc		RLuc/FLuc		RLuc/FLuc	
	10 nM		1 nM		0.1 nM	
	Avg (%)	SD (%)	Avg (%)	SD (%)	Avg (%)	SD (%)
AD-1684598.1	82.26	9.02	100.74	8.99	95.70	14.97
AD-1684638.1	90.83	19.35	99.80	1.21	88.22	5.61
AD-1290599.7	81.02	16.64	88.84	3.66	96.80	4.47
AD-1613400.2	78.98	6.10	101.81	4.90	97.90	11.65
AD-1684615.1	67.00	20.89	97.66	10.46	88.82	5.13
AD-1684630.1	92.58	21.02	102.41	5.76	95.70	6.29
AD-1613072.1	74.57	8.15	92.03	6.87	101.02	3.25
AD-1684632.1	123.67	22.63	120.79	8.89	111.58	5.69
AD-1613242.2	78.42	23.84	97.73	5.29	91.80	1.46
AD-1684605.1	100.37	8.25	97.95	10.50	93.62	9.84
AD-1684594.1	72.68	15.57	112.86	9.89	96.08	5.44
AD-1612957.2	84.90	22.12	94.33	10.29	95.29	8.77
AD-1290971.3	90.45	5.32	92.69	5.86	100.99	5.05
AD-1684595.1	67.25	5.15	83.63	8.61	97.72	8.62
AD-1613371.3	84.73	8.63	93.73	5.20	92.88	3.87
AD-1684593.1	95.59	10.06	105.09	8.84	99.26	9.30
AD-1684639.1	111.42	26.90	100.56	13.89	100.10	10.09
AD-1613094.2	109.88	20.02	106.26	7.18	91.52	4.75
AD-1684597.1	87.17	18.25	98.70	10.75	97.29	11.97
AD-1290563.2	57.60	6.91	70.25	6.46	93.86	10.89
AD-1684599.1	95.44	9.63	99.22	5.79	96.16	3.23
AD-1684640.1	68.26	5.61	95.79	2.54	102.60	4.75
AD-1290584.2	61.38	5.41	94.01	8.50	94.05	2.24
AD-1684627.1	90.44	15.14	92.95	9.50	93.69	9.49
AD-1290969.7	81.86	22.36	100.31	15.03	104.51	10.34
AD-1290651.2	97.29	8.97	93.94	5.58	90.64	2.47
AD-1684628.1	99.71	21.99	94.37	8.89	95.59	1.56
AD-1290884.5	89.60	2.17	98.52	11.66	105.58	5.25
AD-1684633.1	124.09	6.72	124.21	8.35	126.12	7.08
AD-1684637.1	87.99	25.10	99.86	3.94	98.08	2.65
AD-1684629.1	96.24	14.82	108.74	6.76	98.94	1.93
AD-1684635.1	115.43	19.21	110.59	14.86	111.51	5.28
AD-1684613.1	77.44	17.90	86.13	7.31	96.31	11.48
AD-1684604.1	126.73	12.80	104.44	9.66	88.10	9.76
AD-1290666.2	77.77	7.66	85.66	5.31	91.09	7.78
AD-1684634.1	101.54	9.42	112.46	7.92	102.84	8.33
AD-1684600.1	92.36	15.27	102.10	14.83	98.62	7.39
AD-1684644.1	94.78	12.14	105.73	11.26	91.40	7.74
AD-1684643.1	134.90	25.23	106.06	3.63	114.45	5.37
AD-1684601.1	109.99	17.91	106.64	6.25	93.03	6.35
AD-1684626.1	105.90	5.90	97.95	4.84	97.84	3.22

Duplex Name	RLuc/FLuc		RLuc/FLuc		RLuc/FLuc	
	10 nM		1 nM		0.1 nM	
	Avg (%)	SD (%)	Avg (%)	SD (%)	Avg (%)	SD (%)
AD-1684642.1	121.11	34.83	118.91	13.95	106.61	2.62
AD-1684592.1	93.35	12.76	103.28	10.86	103.22	9.57
AD-1684636.1	101.15	23.41	102.25	10.70	108.30	10.50
AD-1684603.1	105.78	12.89	103.83	10.25	94.04	10.93
AD-1684631.1	88.92	2.51	98.87	14.74	103.10	3.82
AD-1684625.1	98.13	10.61	116.53	26.66	103.80	4.63
AD-1290523.2	36.07	3.49	83.69	18.88	78.13	21.59
AD-1684602.1	108.47	14.10	109.97	12.29	100.25	5.84
AD-1290570.2	69.96	7.85	86.80	14.21	101.61	7.01
AD-1684666.1	77.63	4.44	85.12	7.88	89.66	10.91
AD-1290865.2	67.01	0.58	88.22	11.34	96.40	4.28
AD-1290589.2	67.56	4.89	85.24	5.97	97.93	8.15
AD-1684681.1	86.44	3.20	88.04	8.65	103.81	12.28
AD-1684689.1	49.57	6.76	86.48	5.18	90.62	11.35
AD-1684708.1	23.03	1.62	33.48	7.99	57.59	11.14
AD-1290557.2	94.58	3.42	98.87	10.22	103.18	8.22
AD-1290515.2	48.39	6.21	70.61	2.16	86.52	1.87
AD-1290741.2	62.89	8.45	108.61	21.31	83.31	16.19
AD-1684713.1	25.62	2.85	56.78	8.85	73.15	15.46
AD-1290650.2	45.96	4.20	75.32	14.73	88.04	15.00
AD-1290897.2	91.50	12.78	99.78	4.12	95.69	6.37
AD-1290556.2	46.60	6.23	72.83	12.88	95.77	2.43
AD-1290750.2	100.69	11.17	112.50	12.75	98.54	9.04
AD-1684714.1	28.09	1.61	63.87	15.58	58.74	14.71
AD-1290654.2	59.38	5.24	82.45	5.68	92.90	11.63
AD-1290909.2	79.81	7.84	85.50	1.84	99.95	6.60
AD-1684674.1	38.19	5.91	68.84	4.29	86.91	7.62
AD-1684712.1	27.74	1.92	51.61	7.17	81.25	10.84
AD-1290796.2	90.91	8.26	93.92	11.82	98.49	8.90
AD-1290612.2	42.68	2.55	66.55	14.42	68.94	7.63
AD-1290633.2	50.34	3.85	73.42	11.49	83.99	10.78
AD-1684691.1	66.75	8.42	91.12	4.34	97.18	11.63
AD-1290659.2	29.24	3.16	58.78	1.46	83.51	13.24
AD-1684686.1	55.60	5.55	81.33	10.32	90.49	12.00
AD-1290604.2	30.50	1.61	58.09	12.94	75.45	12.12
AD-1290574.2	62.06	4.41	79.92	5.27	89.83	8.75
AD-1290609.2	27.15	4.45	50.65	5.55	73.67	12.54
AD-1290911.2	96.37	7.95	93.75	11.00	96.22	5.42
AD-1290615.2	51.72	2.67	70.39	15.92	77.60	16.60
AD-1684710.1	42.53	5.32	73.27	11.74	68.13	11.94
AD-1684709.1	58.70	4.19	79.18	25.68	86.01	19.30

