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(54) Title: METHODS AND COMPOSITIONS FOR THE SPECIFIC INHIBITION OF ANDROGEN RECEPTOR BY DOUBLE-STRANDED RNA

Figure 1

(57) Abrégé/Abstract:
This invention relates to compounds, compositions, and methods useful for reducing AR target RNA and protein levels via use of dsRNAs, e.g., Dicer substrate siRNA (DsiRNA) agents.

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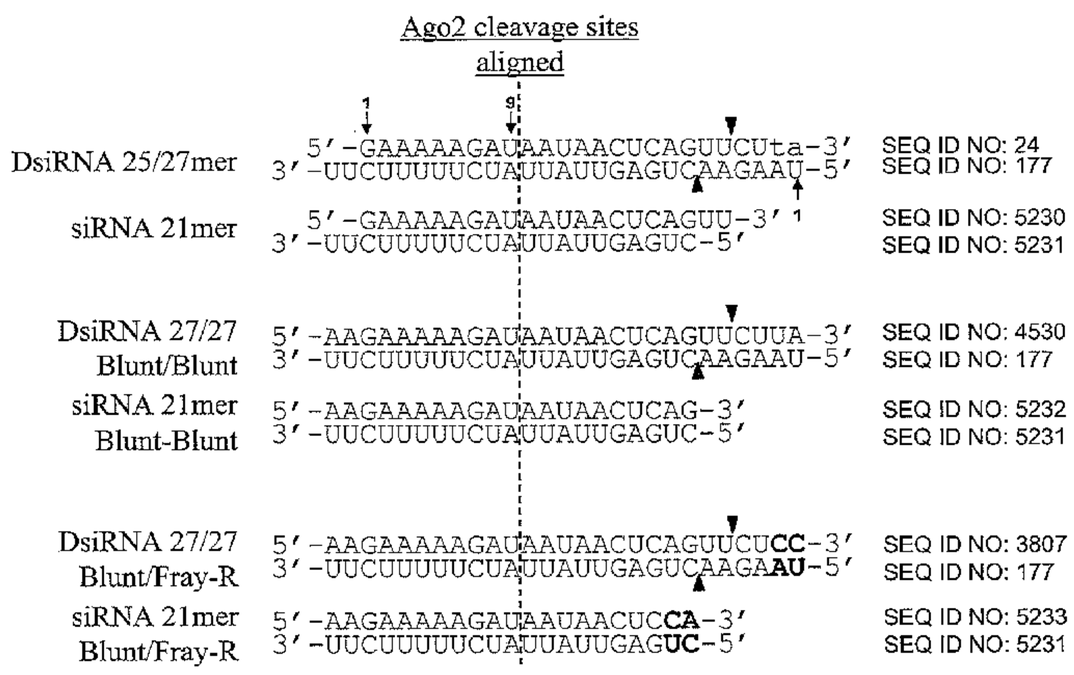

Figure 1

(57) Abstract: This invention relates to compounds, compositions, and methods useful for reducing AR target RNA and protein levels via use of dsRNAs, e.g., Dicer substrate siRNA (DsiRNA) agents.

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METHODS AND COMPOSITIONS FOR THE SPECIFIC INHIBITION OF ANDROGEN RECEPTOR BY DOUBLE-STRANDED RNA

CROSS-REFERENCE TO RELATED APPLICATIONS

The present application claims priority to, and the benefit under 35 U.S.C. §119(e) of, U.S. provisional patent application No. 61/361,759, filed July 6, 2010, entitled "Methods and Compositions for the Specific Inhibition of Androgen Receptor by Double-Stranded RNA". The entire teachings of this application are incorporated herein by reference.

FIELD OF THE INVENTION

The present invention relates to compounds, compositions, and methods for the study, diagnosis, and treatment of traits, diseases and conditions that respond to the modulation of androgen receptor (AR) gene expression and/or activity.

BACKGROUND OF THE INVENTION

AR is a ligand-activated steroid hormone receptor which functions as a transcription factor in prostate cells to regulate myriad genes involved in cell division, apoptosis and angiogenesis (Compagno *et al.*, *PLoS One*, 2: e1006). Prostate carcinomas are initially androgen-dependent and, therefore, responsive to therapies that reduce or eliminate AR activation. Specifically, a variety of approaches aimed at manipulating the effects of androgen have been shown unequivocally to be efficacious in the treatment of prostatic carcinoma. Historically, orchiectomy and the administration of estrogen were first demonstrated to have beneficial effects. However, prostate cancers often escape from such treatments and recur (Heinlein and Chang, *Endocr Rev* 25: 276–308).

Gonadotropin-releasing hormone agonists (GnRH agonists) and antiandrogens have been shown to be safe and effective in multiple settings and have become the standards of care for patients at high risk of recurrence after initial surgery or radiotherapy or who recur after these procedures (Scher and Sawyers. *Journal of Clinical Oncology*, 23: 8253-8261; Baltogiannis *et al. Experimental Oncology*, 26: 185-191; National Comprehensive Cancer Network (2008). Practice guidelines in oncology, 1.2008, 1-44; Bhandari et al. *Journal of Clinical Oncology*, 23: 8212-8218; Clinical Care Options & Postgraduate Institute for Medicine (2006). Recent and Future Directions of Hormonal Therapy in Prostate Cancer. 1-22; Evans *et al. BJU*

International, 95: 743-479; Use of 5-aplha- reductase inhibitors for prostate cancer chemoprevention: American society of clinical oncology/American urological association 2008 clinical practice guideline summary, (2009, May) *Journal of Oncology Practice*, 5: 127-129; O'Connor and Fitzpatrick. *BJU International*, 95: 22-28; Koltz and Schellhammer. Combined androgen blockade: worth a second look. 1-17). Many studies have evaluated the development of resistance in patients receiving endocrine manipulations, and it is clear that potential reasons for the resistance seen with endocrine manipulation therapies include: increased expression of the androgen receptor, increased sensitivity of the androgen receptor, and increased local production of androgens by cells not sensitive to existing inhibitors. Recently, antiandrogens have been shown to have activity in patients with resistance to standard methods of treating prostatic cancer, further validating the role of this receptor even in patients who appear to have "castration-resistant" prostatic cancer. It appears clear that even in patients whose tumors fail to respond to standard therapies, inhibition of the androgen receptor directly by dsRNA agents directed to this target should be active and, because of the increased androgen receptor expression that characterizes prostate cancers resistant to traditional therapies, may be more active in subjects harboring resistant cancers than earlier stages of disease.

Double-stranded RNA (dsRNA) agents possessing strand lengths of 25 to 35 nucleotides have been described as effective inhibitors of target gene expression in mammalian cells (Rossi *et al.*, U.S. Patent Application Nos. 2005/0244858 and US 2005/0277610). dsRNA agents of such length are believed to be processed by the Dicer enzyme of the RNA interference (RNAi) pathway, leading such agents to be termed "Dicer substrate siRNA" ("DsiRNA") agents. Additional modified structures of DsiRNA agents were previously described (Rossi *et al.*, U.S. Patent Application No. 2007/0265220).

BRIEF SUMMARY OF THE INVENTION

The present invention is directed to compositions that contain double stranded RNA ("dsRNA"), and methods for preparing them. The dsRNAs of the invention are capable of reducing the expression of a target AR gene in a cell, either *in vitro* or in a mammalian subject. More particularly, the invention is directed to Dicer substrate siRNAs ("DsiRNAs") with structures and modification patterns that act as effective and highly potent AR inhibitory agents, optionally possessing extended duration of

inhibitory effect. A number of such DsiRNAs possess target-specific inhibitory potencies and efficacies that are significantly enhanced relative to 21 nucleotide siRNAs directed against the same target RNA, as such an effect has been recently documented for DsiRNAs directed against a KRAS target transcript (see U.S. Serial Number 12/754,427).

In one aspect, the invention provides an isolated double stranded ribonucleic acid (dsRNA) comprising first and second nucleic acid strands, wherein the first strand is 15-35 nucleotides in length and the second strand is 19-35 nucleotides in length, wherein the second oligonucleotide strand is sufficiently complementary to a target AR cDNA sequence of Table 13 along at least 19 nucleotides of the second oligonucleotide strand length to reduce AR target gene expression when the double stranded nucleic acid is introduced into a mammalian cell. In certain embodiments, the isolated dsRNA possesses a duplex region of at least 25 base pairs. In one embodiment, the second strand of the isolated dsRNA includes a one to five nucleotide single stranded overhang of the first strand at the 3' terminus of the second strand. In another embodiment, the first strand is 25-35 nucleotides in length. In an additional embodiment, the second strand is 25-35 nucleotides in length. Optionally, the second oligonucleotide strand is complementary to a target AR cDNA sequence of GenBank Accession Nos. NM_000044.2 or NM_001011645.1 along at most 27 nucleotides of the second oligonucleotide strand length.

In one embodiment, starting from the first nucleotide (position 1) at the 3' terminus of the first oligonucleotide strand, position 1, 2 and/or 3 is substituted with a modified nucleotide. In certain embodiments, the modified nucleotide residue of the 3' terminus of the first strand is a deoxyribonucleotide, an acyclonucleotide or a fluorescent molecule. In a related embodiment, position 1 of the 3' terminus of the first oligonucleotide strand is a deoxyribonucleotide.

In an additional embodiment, the 3' terminus of the first strand and the 5' terminus of the second strand form a blunt end.

In another embodiment, the first strand is 25 nucleotides in length and the second strand is 27 nucleotides in length.

In one embodiment, the second strand includes a sequence of SEQ ID NOs: 164, 166, 174, 177, 179, 1975, 1984, 1986, 1987, 1992, 1994, 1998, 224, 2074, 1283, 2136, 246, 2204, 2220, 2227, 2230, 2235 and 2239.

In another embodiment, the first strand includes a sequence of SEQ ID NOs: 11, 13, 21, 24, 26, 1570, 1579, 1581, 1582, 1587, 1589, 1593, 71, 1669, 1220, 1731, 93, 1799, 1815, 1822, 1825, 1830 and 1834.

In an additional embodiment, the dsRNA includes a pair of first strand/second strand sequences as shown for a DsiRNA agent of Tables 2, 3, 5, 7, 9 and 11.

In one embodiment, each of the first and the second strands has a length which is at least 26 nucleotides.

In another embodiment, the nucleotides of the 3' overhang include a modified nucleotide. Optionally, the modified nucleotide of the 3' overhang is a 2'-O-methyl ribonucleotide. In a related embodiment, all nucleotides of the 3' overhang are modified nucleotides.

In an additional embodiment, one or both of the first and second oligonucleotide strands includes a 5' phosphate.

In another embodiment, the modified nucleotide residues of the dsRNA are 2'-O-methyl, 2'-methoxyethoxy, 2'-fluoro, 2'-allyl, 2'-O-[2-(methylamino)-2-oxoethyl], 4'-thio, 4'-CH2-O-2'-bridge, 4'-(CH2)2-O-2'-bridge, 2'-LNA, 2'-amino or 2'-O-(N-methlycarbamate).

In one embodiment, the 3' overhang of the dsRNA is 1-3 nucleotides in length. Optionally, the 3' overhang is 1-2 nucleotides in length. In a related embodiment, the 3' overhang is two nucleotides in length and the modified nucleotide of the 3' overhang is a 2'-O-methyl modified ribonucleotide.

In a further embodiment, the second oligonucleotide strand, starting from the nucleotide residue of the second strand that is complementary to the 5' terminal nucleotide residue of the first oligonucleotide strand, includes alternating modified and unmodified nucleotide residues. In another embodiment, the second oligonucleotide strand, starting from the nucleotide residue of the second strand that is complementary to the 5' terminal nucleotide residue of the first oligonucleotide strand, includes unmodified nucleotide residues at all positions from position 18 to the 5' terminus of the second oligonucleotide strand.

In another embodiment, each of the first and the second strands has a length which is at least 26 and at most 30 nucleotides.

In one embodiment, the dsRNA is cleaved endogenously in the cell by Dicer.

In an additional embodiment, the amount of the isolated double stranded nucleic acid sufficient to reduce expression of the target gene is 1 nanomolar or less,

200 picomolar or less, 100 picomolar or less, 50 picomolar or less, 20 picomolar or less, 10 picomolar or less, 5 picomolar or less, 2 picomolar or less or 1 picomolar or less in the environment of the cell.

In a further embodiment, the isolated dsRNA possesses greater potency than isolated 21mer siRNAs directed to the identical at least 19 nucleotides of the target AR cDNA in reducing target AR gene expression when assayed *in vitro* in a mammalian cell at an effective concentration in the environment of a cell of 1 nanomolar or less, 200 picomolar or less, 100 picomolar or less, 50 picomolar or less, 20 picomolar or less, 10 picomolar or less, 5 picomolar or less, 2 picomolar or less or 1 picomolar or less.

In another embodiment, the isolated dsRNA is sufficiently complementary to the target AR cDNA sequence to reduce AR target gene expression by at least 10%, at least 50%, at least 80-90%, at least 95%, at least 98%, or at least 99% when the double stranded nucleic acid is introduced into a mammalian cell.

In a further embodiment, the first and second strands are joined by a chemical linker. In a related embodiment, the 3' terminus of the first strand and the 5' terminus of the second strand are joined by a chemical linker.

In one embodiment, a nucleotide of the second or first strand is substituted with a modified nucleotide that directs the orientation of Dicer cleavage.

In another embodiment, the dsRNA has a modified nucleotide that is a deoxyribonucleotide, a dideoxyribonucleotide, an acyclonucleotide, a 3'-deoxyadenosine (cordycepin), a 3'-azido-3'-deoxythymidine (AZT), a 2',3'-dideoxyinosine (ddI), a 2',3'-dideoxy-3'-thiacytidine (3TC), a 2',3'-didehydro-2',3'-dideoxythymidine (d4T), a monophosphate nucleotide of 3'-azido-3'-deoxythymidine (AZT), a 2',3'-dideoxy-3'-thiacytidine (3TC) and a monophosphate nucleotide of 2',3'-didehydro-2',3'-dideoxythymidine (d4T), a 4-thiouracil, a 5-bromouracil, a 5-iodouracil, a 5-(3-aminoallyl)-uracil, a 2'-O-alkyl ribonucleotide, a 2'-O-methyl ribonucleotide, a 2'-amino ribonucleotide, a 2'-fluoro ribonucleotide, or a locked nucleic acid.

In an additional embodiment, the dsRNA has a phosphonate, a phosphorothioate or a phosphotriesterphosphate backbone modification.

In a further embodiment, the dsRNA contains a morpholino nucleic acid or oligonucleotide, or a peptide nucleic acid (PNA).

In one embodiment, the invention provides a method for reducing expression of a target AR gene in a mammalian cell having contacting a mammalian cell *in vitro* with an isolated dsRNA as described in an amount sufficient to reduce expression of a target AR gene in the cell.

In one embodiment, target AR gene expression is reduced by at least 10%, at least 50%, or at least 80-90%. In another embodiment, target AR mRNA levels are reduced at least 90% at least 8 days after the cell is contacted with the dsRNA. In a further embodiment, AR mRNA levels are reduced by at least 70% at least 10 days after the cell is contacted with the dsRNA.

In a further embodiment, the invention provides a method for reducing expression of a target AR gene in a mammal by administering an isolated dsRNA as described to a mammal in an amount sufficient to reduce expression of a target AR gene in the mammal.

In one embodiment, the isolated dsRNA is administered at a dosage of 1 microgram to 5 milligrams per kilogram of the mammal per day, 100 micrograms to 0.5 milligrams per kilogram, 0.001 to 0.25 milligrams per kilogram, 0.01 to 20 micrograms per kilogram, 0.01 to 10 micrograms per kilogram, 0.10 to 5 micrograms per kilogram, or 0.1 to 2.5 micrograms per kilogram.

In another embodiment, the isolated dsRNA possesses greater potency than isolated 21mer siRNAs directed to the identical at least 19 nucleotides of the target AR cDNA in reducing target AR gene expression when assayed *in vitro* in a mammalian cell at an effective concentration in the environment of a cell of 1 nanomolar or less.

In an additional embodiment, the administering step includes intravenous injection, intramuscular injection, intraperitoneal injection, infusion, subcutaneous injection, transdermal, aerosol, rectal, vaginal, topical, oral or inhaled delivery.

In a further embodiment, the invention provides a method for selectively inhibiting the growth of a cell by contacting a cell with an amount of an isolated dsRNA as described, in an amount sufficient to inhibit the growth of the cell.

In one embodiment, the cell is a tumor cell of a subject. Optionally, the cell is a tumor cell *in vitro*, *e.g.*, a prostate cancer cell (*e.g.*, 22Rv1 or VCaP) or adenocarcinoma cell (*e.g.*, A549), or other cancer cell. In certain embodiments, the cell is a mammalian prostate cell. In a related embodiment, the cell is a human cell.

In an additional embodiment, the invention provides a formulation which includes an isolated dsRNA as described, where the dsRNA is present in an amount effective to reduce target AR RNA levels when the dsRNA is introduced into a mammalian cell *in vitro* by at least 10%, at least 50% or at least 80-90%, and where the dsRNA possesses greater potency than isolated 21mer siRNAs directed to the identical at least 19 nucleotides of the target AR cDNA in reducing target AR RNA levels when assayed *in vitro* in a mammalian cell at an effective concentration in the environment of a cell of 1 nanomolar or less.

In one embodiment, the effective amount is 1 nanomolar or less, 200 picomolar or less, 100 picomolar or less, 50 picomolar or less, 20 picomolar or less, 10 picomolar or less, 5 picomolar or less, 2 picomolar or less or 1 picomolar or less in the environment of the cell.

In another embodiment, the invention provides a formulation which includes an isolated dsRNA as described, where the dsRNA is present in an amount effective to reduce target RNA levels when the dsRNA is introduced into a cell of a mammalian subject by at least 10%, at least 50% or at least 80-90%, and where the dsRNA possesses greater potency than isolated 21mer siRNAs directed to the identical at least 19 nucleotides of the target AR cDNA in reducing target AR RNA levels when assayed *in vitro* in a mammalian cell at an effective concentration in the environment of a cell of 1 nanomolar or less.

In one embodiment, the effective amount is a dosage of 1 microgram to 5 milligrams per kilogram of the subject per day, 100 micrograms to 0.5 milligrams per kilogram, 0.001 to 0.25 milligrams per kilogram, 0.01 to 20 micrograms per kilogram, 0.01 to 10 micrograms per kilogram, 0.10 to 5 micrograms per kilogram, or 0.1 to 2.5 micrograms per kilogram.

In an additional embodiment, the invention provides a mammalian cell containing an isolated dsRNA as described.

Another embodiment of the invention provides a pharmaceutical composition which includes an isolated dsRNA as described and a pharmaceutically acceptable carrier. A further embodiment of the invention provides a kit having an isolated dsRNA as described and instructions for its use.

In an additional aspect, the invention provides a composition possessing AR inhibitory activity consisiting essentially of an isolated double stranded ribonucleic acid (dsRNA) comprising first and second nucleic acid strands, wherein the first

strand is 15-35 nucleotides in length and the second strand is 19-35 nucleotides in length, wherein the second oligonucleotide strand is sufficiently complementary to a target AR cDNA sequence of Table 13 along at least 19 nucleotides of the second oligonucleotide strand length to reduce AR target gene expression when the double stranded nucleic acid is introduced into a mammalian cell.

In another embodiment, the invention provides a method for treating or preventing an AR-associated disease or disorder in a subject by administering a dsRNA and/or dsRNA-containing composition of the invention and a pharmaceutically acceptable carrier to a subject in an amount sufficient to treat or prevent an AR-associated disease or disorder in the subject. In a related embodiment, the AR-associated disease or disorder is prostate cancer or adenocarcinoma.

In another aspect, the invention provides an isolated double stranded ribonucleic acid (dsRNA) comprising first and second nucleic acid strands, wherein the dsRNA comprises blunt ends, wherein each of the first and second oligonucleotide strands consists of the same number of nucleotide residues and is at most 35 nucleotides in length, wherein the second oligonucleotide strand is sufficiently complementary to a target AR cDNA sequence of Table 13 along at least 19 nucleotides of the second oligonucleotide strand length to reduce AR target gene expression when the double stranded nucleic acid is introduced into a mammalian cell.

In one embodiment, the dsRNA is capable of reducing target gene expression at a concentration of less than 1 nanomolar in the environment of a cell. In another embodiment, each of the first and the second strands has a length which is at least 26 nucleotides. In a related embodiment, each of the first and the second strands has a length which is 26-30 nucleotides. Optionally, each of the first and the second strands has a length which is 27 nucleotides.

In certain embodiments, the second strand of the dsRNA includes a sequence selected from SEQ ID NOs: 164, 166, 174, 177, 179, 1975, 1984, 1986, 1987, 1992, 1994, 1998, 224, 2074, 1283, 2136, 246, 2204, 2220, 2227, 2230, 2235 and 2239. In related embodiments, the first strand of the dsRNA includes a sequence selected from SEQ ID NOs: 4517, 4519, 4527, 4530, 4532, 4876, 4885, 4887, 4888, 4893, 4895, 4899, 4577, 4975, 4778, 5037, 4599, 5105, 5121, 5128, 5131, 5136 and 5140. In a further embodiment, the dsRNA includes a pair of first strand and corresponding second strand sequences selected from Tables 2, 3, 5, 7, 9 and 11.

Another aspect of the invention provides an isolated double stranded ribonucleic acid (dsRNA) comprising first and second nucleic acid strands, wherein the dsRNA comprises a blunt end, wherein each of the first and second oligonucleotide strands consists of the same number of nucleotide residues and is at most 35 nucleotides in length, wherein the ultimate and penultimate residues of the 3' terminus of the first strand and the ultimate and penultimate residues of said 5' terminus of the second strand form one or two mismatched based pairs, wherein the second oligonucleotide strand is sufficiently complementary to a target AR cDNA sequence of Table 13 along at least 19 nucleotides of the second oligonucleotide strand length to reduce AR target gene expression when the double stranded nucleic acid is introduced into a mammalian cell.

In one embodiment, the first strand includes a sequence of SEQ ID NOs: 3794, 3796, 3804, 3807, 3809, 4153, 4162, 4164, 4165, 4170, 4172, 4176, 3854, 4252, 4055, 4314, 3876, 4382, 4398, 4405, 4408, 4413 and 4417.

In an additional aspect, the invention provides a composition possessing AR inhibitory activity consisting essentially of an isolated double stranded ribonucleic acid (dsRNA) comprising first and second nucleic acid strands, wherein the dsRNA comprises blunt ends, wherein each of the first and second oligonucleotide strands consists of the same number of nucleotide residues and is at most 35 nucleotides in length, wherein the second oligonucleotide strand is sufficiently complementary to a target AR cDNA sequence of Table 13 along at least 19 nucleotides of the second oligonucleotide strand length to reduce AR target gene expression when the double stranded nucleic acid is introduced into a mammalian cell.

In another aspect, the invention provides an isolated dsRNA molecule consisting of a sense region and an antisense region, where the sense region and the antisense region together form a duplex region consisting of 15-35 base pairs and the antisense region includes a sequence that is the complement of a sequence of Table 13, and the isolated dsRNA further includes from zero to two 3' overhang regions where each overhang region is six or fewer nucleotides in length. Optionally, the duplex region consists of 19-35 base pairs. In certain embodiments, the duplex region consists of 25-35 base pairs. In additional embodiments, the duplex region consists of 25-30 base pairs.

In a further aspect, the invention provides a siRNA molecule consisting of a sense region and an antisense region, where the sense region and the antisense region

together form a duplex region consisting of 19-23 base pairs and the antisense region includes a sequence that is the complement of a sequence of Table 13, and the isolated dsRNA further includes from zero to four overhang regions, where each overhang region is six or fewer nucleotides in length.

In certain aspects, the invention is directed to Dicer substrate siRNAs ("DsiRNAs") with structures and modification patterns that act as effective and highly potent AR inhibitory agents, optionally possessing extended duration of inhibitory effect. A number of such DsiRNAs possess target-specific inhibitory potencies and efficacies that are significantly enhanced relative to 19-23 base pair double stranded nucleic acids (e.g., 21 nucleotide siRNAs) directed against the same target RNA. In certain such embodiments, such a DsiRNA is more potent at reducing AR target gene expression in a mammalian cell than a 19, 20, 21, 22 or 23 base pair sequence that is contained within it, when suitably formulated at a concentration of 1 nM or less.

In a further aspect, the invention provides an isolated double stranded ribonucleic acid (dsRNA) comprising first and second nucleic acid strands and a duplex region of at least 25 base pairs, wherein the first strand is 25-34 nucleotides in length and the second strand is 26-35 nucleotides in length and comprises 1-5 single-stranded nucleotides at its 3' terminus, wherein the second oligonucleotide strand is sufficiently complementary to a target AR cDNA sequence of SEQ ID NOs: 307-459, 826-915, 1024-1077, 1312-1374, 2311-2715 or 3622-3669 along at least 15 nucleotides of the second oligonucleotide strand length to reduce AR target gene expression when the double stranded nucleic acid is introduced into a mammalian cell. Optionally, the second oligonucleotide strand is complementary to a target AR cDNA sequence of SEQ ID NOs: 3766, 3768 or 3770 along at most 27 nucleotides of the second oligonucleotide strand length.

In one embodiment, starting from the first nucleotide (position 1) at the 3' terminus of the first oligonucleotide strand, position 1, 2 and/or 3 is substituted with a modified nucleotide. In certain embodiments, the modified nucleotide residue of the 3' terminus of the first strand is a deoxyribonucleotide, an acyclonucleotide or a fluorescent molecule. In a related embodiment, position 1 of the 3' terminus of the first oligonucleotide strand is a deoxyribonucleotide.

In an additional embodiment, the 3' terminus of the first strand and the 5' terminus of the second strand form a blunt end.

In another embodiment, the first strand is 25 nucleotides in length and the second strand is 27 nucleotides in length.

In one embodiment, the second strand includes a sequence of SEQ ID NOs: 154-306, 796-825, 970-1023, 1249-1311, 1906-2310 and 3574-3621.

In another embodiment, the first strand includes a sequence of SEQ ID NOs: 1-153, 766-795, 916-969, 1186-1248, 1501-1905 and 3526-3573.

In an additional embodiment, the dsRNA includes a pair of first strand/second strand sequences as shown for a DsiRNA agent of Table 9.

In one embodiment, each of the first and the second strands has a length which is at least 26 nucleotides.

In another embodiment, the nucleotides of the 3' overhang include a modified nucleotide. Optionally, the modified nucleotide of the 3' overhang is a 2'-O-methyl ribonucleotide. In a related embodiment, all nucleotides of the 3' overhang are modified nucleotides.

In an additional embodiment, one or both of the first and second oligonucleotide strands includes a 5' phosphate.

In another embodiment, the modified nucleotide residues of the dsRNA are 2'-O-methyl, 2'-methoxyethoxy, 2'-fluoro, 2'-allyl, 2'-O-[2-(methylamino)-2-oxoethyl], 4'-thio, 4'-CH2-O-2'-bridge, 4'-(CH2)2-O-2'-bridge, 2'-LNA, 2'-amino or 2'-O-(N-methlycarbamate).

In one embodiment, the 3' overhang of the dsRNA is 1-3 nucleotides in length. Optionally, the 3' overhang is 1-2 nucleotides in length. In a related embodiment, the 3' overhang is two nucleotides in length and the modified nucleotide of the 3' overhang is a 2'-O-methyl modified ribonucleotide.

In a further embodiment, the second oligonucleotide strand, starting from the nucleotide residue of the second strand that is complementary to the 5' terminal nucleotide residue of the first oligonucleotide strand, includes alternating modified and unmodified nucleotide residues. In another embodiment, the second oligonucleotide strand, starting from the nucleotide residue of the second strand that is complementary to the 5' terminal nucleotide residue of the first oligonucleotide strand, includes unmodified nucleotide residues at all positions from position 18 to the 5' terminus of the second oligonucleotide strand.

In another embodiment, each of the first and the second strands has a length which is at least 26 and at most 30 nucleotides.

In one embodiment, the dsRNA is cleaved endogenously in the cell by Dicer.

In an additional embodiment, the amount of the isolated double stranded nucleic acid sufficient to reduce expression of the target gene is 1 nanomolar or less, 200 picomolar or less, 100 picomolar or less, 50 picomolar or less, 20 picomolar or less, 10 picomolar or less, 5 picomolar or less, 2 picomolar or less or 1 picomolar or less in the environment of the cell.

In a further embodiment, the isolated dsRNA possesses greater potency than isolated 21mer siRNAs directed to the identical at least 15 nucleotides of the target AR cDNA in reducing target AR gene expression when assayed *in vitro* in a mammalian cell at an effective concentration in the environment of a cell of 1 nanomolar or less, 200 picomolar or less, 100 picomolar or less, 50 picomolar or less, 20 picomolar or less, 10 picomolar or less, 5 picomolar or less, 2 picomolar or less or 1 picomolar or less.

In another embodiment, the isolated dsRNA is sufficiently complementary to the target AR cDNA sequence to reduce AR target gene expression by at least 10%, at least 50%, at least 80-90%, at least 95%, at least 98%, or at least 99% when the double stranded nucleic acid is introduced into a mammalian cell.

In a further embodiment, the first and second strands are joined by a chemical linker. In a related embodiment, the 3' terminus of the first strand and the 5' terminus of the second strand are joined by a chemical linker.

In one embodiment, a nucleotide of the second or first strand is substituted with a modified nucleotide that directs the orientation of Dicer cleavage.

In another embodiment, the dsRNA has a modified nucleotide that is a deoxyribonucleotide, a dideoxyribonucleotide, an acyclonucleotide, a 3'-deoxyadenosine (cordycepin), a 3'-azido-3'-deoxythymidine (AZT), a 2',3'-dideoxyinosine (ddI), a 2',3'-dideoxy-3'-thiacytidine (3TC), a 2',3'-didehydro-2',3'-dideoxythymidine (d4T), a monophosphate nucleotide of 3'-azido-3'-deoxythymidine (AZT), a 2',3'-dideoxy-3'-thiacytidine (3TC) and a monophosphate nucleotide of 2',3'-didehydro-2',3'-dideoxythymidine (d4T), a 4-thiouracil, a 5-bromouracil, a 5-iodouracil, a 5-(3-aminoallyl)-uracil, a 2'-O-alkyl ribonucleotide, a 2'-O-methyl ribonucleotide, a 2'-amino ribonucleotide, a 2'-fluoro ribonucleotide, or a locked nucleic acid.

In an additional embodiment, the dsRNA has a phosphonate, a phosphorothioate or a phosphotriesterphosphate backbone modification.

In one embodiment, the invention provides a method for reducing expression of a target AR gene in a mammalian cell having contacting a mammalian cell *in vitro* with an isolated dsRNA as described in an amount sufficient to reduce expression of a target AR gene in the cell.

In one embodiment, target AR gene expression is reduced by at least 10%, at least 50%, or at least 80-90%. In another embodiment, target AR mRNA levels are reduced at least 90% at least 8 days after the cell is contacted with the dsRNA. In a further embodiment, AR mRNA levels are reduced by at least 70% at least 10 days after the cell is contacted with the dsRNA.

In a further embodiment, the invention provides a method for reducing expression of a target AR gene in a mammal by administering an isolated dsRNA as described to a mammal in an amount sufficient to reduce expression of a target AR gene in the mammal.

In one embodiment, the isolated dsRNA is administered at a dosage of 1 microgram to 5 milligrams per kilogram of the mammal per day, 100 micrograms to 0.5 milligrams per kilogram, 0.001 to 0.25 milligrams per kilogram, 0.01 to 20 micrograms per kilogram, 0.01 to 10 micrograms per kilogram, 0.10 to 5 micrograms per kilogram, or 0.1 to 2.5 micrograms per kilogram.

In another embodiment, the isolated dsRNA possesses greater potency than isolated 21mer siRNAs directed to the identical at least 15 nucleotides of the target AR cDNA in reducing target AR gene expression when assayed *in vitro* in a mammalian cell at an effective concentration in the environment of a cell of 1 nanomolar or less.

In an additional embodiment, the administering step includes intravenous injection, intramuscular injection, intraperitoneal injection, infusion, subcutaneous injection, transdermal, aerosol, rectal, vaginal, topical, oral or inhaled delivery.

In a further embodiment, the invention provides a method for selectively inhibiting the growth of a cell by contacting a cell with an amount of an isolated dsRNA as described, in an amount sufficient to inhibit the growth of the cell.

In one embodiment, the cell is a tumor cell of a subject. Optionally, the cell is a tumor cell *in vitro*. In a related embodiment, the cell is a human cell.

In an additional embodiment, the invention provides a formulation which includes an isolated dsRNA as described, where the dsRNA is present in an amount effective to reduce target AR RNA levels when the dsRNA is introduced into a

mammalian cell *in vitro* by at least 10%, at least 50% or at least 80-90%, and where the dsRNA possesses greater potency than isolated 21mer siRNAs directed to the identical at least 15 nucleotides of the target AR cDNA in reducing target AR RNA levels when assayed *in vitro* in a mammalian cell at an effective concentration in the environment of a cell of 1 nanomolar or less.

In one embodiment, the effective amount is 1 nanomolar or less, 200 picomolar or less, 100 picomolar or less, 50 picomolar or less, 20 picomolar or less, 10 picomolar or less, 5 picomolar or less, 2 picomolar or less or 1 picomolar or less in the environment of the cell.

In another embodiment, the invention provides a formulation which includes an isolated dsRNA as described, where the dsRNA is present in an amount effective to reduce target RNA levels when the dsRNA is introduced into a cell of a mammalian subject by at least 10%, at least 50% or at least 80-90%, and where the dsRNA possesses greater potency than isolated 21mer siRNAs directed to the identical at least 15 nucleotides of the target AR cDNA in reducing target AR RNA levels when assayed *in vitro* in a mammalian cell at an effective concentration in the environment of a cell of 1 nanomolar or less.

In one embodiment, the effective amount is a dosage of 1 microgram to 5 milligrams per kilogram of the subject per day, 100 micrograms to 0.5 milligrams per kilogram, 0.001 to 0.25 milligrams per kilogram, 0.01 to 20 micrograms per kilogram, 0.01 to 10 micrograms per kilogram, 0.10 to 5 micrograms per kilogram, or 0.1 to 2.5 micrograms per kilogram.

In an additional embodiment, the invention provides a mammalian cell containing an isolated dsRNA as described.

Another embodiment of the invention provides a pharmaceutical composition which includes an isolated dsRNA as described and a pharmaceutically acceptable carrier. A further embodiment of the invention provides a kit having an isolated dsRNA as described and instructions for its use.

In an additional aspect, the invention provides a composition possessing AR inhibitory activity consisiting essentially of an isolated double stranded ribonucleic acid (dsRNA) comprising first and second nucleic acid strands and a duplex region of at least 25 base pairs, wherein the first strand is 25-34 nucleotides in length and the second strand is 26-35 nucleotides in length and comprises 1-5 single-stranded nucleotides at its 3' terminus, wherein the second oligonucleotide strand is sufficiently

complementary to a target AR cDNA sequence of SEQ ID NOs: 307-459, 826-915, 1024-1077, 1312-1374, 2311-2715 or 3622-3669 along at least 15 nucleotides of the second oligonucleotide strand length to reduce AR target gene expression when the double stranded nucleic acid is introduced into a mammalian cell.

In another embodiment, the invention provides a method for treating or preventing an AR-associated disease or disorder in a subject by administering a dsRNA and/or dsRNA-containing composition of the invention and a pharmaceutically acceptable carrier to a subject in an amount sufficient to treat or prevent an AR-associated disease or disorder in the subject. In a related embodiment, the AR-associated disease or disorder is prostate cancer.

In another aspect, the invention provides an isolated double stranded ribonucleic acid (dsRNA) comprising first and second nucleic acid strands and a duplex region of at least 25 base pairs, wherein the dsRNA comprises blunt ends, wherein each of the first and second oligonucleotide strands consists of the same number of nucleotide residues and is at most 35 nucleotides in length, wherein the second oligonucleotide strand is sufficiently complementary to a target AR cDNA sequence of SEQ ID NOs: 307-459, 826-915, 1024-1077, 1312-1374, 2311-2715 or 3622-3669 along at least 15 nucleotides of the second oligonucleotide strand length to reduce AR target gene expression when the double stranded nucleic acid is introduced into a mammalian cell.

In one embodiment, the dsRNA is capable of reducing target gene expression at a concentration of less than 1 nanomolar in the environment of a cell. In another embodiment, each of the first and the second strands has a length which is at least 26 nucleotides. In a related embodiment, each of the first and the second strands has a length which is 26-30 nucleotides. Optionally, each of the first and the second strands has a length which is 27 nucleotides.

In certain embodiments, the second strand of the dsRNA includes a sequence selected from SEQ ID NOs: 154-306, 796-825, 970-1023, 1249-1311, 1906-2310 and 3574-3621. (Optionally, the second strand is a sequence selected from SEQ ID NOs: 154-306, 796-825, 970-1023, 1249-1311, 1906-2310 and 3574-3621.) In related embodiments, the first strand of the dsRNA includes a sequence selected from SEQ ID NOs: 3784-5229. (Optionally, the first strand is a sequence selected from SEQ ID NOs: 3784-5229.) In a further embodiment, the dsRNA includes a pair of first strand and corresponding second strand sequences selected from Tables 5-8.

Another aspect of the invention provides an isolated double stranded ribonucleic acid (dsRNA) comprising first and second nucleic acid strands and a duplex region of at least 25 base pairs, wherein the dsRNA comprises a blunt end, wherein each of the first and second oligonucleotide strands consists of the same number of nucleotide residues and is at most 35 nucleotides in length, wherein the ultimate and penultimate residues of the 3' terminus of the first strand and the ultimate and penultimate residues of said 5' terminus of the second strand form one or two mismatched based pairs. wherein the second oligonucleotide strand is sufficiently complementary to a target AR cDNA sequence of SEQ ID NOs: 307-459, 826-915, 1024-1077, 1312-1374, 2311-2715 or 3622-3669 along at least 15 nucleotides of the second oligonucleotide strand length to reduce AR target gene expression when the double stranded nucleic acid is introduced into a mammalian cell.

In one embodiment, the first strand includes a sequence of SEQ ID NOs: 3784-4506.

In an additional aspect, the invention provides a composition possessing AR inhibitory activity consisting essentially of an isolated double stranded ribonucleic acid (dsRNA) comprising first and second nucleic acid strands and a duplex region of at least 25 base pairs, wherein said dsRNA comprises blunt ends, wherein each of the first and second oligonucleotide strands consists of the same number of nucleotide residues and is at most 35 nucleotides in length, wherein the second oligonucleotide strand is sufficiently complementary to a target AR cDNA sequence of SEQ ID NOs: 307-459, 826-915, 1024-1077, 1312-1374, 2311-2715 or 3622-3669 along at least 15 nucleotides of the second oligonucleotide strand length to reduce AR target gene expression when the double stranded nucleic acid is introduced into a mammalian cell.

In another aspect, the invention provides an isolated dsRNA molecule consisting of a sense region and an antisense region, where the sense region and the antisense region together form a duplex region consisting of 19-35 base pairs and the antisense region includes a sequence that is the complement of SEQ ID NOs 613-765, 886-915, 1132-1185, 1438-1500 or 3121-3765, and the isolated dsRNA further includes from zero to two 3' overhang regions where each overhang region is six or fewer nucleotides in length. Optionally, the duplex region consists of 25-35 base pairs.

In a further aspect, the invention provides a siRNA molecule consisting of a sense region and an antisense region, where the sense region and the antisense region together form a duplex region consisting of 19-23 base pairs and the antisense region includes a sequence that is the complement of SEQ ID NOs 613-765, 886-915, 1132-1185, 1438-1500 or 3121-3765, and the isolated dsRNA further includes from zero to four overhang regions, where each overhang region is six or fewer nucleotides in length.

The present invention is also directed to compounds, compositions, and methods relating to traits, diseases and conditions that respond to the modulation of expression and/or activity of genes involved in AR gene expression pathways or other cellular processes that mediate the maintenance or development of such traits, diseases and conditions. Specifically, the invention relates to small nucleic acid molecules that are capable of being processed by the Dicer enzyme, such as Dicer substrate siRNAs (DsiRNAs) capable of mediating RNA interference (RNAi) against AR gene expression. Such anti-AR DsiRNAs are useful, for example, in providing compositions for treatment of traits, diseases and conditions that can respond to modulation of AR in a subject, such as cancer and/or other proliferative diseases, disorders, or conditions. Efficacy, potency, toxicity and other effects of an anti-AR DsiRNA can be examined in one or more animal models of proliferative disease (exemplary animal models of proliferative disease are recited below).

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows the structures of exemplary DsiRNA agents targeting a site in the AR RNA referred to herein as the "AR-770" target site. UPPER case = unmodified RNA, lower case = DNA, **Bold** = mismatch base pair nucleotides; arrowheads indicate projected Dicer enzyme cleavage sites; dashed line indicates sense strand (top strand) sequences corresponding to the projected Argonaute 2 (Ago2) cleavage site within the targeted AR sequence.

Figures 2 and 3 show histograms of human AR inhibitory efficacies observed for indicated DsiRNAs. "P1" indicates phase 1, while "P2" indicates phase 2. In phase 1, DsiRNAs were tested at 1 nM in the environment of 22Rv1 cells. In phase 2, DsiRNAs were tested at 1 nM, at 0.3 nM and at 0.1 nM in the environment of 22Rv1

cells. Individual bars represent average human AR levels observed in triplicate, with standard errors shown. Human AR levels were normalized to HPRT and SFRS9 levels.

Figures 4 and 5 show histograms of mouse AR inhibitory efficacies observed for indicated DsiRNAs. "P1" indicates phase 1, while "P2" indicates phase 2. In phase 1, DsiRNAs were tested at 1 nM in the environment of LMTK- cells. In phase 2, DsiRNAs were tested at 1 nM, at 0.3 nM and at 0.1 nM in the environment of LMTK- cells. Individual bars represent average mouse AR levels observed in triplicate, with standard errors shown. Mouse AR levels were normalized to HPRT and Rpl23 levels.

Figures 6A and 6B show that DsiRNA-mediated AR protein knockdown correlated with location of targeted AR sites within the AR transcript. ***Figure 6A*** shows that proteins corresponding to both long and short forms of AR transcript were effectively knocked down at 24 and 48 hours post-administration by AR-targeting DsiRNAs AR-2224 and AR-2213, whereas only protein corresponding to the long form of the AR transcript was effectively knocked down by AR-targeting DsiRNAs AR-3518 and AR-3242. ***Figure 6B*** depicts DsiRNA Targeted Locations in AR mRNAs expressed in 22Rv1 cells.

Figures 7-1 to 7-32 present bar graphs showing efficacy data for six different modification patterns each across 32 AR-targeting DsiRNAs in human A549 cells at 0.1 nM (parallel assays) and 1 nM.

Figure 8 presents a histogram showing that an exemplary AR-targeting DsiRNA, AR-2813, effectively reduced AR levels in lung tissues of mice administered AR-2813, as compared to mock- and control DsiRNA-treated mice. (Results for each of three parallel qPCR assays of AR levels as indicated are shown.)

Figure 9 demonstrates administration of AR-2813 DsiRNA produced effective inhibition of both AR mRNA (lower panel) and protein (top panels) in the human prostate cancer cell line 22Rv1, with 24h (Day 1) and 48h (Day 2) timepoints post-administration shown.

Figure 10 shows dose-response curves for five DsiRNAs assayed in A549 cells (adenocarcinomic human alveolar basal epithelial cells) for reduction of AR mRNA levels. IC_{50} values were calculated for each of the assayed AR-targeting DsiRNAs:

AR-2813-M25 (IC_{50} = 21 pM), AR-2815-M12 (IC_{50} = 0.7 pM), AR-2874-M12 (IC_{50} = 0.4 pM), AR-3518-M12 (IC_{50} = 0.086 pM) and AR-3599-M25 (IC_{50} = 1.57 pM).

Figure 11 shows that AR-targeting DsiRNAs (here, the AR-2813 DsiRNA) inhibited cell growth following administration to 22Rv1 (human prostate cancer) cells.

Figure 12 shows that AR-targeting DsiRNAs (here, the AR-3599 and AR-2813 DsiRNAs, where the antisense (guide) strand carries the M25 modification pattern as shown in Figure 7) inhibited cell growth following administration to VCaP (human prostate cancer) cells. Cell growth values were assessed at five days post-transfection-mediated administration of DsiRNAs.

Figure 13 demonstrates that four distinct AR-targeting DsiRNAs (AR-2815-M12, AR-2874-M12, AR-3518-M12 and AR3599-M25) each reduced AR mRNA expression in normal liver tissue by at least 80% (in certain cases, at least 90% or even 95%) as compared to a PBS- or control oligonucleotide-treated control. DsiRNAs were formulated in InVivoFectamineTM (InVitrogen) 2.0 transfection agent and were administered to two month old nu/nu male mice (n=7) at 10 mg/kg by i.v. injection on day 1 and day 4, with tissue harvested 48 hours after administration of the second dose.

Figure 14 shows that AR-targeting DsiRNAs (AR-2815-M12 and AR3599-M25) reduced AR mRNA expression in normal liver tissue by at least 80% (in one case, at least 90%) as compared to a saline- or control oligonucleotide-treated control. DsiRNAs were formulated in lipid formulation "DL1" and were administered to mice at 5 mg/kg by i.v. injection in a series of three doses at timepoints 0, 48 hours and 96 hours, with tissue harvested at 48 hours after administration of the final dose.

DETAILED DESCRIPTION OF THE INVENTION

The present invention is directed to compositions that contain double stranded RNA ("dsRNA"), and methods for preparing them, that are capable of reducing the level and/or expression of the AR gene *in vivo* or *in vitro*. One of the strands of the dsRNA contains a region of nucleotide sequence that has a length that ranges from 19 to 35 nucleotides that can direct the destruction and/or translational inhibition of the targeted AR transcript.

Definitions

Unless defined otherwise, all technical and scientific terms used herein have the meaning commonly understood by a person skilled in the art to which this invention belongs. The following references provide one of skill with a general definition of many of the terms used in this invention: Singleton *et al.*, Dictionary of Microbiology and Molecular Biology (2nd ed. 1994); The Cambridge Dictionary of Science and Technology (Walker ed., 1988); The Glossary of Genetics, 5th Ed., R. Rieger et al. (eds.), Springer Verlag (1991); and Hale & Marham, The Harper Collins Dictionary of Biology (1991). As used herein, the following terms have the meanings ascribed to them below, unless specified otherwise.

The present invention features one or more DsiRNA molecules that can modulate (*e.g.*, inhibit) AR expression. The DsiRNAs of the invention optionally can be used in combination with modulators of other genes and/or gene products associated with the maintenance or development of diseases or disorders associated with AR misregulation (*e.g.*, tumor formation and/or growth, etc.). The DsiRNA agents of the invention modulate AR RNAs such as those corresponding to the cDNA sequences referred to by GenBank Accession Nos. NM_000044.2 (human AR, long version), NM_001011645.1 (human AR, short version) and NM_013476.3 (mouse AR), which are recited below and referred to herein generally as "AR."

The below description of the various aspects and embodiments of the invention is provided with reference to exemplary AR RNAs, generally referred to herein as AR. However, such reference is meant to be exemplary only and the various aspects and embodiments of the invention are also directed to alternate AR RNAs, such as mutant AR RNAs or additional AR splice variants. Certain aspects and embodiments are also directed to other genes involved in AR pathways, including genes whose misregulation acts in association with that of AR (or is affected or affects AR regulation) to produce phenotypic effects that may be targeted for treatment (*e.g.*, tumor formation and/or growth, etc.). Such additional genes can be targeted using DsiRNA and the methods described herein for use of AR targeting DsiRNAs. Thus, the inhibition and the effects of such inhibition of the other genes can be performed as described herein.

The term "AR" refers to nucleic acid sequences encoding an AR protein, peptide, or polypeptide (*e.g.*, AR transcripts, such as the sequences of AR Genbank Accession Nos. NM_000044.2, NM_001011645.1 and NM_013476.3). In certain

embodiments, the term "AR" is also meant to include other AR encoding sequence, such as other AR isoforms, mutant AR genes, splice variants of AR genes, and AR gene polymorphisms. The term “AR” is used to refer to the polypeptide gene product of an AR gene/transript, *e.g.*, an AR protein, peptide, or polypeptide, such as those encoded by AR Genbank Accession Nos. NM_000044.2, NM_001011645.1 and NM_013476.3.

As used herein, an “AR-associated disease or disorder” refers to a disease or disorder known in the art to be associated with altered AR expression, level and/or activity. Notably, an “AR-associated disease or disorder” includes cancer and/or proliferative diseases, conditions, or disorders. An exemplary “AR-associated disease or disorder” is prostate cancer.

By "proliferative disease" or "cancer" as used herein is meant, a disease, condition, trait, genotype or phenotype characterized by unregulated cell growth or replication as is known in the art; including leukemias, for example, acute myelogenous leukemia (AML), chronic myelogenous leukemia (CML), acute lymphocytic leukemia (ALL), and chronic lymphocytic leukemia, AIDS related cancers such as Kaposi's sarcoma; breast cancers; bone cancers such as Osteosarcoma, Chondrosarcomas, Ewing's sarcoma, Fibrosarcomas, Giant cell tumors, Adamantinomas, and Chordomas; Brain cancers such as Meningiomas, Glioblastomas, Lower-Grade Astrocytomas, Oligodendrocytomas, Pituitary Tumors, Schwannomas, and Metastatic brain cancers; cancers of the head and neck including various lymphomas such as mantle cell lymphoma, non-Hodgkins lymphoma, adenoma, squamous cell carcinoma, laryngeal carcinoma, gallbladder and bile duct cancers, cancers of the retina such as retinoblastoma, cancers of the esophagus, gastric cancers, multiple myeloma, ovarian cancer, uterine cancer, thyroid cancer, testicular cancer, endometrial cancer, melanoma, colorectal cancer, lung cancer, bladder cancer, prostate cancer, lung cancer (including non-small cell lung carcinoma), pancreatic cancer, sarcomas, Wilms' tumor, cervical cancer, head and neck cancer, skin cancers, nasopharyngeal carcinoma, liposarcoma, epithelial carcinoma, renal cell carcinoma, gallbladder adeno carcinoma, parotid adenocarcinoma, endometrial sarcoma, multidrug resistant cancers; and proliferative diseases and conditions, such as neovascularization associated with tumor angiogenesis, macular degeneration (e.g., wet/dry AMD), corneal neovascularization, diabetic retinopathy, neovascular glaucoma, myopic degeneration and other proliferative diseases and conditions such

as restenosis and polycystic kidney disease, and other cancer or proliferative disease, condition, trait, genotype or phenotype that can respond to the modulation of disease related gene expression in a cell or tissue, alone or in combination with other therapies.

In certain embodiments, dsRNA-mediated inhibition of an AR target sequence is assessed. In such embodiments, AR RNA levels can be assessed by art-recognized methods (*e.g.*, RT-PCR, Northern blot, expression array, etc.), optionally *via* comparison of AR levels in the presence of an anti-AR dsRNA of the invention relative to the absence of such an anti-AR dsRNA. In certain embodiments, AR levels in the presence of an anti-AR dsRNA are compared to those observed in the presence of vehicle alone, in the presence of a dsRNA directed against an unrelated target RNA, or in the absence of any treatment.

It is also recognized that levels of AR protein can be assessed and that AR protein levels are, under different conditions, either directly or indirectly related to AR RNA levels and/or the extent to which a dsRNA inhibits AR expression, thus art-recognized methods of assessing AR protein levels (*e.g.*, Western blot, immunoprecipitation, other antibody-based methods, etc.) can also be employed to examine the inhibitory effect of a dsRNA of the invention.

An anti-AR dsRNA of the invention is deemed to possess "AR inhibitory activity" if a statistically significant reduction in AR RNA (or when the AR protein is assessed, AR protein levels) is seen when an anti-AR dsRNA of the invention is administered to a system (*e.g.*, cell-free *in vitro* system), cell, tissue or organism, as compared to a selected control. The distribution of experimental values and the number of replicate assays performed will tend to dictate the parameters of what levels of reduction in AR RNA (either as a % or in absolute terms) is deemed statistically significant (as assessed by standard methods of determining statistical significance known in the art). However, in certain embodiments, "AR inhibitory activity" is defined based upon a % or absolute level of reduction in the level of AR in a system, cell, tissue or organism. For example, in certain embodiments, a DsiRNA of the invention is deemed to possess AR inhibitory activity if at least a 5% reduction or at least a 10% reduction in AR RNA is observed in the presence of a DsiRNA of the invention relative to AR levels seen for a suitable control. (For example, *in vivo* AR levels in a tissue and/or subject can, in certain embodiments, be deemed to be inhibited by a DsiRNA agent of the invention if, *e.g.*, a 5% or 10% reduction in AR

levels is observed relative to a control.) In certain other embodiments, a DsiRNA of the invention is deemed to possess AR inhibitory activity if AR RNA levels are observed to be reduced by at least 15% relative to a selected control, by at least 20% relative to a selected control, by at least 25% relative to a selected control, by at least 30% relative to a selected control, by at least 35% relative to a selected control, by at least 40% relative to a selected control, by at least 45% relative to a selected control, by at least 50% relative to a selected control, by at least 55% relative to a selected control, by at least 60% relative to a selected control, by at least 65% relative to a selected control, by at least 70% relative to a selected control, by at least 75% relative to a selected control, by at least 80% relative to a selected control, by at least 85% relative to a selected control, by at least 90% relative to a selected control, by at least 95% relative to a selected control, by at least 96% relative to a selected control, by at least 97% relative to a selected control, by at least 98% relative to a selected control or by at least 99% relative to a selected control. In some embodiments, complete inhibition of AR is required for a DsiRNA to be deemed to possess AR inhibitory activity. In certain models (*e.g.*, cell culture), a DsiRNA is deemed to possess AR inhibitory activity if at least a 50% reduction in AR levels is observed relative to a suitable control. In certain other embodiments, a DsiRNA is deemed to possess AR inhibitory activity if at least an 80% reduction in AR levels is observed relative to a suitable control.

By way of specific example, in the Examples below, a series of DsiRNAs targeting AR were tested for the ability to reduce AR mRNA levels in human 22Rv1 or mouse LMTK- cells *in vitro*, at 1 nM concentrations in the environment of such cells and in the presence of a transfection agent (Lipofectamine™ RNAiMAX, Invitrogen). Within the below Examples, AR inhibitory activity was initially ascribed to those DsiRNAs that were observed to effect at least a 70% reduction of AR mRNA levels under the assayed conditions. It is contemplated that AR inhibitory activity could also be attributed to a dsRNA under either more or less stringent conditions than those employed for the Examples below, even when the same or a similar assay and conditions are employed. For example, in certain embodiments, a tested dsRNA of the invention is deemed to possess AR inhibitory activity if at least a 10% reduction, at least a 20% reduction, at least a 30% reduction, at least a 40% reduction, at least a 50% reduction, at least a 60% reduction, at least a 75% reduction, at least an 80% reduction, at least an 85% reduction, at least a 90% reduction, or at least a 95%

reduction in AR mRNA levels is observed in a mammalian cell line *in vitro* at 1 nM dsRNA concentration or lower in the environment of a cell, relative to a suitable control.

Use of other endpoints for determination of whether a double stranded RNA of the invention possesses AR inhibitory activity is also contemplated. Specfically, in one embodiment, in addition to or as an alternative to assessing AR mRNA levels, the ability of a tested dsRNA to reduce AR protein levels (*e.g.*, at 48 hours after contacting a mammalian cell *in vitro* or *in vivo*) is assessed, and a tested dsRNA is deemed to possess AR inhibitory activity if at least a 10% reduction, at least a 20% reduction, at least a 30% reduction, at least a 40% reduction, at least a 50% reduction, at least a 60% reduction, at least a 70% reduction, at least a 75% reduction, at least an 80% reduction, at least an 85% reduction, at least a 90% reduction, or at least a 95% reduction in AR protein levels is observed in a mammalian cell contacted with the assayed double stranded RNA *in vitro* or *in vivo*, relative to a suitable control. Additional endpoints contemplated include, *e.g.*, assessment of a phenotype associated with reduction of AR levels – *e.g.*, reduction of growth of a contacted mammalian cell line *in vitro* and/or reduction of growth of a tumor *in vivo*, including, *e.g.*, halting or reducing the growth of tumor or cancer cell levels as described in greater detail elsewhere herein.

AR inhibitory activity can also be evaluated over time (duration) and over concentration ranges (potency), with assessment of what constitutes a dsRNA possessing AR inhibitory activity adjusted in accordance with concentrations administered and duration of time following administration. Thus, in certain embodiments, a DsiRNA of the invention is deemed to possess AR inhibitory activity if at least a 50% reduction in AR activity is observed at a duration of time of 2 hours, 5 hours, 10 hours, 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 8 days, 9 days, 10 days or more after administration is observed/persists. In additional embodiments, a DsiRNA of the invention is deemed to be a potent AR inhibitory agent if AR inihibitory activity (*e.g.*, in certain embodiments, at least 50% inhibition of AR) is observed at a concentration of 1 nM or less, 500 pM or less, 200 pM or less, 100 pM or less, 50 pM or less, 20 pM or less, 10 pM or less, 5 pM or less, 2 pM or less or even 1 pM or less in the environment of a cell, for example, within an *in vitro* assay for AR inihibitory activity as described herein. In certain embodiments, a potent AR inhibitory dsRNA of the invention is defined as one that is capable of AR inihibitory

activity (*e.g.*, in certain embodiments, at least 20% reduction of AR levels) at a formulated concentration of 10 mg/kg or less when administered to a subject in an effective delivery vehicle (*e.g.*, an effective lipid nanoparticle formulation). Preferably, a potent AR inhibitory dsRNA of the invention is defined as one that is capable of AR inihibitory activity (*e.g.*, in certain embodiments, at least 50% reduction of AR levels) at a formulated concentration of 5 mg/kg or less when administered to a subject in an effective delivery vehicle. More preferably, a potent AR inhibitory dsRNA of the invention is defined as one that is capable of AR inihibitory activity (*e.g.*, in certain embodiments, at least 50% reduction of AR levels) at a formulated concentration of 5 mg/kg or less when administered to a subject in an effective delivery vehicle. Optionally, a potent AR inhibitory dsRNA of the invention is defined as one that is capable of AR inihibitory activity (*e.g.*, in certain embodiments, at least 50% reduction of AR levels) at a formulated concentration of 2 mg/kg or less, or even 1 mg/kg or less, when administered to a subject in an effective delivery vehicle.

In certain embodiments, potency of a dsRNA of the invention is determined in reference to the number of copies of a dsRNA present in the cytoplasm of a target cell that are required to achieve a certain level of target gene knockdown. For example, in certain embodiments, a potent dsRNA is one capable of causing 50% or greater knockdown of a target mRNA when present in the cytoplasm of a target cell at a copy number of 1000 or fewer RISC-loaded antisense strands per cell. More preferably, a potent dsRNA is one capable of producing 50% or greater knockdown of a target mRNA when present in the cytoplasm of a target cell at a copy number of 500 or fewer RISC-loaded antisense strands per cell. Optionally, a potent dsRNA is one capable of producing 50% or greater knockdown of a target mRNA when present in the cytoplasm of a target cell at a copy number of 300 or fewer RISC-loaded antisense strands per cell.

In further embodiments, the potency of a DsiRNA of the invention can be defined in reference to a 19 to 23mer dsRNA directed to the same target sequence within the same target gene. For example, a DsiRNA of the invention that possesses enhanced potency relative to a corresponding 19 to 23mer dsRNA can be a DsiRNA that reduces a target gene by an additional 5% or more, an additional 10% or more, an additional 20% or more, an additional 30% or more, an additional 40% or more, or an additional 50% or more as compared to a corresponding 19 to 23mer dsRNA, when

assayed in an in vitro assay as described herein at a sufficiently low concentration to allow for detection of a potency difference (e.g., transfection concentrations at or below 1 nM in the environment of a cell, at or below 100 pM in the environment of a cell, at or below 10 pM in the environment of a cell, at or below 1 nM in the environment of a cell, in an in vitro assay as described herein; notably, it is recognized that potency differences can be best detected via performance of such assays across a range of concentrations – e.g., 0.1 pM to 10 nM – for purpose of generating a dose-response curve and identifying an IC50 value associated with a DsiRNA/dsRNA).

AR inhibitory levels and/or AR levels may also be assessed indirectly, *e.g.*, measurement of a reduction in PSA levels or reduction of the size or number of polyps or tumors in a subject may be used to assess AR levels and/or AR inhibitory efficacy of a double-stranded nucleic acid of the instant invention.

In certain embodiments, the phrase "consists essentially of" is used in reference to the anti-AR dsRNAs of the invention. In some such embodiments, "consists essentially of" refers to a composition that comprises a dsRNA of the invention which possesse at least a certain level of AR inhibitory activity (*e.g.*, at least 50% AR inhibitory activity) and that also comprises one or more additional components and/or modifications that do not significantly impact the AR inhibitory activity of the dsRNA. For example, in certain embodiments, a composition "consists essentially of" a dsRNA of the invention where modifications of the dsRNA of the invention and/or dsRNA-associated components of the composition do not alter the AR inhibitory activity (optionally including potency or duration of AR inhibitory activity) by greater than 3%, greater than 5%, greater than 10%, greater than 15%, greater than 20%, greater than 25%, greater than 30%, greater than 35%, greater than 40%, greater than 45%, or greater than 50% relative to the dsRNA of the invention in isolation. In certain embodiments, a composition is deemed to consist essentially of a dsRNA of the invention even if more dramatic reduction of AR inhibitory activity (e.g., 80% reduction, 90% reduction, etc. in efficacy, duration and/or potency) occurs in the presence of additional components or modifications, yet where AR inhibitory activity is not significantly elevated (*e.g.*, observed levels of AR inhibitory activity are within 10% those observed for the isolated dsRNA of the invention) in the presence of additional components and/or modifications.

As used herein, the phrase "dsRNA reduces AR mRNA levels by at least X%

when assayed *in vitro* in a mammalian cell at an effective concentration in the environment of said cell of 1 nanomolar or less" refers to a requirement for the dsRNA to reduce the native AR mRNA levels of a HeLa cell population by at least X%, when assayed at a transfection concentration of 1 nanomolar or less in the presence of Lipofectamine™ RNAiMAX (Invitrogen) and following manufacturer's instructions. Such HeLa cells are obtained from ATCC and maintained in DMEM (HyClone) supplemented with 10% fetal bovine serum (HyClone) at 37°C under 5% CO_2. AR mRNA levels are then assayed at 24h or 48h post-transfection to assess % inhibition, with respect to an appropriate control as described elsewhere herein. In certain embodiments, the HeLa cells of such assays are replaced with HepG2, HCT116, HuH7 or other cell line.

As used herein, the term "nucleic acid" refers to deoxyribonucleotides, ribonucleotides, or modified nucleotides, and polymers thereof in single- or double-stranded form. The term encompasses nucleic acids containing known nucleotide analogs or modified backbone residues or linkages, which are synthetic, naturally occurring, and non-naturally occurring, which have similar binding properties as the reference nucleic acid, and which are metabolized in a manner similar to the reference nucleotides. Examples of such analogs include, without limitation, phosphorothioates, phosphoramidates, methyl phosphonates, chiral-methyl phosphonates, 2-O-methyl ribonucleotides, peptide-nucleic acids (PNAs).

As used herein, "nucleotide" is used as recognized in the art to include those with natural bases (standard), and modified bases well known in the art. Such bases are generally located at the 1' position of a nucleotide sugar moiety. Nucleotides generally comprise a base, sugar and a phosphate group. The nucleotides can be unmodified or modified at the sugar, phosphate and/or base moiety, (also referred to interchangeably as nucleotide analogs, modified nucleotides, non-natural nucleotides, non-standard nucleotides and other; see, e.g., Usman and McSwiggen, supra; Eckstein, et al., International PCT Publication No. WO 92/07065; Usman et al, International PCT Publication No. WO 93/15187; Uhlman & Peyman, supra, all are hereby incorporated by reference herein). There are several examples of modified nucleic acid bases known in the art as summarized by Limbach, et al, Nucleic Acids Res. 22:2183, 1994. Some of the non-limiting examples of base modifications that can be introduced into nucleic acid molecules include, hypoxanthine, purine, pyridin-4-one, pyridin-2-one, phenyl, pseudouracil, 2,4,6-trimethoxy benzene, 3-methyl

uracil, dihydrouridine, naphthyl, aminophenyl, 5-alkylcytidines (e.g., 5-methylcytidine), 5-alkyluridines (e.g., ribothymidine), 5-halouridine (e.g., 5-bromouridine) or 6-azapyrimidines or 6-alkylpyrimidines (e.g. 6-methyluridine), propyne, and others (Burgin, et al., Biochemistry 35:14090, 1996; Uhlman & Peyman, supra). By "modified bases" in this aspect is meant nucleotide bases other than adenine, guanine, cytosine and uracil at 1' position or their equivalents.

As used herein, “modified nucleotide” refers to a nucleotide that has one or more modifications to the nucleoside, the nucleobase, pentose ring, or phosphate group. For example, modified nucleotides exclude ribonucleotides containing adenosine monophosphate, guanosine monophosphate, uridine monophosphate, and cytidine monophosphate and deoxyribonucleotides containing deoxyadenosine monophosphate, deoxyguanosine monophosphate, deoxythymidine monophosphate, and deoxycytidine monophosphate. Modifications include those naturally occuring that result from modification by enzymes that modify nucleotides, such as methyltransferases. Modified nucleotides also include synthetic or non-naturally occurring nucleotides. Synthetic or non-naturally occurring modifications in nucleotides include those with 2’ modifications, e.g., 2'-methoxyethoxy, 2'-fluoro, 2'-allyl, 2'-O-[2-(methylamino)-2-oxoethyl], 4'-thio, 4'-CH_2-O-2'-bridge, 4'-$(CH_2)_2$-O-2'-bridge, 2'-LNA, and 2'-O-(N-methylcarbamate) or those comprising base analogs. In connection with 2'-modified nucleotides as described for the present disclosure, by "amino" is meant 2'-NH_2 or 2'-O-NH_2, which can be modified or unmodified. Such modified groups are described, *e.g.*, in Eckstein *et al.*, U.S. Pat. No. 5,672,695 and Matulic-Adamic *et al.*, U.S. Pat. No. 6,248,878.

In reference to the nucleic acid molecules of the present disclosure, modifications may exist upon these agents in patterns on one or both strands of the double stranded ribonucleic acid (dsRNA). As used herein, “alternating positions” refers to a pattern where every other nucleotide is a modified nucleotide or there is an unmodified nucleotide (*e.g.*, an unmodified ribonucleotide) between every modified nucleotide over a defined length of a strand of the dsRNA (*e.g.*, 5’-MNMNMN-3’; 3’-MNMNMN-5’; where M is a modified nucleotide and N is an unmodified nucleotide). The modification pattern starts from the first nucleotide position at either the 5’ or 3’ terminus according to a position numbering convention, e.g., as described herein (in certain embodiments, position 1 is designated in reference to the terminal residue of a strand following a projected Dicer cleavage event of a DsiRNA agent of

the invention; thus, position 1 does not always constitute a 3' terminal or 5' terminal residue of a pre-processed agent of the invention). The pattern of modified nucleotides at alternating positions may run the full length of the strand, but in certain embodiments includes at least 4, 6, 8, 10, 12, 14 nucleotides containing at least 2, 3, 4, 5, 6 or 7 modified nucleotides, respectively. As used herein, "alternating pairs of positions" refers to a pattern where two consecutive modified nucleotides are separated by two consecutive unmodified nucleotides over a defined length of a strand of the dsRNA (e.g., 5'-MMNNMMNNMMNN-3'; 3'-MMNNMMNNMMNN-5'; where M is a modified nucleotide and N is an unmodified nucleotide). The modification pattern starts from the first nucleotide position at either the 5' or 3' terminus according to a position numbering convention such as those described herein. The pattern of modified nucleotides at alternating positions may run the full length of the strand, but preferably includes at least 8, 12, 16, 20, 24, 28 nucleotides containing at least 4, 6, 8, 10, 12 or 14 modified nucleotides, respectively. It is emphasized that the above modification patterns are exemplary and are not intended as limitations on the scope of the invention.

As used herein, "base analog" refers to a heterocyclic moiety which is located at the 1' position of a nucleotide sugar moiety in a modified nucleotide that can be incorporated into a nucleic acid duplex (or the equivalent position in a nucleotide sugar moiety substitution that can be incorporated into a nucleic acid duplex). In the dsRNAs of the invention, a base analog is generally either a purine or pyrimidine base excluding the common bases guanine (G), cytosine (C), adenine (A), thymine (T), and uracil (U). Base analogs can duplex with other bases or base analogs in dsRNAs. Base analogs include those useful in the compounds and methods of the invention., e.g., those disclosed in US Pat. Nos. 5,432,272 and 6,001,983 to Benner and US Patent Publication No. 20080213891 to Manoharan, which are herein incorporated by reference. Non-limiting examples of bases include hypoxanthine (I), xanthine (X), 3β-D-ribofuranosyl-(2,6-diaminopyrimidine) (K), 3-β-D-ribofuranosyl-(1-methyl-pyrazolo[4,3-d]pyrimidine-5,7(4H,6H)-dione) (P), iso-cytosine (iso-C), iso-guanine (iso-G), 1-β-D-ribofuranosyl-(5-nitroindole), 1-β-D-ribofuranosyl-(3-nitropyrrole), 5-bromouracil, 2-aminopurine, 4-thio-dT, 7-(2-thienyl)-imidazo[4,5-b]pyridine (Ds) and pyrrole-2-carbaldehyde (Pa), 2-amino-6-(2-thienyl)purine (S), 2-oxopyridine (Y), difluorotolyl, 4-fluoro-6-methylbenzimidazole, 4-methylbenzimidazole, 3-methyl isocarbostyrilyl, 5-methyl isocarbostyrilyl, and 3-methyl-7-propynyl isocarbostyrilyl,

7-azaindolyl, 6-methyl-7-azaindolyl, imidizopyridinyl, 9-methyl-imidizopyridinyl, pyrrolopyrizinyl, isocarbostyrilyl, 7-propynyl isocarbostyrilyl, propynyl-7-azaindolyl, 2,4,5-trimethylphenyl, 4-methylindolyl, 4,6-dimethylindolyl, phenyl, napthalenyl, anthracenyl, phenanthracenyl, pyrenyl, stilbenzyl, tetracenyl, pentacenyl, and structural derivates thereof (Schweitzer et al., J. Org. Chem., 59:7238-7242 (1994); Berger et al., Nucleic Acids Research, 28(15):2911-2914 (2000); Moran et al., J. Am. Chem. Soc., 119:2056-2057 (1997); Morales et al., J. Am. Chem. Soc., 121:2323-2324 (1999); Guckian et al., J. Am. Chem. Soc., 118:8182-8183 (1996); Morales et al., J. Am. Chem. Soc., 122(6):1001-1007 (2000); McMinn et al., J. Am. Chem. Soc., 121:11585-11586 (1999); Guckian et al., J. Org. Chem., 63:9652-9656 (1998); Moran et al., Proc. Natl. Acad. Sci., 94:10506-10511 (1997); Das et al., J. Chem. Soc., Perkin Trans., 1:197-206 (2002); Shibata et al., J. Chem. Soc., Perkin Trans., 1: 1605-1611 (2001); Wu et al., J. Am. Chem. Soc., 122(32):7621-7632 (2000); O'Neill et al., J. Org. Chem., 67:5869-5875 (2002); Chaudhuri et al., J. Am. Chem. Soc., 117:10434-10442 (1995); and U.S. Pat. No. 6,218,108.). Base analogs may also be a universal base.

As used herein, "universal base" refers to a heterocyclic moiety located at the 1' position of a nucleotide sugar moiety in a modified nucleotide, or the equivalent position in a nucleotide sugar moiety substitution, that, when present in a nucleic acid duplex, can be positioned opposite more than one type of base without altering the double helical structure (e.g., the structure of the phosphate backbone). Additionally, the universal base does not destroy the ability of the single stranded nucleic acid in which it resides to duplex to a target nucleic acid. The ability of a single stranded nucleic acid containing a universal base to duplex a target nucleic can be assayed by methods apparent to one in the art (*e.g.*, UV absorbance, circular dichroism, gel shift, single stranded nuclease sensitivity, etc.). Additionally, conditions under which duplex formation is observed may be varied to determine duplex stability or formation, *e.g.*, temperature, as melting temperature (Tm) correlates with the stability of nucleic acid duplexes. Compared to a reference single stranded nucleic acid that is exactly complementary to a target nucleic acid, the single stranded nucleic acid containing a universal base forms a duplex with the target nucleic acid that has a lower Tm than a duplex formed with the complementary nucleic acid. However, compared to a reference single stranded nucleic acid in which the universal base has been replaced with a base to generate a single mismatch, the single stranded nucleic

acid containing the universal base forms a duplex with the target nucleic acid that has a higher Tm than a duplex formed with the nucleic acid having the mismatched base.

Some universal bases are capable of base pairing by forming hydrogen bonds between the universal base and all of the bases guanine (G), cytosine (C), adenine (A), thymine (T), and uracil (U) under base pair forming conditions. A universal base is not a base that forms a base pair with only one single complementary base. In a duplex, a universal base may form no hydrogen bonds, one hydrogen bond, or more than one hydrogen bond with each of G, C, A, T, and U opposite to it on the opposite strand of a duplex. Preferably, the universal bases does not interact with the base opposite to it on the opposite strand of a duplex. In a duplex, base pairing between a universal base occurs without altering the double helical structure of the phosphate backbone. A universal base may also interact with bases in adjacent nucleotides on the same nucleic acid strand by stacking interactions. Such stacking interactions stabilize the duplex, especially in situations where the universal base does not form any hydrogen bonds with the base positioned opposite to it on the opposite strand of the duplex. Non-limiting examples of universal-binding nucleotides include inosine, 1-β-D-ribofuranosyl-5-nitroindole, and/or 1-β-D-ribofuranosyl-3-nitropyrrole (US Pat. Appl. Publ. No. 20070254362 to Quay et al.; Van Aerschot et al., An acyclic 5-nitroindazole nucleoside analogue as ambiguous nucleoside. Nucleic Acids Res. 1995 Nov 11;23(21):4363-70; Loakes et al., 3-Nitropyrrole and 5-nitroindole as universal bases in primers for DNA sequencing and PCR. Nucleic Acids Res. 1995 Jul 11;23(13):2361-6; Loakes and Brown, 5-Nitroindole as an universal base analogue. Nucleic Acids Res. 1994 Oct 11;22(20):4039-43).

As used herein, "loop" refers to a structure formed by a single strand of a nucleic acid, in which complementary regions that flank a particular single stranded nucleotide region hybridize in a way that the single stranded nucleotide region between the complementary regions is excluded from duplex formation or Watson-Crick base pairing. A loop is a single stranded nucleotide region of any length. Examples of loops include the unpaired nucleotides present in such structures as hairpins, stem loops, or extended loops.

As used herein, "extended loop" in the context of a dsRNA refers to a single stranded loop and in addition 1, 2, 3, 4, 5, 6 or up to 20 base pairs or duplexes flanking the loop. In an extended loop, nucleotides that flank the loop on the 5' side form a duplex with nucleotides that flank the loop on the 3' side. An extended loop

may form a hairpin or stem loop.

As used herein, "tetraloop" in the context of a dsRNA refers to a loop (a single stranded region) consisting of four nucleotides that forms a stable secondary structure that contributes to the stability of an adjacent Watson-Crick hybridized nucleotides. Without being limited to theory, a tetraloop may stabilize an adjacent Watson-Crick base pair by stacking interactions. In addition, interactions among the four nucleotides in a tetraloop include but are not limited to non-Watson-Crick base pairing, stacking interactions, hydrogen bonding, and contact interactions (Cheong *et al.*, *Nature* 1990 Aug 16;346(6285):680-2; Heus and Pardi, *Science* 1991 Jul 12;253(5016):191-4). A tetraloop confers an increase in the melting temperature (Tm) of an adjacent duplex that is higher than expected from a simple model loop sequence consisting of four random bases. For example, a tetraloop can confer a melting temperature of at least 55°C in 10mM $NaHPO_4$ to a hairpin comprising a duplex of at least 2 base pairs in length. A tetraloop may contain ribonucleotides, deoxyribonucleotides, modified nucleotides, and combinations thereof. Examples of RNA tetraloops include the UNCG family of tetraloops (e.g., UUCG), the GNRA family of tetraloops (e.g., GAAA), and the CUUG tetraloop. (Woese et al., Proc Natl Acad Sci U S A. 1990 Nov;87(21):8467-71; Antao et al., Nucleic Acids Res. 1991 Nov 11;19(21):5901-5). Examples of DNA tetraloops include the d(GNNA) family of tetraloops (e.g., d(GTTA), the d(GNRA)) family of tetraloops, the d(GNAB) family of tetraloops, the d(CNNG) family of tetraloops, the d(TNCG) family of tetraloops (e.g., d(TTCG)). (Nakano et al. Biochemistry, 41 (48), 14281 -14292, 2002.; SHINJI et al. Nippon Kagakkai Koen Yokoshu VOL.78th; NO.2; PAGE.731 (2000).)

As used herein, the term "siRNA" refers to a double stranded nucleic acid in which each strand comprises RNA, RNA analog(s) or RNA and DNA. The siRNA comprises between 19 and 23 nucleotides or comprises 21 nucleotides. The siRNA typically has 2 bp overhangs on the 3' ends of each strand such that the duplex region in the siRNA comprises 17-21 nucleotides, or 19 nucleotides. Typically, the antisense strand of the siRNA is sufficiently complementary with the target sequence of the AR gene/RNA.

An anti-AR DsiRNA of the instant invention possesses strand lengths of at least 25 nucleotides. Accordingly, in certain embodiments, an anti-AR DsiRNA contains one oligonucleotide sequence, a first sequence, that is at least 25 nucleotides

in length and no longer than 35 or up to 50 or more nucleotides. This sequence of RNA can be between 26 and 35, 26 and 34, 26 and 33, 26 and 32, 26 and 31, 26 and 30, and 26 and 29 nucleotides in length. This sequence can be 27 or 28 nucleotides in length or 27 nucleotides in length. The second sequence of the DsiRNA agent can be a sequence that anneals to the first sequence under biological conditions, such as within the cytoplasm of a eukaryotic cell. Generally, the second oligonucleotide sequence will have at least 19 complementary base pairs with the first oligonucleotide sequence, more typically the second oligonucleotide sequence will have 21 or more complementary base pairs, or 25 or more complementary base pairs with the first oligonucleotide sequence. In one embodiment, the second sequence is the same length as the first sequence, and the DsiRNA agent is blunt ended. In another embodiment, the ends of the DsiRNA agent have one or more overhangs.

In certain embodiments, the first and second oligonucleotide sequences of the DsiRNA agent exist on separate oligonucleotide strands that can be and typically are chemically synthesized. In some embodiments, both strands are between 26 and 35 nucleotides in length. In other embodiments, both strands are between 25 and 30 or 26 and 30 nucleotides in length. In one embodiment, both strands are 27 nucleotides in length, are completely complementary and have blunt ends. In certain embodiments of the instant invention, the first and second sequences of an anti-AR DsiRNA exist on separate RNA oligonucleotides (strands). In one embodiment, one or both oligonucleotide strands are capable of serving as a substrate for Dicer. In other embodiments, at least one modification is present that promotes Dicer to bind to the double-stranded RNA structure in an orientation that maximizes the double-stranded RNA structure's effectiveness in inhibiting gene expression. In certain embodiments of the instant invention, the anti-AR DsiRNA agent is comprised of two oligonucleotide strands of differing lengths, with the anti-AR DsiRNA possessing a blunt end at the 3' terminus of a first strand (sense strand) and a 3' overhang at the 3' terminus of a second strand (antisense strand). The DsiRNA can also contain one or more deoxyribonucleic acid (DNA) base substitutions.

Suitable DsiRNA compositions that contain two separate oligonucleotides can be chemically linked outside their annealing region by chemical linking groups. Many suitable chemical linking groups are known in the art and can be used. Suitable groups will not block Dicer activity on the DsiRNA and will not interfere with the directed destruction of the RNA transcribed from the target gene. Alternatively, the

two separate oligonucleotides can be linked by a third oligonucleotide such that a hairpin structure is produced upon annealing of the two oligonucleotides making up the DsiRNA composition. The hairpin structure will not block Dicer activity on the DsiRNA and will not interfere with the directed destruction of the target RNA.

As used herein, a dsRNA, *e.g.*, DsiRNA or siRNA, having a sequence "sufficiently complementary" to a target RNA or cDNA sequence (*e.g.*, AR mRNA) means that the dsRNA has a sequence sufficient to trigger the destruction of the target RNA (where a cDNA sequence is recited, the RNA sequence corresponding to the recited cDNA sequence) by the RNAi machinery (*e.g.*, the RISC complex) or process. The dsRNA molecule can be designed such that every residue of the antisense strand is complementary to a residue in the target molecule. Alternatively, substitutions can be made within the molecule to increase stability and/or enhance processing activity of said molecule. Substitutions can be made within the strand or can be made to residues at the ends of the strand. In certain embodiments, substitutions and/or modifications are made at specific residues within a DsiRNA agent. Such substitutions and/or modifications can include, *e.g.*, deoxy- modifications at one or more residues of positions 1, 2 and 3 when numbering from the 3' terminal position of the sense strand of a DsiRNA agent; and introduction of 2'-O-alkyl (e.g., 2'-O-methyl) modifications at the 3' terminal residue of the antisense strand of DsiRNA agents, with such modifications also being performed at overhang positions of the 3' portion of the antisense strand and at alternating residues of the antisense strand of the DsiRNA that are included within the region of a DsiRNA agent that is processed to form an active siRNA agent. The preceding modifications are offered as exemplary, and are not intended to be limiting in any manner. Further consideration of the structure of preferred DsiRNA agents, including further description of the modifications and substitutions that can be performed upon the anti-AR DsiRNA agents of the instant invention, can be found below.

As used herein, a dsRNA, *e.g.*, DsiRNA or siRNA, having a sequence "sufficiently complementary" to a target RNA or cDNA sequence (*e.g.*, AR mRNA) means that the dsRNA has a sequence sufficient to trigger the destruction of the target RNA (where a cDNA sequence is recited, the RNA sequence corresponding to the recited cDNA sequence) by the RNAi machinery (*e.g.*, the RISC complex) or process. For example, a dsRNA that is "sufficiently complementary" to a target RNA or cDNA sequence to trigger the destruction of the target RNA by the RNAi machinery or

process can be identified as a dsRNA that causes a detectable reduction in the level of the target RNA in an appropriate assay of dsRNA activity (*e.g.*, an *in vitro* assay as described in Example 2 below), or, in further examples, a dsRNA that is sufficiently complementary to a target RNA or cDNA sequence to trigger the destruction of the target RNA by the RNAi machinery or process can be identified as a dsRNA that produces at least a 5%, at least a 10%, at least a 15%, at least a 20%, at least a 25%, at least a 30%, at least a 35%, at least a 40%, at least a 45%, at least a 50%, at least a 55%, at least a 60%, at least a 65%, at least a 70%, at least a 75%, at least a 80%, at least a 85%, at least a 90%, at least a 95%, at least a 98% or at least a 99% reduction in the level of the target RNA in an appropriate assay of dsRNA activity. In additional examples, a dsRNA that is sufficiently complementary to a target RNA or cDNA sequence to trigger the destruction of the target RNA by the RNAi machinery or process can be identified based upon assessment of the duration of a certain level of inhibitory activity with respect to the target RNA or protein levels in a cell or organism. For example, a dsRNA that is sufficiently complementary to a target RNA or cDNA sequence to trigger the destruction of the target RNA by the RNAi machinery or process can be identified as a dsRNA capable of reducing target mRNA levels by at least 20% at least 48 hours post-administration of said dsRNA to a cell or organism. Preferably, a dsRNA that is sufficiently complementary to a target RNA or cDNA sequence to trigger the destruction of the target RNA by the RNAi machinery or process is identified as a dsRNA capable of reducing target mRNA levels by at least 40% at least 72 hours post-administration of said dsRNA to a cell or organism, by at least 40% at least four, five or seven days post-administration of said dsRNA to a cell or organism, by at least 50% at least 48 hours post-administration of said dsRNA to a cell or organism, by at least 50% at least 72 hours post-administration of said dsRNA to a cell or organism, by at least 50% at least four, five or seven days post-administration of said dsRNA to a cell or organism, by at least 80% at least 48 hours post-administration of said dsRNA to a cell or organism, by at least 80% at least 72 hours post-administration of said dsRNA to a cell or organism, or by at least 80% at least four, five or seven days post-administration of said dsRNA to a cell or organism.

The dsRNA molecule can be designed such that every residue of the antisense strand is complementary to a residue in the target molecule. Alternatively, substitutions can be made within the molecule to increase stability and/or enhance

processing activity of said molecule. Substitutions can be made within the strand or can be made to residues at the ends of the strand. In certain embodiments, substitutions and/or modifications are made at specific residues within a DsiRNA agent. Such substitutions and/or modifications can include, *e.g.*, deoxy- modifications at one or more residues of positions 1, 2 and 3 when numbering from the 3' terminal position of the sense strand of a DsiRNA agent; and introduction of 2'-O-alkyl (e.g., 2'-O-methyl) modifications at the 3' terminal residue of the antisense strand of DsiRNA agents, with such modifications also being performed at overhang positions of the 3' portion of the antisense strand and at alternating residues of the antisense strand of the DsiRNA that are included within the region of a DsiRNA agent that is processed to form an active siRNA agent. The preceding modifications are offered as exemplary, and are not intended to be limiting in any manner. Further consideration of the structure of preferred DsiRNA agents, including further description of the modifications and substitutions that can be performed upon the anti-AR DsiRNA agents of the instant invention, can be found below.

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 may form one or more, but generally not more than 4, 3 or 2 mismatched base pairs upon hybridization, while retaining the ability to hybridize under the conditions most relevant to their ultimate application. 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, may yet be referred to as "fully complementary" for the purposes of the invention.

The term "double-stranded RNA" or "dsRNA", as used herein, refers to a complex of ribonucleic acid molecules, having a duplex structure comprising two anti-parallel and substantially complementary, as defined above, nucleic acid strands. The two strands forming the duplex structure may be different portions of one larger RNA molecule, or they may be separate RNA molecules. Where separate RNA molecules, such dsRNA are often referred to as siRNA ("short interfering RNA") or DsiRNA ("Dicer substrate siRNAs"). 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", "short hairpin RNA" or "shRNA". Where the two strands are connected covalently by means other than 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 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, a dsRNA may comprise one or more nucleotide overhangs. In addition, as used herein, "dsRNA" may include chemical modifications to ribonucleotides, internucleoside linkages, end-groups, caps, and conjugated moieties, including substantial modifications at multiple nucleotides and including all types of modifications disclosed herein or known in the art. Any such modifications, as used in an siRNA- or DsiRNA-type molecule, are encompassed by "dsRNA" for the purposes of this specification and claims.

The phrase "duplex region" refers to the region in two complementary or substantially complementary oligonucleotides that form base pairs with one another, either by Watson-Crick base pairing or other manner that allows for a duplex between oligonucleotide strands that are complementary or substantially complementary. For example, an oligonucleotide strand having 21 nucleotide units can base pair with another oligonucleotide of 21 nucleotide units, yet only 19 bases on each strand are complementary or substantially complementary, such that the "duplex region" consists of 19 base pairs. The remaining base pairs may, for example, exist as 5' and 3' overhangs. Further, within the duplex region, 100% complementarity is not required; substantial complementarity is allowable within a duplex region. Substantial complementarity refers to complementarity between the strands such that they are capable of annealing under biological conditions. Techniques to empirically determine if two strands are capable of annealing under biological conditions are well know in the art. Alternatively, two strands can be synthesized and added together under biological conditions to determine if they anneal to one another.

Single-stranded nucleic acids that base pair over a number of bases are said to “hybridize.” Hybridization is typically determined under physiological or biologically relevant conditions (e.g., intracellular: pH 7.2, 140 mM potassium ion;

extracellular pH 7.4, 145 mM sodium ion). Hybridization conditions generally contain a monovalent cation and biologically acceptable buffer and may or may not contain a divalent cation, complex anions, e.g. gluconate from potassium gluconate, uncharged species such as sucrose, and inert polymers to reduce the activity of water in the sample, *e.g.* PEG. Such conditions include conditions under which base pairs can form.

Hybridization is measured by the temperature required to dissociate single stranded nucleic acids forming a duplex, *i.e.*, (the melting temperature; Tm). Hybridization conditions are also conditions under which base pairs can form. Various conditions of stringency can be used to determine hybridization (see, e.g., Wahl, G. M. and S. L. Berger (1987) Methods Enzymol. 152:399; Kimmel, A. R. (1987) Methods Enzymol. 152:507). Stringent temperature conditions will ordinarily include temperatures of at least about 30° C, more preferably of at least about 37° C, and most preferably of at least about 42° C. The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (Tm) of the hybrid, where Tm is determined according to the following equations. For hybrids less than 18 base pairs in length, Tm(°C)=2(# of A+T bases)+4(# of G+C bases). For hybrids between 18 and 49 base pairs in length, Tm(°C)=81.5+16.6(log 10[Na+])+0.41 (% G+C)-(600/N), where N is the number of bases in the hybrid, and [Na+] is the concentration of sodium ions in the hybridization buffer ([Na+] for 1xSSC=0.165 M). For example, a hybridization determination buffer is shown in Table 1.

Table 1.

	final conc.	Vender	Cat#	Lot#	m.w./Stock	To make 50 mL solution
NaCl	100 mM	Sigma	S-5150	41K8934	5M	1 mL
KCl	80 mM	Sigma	P-9541	70K0002	74.55	0.298 g
$MgCl_2$	8 mM	Sigma	M-1028	120K8933	1M	0.4 mL
sucrose	2% w/v	Fisher	BP220-212	907105	342.3	1 g
Tris-HCl	16 mM	Fisher	BP1757-500	12419	1M	0.8 mL
NaH_2PO_4	1 mM	Sigma	S-3193	52H-029515	120.0	0.006 g
EDTA	0.02 mM	Sigma	E-7889	110K89271	0.5M	2 µL
H_2O		Sigma	W-4502	51K2359		to 50 mL
pH = 7.0 at 20°C	adjust with HCl					

Useful variations on hybridization conditions will be readily apparent to those

skilled in the art. Hybridization techniques are well known to those skilled in the art and are described, for example, in Benton and Davis (Science 196:180, 1977); Grunstein and Hogness (Proc. Natl. Acad. Sci., USA 72:3961, 1975); Ausubel et al. (Current Protocols in Molecular Biology, Wiley Interscience, New York, 2001); Berger and Kimmel (Antisense to Molecular Cloning Techniques, 1987, Academic Press, New York); and Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, New York.

As used herein, "oligonucleotide strand" is a single stranded nucleic acid molecule. An oligonucleotide may comprise ribonucleotides, deoxyribonucleotides, modified nucleotides (*e.g.*, nucleotides with 2' modifications, synthetic base analogs, etc.) or combinations thereof. Such modified oligonucleotides can be preferred over native forms because of properties such as, for example, enhanced cellular uptake and increased stability in the presence of nucleases.

As used herein, the term "ribonucleotide" encompasses natural and synthetic, unmodified and modified ribonucleotides. Modifications include changes to the sugar moiety, to the base moiety and/or to the linkages between ribonucleotides in the oligonucleotide. As used herein, the term "ribonucleotide" specifically excludes a deoxyribonucleotide, which is a nucleotide possessing a single proton group at the 2' ribose ring position.

As used herein, the term "deoxyribonucleotide" encompasses natural and synthetic, unmodified and modified deoxyribonucleotides. Modifications include changes to the sugar moiety, to the base moiety and/or to the linkages between deoxyribonucleotide in the oligonucleotide. As used herein, the term "deoxyribonucleotide" also includes a modified ribonucleotide that does not permit Dicer cleavage of a dsRNA agent, *e.g.*, a 2'-O-methyl ribonucleotide, a phosphorothioate-modified ribonucleotide residue, etc., that does not permit Dicer cleavage to occur at a bond of such a residue.

As used herein, the term "PS-NA" refers to a phosphorothioate-modified nucleotide residue. The term "PS-NA" therefore encompasses both phosphorothioate-modified ribonucleotides ("PS-RNAs") and phosphorothioate-modified deoxyribonucleotides ("PS-DNAs").

As used herein, "Dicer" refers to an endoribonuclease in the RNase III family that cleaves a dsRNA or dsRNA-containing molecule, *e.g.*, double-stranded RNA (dsRNA) or pre-microRNA (miRNA), into double-stranded nucleic acid fragments

19-25 nucleotides long, usually with a two-base overhang on the 3' end. With respect to the dsRNAs of the invention, the duplex formed by a dsRNA region of an agent of the invention is recognized by Dicer and is a Dicer substrate on at least one strand of the duplex. Dicer catalyzes the first step in the RNA interference pathway, which consequently results in the degradation of a target RNA. The protein sequence of human Dicer is provided at the NCBI database under accession number NP_085124, hereby incorporated by reference.

Dicer "cleavage" is determined as follows (*e.g.*, see Collingwood *et al.*, Oligonucleotides 18:187–200 (2008)). In a Dicer cleavage assay, RNA duplexes (100 pmol) are incubated in 20 μL of 20 mM Tris pH 8.0, 200 mM NaCl, 2.5 mM MgCl2 with or without 1 unit of recombinant human Dicer (Stratagene, La Jolla, CA) at 37°C for 18–24 hours. Samples are desalted using a Performa SR 96-well plate (Edge Biosystems, Gaithersburg, MD). Electrospray-ionization liquid chromatography mass spectroscopy (ESI-LCMS) of duplex RNAs pre- and post-treatment with Dicer is done using an Oligo HTCS system (Novatia, Princeton, NJ; Hail et al., 2004), which consists of a ThermoFinnigan TSQ7000, Xcalibur data system, ProMass data processing software and Paradigm MS4 HPLC (Michrom BioResources, Auburn, CA). In this assay, Dicer cleavage occurs where at least 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, or even 100% of the Dicer substrate dsRNA, (i.e., 25-30 bp, dsRNA, preferably 26-30 bp dsRNA) is cleaved to a shorter dsRNA (e.g., 19-23 bp dsRNA, preferably, 21-23 bp dsRNA).

As used herein, "Dicer cleavage site" refers to the sites at which Dicer cleaves a dsRNA (*e.g.*, the dsRNA region of a DsiRNA agent of the invention). Dicer contains two RNase III domains which typically cleave both the sense and antisense strands of a dsRNA. The average distance between the RNase III domains and the PAZ domain determines the length of the short double-stranded nucleic acid fragments it produces and this distance can vary (Macrae *et al.* (2006) *Science* 311: 195–8). As shown in Figure 1, Dicer is projected to cleave certain double-stranded ribonucleic acids of the instant invention that possess an antisense strand having a 2 nucleotide 3' overhang at a site between the 21st and 22nd nucleotides removed from the 3' terminus of the antisense strand, and at a corresponding site between the 21st and 22nd nucleotides removed from the 5' terminus of the sense strand. The projected and/or prevalent Dicer cleavage site(s) for dsRNA molecules distinct from those depicted in Figure 1 may be similarly identified *via* art-recognized methods, including

those described in Macrae *et al.* While the Dicer cleavage events depicted in Figure 1 generate 21 nucleotide siRNAs, it is noted that Dicer cleavage of a dsRNA (*e.g.*, DsiRNA) can result in generation of Dicer-processed siRNA lengths of 19 to 23 nucleotides in length. Indeed, in certain embodiments, a double-stranded DNA region may be included within a dsRNA for purpose of directing prevalent Dicer excision of a typically non-preferred 19mer or 20mer siRNA, rather than a 21mer.

As used herein, "overhang" refers to unpaired nucleotides, in the context of a duplex having one or more free ends at the 5' terminus or 3' terminus of a dsRNA. In certain embodiments, the overhang is a 3' or 5' overhang on the antisense strand or sense strand. In some embodiments, the overhang is a 3' overhang having a length of between one and six nucleotides, optionally one to five, one to four, one to three, one to two, two to six, two to five, two to four, two to three, three to six, three to five, three to four, four to six, four to five, five to six nucleotides, or one, two, three, four, five or six nucleotides.

A dsRNA of the invention comprises two RNA strands that are sufficiently complementary to hybridize to form a duplex structure. One strand of the dsRNA (the antisense strand) comprises a region of complementarity that is substantially complementary, and generally fully complementary, to a target sequence, derived from the sequence of an mRNA formed during the expression of the AR target gene, the other strand (the sense strand) comprises a region which is complementary to the antisense strand, such that the two strands hybridize and form a duplex structure when combined under suitable conditions. Generally, the duplex structure is between 15 and 35, optionally between 25 and 30, between 26 and 30, between 18 and 25, between 19 and 24, or between 19 and 21 base pairs in length. Similarly, the region of complementarity to the target sequence is between 15 and 35, optionally between 18 and 30, between 25 and 30, between 19 and 24, or between 19 and 21 nucleotides in length. The dsRNA of the invention may further comprise one or more single-stranded nucleotide overhang(s). It has been identified that dsRNAs comprising duplex structures of between 15 and 35 base pairs in length can be effective in inducing RNA interference, including DsiRNAs (generally of at least 25 base pairs in length) and siRNAs (in certain embodiments, duplex structures of siRNAs are between 20 and 23, and optionally, specifically 21 base pairs (Elbashir *et al.*, *EMBO* 20: 6877-6888)). It has also been identified that dsRNAs possessing duplexes shorter than 20 base pairs can be effective as well (*e.g.*, 15, 16, 17, 18 or 19 base pair

duplexes). In certain embodiments, the dsRNAs of the invention can comprise at least one strand of a length of 19 nucleotides or more. In certain embodiments, it can be reasonably expected that shorter dsRNAs comprising a sequence complementary to one of the sequences of Table 10 below, minus only a few nucleotides on one or both ends may be similarly effective as compared to the dsRNAs described above and in Tables 2-5 and 7-10. Hence, dsRNAs comprising a partial sequence of at least 15, 16, 17, 18, 19, 20, or more contiguous nucleotides sufficiently complementary to one of the sequences of Table 10, and differing in their ability to inhibit the expression of the AR target gene in an assay as described herein by not more than 5, 10, 15, 20, 25, or 30% inhibition from a dsRNA comprising the full sequence, are contemplated by the invention. In one embodiment, at least one end of the dsRNA has a single-stranded nucleotide overhang of 1 to 5, optionally 1 to 4, in certain embodiments, 1 or 2 nucleotides. Certain dsRNA structures having at least one nucleotide overhang possess superior inhibitory properties as compared to counterparts possessing base-paired blunt ends at both ends of the dsRNA molecule.

As used herein, the term "RNA processing" refers to processing activities performed by components of the siRNA, miRNA or RNase H pathways (*e.g.*, Drosha, Dicer, Argonaute2 or other RISC endoribonucleases, and RNaseH), which are described in greater detail below (see "RNA Processing" section below). The term is explicitly distinguished from the post-transcriptional processes of 5' capping of RNA and degradation of RNA *via* non-RISC- or non-RNase H-mediated processes. Such "degradation" of an RNA can take several forms, *e.g.* deadenylation (removal of a 3' poly(A) tail), and/or nuclease digestion of part or all of the body of the RNA by one or more of several endo- or exo-nucleases (*e.g.*, RNase III, RNase P, RNase T1, RNase A (1, 2, 3, 4/5), oligonucleotidase, etc.).

By "homologous sequence" is meant, a nucleotide sequence that is shared by one or more polynucleotide sequences, such as genes, gene transcripts and/or non-coding polynucleotides. For example, a homologous sequence can be a nucleotide sequence that is shared by two or more genes encoding related but different proteins, such as different members of a gene family, different protein epitopes, different protein isoforms or completely divergent genes, such as a cytokine and its corresponding receptors. A homologous sequence can be a nucleotide sequence that is shared by two or more non-coding polynucleotides, such as noncoding DNA or RNA, regulatory sequences, introns, and sites of transcriptional control or regulation.

Homologous sequences can also include conserved sequence regions shared by more than one polynucleotide sequence. Homology does not need to be perfect homology (e.g., 100%), as partially homologous sequences are also contemplated by the instant invention (e.g., 99%, 98%, 97%, 96%, 95%, 94%, 93%, 92%, 91%, 90%, 89%, 88%, 87%, 86%, 85%, 84%, 83%, 82%, 81%, 80% etc.). Indeed, design and use of the DsiRNA agents of the instant invention contemplates the possibility of using such DsiRNA agents not only against target RNAs of AR possessing perfect complementarity with the presently described DsiRNA agents, but also against target AR RNAs possessing sequences that are, *e.g.*, only 99%, 98%, 97%, 96%, 95%, 94%, 93%, 92%, 91%, 90%, 89%, 88%, 87%, 86%, 85%, 84%, 83%, 82%, 81%, 80% etc. complementary to said DsiRNA agents. Similarly, it is contemplated that the presently described DsiRNA agents of the instant invention might be readily altered by the skilled artisan to enhance the extent of complementarity between said DsiRNA agents and a target AR RNA, *e.g.*, of a specific allelic variant of AR (*e.g.*, an allele of enhanced therapeutic interest). Indeed, DsiRNA agent sequences with insertions, deletions, and single point mutations relative to the target AR sequence can also be effective for inhibition. Alternatively, DsiRNA agent sequences with nucleotide analog substitutions or insertions can be effective for inhibition.

Sequence identity may be determined by sequence comparison and alignment algorithms known in the art. To determine the percent identity of two nucleic acid sequences (or of two amino acid sequences), the sequences are aligned for comparison purposes (*e.g.*, gaps can be introduced in the first sequence or second sequence for optimal alignment). The nucleotides (or amino acid residues) at corresponding nucleotide (or amino acid) positions are then compared. When a position in the first sequence is occupied by the same residue as the corresponding position in the second sequence, then the molecules are identical at that position. The percent identity between the two sequences is a function of the number of identical positions shared by the sequences (i.e., % homology=# of identical positions/total # of positions.times.100), optionally penalizing the score for the number of gaps introduced and/or length of gaps introduced.

The comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm. In one embodiment, the alignment generated over a certain portion of the sequence aligned having sufficient identity but not over portions having low degree of identity (i.e., a

local alignment). A preferred, non-limiting example of a local alignment algorithm utilized for the comparison of sequences is the algorithm of Karlin and Altschul (1990) Proc. Natl. Acad. Sci. USA 87:2264-68, modified as in Karlin and Altschul (1993) Proc. Natl. Acad. Sci. USA 90:5873-77. Such an algorithm is incorporated into the BLAST programs (version 2.0) of Altschul, et al. (1990) J. Mol. Biol. 215:403-10.

In another embodiment, a gapped alignment the alignment is optimized is formed by introducing appropriate gaps, and percent identity is determined over the length of the aligned sequences (i.e., a gapped alignment). To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al., (1997) Nucleic Acids Res. 25(17):3389-3402. In another embodiment, a global alignment the alignment is optimizedis formed by introducing appropriate gaps, and percent identity is determined over the entire length of the sequences aligned. (i.e., a global alignment). A preferred, non-limiting example of a mathematical algorithm utilized for the global comparison of sequences is the algorithm of Myers and Miller, CABIOS (1989). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used.

Greater than 80% sequence identity, e.g., 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or even 100% sequence identity, between the DsiRNA antisense strand and the portion of the AR RNA sequence is preferred. Alternatively, the DsiRNA may be defined functionally as a nucleotide sequence (or oligonucleotide sequence) that is capable of hybridizing with a portion of the AR RNA (e.g., 400 mM NaCl, 40 mM PIPES pH 6.4, 1 mM EDTA, 50°C or 70°C hybridization for 12-16 hours; followed by washing). Additional preferred hybridization conditions include hybridization at 70°C in 1xSSC or 50°C in 1xSSC, 50% formamide followed by washing at 70°C in 0.3xSSC or hybridization at 70°C. in 4xSSC or 50°C in 4xSSC, 50% formamide followed by washing at 67°C in 1xSSC. The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (Tm) of the hybrid, where Tm is determined according to the following equations. For hybrids less than 18 base pairs in length, Tm(°C)=2(# of A+T

bases)+4(# of G+C bases). For hybrids between 18 and 49 base pairs in length, Tm(°C)=81.5+16.6(log 10[Na+])+0.41 (% G+C)-(600/N), where N is the number of bases in the hybrid, and [Na+] is the concentration of sodium ions in the hybridization buffer ([Na+] for 1xSSC=0.165 M). Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E. F. Fritsch, and T. Maniatis, 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., chapters 9 and 11, and Current Protocols in Molecular Biology, 1995, F. M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4. The length of the identical nucleotide sequences may be at least 10, 12, 15, 17, 20, 22, 25, 27 or 30 bases.

By "conserved sequence region" is meant, a nucleotide sequence of one or more regions in a polynucleotide does not vary significantly between generations or from one biological system, subject, or organism to another biological system, subject, or organism. The polynucleotide can include both coding and non-coding DNA and RNA.

By "sense region" is meant a nucleotide sequence of a DsiRNA molecule having complementarity to an antisense region of the DsiRNA molecule. In addition, the sense region of a DsiRNA molecule can comprise a nucleic acid sequence having homology with a target nucleic acid sequence.

By "antisense region" is meant a nucleotide sequence of a DsiRNA molecule having complementarity to a target nucleic acid sequence. In addition, the antisense region of a DsiRNA molecule comprises a nucleic acid sequence having complementarity to a sense region of the DsiRNA molecule.

As used herein, “antisense strand” refers to a single stranded nucleic acid molecule which has a sequence complementary to that of a target RNA. When the antisense strand contains modified nucleotides with base analogs, it is not necessarily complementary over its entire length, but must at least hybridize with a target RNA.

As used herein, “sense strand” refers to a single stranded nucleic acid molecule which has a sequence complementary to that of an antisense strand. When the antisense strand contains modified nucleotides with base analogs, the sense strand need not be complementary over the entire length of the antisense strand, but must at least duplex with the antisense strand.

As used herein, “guide strand” refers to a single stranded nucleic acid molecule of a dsRNA or dsRNA-containing molecule, which has a sequence

sufficiently complementary to that of a target RNA to result in RNA interference. After cleavage of the dsRNA or dsRNA-containing molecule by Dicer, a fragment of the guide strand remains associated with RISC, binds a target RNA as a component of the RISC complex, and promotes cleavage of a target RNA by RISC. As used herein, the guide strand does not necessarily refer to a continuous single stranded nucleic acid and may comprise a discontinuity, preferably at a site that is cleaved by Dicer. A guide strand is an antisense strand.

As used herein, "passenger strand" refers to an oligonucleotide strand of a dsRNA or dsRNA-containing molecule, which has a sequence that is complementary to that of the guide strand. As used herein, the passenger strand does not necessarily refer to a continuous single stranded nucleic acid and may comprise a discontinuity, preferably at a site that is cleaved by Dicer. A passenger strand is a sense strand.

By "target nucleic acid" is meant a nucleic acid sequence whose expression, level or activity is to be modulated. The target nucleic acid can be DNA or RNA. For agents that target AR, in certain embodiments target nucleic acid is AR RNA. AR RNA target sites can also interchangeably be referenced by corresponding cDNA sequences. Levels of AR may also be targeted *via* targeting of upstream effectors of AR, or the effects of modulated or misregulated AR may also be modulated by targeting of molecules downstream of AR in the AR signalling pathway.

By "complementarity" is meant that a nucleic acid can form hydrogen bond(s) with another nucleic acid sequence by either traditional Watson-Crick or other non-traditional types. In reference to the nucleic molecules of the present invention, the binding free energy for a nucleic acid molecule with its complementary sequence is sufficient to allow the relevant function of the nucleic acid to proceed, e.g., RNAi activity. Determination of binding free energies for nucleic acid molecules is well known in the art (see, e.g., Turner et al., 1987, CSH Symp. Quant. Biol. LII pp. 123-133; Frier et al., 1986, Proc. Nat. Acad. Sci. USA 83:9373-9377; Turner et al., 1987, J. Am. Chem. Soc. 109:3783-3785). A percent complementarity indicates the percentage of contiguous residues in a nucleic acid molecule that can form hydrogen bonds (e.g., Watson-Crick base pairing) with a second nucleic acid sequence (e.g., 5, 6, 7, 8, 9, or 10 nucleotides out of a total of 10 nucleotides in the first oligonucleotide being based paired to a second nucleic acid sequence having 10 nucleotides represents 50%, 60%, 70%, 80%, 90%, and 100% complementary respectively). "Perfectly complementary" means that all the contiguous residues of a nucleic acid sequence will

hydrogen bond with the same number of contiguous residues in a second nucleic acid sequence. In one embodiment, a DsiRNA molecule of the invention comprises 19 to 30 (e.g., 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 or more) nucleotides that are complementary to one or more target nucleic acid molecules or a portion thereof.

In one embodiment, DsiRNA molecules of the invention that down regulate or reduce AR gene expression are used for treating, preventing or reducing AR-related diseases or disorders (*e.g.*, cancer) in a subject or organism.

In one embodiment of the present invention, each sequence of a DsiRNA molecule of the invention is independently 25 to 35 nucleotides in length, in specific embodiments 25, 26, 27, 28, 29, 30, 31, 32, 33, 34 or 35 nucleotides in length. In another embodiment, the DsiRNA duplexes of the invention independently comprise 25 to 30 base pairs (*e.g.*, 25, 26, 27, 28, 29, or 30). In another embodiment, one or more strands of the DsiRNA molecule of the invention independently comprises 19 to 35 nucleotides (e.g., 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34 or 35) that are complementary to a target (AR) nucleic acid molecule. In certain embodiments, a DsiRNA molecule of the invention possesses a length of duplexed nucleotides between 25 and 34 nucleotides in length (*e.g.*, 25, 26, 27, 28, 29, 30, 31, 32, 33 or 34 nucleotides in length; optionally, all such nucleotides base pair with cognate nucleotides of the opposite strand). (Exemplary DsiRNA molecules of the invention are shown in Figure 1, and below.

As used herein "cell" is used in its usual biological sense, and does not refer to an entire multicellular organism, e.g., specifically does not refer to a human. The cell can be present in an organism, e.g., birds, plants and mammals such as humans, cows, sheep, apes, monkeys, swine, dogs, and cats. The cell can be prokaryotic (e.g., bacterial cell) or eukaryotic (e.g., mammalian or plant cell). The cell can be of somatic or germ line origin, totipotent or pluripotent, dividing or non-dividing. The cell can also be derived from or can comprise a gamete or embryo, a stem cell, or a fully differentiated cell. Within certain aspects, the term “cell” refers specifically to mammalian cells, such as human cells, that contain one or more isolated dsRNA molecules of the present disclosure. In particular aspects, a cell processes dsRNAs or dsRNA-containing molecules resulting in RNA intereference of target nucleic acids, and contains proteins and protein complexes required for RNAi, *e.g.*, Dicer and RISC.

In certain embodiments, dsRNAs of the invention are Dicer substrate siRNAs (“DsiRNAs”). DsiRNAs can possess certain advantages as compared to inhibitory

nucleic acids that are not dicer substrates ("non-DsiRNAs"). Such advantages include, but are not limited to, enhanced duration of effect of a DsiRNA relative to a non-DsiRNA, as well as enhanced inhibitory activity of a DsiRNA as compared to a non-DsiRNA (e.g., a 19-23mer siRNA) when each inhibitory nucleic acid is suitably formulated and assessed for inhibitory activity in a mammalian cell at the same concentration (in this latter scenario, the DsiRNA would be identified as more potent than the non-DsiRNA). Detection of the enhanced potency of a DsiRNA relative to a non-DsiRNA is often most readily achieved at a formulated concentration (e.g., transfection concentration of the dsRNA) that results in the DsiRNA eliciting approximately 30-70% knockdown activity upon a target RNA (*e.g.*, a mRNA). For active DsiRNAs, such levels of knockdown activity are most often achieved at *in vitro* mammalian cell DsiRNA transfection concentrations of 1 nM or less of as suitably formulated, and in certain instances are observed at DsiRNA transfection concentrations of 200 pM or less, 100 pM or less, 50pM or less, 20 pM or less, 10 pM or less, 5 pM or less, or even 1 pM or less. Indeed, due to the variability among DsiRNAs of the precise concentration at which 30-70% knockdown of a target RNA is observed, construction of an IC50 curve *via* assessment of the inhibitory activity of DsiRNAs and non-DsiRNAs across a range of effective concentrations is a preferred method for detecting the enhanced potency of a DsiRNA relative to a non-DsiRNA inhibitory agent.

In certain embodiments, a DsiRNA (in a state as initially formed, prior to dicer cleavage) is more potent at reducing AR target gene expression in a mammalian cell than a 19, 20, 21, 22 or 23 base pair sequence that is contained within it. In certain such embodiments, a DsiRNA prior to dicer cleavage is more potent than a 19-21mer contained within it. Optionally, a DsiRNA prior to dicer cleavage is more potent than a 19 base pair duplex contained within it that is synthesized with symmetric dTdT overhangs (thereby forming a siRNA possessing 21 nucleotide strand lengths having dTdT overhangs). In certain embodiments, the DsiRNA is more potent than a 19-23mer siRNA (e.g., a 19 base pair duplex with dTdT overhangs) that targets at least 15 nucleotides of the 21 nucleotide target sequence that is recited for a DsiRNA of the invention (without wishing to be bound by theory, the identity of a such a target site for a DsiRNA is identified *via* identification of the Ago2 cleavage site for the DsiRNA; once the Ago2 cleavage site of a DsiRNA is determined for a DsiRNA, identification of the Ago2 cleavage site for any other inhibitory dsRNA can be

performed and these Ago2 cleavage sites can be aligned, thereby determining the alignment of projected target nucleotide sequences for multiple dsRNAs). In certain related embodiments, the DsiRNA is more potent than a 19-23mer siRNA that targets at least 20 nucleotides of the 21 nucleotide target sequence that is recited for a DsiRNA of the invention. Optionally, the DsiRNA is more potent than a 19-23mer siRNA that targets the same 21 nucleotide target sequence that is recited for a DsiRNA of the invention. In certain embodiments, the DsiRNA is more potent than any 21mer siRNA that targets the same 21 nucleotide target sequence that is recited for a DsiRNA of the invention. Optionally, the DsiRNA is more potent than any 21 or 22mer siRNA that targets the same 21 nucleotide target sequence that is recited for a DsiRNA of the invention. In certain embodiments, the DsiRNA is more potent than any 21, 22 or 23mer siRNA that targets the same 21 nucleotide target sequence that is recited for a DsiRNA of the invention. As noted above, such potency assessments are most effectively performed upon dsRNAs that are suitably formulated (e.g., formulated with an appropriate transfection reagent) at a concentration of 1 nM or less. Optionally, an IC50 assessment is performed to evaluate activity across a range of effective inhibitory concentrations, thereby allowing for robust comparison of the relative potencies of dsRNAs so assayed.

The dsRNA molecules of the invention are added directly, or can be complexed with lipids (*e.g.*, cationic lipids), packaged within liposomes, or otherwise delivered to target cells or tissues. The nucleic acid or nucleic acid complexes can be locally administered to relevant tissues *ex vivo*, or *in vivo* through direct dermal application, transdermal application, or injection, with or without their incorporation in biopolymers. In particular embodiments, the nucleic acid molecules of the invention comprise sequences shown in Figure 1, and the below exemplary structures. Examples of such nucleic acid molecules consist essentially of sequences defined in these figures and exemplary structures. Furthermore, where such agents are modified in accordance with the below description of modification patterning of DsiRNA agents, chemically modified forms of constructs described in Figure 1, and the below exemplary structures can be used in all uses described for the DsiRNA agents of Figure 1, and the below exemplary structures.

In another aspect, the invention provides mammalian cells containing one or more DsiRNA molecules of this invention. The one or more DsiRNA molecules can independently be targeted to the same or different sites.

By "RNA" is meant a molecule comprising at least one, and preferably at least 4 , 8 and 12 ribonucleotide residues. The at least 4, 8 or 12 RNA residues may be contiguous. By "ribonucleotide" is meant a nucleotide with a hydroxyl group at the 2' position of a β-D-ribofuranose moiety. The terms include double-stranded RNA, single-stranded RNA, isolated RNA such as partially purified RNA, essentially pure RNA, synthetic RNA, recombinantly produced RNA, as well as altered RNA that differs from naturally occurring RNA by the addition, deletion, substitution and/or alteration of one or more nucleotides. Such alterations can include addition of non-nucleotide material, such as to the end(s) of the DsiRNA or internally, for example at one or more nucleotides of the RNA. Nucleotides in the RNA molecules of the instant invention can also comprise non-standard nucleotides, such as non-naturally occurring nucleotides or chemically synthesized nucleotides or deoxynucleotides. These altered RNAs can be referred to as analogs or analogs of naturally-occurring RNA.

By "subject" is meant an organism, which is a donor or recipient of explanted cells or the cells themselves. "Subject" also refers to an organism to which the DsiRNA agents of the invention can be administered. A subject can be a mammal or mammalian cells, including a human or human cells.

The phrase "pharmaceutically acceptable carrier" refers to a carrier for the administration of a therapeutic agent. Exemplary carriers include saline, buffered saline, dextrose, water, glycerol, ethanol, and combinations thereof. For drugs administered orally, pharmaceutically acceptable carriers include, but are not limited to pharmaceutically acceptable excipients such as inert diluents, disintegrating agents, binding agents, lubricating agents, sweetening agents, flavoring agents, coloring agents and preservatives. Suitable inert diluents include sodium and calcium carbonate, sodium and calcium phosphate, and lactose, while corn starch and alginic acid are suitable disintegrating agents. Binding agents may include starch and gelatin, while the lubricating agent, if present, will generally be magnesium stearate, stearic acid or talc. If desired, the tablets may be coated with a material such as glyceryl monostearate or glyceryl distearate, to delay absorption in the gastrointestinal tract. The pharmaceutically acceptable carrier of the disclosed dsRNA compositions may be micellar structures, such as a liposomes, capsids, capsoids, polymeric nanocapsules, or polymeric microcapsules.

Polymeric nanocapsules or microcapsules facilitate transport and release of the encapsulated or bound dsRNA into the cell. They include polymeric and monomeric materials, especially including polybutylcyanoacrylate. A summary of materials and fabrication methods has been published (see Kreuter, 1991). The polymeric materials which are formed from monomeric and/or oligomeric precursors in the polymerization/nanoparticle generation step, are *per se* known from the prior art, as are the molecular weights and molecular weight distribution of the polymeric material which a person skilled in the field of manufacturing nanoparticles may suitably select in accordance with the usual skill.

Various methodologies of the instant invention include step that involves comparing a value, level, feature, characteristic, property, etc. to a "suitable control", referred to interchangeably herein as an "appropriate control". A "suitable control" or "appropriate control" is a control or standard familiar to one of ordinary skill in the art useful for comparison purposes. In one embodiment, a "suitable control" or "appropriate control" is a value, level, feature, characteristic, property, etc. determined prior to performing an RNAi methodology, as described herein. For example, a transcription rate, mRNA level, translation rate, protein level, biological activity, cellular characteristic or property, genotype, phenotype, etc. can be determined prior to introducing an RNA silencing agent (*e.g.*, DsiRNA) of the invention into a cell or organism. In another embodiment, a "suitable control" or "appropriate control" is a value, level, feature, characteristic, property, etc. determined in a cell or organism, *e.g.*, a control or normal cell or organism, exhibiting, for example, normal traits. In yet another embodiment, a "suitable control" or "appropriate control" is a predefined value, level, feature, characteristic, property, etc.

The term "*in vitro*" has its art recognized meaning, *e.g.*, involving purified reagents or extracts, *e.g.*, cell extracts. The term "*in vivo*" also has its art recognized meaning, *e.g.*, involving living cells, *e.g.*, immortalized cells, primary cells, cell lines, and/or cells in an organism.

"Treatment", or "treating" as used herein, is defined as the application or administration of a therapeutic agent (*e.g.*, a DsiRNA agent or a vector or transgene encoding same) to a patient, or application or administration of a therapeutic agent to an isolated tissue or cell line from a patient, who has a disorder with the purpose to cure, heal, alleviate, relieve, alter, remedy, ameliorate, improve or affect the disease or disorder, or symptoms of the disease or disorder. The term "treatment" or

"treating" is also used herein in the context of administering agents prophylactically. The term "effective dose" or "effective dosage" is defined as an amount sufficient to achieve or at least partially achieve the desired effect. The term "therapeutically effective dose" is defined as an amount sufficient to cure or at least partially arrest the disease and its complications in a patient already suffering from the disease. The term "patient" includes human and other mammalian subjects that receive either prophylactic or therapeutic treatment.

Structures of Anti-AR DsiRNA Agents

In certain embodiments, the anti-AR DsiRNA agents of the invention can have the following structures:

In one such embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-YXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA and "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers. In a related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-YXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers, and “D”=DNA. In one embodiment, the top strand is the sense strand, and the bottom strand is the antisense strand. Alternatively, the bottom strand is the sense strand and the top strand is the antisense strand.

DsiRNAs of the invention can carry a broad range of modification patterns (*e.g.*, 2'-O-methyl RNA patterns, *e.g.*, within extended DsiRNA agents). Certain modification patterns of the second strand of DsiRNAs of the invention are presented below.

In one embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-YXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers and underlined

residues are 2'-O-methyl RNA monomers. In a related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-Y<u>X</u><u>X</u><u>X</u><u>X</u><u>X</u><u>X</u><u>X</u><u>X</u><u>X</u><u>X</u><u>X</u>XXXXXXXXXX-5′

wherein "X"=RNA, "<u>X</u>"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers and underlined residues are 2'-O-methyl RNA monomers, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand.

In another such embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-Y<u>X</u><u>X</u><u>X</u><u>X</u><u>X</u><u>X</u><u>X</u><u>X</u><u>X</u><u>X</u><u>X</u>XXXXXXXXX-5′

wherein "X"=RNA, "<u>X</u>"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers and underlined residues are 2'-O-methyl RNA monomers. In a related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-Y<u>X</u><u>X</u><u>X</u><u>X</u><u>X</u><u>X</u><u>X</u><u>X</u><u>X</u><u>X</u><u>X</u>XXXXXXXXX-5′

wherein "X"=RNA, "<u>X</u>"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers, underlined residues are 2'-O-methyl RNA monomers, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand.

In another such embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-Y<u>X</u><u>X</u><u>X</u><u>X</u><u>X</u><u>X</u><u>X</u><u>X</u><u>X</u><u>X</u><u>X</u>XXXXXXXXX-5′

wherein "X"=RNA, "<u>X</u>"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers and underlined residues are 2'-O-methyl RNA monomers. In a related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-Y<u>X</u><u>X</u><u>X</u><u>X</u><u>X</u><u>X</u><u>X</u><u>X</u><u>X</u><u>X</u><u>X</u>XXXXXXXXX-5′

wherein "X"=RNA, "<u>X</u>"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers, underlined residues are 2'-O-methyl RNA monomers, and "D"=DNA. The top strand is the

sense strand, and the bottom strand is the antisense strand.

In further embodiments, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-YXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers and underlined residues are 2'-O-methyl RNA monomers. In a related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-YXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers, underlined residues are 2'-O-methyl RNA monomers, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In one related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-XXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA and "X"=2'-O-methyl RNA. In a further related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-XXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand.

In additional embodiments, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-YXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers and underlined residues are 2'-O-methyl RNA monomers. In a related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-YXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of

1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers, underlined residues are 2'-O-methyl RNA monomers, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand. The top strand is the sense strand, and the bottom strand is the antisense strand. In another related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-XXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA and "X"=2'-O-methyl RNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In a further related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-XXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand.

In other embodiments, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-YXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers and underlined residues are 2'-O-methyl RNA monomers. The top strand is the sense strand, and the bottom strand is the antisense strand. In a related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-YXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers, underlined residues are 2'-O-methyl RNA monomers, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In one related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-XXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA and "X"=2'-O-methyl RNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In another related embodiment, the

DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-XXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand.

In further embodiments, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-YXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers and underlined residues are 2'-O-methyl RNA monomers. The top strand is the sense strand, and the bottom strand is the antisense strand. In a related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-YXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers, underlined residues are 2'-O-methyl RNA monomers, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In one related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-XXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA and "X"=2'-O-methyl RNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In a further related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-XXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand.

In additional embodiments, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-YXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of

1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers and underlined residues are 2'-O-methyl RNA monomers. The top strand is the sense strand, and the bottom strand is the antisense strand. In a related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-Y<u>X</u><u>X</u><u>X</u><u>X</u>XXXXXXX<u>X</u><u>X</u>XXXXXXX<u>XXXX</u>-5′

wherein "X"=RNA, "<u>X</u>"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers, underlined residues are 2'-O-methyl RNA monomers, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In another related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-<u>XXXX</u><u>X</u><u>X</u><u>X</u>XXXXXXX<u>X</u><u>X</u>XXXXXXX<u>XXXX</u>-5′

wherein "X"=RNA and "X"=2'-O-methyl RNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In a further related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-<u>XXXX</u><u>X</u><u>X</u><u>X</u>XXXXXXX<u>X</u><u>X</u>XXXXXXX<u>XXXX</u>-5′

wherein "X"=RNA, "<u>X</u>"=2'-O-methyl RNA, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand.

In other embodiments, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-Y<u>X</u><u>X</u><u>X</u><u>X</u>XXXXXXXXXXXXXXXXX<u>XXXX</u>-5′

wherein "X"=RNA, "<u>X</u>"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers and underlined residues are 2'-O-methyl RNA monomers. The top strand is the sense strand, and the bottom strand is the antisense strand. In one related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-Y<u>X</u><u>X</u><u>X</u><u>X</u>XXXXXXXXXXXXXXXXX<u>XXXX</u>-5′

wherein "X"=RNA, "<u>X</u>"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers, underlined residues are 2'-O-methyl RNA monomers, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In another related

embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-XXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA and "X"=2'-O-methyl RNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In a further related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-XXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand.

In additional embodiments, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-YXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers and underlined residues are 2'-O-methyl RNA monomers. The top strand is the sense strand, and the bottom strand is the antisense strand. In a related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-YXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers, underlined residues are 2'-O-methyl RNA monomers, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In another related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-XXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA and "X"=2'-O-methyl RNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In a further related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-XXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, and "D"=DNA. The top strand is the

sense strand, and the bottom strand is the antisense strand.

In further embodiments, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-YXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers and underlined residues are 2'-O-methyl RNA monomers. The top strand is the sense strand, and the bottom strand is the antisense strand. In a related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-YXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers, underlined residues are 2'-O-methyl RNA monomers, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In another related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-XXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA and "X"=2'-O-methyl RNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In a further related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-XXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand.

In additional embodiments, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-YXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers and underlined residues are 2'-O-methyl RNA monomers. The top strand is the sense strand, and the bottom strand is the antisense strand. In one related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-YXXXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers, underlined residues are 2'-O-methyl RNA monomers, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In another related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-XXXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA and "X"=2'-O-methyl RNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In a further related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-XXXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand.

In other embodiments, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-YXXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers and underlined residues are 2'-O-methyl RNA monomers. The top strand is the sense strand, and the bottom strand is the antisense strand. In a related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-YXXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers, underlined residues are 2'-O-methyl RNA monomers, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In another related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-XXXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA and "X"=2'-O-methyl RNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In a further related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-XXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand.

In further embodiments, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-YXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers and underlined residues are 2'-O-methyl RNA monomers. The top strand is the sense strand, and the bottom strand is the antisense strand. In one related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-YXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers, underlined residues are 2'-O-methyl RNA monomers, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In another related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-XXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA and "X"=2'-O-methyl RNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In a further related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-XXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand.

In additional embodiments, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-Y<u>X</u><u>X</u><u>X</u>XXXXXXXXXX<u>X</u><u>X</u><u>X</u>XXXXXX<u>XXXX</u>-5′

wherein "X"=RNA, "<u>X</u>"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers and underlined residues are 2'-O-methyl RNA monomers. The top strand is the sense strand, and the bottom strand is the antisense strand. In one related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-Y<u>X</u><u>X</u><u>X</u>XXXXXXXXXX<u>X</u><u>X</u><u>X</u>XXXXXX<u>XXXX</u>-5′

wherein "X"=RNA, "<u>X</u>"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers, underlined residues are 2'-O-methyl RNA monomers, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In another related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-<u>X</u><u>X</u><u>X</u><u>X</u>XXXXXXXXXX<u>X</u><u>X</u><u>X</u>XXXXXX<u>XXXX</u>-5′

wherein "X"=RNA and "<u>X</u>"=2'-O-methyl RNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In a further related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-<u>X</u><u>X</u><u>X</u><u>X</u>XXXXXXXXXX<u>X</u><u>X</u><u>X</u>XXXXXX<u>XXXX</u>-5′

wherein "X"=RNA, "<u>X</u>"=2'-O-methyl RNA, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand.

In further embodiments, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-Y<u>X</u><u>X</u><u>X</u>XXXXXXXXXX<u>X</u><u>X</u><u>X</u>XXXXXX<u>XX</u>-5′

wherein "X"=RNA, "<u>X</u>"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers and underlined residues are 2'-O-methyl RNA monomers. The top strand is the sense strand, and the bottom strand is the antisense strand. In one related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-Y<u>X</u><u>X</u><u>X</u>XXXXXXXXXX<u>X</u><u>X</u><u>X</u>XXXXXX<u>XX</u>-5′

wherein "X"=RNA, "<u>X</u>"=2'-O-methyl RNA, "Y" is an overhang domain comprised of

1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers, underlined residues are 2'-O-methyl RNA monomers, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In another related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'
3′-XXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA and "X"=2'-O-methyl RNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In a further related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXDD-3'
3′-XXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand.

In other embodiments, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'
3′-YXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers and underlined residues are 2'-O-methyl RNA monomers. The top strand is the sense strand, and the bottom strand is the antisense strand. In another related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXDD-3'
3′-YXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers, underlined residues are 2'-O-methyl RNA monomers, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In another related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'
3′-XXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA and "X"=2'-O-methyl RNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In a further related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXDD-3'
3′-XXXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand.

In further embodiments, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXXX-3'
3′-YXXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers and underlined residues are 2'-O-methyl RNA monomers. The top strand is the sense strand, and the bottom strand is the antisense strand. In one related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXDD-3'
3′-YXXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers, underlined residues are 2'-O-methyl RNA monomers, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In another related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXXX-3'
3′-XXXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA and “X”=2’-O-methyl RNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In a further related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXDD-3'
3′-XXXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand.

In additional embodiments, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXXX-3'
3′-YXXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers and underlined

residues are 2'-O-methyl RNA monomers. The top strand is the sense strand, and the bottom strand is the antisense strand. In one related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-YXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers, underlined residues are 2'-O-methyl RNA monomers, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In another related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-XXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand.

In further embodiments, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-YXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers and underlined residues are 2'-O-methyl RNA monomers. The top strand is the sense strand, and the bottom strand is the antisense strand. In a related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-YXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers, underlined residues are 2'-O-methyl RNA monomers, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In another related

embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-XXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA and “X”=2’-O-methyl RNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In a further related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-XXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand.

In additional embodiments, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-YXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers and underlined residues are 2’-O-methyl RNA monomers. The top strand is the sense strand, and the bottom strand is the antisense strand. In one related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-YXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers, underlined residues are 2’-O-methyl RNA monomers, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In another related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-XXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA and “X”=2’-O-methyl RNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In a further related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-XXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, and "D"=DNA. The top strand is the

sense strand, and the bottom strand is the antisense strand.

In further embodiments, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-YXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers and underlined residues are 2'-O-methyl RNA monomers. The top strand is the sense strand, and the bottom strand is the antisense strand. In one related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-YXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers, underlined residues are 2'-O-methyl RNA monomers, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In another related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-XXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA and "X"=2'-O-methyl RNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In a further related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-XXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand.

In additional embodiments, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-YXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers and underlined residues are 2'-O-methyl RNA monomers. The top strand is the sense strand, and the bottom strand is the antisense strand. In one related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-YXXXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers, underlined residues are 2'-O-methyl RNA monomers, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In another related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-XXXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA and "X"=2'-O-methyl RNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In a further related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-XXXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand.

In further embodiments, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-YXXXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers and underlined residues are 2'-O-methyl RNA monomers. The top strand is the sense strand, and the bottom strand is the antisense strand. In one related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-YXXXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers, underlined residues are 2'-O-methyl RNA monomers, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In another related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-XXXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA and “X”=2’-O-methyl RNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In a further related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-XXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand.

In additional embodiments, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-YXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers and underlined residues are 2’-O-methyl RNA monomers. The top strand is the sense strand, and the bottom strand is the antisense strand. In one related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-YXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers, underlined residues are 2’-O-methyl RNA monomers, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In another related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXXX-3'

3′-XXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA and “X”=2’-O-methyl RNA. The top strand is the sense strand, and the bottom strand is the antisense strand. In a further related embodiment, the DsiRNA comprises:

5′-XXXXXXXXXXXXXXXXXXXXXXXDD-3'

3′-XXXXXXXXXXXXXXXXXXXXXXXXX-5′

wherein "X"=RNA, "X"=2'-O-methyl RNA, and "D"=DNA. The top strand is the sense strand, and the bottom strand is the antisense strand.