Duplex Name	RLuc/FLuc		RLuc/FLuc		RLuc/FLuc	
	10 nM		1 nM		0.1 nM	
	Avg (%)	SD (%)	Avg (%)	SD (%)	Avg (%)	SD (%)
AD-1290533.2	47.59	4.90	68.99	11.94	77.30	6.48
AD-1684671.1	47.59	1.95	61.26	3.20	82.05	10.96
AD-1684650.1	46.11	8.10	76.50	10.07	82.83	4.08
AD-1684711.1	25.37	2.16	39.63	9.66	66.61	6.31
AD-1684670.1	61.98	4.96	79.82	3.32	86.14	2.50
AD-1684692.1	51.68	5.44	73.68	5.82	94.81	6.71
AD-1290939.2	79.47	12.39	91.84	15.17	102.79	10.83
AD-1684662.1	92.36	5.74	89.87	6.57	98.46	7.31
AD-1684700.1	49.06	2.35	66.17	5.75	80.59	11.96
AD-1290742.2	97.05	12.34	108.91	9.16	98.27	8.80
AD-1684715.1	39.93	3.07	71.43	4.49	66.16	5.22
AD-1290894.2	69.53	5.96	86.15	6.51	89.41	8.71
AD-1684718.1	38.19	2.50	56.43	6.04	89.12	4.16
AD-1290702.2	63.45	4.81	94.75	15.47	93.98	25.50
AD-1684688.1	31.21	4.38	62.76	5.56	71.36	5.67
AD-1684690.1	37.78	7.44	65.65	6.32	81.53	5.19
AD-1684672.1	50.47	5.26	77.82	8.07	89.96	7.10
AD-1684684.1	34.84	3.57	66.09	6.84	81.50	13.30
AD-1684723.1	35.25	2.97	68.48	5.60	65.99	9.83
AD-1684651.1	70.03	6.39	85.13	4.79	94.44	5.75
AD-1684683.1	54.95	5.39	77.78	7.33	95.72	7.28
AD-1290973.2	98.50	6.54	92.81	14.03	98.60	4.58
AD-1290857.2	87.52	2.70	96.73	5.63	99.17	2.18
AD-1684649.1	72.47	0.92	84.56	8.23	89.82	2.21
AD-1290516.2	26.76	0.49	42.76	4.24	59.84	6.99
AD-1290554.2	61.58	4.05	88.87	14.21	74.37	3.21
AD-1290509.2	73.11	5.62	99.31	14.02	101.98	16.69
AD-1290660.2	54.56	9.39	83.38	0.31	86.16	6.94
AD-1684698.1	49.13	6.23	101.74	19.35	58.63	21.67
AD-1290670.2	70.45	5.20	85.30	12.39	83.73	9.68
AD-1684673.1	54.65	6.25	78.09	7.36	92.77	10.76
AD-1684646.1	88.86	5.66	109.84	2.99	100.07	6.89
AD-1290597.2	64.33	3.82	104.86	17.05	78.64	14.59
AD-1290573.2	21.93	2.25	51.90	11.20	61.08	10.20
AD-1684707.1	25.65	1.98	47.58	11.42	58.67	13.41
AD-1684722.1	42.02	2.86	72.20	13.41	91.03	17.74
AD-1290639.2	65.65	8.85	106.60	6.21	80.86	3.84
AD-1290551.2	37.93	4.95	63.38	4.48	69.08	10.49
AD-1684655.1	82.73	4.01	88.85	9.58	98.35	13.91
AD-1684678.1	71.26	6.57	96.82	5.79	98.92	5.96
AD-1290800.2	81.68	8.76	95.82	8.76	99.82	11.38

Duplex Name	RLuc/FLuc		RLuc/FLuc		RLuc/FLuc	
	10 nM		1 nM		0.1 nM	
	Avg (%)	SD (%)	Avg (%)	SD (%)	Avg (%)	SD (%)
AD-1684726.1	28.47	1.78	45.62	14.88	47.10	11.51
AD-1290764.2	67.56	8.24	67.75	7.72	79.61	6.78
AD-1290672.2	42.65	3.57	64.81	14.49	73.51	15.34
AD-1684685.1	52.36	4.45	80.46	8.33	90.09	6.80
AD-1290528.2	40.22	5.18	55.62	6.12	74.10	6.88
AD-1684696.1	36.27	4.80	43.87	3.17	104.26	16.60
AD-1290836.2	78.37	9.59	84.56	11.22	101.22	23.26
AD-1684682.1	80.66	18.04	114.19	18.74	92.36	3.20
AD-1684659.1	80.80	5.53	92.64	9.37	100.32	4.86
AD-1684669.1	61.93	5.52	72.55	4.18	83.30	4.78
AD-1684704.1	73.43	3.74	102.98	4.47	82.11	11.96
AD-1684716.1	49.39	6.90	78.93	10.67	88.70	8.71
AD-1684699.1	32.13	1.49	49.17	12.29	88.94	7.66
AD-1290510.2	29.78	2.09	61.76	7.12	57.41	3.23
AD-1290531.2	30.64	2.31	61.41	11.62	88.80	10.45
AD-1684703.1	29.94	4.56	48.74	5.70	64.27	5.80
AD-1290910.2	78.87	4.68	83.35	7.19	102.58	9.62
AD-1684705.1	84.81	5.73	78.46	14.78	108.49	29.28
AD-1290618.2	38.80	2.21	91.85	24.03	70.60	14.74
AD-1684668.1	82.61	3.09	85.84	5.55	102.22	13.23
AD-1684701.1	33.37	3.20	59.65	10.73	79.48	7.48
AD-1290542.2	25.33	4.70	75.56	5.50	43.19	10.83
AD-1290626.2	42.99	7.92	66.24	9.90	78.99	6.15
AD-1684724.1	25.49	3.64	41.90	10.84	75.17	17.57
AD-1290535.2	39.61	4.59	86.53	3.83	75.49	9.54
AD-1290558.2	52.87	4.30	77.41	14.99	88.24	18.29
AD-1684647.1	63.31	20.44	88.14	11.46	99.17	9.42
AD-1290763.2	76.79	3.45	91.24	4.92	100.24	8.61
AD-1684677.1	49.89	7.84	62.12	3.31	80.47	5.14
AD-1684658.1	61.99	9.91	82.39	6.38	93.13	3.41
AD-1684687.1	56.84	10.02	73.94	6.08	90.30	8.39
AD-1684719.1	21.60	1.78	54.66	6.44	49.60	12.61
AD-1290681.2	70.01	13.50	102.05	13.79	97.11	8.26
AD-1684653.1	77.63	3.92	90.78	7.67	107.04	10.77
AD-1290841.2	102.02	12.88	92.72	10.43	92.89	8.78
AD-1290687.2	24.79	5.58	47.49	9.56	54.96	7.96
AD-1290592.2	42.32	3.00	63.61	7.19	81.99	13.27
AD-1290522.2	63.08	8.25	80.77	2.61	89.07	3.72
AD-1290880.2	86.62	8.68	84.96	10.84	112.23	7.89
AD-1684693.1	33.57	4.76	72.88	8.53	56.56	8.52
AD-1684679.1	63.98	10.81	81.92	8.14	99.47	7.56