The above modification patterns can also be incorporated into, *e.g.*, the extended DsiRNA structures and mismatch and/or frayed DsiRNA structures

described below.

In another embodiment, the DsiRNA comprises strands having equal lengths possessing 1-3 mismatched residues that serve to orient Dicer cleavage (specifically, one or more of positions 1, 2 or 3 on the first strand of the DsiRNA, when numbering from the 3'-terminal residue, are mismatched with corresponding residues of the 5'-terminal region on the second strand when first and second strands are annealed to one another). An exemplary 27mer DsiRNA agent with two terminal mismatched residues is shown:

$$5'\text{-}XXXXXXXXXXXXXXXXXXXXXXXXXX^{M}{}^{M-3'}$$

$$3'\text{-}XXXXXXXXXXXXXXXXXXXXXXXXXX_{M}{}_{M-5'}$$

wherein "X"=RNA, "M"=Nucleic acid residues (RNA, DNA or non-natural or modified nucleic acids) that do not base pair (hydrogen bond) with corresponding "M" residues of otherwise complementary strand when strands are annealed. Any of the residues of such agents can optionally be 2'-O-methyl RNA monomers – alternating positioning of 2'-O-methyl RNA monomers that commences from the 3'-terminal residue of the bottom (second) strand, as shown for above asymmetric agents, can also be used in the above "blunt/fray" DsiRNA agent. In one embodiment, the top strand is the sense strand, and the bottom strand is the antisense strand. Alternatively, the bottom strand is the sense strand and the top strand is the antisense strand.

In certain additional embodiments, the present invention provides compositions for RNA interference (RNAi) that possess one or more base paired deoxyribonucleotides within a region of a double stranded ribonucleic acid (dsRNA) that is positioned 3' of a projected sense strand Dicer cleavage site and correspondingly 5' of a projected antisense strand Dicer cleavage site. The compositions of the invention comprise a dsRNA which is a precursor molecule, *i.e.*, the dsRNA of the present invention is processed *in vivo* to produce an active small interfering nucleic acid (siRNA). The dsRNA is processed by Dicer to an active siRNA which is incorporated into RISC.

In certain embodiments, the DsiRNA agents of the invention can have the following exemplary structures (noting that any of the following exemplary structures can be combined, *e.g.*, with the bottom strand modification patterns of the above-described structures – in one specific example, the bottom strand modification pattern

shown in any of the above structures is applied to the 27 most 3' residues of the bottom strand of any of the following structures; in another specific example, the bottom strand modification pattern shown in any of the above structures upon the 23 most 3' residues of the bottom strand is applied to the 23 most 3' residues of the bottom strand of any of the following structures):

In one such embodiment, the DsiRNA comprises the following (an exemplary "right-extended", "DNA extended" DsiRNA):

5'-XXXXXXXXXXXXXXXXXXXXXXXXX$X_{N*}D_NDD$-3'

3'-YXXXXXXXXXXXXXXXXXXXXXXXX$X_{N*}D_NXX$-5'

wherein "X"=RNA, "Y" is an optional overhang domain comprised of 0-10 RNA monomers that are optionally 2'-O-methyl RNA monomers – in certain embodiments, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers, "D"=DNA, and "N"=1 to 50 or more, but is optionally 1-8 or 1-10. "N*"=0 to 15 or more, but is optionally 0, 1, 2, 3, 4, 5 or 6. In one embodiment, the top strand is the sense strand, and the bottom strand is the antisense strand. Alternatively, the bottom strand is the sense strand and the top strand is the antisense strand.

In a related embodiment, the DsiRNA comprises:

5'-XXXXXXXXXXXXXXXXXXXXXXXXX$X_{N*}D_NDD$-3'

3'-YXXXXXXXXXXXXXXXXXXXXXXXX$X_{N*}D_NDD$-5'

wherein "X"=RNA, "Y" is an optional overhang domain comprised of 0-10 RNA monomers that are optionally 2'-O-methyl RNA monomers – in certain embodiments, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers, "D"=DNA, and "N"=1 to 50 or more, but is optionally 1-8 or 1-10. "N*"=0 to 15 or more, but is optionally 0, 1, 2, 3, 4, 5 or 6. In one embodiment, the top strand is the sense strand, and the bottom strand is the antisense strand. Alternatively, the bottom strand is the sense strand and the top strand is the antisense strand.

In an additional embodiment, the DsiRNA comprises:

5'-XXXXXXXXXXXXXXXXXXXXXXXXX$X_{N*}D_NDD$-3'

3'-Y$\underline{X}\underline{X}\underline{X}\underline{X}\underline{X}\underline{X}\underline{X}\underline{X}\underline{X}\underline{X}\underline{X}\underline{X}$XXXXXXXXX$X_{N*}D_NZZ$-5'

wherein "X"=RNA, "$\underline{X}$"=2'-O-methyl RNA, "Y" is an optional overhang domain comprised of 0-10 RNA monomers that are optionally 2'-O-methyl RNA monomers –

in certain embodiments, “Y” is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers, "D"=DNA, “Z”=DNA or RNA, and “N”=1 to 50 or more, but is optionally 1-8 or 1-10. “N*”=0 to 15 or more, but is optionally 0, 1, 2, 3, 4, 5 or 6. In one embodiment, the top strand is the sense strand, and the bottom strand is the antisense strand. Alternatively, the bottom strand is the sense strand and the top strand is the antisense strand, with 2’-O-methyl RNA monomers located at alternating residues along the top strand, rather than the bottom strand presently depicted in the above schematic.

In another such embodiment, the DsiRNA comprises:

5'-XXXXXXXXXXXXXXXXXXXXXXXXX$X_{N*}D_NDD$-3'

3′-Y<u>X</u><u>X</u><u>X</u>

strand presently depicted in the above schematic.

In another embodiment, the DsiRNA comprises:

5'-XXXXXXXXXXXXXXXXXXXXXXXXXX_{N*}[X1/D1]$_N$DD-3'

3′-YXXXXXXXXXXXXXXXXXXXXXXXXX_{N*}[X2/D2]$_N$ZZ-5'

wherein "X"=RNA, "Y" is an optional overhang domain comprised of 0-10 RNA monomers that are optionally 2'-O-methyl RNA monomers – in certain embodiments, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers, "D"=DNA, "Z"=DNA or RNA, and "N"=1 to 50 or more, but is optionally 1-8 or 1-10, where at least one $D1_N$ is present in the top strand and is base paired with a corresponding $D2_N$ in the bottom strand. Optionally, $D1_N$ and $D1_{N+1}$ are base paired with corresponding $D2_N$ and $D2_{N+1}$; $D1_N$, $D1_{N+1}$ and $D1_{N+2}$ are base paired with corresponding $D2_N$, $D1_{N+1}$ and $D1_{N+2}$, etc. "N*"=0 to 15 or more, but is optionally 0, 1, 2, 3, 4, 5 or 6. In one embodiment, the top strand is the sense strand, and the bottom strand is the antisense strand. Alternatively, the bottom strand is the sense strand and the top strand is the antisense strand, with 2'-O-methyl RNA monomers located at alternating residues along the top strand, rather than the bottom strand presently depicted in the above schematic.

In the structures depicted herein, the 5' end of either the sense strand or antisense strand can optionally comprise a phosphate group.

In another embodiment, a DNA:DNA-extended DsiRNA comprises strands having equal lengths possessing 1-3 mismatched residues that serve to orient Dicer cleavage (specifically, one or more of positions 1, 2 or 3 on the first strand of the DsiRNA, when numbering from the 3'-terminal residue, are mismatched with corresponding residues of the 5'-terminal region on the second strand when first and second strands are annealed to one another). An exemplary DNA:DNA-extended DsiRNA agent with two terminal mismatched residues is shown:

5'-D_NXXXXXXXXXXXXXXXXXXXXXXXXX$X_{N*}$$M^{M-3'}$

3′-D_NXXXXXXXXXXXXXXXXXXXXXXXXX$X_{N*}M_{M-5'}$

wherein "X"=RNA, "M"=Nucleic acid residues (RNA, DNA or non-natural or modified nucleic acids) that do not base pair (hydrogen bond) with corresponding "M" residues of otherwise complementary strand when strands are annealed, "D"=DNA and "N"=1 to 50 or more, but is optionally 1-15 or, optionally, 1-8.

"N*"=0 to 15 or more, but is optionally 0, 1, 2, 3, 4, 5 or 6. Any of the residues of such agents can optionally be 2'-O-methyl RNA monomers – alternating positioning of 2'-O-methyl RNA monomers that commences from the 3'-terminal residue of the bottom (second) strand, as shown for above asymmetric agents, can also be used in the above "blunt/fray" DsiRNA agent. In one embodiment, the top strand (first strand) is the sense strand, and the bottom strand (second strand) is the antisense strand. Alternatively, the bottom strand is the sense strand and the top strand is the antisense strand. Modification and DNA:DNA extension patterns paralleling those shown above for asymmetric/overhang agents can also be incorporated into such "blunt/frayed" agents.

In one embodiment, a length-extended DsiRNA agent is provided that comprises deoxyribonucleotides positioned at sites modeled to function *via* specific direction of Dicer cleavage, yet which does not require the presence of a base-paired deoxyribonucleotide in the dsRNA structure. An exemplary structure for such a molecule is shown:

5'-XXXXXXXXXXXXXXXXXXXXDDXX-3'
3'-YXXXXXXXXXXXXXXXXXXDDXXXX-5'

wherein "X"=RNA, "Y" is an optional overhang domain comprised of 0-10 RNA monomers that are optionally 2'-O-methyl RNA monomers – in certain embodiments, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers, and "D"=DNA. In one embodiment, the top strand is the sense strand, and the bottom strand is the antisense strand. Alternatively, the bottom strand is the sense strand and the top strand is the antisense strand. The above structure is modeled to force Dicer to cleave a minimum of a 21mer duplex as its primary post-processing form. In embodiments where the bottom strand of the above structure is the antisense strand, the positioning of two deoxyribonucleotide residues at the ultimate and penultimate residues of the 5' end of the antisense strand will help reduce off-target effects (as prior studies have shown a 2'-O-methyl modification of at least the penultimate position from the 5' terminus of the antisense strand to reduce off-target effects; see, *e.g.*, US 2007/0223427).

In one embodiment, the DsiRNA comprises the following (an exemplary "left-extended", "DNA extended" DsiRNA):

5'-D_NXXXXXXXXXXXXXXXXXXXXXXXX_{N*}Y-3'

3′-D_NXXXXXXXXXXXXXXXXXXXXXXXXX_{N*}-5’

wherein "X"=RNA, "Y" is an optional overhang domain comprised of 0-10 RNA monomers that are optionally 2'-O-methyl RNA monomers – in certain embodiments, “Y” is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers, "D"=DNA, and “N”=1 to 50 or more, but is optionally 1-8 or 1-10. “N*”=0 to 15 or more, but is optionally 0, 1, 2, 3, 4, 5 or 6. In one embodiment, the top strand is the sense strand, and the bottom strand is the antisense strand. Alternatively, the bottom strand is the sense strand and the top strand is the antisense strand.

In a related embodiment, the DsiRNA comprises:

5'-D_NXXXXXXXXXXXXXXXXXXXXXXXXX_{N*}DD-3'

3′-D_NXXXXXXXXXXXXXXXXXXXXXXXXX_{N*}XX-5’

wherein "X"=RNA, optionally a 2'-O-methyl RNA monomers "D"=DNA, “N”=1 to 50 or more, but is optionally 1-8 or 1-10. “N*”=0 to 15 or more, but is optionally 0, 1, 2, 3, 4, 5 or 6. In one embodiment, the top strand is the sense strand, and the bottom strand is the antisense strand. Alternatively, the bottom strand is the sense strand and the top strand is the antisense strand.

In an additional embodiment, the DsiRNA comprises:

5'-D_NXXXXXXXXXXXXXXXXXXXXXXXXX_{N*}DD-3'

3′-D_NXXXXXXXXXXXXXXXXXXXXXXXXX_{N*}ZZ-5’

wherein "X"=RNA, optionally a 2'-O-methyl RNA monomers "D"=DNA, “N”=1 to 50 or more, but is optionally 1-8 or 1-10. “N*”=0 to 15 or more, but is optionally 0, 1, 2, 3, 4, 5 or 6. “Z”=DNA or RNA. In one embodiment, the top strand is the sense strand, and the bottom strand is the antisense strand. Alternatively, the bottom strand is the sense strand and the top strand is the antisense strand, with 2’-O-methyl RNA monomers located at alternating residues along the top strand, rather than the bottom strand presently depicted in the above schematic.

In another such embodiment, the DsiRNA comprises:

5'-D_NXXXXXXXXXXXXXXXXXXXXXXXXX_{N*}DD-3'

3′-D_NXXXXXXXXXXXXXXXXXXXXXXXXX_{N*}ZZ-5’

wherein "X"=RNA, optionally a 2'-O-methyl RNA monomers "D"=DNA, “N”=1 to 50 or more, but is optionally 1-8 or 1-10. “N*”=0 to 15 or more, but is optionally 0, 1, 2, 3, 4, 5 or 6. “Z”=DNA or RNA. In one embodiment, the top strand is the sense

strand, and the bottom strand is the antisense strand. Alternatively, the bottom strand is the sense strand and the top strand is the antisense strand, with 2'-O-methyl RNA monomers located at alternating residues along the top strand, rather than the bottom strand presently depicted in the above schematic.

In another such embodiment, the DsiRNA comprises:

5'-D_NZZXXXXXXXXXXXXXXXXXXXXXXXXX_{N*}DD-3'

3'-D_NXXXXXXXXXXXXXXXXXXXXXXXXX_{N*}ZZ-5'

wherein "X"=RNA, "X"=2'-O-methyl RNA, "D"=DNA, "Z"=DNA or RNA, and "N"=1 to 50 or more, but is optionally 1-8 or 1-10. "N*"=0 to 15 or more, but is optionally 0, 1, 2, 3, 4, 5 or 6. In one embodiment, the top strand is the sense strand, and the bottom strand is the antisense strand. Alternatively, the bottom strand is the sense strand and the top strand is the antisense strand, with 2'-O-methyl RNA monomers located at alternating residues along the top strand, rather than the bottom strand presently depicted in the above schematic.

In another such embodiment, the DsiRNA comprises:

5'-D_NZZXXXXXXXXXXXXXXXXXXXXXXXXX_{N*}Y-3'

3'-D_NXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX_{N*}-5'

wherein "X"=RNA, "X"=2'-O-methyl RNA, "D"=DNA, "Z"=DNA or RNA, and "N"=1 to 50 or more, but is optionally 1-8 or 1-10. "N*"=0 to 15 or more, but is optionally 0, 1, 2, 3, 4, 5 or 6. "Y" is an optional overhang domain comprised of 0-10 RNA monomers that are optionally 2'-O-methyl RNA monomers – in certain embodiments, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers. In one embodiment, the top strand is the sense strand, and the bottom strand is the antisense strand. Alternatively, the bottom strand is the sense strand and the top strand is the antisense strand, with 2'-O-methyl RNA monomers located at alternating residues along the top strand, rather than the bottom strand presently depicted in the above schematic.

In another embodiment, the DsiRNA comprises:

5'-[X1/D1]$_N$XXXXXXXXXXXXXXXXXXXXXXXXX_{N*}DD-3'

3'-[X2/D2]$_N$XXXXXXXXXXXXXXXXXXXXXXXXX_{N*}ZZ-5'

wherein "X"=RNA, "D"=DNA, "Z"=DNA or RNA, and "N"=1 to 50 or more, but is optionally 1-8 or 1-10, where at least one $D1_N$ is present in the top strand and is base paired with a corresponding $D2_N$ in the bottom strand. Optionally, $D1_N$ and $D1_{N+1}$ are

base paired with corresponding $D2_N$ and $D2_{N+1}$; $D1_N$, $D1_{N+1}$ and $D1_{N+2}$ are base paired with corresponding $D2_N$, $D1_{N+1}$ and $D1_{N+2}$, etc. "N*"=0 to 15 or more, but is optionally 0, 1, 2, 3, 4, 5 or 6. In one embodiment, the top strand is the sense strand, and the bottom strand is the antisense strand. Alternatively, the bottom strand is the sense strand and the top strand is the antisense strand, with 2'-O-methyl RNA monomers located at alternating residues along the top strand, rather than the bottom strand presently depicted in the above schematic.

In a related embodiment, the DsiRNA comprises:

5'-[X1/D1]$_N$XXXXXXXXXXXXXXXXXXXXXXXXX$_{N*}$Y-3'

3′-[X2/D2]$_N$XXXXXXXXXXXXXXXXXXXXXXXXX$_{N*}$-5'

wherein "X"=RNA, "D"=DNA, "Y" is an optional overhang domain comprised of 0-10 RNA monomers that are optionally 2'-O-methyl RNA monomers – in certain embodiments, "Y" is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers, and "N"=1 to 50 or more, but is optionally 1-8 or 1-10, where at least one $D1_N$ is present in the top strand and is base paired with a corresponding $D2_N$ in the bottom strand. Optionally, $D1_N$ and $D1_{N+1}$ are base paired with corresponding $D2_N$ and $D2_{N+1}$; $D1_N$, $D1_{N+1}$ and $D1_{N+2}$ are base paired with corresponding $D2_N$, $D1_{N+1}$ and $D1_{N+2}$, etc. "N*"=0 to 15 or more, but is optionally 0, 1, 2, 3, 4, 5 or 6. In one embodiment, the top strand is the sense strand, and the bottom strand is the antisense strand. Alternatively, the bottom strand is the sense strand and the top strand is the antisense strand, with 2'-O-methyl RNA monomers located at alternating residues along the top strand, rather than the bottom strand presently depicted in the above schematic.

In another embodiment, the DNA:DNA-extended DsiRNA comprises strands having equal lengths possessing 1-3 mismatched residues that serve to orient Dicer cleavage (specifically, one or more of positions 1, 2 or 3 on the first strand of the DsiRNA, when numbering from the 3'-terminal residue, are mismatched with corresponding residues of the 5'-terminal region on the second strand when first and second strands are annealed to one another). An exemplary DNA:DNA-extended DsiRNA agent with two terminal mismatched residues is shown:

5'-D_NXXXXXXXXXXXXXXXXXXXXXXXXX$_{N*}$$M^M$-3'

3′-D_NXXXXXXXXXXXXXXXXXXXXXXXXX$_{N*}M_M$-5′

wherein “X”=RNA, “M”=Nucleic acid residues (RNA, DNA or non-natural or modified nucleic acids) that do not base pair (hydrogen bond) with corresponding “M” residues of otherwise complementary strand when strands are annealed, "D"=DNA and “N”=1 to 50 or more, but is optionally 1-8 or 1-10. “N*”=0 to 15 or more, but is optionally 0, 1, 2, 3, 4, 5 or 6. Any of the residues of such agents can optionally be 2'-O-methyl RNA monomers – alternating positioning of 2'-O-methyl RNA monomers that commences from the 3’-terminal residue of the bottom (second) strand, as shown for above asymmetric agents, can also be used in the above “blunt/fray” DsiRNA agent. In one embodiment, the top strand (first strand) is the sense strand, and the bottom strand (second strand) is the antisense strand. Alternatively, the bottom strand is the sense strand and the top strand is the antisense strand. Modification and DNA:DNA extension patterns paralleling those shown above for asymmetric/overhang agents can also be incorporated into such “blunt/frayed” agents.

In another embodiment, a length-extended DsiRNA agent is provided that comprises deoxyribonucleotides positioned at sites modeled to function *via* specific direction of Dicer cleavage, yet which does not require the presence of a base-paired deoxyribonucleotide in the dsRNA structure. Exemplary structures for such a molecule are shown:

5'-XXDDXXXXXXXXXXXXXXXXXXXX$_{N*}$Y-3'

3′-DDXXXXXXXXXXXXXXXXXXXX$_{N*}$-5′

or

5'-XDXDXXXXXXXXXXXXXXXXXXX$_{N*}$Y-3'

3′-DXDXXXXXXXXXXXXXXXXXXX$_{N*}$-5′

wherein "X"=RNA, "Y" is an optional overhang domain comprised of 0-10 RNA monomers that are optionally 2'-O-methyl RNA monomers – in certain embodiments, “Y” is an overhang domain comprised of 1-4 RNA monomers that are optionally 2'-O-methyl RNA monomers, and "D"=DNA. “N*”=0 to 15 or more, but is optionally 0, 1, 2, 3, 4, 5 or 6. In one embodiment, the top strand is the sense strand, and the bottom strand is the antisense strand. Alternatively, the bottom strand is the sense strand and the top strand is the antisense strand.

In any of the above embodiments where the bottom strand of the above structure is the antisense strand, the positioning of two deoxyribonucleotide residues at the ultimate and penultimate residues of the 5’ end of the antisense strand will help

reduce off-target effects (as prior studies have shown a 2'-O-methyl modification of at least the penultimate position from the 5' terminus of the antisense strand to reduce off-target effects; see, *e.g.*, US 2007/0223427).

In certain embodiments, the "D" residues of the above structures include at least one PS-DNA or PS-RNA. Optionally, the "D" residues of the above structures include at least one modified nucleotide that inhibits Dicer cleavage.

While the above-described "DNA-extended" DsiRNA agents can be categorized as either "left extended" or "right extended", DsiRNA agents comprising both left- and right-extended DNA-containing sequences within a single agent (*e.g.*, both flanks surrounding a core dsRNA structure are dsDNA extensions) can also be generated and used in similar manner to those described herein for "right-extended" and "left-extended" agents.

In some embodiments, the DsiRNA of the instant invention further comprises a linking moiety or domain that joins the sense and antisense strands of a DNA:DNA-extended DsiRNA agent. Optionally, such a linking moiety domain joins the 3' end of the sense strand and the 5' end of the antisense strand. The linking moiety may be a chemical (non-nucleotide) linker, such as an oligomethylenediol linker, oligoethylene glycol linker, or other art-recognized linker moiety. Alternatively, the linker can be a nucleotide linker, optionally including an extended loop and/or tetraloop.

In one embodiment, the DsiRNA agent has an asymmetric structure, with the sense strand having a 25-base pair length, and the antisense strand having a 27-base pair length with a 1-4 base 3'-overhang (*e.g.*, a one base 3'-overhang, a two base 3'-overhang, a three base 3'-overhang or a four base 3'-overhang). In another embodiment, this DsiRNA agent has an asymmetric structure further containing 2 deoxynucleotides at the 3' end of the sense strand.

In another embodiment, the DsiRNA agent has an asymmetric structure, with the antisense strand having a 25-base pair length, and the sense strand having a 27-base pair length with a 1-4 base 3'-overhang (*e.g.*, a one base 3'-overhang, a two base 3'-overhang, a three base 3'-overhang or a four base 3'-overhang). In another embodiment, this DsiRNA agent has an asymmetric structure further containing 2 deoxyribonucleotides at the 3' end of the antisense strand.

Exemplary AR targeting DsiRNA agents of the invention include the

following:

Table 2: Selected Anti-AR DsiRNA Agents

5'-AAGUUUUUAAAAGCUGCUAAAGAct-3' (SEQ ID NO: 1)
3'-ACUUCAAAAAUUUUCGACGAUUUCUGA-5' (SEQ ID NO: 154)
AR-252 Target: 5'-TGAAGTTTTTAAAAGCTGCTAAAGACT-3' (SEQ ID NO: 307)

5'-AGUUUUUAAAAGCUGCUAAAGACtc-3' (SEQ ID NO: 2)
3'-CUUCAAAAAUUUUCGACGAUUUCUGAG-5' (SEQ ID NO: 155)
AR-253 Target: 5'-GAAGTTTTTAAAAGCTGCTAAAGACTC-3' (SEQ ID NO: 308)

5'-GUUUUUAAAAGCUGCUAAAGACUcg-3' (SEQ ID NO: 3)
3'-UUCAAAAAUUUUCGACGAUUUCUGAGC-5' (SEQ ID NO: 156)
AR-254 Target: 5'-AAGTTTTTAAAAGCTGCTAAAGACTCG-3' (SEQ ID NO: 309)

5'-CGGAGCCAGAGAUCAAAAGAUGAaa-3' (SEQ ID NO: 4)
3'-ACGCCUCGGUCUCUAGUUUUCUACUUU-5' (SEQ ID NO: 157)
AR-682 Target: 5'-TGCGGAGCCAGAGATCAAAAGATGAAA-3' (SEQ ID NO: 310)

5'-CAGAGAUCAAAAGAUGAAAAGGCag-3' (SEQ ID NO: 5)
3'-CGGUCUCUAGUUUUCUACUUUUCCGUC-5' (SEQ ID NO: 158)
AR-688 Target: 5'-GCCAGAGATCAAAAGATGAAAAGGCAG-3' (SEQ ID NO: 311)

5'-AGAGAUCAAAAGAUGAAAAGGCAgt-3' (SEQ ID NO: 6)
3'-GGUCUCUAGUUUUCUACUUUUCCGUCA-5' (SEQ ID NO: 159)
AR-689 Target: 5'-CCAGAGATCAAAAGATGAAAAGGCAGT-3' (SEQ ID NO: 312)

5'-AAAGAUGAAAAGGCAGUCAGGUCtt-3' (SEQ ID NO: 7)
3'-GUUUUCUACUUUUCCGUCAGUCCAGAA-5' (SEQ ID NO: 160)
AR-697 Target: 5'-CAAAAGATGAAAAGGCAGTCAGGTCTT-3' (SEQ ID NO: 313)

5'-AAGAUGAAAAGGCAGUCAGGUCUtc-3' (SEQ ID NO: 8)
3'-UUUUCUACUUUUCCGUCAGUCCAGAAG-5' (SEQ ID NO: 161)
AR-698 Target: 5'-AAAAGATGAAAAGGCAGTCAGGTCTTC-3' (SEQ ID NO: 314)

5'-CAGGUCUUCAGUAGCCAAAAAACaa-3' (SEQ ID NO: 9)
3'-CAGUCCAGAAGUCAUCGGUUUUUUGUU-5' (SEQ ID NO: 162)
AR-714 Target: 5'-GTCAGGTCTTCAGTAGCCAAAAAACAA-3' (SEQ ID NO: 315)

5'-AGGUCUUCAGUAGCCAAAAAACAaa-3' (SEQ ID NO: 10)
3'-AGUCCAGAAGUCAUCGGUUUUUUGUUU-5' (SEQ ID NO: 163)
AR-715 Target: 5'-TCAGGTCTTCAGTAGCCAAAAAACAAA-3' (SEQ ID NO: 316)

5'-GUAGCCAAAAAACAAAACAAACAaa-3' (SEQ ID NO: 11)
3'-GUCAUCGGUUUUUUGUUUUGUUUGUUU-5' (SEQ ID NO: 164)
AR-724 Target: 5'-CAGTAGCCAAAAAACAAAACAAACAAA-3' (SEQ ID NO: 317)

5'-CAAAAAACAAAACAAACAAAAACaa-3' (SEQ ID NO: 12)

3'-CGGUUUUUUGUUUUGUUUGUUUUUGUU-5' (SEQ ID NO: 165)

AR-729 Target: 5'-GCCAAAAAACAAAACAAACAAAAACAA-3' (SEQ ID NO: 318)

5'-AAAAAACAAAACAAACAAAAACAaa-3' (SEQ ID NO: 13)
3'-GGUUUUUGUUUUGUUUGUUUUUGUUU-5' (SEQ ID NO: 166)

AR-730 Target: 5'-CCAAAAAACAAAACAAACAAAAACAAA-3' (SEQ ID NO: 319)

5'-AAAACAAACAAAAACAAAAAAGCcg-3' (SEQ ID NO: 14)
3'-UGUUUUGUUUGUUUUUGUUUUUUCGGC-5' (SEQ ID NO: 167)

AR-737 Target: 5'-ACAAAACAAACAAAAACAAAAAAGCCG-3' (SEQ ID NO: 320)

5'-CAAAAACAAAAAAGCCGAAAUAAaa-3' (SEQ ID NO: 15)
3'-UUGUUUUUGUUUUUUCGGCUUUAUUUU-5' (SEQ ID NO: 168)

AR-745 Target: 5'-AACAAAAACAAAAAAGCCGAAATAAAA-3' (SEQ ID NO: 321)

5'-AAAAACAAAAAAGCCGAAAUAAAag-3' (SEQ ID NO: 16)
3'-UGUUUUUGUUUUUUCGGCUUUAUUUUC-5' (SEQ ID NO: 169)

AR-746 Target: 5'-ACAAAAACAAAAAAGCCGAAATAAAAG-3' (SEQ ID NO: 322)

5'-AAAACAAAAAAGCCGAAAUAAAAga-3' (SEQ ID NO: 17)
3'-GUUUUUGUUUUUUCGGCUUUAUUUUCU-5' (SEQ ID NO: 170)

AR-747 Target: 5'-CAAAAACAAAAAAGCCGAAATAAAAGA-3' (SEQ ID NO: 323)

5'-AAAAAAGCCGAAAUAAAAGAAAAag-3' (SEQ ID NO: 18)
3'-UGUUUUUCGGCUUUAUUUUCUUUUUC-5' (SEQ ID NO: 171)

AR-752 Target: 5'-ACAAAAAAGCCGAAATAAAAGAAAAAG-3' (SEQ ID NO: 324)

5'-AAAAAGCCGAAAUAAAAGAAAAAga-3' (SEQ ID NO: 19)
3'-GUUUUUUCGGCUUUAUUUUCUUUUUCU-5' (SEQ ID NO: 172)

AR-753 Target: 5'-CAAAAAAGCCGAAATAAAAGAAAAAGA-3' (SEQ ID NO: 325)

5'-AAAGCCGAAAUAAAAGAAAAAGAta-3' (SEQ ID NO: 20)
3'-UUUUUCGGCUUUAUUUUCUUUUUCUAU-5' (SEQ ID NO: 173)

AR-755 Target: 5'-AAAAAGCCGAAATAAAAGAAAAAGATA-3' (SEQ ID NO: 326)

5'-CGAAAUAAAAGAAAAAGAUAAUAac-3' (SEQ ID NO: 21)
3'-CGGCUUUAUUUUCUUUUUCUAUUAUUG-5' (SEQ ID NO: 174)

AR-760 Target: 5'-GCCGAAATAAAAGAAAAAGATAATAAC-3' (SEQ ID NO: 327)

5'-GAAAUAAAAGAAAAAGAUAAUAAct-3' (SEQ ID NO: 22)
3'-GGCUUUAUUUUCUUUUUCUAUUAUUGA-5' (SEQ ID NO: 175)

AR-761 Target: 5'-CCGAAATAAAAGAAAAAGATAATAACT-3' (SEQ ID NO: 328)

5'-AAAUAAAAGAAAAAGAUAAUAACtc-3' (SEQ ID NO: 23)
3'-GCUUUAUUUUCUUUUUCUAUUAUUGAG-5' (SEQ ID NO: 176)

AR-762 Target: 5'-CGAAATAAAAGAAAAAGATAATAACTC-3' (SEQ ID NO: 329)

5'-GAAAAAGAUAAUAACUCAGUUCUta-3' (SEQ ID NO: 24)

3'-UUCUUUUUCUAUUAUUGAGUCAAGAAU-5' (SEQ ID NO: 177)

AR-770 Target: 5'-AAGAAAAAGATAATAACTCAGTTCTTA-3' (SEQ ID NO: 330)

5'-AAGAUAAUAACUCAGUUCUUAUUtg-3' (SEQ ID NO: 25)
3'-UUUUCUAUUAUUGAGUCAAGAAUAAAC-5' (SEQ ID NO: 178)

AR-774 Target: 5'-AAAAGATAATAACTCAGTTCTTATTTG-3' (SEQ ID NO: 331)

5'-AGAUAAUAACUCAGUUCUUAUUUgc-3' (SEQ ID NO: 26)
3'-UUUCUAUUAUUGAGUCAAGAAUAAACG-5' (SEQ ID NO: 179)

AR-775 Target: 5'-AAAGATAATAACTCAGTTCTTATTTGC-3' (SEQ ID NO: 332)

5'-AUAAUAACUCAGUUCUUAUUUGCac-3' (SEQ ID NO: 27)
3'-UCUAUUAUUGAGUCAAGAAUAAACGUG-5' (SEQ ID NO: 180)

AR-777 Target: 5'-AGATAATAACTCAGTTCTTATTTGCAC-3' (SEQ ID NO: 333)

5'-UAAUAACUCAGUUCUUAUUUGCAcc-3' (SEQ ID NO: 28)
3'-CUAUUAUUGAGUCAAGAAUAAACGUGG-5' (SEQ ID NO: 181)

AR-778 Target: 5'-GATAATAACTCAGTTCTTATTTGCACC-3' (SEQ ID NO: 334)

5'-UUAUUUGCACCUACUUCAGUGGAca-3' (SEQ ID NO: 29)
3'-AGAAUAAACGUGGAUGAAGUCACCUGU-5' (SEQ ID NO: 182)

AR-792 Target: 5'-TCTTATTTGCACCTACTTCAGTGGACA-3' (SEQ ID NO: 335)

5'-AGUGGACACUGAAUUUGGAAGGUgg-3' (SEQ ID NO: 30)
3'-AGUCACCUGUGACUUAAACCUUCCACC-5' (SEQ ID NO: 183)

AR-809 Target: 5'-TCAGTGGACACTGAATTTGGAAGGTGG-3' (SEQ ID NO: 336)

5'-CUGAAUUUGGAAGGUGGAGGAUUtt-3' (SEQ ID NO: 31)
3'-GUGACUUAAACCUUCCACCUCCUAAAA-5' (SEQ ID NO: 184)

AR-817 Target: 5'-CACTGAATTTGGAAGGTGGAGGATTTT-3' (SEQ ID NO: 337)

5'-UGGAAGGUGGAGGAUUUUGUUUUtt-3' (SEQ ID NO: 32)
3'-AAACCUUCCACCUCCUAAAACAAAAAA-5' (SEQ ID NO: 185)

AR-824 Target: 5'-TTTGGAAGGTGGAGGATTTTGTTTTTT-3' (SEQ ID NO: 338)

5'-AAGGUGGAGGAUUUUGUUUUUUUct-3' (SEQ ID NO: 33)
3'-CCUUCCACCUCCUAAAACAAAAAAAGA-5' (SEQ ID NO: 186)

AR-827 Target: 5'-GGAAGGTGGAGGATTTTGTTTTTTCT-3' (SEQ ID NO: 339)

5'-GAGGAUUUUGUUUUUUUCUUUUAag-3' (SEQ ID NO: 34)
3'-ACCUCCUAAAACAAAAAAAGAAAAUUC-5' (SEQ ID NO: 187)

AR-833 Target: 5'-TGGAGGATTTTGTTTTTTTCTTTTAAG-3' (SEQ ID NO: 340)

5'-AGGAUUUUGUUUUUUUCUUUUAAga-3' (SEQ ID NO: 35)
3'-CCUCCUAAAACAAAAAAAGAAAAUUCU-5' (SEQ ID NO: 188)

AR-834 Target: 5'-GGAGGATTTTGTTTTTTTCTTTTAAGA-3' (SEQ ID NO: 341)

5'-GAUUUUGUUUUUUUCUUUUAAGAtc-3' (SEQ ID NO: 36)

3'-UCCUAAAACAAAAAAAGAAAAUUCUAG-5' (SEQ ID NO: 189)

AR-836 Target: 5'-AGGATTTTGTTTTTTCTTTTAAGATC-3' (SEQ ID NO: 342)

5'-AUUUUGUUUUUUUCUUUUAAGAUct-3' (SEQ ID NO: 37)
3'-CCUAAAACAAAAAAAGAAAAUUCUAGA-5' (SEQ ID NO: 190)

AR-837 Target: 5'-GGATTTTGTTTTTTCTTTTAAGATCT-3' (SEQ ID NO: 343)

5'-UUUUGUUUUUUUCUUUUAAGAUCtg-3' (SEQ ID NO: 38)
3'-CUAAAACAAAAAAAGAAAAUUCUAGAC-5' (SEQ ID NO: 191)

AR-838 Target: 5'-GATTTTGTTTTTTCTTTTAAGATCTG-3' (SEQ ID NO: 344)

5'-UUUGUUUUUUUCUUUUAAGAUCUgg-3' (SEQ ID NO: 39)
3'-UAAAACAAAAAAAGAAAAUUCUAGACC-5' (SEQ ID NO: 192)

AR-839 Target: 5'-ATTTTGTTTTTTCTTTTAAGATCTGG-3' (SEQ ID NO: 345)

5'-UUUUUUUCUUUUAAGAUCUGGGCat-3' (SEQ ID NO: 40)
3'-ACAAAAAAAGAAAAUUCUAGACCCGUA-5' (SEQ ID NO: 193)

AR-843 Target: 5'-TGTTTTTTCTTTTAAGATCTGGGCAT-3' (SEQ ID NO: 346)

5'-UUUUUUCUUUUAAGAUCUGGGCAtc-3' (SEQ ID NO: 41)
3'-CAAAAAAAGAAAAUUCUAGACCCGUAG-5' (SEQ ID NO: 194)

AR-844 Target: 5'-GTTTTTTCTTTTAAGATCTGGGCATC-3' (SEQ ID NO: 347)

5'-UAAGAUCUGGGCAUCUUUUGAAUct-3' (SEQ ID NO: 42)
3'-AAAUUCUAGACCCGUAGAAAACUUAGA-5' (SEQ ID NO: 195)

AR-854 Target: 5'-TTTAAGATCTGGGCATCTTTTGAATCT-3' (SEQ ID NO: 348)

5'-CUUUUGAAUCUACCCUUCAAGUAtt-3' (SEQ ID NO: 43)
3'-UAGAAAACUUAGAUGGGAAGUUCAUAA-5' (SEQ ID NO: 196)

AR-868 Target: 5'-ATCTTTTGAATCTACCCTTCAAGTATT-3' (SEQ ID NO: 349)

5'-UUUUGAAUCUACCCUUCAAGUAUta-3' (SEQ ID NO: 44)
3'-AGAAAACUUAGAUGGGAAGUUCAUAAU-5' (SEQ ID NO: 197)

AR-869 Target: 5'-TCTTTTGAATCTACCCTTCAAGTATTA-3' (SEQ ID NO: 350)

5'-UUUGAAUCUACCCUUCAAGUAUUaa-3' (SEQ ID NO: 45)
3'-GAAAACUUAGAUGGGAAGUUCAUAAUU-5' (SEQ ID NO: 198)

AR-870 Target: 5'-CTTTTGAATCTACCCTTCAAGTATTAA-3' (SEQ ID NO: 351)

5'-UUGAAUCUACCCUUCAAGUAUUAag-3' (SEQ ID NO: 46)
3'-AAAACUUAGAUGGGAAGUUCAUAAUUC-5' (SEQ ID NO: 199)

AR-871 Target: 5'-TTTTGAATCTACCCTTCAAGTATTAAG-3' (SEQ ID NO: 352)

5'-UGAAUCUACCCUUCAAGUAUUAAga-3' (SEQ ID NO: 47)
3'-AAACUUAGAUGGGAAGUUCAUAAUUCU-5' (SEQ ID NO: 200)

AR-872 Target: 5'-TTTGAATCTACCCTTCAAGTATTAAGA-3' (SEQ ID NO: 353)

5'-AAGUAUUAAGAGACAGACUGUGAgc-3' (SEQ ID NO: 48)

3'-AGUUCAUAAUUCUCUGUCUGACACUCG-5' (SEQ ID NO: 201)

AR-886 Target: 5'-TCAAGTATTAAGAGACAGACTGTGAGC-3' (SEQ ID NO: 354)

5'-UAUUAAGAGACAGACUGUGAGCCta-3' (SEQ ID NO: 49)
3'-UCAUAAUUCUCUGUCUGACACUCGGAU-5' (SEQ ID NO: 202)

AR-889 Target: 5'-AGTATTAAGAGACAGACTGTGAGCCTA-3' (SEQ ID NO: 355)

5'-GUUGAACUCUUCUGAGCAAGAGAag-3' (SEQ ID NO: 50)
3'-GACAACUUGAGAAGACUCGUUCUCUUC-5' (SEQ ID NO: 203)

AR-1067 Target: 5'-CTGTTGAACTCTTCTGAGCAAGAGAAG-3' (SEQ ID NO: 356)

5'-UUGAACUCUUCUGAGCAAGAGAAgg-3' (SEQ ID NO: 51)
3'-ACAACUUGAGAAGACUCGUUCUCUUCC-5' (SEQ ID NO: 204)

AR-1068 Target: 5'-TGTTGAACTCTTCTGAGCAAGAGAAGG-3' (SEQ ID NO: 357)

5'-AGGAUGGAAGUGCAGUUAGGGCUgg-3' (SEQ ID NO: 52)
3'-GUUCCUACCUUCACGUCAAUCCCGACC-5' (SEQ ID NO: 205)

AR-1137 Target: 5'-CAAGGATGGAAGTGCAGTTAGGGCTGG-3' (SEQ ID NO: 358)

5'-GAGGAGCUUUCCAGAAUCUGUUCca-3' (SEQ ID NO: 53)
3'-GGCUCCUCGAAAGGUCUUAGACAAGGU-5' (SEQ ID NO: 206)

AR-1198 Target: 5'-CCGAGGAGCTTTCCAGAATCTGTTCCA-3' (SEQ ID NO: 359)

5'-AGGAGCUUUCCAGAAUCUGUUCCag-3' (SEQ ID NO: 54)
3'-GCUCCUCGAAAGGUCUUAGACAAGGUC-5' (SEQ ID NO: 207)

AR-1199 Target: 5'-CGAGGAGCTTTCCAGAATCTGTTCCAG-3' (SEQ ID NO: 360)

5'-CUGACCUUAAAGACAUCCUGAGCga-3' (SEQ ID NO: 55)
3'-GCGACUGGAAUUUCUGUAGGACUCGCU-5' (SEQ ID NO: 208)

AR-1675 Target: 5'-CGCTGACCTTAAAGACATCCTGAGCGA-3' (SEQ ID NO: 361)

5'-CAAGGACAAUUACUUAGGGGGCAct-3' (SEQ ID NO: 56)
3'-AGGUUCCUGUUAAUGAAUCCCCCGUGA-5' (SEQ ID NO: 209)

AR-1802 Target: 5'-TCCAAGGACAATTACTTAGGGGGCACT-3' (SEQ ID NO: 362)

5'-AAGGAGUUGUGUAAGGCAGUGUCgg-3' (SEQ ID NO: 57)
3'-GGUUCCUCAACACAUUCCGUCACAGCC-5' (SEQ ID NO: 210)

AR-1848 Target: 5'-CCAAGGAGTTGTGTAAGGCAGTGTCGG-3' (SEQ ID NO: 363)

5'-CUGAAGAUACUGCUGAGUAUUCCcc-3' (SEQ ID NO: 58)
3'-GUGACUUCUAUGACGACUCAUAAGGGG-5' (SEQ ID NO: 211)

AR-2047 Target: 5'-CACTGAAGATACTGCTGAGTATTCCCC-3' (SEQ ID NO: 364)

5'-CUGAGUAUUCCCCUUUCAAGGGAgg-3' (SEQ ID NO: 59)
3'-ACGACUCAUAAGGGGAAAGUUCCCUCC-5' (SEQ ID NO: 212)

AR-2059 Target: 5'-TGCTGAGTATTCCCCTTTCAAGGGAGG-3' (SEQ ID NO: 365)

5'-CUUGUGUCAAAAGCGAAAUGGGCcc-3' (SEQ ID NO: 60)

3'-GUGAACACAGUUUUCGCUUUACCCGGG-5' (SEQ ID NO: 213)

AR-2692 Target: 5'-CACTTGTGTCAAAAGCGAAATGGGCCC-3' (SEQ ID NO: 366)

5'-UUGUGUCAAAAGCGAAAUGGGCCcc-3' (SEQ ID NO: 61)
3'-UGAACACAGUUUUCGCUUUACCCGGGG-5' (SEQ ID NO: 214)

AR-2693 Target: 5'-ACTTGTGTCAAAAGCGAAATGGGCCCC-3' (SEQ ID NO: 367)

5'-CAUGUUUUGCCCAUUGACUAUUAct-3' (SEQ ID NO: 62)
3'-UGGUACAAAACGGGUAACUGAUAAUGA-5' (SEQ ID NO: 215)

AR-2775 Target: 5'-ACCATGTTTTGCCCATTGACTATTACT-3' (SEQ ID NO: 368)

5'-UGUUUUGCCCAUUGACUAUUACUtt-3' (SEQ ID NO: 63)
3'-GUACAAAACGGGUAACUGAUAAUGAAA-5' (SEQ ID NO: 216)

AR-2777 Target: 5'-CATGTTTTGCCCATTGACTATTACTTT-3' (SEQ ID NO: 369)

5'-GUGGAGAUGAAGCUUCUGGGUGUca-3' (SEQ ID NO: 64)
3'-GACACCUCUACUUCGAAGACCCACAGU-5' (SEQ ID NO: 217)

AR-2827 Target: 5'-CTGTGGAGATGAAGCTTCTGGGTGTCA-3' (SEQ ID NO: 370)

5'-AAGGGAAACAGAAGUACCUGUGCgc-3' (SEQ ID NO: 65)
3'-ACUUCCCUUUGUCUUCAUGGACACGCG-5' (SEQ ID NO: 218)

AR-2905 Target: 5'-TGAAGGGAAACAGAAGTACCTGTGCGC-3' (SEQ ID NO: 371)

5'-AGAAAUGAUUGCACUAUUGAUAAat-3' (SEQ ID NO: 66)
3'-CGUCUUUACUAACGUGAUAACUAUUUA-5' (SEQ ID NO: 219)

AR-2934 Target: 5'-GCAGAAATGATTGCACTATTGATAAAT-3' (SEQ ID NO: 372)

5'-GAAAUGAUUGCACUAUUGAUAAAtt-3' (SEQ ID NO: 67)
3'-GUCUUUACUAACGUGAUAACUAUUUAA-5' (SEQ ID NO: 220)

AR-2935 Target: 5'-CAGAAATGATTGCACTATTGATAAATT-3' (SEQ ID NO: 373)

5'-AAAUGAUUGCACUAUUGAUAAAUtc-3' (SEQ ID NO: 68)
3'-UCUUUACUAACGUGAUAACUAUUUAAG-5' (SEQ ID NO: 221)

AR-2936 Target: 5'-AGAAATGATTGCACTATTGATAAATTC-3' (SEQ ID NO: 374)

5'-AUGAUUGCACUAUUGAUAAAUUCcg-3' (SEQ ID NO: 69)
3'-UUUACUAACGUGAUAACUAUUUAAGGC-5' (SEQ ID NO: 222)

AR-2938 Target: 5'-AAATGATTGCACTATTGATAAATTCCG-3' (SEQ ID NO: 375)

5'-UGAUUGCACUAUUGAUAAAUUCCga-3' (SEQ ID NO: 70)
3'-UUACUAACGUGAUAACUAUUUAAGGCU-5' (SEQ ID NO: 223)

AR-2939 Target: 5'-AATGATTGCACTATTGATAAATTCCGA-3' (SEQ ID NO: 376)

5'-CUAUUGAUAAAUUCCGAAGGAAAaa-3' (SEQ ID NO: 71)
3'-GUGAUAACUAUUUAAGGCUUCCUUUUU-5' (SEQ ID NO: 224)

AR-2947 Target: 5'-CACTATTGATAAATTCCGAAGGAAAAA-3' (SEQ ID NO: 377)

5'-UAUUGAUAAAUUCCGAAGGAAAAat-3' (SEQ ID NO: 72)

3'-UGAUAACUAUUUAAGGCUUCCUUUUUA-5' (SEQ ID NO: 225)

AR-2948 Target: 5'-ACTATTGATAAATTCCGAAGGAAAAAT-3' (SEQ ID NO: 378)

5'-AUUGAUAAAUUCCGAAGGAAAAAtt-3' (SEQ ID NO: 73)
3'-GAUAACUAUUUAAGGCUUCCUUUUUAA-5' (SEQ ID NO: 226)

AR-2949 Target: 5'-CTATTGATAAATTCCGAAGGAAAAATT-3' (SEQ ID NO: 379)

5'-UUGAUAAAUUCCGAAGGAAAAAUtg-3' (SEQ ID NO: 74)
3'-AUAACUAUUUAAGGCUUCCUUUUUAAC-5' (SEQ ID NO: 227)

AR-2950 Target: 5'-TATTGATAAATTCCGAAGGAAAAATTG-3' (SEQ ID NO: 380)

5'-UGAUAAAUUCCGAAGGAAAAAUUgt-3' (SEQ ID NO: 75)
3'-UAACUAUUUAAGGCUUCCUUUUUAACA-5' (SEQ ID NO: 228)

AR-2951 Target: 5'-ATTGATAAATTCCGAAGGAAAAATTGT-3' (SEQ ID NO: 381)

5'-AUAAAUUCCGAAGGAAAAAUUGUcc-3' (SEQ ID NO: 76)
3'-ACUAUUUAAGGCUUCCUUUUUAACAGG-5' (SEQ ID NO: 229)

AR-2953 Target: 5'-TGATAAATTCCGAAGGAAAAATTGTCC-3' (SEQ ID NO: 382)

5'-UAAAUUCCGAAGGAAAAAUUGUCca-3' (SEQ ID NO: 77)
3'-CUAUUUAAGGCUUCCUUUUUAACAGGU-5' (SEQ ID NO: 230)

AR-2954 Target: 5'-GATAAATTCCGAAGGAAAAATTGTCCA-3' (SEQ ID NO: 383)

5'-AAGGAAAAAUUGUCCAUCUUGUCgt-3' (SEQ ID NO: 78)
3'-GCUUCCUUUUUAACAGGUAGAACAGCA-5' (SEQ ID NO: 231)

AR-2963 Target: 5'-CGAAGGAAAAATTGTCCATCTTGTCGT-3' (SEQ ID NO: 384)

5'-CUUGUCGUCUUCGGAAAUGUUAUga-3' (SEQ ID NO: 79)
3'-UAGAACAGCAGAAGCCUUUACAAUACU-5' (SEQ ID NO: 232)

AR-2980 Target: 5'-ATCTTGTCGTCTTCGGAAATGTTATGA-3' (SEQ ID NO: 385)

5'-GAAAUGUUAUGAAGCAGGGAUGAct-3' (SEQ ID NO: 80)
3'-GCCUUUACAAUACUUCGUCCCUACUGA-5' (SEQ ID NO: 233)

AR-2993 Target: 5'-CGGAAATGTTATGAAGCAGGGATGACT-3' (SEQ ID NO: 386)

5'-AAUGUUAUGAAGCAGGGAUGACUct-3' (SEQ ID NO: 81)
3'-CUUUACAAUACUUCGUCCCUACUGAGA-5' (SEQ ID NO: 234)

AR-2995 Target: 5'-GAAATGTTATGAAGCAGGGATGACTCT-3' (SEQ ID NO: 387)

5'-CGGAAGCUGAAGAAACUUGGUAAtc-3' (SEQ ID NO: 82)
3'-GGGCCUUCGACUUCUUUGAACCAUUAG-5' (SEQ ID NO: 235)

AR-3027 Target: 5'-CCCGGAAGCTGAAGAAACTTGGTAATC-3' (SEQ ID NO: 388)

5'-GAAGCUGAAGAAACUUGGUAAUCtg-3' (SEQ ID NO: 83)
3'-GCCUUCGACUUCUUUGAACCAUUAGAC-5' (SEQ ID NO: 236)

AR-3029 Target: 5'-CGGAAGCTGAAGAAACTTGGTAATCTG-3' (SEQ ID NO: 389)

5'-UGAAGAAACUUGGUAAUCUGAAAct-3' (SEQ ID NO: 84)

3'-CGACUUCUUUGAACCAUUAGACUUUGA-5' (SEQ ID NO: 237)

AR-3034 Target: 5'-GCTGAAGAAACTTGGTAATCTGAAACT-3' (SEQ ID NO: 390)

5'-GAAGAAACUUGGUAAUCUGAAACta-3' (SEQ ID NO: 85)
3'-GACUUCUUUGAACCAUUAGACUUUGAU-5' (SEQ ID NO: 238)

AR-3035 Target: 5'-CTGAAGAAACTTGGTAATCTGAAACTA-3' (SEQ ID NO: 391)

5'-AAGAAACUUGGUAAUCUGAAACUac-3' (SEQ ID NO: 86)
3'-ACUUCUUUGAACCAUUAGACUUUGAUG-5' (SEQ ID NO: 239)

AR-3036 Target: 5'-TGAAGAAACTTGGTAATCTGAAACTAC-3' (SEQ ID NO: 392)

5'-GGUAAUCUGAAACUACAGGAGGAag-3' (SEQ ID NO: 87)
3'-AACCAUUAGACUUUGAUGUCCUCCUUC-5' (SEQ ID NO: 240)

AR-3045 Target: 5'-TTGGTAATCTGAAACTACAGGAGGAAG-3' (SEQ ID NO: 393)

5'-CUGAAACUACAGGAGGAAGGAGAgg-3' (SEQ ID NO: 88)
3'-UAGACUUUGAUGUCCUCCUUCCUCUCC-5' (SEQ ID NO: 241)

AR-3051 Target: 5'-ATCTGAAACTACAGGAGGAAGGAGAGG-3' (SEQ ID NO: 394)

5'-CAGGAAUUCCUGUGCAUGAAAGCac-3' (SEQ ID NO: 89)
3'-GGGUCCUUAAGGACACGUACUUUCGUG-5' (SEQ ID NO: 242)

AR-3546 Target: 5'-CCCAGGAATTCCTGTGCATGAAAGCAC-3' (SEQ ID NO: 395)

5'-AGGAAUUCCUGUGCAUGAAAGCAct-3' (SEQ ID NO: 90)
3'-GGUCCUUAAGGACACGUACUUUCGUGA-5' (SEQ ID NO: 243)

AR-3547 Target: 5'-CCAGGAATTCCTGTGCATGAAAGCACT-3' (SEQ ID NO: 396)

5'-GGAUGGGCUGAAAAAUCAAAAAUtc-3' (SEQ ID NO: 91)
3'-CACCUACCCGACUUUUUAGUUUUUAAG-5' (SEQ ID NO: 244)

AR-3596 Target: 5'-GTGGATGGGCTGAAAAATCAAAAATTC-3' (SEQ ID NO: 397)

5'-GAUGGGCUGAAAAAUCAAAAAUUct-3' (SEQ ID NO: 92)
3'-ACCUACCCGACUUUUUAGUUUUUAAGA-5' (SEQ ID NO: 245)

AR-3597 Target: 5'-TGGATGGGCTGAAAAATCAAAAATTCT-3' (SEQ ID NO: 398)

5'-UGGGCUGAAAAAUCAAAAAUUCUtt-3' (SEQ ID NO: 93)
3'-CUACCCGACUUUUUAGUUUUUAAGAAA-5' (SEQ ID NO: 246)

AR-3599 Target: 5'-GATGGGCTGAAAAATCAAAAATTCTTT-3' (SEQ ID NO: 399)

5'-CUGAAAAAUCAAAAAUUCUUUGAtg-3' (SEQ ID NO: 94)
3'-CCGACUUUUUAGUUUUUAAGAAACUAC-5' (SEQ ID NO: 247)

AR-3603 Target: 5'-GGCTGAAAAATCAAAAATTCTTTGATG-3' (SEQ ID NO: 400)

5'-UGAAAAAUCAAAAAUUCUUUGAUga-3' (SEQ ID NO: 95)
3'-CGACUUUUUAGUUUUUAAGAAACUACU-5' (SEQ ID NO: 248)

AR-3604 Target: 5'-GCTGAAAAATCAAAAATTCTTTGATGA-3' (SEQ ID NO: 401)

5'-AAAAAUCAAAAAUUCUUUGAUGAac-3' (SEQ ID NO: 96)

3'-ACUUUUUAGUUUUUAAGAAACUACUUG-5' (SEQ ID NO: 249)

AR-3606 Target: 5'-TGAAAAATCAAAAATTCTTTGATGAAC-3' (SEQ ID NO: 402)

5'-AAAAUCAAAAAUUCUUUGAUGAAct-3' (SEQ ID NO: 97)
3'-CUUUUUAGUUUUUAAGAAACUACUUGA-5' (SEQ ID NO: 250)

AR-3607 Target: 5'-GAAAAATCAAAAATTCTTTGATGAACT-3' (SEQ ID NO: 403)

5'-AAAUCAAAAAUUCUUUGAUGAACtt-3' (SEQ ID NO: 98)
3'-UUUUUAGUUUUUAAGAAACUACUUGAA-5' (SEQ ID NO: 251)

AR-3608 Target: 5'-AAAAATCAAAAATTCTTTGATGAACTT-3' (SEQ ID NO: 404)

5'-CGAAUGAACUACAUCAAGGAACUcg-3' (SEQ ID NO: 99)
3'-AAGCUUACUUGAUGUAGUUCCUUGAGC-5' (SEQ ID NO: 252)

AR-3633 Target: 5'-TTCGAATGAACTACATCAAGGAACTCG-3' (SEQ ID NO: 405)

5'-AAGGAACUCGAUCGUAUCAUUGCat-3' (SEQ ID NO: 100)
3'-AGUUCCUUGAGCUAGCAUAGUAACGUA-5' (SEQ ID NO: 253)

AR-3648 Target: 5'-TCAAGGAACTCGATCGTATCATTGCAT-3' (SEQ ID NO: 406)

5'-AGGAACUCGAUCGUAUCAUUGCAtg-3' (SEQ ID NO: 101)
3'-GUUCCUUGAGCUAGCAUAGUAACGUAC-5' (SEQ ID NO: 254)

AR-3649 Target: 5'-CAAGGAACTCGATCGTATCATTGCATG-3' (SEQ ID NO: 407)

5'-CGUAUCAUUGCAUGCAAAAGAAAaa-3' (SEQ ID NO: 102)
3'-UAGCAUAGUAACGUACGUUUUCUUUUU-5' (SEQ ID NO: 255)

AR-3660 Target: 5'-ATCGTATCATTGCATGCAAAAGAAAAA-3' (SEQ ID NO: 408)

5'-GUAUCAUUGCAUGCAAAAGAAAAaa-3' (SEQ ID NO: 103)
3'-AGCAUAGUAACGUACGUUUUCUUUUUU-5' (SEQ ID NO: 256)

AR-3661 Target: 5'-TCGTATCATTGCATGCAAAAGAAAAAA-3' (SEQ ID NO: 409)

5'-CAUUGCAUGCAAAAGAAAAAAUCcc-3' (SEQ ID NO: 104)
3'-UAGUAACGUACGUUUUCUUUUUUAGGG-5' (SEQ ID NO: 257)

AR-3665 Target: 5'-ATCATTGCATGCAAAAGAAAAAATCCC-3' (SEQ ID NO: 410)

5'-CUUUUGACCUGCUAAUCAAGUCAca-3' (SEQ ID NO: 105)
3'-GUGAAAACUGGACGAUUAGUUCAGUGU-5' (SEQ ID NO: 258)

AR-3772 Target: 5'-CACTTTTGACCTGCTAATCAAGTCACA-3' (SEQ ID NO: 411)

5'-GUGGACUUUCCGGAAAUGAUGGCag-3' (SEQ ID NO: 106)
3'-CGCACCUGAAAGGCCUUUACUACCGUC-5' (SEQ ID NO: 259)

AR-3807 Target: 5'-GCGTGGACTTTCCGGAAATGATGGCAG-3' (SEQ ID NO: 412)

5'-UGGACUUUCCGGAAAUGAUGGCAga-3' (SEQ ID NO: 107)
3'-GCACCUGAAAGGCCUUUACUACCGUCU-5' (SEQ ID NO: 260)

AR-3808 Target: 5'-CGTGGACTTTCCGGAAATGATGGCAGA-3' (SEQ ID NO: 413)

5'-AUGGCAGAGAUCAUCUCUGUGCAag-3' (SEQ ID NO: 108)

3'-ACUACCGUCUCUAGUAGAGACACGUUC-5' (SEQ ID NO: 261)

AR-3825 Target: 5'-TGATGGCAGAGATCATCTCTGTGCAAG-3' (SEQ ID NO: 414)

5'-AGAGAUCAUCUCUGUGCAAGUGCcc-3' (SEQ ID NO: 109)
3'-CGUCUCUAGUAGAGACACGUUCACGGG-5' (SEQ ID NO: 262)

AR-3830 Target: 5'-GCAGAGATCATCTCTGTGCAAGTGCCC-3' (SEQ ID NO: 415)

5'-GAGAUCAUCUCUGUGCAAGUGCCca-3' (SEQ ID NO: 110)
3'-GUCUCUAGUAGAGACACGUUCACGGGU-5' (SEQ ID NO: 263)

AR-3831 Target: 5'-CAGAGATCATCTCTGTGCAAGTGCCCA-3' (SEQ ID NO: 416)

5'-CAAGAUCCUUUCUGGGAAAGUCAag-3' (SEQ ID NO: 111)
3'-GGGUUCUAGGAAAGACCCUUUCAGUUC-5' (SEQ ID NO: 264)

AR-3854 Target: 5'-CCCAAGATCCTTTCTGGGAAAGTCAAG-3' (SEQ ID NO: 417)

5'-GAAGCAUUGGAAACCCUAUUUCCcc-3' (SEQ ID NO: 112)
3'-CACUUCGUAACCUUUGGGAUAAAGGGG-5' (SEQ ID NO: 265)

AR-3901 Target: 5'-GTGAAGCATTGGAAACCCTATTTCCCC-3' (SEQ ID NO: 418)

5'-GAUGUCUUCUGCCUGUUAUAACUct-3' (SEQ ID NO: 113)
3'-GUCUACAGAAGACGGACAAUAUUGAGA-5' (SEQ ID NO: 266)

AR-3949 Target: 5'-CAGATGTCTTCTGCCTGTTATAACTCT-3' (SEQ ID NO: 419)

5'-CUUGGGGAAUUUCCUCUAUUGAUgt-3' (SEQ ID NO: 114)
3'-CGGAACCCCUUAAAGGAGAUAACUACA-5' (SEQ ID NO: 267)

AR-3994 Target: 5'-GCCTTGGGGAATTTCCTCTATTGATGT-3' (SEQ ID NO: 420)

5'-UGGGGAAUUUCCUCUAUUGAUGUac-3' (SEQ ID NO: 115)
3'-GAACCCCUUAAAGGAGAUAACUACAUG-5' (SEQ ID NO: 268)

AR-3996 Target: 5'-CTTGGGGAATTTCCTCTATTGATGTAC-3' (SEQ ID NO: 421)

5'-GGGGAAUUUCCUCUAUUGAUGUAca-3' (SEQ ID NO: 116)
3'-AACCCCUUAAAGGAGAUAACUACAUGU-5' (SEQ ID NO: 269)

AR-3997 Target: 5'-TTGGGGAATTTCCTCTATTGATGTACA-3' (SEQ ID NO: 422)

5'-GGGAAUUUCCUCUAUUGAUGUACag-3' (SEQ ID NO: 117)
3'-ACCCCUUAAAGGAGAUAACUACAUGUC-5' (SEQ ID NO: 270)

AR-3998 Target: 5'-TGGGGAATTTCCTCTATTGATGTACAG-3' (SEQ ID NO: 423)

5'-GGAAUUUCCUCUAUUGAUGUACAgt-3' (SEQ ID NO: 118)
3'-CCCCUUAAAGGAGAUAACUACAUGUCA-5' (SEQ ID NO: 271)

AR-3999 Target: 5'-GGGGAATTTCCTCTATTGATGTACAGT-3' (SEQ ID NO: 424)

5'-AUUGAUGUACAGUCUGUCAUGAAca-3' (SEQ ID NO: 119)
3'-GAUAACUACAUGUCAGACAGUACUUGU-5' (SEQ ID NO: 272)

AR-4011 Target: 5'-CTATTGATGTACAGTCTGTCATGAACA-3' (SEQ ID NO: 425)

5'-UUGAUGUACAGUCUGUCAUGAACat-3' (SEQ ID NO: 120)

3'-AUAACUACAUGUCAGACAGUACUUGUA-5' (SEQ ID NO: 273)

AR-4012 Target: 5'-TATTGATGTACAGTCTGTCATGAACAT-3' (SEQ ID NO: 426)

5'-UGAUGUACAGUCUGUCAUGAACAtg-3' (SEQ ID NO: 121)
3'-UAACUACAUGUCAGACAGUACUUGUAC-5' (SEQ ID NO: 274)

AR-4013 Target: 5'-ATTGATGTACAGTCTGTCATGAACATG-3' (SEQ ID NO: 427)

5'-CAUGUUCCUGAAUUCUAUUUGCUgg-3' (SEQ ID NO: 122)
3'-UUGUACAAGGACUUAAGAUAAACGACC-5' (SEQ ID NO: 275)

AR-4034 Target: 5'-AACATGTTCCTGAATTCTATTTGCTGG-3' (SEQ ID NO: 428)

5'-CUAUUUGCUGGGCUUUUUUUUUCtc-3' (SEQ ID NO: 123)
3'-AAGAUAAACGACCCGAAAAAAAAAGAG-5' (SEQ ID NO: 276)

AR-4048 Target: 5'-TTCTATTTGCTGGGCTTTTTTTTTCTC-3' (SEQ ID NO: 429)

5'-UAUUUGCUGGGCUUUUUUUUUCUct-3' (SEQ ID NO: 124)
3'-AGAUAAACGACCCGAAAAAAAAAGAGA-5' (SEQ ID NO: 277)

AR-4049 Target: 5'-TCTATTTGCTGGGCTTTTTTTTTCTCT-3' (SEQ ID NO: 430)

5'-CUGGGCUUUUUUUUUCUCUUUCUct-3' (SEQ ID NO: 125)
3'-ACGACCCGAAAAAAAAAGAGAAAGAGA-5' (SEQ ID NO: 278)

AR-4055 Target: 5'-TGCTGGGCTTTTTTTTTCTCTTTCTCT-3' (SEQ ID NO: 431)

5'-UUUUUUCUCUUUCUCUCCUUUCUtt-3' (SEQ ID NO: 126)
3'-AAAAAAAAGAGAAAGAGAGGAAAGAAA-5' (SEQ ID NO: 279)

AR-4064 Target: 5'-TTTTTTTTCTCTTTCTCTCCTTTCTTT-3' (SEQ ID NO: 432)

5'-CAGACUUUGCUUCCCAUUGUGGCtc-3' (SEQ ID NO: 127)
3'-AAGUCUGAAACGAAGGGUAACACCGAG-5' (SEQ ID NO: 280)

AR-4128 Target: 5'-TTCAGACTTTGCTTCCCATTGTGGCTC-3' (SEQ ID NO: 433)

5'-GUGGCUCCUAUCUGUGUUUUGAAtg-3' (SEQ ID NO: 128)
3'-AACACCGAGGAUAGACACAAAACUUAC-5' (SEQ ID NO: 281)

AR-4146 Target: 5'-TTGTGGCTCCTATCTGTGTTTTGAATG-3' (SEQ ID NO: 434)

5'-CUAUCUGUGUUUUGAAUGGUGUUGt-3' (SEQ ID NO: 129)
3'-AGGAUAGACACAAAACUUACCACAACA-5' (SEQ ID NO: 282)

AR-4153 Target: 5'-TCCTATCTGTGTTTTGAATGGTGTTGT-3' (SEQ ID NO: 435)

5'-CUGUGUUUUGAAUGGUGUUGUAUgc-3' (SEQ ID NO: 130)
3'-UAGACACAAAACUUACCACAACAUACG-5' (SEQ ID NO: 283)

AR-4157 Target: 5'-ATCTGTGTTTTGAATGGTGTTGTATGC-3' (SEQ ID NO: 436)

5'-UGUUUUGAAUGGUGUUGUAUGCCtt-3' (SEQ ID NO: 131)
3'-ACACAAAACUUACCACAACAUACGGAA-5' (SEQ ID NO: 284)

AR-4160 Target: 5'-TGTGTTTTGAATGGTGTTGTATGCCTT-3' (SEQ ID NO: 437)

5'-AAUGGUGUUGUAUGCCUUUAAAUct-3' (SEQ ID NO: 132)

3'-ACUUACCACAACAUACGGAAAUUUAGA-5' (SEQ ID NO: 285)

AR-4167 Target: 5'-TGAATGGTGTTGTATGCCTTTAAATCT-3' (SEQ ID NO: 438)

5'-AUGGUGUUGUAUGCCUUUAAAUCtg-3' (SEQ ID NO: 133)
3'-CUUACCACAACAUACGGAAAUUUAGAC-5' (SEQ ID NO: 286)

AR-4168 Target: 5'-GAATGGTGTTGTATGCCTTTAAATCTG-3' (SEQ ID NO: 439)

5'-UUGUAUGCCUUUAAAUCUGUGAUga-3' (SEQ ID NO: 134)
3'-ACAACAUACGGAAAUUUAGACACUACU-5' (SEQ ID NO: 287)

AR-4174 Target: 5'-TGTTGTATGCCTTTAAATCTGTGATGA-3' (SEQ ID NO: 440)

5'-GUAUGCCUUUAAAUCUGUGAUGAtc-3' (SEQ ID NO: 135)
3'-AACAUACGGAAAUUUAGACACUACUAG-5' (SEQ ID NO: 288)

AR-4176 Target: 5'-TTGTATGCCTTTAAATCTGTGATGATC-3' (SEQ ID NO: 441)

5'-UAUGCCUUUAAAUCUGUGAUGAUcc-3' (SEQ ID NO: 136)
3'-ACAUACGGAAAUUUAGACACUACUAGG-5' (SEQ ID NO: 289)

AR-4177 Target: 5'-TGTATGCCTTTAAATCTGTGATGATCC-3' (SEQ ID NO: 442)

5'-CAGUGUCAAGUUGUGCUUGUUUAca-3' (SEQ ID NO: 137)
3'-GGGUCACAGUUCAACACGAACAAAUGU-5' (SEQ ID NO: 290)

AR-4212 Target: 5'-CCCAGTGTCAAGTTGTGCTTGTTTACA-3' (SEQ ID NO: 443)

5'-AGUGUCAAGUUGUGCUUGUUUACag-3' (SEQ ID NO: 138)
3'-GGUCACAGUUCAACACGAACAAAUGUC-5' (SEQ ID NO: 291)

AR-4213 Target: 5'-CCAGTGTCAAGTTGTGCTTGTTTACAG-3' (SEQ ID NO: 444)

5'-UUGUUUACAGCACUACUCUGUGCca-3' (SEQ ID NO: 139)
3'-CGAACAAAUGUCGUGAUGAGACACGGU-5' (SEQ ID NO: 292)

AR-4228 Target: 5'-GCTTGTTTACAGCACTACTCTGTGCCA-3' (SEQ ID NO: 445)

5'-UGUUUACAGCACUACUCUGUGCCag-3' (SEQ ID NO: 140)
3'-GAACAAAUGUCGUGAUGAGACACGGUC-5' (SEQ ID NO: 293)

AR-4229 Target: 5'-CTTGTTTACAGCACTACTCTGTGCCAG-3' (SEQ ID NO: 446)

5'-CAAACGUUUACUUAUCUUAUGCCac-3' (SEQ ID NO: 141)
3'-GUGUUUGCAAAUGAAUAGAAUACGGUG-5' (SEQ ID NO: 294)

AR-4259 Target: 5'-CACAAACGTTTACTTATCTTATGCCAC-3' (SEQ ID NO: 447)

5'-CGGGAAGUUUAGAGAGCUAAGAUta-3' (SEQ ID NO: 142)
3'-GUGCCCUUCAAAUCUCUCGAUUCUAAU-5' (SEQ ID NO: 295)

AR-4283 Target: 5'-CACGGGAAGTTTAGAGAGCTAAGATTA-3' (SEQ ID NO: 448)

5'-GGGAAGUUUAGAGAGCUAAGAUUat-3' (SEQ ID NO: 143)
3'-UGCCCUUCAAAUCUCUCGAUUCUAAUA-5' (SEQ ID NO: 296)

AR-4284 Target: 5'-ACGGGAAGTTTAGAGAGCTAAGATTAT-3' (SEQ ID NO: 449)

5'-GGAAGUUUAGAGAGCUAAGAUUAtc-3' (SEQ ID NO: 144)

3'-GCCCUUCAAAUCUCUCGAUUCUAAUAG-5' (SEQ ID NO: 297)

AR-4285 Target: 5'-CGGGAAGTTTAGAGAGCTAAGATTATC-3' (SEQ ID NO: 450)

5'-GAAGUUUAGAGAGCUAAGAUUAUct-3' (SEQ ID NO: 145)
3'-CCCUUCAAAUCUCUCGAUUCUAAUAGA-5' (SEQ ID NO: 298)

AR-4286 Target: 5'-GGGAAGTTTAGAGAGCTAAGATTATCT-3' (SEQ ID NO: 451)

5'-AGUUUAGAGAGCUAAGAUUAUCUgg-3' (SEQ ID NO: 146)
3'-CUUCAAAUCUCUCGAUUCUAAUAGACC-5' (SEQ ID NO: 299)

AR-4288 Target: 5'-GAAGTTTAGAGAGCTAAGATTATCTGG-3' (SEQ ID NO: 452)

5'-AGAGAGCUAAGAUUAUCUGGGGAaa-3' (SEQ ID NO: 147)
3'-AAUCUCUCGAUUCUAAUAGACCCCUUU-5' (SEQ ID NO: 300)

AR-4293 Target: 5'-TTAGAGAGCTAAGATTATCTGGGGAAA-3' (SEQ ID NO: 453)

5'-GAGAGCUAAGAUUAUCUGGGGAAat-3' (SEQ ID NO: 148)
3'-AUCUCUCGAUUCUAAUAGACCCCUUUA-5' (SEQ ID NO: 301)

AR-4294 Target: 5'-TAGAGAGCTAAGATTATCTGGGGAAAT-3' (SEQ ID NO: 454)

5'-AGAGCUAAGAUUAUCUGGGGAAAtc-3' (SEQ ID NO: 149)
3'-UCUCUCGAUUCUAAUAGACCCCUUUAG-5' (SEQ ID NO: 302)

AR-4295 Target: 5'-AGAGAGCTAAGATTATCTGGGGAAATC-3' (SEQ ID NO: 455)

5'-AGAUUAUCUGGGGAAAUCAAAACaa-3' (SEQ ID NO: 150)
3'-AUUCUAAUAGACCCCUUUAGUUUUGUU-5' (SEQ ID NO: 303)

AR-4302 Target: 5'-TAAGATTATCTGGGGAAATCAAAACAA-3' (SEQ ID NO: 456)

5'-GAUUAUCUGGGGAAAUCAAAACAaa-3' (SEQ ID NO: 151)
3'-UUCUAAUAGACCCCUUUAGUUUUGUUU-5' (SEQ ID NO: 304)

AR-4303 Target: 5'-AAGATTATCTGGGGAAATCAAAACAAA-3' (SEQ ID NO: 457)

5'-CUGGGGAAAUCAAAACAAAAACAag-3' (SEQ ID NO: 152)
3'-UAGACCCCUUUAGUUUUGUUUUGUUC-5' (SEQ ID NO: 305)

AR-4309 Target: 5'-ATCTGGGGAAATCAAAACAAAAACAAG-3' (SEQ ID NO: 458)

5'-GGAAAUCAAAACAAAAACAAGCAaa-3' (SEQ ID NO: 153)
3'-CCCCUUUAGUUUUGUUUUUGUUCGUUU-5' (SEQ ID NO: 306)

AR-4313 Target: 5'-GGGGAAATCAAAACAAAAACAAGCAAA-3' (SEQ ID NO: 459)

5'-GAAGUUUUUAAAAGCUGCUAAAGac-3' (SEQ ID NO: 766)
3'-CACUUCAAAAAUUUUCGACGAUUUCUG-5' (SEQ ID NO: 796)

AR-251 Target: 5'-GTGAAGTTTTTAAAAGCTGCTAAAGAC-3' (SEQ ID NO: 826)

5'-CUAGCUGCACAUUGCAAAGAAGGct-3' (SEQ ID NO: 767)
3'-UCGAUCGACGUGUAACGUUUCUUCCGA-5' (SEQ ID NO: 797)

AR-524 Target: 5'-AGCTAGCTGCACATTGCAAAGAAGGCT-3' (SEQ ID NO: 827)

5'-AUUGCAAAGAAGGCUCUUAGGAGcc-3' (SEQ ID NO: 768)

3'-UGUAACGUUUCUUCCGAGAAUCCUCGG-5' (SEQ ID NO: 798)

AR-534 Target: 5'-ACATTGCAAAGAAGGCTCTTAGGAGCC-3' (SEQ ID NO: 828)

5'-CAAAACAAACAAAAACAAAAAAGcc-3' (SEQ ID NO: 769)
3'-UUGUUUUGUUUGUUUUUGUUUUUCGG-5' (SEQ ID NO: 799)

AR-736 Target: 5'-AACAAAACAAACAAAAACAAAAAAGCC-3' (SEQ ID NO: 829)

5'-GAUAAUAACUCAGUUCUUAUUUGca-3' (SEQ ID NO: 770)
3'-UUCUAUUAUUGAGUCAAGAAUAAACGU-5' (SEQ ID NO: 800)

AR-776 Target: 5'-AAGATAATAACTCAGTTCTTATTTGCA-3' (SEQ ID NO: 830)

5'-CAGUGGACACUGAAUUUGGAAGGtg-3' (SEQ ID NO: 771)
3'-AAGUCACCUGUGACUUAAACCUUCCAC-5' (SEQ ID NO: 801)

AR-808 Target: 5'-TTCAGTGGACACTGAATTTGGAAGGTG-3' (SEQ ID NO: 831)

5'-GUGGACACUGAAUUUGGAAGGUGga-3' (SEQ ID NO: 772)
3'-GUCACCUGUGACUUAAACCUUCCACCU-5' (SEQ ID NO: 802)

AR-810 Target: 5'-CAGTGGACACTGAATTTGGAAGGTGGA-3' (SEQ ID NO: 832)

5'-UGGACACUGAAUUUGGAAGGUGGag-3' (SEQ ID NO: 773)
3'-UCACCUGUGACUUAAACCUUCCACCUC-5' (SEQ ID NO: 803)

AR-811 Target: 5'-AGTGGACACTGAATTTGGAAGGTGGAG-3' (SEQ ID NO: 833)

5'-GAAUCUACCCUUCAAGUAUUAAGag-3' (SEQ ID NO: 774)
3'-AACUUAGAUGGGAAGUUCAUAAUUCUC-5' (SEQ ID NO: 804)

AR-873 Target: 5'-TTGAATCTACCCTTCAAGTATTAAGAG-3' (SEQ ID NO: 834)

5'-AGUAUUAAGAGACAGACUGUGAGcc-3' (SEQ ID NO: 775)
3'-GUUCAUAAUUCUCUGUCUGACACUCGG-5' (SEQ ID NO: 805)

AR-887 Target: 5'-CAAGTATTAAGAGACAGACTGTGAGCC-3' (SEQ ID NO: 835)

5'-UGAGUAUUCCCCUUUCAAGGGAGgt-3' (SEQ ID NO: 776)
3'-CGACUCAUAAGGGGAAAGUUCCCUCCA-5' (SEQ ID NO: 806)

AR-2060 Target: 5'-GCTGAGTATTCCCCTTTCAAGGGAGGT-3' (SEQ ID NO: 836)

5'-GAGUAUUCCCCUUUCAAGGGAGGtt-3' (SEQ ID NO: 777)
3'-GACUCAUAAGGGGAAAGUUCCCUCCAA-5' (SEQ ID NO: 807)

AR-2061 Target: 5'-CTGAGTATTCCCCTTTCAAGGGAGGTT-3' (SEQ ID NO: 837)

5'-UGUGGAGAUGAAGCUUCUGGGUGtc-3' (SEQ ID NO: 778)
3'-AGACACCUCUACUUCGAAGACCCACAG-5' (SEQ ID NO: 808)

AR-2826 Target: 5'-TCTGTGGAGATGAAGCTTCTGGGTGTC-3' (SEQ ID NO: 838)

5'-AGGGAAACAGAAGUACCUGUGCGcc-3' (SEQ ID NO: 779)
3'-CUUCCCUUUGUCUUCAUGGACACGCGG-5' (SEQ ID NO: 809)

AR-2906 Target: 5'-GAAGGGAAACAGAAGTACCTGTGCGCC-3' (SEQ ID NO: 839)

5'-GAUAAAUUCCGAAGGAAAAAUUGtc-3' (SEQ ID NO: 780)

3'-AACUAUUUAAGGCUUCCUUUUUAACAG-5' (SEQ ID NO: 810)

AR-2952 Target: 5'-TTGATAAATTCCGAAGGAAAAATTGTC-3' (SEQ ID NO: 840)

5'-AGGAAAAAUUGUCCAUCUUGUCGtc-3' (SEQ ID NO: 781)
3'-CUUCCUUUUUAACAGGUAGAACAGCAG-5' (SEQ ID NO: 811)

AR-2964 Target: 5'-GAAGGAAAAATTGTCCATCTTGTCGTC-3' (SEQ ID NO: 841)

5'-GGAAAUGUUAUGAAGCAGGGAUGac-3' (SEQ ID NO: 782)
3'-AGCCUUUACAAUACUUCGUCCCUACUG-5' (SEQ ID NO: 812)

AR-2992 Target: 5'-TCGGAAATGTTATGAAGCAGGGATGAC-3' (SEQ ID NO: 842)

5'-UUGGUAAUCUGAAACUACAGGAGga-3' (SEQ ID NO: 783)
3'-UGAACCAUUAGACUUUGAUGUCCUCCU-5' (SEQ ID NO: 813)

AR-3043 Target: 5'-ACTTGGTAATCTGAAACTACAGGAGGA-3' (SEQ ID NO: 843)

5'-UGGUAAUCUGAAACUACAGGAGGaa-3' (SEQ ID NO: 784)
3'-GAACCAUUAGACUUUGAUGUCCUCCUU-5' (SEQ ID NO: 814)

AR-3044 Target: 5'-CTTGGTAATCTGAAACTACAGGAGGAA-3' (SEQ ID NO: 844)

5'-UAAUCUGAAACUACAGGAGGAAGga-3' (SEQ ID NO: 785)
3'-CCAUUAGACUUUGAUGUCCUCCUUCCU-5' (SEQ ID NO: 815)

AR-3047 Target: 5'-GGTAATCTGAAACTACAGGAGGAAGGA-3' (SEQ ID NO: 845)

5'-CUGACAGUGUCACACAUUGAAGGct-3' (SEQ ID NO: 786)
3'-UCGACUGUCACAGUGUGUAACUUCCGA-5' (SEQ ID NO: 816)

AR-3117 Target: 5'-AGCTGACAGTGTCACACATTGAAGGCT-3' (SEQ ID NO: 846)

5'-CUGUCAUUCAGUACUCCUGGAUGgg-3' (SEQ ID NO: 787)
3'-CCGACAGUAAGUCAUGAGGACCUACCC-5' (SEQ ID NO: 817)

AR-3346 Target: 5'-GGCTGTCATTCAGTACTCCTGGATGGG-3' (SEQ ID NO: 847)

5'-GAAAAAUCAAAAAUUCUUUGAUGaa-3' (SEQ ID NO: 788)
3'-GACUUUUUAGUUUUUAAGAAACUACUU-5' (SEQ ID NO: 818)

AR-3605 Target: 5'-CTGAAAAATCAAAAATTCTTTGATGAA-3' (SEQ ID NO: 848)

5'-AAUUCUUUGAUGAACUUCGAAUGaa-3' (SEQ ID NO: 789)
3'-UUUUAAGAAACUACUUGAAGCUUACUU-5' (SEQ ID NO: 819)

AR-3616 Target: 5'-AAAATTCTTTGATGAACTTCGAATGAA-3' (SEQ ID NO: 849)

5'-CUAAUCAAGUCACACAUGGUGAGcg-3' (SEQ ID NO: 790)
3'-ACGAUUAGUUCAGUGUGUACCACUCGC-5' (SEQ ID NO: 820)

AR-3783 Target: 5'-TGCTAATCAAGTCACACATGGTGAGCG-3' (SEQ ID NO: 850)

5'-CGUGGACUUUCCGGAAAUGAUGGca-3' (SEQ ID NO: 791)
3'-UCGCACCUGAAAGGCCUUUACUACCGU-5' (SEQ ID NO: 821)

AR-3806 Target: 5'-AGCGTGGACTTTCCGGAAATGATGGCA-3' (SEQ ID NO: 851)

5'-UUGGGGAAUUUCCUCUAUUGAUGta-3' (SEQ ID NO: 792)

3'-GGAACCCCUUAAAGGAGAUAACUACAU-5' (SEQ ID NO: 822)

AR-3995 Target: 5'-CCTTGGGGAATTTCCTCTATTGATGTA-3' (SEQ ID NO: 852)

5'-UGUGUUUUGAAUGGUGUUGUAUGcc-3' (SEQ ID NO: 793)
3'-AGACACAAAACUUACCACAACAUACGG-5' (SEQ ID NO: 823)

AR-4158 Target: 5'-TCTGTGTTTTGAATGGTGTTGTATGCC-3' (SEQ ID NO: 853)

5'-UGUAUGCCUUUAAAUCUGUGAUGat-3' (SEQ ID NO: 794)
3'-CAACAUACGGAAAUUUAGACACUACUA-5' (SEQ ID NO: 824)

AR-4175 Target: 5'-GTTGTATGCCTTTAAATCTGTGATGAT-3' (SEQ ID NO: 854)

5'-UAGAGAGCUAAGAUUAUCUGGGGaa-3' (SEQ ID NO: 795)
3'-AAAUCUCUCGAUUCUAAUAGACCCCUU-5' (SEQ ID NO: 825)

AR-4292 Target: 5'-TTTAGAGAGCTAAGATTATCTGGGGAA-3' (SEQ ID NO: 855)

5'-GGUGAAGUUUUUAAAAGCUGCUAaa-3' (SEQ ID NO: 916)
3'-AGCCACUUCAAAAAUUUUCGACGAUUU-5' (SEQ ID NO: 970)

AR-248 Target: 5'-TCGGTGAAGTTTTTAAAAGCTGCTAAA-3' (SEQ ID NO: 1024)

5'-UUUUUAAAAGCUGCUAAAGACUCgg-3' (SEQ ID NO: 917)
3'-UCAAAAAUUUUCGACGAUUUCUGAGCC-5' (SEQ ID NO: 971)

AR-255 Target: 5'-AGTTTTTAAAAGCTGCTAAAGACTCGG-3' (SEQ ID NO: 1025)

5'-AGAGAGGUAACUCCCUUUGGCUGcg-3' (SEQ ID NO: 918)
3'-CGUCUCUCCAUUGAGGGAAACCGACGC-5' (SEQ ID NO: 972)

AR-489 Target: 5'-GCAGAGAGGTAACTCCCTTTGGCTGCG-3' (SEQ ID NO: 1026)

5'-GAGAUCAAAAGAUGAAAAGGCAGtc-3' (SEQ ID NO: 919)
3'-GUCUCUAGUUUUCUACUUUUCCGUCAG-5' (SEQ ID NO: 973)

AR-690 Target: 5'-CAGAGATCAAAAGATGAAAAGGCAGTC-3' (SEQ ID NO: 1027)

5'-AAAAACAAAACAAACAAAAACAAaa-3' (SEQ ID NO: 920)
3'-GUUUUUUGUUUUGUUUGUUUUUGUUUU-5' (SEQ ID NO: 974)

AR-731 Target: 5'-CAAAAAACAAAACAAACAAAAACAAAA-3' (SEQ ID NO: 1028)

5'-AUAAAAGAAAAAGAUAAUAACUCag-3' (SEQ ID NO: 921)
3'-UUUAUUUUCUUUUUCUAUUAUUGAGUC-5' (SEQ ID NO: 975)

AR-764 Target: 5'-AAATAAAAGAAAAAGATAATAACTCAG-3' (SEQ ID NO: 1029)

5'-AAAAAGAUAAUAACUCAGUUCUUat-3' (SEQ ID NO: 922)
3'-UCUUUUUCUAUUAUUGAGUCAAGAAUA-5' (SEQ ID NO: 976)

AR-771 Target: 5'-AGAAAAAGATAATAACTCAGTTCTTAT-3' (SEQ ID NO: 1030)

5'-AAUAACUCAGUUCUUAUUUGCACct-3' (SEQ ID NO: 923)
3'-UAUUAUUGAGUCAAGAAUAAACGUGGA-5' (SEQ ID NO: 977)

AR-779 Target: 5'-ATAATAACTCAGTTCTTATTTGCACCT-3' (SEQ ID NO: 1031)

5'-GUGGAGGAUUUUGUUUUUUUCUUtt-3' (SEQ ID NO: 924)

3'-UCCACCUCCUAAAACAAAAAAAGAAAA-5' (SEQ ID NO: 978)

AR-830 Target: 5'-AGGTGGAGGATTTTGTTTTTTCTTTT-3' (SEQ ID NO: 1032)

5'-UUGUUUUUUUCUUUUAAGAUCUGgg-3' (SEQ ID NO: 925)
3'-AAAACAAAAAAAGAAAAUUCUAGACCC-5' (SEQ ID NO: 979)

AR-840 Target: 5'-TTTTGTTTTTTTCTTTTAAGATCTGGG-3' (SEQ ID NO: 1033)

5'-UUUUUCUUUUAAGAUCUGGGCAUct-3' (SEQ ID NO: 926)
3'-AAAAAAAGAAAAUUCUAGACCCGUAGA-5' (SEQ ID NO: 980)

AR-845 Target: 5'-TTTTTTCTTTTAAGATCTGGGCATCT-3' (SEQ ID NO: 1034)

5'-CUGGGCAUCUUUUGAAUCUACCCtt-3' (SEQ ID NO: 927)
3'-UAGACCCGUAGAAAACUUAGAUGGGAA-5' (SEQ ID NO: 981)

AR-860 Target: 5'-ATCTGGGCATCTTTTGAATCTACCCTT-3' (SEQ ID NO: 1035)

5'-AGGGAAGUAGGUGGAAGAUUCAGcc-3' (SEQ ID NO: 928)
3'-AUUCCCUUCAUCCACCUUCUAAGUCGG-5' (SEQ ID NO: 982)

AR-1105 Target: 5'-TAAGGGAAGTAGGTGGAAGATTCAGCC-3' (SEQ ID NO: 1036)

5'-GGAGCUUUCCAGAAUCUGUUCCAga-3' (SEQ ID NO: 929)
3'-CUCCUCGAAAGGUCUUAGACAAGGUCU-5' (SEQ ID NO: 983)

AR-1200 Target: 5'-GAGGAGCTTTCCAGAATCTGTTCCAGA-3' (SEQ ID NO: 1037)

5'-CAGGAAGCAGUAUCCGAAGGCAGca-3' (SEQ ID NO: 930)
3'-UCGUCCUUCGUCAUAGGCUUCCGUCGU-5' (SEQ ID NO: 984)

AR-1734 Target: 5'-AGCAGGAAGCAGTATCCGAAGGCAGCA-3' (SEQ ID NO: 1038)

5'-AAGGACAAUUACUUAGGGGGCACtt-3' (SEQ ID NO: 931)
3'-GGUUCCUGUUAAUGAAUCCCCCGUGAA-5' (SEQ ID NO: 985)

AR-1803 Target: 5'-CCAAGGACAATTACTTAGGGGGCACTT-3' (SEQ ID NO: 1039)

5'-GGAGUUGUGUAAGGCAGUGUCGGtg-3' (SEQ ID NO: 932)
3'-UUCCUCAACACAUUCCGUCACAGCCAC-5' (SEQ ID NO: 986)

AR-1850 Target: 5'-AAGGAGTTGTGTAAGGCAGTGTCGGTG-3' (SEQ ID NO: 1040)

5'-CAAGAGCACUGAAGAUACUGCUGag-3' (SEQ ID NO: 933)
3'-CCGUUCUCGUGACUUCUAUGACGACUC-5' (SEQ ID NO: 987)

AR-2039 Target: 5'-GGCAAGAGCACTGAAGATACTGCTGAG-3' (SEQ ID NO: 1041)

5'-UGAAGAUACUGCUGAGUAUUCCCct-3' (SEQ ID NO: 934)
3'-UGACUUCUAUGACGACUCAUAAGGGGA-5' (SEQ ID NO: 988)

AR-2048 Target: 5'-ACTGAAGATACTGCTGAGTATTCCCCT-3' (SEQ ID NO: 1042)

5'-AGGGAGGUUACACCAAAGGGCUAga-3' (SEQ ID NO: 935)
3'-GUUCCCUCCAAUGUGGUUUCCCGAUCU-5' (SEQ ID NO: 989)

AR-2077 Target: 5'-CAAGGGAGGTTACACCAAAGGGCTAGA-3' (SEQ ID NO: 1043)

5'-UGUGUCAAAAGCGAAAUGGGCCCct-3' (SEQ ID NO: 936)

3'-GAACACAGUUUUCGCUUUACCCGGGGA-5' (SEQ ID NO: 990)

AR-2694 Target: 5'-CTTGTGTCAAAAGCGAAATGGGCCCCT-3' (SEQ ID NO: 1044)

5'-GUUUUGCCCAUUGACUAUUACUUtc-3' (SEQ ID NO: 937)
3'-UACAAAACGGGUAACUGAUAAUGAAAG-5' (SEQ ID NO: 991)

AR-2778 Target: 5'-ATGTTTTGCCCATTGACTATTACTTTC-3' (SEQ ID NO: 1045)

5'-CAAGGUCUUCUUCAAAAGAGCCGct-3' (SEQ ID NO: 938)
3'-ACGUUCCAGAAGAAGUUUUCUCGGCGA-5' (SEQ ID NO: 992)

AR-2879 Target: 5'-TGCAAGGTCTTCTTCAAAAGAGCCGCT-3' (SEQ ID NO: 1046)

5'-GGGAAACAGAAGUACCUGUGCGCca-3' (SEQ ID NO: 939)
3'-UUCCCUUUGUCUUCAUGGACACGCGGU-5' (SEQ ID NO: 993)

AR-2907 Target: 5'-AAGGGAAACAGAAGTACCTGTGCGCCA-3' (SEQ ID NO: 1047)

5'-GAUUGCACUAUUGAUAAAUUCCGaa-3' (SEQ ID NO: 940)
3'-UACUAACGUGAUAACUAUUUAAGGCUU-5' (SEQ ID NO: 994)

AR-2940 Target: 5'-ATGATTGCACTATTGATAAATTCCGAA-3' (SEQ ID NO: 1048)

5'-AAUUCCGAAGGAAAAAUUGUCCAtc-3' (SEQ ID NO: 941)
3'-AUUUAAGGCUUCCUUUUUAACAGGUAG-5' (SEQ ID NO: 995)

AR-2956 Target: 5'-TAAATTCCGAAGGAAAAATTGTCCATC-3' (SEQ ID NO: 1049)

5'-GGAAAAAUUGUCCAUCUUGUCGUct-3' (SEQ ID NO: 942)
3'-UUCCUUUUUAACAGGUAGAACAGCAGA-5' (SEQ ID NO: 996)

AR-2965 Target: 5'-AAGGAAAAATTGTCCATCTTGTCGTCT-3' (SEQ ID NO: 1050)

5'-AAAAUUGUCCAUCUUGUCGUCUUcg-3' (SEQ ID NO: 943)
3'-CUUUUUAACAGGUAGAACAGCAGAAGC-5' (SEQ ID NO: 997)

AR-2968 Target: 5'-GAAAAATTGTCCATCTTGTCGTCTTCG-3' (SEQ ID NO: 1051)

5'-AGAAACUUGGUAAUCUGAAACUAca-3' (SEQ ID NO: 944)
3'-CUUCUUUGAACCAUUAGACUUUGAUGU-5' (SEQ ID NO: 998)

AR-3037 Target: 5'-GAAGAAACTTGGTAATCTGAAACTACA-3' (SEQ ID NO: 1052)

5'-UUGAAGGCUAUGAAUGUCAGCCCat-3' (SEQ ID NO: 945)
3'-GUAACUUCCGAUACUUACAGUCGGGUA-5' (SEQ ID NO: 999)

AR-3133 Target: 5'-CATTGAAGGCTATGAATGTCAGCCCAT-3' (SEQ ID NO: 1053)

5'-GGAAUUCCUGUGCAUGAAAGCACtg-3' (SEQ ID NO: 946)
3'-GUCCUUAAGGACACGUACUUUCGUGAC-5' (SEQ ID NO: 1000)

AR-3548 Target: 5'-CAGGAATTCCTGTGCATGAAAGCACTG-3' (SEQ ID NO: 1054)

5'-AAAAAUUCUUUGAUGAACUUCGAat-3' (SEQ ID NO: 947)
3'-AGUUUUUAAGAAACUACUUGAAGCUUA-5' (SEQ ID NO: 1001)

AR-3613 Target: 5'-TCAAAAATTCTTTGATGAACTTCGAAT-3' (SEQ ID NO: 1055)

5'-UUUGAUGAACUUCGAAUGAACUAca-3' (SEQ ID NO: 948)

3'-AGAAACUACUUGAAGCUUACUUGAUGU-5' (SEQ ID NO: 1002)

AR-3621 Target: 5'-TCTTTGATGAACTTCGAATGAACTACA-3' (SEQ ID NO: 1056)

5'-GAUGAACUUCGAAUGAACUACAUca-3' (SEQ ID NO: 949)
3'-AACUACUUGAAGCUUACUUGAUGUAGU-5' (SEQ ID NO: 1003)

AR-3624 Target: 5'-TTGATGAACTTCGAATGAACTACATCA-3' (SEQ ID NO: 1057)

5'-GAAUGAACUACAUCAAGGAACUCga-3' (SEQ ID NO: 950)
3'-AGCUUACUUGAUGUAGUUCCUUGAGCU-5' (SEQ ID NO: 1004)

AR-3634 Target: 5'-TCGAATGAACTACATCAAGGAACTCGA-3' (SEQ ID NO: 1058)

5'-CAAAAGAAAAAAUCCCACAUCCUgc-3' (SEQ ID NO: 951)
3'-ACGUUUUCUUUUUUAGGGUGUAGGACG-5' (SEQ ID NO: 1005)

AR-3674 Target: 5'-TGCAAAAGAAAAAATCCCACATCCTGC-3' (SEQ ID NO: 1059)

5'-AGAAAAAAUCCCACAUCCUGCUCaa-3' (SEQ ID NO: 952)
3'-UUUCUUUUUUAGGGUGUAGGACGAGUU-5' (SEQ ID NO: 1006)

AR-3678 Target: 5'-AAAGAAAAAATCCCACATCCTGCTCAA-3' (SEQ ID NO: 1060)

5'-UUUUGACCUGCUAAUCAAGUCACac-3' (SEQ ID NO: 953)
3'-UGAAAACUGGACGAUUAGUUCAGUGUG-5' (SEQ ID NO: 1007)

AR-3773 Target: 5'-ACTTTTGACCTGCTAATCAAGTCACAC-3' (SEQ ID NO: 1061)

5'-AAGAUCCUUUCUGGGAAAGUCAAgc-3' (SEQ ID NO: 954)
3'-GGUUCUAGGAAAGACCCUUUCAGUUCG-5' (SEQ ID NO: 1008)

AR-3855 Target: 5'-CCAAGATCCTTTCTGGGAAAGTCAAGC-3' (SEQ ID NO: 1062)

5'-AAAGUCAAGCCCAUCUAUUUCCAca-3' (SEQ ID NO: 955)
3'-CCUUUCAGUUCGGGUAGAUAAAGGUGU-5' (SEQ ID NO: 1009)

AR-3870 Target: 5'-GGAAAGTCAAGCCCATCTATTTCCACA-3' (SEQ ID NO: 1063)

5'-AUGUCUUCUGCCUGUUAUAACUCtg-3' (SEQ ID NO: 956)
3'-UCUACAGAAGACGGACAAUAUUGAGAC-5' (SEQ ID NO: 1010)

AR-3950 Target: 5'-AGATGTCTTCTGCCTGTTATAACTCTG-3' (SEQ ID NO: 1064)

5'-GAAUUUCCUCUAUUGAUGUACAGtc-3' (SEQ ID NO: 957)
3'-CCCUUAAAGGAGAUAACUACAUGUCAG-5' (SEQ ID NO: 1011)

AR-4000 Target: 5'-GGGAATTTCCTCTATTGATGTACAGTC-3' (SEQ ID NO: 1065)

5'-GAUGUACAGUCUGUCAUGAACAUgt-3' (SEQ ID NO: 958)
3'-AACUACAUGUCAGACAGUACUUGUACA-5' (SEQ ID NO: 1012)

AR-4014 Target: 5'-TTGATGTACAGTCTGTCATGAACATGT-3' (SEQ ID NO: 1066)

5'-CAGUCUGUCAUGAACAUGUUCCUga-3' (SEQ ID NO: 959)
3'-AUGUCAGACAGUACUUGUACAAGGACU-5' (SEQ ID NO: 1013)

AR-4020 Target: 5'-TACAGTCTGTCATGAACATGTTCCTGA-3' (SEQ ID NO: 1067)

5'-CAUGAACAUGUUCCUGAAUUCUAtt-3' (SEQ ID NO: 960)

3'-CAGUACUUGUACAAGGACUUAAGAUAA-5' (SEQ ID NO: 1014)

AR-4028 Target: 5'-GTCATGAACATGTTCCTGAATTCTATT-3' (SEQ ID NO: 1068)

5'-AUGUUCCUGAAUUCUAUUUGCUGgg-3' (SEQ ID NO: 961)
3'-UGUACAAGGACUUAAGAUAAACGACCC-5' (SEQ ID NO: 1015)

AR-4035 Target: 5'-ACATGTTCCTGAATTCTATTTGCTGGG-3' (SEQ ID NO: 1069)

5'-UGGGCUUUUUUUUUCUCUUUCUCtc-3' (SEQ ID NO: 962)
3'-CGACCCGAAAAAAAAAGAGAAAGAGAG-5' (SEQ ID NO: 1016)

AR-4056 Target: 5'-GCTGGGCTTTTTTTTCTCTTTCTCTC-3' (SEQ ID NO: 1070)

5'-UUUUUCUCUUUCUCUCCUUUCUUtt-3' (SEQ ID NO: 963)
3'-AAAAAAAAGAGAAAGAGAGGAAAGAAAA-5' (SEQ ID NO: 1017)

AR-4065 Target: 5'-TTTTTTTCTCTTTCTCTCCTTTCTTTT-3' (SEQ ID NO: 1071)

5'-GUUUUGAAUGGUGUUGUAUGCCUtt-3' (SEQ ID NO: 964)
3'-CACAAAACUUACCACAACAUACGGAAA-5' (SEQ ID NO: 1018)

AR-4161 Target: 5'-GTGTTTTGAATGGTGTTGTATGCCTTT-3' (SEQ ID NO: 1072)

5'-GGUGUUGUAUGCCUUUAAAUCUGtg-3' (SEQ ID NO: 965)
3'-UACCACAACAUACGGAAAUUUAGACAC-5' (SEQ ID NO: 1019)

AR-4170 Target: 5'-ATGGTGTTGTATGCCTTTAAATCTGTG-3' (SEQ ID NO: 1073)

5'-CAAGUUGUGCUUGUUUACAGCACta-3' (SEQ ID NO: 966)
3'-CAGUUCAACACGAACAAAUGUCGUGAU-5' (SEQ ID NO: 1020)

AR-4218 Target: 5'-GTCAAGTTGTGCTTGTTTACAGCACTA-3' (SEQ ID NO: 1074)

5'-CUAAGAUUAUCUGGGGAAAUCAAaa-3' (SEQ ID NO: 967)
3'-UCGAUUCUAAUAGACCCCUUUAGUUUU-5' (SEQ ID NO: 1021)

AR-4299 Target: 5'-AGCTAAGATTATCTGGGGAAATCAAAA-3' (SEQ ID NO: 1075)

5'-UGGGGAAAUCAAAACAAAAACAAgc-3' (SEQ ID NO: 968)
3'-AGACCCCUUUAGUUUUGUUUUUGUUCG-5' (SEQ ID NO: 1022)

AR-4310 Target: 5'-TCTGGGGAAATCAAAACAAAAACAAGC-3' (SEQ ID NO: 1076)

5'-GAAAUCAAAACAAAAACAAGCAAac-3' (SEQ ID NO: 969)
3'-CCCUUUAGUUUUGUUUUUGUUCGUUUG-5' (SEQ ID NO: 1023)

AR-4314 Target: 5'-GGGAAATCAAAACAAAAACAAGCAAAC-3' (SEQ ID NO: 1077)

5'-GUGAAGUUUUUAAAAGCUGCUAAag-3' (SEQ ID NO: 1186)
3'-GCCACUUCAAAAAUUUUCGACGAUUUC-5' (SEQ ID NO: 1249)

AR-249 Target: 5'-CGGTGAAGTTTTTAAAAGCTGCTAAAG-3' (SEQ ID NO: 1312)

5'-UUUUAAAAGCUGCUAAAGACUCGga-3' (SEQ ID NO: 1187)
3'-CAAAAAUUUUCGACGAUUUCUGAGCCU-5' (SEQ ID NO: 1250)

AR-256 Target: 5'-GTTTTTAAAAGCTGCTAAAGACTCGGA-3' (SEQ ID NO: 1313)

5'-UUAAAAGCUGCUAAAGACUCGGAgg-3' (SEQ ID NO: 1188)

3'-AAAAUUUUCGACGAUUUCUGAGCCUCC-5' (SEQ ID NO: 1251)

AR-258 Target: 5'-TTTTAAAAGCTGCTAAAGACTCGGAGG-3' (SEQ ID NO: 1314)

5'-GGAGAGAACCCUCUGUUUUCCCCca-3' (SEQ ID NO: 1189)
3'-CGCCUCUCUUGGGAGACAAAAGGGGGU-5' (SEQ ID NO: 1252)

AR-618 Target: 5'-GCGGAGAGAACCCTCTGTTTTCCCCCA-3' (SEQ ID NO: 1315)

5'-AGAUCAAAAGAUGAAAAGGCAGUca-3' (SEQ ID NO: 1190)
3'-UCUCUAGUUUUCUACUUUUCCGUCAGU-5' (SEQ ID NO: 1253)

AR-691 Target: 5'-AGAGATCAAAAGATGAAAAGGCAGTCA-3' (SEQ ID NO: 1316)

5'-CAAAAGAUGAAAAGGCAGUCAGGtc-3' (SEQ ID NO: 1191)
3'-UAGUUUUCUACUUUUCCGUCAGUCCAG-5' (SEQ ID NO: 1254)

AR-695 Target: 5'-ATCAAAAGATGAAAAGGCAGTCAGGTC-3' (SEQ ID NO: 1317)

5'-CAGUAGCCAAAAAACAAAACAAAca-3' (SEQ ID NO: 1192)
3'-AAGUCAUCGGUUUUUUGUUUUGUUUGU-5' (SEQ ID NO: 1255)

AR-722 Target: 5'-TTCAGTAGCCAAAAAACAAAACAAACA-3' (SEQ ID NO: 1318)

5'-AAAACAAAACAAACAAAAACAAAaa-3' (SEQ ID NO: 1193)
3'-UUUUUUGUUUUGUUUGUUUUUGUUUUU-5' (SEQ ID NO: 1256)

AR-732 Target: 5'-AAAAAACAAAACAAACAAAAACAAAAA-3' (SEQ ID NO: 1319)

5'-UAAAAGAAAAAGAUAAUAACUCAgt-3' (SEQ ID NO: 1194)
3'-UUAUUUUCUUUUUCUAUUAUUGAGUCA-5' (SEQ ID NO: 1257)

AR-765 Target: 5'-AATAAAAGAAAAAGATAATAACTCAGT-3' (SEQ ID NO: 1320)

5'-AAAGAAAAAGAUAAUAACUCAGUtc-3' (SEQ ID NO: 1195)
3'-AUUUUCUUUUUCUAUUAUUGAGUCAAG-5' (SEQ ID NO: 1258)

AR-767 Target: 5'-TAAAAGAAAAAGATAATAACTCAGTTC-3' (SEQ ID NO: 1321)

5'-AAAAGAUAAUAACUCAGUUCUUAtt-3' (SEQ ID NO: 1196)
3'-CUUUUUCUAUUAUUGAGUCAAGAAUAA-5' (SEQ ID NO: 1259)

AR-772 Target: 5'-GAAAAAGATAATAACTCAGTTCTTATT-3' (SEQ ID NO: 1322)

5'-AUAACUCAGUUCUUAUUUGCACCta-3' (SEQ ID NO: 1197)
3'-AUUAUUGAGUCAAGAAUAAACGUGGAU-5' (SEQ ID NO: 1260)

AR-780 Target: 5'-TAATAACTCAGTTCTTATTTGCACCTA-3' (SEQ ID NO: 1323)

5'-CAGUUCUUAUUUGCACCUACUUCag-3' (SEQ ID NO: 1198)
3'-GAGUCAAGAAUAAACGUGGAUGAAGUC-5' (SEQ ID NO: 1261)

AR-786 Target: 5'-CTCAGTTCTTATTTGCACCTACTTCAG-3' (SEQ ID NO: 1324)

5'-UGGAGGAUUUUGUUUUUUUCUUUta-3' (SEQ ID NO: 1199)
3'-CCACCUCCUAAAACAAAAAAAGAAAAU-5' (SEQ ID NO: 1262)

AR-831 Target: 5'-GGTGGAGGATTTTGTTTTTTCTTTTA-3' (SEQ ID NO: 1325)

5'-UGUUUUUUUCUUUUAAGAUCUGGgc-3' (SEQ ID NO: 1200)

3'-AAACAAAAAAAGAAAAUUCUAGACCCG-5' (SEQ ID NO: 1263)

AR-841 Target: 5'-TTTGTTTTTTCTTTTAAGATCTGGGC-3' (SEQ ID NO: 1326)

5'-UUUUCUUUUAAGAUCUGGGCAUCtt-3' (SEQ ID NO: 1201)
3'-AAAAAAGAAAAUUCUAGACCCGUAGAA-5' (SEQ ID NO: 1264)

AR-846 Target: 5'-TTTTTTCTTTTAAGATCTGGGCATCTT-3' (SEQ ID NO: 1327)

5'-UGGGCAUCUUUUGAAUCUACCCUtc-3' (SEQ ID NO: 1202)
3'-AGACCCGUAGAAAACUUAGAUGGGAAG-5' (SEQ ID NO: 1265)

AR-861 Target: 5'-TCTGGGCATCTTTTGAATCTACCCTTC-3' (SEQ ID NO: 1328)

5'-CAAGUUUCCUUCUCUGGAGCUUCcc-3' (SEQ ID NO: 1203)
3'-GCGUUCAAAGGAAGAGACCUCGAAGGG-5' (SEQ ID NO: 1266)

AR-997 Target: 5'-CGCAAGTTTCCTTCTCTGGAGCTTCCC-3' (SEQ ID NO: 1329)

5'-GGGAAGUAGGUGGAAGAUUCAGCca-3' (SEQ ID NO: 1204)
3'-UUCCCUUCAUCCACCUUCUAAGUCGGU-5' (SEQ ID NO: 1267)

AR-1106 Target: 5'-AAGGGAAGTAGGTGGAAGATTCAGCCA-3' (SEQ ID NO: 1330)

5'-AAGUAGGUGGAAGAUUCAGCCAAgc-3' (SEQ ID NO: 1205)
3'-CCUUCAUCCACCUUCUAAGUCGGUUCG-5' (SEQ ID NO: 1268)

AR-1109 Target: 5'-GGAAGTAGGTGGAAGATTCAGCCAAGC-3' (SEQ ID NO: 1331)

5'-AGGACAAUUACUUAGGGGGCACUtc-3' (SEQ ID NO: 1206)
3'-GUUCCUGUUAAUGAAUCCCCCGUGAAG-5' (SEQ ID NO: 1269)

AR-1804 Target: 5'-CAAGGACAATTACTTAGGGGGCACTTC-3' (SEQ ID NO: 1332)

5'-CGAAUGCAAAGGUUCUCUGCUAGac-3' (SEQ ID NO: 1207)
3'-CGGCUUACGUUUCCAAGAGACGAUCUG-5' (SEQ ID NO: 1270)

AR-2003 Target: 5'-GCCGAATGCAAAGGTTCTCTGCTAGAC-3' (SEQ ID NO: 1333)

5'-AAGAGCACUGAAGAUACUGCUGAgt-3' (SEQ ID NO: 1208)
3'-CGUUCUCGUGACUUCUAUGACGACUCA-5' (SEQ ID NO: 1271)

AR-2040 Target: 5'-GCAAGAGCACTGAAGATACTGCTGAGT-3' (SEQ ID NO: 1334)

5'-GAAGAUACUGCUGAGUAUUCCCCtt-3' (SEQ ID NO: 1209)
3'-GACUUCUAUGACGACUCAUAAGGGGAA-5' (SEQ ID NO: 1272)

AR-2049 Target: 5'-CTGAAGATACTGCTGAGTATTCCCCTT-3' (SEQ ID NO: 1335)

5'-GUGUCAAAAGCGAAAUGGGCCCCtg-3' (SEQ ID NO: 1210)
3'-AACACAGUUUUCGCUUUACCCGGGGAC-5' (SEQ ID NO: 1273)

AR-2695 Target: 5'-TTGTGTCAAAAGCGAAATGGGCCCCTG-3' (SEQ ID NO: 1336)

5'-UUUUGCCCAUUGACUAUUACUUUcc-3' (SEQ ID NO: 1211)
3'-ACAAAACGGGUAACUGAUAAUGAAAGG-5' (SEQ ID NO: 1274)

AR-2779 Target: 5'-TGTTTTGCCCATTGACTATTACTTTCC-3' (SEQ ID NO: 1337)

5'-CAUUGACUAUUACUUUCCACCCCag-3' (SEQ ID NO: 1212)

3'-GGGUAACUGAUAAUGAAAGGUGGGGUC-5' (SEQ ID NO: 1275)

AR-2786 Target: 5'-CCCATTGACTATTACTTTCCACCCCAG-3' (SEQ ID NO: 1338)

5'-AAGGUCUUCUUCAAAAGAGCCGCtg-3' (SEQ ID NO: 1213)
3'-CGUUCCAGAAGAAGUUUUCUCGGCGAC-5' (SEQ ID NO: 1276)

AR-2880 Target: 5'-GCAAGGTCTTCTTCAAAAGAGCCGCTG-3' (SEQ ID NO: 1339)

5'-AUUGCACUAUUGAUAAAUUCCGAag-3' (SEQ ID NO: 1214)
3'-ACUAACGUGAUAACUAUUUAAGGCUUC-5' (SEQ ID NO: 1277)

AR-2941 Target: 5'-TGATTGCACTATTGATAAATTCCGAAG-3' (SEQ ID NO: 1340)

5'-CGAAGGAAAAAUUGUCCAUCUUGtc-3' (SEQ ID NO: 1215)
3'-AGGCUUCCUUUUUAACAGGUAGAACAG-5' (SEQ ID NO: 1278)

AR-2961 Target: 5'-TCCGAAGGAAAAATTGTCCATCTTGTC-3' (SEQ ID NO: 1341)

5'-GAAAAAUUGUCCAUCUUGUCGUCtt-3' (SEQ ID NO: 1216)
3'-UCCUUUUUAACAGGUAGAACAGCAGAA-5' (SEQ ID NO: 1279)

AR-2966 Target: 5'-AGGAAAAATTGTCCATCTTGTCGTCTT-3' (SEQ ID NO: 1342)

5'-CAGUGUCACACAUUGAAGGCUAUga-3' (SEQ ID NO: 1217)
3'-CUGUCACAGUGUGUAACUUCCGAUACU-5' (SEQ ID NO: 1280)

AR-3121 Target: 5'-GACAGTGTCACACATTGAAGGCTATGA-3' (SEQ ID NO: 1343)

5'-UGAAGGCUAUGAAUGUCAGCCCAtc-3' (SEQ ID NO: 1218)
3'-UAACUUCCGAUACUUACAGUCGGGUAG-5' (SEQ ID NO: 1281)

AR-3134 Target: 5'-ATTGAAGGCTATGAATGTCAGCCCATC-3' (SEQ ID NO: 1344)

5'-AUGGCUGUCAUUCAGUACUCCUGga-3' (SEQ ID NO: 1219)
3'-UCUACCGACAGUAAGUCAUGAGGACCU-5' (SEQ ID NO: 1282)

AR-3342 Target: 5'-AGATGGCTGTCATTCAGTACTCCTGGA-3' (SEQ ID NO: 1345)

5'-UGGUUUUCAAUGAGUACCGCAUGca-3' (SEQ ID NO: 1220)
3'-AGACCAAAAGUUACUCAUGGCGUACGU-5' (SEQ ID NO: 1283)

AR-3445 Target: 5'-TCTGGTTTTCAATGAGTACCGCATGCA-3' (SEQ ID NO: 1346)

5'-GAAUUCCUGUGCAUGAAAGCACUgc-3' (SEQ ID NO: 1221)
3'-UCCUUAAGGACACGUACUUUCGUGACG-5' (SEQ ID NO: 1284)

AR-3549 Target: 5'-AGGAATTCCTGTGCATGAAAGCACTGC-3' (SEQ ID NO: 1347)

5'-AAAAUUCUUUGAUGAACUUCGAAtg-3' (SEQ ID NO: 1222)
3'-GUUUUUAAGAAACUACUUGAAGCUUAC-5' (SEQ ID NO: 1285)

AR-3614 Target: 5'-CAAAAATTCTTTGATGAACTTCGAATG-3' (SEQ ID NO: 1348)

5'-UUGAUGAACUUCGAAUGAACUACat-3' (SEQ ID NO: 1223)
3'-GAAACUACUUGAAGCUUACUUGAUGUA-5' (SEQ ID NO: 1286)

AR-3622 Target: 5'-CTTTGATGAACTTCGAATGAACTACAT-3' (SEQ ID NO: 1349)

5'-AUGAACUUCGAAUGAACUACAUCaa-3' (SEQ ID NO: 1224)

3'-ACUACUUGAAGCUUACUUGAUGUAGUU-5' (SEQ ID NO: 1287)

AR-3625 Target: 5'-TGATGAACTTCGAATGAACTACATCAA-3' (SEQ ID NO: 1350)

5'-AAUGAACUACAUCAAGGAACUCGat-3' (SEQ ID NO: 1225)
3'-GCUUACUUGAUGUAGUUCCUUGAGCUA-5' (SEQ ID NO: 1288)

AR-3635 Target: 5'-CGAATGAACTACATCAAGGAACTCGAT-3' (SEQ ID NO: 1351)

5'-UGAACUACAUCAAGGAACUCGAUcg-3' (SEQ ID NO: 1226)
3'-UUACUUGAUGUAGUUCCUUGAGCUAGC-5' (SEQ ID NO: 1289)

AR-3637 Target: 5'-AATGAACTACATCAAGGAACTCGATCG-3' (SEQ ID NO: 1352)

5'-AAAAGAAAAAAUCCCACAUCCUGct-3' (SEQ ID NO: 1227)
3'-CGUUUUCUUUUUUAGGGUGUAGGACGA-5' (SEQ ID NO: 1290)

AR-3675 Target: 5'-GCAAAAGAAAAAATCCCACATCCTGCT-3' (SEQ ID NO: 1353)

5'-GAAAAAAUCCCACAUCCUGCUCAag-3' (SEQ ID NO: 1228)
3'-UUCUUUUUUAGGGUGUAGGACGAGUUC-5' (SEQ ID NO: 1291)

AR-3679 Target: 5'-AAGAAAAAATCCCACATCCTGCTCAAG-3' (SEQ ID NO: 1354)

5'-UUUGACCUGCUAAUCAAGUCACAca-3' (SEQ ID NO: 1229)
3'-GAAAACUGGACGAUUAGUUCAGUGUGU-5' (SEQ ID NO: 1292)

AR-3774 Target: 5'-CTTTTGACCTGCTAATCAAGTCACACA-3' (SEQ ID NO: 1355)

5'-CUGUUAUAACUCUGCACUACUCCtc-3' (SEQ ID NO: 1230)
3'-CGGACAAUAUUGAGACGUGAUGAGGAG-5' (SEQ ID NO: 1293)

AR-3961 Target: 5'-GCCTGTTATAACTCTGCACTACTCCTC-3' (SEQ ID NO: 1356)

5'-GUUAUAACUCUGCACUACUCCUCtg-3' (SEQ ID NO: 1231)
3'-GACAAUAUUGAGACGUGAUGAGGAGAC-5' (SEQ ID NO: 1294)

AR-3963 Target: 5'-CTGTTATAACTCTGCACTACTCCTCTG-3' (SEQ ID NO: 1357)

5'-AAUUUCCUCUAUUGAUGUACAGUct-3' (SEQ ID NO: 1232)
3'-CCUUAAAGGAGAUAACUACAUGUCAGA-5' (SEQ ID NO: 1295)

AR-4001 Target: 5'-GGAATTTCCTCTATTGATGTACAGTCT-3' (SEQ ID NO: 1358)

5'-CUAUUGAUGUACAGUCUGUCAUGaa-3' (SEQ ID NO: 1233)
3'-GAGAUAACUACAUGUCAGACAGUACUU-5' (SEQ ID NO: 1296)

AR-4009 Target: 5'-CTCTATTGATGTACAGTCTGTCATGAA-3' (SEQ ID NO: 1359)

5'-AUGAACAUGUUCCUGAAUUCUAUtt-3' (SEQ ID NO: 1234)
3'-AGUACUUGUACAAGGACUUAAGAUAAA-5' (SEQ ID NO: 1297)

AR-4029 Target: 5'-TCATGAACATGTTCCTGAATTCTATTT-3' (SEQ ID NO: 1360)

5'-CUGAAUUCUAUUUGCUGGGCUUUtt-3' (SEQ ID NO: 1235)
3'-AGGACUUAAGAUAAACGACCCGAAAAA-5' (SEQ ID NO: 1298)

AR-4041 Target: 5'-TCCTGAATTCTATTTGCTGGGCTTTTT-3' (SEQ ID NO: 1361)

5'-UUUUUUUUUCUCUUUCUCUCCUUtc-3' (SEQ ID NO: 1236)

3'-CGAAAAAAAAAGAGAAAGAGAGGAAAG-5' (SEQ ID NO: 1299)

AR-4061 Target: 5'-GCTTTTTTTTCTCTTTCTCTCCTTTC-3' (SEQ ID NO: 1362)

5'-UUUUCUCUUUCUCUCCUUUCUUUtt-3' (SEQ ID NO: 1237)
3'-AAAAAAGAGAAAGAGAGGAAAGAAAAA-5' (SEQ ID NO: 1300)

AR-4066 Target: 5'-TTTTTTCTCTTTCTCTCCTTTCTTTTT-3' (SEQ ID NO: 1363)

5'-CUUUCUCUCCUUUCUUUUUCUUCtt-3' (SEQ ID NO: 1238)
3'-GAGAAAGAGAGGAAAGAAAAAGAAGAA-5' (SEQ ID NO: 1301)

AR-4072 Target: 5'-CTCTTTCTCTCCTTTCTTTTTCTTCTT-3' (SEQ ID NO: 1364)

5'-AUGGCACCUUCAGACUUUGCUUCcc-3' (SEQ ID NO: 1239)
3'-GGUACCGUGGAAGUCUGAAACGAAGGG-5' (SEQ ID NO: 1302)

AR-4118 Target: 5'-CCATGGCACCTTCAGACTTTGCTTCCC-3' (SEQ ID NO: 1365)

5'-UUUUGAAUGGUGUUGUAUGCCUUta-3' (SEQ ID NO: 1240)
3'-ACAAAACUUACCACAACAUACGGAAAU-5' (SEQ ID NO: 1303)

AR-4162 Target: 5'-TGTTTTGAATGGTGTTGTATGCCTTTA-3' (SEQ ID NO: 1366)

5'-GUGUUGUAUGCCUUUAAAUCUGUga-3' (SEQ ID NO: 1241)
3'-ACCACAACAUACGGAAAUUUAGACACU-5' (SEQ ID NO: 1304)

AR-4171 Target: 5'-TGGTGTTGTATGCCTTTAAATCTGTGA-3' (SEQ ID NO: 1367)

5'-UUAAAUCUGUGAUGAUCCUCAUAtg-3' (SEQ ID NO: 1242)
3'-GAAAUUUAGACACUACUAGGAGUAUAC-5' (SEQ ID NO: 1305)

AR-4184 Target: 5'-CTTTAAATCTGTGATGATCCTCATATG-3' (SEQ ID NO: 1368)

5'-UGUGAUGAUCCUCAUAUGGCCCAgt-3' (SEQ ID NO: 1243)
3'-AGACACUACUAGGAGUAUACCGGGUCA-5' (SEQ ID NO: 1306)

AR-4191 Target: 5'-TCTGTGATGATCCTCATATGGCCCAGT-3' (SEQ ID NO: 1369)

5'-GUUGUGCUUGUUUACAGCACUACtc-3' (SEQ ID NO: 1244)
3'-UUCAACACGAACAAAUGUCGUGAUGAG-5' (SEQ ID NO: 1307)

AR-4221 Target: 5'-AAGTTGTGCTTGTTTACAGCACTACTC-3' (SEQ ID NO: 1370)

5'-GUUUACUUAUCUUAUGCCACGGGaa-3' (SEQ ID NO: 1245)
3'-UGCAAAUGAAUAGAAUACGGUGCCCUU-5' (SEQ ID NO: 1308)

AR-4264 Target: 5'-ACGTTTACTTATCTTATGCCACGGGAA-3' (SEQ ID NO: 1371)

5'-UUUAGAGAGCUAAGAUUAUCUGGgg-3' (SEQ ID NO: 1246)
3'-UCAAAUCUCUCGAUUCUAAUAGACCCC-5' (SEQ ID NO: 1309)

AR-4290 Target: 5'-AGTTTAGAGAGCTAAGATTATCTGGGG-3' (SEQ ID NO: 1372)

5'-UAAGAUUAUCUGGGGAAAUCAAAac-3' (SEQ ID NO: 1247)
3'-CGAUUCUAAUAGACCCCUUUAGUUUUG-5' (SEQ ID NO: 1310)

AR-4300 Target: 5'-GCTAAGATTATCTGGGGAAATCAAAAC-3' (SEQ ID NO: 1373)

5'-GGGGAAAUCAAAACAAAAACAAGca-3' (SEQ ID NO: 1248)

3'-GACCCCUUUAGUUUUGUUUUUGUUCGU-5' (SEQ ID NO: 1311)

AR-4311 Target: 5'-CTGGGGAAATCAAAACAAAAAACAAGCA-3' (SEQ ID NO: 1374)

Table 3: Selected Anti-AR DsiRNA Agents, Unmodified Duplexes

5'-AAGUUUUUAAAAGCUGCUAAAGACU-3' (SEQ ID NO: 460)
3'-ACUUCAAAAAUUUUCGACGAUUUCUGA-5' (SEQ ID NO: 154)

AR-252 Target: 5'-TGAAGTTTTTAAAAGCTGCTAAAGACT-3' (SEQ ID NO: 307)

5'-AGUUUUUAAAAGCUGCUAAAGACUC-3' (SEQ ID NO: 461)
3'-CUUCAAAAAUUUUCGACGAUUUCUGAG-5' (SEQ ID NO: 155)

AR-253 Target: 5'-GAAGTTTTTAAAAGCTGCTAAAGACTC-3' (SEQ ID NO: 308)

5'-GUUUUUAAAAGCUGCUAAAGACUCG-3' (SEQ ID NO: 462)
3'-UUCAAAAAUUUUCGACGAUUUCUGAGC-5' (SEQ ID NO: 156)

AR-254 Target: 5'-AAGTTTTTAAAAGCTGCTAAAGACTCG-3' (SEQ ID NO: 309)

5'-CGGAGCCAGAGAUCAAAAGAUGAAA-3' (SEQ ID NO: 463)
3'-ACGCCUCGGUCUCUAGUUUUCUACUUU-5' (SEQ ID NO: 157)

AR-682 Target: 5'-TGCGGAGCCAGAGATCAAAAGATGAAA-3' (SEQ ID NO: 310)

5'-CAGAGAUCAAAAGAUGAAAAGGCAG-3' (SEQ ID NO: 464)
3'-CGGUCUCUAGUUUUCUACUUUUCCGUC-5' (SEQ ID NO: 158)

AR-688 Target: 5'-GCCAGAGATCAAAAGATGAAAAGGCAG-3' (SEQ ID NO: 311)

5'-AGAGAUCAAAAGAUGAAAAGGCAGU-3' (SEQ ID NO: 465)
3'-GGUCUCUAGUUUUCUACUUUUCCGUCA-5' (SEQ ID NO: 159)

AR-689 Target: 5'-CCAGAGATCAAAAGATGAAAAGGCAGT-3' (SEQ ID NO: 312)

5'-AAAGAUGAAAAGGCAGUCAGGUCUU-3' (SEQ ID NO: 466)
3'-GUUUUCUACUUUUCCGUCAGUCCAGAA-5' (SEQ ID NO: 160)

AR-697 Target: 5'-CAAAAGATGAAAAGGCAGTCAGGTCTT-3' (SEQ ID NO: 313)

5'-AAGAUGAAAAGGCAGUCAGGUCUUC-3' (SEQ ID NO: 467)
3'-UUUUCUACUUUUCCGUCAGUCCAGAAG-5' (SEQ ID NO: 161)

AR-698 Target: 5'-AAAAGATGAAAAGGCAGTCAGGTCTTC-3' (SEQ ID NO: 314)

5'-CAGGUCUUCAGUAGCCAAAAAACAA-3' (SEQ ID NO: 468)
3'-CAGUCCAGAAGUCAUCGGUUUUUUGUU-5' (SEQ ID NO: 162)

AR-714 Target: 5'-GTCAGGTCTTCAGTAGCCAAAAAACAA-3' (SEQ ID NO: 315)

5'-AGGUCUUCAGUAGCCAAAAAACAAA-3' (SEQ ID NO: 469)
3'-AGUCCAGAAGUCAUCGGUUUUUUGUUU-5' (SEQ ID NO: 163)

AR-715 Target: 5'-TCAGGTCTTCAGTAGCCAAAAAACAAA-3' (SEQ ID NO: 316)

5'-GUAGCCAAAAAACAAAACAAACAAA-3' (SEQ ID NO: 470)
3'-GUCAUCGGUUUUUUGUUUUGUUUGUUU-5' (SEQ ID NO: 164)

AR-724 Target: 5'-CAGTAGCCAAAAAACAAAACAAACAAA-3' (SEQ ID NO: 317)

5'-CAAAAAACAAAACAAACAAAAACAA-3' (SEQ ID NO: 471)
3'-CGGUUUUUUGUUUUGUUUGUUUUUGUU-5' (SEQ ID NO: 165)

AR-729 Target: 5'-GCCAAAAAACAAAACAAACAAAAACAA-3' (SEQ ID NO: 318)

5'-AAAAAACAAAACAAACAAAAACAAA-3' (SEQ ID NO: 472)
3'-GGUUUUUUGUUUUGUUUGUUUUUGUUU-5' (SEQ ID NO: 166)

AR-730 Target: 5'-CCAAAAAACAAAACAAACAAAAACAAA-3' (SEQ ID NO: 319)

5'-AAAACAAACAAAAACAAAAAAGCCG-3' (SEQ ID NO: 473)
3'-UGUUUUGUUUGUUUUUGUUUUUUCGGC-5' (SEQ ID NO: 167)

AR-737 Target: 5'-ACAAAACAAACAAAAACAAAAAAGCCG-3' (SEQ ID NO: 320)

5'-CAAAAACAAAAAAGCCGAAAUAAAA-3' (SEQ ID NO: 474)
3'-UUGUUUUUGUUUUUUCGGCUUUAUUUU-5' (SEQ ID NO: 168)

AR-745 Target: 5'-AACAAAAACAAAAAAGCCGAAATAAAA-3' (SEQ ID NO: 321)

5'-AAAAACAAAAAAGCCGAAAUAAAAG-3' (SEQ ID NO: 475)
3'-UGUUUUUGUUUUUUCGGCUUUAUUUUC-5' (SEQ ID NO: 169)

AR-746 Target: 5'-ACAAAAACAAAAAAGCCGAAATAAAAG-3' (SEQ ID NO: 322)

5'-AAAACAAAAAAGCCGAAAUAAAAGA-3' (SEQ ID NO: 476)
3'-GUUUUUGUUUUUUCGGCUUUAUUUUCU-5' (SEQ ID NO: 170)

AR-747 Target: 5'-CAAAAACAAAAAAGCCGAAATAAAAGA-3' (SEQ ID NO: 323)

5'-AAAAAAGCCGAAAUAAAAGAAAAAG-3' (SEQ ID NO: 477)
3'-UGUUUUUUCGGCUUUAUUUUCUUUUUC-5' (SEQ ID NO: 171)

AR-752 Target: 5'-ACAAAAAAGCCGAAATAAAAGAAAAAG-3' (SEQ ID NO: 324)

5'-AAAAAGCCGAAAUAAAAGAAAAAGA-3' (SEQ ID NO: 478)
3'-GUUUUUUCGGCUUUAUUUUCUUUUUCU-5' (SEQ ID NO: 172)

AR-753 Target: 5'-CAAAAAAGCCGAAATAAAAGAAAAAGA-3' (SEQ ID NO: 325)

5'-AAAGCCGAAAUAAAAGAAAAAGAUA-3' (SEQ ID NO: 479)
3'-UUUUUCGGCUUUAUUUUCUUUUUCUAU-5' (SEQ ID NO: 173)

AR-755 Target: 5'-AAAAAGCCGAAATAAAAGAAAAAGATA-3' (SEQ ID NO: 326)

5'-CGAAAUAAAAGAAAAAGAUAAUAAC-3' (SEQ ID NO: 480)
3'-CGGCUUUAUUUUCUUUUUCUAUUAUUG-5' (SEQ ID NO: 174)

AR-760 Target: 5'-GCCGAAATAAAAGAAAAAGATAATAAC-3' (SEQ ID NO: 327)

5'-GAAAUAAAAGAAAAAGAUAAUAACU-3' (SEQ ID NO: 481)
3'-GGCUUUAUUUUCUUUUUCUAUUAUUGA-5' (SEQ ID NO: 175)

AR-761 Target: 5'-CCGAAATAAAAGAAAAAGATAATAACT-3' (SEQ ID NO: 328)

5'-AAAUAAAAGAAAAAGAUAAUAACUC-3' (SEQ ID NO: 482)
3'-GCUUUAUUUUCUUUUUCUAUUAUUGAG-5' (SEQ ID NO: 176)

AR-762 Target: 5'-CGAAATAAAAGAAAAAGATAATAACTC-3' (SEQ ID NO: 329)

5'-GAAAAAGAUAAUAACUCAGUUCUUA-3' (SEQ ID NO: 483)
3'-UUCUUUUUCUAUUAUUGAGUCAAGAAU-5' (SEQ ID NO: 177)

AR-770 Target: 5'-AAGAAAAAGATAATAACTCAGTTCTTA-3' (SEQ ID NO: 330)

5'-AAGAUAAUAACUCAGUUCUUAUUUG-3' (SEQ ID NO: 484)
3'-UUUUCUAUUAUUGAGUCAAGAAUAAAC-5' (SEQ ID NO: 178)

AR-774 Target: 5'-AAAAGATAATAACTCAGTTCTTATTTG-3' (SEQ ID NO: 331)

5'-AGAUAAUAACUCAGUUCUUAUUUGC-3' (SEQ ID NO: 485)
3'-UUUCUAUUAUUGAGUCAAGAAUAAACG-5' (SEQ ID NO: 179)

AR-775 Target: 5'-AAAGATAATAACTCAGTTCTTATTTGC-3' (SEQ ID NO: 332)

5'-AUAAUAACUCAGUUCUUAUUUGCAC-3' (SEQ ID NO: 486)
3'-UCUAUUAUUGAGUCAAGAAUAAACGUG-5' (SEQ ID NO: 180)

AR-777 Target: 5'-AGATAATAACTCAGTTCTTATTTGCAC-3' (SEQ ID NO: 333)

5'-UAAUAACUCAGUUCUUAUUUGCACC-3' (SEQ ID NO: 487)
3'-CUAUUAUUGAGUCAAGAAUAAACGUGG-5' (SEQ ID NO: 181)

AR-778 Target: 5'-GATAATAACTCAGTTCTTATTTGCACC-3' (SEQ ID NO: 334)

5'-UUAUUUGCACCUACUUCAGUGGACA-3' (SEQ ID NO: 488)
3'-AGAAUAAACGUGGAUGAAGUCACCUGU-5' (SEQ ID NO: 182)

AR-792 Target: 5'-TCTTATTTGCACCTACTTCAGTGGACA-3' (SEQ ID NO: 335)

5'-AGUGGACACUGAAUUUGGAAGGUGG-3' (SEQ ID NO: 489)
3'-AGUCACCUGUGACUUAAACCUUCCACC-5' (SEQ ID NO: 183)

AR-809 Target: 5'-TCAGTGGACACTGAATTTGGAAGGTGG-3' (SEQ ID NO: 336)

5'-CUGAAUUUGGAAGGUGGAGGAUUUU-3' (SEQ ID NO: 490)
3'-GUGACUUAAACCUUCCACCUCCUAAAA-5' (SEQ ID NO: 184)

AR-817 Target: 5'-CACTGAATTTGGAAGGTGGAGGATTTT-3' (SEQ ID NO: 337)

5'-UGGAAGGUGGAGGAUUUUGUUUUUU-3' (SEQ ID NO: 491)
3'-AAACCUUCCACCUCCUAAAACAAAAAA-5' (SEQ ID NO: 185)

AR-824 Target: 5'-TTTGGAAGGTGGAGGATTTTGTTTTTT-3' (SEQ ID NO: 338)

5'-AAGGUGGAGGAUUUUGUUUUUUUCU-3' (SEQ ID NO: 492)
3'-CCUUCCACCUCCUAAAACAAAAAAAGA-5' (SEQ ID NO: 186)

AR-827 Target: 5'-GGAAGGTGGAGGATTTTGTTTTTTTCT-3' (SEQ ID NO: 339)

5'-GAGGAUUUUGUUUUUUUCUUUUAAG-3' (SEQ ID NO: 493)
3'-ACCUCCUAAAACAAAAAAAGAAAAUUC-5' (SEQ ID NO: 187)

AR-833 Target: 5'-TGGAGGATTTTGTTTTTTTCTTTTAAG-3' (SEQ ID NO: 340)

5'-AGGAUUUUGUUUUUUUCUUUUAAGA-3' (SEQ ID NO: 494)
3'-CCUCCUAAAACAAAAAAAGAAAAUUCU-5' (SEQ ID NO: 188)

AR-834 Target: 5'-GGAGGATTTTGTTTTTTTCTTTTAAGA-3' (SEQ ID NO: 341)

5'-GAUUUUGUUUUUUUCUUUUAAGAUC-3' (SEQ ID NO: 495)
3'-UCCUAAAACAAAAAAAGAAAAUUCUAG-5' (SEQ ID NO: 189)

AR-836 Target: 5'-AGGATTTTGTTTTTTCTTTTAAGATC-3' (SEQ ID NO: 342)

5'-AUUUUGUUUUUUUCUUUUAAGAUCU-3' (SEQ ID NO: 496)
3'-CCUAAAACAAAAAAAGAAAAUUCUAGA-5' (SEQ ID NO: 190)

AR-837 Target: 5'-GGATTTTGTTTTTTCTTTTAAGATCT-3' (SEQ ID NO: 343)

5'-UUUUGUUUUUUUCUUUUAAGAUCUG-3' (SEQ ID NO: 497)
3'-CUAAAACAAAAAAAGAAAAUUCUAGAC-5' (SEQ ID NO: 191)

AR-838 Target: 5'-GATTTTGTTTTTTCTTTTAAGATCTG-3' (SEQ ID NO: 344)

5'-UUUGUUUUUUUCUUUUAAGAUCUGG-3' (SEQ ID NO: 498)
3'-UAAAACAAAAAAAGAAAAUUCUAGACC-5' (SEQ ID NO: 192)

AR-839 Target: 5'-ATTTTGTTTTTTCTTTTAAGATCTGG-3' (SEQ ID NO: 345)

5'-UUUUUUUCUUUUAAGAUCUGGGCAU-3' (SEQ ID NO: 499)
3'-ACAAAAAAAGAAAAUUCUAGACCCGUA-5' (SEQ ID NO: 193)

AR-843 Target: 5'-TGTTTTTTCTTTTAAGATCTGGGCAT-3' (SEQ ID NO: 346)

5'-UUUUUUCUUUUAAGAUCUGGGCAUC-3' (SEQ ID NO: 500)
3'-CAAAAAAAGAAAAUUCUAGACCCGUAG-5' (SEQ ID NO: 194)

AR-844 Target: 5'-GTTTTTTCTTTTAAGATCTGGGCATC-3' (SEQ ID NO: 347)

5'-UAAGAUCUGGGCAUCUUUUGAAUCU-3' (SEQ ID NO: 501)
3'-AAAUUCUAGACCCGUAGAAAACUUAGA-5' (SEQ ID NO: 195)

AR-854 Target: 5'-TTTAAGATCTGGGCATCTTTTGAATCT-3' (SEQ ID NO: 348)

5'-CUUUUGAAUCUACCCUUCAAGUAUU-3' (SEQ ID NO: 502)
3'-UAGAAAACUUAGAUGGGAAGUUCAUAA-5' (SEQ ID NO: 196)

AR-868 Target: 5'-ATCTTTTGAATCTACCCTTCAAGTATT-3' (SEQ ID NO: 349)

5'-UUUUGAAUCUACCCUUCAAGUAUUA-3' (SEQ ID NO: 503)
3'-AGAAAACUUAGAUGGGAAGUUCAUAAU-5' (SEQ ID NO: 197)

AR-869 Target: 5'-TCTTTTGAATCTACCCTTCAAGTATTA-3' (SEQ ID NO: 350)

5'-UUUGAAUCUACCCUUCAAGUAUUAA-3' (SEQ ID NO: 504)
3'-GAAAACUUAGAUGGGAAGUUCAUAAUU-5' (SEQ ID NO: 198)

AR-870 Target: 5'-CTTTTGAATCTACCCTTCAAGTATTAA-3' (SEQ ID NO: 351)

5'-UUGAAUCUACCCUUCAAGUAUUAAG-3' (SEQ ID NO: 505)
3'-AAAACUUAGAUGGGAAGUUCAUAAUUC-5' (SEQ ID NO: 199)

AR-871 Target: 5'-TTTTGAATCTACCCTTCAAGTATTAAG-3' (SEQ ID NO: 352)

5'-UGAAUCUACCCUUCAAGUAUUAAGA-3' (SEQ ID NO: 506)
3'-AAACUUAGAUGGGAAGUUCAUAAUUCU-5' (SEQ ID NO: 200)

AR-872 Target: 5'-TTTGAATCTACCCTTCAAGTATTAAGA-3' (SEQ ID NO: 353)

5'-AAGUAUUAAGAGACAGACUGUGAGC-3' (SEQ ID NO: 507)
3'-AGUUCAUAAUUCUCUGUCUGACACUCG-5' (SEQ ID NO: 201)

AR-886 Target: 5'-TCAAGTATTAAGAGACAGACTGTGAGC-3' (SEQ ID NO: 354)

5'-UAUUAAGAGACAGACUGUGAGCCUA-3' (SEQ ID NO: 508)
3'-UCAUAAUUCUCUGUCUGACACUCGGAU-5' (SEQ ID NO: 202)

AR-889 Target: 5'-AGTATTAAGAGACAGACTGTGAGCCTA-3' (SEQ ID NO: 355)

5'-GUUGAACUCUUCUGAGCAAGAGAAG-3' (SEQ ID NO: 509)
3'-GACAACUUGAGAAGACUCGUUCUCUUC-5' (SEQ ID NO: 203)

AR-1067 Target: 5'-CTGTTGAACTCTTCTGAGCAAGAGAAG-3' (SEQ ID NO: 356)

5'-UUGAACUCUUCUGAGCAAGAGAAGG-3' (SEQ ID NO: 510)
3'-ACAACUUGAGAAGACUCGUUCUCUUCC-5' (SEQ ID NO: 204)

AR-1068 Target: 5'-TGTTGAACTCTTCTGAGCAAGAGAAGG-3' (SEQ ID NO: 357)

5'-AGGAUGGAAGUGCAGUUAGGGCUGG-3' (SEQ ID NO: 511)
3'-GUUCCUACCUUCACGUCAAUCCCGACC-5' (SEQ ID NO: 205)

AR-1137 Target: 5'-CAAGGATGGAAGTGCAGTTAGGGCTGG-3' (SEQ ID NO: 358)

5'-GAGGAGCUUUCCAGAAUCUGUUCCA-3' (SEQ ID NO: 512)
3'-GGCUCCUCGAAAGGUCUUAGACAAGGU-5' (SEQ ID NO: 206)

AR-1198 Target: 5'-CCGAGGAGCTTTCCAGAATCTGTTCCA-3' (SEQ ID NO: 359)

5'-AGGAGCUUUCCAGAAUCUGUUCCAG-3' (SEQ ID NO: 513)
3'-GCUCCUCGAAAGGUCUUAGACAAGGUC-5' (SEQ ID NO: 207)

AR-1199 Target: 5'-CGAGGAGCTTTCCAGAATCTGTTCCAG-3' (SEQ ID NO: 360)

5'-CUGACCUUAAAGACAUCCUGAGCGA-3' (SEQ ID NO: 514)
3'-GCGACUGGAAUUUCUGUAGGACUCGCU-5' (SEQ ID NO: 208)

AR-1675 Target: 5'-CGCTGACCTTAAAGACATCCTGAGCGA-3' (SEQ ID NO: 361)

5'-CAAGGACAAUUACUUAGGGGGCACU-3' (SEQ ID NO: 515)
3'-AGGUUCCUGUUAAUGAAUCCCCCGUGA-5' (SEQ ID NO: 209)

AR-1802 Target: 5'-TCCAAGGACAATTACTTAGGGGGCACT-3' (SEQ ID NO: 362)

5'-AAGGAGUUGUGUAAGGCAGUGUCGG-3' (SEQ ID NO: 516)
3'-GGUUCCUCAACACAUUCCGUCACAGCC-5' (SEQ ID NO: 210)

AR-1848 Target: 5'-CCAAGGAGTTGTGTAAGGCAGTGTCGG-3' (SEQ ID NO: 363)

5'-CUGAAGAUACUGCUGAGUAUUCCCC-3' (SEQ ID NO: 517)
3'-GUGACUUCUAUGACGACUCAUAAGGGG-5' (SEQ ID NO: 211)

AR-2047 Target: 5'-CACTGAAGATACTGCTGAGTATTCCCC-3' (SEQ ID NO: 364)

5'-CUGAGUAUUCCCCUUUCAAGGGAGG-3' (SEQ ID NO: 518)
3'-ACGACUCAUAAGGGGAAAGUUCCCUCC-5' (SEQ ID NO: 212)

AR-2059 Target: 5'-TGCTGAGTATTCCCCTTTCAAGGGAGG-3' (SEQ ID NO: 365)

5'-CUUGUGUCAAAAGCGAAAUGGGCCC-3' (SEQ ID NO: 519)
3'-GUGAACACAGUUUUCGCUUUACCCGGG-5' (SEQ ID NO: 213)

AR-2692 Target: 5'-CACTTGTGTCAAAAGCGAAATGGGCCC-3' (SEQ ID NO: 366)

5'-UUGUGUCAAAAGCGAAAUGGGCCCC-3' (SEQ ID NO: 520)
3'-UGAACACAGUUUUCGCUUUACCCGGGG-5' (SEQ ID NO: 214)

AR-2693 Target: 5'-ACTTGTGTCAAAAGCGAAATGGGCCCC-3' (SEQ ID NO: 367)

5'-CAUGUUUUGCCCAUUGACUAUUACU-3' (SEQ ID NO: 521)
3'-UGGUACAAAACGGGUAACUGAUAAUGA-5' (SEQ ID NO: 215)

AR-2775 Target: 5'-ACCATGTTTTGCCCATTGACTATTACT-3' (SEQ ID NO: 368)

5'-UGUUUUGCCCAUUGACUAUUACUUU-3' (SEQ ID NO: 522)
3'-GUACAAAACGGGUAACUGAUAAUGAAA-5' (SEQ ID NO: 216)

AR-2777 Target: 5'-CATGTTTTGCCCATTGACTATTACTTT-3' (SEQ ID NO: 369)

5'-GUGGAGAUGAAGCUUCUGGGUGUCA-3' (SEQ ID NO: 523)
3'-GACACCUCUACUUCGAAGACCCACAGU-5' (SEQ ID NO: 217)

AR-2827 Target: 5'-CTGTGGAGATGAAGCTTCTGGGTGTCA-3' (SEQ ID NO: 370)

5'-AAGGGAAACAGAAGUACCUGUGCGC-3' (SEQ ID NO: 524)
3'-ACUUCCCUUUGUCUUCAUGGACACGCG-5' (SEQ ID NO: 218)

AR-2905 Target: 5'-TGAAGGGAAACAGAAGTACCTGTGCGC-3' (SEQ ID NO: 371)

5'-AGAAAUGAUUGCACUAUUGAUAAAU-3' (SEQ ID NO: 525)
3'-CGUCUUUACUAACGUGAUAACUAUUUA-5' (SEQ ID NO: 219)

AR-2934 Target: 5'-GCAGAAATGATTGCACTATTGATAAAT-3' (SEQ ID NO: 372)

5'-GAAAUGAUUGCACUAUUGAUAAAUU-3' (SEQ ID NO: 526)
3'-GUCUUUACUAACGUGAUAACUAUUUAA-5' (SEQ ID NO: 220)

AR-2935 Target: 5'-CAGAAATGATTGCACTATTGATAAATT-3' (SEQ ID NO: 373)

5'-AAAUGAUUGCACUAUUGAUAAAUUC-3' (SEQ ID NO: 527)
3'-UCUUUACUAACGUGAUAACUAUUUAAG-5' (SEQ ID NO: 221)

AR-2936 Target: 5'-AGAAATGATTGCACTATTGATAAATTC-3' (SEQ ID NO: 374)

5'-AUGAUUGCACUAUUGAUAAAUUCCG-3' (SEQ ID NO: 528)
3'-UUUACUAACGUGAUAACUAUUUAAGGC-5' (SEQ ID NO: 222)

AR-2938 Target: 5'-AAATGATTGCACTATTGATAAATTCCG-3' (SEQ ID NO: 375)

5'-UGAUUGCACUAUUGAUAAAUUCCGA-3' (SEQ ID NO: 529)
3'-UUACUAACGUGAUAACUAUUUAAGGCU-5' (SEQ ID NO: 223)

AR-2939 Target: 5'-AATGATTGCACTATTGATAAATTCCGA-3' (SEQ ID NO: 376)

5'-CUAUUGAUAAAUUCCGAAGGAAAAA-3' (SEQ ID NO: 530)
3'-GUGAUAACUAUUUAAGGCUUCCUUUUU-5' (SEQ ID NO: 224)

AR-2947 Target: 5'-CACTATTGATAAATTCCGAAGGAAAAA-3' (SEQ ID NO: 377)

5'-UAUUGAUAAAUUCCGAAGGAAAAAU-3' (SEQ ID NO: 531)
3'-UGAUAACUAUUUAAGGCUUCCUUUUUA-5' (SEQ ID NO: 225)

AR-2948 Target: 5'-ACTATTGATAAATTCCGAAGGAAAAAT-3' (SEQ ID NO: 378)

5'-AUUGAUAAAUUCCGAAGGAAAAAUU-3' (SEQ ID NO: 532)
3'-GAUAACUAUUUAAGGCUUCCUUUUUAA-5' (SEQ ID NO: 226)

AR-2949 Target: 5'-CTATTGATAAATTCCGAAGGAAAAATT-3' (SEQ ID NO: 379)

5'-UUGAUAAAUUCCGAAGGAAAAAUUG-3' (SEQ ID NO: 533)
3'-AUAACUAUUUAAGGCUUCCUUUUUAAC-5' (SEQ ID NO: 227)

AR-2950 Target: 5'-TATTGATAAATTCCGAAGGAAAAATTG-3' (SEQ ID NO: 380)

5'-UGAUAAAUUCCGAAGGAAAAAUUGU-3' (SEQ ID NO: 534)
3'-UAACUAUUUAAGGCUUCCUUUUUAACA-5' (SEQ ID NO: 228)

AR-2951 Target: 5'-ATTGATAAATTCCGAAGGAAAAATTGT-3' (SEQ ID NO: 381)

5'-AUAAAUUCCGAAGGAAAAAUUGUCC-3' (SEQ ID NO: 535)
3'-ACUAUUUAAGGCUUCCUUUUUAACAGG-5' (SEQ ID NO: 229)

AR-2953 Target: 5'-TGATAAATTCCGAAGGAAAAATTGTCC-3' (SEQ ID NO: 382)

5'-UAAAUUCCGAAGGAAAAAUUGUCCA-3' (SEQ ID NO: 536)
3'-CUAUUUAAGGCUUCCUUUUUAACAGGU-5' (SEQ ID NO: 230)

AR-2954 Target: 5'-GATAAATTCCGAAGGAAAAATTGTCCA-3' (SEQ ID NO: 383)

5'-AAGGAAAAAUUGUCCAUCUUGUCGU-3' (SEQ ID NO: 537)
3'-GCUUCCUUUUUAACAGGUAGAACAGCA-5' (SEQ ID NO: 231)

AR-2963 Target: 5'-CGAAGGAAAAATTGTCCATCTTGTCGT-3' (SEQ ID NO: 384)

5'-CUUGUCGUCUUCGGAAAUGUUAUGA-3' (SEQ ID NO: 538)
3'-UAGAACAGCAGAAGCCUUUACAAUACU-5' (SEQ ID NO: 232)

AR-2980 Target: 5'-ATCTTGTCGTCTTCGGAAATGTTATGA-3' (SEQ ID NO: 385)

5'-GAAAUGUUAUGAAGCAGGGAUGACU-3' (SEQ ID NO: 539)
3'-GCCUUUACAAUACUUCGUCCCUACUGA-5' (SEQ ID NO: 233)

AR-2993 Target: 5'-CGGAAATGTTATGAAGCAGGGATGACT-3' (SEQ ID NO: 386)

5'-AAUGUUAUGAAGCAGGGAUGACUCU-3' (SEQ ID NO: 540)
3'-CUUUACAAUACUUCGUCCCUACUGAGA-5' (SEQ ID NO: 234)

AR-2995 Target: 5'-GAAATGTTATGAAGCAGGGATGACTCT-3' (SEQ ID NO: 387)

5'-CGGAAGCUGAAGAAACUUGGUAAUC-3' (SEQ ID NO: 541)
3'-GGGCCUUCGACUUCUUUGAACCAUUAG-5' (SEQ ID NO: 235)

AR-3027 Target: 5'-CCCGGAAGCTGAAGAAACTTGGTAATC-3' (SEQ ID NO: 388)

5'-GAAGCUGAAGAAACUUGGUAAUCUG-3' (SEQ ID NO: 542)
3'-GCCUUCGACUUCUUUGAACCAUUAGAC-5' (SEQ ID NO: 236)

AR-3029 Target: 5'-CGGAAGCTGAAGAAACTTGGTAATCTG-3' (SEQ ID NO: 389)

5'-UGAAGAAACUUGGUAAUCUGAAACU-3' (SEQ ID NO: 543)
3'-CGACUUCUUUGAACCAUUAGACUUUGA-5' (SEQ ID NO: 237)

AR-3034 Target: 5'-GCTGAAGAAACTTGGTAATCTGAAACT-3' (SEQ ID NO: 390)

5'-GAAGAAACUUGGUAAUCUGAAACUA-3' (SEQ ID NO: 544)
3'-GACUUCUUUGAACCAUUAGACUUUGAU-5' (SEQ ID NO: 238)

AR-3035 Target: 5'-CTGAAGAAACTTGGTAATCTGAAACTA-3' (SEQ ID NO: 391)

5'-AAGAAACUUGGUAAUCUGAAACUAC-3' (SEQ ID NO: 545)
3'-ACUUCUUUGAACCAUUAGACUUUGAUG-5' (SEQ ID NO: 239)

AR-3036 Target: 5'-TGAAGAAACTTGGTAATCTGAAACTAC-3' (SEQ ID NO: 392)

5'-GGUAAUCUGAAACUACAGGAGGAAG-3' (SEQ ID NO: 546)
3'-AACCAUUAGACUUUGAUGUCCUCCUUC-5' (SEQ ID NO: 240)

AR-3045 Target: 5'-TTGGTAATCTGAAACTACAGGAGGAAG-3' (SEQ ID NO: 393)

5'-CUGAAACUACAGGAGGAAGGAGAGG-3' (SEQ ID NO: 547)
3'-UAGACUUUGAUGUCCUCCUUCCUCUCC-5' (SEQ ID NO: 241)

AR-3051 Target: 5'-ATCTGAAACTACAGGAGGAAGGAGAGG-3' (SEQ ID NO: 394)

5'-CAGGAAUUCCUGUGCAUGAAAGCAC-3' (SEQ ID NO: 548)
3'-GGGUCCUUAAGGACACGUACUUUCGUG-5' (SEQ ID NO: 242)

AR-3546 Target: 5'-CCCAGGAATTCCTGTGCATGAAAGCAC-3' (SEQ ID NO: 395)

5'-AGGAAUUCCUGUGCAUGAAAGCACU-3' (SEQ ID NO: 549)
3'-GGUCCUUAAGGACACGUACUUUCGUGA-5' (SEQ ID NO: 243)

AR-3547 Target: 5'-CCAGGAATTCCTGTGCATGAAAGCACT-3' (SEQ ID NO: 396)

5'-GGAUGGGCUGAAAAAUCAAAAAUUC-3' (SEQ ID NO: 550)
3'-CACCUACCCGACUUUUUAGUUUUUAAG-5' (SEQ ID NO: 244)

AR-3596 Target: 5'-GTGGATGGGCTGAAAAATCAAAAATTC-3' (SEQ ID NO: 397)

5'-GAUGGGCUGAAAAAUCAAAAAUUCU-3' (SEQ ID NO: 551)
3'-ACCUACCCGACUUUUUAGUUUUUAAGA-5' (SEQ ID NO: 245)

AR-3597 Target: 5'-TGGATGGGCTGAAAAATCAAAAATTCT-3' (SEQ ID NO: 398)

5'-UGGGCUGAAAAAUCAAAAAUUCUUU-3' (SEQ ID NO: 552)
3'-CUACCCGACUUUUUAGUUUUUAAGAAA-5' (SEQ ID NO: 246)

AR-3599 Target: 5'-GATGGGCTGAAAAATCAAAAATTCTTT-3' (SEQ ID NO: 399)

5'-CUGAAAAAUCAAAAAUUCUUUGAUG-3' (SEQ ID NO: 553)
3'-CCGACUUUUUAGUUUUUAAGAAACUAC-5' (SEQ ID NO: 247)

AR-3603 Target: 5'-GGCTGAAAAATCAAAAATTCTTTGATG-3' (SEQ ID NO: 400)

5'-UGAAAAAUCAAAAAUUCUUUGAUGA-3' (SEQ ID NO: 554)
3'-CGACUUUUUAGUUUUUAAGAAACUACU-5' (SEQ ID NO: 248)

AR-3604 Target: 5'-GCTGAAAAATCAAAAATTCTTTGATGA-3' (SEQ ID NO: 401)

5'-AAAAAUCAAAAAUUCUUUGAUGAAC-3' (SEQ ID NO: 555)
3'-ACUUUUUAGUUUUUAAGAAACUACUUG-5' (SEQ ID NO: 249)

AR-3606 Target: 5'-TGAAAAATCAAAAATTCTTTGATGAAC-3' (SEQ ID NO: 402)

5'-AAAAUCAAAAAUUCUUUGAUGAACU-3' (SEQ ID NO: 556)
3'-CUUUUUAGUUUUUAAGAAACUACUUGA-5' (SEQ ID NO: 250)

AR-3607 Target: 5'-GAAAAATCAAAAATTCTTTGATGAACT-3' (SEQ ID NO: 403)

5'-AAAUCAAAAAUUCUUUGAUGAACUU-3' (SEQ ID NO: 557)
3'-UUUUUAGUUUUUAAGAAACUACUUGAA-5' (SEQ ID NO: 251)

AR-3608 Target: 5'-AAAAATCAAAAATTCTTTGATGAACTT-3' (SEQ ID NO: 404)

5'-CGAAUGAACUACAUCAAGGAACUCG-3' (SEQ ID NO: 558)
3'-AAGCUUACUUGAUGUAGUUCCUUGAGC-5' (SEQ ID NO: 252)

AR-3633 Target: 5'-TTCGAATGAACTACATCAAGGAACTCG-3' (SEQ ID NO: 405)

5'-AAGGAACUCGAUCGUAUCAUUGCAU-3' (SEQ ID NO: 559)
3'-AGUUCCUUGAGCUAGCAUAGUAACGUA-5' (SEQ ID NO: 253)

AR-3648 Target: 5'-TCAAGGAACTCGATCGTATCATTGCAT-3' (SEQ ID NO: 406)

5'-AGGAACUCGAUCGUAUCAUUGCAUG-3' (SEQ ID NO: 560)
3'-GUUCCUUGAGCUAGCAUAGUAACGUAC-5' (SEQ ID NO: 254)

AR-3649 Target: 5'-CAAGGAACTCGATCGTATCATTGCATG-3' (SEQ ID NO: 407)

5'-CGUAUCAUUGCAUGCAAAAGAAAAA-3' (SEQ ID NO: 561)
3'-UAGCAUAGUAACGUACGUUUUCUUUUU-5' (SEQ ID NO: 255)

AR-3660 Target: 5'-ATCGTATCATTGCATGCAAAAGAAAAA-3' (SEQ ID NO: 408)

5'-GUAUCAUUGCAUGCAAAAGAAAAAA-3' (SEQ ID NO: 562)
3'-AGCAUAGUAACGUACGUUUUCUUUUUU-5' (SEQ ID NO: 256)

AR-3661 Target: 5'-TCGTATCATTGCATGCAAAAGAAAAAA-3' (SEQ ID NO: 409)

5'-CAUUGCAUGCAAAAGAAAAAAUCCC-3' (SEQ ID NO: 563)
3'-UAGUAACGUACGUUUUCUUUUUUAGGG-5' (SEQ ID NO: 257)

AR-3665 Target: 5'-ATCATTGCATGCAAAAGAAAAAATCCC-3' (SEQ ID NO: 410)

5'-CUUUUGACCUGCUAAUCAAGUCACA-3' (SEQ ID NO: 564)
3'-GUGAAAACUGGACGAUUAGUUCAGUGU-5' (SEQ ID NO: 258)

AR-3772 Target: 5'-CACTTTTGACCTGCTAATCAAGTCACA-3' (SEQ ID NO: 411)

5'-GUGGACUUUCCGGAAAUGAUGGCAG-3' (SEQ ID NO: 565)
3'-CGCACCUGAAAGGCCUUUACUACCGUC-5' (SEQ ID NO: 259)

AR-3807 Target: 5'-GCGTGGACTTTCCGGAAATGATGGCAG-3' (SEQ ID NO: 412)

5'-UGGACUUUCCGGAAAUGAUGGCAGA-3' (SEQ ID NO: 566)
3'-GCACCUGAAAGGCCUUUACUACCGUCU-5' (SEQ ID NO: 260)

AR-3808 Target: 5'-CGTGGACTTTCCGGAAATGATGGCAGA-3' (SEQ ID NO: 413)

5'-AUGGCAGAGAUCAUCUCUGUGCAAG-3' (SEQ ID NO: 567)
3'-ACUACCGUCUCUAGUAGAGACACGUUC-5' (SEQ ID NO: 261)

AR-3825 Target: 5'-TGATGGCAGAGATCATCTCTGTGCAAG-3' (SEQ ID NO: 414)

5'-AGAGAUCAUCUCUGUGCAAGUGCCC-3' (SEQ ID NO: 568)
3'-CGUCUCUAGUAGAGACACGUUCACGGG-5' (SEQ ID NO: 262)

AR-3830 Target: 5'-GCAGAGATCATCTCTGTGCAAGTGCCC-3' (SEQ ID NO: 415)

5'-GAGAUCAUCUCUGUGCAAGUGCCCA-3' (SEQ ID NO: 569)
3'-GUCUCUAGUAGAGACACGUUCACGGGU-5' (SEQ ID NO: 263)

AR-3831 Target: 5'-CAGAGATCATCTCTGTGCAAGTGCCCA-3' (SEQ ID NO: 416)

5'-CAAGAUCCUUUCUGGGAAAGUCAAG-3' (SEQ ID NO: 570)
3'-GGGUUCUAGGAAAGACCCUUUCAGUUC-5' (SEQ ID NO: 264)

AR-3854 Target: 5'-CCCAAGATCCTTTCTGGGAAAGTCAAG-3' (SEQ ID NO: 417)

5'-GAAGCAUUGGAAACCCUAUUUCCCC-3' (SEQ ID NO: 571)
3'-CACUUCGUAACCUUUGGGAUAAAGGGG-5' (SEQ ID NO: 265)

AR-3901 Target: 5'-GTGAAGCATTGGAAACCCTATTTCCCC-3' (SEQ ID NO: 418)

5'-GAUGUCUUCUGCCUGUUAUAACUCU-3' (SEQ ID NO: 572)
3'-GUCUACAGAAGACGGACAAUAUUGAGA-5' (SEQ ID NO: 266)

AR-3949 Target: 5'-CAGATGTCTTCTGCCTGTTATAACTCT-3' (SEQ ID NO: 419)

5'-CUUGGGGAAUUUCCUCUAUUGAUGU-3' (SEQ ID NO: 573)
3'-CGGAACCCCUUAAAGGAGAUAACUACA-5' (SEQ ID NO: 267)

AR-3994 Target: 5'-GCCTTGGGGAATTTCCTCTATTGATGT-3' (SEQ ID NO: 420)

5'-UGGGGAAUUUCCUCUAUUGAUGUAC-3' (SEQ ID NO: 574)
3'-GAACCCCUUAAAGGAGAUAACUACAUG-5' (SEQ ID NO: 268)

AR-3996 Target: 5'-CTTGGGGAATTTCCTCTATTGATGTAC-3' (SEQ ID NO: 421)

5'-GGGGAAUUUCCUCUAUUGAUGUACA-3' (SEQ ID NO: 575)
3'-AACCCCUUAAAGGAGAUAACUACAUGU-5' (SEQ ID NO: 269)

AR-3997 Target: 5'-TTGGGGAATTTCCTCTATTGATGTACA-3' (SEQ ID NO: 422)

5'-GGGAAUUUCCUCUAUUGAUGUACAG-3' (SEQ ID NO: 576)
3'-ACCCCUUAAAGGAGAUAACUACAUGUC-5' (SEQ ID NO: 270)

AR-3998 Target: 5'-TGGGGAATTTCCTCTATTGATGTACAG-3' (SEQ ID NO: 423)

5'-GGAAUUUCCUCUAUUGAUGUACAGU-3' (SEQ ID NO: 577)
3'-CCCCUUAAAGGAGAUAACUACAUGUCA-5' (SEQ ID NO: 271)

AR-3999 Target: 5'-GGGGAATTTCCTCTATTGATGTACAGT-3' (SEQ ID NO: 424)

5'-AUUGAUGUACAGUCUGUCAUGAACA-3' (SEQ ID NO: 578)
3'-GAUAACUACAUGUCAGACAGUACUUGU-5' (SEQ ID NO: 272)

AR-4011 Target: 5'-CTATTGATGTACAGTCTGTCATGAACA-3' (SEQ ID NO: 425)

5'-UUGAUGUACAGUCUGUCAUGAACAU-3' (SEQ ID NO: 579)
3'-AUAACUACAUGUCAGACAGUACUUGUA-5' (SEQ ID NO: 273)

AR-4012 Target: 5'-TATTGATGTACAGTCTGTCATGAACAT-3' (SEQ ID NO: 426)

5'-UGAUGUACAGUCUGUCAUGAACAUG-3' (SEQ ID NO: 580)
3'-UAACUACAUGUCAGACAGUACUUGUAC-5' (SEQ ID NO: 274)

AR-4013 Target: 5'-ATTGATGTACAGTCTGTCATGAACATG-3' (SEQ ID NO: 427)

5'-CAUGUUCCUGAAUUCUAUUUGCUGG-3' (SEQ ID NO: 581)
3'-UUGUACAAGGACUUAAGAUAAACGACC-5' (SEQ ID NO: 275)

AR-4034 Target: 5'-AACATGTTCCTGAATTCTATTTGCTGG-3' (SEQ ID NO: 428)

5'-CUAUUUGCUGGGCUUUUUUUUUCUC-3' (SEQ ID NO: 582)
3'-AAGAUAAACGACCCGAAAAAAAAAGAG-5' (SEQ ID NO: 276)

AR-4048 Target: 5'-TTCTATTTGCTGGGCTTTTTTTTTCTC-3' (SEQ ID NO: 429)

5'-UAUUUGCUGGGCUUUUUUUUUCUCU-3' (SEQ ID NO: 583)
3'-AGAUAAACGACCCGAAAAAAAAAGAGA-5' (SEQ ID NO: 277)

AR-4049 Target: 5'-TCTATTTGCTGGGCTTTTTTTTTCTCT-3' (SEQ ID NO: 430)

5'-CUGGGCUUUUUUUUUCUCUUUCUCU-3' (SEQ ID NO: 584)
3'-ACGACCCGAAAAAAAAAGAGAAAGAGA-5' (SEQ ID NO: 278)

AR-4055 Target: 5'-TGCTGGGCTTTTTTTTCTCTTTCTCT-3' (SEQ ID NO: 431)

5'-UUUUUUCUCUUUCUCUCCUUUCUUU-3' (SEQ ID NO: 585)
3'-AAAAAAAAGAGAAAGAGAGGAAAGAAA-5' (SEQ ID NO: 279)

AR-4064 Target: 5'-TTTTTTTCTCTTTCTCTCCTTTCTTT-3' (SEQ ID NO: 432)

5'-CAGACUUUGCUUCCCAUUGUGGCUC-3' (SEQ ID NO: 586)
3'-AAGUCUGAAACGAAGGGUAACACCGAG-5' (SEQ ID NO: 280)

AR-4128 Target: 5'-TTCAGACTTTGCTTCCCATTGTGGCTC-3' (SEQ ID NO: 433)

5'-GUGGCUCCUAUCUGUGUUUUGAAUG-3' (SEQ ID NO: 587)
3'-AACACCGAGGAUAGACACAAAACUUAC-5' (SEQ ID NO: 281)

AR-4146 Target: 5'-TTGTGGCTCCTATCTGTGTTTTGAATG-3' (SEQ ID NO: 434)

5'-CUAUCUGUGUUUUGAAUGGUGUUGU-3' (SEQ ID NO: 588)
3'-AGGAUAGACACAAAACUUACCACAACA-5' (SEQ ID NO: 282)

AR-4153 Target: 5'-TCCTATCTGTGTTTTGAATGGTGTTGT-3' (SEQ ID NO: 435)

5'-CUGUGUUUUGAAUGGUGUUGUAUGC-3' (SEQ ID NO: 589)
3'-UAGACACAAAACUUACCACAACAUACG-5' (SEQ ID NO: 283)

AR-4157 Target: 5'-ATCTGTGTTTTGAATGGTGTTGTATGC-3' (SEQ ID NO: 436)

5'-UGUUUUGAAUGGUGUUGUAUGCCUU-3' (SEQ ID NO: 590)
3'-ACACAAAACUUACCACAACAUACGGAA-5' (SEQ ID NO: 284)

AR-4160 Target: 5'-TGTGTTTTGAATGGTGTTGTATGCCTT-3' (SEQ ID NO: 437)

5'-AAUGGUGUUGUAUGCCUUUAAAUCU-3' (SEQ ID NO: 591)
3'-ACUUACCACAACAUACGGAAAUUUAGA-5' (SEQ ID NO: 285)

AR-4167 Target: 5'-TGAATGGTGTTGTATGCCTTTAAATCT-3' (SEQ ID NO: 438)

5'-AUGGUGUUGUAUGCCUUUAAAUCUG-3' (SEQ ID NO: 592)
3'-CUUACCACAACAUACGGAAAUUUAGAC-5' (SEQ ID NO: 286)

AR-4168 Target: 5'-GAATGGTGTTGTATGCCTTTAAATCTG-3' (SEQ ID NO: 439)

5'-UUGUAUGCCUUUAAAUCUGUGAUGA-3' (SEQ ID NO: 593)
3'-ACAACAUACGGAAAUUUAGACACUACU-5' (SEQ ID NO: 287)

AR-4174 Target: 5'-TGTTGTATGCCTTTAAATCTGTGATGA-3' (SEQ ID NO: 440)

5'-GUAUGCCUUUAAAUCUGUGAUGAUC-3' (SEQ ID NO: 594)
3'-AACAUACGGAAAUUUAGACACUACUAG-5' (SEQ ID NO: 288)

AR-4176 Target: 5'-TTGTATGCCTTTAAATCTGTGATGATC-3' (SEQ ID NO: 441)

5'-UAUGCCUUUAAAUCUGUGAUGAUCC-3' (SEQ ID NO: 595)
3'-ACAUACGGAAAUUUAGACACUACUAGG-5' (SEQ ID NO: 289)

AR-4177 Target: 5'-TGTATGCCTTTAAATCTGTGATGATCC-3' (SEQ ID NO: 442)

5'-CAGUGUCAAGUUGUGCUUGUUUACA-3' (SEQ ID NO: 596)
3'-GGGUCACAGUUCAACACGAACAAAUGU-5' (SEQ ID NO: 290)

AR-4212 Target: 5'-CCCAGTGTCAAGTTGTGCTTGTTTACA-3' (SEQ ID NO: 443)

5'-AGUGUCAAGUUGUGCUUGUUUACAG-3' (SEQ ID NO: 597)
3'-GGUCACAGUUCAACACGAACAAAUGUC-5' (SEQ ID NO: 291)

AR-4213 Target: 5'-CCAGTGTCAAGTTGTGCTTGTTTACAG-3' (SEQ ID NO: 444)

5'-UUGUUUACAGCACUACUCUGUGCCA-3' (SEQ ID NO: 598)
3'-CGAACAAAUGUCGUGAUGAGACACGGU-5' (SEQ ID NO: 292)

AR-4228 Target: 5'-GCTTGTTTACAGCACTACTCTGTGCCA-3' (SEQ ID NO: 445)

5'-UGUUUACAGCACUACUCUGUGCCAG-3' (SEQ ID NO: 599)
3'-GAACAAAUGUCGUGAUGAGACACGGUC-5' (SEQ ID NO: 293)

AR-4229 Target: 5'-CTTGTTTACAGCACTACTCTGTGCCAG-3' (SEQ ID NO: 446)

5'-CAAACGUUUACUUAUCUUAUGCCAC-3' (SEQ ID NO: 600)
3'-GUGUUUGCAAAUGAAUAGAAUACGGUG-5' (SEQ ID NO: 294)

AR-4259 Target: 5'-CACAAACGTTTACTTATCTTATGCCAC-3' (SEQ ID NO: 447)

5'-CGGGAAGUUUAGAGAGCUAAGAUUA-3' (SEQ ID NO: 601)
3'-GUGCCCUUCAAAUCUCUCGAUUCUAAU-5' (SEQ ID NO: 295)

AR-4283 Target: 5'-CACGGGAAGTTTAGAGAGCTAAGATTA-3' (SEQ ID NO: 448)

5'-GGGAAGUUUAGAGAGCUAAGAUUAU-3' (SEQ ID NO: 602)
3'-UGCCCUUCAAAUCUCUCGAUUCUAAUA-5' (SEQ ID NO: 296)

AR-4284 Target: 5'-ACGGGAAGTTTAGAGAGCTAAGATTAT-3' (SEQ ID NO: 449)

5'-GGAAGUUUAGAGAGCUAAGAUUAUC-3' (SEQ ID NO: 603)
3'-GCCCUUCAAAUCUCUCGAUUCUAAUAG-5' (SEQ ID NO: 297)

AR-4285 Target: 5'-CGGGAAGTTTAGAGAGCTAAGATTATC-3' (SEQ ID NO: 450)

5'-GAAGUUUAGAGAGCUAAGAUUAUCU-3' (SEQ ID NO: 604)
3'-CCCUUCAAAUCUCUCGAUUCUAAUAGA-5' (SEQ ID NO: 298)

AR-4286 Target: 5'-GGGAAGTTTAGAGAGCTAAGATTATCT-3' (SEQ ID NO: 451)

5'-AGUUUAGAGAGCUAAGAUUAUCUGG-3' (SEQ ID NO: 605)
3'-CUUCAAAUCUCUCGAUUCUAAUAGACC-5' (SEQ ID NO: 299)

AR-4288 Target: 5'-GAAGTTTAGAGAGCTAAGATTATCTGG-3' (SEQ ID NO: 452)

5'-AGAGAGCUAAGAUUAUCUGGGGAAA-3' (SEQ ID NO: 606)
3'-AAUCUCUCGAUUCUAAUAGACCCCUUU-5' (SEQ ID NO: 300)

AR-4293 Target: 5'-TTAGAGAGCTAAGATTATCTGGGGAAA-3' (SEQ ID NO: 453)

5'-GAGAGCUAAGAUUAUCUGGGGAAAU-3' (SEQ ID NO: 607)
3'-AUCUCUCGAUUCUAAUAGACCCCUUUA-5' (SEQ ID NO: 301)

AR-4294 Target: 5'-TAGAGAGCTAAGATTATCTGGGGAAAT-3' (SEQ ID NO: 454)

5'-AGAGCUAAGAUUAUCUGGGGAAAUC-3' (SEQ ID NO: 608)
3'-UCUCUCGAUUCUAAUAGACCCCUUUAG-5' (SEQ ID NO: 302)

AR-4295 Target: 5'-AGAGAGCTAAGATTATCTGGGGAAATC-3' (SEQ ID NO: 455)

5'-AGAUUAUCUGGGGAAAUCAAAACAA-3' (SEQ ID NO: 609)
3'-AUUCUAAUAGACCCCUUUAGUUUUGUU-5' (SEQ ID NO: 303)

AR-4302 Target: 5'-TAAGATTATCTGGGGAAATCAAAACAA-3' (SEQ ID NO: 456)

5'-GAUUAUCUGGGGAAAUCAAAACAAA-3' (SEQ ID NO: 610)
3'-UUCUAAUAGACCCCUUUAGUUUUGUUU-5' (SEQ ID NO: 304)

AR-4303 Target: 5'-AAGATTATCTGGGGAAATCAAAACAAA-3' (SEQ ID NO: 457)

5'-CUGGGGAAAUCAAAACAAAAACAAG-3' (SEQ ID NO: 611)
3'-UAGACCCCUUUAGUUUUGUUUUUGUUC-5' (SEQ ID NO: 305)

AR-4309 Target: 5'-ATCTGGGGAAATCAAAACAAAAACAAG-3' (SEQ ID NO: 458)

5'-GGAAAUCAAAACAAAAACAAGCAAA-3' (SEQ ID NO: 612)
3'-CCCCUUUAGUUUUGUUUUUGUUCGUUU-5' (SEQ ID NO: 306)

AR-4313 Target: 5'-GGGGAAATCAAAACAAAAACAAGCAAA-3' (SEQ ID NO: 459)

5'-GAAGUUUUUAAAAGCUGCUAAAGAC-3' (SEQ ID NO: 856)
3'-CACUUCAAAAAUUUUCGACGAUUUCUG-5' (SEQ ID NO: 796)

AR-251 Target: 5'-GTGAAGTTTTTAAAAGCTGCTAAAGAC-3' (SEQ ID NO: 826)

5'-CUAGCUGCACAUUGCAAAGAAGGCU-3' (SEQ ID NO: 857)
3'-UCGAUCGACGUGUAACGUUUCUUCCGA-5' (SEQ ID NO: 797)

AR-524 Target: 5'-AGCTAGCTGCACATTGCAAAGAAGGCT-3' (SEQ ID NO: 827)

5'-AUUGCAAAGAAGGCUCUUAGGAGCC-3' (SEQ ID NO: 858)
3'-UGUAACGUUUCUUCCGAGAAUCCUCGG-5' (SEQ ID NO: 798)

AR-534 Target: 5'-ACATTGCAAAGAAGGCTCTTAGGAGCC-3' (SEQ ID NO: 828)

5'-CAAAACAAACAAAAACAAAAAAGCC-3' (SEQ ID NO: 859)
3'-UUGUUUUGUUUGUUUUUGUUUUUCGG-5' (SEQ ID NO: 799)

AR-736 Target: 5'-AACAAAACAAACAAAAACAAAAAAGCC-3' (SEQ ID NO: 829)

5'-GAUAAUAACUCAGUUCUUAUUUGCA-3' (SEQ ID NO: 860)
3'-UUCUAUUAUUGAGUCAAGAAUAAACGU-5' (SEQ ID NO: 800)

AR-776 Target: 5'-AAGATAATAACTCAGTTCTTATTTGCA-3' (SEQ ID NO: 830)

5'-CAGUGGACACUGAAUUUGGAAGGUG-3' (SEQ ID NO: 861)
3'-AAGUCACCUGUGACUUAAACCUUCCAC-5' (SEQ ID NO: 801)

AR-808 Target: 5'-TTCAGTGGACACTGAATTTGGAAGGTG-3' (SEQ ID NO: 831)

5'-GUGGACACUGAAUUUGGAAGGUGGA-3' (SEQ ID NO: 862)
3'-GUCACCUGUGACUUAAACCUUCCACCU-5' (SEQ ID NO: 802)

AR-810 Target: 5'-CAGTGGACACTGAATTTGGAAGGTGGA-3' (SEQ ID NO: 832)

5'-UGGACACUGAAUUUGGAAGGUGGAG-3' (SEQ ID NO: 863)
3'-UCACCUGUGACUUAAACCUUCCACCUC-5' (SEQ ID NO: 803)

AR-811 Target: 5'-AGTGGACACTGAATTTGGAAGGTGGAG-3' (SEQ ID NO: 833)

5'-GAAUCUACCCUUCAAGUAUUAAGAG-3' (SEQ ID NO: 864)
3'-AACUUAGAUGGGAAGUUCAUAAUUCUC-5' (SEQ ID NO: 804)

AR-873 Target: 5'-TTGAATCTACCCTTCAAGTATTAAGAG-3' (SEQ ID NO: 834)

5'-AGUAUUAAGAGACAGACUGUGAGCC-3' (SEQ ID NO: 865)
3'-GUUCAUAAUUCUCUGUCUGACACUCGG-5' (SEQ ID NO: 805)

AR-887 Target: 5'-CAAGTATTAAGAGACAGACTGTGAGCC-3' (SEQ ID NO: 835)

5'-UGAGUAUUCCCCUUUCAAGGGAGGU-3' (SEQ ID NO: 866)
3'-CGACUCAUAAGGGGAAAGUUCCCUCCA-5' (SEQ ID NO: 806)

AR-2060 Target: 5'-GCTGAGTATTCCCCTTTCAAGGGAGGT-3' (SEQ ID NO: 836)

5'-GAGUAUUCCCCUUUCAAGGGAGGUU-3' (SEQ ID NO: 867)
3'-GACUCAUAAGGGGAAAGUUCCCUCCAA-5' (SEQ ID NO: 807)

AR-2061 Target: 5'-CTGAGTATTCCCCTTTCAAGGGAGGTT-3' (SEQ ID NO: 837)

5'-UGUGGAGAUGAAGCUUCUGGGUGUC-3' (SEQ ID NO: 868)
3'-AGACACCUCUACUUCGAAGACCCACAG-5' (SEQ ID NO: 808)

AR-2826 Target: 5'-TCTGTGGAGATGAAGCTTCTGGGTGTC-3' (SEQ ID NO: 838)

5'-AGGGAAACAGAAGUACCUGUGCGCC-3' (SEQ ID NO: 869)
3'-CUUCCCUUUGUCUUCAUGGACACGCGG-5' (SEQ ID NO: 809)

AR-2906 Target: 5'-GAAGGGAAACAGAAGTACCTGTGCGCC-3' (SEQ ID NO: 839)

5'-GAUAAAUUCCGAAGGAAAAAUUGUC-3' (SEQ ID NO: 870)
3'-AACUAUUUAAGGCUUCCUUUUUAACAG-5' (SEQ ID NO: 810)

AR-2952 Target: 5'-TTGATAAATTCCGAAGGAAAAATTGTC-3' (SEQ ID NO: 840)

5'-AGGAAAAAUUGUCCAUCUUGUCGUC-3' (SEQ ID NO: 871)
3'-CUUCCUUUUUAACAGGUAGAACAGCAG-5' (SEQ ID NO: 811)

AR-2964 Target: 5'-GAAGGAAAAATTGTCCATCTTGTCGTC-3' (SEQ ID NO: 841)

5'-GGAAAUGUUAUGAAGCAGGGAUGAC-3' (SEQ ID NO: 872)
3'-AGCCUUUACAAUACUUCGUCCCUACUG-5' (SEQ ID NO: 812)

AR-2992 Target: 5'-TCGGAAATGTTATGAAGCAGGGATGAC-3' (SEQ ID NO: 842)

5'-UUGGUAAUCUGAAACUACAGGAGGA-3' (SEQ ID NO: 873)
3'-UGAACCAUUAGACUUUGAUGUCCUCCU-5' (SEQ ID NO: 813)

AR-3043 Target: 5'-ACTTGGTAATCTGAAACTACAGGAGGA-3' (SEQ ID NO: 843)

5'-UGGUAAUCUGAAACUACAGGAGGAA-3' (SEQ ID NO: 874)
3'-GAACCAUUAGACUUUGAUGUCCUCCUU-5' (SEQ ID NO: 814)

AR-3044 Target: 5'-CTTGGTAATCTGAAACTACAGGAGGAA-3' (SEQ ID NO: 844)

5'-UAAUCUGAAACUACAGGAGGAAGGA-3' (SEQ ID NO: 875)
3'-CCAUUAGACUUUGAUGUCCUCCUUCCU-5' (SEQ ID NO: 815)

AR-3047 Target: 5'-GGTAATCTGAAACTACAGGAGGAAGGA-3' (SEQ ID NO: 845)

5'-CUGACAGUGUCACACAUUGAAGGCU-3' (SEQ ID NO: 876)
3'-UCGACUGUCACAGUGUGUAACUUCCGA-5' (SEQ ID NO: 816)

AR-3117 Target: 5'-AGCTGACAGTGTCACACATTGAAGGCT-3' (SEQ ID NO: 846)

5'-CUGUCAUUCAGUACUCCUGGAUGGG-3' (SEQ ID NO: 877)
3'-CCGACAGUAAGUCAUGAGGACCUACCC-5' (SEQ ID NO: 817)

AR-3346 Target: 5'-GGCTGTCATTCAGTACTCCTGGATGGG-3' (SEQ ID NO: 847)

5'-GAAAAAUCAAAAAUUCUUUGAUGAA-3' (SEQ ID NO: 878)
3'-GACUUUUUAGUUUUUAAGAAACUACUU-5' (SEQ ID NO: 818)

AR-3605 Target: 5'-CTGAAAAATCAAAAATTCTTTGATGAA-3' (SEQ ID NO: 848)

5'-AAUUCUUUGAUGAACUUCGAAUGAA-3' (SEQ ID NO: 879)
3'-UUUUAAGAAACUACUUGAAGCUUACUU-5' (SEQ ID NO: 819)

AR-3616 Target: 5'-AAAATTCTTTGATGAACTTCGAATGAA-3' (SEQ ID NO: 849)

5'-CUAAUCAAGUCACACAUGGUGAGCG-3' (SEQ ID NO: 880)
3'-ACGAUUAGUUCAGUGUGUACCACUCGC-5' (SEQ ID NO: 820)

AR-3783 Target: 5'-TGCTAATCAAGTCACACATGGTGAGCG-3' (SEQ ID NO: 850)

5'-CGUGGACUUUCCGGAAAUGAUGGCA-3' (SEQ ID NO: 881)
3'-UCGCACCUGAAAGGCCUUUACUACCGU-5' (SEQ ID NO: 821)

AR-3806 Target: 5'-AGCGTGGACTTTCCGGAAATGATGGCA-3' (SEQ ID NO: 851)

5'-UUGGGGAAUUUCCUCUAUUGAUGUA-3' (SEQ ID NO: 882)
3'-GGAACCCCUUAAAGGAGAUAACUACAU-5' (SEQ ID NO: 822)

AR-3995 Target: 5'-CCTTGGGGAATTTCCTCTATTGATGTA-3' (SEQ ID NO: 852)

5'-UGUGUUUUGAAUGGUGUUGUAUGCC-3' (SEQ ID NO: 883)
3'-AGACACAAAACUUACCACAACAUACGG-5' (SEQ ID NO: 823)

AR-4158 Target: 5'-TCTGTGTTTTGAATGGTGTTGTATGCC-3' (SEQ ID NO: 853)

5'-UGUAUGCCUUUAAAUCUGUGAUGAU-3' (SEQ ID NO: 884)
3'-CAACAUACGGAAAUUUAGACACUACUA-5' (SEQ ID NO: 824)

AR-4175 Target: 5'-GTTGTATGCCTTTAAATCTGTGATGAT-3' (SEQ ID NO: 854)

5'-UAGAGAGCUAAGAUUAUCUGGGGAA-3' (SEQ ID NO: 885)
3'-AAAUCUCUCGAUUCUAAUAGACCCCUU-5' (SEQ ID NO: 825)

AR-4292 Target: 5'-TTTAGAGAGCTAAGATTATCTGGGGAA-3' (SEQ ID NO: 855)

5'-GGUGAAGUUUUUAAAAGCUGCUAAA-3' (SEQ ID NO: 1078)
3'-AGCCACUUCAAAAAUUUUCGACGAUUU-5' (SEQ ID NO: 970)

AR-248 Target: 5'-TCGGTGAAGTTTTTAAAAGCTGCTAAA-3' (SEQ ID NO: 1024)

5'-UUUUUAAAAGCUGCUAAAGACUCGG-3' (SEQ ID NO: 1079)
3'-UCAAAAAUUUUCGACGAUUUCUGAGCC-5' (SEQ ID NO: 971)

AR-255 Target: 5'-AGTTTTTAAAAGCTGCTAAAGACTCGG-3' (SEQ ID NO: 1025)

5'-AGAGAGGUAACUCCCUUUGGCUGCG-3' (SEQ ID NO: 1080)
3'-CGUCUCUCCAUUGAGGGAAACCGACGC-5' (SEQ ID NO: 972)

AR-489 Target: 5'-GCAGAGAGGTAACTCCCTTTGGCTGCG-3' (SEQ ID NO: 1026)

5'-GAGAUCAAAAGAUGAAAAGGCAGUC-3' (SEQ ID NO: 1081)
3'-GUCUCUAGUUUUCUACUUUUCCGUCAG-5' (SEQ ID NO: 973)

AR-690 Target: 5'-CAGAGATCAAAAGATGAAAAGGCAGTC-3' (SEQ ID NO: 1027)

5'-AAAAACAAAACAAACAAAAACAAAA-3' (SEQ ID NO: 1082)
3'-GUUUUUUGUUUUGUUUGUUUUUGUUUU-5' (SEQ ID NO: 974)

AR-731 Target: 5'-CAAAAAACAAAACAAACAAAAACAAAA-3' (SEQ ID NO: 1028)

5'-AUAAAAGAAAAAGAUAAUAACUCAG-3' (SEQ ID NO: 1083)
3'-UUUAUUUUCUUUUUCUAUUAUUGAGUC-5' (SEQ ID NO: 975)

AR-764 Target: 5'-AAATAAAAGAAAAAGATAATAACTCAG-3' (SEQ ID NO: 1029)

5'-AAAAAGAUAAUAACUCAGUUCUUAU-3' (SEQ ID NO: 1084)
3'-UCUUUUUCUAUUAUUGAGUCAAGAAUA-5' (SEQ ID NO: 976)

AR-771 Target: 5'-AGAAAAAGATAATAACTCAGTTCTTAT-3' (SEQ ID NO: 1030)

5'-AAUAACUCAGUUCUUAUUUGCACCU-3' (SEQ ID NO: 1085)
3'-UAUUAUUGAGUCAAGAAUAAACGUGGA-5' (SEQ ID NO: 977)

AR-779 Target: 5'-ATAATAACTCAGTTCTTATTTGCACCT-3' (SEQ ID NO: 1031)

5'-GUGGAGGAUUUUGUUUUUUUCUUUU-3' (SEQ ID NO: 1086)
3'-UCCACCUCCUAAAACAAAAAAAGAAAA-5' (SEQ ID NO: 978)

AR-830 Target: 5'-AGGTGGAGGATTTTGTTTTTTTCTTTT-3' (SEQ ID NO: 1032)

5'-UUGUUUUUUUCUUUUAAGAUCUGGG-3' (SEQ ID NO: 1087)
3'-AAAACAAAAAAAGAAAAUUCUAGACCC-5' (SEQ ID NO: 979)

AR-840 Target: 5'-TTTTGTTTTTTTCTTTTAAGATCTGGG-3' (SEQ ID NO: 1033)

5'-UUUUUCUUUUAAGAUCUGGGCAUCU-3' (SEQ ID NO: 1088)
3'-AAAAAAAGAAAAUUCUAGACCCGUAGA-5' (SEQ ID NO: 980)

AR-845 Target: 5'-TTTTTTTCTTTTAAGATCTGGGCATCT-3' (SEQ ID NO: 1034)

5'-CUGGGCAUCUUUUGAAUCUACCCUU-3' (SEQ ID NO: 1089)
3'-UAGACCCGUAGAAAACUUAGAUGGGAA-5' (SEQ ID NO: 981)

AR-860 Target: 5'-ATCTGGGCATCTTTTGAATCTACCCTT-3' (SEQ ID NO: 1035)

5'-AGGGAAGUAGGUGGAAGAUUCAGCC-3' (SEQ ID NO: 1090)
3'-AUUCCCUUCAUCCACCUUCUAAGUCGG-5' (SEQ ID NO: 982)

AR-1105 Target: 5'-TAAGGGAAGTAGGTGGAAGATTCAGCC-3' (SEQ ID NO: 1036)

5'-GGAGCUUUCCAGAAUCUGUUCCAGA-3' (SEQ ID NO: 1091)
3'-CUCCUCGAAAGGUCUUAGACAAGGUCU-5' (SEQ ID NO: 983)

AR-1200 Target: 5'-GAGGAGCTTTCCAGAATCTGTTCCAGA-3' (SEQ ID NO: 1037)

5'-CAGGAAGCAGUAUCCGAAGGCAGCA-3' (SEQ ID NO: 1092)
3'-UCGUCCUUCGUCAUAGGCUUCCGUCGU-5' (SEQ ID NO: 984)

AR-1734 Target: 5'-AGCAGGAAGCAGTATCCGAAGGCAGCA-3' (SEQ ID NO: 1038)

5'-AAGGACAAUUACUUAGGGGGCACUU-3' (SEQ ID NO: 1093)
3'-GGUUCCUGUUAAUGAAUCCCCCGUGAA-5' (SEQ ID NO: 985)

AR-1803 Target: 5'-CCAAGGACAATTACTTAGGGGGCACTT-3' (SEQ ID NO: 1039)

5'-GGAGUUGUGUAAGGCAGUGUCGGUG-3' (SEQ ID NO: 1094)
3'-UUCCUCAACACAUUCCGUCACAGCCAC-5' (SEQ ID NO: 986)

AR-1850 Target: 5'-AAGGAGTTGTGTAAGGCAGTGTCGGTG-3' (SEQ ID NO: 1040)

5'-CAAGAGCACUGAAGAUACUGCUGAG-3' (SEQ ID NO: 1095)
3'-CCGUUCUCGUGACUUCUAUGACGACUC-5' (SEQ ID NO: 987)

AR-2039 Target: 5'-GGCAAGAGCACTGAAGATACTGCTGAG-3' (SEQ ID NO: 1041)

5'-UGAAGAUACUGCUGAGUAUUCCCCU-3' (SEQ ID NO: 1096)
3'-UGACUUCUAUGACGACUCAUAAGGGGA-5' (SEQ ID NO: 988)

AR-2048 Target: 5'-ACTGAAGATACTGCTGAGTATTCCCCT-3' (SEQ ID NO: 1042)

5'-AGGGAGGUUACACCAAAGGGCUAGA-3' (SEQ ID NO: 1097)
3'-GUUCCCUCCAAUGUGGUUUCCCGAUCU-5' (SEQ ID NO: 989)

AR-2077 Target: 5'-CAAGGGAGGTTACACCAAAGGGCTAGA-3' (SEQ ID NO: 1043)

5'-UGUGUCAAAAGCGAAAUGGGCCCCU-3' (SEQ ID NO: 1098)
3'-GAACACAGUUUUCGCUUUACCCGGGGA-5' (SEQ ID NO: 990)

AR-2694 Target: 5'-CTTGTGTCAAAAGCGAAATGGGCCCCT-3' (SEQ ID NO: 1044)

5'-GUUUUGCCCAUUGACUAUUACUUUC-3' (SEQ ID NO: 1099)
3'-UACAAAACGGGUAACUGAUAAUGAAAG-5' (SEQ ID NO: 991)

AR-2778 Target: 5'-ATGTTTTGCCCATTGACTATTACTTTC-3' (SEQ ID NO: 1045)

5'-CAAGGUCUUCUUCAAAAGAGCCGCU-3' (SEQ ID NO: 1100)
3'-ACGUUCCAGAAGAAGUUUUCUCGGCGA-5' (SEQ ID NO: 992)

AR-2879 Target: 5'-TGCAAGGTCTTCTTCAAAAGAGCCGCT-3' (SEQ ID NO: 1046)

5'-GGGAAACAGAAGUACCUGUGCGCCA-3' (SEQ ID NO: 1101)
3'-UUCCCUUUGUCUUCAUGGACACGCGGU-5' (SEQ ID NO: 993)

AR-2907 Target: 5'-AAGGGAAACAGAAGTACCTGTGCGCCA-3' (SEQ ID NO: 1047)

5'-GAUUGCACUAUUGAUAAAUUCCGAA-3' (SEQ ID NO: 1102)
3'-UACUAACGUGAUAACUAUUUAAGGCUU-5' (SEQ ID NO: 994)

AR-2940 Target: 5'-ATGATTGCACTATTGATAAATTCCGAA-3' (SEQ ID NO: 1048)

5'-AAUUCCGAAGGAAAAAUUGUCCAUC-3' (SEQ ID NO: 1103)
3'-AUUUAAGGCUUCCUUUUUAACAGGUAG-5' (SEQ ID NO: 995)

AR-2956 Target: 5'-TAAATTCCGAAGGAAAAATTGTCCATC-3' (SEQ ID NO: 1049)

5'-GGAAAAAUUGUCCAUCUUGUCGUCU-3' (SEQ ID NO: 1104)
3'-UUCCUUUUUAACAGGUAGAACAGCAGA-5' (SEQ ID NO: 996)

AR-2965 Target: 5'-AAGGAAAAATTGTCCATCTTGTCGTCT-3' (SEQ ID NO: 1050)

5'-AAAAUUGUCCAUCUUGUCGUCUUCG-3' (SEQ ID NO: 1105)
3'-CUUUUUAACAGGUAGAACAGCAGAAGC-5' (SEQ ID NO: 997)

AR-2968 Target: 5'-GAAAAATTGTCCATCTTGTCGTCTTCG-3' (SEQ ID NO: 1051)

5'-AGAAACUUGGUAAUCUGAAACUACA-3' (SEQ ID NO: 1106)
3'-CUUCUUUGAACCAUUAGACUUUGAUGU-5' (SEQ ID NO: 998)

AR-3037 Target: 5'-GAAGAAACTTGGTAATCTGAAACTACA-3' (SEQ ID NO: 1052)

5'-UUGAAGGCUAUGAAUGUCAGCCCAU-3' (SEQ ID NO: 1107)
3'-GUAACUUCCGAUACUUACAGUCGGGUA-5' (SEQ ID NO: 999)

AR-3133 Target: 5'-CATTGAAGGCTATGAATGTCAGCCCAT-3' (SEQ ID NO: 1053)

5'-GGAAUUCCUGUGCAUGAAAGCACUG-3' (SEQ ID NO: 1108)
3'-GUCCUUAAGGACACGUACUUUCGUGAC-5' (SEQ ID NO: 1000)

AR-3548 Target: 5'-CAGGAATTCCTGTGCATGAAAGCACTG-3' (SEQ ID NO: 1054)

5'-AAAAAUUCUUUGAUGAACUUCGAAU-3' (SEQ ID NO: 1109)
3'-AGUUUUUAAGAAACUACUUGAAGCUUA-5' (SEQ ID NO: 1001)

AR-3613 Target: 5'-TCAAAAATTCTTTGATGAACTTCGAAT-3' (SEQ ID NO: 1055)

5'-UUUGAUGAACUUCGAAUGAACUACA-3' (SEQ ID NO: 1110)
3'-AGAAACUACUUGAAGCUUACUUGAUGU-5' (SEQ ID NO: 1002)

AR-3621 Target: 5'-TCTTTGATGAACTTCGAATGAACTACA-3' (SEQ ID NO: 1056)

5'-GAUGAACUUCGAAUGAACUACAUCA-3' (SEQ ID NO: 1111)
3'-AACUACUUGAAGCUUACUUGAUGUAGU-5' (SEQ ID NO: 1003)

AR-3624 Target: 5'-TTGATGAACTTCGAATGAACTACATCA-3' (SEQ ID NO: 1057)

5'-GAAUGAACUACAUCAAGGAACUCGA-3' (SEQ ID NO: 1112)
3'-AGCUUACUUGAUGUAGUUCCUUGAGCU-5' (SEQ ID NO: 1004)

AR-3634 Target: 5'-TCGAATGAACTACATCAAGGAACTCGA-3' (SEQ ID NO: 1058)

5'-CAAAAGAAAAAAUCCCACAUCCUGC-3' (SEQ ID NO: 1113)
3'-ACGUUUUCUUUUUUAGGGUGUAGGACG-5' (SEQ ID NO: 1005)

AR-3674 Target: 5'-TGCAAAAGAAAAAATCCCACATCCTGC-3' (SEQ ID NO: 1059)

5'-AGAAAAAAUCCCACAUCCUGCUCAA-3' (SEQ ID NO: 1114)
3'-UUUCUUUUUUAGGGUGUAGGACGAGUU-5' (SEQ ID NO: 1006)

AR-3678 Target: 5'-AAAGAAAAAATCCCACATCCTGCTCAA-3' (SEQ ID NO: 1060)

5'-UUUUGACCUGCUAAUCAAGUCACAC-3' (SEQ ID NO: 1115)
3'-UGAAAACUGGACGAUUAGUUCAGUGUG-5' (SEQ ID NO: 1007)

AR-3773 Target: 5'-ACTTTTGACCTGCTAATCAAGTCACAC-3' (SEQ ID NO: 1061)

5'-AAGAUCCUUUCUGGGAAAGUCAAGC-3' (SEQ ID NO: 1116)
3'-GGUUCUAGGAAAGACCCUUUCAGUUCG-5' (SEQ ID NO: 1008)

AR-3855 Target: 5'-CCAAGATCCTTTCTGGGAAAGTCAAGC-3' (SEQ ID NO: 1062)

5'-AAAGUCAAGCCCAUCUAUUUCCACA-3' (SEQ ID NO: 1117)
3'-CCUUUCAGUUCGGGUAGAUAAAGGUGU-5' (SEQ ID NO: 1009)

AR-3870 Target: 5'-GGAAAGTCAAGCCCATCTATTTCCACA-3' (SEQ ID NO: 1063)

5'-AUGUCUUCUGCCUGUUAUAACUCUG-3' (SEQ ID NO: 1118)
3'-UCUACAGAAGACGGACAAUAUUGAGAC-5' (SEQ ID NO: 1010)

AR-3950 Target: 5'-AGATGTCTTCTGCCTGTTATAACTCTG-3' (SEQ ID NO: 1064)

5'-GAAUUUCCUCUAUUGAUGUACAGUC-3' (SEQ ID NO: 1119)
3'-CCCUUAAAGGAGAUAACUACAUGUCAG-5' (SEQ ID NO: 1011)

AR-4000 Target: 5'-GGGAATTTCCTCTATTGATGTACAGTC-3' (SEQ ID NO: 1065)

5'-GAUGUACAGUCUGUCAUGAACAUGU-3' (SEQ ID NO: 1120)
3'-AACUACAUGUCAGACAGUACUUGUACA-5' (SEQ ID NO: 1012)

AR-4014 Target: 5'-TTGATGTACAGTCTGTCATGAACATGT-3' (SEQ ID NO: 1066)

5'-CAGUCUGUCAUGAACAUGUUCCUGA-3' (SEQ ID NO: 1121)
3'-AUGUCAGACAGUACUUGUACAAGGACU-5' (SEQ ID NO: 1013)

AR-4020 Target: 5'-TACAGTCTGTCATGAACATGTTCCTGA-3' (SEQ ID NO: 1067)

5'-CAUGAACAUGUUCCUGAAUUCUAUU-3' (SEQ ID NO: 1122)
3'-CAGUACUUGUACAAGGACUUAAGAUAA-5' (SEQ ID NO: 1014)

AR-4028 Target: 5'-GTCATGAACATGTTCCTGAATTCTATT-3' (SEQ ID NO: 1068)

5'-AUGUUCCUGAAUUCUAUUUGCUGGG-3' (SEQ ID NO: 1123)
3'-UGUACAAGGACUUAAGAUAAACGACCC-5' (SEQ ID NO: 1015)

AR-4035 Target: 5'-ACATGTTCCTGAATTCTATTTGCTGGG-3' (SEQ ID NO: 1069)

5'-UGGGCUUUUUUUUUCUCUUUCUCUC-3' (SEQ ID NO: 1124)
3'-CGACCCGAAAAAAAAAGAGAAAGAGAG-5' (SEQ ID NO: 1016)

AR-4056 Target: 5'-GCTGGGCTTTTTTTTCTCTTTCTCTC-3' (SEQ ID NO: 1070)

5'-UUUUUCUCUUUCUCUCCUUUCUUUU-3' (SEQ ID NO: 1125)
3'-AAAAAAAGAGAAAGAGAGGAAAGAAAA-5' (SEQ ID NO: 1017)

AR-4065 Target: 5'-TTTTTTCTCTTTCTCTCCTTTCTTTT-3' (SEQ ID NO: 1071)

5'-GUUUUGAAUGGUGUUGUAUGCCUUU-3' (SEQ ID NO: 1126)
3'-CACAAAACUUACCACAACAUACGGAAA-5' (SEQ ID NO: 1018)

AR-4161 Target: 5'-GTGTTTTGAATGGTGTTGTATGCCTTT-3' (SEQ ID NO: 1072)

5'-GGUGUUGUAUGCCUUUAAAUCUGUG-3' (SEQ ID NO: 1127)
3'-UACCACAACAUACGGAAAUUUAGACAC-5' (SEQ ID NO: 1019)

AR-4170 Target: 5'-ATGGTGTTGTATGCCTTTAAATCTGTG-3' (SEQ ID NO: 1073)

5'-CAAGUUGUGCUUGUUUACAGCACUA-3' (SEQ ID NO: 1128)
3'-CAGUUCAACACGAACAAAUGUCGUGAU-5' (SEQ ID NO: 1020)

AR-4218 Target: 5'-GTCAAGTTGTGCTTGTTTACAGCACTA-3' (SEQ ID NO: 1074)

5'-CUAAGAUUAUCUGGGGAAAUCAAAA-3' (SEQ ID NO: 1129)
3'-UCGAUUCUAAUAGACCCCUUUAGUUUU-5' (SEQ ID NO: 1021)

AR-4299 Target: 5'-AGCTAAGATTATCTGGGGAAATCAAAA-3' (SEQ ID NO: 1075)

5'-UGGGGAAAUCAAAACAAAAACAAGC-3' (SEQ ID NO: 1130)
3'-AGACCCCUUUAGUUUUGUUUUUGUUCG-5' (SEQ ID NO: 1022)

AR-4310 Target: 5'-TCTGGGGAAATCAAAACAAAAACAAGC-3' (SEQ ID NO: 1076)

5'-GAAAUCAAAACAAAAACAAGCAAAC-3' (SEQ ID NO: 1131)
3'-CCCUUUAGUUUUGUUUUUGUUCGUUUG-5' (SEQ ID NO: 1023)

AR-4314 Target: 5'-GGGAAATCAAAACAAAAACAAGCAAAC-3' (SEQ ID NO: 1077)

5'-GUGAAGUUUUUAAAAGCUGCUAAAG-3' (SEQ ID NO: 1375)
3'-GCCACUUCAAAAAUUUUCGACGAUUUC-5' (SEQ ID NO: 1249)

AR-249 Target: 5'-CGGTGAAGTTTTTAAAAGCTGCTAAAG-3' (SEQ ID NO: 1312)

5'-UUUUAAAAGCUGCUAAAGACUCGGA-3' (SEQ ID NO: 1376)
3'-CAAAAAUUUUCGACGAUUUCUGAGCCU-5' (SEQ ID NO: 1250)

AR-256 Target: 5'-GTTTTTAAAAGCTGCTAAAGACTCGGA-3' (SEQ ID NO: 1313)

5'-UUAAAAGCUGCUAAAGACUCGGAGG-3' (SEQ ID NO: 1377)
3'-AAAAUUUUCGACGAUUUCUGAGCCUCC-5' (SEQ ID NO: 1251)

AR-258 Target: 5'-TTTTAAAAGCTGCTAAAGACTCGGAGG-3' (SEQ ID NO: 1314)

5'-GGAGAGAACCCUCUGUUUUCCCCCA-3' (SEQ ID NO: 1378)
3'-CGCCUCUCUUGGGAGACAAAAGGGGGU-5' (SEQ ID NO: 1252)

AR-618 Target: 5'-GCGGAGAGAACCCTCTGTTTTCCCCCA-3' (SEQ ID NO: 1315)

5'-AGAUCAAAAGAUGAAAAGGCAGUCA-3' (SEQ ID NO: 1379)
3'-UCUCUAGUUUUCUACUUUUCCGUCAGU-5' (SEQ ID NO: 1253)

AR-691 Target: 5'-AGAGATCAAAAGATGAAAAGGCAGTCA-3' (SEQ ID NO: 1316)

5'-CAAAAGAUGAAAAGGCAGUCAGGUC-3' (SEQ ID NO: 1380)
3'-UAGUUUUCUACUUUUCCGUCAGUCCAG-5' (SEQ ID NO: 1254)

AR-695 Target: 5'-ATCAAAAGATGAAAAGGCAGTCAGGTC-3' (SEQ ID NO: 1317)

5'-CAGUAGCCAAAAAACAAAACAAACA-3' (SEQ ID NO: 1381)
3'-AAGUCAUCGGUUUUUUGUUUUGUUUGU-5' (SEQ ID NO: 1255)

AR-722 Target: 5'-TTCAGTAGCCAAAAAACAAAACAAACA-3' (SEQ ID NO: 1318)

5'-AAAACAAAACAAACAAAAACAAAAA-3' (SEQ ID NO: 1382)
3'-UUUUUUGUUUUGUUUGUUUUUGUUUUU-5' (SEQ ID NO: 1256)

AR-732 Target: 5'-AAAAAACAAAACAAACAAAAACAAAAA-3' (SEQ ID NO: 1319)

5'-UAAAAGAAAAAGAUAAUAACUCAGU-3' (SEQ ID NO: 1383)
3'-UUAUUUUCUUUUUCUAUUAUUGAGUCA-5' (SEQ ID NO: 1257)

AR-765 Target: 5'-AATAAAAGAAAAAGATAATAACTCAGT-3' (SEQ ID NO: 1320)

5'-AAAGAAAAAGAUAAUAACUCAGUUC-3' (SEQ ID NO: 1384)
3'-AUUUUCUUUUUCUAUUAUUGAGUCAAG-5' (SEQ ID NO: 1258)

AR-767 Target: 5'-TAAAAGAAAAAGATAATAACTCAGTTC-3' (SEQ ID NO: 1321)

5'-AAAAGAUAAUAACUCAGUUCUUAUU-3' (SEQ ID NO: 1385)
3'-CUUUUUCUAUUAUUGAGUCAAGAAUAA-5' (SEQ ID NO: 1259)

AR-772 Target: 5'-GAAAAAGATAATAACTCAGTTCTTATT-3' (SEQ ID NO: 1322)

5'-AUAACUCAGUUCUUAUUUGCACCUA-3' (SEQ ID NO: 1386)
3'-AUUAUUGAGUCAAGAAUAAACGUGGAU-5' (SEQ ID NO: 1260)

AR-780 Target: 5'-TAATAACTCAGTTCTTATTTGCACCTA-3' (SEQ ID NO: 1323)

5'-CAGUUCUUAUUUGCACCUACUUCAG-3' (SEQ ID NO: 1387)
3'-GAGUCAAGAAUAAACGUGGAUGAAGUC-5' (SEQ ID NO: 1261)

AR-786 Target: 5'-CTCAGTTCTTATTTGCACCTACTTCAG-3' (SEQ ID NO: 1324)

5'-UGGAGGAUUUUGUUUUUUUCUUUUA-3' (SEQ ID NO: 1388)
3'-CCACCUCCUAAAACAAAAAAAGAAAAU-5' (SEQ ID NO: 1262)

AR-831 Target: 5'-GGTGGAGGATTTTGTTTTTTTCTTTTA-3' (SEQ ID NO: 1325)

5'-UGUUUUUUUCUUUUAAGAUCUGGGC-3' (SEQ ID NO: 1389)
3'-AAACAAAAAAAGAAAAUUCUAGACCCG-5' (SEQ ID NO: 1263)

AR-841 Target: 5'-TTTGTTTTTTCTTTTAAGATCTGGGC-3' (SEQ ID NO: 1326)

5'-UUUUCUUUUAAGAUCUGGGCAUCUU-3' (SEQ ID NO: 1390)
3'-AAAAAAGAAAAUUCUAGACCCGUAGAA-5' (SEQ ID NO: 1264)

AR-846 Target: 5'-TTTTTTCTTTTAAGATCTGGGCATCTT-3' (SEQ ID NO: 1327)

5'-UGGGCAUCUUUUGAAUCUACCCUUC-3' (SEQ ID NO: 1391)
3'-AGACCCGUAGAAAACUUAGAUGGGAAG-5' (SEQ ID NO: 1265)

AR-861 Target: 5'-TCTGGGCATCTTTTGAATCTACCCTTC-3' (SEQ ID NO: 1328)

5'-CAAGUUUCCUUCUCUGGAGCUUCCC-3' (SEQ ID NO: 1392)
3'-GCGUUCAAAGGAAGAGACCUCGAAGGG-5' (SEQ ID NO: 1266)

AR-997 Target: 5'-CGCAAGTTTCCTTCTCTGGAGCTTCCC-3' (SEQ ID NO: 1329)

5'-GGGAAGUAGGUGGAAGAUUCAGCCA-3' (SEQ ID NO: 1393)
3'-UUCCCUUCAUCCACCUUCUAAGUCGGU-5' (SEQ ID NO: 1267)

AR-1106 Target: 5'-AAGGGAAGTAGGTGGAAGATTCAGCCA-3' (SEQ ID NO: 1330)

5'-AAGUAGGUGGAAGAUUCAGCCAAGC-3' (SEQ ID NO: 1394)
3'-CCUUCAUCCACCUUCUAAGUCGGUUCG-5' (SEQ ID NO: 1268)

AR-1109 Target: 5'-GGAAGTAGGTGGAAGATTCAGCCAAGC-3' (SEQ ID NO: 1331)

5'-AGGACAAUUACUUAGGGGGCACUUC-3' (SEQ ID NO: 1395)
3'-GUUCCUGUUAAUGAAUCCCCCGUGAAG-5' (SEQ ID NO: 1269)

AR-1804 Target: 5'-CAAGGACAATTACTTAGGGGGCACTTC-3' (SEQ ID NO: 1332)

5'-CGAAUGCAAAGGUUCUCUGCUAGAC-3' (SEQ ID NO: 1396)
3'-CGGCUUACGUUUCCAAGAGACGAUCUG-5' (SEQ ID NO: 1270)

AR-2003 Target: 5'-GCCGAATGCAAAGGTTCTCTGCTAGAC-3' (SEQ ID NO: 1333)

5'-AAGAGCACUGAAGAUACUGCUGAGU-3' (SEQ ID NO: 1397)
3'-CGUUCUCGUGACUUCUAUGACGACUCA-5' (SEQ ID NO: 1271)

AR-2040 Target: 5'-GCAAGAGCACTGAAGATACTGCTGAGT-3' (SEQ ID NO: 1334)

5'-GAAGAUACUGCUGAGUAUUCCCCUU-3' (SEQ ID NO: 1398)
3'-GACUUCUAUGACGACUCAUAAGGGGAA-5' (SEQ ID NO: 1272)

AR-2049 Target: 5'-CTGAAGATACTGCTGAGTATTCCCCTT-3' (SEQ ID NO: 1335)

5'-GUGUCAAAAGCGAAAUGGGCCCCUG-3' (SEQ ID NO: 1399)
3'-AACACAGUUUUCGCUUUACCCGGGGAC-5' (SEQ ID NO: 1273)

AR-2695 Target: 5'-TTGTGTCAAAAGCGAAATGGGCCCCTG-3' (SEQ ID NO: 1336)

5'-UUUUGCCCAUUGACUAUUACUUUCC-3' (SEQ ID NO: 1400)
3'-ACAAAACGGGUAACUGAUAAUGAAAGG-5' (SEQ ID NO: 1274)

AR-2779 Target: 5'-TGTTTTGCCCATTGACTATTACTTTCC-3' (SEQ ID NO: 1337)

5'-CAUUGACUAUUACUUUCCACCCCAG-3' (SEQ ID NO: 1401)
3'-GGGUAACUGAUAAUGAAAGGUGGGGUC-5' (SEQ ID NO: 1275)

AR-2786 Target: 5'-CCCATTGACTATTACTTTCCACCCCAG-3' (SEQ ID NO: 1338)

5'-AAGGUCUUCUUCAAAAGAGCCGCUG-3' (SEQ ID NO: 1402)
3'-CGUUCCAGAAGAAGUUUUCUCGGCGAC-5' (SEQ ID NO: 1276)

AR-2880 Target: 5'-GCAAGGTCTTCTTCAAAAGAGCCGCTG-3' (SEQ ID NO: 1339)

5'-AUUGCACUAUUGAUAAAUUCCGAAG-3' (SEQ ID NO: 1403)
3'-ACUAACGUGAUAACUAUUUAAGGCUUC-5' (SEQ ID NO: 1277)

AR-2941 Target: 5'-TGATTGCACTATTGATAAATTCCGAAG-3' (SEQ ID NO: 1340)

5'-CGAAGGAAAAAUUGUCCAUCUUGUC-3' (SEQ ID NO: 1404)
3'-AGGCUUCCUUUUUAACAGGUAGAACAG-5' (SEQ ID NO: 1278)

AR-2961 Target: 5'-TCCGAAGGAAAAATTGTCCATCTTGTC-3' (SEQ ID NO: 1341)

5'-GAAAAAUUGUCCAUCUUGUCGUCUU-3' (SEQ ID NO: 1405)
3'-UCCUUUUUAACAGGUAGAACAGCAGAA-5' (SEQ ID NO: 1279)

AR-2966 Target: 5'-AGGAAAAATTGTCCATCTTGTCGTCTT-3' (SEQ ID NO: 1342)

5'-CAGUGUCACACAUUGAAGGCUAUGA-3' (SEQ ID NO: 1406)
3'-CUGUCACAGUGUGUAACUUCCGAUACU-5' (SEQ ID NO: 1280)

AR-3121 Target: 5'-GACAGTGTCACACATTGAAGGCTATGA-3' (SEQ ID NO: 1343)

5'-UGAAGGCUAUGAAUGUCAGCCCAUC-3' (SEQ ID NO: 1407)
3'-UAACUUCCGAUACUUACAGUCGGGUAG-5' (SEQ ID NO: 1281)

AR-3134 Target: 5'-ATTGAAGGCTATGAATGTCAGCCCATC-3' (SEQ ID NO: 1344)

5'-AUGGCUGUCAUUCAGUACUCCUGGA-3' (SEQ ID NO: 1408)
3'-UCUACCGACAGUAAGUCAUGAGGACCU-5' (SEQ ID NO: 1282)

AR-3342 Target: 5'-AGATGGCTGTCATTCAGTACTCCTGGA-3' (SEQ ID NO: 1345)

5'-UGGUUUUCAAUGAGUACCGCAUGCA-3' (SEQ ID NO: 1409)
3'-AGACCAAAAGUUACUCAUGGCGUACGU-5' (SEQ ID NO: 1283)

AR-3445 Target: 5'-TCTGGTTTTCAATGAGTACCGCATGCA-3' (SEQ ID NO: 1346)

5'-GAAUUCCUGUGCAUGAAAGCACUGC-3' (SEQ ID NO: 1410)
3'-UCCUUAAGGACACGUACUUUCGUGACG-5' (SEQ ID NO: 1284)

AR-3549 Target: 5'-AGGAATTCCTGTGCATGAAAGCACTGC-3' (SEQ ID NO: 1347)

5'-AAAAUUCUUUGAUGAACUUCGAAUG-3' (SEQ ID NO: 1411)
3'-GUUUUUAAGAAACUACUUGAAGCUUAC-5' (SEQ ID NO: 1285)

AR-3614 Target: 5'-CAAAAATTCTTTGATGAACTTCGAATG-3' (SEQ ID NO: 1348)

5'-UUGAUGAACUUCGAAUGAACUACAU-3' (SEQ ID NO: 1412)
3'-GAAACUACUUGAAGCUUACUUGAUGUA-5' (SEQ ID NO: 1286)

AR-3622 Target: 5'-CTTTGATGAACTTCGAATGAACTACAT-3' (SEQ ID NO: 1349)

5'-AUGAACUUCGAAUGAACUACAUCAA-3' (SEQ ID NO: 1413)
3'-ACUACUUGAAGCUUACUUGAUGUAGUU-5' (SEQ ID NO: 1287)

AR-3625 Target: 5'-TGATGAACTTCGAATGAACTACATCAA-3' (SEQ ID NO: 1350)

5'-AAUGAACUACAUCAAGGAACUCGAU-3' (SEQ ID NO: 1414)
3'-GCUUACUUGAUGUAGUUCCUUGAGCUA-5' (SEQ ID NO: 1288)

AR-3635 Target: 5'-CGAATGAACTACATCAAGGAACTCGAT-3' (SEQ ID NO: 1351)

5'-UGAACUACAUCAAGGAACUCGAUCG-3' (SEQ ID NO: 1415)
3'-UUACUUGAUGUAGUUCCUUGAGCUAGC-5' (SEQ ID NO: 1289)

AR-3637 Target: 5'-AATGAACTACATCAAGGAACTCGATCG-3' (SEQ ID NO: 1352)

5'-AAAAGAAAAAAUCCCACAUCCUGCU-3' (SEQ ID NO: 1416)
3'-CGUUUUCUUUUUUAGGGUGUAGGACGA-5' (SEQ ID NO: 1290)

AR-3675 Target: 5'-GCAAAAGAAAAAATCCCACATCCTGCT-3' (SEQ ID NO: 1353)

5'-GAAAAAAUCCCACAUCCUGCUCAAG-3' (SEQ ID NO: 1417)
3'-UUCUUUUUUAGGGUGUAGGACGAGUUC-5' (SEQ ID NO: 1291)

AR-3679 Target: 5'-AAGAAAAAATCCCACATCCTGCTCAAG-3' (SEQ ID NO: 1354)

5'-UUUGACCUGCUAAUCAAGUCACACA-3' (SEQ ID NO: 1418)
3'-GAAAACUGGACGAUUAGUUCAGUGUGU-5' (SEQ ID NO: 1292)

AR-3774 Target: 5'-CTTTTGACCTGCTAATCAAGTCACACA-3' (SEQ ID NO: 1355)

5'-CUGUUAUAACUCUGCACUACUCCUC-3' (SEQ ID NO: 1419)
3'-CGGACAAUAUUGAGACGUGAUGAGGAG-5' (SEQ ID NO: 1293)

AR-3961 Target: 5'-GCCTGTTATAACTCTGCACTACTCCTC-3' (SEQ ID NO: 1356)

5'-GUUAUAACUCUGCACUACUCCUCUG-3' (SEQ ID NO: 1420)
3'-GACAAUAUUGAGACGUGAUGAGGAGAC-5' (SEQ ID NO: 1294)

AR-3963 Target: 5'-CTGTTATAACTCTGCACTACTCCTCTG-3' (SEQ ID NO: 1357)

5'-AAUUUCCUCUAUUGAUGUACAGUCU-3' (SEQ ID NO: 1421)
3'-CCUUAAAGGAGAUAACUACAUGUCAGA-5' (SEQ ID NO: 1295)

AR-4001 Target: 5'-GGAATTTCCTCTATTGATGTACAGTCT-3' (SEQ ID NO: 1358)

5'-CUAUUGAUGUACAGUCUGUCAUGAA-3' (SEQ ID NO: 1422)
3'-GAGAUAACUACAUGUCAGACAGUACUU-5' (SEQ ID NO: 1296)

AR-4009 Target: 5'-CTCTATTGATGTACAGTCTGTCATGAA-3' (SEQ ID NO: 1359)

5'-AUGAACAUGUUCCUGAAUUCUAUUU-3' (SEQ ID NO: 1423)
3'-AGUACUUGUACAAGGACUUAAGAUAAA-5' (SEQ ID NO: 1297)

AR-4029 Target: 5'-TCATGAACATGTTCCTGAATTCTATTT-3' (SEQ ID NO: 1360)

5'-CUGAAUUCUAUUUGCUGGGCUUUUU-3' (SEQ ID NO: 1424)
3'-AGGACUUAAGAUAAACGACCCGAAAAA-5' (SEQ ID NO: 1298)

AR-4041 Target: 5'-TCCTGAATTCTATTTGCTGGGCTTTTT-3' (SEQ ID NO: 1361)

5'-UUUUUUUUUCUCUUUCUCUCCUUUC-3' (SEQ ID NO: 1425)
3'-CGAAAAAAAAAGAGAAAGAGAGGAAAG-5' (SEQ ID NO: 1299)

AR-4061 Target: 5'-GCTTTTTTTTCTCTTTCTCTCCTTTC-3' (SEQ ID NO: 1362)

5'-UUUUCUCUUUCUCUCCUUUCUUUUU-3' (SEQ ID NO: 1426)
3'-AAAAAAGAGAAAGAGAGGAAAGAAAAA-5' (SEQ ID NO: 1300)

AR-4066 Target: 5'-TTTTTCTCTTTCTCTCCTTTCTTTTT-3' (SEQ ID NO: 1363)

5'-CUUUCUCUCCUUUCUUUUUCUUCUU-3' (SEQ ID NO: 1427)
3'-GAGAAAGAGAGGAAAGAAAAAGAAGAA-5' (SEQ ID NO: 1301)

AR-4072 Target: 5'-CTCTTTCTCTCCTTTCTTTTTCTTCTT-3' (SEQ ID NO: 1364)

5'-AUGGCACCUUCAGACUUUGCUUCCC-3' (SEQ ID NO: 1428)
3'-GGUACCGUGGAAGUCUGAAACGAAGGG-5' (SEQ ID NO: 1302)

AR-4118 Target: 5'-CCATGGCACCTTCAGACTTTGCTTCCC-3' (SEQ ID NO: 1365)

5'-UUUUGAAUGGUGUUGUAUGCCUUUA-3' (SEQ ID NO: 1429)
3'-ACAAAACUUACCACAACAUACGGAAAU-5' (SEQ ID NO: 1303)

AR-4162 Target: 5'-TGTTTTGAATGGTGTTGTATGCCTTTA-3' (SEQ ID NO: 1366)

5'-GUGUUGUAUGCCUUUAAAUCUGUGA-3' (SEQ ID NO: 1430)
3'-ACCACAACAUACGGAAAUUUAGACACU-5' (SEQ ID NO: 1304)

AR-4171 Target: 5'-TGGTGTTGTATGCCTTTAAATCTGTGA-3' (SEQ ID NO: 1367)

5'-UUAAAUCUGUGAUGAUCCUCAUAUG-3' (SEQ ID NO: 1431)
3'-GAAAUUUAGACACUACUAGGAGUAUAC-5' (SEQ ID NO: 1305)

AR-4184 Target: 5'-CTTTAAATCTGTGATGATCCTCATATG-3' (SEQ ID NO: 1368)

5'-UGUGAUGAUCCUCAUAUGGCCCAGU-3' (SEQ ID NO: 1432)
3'-AGACACUACUAGGAGUAUACCGGGUCA-5' (SEQ ID NO: 1306)

AR-4191 Target: 5'-TCTGTGATGATCCTCATATGGCCCAGT-3' (SEQ ID NO: 1369)

5'-GUUGUGCUUGUUUACAGCACUACUC-3' (SEQ ID NO: 1433)
3'-UUCAACACGAACAAAUGUCGUGAUGAG-5' (SEQ ID NO: 1307)

AR-4221 Target: 5'-AAGTTGTGCTTGTTTACAGCACTACTC-3' (SEQ ID NO: 1370)

5'-GUUUACUUAUCUUAUGCCACGGGAA-3' (SEQ ID NO: 1434)
3'-UGCAAAUGAAUAGAAUACGGUGCCCUU-5' (SEQ ID NO: 1308)

AR-4264 Target: 5'-ACGTTTACTTATCTTATGCCACGGGAA-3' (SEQ ID NO: 1371)

5'-UUUAGAGAGCUAAGAUUAUCUGGGG-3' (SEQ ID NO: 1435)
3'-UCAAAUCUCUCGAUUCUAAUAGACCCC-5' (SEQ ID NO: 1309)

AR-4290 Target: 5'-AGTTTAGAGAGCTAAGATTATCTGGGG-3' (SEQ ID NO: 1372)

5'-UAAGAUUAUCUGGGGAAAUCAAAAC-3' (SEQ ID NO: 1436)
3'-CGAUUCUAAUAGACCCCUUUAGUUUUG-5' (SEQ ID NO: 1310)

AR-4300 Target: 5'-GCTAAGATTATCTGGGGAAATCAAAAC-3' (SEQ ID NO: 1373)

5'-GGGGAAAUCAAAACAAAAACAAGCA-3' (SEQ ID NO: 1437)
3'-GACCCCUUUAGUUUUGUUUUUGUUCGU-5' (SEQ ID NO: 1311)

AR-4311 Target: 5'-CTGGGGAAATCAAAACAAAAACAAGCA-3' (SEQ ID NO: 1374)

Projected 21 nucleotide target sequences for each DsiRNA of Tables 2-3 above and of Tables 5-12 below are presented in Table 4.

Table 4: DsiRNA Target Sequences (21mers)

AR-252	21 nt Target:	5'-TGAAGTTTTTAAAAGCTGCTA-3'	(SEQ ID NO: 613)
AR-253	21 nt Target:	5'-GAAGTTTTTAAAAGCTGCTAA-3'	(SEQ ID NO: 614)
AR-254	21 nt Target:	5'-AAGTTTTTAAAAGCTGCTAAA-3'	(SEQ ID NO: 615)
AR-682	21 nt Target:	5'-TGCGGAGCCAGAGATCAAAAG-3'	(SEQ ID NO: 616)
AR-688	21 nt Target:	5'-GCCAGAGATCAAAAGATGAAA-3'	(SEQ ID NO: 617)
AR-689	21 nt Target:	5'-CCAGAGATCAAAAGATGAAAA-3'	(SEQ ID NO: 618)
AR-697	21 nt Target:	5'-CAAAAGATGAAAAGGCAGTCA-3'	(SEQ ID NO: 619)
AR-698	21 nt Target:	5'-AAAAGATGAAAAGGCAGTCAG-3'	(SEQ ID NO: 620)
AR-714	21 nt Target:	5'-GTCAGGTCTTCAGTAGCCAAA-3'	(SEQ ID NO: 621)
AR-715	21 nt Target:	5'-TCAGGTCTTCAGTAGCCAAAA-3'	(SEQ ID NO: 622)
AR-724	21 nt Target:	5'-CAGTAGCCAAAAAACAAAACA-3'	(SEQ ID NO: 623)
AR-729	21 nt Target:	5'-GCCAAAAAACAAAACAAACAA-3'	(SEQ ID NO: 624)
AR-730	21 nt Target:	5'-CCAAAAAACAAAACAAACAAA-3'	(SEQ ID NO: 625)
AR-737	21 nt Target:	5'-ACAAAACAAACAAAAACAAAA-3'	(SEQ ID NO: 626)
AR-745	21 nt Target:	5'-AACAAAAACAAAAAAGCCGAA-3'	(SEQ ID NO: 627)
AR-746	21 nt Target:	5'-ACAAAAACAAAAAAGCCGAAA-3'	(SEQ ID NO: 628)
AR-747	21 nt Target:	5'-CAAAAACAAAAAAGCCGAAAT-3'	(SEQ ID NO: 629)
AR-752	21 nt Target:	5'-ACAAAAAAGCCGAAATAAAAG-3'	(SEQ ID NO: 630)
AR-753	21 nt Target:	5'-CAAAAAAGCCGAAATAAAAGA-3'	(SEQ ID NO: 631)
AR-755	21 nt Target:	5'-AAAAAGCCGAAATAAAAGAAA-3'	(SEQ ID NO: 632)
AR-760	21 nt Target:	5'-GCCGAAATAAAAGAAAAAGAT-3'	(SEQ ID NO: 633)
AR-761	21 nt Target:	5'-CCGAAATAAAAGAAAAAGATA-3'	(SEQ ID NO: 634)
AR-762	21 nt Target:	5'-CGAAATAAAAGAAAAAGATAA-3'	(SEQ ID NO: 635)
AR-770	21 nt Target:	5'-AAGAAAAAGATAATAACTCAG-3'	(SEQ ID NO: 636)
AR-774	21 nt Target:	5'-AAAAGATAATAACTCAGTTCT-3'	(SEQ ID NO: 637)
AR-775	21 nt Target:	5'-AAAGATAATAACTCAGTTCTT-3'	(SEQ ID NO: 638)
AR-777	21 nt Target:	5'-AGATAATAACTCAGTTCTTAT-3'	(SEQ ID NO: 639)
AR-778	21 nt Target:	5'-GATAATAACTCAGTTCTTATT-3'	(SEQ ID NO: 640)
AR-792	21 nt Target:	5'-TCTTATTTGCACCTACTTCAG-3'	(SEQ ID NO: 641)
AR-809	21 nt Target:	5'-TCAGTGGACACTGAATTTGGA-3'	(SEQ ID NO: 642)
AR-817	21 nt Target:	5'-CACTGAATTTGGAAGGTGGAG-3'	(SEQ ID NO: 643)
AR-824	21 nt Target:	5'-TTTGGAAGGTGGAGGATTTTG-3'	(SEQ ID NO: 644)
AR-827	21 nt Target:	5'-GGAAGGTGGAGGATTTTGTTT-3'	(SEQ ID NO: 645)
AR-833	21 nt Target:	5'-TGGAGGATTTTGTTTTTTTCT-3'	(SEQ ID NO: 646)
AR-834	21 nt Target:	5'-GGAGGATTTTGTTTTTTTCTT-3'	(SEQ ID NO: 647)
AR-836	21 nt Target:	5'-AGGATTTTGTTTTTTTCTTTT-3'	(SEQ ID NO: 648)
AR-837	21 nt Target:	5'-GGATTTTGTTTTTTTCTTTTA-3'	(SEQ ID NO: 649)
AR-838	21 nt Target:	5'-GATTTTGTTTTTTTCTTTTAA-3'	(SEQ ID NO: 650)
AR-839	21 nt Target:	5'-ATTTTGTTTTTTTCTTTTAAG-3'	(SEQ ID NO: 651)
AR-843	21 nt Target:	5'-TGTTTTTTTCTTTTAAGATCT-3'	(SEQ ID NO: 652)
AR-844	21 nt Target:	5'-GTTTTTTTCTTTTAAGATCTG-3'	(SEQ ID NO: 653)
AR-854	21 nt Target:	5'-TTTAAGATCTGGGCATCTTTT-3'	(SEQ ID NO: 654)
AR-868	21 nt Target:	5'-ATCTTTTGAATCTACCCTTCA-3'	(SEQ ID NO: 655)
AR-869	21 nt Target:	5'-TCTTTTGAATCTACCCTTCAA-3'	(SEQ ID NO: 656)
AR-870	21 nt Target:	5'-CTTTTGAATCTACCCTTCAAG-3'	(SEQ ID NO: 657)
AR-871	21 nt Target:	5'-TTTTGAATCTACCCTTCAAGT-3'	(SEQ ID NO: 658)
AR-872	21 nt Target:	5'-TTTGAATCTACCCTTCAAGTA-3'	(SEQ ID NO: 659)
AR-886	21 nt Target:	5'-TCAAGTATTAAGAGACAGACT-3'	(SEQ ID NO: 660)
AR-889	21 nt Target:	5'-AGTATTAAGAGACAGACTGTG-3'	(SEQ ID NO: 661)

AR-1067 21 nt Target: 5'-CTGTTGAACTCTTCTGAGCAA-3' (SEQ ID NO: 662)
AR-1068 21 nt Target: 5'-TGTTGAACTCTTCTGAGCAAG-3' (SEQ ID NO: 663)
AR-1137 21 nt Target: 5'-CAAGGATGGAAGTGCAGTTAG-3' (SEQ ID NO: 664)
AR-1198 21 nt Target: 5'-CCGAGGAGCTTTCCAGAATCT-3' (SEQ ID NO: 665)
AR-1199 21 nt Target: 5'-CGAGGAGCTTTCCAGAATCTG-3' (SEQ ID NO: 666)
AR-1675 21 nt Target: 5'-CGCTGACCTTAAAGACATCCT-3' (SEQ ID NO: 667)
AR-1802 21 nt Target: 5'-TCCAAGGACAATTACTTAGGG-3' (SEQ ID NO: 668)
AR-1848 21 nt Target: 5'-CCAAGGAGTTGTGTAAGGCAG-3' (SEQ ID NO: 669)
AR-2047 21 nt Target: 5'-CACTGAAGATACTGCTGAGTA-3' (SEQ ID NO: 670)
AR-2059 21 nt Target: 5'-TGCTGAGTATTCCCCTTTCAA-3' (SEQ ID NO: 671)
AR-2692 21 nt Target: 5'-CACTTGTGTCAAAAGCGAAAT-3' (SEQ ID NO: 672)
AR-2693 21 nt Target: 5'-ACTTGTGTCAAAAGCGAAATG-3' (SEQ ID NO: 673)
AR-2775 21 nt Target: 5'-ACCATGTTTTGCCCATTGACT-3' (SEQ ID NO: 674)
AR-2777 21 nt Target: 5'-CATGTTTTGCCCATTGACTAT-3' (SEQ ID NO: 675)
AR-2827 21 nt Target: 5'-CTGTGGAGATGAAGCTTCTGG-3' (SEQ ID NO: 676)
AR-2905 21 nt Target: 5'-TGAAGGGAAACAGAAGTACCT-3' (SEQ ID NO: 677)
AR-2934 21 nt Target: 5'-GCAGAAATGATTGCACTATTG-3' (SEQ ID NO: 678)
AR-2935 21 nt Target: 5'-CAGAAATGATTGCACTATTGA-3' (SEQ ID NO: 679)
AR-2936 21 nt Target: 5'-AGAAATGATTGCACTATTGAT-3' (SEQ ID NO: 680)
AR-2938 21 nt Target: 5'-AAATGATTGCACTATTGATAA-3' (SEQ ID NO: 681)
AR-2939 21 nt Target: 5'-AATGATTGCACTATTGATAAA-3' (SEQ ID NO: 682)
AR-2947 21 nt Target: 5'-CACTATTGATAAATTCCGAAG-3' (SEQ ID NO: 683)
AR-2948 21 nt Target: 5'-ACTATTGATAAATTCCGAAGG-3' (SEQ ID NO: 684)
AR-2949 21 nt Target: 5'-CTATTGATAAATTCCGAAGGA-3' (SEQ ID NO: 685)
AR-2950 21 nt Target: 5'-TATTGATAAATTCCGAAGGAA-3' (SEQ ID NO: 686)
AR-2951 21 nt Target: 5'-ATTGATAAATTCCGAAGGAAA-3' (SEQ ID NO: 687)
AR-2953 21 nt Target: 5'-TGATAAATTCCGAAGGAAAAA-3' (SEQ ID NO: 688)
AR-2954 21 nt Target: 5'-GATAAATTCCGAAGGAAAAAT-3' (SEQ ID NO: 689)
AR-2963 21 nt Target: 5'-CGAAGGAAAAATTGTCCATCT-3' (SEQ ID NO: 690)
AR-2980 21 nt Target: 5'-ATCTTGTCGTCTTCGGAAATG-3' (SEQ ID NO: 691)
AR-2993 21 nt Target: 5'-CGGAAATGTTATGAAGCAGGG-3' (SEQ ID NO: 692)
AR-2995 21 nt Target: 5'-GAAATGTTATGAAGCAGGGAT-3' (SEQ ID NO: 693)
AR-3027 21 nt Target: 5'-CCCGGAAGCTGAAGAAACTTG-3' (SEQ ID NO: 694)
AR-3029 21 nt Target: 5'-CGGAAGCTGAAGAAACTTGGT-3' (SEQ ID NO: 695)
AR-3034 21 nt Target: 5'-GCTGAAGAAACTTGGTAATCT-3' (SEQ ID NO: 696)
AR-3035 21 nt Target: 5'-CTGAAGAAACTTGGTAATCTG-3' (SEQ ID NO: 697)
AR-3036 21 nt Target: 5'-TGAAGAAACTTGGTAATCTGA-3' (SEQ ID NO: 698)
AR-3045 21 nt Target: 5'-TTGGTAATCTGAAACTACAGG-3' (SEQ ID NO: 699)
AR-3051 21 nt Target: 5'-ATCTGAAACTACAGGAGGAAG-3' (SEQ ID NO: 700)
AR-3546 21 nt Target: 5'-CCCAGGAATTCCTGTGCATGA-3' (SEQ ID NO: 701)
AR-3547 21 nt Target: 5'-CCAGGAATTCCTGTGCATGAA-3' (SEQ ID NO: 702)
AR-3596 21 nt Target: 5'-GTGGATGGGCTGAAAAATCAA-3' (SEQ ID NO: 703)
AR-3597 21 nt Target: 5'-TGGATGGGCTGAAAAATCAAA-3' (SEQ ID NO: 704)
AR-3599 21 nt Target: 5'-GATGGGCTGAAAAATCAAAAA-3' (SEQ ID NO: 705)
AR-3603 21 nt Target: 5'-GGCTGAAAAATCAAAAATTCT-3' (SEQ ID NO: 706)
AR-3604 21 nt Target: 5'-GCTGAAAAATCAAAAATTCTT-3' (SEQ ID NO: 707)
AR-3606 21 nt Target: 5'-TGAAAAATCAAAAATTCTTTG-3' (SEQ ID NO: 708)
AR-3607 21 nt Target: 5'-GAAAAATCAAAAATTCTTTGA-3' (SEQ ID NO: 709)
AR-3608 21 nt Target: 5'-AAAAATCAAAAATTCTTTGAT-3' (SEQ ID NO: 710)
AR-3633 21 nt Target: 5'-TTCGAATGAACTACATCAAGG-3' (SEQ ID NO: 711)
AR-3648 21 nt Target: 5'-TCAAGGAACTCGATCGTATCA-3' (SEQ ID NO: 712)
AR-3649 21 nt Target: 5'-CAAGGAACTCGATCGTATCAT-3' (SEQ ID NO: 713)
AR-3660 21 nt Target: 5'-ATCGTATCATTGCATGCAAAA-3' (SEQ ID NO: 714)
AR-3661 21 nt Target: 5'-TCGTATCATTGCATGCAAAAG-3' (SEQ ID NO: 715)
AR-3665 21 nt Target: 5'-ATCATTGCATGCAAAAGAAAA-3' (SEQ ID NO: 716)
AR-3772 21 nt Target: 5'-CACTTTTGACCTGCTAATCAA-3' (SEQ ID NO: 717)
AR-3807 21 nt Target: 5'-GCGTGGACTTTCCGGAAATGA-3' (SEQ ID NO: 718)
AR-3808 21 nt Target: 5'-CGTGGACTTTCCGGAAATGAT-3' (SEQ ID NO: 719)
AR-3825 21 nt Target: 5'-TGATGGCAGAGATCATCTCTG-3' (SEQ ID NO: 720)
AR-3830 21 nt Target: 5'-GCAGAGATCATCTCTGTGCAA-3' (SEQ ID NO: 721)
AR-3831 21 nt Target: 5'-CAGAGATCATCTCTGTGCAAG-3' (SEQ ID NO: 722)

AR-3854 21 nt Target: 5'-CCCAAGATCCTTTCTGGGAAA-3' (SEQ ID NO: 723)
AR-3901 21 nt Target: 5'-GTGAAGCATTGGAAACCCTAT-3' (SEQ ID NO: 724)
AR-3949 21 nt Target: 5'-CAGATGTCTTCTGCCTGTTAT-3' (SEQ ID NO: 725)
AR-3994 21 nt Target: 5'-GCCTTGGGGAATTTCCTCTAT-3' (SEQ ID NO: 726)
AR-3996 21 nt Target: 5'-CTTGGGGAATTTCCTCTATTG-3' (SEQ ID NO: 727)
AR-3997 21 nt Target: 5'-TTGGGGAATTTCCTCTATTGA-3' (SEQ ID NO: 728)
AR-3998 21 nt Target: 5'-TGGGGAATTTCCTCTATTGAT-3' (SEQ ID NO: 729)
AR-3999 21 nt Target: 5'-GGGGAATTTCCTCTATTGATG-3' (SEQ ID NO: 730)
AR-4011 21 nt Target: 5'-CTATTGATGTACAGTCTGTCA-3' (SEQ ID NO: 731)
AR-4012 21 nt Target: 5'-TATTGATGTACAGTCTGTCAT-3' (SEQ ID NO: 732)
AR-4013 21 nt Target: 5'-ATTGATGTACAGTCTGTCATG-3' (SEQ ID NO: 733)
AR-4034 21 nt Target: 5'-AACATGTTCCTGAATTCTATT-3' (SEQ ID NO: 734)
AR-4048 21 nt Target: 5'-TTCTATTTGCTGGGCTTTTTT-3' (SEQ ID NO: 735)
AR-4049 21 nt Target: 5'-TCTATTTGCTGGGCTTTTTTT-3' (SEQ ID NO: 736)
AR-4055 21 nt Target: 5'-TGCTGGGCTTTTTTTTCTCT-3' (SEQ ID NO: 737)
AR-4064 21 nt Target: 5'-TTTTTTTCTCTTTCTCTCCT-3' (SEQ ID NO: 738)
AR-4128 21 nt Target: 5'-TTCAGACTTTGCTTCCCATTG-3' (SEQ ID NO: 739)
AR-4146 21 nt Target: 5'-TTGTGGCTCCTATCTGTGTTT-3' (SEQ ID NO: 740)
AR-4153 21 nt Target: 5'-TCCTATCTGTGTTTTGAATGG-3' (SEQ ID NO: 741)
AR-4157 21 nt Target: 5'-ATCTGTGTTTTGAATGGTGTT-3' (SEQ ID NO: 742)
AR-4160 21 nt Target: 5'-TGTGTTTTGAATGGTGTTGTA-3' (SEQ ID NO: 743)
AR-4167 21 nt Target: 5'-TGAATGGTGTTGTATGCCTTT-3' (SEQ ID NO: 744)
AR-4168 21 nt Target: 5'-GAATGGTGTTGTATGCCTTTA-3' (SEQ ID NO: 745)
AR-4174 21 nt Target: 5'-TGTTGTATGCCTTTAAATCTG-3' (SEQ ID NO: 746)
AR-4176 21 nt Target: 5'-TTGTATGCCTTTAAATCTGTG-3' (SEQ ID NO: 747)
AR-4177 21 nt Target: 5'-TGTATGCCTTTAAATCTGTGA-3' (SEQ ID NO: 748)
AR-4212 21 nt Target: 5'-CCCAGTGTCAAGTTGTGCTTG-3' (SEQ ID NO: 749)
AR-4213 21 nt Target: 5'-CCAGTGTCAAGTTGTGCTTGT-3' (SEQ ID NO: 750)
AR-4228 21 nt Target: 5'-GCTTGTTTACAGCACTACTCT-3' (SEQ ID NO: 751)
AR-4229 21 nt Target: 5'-CTTGTTTACAGCACTACTCTG-3' (SEQ ID NO: 752)
AR-4259 21 nt Target: 5'-CACAAACGTTTACTTATCTTA-3' (SEQ ID NO: 753)
AR-4283 21 nt Target: 5'-CACGGGAAGTTTAGAGAGCTA-3' (SEQ ID NO: 754)
AR-4284 21 nt Target: 5'-ACGGGAAGTTTAGAGAGCTAA-3' (SEQ ID NO: 755)
AR-4285 21 nt Target: 5'-CGGGAAGTTTAGAGAGCTAAG-3' (SEQ ID NO: 756)
AR-4286 21 nt Target: 5'-GGGAAGTTTAGAGAGCTAAGA-3' (SEQ ID NO: 757)
AR-4288 21 nt Target: 5'-GAAGTTTAGAGAGCTAAGATT-3' (SEQ ID NO: 758)
AR-4293 21 nt Target: 5'-TTAGAGAGCTAAGATTATCTG-3' (SEQ ID NO: 759)
AR-4294 21 nt Target: 5'-TAGAGAGCTAAGATTATCTGG-3' (SEQ ID NO: 760)
AR-4295 21 nt Target: 5'-AGAGAGCTAAGATTATCTGGG-3' (SEQ ID NO: 761)
AR-4302 21 nt Target: 5'-TAAGATTATCTGGGGAAATCA-3' (SEQ ID NO: 762)
AR-4303 21 nt Target: 5'-AAGATTATCTGGGGAAATCAA-3' (SEQ ID NO: 763)
AR-4309 21 nt Target: 5'-ATCTGGGGAAATCAAAACAAA-3' (SEQ ID NO: 764)
AR-4313 21 nt Target: 5'-GGGGAAATCAAAACAAAAACA-3' (SEQ ID NO: 765)
AR-251 21 nt Target: 5'-GTGAAGTTTTTAAAAGCTGCT-3' (SEQ ID NO: 886)
AR-524 21 nt Target: 5'-AGCTAGCTGCACATTGCAAAG-3' (SEQ ID NO: 887)
AR-534 21 nt Target: 5'-ACATTGCAAAGAAGGCTCTTA-3' (SEQ ID NO: 888)
AR-736 21 nt Target: 5'-AACAAAACAAACAAAAACAAA-3' (SEQ ID NO: 889)
AR-776 21 nt Target: 5'-AAGATAATAACTCAGTTCTTA-3' (SEQ ID NO: 890)
AR-808 21 nt Target: 5'-TTCAGTGGACACTGAATTTGG-3' (SEQ ID NO: 891)
AR-810 21 nt Target: 5'-CAGTGGACACTGAATTTGGAA-3' (SEQ ID NO: 892)
AR-811 21 nt Target: 5'-AGTGGACACTGAATTTGGAAG-3' (SEQ ID NO: 893)
AR-873 21 nt Target: 5'-TTGAATCTACCCTTCAAGTAT-3' (SEQ ID NO: 894)
AR-887 21 nt Target: 5'-CAAGTATTAAGAGACAGACTG-3' (SEQ ID NO: 895)
AR-2060 21 nt Target: 5'-GCTGAGTATTCCCCTTTCAAG-3' (SEQ ID NO: 896)
AR-2061 21 nt Target: 5'-CTGAGTATTCCCCTTTCAAGG-3' (SEQ ID NO: 897)
AR-2826 21 nt Target: 5'-TCTGTGGAGATGAAGCTTCTG-3' (SEQ ID NO: 898)
AR-2906 21 nt Target: 5'-GAAGGGAAACAGAAGTACCTG-3' (SEQ ID NO: 899)
AR-2952 21 nt Target: 5'-TTGATAAATTCCGAAGGAAAA-3' (SEQ ID NO: 900)
AR-2964 21 nt Target: 5'-GAAGGAAAAATTGTCCATCTT-3' (SEQ ID NO: 901)
AR-2992 21 nt Target: 5'-TCGGAAATGTTATGAAGCAGG-3' (SEQ ID NO: 902)
AR-3043 21 nt Target: 5'-ACTTGGTAATCTGAAACTACA-3' (SEQ ID NO: 903)

AR-3044 21 nt Target: 5'-CTTGGTAATCTGAAACTACAG-3' (SEQ ID NO: 904)
AR-3047 21 nt Target: 5'-GGTAATCTGAAACTACAGGAG-3' (SEQ ID NO: 905)
AR-3117 21 nt Target: 5'-AGCTGACAGTGTCACACATTG-3' (SEQ ID NO: 906)
AR-3346 21 nt Target: 5'-GGCTGTCATTCAGTACTCCTG-3' (SEQ ID NO: 907)
AR-3605 21 nt Target: 5'-CTGAAAAATCAAAAATTCTTT-3' (SEQ ID NO: 908)
AR-3616 21 nt Target: 5'-AAAATTCTTTGATGAACTTCG-3' (SEQ ID NO: 909)
AR-3783 21 nt Target: 5'-TGCTAATCAAGTCACACATGG-3' (SEQ ID NO: 910)
AR-3806 21 nt Target: 5'-AGCGTGGACTTTCCGGAAATG-3' (SEQ ID NO: 911)
AR-3995 21 nt Target: 5'-CCTTGGGGAATTTCCTCTATT-3' (SEQ ID NO: 912)
AR-4158 21 nt Target: 5'-TCTGTGTTTTGAATGGTGTTG-3' (SEQ ID NO: 913)
AR-4175 21 nt Target: 5'-GTTGTATGCCTTTAAATCTGT-3' (SEQ ID NO: 914)
AR-4292 21 nt Target: 5'-TTTAGAGAGCTAAGATTATCT-3' (SEQ ID NO: 915)
AR-248 21 nt Target: 5'-TCGGTGAAGTTTTTAAAAGCT-3' (SEQ ID NO: 1132)
AR-255 21 nt Target: 5'-AGTTTTTAAAAGCTGCTAAAG-3' (SEQ ID NO: 1133)
AR-489 21 nt Target: 5'-GCAGAGAGGTAACTCCCTTTG-3' (SEQ ID NO: 1134)
AR-690 21 nt Target: 5'-CAGAGATCAAAAGATGAAAAG-3' (SEQ ID NO: 1135)
AR-731 21 nt Target: 5'-CAAAAAACAAAACAAACAAAA-3' (SEQ ID NO: 1136)
AR-764 21 nt Target: 5'-AAATAAAAGAAAAAGATAATA-3' (SEQ ID NO: 1137)
AR-771 21 nt Target: 5'-AGAAAAAGATAATAACTCAGT-3' (SEQ ID NO: 1138)
AR-779 21 nt Target: 5'-ATAATAACTCAGTTCTTATTT-3' (SEQ ID NO: 1139)
AR-830 21 nt Target: 5'-AGGTGGAGGATTTTGTTTTTT-3' (SEQ ID NO: 1140)
AR-840 21 nt Target: 5'-TTTTGTTTTTTTCTTTTAAGA-3' (SEQ ID NO: 1141)
AR-845 21 nt Target: 5'-TTTTTTTCTTTTAAGATCTGG-3' (SEQ ID NO: 1142)
AR-860 21 nt Target: 5'-ATCTGGGCATCTTTTGAATCT-3' (SEQ ID NO: 1143)
AR-1105 21 nt Target: 5'-TAAGGGAAGTAGGTGGAAGAT-3' (SEQ ID NO: 1144)
AR-1200 21 nt Target: 5'-GAGGAGCTTTCCAGAATCTGT-3' (SEQ ID NO: 1145)
AR-1734 21 nt Target: 5'-AGCAGGAAGCAGTATCCGAAG-3' (SEQ ID NO: 1146)
AR-1803 21 nt Target: 5'-CCAAGGACAATTACTTAGGGG-3' (SEQ ID NO: 1147)
AR-1850 21 nt Target: 5'-AAGGAGTTGTGTAAGGCAGTG-3' (SEQ ID NO: 1148)
AR-2039 21 nt Target: 5'-GGCAAGAGCACTGAAGATACT-3' (SEQ ID NO: 1149)
AR-2048 21 nt Target: 5'-ACTGAAGATACTGCTGAGTAT-3' (SEQ ID NO: 1150)
AR-2077 21 nt Target: 5'-CAAGGGAGGTTACACCAAAGG-3' (SEQ ID NO: 1151)
AR-2694 21 nt Target: 5'-CTTGTGTCAAAAGCGAAATGG-3' (SEQ ID NO: 1152)
AR-2778 21 nt Target: 5'-ATGTTTTGCCCATTGACTATT-3' (SEQ ID NO: 1153)
AR-2879 21 nt Target: 5'-TGCAAGGTCTTCTTCAAAAGA-3' (SEQ ID NO: 1154)
AR-2907 21 nt Target: 5'-AAGGGAAACAGAAGTACCTGT-3' (SEQ ID NO: 1155)
AR-2940 21 nt Target: 5'-ATGATTGCACTATTGATAAAT-3' (SEQ ID NO: 1156)
AR-2956 21 nt Target: 5'-TAAATTCCGAAGGAAAAATTG-3' (SEQ ID NO: 1157)
AR-2965 21 nt Target: 5'-AAGGAAAAATTGTCCATCTTG-3' (SEQ ID NO: 1158)
AR-2968 21 nt Target: 5'-GAAAAATTGTCCATCTTGTCG-3' (SEQ ID NO: 1159)
AR-3037 21 nt Target: 5'-GAAGAAACTTGGTAATCTGAA-3' (SEQ ID NO: 1160)
AR-3133 21 nt Target: 5'-CATTGAAGGCTATGAATGTCA-3' (SEQ ID NO: 1161)
AR-3548 21 nt Target: 5'-CAGGAATTCCTGTGCATGAAA-3' (SEQ ID NO: 1162)
AR-3613 21 nt Target: 5'-TCAAAAATTCTTTGATGAACT-3' (SEQ ID NO: 1163)
AR-3621 21 nt Target: 5'-TCTTTGATGAACTTCGAATGA-3' (SEQ ID NO: 1164)
AR-3624 21 nt Target: 5'-TTGATGAACTTCGAATGAACT-3' (SEQ ID NO: 1165)
AR-3634 21 nt Target: 5'-TCGAATGAACTACATCAAGGA-3' (SEQ ID NO: 1166)
AR-3674 21 nt Target: 5'-TGCAAAAGAAAAAATCCCACA-3' (SEQ ID NO: 1167)
AR-3678 21 nt Target: 5'-AAAGAAAAAATCCCACATCCT-3' (SEQ ID NO: 1168)
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AR-3855 21 nt Target: 5'-CCAAGATCCTTTCTGGGAAAG-3' (SEQ ID NO: 1170)
AR-3870 21 nt Target: 5'-GGAAAGTCAAGCCCATCTATT-3' (SEQ ID NO: 1171)
AR-3950 21 nt Target: 5'-AGATGTCTTCTGCCTGTTATA-3' (SEQ ID NO: 1172)
AR-4000 21 nt Target: 5'-GGGAATTTCCTCTATTGATGT-3' (SEQ ID NO: 1173)
AR-4014 21 nt Target: 5'-TTGATGTACAGTCTGTCATGA-3' (SEQ ID NO: 1174)
AR-4020 21 nt Target: 5'-TACAGTCTGTCATGAACATGT-3' (SEQ ID NO: 1175)
AR-4028 21 nt Target: 5'-GTCATGAACATGTTCCTGAAT-3' (SEQ ID NO: 1176)
AR-4035 21 nt Target: 5'-ACATGTTCCTGAATTCTATTT-3' (SEQ ID NO: 1177)
AR-4056 21 nt Target: 5'-GCTGGGCTTTTTTTTTCTCTT-3' (SEQ ID NO: 1178)
AR-4065 21 nt Target: 5'-TTTTTTTCTCTTTCTCTCCTT-3' (SEQ ID NO: 1179)
AR-4161 21 nt Target: 5'-GTGTTTTGAATGGTGTTGTAT-3' (SEQ ID NO: 1180)

AR-4170 21 nt Target: 5'-ATGGTGTTGTATGCCTTTAAA-3' (SEQ ID NO: 1181)
AR-4218 21 nt Target: 5'-GTCAAGTTGTGCTTGTTTACA-3' (SEQ ID NO: 1182)
AR-4299 21 nt Target: 5'-AGCTAAGATTATCTGGGGAAA-3' (SEQ ID NO: 1183)
AR-4310 21 nt Target: 5'-TCTGGGGAAATCAAAACAAAA-3' (SEQ ID NO: 1184)
AR-4314 21 nt Target: 5'-GGGAAATCAAAACAAAAACAA-3' (SEQ ID NO: 1185)
AR-249 21 nt Target: 5'-CGGTGAAGTTTTTAAAAGCTG-3' (SEQ ID NO: 1438)
AR-256 21 nt Target: 5'-GTTTTTAAAAGCTGCTAAAGA-3' (SEQ ID NO: 1439)
AR-258 21 nt Target: 5'-TTTTAAAAGCTGCTAAAGACT-3' (SEQ ID NO: 1440)
AR-618 21 nt Target: 5'-GCGGAGAGAACCCTCTGTTTT-3' (SEQ ID NO: 1441)
AR-691 21 nt Target: 5'-AGAGATCAAAAGATGAAAAGG-3' (SEQ ID NO: 1442)
AR-695 21 nt Target: 5'-ATCAAAAGATGAAAAGGCAGT-3' (SEQ ID NO: 1443)
AR-722 21 nt Target: 5'-TTCAGTAGCCAAAAAACAAAA-3' (SEQ ID NO: 1444)
AR-732 21 nt Target: 5'-AAAAAACAAAACAAACAAAAA-3' (SEQ ID NO: 1445)
AR-765 21 nt Target: 5'-AATAAAAGAAAAAGATAATAA-3' (SEQ ID NO: 1446)
AR-767 21 nt Target: 5'-TAAAAGAAAAAGATAATAACT-3' (SEQ ID NO: 1447)
AR-772 21 nt Target: 5'-GAAAAAGATAATAACTCAGTT-3' (SEQ ID NO: 1448)
AR-780 21 nt Target: 5'-TAATAACTCAGTTCTTATTTG-3' (SEQ ID NO: 1449)
AR-786 21 nt Target: 5'-CTCAGTTCTTATTTGCACCTA-3' (SEQ ID NO: 1450)
AR-831 21 nt Target: 5'-GGTGGAGGATTTTGTTTTTTT-3' (SEQ ID NO: 1451)
AR-841 21 nt Target: 5'-TTTGTTTTTTTCTTTTAAGAT-3' (SEQ ID NO: 1452)
AR-846 21 nt Target: 5'-TTTTTTCTTTTAAGATCTGGG-3' (SEQ ID NO: 1453)
AR-861 21 nt Target: 5'-TCTGGGCATCTTTTGAATCTA-3' (SEQ ID NO: 1454)
AR-997 21 nt Target: 5'-CGCAAGTTTCCTTCTCTGGAG-3' (SEQ ID NO: 1455)
AR-1106 21 nt Target: 5'-AAGGGAAGTAGGTGGAAGATT-3' (SEQ ID NO: 1456)
AR-1109 21 nt Target: 5'-GGAAGTAGGTGGAAGATTCAG-3' (SEQ ID NO: 1457)
AR-1804 21 nt Target: 5'-CAAGGACAATTACTTAGGGGG-3' (SEQ ID NO: 1458)
AR-2003 21 nt Target: 5'-GCCGAATGCAAAGGTTCTCTG-3' (SEQ ID NO: 1459)
AR-2040 21 nt Target: 5'-GCAAGAGCACTGAAGATACTG-3' (SEQ ID NO: 1460)
AR-2049 21 nt Target: 5'-CTGAAGATACTGCTGAGTATT-3' (SEQ ID NO: 1461)
AR-2695 21 nt Target: 5'-TTGTGTCAAAAGCGAAATGGG-3' (SEQ ID NO: 1462)
AR-2779 21 nt Target: 5'-TGTTTTGCCCATTGACTATTA-3' (SEQ ID NO: 1463)
AR-2786 21 nt Target: 5'-CCCATTGACTATTACTTTCCA-3' (SEQ ID NO: 1464)
AR-2880 21 nt Target: 5'-GCAAGGTCTTCTTCAAAAGAG-3' (SEQ ID NO: 1465)
AR-2941 21 nt Target: 5'-TGATTGCACTATTGATAAATT-3' (SEQ ID NO: 1466)
AR-2961 21 nt Target: 5'-TCCGAAGGAAAAATTGTCCAT-3' (SEQ ID NO: 1467)
AR-2966 21 nt Target: 5'-AGGAAAAATTGTCCATCTTGT-3' (SEQ ID NO: 1468)
AR-3121 21 nt Target: 5'-GACAGTGTCACACATTGAAGG-3' (SEQ ID NO: 1469)
AR-3134 21 nt Target: 5'-ATTGAAGGCTATGAATGTCAG-3' (SEQ ID NO: 1470)
AR-3342 21 nt Target: 5'-AGATGGCTGTCATTCAGTACT-3' (SEQ ID NO: 1471)
AR-3445 21 nt Target: 5'-TCTGGTTTTCAATGAGTACCG-3' (SEQ ID NO: 1472)
AR-3549 21 nt Target: 5'-AGGAATTCCTGTGCATGAAAG-3' (SEQ ID NO: 1473)
AR-3614 21 nt Target: 5'-CAAAAATTCTTTGATGAACTT-3' (SEQ ID NO: 1474)
AR-3622 21 nt Target: 5'-CTTTGATGAACTTCGAATGAA-3' (SEQ ID NO: 1475)
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AR-3635 21 nt Target: 5'-CGAATGAACTACATCAAGGAA-3' (SEQ ID NO: 1477)
AR-3637 21 nt Target: 5'-AATGAACTACATCAAGGAACT-3' (SEQ ID NO: 1478)
AR-3675 21 nt Target: 5'-GCAAAAGAAAAAATCCCACAT-3' (SEQ ID NO: 1479)
AR-3679 21 nt Target: 5'-AAGAAAAAATCCCACATCCTG-3' (SEQ ID NO: 1480)
AR-3774 21 nt Target: 5'-CTTTTGACCTGCTAATCAAGT-3' (SEQ ID NO: 1481)
AR-3961 21 nt Target: 5'-GCCTGTTATAACTCTGCACTA-3' (SEQ ID NO: 1482)
AR-3963 21 nt Target: 5'-CTGTTATAACTCTGCACTACT-3' (SEQ ID NO: 1483)
AR-4001 21 nt Target: 5'-GGAATTTCCTCTATTGATGTA-3' (SEQ ID NO: 1484)
AR-4009 21 nt Target: 5'-CTCTATTGATGTACAGTCTGT-3' (SEQ ID NO: 1485)
AR-4029 21 nt Target: 5'-TCATGAACATGTTCCTGAATT-3' (SEQ ID NO: 1486)
AR-4041 21 nt Target: 5'-TCCTGAATTCTATTTGCTGGG-3' (SEQ ID NO: 1487)
AR-4061 21 nt Target: 5'-GCTTTTTTTTTCTCTTTCTCT-3' (SEQ ID NO: 1488)
AR-4066 21 nt Target: 5'-TTTTTTCTCTTTCTCTCCTTT-3' (SEQ ID NO: 1489)
AR-4072 21 nt Target: 5'-CTCTTTCTCTCCTTTCTTTTT-3' (SEQ ID NO: 1490)
AR-4118 21 nt Target: 5'-CCATGGCACCTTCAGACTTTG-3' (SEQ ID NO: 1491)
AR-4162 21 nt Target: 5'-TGTTTTGAATGGTGTTGTATG-3' (SEQ ID NO: 1492)
AR-4171 21 nt Target: 5'-TGGTGTTGTATGCCTTTAAAT-3' (SEQ ID NO: 1493)