Duplex Name	RLuc/FLuc		RLuc/FLuc		RLuc/FLuc	
	10 nM		1 nM		0.1 nM	
	Avg (%)	SD (%)	Avg (%)	SD (%)	Avg (%)	SD (%)
AD-1290555.2	29.21	2.95	57.32	7.73	76.70	14.67
AD-1684648.1	57.07	4.43	72.65	5.51	90.63	6.01
AD-1684725.1	37.50	5.23	60.12	13.34	75.61	7.15
AD-1684706.1	34.25	5.45	66.03	7.18	61.51	7.34
AD-1684663.1	100.81	7.18	100.10	13.78	98.87	4.95
AD-1684702.1	27.84	1.80	55.04	5.17	62.99	6.59
AD-1291003.2	99.82	7.41	90.75	6.78	96.81	11.67
AD-1684664.1	98.11	1.83	95.21	12.95	100.40	8.82
AD-1684697.1	63.74	8.80	90.40	16.93	79.86	15.55
AD-1290514.2	25.53	1.05	39.72	6.89	59.21	5.46
AD-1290989.2	80.25	6.00	95.06	4.87	94.19	9.09
AD-1684657.1	85.45	4.39	92.61	11.75	107.59	8.01
AD-1684654.1	93.92	6.75	95.83	4.68	99.57	13.80
AD-1684695.1	40.77	3.71	87.34	16.28	65.10	12.55
AD-1290712.2	76.80	6.49	89.36	6.93	97.09	5.67
AD-1290931.2	74.20	8.48	91.78	7.74	93.55	7.40
AD-1684729.1	32.72	5.04	71.92	14.70	63.69	5.82
AD-1290805.2	85.12	3.08	83.71	7.55	90.13	4.27
AD-1290755.2	82.43	5.17	101.69	9.25	96.50	4.82
AD-1290527.2	35.84	2.68	72.84	6.30	61.60	13.91
AD-1684652.1	85.57	2.57	95.34	9.86	91.15	4.65
AD-1290507.2	29.99	3.00	86.33	6.23	57.42	9.02
AD-1290747.2	93.73	11.80	93.12	7.86	93.91	7.92
AD-1290926.2	105.81	5.23	93.36	5.15	101.13	11.67
AD-1290983.2	83.97	2.62	84.46	5.64	102.69	8.80
AD-1684680.1	75.84	12.82	88.75	9.33	92.50	2.09
AD-1290605.2	71.92	10.68	111.52	16.71	79.13	8.92
AD-1290842.2	104.49	5.65	91.21	5.53	95.02	7.94
AD-1290565.2	34.69	2.42	75.14	21.84	83.67	22.69
AD-1290661.2	47.11	5.63	82.93	15.48	77.74	26.12
AD-1684667.1	50.51	6.46	74.42	2.87	89.86	7.71
AD-1290684.2	61.88	5.00	86.54	7.60	91.09	8.89
AD-1290524.2	55.34	5.89	100.08	30.59	97.04	35.30
AD-1290655.2	55.60	8.94	79.31	8.29	86.56	4.09
AD-1684660.1	90.30	7.72	90.68	6.87	89.53	4.84
AD-1684656.1	99.30	6.66	87.28	5.54	93.70	10.20
AD-1684676.1	42.60	3.34	64.98	4.82	81.15	8.48
AD-1684727.1	34.77	9.34	62.64	16.13	56.10	7.77
AD-1684665.1	88.07	7.37	85.96	2.62	96.42	4.35
AD-1290993.2	126.19	4.37	103.72	5.04	100.36	8.22
AD-1684721.1	30.93	4.69	73.02	5.08	74.51	8.53

Duplex Name	RLuc/FLuc		RLuc/FLuc		RLuc/FLuc	
	10 nM		1 nM		0.1 nM	
	Avg (%)	SD (%)	Avg (%)	SD (%)	Avg (%)	SD (%)
AD-1290543.2	60.43	2.14	78.76	1.16	86.30	3.38
AD-1290719.2	72.55	5.47	106.96	11.38	89.56	13.94
AD-1290602.2	36.81	5.78	75.60	6.07	63.11	4.79
AD-1290564.2	46.18	1.47	88.84	15.84	89.88	12.30
AD-1684737.1	19.91	2.75	65.84	2.75	50.34	9.86
AD-1684694.1	37.30	6.64	65.54	8.09	68.75	11.54
AD-1290875.2	88.36	6.67	87.65	4.57	95.91	11.39
AD-1684732.1	21.92	1.86	70.21	17.18	48.70	2.36
AD-1684717.1	20.14	3.23	53.41	2.38	49.49	5.05
AD-1290908.2	69.14	8.90	91.09	8.96	105.33	6.07
AD-1684720.1	25.19	1.57	65.20	9.13	55.67	9.89
AD-1290552.2	60.07	5.86	110.60	5.95	68.03	4.85
AD-1684728.1	32.65	4.26	60.26	10.61	81.39	13.63
AD-1684731.1	71.00	4.39	97.76	10.63	103.47	10.13
AD-1290722.2	56.44	2.77	96.22	25.60	84.59	1.63
AD-1684730.1	55.45	5.72	103.19	33.31	94.48	30.63
AD-1684736.1	22.63	1.19	55.13	6.21	63.03	19.64
AD-1684733.1	31.22	2.64	74.74	15.23	80.11	13.22
AD-1684661.1	88.94	5.85	86.32	8.94	96.70	2.89
AD-1684734.1	24.44	1.34	55.52	4.03	41.46	7.30
AD-1684735.1	27.36	1.31	62.50	9.06	50.38	6.57
AD-1290600.2	63.33	8.27	96.26	30.33	114.38	17.93
AD-1290624.2	34.72	1.33	92.38	34.13	71.36	13.25
AD-1290643.2	31.00	3.54	63.18	15.27	67.58	13.33
AD-1684675.1	43.08	8.00	63.69	6.05	73.37	3.64

Example 6: Effects of siRNA –GalNAC Conjugates in Non-Human Primates

The effect of candidates identified from the *in vitro* studies described above, duplexes AD-1613062, AD-1613073, AD-1613242, AD-1613243, AD-1613246, AD-1613247, AD-1613400, AD-1634397, AD-1634424, and AD-1634425, were further investigated for their effectiveness in non-human primates. Specifically, a single dose of 3 mg/kg of AD-1613062, AD-1613073, AD-1613242, AD-1613243, AD-1613246, AD-1613247, AD-1613400, AD-1634397, AD-1634424, or AD-1634425 was subcutaneously administered to cynomolgous monkeys. Sera and tissue samples were collected at Days 29, 50, and 78 post-dose.

mRNA was extracted from liver tissue by a magnetic bead-based extraction method using the NucleoMag RNA kit by Macherey-Nagel. cDNA was generated using Applied Biosystems SuperScript IV VILO master mix. Taqman probe-based qPCR was used to quantify KHK mRNA which was normalized to the geometric mean of two housekeeping genes, ARL6IP4 and PPIB.