AR-4184 21 nt Target: 5'-CTTTAAATCTGTGATGATCCT-3' (SEQ ID NO: 1494)
AR-4191 21 nt Target: 5'-TCTGTGATGATCCTCATATGG-3' (SEQ ID NO: 1495)
AR-4221 21 nt Target: 5'-AAGTTGTGCTTGTTTACAGCA-3' (SEQ ID NO: 1496)
AR-4264 21 nt Target: 5'-ACGTTTACTTATCTTATGCCA-3' (SEQ ID NO: 1497)
AR-4290 21 nt Target: 5'-AGTTTAGAGAGCTAAGATTAT-3' (SEQ ID NO: 1498)
AR-4300 21 nt Target: 5'-GCTAAGATTATCTGGGGAAAT-3' (SEQ ID NO: 1499)
AR-4311 21 nt Target: 5'-CTGGGGAAATCAAAACAAAAA-3' (SEQ ID NO: 1500)
AR-39 21 nt Target: 5'-GAGCCAGCTTGCTGGGAGAGC-3' (SEQ ID NO: 3121)
AR-174 21 nt Target: 5'-CGGCTCCAGCGACAGCCAACG-3' (SEQ ID NO: 3122)
AR-186 21 nt Target: 5'-CAGCCAACGCCTCTTGCAGCG-3' (SEQ ID NO: 3123)
AR-194 21 nt Target: 5'-GCCTCTTGCAGCGCGGCGGCT-3' (SEQ ID NO: 3124)
AR-200 21 nt Target: 5'-TGCAGCGCGGCGGCTTCGAAG-3' (SEQ ID NO: 3125)
AR-216 21 nt Target: 5'-CGAAGCCGCCGCCCGGAGCTG-3' (SEQ ID NO: 3126)
AR-222 21 nt Target: 5'-CGCCGCCCGGAGCTGCCCTTT-3' (SEQ ID NO: 3127)
AR-252 21 nt Target: 5'-TGAAGTTTTTAAAAGCTGCTA-3' (SEQ ID NO: 3128)
AR-375 21 nt Target: 5'-CCGTCTTCTCTCCCGCAGCTG-3' (SEQ ID NO: 3129)
AR-387 21 nt Target: 5'-CCGCAGCTGCCTCAGTCGGCT-3' (SEQ ID NO: 3130)
AR-506 21 nt Target: 5'-TTTGGCTGCGAGCGGGCGAGC-3' (SEQ ID NO: 3131)
AR-518 21 nt Target: 5'-CGGGCGAGCTAGCTGCACATT-3' (SEQ ID NO: 3132)
AR-646 21 nt Target: 5'-TCTCTCTCCACCTCCTCCTGC-3' (SEQ ID NO: 3133)
AR-689 21 nt Target: 5'-CCAGAGATCAAAAGATGAAAA-3' (SEQ ID NO: 3134)
AR-724 21 nt Target: 5'-CAGTAGCCAAAAAACAAAACA-3' (SEQ ID NO: 3135)
AR-730 21 nt Target: 5'-CCAAAAAACAAAACAAACAAA-3' (SEQ ID NO: 3136)
AR-737 21 nt Target: 5'-ACAAAACAAACAAAAACAAAA-3' (SEQ ID NO: 3137)
AR-752 21 nt Target: 5'-ACAAAAAAGCCGAAATAAAAG-3' (SEQ ID NO: 3138)
AR-760 21 nt Target: 5'-GCCGAAATAAAAGAAAAAGAT-3' (SEQ ID NO: 3139)
AR-770 21 nt Target: 5'-AAGAAAAAGATAATAACTCAG-3' (SEQ ID NO: 3140)
AR-775 21 nt Target: 5'-AAAGATAATAACTCAGTTCTT-3' (SEQ ID NO: 3141)
AR-778 21 nt Target: 5'-GATAATAACTCAGTTCTTATT-3' (SEQ ID NO: 3142)
AR-833 21 nt Target: 5'-TGGAGGATTTTGTTTTTTTCT-3' (SEQ ID NO: 3143)
AR-838 21 nt Target: 5'-GATTTTGTTTTTTTCTTTTAA-3' (SEQ ID NO: 3144)
AR-844 21 nt Target: 5'-GTTTTTTTCTTTTAAGATCTG-3' (SEQ ID NO: 3145)
AR-864 21 nt Target: 5'-GGGCATCTTTTGAATCTACCC-3' (SEQ ID NO: 3146)
AR-971 21 nt Target: 5'-CAGAGCGCTTTTTGCGTGGTT-3' (SEQ ID NO: 3147)
AR-976 21 nt Target: 5'-CGCTTTTTGCGTGGTTGCTCC-3' (SEQ ID NO: 3148)
AR-1000 21 nt Target: 5'-AAGTTTCCTTCTCTGGAGCTT-3' (SEQ ID NO: 3149)
AR-1016 21 nt Target: 5'-AGCTTCCCGCAGGTGGGCAGC-3' (SEQ ID NO: 3150)
AR-1028 21 nt Target: 5'-GTGGGCAGCTAGCTGCAGCGA-3' (SEQ ID NO: 3151)
AR-1146 21 nt Target: 5'-AAGTGCAGTTAGGGCTGGGAA-3' (SEQ ID NO: 3152)
AR-1147 21 nt Target: 5'-AGTGCAGTTAGGGCTGGGAAG-3' (SEQ ID NO: 3153)
AR-1148 21 nt Target: 5'-GTGCAGTTAGGGCTGGGAAGG-3' (SEQ ID NO: 3154)
AR-1149 21 nt Target: 5'-TGCAGTTAGGGCTGGGAAGGG-3' (SEQ ID NO: 3155)
AR-1150 21 nt Target: 5'-GCAGTTAGGGCTGGGAAGGGT-3' (SEQ ID NO: 3156)
AR-1151 21 nt Target: 5'-CAGTTAGGGCTGGGAAGGGTC-3' (SEQ ID NO: 3157)
AR-1152 21 nt Target: 5'-AGTTAGGGCTGGGAAGGGTCT-3' (SEQ ID NO: 3158)
AR-1153 21 nt Target: 5'-GTTAGGGCTGGGAAGGGTCTA-3' (SEQ ID NO: 3159)
AR-1154 21 nt Target: 5'-TTAGGGCTGGGAAGGGTCTAC-3' (SEQ ID NO: 3160)
AR-1155 21 nt Target: 5'-TAGGGCTGGGAAGGGTCTACC-3' (SEQ ID NO: 3161)
AR-1156 21 nt Target: 5'-AGGGCTGGGAAGGGTCTACCC-3' (SEQ ID NO: 3162)
AR-1206 21 nt Target: 5'-CTTTCCAGAATCTGTTCCAGA-3' (SEQ ID NO: 3163)
AR-1207 21 nt Target: 5'-TTTCCAGAATCTGTTCCAGAG-3' (SEQ ID NO: 3164)
AR-1208 21 nt Target: 5'-TTCCAGAATCTGTTCCAGAGC-3' (SEQ ID NO: 3165)
AR-1209 21 nt Target: 5'-TCCAGAATCTGTTCCAGAGCG-3' (SEQ ID NO: 3166)
AR-1210 21 nt Target: 5'-CCAGAATCTGTTCCAGAGCGT-3' (SEQ ID NO: 3167)
AR-1211 21 nt Target: 5'-CAGAATCTGTTCCAGAGCGTG-3' (SEQ ID NO: 3168)
AR-1212 21 nt Target: 5'-AGAATCTGTTCCAGAGCGTGC-3' (SEQ ID NO: 3169)
AR-1213 21 nt Target: 5'-GAATCTGTTCCAGAGCGTGCG-3' (SEQ ID NO: 3170)
AR-1214 21 nt Target: 5'-AATCTGTTCCAGAGCGTGCGC-3' (SEQ ID NO: 3171)
AR-1215 21 nt Target: 5'-ATCTGTTCCAGAGCGTGCGCG-3' (SEQ ID NO: 3172)
AR-1216 21 nt Target: 5'-TCTGTTCCAGAGCGTGCGCGA-3' (SEQ ID NO: 3173)
AR-1217 21 nt Target: 5'-CTGTTCCAGAGCGTGCGCGAA-3' (SEQ ID NO: 3174)

AR-1218 21 nt Target: 5'-TGTTCCAGAGCGTGCGCGAAG-3' (SEQ ID NO: 3175)
AR-1292 21 nt Target: 5'-GGCGCCAGTTTGCTGCTGCTG-3' (SEQ ID NO: 3176)
AR-1301 21 nt Target: 5'-TTGCTGCTGCTGCAGCAGCAG-3' (SEQ ID NO: 3177)
AR-1533 21 nt Target: 5'-GCGTCCCAGAGCCTGGAGCCG-3' (SEQ ID NO: 3178)
AR-1572 21 nt Target: 5'-GGCTGCCGCAGCAGCTGCCAG-3' (SEQ ID NO: 3179)
AR-1578 21 nt Target: 5'-CGCAGCAGCTGCCAGCACCTC-3' (SEQ ID NO: 3180)
AR-1621 21 nt Target: 5'-CCCATCCACGTTGTCCCTGCT-3' (SEQ ID NO: 3181)
AR-1656 21 nt Target: 5'-CCGGCTTAAGCAGCTGCTCCG-3' (SEQ ID NO: 3182)
AR-1657 21 nt Target: 5'-CGGCTTAAGCAGCTGCTCCGC-3' (SEQ ID NO: 3183)
AR-1662 21 nt Target: 5'-TAAGCAGCTGCTCCGCTGACC-3' (SEQ ID NO: 3184)
AR-1712 21 nt Target: 5'-ATGCAACTCCTTCAGCAACAG-3' (SEQ ID NO: 3185)
AR-1832 21 nt Target: 5'-ACCATTTCTGACAACGCCAAG-3' (SEQ ID NO: 3186)
AR-1952 21 nt Target: 5'-CCACTTTTGGGAGTTCCACCC-3' (SEQ ID NO: 3187)
AR-2037 21 nt Target: 5'-CAGGCAAGAGCACTGAAGATA-3' (SEQ ID NO: 3188)
AR-2124 21 nt Target: 5'-CTGGCAGCGCTGCAGCAGGGA-3' (SEQ ID NO: 3189)
AR-2222 21 nt Target: 5'-AGTCGCGACTACTACAACTTT-3' (SEQ ID NO: 3190)
AR-2223 21 nt Target: 5'-GTCGCGACTACTACAACTTTC-3' (SEQ ID NO: 3191)
AR-2224 21 nt Target: 5'-TCGCGACTACTACAACTTTCC-3' (SEQ ID NO: 3192)
AR-2294 21 nt Target: 5'-GCTCGCATCAAGCTGGAGAAC-3' (SEQ ID NO: 3193)
AR-2317 21 nt Target: 5'-GCTGGACTACGGCAGCGCCTG-3' (SEQ ID NO: 3194)
AR-2318 21 nt Target: 5'-CTGGACTACGGCAGCGCCTGG-3' (SEQ ID NO: 3195)
AR-2319 21 nt Target: 5'-TGGACTACGGCAGCGCCTGGG-3' (SEQ ID NO: 3196)
AR-2320 21 nt Target: 5'-GGACTACGGCAGCGCCTGGGC-3' (SEQ ID NO: 3197)
AR-2386 21 nt Target: 5'-TGGCGCGGGTGCAGCGGGACC-3' (SEQ ID NO: 3198)
AR-2607 21 nt Target: 5'-GGCTGGCGGGCCAGGAAAGCG-3' (SEQ ID NO: 3199)
AR-2650 21 nt Target: 5'-GTACCCTGGCGGCATGGTGAG-3' (SEQ ID NO: 3200)
AR-2720 21 nt Target: 5'-TGGATGGATAGCTACTCCGGA-3' (SEQ ID NO: 3201)
AR-2808 21 nt Target: 5'-CCCAGAAGACCTGCCTGATCT-3' (SEQ ID NO: 3202)
AR-2809 21 nt Target: 5'-CCAGAAGACCTGCCTGATCTG-3' (SEQ ID NO: 3203)
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AR-2818 21 nt Target: 5'-CTGCCTGATCTGTGGAGATGA-3' (SEQ ID NO: 3212)
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AR-2822 21 nt Target: 5'-CTGATCTGTGGAGATGAAGCT-3' (SEQ ID NO: 3216)
AR-2823 21 nt Target: 5'-TGATCTGTGGAGATGAAGCTT-3' (SEQ ID NO: 3217)
AR-2824 21 nt Target: 5'-GATCTGTGGAGATGAAGCTTC-3' (SEQ ID NO: 3218)
AR-2825 21 nt Target: 5'-ATCTGTGGAGATGAAGCTTCT-3' (SEQ ID NO: 3219)
AR-2826 21 nt Target: 5'-TCTGTGGAGATGAAGCTTCTG-3' (SEQ ID NO: 3220)
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AR-2840 21 nt Target: 5'-GCTTCTGGGTGTCACTATGGA-3' (SEQ ID NO: 3222)
AR-2857 21 nt Target: 5'-TGGAGCTCTCACATGTGGAAG-3' (SEQ ID NO: 3223)
AR-2874 21 nt Target: 5'-GAAGCTGCAAGGTCTTCTTCA-3' (SEQ ID NO: 3224)
AR-2875 21 nt Target: 5'-AAGCTGCAAGGTCTTCTTCAA-3' (SEQ ID NO: 3225)
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AR-2880 21 nt Target: 5'-GCAAGGTCTTCTTCAAAAGAG-3' (SEQ ID NO: 3230)
AR-2881 21 nt Target: 5'-CAAGGTCTTCTTCAAAAGAGC-3' (SEQ ID NO: 3231)
AR-2882 21 nt Target: 5'-AAGGTCTTCTTCAAAAGAGCC-3' (SEQ ID NO: 3232)
AR-2883 21 nt Target: 5'-AGGTCTTCTTCAAAAGAGCCG-3' (SEQ ID NO: 3233)
AR-2884 21 nt Target: 5'-GGTCTTCTTCAAAAGAGCCGC-3' (SEQ ID NO: 3234)
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AR-2902 21 nt Target: 5'-CGCTGAAGGGAAACAGAAGTA-3' (SEQ ID NO: 3251)
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AR-2934 21 nt Target: 5'-GCAGAAATGATTGCACTATTG-3' (SEQ ID NO: 3253)
AR-2939 21 nt Target: 5'-AATGATTGCACTATTGATAAA-3' (SEQ ID NO: 3254)
AR-2947 21 nt Target: 5'-CACTATTGATAAATTCCGAAG-3' (SEQ ID NO: 3255)
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AR-2995 21 nt Target: 5'-GAAATGTTATGAAGCAGGGAT-3' (SEQ ID NO: 3260)
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AR-2998 21 nt Target: 5'-ATGTTATGAAGCAGGGATGAC-3' (SEQ ID NO: 3263)
AR-2999 21 nt Target: 5'-TGTTATGAAGCAGGGATGACT-3' (SEQ ID NO: 3264)
AR-3000 21 nt Target: 5'-GTTATGAAGCAGGGATGACTC-3' (SEQ ID NO: 3265)
AR-3001 21 nt Target: 5'-TTATGAAGCAGGGATGACTCT-3' (SEQ ID NO: 3266)
AR-3002 21 nt Target: 5'-TATGAAGCAGGGATGACTCTG-3' (SEQ ID NO: 3267)
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AR-3054 21 nt Target: 5'-TGAAACTACAGGAGGAAGGAG-3' (SEQ ID NO: 3274)
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AR-3134 21 nt Target: 5'-ATTGAAGGCTATGAATGTCAG-3' (SEQ ID NO: 3279)
AR-3135 21 nt Target: 5'-TTGAAGGCTATGAATGTCAGC-3' (SEQ ID NO: 3280)
AR-3136 21 nt Target: 5'-TGAAGGCTATGAATGTCAGCC-3' (SEQ ID NO: 3281)
AR-3168 21 nt Target: 5'-ATGTCCTGGAAGCCATTGAGC-3' (SEQ ID NO: 3282)
AR-3169 21 nt Target: 5'-TGTCCTGGAAGCCATTGAGCC-3' (SEQ ID NO: 3283)
AR-3170 21 nt Target: 5'-GTCCTGGAAGCCATTGAGCCA-3' (SEQ ID NO: 3284)
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AR-3457 21 nt Target: 5'-TGAGTACCGCATGCACAAGTC-3' (SEQ ID NO: 3332)
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AR-3514 21 nt Target: 5'-CTCTCAAGAGTTTGGATGGCT-3' (SEQ ID NO: 3334)
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AR-3518 21 nt Target: 5'-CAAGAGTTTGGATGGCTCCAA-3' (SEQ ID NO: 3338)
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AR-3581 21 nt Target: 5'-TTCAGCATTATTCCAGTGGAT-3' (SEQ ID NO: 3356)
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AR-3604 21 nt Target: 5'-GCTGAAAAATCAAAAATTCTT-3' (SEQ ID NO: 3379)
AR-3605 21 nt Target: 5'-CTGAAAAATCAAAAATTCTTT-3' (SEQ ID NO: 3380)
AR-3606 21 nt Target: 5'-TGAAAAATCAAAAATTCTTTG-3' (SEQ ID NO: 3381)
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AR-3613 21 nt Target: 5'-TCAAAAATTCTTTGATGAACT-3' (SEQ ID NO: 3387)
AR-3614 21 nt Target: 5'-CAAAAATTCTTTGATGAACTT-3' (SEQ ID NO: 3388)
AR-3615 21 nt Target: 5'-AAAAATTCTTTGATGAACTTC-3' (SEQ ID NO: 3389)
AR-3616 21 nt Target: 5'-AAAATTCTTTGATGAACTTCG-3' (SEQ ID NO: 3390)
AR-3617 21 nt Target: 5'-AAATTCTTTGATGAACTTCGA-3' (SEQ ID NO: 3391)
AR-3618 21 nt Target: 5'-AATTCTTTGATGAACTTCGAA-3' (SEQ ID NO: 3392)
AR-3619 21 nt Target: 5'-ATTCTTTGATGAACTTCGAAT-3' (SEQ ID NO: 3393)
AR-3620 21 nt Target: 5'-TTCTTTGATGAACTTCGAATG-3' (SEQ ID NO: 3394)
AR-3621 21 nt Target: 5'-TCTTTGATGAACTTCGAATGA-3' (SEQ ID NO: 3395)
AR-3622 21 nt Target: 5'-CTTTGATGAACTTCGAATGAA-3' (SEQ ID NO: 3396)
AR-3623 21 nt Target: 5'-TTTGATGAACTTCGAATGAAC-3' (SEQ ID NO: 3397)
AR-3624 21 nt Target: 5'-TTGATGAACTTCGAATGAACT-3' (SEQ ID NO: 3398)
AR-3625 21 nt Target: 5'-TGATGAACTTCGAATGAACTA-3' (SEQ ID NO: 3399)
AR-3626 21 nt Target: 5'-GATGAACTTCGAATGAACTAC-3' (SEQ ID NO: 3400)
AR-3627 21 nt Target: 5'-ATGAACTTCGAATGAACTACA-3' (SEQ ID NO: 3401)
AR-3628 21 nt Target: 5'-TGAACTTCGAATGAACTACAT-3' (SEQ ID NO: 3402)
AR-3629 21 nt Target: 5'-GAACTTCGAATGAACTACATC-3' (SEQ ID NO: 3403)
AR-3630 21 nt Target: 5'-AACTTCGAATGAACTACATCA-3' (SEQ ID NO: 3404)
AR-3631 21 nt Target: 5'-ACTTCGAATGAACTACATCAA-3' (SEQ ID NO: 3405)
AR-3632 21 nt Target: 5'-CTTCGAATGAACTACATCAAG-3' (SEQ ID NO: 3406)
AR-3633 21 nt Target: 5'-TTCGAATGAACTACATCAAGG-3' (SEQ ID NO: 3407)
AR-3634 21 nt Target: 5'-TCGAATGAACTACATCAAGGA-3' (SEQ ID NO: 3408)
AR-3635 21 nt Target: 5'-CGAATGAACTACATCAAGGAA-3' (SEQ ID NO: 3409)
AR-3636 21 nt Target: 5'-GAATGAACTACATCAAGGAAC-3' (SEQ ID NO: 3410)
AR-3637 21 nt Target: 5'-AATGAACTACATCAAGGAACT-3' (SEQ ID NO: 3411)
AR-3638 21 nt Target: 5'-ATGAACTACATCAAGGAACTC-3' (SEQ ID NO: 3412)
AR-3639 21 nt Target: 5'-TGAACTACATCAAGGAACTCG-3' (SEQ ID NO: 3413)
AR-3640 21 nt Target: 5'-GAACTACATCAAGGAACTCGA-3' (SEQ ID NO: 3414)
AR-3641 21 nt Target: 5'-AACTACATCAAGGAACTCGAT-3' (SEQ ID NO: 3415)
AR-3642 21 nt Target: 5'-ACTACATCAAGGAACTCGATC-3' (SEQ ID NO: 3416)
AR-3643 21 nt Target: 5'-CTACATCAAGGAACTCGATCG-3' (SEQ ID NO: 3417)
AR-3663 21 nt Target: 5'-GTATCATTGCATGCAAAAGAA-3' (SEQ ID NO: 3418)

AR-3664 21 nt Target: 5'-TATCATTGCATGCAAAAGAAA-3' (SEQ ID NO: 3419)
AR-3684 21 nt Target: 5'-AAAATCCCACATCCTGCTCAA-3' (SEQ ID NO: 3420)
AR-3685 21 nt Target: 5'-AAATCCCACATCCTGCTCAAG-3' (SEQ ID NO: 3421)
AR-3705 21 nt Target: 5'-GACGCTTCTACCAGCTCACCA-3' (SEQ ID NO: 3422)
AR-3706 21 nt Target: 5'-ACGCTTCTACCAGCTCACCAA-3' (SEQ ID NO: 3423)
AR-3707 21 nt Target: 5'-CGCTTCTACCAGCTCACCAAG-3' (SEQ ID NO: 3424)
AR-3708 21 nt Target: 5'-GCTTCTACCAGCTCACCAAGC-3' (SEQ ID NO: 3425)
AR-3709 21 nt Target: 5'-CTTCTACCAGCTCACCAAGCT-3' (SEQ ID NO: 3426)
AR-3710 21 nt Target: 5'-TTCTACCAGCTCACCAAGCTC-3' (SEQ ID NO: 3427)
AR-3711 21 nt Target: 5'-TCTACCAGCTCACCAAGCTCC-3' (SEQ ID NO: 3428)
AR-3712 21 nt Target: 5'-CTACCAGCTCACCAAGCTCCT-3' (SEQ ID NO: 3429)
AR-3713 21 nt Target: 5'-TACCAGCTCACCAAGCTCCTG-3' (SEQ ID NO: 3430)
AR-3714 21 nt Target: 5'-ACCAGCTCACCAAGCTCCTGG-3' (SEQ ID NO: 3431)
AR-3715 21 nt Target: 5'-CCAGCTCACCAAGCTCCTGGA-3' (SEQ ID NO: 3432)
AR-3717 21 nt Target: 5'-AGCTCACCAAGCTCCTGGACT-3' (SEQ ID NO: 3433)
AR-3726 21 nt Target: 5'-AGCTCCTGGACTCCGTGCAGC-3' (SEQ ID NO: 3434)
AR-3737 21 nt Target: 5'-TCCGTGCAGCCTATTGCGAGA-3' (SEQ ID NO: 3435)
AR-3753 21 nt Target: 5'-CGAGAGAGCTGCATCAGTTCA-3' (SEQ ID NO: 3436)
AR-3754 21 nt Target: 5'-GAGAGAGCTGCATCAGTTCAC-3' (SEQ ID NO: 3437)
AR-3755 21 nt Target: 5'-AGAGAGCTGCATCAGTTCACT-3' (SEQ ID NO: 3438)
AR-3756 21 nt Target: 5'-GAGAGCTGCATCAGTTCACTT-3' (SEQ ID NO: 3439)
AR-3757 21 nt Target: 5'-AGAGCTGCATCAGTTCACTTT-3' (SEQ ID NO: 3440)
AR-3758 21 nt Target: 5'-GAGCTGCATCAGTTCACTTTT-3' (SEQ ID NO: 3441)
AR-3759 21 nt Target: 5'-AGCTGCATCAGTTCACTTTTG-3' (SEQ ID NO: 3442)
AR-3760 21 nt Target: 5'-GCTGCATCAGTTCACTTTTGA-3' (SEQ ID NO: 3443)
AR-3761 21 nt Target: 5'-CTGCATCAGTTCACTTTTGAC-3' (SEQ ID NO: 3444)
AR-3762 21 nt Target: 5'-TGCATCAGTTCACTTTTGACC-3' (SEQ ID NO: 3445)
AR-3763 21 nt Target: 5'-GCATCAGTTCACTTTTGACCT-3' (SEQ ID NO: 3446)
AR-3764 21 nt Target: 5'-CATCAGTTCACTTTTGACCTG-3' (SEQ ID NO: 3447)
AR-3765 21 nt Target: 5'-ATCAGTTCACTTTTGACCTGC-3' (SEQ ID NO: 3448)
AR-3766 21 nt Target: 5'-TCAGTTCACTTTTGACCTGCT-3' (SEQ ID NO: 3449)
AR-3767 21 nt Target: 5'-CAGTTCACTTTTGACCTGCTA-3' (SEQ ID NO: 3450)
AR-3768 21 nt Target: 5'-AGTTCACTTTTGACCTGCTAA-3' (SEQ ID NO: 3451)
AR-3769 21 nt Target: 5'-GTTCACTTTTGACCTGCTAAT-3' (SEQ ID NO: 3452)
AR-3770 21 nt Target: 5'-TTCACTTTTGACCTGCTAATC-3' (SEQ ID NO: 3453)
AR-3771 21 nt Target: 5'-TCACTTTTGACCTGCTAATCA-3' (SEQ ID NO: 3454)
AR-3772 21 nt Target: 5'-CACTTTTGACCTGCTAATCAA-3' (SEQ ID NO: 3455)
AR-3773 21 nt Target: 5'-ACTTTTGACCTGCTAATCAAG-3' (SEQ ID NO: 3456)
AR-3798 21 nt Target: 5'-ACATGGTGAGCGTGGACTTTC-3' (SEQ ID NO: 3457)
AR-3799 21 nt Target: 5'-CATGGTGAGCGTGGACTTTCC-3' (SEQ ID NO: 3458)
AR-3819 21 nt Target: 5'-CGGAAATGATGGCAGAGATCA-3' (SEQ ID NO: 3459)
AR-3820 21 nt Target: 5'-GGAAATGATGGCAGAGATCAT-3' (SEQ ID NO: 3460)
AR-3821 21 nt Target: 5'-GAAATGATGGCAGAGATCATC-3' (SEQ ID NO: 3461)
AR-3822 21 nt Target: 5'-AAATGATGGCAGAGATCATCT-3' (SEQ ID NO: 3462)
AR-3823 21 nt Target: 5'-AATGATGGCAGAGATCATCTC-3' (SEQ ID NO: 3463)
AR-3824 21 nt Target: 5'-ATGATGGCAGAGATCATCTCT-3' (SEQ ID NO: 3464)
AR-3825 21 nt Target: 5'-TGATGGCAGAGATCATCTCTG-3' (SEQ ID NO: 3465)
AR-3826 21 nt Target: 5'-GATGGCAGAGATCATCTCTGT-3' (SEQ ID NO: 3466)
AR-3827 21 nt Target: 5'-ATGGCAGAGATCATCTCTGTG-3' (SEQ ID NO: 3467)
AR-3828 21 nt Target: 5'-TGGCAGAGATCATCTCTGTGC-3' (SEQ ID NO: 3468)
AR-3829 21 nt Target: 5'-GGCAGAGATCATCTCTGTGCA-3' (SEQ ID NO: 3469)
AR-3830 21 nt Target: 5'-GCAGAGATCATCTCTGTGCAA-3' (SEQ ID NO: 3470)
AR-3831 21 nt Target: 5'-CAGAGATCATCTCTGTGCAAG-3' (SEQ ID NO: 3471)
AR-3832 21 nt Target: 5'-AGAGATCATCTCTGTGCAAGT-3' (SEQ ID NO: 3472)
AR-3833 21 nt Target: 5'-GAGATCATCTCTGTGCAAGTG-3' (SEQ ID NO: 3473)
AR-3834 21 nt Target: 5'-AGATCATCTCTGTGCAAGTGC-3' (SEQ ID NO: 3474)
AR-3835 21 nt Target: 5'-GATCATCTCTGTGCAAGTGCC-3' (SEQ ID NO: 3475)
AR-3836 21 nt Target: 5'-ATCATCTCTGTGCAAGTGCCC-3' (SEQ ID NO: 3476)
AR-3837 21 nt Target: 5'-TCATCTCTGTGCAAGTGCCCA-3' (SEQ ID NO: 3477)
AR-3838 21 nt Target: 5'-CATCTCTGTGCAAGTGCCCAA-3' (SEQ ID NO: 3478)
AR-3839 21 nt Target: 5'-ATCTCTGTGCAAGTGCCCAAG-3' (SEQ ID NO: 3479)

AR-3840 21 nt Target: 5'-TCTCTGTGCAAGTGCCCAAGA-3' (SEQ ID NO: 3480)
AR-3841 21 nt Target: 5'-CTCTGTGCAAGTGCCCAAGAT-3' (SEQ ID NO: 3481)
AR-3842 21 nt Target: 5'-TCTGTGCAAGTGCCCAAGATC-3' (SEQ ID NO: 3482)
AR-3843 21 nt Target: 5'-CTGTGCAAGTGCCCAAGATCC-3' (SEQ ID NO: 3483)
AR-3844 21 nt Target: 5'-TGTGCAAGTGCCCAAGATCCT-3' (SEQ ID NO: 3484)
AR-3845 21 nt Target: 5'-GTGCAAGTGCCCAAGATCCTT-3' (SEQ ID NO: 3485)
AR-3846 21 nt Target: 5'-TGCAAGTGCCCAAGATCCTTT-3' (SEQ ID NO: 3486)
AR-3847 21 nt Target: 5'-GCAAGTGCCCAAGATCCTTTC-3' (SEQ ID NO: 3487)
AR-3848 21 nt Target: 5'-CAAGTGCCCAAGATCCTTTCT-3' (SEQ ID NO: 3488)
AR-3849 21 nt Target: 5'-AAGTGCCCAAGATCCTTTCTG-3' (SEQ ID NO: 3489)
AR-3850 21 nt Target: 5'-AGTGCCCAAGATCCTTTCTGG-3' (SEQ ID NO: 3490)
AR-3851 21 nt Target: 5'-GTGCCCAAGATCCTTTCTGGG-3' (SEQ ID NO: 3491)
AR-3852 21 nt Target: 5'-TGCCCAAGATCCTTTCTGGGA-3' (SEQ ID NO: 3492)
AR-3853 21 nt Target: 5'-GCCCAAGATCCTTTCTGGGAA-3' (SEQ ID NO: 3493)
AR-3854 21 nt Target: 5'-CCCAAGATCCTTTCTGGGAAA-3' (SEQ ID NO: 3494)
AR-3855 21 nt Target: 5'-CCAAGATCCTTTCTGGGAAAG-3' (SEQ ID NO: 3495)
AR-3856 21 nt Target: 5'-CAAGATCCTTTCTGGGAAAGT-3' (SEQ ID NO: 3496)
AR-3857 21 nt Target: 5'-AAGATCCTTTCTGGGAAAGTC-3' (SEQ ID NO: 3497)
AR-3858 21 nt Target: 5'-AGATCCTTTCTGGGAAAGTCA-3' (SEQ ID NO: 3498)
AR-3859 21 nt Target: 5'-GATCCTTTCTGGGAAAGTCAA-3' (SEQ ID NO: 3499)
AR-3860 21 nt Target: 5'-ATCCTTTCTGGGAAAGTCAAG-3' (SEQ ID NO: 3500)
AR-3861 21 nt Target: 5'-TCCTTTCTGGGAAAGTCAAGC-3' (SEQ ID NO: 3501)
AR-3862 21 nt Target: 5'-CCTTTCTGGGAAAGTCAAGCC-3' (SEQ ID NO: 3502)
AR-3863 21 nt Target: 5'-CTTTCTGGGAAAGTCAAGCCC-3' (SEQ ID NO: 3503)
AR-3864 21 nt Target: 5'-TTTCTGGGAAAGTCAAGCCCA-3' (SEQ ID NO: 3504)
AR-3865 21 nt Target: 5'-TTCTGGGAAAGTCAAGCCCAT-3' (SEQ ID NO: 3505)
AR-3866 21 nt Target: 5'-TCTGGGAAAGTCAAGCCCATC-3' (SEQ ID NO: 3506)
AR-3867 21 nt Target: 5'-CTGGGAAAGTCAAGCCCATCT-3' (SEQ ID NO: 3507)
AR-3868 21 nt Target: 5'-TGGGAAAGTCAAGCCCATCTA-3' (SEQ ID NO: 3508)
AR-3869 21 nt Target: 5'-GGGAAAGTCAAGCCCATCTAT-3' (SEQ ID NO: 3509)
AR-3870 21 nt Target: 5'-GGAAAGTCAAGCCCATCTATT-3' (SEQ ID NO: 3510)
AR-3871 21 nt Target: 5'-GAAAGTCAAGCCCATCTATTT-3' (SEQ ID NO: 3511)
AR-3947 21 nt Target: 5'-TTCAGATGTCTTCTGCCTGTT-3' (SEQ ID NO: 3512)
AR-3948 21 nt Target: 5'-TCAGATGTCTTCTGCCTGTTA-3' (SEQ ID NO: 3513)
AR-3949 21 nt Target: 5'-CAGATGTCTTCTGCCTGTTAT-3' (SEQ ID NO: 3514)
AR-3950 21 nt Target: 5'-AGATGTCTTCTGCCTGTTATA-3' (SEQ ID NO: 3515)
AR-3999 21 nt Target: 5'-GGGGAATTTCCTCTATTGATG-3' (SEQ ID NO: 3516)
AR-4054 21 nt Target: 5'-TTGCTGGGCTTTTTTTTTCTC-3' (SEQ ID NO: 3517)
AR-4055 21 nt Target: 5'-TGCTGGGCTTTTTTTTTCTCT-3' (SEQ ID NO: 3518)
AR-4061 21 nt Target: 5'-GCTTTTTTTTTCTCTTTCTCT-3' (SEQ ID NO: 3519)
AR-4066 21 nt Target: 5'-TTTTTTCTCTTTCTCTCCTTT-3' (SEQ ID NO: 3520)
AR-4086 21 nt Target: 5'-TCTTTTTCTTCTTCCCTCCCT-3' (SEQ ID NO: 3521)
AR-4174 21 nt Target: 5'-TGTTGTATGCCTTTAAATCTG-3' (SEQ ID NO: 3522)
AR-4225 21 nt Target: 5'-TGTGCTTGTTTACAGCACTAC-3' (SEQ ID NO: 3523)
AR-4293 21 nt Target: 5'-TTAGAGAGCTAAGATTATCTG-3' (SEQ ID NO: 3524)
AR-4313 21 nt Target: 5'-GGGGAAATCAAAACAAAAACA-3' (SEQ ID NO: 3525)
AR-m258 21 nt Target: 5'-GGCAGCAGCACACTGAGGATG-3' (SEQ ID NO: 3718)
AR-m361 21 nt Target: 5'-CTCCGAGGGCCACCCTGAGAG-3' (SEQ ID NO: 3719)
AR-m367 21 nt Target: 5'-GGGCCACCCTGAGAGCAGCTG-3' (SEQ ID NO: 3720)
AR-m426 21 nt Target: 5'-GGCTGCCGCAGCAGCCACCAG-3' (SEQ ID NO: 3721)
AR-m502 21 nt Target: 5'-CACTTTCCCAGGCTTAAGCAG-3' (SEQ ID NO: 3722)
AR-m566 21 nt Target: 5'-ATGCAACTTCTTCAGCAGCAG-3' (SEQ ID NO: 3723)
AR-m872 21 nt Target: 5'-GTGCGTCCCACTCCTTGTGCG-3' (SEQ ID NO: 3724)
AR-m1020 21 nt Target: 5'-CTGGCAGCAGTGAAGCAGGTA-3' (SEQ ID NO: 3725)
AR-m1136 21 nt Target: 5'-TTTCCGCTGGCTCTGTCCGGG-3' (SEQ ID NO: 3726)
AR-m1224 21 nt Target: 5'-GCAGCGCCTGGGCTGCGGCGG-3' (SEQ ID NO: 3727)
AR-m1229 21 nt Target: 5'-GCCTGGGCTGCGGCGGCAGCG-3' (SEQ ID NO: 3728)
AR-m1236 21 nt Target: 5'-CTGCGGCGGCAGCGCAATGCC-3' (SEQ ID NO: 3729)
AR-m1291 21 nt Target: 5'-TGTAGCCGGGCCCAGCACTGG-3' (SEQ ID NO: 3730)
AR-m1335 21 nt Target: 5'-CTTCCTGGCATACTCTCTTCA-3' (SEQ ID NO: 3731)
AR-m1403 21 nt Target: 5'-AGCAGCCCAAGCGATGCCGGG-3' (SEQ ID NO: 3732)

AR-m1694 21 nt Target: 5'-GCTTCTGGCTGTCACTACGGA-3' (SEQ ID NO: 3733)
AR-m1711 21 nt Target: 5'-CGGAGCTCTCACTTGTGGCAG-3' (SEQ ID NO: 3734)
AR-m1720 21 nt Target: 5'-CACTTGTGGCAGCTGCAAGGT-3' (SEQ ID NO: 3735)
AR-m1725 21 nt Target: 5'-GTGGCAGCTGCAAGGTCTTCT-3' (SEQ ID NO: 3736)
AR-m1865 21 nt Target: 5'-GGGATGACTCTGGGAGCTCGT-3' (SEQ ID NO: 3737)
AR-m1874 21 nt Target: 5'-CTGGGAGCTCGTAAGCTGAAG-3' (SEQ ID NO: 3738)
AR-m2079 21 nt Target: 5'-CAGATTCCTTTGCTGCCTTGT-3' (SEQ ID NO: 3739)
AR-m2086 21 nt Target: 5'-CTTTGCTGCCTTGTTATCTAG-3' (SEQ ID NO: 3740)
AR-m2162 21 nt Target: 5'-TTGCCTGGCTTCCGCAACTTG-3' (SEQ ID NO: 3741)
AR-m2219 21 nt Target: 5'-TGGATGGGACTGATGGTATTT-3' (SEQ ID NO: 3742)
AR-m2275 21 nt Target: 5'-CAGGATGCTCTACTTTGCACC-3' (SEQ ID NO: 3743)
AR-m2280 21 nt Target: 5'-TGCTCTACTTTGCACCTGACT-3' (SEQ ID NO: 3744)
AR-m2287 21 nt Target: 5'-CTTTGCACCTGACTTGGTTTT-3' (SEQ ID NO: 3745)
AR-m2297 21 nt Target: 5'-GACTTGGTTTTCAATGAGTAC-3' (SEQ ID NO: 3746)
AR-m2312 21 nt Target: 5'-GAGTACCGCATGCACAAGTCT-3' (SEQ ID NO: 3747)
AR-m2411 21 nt Target: 5'-CTGTGCATGAAAGCACTGCTG-3' (SEQ ID NO: 3748)
AR-m2416 21 nt Target: 5'-CATGAAAGCACTGCTGCTCTT-3' (SEQ ID NO: 3749)
AR-m2422 21 nt Target: 5'-AGCACTGCTGCTCTTCAGCAT-3' (SEQ ID NO: 3750)
AR-m2427 21 nt Target: 5'-TGCTGCTCTTCAGCATTATTC-3' (SEQ ID NO: 3751)
AR-m2571 21 nt Target: 5'-AGCTCACCAAGCTCCTGGATT-3' (SEQ ID NO: 3752)
AR-m2580 21 nt Target: 5'-AGCTCCTGGATTCTGTGCAGC-3' (SEQ ID NO: 3753)
AR-m2585 21 nt Target: 5'-CTGGATTCTGTGCAGCCTATT-3' (SEQ ID NO: 3754)
AR-m2591 21 nt Target: 5'-TCTGTGCAGCCTATTGCAAGA-3' (SEQ ID NO: 3755)
AR-m2597 21 nt Target: 5'-CAGCCTATTGCAAGAGAGCTG-3' (SEQ ID NO: 3756)
AR-m2661 21 nt Target: 5'-GCGTGGACTTTCCTGAAATGA-3' (SEQ ID NO: 3757)
AR-m2809 21 nt Target: 5'-TCTTCTGCCTGTTATATAACT-3' (SEQ ID NO: 3758)
AR-m2831 21 nt Target: 5'-TGCACTACTTCTCTGCAGTGC-3' (SEQ ID NO: 3759)
AR-m2912 21 nt Target: 5'-TCCTGGGCTTCTCCTTCTTTT-3' (SEQ ID NO: 3760)
AR-m2918 21 nt Target: 5'-GCTTCTCCTTCTTTTTTTTC-3' (SEQ ID NO: 3761)
AR-m2926 21 nt Target: 5'-TTCTTTTTTTTCTTCTTCCC-3' (SEQ ID NO: 3762)
AR-m2981 21 nt Target: 5'-CTGCTGCGTATTGTGGCTCCT-3' (SEQ ID NO: 3763)
AR-m2992 21 nt Target: 5'-TGTGGCTCCTGCCTTTGTTT-3' (SEQ ID NO: 3764)
AR-m2997 21 nt Target: 5'-CTCCTGCCTTTGTTTTGATTT-3' (SEQ ID NO: 3765)

Within Tables 2 and 3 above and Tables 5-12 below, underlined residues indicate 2'-O-methyl residues, UPPER CASE indicates ribonucleotides, and lower case denotes deoxyribonucleotides. The DsiRNA agents of Tables 2-3 above and 9-12 below are 25/27mer agents possessing a blunt end. The structures and/or modification patterning of the agents of Tables 2-3 above and 9-12 below can be readily adapted to the above generic sequence structures, *e.g.*, the 3' overhang of the second strand can be extended or contracted, 2'-O-methylation of the second strand can be expanded towards the 5' end of the second strand, optionally at alternating sites, etc. Such further modifications are optional, as 25/27mer DsiRNAs with such modifications can also be readily designed from the above DsiRNA agents and are also expected to be functional inhibitors of AR expression. Similarly, the 27mer "blunt/fray" and "blunt/blunt" DsiRNA structures and/or modification patterns of the agents of of Tables 5-8 below can also be readily adapted to the above generic sequence structures, *e.g.*, for application of modification patterning of the antisense

strand to such structures and/or adaptation of such sequences to the above generic structures.

In certain embodiments, 27mer DsiRNAs possessing independent strand lengths each of 27 nucleotides are designed and synthesized for targeting of the same sites within the AR transcript as the asymmetric "25/27" structures shown in Tables 2-3 and 9-12 herein. Exemplary "27/27" DsiRNAs are optionally designed with a "blunt/fray" structure as shown for the DsiRNAs of Tables 5 and 6 below, or with a "blunt/blunt" structure as shown for the DsiRNAs of Tables 7 and 8 below.

Table 5: Selected Human Anti-AR 27mer "Blunt/Fray" DsiRNA Agents

5'-UGAAGUUUUUAAAAGCUGCUAAAGA$^{AC-3'}$ (SEQ ID NO: 3784)
3'-ACUUCAAAAAUUUUCGACGAUUUCU$_{GA-5'}$ (SEQ ID NO: 154)

AR-252 Target: 5'-TGAAGTTTTTAAAAGCTGCTAAAGACT-3' (SEQ ID NO: 307)

5'-GAAGUUUUUAAAAGCUGCUAAAGAC$^{CA-3'}$ (SEQ ID NO: 3785)
3'-CUUCAAAAAUUUUCGACGAUUUCUG$_{AG-5'}$ (SEQ ID NO: 155)

AR-253 Target: 5'-GAAGTTTTTAAAAGCTGCTAAAGACTC-3' (SEQ ID NO: 308)

5'-AAGUUUUUAAAAGCUGCUAAAGACU$^{AA-3'}$ (SEQ ID NO: 3786)
3'-UUCAAAAAUUUUCGACGAUUUCUGA$_{GC-5'}$ (SEQ ID NO: 156)

AR-254 Target: 5'-AAGTTTTTAAAAGCTGCTAAAGACTCG-3' (SEQ ID NO: 309)

5'-UGCGGAGCCAGAGAUCAAAAGAUGA$^{CC-3'}$ (SEQ ID NO: 3787)
3'-ACGCCUCGGUCUCUAGUUUUCUACU$_{UU-5'}$ (SEQ ID NO: 157)

AR-682 Target: 5'-TGCGGAGCCAGAGATCAAAAGATGAAA-3' (SEQ ID NO: 310)

5'-GCCAGAGAUCAAAAGAUGAAAAGGC$^{CA-3'}$ (SEQ ID NO: 3788)
3'-CGGUCUCUAGUUUUCUACUUUUCCG$_{UC-5'}$ (SEQ ID NO: 158)

AR-688 Target: 5'-GCCAGAGATCAAAAGATGAAAAGGCAG-3' (SEQ ID NO: 311)

5'-CCAGAGAUCAAAAGAUGAAAAGGCA$^{AC-3'}$ (SEQ ID NO: 3789)
3'-GGUCUCUAGUUUUCUACUUUUCCGU$_{CA-5'}$ (SEQ ID NO: 159)

AR-689 Target: 5'-CCAGAGATCAAAAGATGAAAAGGCAGT-3' (SEQ ID NO: 312)

5'-CAAAAGAUGAAAAGGCAGUCAGGUC$^{CC-3'}$ (SEQ ID NO: 3790)
3'-GUUUUCUACUUUUCCGUCAGUCCAG$_{AA-5'}$ (SEQ ID NO: 160)

AR-697 Target: 5'-CAAAAGATGAAAAGGCAGTCAGGTCTT-3' (SEQ ID NO: 313)

5'-AAAAGAUGAAAAGGCAGUCAGGUCU$^{CA-3'}$ (SEQ ID NO: 3791)
3'-UUUUCUACUUUUCCGUCAGUCCAGA$_{AG-5'}$ (SEQ ID NO: 161)

AR-698 Target: 5'-AAAAGATGAAAAGGCAGTCAGGTCTTC-3' (SEQ ID NO: 314)

5'-GUCAGGUCUUCAGUAGCCAAAAAAC$^{CC-3'}$ (SEQ ID NO: 3792)
3'-CAGUCCAGAAGUCAUCGGUUUUUUG$_{UU-5'}$ (SEQ ID NO: 162)

AR-714 Target: 5'-GTCAGGTCTTCAGTAGCCAAAAAACAA-3' (SEQ ID NO: 315)

5'-UCAGGUCUUCAGUAGCCAAAAAACA$^{CC-3'}$ (SEQ ID NO: 3793)
3'-AGUCCAGAAGUCAUCGGUUUUUUGU$_{UU-5'}$ (SEQ ID NO: 163)

AR-715 Target: 5'-TCAGGTCTTCAGTAGCCAAAAAACAAA-3' (SEQ ID NO: 316)

5'-CAGUAGCCAAAAAACAAAACAAACA$^{CC-3'}$ (SEQ ID NO: 3794)
3'-GUCAUCGGUUUUUUGUUUUGUUUGU$_{UU-5'}$ (SEQ ID NO: 164)

AR-724 Target: 5'-CAGTAGCCAAAAAACAAAACAAACAAA-3' (SEQ ID NO: 317)

5'-GCCAAAAAACAAAACAAACAAAAAC$^{CC-3'}$ (SEQ ID NO: 3795)
3'-CGGUUUUUUGUUUUGUUUGUUUUUG$_{UU-5'}$ (SEQ ID NO: 165)

AR-729 Target: 5'-GCCAAAAAACAAAACAAACAAAAACAA-3' (SEQ ID NO: 318)

5'-CCAAAAAACAAAACAAACAAAAACA$^{CC-3'}$ (SEQ ID NO: 3796)
3'-GGUUUUUUGUUUUGUUUGUUUUUGU$_{UU-5'}$ (SEQ ID NO: 166)

AR-730 Target: 5'-CCAAAAAACAAAACAAACAAAAACAAA-3' (SEQ ID NO: 319)

5'-ACAAAACAAACAAAAACAAAAAAGC$^{AA-3'}$ (SEQ ID NO: 3797)
3'-UGUUUUGUUUGUUUUUGUUUUUUCG$_{GC-5'}$ (SEQ ID NO: 167)

AR-737 Target: 5'-ACAAAACAAACAAAAACAAAAAAGCCG-3' (SEQ ID NO: 320)

5'-AACAAAAACAAAAAAGCCGAAAUAA$^{CC-3'}$ (SEQ ID NO: 3798)
3'-UUGUUUUUGUUUUUUCGGCUUUAUU$_{UU-5'}$ (SEQ ID NO: 168)

AR-745 Target: 5'-AACAAAAACAAAAAAGCCGAAATAAAA-3' (SEQ ID NO: 321)

5'-ACAAAAACAAAAAAGCCGAAAUAAA$^{CA-3'}$ (SEQ ID NO: 3799)
3'-UGUUUUUGUUUUUUCGGCUUUAUUU$_{UC-5'}$ (SEQ ID NO: 169)

AR-746 Target: 5'-ACAAAAACAAAAAAGCCGAAATAAAAG-3' (SEQ ID NO: 322)

5'-CAAAAACAAAAAAGCCGAAAUAAAA$^{AC-3'}$ (SEQ ID NO: 3800)
3'-GUUUUUGUUUUUUCGGCUUUAUUUU$_{CU-5'}$ (SEQ ID NO: 170)

AR-747 Target: 5'-CAAAAACAAAAAAGCCGAAATAAAAGA-3' (SEQ ID NO: 323)

5'-ACAAAAAAGCCGAAAUAAAAGAAAA$^{CA-3'}$ (SEQ ID NO: 3801)
3'-UGUUUUUUCGGCUUUAUUUUCUUUU$_{UC-5'}$ (SEQ ID NO: 171)

AR-752 Target: 5'-ACAAAAAAGCCGAAATAAAAGAAAAAG-3' (SEQ ID NO: 324)

5'-CAAAAAAGCCGAAAUAAAAGAAAAA$^{AC-3'}$ (SEQ ID NO: 3802)
3'-GUUUUUUCGGCUUUAUUUUCUUUUU$_{CU-5'}$ (SEQ ID NO: 172)

AR-753 Target: 5'-CAAAAAAGCCGAAATAAAAGAAAAAAGA-3' (SEQ ID NO: 325)

5'-AAAAAGCCGAAAUAAAAGAAAAAGA$^{CC-3'}$ (SEQ ID NO: 3803)
3'-UUUUUCGGCUUUAUUUUCUUUUUCU$_{AU-5'}$ (SEQ ID NO: 173)

AR-755 Target: 5'-AAAAAGCCGAAATAAAAGAAAAAGATA-3' (SEQ ID NO: 326)

5'-GCCGAAAUAAAAGAAAAAGAUAAUA$^{CA-3'}$ (SEQ ID NO: 3804)
3'-CGGCUUUAUUUUCUUUUUCUAUUAU$_{UG-5'}$ (SEQ ID NO: 174)

AR-760 Target: 5'-GCCGAAATAAAAGAAAAAGATAATAAC-3' (SEQ ID NO: 327)

5'-CCGAAAUAAAAGAAAAAGAUAAUAA$^{AC-3'}$ (SEQ ID NO: 3805)
3'-GGCUUUAUUUUCUUUUUCUAUUAUU$_{GA-5'}$ (SEQ ID NO: 175)

AR-761 Target: 5'-CCGAAATAAAAGAAAAAGATAATAACT-3' (SEQ ID NO: 328)

5'-CGAAAUAAAAGAAAAAGAUAAUAAC$^{CA-3'}$ (SEQ ID NO: 3806)
3'-GCUUUAUUUUCUUUUUCUAUUAUUG$_{AG-5'}$ (SEQ ID NO: 176)

AR-762 Target: 5'-CGAAATAAAAGAAAAAGATAATAACTC-3' (SEQ ID NO: 329)

5'-AAGAAAAAGAUAAUAACUCAGUUCU$^{CC-3'}$ (SEQ ID NO: 3807)
3'-UUCUUUUUCUAUUAUUGAGUCAAGA$_{AU-5'}$ (SEQ ID NO: 177)

AR-770 Target: 5'-AAGAAAAAGATAATAACTCAGTTCTTA-3' (SEQ ID NO: 330)

5'-AAAAGAUAAUAACUCAGUUCUUAUU$^{CA-3'}$ (SEQ ID NO: 3808)
3'-UUUUCUAUUAUUGAGUCAAGAAUAA$_{AC-5'}$ (SEQ ID NO: 178)

AR-774 Target: 5'-AAAAGATAATAACTCAGTTCTTATTTG-3' (SEQ ID NO: 331)

5'-AAAGAUAAUAACUCAGUUCUUAUUU$^{AA-3'}$ (SEQ ID NO: 3809)
3'-UUUCUAUUAUUGAGUCAAGAAUAAA$_{CG-5'}$ (SEQ ID NO: 179)

AR-775 Target: 5'-AAAGATAATAACTCAGTTCTTATTTGC-3' (SEQ ID NO: 332)

5'-AGAUAAUAACUCAGUUCUUAUUUGC$^{CA-3'}$ (SEQ ID NO: 3810)
3'-UCUAUUAUUGAGUCAAGAAUAAACG$_{UG-5'}$ (SEQ ID NO: 180)

AR-777 Target: 5'-AGATAATAACTCAGTTCTTATTTGCAC-3' (SEQ ID NO: 333)

5'-GAUAAUAACUCAGUUCUUAUUUGCA$^{AA-3'}$ (SEQ ID NO: 3811)
3'-CUAUUAUUGAGUCAAGAAUAAACGU$_{GG-5'}$ (SEQ ID NO: 181)

AR-778 Target: 5'-GATAATAACTCAGTTCTTATTTGCACC-3' (SEQ ID NO: 334)

5'-UCUUAUUUGCACCUACUUCAGUGGA$^{AC-3'}$ (SEQ ID NO: 3812)
3'-AGAAUAAACGUGGAUGAAGUCACCU$_{GU-5'}$ (SEQ ID NO: 182)

AR-792 Target: 5'-TCTTATTTGCACCTACTTCAGTGGACA-3' (SEQ ID NO: 335)

5'-UCAGUGGACACUGAAUUUGGAAGGU$^{AA-3'}$ (SEQ ID NO: 3813)
3'-AGUCACCUGUGACUUAAACCUUCCA$_{CC-5'}$ (SEQ ID NO: 183)

AR-809 Target: 5'-TCAGTGGACACTGAATTTGGAAGGTGG-3' (SEQ ID NO: 336)

5'-CACUGAAUUUGGAAGGUGGAGGAUU$^{C}{}^{C-3'}$ (SEQ ID NO: 3814)
3'-GUGACUUAAACCUUCCACCUCCUAA$_{A}{}_{A-5'}$ (SEQ ID NO: 184)

AR-817 Target: 5'-CACTGAATTTGGAAGGTGGAGGATTTT-3' (SEQ ID NO: 337)

5'-UUUGGAAGGUGGAGGAUUUUGUUUU$^{C}{}^{C-3'}$ (SEQ ID NO: 3815)
3'-AAACCUUCCACCUCCUAAAACAAAA$_{A}{}_{A-5'}$ (SEQ ID NO: 185)

AR-824 Target: 5'-TTTGGAAGGTGGAGGATTTTGTTTTTT-3' (SEQ ID NO: 338)

5'-GGAAGGUGGAGGAUUUUGUUUUUUU$^{A}{}^{C-3'}$ (SEQ ID NO: 3816)
3'-CCUUCCACCUCCUAAAACAAAAAAA$_{G}{}_{A-5'}$ (SEQ ID NO: 186)

AR-827 Target: 5'-GGAAGGTGGAGGATTTTGTTTTTTTCT-3' (SEQ ID NO: 339)

5'-UGGAGGAUUUUGUUUUUUUCUUUUA$^{C}{}^{A-3'}$ (SEQ ID NO: 3817)
3'-ACCUCCUAAAACAAAAAAAGAAAAU$_{U}{}_{C-5'}$ (SEQ ID NO: 187)

AR-833 Target: 5'-TGGAGGATTTTGTTTTTTTCTTTTAAG-3' (SEQ ID NO: 340)

5'-GGAGGAUUUUGUUUUUUUCUUUUAA$^{A}{}^{C-3'}$ (SEQ ID NO: 3818)
3'-CCUCCUAAAACAAAAAAAGAAAAUU$_{C}{}_{U-5'}$ (SEQ ID NO: 188)

AR-834 Target: 5'-GGAGGATTTTGTTTTTTTCTTTTAAGA-3' (SEQ ID NO: 341)

5'-AGGAUUUUGUUUUUUUCUUUUAAGA$^{C}{}^{A-3'}$ (SEQ ID NO: 3819)
3'-UCCUAAAACAAAAAAAGAAAAUUCU$_{A}{}_{G-5'}$ (SEQ ID NO: 189)

AR-836 Target: 5'-AGGATTTTGTTTTTTTCTTTTAAGATC-3' (SEQ ID NO: 342)

5'-GGAUUUUGUUUUUUUCUUUUAAGAU$^{A}{}^{C-3'}$ (SEQ ID NO: 3820)
3'-CCUAAAACAAAAAAAGAAAAUUCUA$_{G}{}_{A-5'}$ (SEQ ID NO: 190)

AR-837 Target: 5'-GGATTTTGTTTTTTTCTTTTAAGATCT-3' (SEQ ID NO: 343)

5'-GAUUUUGUUUUUUUCUUUUAAGAUC$^{C}{}^{A-3'}$ (SEQ ID NO: 3821)
3'-CUAAAACAAAAAAAGAAAAUUCUAG$_{A}{}_{C-5'}$ (SEQ ID NO: 191)

AR-838 Target: 5'-GATTTTGTTTTTTTCTTTTAAGATCTG-3' (SEQ ID NO: 344)

5'-AUUUUGUUUUUUUCUUUUAAGAUCU$^{A}{}^{A-3'}$ (SEQ ID NO: 3822)
3'-UAAAACAAAAAAAGAAAAUUCUAGA$_{C}{}_{C-5'}$ (SEQ ID NO: 192)

AR-839 Target: 5'-ATTTTGTTTTTTTCTTTTAAGATCTGG-3' (SEQ ID NO: 345)

5'-UGUUUUUUUCUUUUAAGAUCUGGGC$^{C}{}^{C-3'}$ (SEQ ID NO: 3823)
3'-ACAAAAAAAGAAAAUUCUAGACCCG$_{U}{}_{A-5'}$ (SEQ ID NO: 193)

AR-843 Target: 5'-TGTTTTTTCTTTTAAGATCTGGGCAT-3' (SEQ ID NO: 346)

5'-GUUUUUUUCUUUUAAGAUCUGGGCA$^{C}{}^{A-3'}$ (SEQ ID NO: 3824)
3'-CAAAAAAAGAAAAUUCUAGACCCGU$_{A}{}_{G-5'}$ (SEQ ID NO: 194)

AR-844 Target: 5'-GTTTTTTCTTTTAAGATCTGGGCATC-3' (SEQ ID NO: 347)

5'-UUUAAGAUCUGGGCAUCUUUUGAAU$^{AC-3'}$ (SEQ ID NO: 3825)
3'-AAAUUCUAGACCCGUAGAAAACUUA$_{GA-5'}$ (SEQ ID NO: 195)

AR-854 Target: 5'-TTTAAGATCTGGGCATCTTTTGAATCT-3' (SEQ ID NO: 348)

5'-AUCUUUUGAAUCUACCCUUCAAGUA$^{CC-3'}$ (SEQ ID NO: 3826)
3'-UAGAAAACUUAGAUGGGAAGUUCAU$_{AA-5'}$ (SEQ ID NO: 196)

AR-868 Target: 5'-ATCTTTTGAATCTACCCTTCAAGTATT-3' (SEQ ID NO: 349)

5'-UCUUUUGAAUCUACCCUUCAAGUAU$^{CC-3'}$ (SEQ ID NO: 3827)
3'-AGAAAACUUAGAUGGGAAGUUCAUA$_{AU-5'}$ (SEQ ID NO: 197)

AR-869 Target: 5'-TCTTTTGAATCTACCCTTCAAGTATTA-3' (SEQ ID NO: 350)

5'-CUUUUGAAUCUACCCUUCAAGUAUU$^{CC-3'}$ (SEQ ID NO: 3828)
3'-GAAAACUUAGAUGGGAAGUUCAUAA$_{UU-5'}$ (SEQ ID NO: 198)

AR-870 Target: 5'-CTTTTGAATCTACCCTTCAAGTATTAA-3' (SEQ ID NO: 351)

5'-UUUUGAAUCUACCCUUCAAGUAUUA$^{CA-3'}$ (SEQ ID NO: 3829)
3'-AAAACUUAGAUGGGAAGUUCAUAAU$_{UC-5'}$ (SEQ ID NO: 199)

AR-871 Target: 5'-TTTTGAATCTACCCTTCAAGTATTAAG-3' (SEQ ID NO: 352)

5'-UUUGAAUCUACCCUUCAAGUAUUAA$^{AC-3'}$ (SEQ ID NO: 3830)
3'-AAACUUAGAUGGGAAGUUCAUAAUU$_{CU-5'}$ (SEQ ID NO: 200)

AR-872 Target: 5'-TTTGAATCTACCCTTCAAGTATTAAGA-3' (SEQ ID NO: 353)

5'-UCAAGUAUUAAGAGACAGACUGUGA$^{AA-3'}$ (SEQ ID NO: 3831)
3'-AGUUCAUAAUUCUCUGUCUGACACU$_{CG-5'}$ (SEQ ID NO: 201)

AR-886 Target: 5'-TCAAGTATTAAGAGACAGACTGTGAGC-3' (SEQ ID NO: 354)

5'-AGUAUUAAGAGACAGACUGUGAGCC$^{CC-3'}$ (SEQ ID NO: 3832)
3'-UCAUAAUUCUCUGUCUGACACUCGG$_{AU-5'}$ (SEQ ID NO: 202)

AR-889 Target: 5'-AGTATTAAGAGACAGACTGTGAGCCTA-3' (SEQ ID NO: 355)

5'-CUGUUGAACUCUUCUGAGCAAGAGA$^{CA-3'}$ (SEQ ID NO: 3833)
3'-GACAACUUGAGAAGACUCGUUCUCU$_{UC-5'}$ (SEQ ID NO: 203)

AR-1067 Target: 5'-CTGTTGAACTCTTCTGAGCAAGAGAAG-3' (SEQ ID NO: 356)

5'-UGUUGAACUCUUCUGAGCAAGAGAA$^{AA-3'}$ (SEQ ID NO: 3834)
3'-ACAACUUGAGAAGACUCGUUCUCUU$_{CC-5'}$ (SEQ ID NO: 204)

AR-1068 Target: 5'-TGTTGAACTCTTCTGAGCAAGAGAAGG-3' (SEQ ID NO: 357)

5'-CAAGGAUGGAAGUGCAGUUAGGGCU$^{AA-3'}$ (SEQ ID NO: 3835)
3'-GUUCCUACCUUCACGUCAAUCCCGA$_{CC-5'}$ (SEQ ID NO: 205)

AR-1137 Target: 5'-CAAGGATGGAAGTGCAGTTAGGGCTGG-3' (SEQ ID NO: 358)

5'-CCGAGGAGCUUUCCAGAAUCUGUUC^{A}C-3' (SEQ ID NO: 3836)
3'-GGCUCCUCGAAAGGUCUUAGACAAG$_{G}$$_{U-5'}$ (SEQ ID NO: 206)

AR-1198 Target: 5'-CCGAGGAGCTTTCCAGAATCTGTTCCA-3' (SEQ ID NO: 359)

5'-CGAGGAGCUUUCCAGAAUCUGUUCC^{C}A-3' (SEQ ID NO: 3837)
3'-GCUCCUCGAAAGGUCUUAGACAAGG$_{U}$$_{C-5'}$ (SEQ ID NO: 207)

AR-1199 Target: 5'-CGAGGAGCTTTCCAGAATCTGTTCCAG-3' (SEQ ID NO: 360)

5'-CGCUGACCUUAAAGACAUCCUGAGC^{A}C-3' (SEQ ID NO: 3838)
3'-GCGACUGGAAUUUCUGUAGGACUCG$_{C}$$_{U-5'}$ (SEQ ID NO: 208)

AR-1675 Target: 5'-CGCTGACCTTAAAGACATCCTGAGCGA-3' (SEQ ID NO: 361)

5'-UCCAAGGACAAUUACUUAGGGGGCA^{A}C-3' (SEQ ID NO: 3839)
3'-AGGUUCCUGUUAAUGAAUCCCCCGU$_{G}$$_{A-5'}$ (SEQ ID NO: 209)

AR-1802 Target: 5'-TCCAAGGACAATTACTTAGGGGGCACT-3' (SEQ ID NO: 362)

5'-CCAAGGAGUUGUGUAAGGCAGUGUC^{A}A-3' (SEQ ID NO: 3840)
3'-GGUUCCUCAACACAUUCCGUCACAG$_{C}$$_{C-5'}$ (SEQ ID NO: 210)

AR-1848 Target: 5'-CCAAGGAGTTGTGTAAGGCAGTGTCGG-3' (SEQ ID NO: 363)

5'-CACUGAAGAUACUGCUGAGUAUUCC^{A}A-3' (SEQ ID NO: 3841)
3'-GUGACUUCUAUGACGACUCAUAAGG$_{G}$$_{G-5'}$ (SEQ ID NO: 211)

AR-2047 Target: 5'-CACTGAAGATACTGCTGAGTATTCCCC-3' (SEQ ID NO: 364)

5'-UGCUGAGUAUUCCCCUUUCAAGGGA^{A}A-3' (SEQ ID NO: 3842)
3'-ACGACUCAUAAGGGGAAAGUUCCCU$_{C}$$_{C-5'}$ (SEQ ID NO: 212)

AR-2059 Target: 5'-TGCTGAGTATTCCCCTTTCAAGGGAGG-3' (SEQ ID NO: 365)

5'-CACUUGUGUCAAAAGCGAAAUGGGC^{A}A-3' (SEQ ID NO: 3843)
3'-GUGAACACAGUUUUCGCUUUACCCG$_{G}$$_{G-5'}$ (SEQ ID NO: 213)

AR-2692 Target: 5'-CACTTGTGTCAAAAGCGAAATGGGCCC-3' (SEQ ID NO: 366)

5'-ACUUGUGUCAAAAGCGAAAUGGGCC^{A}A-3' (SEQ ID NO: 3844)
3'-UGAACACAGUUUUCGCUUUACCCGG$_{G}$$_{G-5'}$ (SEQ ID NO: 214)

AR-2693 Target: 5'-ACTTGTGTCAAAAGCGAAATGGGCCCC-3' (SEQ ID NO: 367)

5'-ACCAUGUUUUGCCCAUUGACUAUUA^{A}C-3' (SEQ ID NO: 3845)
3'-UGGUACAAAACGGGUAACUGAUAAU$_{G}$$_{A-5'}$ (SEQ ID NO: 215)

AR-2775 Target: 5'-ACCATGTTTTGCCCATTGACTATTACT-3' (SEQ ID NO: 368)

5'-CAUGUUUUGCCCAUUGACUAUUACU^{C}C-3' (SEQ ID NO: 3846)
3'-GUACAAAACGGGUAACUGAUAAUGA$_{A}$$_{A-5'}$ (SEQ ID NO: 216)

AR-2777 Target: 5'-CATGTTTTGCCCATTGACTATTACTTT-3' (SEQ ID NO: 369)

5'-CUGUGGAGAUGAAGCUUCUGGGUGU^{A}C-3' (SEQ ID NO: 3847)
3'-GACACCUCUACUUCGAAGACCCACA$_{G}$$_{U-5'}$ (SEQ ID NO: 217)

AR-2827 Target: 5'-CTGTGGAGATGAAGCTTCTGGGTGTCA-3' (SEQ ID NO: 370)

5'-UGAAGGGAAACAGAAGUACCUGUGC^{A}A-3' (SEQ ID NO: 3848)
3'-ACUUCCCUUUGUCUUCAUGGACACG$_{C}$$_{G-5'}$ (SEQ ID NO: 218)

AR-2905 Target: 5'-TGAAGGGAAACAGAAGTACCTGTGCGC-3' (SEQ ID NO: 371)

5'-GCAGAAAUGAUUGCACUAUUGAUAA^{C}C-3' (SEQ ID NO: 3849)
3'-CGUCUUUACUAACGUGAUAACUAUU$_{U}$$_{A-5'}$ (SEQ ID NO: 219)

AR-2934 Target: 5'-GCAGAAATGATTGCACTATTGATAAAT-3' (SEQ ID NO: 372)

5'-CAGAAAUGAUUGCACUAUUGAUAAA^{C}C-3' (SEQ ID NO: 3850)
3'-GUCUUUACUAACGUGAUAACUAUUU$_{A}$$_{A-5'}$ (SEQ ID NO: 220)

AR-2935 Target: 5'-CAGAAATGATTGCACTATTGATAAATT-3' (SEQ ID NO: 373)

5'-AGAAAUGAUUGCACUAUUGAUAAAU^{C}A-3' (SEQ ID NO: 3851)
3'-UCUUUACUAACGUGAUAACUAUUUA$_{A}$$_{G-5'}$ (SEQ ID NO: 221)

AR-2936 Target: 5'-AGAAATGATTGCACTATTGATAAATTC-3' (SEQ ID NO: 374)

5'-AAAUGAUUGCACUAUUGAUAAAUUC^{A}A-3' (SEQ ID NO: 3852)
3'-UUUACUAACGUGAUAACUAUUUAAG$_{G}$$_{C-5'}$ (SEQ ID NO: 222)

AR-2938 Target: 5'-AAATGATTGCACTATTGATAAATTCCG-3' (SEQ ID NO: 375)

5'-AAUGAUUGCACUAUUGAUAAAUUCC^{A}C-3' (SEQ ID NO: 3853)
3'-UUACUAACGUGAUAACUAUUUAAGG$_{C}$$_{U-5'}$ (SEQ ID NO: 223)

AR-2939 Target: 5'-AATGATTGCACTATTGATAAATTCCGA-3' (SEQ ID NO: 376)

5'-CACUAUUGAUAAAUUCCGAAGGAAA^{C}C-3' (SEQ ID NO: 3854)
3'-GUGAUAACUAUUUAAGGCUUCCUUU$_{U}$$_{U-5'}$ (SEQ ID NO: 224)

AR-2947 Target: 5'-CACTATTGATAAATTCCGAAGGAAAAA-3' (SEQ ID NO: 377)

5'-ACUAUUGAUAAAUUCCGAAGGAAAA^{C}C-3' (SEQ ID NO: 3855)
3'-UGAUAACUAUUUAAGGCUUCCUUUU$_{U}$$_{A-5'}$ (SEQ ID NO: 225)

AR-2948 Target: 5'-ACTATTGATAAATTCCGAAGGAAAAAT-3' (SEQ ID NO: 378)

5'-CUAUUGAUAAAUUCCGAAGGAAAAA^{C}C-3' (SEQ ID NO: 3856)
3'-GAUAACUAUUUAAGGCUUCCUUUUU$_{A}$$_{A-5'}$ (SEQ ID NO: 226)

AR-2949 Target: 5'-CTATTGATAAATTCCGAAGGAAAAATT-3' (SEQ ID NO: 379)

5'-UAUUGAUAAAUUCCGAAGGAAAAAU^{C}A-3' (SEQ ID NO: 3857)
3'-AUAACUAUUUAAGGCUUCCUUUUUA$_{A}$$_{C-5'}$ (SEQ ID NO: 227)

AR-2950 Target: 5'-TATTGATAAATTCCGAAGGAAAAATTG-3' (SEQ ID NO: 380)

5'-AUUGAUAAAUUCCGAAGGAAAAAUU^{A}C-3' (SEQ ID NO: 3858)
3'-UAACUAUUUAAGGCUUCCUUUUUAA$_{C}A$-5' (SEQ ID NO: 228)

AR-2951 Target: 5'-ATTGATAAATTCCGAAGGAAAAATTGT-3' (SEQ ID NO: 381)

5'-UGAUAAAUUCCGAAGGAAAAAUUGU^{A}A-3' (SEQ ID NO: 3859)
3'-ACUAUUUAAGGCUUCCUUUUUAACA$_{G}G$-5' (SEQ ID NO: 229)

AR-2953 Target: 5'-TGATAAATTCCGAAGGAAAAATTGTCC-3' (SEQ ID NO: 382)

5'-GAUAAAUUCCGAAGGAAAAAUUGUC^{A}C-3' (SEQ ID NO: 3860)
3'-CUAUUUAAGGCUUCCUUUUUAACAG$_{G}U$-5' (SEQ ID NO: 230)

AR-2954 Target: 5'-GATAAATTCCGAAGGAAAAATTGTCCA-3' (SEQ ID NO: 383)

5'-CGAAGGAAAAAUUGUCCAUCUUGUC^{A}C-3' (SEQ ID NO: 3861)
3'-GCUUCCUUUUUAACAGGUAGAACAG$_{C}A$-5' (SEQ ID NO: 231)

AR-2963 Target: 5'-CGAAGGAAAAATTGTCCATCTTGTCGT-3' (SEQ ID NO: 384)

5'-AUCUUGUCGUCUUCGGAAAUGUUAU^{A}C-3' (SEQ ID NO: 3862)
3'-UAGAACAGCAGAAGCCUUUACAAUA$_{C}U$-5' (SEQ ID NO: 232)

AR-2980 Target: 5'-ATCTTGTCGTCTTCGGAAATGTTATGA-3' (SEQ ID NO: 385)

5'-CGGAAAUGUUAUGAAGCAGGGAUGA^{A}C-3' (SEQ ID NO: 3863)
3'-GCCUUUACAAUACUUCGUCCCUACU$_{G}A$-5' (SEQ ID NO: 233)

AR-2993 Target: 5'-CGGAAATGTTATGAAGCAGGGATGACT-3' (SEQ ID NO: 386)

5'-GAAAUGUUAUGAAGCAGGGAUGACU^{A}C-3' (SEQ ID NO: 3864)
3'-CUUUACAAUACUUCGUCCCUACUGA$_{G}A$-5' (SEQ ID NO: 234)

AR-2995 Target: 5'-GAAATGTTATGAAGCAGGGATGACTCT-3' (SEQ ID NO: 387)

5'-CCCGGAAGCUGAAGAAACUUGGUAA^{C}A-3' (SEQ ID NO: 3865)
3'-GGGCCUUCGACUUCUUUGAACCAUU$_{A}G$-5' (SEQ ID NO: 235)

AR-3027 Target: 5'-CCCGGAAGCTGAAGAAACTTGGTAATC-3' (SEQ ID NO: 388)

5'-CGGAAGCUGAAGAAACUUGGUAAUC^{C}A-3' (SEQ ID NO: 3866)
3'-GCCUUCGACUUCUUUGAACCAUUAG$_{A}C$-5' (SEQ ID NO: 236)

AR-3029 Target: 5'-CGGAAGCTGAAGAAACTTGGTAATCTG-3' (SEQ ID NO: 389)

5'-GCUGAAGAAACUUGGUAAUCUGAAA^{A}C-3' (SEQ ID NO: 3867)
3'-CGACUUCUUUGAACCAUUAGACUUU$_{G}A$-5' (SEQ ID NO: 237)

AR-3034 Target: 5'-GCTGAAGAAACTTGGTAATCTGAAACT-3' (SEQ ID NO: 390)

5'-CUGAAGAAACUUGGUAAUCUGAAAC^{C}C-3' (SEQ ID NO: 3868)
3'-GACUUCUUUGAACCAUUAGACUUUG$_{A}U$-5' (SEQ ID NO: 238)

AR-3035 Target: 5'-CTGAAGAAACTTGGTAATCTGAAACTA-3' (SEQ ID NO: 391)

5'-UGAAGAAACUUGGUAAUCUGAAACU$^{CA-3'}$ (SEQ ID NO: 3869)
3'-ACUUCUUUGAACCAUUAGACUUUGA$_{UG-5'}$ (SEQ ID NO: 239)

AR-3036 Target: 5'-TGAAGAAACTTGGTAATCTGAAACTAC-3' (SEQ ID NO: 392)

5'-UUGGUAAUCUGAAACUACAGGAGGA$^{CA-3'}$ (SEQ ID NO: 3870)
3'-AACCAUUAGACUUUGAUGUCCUCCU$_{UC-5'}$ (SEQ ID NO: 240)

AR-3045 Target: 5'-TTGGTAATCTGAAACTACAGGAGGAAG-3' (SEQ ID NO: 393)

5'-AUCUGAAACUACAGGAGGAAGGAGA$^{AA-3'}$ (SEQ ID NO: 3871)
3'-UAGACUUUGAUGUCCUCCUUCCUCU$_{CC-5'}$ (SEQ ID NO: 241)

AR-3051 Target: 5'-ATCTGAAACTACAGGAGGAAGGAGAGG-3' (SEQ ID NO: 394)

5'-CCCAGGAAUUCCUGUGCAUGAAAGC$^{CA-3'}$ (SEQ ID NO: 3872)
3'-GGGUCCUUAAGGACACGUACUUUCG$_{UG-5'}$ (SEQ ID NO: 242)

AR-3546 Target: 5'-CCCAGGAATTCCTGTGCATGAAAGCAC-3' (SEQ ID NO: 395)

5'-CCAGGAAUUCCUGUGCAUGAAAGCA$^{AC-3'}$ (SEQ ID NO: 3873)
3'-GGUCCUUAAGGACACGUACUUUCGU$_{GA-5'}$ (SEQ ID NO: 243)

AR-3547 Target: 5'-CCAGGAATTCCTGTGCATGAAAGCACT-3' (SEQ ID NO: 396)

5'-GUGGAUGGGCUGAAAAAUCAAAAAU$^{CA-3'}$ (SEQ ID NO: 3874)
3'-CACCUACCCGACUUUUUAGUUUUUA$_{AG-5'}$ (SEQ ID NO: 244)

AR-3596 Target: 5'-GTGGATGGGCTGAAAAATCAAAAATTC-3' (SEQ ID NO: 397)

5'-UGGAUGGGCUGAAAAAUCAAAAAUU$^{AC-3'}$ (SEQ ID NO: 3875)
3'-ACCUACCCGACUUUUUAGUUUUUAA$_{GA-5'}$ (SEQ ID NO: 245)

AR-3597 Target: 5'-TGGATGGGCTGAAAAATCAAAAATTCT-3' (SEQ ID NO: 398)

5'-GAUGGGCUGAAAAAUCAAAAAUUCU$^{CC-3'}$ (SEQ ID NO: 3876)
3'-CUACCCGACUUUUUAGUUUUUAAGA$_{AA-5'}$ (SEQ ID NO: 246)

AR-3599 Target: 5'-GATGGGCTGAAAAATCAAAAATTCTTT-3' (SEQ ID NO: 399)

5'-GGCUGAAAAAUCAAAAAUUCUUUGA$^{CA-3'}$ (SEQ ID NO: 3877)
3'-CCGACUUUUUAGUUUUUAAGAAACU$_{AC-5'}$ (SEQ ID NO: 247)

AR-3603 Target: 5'-GGCTGAAAAATCAAAAATTCTTTGATG-3' (SEQ ID NO: 400)

5'-GCUGAAAAAUCAAAAAUUCUUUGAU$^{AC-3'}$ (SEQ ID NO: 3878)
3'-CGACUUUUUAGUUUUUAAGAAACUA$_{CU-5'}$ (SEQ ID NO: 248)

AR-3604 Target: 5'-GCTGAAAAATCAAAAATTCTTTGATGA-3' (SEQ ID NO: 401)

5'-UGAAAAAUCAAAAAUUCUUUGAUGA$^{CA-3'}$ (SEQ ID NO: 3879)
3'-ACUUUUUAGUUUUUAAGAAACUACU$_{UG-5'}$ (SEQ ID NO: 249)

AR-3606 Target: 5'-TGAAAAATCAAAAATTCTTTGATGAAC-3' (SEQ ID NO: 402)

5'-GAAAAAUCAAAAAUUCUUUGAUGAA$^{AC-3'}$ (SEQ ID NO: 3880)
3'-CUUUUUAGUUUUUAAGAAACUACUU$_{GA-5'}$ (SEQ ID NO: 250)

AR-3607 Target: 5'-GAAAAATCAAAAATTCTTTGATGAACT-3' (SEQ ID NO: 403)

5'-AAAAAUCAAAAAUUCUUUGAUGAAC$^{CC-3'}$ (SEQ ID NO: 3881)
3'-UUUUUAGUUUUUAAGAAACUACUUG$_{AA-5'}$ (SEQ ID NO: 251)

AR-3608 Target: 5'-AAAAATCAAAAATTCTTTGATGAACTT-3' (SEQ ID NO: 404)

5'-UUCGAAUGAACUACAUCAAGGAACU$^{AA-3'}$ (SEQ ID NO: 3882)
3'-AAGCUUACUUGAUGUAGUUCCUUGA$_{GC-5'}$ (SEQ ID NO: 252)

AR-3633 Target: 5'-TTCGAATGAACTACATCAAGGAACTCG-3' (SEQ ID NO: 405)

5'-UCAAGGAACUCGAUCGUAUCAUUGC$^{CC-3'}$ (SEQ ID NO: 3883)
3'-AGUUCCUUGAGCUAGCAUAGUAACG$_{UA-5'}$ (SEQ ID NO: 253)

AR-3648 Target: 5'-TCAAGGAACTCGATCGTATCATTGCAT-3' (SEQ ID NO: 406)

5'-CAAGGAACUCGAUCGUAUCAUUGCA$^{CA-3'}$ (SEQ ID NO: 3884)
3'-GUUCCUUGAGCUAGCAUAGUAACGU$_{AC-5'}$ (SEQ ID NO: 254)

AR-3649 Target: 5'-CAAGGAACTCGATCGTATCATTGCATG-3' (SEQ ID NO: 407)

5'-AUCGUAUCAUUGCAUGCAAAAGAAA$^{CC-3'}$ (SEQ ID NO: 3885)
3'-UAGCAUAGUAACGUACGUUUUCUUU$_{UU-5'}$ (SEQ ID NO: 255)

AR-3660 Target: 5'-ATCGTATCATTGCATGCAAAAGAAAAA-3' (SEQ ID NO: 408)

5'-UCGUAUCAUUGCAUGCAAAAGAAAA$^{CC-3'}$ (SEQ ID NO: 3886)
3'-AGCAUAGUAACGUACGUUUUCUUUU$_{UU-5'}$ (SEQ ID NO: 256)

AR-3661 Target: 5'-TCGTATCATTGCATGCAAAAGAAAAAA-3' (SEQ ID NO: 409)

5'-AUCAUUGCAUGCAAAAGAAAAAAUC$^{AA-3'}$ (SEQ ID NO: 3887)
3'-UAGUAACGUACGUUUUCUUUUUUAG$_{GG-5'}$ (SEQ ID NO: 257)

AR-3665 Target: 5'-ATCATTGCATGCAAAAGAAAAAATCCC-3' (SEQ ID NO: 410)

5'-CACUUUUGACCUGCUAAUCAAGUCA$^{AC-3'}$ (SEQ ID NO: 3888)
3'-GUGAAAACUGGACGAUUAGUUCAGU$_{GU-5'}$ (SEQ ID NO: 258)

AR-3772 Target: 5'-CACTTTTGACCTGCTAATCAAGTCACA-3' (SEQ ID NO: 411)

5'-GCGUGGACUUUCCGGAAAUGAUGGC$^{CA-3'}$ (SEQ ID NO: 3889)
3'-CGCACCUGAAAGGCCUUUACUACCG$_{UC-5'}$ (SEQ ID NO: 259)

AR-3807 Target: 5'-GCGTGGACTTTCCGGAAATGATGGCAG-3' (SEQ ID NO: 412)

5'-CGUGGACUUUCCGGAAAUGAUGGCA$^{AC-3'}$ (SEQ ID NO: 3890)
3'-GCACCUGAAAGGCCUUUACUACCGU$_{CU-5'}$ (SEQ ID NO: 260)

AR-3808 Target: 5'-CGTGGACTTTCCGGAAATGATGGCAGA-3' (SEQ ID NO: 413)

5'-UGAUGGCAGAGAUCAUCUCUGUGCA$^{CA-3'}$ (SEQ ID NO: 3891)
3'-ACUACCGUCUCUAGUAGAGACACGU$_{UC-5'}$ (SEQ ID NO: 261)

AR-3825 Target: 5'-TGATGGCAGAGATCATCTCTGTGCAAG-3' (SEQ ID NO: 414)

5'-GCAGAGAUCAUCUCUGUGCAAGUGC$^{AA-3'}$ (SEQ ID NO: 3892)
3'-CGUCUCUAGUAGAGACACGUUCACG$_{GG-5'}$ (SEQ ID NO: 262)

AR-3830 Target: 5'-GCAGAGATCATCTCTGTGCAAGTGCCC-3' (SEQ ID NO: 415)

5'-CAGAGAUCAUCUCUGUGCAAGUGCC$^{AC-3'}$ (SEQ ID NO: 3893)
3'-GUCUCUAGUAGAGACACGUUCACGG$_{GU-5'}$ (SEQ ID NO: 263)

AR-3831 Target: 5'-CAGAGATCATCTCTGTGCAAGTGCCCA-3' (SEQ ID NO: 416)

5'-CCCAAGAUCCUUUCUGGGAAAGUCA$^{CA-3'}$ (SEQ ID NO: 3894)
3'-GGGUUCUAGGAAAGACCCUUUCAGU$_{UC-5'}$ (SEQ ID NO: 264)

AR-3854 Target: 5'-CCCAAGATCCTTTCTGGGAAAGTCAAG-3' (SEQ ID NO: 417)

5'-GUGAAGCAUUGGAAACCCUAUUUCC$^{AA-3'}$ (SEQ ID NO: 3895)
3'-CACUUCGUAACCUUUGGGAUAAAGG$_{GG-5'}$ (SEQ ID NO: 265)

AR-3901 Target: 5'-GTGAAGCATTGGAAACCCTATTTCCCC-3' (SEQ ID NO: 418)

5'-CAGAUGUCUUCUGCCUGUUAUAACU$^{AC-3'}$ (SEQ ID NO: 3896)
3'-GUCUACAGAAGACGGACAAUAUUGA$_{GA-5'}$ (SEQ ID NO: 266)

AR-3949 Target: 5'-CAGATGTCTTCTGCCTGTTATAACTCT-3' (SEQ ID NO: 419)

5'-GCCUUGGGGAAUUUCCUCUAUUGAU$^{AC-3'}$ (SEQ ID NO: 3897)
3'-CGGAACCCCUUAAAGGAGAUAACUA$_{CA-5'}$ (SEQ ID NO: 267)

AR-3994 Target: 5'-GCCTTGGGGAATTTCCTCTATTGATGT-3' (SEQ ID NO: 420)

5'-CUUGGGGAAUUUCCUCUAUUGAUGU$^{CA-3'}$ (SEQ ID NO: 3898)
3'-GAACCCCUUAAAGGAGAUAACUACA$_{UG-5'}$ (SEQ ID NO: 268)

AR-3996 Target: 5'-CTTGGGGAATTTCCTCTATTGATGTAC-3' (SEQ ID NO: 421)

5'-UUGGGGAAUUUCCUCUAUUGAUGUA$^{AC-3'}$ (SEQ ID NO: 3899)
3'-AACCCCUUAAAGGAGAUAACUACAU$_{GU-5'}$ (SEQ ID NO: 269)

AR-3997 Target: 5'-TTGGGGAATTTCCTCTATTGATGTACA-3' (SEQ ID NO: 422)

5'-UGGGGAAUUUCCUCUAUUGAUGUAC$^{CA-3'}$ (SEQ ID NO: 3900)
3'-ACCCCUUAAAGGAGAUAACUACAUG$_{UC-5'}$ (SEQ ID NO: 270)

AR-3998 Target: 5'-TGGGGAATTTCCTCTATTGATGTACAG-3' (SEQ ID NO: 423)

5'-GGGGAAUUUCCUCUAUUGAUGUACA$^{AC-3'}$ (SEQ ID NO: 3901)
3'-CCCCUUAAAGGAGAUAACUACAUGU$_{CA-5'}$ (SEQ ID NO: 271)

AR-3999 Target: 5'-GGGGAATTTCCTCTATTGATGTACAGT-3' (SEQ ID NO: 424)

5'-CUAUUGAUGUACAGUCUGUCAUGAA$^{AC-3'}$ (SEQ ID NO: 3902)
3'-GAUAACUACAUGUCAGACAGUACUU$_{GU-5'}$ (SEQ ID NO: 272)

AR-4011 Target: 5'-CTATTGATGTACAGTCTGTCATGAACA-3' (SEQ ID NO: 425)

5'-UAUUGAUGUACAGUCUGUCAUGAAC$^{CC-3'}$ (SEQ ID NO: 3903)
3'-AUAACUACAUGUCAGACAGUACUUG$_{UA-5'}$ (SEQ ID NO: 273)

AR-4012 Target: 5'-TATTGATGTACAGTCTGTCATGAACAT-3' (SEQ ID NO: 426)

5'-AUUGAUGUACAGUCUGUCAUGAACA$^{CA-3'}$ (SEQ ID NO: 3904)
3'-UAACUACAUGUCAGACAGUACUUGU$_{AC-5'}$ (SEQ ID NO: 274)

AR-4013 Target: 5'-ATTGATGTACAGTCTGTCATGAACATG-3' (SEQ ID NO: 427)

5'-AACAUGUUCCUGAAUUCUAUUUGCU$^{AA-3'}$ (SEQ ID NO: 3905)
3'-UUGUACAAGGACUUAAGAUAAACGA$_{CC-5'}$ (SEQ ID NO: 275)

AR-4034 Target: 5'-AACATGTTCCTGAATTCTATTTGCTGG-3' (SEQ ID NO: 428)

5'-UUCUAUUUGCUGGGCUUUUUUUUUC$^{CA-3'}$ (SEQ ID NO: 3906)
3'-AAGAUAAACGACCCGAAAAAAAAAG$_{AG-5'}$ (SEQ ID NO: 276)

AR-4048 Target: 5'-TTCTATTTGCTGGGCTTTTTTTTTCTC-3' (SEQ ID NO: 429)

5'-UCUAUUUGCUGGGCUUUUUUUUUCU$^{AC-3'}$ (SEQ ID NO: 3907)
3'-AGAUAAACGACCCGAAAAAAAAAAGA$_{GA-5'}$ (SEQ ID NO: 277)

AR-4049 Target: 5'-TCTATTTGCTGGGCTTTTTTTTTCTCT-3' (SEQ ID NO: 430)

5'-UGCUGGGCUUUUUUUUUCUCUUUCU$^{AC-3'}$ (SEQ ID NO: 3908)
3'-ACGACCCGAAAAAAAAAGAGAAAGA$_{GA-5'}$ (SEQ ID NO: 278)

AR-4055 Target: 5'-TGCTGGGCTTTTTTTTTCTCTTTCTCT-3' (SEQ ID NO: 431)

5'-UUUUUUUUCUCUUUCUCUCCUUUCU$^{CC-3'}$ (SEQ ID NO: 3909)
3'-AAAAAAAAGAGAAAGAGAGGAAAGA$_{AA-5'}$ (SEQ ID NO: 279)

AR-4064 Target: 5'-TTTTTTTTCTCTTTCTCTCCTTTCTTT-3' (SEQ ID NO: 432)

5'-UUCAGACUUUGCUUCCCAUUGUGGC$^{CA-3'}$ (SEQ ID NO: 3910)
3'-AAGUCUGAAACGAAGGGUAACACCG$_{AG-5'}$ (SEQ ID NO: 280)

AR-4128 Target: 5'-TTCAGACTTTGCTTCCCATTGTGGCTC-3' (SEQ ID NO: 433)

5'-UUGUGGCUCCUAUCUGUGUUUUGAA$^{CA-3'}$ (SEQ ID NO: 3911)
3'-AACACCGAGGAUAGACACAAAACUU$_{AC-5'}$ (SEQ ID NO: 281)

AR-4146 Target: 5'-TTGTGGCTCCTATCTGTGTTTTGAATG-3' (SEQ ID NO: 434)

5'-UCCUAUCUGUGUUUUGAAUGGUGUU$^{AC-3'}$ (SEQ ID NO: 3912)
3'-AGGAUAGACACAAAACUUACCACAA$_{CA-5'}$ (SEQ ID NO: 282)

AR-4153 Target: 5'-TCCTATCTGTGTTTTGAATGGTGTTGT-3' (SEQ ID NO: 435)

5'-AUCUGUGUUUUGAAUGGUGUUGUAU$^{AA-3'}$ (SEQ ID NO: 3913)
3'-UAGACACAAAACUUACCACAACAUA$_{CG-5'}$ (SEQ ID NO: 283)

AR-4157 Target: 5'-ATCTGTGTTTTGAATGGTGTTGTATGC-3' (SEQ ID NO: 436)

5'-UGUGUUUUGAAUGGUGUUGUAUGCC$^{CC-3'}$ (SEQ ID NO: 3914)
3'-ACACAAAACUUACCACAACAUACGG$_{AA-5'}$ (SEQ ID NO: 284)

AR-4160 Target: 5'-TGTGTTTTGAATGGTGTTGTATGCCTT-3' (SEQ ID NO: 437)

5'-UGAAUGGUGUUGUAUGCCUUUAAAU$^{AC-3'}$ (SEQ ID NO: 3915)
3'-ACUUACCACAACAUACGGAAAUUUA$_{GA-5'}$ (SEQ ID NO: 285)

AR-4167 Target: 5'-TGAATGGTGTTGTATGCCTTTAAATCT-3' (SEQ ID NO: 438)

5'-GAAUGGUGUUGUAUGCCUUUAAAUC$^{CA-3'}$ (SEQ ID NO: 3916)
3'-CUUACCACAACAUACGGAAAUUUAG$_{AC-5'}$ (SEQ ID NO: 286)

AR-4168 Target: 5'-GAATGGTGTTGTATGCCTTTAAATCTG-3' (SEQ ID NO: 439)

5'-UGUUGUAUGCCUUUAAAUCUGUGAU$^{AC-3'}$ (SEQ ID NO: 3917)
3'-ACAACAUACGGAAAUUUAGACACUA$_{CU-5'}$ (SEQ ID NO: 287)

AR-4174 Target: 5'-TGTTGTATGCCTTTAAATCTGTGATGA-3' (SEQ ID NO: 440)

5'-UUGUAUGCCUUUAAAUCUGUGAUGA$^{CA-3'}$ (SEQ ID NO: 3918)
3'-AACAUACGGAAAUUUAGACACUACU$_{AG-5'}$ (SEQ ID NO: 288)

AR-4176 Target: 5'-TTGTATGCCTTTAAATCTGTGATGATC-3' (SEQ ID NO: 441)

5'-UGUAUGCCUUUAAAUCUGUGAUGAU$^{AA-3'}$ (SEQ ID NO: 3919)
3'-ACAUACGGAAAUUUAGACACUACUA$_{GG-5'}$ (SEQ ID NO: 289)

AR-4177 Target: 5'-TGTATGCCTTTAAATCTGTGATGATCC-3' (SEQ ID NO: 442)

5'-CCCAGUGUCAAGUUGUGCUUGUUUA$^{AC-3'}$ (SEQ ID NO: 3920)
3'-GGGUCACAGUUCAACACGAACAAAU$_{GU-5'}$ (SEQ ID NO: 290)

AR-4212 Target: 5'-CCCAGTGTCAAGTTGTGCTTGTTTACA-3' (SEQ ID NO: 443)

5'-CCAGUGUCAAGUUGUGCUUGUUUAC$^{CA-3'}$ (SEQ ID NO: 3921)
3'-GGUCACAGUUCAACACGAACAAAUG$_{UC-5'}$ (SEQ ID NO: 291)

AR-4213 Target: 5'-CCAGTGTCAAGTTGTGCTTGTTTACAG-3' (SEQ ID NO: 444)

5'-GCUUGUUUACAGCACUACUCUGUGC$^{AC-3'}$ (SEQ ID NO: 3922)
3'-CGAACAAAUGUCGUGAUGAGACACG$_{GU-5'}$ (SEQ ID NO: 292)

AR-4228 Target: 5'-GCTTGTTTACAGCACTACTCTGTGCCA-3' (SEQ ID NO: 445)

5'-CUUGUUUACAGCACUACUCUGUGCC$^{CA-3'}$ (SEQ ID NO: 3923)
3'-GAACAAAUGUCGUGAUGAGACACGG$_{UC-5'}$ (SEQ ID NO: 293)

AR-4229 Target: 5'-CTTGTTTACAGCACTACTCTGTGCCAG-3' (SEQ ID NO: 446)

5'-CACAAACGUUUACUUAUCUUAUGCC$^{CA-3'}$ (SEQ ID NO: 3924)
3'-GUGUUUGCAAAUGAAUAGAAUACGG$_{UG-5'}$ (SEQ ID NO: 294)

AR-4259 Target: 5'-CACAAACGTTTACTTATCTTATGCCAC-3' (SEQ ID NO: 447)

5'-CACGGGAAGUUUAGAGAGCUAAGAU$^{CC-3'}$ (SEQ ID NO: 3925)
3'-GUGCCCUUCAAAUCUCUCGAUUCUA$_{AU-5'}$ (SEQ ID NO: 295)

AR-4283 Target: 5'-CACGGGAAGTTTAGAGAGCTAAGATTA-3' (SEQ ID NO: 448)

5'-ACGGGAAGUUUAGAGAGCUAAGAUU$^{CC-3'}$ (SEQ ID NO: 3926)
3'-UGCCCUUCAAAUCUCUCGAUUCUAA$_{UA-5'}$ (SEQ ID NO: 296)

AR-4284 Target: 5'-ACGGGAAGTTTAGAGAGCTAAGATTAT-3' (SEQ ID NO: 449)

5'-CGGGAAGUUUAGAGAGCUAAGAUUA$^{CA-3'}$ (SEQ ID NO: 3927)
3'-GCCCUUCAAAUCUCUCGAUUCUAAU$_{AG-5'}$ (SEQ ID NO: 297)

AR-4285 Target: 5'-CGGGAAGTTTAGAGAGCTAAGATTATC-3' (SEQ ID NO: 450)

5'-GGGAAGUUUAGAGAGCUAAGAUUAU$^{AC-3'}$ (SEQ ID NO: 3928)
3'-CCCUUCAAAUCUCUCGAUUCUAAUA$_{GA-5'}$ (SEQ ID NO: 298)

AR-4286 Target: 5'-GGGAAGTTTAGAGAGCTAAGATTATCT-3' (SEQ ID NO: 451)

5'-GAAGUUUAGAGAGCUAAGAUUAUCU$^{AA-3'}$ (SEQ ID NO: 3929)
3'-CUUCAAAUCUCUCGAUUCUAAUAGA$_{CC-5'}$ (SEQ ID NO: 299)

AR-4288 Target: 5'-GAAGTTTAGAGAGCTAAGATTATCTGG-3' (SEQ ID NO: 452)

5'-UUAGAGAGCUAAGAUUAUCUGGGGA$^{CC-3'}$ (SEQ ID NO: 3930)
3'-AAUCUCUCGAUUCUAAUAGACCCCU$_{UU-5'}$ (SEQ ID NO: 300)

AR-4293 Target: 5'-TTAGAGAGCTAAGATTATCTGGGGAAA-3' (SEQ ID NO: 453)

5'-UAGAGAGCUAAGAUUAUCUGGGGAA$^{CC-3'}$ (SEQ ID NO: 3931)
3'-AUCUCUCGAUUCUAAUAGACCCCUU$_{UA-5'}$ (SEQ ID NO: 301)

AR-4294 Target: 5'-TAGAGAGCTAAGATTATCTGGGGAAAT-3' (SEQ ID NO: 454)

5'-AGAGAGCUAAGAUUAUCUGGGGAAA$^{CA-3'}$ (SEQ ID NO: 3932)
3'-UCUCUCGAUUCUAAUAGACCCCUUU$_{AG-5'}$ (SEQ ID NO: 302)

AR-4295 Target: 5'-AGAGAGCTAAGATTATCTGGGGAAATC-3' (SEQ ID NO: 455)

5'-UAAGAUUAUCUGGGGAAAUCAAAAC$^{CC-3'}$ (SEQ ID NO: 3933)
3'-AUUCUAAUAGACCCCUUUAGUUUUG$_{UU-5'}$ (SEQ ID NO: 303)

AR-4302 Target: 5'-TAAGATTATCTGGGGAAATCAAAACAA-3' (SEQ ID NO: 456)

5'-AAGAUUAUCUGGGGAAAUCAAAACA$^{CC-3'}$ (SEQ ID NO: 3934)
3'-UUCUAAUAGACCCCUUUAGUUUUGU$_{UU-5'}$ (SEQ ID NO: 304)

AR-4303 Target: 5'-AAGATTATCTGGGGAAATCAAAACAAA-3' (SEQ ID NO: 457)

5'-AUCUGGGGAAAUCAAAACAAAAACA$^{CA-3'}$ (SEQ ID NO: 3935)
3'-UAGACCCCUUUAGUUUUGUUUUUGU$_{UC-5'}$ (SEQ ID NO: 305)

AR-4309 Target: 5'-ATCTGGGGAAATCAAAACAAAAACAAG-3' (SEQ ID NO: 458)

5'-GGGGAAAUCAAAACAAAAACAAGCA$^{CC-3'}$ (SEQ ID NO: 3936)
3'-CCCCUUUAGUUUUGUUUUUGUUCGU$_{UU-5'}$ (SEQ ID NO: 306)

AR-4313 Target: 5'-GGGGAAATCAAAACAAAAACAAGCAAA-3' (SEQ ID NO: 459)

5'-GUGAAGUUUUUAAAAGCUGCUAAAG$^{CA-3'}$ (SEQ ID NO: 3937)
3'-CACUUCAAAAAUUUUCGACGAUUUC$_{UG-5'}$ (SEQ ID NO: 796)

AR-251 Target: 5'-GTGAAGTTTTTAAAAGCTGCTAAAGAC-3' (SEQ ID NO: 826)

5'-AGCUAGCUGCACAUUGCAAAGAAGG$^{AC-3'}$ (SEQ ID NO: 3938)
3'-UCGAUCGACGUGUAACGUUUCUUCC$_{GA-5'}$ (SEQ ID NO: 797)

AR-524 Target: 5'-AGCTAGCTGCACATTGCAAAGAAGGCT-3' (SEQ ID NO: 827)

5'-ACAUUGCAAAGAAGGCUCUUAGGAG$^{AA-3'}$ (SEQ ID NO: 3939)
3'-UGUAACGUUUCUUCCGAGAAUCCUC$_{GG-5'}$ (SEQ ID NO: 798)

AR-534 Target: 5'-ACATTGCAAAGAAGGCTCTTAGGAGCC-3' (SEQ ID NO: 828)

5'-AACAAAACAAACAAAAACAAAAAAG$^{AA-3'}$ (SEQ ID NO: 3940)
3'-UUGUUUUGUUUGUUUUUGUUUUUUC$_{GG-5'}$ (SEQ ID NO: 799)

AR-736 Target: 5'-AACAAAACAAACAAAAACAAAAAAGCC-3' (SEQ ID NO: 829)

5'-AAGAUAAUAACUCAGUUCUUAUUUG$^{AC-3'}$ (SEQ ID NO: 3941)
3'-UUCUAUUAUUGAGUCAAGAAUAAAC$_{GU-5'}$ (SEQ ID NO: 800)

AR-776 Target: 5'-AAGATAATAACTCAGTTCTTATTTGCA-3' (SEQ ID NO: 830)

5'-UUCAGUGGACACUGAAUUUGGAAGG$^{CA-3'}$ (SEQ ID NO: 3942)
3'-AAGUCACCUGUGACUUAAACCUUCC$_{AC-5'}$ (SEQ ID NO: 801)

AR-808 Target: 5'-TTCAGTGGACACTGAATTTGGAAGGTG-3' (SEQ ID NO: 831)

5'-CAGUGGACACUGAAUUUGGAAGGUG$^{AC-3'}$ (SEQ ID NO: 3943)
3'-GUCACCUGUGACUUAAACCUUCCAC$_{CU-5'}$ (SEQ ID NO: 802)

AR-810 Target: 5'-CAGTGGACACTGAATTTGGAAGGTGGA-3' (SEQ ID NO: 832)

5'-AGUGGACACUGAAUUUGGAAGGUGG$^{CA-3'}$ (SEQ ID NO: 3944)
3'-UCACCUGUGACUUAAACCUUCCACC$_{UC-5'}$ (SEQ ID NO: 803)

AR-811 Target: 5'-AGTGGACACTGAATTTGGAAGGTGGAG-3' (SEQ ID NO: 833)

5'-UUGAAUCUACCCUUCAAGUAUUAAG$^{CA-3'}$ (SEQ ID NO: 3945)
3'-AACUUAGAUGGGAAGUUCAUAAUUC$_{UC-5'}$ (SEQ ID NO: 804)

AR-873 Target: 5'-TTGAATCTACCCTTCAAGTATTAAGAG-3' (SEQ ID NO: 834)

5'-CAAGUAUUAAGAGACAGACUGUGAG$^{AA-3'}$ (SEQ ID NO: 3946)
3'-GUUCAUAAUUCUCUGUCUGACACUC$_{GG-5'}$ (SEQ ID NO: 805)

AR-887 Target: 5'-CAAGTATTAAGAGACAGACTGTGAGCC-3' (SEQ ID NO: 835)

5'-GCUGAGUAUUCCCCUUUCAAGGGAG$^{AC-3'}$ (SEQ ID NO: 3947)
3'-CGACUCAUAAGGGGAAAGUUCCCUC$_{CA-5'}$ (SEQ ID NO: 806)

AR-2060 Target: 5'-GCTGAGTATTCCCCTTTCAAGGGAGGT-3' (SEQ ID NO: 836)

5'-CUGAGUAUUCCCCUUUCAAGGGAGG$^{CC-3'}$ (SEQ ID NO: 3948)
3'-GACUCAUAAGGGGAAAGUUCCCUCC$_{AA-5'}$ (SEQ ID NO: 807)

AR-2061 Target: 5'-CTGAGTATTCCCCTTTCAAGGGAGGTT-3' (SEQ ID NO: 837)

5'-UCUGUGGAGAUGAAGCUUCUGGGUG$^{CA-3'}$ (SEQ ID NO: 3949)
3'-AGACACCUCUACUUCGAAGACCCAC$_{AG-5'}$ (SEQ ID NO: 808)

AR-2826 Target: 5'-TCTGTGGAGATGAAGCTTCTGGGTGTC-3' (SEQ ID NO: 838)

5'-GAAGGGAAACAGAAGUACCUGUGCG$^{AA-3'}$ (SEQ ID NO: 3950)
3'-CUUCCCUUUGUCUUCAUGGACACGC$_{GG-5'}$ (SEQ ID NO: 809)

AR-2906 Target: 5'-GAAGGGAAACAGAAGTACCTGTGCGCC-3' (SEQ ID NO: 839)

5'-UUGAUAAAUUCCGAAGGAAAAAUUG$^{CA-3'}$ (SEQ ID NO: 3951)
3'-AACUAUUUAAGGCUUCCUUUUUAAC$_{AG-5'}$ (SEQ ID NO: 810)

AR-2952 Target: 5'-TTGATAAATTCCGAAGGAAAAATTGTC-3' (SEQ ID NO: 840)

5'-GAAGGAAAAAUUGUCCAUCUUGUCG$^{CA-3'}$ (SEQ ID NO: 3952)
3'-CUUCCUUUUUAACAGGUAGAACAGC$_{AG-5'}$ (SEQ ID NO: 811)

AR-2964 Target: 5'-GAAGGAAAAATTGTCCATCTTGTCGTC-3' (SEQ ID NO: 841)

5'-UCGGAAAUGUUAUGAAGCAGGGAUG$^{CA-3'}$ (SEQ ID NO: 3953)
3'-AGCCUUUACAAUACUUCGUCCCUAC$_{UG-5'}$ (SEQ ID NO: 812)

AR-2992 Target: 5'-TCGGAAATGTTATGAAGCAGGGATGAC-3' (SEQ ID NO: 842)

5'-ACUUGGUAAUCUGAAACUACAGGAG$^{AC-3'}$ (SEQ ID NO: 3954)
3'-UGAACCAUUAGACUUUGAUGUCCUC$_{CU-5'}$ (SEQ ID NO: 813)

AR-3043 Target: 5'-ACTTGGTAATCTGAAACTACAGGAGGA-3' (SEQ ID NO: 843)

5'-CUUGGUAAUCUGAAACUACAGGAGG$^{CC-3'}$ (SEQ ID NO: 3955)
3'-GAACCAUUAGACUUUGAUGUCCUCC$_{UU-5'}$ (SEQ ID NO: 814)

AR-3044 Target: 5'-CTTGGTAATCTGAAACTACAGGAGGAA-3' (SEQ ID NO: 844)

5'-GGUAAUCUGAAACUACAGGAGGAAG$^{AC-3'}$ (SEQ ID NO: 3956)
3'-CCAUUAGACUUUGAUGUCCUCCUUC$_{CU-5'}$ (SEQ ID NO: 815)

AR-3047 Target: 5'-GGTAATCTGAAACTACAGGAGGAAGGA-3' (SEQ ID NO: 845)

5'-AGCUGACAGUGUCACACAUUGAAGG^{A}C-3' (SEQ ID NO: 3957)
3'-UCGACUGUCACAGUGUGUAACUUCC$_{G}$$_{A-5'}$ (SEQ ID NO: 816)

AR-3117 Target: 5'-AGCTGACAGTGTCACACATTGAAGGCT-3' (SEQ ID NO: 846)

5'-GGCUGUCAUUCAGUACUCCUGGAUG^{A}$^{A-3'}$ (SEQ ID NO: 3958)
3'-CCGACAGUAAGUCAUGAGGACCUAC$_{C}$$_{C-5'}$ (SEQ ID NO: 817)

AR-3346 Target: 5'-GGCTGTCATTCAGTACTCCTGGATGGG-3' (SEQ ID NO: 847)

5'-CUGAAAAAUCAAAAAUUCUUUGAUG^{C}$^{C-3'}$ (SEQ ID NO: 3959)
3'-GACUUUUUAGUUUUUAAGAAACUAC$_{U}$$_{U-5'}$ (SEQ ID NO: 818)

AR-3605 Target: 5'-CTGAAAAATCAAAAATTCTTTGATGAA-3' (SEQ ID NO: 848)

5'-AAAAUUCUUUGAUGAACUUCGAAUG^{C}$^{C-3'}$ (SEQ ID NO: 3960)
3'-UUUUAAGAAACUACUUGAAGCUUAC$_{U}$$_{U-5'}$ (SEQ ID NO: 819)

AR-3616 Target: 5'-AAAATTCTTTGATGAACTTCGAATGAA-3' (SEQ ID NO: 849)

5'-UGCUAAUCAAGUCACACAUGGUGAG^{A}$^{A-3'}$ (SEQ ID NO: 3961)
3'-ACGAUUAGUUCAGUGUGUACCACUC$_{G}$$_{C-5'}$ (SEQ ID NO: 820)

AR-3783 Target: 5'-TGCTAATCAAGTCACACATGGTGAGCG-3' (SEQ ID NO: 850)

5'-AGCGUGGACUUUCCGGAAAUGAUGG^{A}C-3' (SEQ ID NO: 3962)
3'-UCGCACCUGAAAGGCCUUUACUACC$_{G}$$_{U-5'}$ (SEQ ID NO: 821)

AR-3806 Target: 5'-AGCGTGGACTTTCCGGAAATGATGGCA-3' (SEQ ID NO: 851)

5'-CCUUGGGGAAUUUCCUCUAUUGAUG^{C}$^{C-3'}$ (SEQ ID NO: 3963)
3'-GGAACCCCUUAAAGGAGAUAACUAC$_{A}$$_{U-5'}$ (SEQ ID NO: 822)

AR-3995 Target: 5'-CCTTGGGGAATTTCCTCTATTGATGTA-3' (SEQ ID NO: 852)

5'-UCUGUGUUUUGAAUGGUGUUGUAUG^{A}$^{A-3'}$ (SEQ ID NO: 3964)
3'-AGACACAAAACUUACCACAACAUAC$_{G}$$_{G-5'}$ (SEQ ID NO: 823)

AR-4158 Target: 5'-TCTGTGTTTTGAATGGTGTTGTATGCC-3' (SEQ ID NO: 853)

5'-GUUGUAUGCCUUUAAAUCUGUGAUG^{C}$^{C-3'}$ (SEQ ID NO: 3965)
3'-CAACAUACGGAAAUUUAGACACUAC$_{U}$$_{A-5'}$ (SEQ ID NO: 824)

AR-4175 Target: 5'-GTTGTATGCCTTTAAATCTGTGATGAT-3' (SEQ ID NO: 854)

5'-UUUAGAGAGCUAAGAUUAUCUGGGG^{C}$^{C-3'}$ (SEQ ID NO: 3966)
3'-AAAUCUCUCGAUUCUAAUAGACCCC$_{U}$$_{U-5'}$ (SEQ ID NO: 825)

AR-4292 Target: 5'-TTTAGAGAGCTAAGATTATCTGGGGAA-3' (SEQ ID NO: 855)

5'-UCGGUGAAGUUUUUAAAAGCUGCUA^{C}$^{C-3'}$ (SEQ ID NO: 3967)
3'-AGCCACUUCAAAAAUUUUCGACGAU$_{U}$$_{U-5'}$ (SEQ ID NO: 970)

AR-248 Target: 5'-TCGGTGAAGTTTTAAAAGCTGCTAAA-3' (SEQ ID NO: 1024)

5'-AGUUUUUAAAAGCUGCUAAAGACUC$^{AA-3'}$ (SEQ ID NO: 3968)
3'-UCAAAAAUUUUCGACGAUUUCUGAG$_{CC-5'}$ (SEQ ID NO: 971)

AR-255 Target: 5'-AGTTTTTAAAAGCTGCTAAAGACTCGG-3' (SEQ ID NO: 1025)

5'-GCAGAGAGGUAACUCCCUUUGGCUG$^{AA-3'}$ (SEQ ID NO: 3969)
3'-CGUCUCUCCAUUGAGGGAAACCGAC$_{GC-5'}$ (SEQ ID NO: 972)

AR-489 Target: 5'-GCAGAGAGGTAACTCCCTTTGGCTGCG-3' (SEQ ID NO: 1026)

5'-CAGAGAUCAAAAGAUGAAAAGGCAG$^{CA-3'}$ (SEQ ID NO: 3970)
3'-GUCUCUAGUUUUCUACUUUUCCGUC$_{AG-5'}$ (SEQ ID NO: 973)

AR-690 Target: 5'-CAGAGATCAAAAGATGAAAAGGCAGTC-3' (SEQ ID NO: 1027)

5'-CAAAAAACAAAACAAACAAAAACAA$^{CC-3'}$ (SEQ ID NO: 3971)
3'-GUUUUUUGUUUUGUUUGUUUUUGUU$_{UU-5'}$ (SEQ ID NO: 974)

AR-731 Target: 5'-CAAAAAACAAAACAAACAAAAACAAAA-3' (SEQ ID NO: 1028)

5'-AAAUAAAAGAAAAAGAUAAUAACUC$^{CA-3'}$ (SEQ ID NO: 3972)
3'-UUUAUUUUCUUUUUCUAUUAUUGAG$_{UC-5'}$ (SEQ ID NO: 975)

AR-764 Target: 5'-AAATAAAAGAAAAAGATAATAACTCAG-3' (SEQ ID NO: 1029)

5'-AGAAAAAGAUAAUAACUCAGUUCUU$^{CC-3'}$ (SEQ ID NO: 3973)
3'-UCUUUUUCUAUUAUUGAGUCAAGAA$_{UA-5'}$ (SEQ ID NO: 976)

AR-771 Target: 5'-AGAAAAAGATAATAACTCAGTTCTTAT-3' (SEQ ID NO: 1030)

5'-AUAAUAACUCAGUUCUUAUUUGCAC$^{AC-3'}$ (SEQ ID NO: 3974)
3'-UAUUAUUGAGUCAAGAAUAAACGUG$_{GA-5'}$ (SEQ ID NO: 977)

AR-779 Target: 5'-ATAATAACTCAGTTCTTATTTGCACCT-3' (SEQ ID NO: 1031)

5'-AGGUGGAGGAUUUUGUUUUUUUCUU$^{CC-3'}$ (SEQ ID NO: 3975)
3'-UCCACCUCCUAAAACAAAAAAAGAA$_{AA-5'}$ (SEQ ID NO: 978)

AR-830 Target: 5'-AGGTGGAGGATTTTGTTTTTTTCTTTT-3' (SEQ ID NO: 1032)

5'-UUUUGUUUUUUUCUUUUAAGAUCUG$^{AA-3'}$ (SEQ ID NO: 3976)
3'-AAAACAAAAAAAGAAAAUUCUAGAC$_{CC-5'}$ (SEQ ID NO: 979)

AR-840 Target: 5'-TTTTGTTTTTTTCTTTTAAGATCTGGG-3' (SEQ ID NO: 1033)

5'-UUUUUUUCUUUUAAGAUCUGGGCAU$^{AC-3'}$ (SEQ ID NO: 3977)
3'-AAAAAAAGAAAAUUCUAGACCCGUA$_{GA-5'}$ (SEQ ID NO: 980)

AR-845 Target: 5'-TTTTTTTCTTTTAAGATCTGGGCATCT-3' (SEQ ID NO: 1034)

5'-AUCUGGGCAUCUUUUGAAUCUACCC$^{CC-3'}$ (SEQ ID NO: 3978)
3'-UAGACCCGUAGAAAACUUAGAUGGG$_{AA-5'}$ (SEQ ID NO: 981)

AR-860 Target: 5'-ATCTGGGCATCTTTTGAATCTACCCTT-3' (SEQ ID NO: 1035)

5'-UAAGGGAAGUAGGUGGAAGAUUCAG$^{AA-3'}$ (SEQ ID NO: 3979)
3'-AUUCCCUUCAUCCACCUUCUAAGUC$_{GG-5'}$ (SEQ ID NO: 982)

AR-1105 Target: 5'-TAAGGGAAGTAGGTGGAAGATTCAGCC-3' (SEQ ID NO: 1036)

5'-GAGGAGCUUUCCAGAAUCUGUUCCA$^{AC-3'}$ (SEQ ID NO: 3980)
3'-CUCCUCGAAAGGUCUUAGACAAGGU$_{CU-5'}$ (SEQ ID NO: 983)

AR-1200 Target: 5'-GAGGAGCTTTCCAGAATCTGTTCCAGA-3' (SEQ ID NO: 1037)

5'-AGCAGGAAGCAGUAUCCGAAGGCAG$^{AC-3'}$ (SEQ ID NO: 3981)
3'-UCGUCCUUCGUCAUAGGCUUCCGUC$_{GU-5'}$ (SEQ ID NO: 984)

AR-1734 Target: 5'-AGCAGGAAGCAGTATCCGAAGGCAGCA-3' (SEQ ID NO: 1038)

5'-CCAAGGACAAUUACUUAGGGGGCAC$^{CC-3'}$ (SEQ ID NO: 3982)
3'-GGUUCCUGUUAAUGAAUCCCCCGUG$_{AA-5'}$ (SEQ ID NO: 985)

AR-1803 Target: 5'-CCAAGGACAATTACTTAGGGGGCACTT-3' (SEQ ID NO: 1039)

5'-AAGGAGUUGUGUAAGGCAGUGUCGG$^{CA-3'}$ (SEQ ID NO: 3983)
3'-UUCCUCAACACAUUCCGUCACAGCC$_{AC-5'}$ (SEQ ID NO: 986)

AR-1850 Target: 5'-AAGGAGTTGTGTAAGGCAGTGTCGGTG-3' (SEQ ID NO: 1040)

5'-GGCAAGAGCACUGAAGAUACUGCUG$^{CA-3'}$ (SEQ ID NO: 3984)
3'-CCGUUCUCGUGACUUCUAUGACGAC$_{UC-5'}$ (SEQ ID NO: 987)

AR-2039 Target: 5'-GGCAAGAGCACTGAAGATACTGCTGAG-3' (SEQ ID NO: 1041)

5'-ACUGAAGAUACUGCUGAGUAUUCCC$^{AC-3'}$ (SEQ ID NO: 3985)
3'-UGACUUCUAUGACGACUCAUAAGGG$_{GA-5'}$ (SEQ ID NO: 988)

AR-2048 Target: 5'-ACTGAAGATACTGCTGAGTATTCCCCT-3' (SEQ ID NO: 1042)

5'-CAAGGGAGGUUACACCAAAGGGCUA$^{AC-3'}$ (SEQ ID NO: 3986)
3'-GUUCCCUCCAAUGUGGUUUCCCGAU$_{CU-5'}$ (SEQ ID NO: 989)

AR-2077 Target: 5'-CAAGGGAGGTTACACCAAAGGGCTAGA-3' (SEQ ID NO: 1043)

5'-CUUGUGUCAAAAGCGAAAUGGGCCC$^{AC-3'}$ (SEQ ID NO: 3987)
3'-GAACACAGUUUUCGCUUUACCCGGG$_{GA-5'}$ (SEQ ID NO: 990)

AR-2694 Target: 5'-CTTGTGTCAAAAGCGAAATGGGCCCCT-3' (SEQ ID NO: 1044)

5'-AUGUUUUGCCCAUUGACUAUUACUU$^{CA-3'}$ (SEQ ID NO: 3988)
3'-UACAAAACGGGUAACUGAUAAUGAA$_{AG-5'}$ (SEQ ID NO: 991)

AR-2778 Target: 5'-ATGTTTTGCCCATTGACTATTACTTTC-3' (SEQ ID NO: 1045)

5'-UGCAAGGUCUUCUUCAAAAGAGCCG$^{AC-3'}$ (SEQ ID NO: 3989)
3'-ACGUUCCAGAAGAAGUUUUCUCGGC$_{GA-5'}$ (SEQ ID NO: 992)

AR-2879 Target: 5'-TGCAAGGTCTTCTTCAAAAGAGCCGCT-3' (SEQ ID NO: 1046)

5'-AAGGGAAACAGAAGUACCUGUGCGC^{A}C-3′ (SEQ ID NO: 3990)
3'-UUCCCUUUGUCUUCAUGGACACGCG$_{G_{U-5'}}$ (SEQ ID NO: 993)

AR-2907 Target: 5'-AAGGGAAACAGAAGTACCTGTGCGCCA-3' (SEQ ID NO: 1047)

5'-AUGAUUGCACUAUUGAUAAAUUCCG^{C}C-3′ (SEQ ID NO: 3991)
3'-UACUAACGUGAUAACUAUUUAAGGC$_{U_{U-5'}}$ (SEQ ID NO: 994)

AR-2940 Target: 5'-ATGATTGCACTATTGATAAATTCCGAA-3' (SEQ ID NO: 1048)

5'-UAAAUUCCGAAGGAAAAAUUGUCCA^{C}A-3′ (SEQ ID NO: 3992)
3'-AUUUAAGGCUUCCUUUUUAACAGGU$_{A_{G-5'}}$ (SEQ ID NO: 995)

AR-2956 Target: 5'-TAAATTCCGAAGGAAAAATTGTCCATC-3' (SEQ ID NO: 1049)

5'-AAGGAAAAAUUGUCCAUCUUGUCGU^{A}C-3′ (SEQ ID NO: 3993)
3'-UUCCUUUUUAACAGGUAGAACAGCA$_{G_{A-5'}}$ (SEQ ID NO: 996)

AR-2965 Target: 5'-AAGGAAAAATTGTCCATCTTGTCGTCT-3' (SEQ ID NO: 1050)

5'-GAAAAAUUGUCCAUCUUGUCGUCUU^{A}A-3′ (SEQ ID NO: 3994)
3'-CUUUUUAACAGGUAGAACAGCAGAA$_{G_{C-5'}}$ (SEQ ID NO: 997)

AR-2968 Target: 5'-GAAAAATTGTCCATCTTGTCGTCTTCG-3' (SEQ ID NO: 1051)

5'-GAAGAAACUUGGUAAUCUGAAACUA^{A}C-3′ (SEQ ID NO: 3995)
3'-CUUCUUUGAACCAUUAGACUUUGAU$_{G_{U-5'}}$ (SEQ ID NO: 998)

AR-3037 Target: 5'-GAAGAAACTTGGTAATCTGAAACTACA-3' (SEQ ID NO: 1052)

5'-CAUUGAAGGCUAUGAAUGUCAGCCC^{C}C-3′ (SEQ ID NO: 3996)
3'-GUAACUUCCGAUACUUACAGUCGGG$_{U_{A-5'}}$ (SEQ ID NO: 999)

AR-3133 Target: 5'-CATTGAAGGCTATGAATGTCAGCCCAT-3' (SEQ ID NO: 1053)

5'-CAGGAAUUCCUGUGCAUGAAAGCAC^{C}A-3′ (SEQ ID NO: 3997)
3'-GUCCUUAAGGACACGUACUUUCGUG$_{A_{C-5'}}$ (SEQ ID NO: 1000)

AR-3548 Target: 5'-CAGGAATTCCTGTGCATGAAAGCACTG-3' (SEQ ID NO: 1054)

5'-UCAAAAAUUCUUUGAUGAACUUCGA^{C}C-3′ (SEQ ID NO: 3998)
3'-AGUUUUUAAGAAACUACUUGAAGCU$_{U_{A-5'}}$ (SEQ ID NO: 1001)

AR-3613 Target: 5'-TCAAAAATTCTTTGATGAACTTCGAAT-3' (SEQ ID NO: 1055)

5'-UCUUUGAUGAACUUCGAAUGAACUA^{A}C-3′ (SEQ ID NO: 3999)
3'-AGAAACUACUUGAAGCUUACUUGAU$_{G_{U-5'}}$ (SEQ ID NO: 1002)

AR-3621 Target: 5'-TCTTTGATGAACTTCGAATGAACTACA-3' (SEQ ID NO: 1056)

5'-UUGAUGAACUUCGAAUGAACUACAU^{A}C-3′ (SEQ ID NO: 4000)
3'-AACUACUUGAAGCUUACUUGAUGUA$_{G_{U-5'}}$ (SEQ ID NO: 1003)

AR-3624 Target: 5'-TTGATGAACTTCGAATGAACTACATCA-3' (SEQ ID NO: 1057)

5'-UCGAAUGAACUACAUCAAGGAACUC$^{AC-3'}$ (SEQ ID NO: 4001)
3'-AGCUUACUUGAUGUAGUUCCUUGAG$_{CU-5'}$ (SEQ ID NO: 1004)

AR-3634 Target: 5'-TCGAATGAACTACATCAAGGAACTCGA-3' (SEQ ID NO: 1058)

5'-UGCAAAAGAAAAAAUCCCACAUCCU$^{AA-3'}$ (SEQ ID NO: 4002)
3'-ACGUUUUCUUUUUUAGGGUGUAGGA$_{CG-5'}$ (SEQ ID NO: 1005)

AR-3674 Target: 5'-TGCAAAAGAAAAAATCCCACATCCTGC-3' (SEQ ID NO: 1059)

5'-AAAGAAAAAAUCCCACAUCCUGCUC$^{CC-3'}$ (SEQ ID NO: 4003)
3'-UUUCUUUUUUAGGGUGUAGGACGAG$_{UU-5'}$ (SEQ ID NO: 1006)

AR-3678 Target: 5'-AAAGAAAAAATCCCACATCCTGCTCAA-3' (SEQ ID NO: 1060)

5'-ACUUUUGACCUGCUAAUCAAGUCAC$^{CA-3'}$ (SEQ ID NO: 4004)
3'-UGAAAACUGGACGAUUAGUUCAGUG$_{UG-5'}$ (SEQ ID NO: 1007)

AR-3773 Target: 5'-ACTTTTGACCTGCTAATCAAGTCACAC-3' (SEQ ID NO: 1061)

5'-CCAAGAUCCUUUCUGGGAAAGUCAA$^{AA-3'}$ (SEQ ID NO: 4005)
3'-GGUUCUAGGAAAGACCCUUUCAGUU$_{CG-5'}$ (SEQ ID NO: 1008)

AR-3855 Target: 5'-CCAAGATCCTTTCTGGGAAAGTCAAGC-3' (SEQ ID NO: 1062)

5'-GGAAAGUCAAGCCCAUCUAUUUCCA$^{AC-3'}$ (SEQ ID NO: 4006)
3'-CCUUUCAGUUCGGGUAGAUAAAGGU$_{GU-5'}$ (SEQ ID NO: 1009)

AR-3870 Target: 5'-GGAAAGTCAAGCCCATCTATTTCCACA-3' (SEQ ID NO: 1063)

5'-AGAUGUCUUCUGCCUGUUAUAACUC$^{CA-3'}$ (SEQ ID NO: 4007)
3'-UCUACAGAAGACGGACAAUAUUGAG$_{AC-5'}$ (SEQ ID NO: 1010)

AR-3950 Target: 5'-AGATGTCTTCTGCCTGTTATAACTCTG-3' (SEQ ID NO: 1064)

5'-GGGAAUUUCCUCUAUUGAUGUACAG$^{CA-3'}$ (SEQ ID NO: 4008)
3'-CCCUUAAAGGAGAUAACUACAUGUC$_{AG-5'}$ (SEQ ID NO: 1011)

AR-4000 Target: 5'-GGGAATTTCCTCTATTGATGTACAGTC-3' (SEQ ID NO: 1065)

5'-UUGAUGUACAGUCUGUCAUGAACAU$^{AC-3'}$ (SEQ ID NO: 4009)
3'-AACUACAUGUCAGACAGUACUUGUA$_{CA-5'}$ (SEQ ID NO: 1012)

AR-4014 Target: 5'-TTGATGTACAGTCTGTCATGAACATGT-3' (SEQ ID NO: 1066)

5'-UACAGUCUGUCAUGAACAUGUUCCU$^{AC-3'}$ (SEQ ID NO: 4010)
3'-AUGUCAGACAGUACUUGUACAAGGA$_{CU-5'}$ (SEQ ID NO: 1013)

AR-4020 Target: 5'-TACAGTCTGTCATGAACATGTTCCTGA-3' (SEQ ID NO: 1067)

5'-GUCAUGAACAUGUUCCUGAAUUCUA$^{CC-3'}$ (SEQ ID NO: 4011)
3'-CAGUACUUGUACAAGGACUUAAGAU$_{AA-5'}$ (SEQ ID NO: 1014)

AR-4028 Target: 5'-GTCATGAACATGTTCCTGAATTCTATT-3' (SEQ ID NO: 1068)

5'-ACAUGUUCCUGAAUUCUAUUUGCUG$^{AA-3'}$ (SEQ ID NO: 4012)
3'-UGUACAAGGACUUAAGAUAAACGAC$_{CC-5'}$ (SEQ ID NO: 1015)

AR-4035 Target: 5'-ACATGTTCCTGAATTCTATTTGCTGGG-3' (SEQ ID NO: 1069)