Targeted quantitation of KHK protein in cynomolgus monkey liver was performed via liquid chromatography coupled to mass spectrometer (LC-MS) using parallel reaction monitoring (PRM) in positive ion mode. The signature peptide sequence selected for quantitation was HLGFSAGEALR (UniProtKB - A0A2K5V1R8-1, amino acid positions 198-209).

Figure 2 shows the effect of administration of a single 3 mg/kg dose of the selected duplexes on the level of KHK mRNA and protein at Day 29 post-dose.

Figure 3 shows the effect of administration of a single 3 mg/kg dose of the selected duplexes on the level of KHK mRNA at Day 50 post-dose.

Figure 4 shows the effect of administration of a single 3 mg/kg dose of the selected duplexes on the level of KHK mRNA at Day 78 post-dose.

The data demonstrate that the indicated agents, *e.g.*, AD-1613400 and AD-1613243, are effective in durably and potently inhibiting KHK mRNA and protein expression.

EQUIVALENTS

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

We claim:

1. A double stranded ribonucleic acid (dsRNA) agent for inhibiting expression of ketohexokinase (KHK) in a cell, wherein said dsRNA comprises a sense strand and an antisense strand forming a double stranded region, wherein the antisense strand comprises a region of complementarity to an mRNA encoding KHK, and wherein the region of complementarity comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from any one of the antisense nucleotide sequences in any one of Tables 2, 3, 5, 6, and 8-13.
2. The dsRNA agent of claim 1, wherein the dsRNA agent comprises a sense strand comprising at least 15 contiguous nucleotides differing by no more than three nucleotides from any one of the nucleotide sequences of the sense strands in any one of Tables 2, 3, 5, 6, and 8-13 and an antisense strand comprising at least 15 contiguous nucleotides differing by no more than three nucleotides from any one of the nucleotide sequences of the antisense strands in any one of Tables 2, 3, 5, 6, and 8-13.
3. The dsRNA agent of claim 1, wherein the dsRNA agent comprises a sense strand comprising at least 15 contiguous nucleotides differing by no more than two nucleotides from any one of the nucleotide sequences of the sense strands in any one of Tables 2, 3, 5, 6, and 8-13 and an antisense strand comprising at least 15 contiguous nucleotides differing by no more than two nucleotides from any one of the nucleotide sequences of the antisense strands in any one of Tables 2, 3, 5, 6, and 8-13.
4. The dsRNA agent of claim 1, wherein the dsRNA agent comprises a sense strand comprising at least 15 contiguous nucleotides differing by no more than one nucleotide from any one of the nucleotide sequences of the sense strands in any one of Tables 2, 3, 5, 6, and 8-13 and an antisense strand comprising at least 15 contiguous nucleotides differing by no more than one nucleotide from any one of the nucleotide sequences of the antisense strands in any one of Tables 2, 3, 5, 6, and 8-13.
5. The dsRNA agent of claim 1, wherein the dsRNA agent comprises a sense strand comprising a nucleotide sequence selected from the group consisting of any one of the nucleotide sequences of the sense strands in any one of Tables 2, 3, 5, 6, and 8-13 and an antisense strand comprising a nucleotide sequence selected from the group consisting of any one of the nucleotide sequences of the antisense strands in any one of Tables 2, 3, 5, 6, and 8-13.
6. A double stranded ribonucleic acid (dsRNA) agent for inhibiting expression of ketohexokinase (KHK) in a cell, wherein said dsRNA comprises a sense strand and an antisense strand forming a double stranded region, wherein the sense strand comprises at least 15 contiguous nucleotides differing by no more than three nucleotides from any one of the nucleotide sequence of nucleotides 120-162; 164-188; 181-207; 193-217; 209-231; 283-306; 508-546; 568-603; 596-632;

640-674; 746-806; 806-835; 917-942; 936-084; 1016-1041; 1100-1123; 1149-1175; 1160-1193; 1205-1229; 1252-1283; 1334-1356; 1407-1429; 1472-1497; 1506-1533; 1539-1561; 1704-1727; 1747-1787; 1850-1873; 1936-1964; 1960-1990; 2015-2048; 2060-2095; 2090-2118; 2124-2160; 2181-2200; 2221-2262 of SEQ ID NO: 1, and the antisense strand comprises at least 15 contiguous nucleotides differing by no more than three nucleotides from the corresponding nucleotide sequence of SEQ ID NO:2.

7. A double stranded ribonucleic acid (dsRNA) agent for inhibiting expression of ketohexokinase (KHK) in a cell, wherein said dsRNA comprises a sense strand and an antisense strand forming a double stranded region, wherein the sense strand comprises at least 15 contiguous nucleotides differing by no more than three nucleotides from any one of the nucleotide sequence of nucleotides 517-539; 521-543; 524-546; 517-546; 581-603; 610-632; 747-769; 749-771; 752-774; 755-777; 757-779; 758-780; 764-786; 776-798; 781-803; 747-803; 920-942; 941-963; 944-966; 950-972; 962-984; 920-984; 1149-1171; 1161-1183; 1165-1187; 1171-1193; 1149-1193; 1205-1227; 1206-1228; 1205-1228; 1334-1356; 1472-1494; 1475-1497; 1472-1497 of SEQ ID NO: 1, and the antisense strand comprises at least 15 contiguous nucleotides differing by no more than three nucleotides from the corresponding nucleotide sequence of SEQ ID NO:2.

8. A double stranded ribonucleic acid (dsRNA) agent for inhibiting expression of ketohexokinase (KHK) in a cell, wherein said dsRNA comprises a sense strand and an antisense strand forming a double stranded region, wherein the sense strand comprises at least 15 contiguous nucleotides differing by no more than three nucleotides from any one of the nucleotide sequence of nucleotides 517-539; 524-546; 517-546; 753-775; 757-779; 753-779; 764-786; 767-789; 768-790; 769-791; 764-791; 773-795; 781-803; 773-803; 753-803; 808-830; 937-959; 941-963; 944-966; 941-966; 948-970; 950-972; 948-972; 1160-1182; 1161-1183; 1160-1183; and 1207-1229 of SEQ ID NO: 1, and the antisense strand comprises at least 15 contiguous nucleotides differing by no more than three nucleotides from the corresponding nucleotide sequence of SEQ ID NO:2.