5'-GCUGGGCUUUUUUUUUCUCUUUCUC$^{CA-3'}$ (SEQ ID NO: 4013)
3'-CGACCCGAAAAAAAAAGAGAAAGAG$_{AG-5'}$ (SEQ ID NO: 1016)

AR-4056 Target: 5'-GCTGGGCTTTTTTTTCTCTTTCTCTC-3' (SEQ ID NO: 1070)

5'-UUUUUUUCUCUUUCUCUCCUUUCUU$^{CC-3'}$ (SEQ ID NO: 4014)
3'-AAAAAAAGAGAAAGAGAGGAAAGAA$_{AA-5'}$ (SEQ ID NO: 1017)

AR-4065 Target: 5'-TTTTTTTCTCTTTCTCTCCTTTCTTTT-3' (SEQ ID NO: 1071)

5'-GUGUUUUGAAUGGUGUUGUAUGCCU$^{CC-3'}$ (SEQ ID NO: 4015)
3'-CACAAAACUUACCACAACAUACGGA$_{AA-5'}$ (SEQ ID NO: 1018)

AR-4161 Target: 5'-GTGTTTTGAATGGTGTTGTATGCCTTT-3' (SEQ ID NO: 1072)

5'-AUGGUGUUGUAUGCCUUUAAAUCUG$^{CA-3'}$ (SEQ ID NO: 4016)
3'-UACCACAACAUACGGAAAUUUAGAC$_{AC-5'}$ (SEQ ID NO: 1019)

AR-4170 Target: 5'-ATGGTGTTGTATGCCTTTAAATCTGTG-3' (SEQ ID NO: 1073)

5'-GUCAAGUUGUGCUUGUUUACAGCAC$^{CC-3'}$ (SEQ ID NO: 4017)
3'-CAGUUCAACACGAACAAAUGUCGUG$_{AU-5'}$ (SEQ ID NO: 1020)

AR-4218 Target: 5'-GTCAAGTTGTGCTTGTTTACAGCACTA-3' (SEQ ID NO: 1074)

5'-AGCUAAGAUUAUCUGGGGAAAUCAA$^{CC-3'}$ (SEQ ID NO: 4018)
3'-UCGAUUCUAAUAGACCCCUUUAGUU$_{UU-5'}$ (SEQ ID NO: 1021)

AR-4299 Target: 5'-AGCTAAGATTATCTGGGGAAATCAAAA-3' (SEQ ID NO: 1075)

5'-UCUGGGGAAAUCAAAACAAAAACAA$^{AA-3'}$ (SEQ ID NO: 4019)
3'-AGACCCCUUUAGUUUUGUUUUUGUU$_{CG-5'}$ (SEQ ID NO: 1022)

AR-4310 Target: 5'-TCTGGGGAAATCAAAACAAAAACAAGC-3' (SEQ ID NO: 1076)

5'-GGGAAAUCAAAACAAAAACAAGCAA$^{CA-3'}$ (SEQ ID NO: 4020)
3'-CCCUUUAGUUUUGUUUUUGUUCGUU$_{UG-5'}$ (SEQ ID NO: 1023)

AR-4314 Target: 5'-GGGAAATCAAAACAAAAACAAGCAAAC-3' (SEQ ID NO: 1077)

5'-CGGUGAAGUUUUUAAAAGCUGCUAA$^{CA-3'}$ (SEQ ID NO: 4021)
3'-GCCACUUCAAAAAUUUUCGACGAUU$_{UC-5'}$ (SEQ ID NO: 1249)

AR-249 Target: 5'-CGGTGAAGTTTTTAAAAGCTGCTAAAG-3' (SEQ ID NO: 1312)

5'-GUUUUUAAAAGCUGCUAAAGACUCG$^{AC-3'}$ (SEQ ID NO: 4022)
3'-CAAAAAUUUUCGACGAUUUCUGAGC$_{CU-5'}$ (SEQ ID NO: 1250)

AR-256 Target: 5'-GTTTTTAAAAGCTGCTAAAGACTCGGA-3' (SEQ ID NO: 1313)

5'-UUUUAAAAGCUGCUAAAGACUCGGA$^{AA-3'}$ (SEQ ID NO: 4023)
3'-AAAAUUUUCGACGAUUUCUGAGCCU$_{CC-5'}$ (SEQ ID NO: 1251)

AR-258 Target: 5'-TTTTAAAAGCTGCTAAAGACTCGGAGG-3' (SEQ ID NO: 1314)

5'-GCGGAGAGAACCCUCUGUUUUCCCC$^{AC-3'}$ (SEQ ID NO: 4024)
3'-CGCCUCUCUUGGGAGACAAAAGGGG$_{GU-5'}$ (SEQ ID NO: 1252)

AR-618 Target: 5'-GCGGAGAGAACCCTCTGTTTTCCCCCA-3' (SEQ ID NO: 1315)

5'-AGAGAUCAAAAGAUGAAAAGGCAGU$^{AC-3'}$ (SEQ ID NO: 4025)
3'-UCUCUAGUUUUCUACUUUUCCGUCA$_{GU-5'}$ (SEQ ID NO: 1253)

AR-691 Target: 5'-AGAGATCAAAAGATGAAAAGGCAGTCA-3' (SEQ ID NO: 1316)

5'-AUCAAAAGAUGAAAAGGCAGUCAGG$^{CA-3'}$ (SEQ ID NO: 4026)
3'-UAGUUUUCUACUUUUCCGUCAGUCC$_{AG-5'}$ (SEQ ID NO: 1254)

AR-695 Target: 5'-ATCAAAAGATGAAAAGGCAGTCAGGTC-3' (SEQ ID NO: 1317)

5'-UUCAGUAGCCAAAAAACAAAACAAA$^{AC-3'}$ (SEQ ID NO: 4027)
3'-AAGUCAUCGGUUUUUUGUUUUGUUU$_{GU-5'}$ (SEQ ID NO: 1255)

AR-722 Target: 5'-TTCAGTAGCCAAAAAACAAAACAAACA-3' (SEQ ID NO: 1318)

5'-AAAAAACAAAACAAACAAAAACAAA$^{CC-3'}$ (SEQ ID NO: 4028)
3'-UUUUUUGUUUUGUUUGUUUUUGUUU$_{UU-5'}$ (SEQ ID NO: 1256)

AR-732 Target: 5'-AAAAAACAAAACAAACAAAAACAAAAA-3' (SEQ ID NO: 1319)

5'-AAUAAAAGAAAAAGAUAAUAACUCA$^{AC-3'}$ (SEQ ID NO: 4029)
3'-UUAUUUUCUUUUUCUAUUAUUGAGU$_{CA-5'}$ (SEQ ID NO: 1257)

AR-765 Target: 5'-AATAAAAGAAAAAGATAATAACTCAGT-3' (SEQ ID NO: 1320)

5'-UAAAAGAAAAAGAUAAUAACUCAGU$^{CA-3'}$ (SEQ ID NO: 4030)
3'-AUUUUCUUUUUCUAUUAUUGAGUCA$_{AG-5'}$ (SEQ ID NO: 1258)

AR-767 Target: 5'-TAAAAGAAAAAGATAATAACTCAGTTC-3' (SEQ ID NO: 1321)

5'-GAAAAAGAUAAUAACUCAGUUCUUA$^{CC-3'}$ (SEQ ID NO: 4031)
3'-CUUUUUCUAUUAUUGAGUCAAGAAU$_{AA-5'}$ (SEQ ID NO: 1259)

AR-772 Target: 5'-GAAAAAGATAATAACTCAGTTCTTATT-3' (SEQ ID NO: 1322)

5'-UAAUAACUCAGUUCUUAUUUGCACC$^{CC-3'}$ (SEQ ID NO: 4032)
3'-AUUAUUGAGUCAAGAAUAAACGUGG$_{AU-5'}$ (SEQ ID NO: 1260)

AR-780 Target: 5'-TAATAACTCAGTTCTTATTTGCACCTA-3' (SEQ ID NO: 1323)

5'-CUCAGUUCUUAUUUGCACCUACUUC$^{CA-3'}$ (SEQ ID NO: 4033)
3'-GAGUCAAGAAUAAACGUGGAUGAAG$_{UC-5'}$ (SEQ ID NO: 1261)

AR-786 Target: 5'-CTCAGTTCTTATTTGCACCTACTTCAG-3' (SEQ ID NO: 1324)

5'-GGUGGAGGAUUUUGUUUUUUUCUUU$^{C}{}^{C-3'}$ (SEQ ID NO: 4034)
3'-CCACCUCCUAAAACAAAAAAAGAAA$_{A}{}_{U-5'}$ (SEQ ID NO: 1262)

AR-831 Target: 5'-GGTGGAGGATTTTGTTTTTTTCTTTTA-3' (SEQ ID NO: 1325)

5'-UUUGUUUUUUUCUUUUAAGAUCUGG$^{A}{}^{A-3'}$ (SEQ ID NO: 4035)
3'-AAACAAAAAAAAGAAAAUUCUAGACC$_{C}{}_{G-5'}$ (SEQ ID NO: 1263)

AR-841 Target: 5'-TTTGTTTTTTTCTTTTAAGATCTGGGC-3' (SEQ ID NO: 1326)

5'-UUUUUUCUUUUAAGAUCUGGGCAUC$^{C}{}^{C-3'}$ (SEQ ID NO: 4036)
3'-AAAAAAGAAAAUUCUAGACCCGUAG$_{A}{}_{A-5'}$ (SEQ ID NO: 1264)

AR-846 Target: 5'-TTTTTTCTTTTAAGATCTGGGCATCTT-3' (SEQ ID NO: 1327)

5'-UCUGGGCAUCUUUUGAAUCUACCCU$^{C}{}^{A-3'}$ (SEQ ID NO: 4037)
3'-AGACCCGUAGAAAACUUAGAUGGGA$_{A}{}_{G-5'}$ (SEQ ID NO: 1265)

AR-861 Target: 5'-TCTGGGCATCTTTTGAATCTACCCTTC-3' (SEQ ID NO: 1328)

5'-CGCAAGUUUCCUUCUCUGGAGCUUC$^{A}{}^{A-3'}$ (SEQ ID NO: 4038)
3'-GCGUUCAAAGGAAGAGACCUCGAAG$_{G}{}_{G-5'}$ (SEQ ID NO: 1266)

AR-997 Target: 5'-CGCAAGTTTCCTTCTCTGGAGCTTCCC-3' (SEQ ID NO: 1329)

5'-AAGGGAAGUAGGUGGAAGAUUCAGC$^{A}{}^{C-3'}$ (SEQ ID NO: 4039)
3'-UUCCCUUCAUCCACCUUCUAAGUCG$_{G}{}_{U-5'}$ (SEQ ID NO: 1267)

AR-1106 Target: 5'-AAGGGAAGTAGGTGGAAGATTCAGCCA-3' (SEQ ID NO: 1330)

5'-GGAAGUAGGUGGAAGAUUCAGCCAA$^{A}{}^{A-3'}$ (SEQ ID NO: 4040)
3'-CCUUCAUCCACCUUCUAAGUCGGUU$_{C}{}_{G-5'}$ (SEQ ID NO: 1268)

AR-1109 Target: 5'-GGAAGTAGGTGGAAGATTCAGCCAAGC-3' (SEQ ID NO: 1331)

5'-CAAGGACAAUUACUUAGGGGGCACU$^{C}{}^{A-3'}$ (SEQ ID NO: 4041)
3'-GUUCCUGUUAAUGAAUCCCCCGUGA$_{A}{}_{G-5'}$ (SEQ ID NO: 1269)

AR-1804 Target: 5'-CAAGGACAATTACTTAGGGGGCACTTC-3' (SEQ ID NO: 1332)

5'-GCCGAAUGCAAAGGUUCUCUGCUAG$^{C}{}^{A-3'}$ (SEQ ID NO: 4042)
3'-CGGCUUACGUUUCCAAGAGACGAUC$_{U}{}_{G-5'}$ (SEQ ID NO: 1270)

AR-2003 Target: 5'-GCCGAATGCAAAGGTTCTCTGCTAGAC-3' (SEQ ID NO: 1333)

5'-GCAAGAGCACUGAAGAUACUGCUGA$^{A}{}^{C-3'}$ (SEQ ID NO: 4043)
3'-CGUUCUCGUGACUUCUAUGACGACU$_{C}{}_{A-5'}$ (SEQ ID NO: 1271)

AR-2040 Target: 5'-GCAAGAGCACTGAAGATACTGCTGAGT-3' (SEQ ID NO: 1334)

5'-CUGAAGAUACUGCUGAGUAUUCCCC$^{C}{}^{C-3'}$ (SEQ ID NO: 4044)
3'-GACUUCUAUGACGACUCAUAAGGGG$_{A}{}_{A-5'}$ (SEQ ID NO: 1272)

AR-2049 Target: 5'-CTGAAGATACTGCTGAGTATTCCCCTT-3' (SEQ ID NO: 1335)

5'-UUGUGUCAAAAGCGAAAUGGGCCCC$^{CA-3'}$ (SEQ ID NO: 4045)
3'-AACACAGUUUUCGCUUUACCCGGGG$_{AC-5'}$ (SEQ ID NO: 1273)

AR-2695 Target: 5'-TTGTGTCAAAAGCGAAATGGGCCCCTG-3' (SEQ ID NO: 1336)

5'-UGUUUUGCCCAUUGACUAUUACUUU$^{AA-3'}$ (SEQ ID NO: 4046)
3'-ACAAAACGGGUAACUGAUAAUGAAA$_{GG-5'}$ (SEQ ID NO: 1274)

AR-2779 Target: 5'-TGTTTTGCCCATTGACTATTACTTTCC-3' (SEQ ID NO: 1337)

5'-CCCAUUGACUAUUACUUUCCACCCC$^{CA-3'}$ (SEQ ID NO: 4047)
3'-GGGUAACUGAUAAUGAAAGGUGGGG$_{UC-5'}$ (SEQ ID NO: 1275)

AR-2786 Target: 5'-CCCATTGACTATTACTTTCCACCCCAG-3' (SEQ ID NO: 1338)

5'-GCAAGGUCUUCUUCAAAAGAGCCGC$^{CA-3'}$ (SEQ ID NO: 4048)
3'-CGUUCCAGAAGAAGUUUUCUCGGCG$_{AC-5'}$ (SEQ ID NO: 1276)

AR-2880 Target: 5'-GCAAGGTCTTCTTCAAAAGAGCCGCTG-3' (SEQ ID NO: 1339)

5'-UGAUUGCACUAUUGAUAAAUUCCGA$^{CA-3'}$ (SEQ ID NO: 4049)
3'-ACUAACGUGAUAACUAUUUAAGGCU$_{UC-5'}$ (SEQ ID NO: 1277)

AR-2941 Target: 5'-TGATTGCACTATTGATAAATTCCGAAG-3' (SEQ ID NO: 1340)

5'-UCCGAAGGAAAAAUUGUCCAUCUUG$^{CA-3'}$ (SEQ ID NO: 4050)
3'-AGGCUUCCUUUUUAACAGGUAGAAC$_{AG-5'}$ (SEQ ID NO: 1278)

AR-2961 Target: 5'-TCCGAAGGAAAAATTGTCCATCTTGTC-3' (SEQ ID NO: 1341)

5'-AGGAAAAAUUGUCCAUCUUGUCGUC$^{CC-3'}$ (SEQ ID NO: 4051)
3'-UCCUUUUUAACAGGUAGAACAGCAG$_{AA-5'}$ (SEQ ID NO: 1279)

AR-2966 Target: 5'-AGGAAAAATTGTCCATCTTGTCGTCTT-3' (SEQ ID NO: 1342)

5'-GACAGUGUCACACAUUGAAGGCUAU$^{AC-3'}$ (SEQ ID NO: 4052)
3'-CUGUCACAGUGUGUAACUUCCGAUA$_{CU-5'}$ (SEQ ID NO: 1280)

AR-3121 Target: 5'-GACAGTGTCACACATTGAAGGCTATGA-3' (SEQ ID NO: 1343)

5'-AUUGAAGGCUAUGAAUGUCAGCCCA$^{CA-3'}$ (SEQ ID NO: 4053)
3'-UAACUUCCGAUACUUACAGUCGGGU$_{AG-5'}$ (SEQ ID NO: 1281)

AR-3134 Target: 5'-ATTGAAGGCTATGAATGTCAGCCCATC-3' (SEQ ID NO: 1344)

5'-AGAUGGCUGUCAUUCAGUACUCCUG$^{AC-3'}$ (SEQ ID NO: 4054)
3'-UCUACCGACAGUAAGUCAUGAGGAC$_{CU-5'}$ (SEQ ID NO: 1282)

AR-3342 Target: 5'-AGATGGCTGTCATTCAGTACTCCTGGA-3' (SEQ ID NO: 1345)

5'-UCUGGUUUUCAAUGAGUACCGCAUG$^{AC-3'}$ (SEQ ID NO: 4055)
3'-AGACCAAAAGUUACUCAUGGCGUAC$_{GU-5'}$ (SEQ ID NO: 1283)

AR-3445 Target: 5'-TCTGGTTTTCAATGAGTACCGCATGCA-3' (SEQ ID NO: 1346)

5'-AGGAAUUCCUGUGCAUGAAAGCACU$^{A}{}^{A-3'}$ (SEQ ID NO: 4056)
3'-UCCUUAAGGACACGUACUUUCGUGA$_{C}{}_{G-5'}$ (SEQ ID NO: 1284)

AR-3549 Target: 5'-AGGAATTCCTGTGCATGAAAGCACTGC-3' (SEQ ID NO: 1347)

5'-CAAAAAUUCUUUGAUGAACUUCGAA$^{C}{}^{A-3'}$ (SEQ ID NO: 4057)
3'-GUUUUUAAGAAACUACUUGAAGCUU$_{A}{}_{C-5'}$ (SEQ ID NO: 1285)

AR-3614 Target: 5'-CAAAAATTCTTTGATGAACTTCGAATG-3' (SEQ ID NO: 1348)

5'-CUUUGAUGAACUUCGAAUGAACUAC$^{C}{}^{C-3'}$ (SEQ ID NO: 4058)
3'-GAAACUACUUGAAGCUUACUUGAUG$_{U}{}_{A-5'}$ (SEQ ID NO: 1286)

AR-3622 Target: 5'-CTTTGATGAACTTCGAATGAACTACAT-3' (SEQ ID NO: 1349)

5'-UGAUGAACUUCGAAUGAACUACAUC$^{C}{}^{C-3'}$ (SEQ ID NO: 4059)
3'-ACUACUUGAAGCUUACUUGAUGUAG$_{U}{}_{U-5'}$ (SEQ ID NO: 1287)

AR-3625 Target: 5'-TGATGAACTTCGAATGAACTACATCAA-3' (SEQ ID NO: 1350)

5'-CGAAUGAACUACAUCAAGGAACUCG$^{C}{}^{C-3'}$ (SEQ ID NO: 4060)
3'-GCUUACUUGAUGUAGUUCCUUGAGC$_{U}{}_{A-5'}$ (SEQ ID NO: 1288)

AR-3635 Target: 5'-CGAATGAACTACATCAAGGAACTCGAT-3' (SEQ ID NO: 1351)

5'-AAUGAACUACAUCAAGGAACUCGAU$^{A}{}^{A-3'}$ (SEQ ID NO: 4061)
3'-UUACUUGAUGUAGUUCCUUGAGCUA$_{G}{}_{C-5'}$ (SEQ ID NO: 1289)

AR-3637 Target: 5'-AATGAACTACATCAAGGAACTCGATCG-3' (SEQ ID NO: 1352)

5'-GCAAAAGAAAAAAUCCCACAUCCUG$^{A}{}^{C-3'}$ (SEQ ID NO: 4062)
3'-CGUUUUCUUUUUUAGGGUGUAGGAC$_{G}{}_{A-5'}$ (SEQ ID NO: 1290)

AR-3675 Target: 5'-GCAAAAGAAAAAATCCCACATCCTGCT-3' (SEQ ID NO: 1353)

5'-AAGAAAAAAUCCCACAUCCUGCUCA$^{C}{}^{A-3'}$ (SEQ ID NO: 4063)
3'-UUCUUUUUUAGGGUGUAGGACGAGU$_{U}{}_{C-5'}$ (SEQ ID NO: 1291)

AR-3679 Target: 5'-AAGAAAAAATCCCACATCCTGCTCAAG-3' (SEQ ID NO: 1354)

5'-CUUUUGACCUGCUAAUCAAGUCACA$^{A}{}^{C-3'}$ (SEQ ID NO: 4064)
3'-GAAAACUGGACGAUUAGUUCAGUGU$_{G}{}_{U-5'}$ (SEQ ID NO: 1292)

AR-3774 Target: 5'-CTTTTGACCTGCTAATCAAGTCACACA-3' (SEQ ID NO: 1355)

5'-GCCUGUUAUAACUCUGCACUACUCC$^{C}{}^{A-3'}$ (SEQ ID NO: 4065)
3'-CGGACAAUAUUGAGACGUGAUGAGG$_{A}{}_{G-5'}$ (SEQ ID NO: 1293)

AR-3961 Target: 5'-GCCTGTTATAACTCTGCACTACTCCTC-3' (SEQ ID NO: 1356)

5'-CUGUUAUAACUCUGCACUACUCCUC$^{C}{}^{A-3'}$ (SEQ ID NO: 4066)
3'-GACAAUAUUGAGACGUGAUGAGGAG$_{A}{}_{C-5'}$ (SEQ ID NO: 1294)

AR-3963 Target: 5'-CTGTTATAACTCTGCACTACTCCTCTG-3' (SEQ ID NO: 1357)

5'-GGAAUUUCCUCUAUUGAUGUACAGU$^{AC-3'}$ (SEQ ID NO: 4067)
3'-CCUUAAAGGAGAUAACUACAUGUCA$_{GA-5'}$ (SEQ ID NO: 1295)

AR-4001 Target: 5'-GGAATTTCCTCTATTGATGTACAGTCT-3' (SEQ ID NO: 1358)

5'-CUCUAUUGAUGUACAGUCUGUCAUG$^{CC-3'}$ (SEQ ID NO: 4068)
3'-GAGAUAACUACAUGUCAGACAGUAC$_{UU-5'}$ (SEQ ID NO: 1296)

AR-4009 Target: 5'-CTCTATTGATGTACAGTCTGTCATGAA-3' (SEQ ID NO: 1359)

5'-UCAUGAACAUGUUCCUGAAUUCUAU$^{CC-3'}$ (SEQ ID NO: 4069)
3'-AGUACUUGUACAAGGACUUAAGAUA$_{AA-5'}$ (SEQ ID NO: 1297)

AR-4029 Target: 5'-TCATGAACATGTTCCTGAATTCTATTT-3' (SEQ ID NO: 1360)

5'-UCCUGAAUUCUAUUUGCUGGGCUUU$^{CC-3'}$ (SEQ ID NO: 4070)
3'-AGGACUUAAGAUAAACGACCCGAAA$_{AA-5'}$ (SEQ ID NO: 1298)

AR-4041 Target: 5'-TCCTGAATTCTATTTGCTGGGCTTTTT-3' (SEQ ID NO: 1361)

5'-GCUUUUUUUUUCUCUUUCUCUCCUU$^{CA-3'}$ (SEQ ID NO: 4071)
3'-CGAAAAAAAAAGAGAAAGAGAGGAA$_{AG-5'}$ (SEQ ID NO: 1299)

AR-4061 Target: 5'-GCTTTTTTTTCTCTTTCTCTCCTTTC-3' (SEQ ID NO: 1362)

5'-UUUUUUCUCUUUCUCUCCUUUCUUU$^{CC-3'}$ (SEQ ID NO: 4072)
3'-AAAAAAGAGAAAGAGAGGAAAGAAA$_{AA-5'}$ (SEQ ID NO: 1300)

AR-4066 Target: 5'-TTTTTCTCTTTCTCTCCTTTCTTTTT-3' (SEQ ID NO: 1363)

5'-CUCUUUCUCUCCUUUCUUUUUCUUC$^{CC-3'}$ (SEQ ID NO: 4073)
3'-GAGAAAGAGAGGAAAGAAAAAGAAG$_{AA-5'}$ (SEQ ID NO: 1301)

AR-4072 Target: 5'-CTCTTTCTCTCCTTTCTTTTTCTTCTT-3' (SEQ ID NO: 1364)

5'-CCAUGGCACCUUCAGACUUUGCUUC$^{AA-3'}$ (SEQ ID NO: 4074)
3'-GGUACCGUGGAAGUCUGAAACGAAG$_{GG-5'}$ (SEQ ID NO: 1302)

AR-4118 Target: 5'-CCATGGCACCTTCAGACTTTGCTTCCC-3' (SEQ ID NO: 1365)

5'-UGUUUUGAAUGGUGUUGUAUGCCUU$^{CC-3'}$ (SEQ ID NO: 4075)
3'-ACAAAACUUACCACAACAUACGGAA$_{AU-5'}$ (SEQ ID NO: 1303)

AR-4162 Target: 5'-TGTTTTGAATGGTGTTGTATGCCTTTA-3' (SEQ ID NO: 1366)

5'-UGGUGUUGUAUGCCUUUAAAUCUGU$^{AC-3'}$ (SEQ ID NO: 4076)
3'-ACCACAACAUACGGAAAUUUAGACA$_{CU-5'}$ (SEQ ID NO: 1304)

AR-4171 Target: 5'-TGGTGTTGTATGCCTTTAAATCTGTGA-3' (SEQ ID NO: 1367)

5'-CUUUAAAUCUGUGAUGAUCCUCAUA$^{CA-3'}$ (SEQ ID NO: 4077)
3'-GAAAUUUAGACACUACUAGGAGUAU$_{AC-5'}$ (SEQ ID NO: 1305)

AR-4184 Target: 5'-CTTTAAATCTGTGATGATCCTCATATG-3' (SEQ ID NO: 1368)

5'-UCUGUGAUGAUCCUCAUAUGGCCCA$^{AC-3'}$ (SEQ ID NO: 4078)
3'-AGACACUACUAGGAGUAUACCGGGU$_{CA-5'}$ (SEQ ID NO: 1306)

AR-4191 Target: 5'-TCTGTGATGATCCTCATATGGCCCAGT-3' (SEQ ID NO: 1369)

5'-AAGUUGUGCUUGUUUACAGCACUAC$^{CA-3'}$ (SEQ ID NO: 4079)
3'-UUCAACACGAACAAAUGUCGUGAUG$_{AG-5'}$ (SEQ ID NO: 1307)

AR-4221 Target: 5'-AAGTTGTGCTTGTTTACAGCACTACTC-3' (SEQ ID NO: 1370)

5'-ACGUUUACUUAUCUUAUGCCACGGG$^{CC-3'}$ (SEQ ID NO: 4080)
3'-UGCAAAUGAAUAGAAUACGGUGCCC$_{UU-5'}$ (SEQ ID NO: 1308)

AR-4264 Target: 5'-ACGTTTACTTATCTTATGCCACGGGAA-3' (SEQ ID NO: 1371)

5'-AGUUUAGAGAGCUAAGAUUAUCUGG$^{AA-3'}$ (SEQ ID NO: 4081)
3'-UCAAAUCUCUCGAUUCUAAUAGACC$_{CC-5'}$ (SEQ ID NO: 1309)

AR-4290 Target: 5'-AGTTTAGAGAGCTAAGATTATCTGGGG-3' (SEQ ID NO: 1372)

5'-GCUAAGAUUAUCUGGGGAAAUCAAA$^{CA-3'}$ (SEQ ID NO: 4082)
3'-CGAUUCUAAUAGACCCCUUUAGUUU$_{UG-5'}$ (SEQ ID NO: 1310)

AR-4300 Target: 5'-GCTAAGATTATCTGGGGAAATCAAAAC-3' (SEQ ID NO: 1373)

5'-CUGGGGAAAUCAAAACAAAAACAAG$^{AC-3'}$ (SEQ ID NO: 4083)
3'-GACCCCUUUAGUUUUGUUUUUGUUC$_{GU-5'}$ (SEQ ID NO: 1311)

AR-4311 Target: 5'-CTGGGGAAATCAAAACAAAAACAAGCA-3' (SEQ ID NO: 1374)

5'-GAGCCAGCUUGCUGGGAGAGCGGGA$^{AA-3'}$ (SEQ ID NO: 4084)
3'-CUCGGUCGAACGACCCUCUCGCCCU$_{GC-5'}$ (SEQ ID NO: 1906)

AR-39 Target: 5'-GAGCCAGCTTGCTGGGAGAGCGGGACG-3' (SEQ ID NO: 2311)

5'-CGGCUCCAGCGACAGCCAACGCCUC$^{CC-3'}$ (SEQ ID NO: 4085)
3'-GCCGAGGUCGCUGUCGGUUGCGGAG$_{AA-5'}$ (SEQ ID NO: 1907)

AR-174 Target: 5'-CGGCTCCAGCGACAGCCAACGCCTCTT-3' (SEQ ID NO: 2312)

5'-CAGCCAACGCCUCUUGCAGCGCGGC$^{AA-3'}$ (SEQ ID NO: 4086)
3'-GUCGGUUGCGGAGAACGUCGCGCCG$_{CC-5'}$ (SEQ ID NO: 1908)

AR-186 Target: 5'-CAGCCAACGCCTCTTGCAGCGCGGCGG-3' (SEQ ID NO: 2313)

5'-GCCUCUUGCAGCGCGGCGGCUUCGA$^{CA-3'}$ (SEQ ID NO: 4087)
3'-CGGAGAACGUCGCGCCGCCGAAGCU$_{UC-5'}$ (SEQ ID NO: 1909)

AR-194 Target: 5'-GCCTCTTGCAGCGCGGCGGCTTCGAAG-3' (SEQ ID NO: 2314)

5'-UGCAGCGCGGCGGCUUCGAAGCCGC$^{AA-3'}$ (SEQ ID NO: 4088)
3'-ACGUCGCGCCGCCGAAGCUUCGGCG$_{GC-5'}$ (SEQ ID NO: 1910)

AR-200 Target: 5'-TGCAGCGCGGCGGCTTCGAAGCCGCCG-3' (SEQ ID NO: 2315)

5'-CGAAGCCGCCGCCCGGAGCUGCCCU$^{C}{}^{C-3'}$ (SEQ ID NO: 4089)
3'-GCUUCGGCGGCGGGCCUCGACGGGA$_{A}{}_{A-5'}$ (SEQ ID NO: 1911)

AR-216 Target: 5'-CGAAGCCGCCGCCCGGAGCTGCCCTTT-3' (SEQ ID NO: 2316)

5'-CGCCGCCCGGAGCUGCCCUUUCCUC$^{C}{}^{C-3'}$ (SEQ ID NO: 4090)
3'-GCGGCGGGCCUCGACGGGAAAGGAG$_{A}{}_{A-5'}$ (SEQ ID NO: 1912)

AR-222 Target: 5'-CGCCGCCCGGAGCTGCCCTTTCCTCTT-3' (SEQ ID NO: 2317)

5'-UGAAGUUUUUAAAAGCUGCUAAAGA$^{A}{}^{C-3'}$ (SEQ ID NO: 4091)
3'-ACUUCAAAAAUUUUCGACGAUUUCU$_{G}{}_{A-5'}$ (SEQ ID NO: 1913)

AR-252 Target: 5'-TGAAGTTTTTAAAAGCTGCTAAAGACT-3' (SEQ ID NO: 2318)

5'-CCGUCUUCUCUCCCGCAGCUGCCUC$^{C}{}^{A-3'}$ (SEQ ID NO: 4092)
3'-GGCAGAAGAGAGGGCGUCGACGGAG$_{U}{}_{C-5'}$ (SEQ ID NO: 1914)

AR-375 Target: 5'-CCGTCTTCTCTCCCGCAGCTGCCTCAG-3' (SEQ ID NO: 2319)

5'-CCGCAGCUGCCUCAGUCGGCUACUC$^{C}{}^{A-3'}$ (SEQ ID NO: 4093)
3'-GGCGUCGACGGAGUCAGCCGAUGAG$_{A}{}_{G-5'}$ (SEQ ID NO: 1915)

AR-387 Target: 5'-CCGCAGCTGCCTCAGTCGGCTACTCTC-3' (SEQ ID NO: 2320)

5'-UUUGGCUGCGAGCGGGCGAGCUAGC$^{C}{}^{A-3'}$ (SEQ ID NO: 4094)
3'-AAACCGACGCUCGCCCGCUCGAUCG$_{A}{}_{C-5'}$ (SEQ ID NO: 1916)

AR-506 Target: 5'-TTTGGCTGCGAGCGGGCGAGCTAGCTG-3' (SEQ ID NO: 2321)

5'-CGGGCGAGCUAGCUGCACAUUGCAA$^{C}{}^{A-3'}$ (SEQ ID NO: 4095)
3'-GCCCGCUCGAUCGACGUGUAACGUU$_{U}{}_{C-5'}$ (SEQ ID NO: 1917)

AR-518 Target: 5'-CGGGCGAGCTAGCTGCACATTGCAAAG-3' (SEQ ID NO: 2322)

5'-UCUCUCUCCACCUCCUCCUGCCUUC$^{A}{}^{A-3'}$ (SEQ ID NO: 4096)
3'-AGAGAGAGGUGGAGGAGGACGGAAG$_{G}{}_{G-5'}$ (SEQ ID NO: 1918)

AR-646 Target: 5'-TCTCTCTCCACCTCCTCCTGCCTTCCC-3' (SEQ ID NO: 2323)

5'-CCAGAGAUCAAAAGAUGAAAAGGCA$^{A}{}^{C-3'}$ (SEQ ID NO: 4097)
3'-GGUCUCUAGUUUUCUACUUUUCCGU$_{C}{}_{A-5'}$ (SEQ ID NO: 1919)

AR-689 Target: 5'-CCAGAGATCAAAAGATGAAAAGGCAGT-3' (SEQ ID NO: 2324)

5'-CAGUAGCCAAAAAACAAAACAAACA$^{C}{}^{C-3'}$ (SEQ ID NO: 4098)
3'-GUCAUCGGUUUUUUGUUUUGUUUGU$_{U}{}_{U-5'}$ (SEQ ID NO: 1920)

AR-724 Target: 5'-CAGTAGCCAAAAAACAAAACAAACAAA-3' (SEQ ID NO: 2325)

5'-CCAAAAAACAAAACAAACAAAAACA$^{C}{}^{C-3'}$ (SEQ ID NO: 4099)
3'-GGUUUUUUGUUUUGUUUGUUUUUGU$_{U}{}_{U-5'}$ (SEQ ID NO: 1921)

AR-730 Target: 5'-CCAAAAAACAAAACAAACAAAAACAAA-3' (SEQ ID NO: 2326)

5'-ACAAAACAAACAAAAACAAAAAAGC$^{AA-3'}$ (SEQ ID NO: 4100)
3'-UGUUUUGUUUGUUUUUGUUUUUUCG$_{GC-5'}$ (SEQ ID NO: 1922)

AR-737 Target: 5'-ACAAAACAAACAAAAACAAAAAAGCCG-3' (SEQ ID NO: 2327)

5'-ACAAAAAAGCCGAAAUAAAAGAAAA$^{CA-3'}$ (SEQ ID NO: 4101)
3'-UGUUUUUUCGGCUUUAUUUUCUUUU$_{UC-5'}$ (SEQ ID NO: 1923)

AR-752 Target: 5'-ACAAAAAAGCCGAAATAAAAGAAAAAG-3' (SEQ ID NO: 2328)

5'-GCCGAAAUAAAAGAAAAAGAUAAUA$^{CA-3'}$ (SEQ ID NO: 4102)
3'-CGGCUUUAUUUUCUUUUUCUAUUAU$_{UG-5'}$ (SEQ ID NO: 1924)

AR-760 Target: 5'-GCCGAAATAAAAGAAAAAGATAATAAC-3' (SEQ ID NO: 2329)

5'-AAGAAAAAGAUAAUAACUCAGUUCU$^{CC-3'}$ (SEQ ID NO: 4103)
3'-UUCUUUUUCUAUUAUUGAGUCAAGA$_{AU-5'}$ (SEQ ID NO: 1925)

AR-770 Target: 5'-AAGAAAAAGATAATAACTCAGTTCTTA-3' (SEQ ID NO: 2330)

5'-AAAGAUAAUAACUCAGUUCUUAUUU$^{AA-3'}$ (SEQ ID NO: 4104)
3'-UUUCUAUUAUUGAGUCAAGAAUAAA$_{CG-5'}$ (SEQ ID NO: 1926)

AR-775 Target: 5'-AAAGATAATAACTCAGTTCTTATTTGC-3' (SEQ ID NO: 2331)

5'-GAUAAUAACUCAGUUCUUAUUUGCA$^{AA-3'}$ (SEQ ID NO: 4105)
3'-CUAUUAUUGAGUCAAGAAUAAACGU$_{GG-5'}$ (SEQ ID NO: 1927)

AR-778 Target: 5'-GATAATAACTCAGTTCTTATTTGCACC-3' (SEQ ID NO: 2332)

5'-UGGAGGAUUUUGUUUUUUUCUUUUA$^{CA-3'}$ (SEQ ID NO: 4106)
3'-ACCUCCUAAAACAAAAAAAGAAAAU$_{UC-5'}$ (SEQ ID NO: 1928)

AR-833 Target: 5'-TGGAGGATTTTGTTTTTTTCTTTTAAG-3' (SEQ ID NO: 2333)

5'-GAUUUUGUUUUUUUCUUUUAAGAUC$^{CA-3'}$ (SEQ ID NO: 4107)
3'-CUAAAACAAAAAAAAGAAAAUUCUAG$_{AC-5'}$ (SEQ ID NO: 1929)

AR-838 Target: 5'-GATTTTGTTTTTTTCTTTTAAGATCTG-3' (SEQ ID NO: 2334)

5'-GUUUUUUUCUUUUAAGAUCUGGGCA$^{CA-3'}$ (SEQ ID NO: 4108)
3'-CAAAAAAAGAAAAUUCUAGACCCGU$_{AG-5'}$ (SEQ ID NO: 1930)

AR-844 Target: 5'-GTTTTTTTCTTTTAAGATCTGGGCATC-3' (SEQ ID NO: 2335)

5'-GGGCAUCUUUUGAAUCUACCCUUCA$^{CA-3'}$ (SEQ ID NO: 4109)
3'-CCCGUAGAAAACUUAGAUGGGAAGU$_{UC-5'}$ (SEQ ID NO: 1931)

AR-864 Target: 5'-GGGCATCTTTTGAATCTACCCTTCAAG-3' (SEQ ID NO: 2336)

5'-CAGAGCGCUUUUUGCGUGGUUGCUC$^{AA-3'}$ (SEQ ID NO: 4110)
3'-GUCUCGCGAAAAACGCACCAACGAG$_{GG-5'}$ (SEQ ID NO: 1932)

AR-971 Target: 5'-CAGAGCGCTTTTTGCGTGGTTGCTCCC-3' (SEQ ID NO: 2337)

5'-CGCUUUUUGCGUGGUUGCUCCCGCA$^{CA-3'}$ (SEQ ID NO: 4111)
3'-GCGAAAAACGCACCAACGAGGGCGU$_{UC-5'}$ (SEQ ID NO: 1933)

AR-976 Target: 5'-CGCTTTTTGCGTGGTTGCTCCCGCAAG-3' (SEQ ID NO: 2338)

5'-AAGUUUCCUUCUCUGGAGCUUCCCG$^{AC-3'}$ (SEQ ID NO: 4112)
3'-UUCAAAGGAAGAGACCUCGAAGGGC$_{GU-5'}$ (SEQ ID NO: 1934)

AR-1000 Target: 5'-AAGTTTCCTTCTCTGGAGCTTCCCGCA-3' (SEQ ID NO: 2339)

5'-AGCUUCCCGCAGGUGGGCAGCUAGC$^{CA-3'}$ (SEQ ID NO: 4113)
3'-UCGAAGGGCGUCCACCCGUCGAUCG$_{AC-5'}$ (SEQ ID NO: 1935)

AR-1016 Target: 5'-AGCTTCCCGCAGGTGGGCAGCTAGCTG-3' (SEQ ID NO: 2340)

5'-GUGGGCAGCUAGCUGCAGCGACUAC$^{AA-3'}$ (SEQ ID NO: 4114)
3'-CACCCGUCGAUCGACGUCGCUGAUG$_{GC-5'}$ (SEQ ID NO: 1936)

AR-1028 Target: 5'-GTGGGCAGCTAGCTGCAGCGACTACCG-3' (SEQ ID NO: 2341)

5'-AAGUGCAGUUAGGGCUGGGAAGGGU$^{AC-3'}$ (SEQ ID NO: 4115)
3'-UUCACGUCAAUCCCGACCCUUCCCA$_{GA-5'}$ (SEQ ID NO: 1937)

AR-1146 Target: 5'-AAGTGCAGTTAGGGCTGGGAAGGGTCT-3' (SEQ ID NO: 2342)

5'-AGUGCAGUUAGGGCUGGGAAGGGUC$^{CC-3'}$ (SEQ ID NO: 4116)
3'-UCACGUCAAUCCCGACCCUUCCCAG$_{AU-5'}$ (SEQ ID NO: 1938)

AR-1147 Target: 5'-AGTGCAGTTAGGGCTGGGAAGGGTCTA-3' (SEQ ID NO: 2343)

5'-GUGCAGUUAGGGCUGGGAAGGGUCU$^{CA-3'}$ (SEQ ID NO: 4117)
3'-CACGUCAAUCCCGACCCUUCCCAGA$_{UG-5'}$ (SEQ ID NO: 1939)

AR-1148 Target: 5'-GTGCAGTTAGGGCTGGGAAGGGTCTAC-3' (SEQ ID NO: 2344)

5'-UGCAGUUAGGGCUGGGAAGGGUCUA$^{AA-3'}$ (SEQ ID NO: 4118)
3'-ACGUCAAUCCCGACCCUUCCCAGAU$_{GG-5'}$ (SEQ ID NO: 1940)

AR-1149 Target: 5'-TGCAGTTAGGGCTGGGAAGGGTCTACC-3' (SEQ ID NO: 2345)

5'-GCAGUUAGGGCUGGGAAGGGUCUAC$^{AA-3'}$ (SEQ ID NO: 4119)
3'-CGUCAAUCCCGACCCUUCCCAGAUG$_{GG-5'}$ (SEQ ID NO: 1941)

AR-1150 Target: 5'-GCAGTTAGGGCTGGGAAGGGTCTACCC-3' (SEQ ID NO: 2346)

5'-CAGUUAGGGCUGGGAAGGGUCUACC$^{AC-3'}$ (SEQ ID NO: 4120)
3'-GUCAAUCCCGACCCUUCCCAGAUGG$_{GA-5'}$ (SEQ ID NO: 1942)

AR-1151 Target: 5'-CAGTTAGGGCTGGGAAGGGTCTACCCT-3' (SEQ ID NO: 2347)

5'-AGUUAGGGCUGGGAAGGGUCUACCC$^{CA-3'}$ (SEQ ID NO: 4121)
3'-UCAAUCCCGACCCUUCCCAGAUGGG$_{AG-5'}$ (SEQ ID NO: 1943)

AR-1152 Target: 5'-AGTTAGGGCTGGGAAGGGTCTACCCTC-3' (SEQ ID NO: 2348)

5'-GUUAGGGCUGGGAAGGGUCUACCCU$^{AA-3'}$ (SEQ ID NO: 4122)
3'-CAAUCCCGACCCUUCCCAGAUGGGA$_{GC-5'}$ (SEQ ID NO: 1944)

AR-1153 Target: 5'-GTTAGGGCTGGGAAGGGTCTACCCTCG-3' (SEQ ID NO: 2349)

5'-UUAGGGCUGGGAAGGGUCUACCCUC$^{AA-3'}$ (SEQ ID NO: 4123)
3'-AAUCCCGACCCUUCCCAGAUGGGAG$_{CC-5'}$ (SEQ ID NO: 1945)

AR-1154 Target: 5'-TTAGGGCTGGGAAGGGTCTACCCTCGG-3' (SEQ ID NO: 2350)

5'-UAGGGCUGGGAAGGGUCUACCCUCG$^{AA-3'}$ (SEQ ID NO: 4124)
3'-AUCCCGACCCUUCCCAGAUGGGAGC$_{CG-5'}$ (SEQ ID NO: 1946)

AR-1155 Target: 5'-TAGGGCTGGGAAGGGTCTACCCTCGGC-3' (SEQ ID NO: 2351)

5'-AGGGCUGGGAAGGGUCUACCCUCGG$^{AA-3'}$ (SEQ ID NO: 4125)
3'-UCCCGACCCUUCCCAGAUGGGAGCC$_{GG-5'}$ (SEQ ID NO: 1947)

AR-1156 Target: 5'-AGGGCTGGGAAGGGTCTACCCTCGGCC-3' (SEQ ID NO: 2352)

5'-CUUUCCAGAAUCUGUUCCAGAGCGU$^{AA-3'}$ (SEQ ID NO: 4126)
3'-GAAAGGUCUUAGACAAGGUCUCGCA$_{CG-5'}$ (SEQ ID NO: 1948)

AR-1206 Target: 5'-CTTTCCAGAATCTGTTCCAGAGCGTGC-3' (SEQ ID NO: 2353)

5'-UUUCCAGAAUCUGUUCCAGAGCGUG$^{AA-3'}$ (SEQ ID NO: 4127)
3'-AAAGGUCUUAGACAAGGUCUCGCAC$_{GC-5'}$ (SEQ ID NO: 1949)

AR-1207 Target: 5'-TTTCCAGAATCTGTTCCAGAGCGTGCG-3' (SEQ ID NO: 2354)

5'-UUCCAGAAUCUGUUCCAGAGCGUGC$^{AA-3'}$ (SEQ ID NO: 4128)
3'-AAGGUCUUAGACAAGGUCUCGCACG$_{CG-5'}$ (SEQ ID NO: 1950)

AR-1208 Target: 5'-TTCCAGAATCTGTTCCAGAGCGTGCGC-3' (SEQ ID NO: 2355)

5'-UCCAGAAUCUGUUCCAGAGCGUGCG$^{AA-3'}$ (SEQ ID NO: 4129)
3'-AGGUCUUAGACAAGGUCUCGCACGC$_{GC-5'}$ (SEQ ID NO: 1951)

AR-1209 Target: 5'-TCCAGAATCTGTTCCAGAGCGTGCGCG-3' (SEQ ID NO: 2356)

5'-CCAGAAUCUGUUCCAGAGCGUGCGC$^{AC-3'}$ (SEQ ID NO: 4130)
3'-GGUCUUAGACAAGGUCUCGCACGCG$_{CU-5'}$ (SEQ ID NO: 1952)

AR-1210 Target: 5'-CCAGAATCTGTTCCAGAGCGTGCGCGA-3' (SEQ ID NO: 2357)

5'-CAGAAUCUGUUCCAGAGCGUGCGCG$^{CC-3'}$ (SEQ ID NO: 4131)
3'-GUCUUAGACAAGGUCUCGCACGCGC$_{UU-5'}$ (SEQ ID NO: 1953)

AR-1211 Target: 5'-CAGAATCTGTTCCAGAGCGTGCGCGAA-3' (SEQ ID NO: 2358)

5'-AGAAUCUGUUCCAGAGCGUGCGCGA$^{CA-3'}$ (SEQ ID NO: 4132)
3'-UCUUAGACAAGGUCUCGCACGCGCU$_{UC-5'}$ (SEQ ID NO: 1954)

AR-1212 Target: 5'-AGAATCTGTTCCAGAGCGTGCGCGAAG-3' (SEQ ID NO: 2359)

5'-GAAUCUGUUCCAGAGCGUGCGCGAA$^{AC-3'}$ (SEQ ID NO: 4133)
3'-CUUAGACAAGGUCUCGCACGCGCUU$_{CA-5'}$ (SEQ ID NO: 1955)

AR-1213 Target: 5'-GAATCTGTTCCAGAGCGTGCGCGAAGT-3' (SEQ ID NO: 2360)

5'-AAUCUGUUCCAGAGCGUGCGCGAAG$^{CA-3'}$ (SEQ ID NO: 4134)
3'-UUAGACAAGGUCUCGCACGCGCUUC$_{AC-5'}$ (SEQ ID NO: 1956)

AR-1214 Target: 5'-AATCTGTTCCAGAGCGTGCGCGAAGTG-3' (SEQ ID NO: 2361)

5'-AUCUGUUCCAGAGCGUGCGCGAAGU$^{AC-3'}$ (SEQ ID NO: 4135)
3'-UAGACAAGGUCUCGCACGCGCUUCA$_{CU-5'}$ (SEQ ID NO: 1957)

AR-1215 Target: 5'-ATCTGTTCCAGAGCGTGCGCGAAGTGA-3' (SEQ ID NO: 2362)

5'-UCUGUUCCAGAGCGUGCGCGAAGUG$^{CC-3'}$ (SEQ ID NO: 4136)
3'-AGACAAGGUCUCGCACGCGCUUCAC$_{UA-5'}$ (SEQ ID NO: 1958)

AR-1216 Target: 5'-TCTGTTCCAGAGCGTGCGCGAAGTGAT-3' (SEQ ID NO: 2363)

5'-CUGUUCCAGAGCGUGCGCGAAGUGA$^{CA-3'}$ (SEQ ID NO: 4137)
3'-GACAAGGUCUCGCACGCGCUUCACU$_{AG-5'}$ (SEQ ID NO: 1959)

AR-1217 Target: 5'-CTGTTCCAGAGCGTGCGCGAAGTGATC-3' (SEQ ID NO: 2364)

5'-UGUUCCAGAGCGUGCGCGAAGUGAU$^{AA-3'}$ (SEQ ID NO: 4138)
3'-ACAAGGUCUCGCACGCGCUUCACUA$_{GG-5'}$ (SEQ ID NO: 1960)

AR-1218 Target: 5'-TGTTCCAGAGCGTGCGCGAAGTGATCC-3' (SEQ ID NO: 2365)

5'-GGCGCCAGUUUGCUGCUGCUGCAGC$^{CA-3'}$ (SEQ ID NO: 4139)
3'-CCGCGGUCAAACGACGACGACGUCG$_{UC-5'}$ (SEQ ID NO: 1961)

AR-1292 Target: 5'-GGCGCCAGTTTGCTGCTGCTGCAGCAG-3' (SEQ ID NO: 2366)

5'-UUGCUGCUGCUGCAGCAGCAGCAGC$^{CA-3'}$ (SEQ ID NO: 4140)
3'-AACGACGACGACGUCGUCGUCGUCG$_{UC-5'}$ (SEQ ID NO: 1962)

AR-1301 Target: 5'-TTGCTGCTGCTGCAGCAGCAGCAGCAG-3' (SEQ ID NO: 2367)

5'-GCGUCCCAGAGCCUGGAGCCGCCGU$^{AA-3'}$ (SEQ ID NO: 4141)
3'-CGCAGGGUCUCGGACCUCGGCGGCA$_{CC-5'}$ (SEQ ID NO: 1963)

AR-1533 Target: 5'-GCGTCCCAGAGCCTGGAGCCGCCGTGG-3' (SEQ ID NO: 2368)

5'-GGCUGCCGCAGCAGCUGCCAGCACC$^{CA-3'}$ (SEQ ID NO: 4142)
3'-CCGACGGCGUCGUCGACGGUCGUGG$_{AG-5'}$ (SEQ ID NO: 1964)

AR-1572 Target: 5'-GGCTGCCGCAGCAGCTGCCAGCACCTC-3' (SEQ ID NO: 2369)

5'-CGCAGCAGCUGCCAGCACCUCCGGA$^{AA-3'}$ (SEQ ID NO: 4143)
3'-GCGUCGUCGACGGUCGUGGAGGCCU$_{GC-5'}$ (SEQ ID NO: 1965)

AR-1578 Target: 5'-CGCAGCAGCTGCCAGCACCTCCGGACG-3' (SEQ ID NO: 2370)

5'-CCCAUCCACGUUGUCCCUGCUGGGC$^{AA-3'}$ (SEQ ID NO: 4144)
3'-GGGUAGGUGCAACAGGGACGACCCG$_{GG-5'}$ (SEQ ID NO: 1966)

AR-1621 Target: 5'-CCCATCCACGTTGTCCCTGCTGGGCCC-3' (SEQ ID NO: 2371)

5'-CCGGCUUAAGCAGCUGCUCCGCUGA$^{AA-3'}$ (SEQ ID NO: 4145)
3'-GGCCGAAUUCGUCGACGAGGCGACU$_{GG-5'}$ (SEQ ID NO: 1967)

AR-1656 Target: 5'-CCGGCTTAAGCAGCTGCTCCGCTGACC-3' (SEQ ID NO: 2372)

5'-CGGCUUAAGCAGCUGCUCCGCUGAC$^{AC-3'}$ (SEQ ID NO: 4146)
3'-GCCGAAUUCGUCGACGAGGCGACUG$_{GA-5'}$ (SEQ ID NO: 1968)

AR-1657 Target: 5'-CGGCTTAAGCAGCTGCTCCGCTGACCT-3' (SEQ ID NO: 2373)

5'-UAAGCAGCUGCUCCGCUGACCUUAA$^{CA-3'}$ (SEQ ID NO: 4147)
3'-AUUCGUCGACGAGGCGACUGGAAUU$_{UC-5'}$ (SEQ ID NO: 1969)

AR-1662 Target: 5'-TAAGCAGCTGCTCCGCTGACCTTAAAG-3' (SEQ ID NO: 2374)

5'-AUGCAACUCCUUCAGCAACAGCAGC$^{CA-3'}$ (SEQ ID NO: 4148)
3'-UACGUUGAGGAAGUCGUUGUCGUCG$_{UC-5'}$ (SEQ ID NO: 1970)

AR-1712 Target: 5'-ATGCAACTCCTTCAGCAACAGCAGCAG-3' (SEQ ID NO: 2375)

5'-ACCAUUUCUGACAACGCCAAGGAGU$^{CA-3'}$ (SEQ ID NO: 4149)
3'-UGGUAAAGACUGUUGCGGUUCCUCA$_{AC-5'}$ (SEQ ID NO: 1971)

AR-1832 Target: 5'-ACCATTTCTGACAACGCCAAGGAGTTG-3' (SEQ ID NO: 2376)

5'-CCACUUUUGGGAGUUCCACCCGCUG$^{CA-3'}$ (SEQ ID NO: 4150)
3'-GGUGAAAACCCUCAAGGUGGGCGAC$_{AC-5'}$ (SEQ ID NO: 1972)

AR-1952 Target: 5'-CCACTTTTGGGAGTTCCACCCGCTGTG-3' (SEQ ID NO: 2377)

5'-CAGGCAAGAGCACUGAAGAUACUGC$^{CA-3'}$ (SEQ ID NO: 4151)
3'-GUCCGUUCUCGUGACUUCUAUGACG$_{AC-5'}$ (SEQ ID NO: 1973)

AR-2037 Target: 5'-CAGGCAAGAGCACTGAAGATACTGCTG-3' (SEQ ID NO: 2378)

5'-CUGGCAGCGCUGCAGCAGGGAGCUC$^{AA-3'}$ (SEQ ID NO: 4152)
3'-GACCGUCGCGACGUCGUCCCUCGAG$_{GC-5'}$ (SEQ ID NO: 1974)

AR-2124 Target: 5'-CTGGCAGCGCTGCAGCAGGGAGCTCCG-3' (SEQ ID NO: 2379)

5'-AGUCGCGACUACUACAACUUUCCAC$^{CA-3'}$ (SEQ ID NO: 4153)
3'-UCAGCGCUGAUGAUGUUGAAAGGUG$_{AC-5'}$ (SEQ ID NO: 1975)

AR-2222 Target: 5'-AGTCGCGACTACTACAACTTTCCACTG-3' (SEQ ID NO: 2380)

5'-GUCGCGACUACUACAACUUUCCACU$^{AA-3'}$ (SEQ ID NO: 4154)
3'-CAGCGCUGAUGAUGUUGAAAGGUGA$_{CC-5'}$ (SEQ ID NO: 1976)

AR-2223 Target: 5'-GTCGCGACTACTACAACTTTCCACTGG-3' (SEQ ID NO: 2381)

5'-UCGCGACUACUACAACUUUCCACUG$^{AA-3'}$ (SEQ ID NO: 4155)
3'-AGCGCUGAUGAUGUUGAAAGGUGAC$_{CG-5'}$ (SEQ ID NO: 1977)

AR-2224 Target: 5'-TCGCGACTACTACAACTTTCCACTGGC-3' (SEQ ID NO: 2382)

5'-GCUCGCAUCAAGCUGGAGAACCCGC$^{CA-3'}$ (SEQ ID NO: 4156)
3'-CGAGCGUAGUUCGACCUCUUGGGCG$_{AC-5'}$ (SEQ ID NO: 1978)

AR-2294 Target: 5'-GCTCGCATCAAGCTGGAGAACCCGCTG-3' (SEQ ID NO: 2383)

5'-GCUGGACUACGGCAGCGCCUGGGCG$^{AA-3'}$ (SEQ ID NO: 4157)
3'-CGACCUGAUGCCGUCGCGGACCCGC$_{CG-5'}$ (SEQ ID NO: 1979)

AR-2317 Target: 5'-GCTGGACTACGGCAGCGCCTGGGCGGC-3' (SEQ ID NO: 2384)

5'-CUGGACUACGGCAGCGCCUGGGCGG$^{AC-3'}$ (SEQ ID NO: 4158)
3'-GACCUGAUGCCGUCGCGGACCCGCC$_{GA-5'}$ (SEQ ID NO: 1980)

AR-2318 Target: 5'-CTGGACTACGGCAGCGCCTGGGCGGCT-3' (SEQ ID NO: 2385)

5'-UGGACUACGGCAGCGCCUGGGCGGC$^{CA-3'}$ (SEQ ID NO: 4159)
3'-ACCUGAUGCCGUCGCGGACCCGCCG$_{AC-5'}$ (SEQ ID NO: 1981)

AR-2319 Target: 5'-TGGACTACGGCAGCGCCTGGGCGGCTG-3' (SEQ ID NO: 2386)

5'-GGACUACGGCAGCGCCUGGGCGGCU$^{AA-3'}$ (SEQ ID NO: 4160)
3'-CCUGAUGCCGUCGCGGACCCGCCGA$_{CG-5'}$ (SEQ ID NO: 1982)

AR-2320 Target: 5'-GGACTACGGCAGCGCCTGGGCGGCTGC-3' (SEQ ID NO: 2387)

5'-UGGCGCGGGUGCAGCGGGACCCGGU$^{CA-3'}$ (SEQ ID NO: 4161)
3'-ACCGCGCCCACGUCGCCCUGGGCCA$_{AG-5'}$ (SEQ ID NO: 1983)

AR-2386 Target: 5'-TGGCGCGGGTGCAGCGGGACCCGGTTC-3' (SEQ ID NO: 2388)

5'-GGCUGGCGGGCCAGGAAAGCGACUU$^{AC-3'}$ (SEQ ID NO: 4162)
3'-CCGACCGCCCGGUCCUUUCGCUGAA$_{GU-5'}$ (SEQ ID NO: 1984)

AR-2607 Target: 5'-GGCTGGCGGGCCAGGAAAGCGACTTCA-3' (SEQ ID NO: 2389)

5'-GUACCCUGGCGGCAUGGUGAGCAGA$^{AC-3'}$ (SEQ ID NO: 4163)
3'-CAUGGGACCGCCGUACCACUCGUCU$_{CA-5'}$ (SEQ ID NO: 1985)

AR-2650 Target: 5'-GTACCCTGGCGGCATGGTGAGCAGAGT-3' (SEQ ID NO: 2390)

5'-UGGAUGGAUAGCUACUCCGGACCUU$^{CA-3'}$ (SEQ ID NO: 4164)
3'-ACCUACCUAUCGAUGAGGCCUGGAA$_{UG-5'}$ (SEQ ID NO: 1986)

AR-2720 Target: 5'-TGGATGGATAGCTACTCCGGACCTTAC-3' (SEQ ID NO: 2391)

5'-CCCAGAAGACCUGCCUGAUCUGUGG$^{CA-3'}$ (SEQ ID NO: 4165)
3'-GGGUCUUCUGGACGGACUAGACACC$_{UC-5'}$ (SEQ ID NO: 1987)

AR-2808 Target: 5'-CCCAGAAGACCTGCCTGATCTGTGGAG-3' (SEQ ID NO: 2392)

5'-CCAGAAGACCUGCCUGAUCUGUGGA^{A}C-3′ (SEQ ID NO: 4166)
3'-GGUCUUCUGGACGGACUAGACACCU$_{C}$U-5′, (SEQ ID NO: 1988)

AR-2809 Target: 5'-CCAGAAGACCTGCCTGATCTGTGGAGA-3' (SEQ ID NO: 2393)

5'-CAGAAGACCUGCCUGAUCUGUGGAG^{C}C-3′ (SEQ ID NO: 4167)
3'-GUCUUCUGGACGGACUAGACACCUC$_{U}$A-5′, (SEQ ID NO: 1989)

AR-2810 Target: 5'-CAGAAGACCTGCCTGATCTGTGGAGAT-3' (SEQ ID NO: 2394)

5'-AGAAGACCUGCCUGAUCUGUGGAGA^{C}A-3′ (SEQ ID NO: 4168)
3'-UCUUCUGGACGGACUAGACACCUCU$_{A}$C-5′, (SEQ ID NO: 1990)

AR-2811 Target: 5'-AGAAGACCTGCCTGATCTGTGGAGATG-3' (SEQ ID NO: 2395)

5'-GAAGACCUGCCUGAUCUGUGGAGAU^{A}C-3′ (SEQ ID NO: 4169)
3'-CUUCUGGACGGACUAGACACCUCUA$_{C}$U-5′, (SEQ ID NO: 1991)

AR-2812 Target: 5'-GAAGACCTGCCTGATCTGTGGAGATGA-3' (SEQ ID NO: 2396)

5'-AAGACCUGCCUGAUCUGUGGAGAUG^{C}C-3′ (SEQ ID NO: 4170)
3'-UUCUGGACGGACUAGACACCUCUAC$_{U}$U-5′, (SEQ ID NO: 1992)

AR-2813 Target: 5'-AAGACCTGCCTGATCTGTGGAGATGAA-3' (SEQ ID NO: 2397)

5'-AGACCUGCCUGAUCUGUGGAGAUGA^{C}A-3′ (SEQ ID NO: 4171)
3'-UCUGGACGGACUAGACACCUCUACU$_{U}$C-5′, (SEQ ID NO: 1993)

AR-2814 Target: 5'-AGACCTGCCTGATCTGTGGAGATGAAG-3' (SEQ ID NO: 2398)

5'-GACCUGCCUGAUCUGUGGAGAUGAA^{A}A-3′ (SEQ ID NO: 4172)
3'-CUGGACGGACUAGACACCUCUACUU$_{C}$G-5′, (SEQ ID NO: 1994)

AR-2815 Target: 5'-GACCTGCCTGATCTGTGGAGATGAAGC-3' (SEQ ID NO: 2399)

5'-ACCUGCCUGAUCUGUGGAGAUGAAG^{A}C-3′ (SEQ ID NO: 4173)
3'-UGGACGGACUAGACACCUCUACUUC$_{G}$A-5′, (SEQ ID NO: 1995)

AR-2816 Target: 5'-ACCTGCCTGATCTGTGGAGATGAAGCT-3' (SEQ ID NO: 2400)

5'-CCUGCCUGAUCUGUGGAGAUGAAGC^{C}C-3′ (SEQ ID NO: 4174)
3'-GGACGGACUAGACACCUCUACUUCG$_{A}$A-5′, (SEQ ID NO: 1996)

AR-2817 Target: 5'-CCTGCCTGATCTGTGGAGATGAAGCTT-3' (SEQ ID NO: 2401)

5'-CUGCCUGAUCUGUGGAGAUGAAGCU^{C}A-3′ (SEQ ID NO: 4175)
3'-GACGGACUAGACACCUCUACUUCGA$_{A}$G-5′, (SEQ ID NO: 1997)

AR-2818 Target: 5'-CTGCCTGATCTGTGGAGATGAAGCTTC-3' (SEQ ID NO: 2402)

5'-UGCCUGAUCUGUGGAGAUGAAGCUU^{A}C-3′ (SEQ ID NO: 4176)
3'-ACGGACUAGACACCUCUACUUCGAA$_{G}$A-5′, (SEQ ID NO: 1998)

AR-2819 Target: 5'-TGCCTGATCTGTGGAGATGAAGCTTCT-3' (SEQ ID NO: 2403)

5'-GCCUGAUCUGUGGAGAUGAAGCUUC$^{CA-3'}$ (SEQ ID NO: 4177)
3'-CGGACUAGACACCUCUACUUCGAAG$_{AC-5'}$ (SEQ ID NO: 1999)

AR-2820 Target: 5'-GCCTGATCTGTGGAGATGAAGCTTCTG-3' (SEQ ID NO: 2404)

5'-CCUGAUCUGUGGAGAUGAAGCUUCU$^{AA-3'}$ (SEQ ID NO: 4178)
3'-GGACUAGACACCUCUACUUCGAAGA$_{CC-5'}$ (SEQ ID NO: 2000)

AR-2821 Target: 5'-CCTGATCTGTGGAGATGAAGCTTCTGG-3' (SEQ ID NO: 2405)

5'-CUGAUCUGUGGAGAUGAAGCUUCUG$^{AA-3'}$ (SEQ ID NO: 4179)
3'-GACUAGACACCUCUACUUCGAAGAC$_{CC-5'}$ (SEQ ID NO: 2001)

AR-2822 Target: 5'-CTGATCTGTGGAGATGAAGCTTCTGGG-3' (SEQ ID NO: 2406)

5'-UGAUCUGUGGAGAUGAAGCUUCUGG$^{AC-3'}$ (SEQ ID NO: 4180)
3'-ACUAGACACCUCUACUUCGAAGACC$_{CA-5'}$ (SEQ ID NO: 2002)

AR-2823 Target: 5'-TGATCTGTGGAGATGAAGCTTCTGGGT-3' (SEQ ID NO: 2407)

5'-GAUCUGUGGAGAUGAAGCUUCUGGG$^{CA-3'}$ (SEQ ID NO: 4181)
3'-CUAGACACCUCUACUUCGAAGACCC$_{AC-5'}$ (SEQ ID NO: 2003)

AR-2824 Target: 5'-GATCTGTGGAGATGAAGCTTCTGGGTG-3' (SEQ ID NO: 2408)

5'-AUCUGUGGAGAUGAAGCUUCUGGGU$^{AC-3'}$ (SEQ ID NO: 4182)
3'-UAGACACCUCUACUUCGAAGACCCA$_{CA-5'}$ (SEQ ID NO: 2004)

AR-2825 Target: 5'-ATCTGTGGAGATGAAGCTTCTGGGTGT-3' (SEQ ID NO: 2409)

5'-UCUGUGGAGAUGAAGCUUCUGGGUG$^{CA-3'}$ (SEQ ID NO: 4183)
3'-AGACACCUCUACUUCGAAGACCCAC$_{AG-5'}$ (SEQ ID NO: 2005)

AR-2826 Target: 5'-TCTGTGGAGATGAAGCTTCTGGGTGTC-3' (SEQ ID NO: 2410)

5'-CUGUGGAGAUGAAGCUUCUGGGUGU$^{AC-3'}$ (SEQ ID NO: 4184)
3'-GACACCUCUACUUCGAAGACCCACA$_{GU-5'}$ (SEQ ID NO: 2006)

AR-2827 Target: 5'-CTGTGGAGATGAAGCTTCTGGGTGTCA-3' (SEQ ID NO: 2411)

5'-GCUUCUGGGUGUCACUAUGGAGCUC$^{CA-3'}$ (SEQ ID NO: 4185)
3'-CGAAGACCCACAGUGAUACCUCGAG$_{AG-5'}$ (SEQ ID NO: 2007)

AR-2840 Target: 5'-GCTTCTGGGTGTCACTATGGAGCTCTC-3' (SEQ ID NO: 2412)

5'-UGGAGCUCUCACAUGUGGAAGCUGC$^{CC-3'}$ (SEQ ID NO: 4186)
3'-ACCUCGAGAGUGUACACCUUCGACG$_{UU-5'}$ (SEQ ID NO: 2008)

AR-2857 Target: 5'-TGGAGCTCTCACATGTGGAAGCTGCAA-3' (SEQ ID NO: 2413)

5'-GAAGCUGCAAGGUCUUCUUCAAAAG$^{CA-3'}$ (SEQ ID NO: 4187)
3'-CUUCGACGUUCCAGAAGAAGUUUUC$_{UC-5'}$ (SEQ ID NO: 2009)

AR-2874 Target: 5'-GAAGCTGCAAGGTCTTCTTCAAAAGAG-3' (SEQ ID NO: 2414)

5'-AAGCUGCAAGGUCUUCUUCAAAAGA$^{AA-3'}$ (SEQ ID NO: 4188)
3'-UUCGACGUUCCAGAAGAAGUUUUCU$_{CG-5'}$ (SEQ ID NO: 2010)

AR-2875 Target: 5'-AAGCTGCAAGGTCTTCTTCAAAAGAGC-3' (SEQ ID NO: 2415)

5'-AGCUGCAAGGUCUUCUUCAAAAGAG$^{AA-3'}$ (SEQ ID NO: 4189)
3'-UCGACGUUCCAGAAGAAGUUUUCUC$_{GG-5'}$ (SEQ ID NO: 2011)

AR-2876 Target: 5'-AGCTGCAAGGTCTTCTTCAAAAGAGCC-3' (SEQ ID NO: 2416)

5'-GCUGCAAGGUCUUCUUCAAAAGAGC$^{AA-3'}$ (SEQ ID NO: 4190)
3'-CGACGUUCCAGAAGAAGUUUUCUCG$_{GC-5'}$ (SEQ ID NO: 2012)

AR-2877 Target: 5'-GCTGCAAGGTCTTCTTCAAAAGAGCCG-3' (SEQ ID NO: 2417)

5'-CUGCAAGGUCUUCUUCAAAAGAGCC$^{AA-3'}$ (SEQ ID NO: 4191)
3'-GACGUUCCAGAAGAAGUUUUCUCGG$_{CG-5'}$ (SEQ ID NO: 2013)

AR-2878 Target: 5'-CTGCAAGGTCTTCTTCAAAAGAGCCGC-3' (SEQ ID NO: 2418)

5'-UGCAAGGUCUUCUUCAAAAGAGCCG$^{AC-3'}$ (SEQ ID NO: 4192)
3'-ACGUUCCAGAAGAAGUUUUCUCGGC$_{GA-5'}$ (SEQ ID NO: 2014)

AR-2879 Target: 5'-TGCAAGGTCTTCTTCAAAAGAGCCGCT-3' (SEQ ID NO: 2419)

5'-GCAAGGUCUUCUUCAAAAGAGCCGC$^{CA-3'}$ (SEQ ID NO: 4193)
3'-CGUUCCAGAAGAAGUUUUCUCGGCG$_{AC-5'}$ (SEQ ID NO: 2015)

AR-2880 Target: 5'-GCAAGGTCTTCTTCAAAAGAGCCGCTG-3' (SEQ ID NO: 2420)

5'-CAAGGUCUUCUUCAAAAGAGCCGCU$^{AC-3'}$ (SEQ ID NO: 4194)
3'-GUUCCAGAAGAAGUUUUCUCGGCGA$_{CU-5'}$ (SEQ ID NO: 2016)

AR-2881 Target: 5'-CAAGGTCTTCTTCAAAAGAGCCGCTGA-3' (SEQ ID NO: 2421)

5'-AAGGUCUUCUUCAAAAGAGCCGCUG$^{CC-3'}$ (SEQ ID NO: 4195)
3'-UUCCAGAAGAAGUUUUCUCGGCGAC$_{UU-5'}$ (SEQ ID NO: 2017)

AR-2882 Target: 5'-AAGGTCTTCTTCAAAAGAGCCGCTGAA-3' (SEQ ID NO: 2422)

5'-AGGUCUUCUUCAAAAGAGCCGCUGA$^{CA-3'}$ (SEQ ID NO: 4196)
3'-UCCAGAAGAAGUUUUCUCGGCGACU$_{UC-5'}$ (SEQ ID NO: 2018)

AR-2883 Target: 5'-AGGTCTTCTTCAAAAGAGCCGCTGAAG-3' (SEQ ID NO: 2423)

5'-GGUCUUCUUCAAAAGAGCCGCUGAA$^{AA-3'}$ (SEQ ID NO: 4197)
3'-CCAGAAGAAGUUUUCUCGGCGACUU$_{CC-5'}$ (SEQ ID NO: 2019)

AR-2884 Target: 5'-GGTCTTCTTCAAAAGAGCCGCTGAAGG-3' (SEQ ID NO: 2424)

5'-GUCUUCUUCAAAAGAGCCGCUGAAG$^{AA-3'}$ (SEQ ID NO: 4198)
3'-CAGAAGAAGUUUUCUCGGCGACUUC$_{CC-5'}$ (SEQ ID NO: 2020)

AR-2885 Target: 5'-GTCTTCTTCAAAAGAGCCGCTGAAGGG-3' (SEQ ID NO: 2425)

5'-UCUUCUUCAAAAGAGCCGCUGAAGG$^{AC-3'}$ (SEQ ID NO: 4199)
3'-AGAAGAAGUUUUCUCGGCGACUUCC$_{CU-5'}$ (SEQ ID NO: 2021)

AR-2886 Target: 5'-TCTTCTTCAAAAGAGCCGCTGAAGGGA-3' (SEQ ID NO: 2426)

5'-CUUCUUCAAAAGAGCCGCUGAAGGG$^{CC-3'}$ (SEQ ID NO: 4200)
3'-GAAGAAGUUUUCUCGGCGACUUCCC$_{UU-5'}$ (SEQ ID NO: 2022)

AR-2887 Target: 5'-CTTCTTCAAAAGAGCCGCTGAAGGGAA-3' (SEQ ID NO: 2427)

5'-UUCUUCAAAAGAGCCGCUGAAGGGA$^{CC-3'}$ (SEQ ID NO: 4201)
3'-AAGAAGUUUUCUCGGCGACUUCCCU$_{UU-5'}$ (SEQ ID NO: 2023)

AR-2888 Target: 5'-TTCTTCAAAAGAGCCGCTGAAGGGAAA-3' (SEQ ID NO: 2428)

5'-UCUUCAAAAGAGCCGCUGAAGGGAA$^{CA-3'}$ (SEQ ID NO: 4202)
3'-AGAAGUUUUCUCGGCGACUUCCCUU$_{UG-5'}$ (SEQ ID NO: 2024)

AR-2889 Target: 5'-TCTTCAAAAGAGCCGCTGAAGGGAAAC-3' (SEQ ID NO: 2429)

5'-CUUCAAAAGAGCCGCUGAAGGGAAA$^{AC-3'}$ (SEQ ID NO: 4203)
3'-GAAGUUUUCUCGGCGACUUCCCUUU$_{GU-5'}$ (SEQ ID NO: 2025)

AR-2890 Target: 5'-CTTCAAAAGAGCCGCTGAAGGGAAACA-3' (SEQ ID NO: 2430)

5'-UUCAAAAGAGCCGCUGAAGGGAAAC$^{CA-3'}$ (SEQ ID NO: 4204)
3'-AAGUUUUCUCGGCGACUUCCCUUUG$_{UC-5'}$ (SEQ ID NO: 2026)

AR-2891 Target: 5'-TTCAAAAGAGCCGCTGAAGGGAAACAG-3' (SEQ ID NO: 2431)

5'-UCAAAAGAGCCGCUGAAGGGAAACA$^{AC-3'}$ (SEQ ID NO: 4205)
3'-AGUUUUCUCGGCGACUUCCCUUUGU$_{CU-5'}$ (SEQ ID NO: 2027)

AR-2892 Target: 5'-TCAAAAGAGCCGCTGAAGGGAAACAGA-3' (SEQ ID NO: 2432)

5'-CAAAAGAGCCGCUGAAGGGAAACAG$^{CC-3'}$ (SEQ ID NO: 4206)
3'-GUUUUCUCGGCGACUUCCCUUUGUC$_{UU-5'}$ (SEQ ID NO: 2028)

AR-2893 Target: 5'-CAAAAGAGCCGCTGAAGGGAAACAGAA-3' (SEQ ID NO: 2433)

5'-AAAAGAGCCGCUGAAGGGAAACAGA$^{CA-3'}$ (SEQ ID NO: 4207)
3'-UUUUCUCGGCGACUUCCCUUUGUCU$_{UC-5'}$ (SEQ ID NO: 2029)

AR-2894 Target: 5'-AAAAGAGCCGCTGAAGGGAAACAGAAG-3' (SEQ ID NO: 2434)

5'-AAAGAGCCGCUGAAGGGAAACAGAA$^{AC-3'}$ (SEQ ID NO: 4208)
3'-UUUCUCGGCGACUUCCCUUUGUCUU$_{CA-5'}$ (SEQ ID NO: 2030)

AR-2895 Target: 5'-AAAGAGCCGCTGAAGGGAAACAGAAGT-3' (SEQ ID NO: 2435)

5'-AAGAGCCGCUGAAGGGAAACAGAAG$^{CC-3'}$ (SEQ ID NO: 4209)
3'-UUCUCGGCGACUUCCCUUUGUCUUC$_{AU-5'}$ (SEQ ID NO: 2031)

AR-2896 Target: 5'-AAGAGCCGCTGAAGGGAAACAGAAGTA-3' (SEQ ID NO: 2436)

5'-AGAGCCGCUGAAGGGAAACAGAAGU$^{CA-3'}$ (SEQ ID NO: 4210)
3'-UCUCGGCGACUUCCCUUUGUCUUCA$_{UG-5'}$ (SEQ ID NO: 2032)

AR-2897 Target: 5'-AGAGCCGCTGAAGGGAAACAGAAGTAC-3' (SEQ ID NO: 2437)

5'-GAGCCGCUGAAGGGAAACAGAAGUA$^{AA-3'}$ (SEQ ID NO: 4211)
3'-CUCGGCGACUUCCCUUUGUCUUCAU$_{GG-5'}$ (SEQ ID NO: 2033)

AR-2898 Target: 5'-GAGCCGCTGAAGGGAAACAGAAGTACC-3' (SEQ ID NO: 2438)

5'-AGCCGCUGAAGGGAAACAGAAGUAC$^{AC-3'}$ (SEQ ID NO: 4212)
3'-UCGGCGACUUCCCUUUGUCUUCAUG$_{GA-5'}$ (SEQ ID NO: 2034)

AR-2899 Target: 5'-AGCCGCTGAAGGGAAACAGAAGTACCT-3' (SEQ ID NO: 2439)

5'-CCGCUGAAGGGAAACAGAAGUACCU$^{AC-3'}$ (SEQ ID NO: 4213)
3'-GGCGACUUCCCUUUGUCUUCAUGGA$_{CA-5'}$ (SEQ ID NO: 2035)

AR-2901 Target: 5'-CCGCTGAAGGGAAACAGAAGTACCTGT-3' (SEQ ID NO: 2440)

5'-CGCUGAAGGGAAACAGAAGUACCUG$^{CA-3'}$ (SEQ ID NO: 4214)
3'-GCGACUUCCCUUUGUCUUCAUGGAC$_{AC-5'}$ (SEQ ID NO: 2036)

AR-2902 Target: 5'-CGCTGAAGGGAAACAGAAGTACCTGTG-3' (SEQ ID NO: 2441)

5'-CCUGUGCGCCAGCAGAAAUGAUUGC$^{CA-3'}$ (SEQ ID NO: 4215)
3'-GGACACGCGGUCGUCUUUACUAACG$_{UG-5'}$ (SEQ ID NO: 2037)

AR-2923 Target: 5'-CCTGTGCGCCAGCAGAAATGATTGCAC-3' (SEQ ID NO: 2442)

5'-GCAGAAAUGAUUGCACUAUUGAUAA$^{CC-3'}$ (SEQ ID NO: 4216)
3'-CGUCUUUACUAACGUGAUAACUAUU$_{UA-5'}$ (SEQ ID NO: 2038)

AR-2934 Target: 5'-GCAGAAATGATTGCACTATTGATAAAT-3' (SEQ ID NO: 2443)

5'-AAUGAUUGCACUAUUGAUAAAUUCC$^{AC-3'}$ (SEQ ID NO: 4217)
3'-UUACUAACGUGAUAACUAUUUAAGG$_{CU-5'}$ (SEQ ID NO: 2039)

AR-2939 Target: 5'-AATGATTGCACTATTGATAAATTCCGA-3' (SEQ ID NO: 2444)

5'-CACUAUUGAUAAAUUCCGAAGGAAA$^{CC-3'}$ (SEQ ID NO: 4218)
3'-GUGAUAACUAUUUAAGGCUUCCUUU$_{UU-5'}$ (SEQ ID NO: 2040)

AR-2947 Target: 5'-CACTATTGATAAATTCCGAAGGAAAAA-3' (SEQ ID NO: 2445)

5'-UUCGGAAAUGUUAUGAAGCAGGGAU$^{AC-3'}$ (SEQ ID NO: 4219)
3'-AAGCCUUUACAAUACUUCGUCCCUA$_{CU-5'}$ (SEQ ID NO: 2041)

AR-2991 Target: 5'-TTCGGAAATGTTATGAAGCAGGGATGA-3' (SEQ ID NO: 2446)

5'-UCGGAAAUGUUAUGAAGCAGGGAUG$^{CA-3'}$ (SEQ ID NO: 4220)
3'-AGCCUUUACAAUACUUCGUCCCUAC$_{UG-5'}$ (SEQ ID NO: 2042)

AR-2992 Target: 5'-TCGGAAATGTTATGAAGCAGGGATGAC-3' (SEQ ID NO: 2447)

5'-CGGAAAUGUUAUGAAGCAGGGAUGA$^{AC-3'}$ (SEQ ID NO: 4221)
3'-GCCUUUACAAUACUUCGUCCCUACU$_{GA-5'}$ (SEQ ID NO: 2043)

AR-2993 Target: 5'-CGGAAATGTTATGAAGCAGGGATGACT-3' (SEQ ID NO: 2448)

5'-GGAAAUGUUAUGAAGCAGGGAUGAC$^{CA-3'}$ (SEQ ID NO: 4222)
3'-CCUUUACAAUACUUCGUCCCUACUG$_{AG-5'}$ (SEQ ID NO: 2044)

AR-2994 Target: 5'-GGAAATGTTATGAAGCAGGGATGACTC-3' (SEQ ID NO: 2449)

5'-GAAAUGUUAUGAAGCAGGGAUGACU$^{AC-3'}$ (SEQ ID NO: 4223)
3'-CUUUACAAUACUUCGUCCCUACUGA$_{GA-5'}$ (SEQ ID NO: 2045)

AR-2995 Target: 5'-GAAATGTTATGAAGCAGGGATGACTCT-3' (SEQ ID NO: 2450)

5'-AAAUGUUAUGAAGCAGGGAUGACUC$^{CA-3'}$ (SEQ ID NO: 4224)
3'-UUUACAAUACUUCGUCCCUACUGAG$_{AC-5'}$ (SEQ ID NO: 2046)

AR-2996 Target: 5'-AAATGTTATGAAGCAGGGATGACTCTG-3' (SEQ ID NO: 2451)

5'-AAUGUUAUGAAGCAGGGAUGACUCU$^{AA-3'}$ (SEQ ID NO: 4225)
3'-UUACAAUACUUCGUCCCUACUGAGA$_{CC-5'}$ (SEQ ID NO: 2047)

AR-2997 Target: 5'-AATGTTATGAAGCAGGGATGACTCTGG-3' (SEQ ID NO: 2452)

5'-AUGUUAUGAAGCAGGGAUGACUCUG$^{AA-3'}$ (SEQ ID NO: 4226)
3'-UACAAUACUUCGUCCCUACUGAGAC$_{CC-5'}$ (SEQ ID NO: 2048)

AR-2998 Target: 5'-ATGTTATGAAGCAGGGATGACTCTGGG-3' (SEQ ID NO: 2453)

5'-UGUUAUGAAGCAGGGAUGACUCUGG$^{AC-3'}$ (SEQ ID NO: 4227)
3'-ACAAUACUUCGUCCCUACUGAGACC$_{CU-5'}$ (SEQ ID NO: 2049)

AR-2999 Target: 5'-TGTTATGAAGCAGGGATGACTCTGGGA-3' (SEQ ID NO: 2454)

5'-GUUAUGAAGCAGGGAUGACUCUGGG$^{CA-3'}$ (SEQ ID NO: 4228)
3'-CAAUACUUCGUCCCUACUGAGACCC$_{UC-5'}$ (SEQ ID NO: 2050)

AR-3000 Target: 5'-GTTATGAAGCAGGGATGACTCTGGGAG-3' (SEQ ID NO: 2455)

5'-UUAUGAAGCAGGGAUGACUCUGGGA$^{AA-3'}$ (SEQ ID NO: 4229)
3'-AAUACUUCGUCCCUACUGAGACCCU$_{CG-5'}$ (SEQ ID NO: 2051)

AR-3001 Target: 5'-TTATGAAGCAGGGATGACTCTGGGAGC-3' (SEQ ID NO: 2456)

5'-UAUGAAGCAGGGAUGACUCUGGGAG$^{AA-3'}$ (SEQ ID NO: 4230)
3'-AUACUUCGUCCCUACUGAGACCCUC$_{GG-5'}$ (SEQ ID NO: 2052)

AR-3002 Target: 5'-TATGAAGCAGGGATGACTCTGGGAGCC-3' (SEQ ID NO: 2457)

5'-AUGAAGCAGGGAUGACUCUGGGAGC$^{AA-3'}$ (SEQ ID NO: 4231)
3'-UACUUCGUCCCUACUGAGACCCUCG$_{GG-5'}$ (SEQ ID NO: 2053)

AR-3003 Target: 5'-ATGAAGCAGGGATGACTCTGGGAGCCC-3' (SEQ ID NO: 2458)

5'-UGAAGCAGGGAUGACUCUGGGAGCC$^{A}{}^{A-3'}$ (SEQ ID NO: 4232)
3'-ACUUCGUCCCUACUGAGACCCUCGG$_{G}{}_{C-5'}$ (SEQ ID NO: 2054)

AR-3004 Target: 5'-TGAAGCAGGGATGACTCTGGGAGCCCG-3' (SEQ ID NO: 2459)

5'-GAAGCAGGGAUGACUCUGGGAGCCC$^{A}{}^{A-3'}$ (SEQ ID NO: 4233)
3'-CUUCGUCCCUACUGAGACCCUCGGG$_{C}{}_{C-5'}$ (SEQ ID NO: 2055)

AR-3005 Target: 5'-GAAGCAGGGATGACTCTGGGAGCCCGG-3' (SEQ ID NO: 2460)

5'-AAGCAGGGAUGACUCUGGGAGCCCG$^{A}{}^{C-3'}$ (SEQ ID NO: 4234)
3'-UUCGUCCCUACUGAGACCCUCGGGC$_{C}{}_{U-5'}$ (SEQ ID NO: 2056)

AR-3006 Target: 5'-AAGCAGGGATGACTCTGGGAGCCCGGA-3' (SEQ ID NO: 2461)

5'-AGCAGGGAUGACUCUGGGAGCCCGG$^{C}{}^{C-3'}$ (SEQ ID NO: 4235)
3'-UCGUCCCUACUGAGACCCUCGGGCC$_{U}{}_{U-5'}$ (SEQ ID NO: 2057)

AR-3007 Target: 5'-AGCAGGGATGACTCTGGGAGCCCGGAA-3' (SEQ ID NO: 2462)

5'-CUGAAGAAACUUGGUAAUCUGAAAC$^{C}{}^{C-3'}$ (SEQ ID NO: 4236)
3'-GACUUCUUUGAACCAUUAGACUUUG$_{A}{}_{U-5'}$ (SEQ ID NO: 2058)

AR-3035 Target: 5'-CTGAAGAAACTTGGTAATCTGAAACTA-3' (SEQ ID NO: 2463)

5'-UGAAACUACAGGAGGAAGGAGAGGC$^{C}{}^{C-3'}$ (SEQ ID NO: 4237)
3'-ACUUUGAUGUCCUCCUUCCUCUCCG$_{A}{}_{A-5'}$ (SEQ ID NO: 2059)

AR-3054 Target: 5'-TGAAACTACAGGAGGAAGGAGAGGCTT-3' (SEQ ID NO: 2464)

5'-GAAACUACAGGAGGAAGGAGAGGCU$^{C}{}^{A-3'}$ (SEQ ID NO: 4238)
3'-CUUUGAUGUCCUCCUUCCUCUCCGA$_{A}{}_{G-5'}$ (SEQ ID NO: 2060)

AR-3055 Target: 5'-GAAACTACAGGAGGAAGGAGAGGCTTC-3' (SEQ ID NO: 2465)

5'-CACAUUGAAGGCUAUGAAUGUCAGC$^{A}{}^{A-3'}$ (SEQ ID NO: 4239)
3'-GUGUAACUUCCGAUACUUACAGUCG$_{G}{}_{G-5'}$ (SEQ ID NO: 2061)

AR-3131 Target: 5'-CACATTGAAGGCTATGAATGTCAGCCC-3' (SEQ ID NO: 2466)

5'-ACAUUGAAGGCUAUGAAUGUCAGCC$^{A}{}^{C-3'}$ (SEQ ID NO: 4240)
3'-UGUAACUUCCGAUACUUACAGUCGG$_{G}{}_{U-5'}$ (SEQ ID NO: 2062)

AR-3132 Target: 5'-ACATTGAAGGCTATGAATGTCAGCCCA-3' (SEQ ID NO: 2467)

5'-CAUUGAAGGCUAUGAAUGUCAGCCC$^{C}{}^{C-3'}$ (SEQ ID NO: 4241)
3'-GUAACUUCCGAUACUUACAGUCGGG$_{U}{}_{A-5'}$ (SEQ ID NO: 2063)

AR-3133 Target: 5'-CATTGAAGGCTATGAATGTCAGCCCAT-3' (SEQ ID NO: 2468)

5'-AUUGAAGGCUAUGAAUGUCAGCCCA$^{C}{}^{A-3'}$ (SEQ ID NO: 4242)
3'-UAACUUCCGAUACUUACAGUCGGGU$_{A}{}_{G-5'}$ (SEQ ID NO: 2064)

AR-3134 Target: 5'-ATTGAAGGCTATGAATGTCAGCCCATC-3' (SEQ ID NO: 2469)

5'-UUGAAGGCUAUGAAUGUCAGCCCAU$^{A}C_{A-5'}$ (SEQ ID NO: 4243)
3'-AACUUCCGAUACUUACAGUCGGGUA$_{G}$ (SEQ ID NO: 2065)

AR-3135 Target: 5'-TTGAAGGCTATGAATGTCAGCCCATCT-3' (SEQ ID NO: 2470)

5'-UGAAGGCUAUGAAUGUCAGCCCAUC$^{C}C_{A-5'}$ (SEQ ID NO: 4244)
3'-ACUUCCGAUACUUACAGUCGGGUAG$_{A}$ (SEQ ID NO: 2066)

AR-3136 Target: 5'-TGAAGGCTATGAATGTCAGCCCATCTT-3' (SEQ ID NO: 2471)

5'-AUGUCCUGGAAGCCAUUGAGCCAGG$^{C}C_{A-5'}$ (SEQ ID NO: 4245)
3'-UACAGGACCUUCGGUAACUCGGUCC$_{A}$ (SEQ ID NO: 2067)

AR-3168 Target: 5'-ATGTCCTGGAAGCCATTGAGCCAGGTG-3' (SEQ ID NO: 2472)

5'-UGUCCUGGAAGCCAUUGAGCCAGGU$^{A}C_{A-5'}$ (SEQ ID NO: 4246)
3'-ACAGGACCUUCGGUAACUCGGUCCA$_{C}$ (SEQ ID NO: 2068)

AR-3169 Target: 5'-TGTCCTGGAAGCCATTGAGCCAGGTGT-3' (SEQ ID NO: 2473)

5'-GUCCUGGAAGCCAUUGAGCCAGGUG$^{C}C_{A-5'}$ (SEQ ID NO: 4247)
3'-CAGGACCUUCGGUAACUCGGUCCAC$_{A}$ (SEQ ID NO: 2069)

AR-3170 Target: 5'-GTCCTGGAAGCCATTGAGCCAGGTGTA-3' (SEQ ID NO: 2474)

5'-UCCUGGAAGCCAUUGAGCCAGGUGU$^{C}A_{A-5'}$ (SEQ ID NO: 4248)
3'-AGGACCUUCGGUAACUCGGUCCACA$_{U}$ (SEQ ID NO: 2070)

AR-3171 Target: 5'-TCCTGGAAGCCATTGAGCCAGGTGTAG-3' (SEQ ID NO: 2475)

5'-CCUGGAAGCCAUUGAGCCAGGUGUA$^{A}C_{A-5'}$ (SEQ ID NO: 4249)
3'-GGACCUUCGGUAACUCGGUCCACAU$_{C}$ (SEQ ID NO: 2071)

AR-3172 Target: 5'-CCTGGAAGCCATTGAGCCAGGTGTAGT-3' (SEQ ID NO: 2476)

5'-ACCAGCCCGACUCCUUUGCAGCCUU$^{A}A_{G-5'}$ (SEQ ID NO: 4250)
3'-UGGUCGGGCUGAGGAAACGUCGGAA$_{C}$ (SEQ ID NO: 2072)

AR-3219 Target: 5'-ACCAGCCCGACTCCTTTGCAGCCTTGC-3' (SEQ ID NO: 2477)

5'-CCGACUCCUUUGCAGCCUUGCUCUC$^{C}C_{A-5'}$ (SEQ ID NO: 4251)
3'-GGCUGAGGAAACGUCGGAACGAGAG$_{A}$ (SEQ ID NO: 2073)

AR-3225 Target: 5'-CCGACTCCTTTGCAGCCTTGCTCTCTA-3' (SEQ ID NO: 2478)

5'-UGCAGCCUUGCUCUCUAGCCUCAAU$^{A}C_{A-5'}$ (SEQ ID NO: 4252)
3'-ACGUCGGAACGAGAGAUCGGAGUUA$_{C}$ (SEQ ID NO: 2074)

AR-3235 Target: 5'-TGCAGCCTTGCTCTCTAGCCTCAATGA-3' (SEQ ID NO: 2479)

5'-ACGUGGUCAAGUGGGCCAAGGCCUU$^{A}A_{G-5'}$ (SEQ ID NO: 4253)
3'-UGCACCAGUUCACCCGGUUCCGGAA$_{C}$ (SEQ ID NO: 2075)

AR-3285 Target: 5'-ACGTGGTCAAGTGGGCCAAGGCCTTGC-3' (SEQ ID NO: 2480)

5'-CGUGGUCAAGUGGGCCAAGGCCUUG^{A}$^{A-3'}$ (SEQ ID NO: 4254)
3'-GCACCAGUUCACCCGGUUCCGGAAC$_{G}$$_{G-5'}$ (SEQ ID NO: 2076)

AR-3286 Target: 5'-CGTGGTCAAGTGGGCCAAGGCCTTGCC-3' (SEQ ID NO: 2481)

5'-GUGGUCAAGUGGGCCAAGGCCUUGC^{A}$^{C-3'}$ (SEQ ID NO: 4255)
3'-CACCAGUUCACCCGGUUCCGGAACG$_{G}$$_{A-5'}$ (SEQ ID NO: 2077)

AR-3287 Target: 5'-GTGGTCAAGTGGGCCAAGGCCTTGCCT-3' (SEQ ID NO: 2482)

5'-UGGUCAAGUGGGCCAAGGCCUUGCC^{C}$^{A-3'}$ (SEQ ID NO: 4256)
3'-ACCAGUUCACCCGGUUCCGGAACGG$_{A}$$_{C-5'}$ (SEQ ID NO: 2078)

AR-3288 Target: 5'-TGGTCAAGTGGGCCAAGGCCTTGCCTG-3' (SEQ ID NO: 2483)

5'-GGUCAAGUGGGCCAAGGCCUUGCCU^{A}$^{A-3'}$ (SEQ ID NO: 4257)
3'-CCAGUUCACCCGGUUCCGGAACGGA$_{C}$$_{C-5'}$ (SEQ ID NO: 2079)

AR-3289 Target: 5'-GGTCAAGTGGGCCAAGGCCTTGCCTGG-3' (SEQ ID NO: 2484)

5'-GUCAAGUGGGCCAAGGCCUUGCCUG^{A}$^{A-3'}$ (SEQ ID NO: 4258)
3'-CAGUUCACCCGGUUCCGGAACGGAC$_{C}$$_{G-5'}$ (SEQ ID NO: 2080)

AR-3290 Target: 5'-GTCAAGTGGGCCAAGGCCTTGCCTGGC-3' (SEQ ID NO: 2485)

5'-UCAAGUGGGCCAAGGCCUUGCCUGG^{A}$^{C-3'}$ (SEQ ID NO: 4259)
3'-AGUUCACCCGGUUCCGGAACGGACC$_{G}$$_{A-5'}$ (SEQ ID NO: 2081)

AR-3291 Target: 5'-TCAAGTGGGCCAAGGCCTTGCCTGGCT-3' (SEQ ID NO: 2486)

5'-CAAGUGGGCCAAGGCCUUGCCUGGC^{C}$^{C-3'}$ (SEQ ID NO: 4260)
3'-GUUCACCCGGUUCCGGAACGGACCG$_{A}$$_{A-5'}$ (SEQ ID NO: 2082)

AR-3292 Target: 5'-CAAGTGGGCCAAGGCCTTGCCTGGCTT-3' (SEQ ID NO: 2487)

5'-AAGUGGGCCAAGGCCUUGCCUGGCU^{C}$^{A-3'}$ (SEQ ID NO: 4261)
3'-UUCACCCGGUUCCGGAACGGACCGA$_{A}$$_{G-5'}$ (SEQ ID NO: 2083)

AR-3293 Target: 5'-AAGTGGGCCAAGGCCTTGCCTGGCTTC-3' (SEQ ID NO: 2488)

5'-AGUGGGCCAAGGCCUUGCCUGGCUU^{A}$^{A-3'}$ (SEQ ID NO: 4262)
3'-UCACCCGGUUCCGGAACGGACCGAA$_{G}$$_{G-5'}$ (SEQ ID NO: 2084)

AR-3294 Target: 5'-AGTGGGCCAAGGCCTTGCCTGGCTTCC-3' (SEQ ID NO: 2489)

5'-GUGGGCCAAGGCCUUGCCUGGCUUC^{A}$^{A-3'}$ (SEQ ID NO: 4263)
3'-CACCCGGUUCCGGAACGGACCGAAG$_{G}$$_{C-5'}$ (SEQ ID NO: 2085)

AR-3295 Target: 5'-GTGGGCCAAGGCCTTGCCTGGCTTCCG-3' (SEQ ID NO: 2490)

5'-UGGGCCAAGGCCUUGCCUGGCUUCC^{A}$^{A-3'}$ (SEQ ID NO: 4264)
3'-ACCCGGUUCCGGAACGGACCGAAGG$_{C}$$_{G-5'}$ (SEQ ID NO: 2086)

AR-3296 Target: 5'-TGGGCCAAGGCCTTGCCTGGCTTCCGC-3' (SEQ ID NO: 2491)

5'-GGGCCAAGGCCUUGCCUGGCUUCCG^{A}C-3' (SEQ ID NO: 4265)
3'-CCCGGUUCCGGAACGGACCGAAGGC$_{G}$$_{U-5'}$ (SEQ ID NO: 2087)

AR-3297 Target: 5'-GGGCCAAGGCCTTGCCTGGCTTCCGCA-3' (SEQ ID NO: 2492)

5'-GGCCAAGGCCUUGCCUGGCUUCCGC^{C}C-3' (SEQ ID NO: 4266)
3'-CCGGUUCCGGAACGGACCGAAGGCG$_{U}$$_{U-5'}$ (SEQ ID NO: 2088)

AR-3298 Target: 5'-GGCCAAGGCCTTGCCTGGCTTCCGCAA-3' (SEQ ID NO: 2493)

5'-GCCAAGGCCUUGCCUGGCUUCCGCA^{C}C-3' (SEQ ID NO: 4267)
3'-CGGUUCCGGAACGGACCGAAGGCGU$_{U}$$_{G-5'}$ (SEQ ID NO: 2089)

AR-3299 Target: 5'-GCCAAGGCCTTGCCTGGCTTCCGCAAC-3' (SEQ ID NO: 2494)

5'-CCAAGGCCUUGCCUGGCUUCCGCAA^{A}C-3' (SEQ ID NO: 4268)
3'-GGUUCCGGAACGGACCGAAGGCGUU$_{G}$$_{A-5'}$ (SEQ ID NO: 2090)

AR-3300 Target: 5'-CCAAGGCCTTGCCTGGCTTCCGCAACT-3' (SEQ ID NO: 2495)

5'-CAAGGCCUUGCCUGGCUUCCGCAAC^{C}C-3' (SEQ ID NO: 4269)
3'-GUUCCGGAACGGACCGAAGGCGUUG$_{A}$$_{A-5'}$ (SEQ ID NO: 2091)

AR-3301 Target: 5'-CAAGGCCTTGCCTGGCTTCCGCAACTT-3' (SEQ ID NO: 2496)

5'-AAGGCCUUGCCUGGCUUCCGCAACU^{C}C-3' (SEQ ID NO: 4270)
3'-UUCCGGAACGGACCGAAGGCGUUGA$_{A}$$_{U-5'}$ (SEQ ID NO: 2092)

AR-3302 Target: 5'-AAGGCCTTGCCTGGCTTCCGCAACTTA-3' (SEQ ID NO: 2497)

5'-AGGCCUUGCCUGGCUUCCGCAACUU^{C}A-3' (SEQ ID NO: 4271)
3'-UCCGGAACGGACCGAAGGCGUUGAA$_{U}$$_{G-5'}$ (SEQ ID NO: 2093)

AR-3303 Target: 5'-AGGCCTTGCCTGGCTTCCGCAACTTAC-3' (SEQ ID NO: 2498)

5'-GGCCUUGCCUGGCUUCCGCAACUUA^{A}C-3' (SEQ ID NO: 4272)
3'-CCGGAACGGACCGAAGGCGUUGAAU$_{G}$$_{U-5'}$ (SEQ ID NO: 2094)

AR-3304 Target: 5'-GGCCTTGCCTGGCTTCCGCAACTTACA-3' (SEQ ID NO: 2499)

5'-GCCUUGCCUGGCUUCCGCAACUUAC^{C}A-3' (SEQ ID NO: 4273)
3'-CGGAACGGACCGAAGGCGUUGAAUG$_{U}$$_{G-5'}$ (SEQ ID NO: 2095)

AR-3305 Target: 5'-GCCTTGCCTGGCTTCCGCAACTTACAC-3' (SEQ ID NO: 2500)

5'-CCUUGCCUGGCUUCCGCAACUUACA^{A}A-3' (SEQ ID NO: 4274)
3'-GGAACGGACCGAAGGCGUUGAAUGU$_{G}$$_{C-5'}$ (SEQ ID NO: 2096)

AR-3306 Target: 5'-CCTTGCCTGGCTTCCGCAACTTACACG-3' (SEQ ID NO: 2501)

5'-CUUGCCUGGCUUCCGCAACUUACAC^{A}C-3' (SEQ ID NO: 4275)
3'-GAACGGACCGAAGGCGUUGAAUGUG$_{C}$$_{A-5'}$ (SEQ ID NO: 2097)

AR-3307 Target: 5'-CTTGCCTGGCTTCCGCAACTTACACGT-3' (SEQ ID NO: 2502)

5'-CCAAUGUCAACUCCAGGAUGCUCUA$^{AC-3'}$ (SEQ ID NO: 4276)
3'-GGUUACAGUUGAGGUCCUACGAGAU$_{GA-5'}$ (SEQ ID NO: 2098)

AR-3408 Target: 5'-CCAATGTCAACTCCAGGATGCTCTACT-3' (SEQ ID NO: 2503)

5'-CAAUGUCAACUCCAGGAUGCUCUAC$^{CC-3'}$ (SEQ ID NO: 4277)
3'-GUUACAGUUGAGGUCCUACGAGAUG$_{AA-5'}$ (SEQ ID NO: 2099)

AR-3409 Target: 5'-CAATGTCAACTCCAGGATGCTCTACTT-3' (SEQ ID NO: 2504)

5'-AAUGUCAACUCCAGGAUGCUCUACU$^{CA-3'}$ (SEQ ID NO: 4278)
3'-UUACAGUUGAGGUCCUACGAGAUGA$_{AG-5'}$ (SEQ ID NO: 2100)

AR-3410 Target: 5'-AATGTCAACTCCAGGATGCTCTACTTC-3' (SEQ ID NO: 2505)

5'-AUGUCAACUCCAGGAUGCUCUACUU$^{AA-3'}$ (SEQ ID NO: 4279)
3'-UACAGUUGAGGUCCUACGAGAUGAA$_{GC-5'}$ (SEQ ID NO: 2101)

AR-3411 Target: 5'-ATGTCAACTCCAGGATGCTCTACTTCG-3' (SEQ ID NO: 2506)

5'-UGUCAACUCCAGGAUGCUCUACUUC$^{AA-3'}$ (SEQ ID NO: 4280)
3'-ACAGUUGAGGUCCUACGAGAUGAAG$_{CG-5'}$ (SEQ ID NO: 2102)

AR-3412 Target: 5'-TGTCAACTCCAGGATGCTCTACTTCGC-3' (SEQ ID NO: 2507)

5'-GUCAACUCCAGGAUGCUCUACUUCG$^{AA-3'}$ (SEQ ID NO: 4281)
3'-CAGUUGAGGUCCUACGAGAUGAAGC$_{GG-5'}$ (SEQ ID NO: 2103)

AR-3413 Target: 5'-GTCAACTCCAGGATGCTCTACTTCGCC-3' (SEQ ID NO: 2508)

5'-UCAACUCCAGGAUGCUCUACUUCGC$^{AA-3'}$ (SEQ ID NO: 4282)
3'-AGUUGAGGUCCUACGAGAUGAAGCG$_{GG-5'}$ (SEQ ID NO: 2104)

AR-3414 Target: 5'-TCAACTCCAGGATGCTCTACTTCGCCC-3' (SEQ ID NO: 2509)

5'-UCUGGUUUUCAAUGAGUACCGCAUG$^{AC-3'}$ (SEQ ID NO: 4283)
3'-AGACCAAAAGUUACUCAUGGCGUAC$_{GU-5'}$ (SEQ ID NO: 2105)

AR-3445 Target: 5'-TCTGGTTTTCAATGAGTACCGCATGCA-3' (SEQ ID NO: 2510)

5'-CUGGUUUUCAAUGAGUACCGCAUGC$^{CA-3'}$ (SEQ ID NO: 4284)
3'-GACCAAAAGUUACUCAUGGCGUACG$_{UG-5'}$ (SEQ ID NO: 2106)

AR-3446 Target: 5'-CTGGTTTTCAATGAGTACCGCATGCAC-3' (SEQ ID NO: 2511)

5'-UGGUUUUCAAUGAGUACCGCAUGCA$^{AC-3'}$ (SEQ ID NO: 4285)
3'-ACCAAAAGUUACUCAUGGCGUACGU$_{GU-5'}$ (SEQ ID NO: 2107)

AR-3447 Target: 5'-TGGTTTTCAATGAGTACCGCATGCACA-3' (SEQ ID NO: 2512)

5'-GGUUUUCAAUGAGUACCGCAUGCAC$^{CC-3'}$ (SEQ ID NO: 4286)
3'-CCAAAAGUUACUCAUGGCGUACGUG$_{UU-5'}$ (SEQ ID NO: 2108)

AR-3448 Target: 5'-GGTTTTCAATGAGTACCGCATGCACAA-3' (SEQ ID NO: 2513)

5'-GUUUUCAAUGAGUACCGCAUGCACA$^{CA-3'}$ (SEQ ID NO: 4287)
3'-CAAAAGUUACUCAUGGCGUACGUGU$_{UC-5'}$ (SEQ ID NO: 2109)

AR-3449 Target: 5'-GTTTTCAATGAGTACCGCATGCACAAG-3' (SEQ ID NO: 2514)

5'-UUUUCAAUGAGUACCGCAUGCACAA$^{AC-3'}$ (SEQ ID NO: 4288)
3'-AAAAGUUACUCAUGGCGUACGUGUU$_{CA-5'}$ (SEQ ID NO: 2110)

AR-3450 Target: 5'-TTTTCAATGAGTACCGCATGCACAAGT-3' (SEQ ID NO: 2515)

5'-UUUCAAUGAGUACCGCAUGCACAAG$^{CA-3'}$ (SEQ ID NO: 4289)
3'-AAAGUUACUCAUGGCGUACGUGUUC$_{AG-5'}$ (SEQ ID NO: 2111)

AR-3451 Target: 5'-TTTCAATGAGTACCGCATGCACAAGTC-3' (SEQ ID NO: 2516)

5'-UUCAAUGAGUACCGCAUGCACAAGU$^{AA-3'}$ (SEQ ID NO: 4290)
3'-AAGUUACUCAUGGCGUACGUGUUCA$_{GG-5'}$ (SEQ ID NO: 2112)

AR-3452 Target: 5'-TTCAATGAGTACCGCATGCACAAGTCC-3' (SEQ ID NO: 2517)

5'-UCAAUGAGUACCGCAUGCACAAGUC$^{AA-3'}$ (SEQ ID NO: 4291)
3'-AGUUACUCAUGGCGUACGUGUUCAG$_{GG-5'}$ (SEQ ID NO: 2113)

AR-3453 Target: 5'-TCAATGAGTACCGCATGCACAAGTCCC-3' (SEQ ID NO: 2518)

5'-CAAUGAGUACCGCAUGCACAAGUCC$^{AA-3'}$ (SEQ ID NO: 4292)
3'-GUUACUCAUGGCGUACGUGUUCAGG$_{GC-5'}$ (SEQ ID NO: 2114)

AR-3454 Target: 5'-CAATGAGTACCGCATGCACAAGTCCCG-3' (SEQ ID NO: 2519)

5'-AAUGAGUACCGCAUGCACAAGUCCC$^{AA-3'}$ (SEQ ID NO: 4293)
3'-UUACUCAUGGCGUACGUGUUCAGGG$_{CC-5'}$ (SEQ ID NO: 2115)

AR-3455 Target: 5'-AATGAGTACCGCATGCACAAGTCCCGG-3' (SEQ ID NO: 2520)

5'-AUGAGUACCGCAUGCACAAGUCCCG$^{AC-3'}$ (SEQ ID NO: 4294)
3'-UACUCAUGGCGUACGUGUUCAGGGC$_{CU-5'}$ (SEQ ID NO: 2116)

AR-3456 Target: 5'-ATGAGTACCGCATGCACAAGTCCCGGA-3' (SEQ ID NO: 2521)

5'-UGAGUACCGCAUGCACAAGUCCCGG$^{CC-3'}$ (SEQ ID NO: 4295)
3'-ACUCAUGGCGUACGUGUUCAGGGCC$_{UA-5'}$ (SEQ ID NO: 2117)

AR-3457 Target: 5'-TGAGTACCGCATGCACAAGTCCCGGAT-3' (SEQ ID NO: 2522)

5'-UCUCUCAAGAGUUUGGAUGGCUCCA$^{CC-3'}$ (SEQ ID NO: 4296)
3'-AGAGAGUUCUCAAACCUACCGAGGU$_{UU-5'}$ (SEQ ID NO: 2118)

AR-3513 Target: 5'-TCTCTCAAGAGTTTGGATGGCTCCAAA-3' (SEQ ID NO: 2523)

5'-CUCUCAAGAGUUUGGAUGGCUCCAA$^{CC-3'}$ (SEQ ID NO: 4297)
3'-GAGAGUUCUCAAACCUACCGAGGUU$_{UA-5'}$ (SEQ ID NO: 2119)

AR-3514 Target: 5'-CTCTCAAGAGTTTGGATGGCTCCAAAT-3' (SEQ ID NO: 2524)

5'-UCUCAAGAGUUUGGAUGGCUCCAAA$^{CA-3'}$ (SEQ ID NO: 4298)
3'-AGAGUUCUCAAACCUACCGAGGUUU$_{AG-5'}$ (SEQ ID NO: 2120)

AR-3515 Target: 5'-TCTCAAGAGTTTGGATGGCTCCAAATC-3' (SEQ ID NO: 2525)

5'-CUCAAGAGUUUGGAUGGCUCCAAAU$^{AC-3'}$ (SEQ ID NO: 4299)
3'-GAGUUCUCAAACCUACCGAGGUUUA$_{GU-5'}$ (SEQ ID NO: 2121)

AR-3516 Target: 5'-CTCAAGAGTTTGGATGGCTCCAAATCA-3' (SEQ ID NO: 2526)

5'-UCAAGAGUUUGGAUGGCUCCAAAUC$^{CA-3'}$ (SEQ ID NO: 4300)
3'-AGUUCUCAAACCUACCGAGGUUUAG$_{UG-5'}$ (SEQ ID NO: 2122)

AR-3517 Target: 5'-TCAAGAGTTTGGATGGCTCCAAATCAC-3' (SEQ ID NO: 2527)

5'-CAAGAGUUUGGAUGGCUCCAAAUCA$^{AA-3'}$ (SEQ ID NO: 4301)
3'-GUUCUCAAACCUACCGAGGUUUAGU$_{GG-5'}$ (SEQ ID NO: 2123)

AR-3518 Target: 5'-CAAGAGTTTGGATGGCTCCAAATCACC-3' (SEQ ID NO: 2528)

5'-AAGAGUUUGGAUGGCUCCAAAUCAC$^{AA-3'}$ (SEQ ID NO: 4302)
3'-UUCUCAAACCUACCGAGGUUUAGUG$_{GG-5'}$ (SEQ ID NO: 2124)

AR-3519 Target: 5'-AAGAGTTTGGATGGCTCCAAATCACCC-3' (SEQ ID NO: 2529)

5'-CCCAGGAAUUCCUGUGCAUGAAAGC$^{CA-3'}$ (SEQ ID NO: 4303)
3'-GGGUCCUUAAGGACACGUACUUUCG$_{UG-5'}$ (SEQ ID NO: 2125)

AR-3546 Target: 5'-CCCAGGAATTCCTGTGCATGAAAGCAC-3' (SEQ ID NO: 2530)

5'-CCAGGAAUUCCUGUGCAUGAAAGCA$^{AC-3'}$ (SEQ ID NO: 4304)
3'-GGUCCUUAAGGACACGUACUUUCGU$_{GA-5'}$ (SEQ ID NO: 2126)

AR-3547 Target: 5'-CCAGGAATTCCTGTGCATGAAAGCACT-3' (SEQ ID NO: 2531)

5'-CAGGAAUUCCUGUGCAUGAAAGCAC$^{CA-3'}$ (SEQ ID NO: 4305)
3'-GUCCUUAAGGACACGUACUUUCGUG$_{AC-5'}$ (SEQ ID NO: 2127)

AR-3548 Target: 5'-CAGGAATTCCTGTGCATGAAAGCACTG-3' (SEQ ID NO: 2532)

5'-AGGAAUUCCUGUGCAUGAAAGCACU$^{AA-3'}$ (SEQ ID NO: 4306)
3'-UCCUUAAGGACACGUACUUUCGUGA$_{CG-5'}$ (SEQ ID NO: 2128)

AR-3549 Target: 5'-AGGAATTCCTGTGCATGAAAGCACTGC-3' (SEQ ID NO: 2533)

5'-GGAAUUCCUGUGCAUGAAAGCACUG$^{AC-3'}$ (SEQ ID NO: 4307)
3'-CCUUAAGGACACGUACUUUCGUGAC$_{GA-5'}$ (SEQ ID NO: 2129)

AR-3550 Target: 5'-GGAATTCCTGTGCATGAAAGCACTGCT-3' (SEQ ID NO: 2534)

5'-GAAUUCCUGUGCAUGAAAGCACUGC$^{CC-3'}$ (SEQ ID NO: 4308)
3'-CUUAAGGACACGUACUUUCGUGACG$_{AU-5'}$ (SEQ ID NO: 2130)

AR-3551 Target: 5'-GAATTCCTGTGCATGAAAGCACTGCTA-3' (SEQ ID NO: 2535)

5'-AAUUCCUGUGCAUGAAAGCACUGCU$^{C}{}^{A-3'}$ (SEQ ID NO: 4309)
3'-UUAAGGACACGUACUUUCGUGACGA$_{U}{}_{G-5'}$ (SEQ ID NO: 2131)

AR-3552 Target: 5'-AATTCCTGTGCATGAAAGCACTGCTAC-3' (SEQ ID NO: 2536)

5'-AUUCCUGUGCAUGAAAGCACUGCUA$^{A}{}^{C-3'}$ (SEQ ID NO: 4310)
3'-UAAGGACACGUACUUUCGUGACGAU$_{G}{}_{A-5'}$ (SEQ ID NO: 2132)

AR-3553 Target: 5'-ATTCCTGTGCATGAAAGCACTGCTACT-3' (SEQ ID NO: 2537)

5'-UUCCUGUGCAUGAAAGCACUGCUAC$^{C}{}^{A-3'}$ (SEQ ID NO: 4311)
3'-AAGGACACGUACUUUCGUGACGAUG$_{A}{}_{G-5'}$ (SEQ ID NO: 2133)

AR-3554 Target: 5'-TTCCTGTGCATGAAAGCACTGCTACTC-3' (SEQ ID NO: 2538)

5'-UCCUGUGCAUGAAAGCACUGCUACU$^{A}{}^{C-3'}$ (SEQ ID NO: 4312)
3'-AGGACACGUACUUUCGUGACGAUGA$_{G}{}_{A-5'}$ (SEQ ID NO: 2134)

AR-3555 Target: 5'-TCCTGTGCATGAAAGCACTGCTACTCT-3' (SEQ ID NO: 2539)

5'-CCUGUGCAUGAAAGCACUGCUACUC$^{C}{}^{C-3'}$ (SEQ ID NO: 4313)
3'-GGACACGUACUUUCGUGACGAUGAG$_{A}{}_{A-5'}$ (SEQ ID NO: 2135)

AR-3556 Target: 5'-CCTGTGCATGAAAGCACTGCTACTCTT-3' (SEQ ID NO: 2540)

5'-UACUCUUCAGCAUUAUUCCAGUGGA$^{C}{}^{A-3'}$ (SEQ ID NO: 4314)
3'-AUGAGAAGUCGUAAUAAGGUCACCU$_{A}{}_{C-5'}$ (SEQ ID NO: 2136)

AR-3576 Target: 5'-TACTCTTCAGCATTATTCCAGTGGATG-3' (SEQ ID NO: 2541)

5'-ACUCUUCAGCAUUAUUCCAGUGGAU$^{A}{}^{A-3'}$ (SEQ ID NO: 4315)
3'-UGAGAAGUCGUAAUAAGGUCACCUA$_{C}{}_{C-5'}$ (SEQ ID NO: 2137)

AR-3577 Target: 5'-ACTCTTCAGCATTATTCCAGTGGATGG-3' (SEQ ID NO: 2542)

5'-CUCUUCAGCAUUAUUCCAGUGGAUG$^{A}{}^{A-3'}$ (SEQ ID NO: 4316)
3'-GAGAAGUCGUAAUAAGGUCACCUAC$_{C}{}_{C-5'}$ (SEQ ID NO: 2138)

AR-3578 Target: 5'-CTCTTCAGCATTATTCCAGTGGATGGG-3' (SEQ ID NO: 2543)

5'-UCUUCAGCAUUAUUCCAGUGGAUGG$^{A}{}^{A-3'}$ (SEQ ID NO: 4317)
3'-AGAAGUCGUAAUAAGGUCACCUACC$_{C}{}_{G-5'}$ (SEQ ID NO: 2139)

AR-3579 Target: 5'-TCTTCAGCATTATTCCAGTGGATGGGC-3' (SEQ ID NO: 2544)

5'-CUUCAGCAUUAUUCCAGUGGAUGGG$^{A}{}^{C-3'}$ (SEQ ID NO: 4318)
3'-GAAGUCGUAAUAAGGUCACCUACCC$_{G}{}_{A-5'}$ (SEQ ID NO: 2140)

AR-3580 Target: 5'-CTTCAGCATTATTCCAGTGGATGGGCT-3' (SEQ ID NO: 2545)

5'-UUCAGCAUUAUUCCAGUGGAUGGGC$^{C}{}^{A-3'}$ (SEQ ID NO: 4319)
3'-AAGUCGUAAUAAGGUCACCUACCCG$_{A}{}_{C-5'}$ (SEQ ID NO: 2141)

AR-3581 Target: 5'-TTCAGCATTATTCCAGTGGATGGGCTG-3' (SEQ ID NO: 2546)

5'-UCAGCAUUAUUCCAGUGGAUGGGCU^{A}C-3′ (SEQ ID NO: 4320)
3'-AGUCGUAAUAAGGUCACCUACCCGA$_{C}$$_{U-5′}$ (SEQ ID NO: 2142)

AR-3582 Target: 5'-TCAGCATTATTCCAGTGGATGGGCTGA-3' (SEQ ID NO: 2547)

5'-CAGCAUUAUUCCAGUGGAUGGGCUG^{C}C-3′ (SEQ ID NO: 4321)
3'-GUCGUAAUAAGGUCACCUACCCGAC$_{U}$$_{U-5′}$ (SEQ ID NO: 2143)

AR-3583 Target: 5'-CAGCATTATTCCAGTGGATGGGCTGAA-3' (SEQ ID NO: 2548)

5'-AGCAUUAUUCCAGUGGAUGGGCUGA^{C}C-3′ (SEQ ID NO: 4322)
3'-UCGUAAUAAGGUCACCUACCCGACU$_{U}$$_{U-5′}$ (SEQ ID NO: 2144)

AR-3584 Target: 5'-AGCATTATTCCAGTGGATGGGCTGAAA-3' (SEQ ID NO: 2549)

5'-GCAUUAUUCCAGUGGAUGGGCUGAA^{C}C-3′ (SEQ ID NO: 4323)
3'-CGUAAUAAGGUCACCUACCCGACUU$_{U}$$_{U-5′}$ (SEQ ID NO: 2145)

AR-3585 Target: 5'-GCATTATTCCAGTGGATGGGCTGAAAA-3' (SEQ ID NO: 2550)

5'-CAUUAUUCCAGUGGAUGGGCUGAAA^{C}C-3′ (SEQ ID NO: 4324)
3'-GUAAUAAGGUCACCUACCCGACUUU$_{U}$$_{U-5′}$ (SEQ ID NO: 2146)

AR-3586 Target: 5'-CATTATTCCAGTGGATGGGCTGAAAAA-3' (SEQ ID NO: 2551)

5'-AUUAUUCCAGUGGAUGGGCUGAAAA^{C}C-3′ (SEQ ID NO: 4325)
3'-UAAUAAGGUCACCUACCCGACUUUU$_{U}$$_{A-5′}$ (SEQ ID NO: 2147)

AR-3587 Target: 5'-ATTATTCCAGTGGATGGGCTGAAAAAT-3' (SEQ ID NO: 2552)

5'-UUAUUCCAGUGGAUGGGCUGAAAAA^{C}A-3′ (SEQ ID NO: 4326)
3'-AAUAAGGUCACCUACCCGACUUUUU$_{A}$$_{G-5′}$ (SEQ ID NO: 2148)

AR-3588 Target: 5'-TTATTCCAGTGGATGGGCTGAAAAATC-3' (SEQ ID NO: 2553)

5'-UAUUCCAGUGGAUGGGCUGAAAAAU^{A}C-3′ (SEQ ID NO: 4327)
3'-AUAAGGUCACCUACCCGACUUUUUA$_{G}$$_{U-5′}$ (SEQ ID NO: 2149)

AR-3589 Target: 5'-TATTCCAGTGGATGGGCTGAAAAATCA-3' (SEQ ID NO: 2554)

5'-AUUCCAGUGGAUGGGCUGAAAAAUC^{C}C-3′ (SEQ ID NO: 4328)
3'-UAAGGUCACCUACCCGACUUUUUAG$_{U}$$_{U-5′}$ (SEQ ID NO: 2150)

AR-3590 Target: 5'-ATTCCAGTGGATGGGCTGAAAAATCAA-3' (SEQ ID NO: 2555)

5'-UUCCAGUGGAUGGGCUGAAAAAUCA^{C}C-3′ (SEQ ID NO: 4329)
3'-AAGGUCACCUACCCGACUUUUUAGU$_{U}$$_{U-5′}$ (SEQ ID NO: 2151)

AR-3591 Target: 5'-TTCCAGTGGATGGGCTGAAAAATCAAA-3' (SEQ ID NO: 2556)

5'-UCCAGUGGAUGGGCUGAAAAAUCAA^{C}C-3′ (SEQ ID NO: 4330)
3'-AGGUCACCUACCCGACUUUUUAGUU$_{U}$$_{U-5′}$ (SEQ ID NO: 2152)

AR-3592 Target: 5'-TCCAGTGGATGGGCTGAAAAATCAAAA-3' (SEQ ID NO: 2557)

5'-CCAGUGGAUGGGCUGAAAAAUCAAA$^{C}C_{C-3'}$ (SEQ ID NO: 4331)
3'-GGUCACCUACCCGACUUUUUAGUUU$_{U}U_{U-5'}$ (SEQ ID NO: 2153)

AR-3593 Target: 5'-CCAGTGGATGGGCTGAAAAATCAAAAA-3' (SEQ ID NO: 2558)

5'-CAGUGGAUGGGCUGAAAAAUCAAAA$^{C}C_{C-3'}$ (SEQ ID NO: 4332)
3'-GUCACCUACCCGACUUUUUAGUUUU$_{U}U_{A-5'}$ (SEQ ID NO: 2154)

AR-3594 Target: 5'-CAGTGGATGGGCTGAAAAATCAAAAAT-3' (SEQ ID NO: 2559)

5'-AGUGGAUGGGCUGAAAAAUCAAAAA$^{C}C_{C-3'}$ (SEQ ID NO: 4333)
3'-UCACCUACCCGACUUUUUAGUUUUU$_{A}A_{A-5'}$ (SEQ ID NO: 2155)

AR-3595 Target: 5'-AGTGGATGGGCTGAAAAATCAAAAATT-3' (SEQ ID NO: 2560)

5'-GUGGAUGGGCUGAAAAAUCAAAAAU$^{C}C_{A-3'}$ (SEQ ID NO: 4334)
3'-CACCUACCCGACUUUUUAGUUUUUA$_{A}A_{G-5'}$ (SEQ ID NO: 2156)

AR-3596 Target: 5'-GTGGATGGGCTGAAAAATCAAAAATTC-3' (SEQ ID NO: 2561)

5'-UGGAUGGGCUGAAAAAUCAAAAAUU$^{A}C_{C-3'}$ (SEQ ID NO: 4335)
3'-ACCUACCCGACUUUUUAGUUUUUAA$_{G}A_{A-5'}$ (SEQ ID NO: 2157)

AR-3597 Target: 5'-TGGATGGGCTGAAAAATCAAAAATTCT-3' (SEQ ID NO: 2562)

5'-GGAUGGGCUGAAAAAUCAAAAAUUC$^{C}C_{C-3'}$ (SEQ ID NO: 4336)
3'-CCUACCCGACUUUUUAGUUUUUAAG$_{A}A_{A-5'}$ (SEQ ID NO: 2158)

AR-3598 Target: 5'-GGATGGGCTGAAAAATCAAAAATTCTT-3' (SEQ ID NO: 2563)

5'-GAUGGGCUGAAAAAUCAAAAAUUCU$^{C}C_{C-3'}$ (SEQ ID NO: 4337)
3'-CUACCCGACUUUUUAGUUUUUAAGA$_{A}A_{A-5'}$ (SEQ ID NO: 2159)

AR-3599 Target: 5'-GATGGGCTGAAAAATCAAAAATTCTTT-3' (SEQ ID NO: 2564)

5'-AUGGGCUGAAAAAUCAAAAAUUCUU$^{C}C_{A-3'}$ (SEQ ID NO: 4338)
3'-UACCCGACUUUUUAGUUUUUAAGAA$_{A}A_{C-5'}$ (SEQ ID NO: 2160)

AR-3600 Target: 5'-ATGGGCTGAAAAATCAAAAATTCTTTG-3' (SEQ ID NO: 2565)

5'-UGGGCUGAAAAAUCAAAAAUUCUUU$^{A}C_{C-3'}$ (SEQ ID NO: 4339)
3'-ACCCGACUUUUUAGUUUUUAAGAAA$_{C}U_{U-5'}$ (SEQ ID NO: 2161)

AR-3601 Target: 5'-TGGGCTGAAAAATCAAAAATTCTTTGA-3' (SEQ ID NO: 2566)

5'-GGGCUGAAAAAUCAAAAAUUCUUUG$^{C}C_{C-3'}$ (SEQ ID NO: 4340)
3'-CCCGACUUUUUAGUUUUUAAGAAAC$_{U}U_{A-5'}$ (SEQ ID NO: 2162)

AR-3602 Target: 5'-GGGCTGAAAAATCAAAAATTCTTTGAT-3' (SEQ ID NO: 2567)

5'-GGCUGAAAAAUCAAAAAUUCUUUGA$^{C}C_{A-3'}$ (SEQ ID NO: 4341)
3'-CCGACUUUUUAGUUUUUAAGAAACU$_{A}A_{C-5'}$ (SEQ ID NO: 2163)

AR-3603 Target: 5'-GGCTGAAAAATCAAAAATTCTTTGATG-3' (SEQ ID NO: 2568)

5'-GCUGAAAAAUCAAAAAUUCUUUGAU^{A}C-3' (SEQ ID NO: 4342)
3'-CGACUUUUUAGUUUUUAAGAAACUA$_{C}U$-5' (SEQ ID NO: 2164)

AR-3604 Target: 5'-GCTGAAAAATCAAAAATTCTTTGATGA-3' (SEQ ID NO: 2569)

5'-CUGAAAAAUCAAAAAUUCUUUGAUG^{C}C-3' (SEQ ID NO: 4343)
3'-GACUUUUUAGUUUUUAAGAAACUAC$_{U}U$-5' (SEQ ID NO: 2165)

AR-3605 Target: 5'-CTGAAAAATCAAAAATTCTTTGATGAA-3' (SEQ ID NO: 2570)

5'-UGAAAAAUCAAAAAUUCUUUGAUGA^{C}A-3' (SEQ ID NO: 4344)
3'-ACUUUUUAGUUUUUAAGAAACUACU$_{U}G$-5' (SEQ ID NO: 2166)

AR-3606 Target: 5'-TGAAAAATCAAAAATTCTTTGATGAAC-3' (SEQ ID NO: 2571)

5'-AAAAAUCAAAAAUUCUUUGAUGAAC^{C}C-3' (SEQ ID NO: 4345)
3'-UUUUUAGUUUUUAAGAAACUACUUG$_{A}A$-5' (SEQ ID NO: 2167)

AR-3608 Target: 5'-AAAAATCAAAAATTCTTTGATGAACTT-3' (SEQ ID NO: 2572)

5'-AAAAUCAAAAAUUCUUUGAUGAACU^{C}A-3' (SEQ ID NO: 4346)
3'-UUUUAGUUUUUAAGAAACUACUUGA$_{A}G$-5' (SEQ ID NO: 2168)

AR-3609 Target: 5'-AAAATCAAAAATTCTTTGATGAACTTC-3' (SEQ ID NO: 2573)

5'-AAAUCAAAAAUUCUUUGAUGAACUU^{A}A-3' (SEQ ID NO: 4347)
3'-UUUAGUUUUUAAGAAACUACUUGAA$_{G}C$-5' (SEQ ID NO: 2169)

AR-3610 Target: 5'-AAATCAAAAATTCTTTGATGAACTTCG-3' (SEQ ID NO: 2574)

5'-AAUCAAAAAUUCUUUGAUGAACUUC^{A}C-3' (SEQ ID NO: 4348)
3'-UUAGUUUUUAAGAAACUACUUGAAG$_{C}U$-5' (SEQ ID NO: 2170)

AR-3611 Target: 5'-AATCAAAAATTCTTTGATGAACTTCGA-3' (SEQ ID NO: 2575)

5'-AUCAAAAAUUCUUUGAUGAACUUCG^{C}C-3' (SEQ ID NO: 4349)
3'-UAGUUUUUAAGAAACUACUUGAAGC$_{U}U$-5' (SEQ ID NO: 2171)

AR-3612 Target: 5'-ATCAAAAATTCTTTGATGAACTTCGAA-3' (SEQ ID NO: 2576)

5'-UCAAAAAUUCUUUGAUGAACUUCGA^{C}C-3' (SEQ ID NO: 4350)
3'-AGUUUUUAAGAAACUACUUGAAGCU$_{U}A$-5' (SEQ ID NO: 2172)

AR-3613 Target: 5'-TCAAAAATTCTTTGATGAACTTCGAAT-3' (SEQ ID NO: 2577)

5'-CAAAAAUUCUUUGAUGAACUUCGAA^{C}A-3' (SEQ ID NO: 4351)
3'-GUUUUUAAGAAACUACUUGAAGCUU$_{A}C$-5' (SEQ ID NO: 2173)