9. The dsRNA agent of any one of claims 1-8, wherein the antisense strand comprises at least 15 contiguous nucleotides differing by no more than three nucleotides from any one of the antisense strand nucleotide sequences of a duplex selected from the group consisting of AD-1613400; AD-1613243; AD-1290757.3; AD-1290878.3; AD-1290969.3; AD-1423317.2; AD-1423327.2; AD-1423336.2; AD-1290599.3; AD-1523172.1; AD-1290837.3; AD-1523173.1; AD-1290884.3; AD-1523174.1; AD-1290959.3; AD-1523175.1; AD-1423311.2; AD-1423324.2; AD-1523176.1; AD-1423329.2; AD-1423333.2; AD-1423330.2; AD-1523177.1; AD-1290885.3; AD-1523178.1; AD-1423334.2; AD-1523179.1; AD-1523180.1; AD-1290539.3; and AD-1523181.1.

10. A double stranded ribonucleic acid (dsRNA) agent for inhibiting expression of ketohexokinase (KHK) in a cell, wherein said dsRNA comprises a sense strand and an antisense

strand forming a double stranded region, wherein the sense strand comprises at least 15 contiguous nucleotides differing by no more than three nucleotides from any one of the nucleotide sequence of nucleotides 495-517, 492-517, 500-529, 514-551, 517-539, 524-546, 517-548, 614-643, 625-647, 625-660, 642-664, 642-672, 753-811, 754-780, 762-791, 764-786, 772-800, 781-803, 805-827, 808-830, 809-831, 792-838, 931-982, 944-966, 947-969, 948-970, 948-982, 1011-1035, 1021-1043, 1019-1050, 1063-1091, 1150-1192, 1152-1176, 1160-1192, 1160-1182, 1162-1184, 1198-1230, 1198-1221, and 1202-1230 of SEQ ID NO: 1, and the antisense strand comprises at least 15 contiguous nucleotides differing by no more than three nucleotides from the corresponding nucleotide sequence of SEQ ID NO:2.

11. A double stranded ribonucleic acid (dsRNA) agent for inhibiting expression of ketohexokinase (KHK) in a cell, wherein said dsRNA comprises a sense strand and an antisense strand forming a double stranded region, wherein the sense strand comprises at least 15 contiguous nucleotides differing by no more than three nucleotides from any one of the nucleotide sequence of nucleotides 513-556, 753-813, 936-981, 1155-1193, 1200-1229, 1704-1727, 1747-1787, 1850-1873, 1936-1964, 1960-1990, 1936-1990, 2015-2048, 2060-2095, 2090-2118, 2060-2118, 2124-2160, 2181-2220, 2221-2249, 2181-2249, 2240-2262, 2221-2262, and 2181-2262 of SEQ ID NO: 1, and the antisense strand comprises at least 15 contiguous nucleotides differing by no more than three nucleotides from the corresponding nucleotide sequence of SEQ ID NO:2.

12. A double stranded ribonucleic acid (dsRNA) agent for inhibiting expression of ketohexokinase (KHK) in a cell, wherein said dsRNA comprises a sense strand and an antisense strand forming a double stranded region, wherein the sense strand comprises at least 15 contiguous nucleotides differing by no more than three nucleotides from the nucleotide sequence of nucleotides 1207-1229 or 937-959 of SEQ ID NO: 1, and the antisense strand comprises at least 15 contiguous nucleotides differing by no more than three nucleotides from the corresponding nucleotide sequence of SEQ ID NO:2.

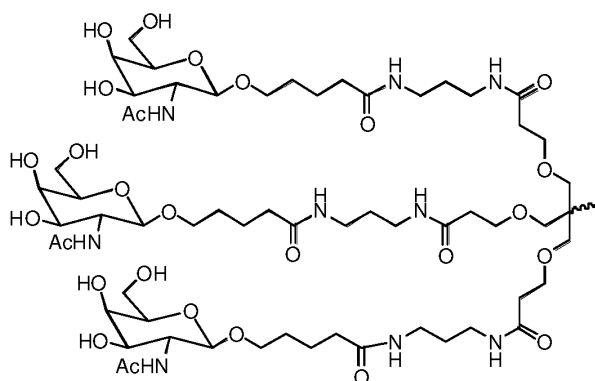
13. The dsRNA agent of claim 12, wherein the sense strand comprises at least 15 contiguous nucleotides differing by no more than three nucleotides from the nucleotide sequence of nucleotides 1207-1229 of SEQ ID NO: 1, and the antisense strand comprises at least 15 contiguous nucleotides differing by no more than three nucleotides from the corresponding nucleotide sequence of SEQ ID NO:2.

14. The dsRNA agent of any one of claims 1-13, wherein the dsRNA agent comprises at least one modified nucleotide.

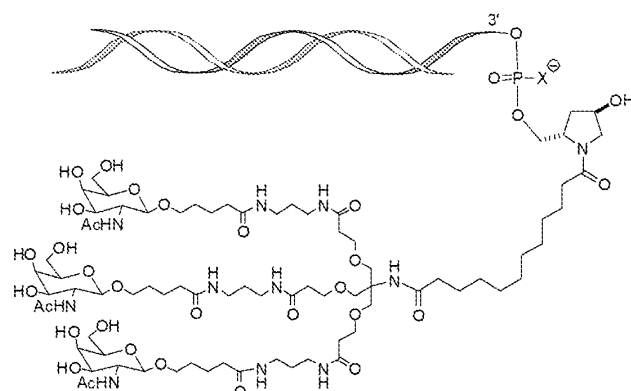
15. The dsRNA agent of any one of claims 1-14, wherein substantially all of the nucleotides of the sense strand; substantially all of the nucleotides of the antisense strand comprise a modification; or substantially all of the nucleotides of the sense strand and substantially all of the nucleotides of the antisense strand comprise a modification.
16. The dsRNA agent of any one of claims 1-15, wherein all of the nucleotides of the sense strand comprise a modification; all of the nucleotides of the antisense strand comprise a modification; or all of the nucleotides of the sense strand and all of the nucleotides of the antisense strand comprise a modification.
17. The dsRNA agent of any one of claims 14-16, wherein at least one of the modified nucleotides is selected from the group consisting of a deoxy-nucleotide, a 3'-terminal deoxythymidine (dT) nucleotide, a 2'-O-methyl modified nucleotide, a 2'-fluoro modified nucleotide, a 2'-deoxy-modified nucleotide, a locked nucleotide, an unlocked nucleotide, a conformationally restricted nucleotide, a constrained ethyl nucleotide, an abasic nucleotide, a 2'-amino-modified nucleotide, a 2'-O-allyl-modified nucleotide, 2'-C-alkyl-modified nucleotide, 2'-hydroxly-modified nucleotide, a 2'-methoxyethyl modified nucleotide, a 2'-O-alkyl-modified nucleotide, a morpholino nucleotide, a phosphoramidate, a non-natural base comprising nucleotide, a tetrahydropyran modified nucleotide, a 1,5-anhydrohexitol modified nucleotide, a cyclohexenyl modified nucleotide, a nucleotide comprising a phosphorothioate group, a nucleotide comprising a methylphosphonate group, a nucleotide comprising a 5'-phosphate, a nucleotide comprising a 5'-phosphate mimic, a nucleotide comprising a 2' phosphate, a thermally destabilizing nucleotide, a glycol modified nucleotide (GNA), a nucleotide comprising a 2' phosphate, and a 2-O-(N-methylacetamide) modified nucleotide; and combinations thereof.
18. The dsRNA agent of any one of claims 14-16, wherein the modifications on the nucleotides are selected from the group consisting of LNA, HNA, CeNA, 2'-methoxyethyl, 2'-O-alkyl, 2'-O-allyl, 2'-C-allyl, 2'-fluoro, 2'-deoxy, 2'-hydroxyl, and glycol; and combinations thereof.
19. The dsRNA agent of any one of claims 14-16, wherein at least one of the modified nucleotides is selected from the group consisting of a deoxy-nucleotide, a 2'-O-methyl modified nucleotide, a 2'-fluoro modified nucleotide, a 2'-deoxy-modified nucleotide, a glycol modified nucleotide (GNA), a nucleotide comprising a 2' phosphate, a vinyl-phosphonate nucleotide; and combinations thereof.