AR-3614 Target: 5'-CAAAAATTCTTTGATGAACTTCGAATG-3' (SEQ ID NO: 2578)

5'-AAAAAUUCUUUGAUGAACUUCGAAU^{A}C-3' (SEQ ID NO: 4352)
3'-UUUUUAAGAAACUACUUGAAGCUUA$_{C}U$-5' (SEQ ID NO: 2174)

AR-3615 Target: 5'-AAAAATTCTTTGATGAACTTCGAATGA-3' (SEQ ID NO: 2579)

5'-AAAAUUCUUUGAUGAACUUCGAAUG^{C}C-3′ (SEQ ID NO: 4353)
3'-UUUUAAGAAACUACUUGAAGCUUAC$_{U}U$-5′ (SEQ ID NO: 2175)

AR-3616 Target: 5'-AAAATTCTTTGATGAACTTCGAATGAA-3' (SEQ ID NO: 2580)

5'-AAAUUCUUUGAUGAACUUCGAAUGA^{C}C-3′ (SEQ ID NO: 4354)
3'-UUUAAGAAACUACUUGAAGCUUACU$_{U}G$-5′ (SEQ ID NO: 2176)

AR-3617 Target: 5'-AAATTCTTTGATGAACTTCGAATGAAC-3' (SEQ ID NO: 2581)

5'-AAUUCUUUGAUGAACUUCGAAUGAA^{A}C-3′ (SEQ ID NO: 4355)
3'-UUAAGAAACUACUUGAAGCUUACUU$_{G}A$-5′ (SEQ ID NO: 2177)

AR-3618 Target: 5'-AATTCTTTGATGAACTTCGAATGAACT-3' (SEQ ID NO: 2582)

5'-AUUCUUUGAUGAACUUCGAAUGAAC^{C}C-3′ (SEQ ID NO: 4356)
3'-UAAGAAACUACUUGAAGCUUACUUG$_{A}U$-5′ (SEQ ID NO: 2178)

AR-3619 Target: 5'-ATTCTTTGATGAACTTCGAATGAACTA-3' (SEQ ID NO: 2583)

5'-UUCUUUGAUGAACUUCGAAUGAACU^{C}A-3′ (SEQ ID NO: 4357)
3'-AAGAAACUACUUGAAGCUUACUUGA$_{U}G$-5′ (SEQ ID NO: 2179)

AR-3620 Target: 5'-TTCTTTGATGAACTTCGAATGAACTAC-3' (SEQ ID NO: 2584)

5'-UCUUUGAUGAACUUCGAAUGAACUA^{A}C-3′ (SEQ ID NO: 4358)
3'-AGAAACUACUUGAAGCUUACUUGAU$_{G}U$-5′ (SEQ ID NO: 2180)

AR-3621 Target: 5'-TCTTTGATGAACTTCGAATGAACTACA-3' (SEQ ID NO: 2585)

5'-CUUUGAUGAACUUCGAAUGAACUAC^{C}C-3′ (SEQ ID NO: 4359)
3'-GAAACUACUUGAAGCUUACUUGAUG$_{U}A$-5′ (SEQ ID NO: 2181)

AR-3622 Target: 5'-CTTTGATGAACTTCGAATGAACTACAT-3' (SEQ ID NO: 2586)

5'-UUUGAUGAACUUCGAAUGAACUACA^{C}A-3′ (SEQ ID NO: 4360)
3'-AAACUACUUGAAGCUUACUUGAUGU$_{A}G$-5′ (SEQ ID NO: 2182)

AR-3623 Target: 5'-TTTGATGAACTTCGAATGAACTACATC-3' (SEQ ID NO: 2587)

5'-UUGAUGAACUUCGAAUGAACUACAU^{A}C-3′ (SEQ ID NO: 4361)
3'-AACUACUUGAAGCUUACUUGAUGUA$_{G}U$-5′ (SEQ ID NO: 2183)

AR-3624 Target: 5'-TTGATGAACTTCGAATGAACTACATCA-3' (SEQ ID NO: 2588)

5'-UGAUGAACUUCGAAUGAACUACAUC^{C}C-3′ (SEQ ID NO: 4362)
3'-ACUACUUGAAGCUUACUUGAUGUAG$_{U}U$-5′ (SEQ ID NO: 2184)

AR-3625 Target: 5'-TGATGAACTTCGAATGAACTACATCAA-3' (SEQ ID NO: 2589)

5'-GAUGAACUUCGAAUGAACUACAUCA^{C}A-3′ (SEQ ID NO: 4363)
3'-CUACUUGAAGCUUACUUGAUGUAGU$_{U}C$-5′ (SEQ ID NO: 2185)

AR-3626 Target: 5'-GATGAACTTCGAATGAACTACATCAAG-3' (SEQ ID NO: 2590)

5'-AUGAACUUCGAAUGAACUACAUCAA$^{A}A_{A-3'}$ (SEQ ID NO: 4364)
3'-UACUUGAAGCUUACUUGAUGUAGUU$_{C}C_{C-5'}$ (SEQ ID NO: 2186)

AR-3627 Target: 5'-ATGAACTTCGAATGAACTACATCAAGG-3' (SEQ ID NO: 2591)

5'-UGAACUUCGAAUGAACUACAUCAAG$^{A}C_{A-3'}$ (SEQ ID NO: 4365)
3'-ACUUGAAGCUUACUUGAUGUAGUUC$_{C}C_{U-5'}$ (SEQ ID NO: 2187)

AR-3628 Target: 5'-TGAACTTCGAATGAACTACATCAAGGA-3' (SEQ ID NO: 2592)

5'-GAACUUCGAAUGAACUACAUCAAGG$^{C}C_{C-3'}$ (SEQ ID NO: 4366)
3'-CUUGAAGCUUACUUGAUGUAGUUCC$_{U}U_{U-5'}$ (SEQ ID NO: 2188)

AR-3629 Target: 5'-GAACTTCGAATGAACTACATCAAGGAA-3' (SEQ ID NO: 2593)

5'-AACUUCGAAUGAACUACAUCAAGGA$^{C}A_{A-3'}$ (SEQ ID NO: 4367)
3'-UUGAAGCUUACUUGAUGUAGUUCCU$_{U}G_{G-5'}$ (SEQ ID NO: 2189)

AR-3630 Target: 5'-AACTTCGAATGAACTACATCAAGGAAC-3' (SEQ ID NO: 2594)

5'-ACUUCGAAUGAACUACAUCAAGGAA$^{A}C_{A-3'}$ (SEQ ID NO: 4368)
3'-UGAAGCUUACUUGAUGUAGUUCCUU$_{G}A_{A-5'}$ (SEQ ID NO: 2190)

AR-3631 Target: 5'-ACTTCGAATGAACTACATCAAGGAACT-3' (SEQ ID NO: 2595)

5'-CUUCGAAUGAACUACAUCAAGGAAC$^{C}A_{A-3'}$ (SEQ ID NO: 4369)
3'-GAAGCUUACUUGAUGUAGUUCCUUG$_{A}G_{G-5'}$ (SEQ ID NO: 2191)

AR-3632 Target: 5'-CTTCGAATGAACTACATCAAGGAACTC-3' (SEQ ID NO: 2596)

5'-UUCGAAUGAACUACAUCAAGGAACU$^{A}A_{A-3'}$ (SEQ ID NO: 4370)
3'-AAGCUUACUUGAUGUAGUUCCUUGA$_{G}G_{C-5'}$ (SEQ ID NO: 2192)

AR-3633 Target: 5'-TTCGAATGAACTACATCAAGGAACTCG-3' (SEQ ID NO: 2597)

5'-UCGAAUGAACUACAUCAAGGAACUC$^{A}C_{A-3'}$ (SEQ ID NO: 4371)
3'-AGCUUACUUGAUGUAGUUCCUUGAG$_{C}C_{U-5'}$ (SEQ ID NO: 2193)

AR-3634 Target: 5'-TCGAATGAACTACATCAAGGAACTCGA-3' (SEQ ID NO: 2598)

5'-CGAAUGAACUACAUCAAGGAACUCG$^{C}C_{C-3'}$ (SEQ ID NO: 4372)
3'-GCUUACUUGAUGUAGUUCCUUGAGC$_{U}A_{A-5'}$ (SEQ ID NO: 2194)

AR-3635 Target: 5'-CGAATGAACTACATCAAGGAACTCGAT-3' (SEQ ID NO: 2599)

5'-GAAUGAACUACAUCAAGGAACUCGA$^{C}A_{A-3'}$ (SEQ ID NO: 4373)
3'-CUUACUUGAUGUAGUUCCUUGAGCU$_{A}G_{G-5'}$ (SEQ ID NO: 2195)

AR-3636 Target: 5'-GAATGAACTACATCAAGGAACTCGATC-3' (SEQ ID NO: 2600)

5'-AAUGAACUACAUCAAGGAACUCGAU$^{A}A_{A-3'}$ (SEQ ID NO: 4374)
3'-UUACUUGAUGUAGUUCCUUGAGCUA$_{G}G_{C-5'}$ (SEQ ID NO: 2196)

AR-3637 Target: 5'-AATGAACTACATCAAGGAACTCGATCG-3' (SEQ ID NO: 2601)

5'-AUGAACUACAUCAAGGAACUCGAUC$^{AC-3'}$ (SEQ ID NO: 4375)
3'-UACUUGAUGUAGUUCCUUGAGCUAG$_{CA-5'}$ (SEQ ID NO: 2197)

AR-3638 Target: 5'-ATGAACTACATCAAGGAACTCGATCGT-3' (SEQ ID NO: 2602)

5'-UGAACUACAUCAAGGAACUCGAUCG$^{CC-3'}$ (SEQ ID NO: 4376)
3'-ACUUGAUGUAGUUCCUUGAGCUAGC$_{AU-5'}$ (SEQ ID NO: 2198)

AR-3639 Target: 5'-TGAACTACATCAAGGAACTCGATCGTA-3' (SEQ ID NO: 2603)

5'-GAACUACAUCAAGGAACUCGAUCGU$^{CC-3'}$ (SEQ ID NO: 4377)
3'-CUUGAUGUAGUUCCUUGAGCUAGCA$_{UA-5'}$ (SEQ ID NO: 2199)

AR-3640 Target: 5'-GAACTACATCAAGGAACTCGATCGTAT-3' (SEQ ID NO: 2604)

5'-AACUACAUCAAGGAACUCGAUCGUA$^{CA-3'}$ (SEQ ID NO: 4378)
3'-UUGAUGUAGUUCCUUGAGCUAGCAU$_{AG-5'}$ (SEQ ID NO: 2200)

AR-3641 Target: 5'-AACTACATCAAGGAACTCGATCGTATC-3' (SEQ ID NO: 2605)

5'-ACUACAUCAAGGAACUCGAUCGUAU$^{AC-3'}$ (SEQ ID NO: 4379)
3'-UGAUGUAGUUCCUUGAGCUAGCAUA$_{GU-5'}$ (SEQ ID NO: 2201)

AR-3642 Target: 5'-ACTACATCAAGGAACTCGATCGTATCA-3' (SEQ ID NO: 2606)

5'-CUACAUCAAGGAACUCGAUCGUAUC$^{CC-3'}$ (SEQ ID NO: 4380)
3'-GAUGUAGUUCCUUGAGCUAGCAUAG$_{UA-5'}$ (SEQ ID NO: 2202)

AR-3643 Target: 5'-CTACATCAAGGAACTCGATCGTATCAT-3' (SEQ ID NO: 2607)

5'-GUAUCAUUGCAUGCAAAAGAAAAAA$^{CA-3'}$ (SEQ ID NO: 4381)
3'-CAUAGUAACGUACGUUUUCUUUUUU$_{AG-5'}$ (SEQ ID NO: 2203)

AR-3663 Target: 5'-GTATCATTGCATGCAAAAGAAAAAATC-3' (SEQ ID NO: 2608)

5'-UAUCAUUGCAUGCAAAAGAAAAAAU$^{AA-3'}$ (SEQ ID NO: 4382)
3'-AUAGUAACGUACGUUUUCUUUUUUA$_{GG-5'}$ (SEQ ID NO: 2204)

AR-3664 Target: 5'-TATCATTGCATGCAAAAGAAAAAATCC-3' (SEQ ID NO: 2609)

5'-AAAAUCCCACAUCCUGCUCAAGACG$^{AC-3'}$ (SEQ ID NO: 4383)
3'-UUUUAGGGUGUAGGACGAGUUCUGC$_{GA-5'}$ (SEQ ID NO: 2205)

AR-3684 Target: 5'-AAAATCCCACATCCTGCTCAAGACGCT-3' (SEQ ID NO: 2610)

5'-AAAUCCCACAUCCUGCUCAAGACGC$^{CC-3'}$ (SEQ ID NO: 4384)
3'-UUUAGGGUGUAGGACGAGUUCUGCG$_{AA-5'}$ (SEQ ID NO: 2206)

AR-3685 Target: 5'-AAATCCCACATCCTGCTCAAGACGCTT-3' (SEQ ID NO: 2611)

5'-GACGCUUCUACCAGCUCACCAAGCU$^{AA-3'}$ (SEQ ID NO: 4385)
3'-CUGCGAAGAUGGUCGAGUGGUUCGA$_{GG-5'}$ (SEQ ID NO: 2207)

AR-3705 Target: 5'-GACGCTTCTACCAGCTCACCAAGCTCC-3' (SEQ ID NO: 2612)

5'-ACGCUUCUACCAGCUCACCAAGCUC^{A}C-3′ (SEQ ID NO: 4386)
3'-UGCGAAGAUGGUCGAGUGGUUCGAG$_{G}$$_{A-5′}$ (SEQ ID NO: 2208)

AR-3706 Target: 5'-ACGCTTCTACCAGCTCACCAAGCTCCT-3' (SEQ ID NO: 2613)

5'-CGCUUCUACCAGCUCACCAAGCUCC^{C}A-3′ (SEQ ID NO: 4387)
3'-GCGAAGAUGGUCGAGUGGUUCGAGG$_{A}$$_{C-5′}$ (SEQ ID NO: 2209)

AR-3707 Target: 5'-CGCTTCTACCAGCTCACCAAGCTCCTG-3' (SEQ ID NO: 2614)

5'-GCUUCUACCAGCUCACCAAGCUCCU^{A}A-3′ (SEQ ID NO: 4388)
3'-CGAAGAUGGUCGAGUGGUUCGAGGA$_{C}$$_{C-5′}$ (SEQ ID NO: 2210)

AR-3708 Target: 5'-GCTTCTACCAGCTCACCAAGCTCCTGG-3' (SEQ ID NO: 2615)

5'-CUUCUACCAGCUCACCAAGCUCCUG^{A}C-3′ (SEQ ID NO: 4389)
3'-GAAGAUGGUCGAGUGGUUCGAGGAC$_{C}$$_{U-5′}$ (SEQ ID NO: 2211)

AR-3709 Target: 5'-CTTCTACCAGCTCACCAAGCTCCTGGA-3' (SEQ ID NO: 2616)

5'-UUCUACCAGCUCACCAAGCUCCUGG^{C}A-3′ (SEQ ID NO: 4390)
3'-AAGAUGGUCGAGUGGUUCGAGGACC$_{U}$$_{G-5′}$ (SEQ ID NO: 2212)

AR-3710 Target: 5'-TTCTACCAGCTCACCAAGCTCCTGGAC-3' (SEQ ID NO: 2617)

5'-UCUACCAGCUCACCAAGCUCCUGGA^{A}C-3′ (SEQ ID NO: 4391)
3'-AGAUGGUCGAGUGGUUCGAGGACCU$_{G}$$_{A-5′}$ (SEQ ID NO: 2213)

AR-3711 Target: 5'-TCTACCAGCTCACCAAGCTCCTGGACT-3' (SEQ ID NO: 2618)

5'-CUACCAGCUCACCAAGCUCCUGGAC^{C}A-3′ (SEQ ID NO: 4392)
3'-GAUGGUCGAGUGGUUCGAGGACCUG$_{A}$$_{G-5′}$ (SEQ ID NO: 2214)

AR-3712 Target: 5'-CTACCAGCTCACCAAGCTCCTGGACTC-3' (SEQ ID NO: 2619)

5'-UACCAGCUCACCAAGCUCCUGGACU^{A}A-3′ (SEQ ID NO: 4393)
3'-AUGGUCGAGUGGUUCGAGGACCUGA$_{G}$$_{G-5′}$ (SEQ ID NO: 2215)

AR-3713 Target: 5'-TACCAGCTCACCAAGCTCCTGGACTCC-3' (SEQ ID NO: 2620)

5'-ACCAGCUCACCAAGCUCCUGGACUC^{A}A-3′ (SEQ ID NO: 4394)
3'-UGGUCGAGUGGUUCGAGGACCUGAG$_{G}$$_{C-5′}$ (SEQ ID NO: 2216)

AR-3714 Target: 5'-ACCAGCTCACCAAGCTCCTGGACTCCG-3' (SEQ ID NO: 2621)

5'-CCAGCUCACCAAGCUCCUGGACUCC^{A}C-3′ (SEQ ID NO: 4395)
3'-GGUCGAGUGGUUCGAGGACCUGAGG$_{C}$$_{A-5′}$ (SEQ ID NO: 2217)

AR-3715 Target: 5'-CCAGCTCACCAAGCTCCTGGACTCCGT-3' (SEQ ID NO: 2622)

5'-AGCUCACCAAGCUCCUGGACUCCGU^{A}A-3′ (SEQ ID NO: 4396)
3'-UCGAGUGGUUCGAGGACCUGAGGCA$_{C}$$_{G-5′}$ (SEQ ID NO: 2218)

AR-3717 Target: 5'-AGCTCACCAAGCTCCTGGACTCCGTGC-3' (SEQ ID NO: 2623)

5'-AGCUCCUGGACUCCGUGCAGCCUAU$^{CA-3'}$ (SEQ ID NO: 4397)
3'-UCGAGGACCUGAGGCACGUCGGAUA$_{AC-5'}$ (SEQ ID NO: 2219)

AR-3726 Target: 5'-AGCTCCTGGACTCCGTGCAGCCTATTG-3' (SEQ ID NO: 2624)

5'-UCCGUGCAGCCUAUUGCGAGAGAGC$^{CA-3'}$ (SEQ ID NO: 4398)
3'-AGGCACGUCGGAUAACGCUCUCUCG$_{AC-5'}$ (SEQ ID NO: 2220)

AR-3737 Target: 5'-TCCGTGCAGCCTATTGCGAGAGAGCTG-3' (SEQ ID NO: 2625)

5'-CGAGAGAGCUGCAUCAGUUCACUUU$^{CA-3'}$ (SEQ ID NO: 4399)
3'-GCUCUCUCGACGUAGUCAAGUGAAA$_{AC-5'}$ (SEQ ID NO: 2221)

AR-3753 Target: 5'-CGAGAGAGCTGCATCAGTTCACTTTTG-3' (SEQ ID NO: 2626)

5'-GAGAGAGCUGCAUCAGUUCACUUUU$^{AC-3'}$ (SEQ ID NO: 4400)
3'-CUCUCUCGACGUAGUCAAGUGAAAA$_{CU-5'}$ (SEQ ID NO: 2222)

AR-3754 Target: 5'-GAGAGAGCTGCATCAGTTCACTTTTGA-3' (SEQ ID NO: 2627)

5'-AGAGAGCUGCAUCAGUUCACUUUUG$^{CA-3'}$ (SEQ ID NO: 4401)
3'-UCUCUCGACGUAGUCAAGUGAAAAC$_{UG-5'}$ (SEQ ID NO: 2223)

AR-3755 Target: 5'-AGAGAGCTGCATCAGTTCACTTTTGAC-3' (SEQ ID NO: 2628)

5'-GAGAGCUGCAUCAGUUCACUUUUGA$^{AA-3'}$ (SEQ ID NO: 4402)
3'-CUCUCGACGUAGUCAAGUGAAAACU$_{GG-5'}$ (SEQ ID NO: 2224)

AR-3756 Target: 5'-GAGAGCTGCATCAGTTCACTTTTGACC-3' (SEQ ID NO: 2629)

5'-AGAGCUGCAUCAGUUCACUUUUGAC$^{AC-3'}$ (SEQ ID NO: 4403)
3'-UCUCGACGUAGUCAAGUGAAAACUG$_{GA-5'}$ (SEQ ID NO: 2225)

AR-3757 Target: 5'-AGAGCTGCATCAGTTCACTTTTGACCT-3' (SEQ ID NO: 2630)

5'-GAGCUGCAUCAGUUCACUUUUGACC$^{CA-3'}$ (SEQ ID NO: 4404)
3'-CUCGACGUAGUCAAGUGAAAACUGG$_{AC-5'}$ (SEQ ID NO: 2226)

AR-3758 Target: 5'-GAGCTGCATCAGTTCACTTTTGACCTG-3' (SEQ ID NO: 2631)

5'-AGCUGCAUCAGUUCACUUUUGACCU$^{AA-3'}$ (SEQ ID NO: 4405)
3'-UCGACGUAGUCAAGUGAAAACUGGA$_{CG-5'}$ (SEQ ID NO: 2227)

AR-3759 Target: 5'-AGCTGCATCAGTTCACTTTTGACCTGC-3' (SEQ ID NO: 2632)

5'-GCUGCAUCAGUUCACUUUUGACCUG$^{AC-3'}$ (SEQ ID NO: 4406)
3'-CGACGUAGUCAAGUGAAAACUGGAC$_{GA-5'}$ (SEQ ID NO: 2228)

AR-3760 Target: 5'-GCTGCATCAGTTCACTTTTGACCTGCT-3' (SEQ ID NO: 2633)

5'-CUGCAUCAGUUCACUUUUGACCUGC$^{CC-3'}$ (SEQ ID NO: 4407)
3'-GACGUAGUCAAGUGAAAACUGGACG$_{AU-5'}$ (SEQ ID NO: 2229)

AR-3761 Target: 5'-CTGCATCAGTTCACTTTTGACCTGCTA-3' (SEQ ID NO: 2634)

5'-UGCAUCAGUUCACUUUUGACCUGCU$^{C}C_{C-3'}$ (SEQ ID NO: 4408)
3'-ACGUAGUCAAGUGAAAACUGGACGA$_{U}U_{U-5'}$ (SEQ ID NO: 2230)

AR-3762 Target: 5'-TGCATCAGTTCACTTTTGACCTGCTAA-3' (SEQ ID NO: 2635)

5'-GCAUCAGUUCACUUUUGACCUGCUA$^{C}C_{C-3'}$ (SEQ ID NO: 4409)
3'-CGUAGUCAAGUGAAAACUGGACGAU$_{U}U_{A-5'}$ (SEQ ID NO: 2231)

AR-3763 Target: 5'-GCATCAGTTCACTTTTGACCTGCTAAT-3' (SEQ ID NO: 2636)

5'-CAUCAGUUCACUUUUGACCUGCUAA$^{C}C_{A-3'}$ (SEQ ID NO: 4410)
3'-GUAGUCAAGUGAAAACUGGACGAUU$_{A}G_{G-5'}$ (SEQ ID NO: 2232)

AR-3764 Target: 5'-CATCAGTTCACTTTTGACCTGCTAATC-3' (SEQ ID NO: 2637)

5'-AUCAGUUCACUUUUGACCUGCUAAU$^{A}C_{C-3'}$ (SEQ ID NO: 4411)
3'-UAGUCAAGUGAAAACUGGACGAUUA$_{G}U_{U-5'}$ (SEQ ID NO: 2233)

AR-3765 Target: 5'-ATCAGTTCACTTTTGACCTGCTAATCA-3' (SEQ ID NO: 2638)

5'-UCAGUUCACUUUUGACCUGCUAAUC$^{C}C_{C-3'}$ (SEQ ID NO: 4412)
3'-AGUCAAGUGAAAACUGGACGAUUAG$_{U}U_{U-5'}$ (SEQ ID NO: 2234)

AR-3766 Target: 5'-TCAGTTCACTTTTGACCTGCTAATCAA-3' (SEQ ID NO: 2639)

5'-CAGUUCACUUUUGACCUGCUAAUCA$^{C}C_{A-3'}$ (SEQ ID NO: 4413)
3'-GUCAAGUGAAAACUGGACGAUUAGU$_{U}U_{C-5'}$ (SEQ ID NO: 2235)

AR-3767 Target: 5'-CAGTTCACTTTTGACCTGCTAATCAAG-3' (SEQ ID NO: 2640)

5'-AGUUCACUUUUGACCUGCUAAUCAA$^{A}C_{C-3'}$ (SEQ ID NO: 4414)
3'-UCAAGUGAAAACUGGACGAUUAGUU$_{C}A_{A-5'}$ (SEQ ID NO: 2236)

AR-3768 Target: 5'-AGTTCACTTTTGACCTGCTAATCAAGT-3' (SEQ ID NO: 2641)

5'-GUUCACUUUUGACCUGCUAAUCAAG$^{C}C_{A-3'}$ (SEQ ID NO: 4415)
3'-CAAGUGAAAACUGGACGAUUAGUUC$_{A}G_{G-5'}$ (SEQ ID NO: 2237)

AR-3769 Target: 5'-GTTCACTTTTGACCTGCTAATCAAGTC-3' (SEQ ID NO: 2642)

5'-UUCACUUUUGACCUGCUAAUCAAGU$^{A}C_{C-3'}$ (SEQ ID NO: 4416)
3'-AAGUGAAAACUGGACGAUUAGUUCA$_{G}U_{U-5'}$ (SEQ ID NO: 2238)

AR-3770 Target: 5'-TTCACTTTTGACCTGCTAATCAAGTCA-3' (SEQ ID NO: 2643)

5'-UCACUUUUGACCUGCUAAUCAAGUC$^{C}C_{A-3'}$ (SEQ ID NO: 4417)
3'-AGUGAAAACUGGACGAUUAGUUCAG$_{U}U_{G-5'}$ (SEQ ID NO: 2239)

AR-3771 Target: 5'-TCACTTTTGACCTGCTAATCAAGTCAC-3' (SEQ ID NO: 2644)

5'-CACUUUUGACCUGCUAAUCAAGUCA$^{A}C_{C-3'}$ (SEQ ID NO: 4418)
3'-GUGAAAACUGGACGAUUAGUUCAGU$_{G}U_{U-5'}$ (SEQ ID NO: 2240)

AR-3772 Target: 5'-CACTTTTGACCTGCTAATCAAGTCACA-3' (SEQ ID NO: 2645)

5'-ACUUUUGACCUGCUAAUCAAGUCAC$^{CA-3'}$ (SEQ ID NO: 4419)
3'-UGAAAACUGGACGAUUAGUUCAGUG$_{UG-5'}$ (SEQ ID NO: 2241)

AR-3773 Target: 5'-ACTTTTGACCTGCTAATCAAGTCACAC-3' (SEQ ID NO: 2646)

5'-ACAUGGUGAGCGUGGACUUUCCGGA$^{CC-3'}$ (SEQ ID NO: 4420)
3'-UGUACCACUCGCACCUGAAAGGCCU$_{UU-5'}$ (SEQ ID NO: 2242)

AR-3798 Target: 5'-ACATGGTGAGCGTGGACTTTCCGGAAA-3' (SEQ ID NO: 2647)

5'-CAUGGUGAGCGUGGACUUUCCGGAA$^{CC-3'}$ (SEQ ID NO: 4421)
3'-GUACCACUCGCACCUGAAAGGCCUU$_{UA-5'}$ (SEQ ID NO: 2243)

AR-3799 Target: 5'-CATGGTGAGCGTGGACTTTCCGGAAAT-3' (SEQ ID NO: 2648)

5'-CGGAAAUGAUGGCAGAGAUCAUCUC$^{CA-3'}$ (SEQ ID NO: 4422)
3'-GCCUUUACUACCGUCUCUAGUAGAG$_{AC-5'}$ (SEQ ID NO: 2244)

AR-3819 Target: 5'-CGGAAATGATGGCAGAGATCATCTCTG-3' (SEQ ID NO: 2649)

5'-GGAAAUGAUGGCAGAGAUCAUCUCU$^{AC-3'}$ (SEQ ID NO: 4423)
3'-CCUUUACUACCGUCUCUAGUAGAGA$_{CA-5'}$ (SEQ ID NO: 2245)

AR-3820 Target: 5'-GGAAATGATGGCAGAGATCATCTCTGT-3' (SEQ ID NO: 2650)

5'-GAAAUGAUGGCAGAGAUCAUCUCUG$^{CA-3'}$ (SEQ ID NO: 4424)
3'-CUUUACUACCGUCUCUAGUAGAGAC$_{AC-5'}$ (SEQ ID NO: 2246)

AR-3821 Target: 5'-GAAATGATGGCAGAGATCATCTCTGTG-3' (SEQ ID NO: 2651)

5'-AAAUGAUGGCAGAGAUCAUCUCUGU$^{AA-3'}$ (SEQ ID NO: 4425)
3'-UUUACUACCGUCUCUAGUAGAGACA$_{CG-5'}$ (SEQ ID NO: 2247)

AR-3822 Target: 5'-AAATGATGGCAGAGATCATCTCTGTGC-3' (SEQ ID NO: 2652)

5'-AAUGAUGGCAGAGAUCAUCUCUGUG$^{AC-3'}$ (SEQ ID NO: 4426)
3'-UUACUACCGUCUCUAGUAGAGACAC$_{GU-5'}$ (SEQ ID NO: 2248)

AR-3823 Target: 5'-AATGATGGCAGAGATCATCTCTGTGCA-3' (SEQ ID NO: 2653)

5'-AUGAUGGCAGAGAUCAUCUCUGUGC$^{CC-3'}$ (SEQ ID NO: 4427)
3'-UACUACCGUCUCUAGUAGAGACACG$_{UU-5'}$ (SEQ ID NO: 2249)

AR-3824 Target: 5'-ATGATGGCAGAGATCATCTCTGTGCAA-3' (SEQ ID NO: 2654)

5'-UGAUGGCAGAGAUCAUCUCUGUGCA$^{CA-3'}$ (SEQ ID NO: 4428)
3'-ACUACCGUCUCUAGUAGAGACACGU$_{UC-5'}$ (SEQ ID NO: 2250)

AR-3825 Target: 5'-TGATGGCAGAGATCATCTCTGTGCAAG-3' (SEQ ID NO: 2655)

5'-GAUGGCAGAGAUCAUCUCUGUGCAA$^{AC-3'}$ (SEQ ID NO: 4429)
3'-CUACCGUCUCUAGUAGAGACACGUU$_{CA-5'}$ (SEQ ID NO: 2251)

AR-3826 Target: 5'-GATGGCAGAGATCATCTCTGTGCAAGT-3' (SEQ ID NO: 2656)

5'-AUGGCAGAGAUCAUCUCUGUGCAAG$^{C}{}^{A-3'}$ (SEQ ID NO: 4430)
3'-UACCGUCUCUAGUAGAGACACGUUC$_{A}{}_{C-5'}$ (SEQ ID NO: 2252)

AR-3827 Target: 5'-ATGGCAGAGATCATCTCTGTGCAAGTG-3' (SEQ ID NO: 2657)

5'-UGGCAGAGAUCAUCUCUGUGCAAGU$^{A}{}^{A-3'}$ (SEQ ID NO: 4431)
3'-ACCGUCUCUAGUAGAGACACGUUCA$_{C}{}_{G-5'}$ (SEQ ID NO: 2253)

AR-3828 Target: 5'-TGGCAGAGATCATCTCTGTGCAAGTGC-3' (SEQ ID NO: 2658)

5'-GGCAGAGAUCAUCUCUGUGCAAGUG$^{A}{}^{A-3'}$ (SEQ ID NO: 4432)
3'-CCGUCUCUAGUAGAGACACGUUCAC$_{G}{}_{G-5'}$ (SEQ ID NO: 2254)

AR-3829 Target: 5'-GGCAGAGATCATCTCTGTGCAAGTGCC-3' (SEQ ID NO: 2659)

5'-GCAGAGAUCAUCUCUGUGCAAGUGC$^{A}{}^{A-3'}$ (SEQ ID NO: 4433)
3'-CGUCUCUAGUAGAGACACGUUCACG$_{G}{}_{G-5'}$ (SEQ ID NO: 2255)

AR-3830 Target: 5'-GCAGAGATCATCTCTGTGCAAGTGCCC-3' (SEQ ID NO: 2660)

5'-CAGAGAUCAUCUCUGUGCAAGUGCC$^{A}{}^{C-3'}$ (SEQ ID NO: 4434)
3'-GUCUCUAGUAGAGACACGUUCACGG$_{G}{}_{U-5'}$ (SEQ ID NO: 2256)

AR-3831 Target: 5'-CAGAGATCATCTCTGTGCAAGTGCCCA-3' (SEQ ID NO: 2661)

5'-AGAGAUCAUCUCUGUGCAAGUGCCC$^{C}{}^{C-3'}$ (SEQ ID NO: 4435)
3'-UCUCUAGUAGAGACACGUUCACGGG$_{U}{}_{U-5'}$ (SEQ ID NO: 2257)

AR-3832 Target: 5'-AGAGATCATCTCTGTGCAAGTGCCCAA-3' (SEQ ID NO: 2662)

5'-GAGAUCAUCUCUGUGCAAGUGCCCA$^{C}{}^{A-3'}$ (SEQ ID NO: 4436)
3'-CUCUAGUAGAGACACGUUCACGGGU$_{U}{}_{C-5'}$ (SEQ ID NO: 2258)

AR-3833 Target: 5'-GAGATCATCTCTGTGCAAGTGCCCAAG-3' (SEQ ID NO: 2663)

5'-AGAUCAUCUCUGUGCAAGUGCCCAA$^{A}{}^{C-3'}$ (SEQ ID NO: 4437)
3'-UCUAGUAGAGACACGUUCACGGGUU$_{C}{}_{U-5'}$ (SEQ ID NO: 2259)

AR-3834 Target: 5'-AGATCATCTCTGTGCAAGTGCCCAAGA-3' (SEQ ID NO: 2664)

5'-GAUCAUCUCUGUGCAAGUGCCCAAG$^{C}{}^{C-3'}$ (SEQ ID NO: 4438)
3'-CUAGUAGAGACACGUUCACGGGUUC$_{U}{}_{A-5'}$ (SEQ ID NO: 2260)

AR-3835 Target: 5'-GATCATCTCTGTGCAAGTGCCCAAGAT-3' (SEQ ID NO: 2665)

5'-AUCAUCUCUGUGCAAGUGCCCAAGA$^{C}{}^{A-3'}$ (SEQ ID NO: 4439)
3'-UAGUAGAGACACGUUCACGGGUUCU$_{A}{}_{G-5'}$ (SEQ ID NO: 2261)

AR-3836 Target: 5'-ATCATCTCTGTGCAAGTGCCCAAGATC-3' (SEQ ID NO: 2666)

5'-UCAUCUCUGUGCAAGUGCCCAAGAU$^{A}{}^{A-3'}$ (SEQ ID NO: 4440)
3'-AGUAGAGACACGUUCACGGGUUCUA$_{G}{}_{G-5'}$ (SEQ ID NO: 2262)

AR-3837 Target: 5'-TCATCTCTGTGCAAGTGCCCAAGATCC-3' (SEQ ID NO: 2667)

5'-CAUCUCUGUGCAAGUGCCCAAGAUC$^{AC-3'}$ (SEQ ID NO: 4441)
3'-GUAGAGACACGUUCACGGGUUCUAG$_{GA-5'}$ (SEQ ID NO: 2263)

AR-3838 Target: 5'-CATCTCTGTGCAAGTGCCCAAGATCCT-3' (SEQ ID NO: 2668)

5'-AUCUCUGUGCAAGUGCCCAAGAUCC$^{CC-3'}$ (SEQ ID NO: 4442)
3'-UAGAGACACGUUCACGGGUUCUAGG$_{AA-5'}$ (SEQ ID NO: 2264)

AR-3839 Target: 5'-ATCTCTGTGCAAGTGCCCAAGATCCTT-3' (SEQ ID NO: 2669)

5'-UCUCUGUGCAAGUGCCCAAGAUCCU$^{CC-3'}$ (SEQ ID NO: 4443)
3'-AGAGACACGUUCACGGGUUCUAGGA$_{AA-5'}$ (SEQ ID NO: 2265)

AR-3840 Target: 5'-TCTCTGTGCAAGTGCCCAAGATCCTTT-3' (SEQ ID NO: 2670)

5'-CUCUGUGCAAGUGCCCAAGAUCCUU$^{CA-3'}$ (SEQ ID NO: 4444)
3'-GAGACACGUUCACGGGUUCUAGGAA$_{AG-5'}$ (SEQ ID NO: 2266)

AR-3841 Target: 5'-CTCTGTGCAAGTGCCCAAGATCCTTTC-3' (SEQ ID NO: 2671)

5'-UCUGUGCAAGUGCCCAAGAUCCUUU$^{AC-3'}$ (SEQ ID NO: 4445)
3'-AGACACGUUCACGGGUUCUAGGAAA$_{GA-5'}$ (SEQ ID NO: 2267)

AR-3842 Target: 5'-TCTGTGCAAGTGCCCAAGATCCTTTCT-3' (SEQ ID NO: 2672)

5'-CUGUGCAAGUGCCCAAGAUCCUUUC$^{CA-3'}$ (SEQ ID NO: 4446)
3'-GACACGUUCACGGGUUCUAGGAAAG$_{AC-5'}$ (SEQ ID NO: 2268)

AR-3843 Target: 5'-CTGTGCAAGTGCCCAAGATCCTTTCTG-3' (SEQ ID NO: 2673)

5'-UGUGCAAGUGCCCAAGAUCCUUUCU$^{AA-3'}$ (SEQ ID NO: 4447)
3'-ACACGUUCACGGGUUCUAGGAAAGA$_{CC-5'}$ (SEQ ID NO: 2269)

AR-3844 Target: 5'-TGTGCAAGTGCCCAAGATCCTTTCTGG-3' (SEQ ID NO: 2674)

5'-GUGCAAGUGCCCAAGAUCCUUUCUG$^{AA-3'}$ (SEQ ID NO: 4448)
3'-CACGUUCACGGGUUCUAGGAAAGAC$_{CC-5'}$ (SEQ ID NO: 2270)

AR-3845 Target: 5'-GTGCAAGTGCCCAAGATCCTTTCTGGG-3' (SEQ ID NO: 2675)

5'-UGCAAGUGCCCAAGAUCCUUUCUGG$^{AC-3'}$ (SEQ ID NO: 4449)
3'-ACGUUCACGGGUUCUAGGAAAGACC$_{CU-5'}$ (SEQ ID NO: 2271)

AR-3846 Target: 5'-TGCAAGTGCCCAAGATCCTTTCTGGGA-3' (SEQ ID NO: 2676)

5'-GCAAGUGCCCAAGAUCCUUUCUGGG$^{CC-3'}$ (SEQ ID NO: 4450)
3'-CGUUCACGGGUUCUAGGAAAGACCC$_{UU-5'}$ (SEQ ID NO: 2272)

AR-3847 Target: 5'-GCAAGTGCCCAAGATCCTTTCTGGGAA-3' (SEQ ID NO: 2677)

5'-CAAGUGCCCAAGAUCCUUUCUGGGA$^{CC-3'}$ (SEQ ID NO: 4451)
3'-GUUCACGGGUUCUAGGAAAGACCCU$_{UU-5'}$ (SEQ ID NO: 2273)

AR-3848 Target: 5'-CAAGTGCCCAAGATCCTTTCTGGGAAA-3' (SEQ ID NO: 2678)

5'-AAGUGCCCAAGAUCCUUUCUGGGAA$^{C}{}^{A-3'}$ (SEQ ID NO: 4452)
3'-UUCACGGGUUCUAGGAAAGACCCUU$_{U}{}_{C-5'}$ (SEQ ID NO: 2274)

AR-3849 Target: 5'-AAGTGCCCAAGATCCTTTCTGGGAAAG-3' (SEQ ID NO: 2679)

5'-AGUGCCCAAGAUCCUUUCUGGGAAA$^{A}{}^{C-3'}$ (SEQ ID NO: 4453)
3'-UCACGGGUUCUAGGAAAGACCCUUU$_{C}{}_{A-5'}$ (SEQ ID NO: 2275)

AR-3850 Target: 5'-AGTGCCCAAGATCCTTTCTGGGAAAGT-3' (SEQ ID NO: 2680)

5'-GUGCCCAAGAUCCUUUCUGGGAAAG$^{C}{}^{A-3'}$ (SEQ ID NO: 4454)
3'-CACGGGUUCUAGGAAAGACCCUUUC$_{A}{}_{G-5'}$ (SEQ ID NO: 2276)

AR-3851 Target: 5'-GTGCCCAAGATCCTTTCTGGGAAAGTC-3' (SEQ ID NO: 2681)

5'-UGCCCAAGAUCCUUUCUGGGAAAGU$^{A}{}^{C-3'}$ (SEQ ID NO: 4455)
3'-ACGGGUUCUAGGAAAGACCCUUUCA$_{G}{}_{U-5'}$ (SEQ ID NO: 2277)

AR-3852 Target: 5'-TGCCCAAGATCCTTTCTGGGAAAGTCA-3' (SEQ ID NO: 2682)

5'-GCCCAAGAUCCUUUCUGGGAAAGUC$^{C}{}^{C-3'}$ (SEQ ID NO: 4456)
3'-CGGGUUCUAGGAAAGACCCUUUCAG$_{U}{}_{U-5'}$ (SEQ ID NO: 2278)

AR-3853 Target: 5'-GCCCAAGATCCTTTCTGGGAAAGTCAA-3' (SEQ ID NO: 2683)

5'-CCCAAGAUCCUUUCUGGGAAAGUCA$^{C}{}^{A-3'}$ (SEQ ID NO: 4457)
3'-GGGUUCUAGGAAAGACCCUUUCAGU$_{U}{}_{C-5'}$ (SEQ ID NO: 2279)

AR-3854 Target: 5'-CCCAAGATCCTTTCTGGGAAAGTCAAG-3' (SEQ ID NO: 2684)

5'-CCAAGAUCCUUUCUGGGAAAGUCAA$^{A}{}^{A-3'}$ (SEQ ID NO: 4458)
3'-GGUUCUAGGAAAGACCCUUUCAGUU$_{C}{}_{G-5'}$ (SEQ ID NO: 2280)

AR-3855 Target: 5'-CCAAGATCCTTTCTGGGAAAGTCAAGC-3' (SEQ ID NO: 2685)

5'-CAAGAUCCUUUCUGGGAAAGUCAAG$^{A}{}^{A-3'}$ (SEQ ID NO: 4459)
3'-GUUCUAGGAAAGACCCUUUCAGUUC$_{G}{}_{G-5'}$ (SEQ ID NO: 2281)

AR-3856 Target: 5'-CAAGATCCTTTCTGGGAAAGTCAAGCC-3' (SEQ ID NO: 2686)

5'-AAGAUCCUUUCUGGGAAAGUCAAGC$^{A}{}^{A-3'}$ (SEQ ID NO: 4460)
3'-UUCUAGGAAAGACCCUUUCAGUUCG$_{G}{}_{G-5'}$ (SEQ ID NO: 2282)

AR-3857 Target: 5'-AAGATCCTTTCTGGGAAAGTCAAGCCC-3' (SEQ ID NO: 2687)

5'-AGAUCCUUUCUGGGAAAGUCAAGCC$^{A}{}^{C-3'}$ (SEQ ID NO: 4461)
3'-UCUAGGAAAGACCCUUUCAGUUCGG$_{G}{}_{U-5'}$ (SEQ ID NO: 2283)

AR-3858 Target: 5'-AGATCCTTTCTGGGAAAGTCAAGCCCA-3' (SEQ ID NO: 2688)

5'-GAUCCUUUCUGGGAAAGUCAAGCCC$^{C}{}^{C-3'}$ (SEQ ID NO: 4462)
3'-CUAGGAAAGACCCUUUCAGUUCGGG$_{U}{}_{A-5'}$ (SEQ ID NO: 2284)

AR-3859 Target: 5'-GATCCTTTCTGGGAAAGTCAAGCCCAT-3' (SEQ ID NO: 2689)

5'-AUCCUUUCUGGGAAAGUCAAGCCCA$^{CA-3'}$ (SEQ ID NO: 4463)
3'-UAGGAAAGACCCUUUCAGUUCGGGU$_{AG-5'}$ (SEQ ID NO: 2285)

AR-3860 Target: 5'-ATCCTTTCTGGGAAAGTCAAGCCCATC-3' (SEQ ID NO: 2690)

5'-UCCUUUCUGGGAAAGUCAAGCCCAU$^{AC-3'}$ (SEQ ID NO: 4464)
3'-AGGAAAGACCCUUUCAGUUCGGGUA$_{GA-5'}$ (SEQ ID NO: 2286)

AR-3861 Target: 5'-TCCTTTCTGGGAAAGTCAAGCCCATCT-3' (SEQ ID NO: 2691)

5'-CCUUUCUGGGAAAGUCAAGCCCAUC$^{CC-3'}$ (SEQ ID NO: 4465)
3'-GGAAAGACCCUUUCAGUUCGGGUAG$_{AU-5'}$ (SEQ ID NO: 2287)

AR-3862 Target: 5'-CCTTTCTGGGAAAGTCAAGCCCATCTA-3' (SEQ ID NO: 2692)

5'-CUUUCUGGGAAAGUCAAGCCCAUCU$^{CC-3'}$ (SEQ ID NO: 4466)
3'-GAAAGACCCUUUCAGUUCGGGUAGA$_{UA-5'}$ (SEQ ID NO: 2288)

AR-3863 Target: 5'-CTTTCTGGGAAAGTCAAGCCCATCTAT-3' (SEQ ID NO: 2693)

5'-UUUCUGGGAAAGUCAAGCCCAUCUA$^{CC-3'}$ (SEQ ID NO: 4467)
3'-AAAGACCCUUUCAGUUCGGGUAGAU$_{AA-5'}$ (SEQ ID NO: 2289)

AR-3864 Target: 5'-TTTCTGGGAAAGTCAAGCCCATCTATT-3' (SEQ ID NO: 2694)

5'-UUCUGGGAAAGUCAAGCCCAUCUAU$^{CC-3'}$ (SEQ ID NO: 4468)
3'-AAGACCCUUUCAGUUCGGGUAGAUA$_{AA-5'}$ (SEQ ID NO: 2290)

AR-3865 Target: 5'-TTCTGGGAAAGTCAAGCCCATCTATTT-3' (SEQ ID NO: 2695)

5'-UCUGGGAAAGUCAAGCCCAUCUAUU$^{CA-3'}$ (SEQ ID NO: 4469)
3'-AGACCCUUUCAGUUCGGGUAGAUAA$_{AG-5'}$ (SEQ ID NO: 2291)

AR-3866 Target: 5'-TCTGGGAAAGTCAAGCCCATCTATTTC-3' (SEQ ID NO: 2696)

5'-CUGGGAAAGUCAAGCCCAUCUAUUU$^{AA-3'}$ (SEQ ID NO: 4470)
3'-GACCCUUUCAGUUCGGGUAGAUAAA$_{GG-5'}$ (SEQ ID NO: 2292)

AR-3867 Target: 5'-CTGGGAAAGTCAAGCCCATCTATTTCC-3' (SEQ ID NO: 2697)

5'-UGGGAAAGUCAAGCCCAUCUAUUUC$^{AC-3'}$ (SEQ ID NO: 4471)
3'-ACCCUUUCAGUUCGGGUAGAUAAAG$_{GU-5'}$ (SEQ ID NO: 2293)

AR-3868 Target: 5'-TGGGAAAGTCAAGCCCATCTATTTCCA-3' (SEQ ID NO: 2698)

5'-GGGAAAGUCAAGCCCAUCUAUUUCC$^{CA-3'}$ (SEQ ID NO: 4472)
3'-CCCUUUCAGUUCGGGUAGAUAAAGG$_{UG-5'}$ (SEQ ID NO: 2294)

AR-3869 Target: 5'-GGGAAAGTCAAGCCCATCTATTTCCAC-3' (SEQ ID NO: 2699)

5'-GGAAAGUCAAGCCCAUCUAUUUCCA$^{AC-3'}$ (SEQ ID NO: 4473)
3'-CCUUUCAGUUCGGGUAGAUAAAGGU$_{GU-5'}$ (SEQ ID NO: 2295)

AR-3870 Target: 5'-GGAAAGTCAAGCCCATCTATTTCCACA-3' (SEQ ID NO: 2700)

5'-GAAAGUCAAGCCCAUCUAUUUCCAC$^{CA-3'}$ (SEQ ID NO: 4474)
3'-CUUUCAGUUCGGGUAGAUAAAGGUG$_{UG-5'}$ (SEQ ID NO: 2296)

AR-3871 Target: 5'-GAAAGTCAAGCCCATCTATTTCCACAC-3' (SEQ ID NO: 2701)

5'-UUCAGAUGUCUUCUGCCUGUUAUAA$^{AC-3'}$ (SEQ ID NO: 4475)
3'-AAGUCUACAGAAGACGGACAAUAUU$_{GA-5'}$ (SEQ ID NO: 2297)

AR-3947 Target: 5'-TTCAGATGTCTTCTGCCTGTTATAACT-3' (SEQ ID NO: 2702)

5'-UCAGAUGUCUUCUGCCUGUUAUAAC$^{CA-3'}$ (SEQ ID NO: 4476)
3'-AGUCUACAGAAGACGGACAAUAUUG$_{AG-5'}$ (SEQ ID NO: 2298)

AR-3948 Target: 5'-TCAGATGTCTTCTGCCTGTTATAACTC-3' (SEQ ID NO: 2703)

5'-CAGAUGUCUUCUGCCUGUUAUAACU$^{AC-3'}$ (SEQ ID NO: 4477)
3'-GUCUACAGAAGACGGACAAUAUUGA$_{GA-5'}$ (SEQ ID NO: 2299)

AR-3949 Target: 5'-CAGATGTCTTCTGCCTGTTATAACTCT-3' (SEQ ID NO: 2704)

5'-AGAUGUCUUCUGCCUGUUAUAACUC$^{CA-3'}$ (SEQ ID NO: 4478)
3'-UCUACAGAAGACGGACAAUAUUGAG$_{AC-5'}$ (SEQ ID NO: 2300)

AR-3950 Target: 5'-AGATGTCTTCTGCCTGTTATAACTCTG-3' (SEQ ID NO: 2705)

5'-GGGGAAUUUCCUCUAUUGAUGUACA$^{AC-3'}$ (SEQ ID NO: 4479)
3'-CCCCUUAAAGGAGAUAACUACAUGU$_{CA-5'}$ (SEQ ID NO: 2301)

AR-3999 Target: 5'-GGGGAATTTCCTCTATTGATGTACAGT-3' (SEQ ID NO: 2706)

5'-UUGCUGGGCUUUUUUUUUCUCUUUC$^{CA-3'}$ (SEQ ID NO: 4480)
3'-AACGACCCGAAAAAAAAAGAGAAAG$_{AG-5'}$ (SEQ ID NO: 2302)

AR-4054 Target: 5'-TTGCTGGGCTTTTTTTTCTCTTTCTC-3' (SEQ ID NO: 2707)

5'-UGCUGGGCUUUUUUUUUCUCUUUCU$^{AC-3'}$ (SEQ ID NO: 4481)
3'-ACGACCCGAAAAAAAAAGAGAAAGA$_{GA-5'}$ (SEQ ID NO: 2303)

AR-4055 Target: 5'-TGCTGGGCTTTTTTTTCTCTTTCTCT-3' (SEQ ID NO: 2708)

5'-GCUUUUUUUUUCUCUUUCUCUCCUU$^{CA-3'}$ (SEQ ID NO: 4482)
3'-CGAAAAAAAAAGAGAAAGAGAGGAA$_{AG-5'}$ (SEQ ID NO: 2304)

AR-4061 Target: 5'-GCTTTTTTTTCTCTTTCTCTCCTTTC-3' (SEQ ID NO: 2709)

5'-UUUUUUCUCUUUCUCUCCUUUCUUU$^{CC-3'}$ (SEQ ID NO: 4483)
3'-AAAAAAGAGAAAGAGAGGAAAGAAA$_{AA-5'}$ (SEQ ID NO: 2305)

AR-4066 Target: 5'-TTTTTCTCTTTCTCTCCTTTCTTTTT-3' (SEQ ID NO: 2710)

5'-UCUUUUUCUUCUUCCCUCCCUAUCU$^{CC-3'}$ (SEQ ID NO: 4484)
3'-AGAAAAAGAAGAAGGGAGGGAUAGA$_{UU-5'}$ (SEQ ID NO: 2306)

AR-4086 Target: 5'-TCTTTTTCTTCTTCCCTCCCTATCTAA-3' (SEQ ID NO: 2711)

5'-UGUUGUAUGCCUUUAAAUCUGUGAU^{A}C-3′ (SEQ ID NO: 4485)
3'-ACAACAUACGGAAAUUUAGACACUA$_{C}U$-5′, (SEQ ID NO: 2307)

AR-4174 Target: 5'-TGTTGTATGCCTTTAAATCTGTGATGA-3' (SEQ ID NO: 2712)

5'-UGUGCUUGUUUACAGCACUACUCUG^{C}A-3′ (SEQ ID NO: 4486)
3'-ACACGAACAAAUGUCGUGAUGAGAC$_{A}C$-5′, (SEQ ID NO: 2308)

AR-4225 Target: 5'-TGTGCTTGTTTACAGCACTACTCTGTG-3' (SEQ ID NO: 2713)

5'-UUAGAGAGCUAAGAUUAUCUGGGGA^{C}C-3′ (SEQ ID NO: 4487)
3'-AAUCUCUCGAUUCUAAUAGACCCCU$_{U}U$-5′, (SEQ ID NO: 2309)

AR-4293 Target: 5'-TTAGAGAGCTAAGATTATCTGGGGAAA-3' (SEQ ID NO: 2714)

5'-GGGGAAAUCAAAACAAAAACAAGCA^{C}C-3′ (SEQ ID NO: 4488)
3'-CCCCUUUAGUUUUGUUUUUGUUCGU$_{U}U$-5′, (SEQ ID NO: 2310)

AR-4313 Target: 5'-GGGGAAATCAAAACAAAAACAAGCAAA-3' (SEQ ID NO: 2715)

Table 6: Selected Mouse Anti-AR 27mer "Blunt/Fray" DsiRNA Agents

5'-GGCAGCAGCACACUGAGGAUGGUUC^{C}A-3′ (SEQ ID NO: 4459)
3'-CCGUCGUCGUGUGACUCCUACCAAG$_{A}G$-5′, (SEQ ID NO: 3574)

AR-m258 Target: 5'-GGCAGCAGCACACTGAGGATGGTTCTC-3' (SEQ ID NO: 3622)

5'-CUCCGAGGGCCACCCUGAGAGCAGC^{C}A-3′ (SEQ ID NO: 4460)
3'-GAGGCUCCCGGUGGGACUCUCGUCG$_{A}C$-5′, (SEQ ID NO: 3575)

AR-m361 Target: 5'-CTCCGAGGGCCACCCTGAGAGCAGCTG-3' (SEQ ID NO: 3623)

5'-GGGCCACCCUGAGAGCAGCUGCCUC^{A}A-3′ (SEQ ID NO: 4461)
3'-CCCGGUGGGACUCUCGUCGACGGAG$_{G}G$-5′, (SEQ ID NO: 3576)

AR-m367 Target: 5'-GGGCCACCCTGAGAGCAGCTGCCTCCC-3' (SEQ ID NO: 3624)

5'-GGCUGCCGCAGCAGCCACCAGCUCC^{C}A-3′ (SEQ ID NO: 4462)
3'-CCGACGGCGUCGUCGGUGGUCGAGG$_{A}G$-5′, (SEQ ID NO: 3577)

AR-m426 Target: 5'-GGCTGCCGCAGCAGCCACCAGCTCCTC-3' (SEQ ID NO: 3625)

5'-CACUUUCCCAGGCUUAAGCAGCUGC^{C}A-3′ (SEQ ID NO: 4463)
3'-GUGAAAGGGUCCGAAUUCGUCGACG$_{A}G$-5′, (SEQ ID NO: 3578)

AR-m502 Target: 5'-CACTTTCCCAGGCTTAAGCAGCTGCTC-3' (SEQ ID NO: 3626)

5'-AUGCAACUUCUUCAGCAGCAGCAAC^{C}C-3′ (SEQ ID NO: 4464)
3'-UACGUUGAAGAAGUCGUCGUCGUUG$_{U}U$-5′, (SEQ ID NO: 3579)

AR-m566 Target: 5'-ATGCAACTTCTTCAGCAGCAGCAACAA-3' (SEQ ID NO: 3627)

5'-GUGCGUCCCACUCCUUGUGCGCCGC$^{CA-3'}$ (SEQ ID NO: 4465)
3'-CACGCAGGGUGAGGAACACGCGGCG$_{AC-5'}$ (SEQ ID NO: 3580)

AR-m872 Target: 5'-GTGCGTCCCACTCCTTGTGCGCCGCTG-3' (SEQ ID NO: 3628)

5'-CUGGCAGCAGUGAAGCAGGUAGCUC$^{CA-3'}$ (SEQ ID NO: 4466)
3'-GACCGUCGUCACUUCGUCCAUCGAG$_{AC-5'}$ (SEQ ID NO: 3581)

AR-m1020 Target: 5'-CTGGCAGCAGTGAAGCAGGTAGCTCTG-3' (SEQ ID NO: 3629)

5'-UUUCCGCUGGCUCUGUCCGGGCCGC$^{AA-3'}$ (SEQ ID NO: 4467)
3'-AAAGGCGACCGAGACAGGCCCGGCG$_{GC-5'}$ (SEQ ID NO: 3582)

AR-m1136 Target: 5'-TTTCCGCTGGCTCTGTCCGGGCCGCCG-3' (SEQ ID NO: 3630)

5'-GCAGCGCCUGGGCUGCGGCGGCAGC$^{AA-3'}$ (SEQ ID NO: 4468)
3'-CGUCGCGGACCCGACGCCGCCGUCG$_{CG-5'}$ (SEQ ID NO: 3583)

AR-m1224 Target: 5'-GCAGCGCCTGGGCTGCGGCGGCAGCGC-3' (SEQ ID NO: 3631)

5'-GCCUGGGCUGCGGCGGCAGCGCAAU$^{AA-3'}$ (SEQ ID NO: 4469)
3'-CGGACCCGACGCCGCCGUCGCGUUA$_{CG-5'}$ (SEQ ID NO: 3584)

AR-m1229 Target: 5'-GCCTGGGCTGCGGCGGCAGCGCAATGC-3' (SEQ ID NO: 3632)

5'-CUGCGGCGGCAGCGCAAUGCCGCUA$^{CA-3'}$ (SEQ ID NO: 4470)
3'-GACGCCGCCGUCGCGUUACGGCGAU$_{AC-5'}$ (SEQ ID NO: 3585)

AR-m1236 Target: 5'-CTGCGGCGGCAGCGCAATGCCGCTATG-3' (SEQ ID NO: 3633)

5'-UGUAGCCGGGCCCAGCACUGGAUCG$^{AA-3'}$ (SEQ ID NO: 4471)
3'-ACAUCGGCCCGGGUCGUGACCUAGC$_{GG-5'}$ (SEQ ID NO: 3586)

AR-m1291 Target: 5'-TGTAGCCGGGCCCAGCACTGGATCGCC-3' (SEQ ID NO: 3634)

5'-CUUCCUGGCAUACUCUCUUCACAGC$^{CA-3'}$ (SEQ ID NO: 4472)
3'-GAAGGACCGUAUGAGAGAAGUGUCG$_{AC-5'}$ (SEQ ID NO: 3587)

AR-m1335 Target: 5'-CTTCCTGGCATACTCTCTTCACAGCTG-3' (SEQ ID NO: 3635)

5'-AGCAGCCCAAGCGAUGCCGGGCCUG$^{CC-3'}$ (SEQ ID NO: 4473)
3'-UCGUCGGGUUCGCUACGGCCCGGAC$_{AU-5'}$ (SEQ ID NO: 3588)

AR-m1403 Target: 5'-AGCAGCCCAAGCGATGCCGGGCCTGTA-3' (SEQ ID NO: 3636)

5'-GCUUCUGGCUGUCACUACGGAGCUC$^{CA-3'}$ (SEQ ID NO: 4474)
3'-CGAAGACCGACAGUGAUGCCUCGAG$_{AG-5'}$ (SEQ ID NO: 3589)

AR-m1694 Target: 5'-GCTTCTGGCTGTCACTACGGAGCTCTC-3' (SEQ ID NO: 3637)

5'-CGGAGCUCUCACUUGUGGCAGCUGC$^{CC-3'}$ (SEQ ID NO: 4475)
3'-GCCUCGAGAGUGAACACCGUCGACG$_{UU-5'}$ (SEQ ID NO: 3590)

AR-m1711 Target: 5'-CGGAGCTCTCACTTGTGGCAGCTGCAA-3' (SEQ ID NO: 3638)

5'-CACUUGUGGCAGCUGCAAGGUCUUC^{C}C-3′ (SEQ ID NO: 4476)
3'-GUGAACACCGUCGACGUUCCAGAAG$_{A}A$-5′, (SEQ ID NO: 3591)

AR-m1720 Target: 5'-CACTTGTGGCAGCTGCAAGGTCTTCTT-3' (SEQ ID NO: 3639)

5'-GUGGCAGCUGCAAGGUCUUCUUCAA^{C}C-3′ (SEQ ID NO: 4477)
3'-CACCGUCGACGUUCCAGAAGAAGUU$_{U}U$-5′, (SEQ ID NO: 3592)

AR-m1725 Target: 5'-GTGGCAGCTGCAAGGTCTTCTTCAAAA-3' (SEQ ID NO: 3640)

5'-GGGAUGACUCUGGGAGCUCGUAAGC^{C}A-3′ (SEQ ID NO: 4478)
3'-CCCUACUGAGACCCUCGAGCAUUCG$_{A}C$-5′, (SEQ ID NO: 3593)

AR-m1865 Target: 5'-GGGATGACTCTGGGAGCTCGTAAGCTG-3' (SEQ ID NO: 3641)

5'-CUGGGAGCUCGUAAGCUGAAGAAAC^{C}C-3′ (SEQ ID NO: 4479)
3'-GACCCUCGAGCAUUCGACUUCUUUG$_{A}A$-5′, (SEQ ID NO: 3594)

AR-m1874 Target: 5'-CTGGGAGCTCGTAAGCTGAAGAAACTT-3' (SEQ ID NO: 3642)

5'-CAGAUUCCUUUGCUGCCUUGUUAUC^{C}C-3′ (SEQ ID NO: 4480)
3'-GUCUAAGGAAACGACGGAACAAUAG$_{A}U$-5′, (SEQ ID NO: 3595)

AR-m2079 Target: 5'-CAGATTCCTTTGCTGCCTTGTTATCTA-3' (SEQ ID NO: 3643)

5'-CUUUGCUGCCUUGUUAUCUAGCCUC^{C}C-3′ (SEQ ID NO: 4481)
3'-GAAACGACGGAACAAUAGAUCGGAG$_{U}U$-5′, (SEQ ID NO: 3596)

AR-m2086 Target: 5'-CTTTGCTGCCTTGTTATCTAGCCTCAA-3' (SEQ ID NO: 3644)

5'-UUGCCUGGCUUCCGCAACUUGCAUG^{C}A-3′ (SEQ ID NO: 4482)
3'-AACGGACCGAAGGCGUUGAACGUAC$_{A}C$-5′, (SEQ ID NO: 3597)

AR-m2162 Target: 5'-TTGCCTGGCTTCCGCAACTTGCATGTG-3' (SEQ ID NO: 3645)

5'-UGGAUGGGACUGAUGGUAUUUGCCA^{C}A-3′ (SEQ ID NO: 4483)
3'-ACCUACCCUGACUACCAUAAACGGU$_{A}C$-5′, (SEQ ID NO: 3598)

AR-m2219 Target: 5'-TGGATGGGACTGATGGTATTTGCCATG-3' (SEQ ID NO: 3646)

5'-CAGGAUGCUCUACUUUGCACCUGAC^{C}C-3′ (SEQ ID NO: 4484)
3'-GUCCUACGAGAUGAAACGUGGACUG$_{A}A$-5′, (SEQ ID NO: 3599)

AR-m2275 Target: 5'-CAGGATGCTCTACTTTGCACCTGACTT-3' (SEQ ID NO: 3647)

5'-UGCUCUACUUUGCACCUGACUUGGU^{C}C-3′ (SEQ ID NO: 4485)
3'-ACGAGAUGAAACGUGGACUGAACCA$_{A}A$-5′, (SEQ ID NO: 3600)

AR-m2280 Target: 5'-TGCTCTACTTTGCACCTGACTTGGTTT-3' (SEQ ID NO: 3648)

5'-CUUUGCACCUGACUUGGUUUUCAAU^{A}C-3′ (SEQ ID NO: 4486)
3'-GAAACGUGGACUGAACCAAAAGUUA$_{C}U$-5′, (SEQ ID NO: 3601)

AR-m2287 Target: 5'-CTTTGCACCTGACTTGGTTTTCAATGA-3' (SEQ ID NO: 3649)

5'-GACUUGGUUUUCAAUGAGUACCGCA$^{CA-3'}$ (SEQ ID NO: 4487)
3'-CUGAACCAAAAGUUACUCAUGGCGU$_{AC-5'}$ (SEQ ID NO: 3602)

AR-m2297 Target: 5'-GACTTGGTTTTCAATGAGTACCGCATG-3' (SEQ ID NO: 3650)

5'-GAGUACCGCAUGCACAAGUCUCGGA$^{CA-3'}$ (SEQ ID NO: 4488)
3'-CUCAUGGCGUACGUGUUCAGAGCCU$_{AC-5'}$ (SEQ ID NO: 3603)

AR-m2312 Target: 5'-GAGTACCGCATGCACAAGTCTCGGATG-3' (SEQ ID NO: 3651)

5'-CUGUGCAUGAAAGCACUGCUGCUCU$^{CA-3'}$ (SEQ ID NO: 4489)
3'-GACACGUACUUUCGUGACGACGAGA$_{AG-5'}$ (SEQ ID NO: 3604)

AR-m2411 Target: 5'-CTGTGCATGAAAGCACTGCTGCTCTTC-3' (SEQ ID NO: 3652)

5'-CAUGAAAGCACUGCUGCUCUUCAGC$^{CC-3'}$ (SEQ ID NO: 4490)
3'-GUACUUUCGUGACGACGAGAAGUCG$_{UA-5'}$ (SEQ ID NO: 3605)

AR-m2416 Target: 5'-CATGAAAGCACTGCTGCTCTTCAGCAT-3' (SEQ ID NO: 3653)

5'-AGCACUGCUGCUCUUCAGCAUUAUU$^{AA-3'}$ (SEQ ID NO: 4491)
3'-UCGUGACGACGAGAAGUCGUAAUAA$_{GG-5'}$ (SEQ ID NO: 3606)

AR-m2422 Target: 5'-AGCACTGCTGCTCTTCAGCATTATTCC-3' (SEQ ID NO: 3654)

5'-UGCUGCUCUUCAGCAUUAUUCCAGU$^{AA-3'}$ (SEQ ID NO: 4492)
3'-ACGACGAGAAGUCGUAAUAAGGUCA$_{CC-5'}$ (SEQ ID NO: 3607)

AR-m2427 Target: 5'-TGCTGCTCTTCAGCATTATTCCAGTGG-3' (SEQ ID NO: 3655)

5'-AGCUCACCAAGCUCCUGGAUUCUGU$^{AA-3'}$ (SEQ ID NO: 4493)
3'-UCGAGUGGUUCGAGGACCUAAGACA$_{CG-5'}$ (SEQ ID NO: 3608)

AR-m2571 Target: 5'-AGCTCACCAAGCTCCTGGATTCTGTGC-3' (SEQ ID NO: 3656)

5'-AGCUCCUGGAUUCUGUGCAGCCUAU$^{CA-3'}$ (SEQ ID NO: 4494)
3'-UCGAGGACCUAAGACACGUCGGAUA$_{AC-5'}$ (SEQ ID NO: 3609)

AR-m2580 Target: 5'-AGCTCCTGGATTCTGTGCAGCCTATTG-3' (SEQ ID NO: 3657)

5'-CUGGAUUCUGUGCAGCCUAUUGCAA$^{AC-3'}$ (SEQ ID NO: 4495)
3'-GACCUAAGACACGUCGGAUAACGUU$_{CU-5'}$ (SEQ ID NO: 3610)

AR-m2585 Target: 5'-CTGGATTCTGTGCAGCCTATTGCAAGA-3' (SEQ ID NO: 3658)

5'-UCUGUGCAGCCUAUUGCAAGAGAGC$^{CA-3'}$ (SEQ ID NO: 4496)
3'-AGACACGUCGGAUAACGUUCUCUCG$_{AC-5'}$ (SEQ ID NO: 3611)

AR-m2591 Target: 5'-TCTGTGCAGCCTATTGCAAGAGAGCTG-3' (SEQ ID NO: 3659)

5'-CAGCCUAUUGCAAGAGAGCUGCAUC$^{CA-3'}$ (SEQ ID NO: 4497)
3'-GUCGGAUAACGUUCUCUCGACGUAG$_{UC-5'}$ (SEQ ID NO: 3612)

AR-m2597 Target: 5'-CAGCCTATTGCAAGAGAGCTGCATCAG-3' (SEQ ID NO: 3660)

5'-GCGUGGACUUUCCUGAAAUGAUGGC^{CA}-3′ (SEQ ID NO: 4498)
3'-CGCACCUGAAAGGACUUUACUACCG$_{UC}$-5′ (SEQ ID NO: 3613)

AR-m2661 Target: 5'-GCGTGGACTTTCCTGAAATGATGGCAG-3' (SEQ ID NO: 3661)

5'-UCUUCUGCCUGUUAUAUAACUCUGC^{CA}-3′ (SEQ ID NO: 4499)
3'-AGAAGACGGACAAUAUAUUGAGACG$_{UG}$-5′ (SEQ ID NO: 3614)

AR-m2809 Target: 5'-TCTTCTGCCTGTTATATAACTCTGCAC-3' (SEQ ID NO: 3662)

5'-UGCACUACUUCUCUGCAGUGCCUUG^{AA}-3′ (SEQ ID NO: 4500)
3'-ACGUGAUGAAGAGACGUCACGGAAC$_{CC}$-5′ (SEQ ID NO: 3615)

AR-m2831 Target: 5'-TGCACTACTTCTCTGCAGTGCCTTGGG-3' (SEQ ID NO: 3663)

5'-UCCUGGGCUUCUCCUUCUUUUUUUU^{CA}-3′ (SEQ ID NO: 4501)
3'-AGGACCCGAAGAGGAAGAAAAAAAA$_{AG}$-5′ (SEQ ID NO: 3616)

AR-m2912 Target: 5'-TCCTGGGCTTCTCCTTCTTTTTTTTC-3' (SEQ ID NO: 3664)

5'-GCUUCUCCUUCUUUUUUUUUCUUCU^{CA}-3′ (SEQ ID NO: 4502)
3'-CGAAGAGGAAGAAAAAAAAAGAAGA$_{AG}$-5′ (SEQ ID NO: 3617)

AR-m2918 Target: 5'-GCTTCTCCTTCTTTTTTTTCTTCTTC-3' (SEQ ID NO: 3665)

5'-UUCUUUUUUUUUCUUCUUCCCUCCC^{CA}-3′ (SEQ ID NO: 4503)
3'-AAGAAAAAAAAAGAAGAAGGGAGGG$_{AG}$-5′ (SEQ ID NO: 3618)

AR-m2926 Target: 5'-TTCTTTTTTTTTCTTCTTCCCTCCCTC-3' (SEQ ID NO: 3666)

5'-CUGCUGCGUAUUGUGGCUCCUGCCU^{CC}-3′ (SEQ ID NO: 4504)
3'-GACGACGCAUAACACCGAGGACGGA$_{AA}$-5′ (SEQ ID NO: 3619)

AR-m2981 Target: 5'-CTGCTGCGTATTGTGGCTCCTGCCTTT-3' (SEQ ID NO: 3667)

5'-UGUGGCUCCUGCCUUUGUUUUGAUU^{CA}-3′ (SEQ ID NO: 4505)
3'-ACACCGAGGACGGAAACAAAACUAA$_{AG}$-5′ (SEQ ID NO: 3620)

AR-m2992 Target: 5'-TGTGGCTCCTGCCTTTGTTTTGATTTC-3' (SEQ ID NO: 3668)

5'-CUCCUGCCUUUGUUUUGAUUUCUGU^{CA}-3′ (SEQ ID NO: 4506)
3'-GAGGACGGAAACAAAACUAAAGACA$_{AC}$-5′ (SEQ ID NO: 3621)

AR-m2997 Target: 5'-CTCCTGCCTTTGTTTTGATTTCTGTTG-3' (SEQ ID NO: 3669)

Table 7: Selected Human Anti-AR 27mer "Blunt/Blunt" DsiRNA Agents

5'-UGAAGUUUUUAAAAGCUGCUAAAGACU-3' (SEQ ID NO: 4507)
3'-ACUUCAAAAAUUUUCGACGAUUUCUGA-5' (SEQ ID NO: 154)

AR-252 Target: 5'-TGAAGTTTTTAAAAGCTGCTAAAGACT-3' (SEQ ID NO: 307)

5'-GAAGUUUUUAAAAGCUGCUAAAGACUC-3' (SEQ ID NO: 4508)
3'-CUUCAAAAAUUUUCGACGAUUUCUGAG-5' (SEQ ID NO: 155)

AR-253 Target: 5'-GAAGTTTTTAAAAGCTGCTAAAGACTC-3' (SEQ ID NO: 308)

5'-AAGUUUUUAAAAGCUGCUAAAGACUCG-3' (SEQ ID NO: 4509)
3'-UUCAAAAAUUUUCGACGAUUUCUGAGC-5' (SEQ ID NO: 156)

AR-254 Target: 5'-AAGTTTTTAAAAGCTGCTAAAGACTCG-3' (SEQ ID NO: 309)

5'-UGCGGAGCCAGAGAUCAAAAGAUGAAA-3' (SEQ ID NO: 4510)
3'-ACGCCUCGGUCUCUAGUUUUCUACUUU-5' (SEQ ID NO: 157)

AR-682 Target: 5'-TGCGGAGCCAGAGATCAAAAGATGAAA-3' (SEQ ID NO: 310)

5'-GCCAGAGAUCAAAAGAUGAAAAGGCAG-3' (SEQ ID NO: 4511)
3'-CGGUCUCUAGUUUUCUACUUUUCCGUC-5' (SEQ ID NO: 158)

AR-688 Target: 5'-GCCAGAGATCAAAAGATGAAAAGGCAG-3' (SEQ ID NO: 311)

5'-CCAGAGAUCAAAAGAUGAAAAGGCAGU-3' (SEQ ID NO: 4512)
3'-GGUCUCUAGUUUUCUACUUUUCCGUCA-5' (SEQ ID NO: 159)

AR-689 Target: 5'-CCAGAGATCAAAAGATGAAAAGGCAGT-3' (SEQ ID NO: 312)

5'-CAAAAGAUGAAAAGGCAGUCAGGUCUU-3' (SEQ ID NO: 4513)
3'-GUUUUCUACUUUUCCGUCAGUCCAGAA-5' (SEQ ID NO: 160)

AR-697 Target: 5'-CAAAAGATGAAAAGGCAGTCAGGTCTT-3' (SEQ ID NO: 313)

5'-AAAAGAUGAAAAGGCAGUCAGGUCUUC-3' (SEQ ID NO: 4514)
3'-UUUUCUACUUUUCCGUCAGUCCAGAAG-5' (SEQ ID NO: 161)

AR-698 Target: 5'-AAAAGATGAAAAGGCAGTCAGGTCTTC-3' (SEQ ID NO: 314)

5'-GUCAGGUCUUCAGUAGCCAAAAAACAA-3' (SEQ ID NO: 4515)
3'-CAGUCCAGAAGUCAUCGGUUUUUUGUU-5' (SEQ ID NO: 162)

AR-714 Target: 5'-GTCAGGTCTTCAGTAGCCAAAAAACAA-3' (SEQ ID NO: 315)

5'-UCAGGUCUUCAGUAGCCAAAAAACAAA-3' (SEQ ID NO: 4516)
3'-AGUCCAGAAGUCAUCGGUUUUUUGUUU-5' (SEQ ID NO: 163)

AR-715 Target: 5'-TCAGGTCTTCAGTAGCCAAAAAACAAA-3' (SEQ ID NO: 316)

5'-CAGUAGCCAAAAAACAAAACAAACAAA-3' (SEQ ID NO: 4517)
3'-GUCAUCGGUUUUUUGUUUUGUUUGUUU-5' (SEQ ID NO: 164)

AR-724 Target: 5'-CAGTAGCCAAAAAACAAAACAAACAAA-3' (SEQ ID NO: 317)

5'-GCCAAAAAACAAAACAAACAAAAACAA-3' (SEQ ID NO: 4518)
3'-CGGUUUUUUGUUUUGUUUGUUUUUGUU-5' (SEQ ID NO: 165)

AR-729 Target: 5'-GCCAAAAAACAAAACAAACAAAAACAA-3' (SEQ ID NO: 318)

5'-CCAAAAAACAAAACAAACAAAAACAAA-3' (SEQ ID NO: 4519)
3'-GGUUUUUUGUUUUGUUUGUUUUUGUUU-5' (SEQ ID NO: 166)

AR-730 Target: 5'-CCAAAAAACAAAACAAACAAAAACAAA-3' (SEQ ID NO: 319)

5'-ACAAAACAAACAAAAACAAAAAAGCCG-3' (SEQ ID NO: 4520)
3'-UGUUUUGUUUGUUUUUGUUUUUUCGGC-5' (SEQ ID NO: 167)

AR-737 Target: 5'-ACAAAACAAACAAAAACAAAAAAGCCG-3' (SEQ ID NO: 320)

5'-AACAAAAACAAAAAAGCCGAAAUAAAA-3' (SEQ ID NO: 4521)
3'-UUGUUUUUGUUUUUUCGGCUUUAUUUU-5' (SEQ ID NO: 168)

AR-745 Target: 5'-AACAAAAACAAAAAAGCCGAAATAAAA-3' (SEQ ID NO: 321)

5'-ACAAAAACAAAAAAGCCGAAAUAAAAG-3' (SEQ ID NO: 4522)

3'-UGUUUUUGUUUUUUCGGCUUUAUUUUC-5' (SEQ ID NO: 169)

AR-746 Target: 5'-ACAAAAACAAAAAAGCCGAAATAAAAG-3' (SEQ ID NO: 322)

5'-CAAAAACAAAAAAGCCGAAAUAAAAGA-3' (SEQ ID NO: 4523)
3'-GUUUUUGUUUUUUCGGCUUUAUUUUCU-5' (SEQ ID NO: 170)

AR-747 Target: 5'-CAAAAACAAAAAAGCCGAAATAAAAGA-3' (SEQ ID NO: 323)

5'-ACAAAAAAGCCGAAAUAAAAGAAAAAG-3' (SEQ ID NO: 4524)
3'-UGUUUUUUCGGCUUUAUUUUCUUUUUC-5' (SEQ ID NO: 171)

AR-752 Target: 5'-ACAAAAAAGCCGAAATAAAAGAAAAAG-3' (SEQ ID NO: 324)

5'-CAAAAAAGCCGAAAUAAAAGAAAAAGA-3' (SEQ ID NO: 4525)
3'-GUUUUUUCGGCUUUAUUUUCUUUUUCU-5' (SEQ ID NO: 172)

AR-753 Target: 5'-CAAAAAAGCCGAAATAAAAGAAAAAGA-3' (SEQ ID NO: 325)

5'-AAAAAGCCGAAAUAAAAGAAAAAGAUA-3' (SEQ ID NO: 4526)
3'-UUUUUCGGCUUUAUUUUCUUUUUCUAU-5' (SEQ ID NO: 173)

AR-755 Target: 5'-AAAAAGCCGAAATAAAAGAAAAAGATA-3' (SEQ ID NO: 326)

5'-GCCGAAAUAAAAGAAAAAGAUAAUAAC-3' (SEQ ID NO: 4527)
3'-CGGCUUUAUUUUCUUUUUCUAUUAUUG-5' (SEQ ID NO: 174)

AR-760 Target: 5'-GCCGAAATAAAAGAAAAAGATAATAAC-3' (SEQ ID NO: 327)

5'-CCGAAAUAAAAGAAAAAGAUAAUAACU-3' (SEQ ID NO: 4528)
3'-GGCUUUAUUUUCUUUUUCUAUUAUUGA-5' (SEQ ID NO: 175)

AR-761 Target: 5'-CCGAAATAAAAGAAAAAGATAATAACT-3' (SEQ ID NO: 328)

5'-CGAAAUAAAAGAAAAAGAUAAUAACUC-3' (SEQ ID NO: 4529)
3'-GCUUUAUUUUCUUUUUCUAUUAUUGAG-5' (SEQ ID NO: 176)

AR-762 Target: 5'-CGAAATAAAAGAAAAAGATAATAACTC-3' (SEQ ID NO: 329)

5'-AAGAAAAAGAUAAUAACUCAGUUCUUA-3' (SEQ ID NO: 4530)
3'-UUCUUUUUCUAUUAUUGAGUCAAGAAU-5' (SEQ ID NO: 177)

AR-770 Target: 5'-AAGAAAAAGATAATAACTCAGTTCTTA-3' (SEQ ID NO: 330)

5'-AAAAGAUAAUAACUCAGUUCUUAUUUG-3' (SEQ ID NO: 4531)
3'-UUUUCUAUUAUUGAGUCAAGAAUAAAC-5' (SEQ ID NO: 178)

AR-774 Target: 5'-AAAAGATAATAACTCAGTTCTTATTTG-3' (SEQ ID NO: 331)

5'-AAAGAUAAUAACUCAGUUCUUAUUUGC-3' (SEQ ID NO: 4532)
3'-UUUCUAUUAUUGAGUCAAGAAUAAACG-5' (SEQ ID NO: 179)

AR-775 Target: 5'-AAAGATAATAACTCAGTTCTTATTTGC-3' (SEQ ID NO: 332)

5'-AGAUAAUAACUCAGUUCUUAUUUGCAC-3' (SEQ ID NO: 4533)
3'-UCUAUUAUUGAGUCAAGAAUAAACGUG-5' (SEQ ID NO: 180)

AR-777 Target: 5'-AGATAATAACTCAGTTCTTATTTGCAC-3' (SEQ ID NO: 333)

5'-GAUAAUAACUCAGUUCUUAUUUGCACC-3' (SEQ ID NO: 4534)
3'-CUAUUAUUGAGUCAAGAAUAAACGUGG-5' (SEQ ID NO: 181)

AR-778 Target: 5'-GATAATAACTCAGTTCTTATTTGCACC-3' (SEQ ID NO: 334)

5'-UCUUAUUUGCACCUACUUCAGUGGACA-3' (SEQ ID NO: 4535)
3'-AGAAUAAACGUGGAUGAAGUCACCUGU-5' (SEQ ID NO: 182)

AR-792 Target: 5'-TCTTATTTGCACCTACTTCAGTGGACA-3' (SEQ ID NO: 335)

5'-UCAGUGGACACUGAAUUUGGAAGGUGG-3' (SEQ ID NO: 4536)
3'-AGUCACCUGUGACUUAAACCUUCCACC-5' (SEQ ID NO: 183)

AR-809 Target: 5'-TCAGTGGACACTGAATTTGGAAGGTGG-3' (SEQ ID NO: 336)

5'-CACUGAAUUUGGAAGGUGGAGGAUUUU-3' (SEQ ID NO: 4537)
3'-GUGACUUAAACCUUCCACCUCCUAAAA-5' (SEQ ID NO: 184)

AR-817 Target: 5'-CACTGAATTTGGAAGGTGGAGGATTTT-3' (SEQ ID NO: 337)

5'-UUUGGAAGGUGGAGGAUUUUGUUUUUU-3' (SEQ ID NO: 4538)
3'-AAACCUUCCACCUCCUAAAACAAAAAA-5' (SEQ ID NO: 185)

AR-824 Target: 5'-TTTGGAAGGTGGAGGATTTTGTTTTTT-3' (SEQ ID NO: 338)

5'-GGAAGGUGGAGGAUUUUGUUUUUUUCU-3' (SEQ ID NO: 4539)
3'-CCUUCCACCUCCUAAAACAAAAAAAGA-5' (SEQ ID NO: 186)

AR-827 Target: 5'-GGAAGGTGGAGGATTTTGTTTTTTTCT-3' (SEQ ID NO: 339)

5'-UGGAGGAUUUUGUUUUUUUCUUUUAAG-3' (SEQ ID NO: 4540)
3'-ACCUCCUAAAACAAAAAAAGAAAAUUC-5' (SEQ ID NO: 187)

AR-833 Target: 5'-TGGAGGATTTTGTTTTTTTCTTTTAAG-3' (SEQ ID NO: 340)

5'-GGAGGAUUUUGUUUUUUUCUUUUAAGA-3' (SEQ ID NO: 4541)
3'-CCUCCUAAAACAAAAAAAGAAAAUUCU-5' (SEQ ID NO: 188)

AR-834 Target: 5'-GGAGGATTTTGTTTTTTTCTTTTAAGA-3' (SEQ ID NO: 341)

5'-AGGAUUUUGUUUUUUUCUUUUAAGAUC-3' (SEQ ID NO: 4542)
3'-UCCUAAAACAAAAAAAGAAAAUUCUAG-5' (SEQ ID NO: 189)

AR-836 Target: 5'-AGGATTTTGTTTTTTTCTTTTAAGATC-3' (SEQ ID NO: 342)

5'-GGAUUUUGUUUUUUUCUUUUAAGAUCU-3' (SEQ ID NO: 4543)
3'-CCUAAAACAAAAAAAGAAAAUUCUAGA-5' (SEQ ID NO: 190)

AR-837 Target: 5'-GGATTTTGTTTTTTTCTTTTAAGATCT-3' (SEQ ID NO: 343)

5'-GAUUUUGUUUUUUUCUUUUAAGAUCUG-3' (SEQ ID NO: 4544)
3'-CUAAAACAAAAAAAGAAAAUUCUAGAC-5' (SEQ ID NO: 191)

AR-838 Target: 5'-GATTTTGTTTTTTTCTTTTAAGATCTG-3' (SEQ ID NO: 344)

5'-AUUUUGUUUUUUUCUUUUAAGAUCUGG-3' (SEQ ID NO: 4545)
3'-UAAAACAAAAAAAGAAAAUUCUAGACC-5' (SEQ ID NO: 192)

AR-839 Target: 5'-ATTTTGTTTTTTTCTTTTAAGATCTGG-3' (SEQ ID NO: 345)

5'-UGUUUUUUUCUUUUAAGAUCUGGGCAU-3' (SEQ ID NO: 4546)
3'-ACAAAAAAAGAAAAUUCUAGACCCGUA-5' (SEQ ID NO: 193)

AR-843 Target: 5'-TGTTTTTTTCTTTTAAGATCTGGGCAT-3' (SEQ ID NO: 346)

5'-GUUUUUUUCUUUUAAGAUCUGGGCAUC-3' (SEQ ID NO: 4547)
3'-CAAAAAAAGAAAAUUCUAGACCCGUAG-5' (SEQ ID NO: 194)

AR-844 Target: 5'-GTTTTTTTCTTTTAAGATCTGGGCATC-3' (SEQ ID NO: 347)

5'-UUUAAGAUCUGGGCAUCUUUUGAAUCU-3' (SEQ ID NO: 4548)
3'-AAAUUCUAGACCCGUAGAAAACUUAGA-5' (SEQ ID NO: 195)

AR-854 Target: 5'-TTTAAGATCTGGGCATCTTTTGAATCT-3' (SEQ ID NO: 348)

5'-AUCUUUUGAAUCUACCCUUCAAGUAUU-3' (SEQ ID NO: 4549)

3'-UAGAAAACUUAGAUGGGAAGUUCAUAA-5' (SEQ ID NO: 196)

AR-868 Target: 5'-ATCTTTTGAATCTACCCTTCAAGTATT-3' (SEQ ID NO: 349)

5'-UCUUUUGAAUCUACCCUUCAAGUAUUA-3' (SEQ ID NO: 4550)
3'-AGAAAACUUAGAUGGGAAGUUCAUAAU-5' (SEQ ID NO: 197)

AR-869 Target: 5'-TCTTTTGAATCTACCCTTCAAGTATTA-3' (SEQ ID NO: 350)

5'-CUUUUGAAUCUACCCUUCAAGUAUUAA-3' (SEQ ID NO: 4551)
3'-GAAAACUUAGAUGGGAAGUUCAUAAUU-5' (SEQ ID NO: 198)

AR-870 Target: 5'-CTTTTGAATCTACCCTTCAAGTATTAA-3' (SEQ ID NO: 351)

5'-UUUUGAAUCUACCCUUCAAGUAUUAAG-3' (SEQ ID NO: 4552)
3'-AAAACUUAGAUGGGAAGUUCAUAAUUC-5' (SEQ ID NO: 199)

AR-871 Target: 5'-TTTTGAATCTACCCTTCAAGTATTAAG-3' (SEQ ID NO: 352)

5'-UUUGAAUCUACCCUUCAAGUAUUAAGA-3' (SEQ ID NO: 4553)
3'-AAACUUAGAUGGGAAGUUCAUAAUUCU-5' (SEQ ID NO: 200)

AR-872 Target: 5'-TTTGAATCTACCCTTCAAGTATTAAGA-3' (SEQ ID NO: 353)

5'-UCAAGUAUUAAGAGACAGACUGUGAGC-3' (SEQ ID NO: 4554)
3'-AGUUCAUAAUUCUCUGUCUGACACUCG-5' (SEQ ID NO: 201)

AR-886 Target: 5'-TCAAGTATTAAGAGACAGACTGTGAGC-3' (SEQ ID NO: 354)

5'-AGUAUUAAGAGACAGACUGUGAGCCUA-3' (SEQ ID NO: 4555)
3'-UCAUAAUUCUCUGUCUGACACUCGGAU-5' (SEQ ID NO: 202)

AR-889 Target: 5'-AGTATTAAGAGACAGACTGTGAGCCTA-3' (SEQ ID NO: 355)

5'-CUGUUGAACUCUUCUGAGCAAGAGAAG-3' (SEQ ID NO: 4556)
3'-GACAACUUGAGAAGACUCGUUCUCUUC-5' (SEQ ID NO: 203)

AR-1067 Target: 5'-CTGTTGAACTCTTCTGAGCAAGAGAAG-3' (SEQ ID NO: 356)

5'-UGUUGAACUCUUCUGAGCAAGAGAAGG-3' (SEQ ID NO: 4557)
3'-ACAACUUGAGAAGACUCGUUCUCUUCC-5' (SEQ ID NO: 204)

AR-1068 Target: 5'-TGTTGAACTCTTCTGAGCAAGAGAAGG-3' (SEQ ID NO: 357)

5'-CAAGGAUGGAAGUGCAGUUAGGGCUGG-3' (SEQ ID NO: 4558)
3'-GUUCCUACCUUCACGUCAAUCCCGACC-5' (SEQ ID NO: 205)

AR-1137 Target: 5'-CAAGGATGGAAGTGCAGTTAGGGCTGG-3' (SEQ ID NO: 358)

5'-CCGAGGAGCUUUCCAGAAUCUGUUCCA-3' (SEQ ID NO: 4559)
3'-GGCUCCUCGAAAGGUCUUAGACAAGGU-5' (SEQ ID NO: 206)

AR-1198 Target: 5'-CCGAGGAGCTTTCCAGAATCTGTTCCA-3' (SEQ ID NO: 359)

5'-CGAGGAGCUUUCCAGAAUCUGUUCCAG-3' (SEQ ID NO: 4560)
3'-GCUCCUCGAAAGGUCUUAGACAAGGUC-5' (SEQ ID NO: 207)

AR-1199 Target: 5'-CGAGGAGCTTTCCAGAATCTGTTCCAG-3' (SEQ ID NO: 360)

5'-CGCUGACCUUAAAGACAUCCUGAGCGA-3' (SEQ ID NO: 4561)
3'-GCGACUGGAAUUUCUGUAGGACUCGCU-5' (SEQ ID NO: 208)

AR-1675 Target: 5'-CGCTGACCTTAAAGACATCCTGAGCGA-3' (SEQ ID NO: 361)

5'-UCCAAGGACAAUUACUUAGGGGGCACU-3' (SEQ ID NO: 4562)
3'-AGGUUCCUGUUAAUGAAUCCCCCGUGA-5' (SEQ ID NO: 209)

AR-1802 Target: 5'-TCCAAGGACAATTACTTAGGGGGCACT-3' (SEQ ID NO: 362)

5'-CCAAGGAGUUGUGUAAGGCAGUGUCGG-3' (SEQ ID NO: 4563)
3'-GGUUCCUCAACACAUUCCGUCACAGCC-5' (SEQ ID NO: 210)

AR-1848 Target: 5'-CCAAGGAGTTGTGTAAGGCAGTGTCGG-3' (SEQ ID NO: 363)

5'-CACUGAAGAUACUGCUGAGUAUUCCCC-3' (SEQ ID NO: 4564)
3'-GUGACUUCUAUGACGACUCAUAAGGGG-5' (SEQ ID NO: 211)

AR-2047 Target: 5'-CACTGAAGATACTGCTGAGTATTCCCC-3' (SEQ ID NO: 364)

5'-UGCUGAGUAUUCCCCUUUCAAGGGAGG-3' (SEQ ID NO: 4565)
3'-ACGACUCAUAAGGGGAAAGUUCCCUCC-5' (SEQ ID NO: 212)

AR-2059 Target: 5'-TGCTGAGTATTCCCCTTTCAAGGGAGG-3' (SEQ ID NO: 365)

5'-CACUUGUGUCAAAAGCGAAAUGGGCCC-3' (SEQ ID NO: 4566)
3'-GUGAACACAGUUUUCGCUUUACCCGGG-5' (SEQ ID NO: 213)

AR-2692 Target: 5'-CACTTGTGTCAAAAGCGAAATGGGCCC-3' (SEQ ID NO: 366)

5'-ACUUGUGUCAAAAGCGAAAUGGGCCCC-3' (SEQ ID NO: 4567)
3'-UGAACACAGUUUUCGCUUUACCCGGGG-5' (SEQ ID NO: 214)

AR-2693 Target: 5'-ACTTGTGTCAAAAGCGAAATGGGCCCC-3' (SEQ ID NO: 367)

5'-ACCAUGUUUUGCCCAUUGACUAUUACU-3' (SEQ ID NO: 4568)
3'-UGGUACAAAACGGGUAACUGAUAAUGA-5' (SEQ ID NO: 215)

AR-2775 Target: 5'-ACCATGTTTTGCCCATTGACTATTACT-3' (SEQ ID NO: 368)

5'-CAUGUUUUGCCCAUUGACUAUUACUUU-3' (SEQ ID NO: 4569)
3'-GUACAAAACGGGUAACUGAUAAUGAAA-5' (SEQ ID NO: 216)

AR-2777 Target: 5'-CATGTTTTGCCCATTGACTATTACTTT-3' (SEQ ID NO: 369)

5'-CUGUGGAGAUGAAGCUUCUGGGUGUCA-3' (SEQ ID NO: 4570)
3'-GACACCUCUACUUCGAAGACCCACAGU-5' (SEQ ID NO: 217)

AR-2827 Target: 5'-CTGTGGAGATGAAGCTTCTGGGTGTCA-3' (SEQ ID NO: 370)

5'-UGAAGGGAAACAGAAGUACCUGUGCGC-3' (SEQ ID NO: 4571)
3'-ACUUCCCUUUGUCUUCAUGGACACGCG-5' (SEQ ID NO: 218)

AR-2905 Target: 5'-TGAAGGGAAACAGAAGTACCTGTGCGC-3' (SEQ ID NO: 371)

5'-GCAGAAAUGAUUGCACUAUUGAUAAAU-3' (SEQ ID NO: 4572)
3'-CGUCUUUACUAACGUGAUAACUAUUUA-5' (SEQ ID NO: 219)

AR-2934 Target: 5'-GCAGAAATGATTGCACTATTGATAAAT-3' (SEQ ID NO: 372)

5'-CAGAAAUGAUUGCACUAUUGAUAAAUU-3' (SEQ ID NO: 4573)
3'-GUCUUUACUAACGUGAUAACUAUUUAA-5' (SEQ ID NO: 220)

AR-2935 Target: 5'-CAGAAATGATTGCACTATTGATAAATT-3' (SEQ ID NO: 373)

5'-AGAAAUGAUUGCACUAUUGAUAAAUUC-3' (SEQ ID NO: 4574)
3'-UCUUUACUAACGUGAUAACUAUUUAAG-5' (SEQ ID NO: 221)

AR-2936 Target: 5'-AGAAATGATTGCACTATTGATAAATTC-3' (SEQ ID NO: 374)

5'-AAAUGAUUGCACUAUUGAUAAAUUCCG-3' (SEQ ID NO: 4575)
3'-UUUACUAACGUGAUAACUAUUUAAGGC-5' (SEQ ID NO: 222)

AR-2938 Target: 5'-AAATGATTGCACTATTGATAAATTCCG-3' (SEQ ID NO: 375)

5'-AAUGAUUGCACUAUUGAUAAAUUCCGA-3' (SEQ ID NO: 4576)

3'-UUACUAACGUGAUAACUAUUUAAGGCU-5' (SEQ ID NO: 223)

AR-2939 Target: 5'-AATGATTGCACTATTGATAAATTCCGA-3' (SEQ ID NO: 376)

5'-CACUAUUGAUAAAUUCCGAAGGAAAAA-3' (SEQ ID NO: 4577)
3'-GUGAUAACUAUUUAAGGCUUCCUUUUU-5' (SEQ ID NO: 224)

AR-2947 Target: 5'-CACTATTGATAAATTCCGAAGGAAAAA-3' (SEQ ID NO: 377)

5'-ACUAUUGAUAAAUUCCGAAGGAAAAAU-3' (SEQ ID NO: 4578)
3'-UGAUAACUAUUUAAGGCUUCCUUUUUA-5' (SEQ ID NO: 225)

AR-2948 Target: 5'-ACTATTGATAAATTCCGAAGGAAAAAT-3' (SEQ ID NO: 378)

5'-CUAUUGAUAAAUUCCGAAGGAAAAAUU-3' (SEQ ID NO: 4579)
3'-GAUAACUAUUUAAGGCUUCCUUUUUAA-5' (SEQ ID NO: 226)

AR-2949 Target: 5'-CTATTGATAAATTCCGAAGGAAAAATT-3' (SEQ ID NO: 379)

5'-UAUUGAUAAAUUCCGAAGGAAAAAUUG-3' (SEQ ID NO: 4580)
3'-AUAACUAUUUAAGGCUUCCUUUUUAAC-5' (SEQ ID NO: 227)

AR-2950 Target: 5'-TATTGATAAATTCCGAAGGAAAAATTG-3' (SEQ ID NO: 380)

5'-AUUGAUAAAUUCCGAAGGAAAAAUUGU-3' (SEQ ID NO: 4581)
3'-UAACUAUUUAAGGCUUCCUUUUUAACA-5' (SEQ ID NO: 228)

AR-2951 Target: 5'-ATTGATAAATTCCGAAGGAAAAATTGT-3' (SEQ ID NO: 381)

5'-UGAUAAAUUCCGAAGGAAAAAUUGUCC-3' (SEQ ID NO: 4582)
3'-ACUAUUUAAGGCUUCCUUUUUAACAGG-5' (SEQ ID NO: 229)

AR-2953 Target: 5'-TGATAAATTCCGAAGGAAAAATTGTCC-3' (SEQ ID NO: 382)

5'-GAUAAAUUCCGAAGGAAAAAUUGUCCA-3' (SEQ ID NO: 4583)
3'-CUAUUUAAGGCUUCCUUUUUAACAGGU-5' (SEQ ID NO: 230)

AR-2954 Target: 5'-GATAAATTCCGAAGGAAAAATTGTCCA-3' (SEQ ID NO: 383)

5'-CGAAGGAAAAAUUGUCCAUCUUGUCGU-3' (SEQ ID NO: 4584)
3'-GCUUCCUUUUUAACAGGUAGAACAGCA-5' (SEQ ID NO: 231)

AR-2963 Target: 5'-CGAAGGAAAAATTGTCCATCTTGTCGT-3' (SEQ ID NO: 384)

5'-AUCUUGUCGUCUUCGGAAAUGUUAUGA-3' (SEQ ID NO: 4585)
3'-UAGAACAGCAGAAGCCUUUACAAUACU-5' (SEQ ID NO: 232)

AR-2980 Target: 5'-ATCTTGTCGTCTTCGGAAATGTTATGA-3' (SEQ ID NO: 385)

5'-CGGAAAUGUUAUGAAGCAGGGAUGACU-3' (SEQ ID NO: 4586)
3'-GCCUUUACAAUACUUCGUCCCUACUGA-5' (SEQ ID NO: 233)

AR-2993 Target: 5'-CGGAAATGTTATGAAGCAGGGATGACT-3' (SEQ ID NO: 386)

5'-GAAAUGUUAUGAAGCAGGGAUGACUCU-3' (SEQ ID NO: 4587)
3'-CUUUACAAUACUUCGUCCCUACUGAGA-5' (SEQ ID NO: 234)

AR-2995 Target: 5'-GAAATGTTATGAAGCAGGGATGACTCT-3' (SEQ ID NO: 387)

5'-CCCGGAAGCUGAAGAAACUUGGUAAUC-3' (SEQ ID NO: 4588)
3'-GGGCCUUCGACUUCUUUGAACCAUUAG-5' (SEQ ID NO: 235)

AR-3027 Target: 5'-CCCGGAAGCTGAAGAAACTTGGTAATC-3' (SEQ ID NO: 388)

5'-CGGAAGCUGAAGAAACUUGGUAAUCUG-3' (SEQ ID NO: 4589)
3'-GCCUUCGACUUCUUUGAACCAUUAGAC-5' (SEQ ID NO: 236)

AR-3029 Target: 5'-CGGAAGCTGAAGAAACTTGGTAATCTG-3' (SEQ ID NO: 389)

5'-GCUGAAGAAACUUGGUAAUCUGAAACU-3' (SEQ ID NO: 4590)
3'-CGACUUCUUUGAACCAUUAGACUUUGA-5' (SEQ ID NO: 237)

AR-3034 Target: 5'-GCTGAAGAAACTTGGTAATCTGAAACT-3' (SEQ ID NO: 390)

5'-CUGAAGAAACUUGGUAAUCUGAAACUA-3' (SEQ ID NO: 4591)
3'-GACUUCUUUGAACCAUUAGACUUUGAU-5' (SEQ ID NO: 238)

AR-3035 Target: 5'-CTGAAGAAACTTGGTAATCTGAAACTA-3' (SEQ ID NO: 391)

5'-UGAAGAAACUUGGUAAUCUGAAACUAC-3' (SEQ ID NO: 4592)
3'-ACUUCUUUGAACCAUUAGACUUUGAUG-5' (SEQ ID NO: 239)

AR-3036 Target: 5'-TGAAGAAACTTGGTAATCTGAAACTAC-3' (SEQ ID NO: 392)

5'-UUGGUAAUCUGAAACUACAGGAGGAAG-3' (SEQ ID NO: 4593)
3'-AACCAUUAGACUUUGAUGUCCUCCUUC-5' (SEQ ID NO: 240)

AR-3045 Target: 5'-TTGGTAATCTGAAACTACAGGAGGAAG-3' (SEQ ID NO: 393)

5'-AUCUGAAACUACAGGAGGAAGGAGAGG-3' (SEQ ID NO: 4594)
3'-UAGACUUUGAUGUCCUCCUUCCUCUCC-5' (SEQ ID NO: 241)

AR-3051 Target: 5'-ATCTGAAACTACAGGAGGAAGGAGAGG-3' (SEQ ID NO: 394)

5'-CCCAGGAAUUCCUGUGCAUGAAAGCAC-3' (SEQ ID NO: 4595)
3'-GGGUCCUUAAGGACACGUACUUUCGUG-5' (SEQ ID NO: 242)

AR-3546 Target: 5'-CCCAGGAATTCCTGTGCATGAAAGCAC-3' (SEQ ID NO: 395)

5'-CCAGGAAUUCCUGUGCAUGAAAGCACU-3' (SEQ ID NO: 4596)
3'-GGUCCUUAAGGACACGUACUUUCGUGA-5' (SEQ ID NO: 243)

AR-3547 Target: 5'-CCAGGAATTCCTGTGCATGAAAGCACT-3' (SEQ ID NO: 396)

5'-GUGGAUGGGCUGAAAAAUCAAAAAUUC-3' (SEQ ID NO: 4597)
3'-CACCUACCCGACUUUUUAGUUUUUAAG-5' (SEQ ID NO: 244)

AR-3596 Target: 5'-GTGGATGGGCTGAAAAATCAAAAATTC-3' (SEQ ID NO: 397)

5'-UGGAUGGGCUGAAAAAUCAAAAAUUCU-3' (SEQ ID NO: 4598)
3'-ACCUACCCGACUUUUUAGUUUUUAAGA-5' (SEQ ID NO: 245)

AR-3597 Target: 5'-TGGATGGGCTGAAAAATCAAAAATTCT-3' (SEQ ID NO: 398)

5'-GAUGGGCUGAAAAAUCAAAAAUUCUUU-3' (SEQ ID NO: 4599)
3'-CUACCCGACUUUUUAGUUUUUAAGAAA-5' (SEQ ID NO: 246)

AR-3599 Target: 5'-GATGGGCTGAAAAATCAAAAATTCTTT-3' (SEQ ID NO: 399)

5'-GGCUGAAAAAUCAAAAAUUCUUUGAUG-3' (SEQ ID NO: 4600)
3'-CCGACUUUUUAGUUUUUAAGAAACUAC-5' (SEQ ID NO: 247)

AR-3603 Target: 5'-GGCTGAAAAATCAAAAATTCTTTGATG-3' (SEQ ID NO: 400)

5'-GCUGAAAAAUCAAAAAUUCUUUGAUGA-3' (SEQ ID NO: 4601)
3'-CGACUUUUUAGUUUUUAAGAAACUACU-5' (SEQ ID NO: 248)

AR-3604 Target: 5'-GCTGAAAAATCAAAAATTCTTTGATGA-3' (SEQ ID NO: 401)

5'-UGAAAAAUCAAAAAUUCUUUGAUGAAC-3' (SEQ ID NO: 4602)
3'-ACUUUUUAGUUUUUAAGAAACUACUUG-5' (SEQ ID NO: 249)

AR-3606 Target: 5'-TGAAAAATCAAAAATTCTTTGATGAAC-3' (SEQ ID NO: 402)

5'-GAAAAAUCAAAAAUUCUUUGAUGAACU-3' (SEQ ID NO: 4603)

3'-CUUUUUAGUUUUUAAGAAACUACUUGA-5' (SEQ ID NO: 250)

AR-3607 Target: 5'-GAAAAATCAAAAATTCTTTGATGAACT-3' (SEQ ID NO: 403)

5'-AAAAAUCAAAAAUUCUUUGAUGAACUU-3' (SEQ ID NO: 4604)
3'-UUUUUAGUUUUUAAGAAACUACUUGAA-5' (SEQ ID NO: 251)

AR-3608 Target: 5'-AAAAATCAAAAATTCTTTGATGAACTT-3' (SEQ ID NO: 404)

5'-UUCGAAUGAACUACAUCAAGGAACUCG-3' (SEQ ID NO: 4605)
3'-AAGCUUACUUGAUGUAGUUCCUUGAGC-5' (SEQ ID NO: 252)

AR-3633 Target: 5'-TTCGAATGAACTACATCAAGGAACTCG-3' (SEQ ID NO: 405)

5'-UCAAGGAACUCGAUCGUAUCAUUGCAU-3' (SEQ ID NO: 4606)
3'-AGUUCCUUGAGCUAGCAUAGUAACGUA-5' (SEQ ID NO: 253)

AR-3648 Target: 5'-TCAAGGAACTCGATCGTATCATTGCAT-3' (SEQ ID NO: 406)

5'-CAAGGAACUCGAUCGUAUCAUUGCAUG-3' (SEQ ID NO: 4607)
3'-GUUCCUUGAGCUAGCAUAGUAACGUAC-5' (SEQ ID NO: 254)

AR-3649 Target: 5'-CAAGGAACTCGATCGTATCATTGCATG-3' (SEQ ID NO: 407)

5'-AUCGUAUCAUUGCAUGCAAAAGAAAAA-3' (SEQ ID NO: 4608)
3'-UAGCAUAGUAACGUACGUUUUCUUUUU-5' (SEQ ID NO: 255)

AR-3660 Target: 5'-ATCGTATCATTGCATGCAAAAGAAAAA-3' (SEQ ID NO: 408)

5'-UCGUAUCAUUGCAUGCAAAAGAAAAAA-3' (SEQ ID NO: 4609)
3'-AGCAUAGUAACGUACGUUUUCUUUUUU-5' (SEQ ID NO: 256)

AR-3661 Target: 5'-TCGTATCATTGCATGCAAAAGAAAAAA-3' (SEQ ID NO: 409)

5'-AUCAUUGCAUGCAAAAGAAAAAAUCCC-3' (SEQ ID NO: 4610)
3'-UAGUAACGUACGUUUUCUUUUUUAGGG-5' (SEQ ID NO: 257)

AR-3665 Target: 5'-ATCATTGCATGCAAAAGAAAAAATCCC-3' (SEQ ID NO: 410)

5'-CACUUUUGACCUGCUAAUCAAGUCACA-3' (SEQ ID NO: 4611)
3'-GUGAAAACUGGACGAUUAGUUCAGUGU-5' (SEQ ID NO: 258)

AR-3772 Target: 5'-CACTTTTGACCTGCTAATCAAGTCACA-3' (SEQ ID NO: 411)

5'-GCGUGGACUUUCCGGAAAUGAUGGCAG-3' (SEQ ID NO: 4612)
3'-CGCACCUGAAAGGCCUUUACUACCGUC-5' (SEQ ID NO: 259)

AR-3807 Target: 5'-GCGTGGACTTTCCGGAAATGATGGCAG-3' (SEQ ID NO: 412)

5'-CGUGGACUUUCCGGAAAUGAUGGCAGA-3' (SEQ ID NO: 4613)
3'-GCACCUGAAAGGCCUUUACUACCGUCU-5' (SEQ ID NO: 260)

AR-3808 Target: 5'-CGTGGACTTTCCGGAAATGATGGCAGA-3' (SEQ ID NO: 413)

5'-UGAUGGCAGAGAUCAUCUCUGUGCAAG-3' (SEQ ID NO: 4614)
3'-ACUACCGUCUCUAGUAGAGACACGUUC-5' (SEQ ID NO: 261)

AR-3825 Target: 5'-TGATGGCAGAGATCATCTCTGTGCAAG-3' (SEQ ID NO: 414)

5'-GCAGAGAUCAUCUCUGUGCAAGUGCCC-3' (SEQ ID NO: 4615)
3'-CGUCUCUAGUAGAGACACGUUCACGGG-5' (SEQ ID NO: 262)

AR-3830 Target: 5'-GCAGAGATCATCTCTGTGCAAGTGCCC-3' (SEQ ID NO: 415)

5'-CAGAGAUCAUCUCUGUGCAAGUGCCCA-3' (SEQ ID NO: 4616)
3'-GUCUCUAGUAGAGACACGUUCACGGGU-5' (SEQ ID NO: 263)

AR-3831 Target: 5'-CAGAGATCATCTCTGTGCAAGTGCCCA-3' (SEQ ID NO: 416)

5'-CCCAAGAUCCUUUCUGGGAAAGUCAAG-3' (SEQ ID NO: 4617)
3'-GGGUUCUAGGAAAGACCCUUUCAGUUC-5' (SEQ ID NO: 264)

AR-3854 Target: 5'-CCCAAGATCCTTTCTGGGAAAGTCAAG-3' (SEQ ID NO: 417)

5'-GUGAAGCAUUGGAAACCCUAUUUCCCC-3' (SEQ ID NO: 4618)
3'-CACUUCGUAACCUUUGGGAUAAAGGGG-5' (SEQ ID NO: 265)

AR-3901 Target: 5'-GTGAAGCATTGGAAACCCTATTTCCCC-3' (SEQ ID NO: 418)

5'-CAGAUGUCUUCUGCCUGUUAUAACUCU-3' (SEQ ID NO: 4619)
3'-GUCUACAGAAGACGGACAAUAUUGAGA-5' (SEQ ID NO: 266)

AR-3949 Target: 5'-CAGATGTCTTCTGCCTGTTATAACTCT-3' (SEQ ID NO: 419)

5'-GCCUUGGGGAAUUUCCUCUAUUGAUGU-3' (SEQ ID NO: 4620)
3'-CGGAACCCCUUAAAGGAGAUAACUACA-5' (SEQ ID NO: 267)

AR-3994 Target: 5'-GCCTTGGGGAATTTCCTCTATTGATGT-3' (SEQ ID NO: 420)

5'-CUUGGGGAAUUUCCUCUAUUGAUGUAC-3' (SEQ ID NO: 4621)
3'-GAACCCCUUAAAGGAGAUAACUACAUG-5' (SEQ ID NO: 268)

AR-3996 Target: 5'-CTTGGGGAATTTCCTCTATTGATGTAC-3' (SEQ ID NO: 421)

5'-UUGGGGAAUUUCCUCUAUUGAUGUACA-3' (SEQ ID NO: 4622)
3'-AACCCCUUAAAGGAGAUAACUACAUGU-5' (SEQ ID NO: 269)

AR-3997 Target: 5'-TTGGGGAATTTCCTCTATTGATGTACA-3' (SEQ ID NO: 422)

5'-UGGGGAAUUUCCUCUAUUGAUGUACAG-3' (SEQ ID NO: 4623)
3'-ACCCCUUAAAGGAGAUAACUACAUGUC-5' (SEQ ID NO: 270)

AR-3998 Target: 5'-TGGGGAATTTCCTCTATTGATGTACAG-3' (SEQ ID NO: 423)

5'-GGGGAAUUUCCUCUAUUGAUGUACAGU-3' (SEQ ID NO: 4624)
3'-CCCCUUAAAGGAGAUAACUACAUGUCA-5' (SEQ ID NO: 271)

AR-3999 Target: 5'-GGGGAATTTCCTCTATTGATGTACAGT-3' (SEQ ID NO: 424)

5'-CUAUUGAUGUACAGUCUGUCAUGAACA-3' (SEQ ID NO: 4625)
3'-GAUAACUACAUGUCAGACAGUACUUGU-5' (SEQ ID NO: 272)

AR-4011 Target: 5'-CTATTGATGTACAGTCTGTCATGAACA-3' (SEQ ID NO: 425)

5'-UAUUGAUGUACAGUCUGUCAUGAACAU-3' (SEQ ID NO: 4626)
3'-AUAACUACAUGUCAGACAGUACUUGUA-5' (SEQ ID NO: 273)

AR-4012 Target: 5'-TATTGATGTACAGTCTGTCATGAACAT-3' (SEQ ID NO: 426)

5'-AUUGAUGUACAGUCUGUCAUGAACAUG-3' (SEQ ID NO: 4627)
3'-UAACUACAUGUCAGACAGUACUUGUAC-5' (SEQ ID NO: 274)

AR-4013 Target: 5'-ATTGATGTACAGTCTGTCATGAACATG-3' (SEQ ID NO: 427)

5'-AACAUGUUCCUGAAUUCUAUUUGCUGG-3' (SEQ ID NO: 4628)
3'-UUGUACAAGGACUUAAGAUAAACGACC-5' (SEQ ID NO: 275)

AR-4034 Target: 5'-AACATGTTCCTGAATTCTATTTGCTGG-3' (SEQ ID NO: 428)

5'-UUCUAUUUGCUGGGCUUUUUUUUUCUC-3' (SEQ ID NO: 4629)
3'-AAGAUAAACGACCCGAAAAAAAAAGAG-5' (SEQ ID NO: 276)

AR-4048 Target: 5'-TTCTATTTGCTGGGCTTTTTTTTTCTC-3' (SEQ ID NO: 429)

5'-UCUAUUUGCUGGGCUUUUUUUUUCUCU-3' (SEQ ID NO: 4630)

3'-AGAUAAACGACCCGAAAAAAAAAGAGA-5' (SEQ ID NO: 277)

AR-4049 Target: 5'-TCTATTTGCTGGGCTTTTTTTTCTCT-3' (SEQ ID NO: 430)

5'-UGCUGGGCUUUUUUUUUCUCUUUCUCU-3' (SEQ ID NO: 4631)
3'-ACGACCCGAAAAAAAAAGAGAAAGAGA-5' (SEQ ID NO: 278)

AR-4055 Target: 5'-TGCTGGGCTTTTTTTTCTCTTTCTCT-3' (SEQ ID NO: 431)

5'-UUUUUUUUCUCUUUCUCUCCUUUCUUU-3' (SEQ ID NO: 4632)
3'-AAAAAAAAGAGAAAGAGAGGAAAGAAA-5' (SEQ ID NO: 279)

AR-4064 Target: 5'-TTTTTTTCTCTTTCTCTCCTTTCTTT-3' (SEQ ID NO: 432)

5'-UUCAGACUUUGCUUCCCAUUGUGGCUC-3' (SEQ ID NO: 4633)
3'-AAGUCUGAAACGAAGGGUAACACCGAG-5' (SEQ ID NO: 280)

AR-4128 Target: 5'-TTCAGACTTTGCTTCCCATTGTGGCTC-3' (SEQ ID NO: 433)

5'-UUGUGGCUCCUAUCUGUGUUUUGAAUG-3' (SEQ ID NO: 4634)
3'-AACACCGAGGAUAGACACAAAACUUAC-5' (SEQ ID NO: 281)

AR-4146 Target: 5'-TTGTGGCTCCTATCTGTGTTTTGAATG-3' (SEQ ID NO: 434)

5'-UCCUAUCUGUGUUUUGAAUGGUGUUGU-3' (SEQ ID NO: 4635)
3'-AGGAUAGACACAAAACUUACCACAACA-5' (SEQ ID NO: 282)

AR-4153 Target: 5'-TCCTATCTGTGTTTTGAATGGTGTTGT-3' (SEQ ID NO: 435)

5'-AUCUGUGUUUUGAAUGGUGUUGUAUGC-3' (SEQ ID NO: 4636)
3'-UAGACACAAAACUUACCACAACAUACG-5' (SEQ ID NO: 283)

AR-4157 Target: 5'-ATCTGTGTTTTGAATGGTGTTGTATGC-3' (SEQ ID NO: 436)

5'-UGUGUUUUGAAUGGUGUUGUAUGCCUU-3' (SEQ ID NO: 4637)
3'-ACACAAAACUUACCACAACAUACGGAA-5' (SEQ ID NO: 284)

AR-4160 Target: 5'-TGTGTTTTGAATGGTGTTGTATGCCTT-3' (SEQ ID NO: 437)

5'-UGAAUGGUGUUGUAUGCCUUUAAAUCU-3' (SEQ ID NO: 4638)
3'-ACUUACCACAACAUACGGAAAUUUAGA-5' (SEQ ID NO: 285)

AR-4167 Target: 5'-TGAATGGTGTTGTATGCCTTTAAATCT-3' (SEQ ID NO: 438)

5'-GAAUGGUGUUGUAUGCCUUUAAAUCUG-3' (SEQ ID NO: 4639)
3'-CUUACCACAACAUACGGAAAUUUAGAC-5' (SEQ ID NO: 286)

AR-4168 Target: 5'-GAATGGTGTTGTATGCCTTTAAATCTG-3' (SEQ ID NO: 439)

5'-UGUUGUAUGCCUUUAAAUCUGUGAUGA-3' (SEQ ID NO: 4640)
3'-ACAACAUACGGAAAUUUAGACACUACU-5' (SEQ ID NO: 287)

AR-4174 Target: 5'-TGTTGTATGCCTTTAAATCTGTGATGA-3' (SEQ ID NO: 440)

5'-UUGUAUGCCUUUAAAUCUGUGAUGAUC-3' (SEQ ID NO: 4641)
3'-AACAUACGGAAAUUUAGACACUACUAG-5' (SEQ ID NO: 288)

AR-4176 Target: 5'-TTGTATGCCTTTAAATCTGTGATGATC-3' (SEQ ID NO: 441)

5'-UGUAUGCCUUUAAAUCUGUGAUGAUCC-3' (SEQ ID NO: 4642)
3'-ACAUACGGAAAUUUAGACACUACUAGG-5' (SEQ ID NO: 289)

AR-4177 Target: 5'-TGTATGCCTTTAAATCTGTGATGATCC-3' (SEQ ID NO: 442)

5'-CCCAGUGUCAAGUUGUGCUUGUUUACA-3' (SEQ ID NO: 4643)
3'-GGGUCACAGUUCAACACGAACAAAUGU-5' (SEQ ID NO: 290)

AR-4212 Target: 5'-CCCAGTGTCAAGTTGTGCTTGTTTACA-3' (SEQ ID NO: 443)

5'-CCAGUGUCAAGUUGUGCUUGUUUACAG-3' (SEQ ID NO: 4644)
3'-GGUCACAGUUCAACACGAACAAAUGUC-5' (SEQ ID NO: 291)

AR-4213 Target: 5'-CCAGTGTCAAGTTGTGCTTGTTTACAG-3' (SEQ ID NO: 444)

5'-GCUUGUUUACAGCACUACUCUGUGCCA-3' (SEQ ID NO: 4645)
3'-CGAACAAAUGUCGUGAUGAGACACGGU-5' (SEQ ID NO: 292)

AR-4228 Target: 5'-GCTTGTTTACAGCACTACTCTGTGCCA-3' (SEQ ID NO: 445)

5'-CUUGUUUACAGCACUACUCUGUGCCAG-3' (SEQ ID NO: 4646)
3'-GAACAAAUGUCGUGAUGAGACACGGUC-5' (SEQ ID NO: 293)

AR-4229 Target: 5'-CTTGTTTACAGCACTACTCTGTGCCAG-3' (SEQ ID NO: 446)

5'-CACAAACGUUUACUUAUCUUAUGCCAC-3' (SEQ ID NO: 4647)
3'-GUGUUUGCAAAUGAAUAGAAUACGGUG-5' (SEQ ID NO: 294)

AR-4259 Target: 5'-CACAAACGTTTACTTATCTTATGCCAC-3' (SEQ ID NO: 447)

5'-CACGGGAAGUUUAGAGAGCUAAGAUUA-3' (SEQ ID NO: 4648)
3'-GUGCCCUUCAAAUCUCUCGAUUCUAAU-5' (SEQ ID NO: 295)

AR-4283 Target: 5'-CACGGGAAGTTTAGAGAGCTAAGATTA-3' (SEQ ID NO: 448)

5'-ACGGGAAGUUUAGAGAGCUAAGAUUAU-3' (SEQ ID NO: 4649)
3'-UGCCCUUCAAAUCUCUCGAUUCUAAUA-5' (SEQ ID NO: 296)

AR-4284 Target: 5'-ACGGGAAGTTTAGAGAGCTAAGATTAT-3' (SEQ ID NO: 449)

5'-CGGGAAGUUUAGAGAGCUAAGAUUAUC-3' (SEQ ID NO: 4650)
3'-GCCCUUCAAAUCUCUCGAUUCUAAUAG-5' (SEQ ID NO: 297)

AR-4285 Target: 5'-CGGGAAGTTTAGAGAGCTAAGATTATC-3' (SEQ ID NO: 450)

5'-GGGAAGUUUAGAGAGCUAAGAUUAUCU-3' (SEQ ID NO: 4651)
3'-CCCUUCAAAUCUCUCGAUUCUAAUAGA-5' (SEQ ID NO: 298)

AR-4286 Target: 5'-GGGAAGTTTAGAGAGCTAAGATTATCT-3' (SEQ ID NO: 451)

5'-GAAGUUUAGAGAGCUAAGAUUAUCUGG-3' (SEQ ID NO: 4652)
3'-CUUCAAAUCUCUCGAUUCUAAUAGACC-5' (SEQ ID NO: 299)

AR-4288 Target: 5'-GAAGTTTAGAGAGCTAAGATTATCTGG-3' (SEQ ID NO: 452)

5'-UUAGAGAGCUAAGAUUAUCUGGGGAAA-3' (SEQ ID NO: 4653)
3'-AAUCUCUCGAUUCUAAUAGACCCCUUU-5' (SEQ ID NO: 300)

AR-4293 Target: 5'-TTAGAGAGCTAAGATTATCTGGGGAAA-3' (SEQ ID NO: 453)

5'-UAGAGAGCUAAGAUUAUCUGGGGAAAU-3' (SEQ ID NO: 4654)
3'-AUCUCUCGAUUCUAAUAGACCCCUUUA-5' (SEQ ID NO: 301)

AR-4294 Target: 5'-TAGAGAGCTAAGATTATCTGGGGAAAT-3' (SEQ ID NO: 454)

5'-AGAGAGCUAAGAUUAUCUGGGGAAAUC-3' (SEQ ID NO: 4655)
3'-UCUCUCGAUUCUAAUAGACCCCUUUAG-5' (SEQ ID NO: 302)

AR-4295 Target: 5'-AGAGAGCTAAGATTATCTGGGGAAATC-3' (SEQ ID NO: 455)

5'-UAAGAUUAUCUGGGGAAAUCAAAACAA-3' (SEQ ID NO: 4656)
3'-AUUCUAAUAGACCCCUUUAGUUUUGUU-5' (SEQ ID NO: 303)

AR-4302 Target: 5'-TAAGATTATCTGGGGAAATCAAAACAA-3' (SEQ ID NO: 456)

5'-AAGAUUAUCUGGGGAAAUCAAAACAAA-3' (SEQ ID NO: 4657)

3'-UUCUAAUAGACCCCUUUAGUUUUGUUU-5' (SEQ ID NO: 304)

AR-4303 Target: 5'-AAGATTATCTGGGGAAATCAAAACAAA-3' (SEQ ID NO: 457)

5'-AUCUGGGGAAAUCAAAACAAAAACAAG-3' (SEQ ID NO: 4658)
3'-UAGACCCCUUUAGUUUUGUUUUUGUUC-5' (SEQ ID NO: 305)

AR-4309 Target: 5'-ATCTGGGGAAATCAAAACAAAAACAAG-3' (SEQ ID NO: 458)

5'-GGGGAAAUCAAAACAAAAACAAGCAAA-3' (SEQ ID NO: 4659)
3'-CCCCUUUAGUUUUGUUUUUGUUCGUUU-5' (SEQ ID NO: 306)

AR-4313 Target: 5'-GGGGAAATCAAAACAAAAACAAGCAAA-3' (SEQ ID NO: 459)

5'-GUGAAGUUUUUAAAAGCUGCUAAAGAC-3' (SEQ ID NO: 4660)
3'-CACUUCAAAAAUUUUCGACGAUUUCUG-5' (SEQ ID NO: 796)

AR-251 Target: 5'-GTGAAGTTTTTAAAAGCTGCTAAAGAC-3' (SEQ ID NO: 826)

5'-AGCUAGCUGCACAUUGCAAAGAAGGCU-3' (SEQ ID NO: 4661)
3'-UCGAUCGACGUGUAACGUUUCUUCCGA-5' (SEQ ID NO: 797)

AR-524 Target: 5'-AGCTAGCTGCACATTGCAAAGAAGGCT-3' (SEQ ID NO: 827)

5'-ACAUUGCAAAGAAGGCUCUUAGGAGCC-3' (SEQ ID NO: 4662)
3'-UGUAACGUUUCUUCCGAGAAUCCUCGG-5' (SEQ ID NO: 798)

AR-534 Target: 5'-ACATTGCAAAGAAGGCTCTTAGGAGCC-3' (SEQ ID NO: 828)

5'-AACAAAACAAACAAAAACAAAAAAGCC-3' (SEQ ID NO: 4663)
3'-UUGUUUUGUUUGUUUUUGUUUUUUCGG-5' (SEQ ID NO: 799)

AR-736 Target: 5'-AACAAAACAAACAAAAACAAAAAAGCC-3' (SEQ ID NO: 829)

5'-AAGAUAAUAACUCAGUUCUUAUUUGCA-3' (SEQ ID NO: 4664)
3'-UUCUAUUAUUGAGUCAAGAAUAAACGU-5' (SEQ ID NO: 800)

AR-776 Target: 5'-AAGATAATAACTCAGTTCTTATTTGCA-3' (SEQ ID NO: 830)

5'-UUCAGUGGACACUGAAUUUGGAAGGUG-3' (SEQ ID NO: 4665)
3'-AAGUCACCUGUGACUUAAACCUUCCAC-5' (SEQ ID NO: 801)

AR-808 Target: 5'-TTCAGTGGACACTGAATTTGGAAGGTG-3' (SEQ ID NO: 831)

5'-CAGUGGACACUGAAUUUGGAAGGUGGA-3' (SEQ ID NO: 4666)
3'-GUCACCUGUGACUUAAACCUUCCACCU-5' (SEQ ID NO: 802)

AR-810 Target: 5'-CAGTGGACACTGAATTTGGAAGGTGGA-3' (SEQ ID NO: 832)

5'-AGUGGACACUGAAUUUGGAAGGUGGAG-3' (SEQ ID NO: 4667)
3'-UCACCUGUGACUUAAACCUUCCACCUC-5' (SEQ ID NO: 803)

AR-811 Target: 5'-AGTGGACACTGAATTTGGAAGGTGGAG-3' (SEQ ID NO: 833)

5'-UUGAAUCUACCCUUCAAGUAUUAAGAG-3' (SEQ ID NO: 4668)
3'-AACUUAGAUGGGAAGUUCAUAAUUCUC-5' (SEQ ID NO: 804)

AR-873 Target: 5'-TTGAATCTACCCTTCAAGTATTAAGAG-3' (SEQ ID NO: 834)

5'-CAAGUAUUAAGAGACAGACUGUGAGCC-3' (SEQ ID NO: 4669)
3'-GUUCAUAAUUCUCUGUCUGACACUCGG-5' (SEQ ID NO: 805)

AR-887 Target: 5'-CAAGTATTAAGAGACAGACTGTGAGCC-3' (SEQ ID NO: 835)

5'-GCUGAGUAUUCCCCUUUCAAGGGAGGU-3' (SEQ ID NO: 4670)
3'-CGACUCAUAAGGGGAAAGUUCCCUCCA-5' (SEQ ID NO: 806)

AR-2060 Target: 5'-GCTGAGTATTCCCCTTTCAAGGGAGGT-3' (SEQ ID NO: 836)

5'-CUGAGUAUUCCCCUUUCAAGGGAGGUU-3' (SEQ ID NO: 4671)
3'-GACUCAUAAGGGGAAAGUUCCCUCCAA-5' (SEQ ID NO: 807)

AR-2061 Target: 5'-CTGAGTATTCCCCTTTCAAGGGAGGTT-3' (SEQ ID NO: 837)

5'-UCUGUGGAGAUGAAGCUUCUGGGUGUC-3' (SEQ ID NO: 4672)
3'-AGACACCUCUACUUCGAAGACCCACAG-5' (SEQ ID NO: 808)

AR-2826 Target: 5'-TCTGTGGAGATGAAGCTTCTGGGTGTC-3' (SEQ ID NO: 838)

5'-GAAGGGAAACAGAAGUACCUGUGCGCC-3' (SEQ ID NO: 4673)
3'-CUUCCCUUUGUCUUCAUGGACACGCGG-5' (SEQ ID NO: 809)

AR-2906 Target: 5'-GAAGGGAAACAGAAGTACCTGTGCGCC-3' (SEQ ID NO: 839)

5'-UUGAUAAAUUCCGAAGGAAAAAUUGUC-3' (SEQ ID NO: 4674)
3'-AACUAUUUAAGGCUUCCUUUUUAACAG-5' (SEQ ID NO: 810)

AR-2952 Target: 5'-TTGATAAATTCCGAAGGAAAAATTGTC-3' (SEQ ID NO: 840)

5'-GAAGGAAAAAUUGUCCAUCUUGUCGUC-3' (SEQ ID NO: 4675)
3'-CUUCCUUUUUAACAGGUAGAACAGCAG-5' (SEQ ID NO: 811)

AR-2964 Target: 5'-GAAGGAAAAATTGTCCATCTTGTCGTC-3' (SEQ ID NO: 841)

5'-UCGGAAAUGUUAUGAAGCAGGGAUGAC-3' (SEQ ID NO: 4676)
3'-AGCCUUUACAAUACUUCGUCCCUACUG-5' (SEQ ID NO: 812)

AR-2992 Target: 5'-TCGGAAATGTTATGAAGCAGGGATGAC-3' (SEQ ID NO: 842)

5'-ACUUGGUAAUCUGAAACUACAGGAGGA-3' (SEQ ID NO: 4677)
3'-UGAACCAUUAGACUUUGAUGUCCUCCU-5' (SEQ ID NO: 813)

AR-3043 Target: 5'-ACTTGGTAATCTGAAACTACAGGAGGA-3' (SEQ ID NO: 843)