20. The dsRNA agent of any one of claims 14-16, wherein at least one of the modifications on the nucleotides is a thermally destabilizing nucleotide modification.
21. The dsRNA agent of claim 20, wherein the thermally destabilizing nucleotide modification is selected from the group consisting of an abasic modification; a mismatch with the opposing nucleotide in the duplex; and destabilizing sugar modification, a 2'-deoxy modification, an acyclic nucleotide, an unlocked nucleic acids (UNA), and a glycerol nucleic acid (GNA).
22. The dsRNA agent of any one of claims 1-21, wherein the double stranded region is 19-30 nucleotide pairs in length.
23. The dsRNA agent of claim 22, wherein the double stranded region is 19-25 nucleotide pairs in length.
24. The dsRNA agent of claim 22, wherein the double stranded region is 19-23 nucleotide pairs in length.
25. The dsRNA agent of claim 22, wherein the double stranded region is 23-27 nucleotide pairs in length.
26. The dsRNA agent of claim 22, wherein the double stranded region is 21-23 nucleotide pairs in length.
27. The dsRNA agent of any one of claims 1-26, wherein each strand is independently no more than 30 nucleotides in length.
28. The dsRNA agent of any one of claims 1-27, wherein the sense strand is 21 nucleotides in length and the antisense strand is 23 nucleotides in length.
29. The dsRNA agent of any one of claims 1-28, wherein the region of complementarity is at least 17 nucleotides in length.
30. The dsRNA agent of any one of claims 1-29, wherein the region of complementarity is between 19 and 23 nucleotides in length.
31. The dsRNA agent of any one of claims 1-30, wherein the region of complementarity is 19 nucleotides in length.

32. The dsRNA agent of any one of claims 1-31, wherein at least one strand comprises a 3' overhang of at least 1 nucleotide.
33. The dsRNA agent of any one of claims 1-31, wherein at least one strand comprises a 3' overhang of at least 2 nucleotides.
34. The dsRNA agent of any one of claims 1-33, further comprising a ligand.
35. The dsRNA agent of claim 34, wherein the ligand is conjugated to the 3' end of the sense strand of the dsRNA agent.
36. The dsRNA agent of claim 34 or 35, wherein the ligand is an N-acetylgalactosamine (GalNAc) derivative.
37. The dsRNA agent of any one of claims 34-36, wherein the ligand is one or more GalNAc derivatives attached through a monovalent, bivalent, or trivalent branched linker.
38. The dsRNA agent of claim 36 or 37, wherein the ligand is



39. The dsRNA agent of claim 38, wherein the dsRNA agent is conjugated to the ligand as shown in the following schematic



and, wherein X is O or S.

40. The dsRNA agent of claim 39, wherein the X is O.

41. The dsRNA agent of any one of claims 1-40, wherein the dsRNA agent further comprises at least one phosphorothioate or methylphosphonate internucleotide linkage.

42. The dsRNA agent of claim 41, wherein the phosphorothioate or methylphosphonate internucleotide linkage is at the 3'-terminus of one strand.

43. The dsRNA agent of claim 42, wherein the strand is the antisense strand.

44. The dsRNA agent of claim 42, wherein the strand is the sense strand.

45. The dsRNA agent of claim 41, wherein the phosphorothioate or methylphosphonate internucleotide linkage is at the 5'-terminus of one strand.

46. The dsRNA agent of claim 45, wherein the strand is the antisense strand.

47. The dsRNA agent of claim 45, wherein the strand is the sense strand.

48. The dsRNA agent of claim 41, wherein the phosphorothioate or methylphosphonate internucleotide linkage is at the both the 5'- and 3'-terminus of one strand.

49. The dsRNA agent of claim 48, wherein the strand is the antisense strand.

50. The dsRNA agent of any one of claims 1-49, wherein the base pair at the 1 position of the 5'-end of the antisense strand of the duplex is an AU base pair.

51. A double stranded ribonucleic acid (dsRNA) agent for inhibiting expression of ketohexokinase (KHK) in a cell, or a pharmaceutically acceptable salt thereof, comprising a sense strand and an antisense strand forming a double stranded region, wherein

a) the nucleotide sequence of the sense strand differs by no more than 4 bases from the nucleotide sequence 5'-gscsaggaagCfAfCfugagauucgu-3' and the nucleotide sequence of the antisense strand differs by no more than 4 bases from the nucleotide sequence 5'-asdCsgadAudCucagdTgCfuuccugcsasc-3',

wherein a, g, c and u are 2'-O-methyl (2'-OMe) A, G, C, and U; Cf and Uf are 2'-deoxy-2'-fluoro (2'-F) C and U; dC, dA, and dT are 2'-deoxy C, A, and T; and s is a phosphorothioate linkage; or

b) the nucleotide sequence of the sense strand differs by no more than 4 bases from the nucleotide sequence 5'-csusacggagAfCfGfugguguuugu-3' and the nucleotide sequence of the antisense strand differs by no more than 4 bases from the nucleotide sequence 5'-asdCsaadAcdAccacdGuCfuccguagscsc-3',

wherein a, g, c and u are 2'-O-methyl (2'-OMe) A, G, C, and U; Cf and Uf are 2'-deoxy-2'-fluoro (2'-F) C and U; dC, dA, and dG are 2'-deoxy C, A, and G; and s is a phosphorothioate linkage.

52. The dsRNA agent of claim 51, wherein

a) the nucleotide sequence of the sense strand differs by no more than 3 bases from the nucleotide sequence 5'-gscsaggaagCfAfCfugagauucgu-3' and the nucleotide sequence of the antisense strand differs by no more than 3 bases from the nucleotide sequence 5'-asdCsgadAudCucagdTgCfuuccugcsasc-3',

wherein a, g, c and u are 2'-O-methyl (2'-OMe) A, G, C, and U; Cf and Uf are 2'-deoxy-2'-fluoro (2'-F) C and U; dC, dA, and dT are 2'-deoxy C, A, and T; and s is a phosphorothioate linkage; or

b) the nucleotide sequence of the sense strand differs by no more than 3 bases from the nucleotide sequence 5'-csusacggagAfCfGfugguguuugu-3' and the nucleotide sequence of the antisense strand differs by no more than 3 bases from the nucleotide sequence 5'-asdCsaadAcdAccacdGuCfuccguagscsc-3',

wherein a, g, c and u are 2'-O-methyl (2'-OMe) A, G, C, and U; Cf and Uf are 2'-deoxy-2'-fluoro (2'-F) C and U; dC, dA, and dG are 2'-deoxy C, A, and G; and s is a phosphorothioate linkage.

53. The dsRNA agent of claim 51, wherein

a) the nucleotide sequence of the sense strand differs by no more than 2 bases from the nucleotide sequence 5'-gscsaggaagCfAfCfugagauucgu-3' and the nucleotide sequence of the antisense strand differs by no more than 2 bases from the nucleotide sequence 5'-asdCsgadAudCucagdTgCfuuccugcsasc-3',

wherein a, g, c and u are 2'-O-methyl (2'-OMe) A, G, C, and U; Cf and Uf are 2'-deoxy-2'-fluoro (2'-F) C and U; dC, dA, and dT are 2'-deoxy C, A, and T; and s is a phosphorothioate linkage; or

b) the nucleotide sequence of the sense strand differs by no more than 2 bases from the nucleotide sequence 5'-csusacggagAfCfGfugguguuugu-3' and the nucleotide sequence of the antisense strand differs by no more than 2 bases from the nucleotide sequence 5'-asdCsaadAcdAccacdGuCfuccguagscsc-3',

wherein a, g, c and u are 2'-O-methyl (2'-OMe) A, G, C, and U; Cf and Uf are 2'-deoxy-2'-fluoro (2'-F) C and U; dC, dA, and dG are 2'-deoxy C, A, and G; and s is a phosphorothioate linkage.

54. The dsRNA agent of claim 51, wherein

a) the nucleotide sequence of the sense strand differs by no more than 1 base from the nucleotide sequence 5'-gscsaggaagCfAfCfugagauucgu-3' and the nucleotide sequence of the antisense strand differs by no more than 1 base from the nucleotide sequence 5'-asdCsgadAudCucagdTgCfuuccugcsasc-3',

wherein a, g, c and u are 2'-O-methyl (2'-OMe) A, G, C, and U; Cf and Uf are 2'-deoxy-2'-fluoro (2'-F) C and U; dC, dA, and dT are 2'-deoxy C, A, and T; and s is a phosphorothioate linkage; or

b) the nucleotide sequence of the sense strand differs by no more than 1 base from the nucleotide sequence 5'-csusacggagAfCfGfugguguuugu-3' and the nucleotide sequence of the antisense strand differs by no more than 1 base from the nucleotide sequence 5'-asdCsaadAcdAccacdGuCfuccguagscsc-3',

wherein a, g, c and u are 2'-O-methyl (2'-OMe) A, G, C, and U; Cf and Uf are 2'-deoxy-2'-fluoro (2'-F) C and U; dC, dA, and dG are 2'-deoxy C, A, and G; and s is a phosphorothioate linkage.

55. The dsRNA agent of claim 51, wherein

a) the nucleotide sequence of the sense strand comprises the nucleotide sequence 5'-gscsaggaagCfAfCfugagauucgu-3' and the nucleotide sequence of the antisense strand comprises the nucleotide sequence 5'-asdCsgadAudCucagdTgCfuuccugcsasc-3',

wherein a, g, c and u are 2'-O-methyl (2'-OMe) A, G, C, and U; Cf and Uf are 2'-deoxy-2'-fluoro (2'-F) C and U; dC, dA, and dT are 2'-deoxy C, A, and T; and s is a phosphorothioate linkage; or

b) the nucleotide sequence of the sense strand comprises the nucleotide sequence 5'-csusacggagAfCfGfugguguugu-3' and the nucleotide sequence of the antisense strand comprises the nucleotide sequence 5'-asdCsaadAcdAccacdGuCfuccguagscsc-3',

wherein a, g, c and u are 2'-O-methyl (2'-OMe) A, G, C, and U; Cf and Uf are 2'-deoxy-2'-fluoro (2'-F) C and U; dC, dA, and dG are 2'-deoxy C, A, and G; and s is a phosphorothioate linkage.

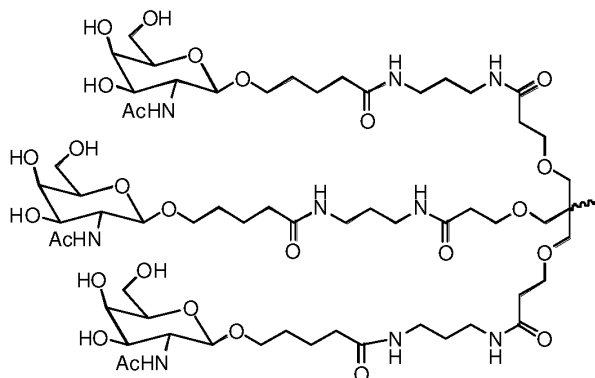
56. The dsRNA agent of any one of claims 50-55, further comprising a ligand.

57. The dsRNA agent of claim 56, wherein the ligand is conjugated to the 3' end of the sense strand of the dsRNA agent.

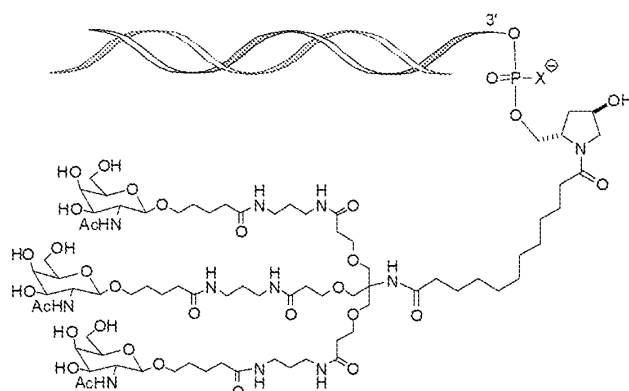
58. The dsRNA agent of claim 56 or 57, wherein the ligand is an N-acetylgalactosamine (GalNAc) derivative.

59. The dsRNA agent of any one of claims 56-58, wherein the ligand is one or more GalNAc derivatives attached through a monovalent, bivalent, or trivalent branched linker.