5'-CUUGGUAAUCUGAAACUACAGGAGGAA-3' (SEQ ID NO: 4678)
3'-GAACCAUUAGACUUUGAUGUCCUCCUU-5' (SEQ ID NO: 814)

AR-3044 Target: 5'-CTTGGTAATCTGAAACTACAGGAGGAA-3' (SEQ ID NO: 844)

5'-GGUAAUCUGAAACUACAGGAGGAAGGA-3' (SEQ ID NO: 4679)
3'-CCAUUAGACUUUGAUGUCCUCCUUCCU-5' (SEQ ID NO: 815)

AR-3047 Target: 5'-GGTAATCTGAAACTACAGGAGGAAGGA-3' (SEQ ID NO: 845)

5'-AGCUGACAGUGUCACACAUUGAAGGCU-3' (SEQ ID NO: 4680)
3'-UCGACUGUCACAGUGUGUAACUUCCGA-5' (SEQ ID NO: 816)

AR-3117 Target: 5'-AGCTGACAGTGTCACACATTGAAGGCT-3' (SEQ ID NO: 846)

5'-GGCUGUCAUUCAGUACUCCUGGAUGGG-3' (SEQ ID NO: 4681)
3'-CCGACAGUAAGUCAUGAGGACCUACCC-5' (SEQ ID NO: 817)

AR-3346 Target: 5'-GGCTGTCATTCAGTACTCCTGGATGGG-3' (SEQ ID NO: 847)

5'-CUGAAAAAUCAAAAAUUCUUUGAUGAA-3' (SEQ ID NO: 4682)
3'-GACUUUUUAGUUUUUAAGAAACUACUU-5' (SEQ ID NO: 818)

AR-3605 Target: 5'-CTGAAAAATCAAAAATTCTTTGATGAA-3' (SEQ ID NO: 848)

5'-AAAAUUCUUUGAUGAACUUCGAAUGAA-3' (SEQ ID NO: 4683)
3'-UUUUAAGAAACUACUUGAAGCUUACUU-5' (SEQ ID NO: 819)

AR-3616 Target: 5'-AAAATTCTTTGATGAACTTCGAATGAA-3' (SEQ ID NO: 849)

5'-UGCUAAUCAAGUCACACAUGGUGAGCG-3' (SEQ ID NO: 4684)

3'-ACGAUUAGUUCAGUGUGUACCACUCGC-5' (SEQ ID NO: 820)

AR-3783 Target: 5'-TGCTAATCAAGTCACACATGGTGAGCG-3' (SEQ ID NO: 850)

5'-AGCGUGGACUUUCCGGAAAUGAUGGCA-3' (SEQ ID NO: 4685)
3'-UCGCACCUGAAAGGCCUUUACUACCGU-5' (SEQ ID NO: 821)

AR-3806 Target: 5'-AGCGTGGACTTTCCGGAAATGATGGCA-3' (SEQ ID NO: 851)

5'-CCUUGGGGAAUUUCCUCUAUUGAUGUA-3' (SEQ ID NO: 4686)
3'-GGAACCCCUUAAAGGAGAUAACUACAU-5' (SEQ ID NO: 822)

AR-3995 Target: 5'-CCTTGGGGAATTTCCTCTATTGATGTA-3' (SEQ ID NO: 852)

5'-UCUGUGUUUUGAAUGGUGUUGUAUGCC-3' (SEQ ID NO: 4687)
3'-AGACACAAAACUUACCACAACAUACGG-5' (SEQ ID NO: 823)

AR-4158 Target: 5'-TCTGTGTTTTGAATGGTGTTGTATGCC-3' (SEQ ID NO: 853)

5'-GUUGUAUGCCUUUAAAUCUGUGAUGAU-3' (SEQ ID NO: 4688)
3'-CAACAUACGGAAAUUUAGACACUACUA-5' (SEQ ID NO: 824)

AR-4175 Target: 5'-GTTGTATGCCTTTAAATCTGTGATGAT-3' (SEQ ID NO: 854)

5'-UUUAGAGAGCUAAGAUUAUCUGGGGAA-3' (SEQ ID NO: 4689)
3'-AAAUCUCUCGAUUCUAAUAGACCCCUU-5' (SEQ ID NO: 825)

AR-4292 Target: 5'-TTTAGAGAGCTAAGATTATCTGGGGAA-3' (SEQ ID NO: 855)

5'-UCGGUGAAGUUUUUAAAAGCUGCUAAA-3' (SEQ ID NO: 4690)
3'-AGCCACUUCAAAAAUUUUCGACGAUUU-5' (SEQ ID NO: 970)

AR-248 Target: 5'-TCGGTGAAGTTTTTAAAAGCTGCTAAA-3' (SEQ ID NO: 1024)

5'-AGUUUUUAAAAGCUGCUAAAGACUCGG-3' (SEQ ID NO: 4691)
3'-UCAAAAAUUUUCGACGAUUUCUGAGCC-5' (SEQ ID NO: 971)

AR-255 Target: 5'-AGTTTTTAAAAGCTGCTAAAGACTCGG-3' (SEQ ID NO: 1025)

5'-GCAGAGAGGUAACUCCCUUUGGCUGCG-3' (SEQ ID NO: 4692)
3'-CGUCUCUCCAUUGAGGGAAACCGACGC-5' (SEQ ID NO: 972)

AR-489 Target: 5'-GCAGAGAGGTAACTCCCTTTGGCTGCG-3' (SEQ ID NO: 1026)

5'-CAGAGAUCAAAAGAUGAAAAGGCAGUC-3' (SEQ ID NO: 4693)
3'-GUCUCUAGUUUUCUACUUUUCCGUCAG-5' (SEQ ID NO: 973)

AR-690 Target: 5'-CAGAGATCAAAAGATGAAAAGGCAGTC-3' (SEQ ID NO: 1027)

5'-CAAAAAACAAAACAAACAAAAACAAAA-3' (SEQ ID NO: 4694)
3'-GUUUUUUGUUUUGUUUGUUUUUGUUUU-5' (SEQ ID NO: 974)

AR-731 Target: 5'-CAAAAAACAAAACAAACAAAAACAAAA-3' (SEQ ID NO: 1028)

5'-AAAUAAAAGAAAAAGAUAAUAACUCAG-3' (SEQ ID NO: 4695)
3'-UUUAUUUUCUUUUUCUAUUAUUGAGUC-5' (SEQ ID NO: 975)

AR-764 Target: 5'-AAATAAAAGAAAAAGATAATAACTCAG-3' (SEQ ID NO: 1029)

5'-AGAAAAAGAUAAUAACUCAGUUCUUAU-3' (SEQ ID NO: 4696)
3'-UCUUUUUCUAUUAUUGAGUCAAGAAUA-5' (SEQ ID NO: 976)

AR-771 Target: 5'-AGAAAAAGATAATAACTCAGTTCTTAT-3' (SEQ ID NO: 1030)

5'-AUAAUAACUCAGUUCUUAUUUGCACCU-3' (SEQ ID NO: 4697)
3'-UAUUAUUGAGUCAAGAAUAAACGUGGA-5' (SEQ ID NO: 977)

AR-779 Target: 5'-ATAATAACTCAGTTCTTATTTGCACCT-3' (SEQ ID NO: 1031)

5'-AGGUGGAGGAUUUUGUUUUUUUCUUUU-3' (SEQ ID NO: 4698)
3'-UCCACCUCCUAAAACAAAAAAAGAAAA-5' (SEQ ID NO: 978)

AR-830 Target: 5'-AGGTGGAGGATTTTGTTTTTTTCTTTT-3' (SEQ ID NO: 1032)

5'-UUUUGUUUUUUUCUUUUAAGAUCUGGG-3' (SEQ ID NO: 4699)
3'-AAAACAAAAAAAGAAAAUUCUAGACCC-5' (SEQ ID NO: 979)

AR-840 Target: 5'-TTTTGTTTTTTTCTTTTAAGATCTGGG-3' (SEQ ID NO: 1033)

5'-UUUUUUUCUUUUAAGAUCUGGGCAUCU-3' (SEQ ID NO: 4700)
3'-AAAAAAAGAAAAUUCUAGACCCGUAGA-5' (SEQ ID NO: 980)

AR-845 Target: 5'-TTTTTTTCTTTTAAGATCTGGGCATCT-3' (SEQ ID NO: 1034)

5'-AUCUGGGCAUCUUUUGAAUCUACCCUU-3' (SEQ ID NO: 4701)
3'-UAGACCCGUAGAAAACUUAGAUGGGAA-5' (SEQ ID NO: 981)

AR-860 Target: 5'-ATCTGGGCATCTTTTGAATCTACCCTT-3' (SEQ ID NO: 1035)

5'-UAAGGGAAGUAGGUGGAAGAUUCAGCC-3' (SEQ ID NO: 4702)
3'-AUUCCCUUCAUCCACCUUCUAAGUCGG-5' (SEQ ID NO: 982)

AR-1105 Target: 5'-TAAGGGAAGTAGGTGGAAGATTCAGCC-3' (SEQ ID NO: 1036)

5'-GAGGAGCUUUCCAGAAUCUGUUCCAGA-3' (SEQ ID NO: 4703)
3'-CUCCUCGAAAGGUCUUAGACAAGGUCU-5' (SEQ ID NO: 983)

AR-1200 Target: 5'-GAGGAGCTTTCCAGAATCTGTTCCAGA-3' (SEQ ID NO: 1037)

5'-AGCAGGAAGCAGUAUCCGAAGGCAGCA-3' (SEQ ID NO: 4704)
3'-UCGUCCUUCGUCAUAGGCUUCCGUCGU-5' (SEQ ID NO: 984)

AR-1734 Target: 5'-AGCAGGAAGCAGTATCCGAAGGCAGCA-3' (SEQ ID NO: 1038)

5'-CCAAGGACAAUUACUUAGGGGGCACUU-3' (SEQ ID NO: 4705)
3'-GGUUCCUGUUAAUGAAUCCCCCGUGAA-5' (SEQ ID NO: 985)

AR-1803 Target: 5'-CCAAGGACAATTACTTAGGGGGCACTT-3' (SEQ ID NO: 1039)

5'-AAGGAGUUGUGUAAGGCAGUGUCGGUG-3' (SEQ ID NO: 4706)
3'-UUCCUCAACACAUUCCGUCACAGCCAC-5' (SEQ ID NO: 986)

AR-1850 Target: 5'-AAGGAGTTGTGTAAGGCAGTGTCGGTG-3' (SEQ ID NO: 1040)

5'-GGCAAGAGCACUGAAGAUACUGCUGAG-3' (SEQ ID NO: 4707)
3'-CCGUUCUCGUGACUUCUAUGACGACUC-5' (SEQ ID NO: 987)

AR-2039 Target: 5'-GGCAAGAGCACTGAAGATACTGCTGAG-3' (SEQ ID NO: 1041)

5'-ACUGAAGAUACUGCUGAGUAUUCCCCU-3' (SEQ ID NO: 4708)
3'-UGACUUCUAUGACGACUCAUAAGGGGA-5' (SEQ ID NO: 988)

AR-2048 Target: 5'-ACTGAAGATACTGCTGAGTATTCCCCT-3' (SEQ ID NO: 1042)

5'-CAAGGGAGGUUACACCAAAGGGCUAGA-3' (SEQ ID NO: 4709)
3'-GUUCCCUCCAAUGUGGUUUCCCGAUCU-5' (SEQ ID NO: 989)

AR-2077 Target: 5'-CAAGGGAGGTTACACCAAAGGGCTAGA-3' (SEQ ID NO: 1043)

5'-CUUGUGUCAAAAGCGAAAUGGGCCCCU-3' (SEQ ID NO: 4710)
3'-GAACACAGUUUUCGCUUUACCCGGGGA-5' (SEQ ID NO: 990)

AR-2694 Target: 5'-CTTGTGTCAAAAGCGAAATGGGCCCCT-3' (SEQ ID NO: 1044)

5'-AUGUUUUGCCCAUUGACUAUUACUUUC-3' (SEQ ID NO: 4711)

3'-UACAAAACGGGUAACUGAUAAUGAAAG-5' (SEQ ID NO: 991)

AR-2778 Target: 5'-ATGTTTTGCCCATTGACTATTACTTTC-3' (SEQ ID NO: 1045)

5'-UGCAAGGUCUUCUUCAAAAGAGCCGCU-3' (SEQ ID NO: 4712)
3'-ACGUUCCAGAAGAAGUUUUCUCGGCGA-5' (SEQ ID NO: 992)

AR-2879 Target: 5'-TGCAAGGTCTTCTTCAAAAGAGCCGCT-3' (SEQ ID NO: 1046)

5'-AAGGGAAACAGAAGUACCUGUGCGCCA-3' (SEQ ID NO: 4713)
3'-UUCCCUUUGUCUUCAUGGACACGCGGU-5' (SEQ ID NO: 993)

AR-2907 Target: 5'-AAGGGAAACAGAAGTACCTGTGCGCCA-3' (SEQ ID NO: 1047)

5'-AUGAUUGCACUAUUGAUAAAUUCCGAA-3' (SEQ ID NO: 4714)
3'-UACUAACGUGAUAACUAUUUAAGGCUU-5' (SEQ ID NO: 994)

AR-2940 Target: 5'-ATGATTGCACTATTGATAAATTCCGAA-3' (SEQ ID NO: 1048)

5'-UAAAUUCCGAAGGAAAAAUUGUCCAUC-3' (SEQ ID NO: 4715)
3'-AUUUAAGGCUUCCUUUUUAACAGGUAG-5' (SEQ ID NO: 995)

AR-2956 Target: 5'-TAAATTCCGAAGGAAAAATTGTCCATC-3' (SEQ ID NO: 1049)

5'-AAGGAAAAAUUGUCCAUCUUGUCGUCU-3' (SEQ ID NO: 4716)
3'-UUCCUUUUUAACAGGUAGAACAGCAGA-5' (SEQ ID NO: 996)

AR-2965 Target: 5'-AAGGAAAAATTGTCCATCTTGTCGTCT-3' (SEQ ID NO: 1050)

5'-GAAAAAUUGUCCAUCUUGUCGUCUUCG-3' (SEQ ID NO: 4717)
3'-CUUUUUAACAGGUAGAACAGCAGAAGC-5' (SEQ ID NO: 997)

AR-2968 Target: 5'-GAAAAATTGTCCATCTTGTCGTCTTCG-3' (SEQ ID NO: 1051)

5'-GAAGAAACUUGGUAAUCUGAAACUACA-3' (SEQ ID NO: 4718)
3'-CUUCUUUGAACCAUUAGACUUUGAUGU-5' (SEQ ID NO: 998)

AR-3037 Target: 5'-GAAGAAACTTGGTAATCTGAAACTACA-3' (SEQ ID NO: 1052)

5'-CAUUGAAGGCUAUGAAUGUCAGCCCAU-3' (SEQ ID NO: 4719)
3'-GUAACUUCCGAUACUUACAGUCGGGUA-5' (SEQ ID NO: 999)

AR-3133 Target: 5'-CATTGAAGGCTATGAATGTCAGCCCAT-3' (SEQ ID NO: 1053)

5'-CAGGAAUUCCUGUGCAUGAAAGCACUG-3' (SEQ ID NO: 4720)
3'-GUCCUUAAGGACACGUACUUUCGUGAC-5' (SEQ ID NO: 1000)

AR-3548 Target: 5'-CAGGAATTCCTGTGCATGAAAGCACTG-3' (SEQ ID NO: 1054)

5'-UCAAAAAUUCUUUGAUGAACUUCGAAU-3' (SEQ ID NO: 4721)
3'-AGUUUUUAAGAAACUACUUGAAGCUUA-5' (SEQ ID NO: 1001)

AR-3613 Target: 5'-TCAAAAATTCTTTGATGAACTTCGAAT-3' (SEQ ID NO: 1055)

5'-UCUUUGAUGAACUUCGAAUGAACUACA-3' (SEQ ID NO: 4722)
3'-AGAAACUACUUGAAGCUUACUUGAUGU-5' (SEQ ID NO: 1002)

AR-3621 Target: 5'-TCTTTGATGAACTTCGAATGAACTACA-3' (SEQ ID NO: 1056)

5'-UUGAUGAACUUCGAAUGAACUACAUCA-3' (SEQ ID NO: 4723)
3'-AACUACUUGAAGCUUACUUGAUGUAGU-5' (SEQ ID NO: 1003)

AR-3624 Target: 5'-TTGATGAACTTCGAATGAACTACATCA-3' (SEQ ID NO: 1057)

5'-UCGAAUGAACUACAUCAAGGAACUCGA-3' (SEQ ID NO: 4724)
3'-AGCUUACUUGAUGUAGUUCCUUGAGCU-5' (SEQ ID NO: 1004)

AR-3634 Target: 5'-TCGAATGAACTACATCAAGGAACTCGA-3' (SEQ ID NO: 1058)

5'-UGCAAAAGAAAAAAUCCCACAUCCUGC-3' (SEQ ID NO: 4725)
3'-ACGUUUUCUUUUUUAGGGUGUAGGACG-5' (SEQ ID NO: 1005)

AR-3674 Target: 5'-TGCAAAAGAAAAAATCCCACATCCTGC-3' (SEQ ID NO: 1059)

5'-AAAGAAAAAAUCCCACAUCCUGCUCAA-3' (SEQ ID NO: 4726)
3'-UUUCUUUUUUAGGGUGUAGGACGAGUU-5' (SEQ ID NO: 1006)

AR-3678 Target: 5'-AAAGAAAAAATCCCACATCCTGCTCAA-3' (SEQ ID NO: 1060)

5'-ACUUUUGACCUGCUAAUCAAGUCACAC-3' (SEQ ID NO: 4727)
3'-UGAAAACUGGACGAUUAGUUCAGUGUG-5' (SEQ ID NO: 1007)

AR-3773 Target: 5'-ACTTTTGACCTGCTAATCAAGTCACAC-3' (SEQ ID NO: 1061)

5'-CCAAGAUCCUUUCUGGGAAAGUCAAGC-3' (SEQ ID NO: 4728)
3'-GGUUCUAGGAAAGACCCUUUCAGUUCG-5' (SEQ ID NO: 1008)

AR-3855 Target: 5'-CCAAGATCCTTTCTGGGAAAGTCAAGC-3' (SEQ ID NO: 1062)

5'-GGAAAGUCAAGCCCAUCUAUUUCCACA-3' (SEQ ID NO: 4729)
3'-CCUUUCAGUUCGGGUAGAUAAAGGUGU-5' (SEQ ID NO: 1009)

AR-3870 Target: 5'-GGAAAGTCAAGCCCATCTATTTCCACA-3' (SEQ ID NO: 1063)

5'-AGAUGUCUUCUGCCUGUUAUAACUCUG-3' (SEQ ID NO: 4730)
3'-UCUACAGAAGACGGACAAUAUUGAGAC-5' (SEQ ID NO: 1010)

AR-3950 Target: 5'-AGATGTCTTCTGCCTGTTATAACTCTG-3' (SEQ ID NO: 1064)

5'-GGGAAUUUCCUCUAUUGAUGUACAGUC-3' (SEQ ID NO: 4731)
3'-CCCUUAAAGGAGAUAACUACAUGUCAG-5' (SEQ ID NO: 1011)

AR-4000 Target: 5'-GGGAATTTCCTCTATTGATGTACAGTC-3' (SEQ ID NO: 1065)

5'-UUGAUGUACAGUCUGUCAUGAACAUGU-3' (SEQ ID NO: 4732)
3'-AACUACAUGUCAGACAGUACUUGUACA-5' (SEQ ID NO: 1012)

AR-4014 Target: 5'-TTGATGTACAGTCTGTCATGAACATGT-3' (SEQ ID NO: 1066)

5'-UACAGUCUGUCAUGAACAUGUUCCUGA-3' (SEQ ID NO: 4733)
3'-AUGUCAGACAGUACUUGUACAAGGACU-5' (SEQ ID NO: 1013)

AR-4020 Target: 5'-TACAGTCTGTCATGAACATGTTCCTGA-3' (SEQ ID NO: 1067)

5'-GUCAUGAACAUGUUCCUGAAUUCUAUU-3' (SEQ ID NO: 4734)
3'-CAGUACUUGUACAAGGACUUAAGAUAA-5' (SEQ ID NO: 1014)

AR-4028 Target: 5'-GTCATGAACATGTTCCTGAATTCTATT-3' (SEQ ID NO: 1068)

5'-ACAUGUUCCUGAAUUCUAUUUGCUGGG-3' (SEQ ID NO: 4735)
3'-UGUACAAGGACUUAAGAUAAACGACCC-5' (SEQ ID NO: 1015)

AR-4035 Target: 5'-ACATGTTCCTGAATTCTATTTGCTGGG-3' (SEQ ID NO: 1069)

5'-GCUGGGCUUUUUUUUUCUCUUUCUCUC-3' (SEQ ID NO: 4736)
3'-CGACCCGAAAAAAAAAGAGAAAGAGAG-5' (SEQ ID NO: 1016)

AR-4056 Target: 5'-GCTGGGCTTTTTTTTCTCTTTCTCTC-3' (SEQ ID NO: 1070)

5'-UUUUUUUCUCUUUCUCUCCUUUCUUUU-3' (SEQ ID NO: 4737)
3'-AAAAAAAGAGAAAGAGAGGAAAGAAAA-5' (SEQ ID NO: 1017)

AR-4065 Target: 5'-TTTTTTTCTCTTTCTCTCCTTTCTTTT-3' (SEQ ID NO: 1071)

5'-GUGUUUUGAAUGGUGUUGUAUGCCUUU-3' (SEQ ID NO: 4738)

3'-CACAAAACUUACCACAACAUACGGAAA-5' (SEQ ID NO: 1018)

AR-4161 Target: 5'-GTGTTTTGAATGGTGTTGTATGCCTTT-3' (SEQ ID NO: 1072)

5'-AUGGUGUUGUAUGCCUUUAAAUCUGUG-3' (SEQ ID NO: 4739)
3'-UACCACAACAUACGGAAAUUUAGACAC-5' (SEQ ID NO: 1019)

AR-4170 Target: 5'-ATGGTGTTGTATGCCTTTAAATCTGTG-3' (SEQ ID NO: 1073)

5'-GUCAAGUUGUGCUUGUUUACAGCACUA-3' (SEQ ID NO: 4740)
3'-CAGUUCAACACGAACAAAUGUCGUGAU-5' (SEQ ID NO: 1020)

AR-4218 Target: 5'-GTCAAGTTGTGCTTGTTTACAGCACTA-3' (SEQ ID NO: 1074)

5'-AGCUAAGAUUAUCUGGGGAAAUCAAAA-3' (SEQ ID NO: 4741)
3'-UCGAUUCUAAUAGACCCCUUUAGUUUU-5' (SEQ ID NO: 1021)

AR-4299 Target: 5'-AGCTAAGATTATCTGGGGAAATCAAAA-3' (SEQ ID NO: 1075)

5'-UCUGGGGAAAUCAAAACAAAAACAAGC-3' (SEQ ID NO: 4742)
3'-AGACCCCUUUAGUUUUGUUUUUGUUCG-5' (SEQ ID NO: 1022)

AR-4310 Target: 5'-TCTGGGGAAATCAAAACAAAAACAAGC-3' (SEQ ID NO: 1076)

5'-GGGAAAUCAAAACAAAAACAAGCAAAC-3' (SEQ ID NO: 4743)
3'-CCCUUUAGUUUUGUUUUUGUUCGUUUG-5' (SEQ ID NO: 1023)

AR-4314 Target: 5'-GGGAAATCAAAACAAAAACAAGCAAAC-3' (SEQ ID NO: 1077)

5'-CGGUGAAGUUUUUAAAAGCUGCUAAAG-3' (SEQ ID NO: 4744)
3'-GCCACUUCAAAAAUUUUCGACGAUUUC-5' (SEQ ID NO: 1249)

AR-249 Target: 5'-CGGTGAAGTTTTTAAAAGCTGCTAAAG-3' (SEQ ID NO: 1312)

5'-GUUUUUAAAAGCUGCUAAAGACUCGGA-3' (SEQ ID NO: 4745)
3'-CAAAAAUUUUCGACGAUUUCUGAGCCU-5' (SEQ ID NO: 1250)

AR-256 Target: 5'-GTTTTTAAAAGCTGCTAAAGACTCGGA-3' (SEQ ID NO: 1313)

5'-UUUUAAAAGCUGCUAAAGACUCGGAGG-3' (SEQ ID NO: 4746)
3'-AAAAUUUUCGACGAUUUCUGAGCCUCC-5' (SEQ ID NO: 1251)

AR-258 Target: 5'-TTTTAAAAGCTGCTAAAGACTCGGAGG-3' (SEQ ID NO: 1314)

5'-GCGGAGAGAACCCUCUGUUUUCCCCCA-3' (SEQ ID NO: 4747)
3'-CGCCUCUCUUGGGAGACAAAAGGGGGU-5' (SEQ ID NO: 1252)

AR-618 Target: 5'-GCGGAGAGAACCCTCTGTTTTCCCCCA-3' (SEQ ID NO: 1315)

5'-AGAGAUCAAAAGAUGAAAAGGCAGUCA-3' (SEQ ID NO: 4748)
3'-UCUCUAGUUUUCUACUUUUCCGUCAGU-5' (SEQ ID NO: 1253)

AR-691 Target: 5'-AGAGATCAAAAGATGAAAAGGCAGTCA-3' (SEQ ID NO: 1316)

5'-AUCAAAAGAUGAAAAGGCAGUCAGGUC-3' (SEQ ID NO: 4749)
3'-UAGUUUUCUACUUUUCCGUCAGUCCAG-5' (SEQ ID NO: 1254)

AR-695 Target: 5'-ATCAAAAGATGAAAAGGCAGTCAGGTC-3' (SEQ ID NO: 1317)

5'-UUCAGUAGCCAAAAAACAAAACAAACA-3' (SEQ ID NO: 4750)
3'-AAGUCAUCGGUUUUUUGUUUUGUUUGU-5' (SEQ ID NO: 1255)

AR-722 Target: 5'-TTCAGTAGCCAAAAAACAAAACAAACA-3' (SEQ ID NO: 1318)

5'-AAAAAACAAAACAAACAAAAACAAAAA-3' (SEQ ID NO: 4751)
3'-UUUUUUGUUUUGUUUGUUUUUGUUUUU-5' (SEQ ID NO: 1256)

AR-732 Target: 5'-AAAAAACAAAACAAACAAAAACAAAAA-3' (SEQ ID NO: 1319)

5'-AAUAAAAGAAAAAGAUAAUAACUCAGU-3' (SEQ ID NO: 4752)
3'-UUAUUUUCUUUUUCUAUUAUUGAGUCA-5' (SEQ ID NO: 1257)

AR-765 Target: 5'-AATAAAAGAAAAAGATAATAACTCAGT-3' (SEQ ID NO: 1320)

5'-UAAAAGAAAAAGAUAAUAACUCAGUUC-3' (SEQ ID NO: 4753)
3'-AUUUUCUUUUUCUAUUAUUGAGUCAAG-5' (SEQ ID NO: 1258)

AR-767 Target: 5'-TAAAAGAAAAAGATAATAACTCAGTTC-3' (SEQ ID NO: 1321)

5'-GAAAAAGAUAAUAACUCAGUUCUUAUU-3' (SEQ ID NO: 4754)
3'-CUUUUUCUAUUAUUGAGUCAAGAAUAA-5' (SEQ ID NO: 1259)

AR-772 Target: 5'-GAAAAAGATAATAACTCAGTTCTTATT-3' (SEQ ID NO: 1322)

5'-UAAUAACUCAGUUCUUAUUUGCACCUA-3' (SEQ ID NO: 4755)
3'-AUUAUUGAGUCAAGAAUAAACGUGGAU-5' (SEQ ID NO: 1260)

AR-780 Target: 5'-TAATAACTCAGTTCTTATTTGCACCTA-3' (SEQ ID NO: 1323)

5'-CUCAGUUCUUAUUUGCACCUACUUCAG-3' (SEQ ID NO: 4756)
3'-GAGUCAAGAAUAAACGUGGAUGAAGUC-5' (SEQ ID NO: 1261)

AR-786 Target: 5'-CTCAGTTCTTATTTGCACCTACTTCAG-3' (SEQ ID NO: 1324)

5'-GGUGGAGGAUUUUGUUUUUUUCUUUUA-3' (SEQ ID NO: 4757)
3'-CCACCUCCUAAAACAAAAAAAGAAAAU-5' (SEQ ID NO: 1262)

AR-831 Target: 5'-GGTGGAGGATTTTGTTTTTTTCTTTTA-3' (SEQ ID NO: 1325)

5'-UUUGUUUUUUUCUUUUAAGAUCUGGGC-3' (SEQ ID NO: 4758)
3'-AAACAAAAAAAAGAAAAUUCUAGACCCG-5' (SEQ ID NO: 1263)

AR-841 Target: 5'-TTTGTTTTTTTCTTTTAAGATCTGGGC-3' (SEQ ID NO: 1326)

5'-UUUUUUCUUUUAAGAUCUGGGCAUCUU-3' (SEQ ID NO: 4759)
3'-AAAAAAGAAAAUUCUAGACCCGUAGAA-5' (SEQ ID NO: 1264)

AR-846 Target: 5'-TTTTTTCTTTTAAGATCTGGGCATCTT-3' (SEQ ID NO: 1327)

5'-UCUGGGCAUCUUUUGAAUCUACCCUUC-3' (SEQ ID NO: 4760)
3'-AGACCCGUAGAAAACUUAGAUGGGAAG-5' (SEQ ID NO: 1265)

AR-861 Target: 5'-TCTGGGCATCTTTTGAATCTACCCTTC-3' (SEQ ID NO: 1328)

5'-CGCAAGUUUCCUUCUCUGGAGCUUCCC-3' (SEQ ID NO: 4761)
3'-GCGUUCAAAGGAAGAGACCUCGAAGGG-5' (SEQ ID NO: 1266)

AR-997 Target: 5'-CGCAAGTTTCCTTCTCTGGAGCTTCCC-3' (SEQ ID NO: 1329)

5'-AAGGGAAGUAGGUGGAAGAUUCAGCCA-3' (SEQ ID NO: 4762)
3'-UUCCCUUCAUCCACCUUCUAAGUCGGU-5' (SEQ ID NO: 1267)

AR-1106 Target: 5'-AAGGGAAGTAGGTGGAAGATTCAGCCA-3' (SEQ ID NO: 1330)

5'-GGAAGUAGGUGGAAGAUUCAGCCAAGC-3' (SEQ ID NO: 4763)
3'-CCUUCAUCCACCUUCUAAGUCGGUUCG-5' (SEQ ID NO: 1268)

AR-1109 Target: 5'-GGAAGTAGGTGGAAGATTCAGCCAAGC-3' (SEQ ID NO: 1331)

5'-CAAGGACAAUUACUUAGGGGGCACUUC-3' (SEQ ID NO: 4764)
3'-GUUCCUGUUAAUGAAUCCCCCGUGAAG-5' (SEQ ID NO: 1269)

AR-1804 Target: 5'-CAAGGACAATTACTTAGGGGGCACTTC-3' (SEQ ID NO: 1332)

5'-GCCGAAUGCAAAGGUUCUCUGCUAGAC-3' (SEQ ID NO: 4765)

3'-CGGCUUACGUUUCCAAGAGACGAUCUG-5' (SEQ ID NO: 1270)

AR-2003 Target: 5'-GCCGAATGCAAAGGTTCTCTGCTAGAC-3' (SEQ ID NO: 1333)

5'-GCAAGAGCACUGAAGAUACUGCUGAGU-3' (SEQ ID NO: 4766)
3'-CGUUCUCGUGACUUCUAUGACGACUCA-5' (SEQ ID NO: 1271)

AR-2040 Target: 5'-GCAAGAGCACTGAAGATACTGCTGAGT-3' (SEQ ID NO: 1334)

5'-CUGAAGAUACUGCUGAGUAUUCCCCUU-3' (SEQ ID NO: 4767)
3'-GACUUCUAUGACGACUCAUAAGGGGAA-5' (SEQ ID NO: 1272)

AR-2049 Target: 5'-CTGAAGATACTGCTGAGTATTCCCCTT-3' (SEQ ID NO: 1335)

5'-UUGUGUCAAAAGCGAAAUGGGCCCCUG-3' (SEQ ID NO: 4768)
3'-AACACAGUUUUCGCUUUACCCGGGGAC-5' (SEQ ID NO: 1273)

AR-2695 Target: 5'-TTGTGTCAAAAGCGAAATGGGCCCCTG-3' (SEQ ID NO: 1336)

5'-UGUUUUGCCCAUUGACUAUUACUUUCC-3' (SEQ ID NO: 4769)
3'-ACAAAACGGGUAACUGAUAAUGAAAGG-5' (SEQ ID NO: 1274)

AR-2779 Target: 5'-TGTTTTGCCCATTGACTATTACTTTCC-3' (SEQ ID NO: 1337)

5'-CCCAUUGACUAUUACUUUCCACCCCAG-3' (SEQ ID NO: 4770)
3'-GGGUAACUGAUAAUGAAAGGUGGGGUC-5' (SEQ ID NO: 1275)

AR-2786 Target: 5'-CCCATTGACTATTACTTTCCACCCCAG-3' (SEQ ID NO: 1338)

5'-GCAAGGUCUUCUUCAAAAGAGCCGCUG-3' (SEQ ID NO: 4771)
3'-CGUUCCAGAAGAAGUUUUCUCGGCGAC-5' (SEQ ID NO: 1276)

AR-2880 Target: 5'-GCAAGGTCTTCTTCAAAAGAGCCGCTG-3' (SEQ ID NO: 1339)

5'-UGAUUGCACUAUUGAUAAAUUCCGAAG-3' (SEQ ID NO: 4772)
3'-ACUAACGUGAUAACUAUUUAAGGCUUC-5' (SEQ ID NO: 1277)

AR-2941 Target: 5'-TGATTGCACTATTGATAAATTCCGAAG-3' (SEQ ID NO: 1340)

5'-UCCGAAGGAAAAAUUGUCCAUCUUGUC-3' (SEQ ID NO: 4773)
3'-AGGCUUCCUUUUUAACAGGUAGAACAG-5' (SEQ ID NO: 1278)

AR-2961 Target: 5'-TCCGAAGGAAAAATTGTCCATCTTGTC-3' (SEQ ID NO: 1341)

5'-AGGAAAAAUUGUCCAUCUUGUCGUCUU-3' (SEQ ID NO: 4774)
3'-UCCUUUUUAACAGGUAGAACAGCAGAA-5' (SEQ ID NO: 1279)

AR-2966 Target: 5'-AGGAAAAATTGTCCATCTTGTCGTCTT-3' (SEQ ID NO: 1342)

5'-GACAGUGUCACACAUUGAAGGCUAUGA-3' (SEQ ID NO: 4775)
3'-CUGUCACAGUGUGUAACUUCCGAUACU-5' (SEQ ID NO: 1280)

AR-3121 Target: 5'-GACAGTGTCACACATTGAAGGCTATGA-3' (SEQ ID NO: 1343)

5'-AUUGAAGGCUAUGAAUGUCAGCCCAUC-3' (SEQ ID NO: 4776)
3'-UAACUUCCGAUACUUACAGUCGGGUAG-5' (SEQ ID NO: 1281)

AR-3134 Target: 5'-ATTGAAGGCTATGAATGTCAGCCCATC-3' (SEQ ID NO: 1344)

5'-AGAUGGCUGUCAUUCAGUACUCCUGGA-3' (SEQ ID NO: 4777)
3'-UCUACCGACAGUAAGUCAUGAGGACCU-5' (SEQ ID NO: 1282)

AR-3342 Target: 5'-AGATGGCTGTCATTCAGTACTCCTGGA-3' (SEQ ID NO: 1345)

5'-UCUGGUUUUCAAUGAGUACCGCAUGCA-3' (SEQ ID NO: 4778)
3'-AGACCAAAAGUUACUCAUGGCGUACGU-5' (SEQ ID NO: 1283)

AR-3445 Target: 5'-TCTGGTTTTCAATGAGTACCGCATGCA-3' (SEQ ID NO: 1346)

5'-AGGAAUUCCUGUGCAUGAAAGCACUGC-3' (SEQ ID NO: 4779)
3'-UCCUUAAGGACACGUACUUUCGUGACG-5' (SEQ ID NO: 1284)

AR-3549 Target: 5'-AGGAATTCCTGTGCATGAAAGCACTGC-3' (SEQ ID NO: 1347)

5'-CAAAAAUUCUUUGAUGAACUUCGAAUG-3' (SEQ ID NO: 4780)
3'-GUUUUUAAGAAACUACUUGAAGCUUAC-5' (SEQ ID NO: 1285)

AR-3614 Target: 5'-CAAAAATTCTTTGATGAACTTCGAATG-3' (SEQ ID NO: 1348)

5'-CUUUGAUGAACUUCGAAUGAACUACAU-3' (SEQ ID NO: 4781)
3'-GAAACUACUUGAAGCUUACUUGAUGUA-5' (SEQ ID NO: 1286)

AR-3622 Target: 5'-CTTTGATGAACTTCGAATGAACTACAT-3' (SEQ ID NO: 1349)

5'-UGAUGAACUUCGAAUGAACUACAUCAA-3' (SEQ ID NO: 4782)
3'-ACUACUUGAAGCUUACUUGAUGUAGUU-5' (SEQ ID NO: 1287)

AR-3625 Target: 5'-TGATGAACTTCGAATGAACTACATCAA-3' (SEQ ID NO: 1350)

5'-CGAAUGAACUACAUCAAGGAACUCGAU-3' (SEQ ID NO: 4783)
3'-GCUUACUUGAUGUAGUUCCUUGAGCUA-5' (SEQ ID NO: 1288)

AR-3635 Target: 5'-CGAATGAACTACATCAAGGAACTCGAT-3' (SEQ ID NO: 1351)

5'-AAUGAACUACAUCAAGGAACUCGAUCG-3' (SEQ ID NO: 4784)
3'-UUACUUGAUGUAGUUCCUUGAGCUAGC-5' (SEQ ID NO: 1289)

AR-3637 Target: 5'-AATGAACTACATCAAGGAACTCGATCG-3' (SEQ ID NO: 1352)

5'-GCAAAAGAAAAAAUCCCACAUCCUGCU-3' (SEQ ID NO: 4785)
3'-CGUUUUCUUUUUUAGGGUGUAGGACGA-5' (SEQ ID NO: 1290)

AR-3675 Target: 5'-GCAAAAGAAAAAATCCCACATCCTGCT-3' (SEQ ID NO: 1353)

5'-AAGAAAAAAUCCCACAUCCUGCUCAAG-3' (SEQ ID NO: 4786)
3'-UUCUUUUUUAGGGUGUAGGACGAGUUC-5' (SEQ ID NO: 1291)

AR-3679 Target: 5'-AAGAAAAAATCCCACATCCTGCTCAAG-3' (SEQ ID NO: 1354)

5'-CUUUUGACCUGCUAAUCAAGUCACACA-3' (SEQ ID NO: 4787)
3'-GAAAACUGGACGAUUAGUUCAGUGUGU-5' (SEQ ID NO: 1292)

AR-3774 Target: 5'-CTTTTGACCTGCTAATCAAGTCACACA-3' (SEQ ID NO: 1355)

5'-GCCUGUUAUAACUCUGCACUACUCCUC-3' (SEQ ID NO: 4788)
3'-CGGACAAUAUUGAGACGUGAUGAGGAG-5' (SEQ ID NO: 1293)

AR-3961 Target: 5'-GCCTGTTATAACTCTGCACTACTCCTC-3' (SEQ ID NO: 1356)

5'-CUGUUAUAACUCUGCACUACUCCUCUG-3' (SEQ ID NO: 4789)
3'-GACAAUAUUGAGACGUGAUGAGGAGAC-5' (SEQ ID NO: 1294)

AR-3963 Target: 5'-CTGTTATAACTCTGCACTACTCCTCTG-3' (SEQ ID NO: 1357)

5'-GGAAUUUCCUCUAUUGAUGUACAGUCU-3' (SEQ ID NO: 4790)
3'-CCUUAAAGGAGAUAACUACAUGUCAGA-5' (SEQ ID NO: 1295)

AR-4001 Target: 5'-GGAATTTCCTCTATTGATGTACAGTCT-3' (SEQ ID NO: 1358)

5'-CUCUAUUGAUGUACAGUCUGUCAUGAA-3' (SEQ ID NO: 4791)
3'-GAGAUAACUACAUGUCAGACAGUACUU-5' (SEQ ID NO: 1296)

AR-4009 Target: 5'-CTCTATTGATGTACAGTCTGTCATGAA-3' (SEQ ID NO: 1359)

5'-UCAUGAACAUGUUCCUGAAUUCUAUUU-3' (SEQ ID NO: 4792)

3'-AGUACUUGUACAAGGACUUAAGAUAAA-5' (SEQ ID NO: 1297)

AR-4029 Target: 5'-TCATGAACATGTTCCTGAATTCTATTT-3' (SEQ ID NO: 1360)

5'-UCCUGAAUUCUAUUUGCUGGGCUUUUU-3' (SEQ ID NO: 4793)
3'-AGGACUUAAGAUAAACGACCCGAAAAA-5' (SEQ ID NO: 1298)

AR-4041 Target: 5'-TCCTGAATTCTATTTGCTGGGCTTTTT-3' (SEQ ID NO: 1361)

5'-GCUUUUUUUUUCUCUUUCUCUCCUUUC-3' (SEQ ID NO: 4794)
3'-CGAAAAAAAAAGAGAAAGAGAGGAAAG-5' (SEQ ID NO: 1299)

AR-4061 Target: 5'-GCTTTTTTTTTCTCTTTCTCTCCTTTC-3' (SEQ ID NO: 1362)

5'-UUUUUUCUCUUUCUCUCCUUUCUUUUU-3' (SEQ ID NO: 4795)
3'-AAAAAAGAGAAAGAGAGGAAAGAAAAA-5' (SEQ ID NO: 1300)

AR-4066 Target: 5'-TTTTTTCTCTTTCTCTCCTTTCTTTTT-3' (SEQ ID NO: 1363)

5'-CUCUUUCUCUCCUUUCUUUUUCUUCUU-3' (SEQ ID NO: 4796)
3'-GAGAAAGAGAGGAAAGAAAAAGAAGAA-5' (SEQ ID NO: 1301)

AR-4072 Target: 5'-CTCTTTCTCTCCTTTCTTTTTCTTCTT-3' (SEQ ID NO: 1364)

5'-CCAUGGCACCUUCAGACUUUGCUUCCC-3' (SEQ ID NO: 4797)
3'-GGUACCGUGGAAGUCUGAAACGAAGGG-5' (SEQ ID NO: 1302)

AR-4118 Target: 5'-CCATGGCACCTTCAGACTTTGCTTCCC-3' (SEQ ID NO: 1365)

5'-UGUUUUGAAUGGUGUUGUAUGCCUUUA-3' (SEQ ID NO: 4798)
3'-ACAAAACUUACCACAACAUACGGAAAU-5' (SEQ ID NO: 1303)

AR-4162 Target: 5'-TGTTTTGAATGGTGTTGTATGCCTTTA-3' (SEQ ID NO: 1366)

5'-UGGUGUUGUAUGCCUUUAAAUCUGUGA-3' (SEQ ID NO: 4799)
3'-ACCACAACAUACGGAAAUUUAGACACU-5' (SEQ ID NO: 1304)

AR-4171 Target: 5'-TGGTGTTGTATGCCTTTAAATCTGTGA-3' (SEQ ID NO: 1367)

5'-CUUUAAAUCUGUGAUGAUCCUCAUAUG-3' (SEQ ID NO: 4800)
3'-GAAAUUUAGACACUACUAGGAGUAUAC-5' (SEQ ID NO: 1305)

AR-4184 Target: 5'-CTTTAAATCTGTGATGATCCTCATATG-3' (SEQ ID NO: 1368)

5'-UCUGUGAUGAUCCUCAUAUGGCCCAGU-3' (SEQ ID NO: 4801)
3'-AGACACUACUAGGAGUAUACCGGGUCA-5' (SEQ ID NO: 1306)

AR-4191 Target: 5'-TCTGTGATGATCCTCATATGGCCCAGT-3' (SEQ ID NO: 1369)

5'-AAGUUGUGCUUGUUUACAGCACUACUC-3' (SEQ ID NO: 4802)
3'-UUCAACACGAACAAAUGUCGUGAUGAG-5' (SEQ ID NO: 1307)

AR-4221 Target: 5'-AAGTTGTGCTTGTTTACAGCACTACTC-3' (SEQ ID NO: 1370)

5'-ACGUUUACUUAUCUUAUGCCACGGGAA-3' (SEQ ID NO: 4803)
3'-UGCAAAUGAAUAGAAUACGGUGCCCUU-5' (SEQ ID NO: 1308)

AR-4264 Target: 5'-ACGTTTACTTATCTTATGCCACGGGAA-3' (SEQ ID NO: 1371)

5'-AGUUUAGAGAGCUAAGAUUAUCUGGGG-3' (SEQ ID NO: 4804)
3'-UCAAAUCUCUCGAUUCUAAUAGACCCC-5' (SEQ ID NO: 1309)

AR-4290 Target: 5'-AGTTTAGAGAGCTAAGATTATCTGGGG-3' (SEQ ID NO: 1372)

5'-GCUAAGAUUAUCUGGGGAAAUCAAAAC-3' (SEQ ID NO: 4805)
3'-CGAUUCUAAUAGACCCCUUUAGUUUUG-5' (SEQ ID NO: 1310)

AR-4300 Target: 5'-GCTAAGATTATCTGGGGAAATCAAAAC-3' (SEQ ID NO: 1373)

5'-CUGGGGAAAUCAAAACAAAAACAAGCA-3' (SEQ ID NO: 4806)
3'-GACCCCUUUAGUUUUGUUUUUGUUCGU-5' (SEQ ID NO: 1311)

AR-4311 Target: 5'-CTGGGGAAATCAAAACAAAAACAAGCA-3' (SEQ ID NO: 1374)

5'-GAGCCAGCUUGCUGGGAGAGCGGGACG-3' (SEQ ID NO: 4807)
3'-CUCGGUCGAACGACCCUCUCGCCCUGC-5' (SEQ ID NO: 1906)

AR-39 Target: 5'-GAGCCAGCTTGCTGGGAGAGCGGGACG-3' (SEQ ID NO: 2311)

5'-CGGCUCCAGCGACAGCCAACGCCUCUU-3' (SEQ ID NO: 4808)
3'-GCCGAGGUCGCUGUCGGUUGCGGAGAA-5' (SEQ ID NO: 1907)

AR-174 Target: 5'-CGGCTCCAGCGACAGCCAACGCCTCTT-3' (SEQ ID NO: 2312)

5'-CAGCCAACGCCUCUUGCAGCGCGGCGG-3' (SEQ ID NO: 4809)
3'-GUCGGUUGCGGAGAACGUCGCGCCGCC-5' (SEQ ID NO: 1908)

AR-186 Target: 5'-CAGCCAACGCCTCTTGCAGCGCGGCGG-3' (SEQ ID NO: 2313)

5'-GCCUCUUGCAGCGCGGCGGCUUCGAAG-3' (SEQ ID NO: 4810)
3'-CGGAGAACGUCGCGCCGCCGAAGCUUC-5' (SEQ ID NO: 1909)

AR-194 Target: 5'-GCCTCTTGCAGCGCGGCGGCTTCGAAG-3' (SEQ ID NO: 2314)

5'-UGCAGCGCGGCGGCUUCGAAGCCGCCG-3' (SEQ ID NO: 4811)
3'-ACGUCGCGCCGCCGAAGCUUCGGCGGC-5' (SEQ ID NO: 1910)

AR-200 Target: 5'-TGCAGCGCGGCGGCTTCGAAGCCGCCG-3' (SEQ ID NO: 2315)

5'-CGAAGCCGCCGCCCGGAGCUGCCCUUU-3' (SEQ ID NO: 4812)
3'-GCUUCGGCGGCGGGCCUCGACGGGAAA-5' (SEQ ID NO: 1911)

AR-216 Target: 5'-CGAAGCCGCCGCCCGGAGCTGCCCTTT-3' (SEQ ID NO: 2316)

5'-CGCCGCCCGGAGCUGCCCUUUCCUCUU-3' (SEQ ID NO: 4813)
3'-GCGGCGGGCCUCGACGGGAAAGGAGAA-5' (SEQ ID NO: 1912)

AR-222 Target: 5'-CGCCGCCCGGAGCTGCCCTTTCCTCTT-3' (SEQ ID NO: 2317)

5'-UGAAGUUUUUAAAAGCUGCUAAAGACU-3' (SEQ ID NO: 4814)
3'-ACUUCAAAAAUUUUCGACGAUUUCUGA-5' (SEQ ID NO: 1913)

AR-252 Target: 5'-TGAAGTTTTTAAAAGCTGCTAAAGACT-3' (SEQ ID NO: 2318)

5'-CCGUCUUCUCUCCCGCAGCUGCCUCAG-3' (SEQ ID NO: 4815)
3'-GGCAGAAGAGAGGGCGUCGACGGAGUC-5' (SEQ ID NO: 1914)

AR-375 Target: 5'-CCGTCTTCTCTCCCGCAGCTGCCTCAG-3' (SEQ ID NO: 2319)

5'-CCGCAGCUGCCUCAGUCGGCUACUCUC-3' (SEQ ID NO: 4816)
3'-GGCGUCGACGGAGUCAGCCGAUGAGAG-5' (SEQ ID NO: 1915)

AR-387 Target: 5'-CCGCAGCTGCCTCAGTCGGCTACTCTC-3' (SEQ ID NO: 2320)

5'-UUUGGCUGCGAGCGGGCGAGCUAGCUG-3' (SEQ ID NO: 4817)
3'-AAACCGACGCUCGCCCGCUCGAUCGAC-5' (SEQ ID NO: 1916)

AR-506 Target: 5'-TTTGGCTGCGAGCGGGCGAGCTAGCTG-3' (SEQ ID NO: 2321)

5'-CGGGCGAGCUAGCUGCACAUUGCAAAG-3' (SEQ ID NO: 4818)
3'-GCCCGCUCGAUCGACGUGUAACGUUUC-5' (SEQ ID NO: 1917)

AR-518 Target: 5'-CGGGCGAGCTAGCTGCACATTGCAAAG-3' (SEQ ID NO: 2322)

5'-UCUCUCUCCACCUCCUCCUGCCUUCCC-3' (SEQ ID NO: 4819)

3'-AGAGAGAGGUGGAGGAGGACGGAAGGG-5' (SEQ ID NO: 1918)

AR-646 Target: 5'-TCTCTCTCCACCTCCTCCTGCCTTCCC-3' (SEQ ID NO: 2323)

5'-CCAGAGAUCAAAAGAUGAAAAGGCAGU-3' (SEQ ID NO: 4820)
3'-GGUCUCUAGUUUUCUACUUUUCCGUCA-5' (SEQ ID NO: 1919)

AR-689 Target: 5'-CCAGAGATCAAAAGATGAAAAGGCAGT-3' (SEQ ID NO: 2324)

5'-CAGUAGCCAAAAAACAAAACAAACAAA-3' (SEQ ID NO: 4821)
3'-GUCAUCGGUUUUUUGUUUUGUUUGUUU-5' (SEQ ID NO: 1920)

AR-724 Target: 5'-CAGTAGCCAAAAAACAAAACAAACAAA-3' (SEQ ID NO: 2325)

5'-CCAAAAAACAAAACAAACAAAAACAAA-3' (SEQ ID NO: 4822)
3'-GGUUUUUGUUUUGUUUGUUUUUGUUU-5' (SEQ ID NO: 1921)

AR-730 Target: 5'-CCAAAAAACAAAACAAACAAAAACAAA-3' (SEQ ID NO: 2326)

5'-ACAAAACAAACAAAAACAAAAAAGCCG-3' (SEQ ID NO: 4823)
3'-UGUUUUGUUUGUUUUUGUUUUUUCGGC-5' (SEQ ID NO: 1922)

AR-737 Target: 5'-ACAAAACAAACAAAAACAAAAAAGCCG-3' (SEQ ID NO: 2327)

5'-ACAAAAAAGCCGAAAUAAAAGAAAAAG-3' (SEQ ID NO: 4824)
3'-UGUUUUUUCGGCUUUAUUUUCUUUUUC-5' (SEQ ID NO: 1923)

AR-752 Target: 5'-ACAAAAAAGCCGAAATAAAAGAAAAAG-3' (SEQ ID NO: 2328)

5'-GCCGAAAUAAAAGAAAAAGAUAAUAAC-3' (SEQ ID NO: 4825)
3'-CGGCUUUAUUUUCUUUUUCUAUUAUUG-5' (SEQ ID NO: 1924)

AR-760 Target: 5'-GCCGAAATAAAAGAAAAAGATAATAAC-3' (SEQ ID NO: 2329)

5'-AAGAAAAAGAUAAUAACUCAGUUCUUA-3' (SEQ ID NO: 4826)
3'-UUCUUUUUCUAUUAUUGAGUCAAGAAU-5' (SEQ ID NO: 1925)

AR-770 Target: 5'-AAGAAAAAGATAATAACTCAGTTCTTA-3' (SEQ ID NO: 2330)

5'-AAAGAUAAUAACUCAGUUCUUAUUUGC-3' (SEQ ID NO: 4827)
3'-UUUCUAUUAUUGAGUCAAGAAUAAACG-5' (SEQ ID NO: 1926)

AR-775 Target: 5'-AAAGATAATAACTCAGTTCTTATTTGC-3' (SEQ ID NO: 2331)

5'-GAUAAUAACUCAGUUCUUAUUUGCACC-3' (SEQ ID NO: 4828)
3'-CUAUUAUUGAGUCAAGAAUAAACGUGG-5' (SEQ ID NO: 1927)

AR-778 Target: 5'-GATAATAACTCAGTTCTTATTTGCACC-3' (SEQ ID NO: 2332)

5'-UGGAGGAUUUUGUUUUUUUCUUUUAAG-3' (SEQ ID NO: 4829)
3'-ACCUCCUAAAACAAAAAAAGAAAAUUC-5' (SEQ ID NO: 1928)

AR-833 Target: 5'-TGGAGGATTTTGTTTTTTTCTTTTAAG-3' (SEQ ID NO: 2333)

5'-GAUUUUGUUUUUUUCUUUUAAGAUCUG-3' (SEQ ID NO: 4830)
3'-CUAAAACAAAAAAAGAAAAUUCUAGAC-5' (SEQ ID NO: 1929)

AR-838 Target: 5'-GATTTTGTTTTTTTCTTTTAAGATCTG-3' (SEQ ID NO: 2334)

5'-GUUUUUUUCUUUUAAGAUCUGGGCAUC-3' (SEQ ID NO: 4831)
3'-CAAAAAAAGAAAAUUCUAGACCCGUAG-5' (SEQ ID NO: 1930)

AR-844 Target: 5'-GTTTTTTTCTTTTAAGATCTGGGCATC-3' (SEQ ID NO: 2335)

5'-GGGCAUCUUUUGAAUCUACCCUUCAAG-3' (SEQ ID NO: 4832)
3'-CCCGUAGAAAACUUAGAUGGGAAGUUC-5' (SEQ ID NO: 1931)

AR-864 Target: 5'-GGGCATCTTTTGAATCTACCCTTCAAG-3' (SEQ ID NO: 2336)

5'-CAGAGCGCUUUUUGCGUGGUUGCUCCC-3' (SEQ ID NO: 4833)
3'-GUCUCGCGAAAAACGCACCAACGAGGG-5' (SEQ ID NO: 1932)

AR-971 Target: 5'-CAGAGCGCTTTTTGCGTGGTTGCTCCC-3' (SEQ ID NO: 2337)

5'-CGCUUUUUGCGUGGUUGCUCCCGCAAG-3' (SEQ ID NO: 4834)
3'-GCGAAAAACGCACCAACGAGGGCGUUC-5' (SEQ ID NO: 1933)

AR-976 Target: 5'-CGCTTTTTGCGTGGTTGCTCCCGCAAG-3' (SEQ ID NO: 2338)

5'-AAGUUUCCUUCUCUGGAGCUUCCCGCA-3' (SEQ ID NO: 4835)
3'-UUCAAAGGAAGAGACCUCGAAGGGCGU-5' (SEQ ID NO: 1934)

AR-1000 Target: 5'-AAGTTTCCTTCTCTGGAGCTTCCCGCA-3' (SEQ ID NO: 2339)

5'-AGCUUCCCGCAGGUGGGCAGCUAGCUG-3' (SEQ ID NO: 4836)
3'-UCGAAGGGCGUCCACCCGUCGAUCGAC-5' (SEQ ID NO: 1935)

AR-1016 Target: 5'-AGCTTCCCGCAGGTGGGCAGCTAGCTG-3' (SEQ ID NO: 2340)

5'-GUGGGCAGCUAGCUGCAGCGACUACCG-3' (SEQ ID NO: 4837)
3'-CACCCGUCGAUCGACGUCGCUGAUGGC-5' (SEQ ID NO: 1936)

AR-1028 Target: 5'-GTGGGCAGCTAGCTGCAGCGACTACCG-3' (SEQ ID NO: 2341)

5'-AAGUGCAGUUAGGGCUGGGAAGGGUCU-3' (SEQ ID NO: 4838)
3'-UUCACGUCAAUCCCGACCCUUCCCAGA-5' (SEQ ID NO: 1937)

AR-1146 Target: 5'-AAGTGCAGTTAGGGCTGGGAAGGGTCT-3' (SEQ ID NO: 2342)

5'-AGUGCAGUUAGGGCUGGGAAGGGUCUA-3' (SEQ ID NO: 4839)
3'-UCACGUCAAUCCCGACCCUUCCCAGAU-5' (SEQ ID NO: 1938)

AR-1147 Target: 5'-AGTGCAGTTAGGGCTGGGAAGGGTCTA-3' (SEQ ID NO: 2343)

5'-GUGCAGUUAGGGCUGGGAAGGGUCUAC-3' (SEQ ID NO: 4840)
3'-CACGUCAAUCCCGACCCUUCCCAGAUG-5' (SEQ ID NO: 1939)

AR-1148 Target: 5'-GTGCAGTTAGGGCTGGGAAGGGTCTAC-3' (SEQ ID NO: 2344)

5'-UGCAGUUAGGGCUGGGAAGGGUCUACC-3' (SEQ ID NO: 4841)
3'-ACGUCAAUCCCGACCCUUCCCAGAUGG-5' (SEQ ID NO: 1940)

AR-1149 Target: 5'-TGCAGTTAGGGCTGGGAAGGGTCTACC-3' (SEQ ID NO: 2345)

5'-GCAGUUAGGGCUGGGAAGGGUCUACCC-3' (SEQ ID NO: 4842)
3'-CGUCAAUCCCGACCCUUCCCAGAUGGG-5' (SEQ ID NO: 1941)

AR-1150 Target: 5'-GCAGTTAGGGCTGGGAAGGGTCTACCC-3' (SEQ ID NO: 2346)

5'-CAGUUAGGGCUGGGAAGGGUCUACCCU-3' (SEQ ID NO: 4843)
3'-GUCAAUCCCGACCCUUCCCAGAUGGGA-5' (SEQ ID NO: 1942)

AR-1151 Target: 5'-CAGTTAGGGCTGGGAAGGGTCTACCCT-3' (SEQ ID NO: 2347)

5'-AGUUAGGGCUGGGAAGGGUCUACCCUC-3' (SEQ ID NO: 4844)
3'-UCAAUCCCGACCCUUCCCAGAUGGGAG-5' (SEQ ID NO: 1943)

AR-1152 Target: 5'-AGTTAGGGCTGGGAAGGGTCTACCCTC-3' (SEQ ID NO: 2348)

5'-GUUAGGGCUGGGAAGGGUCUACCCUCG-3' (SEQ ID NO: 4845)
3'-CAAUCCCGACCCUUCCCAGAUGGGAGC-5' (SEQ ID NO: 1944)

AR-1153 Target: 5'-GTTAGGGCTGGGAAGGGTCTACCCTCG-3' (SEQ ID NO: 2349)

5'-UUAGGGCUGGGAAGGGUCUACCCUCGG-3' (SEQ ID NO: 4846)

3'-AAUCCCGACCCUUCCCAGAUGGGAGCC-5' (SEQ ID NO: 1945)

AR-1154 Target: 5'-TTAGGGCTGGGAAGGGTCTACCCTCGG-3' (SEQ ID NO: 2350)

5'-UAGGGCUGGGAAGGGUCUACCCUCGGC-3' (SEQ ID NO: 4847)
3'-AUCCCGACCCUUCCCAGAUGGGAGCCG-5' (SEQ ID NO: 1946)

AR-1155 Target: 5'-TAGGGCTGGGAAGGGTCTACCCTCGGC-3' (SEQ ID NO: 2351)

5'-AGGGCUGGGAAGGGUCUACCCUCGGCC-3' (SEQ ID NO: 4848)
3'-UCCCGACCCUUCCCAGAUGGGAGCCGG-5' (SEQ ID NO: 1947)

AR-1156 Target: 5'-AGGGCTGGGAAGGGTCTACCCTCGGCC-3' (SEQ ID NO: 2352)

5'-CUUUCCAGAAUCUGUUCCAGAGCGUGC-3' (SEQ ID NO: 4849)
3'-GAAAGGUCUUAGACAAGGUCUCGCACG-5' (SEQ ID NO: 1948)

AR-1206 Target: 5'-CTTTCCAGAATCTGTTCCAGAGCGTGC-3' (SEQ ID NO: 2353)

5'-UUUCCAGAAUCUGUUCCAGAGCGUGCG-3' (SEQ ID NO: 4850)
3'-AAAGGUCUUAGACAAGGUCUCGCACGC-5' (SEQ ID NO: 1949)

AR-1207 Target: 5'-TTTCCAGAATCTGTTCCAGAGCGTGCG-3' (SEQ ID NO: 2354)

5'-UUCCAGAAUCUGUUCCAGAGCGUGCGC-3' (SEQ ID NO: 4851)
3'-AAGGUCUUAGACAAGGUCUCGCACGCG-5' (SEQ ID NO: 1950)

AR-1208 Target: 5'-TTCCAGAATCTGTTCCAGAGCGTGCGC-3' (SEQ ID NO: 2355)

5'-UCCAGAAUCUGUUCCAGAGCGUGCGCG-3' (SEQ ID NO: 4852)
3'-AGGUCUUAGACAAGGUCUCGCACGCGC-5' (SEQ ID NO: 1951)

AR-1209 Target: 5'-TCCAGAATCTGTTCCAGAGCGTGCGCG-3' (SEQ ID NO: 2356)

5'-CCAGAAUCUGUUCCAGAGCGUGCGCGA-3' (SEQ ID NO: 4853)
3'-GGUCUUAGACAAGGUCUCGCACGCGCU-5' (SEQ ID NO: 1952)

AR-1210 Target: 5'-CCAGAATCTGTTCCAGAGCGTGCGCGA-3' (SEQ ID NO: 2357)

5'-CAGAAUCUGUUCCAGAGCGUGCGCGAA-3' (SEQ ID NO: 4854)
3'-GUCUUAGACAAGGUCUCGCACGCGCUU-5' (SEQ ID NO: 1953)

AR-1211 Target: 5'-CAGAATCTGTTCCAGAGCGTGCGCGAA-3' (SEQ ID NO: 2358)

5'-AGAAUCUGUUCCAGAGCGUGCGCGAAG-3' (SEQ ID NO: 4855)
3'-UCUUAGACAAGGUCUCGCACGCGCUUC-5' (SEQ ID NO: 1954)

AR-1212 Target: 5'-AGAATCTGTTCCAGAGCGTGCGCGAAG-3' (SEQ ID NO: 2359)

5'-GAAUCUGUUCCAGAGCGUGCGCGAAGU-3' (SEQ ID NO: 4856)
3'-CUUAGACAAGGUCUCGCACGCGCUUCA-5' (SEQ ID NO: 1955)

AR-1213 Target: 5'-GAATCTGTTCCAGAGCGTGCGCGAAGT-3' (SEQ ID NO: 2360)

5'-AAUCUGUUCCAGAGCGUGCGCGAAGUG-3' (SEQ ID NO: 4857)
3'-UUAGACAAGGUCUCGCACGCGCUUCAC-5' (SEQ ID NO: 1956)

AR-1214 Target: 5'-AATCTGTTCCAGAGCGTGCGCGAAGTG-3' (SEQ ID NO: 2361)

5'-AUCUGUUCCAGAGCGUGCGCGAAGUGA-3' (SEQ ID NO: 4858)
3'-UAGACAAGGUCUCGCACGCGCUUCACU-5' (SEQ ID NO: 1957)

AR-1215 Target: 5'-ATCTGTTCCAGAGCGTGCGCGAAGTGA-3' (SEQ ID NO: 2362)

5'-UCUGUUCCAGAGCGUGCGCGAAGUGAU-3' (SEQ ID NO: 4859)
3'-AGACAAGGUCUCGCACGCGCUUCACUA-5' (SEQ ID NO: 1958)

AR-1216 Target: 5'-TCTGTTCCAGAGCGTGCGCGAAGTGAT-3' (SEQ ID NO: 2363)

5'-CUGUUCCAGAGCGUGCGCGAAGUGAUC-3' (SEQ ID NO: 4860)
3'-GACAAGGUCUCGCACGCGCUUCACUAG-5' (SEQ ID NO: 1959)

AR-1217 Target: 5'-CTGTTCCAGAGCGTGCGCGAAGTGATC-3' (SEQ ID NO: 2364)

5'-UGUUCCAGAGCGUGCGCGAAGUGAUCC-3' (SEQ ID NO: 4861)
3'-ACAAGGUCUCGCACGCGCUUCACUAGG-5' (SEQ ID NO: 1960)

AR-1218 Target: 5'-TGTTCCAGAGCGTGCGCGAAGTGATCC-3' (SEQ ID NO: 2365)

5'-GGCGCCAGUUUGCUGCUGCUGCAGCAG-3' (SEQ ID NO: 4862)
3'-CCGCGGUCAAACGACGACGACGUCGUC-5' (SEQ ID NO: 1961)

AR-1292 Target: 5'-GGCGCCAGTTTGCTGCTGCTGCAGCAG-3' (SEQ ID NO: 2366)

5'-UUGCUGCUGCUGCAGCAGCAGCAGCAG-3' (SEQ ID NO: 4863)
3'-AACGACGACGACGUCGUCGUCGUCGUC-5' (SEQ ID NO: 1962)

AR-1301 Target: 5'-TTGCTGCTGCTGCAGCAGCAGCAGCAG-3' (SEQ ID NO: 2367)

5'-GCGUCCCAGAGCCUGGAGCCGCCGUGG-3' (SEQ ID NO: 4864)
3'-CGCAGGGUCUCGGACCUCGGCGGCACC-5' (SEQ ID NO: 1963)

AR-1533 Target: 5'-GCGTCCCAGAGCCTGGAGCCGCCGTGG-3' (SEQ ID NO: 2368)

5'-GGCUGCCGCAGCAGCUGCCAGCACCUC-3' (SEQ ID NO: 4865)
3'-CCGACGGCGUCGUCGACGGUCGUGGAG-5' (SEQ ID NO: 1964)

AR-1572 Target: 5'-GGCTGCCGCAGCAGCTGCCAGCACCTC-3' (SEQ ID NO: 2369)

5'-CGCAGCAGCUGCCAGCACCUCCGGACG-3' (SEQ ID NO: 4866)
3'-GCGUCGUCGACGGUCGUGGAGGCCUGC-5' (SEQ ID NO: 1965)

AR-1578 Target: 5'-CGCAGCAGCTGCCAGCACCTCCGGACG-3' (SEQ ID NO: 2370)

5'-CCCAUCCACGUUGUCCCUGCUGGGCCC-3' (SEQ ID NO: 4867)
3'-GGGUAGGUGCAACAGGGACGACCCGGG-5' (SEQ ID NO: 1966)

AR-1621 Target: 5'-CCCATCCACGTTGTCCCTGCTGGGCCC-3' (SEQ ID NO: 2371)

5'-CCGGCUUAAGCAGCUGCUCCGCUGACC-3' (SEQ ID NO: 4868)
3'-GGCCGAAUUCGUCGACGAGGCGACUGG-5' (SEQ ID NO: 1967)

AR-1656 Target: 5'-CCGGCTTAAGCAGCTGCTCCGCTGACC-3' (SEQ ID NO: 2372)

5'-CGGCUUAAGCAGCUGCUCCGCUGACCU-3' (SEQ ID NO: 4869)
3'-GCCGAAUUCGUCGACGAGGCGACUGGA-5' (SEQ ID NO: 1968)

AR-1657 Target: 5'-CGGCTTAAGCAGCTGCTCCGCTGACCT-3' (SEQ ID NO: 2373)

5'-UAAGCAGCUGCUCCGCUGACCUUAAAG-3' (SEQ ID NO: 4870)
3'-AUUCGUCGACGAGGCGACUGGAAUUUC-5' (SEQ ID NO: 1969)

AR-1662 Target: 5'-TAAGCAGCTGCTCCGCTGACCTTAAAG-3' (SEQ ID NO: 2374)

5'-AUGCAACUCCUUCAGCAACAGCAGCAG-3' (SEQ ID NO: 4871)
3'-UACGUUGAGGAAGUCGUUGUCGUCGUC-5' (SEQ ID NO: 1970)

AR-1712 Target: 5'-ATGCAACTCCTTCAGCAACAGCAGCAG-3' (SEQ ID NO: 2375)

5'-ACCAUUUCUGACAACGCCAAGGAGUUG-3' (SEQ ID NO: 4872)
3'-UGGUAAAGACUGUUGCGGUUCCUCAAC-5' (SEQ ID NO: 1971)

AR-1832 Target: 5'-ACCATTTCTGACAACGCCAAGGAGTTG-3' (SEQ ID NO: 2376)

5'-CCACUUUUGGGAGUUCCACCCGCUGUG-3' (SEQ ID NO: 4873)

3'-GGUGAAAACCCUCAAGGUGGGCGACAC-5' (SEQ ID NO: 1972)

AR-1952 Target: 5'-CCACTTTTGGGAGTTCCACCCGCTGTG-3' (SEQ ID NO: 2377)

5'-CAGGCAAGAGCACUGAAGAUACUGCUG-3' (SEQ ID NO: 4874)
3'-GUCCGUUCUCGUGACUUCUAUGACGAC-5' (SEQ ID NO: 1973)

AR-2037 Target: 5'-CAGGCAAGAGCACTGAAGATACTGCTG-3' (SEQ ID NO: 2378)

5'-CUGGCAGCGCUGCAGCAGGGAGCUCCG-3' (SEQ ID NO: 4875)
3'-GACCGUCGCGACGUCGUCCCUCGAGGC-5' (SEQ ID NO: 1974)

AR-2124 Target: 5'-CTGGCAGCGCTGCAGCAGGGAGCTCCG-3' (SEQ ID NO: 2379)

5'-AGUCGCGACUACUACAACUUUCCACUG-3' (SEQ ID NO: 4876)
3'-UCAGCGCUGAUGAUGUUGAAAGGUGAC-5' (SEQ ID NO: 1975)

AR-2222 Target: 5'-AGTCGCGACTACTACAACTTTCCACTG-3' (SEQ ID NO: 2380)

5'-GUCGCGACUACUACAACUUUCCACUGG-3' (SEQ ID NO: 4877)
3'-CAGCGCUGAUGAUGUUGAAAGGUGACC-5' (SEQ ID NO: 1976)

AR-2223 Target: 5'-GTCGCGACTACTACAACTTTCCACTGG-3' (SEQ ID NO: 2381)

5'-UCGCGACUACUACAACUUUCCACUGGC-3' (SEQ ID NO: 4878)
3'-AGCGCUGAUGAUGUUGAAAGGUGACCG-5' (SEQ ID NO: 1977)

AR-2224 Target: 5'-TCGCGACTACTACAACTTTCCACTGGC-3' (SEQ ID NO: 2382)

5'-GCUCGCAUCAAGCUGGAGAACCCGCUG-3' (SEQ ID NO: 4879)
3'-CGAGCGUAGUUCGACCUCUUGGGCGAC-5' (SEQ ID NO: 1978)

AR-2294 Target: 5'-GCTCGCATCAAGCTGGAGAACCCGCTG-3' (SEQ ID NO: 2383)

5'-GCUGGACUACGGCAGCGCCUGGGCGGC-3' (SEQ ID NO: 4880)
3'-CGACCUGAUGCCGUCGCGGACCCGCCG-5' (SEQ ID NO: 1979)

AR-2317 Target: 5'-GCTGGACTACGGCAGCGCCTGGGCGGC-3' (SEQ ID NO: 2384)

5'-CUGGACUACGGCAGCGCCUGGGCGGCU-3' (SEQ ID NO: 4881)
3'-GACCUGAUGCCGUCGCGGACCCGCCGA-5' (SEQ ID NO: 1980)

AR-2318 Target: 5'-CTGGACTACGGCAGCGCCTGGGCGGCT-3' (SEQ ID NO: 2385)

5'-UGGACUACGGCAGCGCCUGGGCGGCUG-3' (SEQ ID NO: 4882)
3'-ACCUGAUGCCGUCGCGGACCCGCCGAC-5' (SEQ ID NO: 1981)

AR-2319 Target: 5'-TGGACTACGGCAGCGCCTGGGCGGCTG-3' (SEQ ID NO: 2386)

5'-GGACUACGGCAGCGCCUGGGCGGCUGC-3' (SEQ ID NO: 4883)
3'-CCUGAUGCCGUCGCGGACCCGCCGACG-5' (SEQ ID NO: 1982)

AR-2320 Target: 5'-GGACTACGGCAGCGCCTGGGCGGCTGC-3' (SEQ ID NO: 2387)

5'-UGGCGCGGGUGCAGCGGGACCCGGUUC-3' (SEQ ID NO: 4884)
3'-ACCGCGCCCACGUCGCCCUGGGCCAAG-5' (SEQ ID NO: 1983)

AR-2386 Target: 5'-TGGCGCGGGTGCAGCGGGACCCGGTTC-3' (SEQ ID NO: 2388)

5'-GGCUGGCGGGCCAGGAAAGCGACUUCA-3' (SEQ ID NO: 4885)
3'-CCGACCGCCCGGUCCUUUCGCUGAAGU-5' (SEQ ID NO: 1984)

AR-2607 Target: 5'-GGCTGGCGGGCCAGGAAAGCGACTTCA-3' (SEQ ID NO: 2389)

5'-GUACCCUGGCGGCAUGGUGAGCAGAGU-3' (SEQ ID NO: 4886)
3'-CAUGGGACCGCCGUACCACUCGUCUCA-5' (SEQ ID NO: 1985)

AR-2650 Target: 5'-GTACCCTGGCGGCATGGTGAGCAGAGT-3' (SEQ ID NO: 2390)

5'-UGGAUGGAUAGCUACUCCGGACCUUAC-3' (SEQ ID NO: 4887)
3'-ACCUACCUAUCGAUGAGGCCUGGAAUG-5' (SEQ ID NO: 1986)

AR-2720 Target: 5'-TGGATGGATAGCTACTCCGGACCTTAC-3' (SEQ ID NO: 2391)

5'-CCCAGAAGACCUGCCUGAUCUGUGGAG-3' (SEQ ID NO: 4888)
3'-GGGUCUUCUGGACGGACUAGACACCUC-5' (SEQ ID NO: 1987)

AR-2808 Target: 5'-CCCAGAAGACCTGCCTGATCTGTGGAG-3' (SEQ ID NO: 2392)

5'-CCAGAAGACCUGCCUGAUCUGUGGAGA-3' (SEQ ID NO: 4889)
3'-GGUCUUCUGGACGGACUAGACACCUCU-5' (SEQ ID NO: 1988)

AR-2809 Target: 5'-CCAGAAGACCTGCCTGATCTGTGGAGA-3' (SEQ ID NO: 2393)

5'-CAGAAGACCUGCCUGAUCUGUGGAGAU-3' (SEQ ID NO: 4890)
3'-GUCUUCUGGACGGACUAGACACCUCUA-5' (SEQ ID NO: 1989)

AR-2810 Target: 5'-CAGAAGACCTGCCTGATCTGTGGAGAT-3' (SEQ ID NO: 2394)

5'-AGAAGACCUGCCUGAUCUGUGGAGAUG-3' (SEQ ID NO: 4891)
3'-UCUUCUGGACGGACUAGACACCUCUAC-5' (SEQ ID NO: 1990)

AR-2811 Target: 5'-AGAAGACCTGCCTGATCTGTGGAGATG-3' (SEQ ID NO: 2395)

5'-GAAGACCUGCCUGAUCUGUGGAGAUGA-3' (SEQ ID NO: 4892)
3'-CUUCUGGACGGACUAGACACCUCUACU-5' (SEQ ID NO: 1991)

AR-2812 Target: 5'-GAAGACCTGCCTGATCTGTGGAGATGA-3' (SEQ ID NO: 2396)

5'-AAGACCUGCCUGAUCUGUGGAGAUGAA-3' (SEQ ID NO: 4893)
3'-UUCUGGACGGACUAGACACCUCUACUU-5' (SEQ ID NO: 1992)

AR-2813 Target: 5'-AAGACCTGCCTGATCTGTGGAGATGAA-3' (SEQ ID NO: 2397)

5'-AGACCUGCCUGAUCUGUGGAGAUGAAG-3' (SEQ ID NO: 4894)
3'-UCUGGACGGACUAGACACCUCUACUUC-5' (SEQ ID NO: 1993)

AR-2814 Target: 5'-AGACCTGCCTGATCTGTGGAGATGAAG-3' (SEQ ID NO: 2398)

5'-GACCUGCCUGAUCUGUGGAGAUGAAGC-3' (SEQ ID NO: 4895)
3'-CUGGACGGACUAGACACCUCUACUUCG-5' (SEQ ID NO: 1994)

AR-2815 Target: 5'-GACCTGCCTGATCTGTGGAGATGAAGC-3' (SEQ ID NO: 2399)

5'-ACCUGCCUGAUCUGUGGAGAUGAAGCU-3' (SEQ ID NO: 4896)
3'-UGGACGGACUAGACACCUCUACUUCGA-5' (SEQ ID NO: 1995)

AR-2816 Target: 5'-ACCTGCCTGATCTGTGGAGATGAAGCT-3' (SEQ ID NO: 2400)

5'-CCUGCCUGAUCUGUGGAGAUGAAGCUU-3' (SEQ ID NO: 4897)
3'-GGACGGACUAGACACCUCUACUUCGAA-5' (SEQ ID NO: 1996)

AR-2817 Target: 5'-CCTGCCTGATCTGTGGAGATGAAGCTT-3' (SEQ ID NO: 2401)

5'-CUGCCUGAUCUGUGGAGAUGAAGCUUC-3' (SEQ ID NO: 4898)
3'-GACGGACUAGACACCUCUACUUCGAAG-5' (SEQ ID NO: 1997)

AR-2818 Target: 5'-CTGCCTGATCTGTGGAGATGAAGCTTC-3' (SEQ ID NO: 2402)

5'-UGCCUGAUCUGUGGAGAUGAAGCUUCU-3' (SEQ ID NO: 4899)
3'-ACGGACUAGACACCUCUACUUCGAAGA-5' (SEQ ID NO: 1998)

AR-2819 Target: 5'-TGCCTGATCTGTGGAGATGAAGCTTCT-3' (SEQ ID NO: 2403)

5'-GCCUGAUCUGUGGAGAUGAAGCUUCUG-3' (SEQ ID NO: 4900)

3'-CGGACUAGACACCUCUACUUCGAAGAC-5' (SEQ ID NO: 1999)

AR-2820 Target: 5'-GCCTGATCTGTGGAGATGAAGCTTCTG-3' (SEQ ID NO: 2404)

5'-CCUGAUCUGUGGAGAUGAAGCUUCUGG-3' (SEQ ID NO: 4901)
3'-GGACUAGACACCUCUACUUCGAAGACC-5' (SEQ ID NO: 2000)

AR-2821 Target: 5'-CCTGATCTGTGGAGATGAAGCTTCTGG-3' (SEQ ID NO: 2405)

5'-CUGAUCUGUGGAGAUGAAGCUUCUGGG-3' (SEQ ID NO: 4902)
3'-GACUAGACACCUCUACUUCGAAGACCC-5' (SEQ ID NO: 2001)

AR-2822 Target: 5'-CTGATCTGTGGAGATGAAGCTTCTGGG-3' (SEQ ID NO: 2406)

5'-UGAUCUGUGGAGAUGAAGCUUCUGGGU-3' (SEQ ID NO: 4903)
3'-ACUAGACACCUCUACUUCGAAGACCCA-5' (SEQ ID NO: 2002)

AR-2823 Target: 5'-TGATCTGTGGAGATGAAGCTTCTGGGT-3' (SEQ ID NO: 2407)

5'-GAUCUGUGGAGAUGAAGCUUCUGGGUG-3' (SEQ ID NO: 4904)
3'-CUAGACACCUCUACUUCGAAGACCCAC-5' (SEQ ID NO: 2003)

AR-2824 Target: 5'-GATCTGTGGAGATGAAGCTTCTGGGTG-3' (SEQ ID NO: 2408)

5'-AUCUGUGGAGAUGAAGCUUCUGGGUGU-3' (SEQ ID NO: 4905)
3'-UAGACACCUCUACUUCGAAGACCCACA-5' (SEQ ID NO: 2004)

AR-2825 Target: 5'-ATCTGTGGAGATGAAGCTTCTGGGTGT-3' (SEQ ID NO: 2409)

5'-UCUGUGGAGAUGAAGCUUCUGGGUGUC-3' (SEQ ID NO: 4906)
3'-AGACACCUCUACUUCGAAGACCCACAG-5' (SEQ ID NO: 2005)

AR-2826 Target: 5'-TCTGTGGAGATGAAGCTTCTGGGTGTC-3' (SEQ ID NO: 2410)

5'-CUGUGGAGAUGAAGCUUCUGGGUGUCA-3' (SEQ ID NO: 4907)
3'-GACACCUCUACUUCGAAGACCCACAGU-5' (SEQ ID NO: 2006)

AR-2827 Target: 5'-CTGTGGAGATGAAGCTTCTGGGTGTCA-3' (SEQ ID NO: 2411)

5'-GCUUCUGGGUGUCACUAUGGAGCUCUC-3' (SEQ ID NO: 4908)
3'-CGAAGACCCACAGUGAUACCUCGAGAG-5' (SEQ ID NO: 2007)

AR-2840 Target: 5'-GCTTCTGGGTGTCACTATGGAGCTCTC-3' (SEQ ID NO: 2412)

5'-UGGAGCUCUCACAUGUGGAAGCUGCAA-3' (SEQ ID NO: 4909)
3'-ACCUCGAGAGUGUACACCUUCGACGUU-5' (SEQ ID NO: 2008)

AR-2857 Target: 5'-TGGAGCTCTCACATGTGGAAGCTGCAA-3' (SEQ ID NO: 2413)

5'-GAAGCUGCAAGGUCUUCUUCAAAAGAG-3' (SEQ ID NO: 4910)
3'-CUUCGACGUUCCAGAAGAAGUUUUCUC-5' (SEQ ID NO: 2009)

AR-2874 Target: 5'-GAAGCTGCAAGGTCTTCTTCAAAAGAG-3' (SEQ ID NO: 2414)

5'-AAGCUGCAAGGUCUUCUUCAAAAGAGC-3' (SEQ ID NO: 4911)
3'-UUCGACGUUCCAGAAGAAGUUUUCUCG-5' (SEQ ID NO: 2010)

AR-2875 Target: 5'-AAGCTGCAAGGTCTTCTTCAAAAGAGC-3' (SEQ ID NO: 2415)

5'-AGCUGCAAGGUCUUCUUCAAAAGAGCC-3' (SEQ ID NO: 4912)
3'-UCGACGUUCCAGAAGAAGUUUUCUCGG-5' (SEQ ID NO: 2011)

AR-2876 Target: 5'-AGCTGCAAGGTCTTCTTCAAAAGAGCC-3' (SEQ ID NO: 2416)

5'-GCUGCAAGGUCUUCUUCAAAAGAGCCG-3' (SEQ ID NO: 4913)
3'-CGACGUUCCAGAAGAAGUUUUCUCGGC-5' (SEQ ID NO: 2012)

AR-2877 Target: 5'-GCTGCAAGGTCTTCTTCAAAAGAGCCG-3' (SEQ ID NO: 2417)

5'-CUGCAAGGUCUUCUUCAAAAGAGCCGC-3' (SEQ ID NO: 4914)
3'-GACGUUCCAGAAGAAGUUUUCUCGGCG-5' (SEQ ID NO: 2013)

AR-2878 Target: 5'-CTGCAAGGTCTTCTTCAAAAGAGCCGC-3' (SEQ ID NO: 2418)

5'-UGCAAGGUCUUCUUCAAAAGAGCCGCU-3' (SEQ ID NO: 4915)
3'-ACGUUCCAGAAGAAGUUUUCUCGGCGA-5' (SEQ ID NO: 2014)

AR-2879 Target: 5'-TGCAAGGTCTTCTTCAAAAGAGCCGCT-3' (SEQ ID NO: 2419)

5'-GCAAGGUCUUCUUCAAAAGAGCCGCUG-3' (SEQ ID NO: 4916)
3'-CGUUCCAGAAGAAGUUUUCUCGGCGAC-5' (SEQ ID NO: 2015)

AR-2880 Target: 5'-GCAAGGTCTTCTTCAAAAGAGCCGCTG-3' (SEQ ID NO: 2420)

5'-CAAGGUCUUCUUCAAAAGAGCCGCUGA-3' (SEQ ID NO: 4917)
3'-GUUCCAGAAGAAGUUUUCUCGGCGACU-5' (SEQ ID NO: 2016)

AR-2881 Target: 5'-CAAGGTCTTCTTCAAAAGAGCCGCTGA-3' (SEQ ID NO: 2421)

5'-AAGGUCUUCUUCAAAAGAGCCGCUGAA-3' (SEQ ID NO: 4918)
3'-UUCCAGAAGAAGUUUUCUCGGCGACUU-5' (SEQ ID NO: 2017)

AR-2882 Target: 5'-AAGGTCTTCTTCAAAAGAGCCGCTGAA-3' (SEQ ID NO: 2422)

5'-AGGUCUUCUUCAAAAGAGCCGCUGAAG-3' (SEQ ID NO: 4919)
3'-UCCAGAAGAAGUUUUCUCGGCGACUUC-5' (SEQ ID NO: 2018)

AR-2883 Target: 5'-AGGTCTTCTTCAAAAGAGCCGCTGAAG-3' (SEQ ID NO: 2423)

5'-GGUCUUCUUCAAAAGAGCCGCUGAAGG-3' (SEQ ID NO: 4920)
3'-CCAGAAGAAGUUUUCUCGGCGACUUCC-5' (SEQ ID NO: 2019)

AR-2884 Target: 5'-GGTCTTCTTCAAAAGAGCCGCTGAAGG-3' (SEQ ID NO: 2424)

5'-GUCUUCUUCAAAAGAGCCGCUGAAGGG-3' (SEQ ID NO: 4921)
3'-CAGAAGAAGUUUUCUCGGCGACUUCCC-5' (SEQ ID NO: 2020)

AR-2885 Target: 5'-GTCTTCTTCAAAAGAGCCGCTGAAGGG-3' (SEQ ID NO: 2425)

5'-UCUUCUUCAAAAGAGCCGCUGAAGGGA-3' (SEQ ID NO: 4922)
3'-AGAAGAAGUUUUCUCGGCGACUUCCCU-5' (SEQ ID NO: 2021)

AR-2886 Target: 5'-TCTTCTTCAAAAGAGCCGCTGAAGGGA-3' (SEQ ID NO: 2426)

5'-CUUCUUCAAAAGAGCCGCUGAAGGGAA-3' (SEQ ID NO: 4923)
3'-GAAGAAGUUUUCUCGGCGACUUCCCUU-5' (SEQ ID NO: 2022)

AR-2887 Target: 5'-CTTCTTCAAAAGAGCCGCTGAAGGGAA-3' (SEQ ID NO: 2427)

5'-UUCUUCAAAAGAGCCGCUGAAGGGAAA-3' (SEQ ID NO: 4924)
3'-AAGAAGUUUUCUCGGCGACUUCCCUUU-5' (SEQ ID NO: 2023)

AR-2888 Target: 5'-TTCTTCAAAAGAGCCGCTGAAGGGAAA-3' (SEQ ID NO: 2428)

5'-UCUUCAAAAGAGCCGCUGAAGGGAAAC-3' (SEQ ID NO: 4925)
3'-AGAAGUUUUCUCGGCGACUUCCCUUUG-5' (SEQ ID NO: 2024)

AR-2889 Target: 5'-TCTTCAAAAGAGCCGCTGAAGGGAAAC-3' (SEQ ID NO: 2429)

5'-CUUCAAAAGAGCCGCUGAAGGGAAACA-3' (SEQ ID NO: 4926)
3'-GAAGUUUUCUCGGCGACUUCCCUUUGU-5' (SEQ ID NO: 2025)

AR-2890 Target: 5'-CTTCAAAAGAGCCGCTGAAGGGAAACA-3' (SEQ ID NO: 2430)

5'-UUCAAAAGAGCCGCUGAAGGGAAACAG-3' (SEQ ID NO: 4927)

3'-AAGUUUUCUCGGCGACUUCCCUUUGUC-5' (SEQ ID NO: 2026)

AR-2891 Target: 5'-TTCAAAAGAGCCGCTGAAGGGAAACAG-3' (SEQ ID NO: 2431)

5'-UCAAAAGAGCCGCUGAAGGGAAACAGA-3' (SEQ ID NO: 4928)
3'-AGUUUUCUCGGCGACUUCCCUUUGUCU-5' (SEQ ID NO: 2027)

AR-2892 Target: 5'-TCAAAAGAGCCGCTGAAGGGAAACAGA-3' (SEQ ID NO: 2432)

5'-CAAAAGAGCCGCUGAAGGGAAACAGAA-3' (SEQ ID NO: 4929)
3'-GUUUUCUCGGCGACUUCCCUUUGUCUU-5' (SEQ ID NO: 2028)

AR-2893 Target: 5'-CAAAAGAGCCGCTGAAGGGAAACAGAA-3' (SEQ ID NO: 2433)

5'-AAAAGAGCCGCUGAAGGGAAACAGAAG-3' (SEQ ID NO: 4930)
3'-UUUUCUCGGCGACUUCCCUUUGUCUUC-5' (SEQ ID NO: 2029)

AR-2894 Target: 5'-AAAAGAGCCGCTGAAGGGAAACAGAAG-3' (SEQ ID NO: 2434)

5'-AAAGAGCCGCUGAAGGGAAACAGAAGU-3' (SEQ ID NO: 4931)
3'-UUUCUCGGCGACUUCCCUUUGUCUUCA-5' (SEQ ID NO: 2030)

AR-2895 Target: 5'-AAAGAGCCGCTGAAGGGAAACAGAAGT-3' (SEQ ID NO: 2435)

5'-AAGAGCCGCUGAAGGGAAACAGAAGUA-3' (SEQ ID NO: 4932)
3'-UUCUCGGCGACUUCCCUUUGUCUUCAU-5' (SEQ ID NO: 2031)

AR-2896 Target: 5'-AAGAGCCGCTGAAGGGAAACAGAAGTA-3' (SEQ ID NO: 2436)

5'-AGAGCCGCUGAAGGGAAACAGAAGUAC-3' (SEQ ID NO: 4933)
3'-UCUCGGCGACUUCCCUUUGUCUUCAUG-5' (SEQ ID NO: 2032)

AR-2897 Target: 5'-AGAGCCGCTGAAGGGAAACAGAAGTAC-3' (SEQ ID NO: 2437)

5'-GAGCCGCUGAAGGGAAACAGAAGUACC-3' (SEQ ID NO: 4934)
3'-CUCGGCGACUUCCCUUUGUCUUCAUGG-5' (SEQ ID NO: 2033)

AR-2898 Target: 5'-GAGCCGCTGAAGGGAAACAGAAGTACC-3' (SEQ ID NO: 2438)

5'-AGCCGCUGAAGGGAAACAGAAGUACCU-3' (SEQ ID NO: 4935)
3'-UCGGCGACUUCCCUUUGUCUUCAUGGA-5' (SEQ ID NO: 2034)

AR-2899 Target: 5'-AGCCGCTGAAGGGAAACAGAAGTACCT-3' (SEQ ID NO: 2439)

5'-CCGCUGAAGGGAAACAGAAGUACCUGU-3' (SEQ ID NO: 4936)
3'-GGCGACUUCCCUUUGUCUUCAUGGACA-5' (SEQ ID NO: 2035)

AR-2901 Target: 5'-CCGCTGAAGGGAAACAGAAGTACCTGT-3' (SEQ ID NO: 2440)

5'-CGCUGAAGGGAAACAGAAGUACCUGUG-3' (SEQ ID NO: 4937)
3'-GCGACUUCCCUUUGUCUUCAUGGACAC-5' (SEQ ID NO: 2036)

AR-2902 Target: 5'-CGCTGAAGGGAAACAGAAGTACCTGTG-3' (SEQ ID NO: 2441)

5'-CCUGUGCGCCAGCAGAAAUGAUUGCAC-3' (SEQ ID NO: 4938)
3'-GGACACGCGGUCGUCUUUACUAACGUG-5' (SEQ ID NO: 2037)

AR-2923 Target: 5'-CCTGTGCGCCAGCAGAAATGATTGCAC-3' (SEQ ID NO: 2442)

5'-GCAGAAAUGAUUGCACUAUUGAUAAAU-3' (SEQ ID NO: 4939)
3'-CGUCUUUACUAACGUGAUAACUAUUUA-5' (SEQ ID NO: 2038)

AR-2934 Target: 5'-GCAGAAATGATTGCACTATTGATAAAT-3' (SEQ ID NO: 2443)

5'-AAUGAUUGCACUAUUGAUAAAUUCCGA-3' (SEQ ID NO: 4940)
3'-UUACUAACGUGAUAACUAUUUAAGGCU-5' (SEQ ID NO: 2039)

AR-2939 Target: 5'-AATGATTGCACTATTGATAAATTCCGA-3' (SEQ ID NO: 2444)

5'-CACUAUUGAUAAAUUCCGAAGGAAAAA-3' (SEQ ID NO: 4941)
3'-GUGAUAACUAUUUAAGGCUUCCUUUUU-5' (SEQ ID NO: 2040)

AR-2947 Target: 5'-CACTATTGATAAATTCCGAAGGAAAAA-3' (SEQ ID NO: 2445)

5'-UUCGGAAAUGUUAUGAAGCAGGGAUGA-3' (SEQ ID NO: 4942)
3'-AAGCCUUUACAAUACUUCGUCCCUACU-5' (SEQ ID NO: 2041)

AR-2991 Target: 5'-TTCGGAAATGTTATGAAGCAGGGATGA-3' (SEQ ID NO: 2446)

5'-UCGGAAAUGUUAUGAAGCAGGGAUGAC-3' (SEQ ID NO: 4943)
3'-AGCCUUUACAAUACUUCGUCCCUACUG-5' (SEQ ID NO: 2042)

AR-2992 Target: 5'-TCGGAAATGTTATGAAGCAGGGATGAC-3' (SEQ ID NO: 2447)

5'-CGGAAAUGUUAUGAAGCAGGGAUGACU-3' (SEQ ID NO: 4944)
3'-GCCUUUACAAUACUUCGUCCCUACUGA-5' (SEQ ID NO: 2043)

AR-2993 Target: 5'-CGGAAATGTTATGAAGCAGGGATGACT-3' (SEQ ID NO: 2448)

5'-GGAAAUGUUAUGAAGCAGGGAUGACUC-3' (SEQ ID NO: 4945)
3'-CCUUUACAAUACUUCGUCCCUACUGAG-5' (SEQ ID NO: 2044)

AR-2994 Target: 5'-GGAAATGTTATGAAGCAGGGATGACTC-3' (SEQ ID NO: 2449)

5'-GAAAUGUUAUGAAGCAGGGAUGACUCU-3' (SEQ ID NO: 4946)
3'-CUUUACAAUACUUCGUCCCUACUGAGA-5' (SEQ ID NO: 2045)

AR-2995 Target: 5'-GAAATGTTATGAAGCAGGGATGACTCT-3' (SEQ ID NO: 2450)

5'-AAAUGUUAUGAAGCAGGGAUGACUCUG-3' (SEQ ID NO: 4947)
3'-UUUACAAUACUUCGUCCCUACUGAGAC-5' (SEQ ID NO: 2046)

AR-2996 Target: 5'-AAATGTTATGAAGCAGGGATGACTCTG-3' (SEQ ID NO: 2451)

5'-AAUGUUAUGAAGCAGGGAUGACUCUGG-3' (SEQ ID NO: 4948)
3'-UUACAAUACUUCGUCCCUACUGAGACC-5' (SEQ ID NO: 2047)

AR-2997 Target: 5'-AATGTTATGAAGCAGGGATGACTCTGG-3' (SEQ ID NO: 2452)

5'-AUGUUAUGAAGCAGGGAUGACUCUGGG-3' (SEQ ID NO: 4949)
3'-UACAAUACUUCGUCCCUACUGAGACCC-5' (SEQ ID NO: 2048)

AR-2998 Target: 5'-ATGTTATGAAGCAGGGATGACTCTGGG-3' (SEQ ID NO: 2453)

5'-UGUUAUGAAGCAGGGAUGACUCUGGGA-3' (SEQ ID NO: 4950)
3'-ACAAUACUUCGUCCCUACUGAGACCCU-5' (SEQ ID NO: 2049)

AR-2999 Target: 5'-TGTTATGAAGCAGGGATGACTCTGGGA-3' (SEQ ID NO: 2454)

5'-GUUAUGAAGCAGGGAUGACUCUGGGAG-3' (SEQ ID NO: 4951)
3'-CAAUACUUCGUCCCUACUGAGACCCUC-5' (SEQ ID NO: 2050)

AR-3000 Target: 5'-GTTATGAAGCAGGGATGACTCTGGGAG-3' (SEQ ID NO: 2455)

5'-UUAUGAAGCAGGGAUGACUCUGGGAGC-3' (SEQ ID NO: 4952)
3'-AAUACUUCGUCCCUACUGAGACCCUCG-5' (SEQ ID NO: 2051)

AR-3001 Target: 5'-TTATGAAGCAGGGATGACTCTGGGAGC-3' (SEQ ID NO: 2456)

5'-UAUGAAGCAGGGAUGACUCUGGGAGCC-3' (SEQ ID NO: 4953)
3'-AUACUUCGUCCCUACUGAGACCCUCGG-5' (SEQ ID NO: 2052)

AR-3002 Target: 5'-TATGAAGCAGGGATGACTCTGGGAGCC-3' (SEQ ID NO: 2457)

5'-AUGAAGCAGGGAUGACUCUGGGAGCCC-3' (SEQ ID NO: 4954)

3'-UACUUCGUCCCUACUGAGACCCUCGGG-5' (SEQ ID NO: 2053)

AR-3003 Target: 5'-ATGAAGCAGGGATGACTCTGGGAGCCC-3' (SEQ ID NO: 2458)

5'-UGAAGCAGGGAUGACUCUGGGAGCCCG-3' (SEQ ID NO: 4955)
3'-ACUUCGUCCCUACUGAGACCCUCGGGC-5' (SEQ ID NO: 2054)

AR-3004 Target: 5'-TGAAGCAGGGATGACTCTGGGAGCCCG-3' (SEQ ID NO: 2459)

5'-GAAGCAGGGAUGACUCUGGGAGCCCGG-3' (SEQ ID NO: 4956)
3'-CUUCGUCCCUACUGAGACCCUCGGGCC-5' (SEQ ID NO: 2055)

AR-3005 Target: 5'-GAAGCAGGGATGACTCTGGGAGCCCGG-3' (SEQ ID NO: 2460)

5'-AAGCAGGGAUGACUCUGGGAGCCCGGA-3' (SEQ ID NO: 4957)
3'-UUCGUCCCUACUGAGACCCUCGGGCCU-5' (SEQ ID NO: 2056)

AR-3006 Target: 5'-AAGCAGGGATGACTCTGGGAGCCCGGA-3' (SEQ ID NO: 2461)

5'-AGCAGGGAUGACUCUGGGAGCCCGGAA-3' (SEQ ID NO: 4958)
3'-UCGUCCCUACUGAGACCCUCGGGCCUU-5' (SEQ ID NO: 2057)

AR-3007 Target: 5'-AGCAGGGATGACTCTGGGAGCCCGGAA-3' (SEQ ID NO: 2462)

5'-CUGAAGAAACUUGGUAAUCUGAAACUA-3' (SEQ ID NO: 4959)
3'-GACUUCUUUGAACCAUUAGACUUUGAU-5' (SEQ ID NO: 2058)

AR-3035 Target: 5'-CTGAAGAAACTTGGTAATCTGAAACTA-3' (SEQ ID NO: 2463)

5'-UGAAACUACAGGAGGAAGGAGAGGCUU-3' (SEQ ID NO: 4960)
3'-ACUUUGAUGUCCUCCUUCCUCUCCGAA-5' (SEQ ID NO: 2059)

AR-3054 Target: 5'-TGAAACTACAGGAGGAAGGAGAGGCTT-3' (SEQ ID NO: 2464)

5'-GAAACUACAGGAGGAAGGAGAGGCUUC-3' (SEQ ID NO: 4961)
3'-CUUUGAUGUCCUCCUUCCUCUCCGAAG-5' (SEQ ID NO: 2060)

AR-3055 Target: 5'-GAAACTACAGGAGGAAGGAGAGGCTTC-3' (SEQ ID NO: 2465)

5'-CACAUUGAAGGCUAUGAAUGUCAGCCC-3' (SEQ ID NO: 4962)
3'-GUGUAACUUCCGAUACUUACAGUCGGG-5' (SEQ ID NO: 2061)

AR-3131 Target: 5'-CACATTGAAGGCTATGAATGTCAGCCC-3' (SEQ ID NO: 2466)

5'-ACAUUGAAGGCUAUGAAUGUCAGCCCA-3' (SEQ ID NO: 4963)
3'-UGUAACUUCCGAUACUUACAGUCGGGU-5' (SEQ ID NO: 2062)

AR-3132 Target: 5'-ACATTGAAGGCTATGAATGTCAGCCCA-3' (SEQ ID NO: 2467)

5'-CAUUGAAGGCUAUGAAUGUCAGCCCAU-3' (SEQ ID NO: 4964)
3'-GUAACUUCCGAUACUUACAGUCGGGUA-5' (SEQ ID NO: 2063)

AR-3133 Target: 5'-CATTGAAGGCTATGAATGTCAGCCCAT-3' (SEQ ID NO: 2468)

5'-AUUGAAGGCUAUGAAUGUCAGCCCAUC-3' (SEQ ID NO: 4965)
3'-UAACUUCCGAUACUUACAGUCGGGUAG-5' (SEQ ID NO: 2064)

AR-3134 Target: 5'-ATTGAAGGCTATGAATGTCAGCCCATC-3' (SEQ ID NO: 2469)

5'-UUGAAGGCUAUGAAUGUCAGCCCAUCU-3' (SEQ ID NO: 4966)
3'-AACUUCCGAUACUUACAGUCGGGUAGA-5' (SEQ ID NO: 2065)

AR-3135 Target: 5'-TTGAAGGCTATGAATGTCAGCCCATCT-3' (SEQ ID NO: 2470)

5'-UGAAGGCUAUGAAUGUCAGCCCAUCUU-3' (SEQ ID NO: 4967)
3'-ACUUCCGAUACUUACAGUCGGGUAGAA-5' (SEQ ID NO: 2066)

AR-3136 Target: 5'-TGAAGGCTATGAATGTCAGCCCATCTT-3' (SEQ ID NO: 2471)

5'-AUGUCCUGGAAGCCAUUGAGCCAGGUG-3' (SEQ ID NO: 4968)
3'-UACAGGACCUUCGGUAACUCGGUCCAC-5' (SEQ ID NO: 2067)

AR-3168 Target: 5'-ATGTCCTGGAAGCCATTGAGCCAGGTG-3' (SEQ ID NO: 2472)

5'-UGUCCUGGAAGCCAUUGAGCCAGGUGU-3' (SEQ ID NO: 4969)
3'-ACAGGACCUUCGGUAACUCGGUCCACA-5' (SEQ ID NO: 2068)

AR-3169 Target: 5'-TGTCCTGGAAGCCATTGAGCCAGGTGT-3' (SEQ ID NO: 2473)

5'-GUCCUGGAAGCCAUUGAGCCAGGUGUA-3' (SEQ ID NO: 4970)
3'-CAGGACCUUCGGUAACUCGGUCCACAU-5' (SEQ ID NO: 2069)

AR-3170 Target: 5'-GTCCTGGAAGCCATTGAGCCAGGTGTA-3' (SEQ ID NO: 2474)

5'-UCCUGGAAGCCAUUGAGCCAGGUGUAG-3' (SEQ ID NO: 4971)
3'-AGGACCUUCGGUAACUCGGUCCACAUC-5' (SEQ ID NO: 2070)

AR-3171 Target: 5'-TCCTGGAAGCCATTGAGCCAGGTGTAG-3' (SEQ ID NO: 2475)

5'-CCUGGAAGCCAUUGAGCCAGGUGUAGU-3' (SEQ ID NO: 4972)
3'-GGACCUUCGGUAACUCGGUCCACAUCA-5' (SEQ ID NO: 2071)

AR-3172 Target: 5'-CCTGGAAGCCATTGAGCCAGGTGTAGT-3' (SEQ ID NO: 2476)

5'-ACCAGCCCGACUCCUUUGCAGCCUUGC-3' (SEQ ID NO: 4973)
3'-UGGUCGGGCUGAGGAAACGUCGGAACG-5' (SEQ ID NO: 2072)

AR-3219 Target: 5'-ACCAGCCCGACTCCTTTGCAGCCTTGC-3' (SEQ ID NO: 2477)

5'-CCGACUCCUUUGCAGCCUUGCUCUCUA-3' (SEQ ID NO: 4974)
3'-GGCUGAGGAAACGUCGGAACGAGAGAU-5' (SEQ ID NO: 2073)

AR-3225 Target: 5'-CCGACTCCTTTGCAGCCTTGCTCTCTA-3' (SEQ ID NO: 2478)

5'-UGCAGCCUUGCUCUCUAGCCUCAAUGA-3' (SEQ ID NO: 4975)
3'-ACGUCGGAACGAGAGAUCGGAGUUACU-5' (SEQ ID NO: 2074)

AR-3235 Target: 5'-TGCAGCCTTGCTCTCTAGCCTCAATGA-3' (SEQ ID NO: 2479)

5'-ACGUGGUCAAGUGGGCCAAGGCCUUGC-3' (SEQ ID NO: 4976)
3'-UGCACCAGUUCACCCGGUUCCGGAACG-5' (SEQ ID NO: 2075)

AR-3285 Target: 5'-ACGTGGTCAAGTGGGCCAAGGCCTTGC-3' (SEQ ID NO: 2480)

5'-CGUGGUCAAGUGGGCCAAGGCCUUGCC-3' (SEQ ID NO: 4977)
3'-GCACCAGUUCACCCGGUUCCGGAACGG-5' (SEQ ID NO: 2076)

AR-3286 Target: 5'-CGTGGTCAAGTGGGCCAAGGCCTTGCC-3' (SEQ ID NO: 2481)

5'-GUGGUCAAGUGGGCCAAGGCCUUGCCU-3' (SEQ ID NO: 4978)
3'-CACCAGUUCACCCGGUUCCGGAACGGA-5' (SEQ ID NO: 2077)

AR-3287 Target: 5'-GTGGTCAAGTGGGCCAAGGCCTTGCCT-3' (SEQ ID NO: 2482)

5'-UGGUCAAGUGGGCCAAGGCCUUGCCUG-3' (SEQ ID NO: 4979)
3'-ACCAGUUCACCCGGUUCCGGAACGGAC-5' (SEQ ID NO: 2078)

AR-3288 Target: 5'-TGGTCAAGTGGGCCAAGGCCTTGCCTG-3' (SEQ ID NO: 2483)

5'-GGUCAAGUGGGCCAAGGCCUUGCCUGG-3' (SEQ ID NO: 4980)
3'-CCAGUUCACCCGGUUCCGGAACGGACC-5' (SEQ ID NO: 2079)

AR-3289 Target: 5'-GGTCAAGTGGGCCAAGGCCTTGCCTGG-3' (SEQ ID NO: 2484)

5'-GUCAAGUGGGCCAAGGCCUUGCCUGGC-3' (SEQ ID NO: 4981)

3'-CAGUUCACCCGGUUCCGGAACGGACCG-5' (SEQ ID NO: 2080)

AR-3290 Target: 5'-GTCAAGTGGGCCAAGGCCTTGCCTGGC-3' (SEQ ID NO: 2485)

5'-UCAAGUGGGCCAAGGCCUUGCCUGGCU-3' (SEQ ID NO: 4982)
3'-AGUUCACCCGGUUCCGGAACGGACCGA-5' (SEQ ID NO: 2081)

AR-3291 Target: 5'-TCAAGTGGGCCAAGGCCTTGCCTGGCT-3' (SEQ ID NO: 2486)

5'-CAAGUGGGCCAAGGCCUUGCCUGGCUU-3' (SEQ ID NO: 4983)
3'-GUUCACCCGGUUCCGGAACGGACCGAA-5' (SEQ ID NO: 2082)

AR-3292 Target: 5'-CAAGTGGGCCAAGGCCTTGCCTGGCTT-3' (SEQ ID NO: 2487)

5'-AAGUGGGCCAAGGCCUUGCCUGGCUUC-3' (SEQ ID NO: 4984)
3'-UUCACCCGGUUCCGGAACGGACCGAAG-5' (SEQ ID NO: 2083)

AR-3293 Target: 5'-AAGTGGGCCAAGGCCTTGCCTGGCTTC-3' (SEQ ID NO: 2488)

5'-AGUGGGCCAAGGCCUUGCCUGGCUUCC-3' (SEQ ID NO: 4985)
3'-UCACCCGGUUCCGGAACGGACCGAAGG-5' (SEQ ID NO: 2084)

AR-3294 Target: 5'-AGTGGGCCAAGGCCTTGCCTGGCTTCC-3' (SEQ ID NO: 2489)

5'-GUGGGCCAAGGCCUUGCCUGGCUUCCG-3' (SEQ ID NO: 4986)
3'-CACCCGGUUCCGGAACGGACCGAAGGC-5' (SEQ ID NO: 2085)

AR-3295 Target: 5'-GTGGGCCAAGGCCTTGCCTGGCTTCCG-3' (SEQ ID NO: 2490)

5'-UGGGCCAAGGCCUUGCCUGGCUUCCGC-3' (SEQ ID NO: 4987)
3'-ACCCGGUUCCGGAACGGACCGAAGGCG-5' (SEQ ID NO: 2086)

AR-3296 Target: 5'-TGGGCCAAGGCCTTGCCTGGCTTCCGC-3' (SEQ ID NO: 2491)

5'-GGGCCAAGGCCUUGCCUGGCUUCCGCA-3' (SEQ ID NO: 4988)
3'-CCCGGUUCCGGAACGGACCGAAGGCGU-5' (SEQ ID NO: 2087)

AR-3297 Target: 5'-GGGCCAAGGCCTTGCCTGGCTTCCGCA-3' (SEQ ID NO: 2492)

5'-GGCCAAGGCCUUGCCUGGCUUCCGCAA-3' (SEQ ID NO: 4989)
3'-CCGGUUCCGGAACGGACCGAAGGCGUU-5' (SEQ ID NO: 2088)

AR-3298 Target: 5'-GGCCAAGGCCTTGCCTGGCTTCCGCAA-3' (SEQ ID NO: 2493)

5'-GCCAAGGCCUUGCCUGGCUUCCGCAAC-3' (SEQ ID NO: 4990)
3'-CGGUUCCGGAACGGACCGAAGGCGUUG-5' (SEQ ID NO: 2089)

AR-3299 Target: 5'-GCCAAGGCCTTGCCTGGCTTCCGCAAC-3' (SEQ ID NO: 2494)

5'-CCAAGGCCUUGCCUGGCUUCCGCAACU-3' (SEQ ID NO: 4991)
3'-GGUUCCGGAACGGACCGAAGGCGUUGA-5' (SEQ ID NO: 2090)

AR-3300 Target: 5'-CCAAGGCCTTGCCTGGCTTCCGCAACT-3' (SEQ ID NO: 2495)

5'-CAAGGCCUUGCCUGGCUUCCGCAACUU-3' (SEQ ID NO: 4992)
3'-GUUCCGGAACGGACCGAAGGCGUUGAA-5' (SEQ ID NO: 2091)

AR-3301 Target: 5'-CAAGGCCTTGCCTGGCTTCCGCAACTT-3' (SEQ ID NO: 2496)

5'-AAGGCCUUGCCUGGCUUCCGCAACUUA-3' (SEQ ID NO: 4993)
3'-UUCCGGAACGGACCGAAGGCGUUGAAU-5' (SEQ ID NO: 2092)

AR-3302 Target: 5'-AAGGCCTTGCCTGGCTTCCGCAACTTA-3' (SEQ ID NO: 2497)

5'-AGGCCUUGCCUGGCUUCCGCAACUUAC-3' (SEQ ID NO: 4994)
3'-UCCGGAACGGACCGAAGGCGUUGAAUG-5' (SEQ ID NO: 2093)

AR-3303 Target: 5'-AGGCCTTGCCTGGCTTCCGCAACTTAC-3' (SEQ ID NO: 2498)

5'-GGCCUUGCCUGGCUUCCGCAACUUACA-3' (SEQ ID NO: 4995)
3'-CCGGAACGGACCGAAGGCGUUGAAUGU-5' (SEQ ID NO: 2094)

AR-3304 Target: 5'-GGCCTTGCCTGGCTTCCGCAACTTACA-3' (SEQ ID NO: 2499)

5'-GCCUUGCCUGGCUUCCGCAACUUACAC-3' (SEQ ID NO: 4996)
3'-CGGAACGGACCGAAGGCGUUGAAUGUG-5' (SEQ ID NO: 2095)

AR-3305 Target: 5'-GCCTTGCCTGGCTTCCGCAACTTACAC-3' (SEQ ID NO: 2500)

5'-CCUUGCCUGGCUUCCGCAACUUACACG-3' (SEQ ID NO: 4997)
3'-GGAACGGACCGAAGGCGUUGAAUGUGC-5' (SEQ ID NO: 2096)

AR-3306 Target: 5'-CCTTGCCTGGCTTCCGCAACTTACACG-3' (SEQ ID NO: 2501)

5'-CUUGCCUGGCUUCCGCAACUUACACGU-3' (SEQ ID NO: 4998)
3'-GAACGGACCGAAGGCGUUGAAUGUGCA-5' (SEQ ID NO: 2097)

AR-3307 Target: 5'-CTTGCCTGGCTTCCGCAACTTACACGT-3' (SEQ ID NO: 2502)

5'-CCAAUGUCAACUCCAGGAUGCUCUACU-3' (SEQ ID NO: 4999)
3'-GGUUACAGUUGAGGUCCUACGAGAUGA-5' (SEQ ID NO: 2098)

AR-3408 Target: 5'-CCAATGTCAACTCCAGGATGCTCTACT-3' (SEQ ID NO: 2503)

5'-CAAUGUCAACUCCAGGAUGCUCUACUU-3' (SEQ ID NO: 5000)
3'-GUUACAGUUGAGGUCCUACGAGAUGAA-5' (SEQ ID NO: 2099)

AR-3409 Target: 5'-CAATGTCAACTCCAGGATGCTCTACTT-3' (SEQ ID NO: 2504)

5'-AAUGUCAACUCCAGGAUGCUCUACUUC-3' (SEQ ID NO: 5001)
3'-UUACAGUUGAGGUCCUACGAGAUGAAG-5' (SEQ ID NO: 2100)

AR-3410 Target: 5'-AATGTCAACTCCAGGATGCTCTACTTC-3' (SEQ ID NO: 2505)

5'-AUGUCAACUCCAGGAUGCUCUACUUCG-3' (SEQ ID NO: 5002)
3'-UACAGUUGAGGUCCUACGAGAUGAAGC-5' (SEQ ID NO: 2101)

AR-3411 Target: 5'-ATGTCAACTCCAGGATGCTCTACTTCG-3' (SEQ ID NO: 2506)

5'-UGUCAACUCCAGGAUGCUCUACUUCGC-3' (SEQ ID NO: 5003)
3'-ACAGUUGAGGUCCUACGAGAUGAAGCG-5' (SEQ ID NO: 2102)

AR-3412 Target: 5'-TGTCAACTCCAGGATGCTCTACTTCGC-3' (SEQ ID NO: 2507)

5'-GUCAACUCCAGGAUGCUCUACUUCGCC-3' (SEQ ID NO: 5004)
3'-CAGUUGAGGUCCUACGAGAUGAAGCGG-5' (SEQ ID NO: 2103)

AR-3413 Target: 5'-GTCAACTCCAGGATGCTCTACTTCGCC-3' (SEQ ID NO: 2508)

5'-UCAACUCCAGGAUGCUCUACUUCGCCC-3' (SEQ ID NO: 5005)
3'-AGUUGAGGUCCUACGAGAUGAAGCGGG-5' (SEQ ID NO: 2104)

AR-3414 Target: 5'-TCAACTCCAGGATGCTCTACTTCGCCC-3' (SEQ ID NO: 2509)

5'-UCUGGUUUUCAAUGAGUACCGCAUGCA-3' (SEQ ID NO: 5006)
3'-AGACCAAAAGUUACUCAUGGCGUACGU-5' (SEQ ID NO: 2105)

AR-3445 Target: 5'-TCTGGTTTTCAATGAGTACCGCATGCA-3' (SEQ ID NO: 2510)

5'-CUGGUUUUCAAUGAGUACCGCAUGCAC-3' (SEQ ID NO: 5007)
3'-GACCAAAAGUUACUCAUGGCGUACGUG-5' (SEQ ID NO: 2106)

AR-3446 Target: 5'-CTGGTTTTCAATGAGTACCGCATGCAC-3' (SEQ ID NO: 2511)

5'-UGGUUUUCAAUGAGUACCGCAUGCACA-3' (SEQ ID NO: 5008)

3'-ACCAAAAGUUACUCAUGGCGUACGUGU-5' (SEQ ID NO: 2107)

AR-3447 Target: 5'-TGGTTTTCAATGAGTACCGCATGCACA-3' (SEQ ID NO: 2512)

5'-GGUUUUCAAUGAGUACCGCAUGCACAA-3' (SEQ ID NO: 5009)
3'-CCAAAAGUUACUCAUGGCGUACGUGUU-5' (SEQ ID NO: 2108)

AR-3448 Target: 5'-GGTTTTCAATGAGTACCGCATGCACAA-3' (SEQ ID NO: 2513)

5'-GUUUUCAAUGAGUACCGCAUGCACAAG-3' (SEQ ID NO: 5010)
3'-CAAAAGUUACUCAUGGCGUACGUGUUC-5' (SEQ ID NO: 2109)

AR-3449 Target: 5'-GTTTTCAATGAGTACCGCATGCACAAG-3' (SEQ ID NO: 2514)

5'-UUUUCAAUGAGUACCGCAUGCACAAGU-3' (SEQ ID NO: 5011)
3'-AAAAGUUACUCAUGGCGUACGUGUUCA-5' (SEQ ID NO: 2110)

AR-3450 Target: 5'-TTTTCAATGAGTACCGCATGCACAAGT-3' (SEQ ID NO: 2515)

5'-UUUCAAUGAGUACCGCAUGCACAAGUC-3' (SEQ ID NO: 5012)
3'-AAAGUUACUCAUGGCGUACGUGUUCAG-5' (SEQ ID NO: 2111)

AR-3451 Target: 5'-TTTCAATGAGTACCGCATGCACAAGTC-3' (SEQ ID NO: 2516)

5'-UUCAAUGAGUACCGCAUGCACAAGUCC-3' (SEQ ID NO: 5013)
3'-AAGUUACUCAUGGCGUACGUGUUCAGG-5' (SEQ ID NO: 2112)

AR-3452 Target: 5'-TTCAATGAGTACCGCATGCACAAGTCC-3' (SEQ ID NO: 2517)

5'-UCAAUGAGUACCGCAUGCACAAGUCCC-3' (SEQ ID NO: 5014)
3'-AGUUACUCAUGGCGUACGUGUUCAGGG-5' (SEQ ID NO: 2113)

AR-3453 Target: 5'-TCAATGAGTACCGCATGCACAAGTCCC-3' (SEQ ID NO: 2518)

5'-CAAUGAGUACCGCAUGCACAAGUCCCG-3' (SEQ ID NO: 5015)
3'-GUUACUCAUGGCGUACGUGUUCAGGGC-5' (SEQ ID NO: 2114)

AR-3454 Target: 5'-CAATGAGTACCGCATGCACAAGTCCCG-3' (SEQ ID NO: 2519)

5'-AAUGAGUACCGCAUGCACAAGUCCCGG-3' (SEQ ID NO: 5016)
3'-UUACUCAUGGCGUACGUGUUCAGGGCC-5' (SEQ ID NO: 2115)

AR-3455 Target: 5'-AATGAGTACCGCATGCACAAGTCCCGG-3' (SEQ ID NO: 2520)

5'-AUGAGUACCGCAUGCACAAGUCCCGGA-3' (SEQ ID NO: 5017)
3'-UACUCAUGGCGUACGUGUUCAGGGCCU-5' (SEQ ID NO: 2116)

AR-3456 Target: 5'-ATGAGTACCGCATGCACAAGTCCCGGA-3' (SEQ ID NO: 2521)

5'-UGAGUACCGCAUGCACAAGUCCCGGAU-3' (SEQ ID NO: 5018)
3'-ACUCAUGGCGUACGUGUUCAGGGCCUA-5' (SEQ ID NO: 2117)

AR-3457 Target: 5'-TGAGTACCGCATGCACAAGTCCCGGAT-3' (SEQ ID NO: 2522)

5'-UCUCUCAAGAGUUUGGAUGGCUCCAAA-3' (SEQ ID NO: 5019)
3'-AGAGAGUUCUCAAACCUACCGAGGUUU-5' (SEQ ID NO: 2118)

AR-3513 Target: 5'-TCTCTCAAGAGTTTGGATGGCTCCAAA-3' (SEQ ID NO: 2523)

5'-CUCUCAAGAGUUUGGAUGGCUCCAAAU-3' (SEQ ID NO: 5020)
3'-GAGAGUUCUCAAACCUACCGAGGUUUA-5' (SEQ ID NO: 2119)

AR-3514 Target: 5'-CTCTCAAGAGTTTGGATGGCTCCAAAT-3' (SEQ ID NO: 2524)

5'-UCUCAAGAGUUUGGAUGGCUCCAAAUC-3' (SEQ ID NO: 5021)
3'-AGAGUUCUCAAACCUACCGAGGUUUAG-5' (SEQ ID NO: 2120)

AR-3515 Target: 5'-TCTCAAGAGTTTGGATGGCTCCAAATC-3' (SEQ ID NO: 2525)

5'-CUCAAGAGUUUGGAUGGCUCCAAAUCA-3' (SEQ ID NO: 5022)
3'-GAGUUCUCAAACCUACCGAGGUUUAGU-5' (SEQ ID NO: 2121)

AR-3516 Target: 5'-CTCAAGAGTTTGGATGGCTCCAAATCA-3' (SEQ ID NO: 2526)

5'-UCAAGAGUUUGGAUGGCUCCAAAUCAC-3' (SEQ ID NO: 5023)
3'-AGUUCUCAAACCUACCGAGGUUUAGUG-5' (SEQ ID NO: 2122)

AR-3517 Target: 5'-TCAAGAGTTTGGATGGCTCCAAATCAC-3' (SEQ ID NO: 2527)

5'-CAAGAGUUUGGAUGGCUCCAAAUCACC-3' (SEQ ID NO: 5024)
3'-GUUCUCAAACCUACCGAGGUUUAGUGG-5' (SEQ ID NO: 2123)

AR-3518 Target: 5'-CAAGAGTTTGGATGGCTCCAAATCACC-3' (SEQ ID NO: 2528)

5'-AAGAGUUUGGAUGGCUCCAAAUCACCC-3' (SEQ ID NO: 5025)
3'-UUCUCAAACCUACCGAGGUUUAGUGGG-5' (SEQ ID NO: 2124)

AR-3519 Target: 5'-AAGAGTTTGGATGGCTCCAAATCACCC-3' (SEQ ID NO: 2529)

5'-CCCAGGAAUUCCUGUGCAUGAAAGCAC-3' (SEQ ID NO: 5026)
3'-GGGUCCUUAAGGACACGUACUUUCGUG-5' (SEQ ID NO: 2125)

AR-3546 Target: 5'-CCCAGGAATTCCTGTGCATGAAAGCAC-3' (SEQ ID NO: 2530)

5'-CCAGGAAUUCCUGUGCAUGAAAGCACU-3' (SEQ ID NO: 5027)
3'-GGUCCUUAAGGACACGUACUUUCGUGA-5' (SEQ ID NO: 2126)

AR-3547 Target: 5'-CCAGGAATTCCTGTGCATGAAAGCACT-3' (SEQ ID NO: 2531)

5'-CAGGAAUUCCUGUGCAUGAAAGCACUG-3' (SEQ ID NO: 5028)
3'-GUCCUUAAGGACACGUACUUUCGUGAC-5' (SEQ ID NO: 2127)

AR-3548 Target: 5'-CAGGAATTCCTGTGCATGAAAGCACTG-3' (SEQ ID NO: 2532)

5'-AGGAAUUCCUGUGCAUGAAAGCACUGC-3' (SEQ ID NO: 5029)
3'-UCCUUAAGGACACGUACUUUCGUGACG-5' (SEQ ID NO: 2128)

AR-3549 Target: 5'-AGGAATTCCTGTGCATGAAAGCACTGC-3' (SEQ ID NO: 2533)

5'-GGAAUUCCUGUGCAUGAAAGCACUGCU-3' (SEQ ID NO: 5030)
3'-CCUUAAGGACACGUACUUUCGUGACGA-5' (SEQ ID NO: 2129)

AR-3550 Target: 5'-GGAATTCCTGTGCATGAAAGCACTGCT-3' (SEQ ID NO: 2534)

5'-GAAUUCCUGUGCAUGAAAGCACUGCUA-3' (SEQ ID NO: 5031)
3'-CUUAAGGACACGUACUUUCGUGACGAU-5' (SEQ ID NO: 2130)

AR-3551 Target: 5'-GAATTCCTGTGCATGAAAGCACTGCTA-3' (SEQ ID NO: 2535)

5'-AAUUCCUGUGCAUGAAAGCACUGCUAC-3' (SEQ ID NO: 5032)
3'-UUAAGGACACGUACUUUCGUGACGAUG-5' (SEQ ID NO: 2131)

AR-3552 Target: 5'-AATTCCTGTGCATGAAAGCACTGCTAC-3' (SEQ ID NO: 2536)

5'-AUUCCUGUGCAUGAAAGCACUGCUACU-3' (SEQ ID NO: 5033)
3'-UAAGGACACGUACUUUCGUGACGAUGA-5' (SEQ ID NO: 2132)

AR-3553 Target: 5'-ATTCCTGTGCATGAAAGCACTGCTACT-3' (SEQ ID NO: 2537)

5'-UUCCUGUGCAUGAAAGCACUGCUACUC-3' (SEQ ID NO: 5034)
3'-AAGGACACGUACUUUCGUGACGAUGAG-5' (SEQ ID NO: 2133)

AR-3554 Target: 5'-TTCCTGTGCATGAAAGCACTGCTACTC-3' (SEQ ID NO: 2538)

5'-UCCUGUGCAUGAAAGCACUGCUACUCU-3' (SEQ ID NO: 5035)

3'-AGGACACGUACUUUCGUGACGAUGAGA-5' (SEQ ID NO: 2134)

AR-3555 Target: 5'-TCCTGTGCATGAAAGCACTGCTACTCT-3' (SEQ ID NO: 2539)

5'-CCUGUGCAUGAAAGCACUGCUACUCUU-3' (SEQ ID NO: 5036)
3'-GGACACGUACUUUCGUGACGAUGAGAA-5' (SEQ ID NO: 2135)

AR-3556 Target: 5'-CCTGTGCATGAAAGCACTGCTACTCTT-3' (SEQ ID NO: 2540)

5'-UACUCUUCAGCAUUAUUCCAGUGGAUG-3' (SEQ ID NO: 5037)
3'-AUGAGAAGUCGUAAUAAGGUCACCUAC-5' (SEQ ID NO: 2136)

AR-3576 Target: 5'-TACTCTTCAGCATTATTCCAGTGGATG-3' (SEQ ID NO: 2541)

5'-ACUCUUCAGCAUUAUUCCAGUGGAUGG-3' (SEQ ID NO: 5038)
3'-UGAGAAGUCGUAAUAAGGUCACCUACC-5' (SEQ ID NO: 2137)

AR-3577 Target: 5'-ACTCTTCAGCATTATTCCAGTGGATGG-3' (SEQ ID NO: 2542)

5'-CUCUUCAGCAUUAUUCCAGUGGAUGGG-3' (SEQ ID NO: 5039)
3'-GAGAAGUCGUAAUAAGGUCACCUACCC-5' (SEQ ID NO: 2138)

AR-3578 Target: 5'-CTCTTCAGCATTATTCCAGTGGATGGG-3' (SEQ ID NO: 2543)

5'-UCUUCAGCAUUAUUCCAGUGGAUGGGC-3' (SEQ ID NO: 5040)
3'-AGAAGUCGUAAUAAGGUCACCUACCCG-5' (SEQ ID NO: 2139)

AR-3579 Target: 5'-TCTTCAGCATTATTCCAGTGGATGGGC-3' (SEQ ID NO: 2544)

5'-CUUCAGCAUUAUUCCAGUGGAUGGGCU-3' (SEQ ID NO: 5041)
3'-GAAGUCGUAAUAAGGUCACCUACCCGA-5' (SEQ ID NO: 2140)

AR-3580 Target: 5'-CTTCAGCATTATTCCAGTGGATGGGCT-3' (SEQ ID NO: 2545)

5'-UUCAGCAUUAUUCCAGUGGAUGGGCUG-3' (SEQ ID NO: 5042)
3'-AAGUCGUAAUAAGGUCACCUACCCGAC-5' (SEQ ID NO: 2141)

AR-3581 Target: 5'-TTCAGCATTATTCCAGTGGATGGGCTG-3' (SEQ ID NO: 2546)

5'-UCAGCAUUAUUCCAGUGGAUGGGCUGA-3' (SEQ ID NO: 5043)
3'-AGUCGUAAUAAGGUCACCUACCCGACU-5' (SEQ ID NO: 2142)

AR-3582 Target: 5'-TCAGCATTATTCCAGTGGATGGGCTGA-3' (SEQ ID NO: 2547)

5'-CAGCAUUAUUCCAGUGGAUGGGCUGAA-3' (SEQ ID NO: 5044)
3'-GUCGUAAUAAGGUCACCUACCCGACUU-5' (SEQ ID NO: 2143)

AR-3583 Target: 5'-CAGCATTATTCCAGTGGATGGGCTGAA-3' (SEQ ID NO: 2548)

5'-AGCAUUAUUCCAGUGGAUGGGCUGAAA-3' (SEQ ID NO: 5045)
3'-UCGUAAUAAGGUCACCUACCCGACUUU-5' (SEQ ID NO: 2144)

AR-3584 Target: 5'-AGCATTATTCCAGTGGATGGGCTGAAA-3' (SEQ ID NO: 2549)

5'-GCAUUAUUCCAGUGGAUGGGCUGAAAA-3' (SEQ ID NO: 5046)
3'-CGUAAUAAGGUCACCUACCCGACUUUU-5' (SEQ ID NO: 2145)

AR-3585 Target: 5'-GCATTATTCCAGTGGATGGGCTGAAAA-3' (SEQ ID NO: 2550)

5'-CAUUAUUCCAGUGGAUGGGCUGAAAAA-3' (SEQ ID NO: 5047)
3'-GUAAUAAGGUCACCUACCCGACUUUUU-5' (SEQ ID NO: 2146)

AR-3586 Target: 5'-CATTATTCCAGTGGATGGGCTGAAAAA-3' (SEQ ID NO: 2551)

5'-AUUAUUCCAGUGGAUGGGCUGAAAAAU-3' (SEQ ID NO: 5048)
3'-UAAUAAGGUCACCUACCCGACUUUUUA-5' (SEQ ID NO: 2147)

AR-3587 Target: 5'-ATTATTCCAGTGGATGGGCTGAAAAAT-3' (SEQ ID NO: 2552)

5'-UUAUUCCAGUGGAUGGGCUGAAAAAUC-3' (SEQ ID NO: 5049)
3'-AAUAAGGUCACCUACCCGACUUUUUAG-5' (SEQ ID NO: 2148)

AR-3588 Target: 5'-TTATTCCAGTGGATGGGCTGAAAAATC-3' (SEQ ID NO: 2553)

5'-UAUUCCAGUGGAUGGGCUGAAAAAUCA-3' (SEQ ID NO: 5050)
3'-AUAAGGUCACCUACCCGACUUUUUAGU-5' (SEQ ID NO: 2149)