60. The dsRNA agent of claim 58 or 59, wherein the ligand is



61. The dsRNA agent of claim 60, wherein the dsRNA agent is conjugated to the ligand as shown in the following schematic



and, wherein X is O or S.

62. The dsRNA agent of claim 61, wherein the X is O.

63. A cell containing the dsRNA agent of any one of claims 1-62.

64. A pharmaceutical composition for inhibiting expression of a gene encoding ketohexokinase (KHK) comprising the dsRNA agent of any one of claims 1-62.

65. The pharmaceutical composition of claim 64, wherein dsRNA agent is in an unbuffered solution.

66. The pharmaceutical composition of claim 65, wherein the unbuffered solution is saline or water.

67. The pharmaceutical composition of claim 64, wherein said dsRNA agent is in a buffer solution.

68. The pharmaceutical composition of claim 67, wherein the buffer solution comprises acetate, citrate, prolamine, carbonate, or phosphate or any combination thereof.

69. The pharmaceutical composition of claim 68, wherein the buffer solution is phosphate buffered saline (PBS).

70. A method of inhibiting expression of a ketohexokinase (KHK) gene in a cell, the method comprising contacting the cell with the dsRNA agent of any one of claims 1-62, or the pharmaceutical composition of any one of claims 64-69, thereby inhibiting expression of the KHK gene in the cell.
71. The method of claim 70, wherein the cell is within a subject.
72. The method of claim 71, wherein the subject is a human.
73. The method of claim 71 or 72, wherein the subject has a KHK-associated disorder.
74. The method of claim 73, wherein the KHK-associated disorder is a liver disease selected from the group consisting of non-alcoholic fatty liver disease (NAFLD) and non-alcoholic steatohepatitis (NASH).
75. The method of claim 73, wherein the KHK-associated disorder is dyslipidemia selected from the group consisting of hyperlipidemia, high LDL cholesterol, low HDL cholesterol, hypertriglyceridemia, postprandial hypertriglyceridemia, adipocyte dysfunction, visceral adipose deposition, obesity, and metabolic syndrome.
76. The method of claim 73, wherein the KHK-associated disorder is a disorder of glycemic control selected from the group consisting of insulin resistance, type 2 diabetes, and glucose intolerance.
77. The method of claim 73, wherein the KHK-associated disorder is a cardiovascular disease selected from the group consisting of hypertension and endothelial cell dysfunction.
78. The method of claim 73, wherein the KHK-associated disorder is a kidney disease selected from the group consisting of acute kidney disorder, tubular dysfunction, proinflammatory changes to the proximal tubules, and chronic kidney disease.
79. The method of claim 73, wherein the KHK-associated disorder is hyperuricemia.
80. The method of claim 73, wherein the KHK-associated disorder is gout.
81. The method of any one of claims 56-66, wherein contacting the cell with the dsRNA agent inhibits the expression of KHK by at least 50%, 60%, 70%, 80%, 90%, or 95%.

82. The method of any one of claims 70-81, wherein inhibiting expression of KHK decreases KHK protein level in serum of the subject by at least 50%, 60%, 70%, 80%, 90%, or 95%.
83. A method of treating a subject having a disease or disorder that would benefit from reduction in ketohexokinase (KHK) expression, comprising administering to the subject a therapeutically effective amount of the dsRNA agent of any one of claims 1-62 or the pharmaceutical composition of any one of claims 64-69, thereby treating the subject having the disorder that would benefit from reduction in KHK expression.
84. A method of preventing at least one symptom in a subject having a disorder that would benefit from reduction in ketohexokinase (KHK) expression, comprising administering to the subject a prophylactically effective amount of the dsRNA agent of any one of claims 1-62 or the pharmaceutical composition of any one of claims 64-69, thereby preventing at least one symptom in the subject having the disorder that would benefit from reduction in KHK expression.
85. The method of claim 83 or 84, wherein the disorder is a KHK-associated disorder.
86. The method of claim 85, wherein the KHK-associated disorder is a liver disease selected from the group consisting of non-alcoholic fatty liver disease (NAFLD) and non-alcoholic steatohepatitis (NASH).
87. The method of claim 85, wherein the KHK-associated disorder is dyslipidemia selected from the group consisting of hyperlipidemia, high LDL cholesterol, low HDL cholesterol, hypertriglyceridemia, postprandial hypertriglyceridemia, adipocyte dysfunction, visceral adipose deposition, obesity, and metabolic syndrome.
88. The method of claim 85, wherein the KHK-associated disorder is a disorder of glycemic control selected from the group consisting of insulin resistance, type 2 diabetes, and glucose intolerance.
89. The method of claim 85, wherein the KHK-associated disorder is a cardiovascular disease selected from the group consisting of hypertension and endothelial cell dysfunction.
90. The method of claim 85, wherein the KHK-associated disorder is a kidney disease selected from the group consisting of acute kidney disorder, tubular dysfunction, proinflammatory changes to the proximal tubules, and chronic kidney disease.

91. The method of claim 85, wherein the KHK-associated disorder is hyperuricemia.
92. The method of claim 85, wherein the KHK-associated disorder is gout.
93. The method of any one of claims 83-92, wherein the subject is human.
94. The method of claim 93, wherein the subject has or is prone to compromised renal function.
95. The method of any one of claims 83-94, wherein the administration of the dsRNA agent to the subject causes a decrease in one or more serum lipid and/or a decrease in KHK protein accumulation.
96. The method of any one of claims 83-95, wherein the administration of the dsRNA agent to the subject causes a decrease in fructose metabolism.
97. The method of any one of claims 83-96, wherein the dsRNA agent is administered to the subject at a dose of about 0.01 mg/kg to about 50 mg/kg.
98. The method of any one of claims 83-97, wherein the dsRNA agent is administered to the subject subcutaneously.
99. The method of any one of claims 83-98, further comprising determining the level of KHK in a sample(s) from the subject.
100. The method of claim 99, wherein the level of KHK in the subject sample(s) is a KHK protein level in a blood or serum sample(s).
101. The method of claim 83-100, further comprising determining a level of fructose metabolism in a sample(s) from the subject.
102. The method of claim 83-101, further comprising determining a level of uric acid in a sample(s) from the subject.
103. The method of claim 83-102, further comprising determining a level of serum lipid in a sample(s) from the subject.
104. The method of any one of claims 83-103, further comprising administering to the subject an additional therapeutic agent for treatment of a KHK-associated disorder.

105. A kit comprising the dsRNA agent of any one of claims 1-62 or the pharmaceutical composition of any one of claims 64-69.
106. A vial comprising the dsRNA agent of any one of claims 1-62 or the pharmaceutical composition of any one of claims 64-69.
107. A syringe comprising the dsRNA agent of any one of claims 1-62 or the pharmaceutical composition of any one of claims 64-69.
108. An RNA-induced silencing complex (RISC) comprising an antisense strand of any of the dsRNA agents of claims 1-62.