AR-3589 Target: 5'-TATTCCAGTGGATGGGCTGAAAAATCA-3' (SEQ ID NO: 2554)

5'-AUUCCAGUGGAUGGGCUGAAAAAUCAA-3' (SEQ ID NO: 5051)
3'-UAAGGUCACCUACCCGACUUUUUAGUU-5' (SEQ ID NO: 2150)

AR-3590 Target: 5'-ATTCCAGTGGATGGGCTGAAAAATCAA-3' (SEQ ID NO: 2555)

5'-UUCCAGUGGAUGGGCUGAAAAAUCAAA-3' (SEQ ID NO: 5052)
3'-AAGGUCACCUACCCGACUUUUUAGUUU-5' (SEQ ID NO: 2151)

AR-3591 Target: 5'-TTCCAGTGGATGGGCTGAAAAATCAAA-3' (SEQ ID NO: 2556)

5'-UCCAGUGGAUGGGCUGAAAAAUCAAAA-3' (SEQ ID NO: 5053)
3'-AGGUCACCUACCCGACUUUUUAGUUUU-5' (SEQ ID NO: 2152)

AR-3592 Target: 5'-TCCAGTGGATGGGCTGAAAAATCAAAA-3' (SEQ ID NO: 2557)

5'-CCAGUGGAUGGGCUGAAAAAUCAAAAA-3' (SEQ ID NO: 5054)
3'-GGUCACCUACCCGACUUUUUAGUUUUU-5' (SEQ ID NO: 2153)

AR-3593 Target: 5'-CCAGTGGATGGGCTGAAAAATCAAAAA-3' (SEQ ID NO: 2558)

5'-CAGUGGAUGGGCUGAAAAAUCAAAAAU-3' (SEQ ID NO: 5055)
3'-GUCACCUACCCGACUUUUUAGUUUUUA-5' (SEQ ID NO: 2154)

AR-3594 Target: 5'-CAGTGGATGGGCTGAAAAATCAAAAAT-3' (SEQ ID NO: 2559)

5'-AGUGGAUGGGCUGAAAAAUCAAAAAUU-3' (SEQ ID NO: 5056)
3'-UCACCUACCCGACUUUUUAGUUUUUAA-5' (SEQ ID NO: 2155)

AR-3595 Target: 5'-AGTGGATGGGCTGAAAAATCAAAAATT-3' (SEQ ID NO: 2560)

5'-GUGGAUGGGCUGAAAAAUCAAAAAUUC-3' (SEQ ID NO: 5057)
3'-CACCUACCCGACUUUUUAGUUUUUAAG-5' (SEQ ID NO: 2156)

AR-3596 Target: 5'-GTGGATGGGCTGAAAAATCAAAAATTC-3' (SEQ ID NO: 2561)

5'-UGGAUGGGCUGAAAAAUCAAAAAUUCU-3' (SEQ ID NO: 5058)
3'-ACCUACCCGACUUUUUAGUUUUUAAGA-5' (SEQ ID NO: 2157)

AR-3597 Target: 5'-TGGATGGGCTGAAAAATCAAAAATTCT-3' (SEQ ID NO: 2562)

5'-GGAUGGGCUGAAAAAUCAAAAAUUCUU-3' (SEQ ID NO: 5059)
3'-CCUACCCGACUUUUUAGUUUUUAAGAA-5' (SEQ ID NO: 2158)

AR-3598 Target: 5'-GGATGGGCTGAAAAATCAAAAATTCTT-3' (SEQ ID NO: 2563)

5'-GAUGGGCUGAAAAAUCAAAAAUUCUUU-3' (SEQ ID NO: 5060)
3'-CUACCCGACUUUUUAGUUUUUAAGAAA-5' (SEQ ID NO: 2159)

AR-3599 Target: 5'-GATGGGCTGAAAAATCAAAAATTCTTT-3' (SEQ ID NO: 2564)

5'-AUGGGCUGAAAAAUCAAAAAUUCUUUG-3' (SEQ ID NO: 5061)
3'-UACCCGACUUUUUAGUUUUUAAGAAAC-5' (SEQ ID NO: 2160)

AR-3600 Target: 5'-ATGGGCTGAAAAATCAAAAATTCTTTG-3' (SEQ ID NO: 2565)

5'-UGGGCUGAAAAAUCAAAAAUUCUUUGA-3' (SEQ ID NO: 5062)

3'-ACCCGACUUUUUAGUUUUUAAGAAACU-5' (SEQ ID NO: 2161)

AR-3601 Target: 5'-TGGGCTGAAAAATCAAAAATTCTTTGA-3' (SEQ ID NO: 2566)

5'-GGGCUGAAAAAUCAAAAAUUCUUUGAU-3' (SEQ ID NO: 5063)
3'-CCCGACUUUUUAGUUUUUAAGAAACUA-5' (SEQ ID NO: 2162)

AR-3602 Target: 5'-GGGCTGAAAAATCAAAAATTCTTTGAT-3' (SEQ ID NO: 2567)

5'-GGCUGAAAAAUCAAAAAUUCUUUGAUG-3' (SEQ ID NO: 5064)
3'-CCGACUUUUUAGUUUUUAAGAAACUAC-5' (SEQ ID NO: 2163)

AR-3603 Target: 5'-GGCTGAAAAATCAAAAATTCTTTGATG-3' (SEQ ID NO: 2568)

5'-GCUGAAAAAUCAAAAAUUCUUUGAUGA-3' (SEQ ID NO: 5065)
3'-CGACUUUUUAGUUUUUAAGAAACUACU-5' (SEQ ID NO: 2164)

AR-3604 Target: 5'-GCTGAAAAATCAAAAATTCTTTGATGA-3' (SEQ ID NO: 2569)

5'-CUGAAAAAUCAAAAAUUCUUUGAUGAA-3' (SEQ ID NO: 5066)
3'-GACUUUUUAGUUUUUAAGAAACUACUU-5' (SEQ ID NO: 2165)

AR-3605 Target: 5'-CTGAAAAATCAAAAATTCTTTGATGAA-3' (SEQ ID NO: 2570)

5'-UGAAAAAUCAAAAAUUCUUUGAUGAAC-3' (SEQ ID NO: 5067)
3'-ACUUUUUAGUUUUUAAGAAACUACUUG-5' (SEQ ID NO: 2166)

AR-3606 Target: 5'-TGAAAAATCAAAAATTCTTTGATGAAC-3' (SEQ ID NO: 2571)

5'-AAAAAUCAAAAAUUCUUUGAUGAACUU-3' (SEQ ID NO: 5068)
3'-UUUUUAGUUUUUAAGAAACUACUUGAA-5' (SEQ ID NO: 2167)

AR-3608 Target: 5'-AAAAATCAAAAATTCTTTGATGAACTT-3' (SEQ ID NO: 2572)

5'-AAAAUCAAAAAUUCUUUGAUGAACUUC-3' (SEQ ID NO: 5069)
3'-UUUUAGUUUUUAAGAAACUACUUGAAG-5' (SEQ ID NO: 2168)

AR-3609 Target: 5'-AAAATCAAAAATTCTTTGATGAACTTC-3' (SEQ ID NO: 2573)

5'-AAAUCAAAAAUUCUUUGAUGAACUUCG-3' (SEQ ID NO: 5070)
3'-UUUAGUUUUUAAGAAACUACUUGAAGC-5' (SEQ ID NO: 2169)

AR-3610 Target: 5'-AAATCAAAAATTCTTTGATGAACTTCG-3' (SEQ ID NO: 2574)

5'-AAUCAAAAAUUCUUUGAUGAACUUCGA-3' (SEQ ID NO: 5071)
3'-UUAGUUUUUAAGAAACUACUUGAAGCU-5' (SEQ ID NO: 2170)

AR-3611 Target: 5'-AATCAAAAATTCTTTGATGAACTTCGA-3' (SEQ ID NO: 2575)

5'-AUCAAAAAUUCUUUGAUGAACUUCGAA-3' (SEQ ID NO: 5072)
3'-UAGUUUUUAAGAAACUACUUGAAGCUU-5' (SEQ ID NO: 2171)

AR-3612 Target: 5'-ATCAAAAATTCTTTGATGAACTTCGAA-3' (SEQ ID NO: 2576)

5'-UCAAAAAUUCUUUGAUGAACUUCGAAU-3' (SEQ ID NO: 5073)
3'-AGUUUUUAAGAAACUACUUGAAGCUUA-5' (SEQ ID NO: 2172)

AR-3613 Target: 5'-TCAAAAATTCTTTGATGAACTTCGAAT-3' (SEQ ID NO: 2577)

5'-CAAAAAUUCUUUGAUGAACUUCGAAUG-3' (SEQ ID NO: 5074)
3'-GUUUUUAAGAAACUACUUGAAGCUUAC-5' (SEQ ID NO: 2173)

AR-3614 Target: 5'-CAAAAATTCTTTGATGAACTTCGAATG-3' (SEQ ID NO: 2578)

5'-AAAAAUUCUUUGAUGAACUUCGAAUGA-3' (SEQ ID NO: 5075)
3'-UUUUUAAGAAACUACUUGAAGCUUACU-5' (SEQ ID NO: 2174)

AR-3615 Target: 5'-AAAAATTCTTTGATGAACTTCGAATGA-3' (SEQ ID NO: 2579)

5'-AAAAUUCUUUGAUGAACUUCGAAUGAA-3' (SEQ ID NO: 5076)
3'-UUUUAAGAAACUACUUGAAGCUUACUU-5' (SEQ ID NO: 2175)

AR-3616 Target: 5'-AAAATTCTTTGATGAACTTCGAATGAA-3' (SEQ ID NO: 2580)

5'-AAAUUCUUUGAUGAACUUCGAAUGAAC-3' (SEQ ID NO: 5077)
3'-UUUAAGAAACUACUUGAAGCUUACUUG-5' (SEQ ID NO: 2176)

AR-3617 Target: 5'-AAATTCTTTGATGAACTTCGAATGAAC-3' (SEQ ID NO: 2581)

5'-AAUUCUUUGAUGAACUUCGAAUGAACU-3' (SEQ ID NO: 5078)
3'-UUAAGAAACUACUUGAAGCUUACUUGA-5' (SEQ ID NO: 2177)

AR-3618 Target: 5'-AATTCTTTGATGAACTTCGAATGAACT-3' (SEQ ID NO: 2582)

5'-AUUCUUUGAUGAACUUCGAAUGAACUA-3' (SEQ ID NO: 5079)
3'-UAAGAAACUACUUGAAGCUUACUUGAU-5' (SEQ ID NO: 2178)

AR-3619 Target: 5'-ATTCTTTGATGAACTTCGAATGAACTA-3' (SEQ ID NO: 2583)

5'-UUCUUUGAUGAACUUCGAAUGAACUAC-3' (SEQ ID NO: 5080)
3'-AAGAAACUACUUGAAGCUUACUUGAUG-5' (SEQ ID NO: 2179)

AR-3620 Target: 5'-TTCTTTGATGAACTTCGAATGAACTAC-3' (SEQ ID NO: 2584)

5'-UCUUUGAUGAACUUCGAAUGAACUACA-3' (SEQ ID NO: 5081)
3'-AGAAACUACUUGAAGCUUACUUGAUGU-5' (SEQ ID NO: 2180)

AR-3621 Target: 5'-TCTTTGATGAACTTCGAATGAACTACA-3' (SEQ ID NO: 2585)

5'-CUUUGAUGAACUUCGAAUGAACUACAU-3' (SEQ ID NO: 5082)
3'-GAAACUACUUGAAGCUUACUUGAUGUA-5' (SEQ ID NO: 2181)

AR-3622 Target: 5'-CTTTGATGAACTTCGAATGAACTACAT-3' (SEQ ID NO: 2586)

5'-UUUGAUGAACUUCGAAUGAACUACAUC-3' (SEQ ID NO: 5083)
3'-AAACUACUUGAAGCUUACUUGAUGUAG-5' (SEQ ID NO: 2182)

AR-3623 Target: 5'-TTTGATGAACTTCGAATGAACTACATC-3' (SEQ ID NO: 2587)

5'-UUGAUGAACUUCGAAUGAACUACAUCA-3' (SEQ ID NO: 5084)
3'-AACUACUUGAAGCUUACUUGAUGUAGU-5' (SEQ ID NO: 2183)

AR-3624 Target: 5'-TTGATGAACTTCGAATGAACTACATCA-3' (SEQ ID NO: 2588)

5'-UGAUGAACUUCGAAUGAACUACAUCAA-3' (SEQ ID NO: 5085)
3'-ACUACUUGAAGCUUACUUGAUGUAGUU-5' (SEQ ID NO: 2184)

AR-3625 Target: 5'-TGATGAACTTCGAATGAACTACATCAA-3' (SEQ ID NO: 2589)

5'-GAUGAACUUCGAAUGAACUACAUCAAG-3' (SEQ ID NO: 5086)
3'-CUACUUGAAGCUUACUUGAUGUAGUUC-5' (SEQ ID NO: 2185)

AR-3626 Target: 5'-GATGAACTTCGAATGAACTACATCAAG-3' (SEQ ID NO: 2590)

5'-AUGAACUUCGAAUGAACUACAUCAAGG-3' (SEQ ID NO: 5087)
3'-UACUUGAAGCUUACUUGAUGUAGUUCC-5' (SEQ ID NO: 2186)

AR-3627 Target: 5'-ATGAACTTCGAATGAACTACATCAAGG-3' (SEQ ID NO: 2591)

5'-UGAACUUCGAAUGAACUACAUCAAGGA-3' (SEQ ID NO: 5088)
3'-ACUUGAAGCUUACUUGAUGUAGUUCCU-5' (SEQ ID NO: 2187)

AR-3628 Target: 5'-TGAACTTCGAATGAACTACATCAAGGA-3' (SEQ ID NO: 2592)

5'-GAACUUCGAAUGAACUACAUCAAGGAA-3' (SEQ ID NO: 5089)

3'-CUUGAAGCUUACUUGAUGUAGUUCCUU-5' (SEQ ID NO: 2188)

AR-3629 Target: 5'-GAACTTCGAATGAACTACATCAAGGAA-3' (SEQ ID NO: 2593)

5'-AACUUCGAAUGAACUACAUCAAGGAAC-3' (SEQ ID NO: 5090)
3'-UUGAAGCUUACUUGAUGUAGUUCCUUG-5' (SEQ ID NO: 2189)

AR-3630 Target: 5'-AACTTCGAATGAACTACATCAAGGAAC-3' (SEQ ID NO: 2594)

5'-ACUUCGAAUGAACUACAUCAAGGAACU-3' (SEQ ID NO: 5091)
3'-UGAAGCUUACUUGAUGUAGUUCCUUGA-5' (SEQ ID NO: 2190)

AR-3631 Target: 5'-ACTTCGAATGAACTACATCAAGGAACT-3' (SEQ ID NO: 2595)

5'-CUUCGAAUGAACUACAUCAAGGAACUC-3' (SEQ ID NO: 5092)
3'-GAAGCUUACUUGAUGUAGUUCCUUGAG-5' (SEQ ID NO: 2191)

AR-3632 Target: 5'-CTTCGAATGAACTACATCAAGGAACTC-3' (SEQ ID NO: 2596)

5'-UUCGAAUGAACUACAUCAAGGAACUCG-3' (SEQ ID NO: 5093)
3'-AAGCUUACUUGAUGUAGUUCCUUGAGC-5' (SEQ ID NO: 2192)

AR-3633 Target: 5'-TTCGAATGAACTACATCAAGGAACTCG-3' (SEQ ID NO: 2597)

5'-UCGAAUGAACUACAUCAAGGAACUCGA-3' (SEQ ID NO: 5094)
3'-AGCUUACUUGAUGUAGUUCCUUGAGCU-5' (SEQ ID NO: 2193)

AR-3634 Target: 5'-TCGAATGAACTACATCAAGGAACTCGA-3' (SEQ ID NO: 2598)

5'-CGAAUGAACUACAUCAAGGAACUCGAU-3' (SEQ ID NO: 5095)
3'-GCUUACUUGAUGUAGUUCCUUGAGCUA-5' (SEQ ID NO: 2194)

AR-3635 Target: 5'-CGAATGAACTACATCAAGGAACTCGAT-3' (SEQ ID NO: 2599)

5'-GAAUGAACUACAUCAAGGAACUCGAUC-3' (SEQ ID NO: 5096)
3'-CUUACUUGAUGUAGUUCCUUGAGCUAG-5' (SEQ ID NO: 2195)

AR-3636 Target: 5'-GAATGAACTACATCAAGGAACTCGATC-3' (SEQ ID NO: 2600)

5'-AAUGAACUACAUCAAGGAACUCGAUCG-3' (SEQ ID NO: 5097)
3'-UUACUUGAUGUAGUUCCUUGAGCUAGC-5' (SEQ ID NO: 2196)

AR-3637 Target: 5'-AATGAACTACATCAAGGAACTCGATCG-3' (SEQ ID NO: 2601)

5'-AUGAACUACAUCAAGGAACUCGAUCGU-3' (SEQ ID NO: 5098)
3'-UACUUGAUGUAGUUCCUUGAGCUAGCA-5' (SEQ ID NO: 2197)

AR-3638 Target: 5'-ATGAACTACATCAAGGAACTCGATCGT-3' (SEQ ID NO: 2602)

5'-UGAACUACAUCAAGGAACUCGAUCGUA-3' (SEQ ID NO: 5099)
3'-ACUUGAUGUAGUUCCUUGAGCUAGCAU-5' (SEQ ID NO: 2198)

AR-3639 Target: 5'-TGAACTACATCAAGGAACTCGATCGTA-3' (SEQ ID NO: 2603)

5'-GAACUACAUCAAGGAACUCGAUCGUAU-3' (SEQ ID NO: 5100)
3'-CUUGAUGUAGUUCCUUGAGCUAGCAUA-5' (SEQ ID NO: 2199)

AR-3640 Target: 5'-GAACTACATCAAGGAACTCGATCGTAT-3' (SEQ ID NO: 2604)

5'-AACUACAUCAAGGAACUCGAUCGUAUC-3' (SEQ ID NO: 5101)
3'-UUGAUGUAGUUCCUUGAGCUAGCAUAG-5' (SEQ ID NO: 2200)

AR-3641 Target: 5'-AACTACATCAAGGAACTCGATCGTATC-3' (SEQ ID NO: 2605)

5'-ACUACAUCAAGGAACUCGAUCGUAUCA-3' (SEQ ID NO: 5102)
3'-UGAUGUAGUUCCUUGAGCUAGCAUAGU-5' (SEQ ID NO: 2201)

AR-3642 Target: 5'-ACTACATCAAGGAACTCGATCGTATCA-3' (SEQ ID NO: 2606)

5'-CUACAUCAAGGAACUCGAUCGUAUCAU-3' (SEQ ID NO: 5103)
3'-GAUGUAGUUCCUUGAGCUAGCAUAGUA-5' (SEQ ID NO: 2202)

AR-3643 Target: 5'-CTACATCAAGGAACTCGATCGTATCAT-3' (SEQ ID NO: 2607)

5'-GUAUCAUUGCAUGCAAAAGAAAAAAUC-3' (SEQ ID NO: 5104)
3'-CAUAGUAACGUACGUUUUCUUUUUUAG-5' (SEQ ID NO: 2203)

AR-3663 Target: 5'-GTATCATTGCATGCAAAAGAAAAAATC-3' (SEQ ID NO: 2608)

5'-UAUCAUUGCAUGCAAAAGAAAAAAUCC-3' (SEQ ID NO: 5105)
3'-AUAGUAACGUACGUUUUCUUUUUUAGG-5' (SEQ ID NO: 2204)

AR-3664 Target: 5'-TATCATTGCATGCAAAAGAAAAAATCC-3' (SEQ ID NO: 2609)

5'-AAAAUCCCACAUCCUGCUCAAGACGCU-3' (SEQ ID NO: 5106)
3'-UUUUAGGGUGUAGGACGAGUUCUGCGA-5' (SEQ ID NO: 2205)

AR-3684 Target: 5'-AAAATCCCACATCCTGCTCAAGACGCT-3' (SEQ ID NO: 2610)

5'-AAAUCCCACAUCCUGCUCAAGACGCUU-3' (SEQ ID NO: 5107)
3'-UUUAGGGUGUAGGACGAGUUCUGCGAA-5' (SEQ ID NO: 2206)

AR-3685 Target: 5'-AAATCCCACATCCTGCTCAAGACGCTT-3' (SEQ ID NO: 2611)

5'-GACGCUUCUACCAGCUCACCAAGCUCC-3' (SEQ ID NO: 5108)
3'-CUGCGAAGAUGGUCGAGUGGUUCGAGG-5' (SEQ ID NO: 2207)

AR-3705 Target: 5'-GACGCTTCTACCAGCTCACCAAGCTCC-3' (SEQ ID NO: 2612)

5'-ACGCUUCUACCAGCUCACCAAGCUCCU-3' (SEQ ID NO: 5109)
3'-UGCGAAGAUGGUCGAGUGGUUCGAGGA-5' (SEQ ID NO: 2208)

AR-3706 Target: 5'-ACGCTTCTACCAGCTCACCAAGCTCCT-3' (SEQ ID NO: 2613)

5'-CGCUUCUACCAGCUCACCAAGCUCCUG-3' (SEQ ID NO: 5110)
3'-GCGAAGAUGGUCGAGUGGUUCGAGGAC-5' (SEQ ID NO: 2209)

AR-3707 Target: 5'-CGCTTCTACCAGCTCACCAAGCTCCTG-3' (SEQ ID NO: 2614)

5'-GCUUCUACCAGCUCACCAAGCUCCUGG-3' (SEQ ID NO: 5111)
3'-CGAAGAUGGUCGAGUGGUUCGAGGACC-5' (SEQ ID NO: 2210)

AR-3708 Target: 5'-GCTTCTACCAGCTCACCAAGCTCCTGG-3' (SEQ ID NO: 2615)

5'-CUUCUACCAGCUCACCAAGCUCCUGGA-3' (SEQ ID NO: 5112)
3'-GAAGAUGGUCGAGUGGUUCGAGGACCU-5' (SEQ ID NO: 2211)

AR-3709 Target: 5'-CTTCTACCAGCTCACCAAGCTCCTGGA-3' (SEQ ID NO: 2616)

5'-UUCUACCAGCUCACCAAGCUCCUGGAC-3' (SEQ ID NO: 5113)
3'-AAGAUGGUCGAGUGGUUCGAGGACCUG-5' (SEQ ID NO: 2212)

AR-3710 Target: 5'-TTCTACCAGCTCACCAAGCTCCTGGAC-3' (SEQ ID NO: 2617)

5'-UCUACCAGCUCACCAAGCUCCUGGACU-3' (SEQ ID NO: 5114)
3'-AGAUGGUCGAGUGGUUCGAGGACCUGA-5' (SEQ ID NO: 2213)

AR-3711 Target: 5'-TCTACCAGCTCACCAAGCTCCTGGACT-3' (SEQ ID NO: 2618)

5'-CUACCAGCUCACCAAGCUCCUGGACUC-3' (SEQ ID NO: 5115)
3'-GAUGGUCGAGUGGUUCGAGGACCUGAG-5' (SEQ ID NO: 2214)

AR-3712 Target: 5'-CTACCAGCTCACCAAGCTCCTGGACTC-3' (SEQ ID NO: 2619)

5'-UACCAGCUCACCAAGCUCCUGGACUCC-3' (SEQ ID NO: 5116)

3'-AUGGUCGAGUGGUUCGAGGACCUGAGG-5' (SEQ ID NO: 2215)

AR-3713 Target: 5'-TACCAGCTCACCAAGCTCCTGGACTCC-3' (SEQ ID NO: 2620)

5'-ACCAGCUCACCAAGCUCCUGGACUCCG-3' (SEQ ID NO: 5117)
3'-UGGUCGAGUGGUUCGAGGACCUGAGGC-5' (SEQ ID NO: 2216)

AR-3714 Target: 5'-ACCAGCTCACCAAGCTCCTGGACTCCG-3' (SEQ ID NO: 2621)

5'-CCAGCUCACCAAGCUCCUGGACUCCGU-3' (SEQ ID NO: 5118)
3'-GGUCGAGUGGUUCGAGGACCUGAGGCA-5' (SEQ ID NO: 2217)

AR-3715 Target: 5'-CCAGCTCACCAAGCTCCTGGACTCCGT-3' (SEQ ID NO: 2622)

5'-AGCUCACCAAGCUCCUGGACUCCGUGC-3' (SEQ ID NO: 5119)
3'-UCGAGUGGUUCGAGGACCUGAGGCACG-5' (SEQ ID NO: 2218)

AR-3717 Target: 5'-AGCTCACCAAGCTCCTGGACTCCGTGC-3' (SEQ ID NO: 2623)

5'-AGCUCCUGGACUCCGUGCAGCCUAUUG-3' (SEQ ID NO: 5120)
3'-UCGAGGACCUGAGGCACGUCGGAUAAC-5' (SEQ ID NO: 2219)

AR-3726 Target: 5'-AGCTCCTGGACTCCGTGCAGCCTATTG-3' (SEQ ID NO: 2624)

5'-UCCGUGCAGCCUAUUGCGAGAGAGCUG-3' (SEQ ID NO: 5121)
3'-AGGCACGUCGGAUAACGCUCUCUCGAC-5' (SEQ ID NO: 2220)

AR-3737 Target: 5'-TCCGTGCAGCCTATTGCGAGAGAGCTG-3' (SEQ ID NO: 2625)

5'-CGAGAGAGCUGCAUCAGUUCACUUUUG-3' (SEQ ID NO: 5122)
3'-GCUCUCUCGACGUAGUCAAGUGAAAAC-5' (SEQ ID NO: 2221)

AR-3753 Target: 5'-CGAGAGAGCTGCATCAGTTCACTTTTG-3' (SEQ ID NO: 2626)

5'-GAGAGAGCUGCAUCAGUUCACUUUUGA-3' (SEQ ID NO: 5123)
3'-CUCUCUCGACGUAGUCAAGUGAAAACU-5' (SEQ ID NO: 2222)

AR-3754 Target: 5'-GAGAGAGCTGCATCAGTTCACTTTTGA-3' (SEQ ID NO: 2627)

5'-AGAGAGCUGCAUCAGUUCACUUUUGAC-3' (SEQ ID NO: 5124)
3'-UCUCUCGACGUAGUCAAGUGAAAACUG-5' (SEQ ID NO: 2223)

AR-3755 Target: 5'-AGAGAGCTGCATCAGTTCACTTTTGAC-3' (SEQ ID NO: 2628)

5'-GAGAGCUGCAUCAGUUCACUUUUGACC-3' (SEQ ID NO: 5125)
3'-CUCUCGACGUAGUCAAGUGAAAACUGG-5' (SEQ ID NO: 2224)

AR-3756 Target: 5'-GAGAGCTGCATCAGTTCACTTTTGACC-3' (SEQ ID NO: 2629)

5'-AGAGCUGCAUCAGUUCACUUUUGACCU-3' (SEQ ID NO: 5126)
3'-UCUCGACGUAGUCAAGUGAAAACUGGA-5' (SEQ ID NO: 2225)

AR-3757 Target: 5'-AGAGCTGCATCAGTTCACTTTTGACCT-3' (SEQ ID NO: 2630)

5'-GAGCUGCAUCAGUUCACUUUUGACCUG-3' (SEQ ID NO: 5127)
3'-CUCGACGUAGUCAAGUGAAAACUGGAC-5' (SEQ ID NO: 2226)

AR-3758 Target: 5'-GAGCTGCATCAGTTCACTTTTGACCTG-3' (SEQ ID NO: 2631)

5'-AGCUGCAUCAGUUCACUUUUGACCUGC-3' (SEQ ID NO: 5128)
3'-UCGACGUAGUCAAGUGAAAACUGGACG-5' (SEQ ID NO: 2227)

AR-3759 Target: 5'-AGCTGCATCAGTTCACTTTTGACCTGC-3' (SEQ ID NO: 2632)

5'-GCUGCAUCAGUUCACUUUUGACCUGCU-3' (SEQ ID NO: 5129)
3'-CGACGUAGUCAAGUGAAAACUGGACGA-5' (SEQ ID NO: 2228)

AR-3760 Target: 5'-GCTGCATCAGTTCACTTTTGACCTGCT-3' (SEQ ID NO: 2633)

5'-CUGCAUCAGUUCACUUUUGACCUGCUA-3' (SEQ ID NO: 5130)
3'-GACGUAGUCAAGUGAAAACUGGACGAU-5' (SEQ ID NO: 2229)

AR-3761 Target: 5'-CTGCATCAGTTCACTTTTGACCTGCTA-3' (SEQ ID NO: 2634)

5'-UGCAUCAGUUCACUUUUGACCUGCUAA-3' (SEQ ID NO: 5131)
3'-ACGUAGUCAAGUGAAAACUGGACGAUU-5' (SEQ ID NO: 2230)

AR-3762 Target: 5'-TGCATCAGTTCACTTTTGACCTGCTAA-3' (SEQ ID NO: 2635)

5'-GCAUCAGUUCACUUUUGACCUGCUAAU-3' (SEQ ID NO: 5132)
3'-CGUAGUCAAGUGAAAACUGGACGAUUA-5' (SEQ ID NO: 2231)

AR-3763 Target: 5'-GCATCAGTTCACTTTTGACCTGCTAAT-3' (SEQ ID NO: 2636)

5'-CAUCAGUUCACUUUUGACCUGCUAAUC-3' (SEQ ID NO: 5133)
3'-GUAGUCAAGUGAAAACUGGACGAUUAG-5' (SEQ ID NO: 2232)

AR-3764 Target: 5'-CATCAGTTCACTTTTGACCTGCTAATC-3' (SEQ ID NO: 2637)

5'-AUCAGUUCACUUUUGACCUGCUAAUCA-3' (SEQ ID NO: 5134)
3'-UAGUCAAGUGAAAACUGGACGAUUAGU-5' (SEQ ID NO: 2233)

AR-3765 Target: 5'-ATCAGTTCACTTTTGACCTGCTAATCA-3' (SEQ ID NO: 2638)

5'-UCAGUUCACUUUUGACCUGCUAAUCAA-3' (SEQ ID NO: 5135)
3'-AGUCAAGUGAAAACUGGACGAUUAGUU-5' (SEQ ID NO: 2234)

AR-3766 Target: 5'-TCAGTTCACTTTTGACCTGCTAATCAA-3' (SEQ ID NO: 2639)

5'-CAGUUCACUUUUGACCUGCUAAUCAAG-3' (SEQ ID NO: 5136)
3'-GUCAAGUGAAAACUGGACGAUUAGUUC-5' (SEQ ID NO: 2235)

AR-3767 Target: 5'-CAGTTCACTTTTGACCTGCTAATCAAG-3' (SEQ ID NO: 2640)

5'-AGUUCACUUUUGACCUGCUAAUCAAGU-3' (SEQ ID NO: 5137)
3'-UCAAGUGAAAACUGGACGAUUAGUUCA-5' (SEQ ID NO: 2236)

AR-3768 Target: 5'-AGTTCACTTTTGACCTGCTAATCAAGT-3' (SEQ ID NO: 2641)

5'-GUUCACUUUUGACCUGCUAAUCAAGUC-3' (SEQ ID NO: 5138)
3'-CAAGUGAAAACUGGACGAUUAGUUCAG-5' (SEQ ID NO: 2237)

AR-3769 Target: 5'-GTTCACTTTTGACCTGCTAATCAAGTC-3' (SEQ ID NO: 2642)

5'-UUCACUUUUGACCUGCUAAUCAAGUCA-3' (SEQ ID NO: 5139)
3'-AAGUGAAAACUGGACGAUUAGUUCAGU-5' (SEQ ID NO: 2238)

AR-3770 Target: 5'-TTCACTTTTGACCTGCTAATCAAGTCA-3' (SEQ ID NO: 2643)

5'-UCACUUUUGACCUGCUAAUCAAGUCAC-3' (SEQ ID NO: 5140)
3'-AGUGAAAACUGGACGAUUAGUUCAGUG-5' (SEQ ID NO: 2239)

AR-3771 Target: 5'-TCACTTTTGACCTGCTAATCAAGTCAC-3' (SEQ ID NO: 2644)

5'-CACUUUUGACCUGCUAAUCAAGUCACA-3' (SEQ ID NO: 5141)
3'-GUGAAAACUGGACGAUUAGUUCAGUGU-5' (SEQ ID NO: 2240)

AR-3772 Target: 5'-CACTTTTGACCTGCTAATCAAGTCACA-3' (SEQ ID NO: 2645)

5'-ACUUUUGACCUGCUAAUCAAGUCACAC-3' (SEQ ID NO: 5142)
3'-UGAAAACUGGACGAUUAGUUCAGUGUG-5' (SEQ ID NO: 2241)

AR-3773 Target: 5'-ACTTTTGACCTGCTAATCAAGTCACAC-3' (SEQ ID NO: 2646)

5'-ACAUGGUGAGCGUGGACUUUCCGGAAA-3' (SEQ ID NO: 5143)

3'-UGUACCACUCGCACCUGAAAGGCCUUU-5' (SEQ ID NO: 2242)

AR-3798 Target: 5'-ACATGGTGAGCGTGGACTTTCCGGAAA-3' (SEQ ID NO: 2647)

5'-CAUGGUGAGCGUGGACUUUCCGGAAAU-3' (SEQ ID NO: 5144)
3'-GUACCACUCGCACCUGAAAGGCCUUUA-5' (SEQ ID NO: 2243)

AR-3799 Target: 5'-CATGGTGAGCGTGGACTTTCCGGAAAT-3' (SEQ ID NO: 2648)

5'-CGGAAAUGAUGGCAGAGAUCAUCUCUG-3' (SEQ ID NO: 5145)
3'-GCCUUUACUACCGUCUCUAGUAGAGAC-5' (SEQ ID NO: 2244)

AR-3819 Target: 5'-CGGAAATGATGGCAGAGATCATCTCTG-3' (SEQ ID NO: 2649)

5'-GGAAAUGAUGGCAGAGAUCAUCUCUGU-3' (SEQ ID NO: 5146)
3'-CCUUUACUACCGUCUCUAGUAGAGACA-5' (SEQ ID NO: 2245)

AR-3820 Target: 5'-GGAAATGATGGCAGAGATCATCTCTGT-3' (SEQ ID NO: 2650)

5'-GAAAUGAUGGCAGAGAUCAUCUCUGUG-3' (SEQ ID NO: 5147)
3'-CUUUACUACCGUCUCUAGUAGAGACAC-5' (SEQ ID NO: 2246)

AR-3821 Target: 5'-GAAATGATGGCAGAGATCATCTCTGTG-3' (SEQ ID NO: 2651)

5'-AAAUGAUGGCAGAGAUCAUCUCUGUGC-3' (SEQ ID NO: 5148)
3'-UUUACUACCGUCUCUAGUAGAGACACG-5' (SEQ ID NO: 2247)

AR-3822 Target: 5'-AAATGATGGCAGAGATCATCTCTGTGC-3' (SEQ ID NO: 2652)

5'-AAUGAUGGCAGAGAUCAUCUCUGUGCA-3' (SEQ ID NO: 5149)
3'-UUACUACCGUCUCUAGUAGAGACACGU-5' (SEQ ID NO: 2248)

AR-3823 Target: 5'-AATGATGGCAGAGATCATCTCTGTGCA-3' (SEQ ID NO: 2653)

5'-AUGAUGGCAGAGAUCAUCUCUGUGCAA-3' (SEQ ID NO: 5150)
3'-UACUACCGUCUCUAGUAGAGACACGUU-5' (SEQ ID NO: 2249)

AR-3824 Target: 5'-ATGATGGCAGAGATCATCTCTGTGCAA-3' (SEQ ID NO: 2654)

5'-UGAUGGCAGAGAUCAUCUCUGUGCAAG-3' (SEQ ID NO: 5151)
3'-ACUACCGUCUCUAGUAGAGACACGUUC-5' (SEQ ID NO: 2250)

AR-3825 Target: 5'-TGATGGCAGAGATCATCTCTGTGCAAG-3' (SEQ ID NO: 2655)

5'-GAUGGCAGAGAUCAUCUCUGUGCAAGU-3' (SEQ ID NO: 5152)
3'-CUACCGUCUCUAGUAGAGACACGUUCA-5' (SEQ ID NO: 2251)

AR-3826 Target: 5'-GATGGCAGAGATCATCTCTGTGCAAGT-3' (SEQ ID NO: 2656)

5'-AUGGCAGAGAUCAUCUCUGUGCAAGUG-3' (SEQ ID NO: 5153)
3'-UACCGUCUCUAGUAGAGACACGUUCAC-5' (SEQ ID NO: 2252)

AR-3827 Target: 5'-ATGGCAGAGATCATCTCTGTGCAAGTG-3' (SEQ ID NO: 2657)

5'-UGGCAGAGAUCAUCUCUGUGCAAGUGC-3' (SEQ ID NO: 5154)
3'-ACCGUCUCUAGUAGAGACACGUUCACG-5' (SEQ ID NO: 2253)

AR-3828 Target: 5'-TGGCAGAGATCATCTCTGTGCAAGTGC-3' (SEQ ID NO: 2658)

5'-GGCAGAGAUCAUCUCUGUGCAAGUGCC-3' (SEQ ID NO: 5155)
3'-CCGUCUCUAGUAGAGACACGUUCACGG-5' (SEQ ID NO: 2254)

AR-3829 Target: 5'-GGCAGAGATCATCTCTGTGCAAGTGCC-3' (SEQ ID NO: 2659)

5'-GCAGAGAUCAUCUCUGUGCAAGUGCCC-3' (SEQ ID NO: 5156)
3'-CGUCUCUAGUAGAGACACGUUCACGGG-5' (SEQ ID NO: 2255)

AR-3830 Target: 5'-GCAGAGATCATCTCTGTGCAAGTGCCC-3' (SEQ ID NO: 2660)

5'-CAGAGAUCAUCUCUGUGCAAGUGCCCA-3' (SEQ ID NO: 5157)
3'-GUCUCUAGUAGAGACACGUUCACGGGU-5' (SEQ ID NO: 2256)

AR-3831 Target: 5'-CAGAGATCATCTCTGTGCAAGTGCCCA-3' (SEQ ID NO: 2661)

5'-AGAGAUCAUCUCUGUGCAAGUGCCCAA-3' (SEQ ID NO: 5158)
3'-UCUCUAGUAGAGACACGUUCACGGGUU-5' (SEQ ID NO: 2257)

AR-3832 Target: 5'-AGAGATCATCTCTGTGCAAGTGCCCAA-3' (SEQ ID NO: 2662)

5'-GAGAUCAUCUCUGUGCAAGUGCCCAAG-3' (SEQ ID NO: 5159)
3'-CUCUAGUAGAGACACGUUCACGGGUUC-5' (SEQ ID NO: 2258)

AR-3833 Target: 5'-GAGATCATCTCTGTGCAAGTGCCCAAG-3' (SEQ ID NO: 2663)

5'-AGAUCAUCUCUGUGCAAGUGCCCAAGA-3' (SEQ ID NO: 5160)
3'-UCUAGUAGAGACACGUUCACGGGUUCU-5' (SEQ ID NO: 2259)

AR-3834 Target: 5'-AGATCATCTCTGTGCAAGTGCCCAAGA-3' (SEQ ID NO: 2664)

5'-GAUCAUCUCUGUGCAAGUGCCCAAGAU-3' (SEQ ID NO: 5161)
3'-CUAGUAGAGACACGUUCACGGGUUCUA-5' (SEQ ID NO: 2260)

AR-3835 Target: 5'-GATCATCTCTGTGCAAGTGCCCAAGAT-3' (SEQ ID NO: 2665)

5'-AUCAUCUCUGUGCAAGUGCCCAAGAUC-3' (SEQ ID NO: 5162)
3'-UAGUAGAGACACGUUCACGGGUUCUAG-5' (SEQ ID NO: 2261)

AR-3836 Target: 5'-ATCATCTCTGTGCAAGTGCCCAAGATC-3' (SEQ ID NO: 2666)

5'-UCAUCUCUGUGCAAGUGCCCAAGAUCC-3' (SEQ ID NO: 5163)
3'-AGUAGAGACACGUUCACGGGUUCUAGG-5' (SEQ ID NO: 2262)

AR-3837 Target: 5'-TCATCTCTGTGCAAGTGCCCAAGATCC-3' (SEQ ID NO: 2667)

5'-CAUCUCUGUGCAAGUGCCCAAGAUCCU-3' (SEQ ID NO: 5164)
3'-GUAGAGACACGUUCACGGGUUCUAGGA-5' (SEQ ID NO: 2263)

AR-3838 Target: 5'-CATCTCTGTGCAAGTGCCCAAGATCCT-3' (SEQ ID NO: 2668)

5'-AUCUCUGUGCAAGUGCCCAAGAUCCUU-3' (SEQ ID NO: 5165)
3'-UAGAGACACGUUCACGGGUUCUAGGAA-5' (SEQ ID NO: 2264)

AR-3839 Target: 5'-ATCTCTGTGCAAGTGCCCAAGATCCTT-3' (SEQ ID NO: 2669)

5'-UCUCUGUGCAAGUGCCCAAGAUCCUUU-3' (SEQ ID NO: 5166)
3'-AGAGACACGUUCACGGGUUCUAGGAAA-5' (SEQ ID NO: 2265)

AR-3840 Target: 5'-TCTCTGTGCAAGTGCCCAAGATCCTTT-3' (SEQ ID NO: 2670)

5'-CUCUGUGCAAGUGCCCAAGAUCCUUUC-3' (SEQ ID NO: 5167)
3'-GAGACACGUUCACGGGUUCUAGGAAAG-5' (SEQ ID NO: 2266)

AR-3841 Target: 5'-CTCTGTGCAAGTGCCCAAGATCCTTTC-3' (SEQ ID NO: 2671)

5'-UCUGUGCAAGUGCCCAAGAUCCUUUCU-3' (SEQ ID NO: 5168)
3'-AGACACGUUCACGGGUUCUAGGAAAGA-5' (SEQ ID NO: 2267)

AR-3842 Target: 5'-TCTGTGCAAGTGCCCAAGATCCTTTCT-3' (SEQ ID NO: 2672)

5'-CUGUGCAAGUGCCCAAGAUCCUUUCUG-3' (SEQ ID NO: 5169)
3'-GACACGUUCACGGGUUCUAGGAAAGAC-5' (SEQ ID NO: 2268)

AR-3843 Target: 5'-CTGTGCAAGTGCCCAAGATCCTTTCTG-3' (SEQ ID NO: 2673)

5'-UGUGCAAGUGCCCAAGAUCCUUUCUGG-3' (SEQ ID NO: 5170)

3'-ACACGUUCACGGGUUCUAGGAAAGACC-5' (SEQ ID NO: 2269)

AR-3844 Target: 5'-TGTGCAAGTGCCCAAGATCCTTTCTGG-3' (SEQ ID NO: 2674)

5'-GUGCAAGUGCCCAAGAUCCUUUCUGGG-3' (SEQ ID NO: 5171)
3'-CACGUUCACGGGUUCUAGGAAAGACCC-5' (SEQ ID NO: 2270)

AR-3845 Target: 5'-GTGCAAGTGCCCAAGATCCTTTCTGGG-3' (SEQ ID NO: 2675)

5'-UGCAAGUGCCCAAGAUCCUUUCUGGGA-3' (SEQ ID NO: 5172)
3'-ACGUUCACGGGUUCUAGGAAAGACCCU-5' (SEQ ID NO: 2271)

AR-3846 Target: 5'-TGCAAGTGCCCAAGATCCTTTCTGGGA-3' (SEQ ID NO: 2676)

5'-GCAAGUGCCCAAGAUCCUUUCUGGGAA-3' (SEQ ID NO: 5173)
3'-CGUUCACGGGUUCUAGGAAAGACCCUU-5' (SEQ ID NO: 2272)

AR-3847 Target: 5'-GCAAGTGCCCAAGATCCTTTCTGGGAA-3' (SEQ ID NO: 2677)

5'-CAAGUGCCCAAGAUCCUUUCUGGGAAA-3' (SEQ ID NO: 5174)
3'-GUUCACGGGUUCUAGGAAAGACCCUUU-5' (SEQ ID NO: 2273)

AR-3848 Target: 5'-CAAGTGCCCAAGATCCTTTCTGGGAAA-3' (SEQ ID NO: 2678)

5'-AAGUGCCCAAGAUCCUUUCUGGGAAAG-3' (SEQ ID NO: 5175)
3'-UUCACGGGUUCUAGGAAAGACCCUUUC-5' (SEQ ID NO: 2274)

AR-3849 Target: 5'-AAGTGCCCAAGATCCTTTCTGGGAAAG-3' (SEQ ID NO: 2679)

5'-AGUGCCCAAGAUCCUUUCUGGGAAAGU-3' (SEQ ID NO: 5176)
3'-UCACGGGUUCUAGGAAAGACCCUUUCA-5' (SEQ ID NO: 2275)

AR-3850 Target: 5'-AGTGCCCAAGATCCTTTCTGGGAAAGT-3' (SEQ ID NO: 2680)

5'-GUGCCCAAGAUCCUUUCUGGGAAAGUC-3' (SEQ ID NO: 5177)
3'-CACGGGUUCUAGGAAAGACCCUUUCAG-5' (SEQ ID NO: 2276)

AR-3851 Target: 5'-GTGCCCAAGATCCTTTCTGGGAAAGTC-3' (SEQ ID NO: 2681)

5'-UGCCCAAGAUCCUUUCUGGGAAAGUCA-3' (SEQ ID NO: 5178)
3'-ACGGGUUCUAGGAAAGACCCUUUCAGU-5' (SEQ ID NO: 2277)

AR-3852 Target: 5'-TGCCCAAGATCCTTTCTGGGAAAGTCA-3' (SEQ ID NO: 2682)

5'-GCCCAAGAUCCUUUCUGGGAAAGUCAA-3' (SEQ ID NO: 5179)
3'-CGGGUUCUAGGAAAGACCCUUUCAGUU-5' (SEQ ID NO: 2278)

AR-3853 Target: 5'-GCCCAAGATCCTTTCTGGGAAAGTCAA-3' (SEQ ID NO: 2683)

5'-CCCAAGAUCCUUUCUGGGAAAGUCAAG-3' (SEQ ID NO: 5180)
3'-GGGUUCUAGGAAAGACCCUUUCAGUUC-5' (SEQ ID NO: 2279)

AR-3854 Target: 5'-CCCAAGATCCTTTCTGGGAAAGTCAAG-3' (SEQ ID NO: 2684)

5'-CCAAGAUCCUUUCUGGGAAAGUCAAGC-3' (SEQ ID NO: 5181)
3'-GGUUCUAGGAAAGACCCUUUCAGUUCG-5' (SEQ ID NO: 2280)

AR-3855 Target: 5'-CCAAGATCCTTTCTGGGAAAGTCAAGC-3' (SEQ ID NO: 2685)

5'-CAAGAUCCUUUCUGGGAAAGUCAAGCC-3' (SEQ ID NO: 5182)
3'-GUUCUAGGAAAGACCCUUUCAGUUCGG-5' (SEQ ID NO: 2281)

AR-3856 Target: 5'-CAAGATCCTTTCTGGGAAAGTCAAGCC-3' (SEQ ID NO: 2686)

5'-AAGAUCCUUUCUGGGAAAGUCAAGCCC-3' (SEQ ID NO: 5183)
3'-UUCUAGGAAAGACCCUUUCAGUUCGGG-5' (SEQ ID NO: 2282)

AR-3857 Target: 5'-AAGATCCTTTCTGGGAAAGTCAAGCCC-3' (SEQ ID NO: 2687)

5'-AGAUCCUUUCUGGGAAAGUCAAGCCCA-3' (SEQ ID NO: 5184)
3'-UCUAGGAAAGACCCUUUCAGUUCGGGU-5' (SEQ ID NO: 2283)

AR-3858 Target: 5'-AGATCCTTTCTGGGAAAGTCAAGCCCA-3' (SEQ ID NO: 2688)

5'-GAUCCUUUCUGGGAAAGUCAAGCCCAU-3' (SEQ ID NO: 5185)
3'-CUAGGAAAGACCCUUUCAGUUCGGGUA-5' (SEQ ID NO: 2284)

AR-3859 Target: 5'-GATCCTTTCTGGGAAAGTCAAGCCCAT-3' (SEQ ID NO: 2689)

5'-AUCCUUUCUGGGAAAGUCAAGCCCAUC-3' (SEQ ID NO: 5186)
3'-UAGGAAAGACCCUUUCAGUUCGGGUAG-5' (SEQ ID NO: 2285)

AR-3860 Target: 5'-ATCCTTTCTGGGAAAGTCAAGCCCATC-3' (SEQ ID NO: 2690)

5'-UCCUUUCUGGGAAAGUCAAGCCCAUCU-3' (SEQ ID NO: 5187)
3'-AGGAAAGACCCUUUCAGUUCGGGUAGA-5' (SEQ ID NO: 2286)

AR-3861 Target: 5'-TCCTTTCTGGGAAAGTCAAGCCCATCT-3' (SEQ ID NO: 2691)

5'-CCUUUCUGGGAAAGUCAAGCCCAUCUA-3' (SEQ ID NO: 5188)
3'-GGAAAGACCCUUUCAGUUCGGGUAGAU-5' (SEQ ID NO: 2287)

AR-3862 Target: 5'-CCTTTCTGGGAAAGTCAAGCCCATCTA-3' (SEQ ID NO: 2692)

5'-CUUUCUGGGAAAGUCAAGCCCAUCUAU-3' (SEQ ID NO: 5189)
3'-GAAAGACCCUUUCAGUUCGGGUAGAUA-5' (SEQ ID NO: 2288)

AR-3863 Target: 5'-CTTTCTGGGAAAGTCAAGCCCATCTAT-3' (SEQ ID NO: 2693)

5'-UUUCUGGGAAAGUCAAGCCCAUCUAUU-3' (SEQ ID NO: 5190)
3'-AAAGACCCUUUCAGUUCGGGUAGAUAA-5' (SEQ ID NO: 2289)

AR-3864 Target: 5'-TTTCTGGGAAAGTCAAGCCCATCTATT-3' (SEQ ID NO: 2694)

5'-UUCUGGGAAAGUCAAGCCCAUCUAUUU-3' (SEQ ID NO: 5191)
3'-AAGACCCUUUCAGUUCGGGUAGAUAAA-5' (SEQ ID NO: 2290)

AR-3865 Target: 5'-TTCTGGGAAAGTCAAGCCCATCTATTT-3' (SEQ ID NO: 2695)

5'-UCUGGGAAAGUCAAGCCCAUCUAUUUC-3' (SEQ ID NO: 5192)
3'-AGACCCUUUCAGUUCGGGUAGAUAAAG-5' (SEQ ID NO: 2291)

AR-3866 Target: 5'-TCTGGGAAAGTCAAGCCCATCTATTTC-3' (SEQ ID NO: 2696)

5'-CUGGGAAAGUCAAGCCCAUCUAUUUCC-3' (SEQ ID NO: 5193)
3'-GACCCUUUCAGUUCGGGUAGAUAAAGG-5' (SEQ ID NO: 2292)

AR-3867 Target: 5'-CTGGGAAAGTCAAGCCCATCTATTTCC-3' (SEQ ID NO: 2697)

5'-UGGGAAAGUCAAGCCCAUCUAUUUCCA-3' (SEQ ID NO: 5194)
3'-ACCCUUUCAGUUCGGGUAGAUAAAGGU-5' (SEQ ID NO: 2293)

AR-3868 Target: 5'-TGGGAAAGTCAAGCCCATCTATTTCCA-3' (SEQ ID NO: 2698)

5'-GGGAAAGUCAAGCCCAUCUAUUUCCAC-3' (SEQ ID NO: 5195)
3'-CCCUUUCAGUUCGGGUAGAUAAAGGUG-5' (SEQ ID NO: 2294)

AR-3869 Target: 5'-GGGAAAGTCAAGCCCATCTATTTCCAC-3' (SEQ ID NO: 2699)

5'-GGAAAGUCAAGCCCAUCUAUUUCCACA-3' (SEQ ID NO: 5196)
3'-CCUUUCAGUUCGGGUAGAUAAAGGUGU-5' (SEQ ID NO: 2295)

AR-3870 Target: 5'-GGAAAGTCAAGCCCATCTATTTCCACA-3' (SEQ ID NO: 2700)

5'-GAAAGUCAAGCCCAUCUAUUUCCACAC-3' (SEQ ID NO: 5197)

3'-CUUUCAGUUCGGGUAGAUAAAGGUGUG-5' (SEQ ID NO: 2296)

AR-3871 Target: 5'-GAAAGTCAAGCCCATCTATTTCCACAC-3' (SEQ ID NO: 2701)

5'-UUCAGAUGUCUUCUGCCUGUUAUAACU-3' (SEQ ID NO: 5198)
3'-AAGUCUACAGAAGACGGACAAUAUUGA-5' (SEQ ID NO: 2297)

AR-3947 Target: 5'-TTCAGATGTCTTCTGCCTGTTATAACT-3' (SEQ ID NO: 2702)

5'-UCAGAUGUCUUCUGCCUGUUAUAACUC-3' (SEQ ID NO: 5199)
3'-AGUCUACAGAAGACGGACAAUAUUGAG-5' (SEQ ID NO: 2298)

AR-3948 Target: 5'-TCAGATGTCTTCTGCCTGTTATAACTC-3' (SEQ ID NO: 2703)

5'-CAGAUGUCUUCUGCCUGUUAUAACUCU-3' (SEQ ID NO: 5200)
3'-GUCUACAGAAGACGGACAAUAUUGAGA-5' (SEQ ID NO: 2299)

AR-3949 Target: 5'-CAGATGTCTTCTGCCTGTTATAACTCT-3' (SEQ ID NO: 2704)

5'-AGAUGUCUUCUGCCUGUUAUAACUCUG-3' (SEQ ID NO: 5201)
3'-UCUACAGAAGACGGACAAUAUUGAGAC-5' (SEQ ID NO: 2300)

AR-3950 Target: 5'-AGATGTCTTCTGCCTGTTATAACTCTG-3' (SEQ ID NO: 2705)

5'-GGGGAAUUUCCUCUAUUGAUGUACAGU-3' (SEQ ID NO: 5202)
3'-CCCCUUAAAGGAGAUAACUACAUGUCA-5' (SEQ ID NO: 2301)

AR-3999 Target: 5'-GGGGAATTTCCTCTATTGATGTACAGT-3' (SEQ ID NO: 2706)

5'-UUGCUGGGCUUUUUUUUUCUCUUUCUC-3' (SEQ ID NO: 5203)
3'-AACGACCCGAAAAAAAAAGAGAAAGAG-5' (SEQ ID NO: 2302)

AR-4054 Target: 5'-TTGCTGGGCTTTTTTTTCTCTTTCTC-3' (SEQ ID NO: 2707)

5'-UGCUGGGCUUUUUUUUUCUCUUUCUCU-3' (SEQ ID NO: 5204)
3'-ACGACCCGAAAAAAAAAGAGAAAGAGA-5' (SEQ ID NO: 2303)

AR-4055 Target: 5'-TGCTGGGCTTTTTTTTCTCTTTCTCT-3' (SEQ ID NO: 2708)

5'-GCUUUUUUUUUCUCUUUCUCUCCUUUC-3' (SEQ ID NO: 5205)
3'-CGAAAAAAAAAGAGAAAGAGAGGAAAG-5' (SEQ ID NO: 2304)

AR-4061 Target: 5'-GCTTTTTTTTCTCTTTCTCTCCTTTC-3' (SEQ ID NO: 2709)

5'-UUUUUUCUCUUUCUCUCCUUUCUUUUU-3' (SEQ ID NO: 5206)
3'-AAAAAAGAGAAAGAGAGGAAAGAAAAA-5' (SEQ ID NO: 2305)

AR-4066 Target: 5'-TTTTTCTCTTTCTCTCCTTTCTTTTT-3' (SEQ ID NO: 2710)

5'-UCUUUUUCUUCUUCCCUCCCUAUCUAA-3' (SEQ ID NO: 5207)
3'-AGAAAAAGAAGAAGGGAGGGAUAGAUU-5' (SEQ ID NO: 2306)

AR-4086 Target: 5'-TCTTTTTCTTCTTCCCTCCCTATCTAA-3' (SEQ ID NO: 2711)

5'-UGUUGUAUGCCUUUAAAUCUGUGAUGA-3' (SEQ ID NO: 5208)
3'-ACAACAUACGGAAAUUUAGACACUACU-5' (SEQ ID NO: 2307)

AR-4174 Target: 5'-TGTTGTATGCCTTTAAATCTGTGATGA-3' (SEQ ID NO: 2712)

5'-UGUGCUUGUUUACAGCACUACUCUGUG-3' (SEQ ID NO: 5209)
3'-ACACGAACAAAUGUCGUGAUGAGACAC-5' (SEQ ID NO: 2308)

AR-4225 Target: 5'-TGTGCTTGTTTACAGCACTACTCTGTG-3' (SEQ ID NO: 2713)

5'-UUAGAGAGCUAAGAUUAUCUGGGGAAA-3' (SEQ ID NO: 5210)
3'-AAUCUCUCGAUUCUAAUAGACCCCUUU-5' (SEQ ID NO: 2309)

AR-4293 Target: 5'-TTAGAGAGCTAAGATTATCTGGGGAAA-3' (SEQ ID NO: 2714)

5'-GGGGAAAUCAAAACAAAAACAAGCAAA-3' (SEQ ID NO: 5211)
3'-CCCCUUUAGUUUUGUUUUUGUUCGUUU-5' (SEQ ID NO: 2310)

AR-4313 Target: 5'-GGGGAAATCAAAACAAAAACAAGCAAA-3' (SEQ ID NO: 2715)

Table 8: Selected Mouse Anti-AR 27mer "Blunt/Blunt" DsiRNA Agents

5'-GGCAGCAGCACACUGAGGAUGGUUCUC-3' (SEQ ID NO: 5182)
3'-CCGUCGUCGUGUGACUCCUACCAAGAG-5' (SEQ ID NO: 3574)

AR-m258 Target: 5'-GGCAGCAGCACACTGAGGATGGTTCTC-3' (SEQ ID NO: 3622)

5'-CUCCGAGGGCCACCCUGAGAGCAGCUG-3' (SEQ ID NO: 5183)
3'-GAGGCUCCCGGUGGGACUCUCGUCGAC-5' (SEQ ID NO: 3575)

AR-m361 Target: 5'-CTCCGAGGGCCACCCTGAGAGCAGCTG-3' (SEQ ID NO: 3623)

5'-GGGCCACCCUGAGAGCAGCUGCCUCCC-3' (SEQ ID NO: 5184)
3'-CCCGGUGGGACUCUCGUCGACGGAGGG-5' (SEQ ID NO: 3576)

AR-m367 Target: 5'-GGGCCACCCTGAGAGCAGCTGCCTCCC-3' (SEQ ID NO: 3624)

5'-GGCUGCCGCAGCAGCCACCAGCUCCUC-3' (SEQ ID NO: 5185)
3'-CCGACGGCGUCGUCGGUGGUCGAGGAG-5' (SEQ ID NO: 3577)

AR-m426 Target: 5'-GGCTGCCGCAGCAGCCACCAGCTCCTC-3' (SEQ ID NO: 3625)

5'-CACUUUCCCAGGCUUAAGCAGCUGCUC-3' (SEQ ID NO: 5186)
3'-GUGAAAGGGUCCGAAUUCGUCGACGAG-5' (SEQ ID NO: 3578)

AR-m502 Target: 5'-CACTTTCCCAGGCTTAAGCAGCTGCTC-3' (SEQ ID NO: 3626)

5'-AUGCAACUUCUUCAGCAGCAGCAACAA-3' (SEQ ID NO: 5187)
3'-UACGUUGAAGAAGUCGUCGUCGUUGUU-5' (SEQ ID NO: 3579)

AR-m566 Target: 5'-ATGCAACTTCTTCAGCAGCAGCAACAA-3' (SEQ ID NO: 3627)

5'-GUGCGUCCCACUCCUUGUGCGCCGCUG-3' (SEQ ID NO: 5188)
3'-CACGCAGGGUGAGGAACACGCGGCGAC-5' (SEQ ID NO: 3580)

AR-m872 Target: 5'-GTGCGTCCCACTCCTTGTGCGCCGCTG-3' (SEQ ID NO: 3628)

5'-CUGGCAGCAGUGAAGCAGGUAGCUCUG-3' (SEQ ID NO: 5189)
3'-GACCGUCGUCACUUCGUCCAUCGAGAC-5' (SEQ ID NO: 3581)

AR-m1020 Target: 5'-CTGGCAGCAGTGAAGCAGGTAGCTCTG-3' (SEQ ID NO: 3629)

5'-UUUCCGCUGGCUCUGUCCGGGCCGCCG-3' (SEQ ID NO: 5190)
3'-AAAGGCGACCGAGACAGGCCCGGCGGC-5' (SEQ ID NO: 3582)

AR-m1136 Target: 5'-TTTCCGCTGGCTCTGTCCGGGCCGCCG-3' (SEQ ID NO: 3630)

5'-GCAGCGCCUGGGCUGCGGCGGCAGCGC-3' (SEQ ID NO: 5191)
3'-CGUCGCGGACCCGACGCCGCCGUCGCG-5' (SEQ ID NO: 3583)

AR-m1224 Target: 5'-GCAGCGCCTGGGCTGCGGCGGCAGCGC-3' (SEQ ID NO: 3631)

5'-GCCUGGGCUGCGGCGGCAGCGCAAUGC-3' (SEQ ID NO: 5192)
3'-CGGACCCGACGCCGCCGUCGCGUUACG-5' (SEQ ID NO: 3584)

AR-m1229 Target: 5'-GCCTGGGCTGCGGCGGCAGCGCAATGC-3' (SEQ ID NO: 3632)

5'-CUGCGGCGGCAGCGCAAUGCCGCUAUG-3' (SEQ ID NO: 5193)
3'-GACGCCGCCGUCGCGUUACGGCGAUAC-5' (SEQ ID NO: 3585)

AR-m1236 Target: 5'-CTGCGGCGGCAGCGCAATGCCGCTATG-3' (SEQ ID NO: 3633)

5'-UGUAGCCGGGCCCAGCACUGGAUCGCC-3' (SEQ ID NO: 5194)
3'-ACAUCGGCCCGGGUCGUGACCUAGCGG-5' (SEQ ID NO: 3586)

AR-m1291 Target: 5'-TGTAGCCGGGCCCAGCACTGGATCGCC-3' (SEQ ID NO: 3634)

5'-CUUCCUGGCAUACUCUCUUCACAGCUG-3' (SEQ ID NO: 5195)
3'-GAAGGACCGUAUGAGAGAAGUGUCGAC-5' (SEQ ID NO: 3587)

AR-m1335 Target: 5'-CTTCCTGGCATACTCTCTTCACAGCTG-3' (SEQ ID NO: 3635)

5'-AGCAGCCCAAGCGAUGCCGGGCCUGUA-3' (SEQ ID NO: 5196)
3'-UCGUCGGGUUCGCUACGGCCCGGACAU-5' (SEQ ID NO: 3588)

AR-m1403 Target: 5'-AGCAGCCCAAGCGATGCCGGGCCTGTA-3' (SEQ ID NO: 3636)

5'-GCUUCUGGCUGUCACUACGGAGCUCUC-3' (SEQ ID NO: 5197)
3'-CGAAGACCGACAGUGAUGCCUCGAGAG-5' (SEQ ID NO: 3589)

AR-m1694 Target: 5'-GCTTCTGGCTGTCACTACGGAGCTCTC-3' (SEQ ID NO: 3637)

5'-CGGAGCUCUCACUUGUGGCAGCUGCAA-3' (SEQ ID NO: 5198)
3'-GCCUCGAGAGUGAACACCGUCGACGUU-5' (SEQ ID NO: 3590)

AR-m1711 Target: 5'-CGGAGCTCTCACTTGTGGCAGCTGCAA-3' (SEQ ID NO: 3638)

5'-CACUUGUGGCAGCUGCAAGGUCUUCUU-3' (SEQ ID NO: 5199)
3'-GUGAACACCGUCGACGUUCCAGAAGAA-5' (SEQ ID NO: 3591)

AR-m1720 Target: 5'-CACTTGTGGCAGCTGCAAGGTCTTCTT-3' (SEQ ID NO: 3639)

5'-GUGGCAGCUGCAAGGUCUUCUUCAAAA-3' (SEQ ID NO: 5200)
3'-CACCGUCGACGUUCCAGAAGAAGUUUU-5' (SEQ ID NO: 3592)

AR-m1725 Target: 5'-GTGGCAGCTGCAAGGTCTTCTTCAAAA-3' (SEQ ID NO: 3640)

5'-GGGAUGACUCUGGGAGCUCGUAAGCUG-3' (SEQ ID NO: 5201)
3'-CCCUACUGAGACCCUCGAGCAUUCGAC-5' (SEQ ID NO: 3593)

AR-m1865 Target: 5'-GGGATGACTCTGGGAGCTCGTAAGCTG-3' (SEQ ID NO: 3641)

5'-CUGGGAGCUCGUAAGCUGAAGAAACUU-3' (SEQ ID NO: 5202)
3'-GACCCUCGAGCAUUCGACUUCUUUGAA-5' (SEQ ID NO: 3594)

AR-m1874 Target: 5'-CTGGGAGCTCGTAAGCTGAAGAAACTT-3' (SEQ ID NO: 3642)

5'-CAGAUUCCUUUGCUGCCUUGUUAUCUA-3' (SEQ ID NO: 5203)
3'-GUCUAAGGAAACGACGGAACAAUAGAU-5' (SEQ ID NO: 3595)

AR-m2079 Target: 5'-CAGATTCCTTTGCTGCCTTGTTATCTA-3' (SEQ ID NO: 3643)

5'-CUUUGCUGCCUUGUUAUCUAGCCUCAA-3' (SEQ ID NO: 5204)
3'-GAAACGACGGAACAAUAGAUCGGAGUU-5' (SEQ ID NO: 3596)

AR-m2086 Target: 5'-CTTTGCTGCCTTGTTATCTAGCCTCAA-3' (SEQ ID NO: 3644)

5'-UUGCCUGGCUUCCGCAACUUGCAUGUG-3' (SEQ ID NO: 5205)
3'-AACGGACCGAAGGCGUUGAACGUACAC-5' (SEQ ID NO: 3597)

AR-m2162 Target: 5'-TTGCCTGGCTTCCGCAACTTGCATGTG-3' (SEQ ID NO: 3645)

5'-UGGAUGGGACUGAUGGUAUUUGCCAUG-3' (SEQ ID NO: 5206)
3'-ACCUACCCUGACUACCAUAAACGGUAC-5' (SEQ ID NO: 3598)

AR-m2219 Target: 5'-TGGATGGGACTGATGGTATTTGCCATG-3' (SEQ ID NO: 3646)

5'-CAGGAUGCUCUACUUUGCACCUGACUU-3' (SEQ ID NO: 5207)
3'-GUCCUACGAGAUGAAACGUGGACUGAA-5' (SEQ ID NO: 3599)

AR-m2275 Target: 5'-CAGGATGCTCTACTTTGCACCTGACTT-3' (SEQ ID NO: 3647)

5'-UGCUCUACUUUGCACCUGACUUGGUUU-3' (SEQ ID NO: 5208)
3'-ACGAGAUGAAACGUGGACUGAACCAAA-5' (SEQ ID NO: 3600)

AR-m2280 Target: 5'-TGCTCTACTTTGCACCTGACTTGGTTT-3' (SEQ ID NO: 3648)

5'-CUUUGCACCUGACUUGGUUUUCAAUGA-3' (SEQ ID NO: 5209)
3'-GAAACGUGGACUGAACCAAAAGUUACU-5' (SEQ ID NO: 3601)

AR-m2287 Target: 5'-CTTTGCACCTGACTTGGTTTTCAATGA-3' (SEQ ID NO: 3649)

5'-GACUUGGUUUUCAAUGAGUACCGCAUG-3' (SEQ ID NO: 5210)
3'-CUGAACCAAAAGUUACUCAUGGCGUAC-5' (SEQ ID NO: 3602)

AR-m2297 Target: 5'-GACTTGGTTTTCAATGAGTACCGCATG-3' (SEQ ID NO: 3650)

5'-GAGUACCGCAUGCACAAGUCUCGGAUG-3' (SEQ ID NO: 5211)
3'-CUCAUGGCGUACGUGUUCAGAGCCUAC-5' (SEQ ID NO: 3603)

AR-m2312 Target: 5'-GAGTACCGCATGCACAAGTCTCGGATG-3' (SEQ ID NO: 3651)

5'-CUGUGCAUGAAAGCACUGCUGCUCUUC-3' (SEQ ID NO: 5212)
3'-GACACGUACUUUCGUGACGACGAGAAG-5' (SEQ ID NO: 3604)

AR-m2411 Target: 5'-CTGTGCATGAAAGCACTGCTGCTCTTC-3' (SEQ ID NO: 3652)

5'-CAUGAAAGCACUGCUGCUCUUCAGCAU-3' (SEQ ID NO: 5213)
3'-GUACUUUCGUGACGACGAGAAGUCGUA-5' (SEQ ID NO: 3605)

AR-m2416 Target: 5'-CATGAAAGCACTGCTGCTCTTCAGCAT-3' (SEQ ID NO: 3653)

5'-AGCACUGCUGCUCUUCAGCAUUAUUCC-3' (SEQ ID NO: 5214)
3'-UCGUGACGACGAGAAGUCGUAAUAAGG-5' (SEQ ID NO: 3606)

AR-m2422 Target: 5'-AGCACTGCTGCTCTTCAGCATTATTCC-3' (SEQ ID NO: 3654)

5'-UGCUGCUCUUCAGCAUUAUUCCAGUGG-3' (SEQ ID NO: 5215)
3'-ACGACGAGAAGUCGUAAUAAGGUCACC-5' (SEQ ID NO: 3607)

AR-m2427 Target: 5'-TGCTGCTCTTCAGCATTATTCCAGTGG-3' (SEQ ID NO: 3655)

5'-AGCUCACCAAGCUCCUGGAUUCUGUGC-3' (SEQ ID NO: 5216)
3'-UCGAGUGGUUCGAGGACCUAAGACACG-5' (SEQ ID NO: 3608)

AR-m2571 Target: 5'-AGCTCACCAAGCTCCTGGATTCTGTGC-3' (SEQ ID NO: 3656)

5'-AGCUCCUGGAUUCUGUGCAGCCUAUUG-3' (SEQ ID NO: 5217)
3'-UCGAGGACCUAAGACACGUCGGAUAAC-5' (SEQ ID NO: 3609)

AR-m2580 Target: 5'-AGCTCCTGGATTCTGTGCAGCCTATTG-3' (SEQ ID NO: 3657)

5'-CUGGAUUCUGUGCAGCCUAUUGCAAGA-3' (SEQ ID NO: 5218)
3'-GACCUAAGACACGUCGGAUAACGUUCU-5' (SEQ ID NO: 3610)

AR-m2585 Target: 5'-CTGGATTCTGTGCAGCCTATTGCAAGA-3' (SEQ ID NO: 3658)

5'-UCUGUGCAGCCUAUUGCAAGAGAGCUG-3' (SEQ ID NO: 5219)
3'-AGACACGUCGGAUAACGUUCUCUCGAC-5' (SEQ ID NO: 3611)

AR-m2591 Target: 5'-TCTGTGCAGCCTATTGCAAGAGAGCTG-3' (SEQ ID NO: 3659)

5'-CAGCCUAUUGCAAGAGAGCUGCAUCAG-3' (SEQ ID NO: 5220)
3'-GUCGGAUAACGUUCUCUCGACGUAGUC-5' (SEQ ID NO: 3612)

AR-m2597 Target: 5'-CAGCCTATTGCAAGAGAGCTGCATCAG-3' (SEQ ID NO: 3660)

5'-GCGUGGACUUUCCUGAAAUGAUGGCAG-3' (SEQ ID NO: 5221)
3'-CGCACCUGAAAGGACUUUACUACCGUC-5' (SEQ ID NO: 3613)

AR-m2661 Target: 5'-GCGTGGACTTTCCTGAAATGATGGCAG-3' (SEQ ID NO: 3661)

5'-UCUUCUGCCUGUUAUAUAACUCUGCAC-3' (SEQ ID NO: 5222)
3'-AGAAGACGGACAAUAUAUUGAGACGUG-5' (SEQ ID NO: 3614)

AR-m2809 Target: 5'-TCTTCTGCCTGTTATATAACTCTGCAC-3' (SEQ ID NO: 3662)

5'-UGCACUACUUCUCUGCAGUGCCUUGGG-3' (SEQ ID NO: 5223)
3'-ACGUGAUGAAGAGACGUCACGGAACCC-5' (SEQ ID NO: 3615)

AR-m2831 Target: 5'-TGCACTACTTCTCTGCAGTGCCTTGGG-3' (SEQ ID NO: 3663)

5'-UCCUGGGCUUCUCCUUCUUUUUUUUUC-3' (SEQ ID NO: 5224)
3'-AGGACCCGAAGAGGAAGAAAAAAAAAG-5' (SEQ ID NO: 3616)

AR-m2912 Target: 5'-TCCTGGGCTTCTCCTTCTTTTTTTTC-3' (SEQ ID NO: 3664)

5'-GCUUCUCCUUCUUUUUUUUUCUUCUUC-3' (SEQ ID NO: 5225)
3'-CGAAGAGGAAGAAAAAAAAAAGAAGAAG-5' (SEQ ID NO: 3617)

AR-m2918 Target: 5'-GCTTCTCCTTCTTTTTTTTCTTCTTC-3' (SEQ ID NO: 3665)

5'-UUCUUUUUUUUUCUUCUUCCCUCCCUC-3' (SEQ ID NO: 5226)
3'-AAGAAAAAAAAAAGAAGAAGGGAGGGAG-5' (SEQ ID NO: 3618)

AR-m2926 Target: 5'-TTCTTTTTTTTTCTTCTTCCCTCCCTC-3' (SEQ ID NO: 3666)

5'-CUGCUGCGUAUUGUGGCUCCUGCCUUU-3' (SEQ ID NO: 5227)
3'-GACGACGCAUAACACCGAGGACGGAAA-5' (SEQ ID NO: 3619)

AR-m2981 Target: 5'-CTGCTGCGTATTGTGGCTCCTGCCTTT-3' (SEQ ID NO: 3667)

5'-UGUGGCUCCUGCCUUUGUUUUGAUUUC-3' (SEQ ID NO: 5228)
3'-ACACCGAGGACGGAAACAAAACUAAAG-5' (SEQ ID NO: 3620)

AR-m2992 Target: 5'-TGTGGCTCCTGCCTTTGTTTTGATTTC-3' (SEQ ID NO: 3668)

5'-CUCCUGCCUUUGUUUUGAUUUCUGUUG-3' (SEQ ID NO: 5229)
3'-GAGGACGGAAACAAAACUAAAGACAAC-5' (SEQ ID NO: 3621)

AR-m2997 Target: 5'-CTCCTGCCTTTGTTTTGATTTCTGTTG-3' (SEQ ID NO: 3669)

In certain embodiments, the DsiRNA agents of the invention require, *e.g.*, at least 19, at least 20, at least 21, at least 22, at least 23, at least 24, at least 25 or at least 26 residues of the first strand to be complementary to corresponding residues of the second strand. In certain related embodiments, these first strand residues complementary to corresponding residues of of the second strand are optionally consecutive residues.

As used herein "DsiRNAmm" refers to a DisRNA having a "mismatch tolerant region" containing one, two, three or four mismatched base pairs of the duplex formed by the sense and antisense strands of the DsiRNA, where such

mismatches are positioned within the DsiRNA at a location(s) lying between (and thus not including) the two terminal base pairs of either end of the DsiRNA. The mismatched base pairs are located within a "mismatch-tolerant region" which is defined herein with respect to the location of the projected Ago2 cut site of the corresponding target nucleic acid. The mismatch tolerant region is located "upstream of" the projected Ago2 cut site of the target strand. "Upstream" in this context will be understood as the 5'-most portion of the DsiRNAmm duplex, where 5' refers to the orientation of the sense strand of the DsiRNA duplex. Therefore, the mismatch tolerant region is upstream of the base on the sense (passenger) strand that corresponds to the projected Ago2 cut site of the target nucleic acid (see Figure 1); alternatively, when referring to the antisense (guide) strand of the DsiRNAmm, the mismatch tolerant region can also be described as positioned downstream of the base that is complementary to the projected Ago2 cut site of the target nucleic acid, that is, the 3'-most portion of the antisense strand of the DsiRNAmm (where position 1 of the antisense strand is the 5' terminal nucleotide of the antisense strand, see Figure 1).

In one embodiment, for example with numbering as depicted in Figure 1, the mismatch tolerant region is positioned between and including base pairs 3-9 when numbered from the nucleotide starting at the 5' end of the sense strand of the duplex. Therefore, a DsiRNAmm of the invention possesses a single mismatched base pair at any one of positions 3, 4, 5, 6, 7, 8 or 9 of the sense strand of a right-hand extended DsiRNA (where position 1 is the 5' terminal nucleotide of the sense strand and position 9 is the nucleotide residue of the sense strand that is immediately 5' of the projected Ago2 cut site of the target AR RNA sequence corresponding to the sense strand sequence). In certain embodiments, for a DsiRNAmm that possesses a mismatched base pair nucleotide at any of positions 3, 4, 5, 6, 7, 8 or 9 of the sense strand, the corresponding mismatched base pair nucleotide of the antisense strand not only forms a mismatched base pair with the DsiRNAmm sense strand sequence, but also forms a mismatched base pair with a DsiRNAmm target AR RNA sequence (thus, complementarity between the antisense strand sequence and the sense strand sequence is disrupted at the mismatched base pair within the DsiRNAmm, and complementarity is similarly disrupted between the antisense strand sequence of the DsiRNAmm and the target AR RNA sequence). In alternative embodiments, the mismatch base pair nucleotide of the antisense strand of a DsiRNAmm only form a mismatched base pair with a corresponding nucleotide of the sense strand sequence of

the DsiRNAmm, yet base pairs with its corresponding target AR RNA sequence nucleotide (thus, complementarity between the antisense strand sequence and the sense strand sequence is disrupted at the mismatched base pair within the DsiRNAmm, yet complementarity is maintained between the antisense strand sequence of the DsiRNAmm and the target AR RNA sequence).

A DsiRNAmm of the invention that possesses a single mismatched base pair within the mismatch-tolerant region (mismatch region) as described above (*e.g.*, a DsiRNAmm harboring a mismatched nucleotide residue at any one of positions 3, 4, 5, 6, 7, 8 or 9 of the sense strand) can further include one, two or even three additional mismatched base pairs. In preferred embodiments, these one, two or three additional mismatched base pairs of the DsiRNAmm occur at position(s) 3, 4, 5, 6, 7, 8 and/or 9 of the sense strand (and at corresponding residues of the antisense strand). In one embodiment where one additional mismatched base pair is present within a DsiRNAmm, the two mismatched base pairs of the sense strand can occur, *e.g.*, at nucleotides of both position 4 and position 6 of the sense strand (with mismatch also occurring at corresponding nucleotide residues of the antisense strand).

In DsiRNAmm agents possessing two mismatched base pairs, mismatches can occur consecutively (*e.g.*, at consecutive positions along the sense strand nucleotide sequence). Alternatively, nucleotides of the sense strand that form mismatched base pairs with the antisense strand sequence can be interspersed by nucleotides that base pair with the antisense strand sequence (*e.g.*, for a DsiRNAmm possessing mismatched nucleotides at positions 3 and 6, but not at positions 4 and 5, the mismatched residues of sense strand positions 3 and 6 are interspersed by two nucleotides that form matched base pairs with corresponding residues of the antisense strand). For example, two residues of the sense strand (located within the mismatch-tolerant region of the sense strand) that form mismatched base pairs with the corresponding antisense strand sequence can occur with zero, one, two, three, four or five matched base pairs located between these mismatched base pairs.

For certain DsiRNAmm agents possessing three mismatched base pairs, mismatches can occur consecutively (*e.g.*, in a triplet along the sense strand nucleotide sequence). Alternatively, nucleotides of the sense strand that form mismatched base pairs with the antisense strand sequence can be interspersed by nucleotides that form matched base pairs with the antisense strand sequence (*e.g.*, for a DsiRNAmm possessing mismatched nucleotides at positions 3, 4 and 8, but not at

positions 5, 6 and 7, the mismatched residues of sense strand positions 3 and 4 are adjacent to one another, while the mismatched residues of sense strand positions 4 and 8 are interspersed by three nucleotides that form matched base pairs with corresponding residues of the antisense strand). For example, three residues of the sense strand (located within the mismatch-tolerant region of the sense strand) that form mismatched base pairs with the corresponding antisense strand sequence can occur with zero, one, two, three or four matched base pairs located between any two of these mismatched base pairs.

For certain DsiRNAmm agents possessing four mismatched base pairs, mismatches can occur consecutively (*e.g.*, in a quadruplet along the sense strand nucleotide sequence). Alternatively, nucleotides of the sense strand that form mismatched base pairs with the antisense strand sequence can be interspersed by nucleotides that form matched base pairs with the antisense strand sequence (*e.g.*, for a DsiRNAmm possessing mismatched nucleotides at positions 3, 5, 7 and 8, but not at positions 4 and 6, the mismatched residues of sense strand positions 7 and 8 are adjacent to one another, while the mismatched residues of sense strand positions 3 and 5 are interspersed by one nucleotide that forms a matched base pair with the corresponding residue of the antisense strand – similarly, the the mismatched residues of sense strand positions 5 and 7 are also interspersed by one nucleotide that forms a matched base pair with the corresponding residue of the antisense strand). For example, four residues of the sense strand (located within the mismatch-tolerant region of the sense strand) that form mismatched base pairs with the corresponding antisense strand sequence can occur with zero, one, two or three matched base pairs located between any two of these mismatched base pairs.

In another embodiment, for example with numbering also as depicted in Figure 1, a DsiRNAmm of the invention comprises a mismatch tolerant region which possesses a single mismatched base pair nucleotide at any one of positions 17, 18, 19, 20, 21, 22 or 23 of the antisense strand of the DsiRNA (where position 1 is the 5' terminal nucleotide of the antisense strand and position 17 is the nucleotide residue of the antisense strand that is immediately 3' (downstream) in the antisense strand of the projected Ago2 cut site of the target AR RNA sequence sufficiently complementary to the antisense strand sequence). In certain embodiments, for a DsiRNAmm that possesses a mismatched base pair nucleotide at any of positions 17, 18, 19, 20, 21, 22 or 23 of the antisense strand with respect to the sense strand of the DsiRNAmm, the

mismatched base pair nucleotide of the antisense strand not only forms a mismatched base pair with the DsiRNAmm sense strand sequence, but also forms a mismatched base pair with a DsiRNAmm target AR RNA sequence (thus, complementarity between the antisense strand sequence and the sense strand sequence is disrupted at the mismatched base pair within the DsiRNAmm, and complementarity is similarly disrupted between the antisense strand sequence of the DsiRNAmm and the target AR RNA sequence). In alternative embodiments, the mismatch base pair nucleotide of the antisense strand of a DsiRNAmm only forms a mismatched base pair with a corresponding nucleotide of the sense strand sequence of the DsiRNAmm, yet base pairs with its corresponding target AR RNA sequence nucleotide (thus, complementarity between the antisense strand sequence and the sense strand sequence is disrupted at the mismatched base pair within the DsiRNAmm, yet complementarity is maintained between the antisense strand sequence of the DsiRNAmm and the target AR RNA sequence).

A DsiRNAmm of the invention that possesses a single mismatched base pair within the mismatch-tolerant region as described above (*e.g.*, a DsiRNAmm harboring a mismatched nucleotide residue at positions 17, 18, 19, 20, 21, 22 or 23 of the antisense strand) can further include one, two or even three additional mismatched base pairs. In preferred embodiments, these one, two or three additional mismatched base pairs of the DsiRNAmm occur at position(s) 17, 18, 19, 20, 21, 22 and/or 23 of the antisense strand (and at corresponding residues of the sense strand). In one embodiment where one additional mismatched base pair is present within a DsiRNAmm, the two mismatched base pairs of the antisense strand can occur, *e.g.*, at nucleotides of both position 18 and position 20 of the antisense strand (with mismatch also occurring at corresponding nucleotide residues of the sense strand).

In DsiRNAmm agents possessing two mismatched base pairs, mismatches can occur consecutively (*e.g.*, at consecutive positions along the antisense strand nucleotide sequence). Alternatively, nucleotides of the antisense strand that form mismatched base pairs with the sense strand sequence can be interspersed by nucleotides that base pair with the sense strand sequence (*e.g.*, for a DsiRNAmm possessing mismatched nucleotides at positions 17 and 20, but not at positions 18 and 19, the mismatched residues of antisense strand positions 17 and 20 are interspersed by two nucleotides that form matched base pairs with corresponding residues of the sense strand). For example, two residues of the antisense strand (located within the

mismatch-tolerant region of the sense strand) that form mismatched base pairs with the corresponding sense strand sequence can occur with zero, one, two, three, four, five, six or seven matched base pairs located between these mismatched base pairs.

For certain DsiRNAmm agents possessing three mismatched base pairs, mismatches can occur consecutively (*e.g.*, in a triplet along the antisense strand nucleotide sequence). Alternatively, nucleotides of the antisense strand that form mismatched base pairs with the sense strand sequence can be interspersed by nucleotides that form matched base pairs with the sense strand sequence (*e.g.*, for a DsiRNAmm possessing mismatched nucleotides at positions 17, 18 and 22, but not at positions 19, 20 and 21, the mismatched residues of antisense strand positions 17 and 18 are adjacent to one another, while the mismatched residues of antisense strand positions 18 and 122 are interspersed by three nucleotides that form matched base pairs with corresponding residues of the sense strand). For example, three residues of the antisense strand (located within the mismatch-tolerant region of the antisense strand) that form mismatched base pairs with the corresponding sense strand sequence can occur with zero, one, two, three, four, five or six matched base pairs located between any two of these mismatched base pairs.

For certain DsiRNAmm agents possessing four mismatched base pairs, mismatches can occur consecutively (*e.g.*, in a quadruplet along the antisense strand nucleotide sequence). Alternatively, nucleotides of the antisense strand that form mismatched base pairs with the sense strand sequence can be interspersed by nucleotides that form matched base pairs with the sense strand sequence (*e.g.*, for a DsiRNAmm possessing mismatched nucleotides at positions 18, 20, 22 and 23, but not at positions 19 and 21, the mismatched residues of antisense strand positions 22 and 23 are adjacent to one another, while the mismatched residues of antisense strand positions 18 and 20 are interspersed by one nucleotide that forms a matched base pair with the corresponding residue of the sense strand – similarly, the the mismatched residues of antisense strand positions 20 and 22 are also interspersed by one nucleotide that forms a matched base pair with the corresponding residue of the sense strand). For example, four residues of the antisense strand (located within the mismatch-tolerant region of the antisense strand) that form mismatched base pairs with the corresponding sense strand sequence can occur with zero, one, two, three, four or five matched base pairs located between any two of these mismatched base pairs.

For reasons of clarity, the location(s) of mismatched nucleotide residues within the above DsiRNAmm agents are numbered in reference to the 5' terminal residue of either sense or antisense strands of the DsiRNAmm. The numbering of positions located within the mismatch-tolerant region (mismatch region) of the antisense strand can shift with variations in the proximity of the 5' terminus of the sense or antisense strand to the projected Ago2 cleavage site. Thus, the location(s) of preferred mismatch sites within either antisense strand or sense strand can also be identified as the permissible proximity of such mismatches to the projected Ago2 cut site. Accordingly, in one preferred embodiment, the position of a mismatch nucleotide of the sense strand of a DsiRNAmm is the nucleotide residue of the sense strand that is located immediately 5' (upstream) of the projected Ago2 cleavage site of the corresponding target AR RNA sequence. In other preferred embodiments, a mismatch nucleotide of the sense strand of a DsiRNAmm is positioned at the nucleotide residue of the sense strand that is located two nucleotides 5' (upstream) of the projected Ago2 cleavage site, three nucleotides 5' (upstream) of the projected Ago2 cleavage site, four nucleotides 5' (upstream) of the projected Ago2 cleavage site, five nucleotides 5' (upstream) of the projected Ago2 cleavage site, six nucleotides 5' (upstream) of the projected Ago2 cleavage site, seven nucleotides 5' (upstream) of the projected Ago2 cleavage site, eight nucleotides 5' (upstream) of the projected Ago2 cleavage site, or nine nucleotides 5' (upstream) of the projected Ago2 cleavage site.

Exemplary single mismatch-containing 25/27mer DsiRNAs (DsiRNAmm) include the following structures (such mismatch-containing structures may also be incorporated into other exemplary DsiRNA structures shown herein).

5'-XX^{M}XXXXXXXXXXXXXXXXXXXXDD-3'
3'-XXXX$_{M}$XXXXXXXXXXXXXXXXXXXXX-5'

5'-XXX^{M}XXXXXXXXXXXXXXXXXXXXDD-3'
3'-XXXXX$_{M}$XXXXXXXXXXXXXXXXXXXXX-5'

5′-XXXX^{M}XXXXXXXXXXXXXXXXXXXDD-3'
3′-XXXXXX$_{M}$XXXXXXXXXXXXXXXXXXXX-5′

5′-XXXXX^{M}XXXXXXXXXXXXXXXXXXXDD-3'
3′-XXXXXXX$_{M}$XXXXXXXXXXXXXXXXXXXX-5′

5′-XXXXXX^{M}XXXXXXXXXXXXXXXXXXXDD-3'
3′-XXXXXXXX$_{M}$XXXXXXXXXXXXXXXXXXXX-5′

5′-XXXXXXX^{M}XXXXXXXXXXXXXXXXXXXDD-3'
3′-XXXXXXXXX$_{M}$XXXXXXXXXXXXXXXXXXXX-5′

5′-XXXXXXXX^{M}XXXXXXXXXXXXXXXXXXXDD-3'
3′-XXXXXXXXXX$_{M}$XXXXXXXXXXXXXXXXXXXX-5′

wherein “X”=RNA, "D"=DNA and “M”=Nucleic acid residues (RNA, DNA or non-natural or modified nucleic acids) that do not base pair (hydrogen bond) with corresponding “M” residues of otherwise complementary strand when strands are annealed. Any of the residues of such agents can optionally be 2'-O-methyl RNA monomers – alternating positioning of 2'-O-methyl RNA monomers that commences from the 3’-terminal residue of the bottom (second) strand, as shown above, can also be used in the above DsiRNAmm agents. For the above mismatch structures, the top strand is the sense strand, and the bottom strand is the antisense strand.

In certain embodiments, a DsiRNA of the invention can contain mismatches that exist in reference to the target AR RNA sequence yet do not necessarily exist as mismatched base pairs within the two strands of the DsiRNA – thus, a DsiRNA can possess perfect complementarity between first and second strands of a DsiRNA, yet still possess mismatched residues in reference to a target AR RNA (which, in certain embodiments, may be advantageous in promoting efficacy and/or potency and/or duration of effect). In certain embodiments, where mismatches occur between

antisense strand and target AR RNA sequence, the position of a mismatch is located within the antisense strand at a position(s) that corresponds to a sequence of the sense strand located 5' of the projected Ago2 cut site of the target region – *e.g.*, antisense strand residue(s) positioned within the antisense strand to the 3' of the antisense residue which is complementary to the projected Ago2 cut site of the target sequence.

Exemplary 25/27mer DsiRNAs that harbor a single mismatched residue in reference to target sequences include the following structures.

```
Target RNA Sequence: 5′-. . . AXXXXXXXXXXXXXXXXXXXX . . .-3′
DsiRNAmm Sense Strand:       5′-XXXXXXXXXXXXXXXXXXXXXXDD-3'
DsiRNAmm Antisense Strand: 3′-EXXXXXXXXXXXXXXXXXXXXXXXX-5′

Target RNA Sequence: 5′-. . . XAXXXXXXXXXXXXXXXXXX . . .-3′
DsiRNAmm Sense Strand:       5′-XXXXXXXXXXXXXXXXXXXXXXDD-3'
DsiRNAmm Antisense Strand: 3′-XEXXXXXXXXXXXXXXXXXXXXXX-5′

Target RNA Sequence:   5′-. . . AXXXXXXXXXXXXXXXXXX . . .-3′
DsiRNAmm Sense Strand:       5′-BXXXXXXXXXXXXXXXXXXXXXXDD-3'
DsiRNAmm Antisense Strand: 3′-XXEXXXXXXXXXXXXXXXXXXXXX-5′

Target RNA Sequence:   5′-. . . XAXXXXXXXXXXXXXXXXX . . .-3′
DsiRNAmm Sense Strand:       5′-XBXXXXXXXXXXXXXXXXXXXXDD-3'
DsiRNAmm Antisense Strand: 3′-XXXEXXXXXXXXXXXXXXXXXXX-5′

Target RNA Sequence:   5′-. . . XXAXXXXXXXXXXXXXXXX . . .-3′
DsiRNAmm Sense Strand:       5′-XXBXXXXXXXXXXXXXXXXXXDD-3'
DsiRNAmm Antisense Strand: 3′-XXXXEXXXXXXXXXXXXXXXXXX-5′

Target RNA Sequence:   5′-. . . XXXAXXXXXXXXXXXXXXX . . .-3′
DsiRNAmm Sense Strand:       5′-XXXBXXXXXXXXXXXXXXXXXXDD-3'
DsiRNAmm Antisense Strand: 3′-XXXXXEXXXXXXXXXXXXXXXXX-5′

Target RNA Sequence:   5′-. . . XXXXAXXXXXXXXXXXXXX . . .-3′
DsiRNAmm Sense Strand:       5′-XXXXBXXXXXXXXXXXXXXXXXDD-3'
DsiRNAmm Antisense Strand: 3′-XXXXXXEXXXXXXXXXXXXXXXXX-5′

Target RNA Sequence:   5′-. . . XXXXXAXXXXXXXXXXXXX . . .-3′
```

DsiRNAmm Sense Strand: 5′-XXXXXBXXXXXXXXXXXXXXXXXDD-3'
DsiRNAmm Antisense Strand: 3′-XXXXXXXEXXXXXXXXXXXXXXXXXX-5′

Target RNA Sequence: 5′-. . . XXXXXXAXXXXXXXXXXXX . . .-3′
DsiRNAmm Sense Strand: 5′-XXXXXXBXXXXXXXXXXXXXXXXXDD-3'
DsiRNAmm Antisense Strand: 3′-XXXXXXXEXXXXXXXXXXXXXXXXXX-5′

Target RNA Sequence: 5′-. . . XXXXXXXAXXXXXXXXXXX . . .-3′
DsiRNAmm Sense Strand: 5′-XXXXXXXBXXXXXXXXXXXXXXXXXDD-3'
DsiRNAmm Antisense Strand: 3′-XXXXXXXXEXXXXXXXXXXXXXXXXXX-5′

Target RNA Sequence: 5′-. . . XXXXXXXXAXXXXXXXXXXX . . .-3′
DsiRNAmm Sense Strand: 5′-XXXXXXXXBXXXXXXXXXXXXXXXXXDD-3'
DsiRNAmm Antisense Strand: 3′-XXXXXXXXXEXXXXXXXXXXXXXXXXXX-5′

wherein “X”=RNA, “D”=DNA and “E”=Nucleic acid residues (RNA, DNA or non-natural or modified nucleic acids) that do not base pair (hydrogen bond) with corresponding “A” RNA residues of otherwise complementary (target) strand when strands are annealed, yet optionally do base pair with corresponding “B” residues (“B” residues are also RNA, DNA or non-natural or modified nucleic acids). Any of the residues of such agents can optionally be 2'-O-methyl RNA monomers – alternating positioning of 2'-O-methyl RNA monomers that commences from the 3’-terminal residue of the bottom (second) strand, as shown above, can also be used in the above DsiRNA agents.

In addition to the above-exemplified structures, DsiRNAs of the invention can also possess one, two or three additional residues that form further mismatches with the target AR RNA sequence. Such mismatches can be consecutive, or can be interspersed by nucleotides that form matched base pairs with the target AR RNA sequence. Where interspersed by nucleotides that form matched base pairs, mismatched residues can be spaced apart from each other within a single strand at an interval of one, two, three, four, five, six, seven or even eight base paired nucleotides between such mismatch-forming residues.

As for the above-described DsiRNAmm agents, a preferred location within DsiRNAs for antisense strand nucleotides that form mismatched base pairs with target AR RNA sequence (yet may or may not form mismatches with corresponding sense

strand nucleotides) is within the antisense strand region that is located 3' (downstream) of the antisense strand sequence which is complementary to the projected Ago2 cut site of the DsiRNA (*e.g.*, in Figure 1, the region of the antisense strand which is 3' of the projected Ago2 cut site is preferred for mismatch-forming residues and happens to be located at positions 17-23 of the antisense strand for the 25/27mer agent shown in Figure 1). Thus, in one embodiment, the position of a mismatch nucleotide (in relation to the target AR RNA sequence) of the antisense strand of a DsiRNAmm is the nucleotide residue of the antisense strand that is located immediately 3' (downstream) within the antisense strand sequence of the projected Ago2 cleavage site of the corresponding target AR RNA sequence. In other preferred embodiments, a mismatch nucleotide of the antisense strand of a DsiRNAmm (in relation to the target AR RNA sequence) is positioned at the nucleotide residue of the antisense strand that is located two nucleotides 3' (downstream) of the corresponding projected Ago2 cleavage site, three nucleotides 3' (downstream) of the corresponding projected Ago2 cleavage site, four nucleotides 3' (downstream) of the corresponding projected Ago2 cleavage site, five nucleotides 3' (downstream) of the corresponding projected Ago2 cleavage site, six nucleotides 3' (downstream) of the projected Ago2 cleavage site, seven nucleotides 3' (downstream) of the projected Ago2 cleavage site, eight nucleotides 3' (downstream) of the projected Ago2 cleavage site, or nine nucleotides 3' (downstream) of the projected Ago2 cleavage site.

In DsiRNA agents possessing two mismatch-forming nucleotides of the antisense strand (where mismatch-forming nucleotides are mismatch forming in relation to target AR RNA sequence), mismatches can occur consecutively (*e.g.*, at consecutive positions along the antisense strand nucleotide sequence). Alternatively, nucleotides of the antisense strand that form mismatched base pairs with the target AR RNA sequence can be interspersed by nucleotides that base pair with the target AR RNA sequence (*e.g.*, for a DsiRNA possessing mismatch-forming nucleotides at positions 17 and 20 (starting from the 5' terminus (position 1) of the antisense strand of the 25/27mer agent shown in Figure 1), but not at positions 18 and 19, the mismatched residues of sense strand positions 17 and 20 are interspersed by two nucleotides that form matched base pairs with corresponding residues of the target AR RNA sequence). For example, two residues of the antisense strand (located within the mismatch-tolerant region of the antisense strand) that form mismatched base pairs with the corresponding target AR RNA sequence can occur with zero, one, two, three,

four or five matched base pairs (with respect to target AR RNA sequence) located between these mismatch-forming base pairs.

For certain DsiRNAs possessing three mismatch-forming base pairs (mismatch-forming with respect to target AR RNA sequence), mismatch-forming nucleotides can occur consecutively (*e.g.*, in a triplet along the antisense strand nucleotide sequence). Alternatively, nucleotides of the antisense strand that form mismatched base pairs with the target AR RNA sequence can be interspersed by nucleotides that form matched base pairs with the target AR RNA sequence (*e.g.*, for a DsiRNA possessing mismatched nucleotides at positions 17, 18 and 22, but not at positions 19, 20 and 21, the mismatch-forming residues of antisense strand positions 17 and 18 are adjacent to one another, while the mismatch-forming residues of antisense strand positions 18 and 22 are interspersed by three nucleotides that form matched base pairs with corresponding residues of the target AR RNA). For example, three residues of the antisense strand (located within the mismatch-tolerant region of the antisense strand) that form mismatched base pairs with the corresponding target AR RNA sequence can occur with zero, one, two, three or four matched base pairs located between any two of these mismatch-forming base pairs.

For certain DsiRNAs possessing four mismatch-forming base pairs (mismatch-forming with respect to target AR RNA sequence), mismatch-forming nucleotides can occur consecutively (*e.g.*, in a quadruplet along the sense strand nucleotide sequence). Alternatively, nucleotides of the antisense strand that form mismatched base pairs with the target AR RNA sequence can be interspersed by nucleotides that form matched base pairs with the target AR RNA sequence (*e.g.*, for a DsiRNA possessing mismatch-forming nucleotides at positions 17, 19, 21 and 22, but not at positions 18 and 20, the mismatch-forming residues of antisense strand positions 21 and 22 are adjacent to one another, while the mismatch-forming residues of antisense strand positions 17 and 19 are interspersed by one nucleotide that forms a matched base pair with the corresponding residue of the target AR RNA sequence – similarly, the mismatch-forming residues of antisense strand positions 19 and 21 are also interspersed by one nucleotide that forms a matched base pair with the corresponding residue of the target AR RNA sequence). For example, four residues of the antisense strand (located within the mismatch-tolerant region of the antisense strand) that form mismatched base pairs with the corresponding target AR RNA

sequence can occur with zero, one, two or three matched base pairs located between any two of these mismatch-forming base pairs.

The above DsiRNAmm and other DsiRNA structures are described in order to exemplify certain structures of DsiRNAmm and DsiRNA agents. Design of the above DsiRNAmm and DsiRNA structures can be adapted to generate, *e.g.*, DsiRNAmm forms of other DsiRNA structures shown *infra*. As exemplified above, DsiRNAs can also be designed that possess single mismatches (or two, three or four mismatches) between the antisense strand of the DsiRNA and a target sequence, yet optionally can retain perfect complementarity between sense and antisense strand sequences of a DsiRNA.

It is further noted that the DsiRNA agents exemplified *infra* can also possess insertion/deletion (in/del) structures within their double-stranded and/or target AR RNA-aligned structures. Accordingly, the DsiRNAs of the invention can be designed to possess in/del variations in, *e.g.*, antisense strand sequence as compared to target AR RNA sequence and/or antisense strand sequence as compared to sense strand sequence, with preferred location(s) for placement of such in/del nucleotides corresponding to those locations described above for positioning of mismatched and/or mismatch-forming base pairs.

It is also noted that the DsiRNAs of the instant invention can tolerate mismatches within the 3'-terminal region of the sense strand/5'-terminal region of the antisense strand, as this region is modeled to be processed by Dicer and liberated from the guide strand sequence that loads into RISC. Exemplary DsiRNA structures of the invention that harbor such mismatches include the following:

```
Target RNA Sequence: 5′-. . . XXXXXXXXXXXXXXXXXXXXXHXXX .
. .-3′
DsiRNA Sense Strand:        5′-XXXXXXXXXXXXXXXXXXXXXIXDD-
3'
DsiRNA Antisense Strand: 3′-XXXXXXXXXXXXXXXXXXXXXJXXX-
5′
```

```
Target RNA Sequence: 5′-. . . XXXXXXXXXXXXXXXXXXXXXHXX .
. .-3′
DsiRNA Sense Strand:        5′-XXXXXXXXXXXXXXXXXXXXXIDD-
3'
```

DsiRNA Antisense Strand: 3′-XXXXXXXXXXXXXXXXXXXXXXXXXJXX-5′

Target RNA Sequence: 5′-. . . XXXXXXXXXXXXXXXXXXXXXXXXXHX . . .-3′

DsiRNA Sense Strand: 5′-XXXXXXXXXXXXXXXXXXXXXXXXXID-3'

DsiRNA Antisense Strand: 3′-XXXXXXXXXXXXXXXXXXXXXXXXXJX-5′

Target RNA Sequence: 5′-. . . XXXXXXXXXXXXXXXXXXXXXXXXXH . . .-3′

DsiRNA Sense Strand: 5′-XXXXXXXXXXXXXXXXXXXXXXXXXDI-3'

DsiRNA Antisense Strand: 3′-XXXXXXXXXXXXXXXXXXXXXXXXXXJ-5′

wherein "X"=RNA, "D"=DNA and "I" and "J"=Nucleic acid residues (RNA, DNA or non-natural or modified nucleic acids) that do not base pair (hydrogen bond) with one another, yet optionally "J" is complementary to target RNA sequence nucleotide "H". Any of the residues of such agents can optionally be 2'-O-methyl RNA monomers – alternating positioning of 2'-O-methyl RNA monomers that commences from the 3'-terminal residue of the bottom (second) strand, as shown above – or any of the above-described methylation patterns – can also be used in the above DsiRNA agents. The above mismatches can also be combined within the DsiRNAs of the instant invention.

In the below structures, such mismatches are introduced within the asymmetric AR-770 DsiRNA (newly-introduced mismatch residues are *italicized*):

AR-770 25/27mer DsiRNA, mismatch position = 22 of sense strand (from 5'-terminus)

5′-GAAAAAGAUAAUAACUCAGUU^{A}Uta-3′ (SEQ ID NO: 3772)

3′-UUCUUUUUCUAUUAUUGAGUCAA$_{G}$AAU-5′ (SEQ ID NO: 177)

Optionally, the mismatched "A" residue of position 22 of the sense strand is alternatively "U" or "G".

AR-770 25/27mer DsiRNA, mismatch position = 23 of sense strand

5′-GAAAAAGAUAAUAACUCAGUUC^{G}ta-3′ (SEQ ID NO: 3773)
3′-UUCUUUUUCUAUUAUUGAGUCAAG$_{A}$AU-5′ (SEQ ID NO: 177)

Optionally, the mismatched "G" residue of position 23 of the sense strand is alternatively "A" or "C".

AR-770 25/27mer DsiRNA, mismatch position = 24 of sense strand

5′-GAAAAAGAUAAUAACUCAGUUCU^{g}a-3′ (SEQ ID NO: 3774)
3′-UUCUUUUUCUAUUAUUGAGUCAAGA$_{A}$U-5′ (SEQ ID NO: 177)

Optionally, the mismatched "g" residue of position 24 of the sense strand is alternatively "a" or "c".

AR-770 25/27mer DsiRNA, mismatch position = 25 of sense strand

5′-GAAAAAGAUAAUAACUCAGUUCUt^{c}-3′ (SEQ ID NO: 3775)
3′-UUCUUUUUCUAUUAUUGAGUCAAGAA$_{U}$-5′ (SEQ ID NO: 177)

Optionally, the mismatched "c" residue of position 25 of the sense strand is alternatively "t" or "g".

AR-770 25/27mer DsiRNA, mismatch position = 1 of antisense strand

5′-GAAAAAGAUAAUAACUCAGUUCUt^{a}-3′ (SEQ ID NO: 24)
3′-UUCUUUUUCUAUUAUUGAGUCAAGAA$_{G}$-5′ (SEQ ID NO: 3776)

Optionally, the mismatched "G" residue of position 1 of the antisense strand is alternatively "A" or "C".

AR-770 25/27mer DsiRNA, mismatch position = 2 of antisense strand

5′-GAAAAAGAUAAUAACUCAGUUCU^{t}a-3′ (SEQ ID NO: 24)
3′-UUCUUUUUCUAUUAUUGAGUCAAGA$_{C}$U-5′ (SEQ ID NO: 3777)

Optionally, the mismatched "C" residue of position 2 of the antisense strand is alternatively "G" or "U".

AR-770 25/27mer DsiRNA, mismatch position = 3 of antisense strand

5′-GAAAAAGAUAAUAACUCAGUUC^{U}ta-3′ (SEQ ID NO: 24)

3′-UUCUUUUUCUAUUAUUGAGUCAAG$_{C}$AU-5′ (SEQ ID NO: 3778)

Optionally, the mismatched "C" residue of position 3 of the antisense strand is alternatively "U" or "G".

AR-770 25/27mer DsiRNA, mismatch position = 4 of antisense strand

5′-GAAAAAGAUAAUAACUCAGUU^{C}Uta-3′ (SEQ ID NO: 24)

3′-UUCUUUUUCUAUUAUUGAGUCAA$_{U}$AAU-5′ (SEQ ID NO: 3779)

Optionally, the mismatched "U" residue of position 4 of the antisense strand is alternatively "A" or "C".

As further examples, such mismatches are introduced within the asymmetric AR-2813, AR-2815 and AR-3599 DsiRNAs (newly-introduced mismatch residues are *italicized*):

AR-2813 25/27mer DsiRNA, mismatch position = 22 of sense strand (from 5'-terminus)

5'-GACCUGCCUGAUCUGUGGAGA^{C}Gaa-3' (SEQ ID NO: 5230)

3'-UUCUGGACGGACUAGACACCUCU$_{A}$CUU-5' (SEQ ID NO: 1992)

Optionally, the mismatched "C" residue of position 22 of the sense strand is alternatively "A" or "G".

AR-2813 25/27mer DsiRNA, mismatch position = 23 of sense strand

5'-GACCUGCCUGAUCUGUGGAGAU^{A}aa-3' (SEQ ID NO: 5231)

3'-UUCUGGACGGACUAGACACCUCUA$_{C}$UU-5' (SEQ ID NO: 1992)

Optionally, the mismatched "A" residue of position 23 of the sense strand is alternatively "C" or "U".

AR-2813 25/27mer DsiRNA, mismatch position = 24 of sense strand

5'-GACCUGCCUGAUCUGUGGAGAUG^{C}a-3' (SEQ ID NO: 5232)

3'-UUCUGGACGGACUAGACACCUCUAC$_{U}$U-5' (SEQ ID NO: 1992)

Optionally, the mismatched "c" residue of position 24 of the sense strand is alternatively "t" or "g".

AR-2813 25/27mer DsiRNA, mismatch position = 25 of sense strand

5'-GACCUGCCUGAUCUGUGGAGAUGa^{c}-3' (SEQ ID NO: 5233)
3'-UUCUGGACGGACUAGACACCUCUACU$_{U}$-5' (SEQ ID NO: 1992)

Optionally, the mismatched "c" residue of position 25 of the sense strand is alternatively "t" or "g".

AR-2813 25/27mer DsiRNA, mismatch position = 1 of antisense strand

5'-GACCUGCCUGAUCUGUGGAGAUGa^{a}-3' (SEQ ID NO: 1587)
3'-UUCUGGACGGACUAGACACCUCUACU$_{C}$-5' (SEQ ID NO: 5234)

Optionally, the mismatched "C" residue of position 1 of the antisense strand is alternatively "A" or "G".

AR-2813 25/27mer DsiRNA, mismatch position = 2 of antisense strand

5'-GACCUGCCUGAUCUGUGGAGAUG^{a}a-3' (SEQ ID NO: 1587)
3'-UUCUGGACGGACUAGACACCUCUAC$_{C}$U-5' (SEQ ID NO: 5235)

Optionally, the mismatched "C" residue of position 2 of the antisense strand is alternatively "G" or "A".

AR-2813 25/27mer DsiRNA, mismatch position = 3 of antisense strand

5'-GACCUGCCUGAUCUGUGGAGAU^{G}aa-3' (SEQ ID NO: 1587)
3'-UUCUGGACGGACUAGACACCUCUA$_{A}$UU-5' (SEQ ID NO: 5236)

Optionally, the mismatched "A" residue of position 3 of the antisense strand is alternatively "U" or "G".

AR-2813 25/27mer DsiRNA, mismatch position = 4 of antisense strand

5'-GACCUGCCUGAUCUGUGGAGA^{U}Gaa-3' (SEQ ID NO: 1587)
3'-UUCUGGACGGACUAGACACCUCU$_{C}$CUU-5' (SEQ ID NO: 5237)

Optionally, the mismatched "C" residue of position 4 of the antisense strand is alternatively "U" or "G".

AR-2815 25/27mer DsiRNA, mismatch position = 22 of sense strand (from 5'-terminus)

5'-CCUGCCUGAUCUGUGGAGAUG^{C}Agc-3' (SEQ ID NO: 5238)
3'-CUGGACGGACUAGACACCUCUAC$_{U}$UCG-5' (SEQ ID NO: 1994)

Optionally, the mismatched "C" residue of position 22 of the sense strand is alternatively "U" or "G".

AR-2815 25/27mer DsiRNA, mismatch position = 23 of sense strand

5'-CCUGCCUGAUCUGUGGAGAUGA^{C}gc-3' (SEQ ID NO: 5239)
3'-CUGGACGGACUAGACACCUCUACU$_{U}$CG-5' (SEQ ID NO: 1994)

Optionally, the mismatched "C" residue of position 23 of the sense strand is alternatively "G" or "U".

AR-2815 25/27mer DsiRNA, mismatch position = 24 of sense strand

5'-CCUGCCUGAUCUGUGGAGAUGAA^{a}c-3' (SEQ ID NO: 5240)
3'-CUGGACGGACUAGACACCUCUACUU$_{C}$G-5' (SEQ ID NO: 1994)

Optionally, the mismatched "a" residue of position 24 of the sense strand is alternatively "t" or "c".

AR-2815 25/27mer DsiRNA, mismatch position = 25 of sense strand

5'-CCUGCCUGAUCUGUGGAGAUGAAg^{a}-3' (SEQ ID NO: 5241)
3'-CUGGACGGACUAGACACCUCUACUUC$_{G}$-5' (SEQ ID NO: 1994)

Optionally, the mismatched "a" residue of position 25 of the sense strand is alternatively "t" or "g".

AR-2815 25/27mer DsiRNA, mismatch position = 1 of antisense strand

5'-CCUGCCUGAUCUGUGGAGAUGAAg^{C}-3' (SEQ ID NO: 1589)
3'-CUGGACGGACUAGACACCUCUACUUC$_{A}$-5' (SEQ ID NO: 5242)

Optionally, the mismatched "A" residue of position 1 of the antisense strand is alternatively "U" or "C".

AR-2815 25/27mer DsiRNA, mismatch position = 2 of antisense strand

5'-CCUGCCUGAUCUGUGGAGAUGAA^{g}c-3' (SEQ ID NO: 1589)
3'-CUGGACGGACUAGACACCUCUACUU$_{A}$G-5' (SEQ ID NO: 5243)

Optionally, the mismatched "A" residue of position 2 of the antisense strand is alternatively "G" or "U".

AR-2815 25/27mer DsiRNA, mismatch position = 3 of antisense strand

5'-CCUGCCUGAUCUGUGGAGAUGA^{A}gc-3' (SEQ ID NO: 1589)
3'-CUGGACGGACUAGACACCUCUACU$_{C}$CG-5' (SEQ ID NO: 5244)

Optionally, the mismatched "C" residue of position 3 of the antisense strand is alternatively "G" or "A".

AR-2815 25/27mer DsiRNA, mismatch position = 4 of antisense strand

5'-CCUGCCUGAUCUGUGGAGAUG^{A}Agc-3' (SEQ ID NO: 1589)
3'-CUGGACGGACUAGACACCUCUAC$_{C}$UCG-5' (SEQ ID NO: 5245)

Optionally, the mismatched "C" residue of position 4 of the antisense strand is alternatively "G" or "A".

AR-3599 25/27mer DsiRNA, mismatch position = 22 of sense strand (from 5'-terminus)

5'-UGGGCUGAAAAAUCAAAAAUU^{A}Utt-3' (SEQ ID NO: 5246)
3'-CUACCCGACUUUUUAGUUUUUAA$_{G}$AAA-5' (SEQ ID NO: 2159)

Optionally, the mismatched "A" residue of position 22 of the sense strand is alternatively "U" or "G".

AR-3599 25/27mer DsiRNA, mismatch position = 23 of sense strand

5'-UGGGCUGAAAAAUCAAAAAUUC^{C}tt-3' (SEQ ID NO: 5247)
3'-CUACCCGACUUUUUAGUUUUUAAG$_{A}$AA-5' (SEQ ID NO: 2159)

Optionally, the mismatched "C" residue of position 23 of the sense strand is alternatively "G" or "A".

AR-3599 25/27mer DsiRNA, mismatch position = 24 of sense strand

5'-UGGGCUGAAAAAUCAAAAAUUCU^{C}t-3' (SEQ ID NO: 5248)
3'-CUACCCGACUUUUUAGUUUUUAAGA$_{A}$A-5' (SEQ ID NO: 2159)

Optionally, the mismatched “c” residue of position 24 of the sense strand is alternatively “a” or “g”.

AR-3599 25/27mer DsiRNA, mismatch position = 25 of sense strand

5'-UGGGCUGAAAAAUCAAAAAUUCUt^{c}-3' (SEQ ID NO: 5249)
3'-CUACCCGACUUUUUAGUUUUUAAGAA$_{A}$-5' (SEQ ID NO: 2159)

Optionally, the mismatched “c” residue of position 25 of the sense strand is alternatively “a” or “g”.

AR-3599 25/27mer DsiRNA, mismatch position = 1 of antisense strand

5'-UGGGCUGAAAAAUCAAAAAUUCUt^{t}-3' (SEQ ID NO: 1754)
3'-CUACCCGACUUUUUAGUUUUUAAGAA$_{C}$-5' (SEQ ID NO: 5250)

Optionally, the mismatched “C” residue of position 1 of the antisense strand is alternatively “U” or “G”.

AR-3599 25/27mer DsiRNA, mismatch position = 2 of antisense strand

5'-UGGGCUGAAAAAUCAAAAAUUCU^{t}t-3' (SEQ ID NO: 1754)
3'-CUACCCGACUUUUUAGUUUUUAAGA$_{C}$A-5' (SEQ ID NO: 5251)

Optionally, the mismatched “C” residue of position 2 of the antisense strand is alternatively “G” or “U”.

AR-3599 25/27mer DsiRNA, mismatch position = 3 of antisense strand

5'-UGGGCUGAAAAAUCAAAAAUUC^{U}tt-3' (SEQ ID NO: 1754)
3'-CUACCCGACUUUUUAGUUUUUAAG$_{C}$AA-5' (SEQ ID NO: 5252)

Optionally, the mismatched “C” residue of position 3 of the antisense strand is alternatively “U” or “G”.

AR-3599 25/27mer DsiRNA, mismatch position = 4 of antisense strand

5'-UGGGCUGAAAAAUCAAAAAUU^{C}Utt-3' (SEQ ID NO: 1754)
3'-CUACCCGACUUUUUAGUUUUUAA$_{A}$AAA-5' (SEQ ID NO: 5253)

Optionally, the mismatched “A” residue of position 4 of the antisense strand is alternatively “U” or “C”.

As noted above, introduction of such mismatches can be performed upon any of the DsiRNAs described herein.

The mismatches of such DsiRNA structures can be combined to produce a DsiRNA possessing, *e.g.*, two, three or even four mismatches within the 3'-terminal four nucleotides of the sense strand/5'-terminal four nucleotides of the antisense strand.

Indeed, in view of the flexibility of sequences which can be incorporated into DsiRNAs at the 3'-terminal residues of the sense strand/5'-terminal residues of the antisense strand, in certain embodiments, the sequence requirements of an asymmetric DsiRNA of the instant invention can be represented as the following (minimalist) structure (shown for an exemplary AR-770 DsiRNA sequence):

5′-GAAAAAGAUAAUAACUCAGUUXXX[X]$_n$-3′ (SEQ ID NO: 3780)
3′-UUCUUUUUCUAUUAUUGAGUCXXXXX[X]$_n$-5′ (SEQ ID NO: 3781)

where n= 1 to 5, 1 to 10, 1 to 20, 1 to 30, 1 to 50, or 1 to 80 or more.

AR-770 Target: 5′-AAGAAAAAGATAATAACTCAGXXXXXX-3′ (SEQ ID NO: 3782)

The AR target sight may also be a site which is targeted by one or more of several oligonucleotides whose complementary target sites overlap with a stated target site. For example, for an exemplary AR-2813 DsiRNA, it is noted that certain DsiRNAs targeting overlapping and only slightly offset AR sequences can exhibit activity levels similar to that of AR-2808 (specifically, see AR-2815 and AR-2808 DsiRNAs of Figure 2. Thus, in certain embodiments, a designated target sequence region can be effectively targeted by a series of DsiRNAs possessing largely overlapping sequences. (*E.g.*, if considering DsiRNAs surrounding the AR-2813 site, a more encompassing AR target sequence might be recited as, e.g., 5'-CCCAGAAGACCTGCCTGATCTGTGGAGATGAAGC-3' (SEQ ID NO: 3783), wherein any given DsiRNA (*e.g.*, a DsiRNA selected from AR-2808, AR-2809, AR-2810, AR-2811, AR-2812, AR-2813, AR-2814 and AR-2815) only targets a sub-sequence within such a sequence region, yet the entire sequence can be considered a viable target for such a series of DsiRNAs).

Additionally and/or alternatively, mismatches within the 3'-terminal four nucleotides of the sense strand/5'-terminal four nucleotides of the antisense strand can

be combined with mismatches positioned at other mismatch-tolerant positions, as described above.

In view of the present identification of the above-described Dicer substrate agents (DsiRNAs) as inhibitors of AR levels *via* targeting of specific AR sequences, it is also recognized that DsiRNAs having structures similar to those described herein can also be synthesized which target other sequences within the AR sequence of SEQ ID NO: 3766, SEQ ID NO: 3768 or SEQ ID NO: 3770, or within variants thereof (*e.g.*, target sequences possessing 80% identity, 90% identity, 95% identity, 96% identity, 97% identity, 98% identity, 99% or more identity to a sequence of SEQ ID NO: 3766, SEQ ID NO: 3768 and/or SEQ ID NO: 3770).

Anti-AR DsiRNA Design/Synthesis

It has been found empirically that longer dsRNA species of from 25 to 35 nucleotides (DsiRNAs) and especially from 25 to 30 nucleotides give unexpectedly effective results in terms of potency and duration of action, as compared to 19-23mer siRNA agents. Without wishing to be bound by the underlying theory of the dsRNA processing mechanism, it is thought that the longer dsRNA species serve as a substrate for the Dicer enzyme in the cytoplasm of a cell. In addition to cleaving the dsRNA of the invention into shorter segments, Dicer is thought to facilitate the incorporation of a single-stranded cleavage product derived from the cleaved dsRNA into the RISC complex that is responsible for the destruction of the cytoplasmic RNA (*e.g.*, AR RNA) of or derived from the target gene, AR (or other gene associated with an AR-associated disease or disorder). Prior studies (Rossi *et al.*, U.S. Patent Application No. 2007/0265220) have shown that the cleavability of a dsRNA species (specifically, a DsiRNA agent) by Dicer corresponds with increased potency and duration of action of the dsRNA species.

Certain preferred anti-AR DsiRNA agents were selected from a pre-screened population. Design of DsiRNAs can optionally involve use of predictive scoring algorithms that perform *in silico* assessments of the projected activity/efficacy of a number of possible DsiRNA agents spanning a region of sequence. Information regarding the design of such scoring algorithms can be found, *e.g.*, in Gong *et al.* (*BMC Bioinformatics* 2006, **7:**516), though a more recent "v3" algorithm represents a theoretically improved algorithm relative to siRNA scoring algorithms previously

available in the art. (E.g., the "v3" and "v4" scoring algorithms are machine learning algorithms that are not reliant upon any biases in human sequence. In addition, the "v3" and "v4" algorithms derive from data sets that are many-fold larger than that from which an older "v2" algorithm such as that described in Gong *et al*. derives.)

The first and second oligonucleotides of the DsiRNA agents of the instant invention are not required to be completely complementary. In fact, in one embodiment, the 3'-terminus of the sense strand contains one or more mismatches. In one aspect, two mismatches are incorporated at the 3' terminus of the sense strand. In another embodiment, the DsiRNA of the invention is a double stranded RNA molecule containing two RNA oligonucleotides each of which is 27 nucleotides in length and, when annealed to each other, have blunt ends and a two nucleotide mismatch on the 3'-terminus of the sense strand (the 5'-terminus of the antisense strand). The use of mismatches or decreased thermodynamic stability (specifically at the 3'-sense/5'-antisense position) has been proposed to facilitate or favor entry of the antisense strand into RISC (Schwarz *et al*., 2003, *Cell* 115: 199-208; Khvorova *et al*., 2003, *Cell* 115: 209-216), presumably by affecting some rate-limiting unwinding steps that occur with entry of the siRNA into RISC. Thus, terminal base composition has been included in design algorithms for selecting active 21mer siRNA duplexes (Ui-Tei *et al*., 2004, *Nucleic Acids Res* 32: 936-948; Reynolds *et al*., 2004, *Nat Biotechnol* 22: 326-330). With Dicer cleavage of the dsRNA of this embodiment, the small end-terminal sequence which contains the mismatches will either be left unpaired with the antisense strand (become part of a 3'-overhang) or be cleaved entirely off the final 21-mer siRNA. These "mismatches", therefore, do not persist as mismatches in the final RNA component of RISC. The finding that base mismatches or destabilization of segments at the 3'-end of the sense strand of Dicer substrate improved the potency of synthetic duplexes in RNAi, presumably by facilitating processing by Dicer, was a surprising finding of past works describing the design and use of 25-30mer dsRNAs (also termed "DsiRNAs" herein; Rossi *et al*., U.S. Patent Application Nos. 2005/0277610, 2005/0244858 and 2007/0265220).

Modification of Anti-AR DsiRNAs

One major factor that inhibits the effect of double stranded RNAs ("dsRNAs") is the degradation of dsRNAs (*e.g*., siRNAs and DsiRNAs) by nucleases. A 3'-

exonuclease is the primary nuclease activity present in serum and modification of the 3'-ends of antisense DNA oligonucleotides is crucial to prevent degradation (Eder *et al.*, 1991, *Antisense Res Dev*, 1: 141-151). An RNase-T family nuclease has been identified called ERI-1 which has 3' to 5' exonuclease activity that is involved in regulation and degradation of siRNAs (Kennedy *et al.*, 2004, *Nature* 427: 645-649; Hong *et al.*, 2005, *Biochem J*, 390: 675-679). This gene is also known as Thex1 (NM_02067) in mice or THEX1 (NM_153332) in humans and is involved in degradation of histone mRNA; it also mediates degradation of 3'-overhangs in siRNAs, but does not degrade duplex RNA (Yang *et al.*, 2006, *J Biol Chem*, 281: 30447-30454). It is therefore reasonable to expect that 3'-end-stabilization of dsRNAs, including the DsiRNAs of the instant invention, will improve stability.

XRN1 (NM_019001) is a 5' to 3' exonuclease that resides in P-bodies and has been implicated in degradation of mRNA targeted by miRNA (Rehwinkel *et al.*, 2005, *RNA* 11: 1640-1647) and may also be responsible for completing degradation initiated by internal cleavage as directed by a siRNA. XRN2 (NM _012255) is a distinct 5' to 3' exonuclease that is involved in nuclear RNA processing.

RNase A is a major endonuclease activity in mammals that degrades RNAs. It is specific for ssRNA and cleaves at the 3'-end of pyrimidine bases. SiRNA degradation products consistent with RNase A cleavage can be detected by mass spectrometry after incubation in serum (Turner *et al.*, 2007, *Mol Biosyst* 3: 43-50). The 3'-overhangs enhance the susceptibility of siRNAs to RNase degradation. Depletion of RNase A from serum reduces degradation of siRNAs; this degradation does show some sequence preference and is worse for sequences having poly A/U sequence on the ends (Haupenthal *et al.*, 2006 *Biochem Pharmacol* 71: 702-710). This suggests the possibility that lower stability regions of the duplex may "breathe" and offer transient single-stranded species available for degradation by RNase A. RNase A inhibitors can be added to serum and improve siRNA longevity and potency (Haupenthal *et al.*, 2007, *Int J. Cancer* 121: 206-210).

In 21mers, phosphorothioate or boranophosphate modifications directly stabilize the internucleoside phosphate linkage. Boranophosphate modified RNAs are highly nuclease resistant, potent as silencing agents, and are relatively non-toxic. Boranophosphate modified RNAs cannot be manufactured using standard chemical synthesis methods and instead are made by in vitro transcription (IVT) (Hall *et al.*, 2004, *Nucleic Acids Res* 32: 5991-6000; Hall *et al.*, 2006, *Nucleic Acids Res* 34:

2773-2781). Phosphorothioate (PS) modifications can be easily placed in the RNA duplex at any desired position and can be made using standard chemical synthesis methods. The PS modification shows dose-dependent toxicity, so most investigators have recommended limited incorporation in siRNAs, favoring the 3'-ends where protection from nucleases is most important (Harborth *et al.*, 2003, *Antisense Nucleic Acid Drug Dev* 13: 83-105; Chiu and Rana, 2003, *Mol Cell* 10: 549-561; Braasch *et al.*, 2003, *Biochemistry* 42: 7967-7975; Amarzguioui *et al.*, 2003, *Nucleic Acids Research* 31: 589-595). More extensive PS modification can be compatible with potent RNAi activity; however, use of sugar modifications (such as 2'-O-methyl RNA) may be superior (Choung *et al.*, 2006, *Biochem Biophys Res Commun* 342: 919-927).

A variety of substitutions can be placed at the 2'-position of the ribose which generally increases duplex stability (T_m) and can greatly improve nuclease resistance. 2'-O-methyl RNA is a naturally occurring modification found in mammalian ribosomal RNAs and transfer RNAs. 2'-O-methyl modification in siRNAs is known, but the precise position of modified bases within the duplex is important to retain potency and complete substitution of 2'-O-methyl RNA for RNA will inactivate the siRNA. For example, a pattern that employs alternating 2'-O-methyl bases can have potency equivalent to unmodified RNA and is quite stable in serum (Choung *et al.*, 2006, *Biochem Biophys Res Commun* 342: 919-927; Czauderna *et al.*, 2003, *Nucleic Acids Research* 31: 2705-2716).

The 2'-fluoro (2'-F) modification is also compatible with dsRNA (*e.g.*, siRNA and DsiRNA) function; it is most commonly placed at pyrimidine sites (due to reagent cost and availability) and can be combined with 2'-O-methyl modification at purine positions; 2'-F purines are available and can also be used. Heavily modified duplexes of this kind can be potent triggers of RNAi in vitro (Allerson *et al.*, 2005, *J Med Chem* 48: 901-904; Prakash *et al.*, 2005, *J Med Chem* 48: 4247-4253; Kraynack and Baker, 2006, *RNA* 12: 163-176) and can improve performance and extend duration of action when used in vivo (Morrissey *et al.*, 2005, *Hepatology* 41: 1349-1356; Morrissey *et al.*, 2005, *Nat Biotechnol* 23: 1002-1007). A highly potent, nuclease stable, blunt 19mer duplex containing alternative 2'-F and 2'-O-Me bases is taught by Allerson. In this design, alternating 2'-O-Me residues are positioned in an identical pattern to that employed by Czauderna, however the remaining RNA residues are converted to 2'-F modified bases. A highly potent, nuclease resistant siRNA

employed by Morrissey employed a highly potent, nuclease resistant siRNA *in vivo*. In addition to 2'-O-Me RNA and 2'-F RNA, this duplex includes DNA, RNA, inverted abasic residues, and a 3'-terminal PS internucleoside linkage. While extensive modification has certain benefits, more limited modification of the duplex can also improve in vivo performance and is both simpler and less costly to manufacture. Soutschek *et al.* (2004, *Nature* 432: 173-178) employed a duplex *in vivo* and was mostly RNA with two 2'-O-Me RNA bases and limited 3'-terminal PS internucleoside linkages.

Locked nucleic acids (LNAs) are a different class of 2'-modification that can be used to stabilize dsRNA (*e.g.*, siRNA and DsiRNA). Patterns of LNA incorporation that retain potency are more restricted than 2'-O-methyl or 2'-F bases, so limited modification is preferred (Braasch *et al.*, 2003, *Biochemistry* 42: 7967-7975; Grunweller *et al.*, 2003, *Nucleic Acids Res* 31: 3185-3193; Elmen *et al.*, 2005, *Nucleic Acids Res* 33: 439-447). Even with limited incorporation, the use of LNA modifications can improve dsRNA performance *in vivo* and may also alter or improve off target effect profiles (Mook *et al.*, 2007, *Mol Cancer Ther* 6: 833-843).

Synthetic nucleic acids introduced into cells or live animals can be recognized as "foreign" and trigger an immune response. Immune stimulation constitutes a major class of off-target effects which can dramatically change experimental results and even lead to cell death. The innate immune system includes a collection of receptor molecules that specifically interact with DNA and RNA that mediate these responses, some of which are located in the cytoplasm and some of which reside in endosomes (Marques and Williams, 2005, *Nat Biotechnol* 23: 1399-1405; Schlee *et al.*, 2006, *Mol Ther* 14: 463-470). Delivery of siRNAs by cationic lipids or liposomes exposes the siRNA to both cytoplasmic and endosomal compartments, maximizing the risk for triggering a type 1 interferon (IFN) response both *in vitro* and *in vivo* (Morrissey *et al.*, 2005, *Nat Biotechnol* 23: 1002-1007; Sioud and Sorensen, 2003, *Biochem Biophys Res Commun* 312: 1220-1225; Sioud, 2005, *J Mol Biol* 348: 1079-1090; Ma *et al.*, 2005, *Biochem Biophys Res Commun* 330: 755-759). RNAs transcribed within the cell are less immunogenic (Robbins *et al.*, 2006, *Nat Biotechnol* 24: 566-571) and synthetic RNAs that are immunogenic when delivered using lipid-based methods can evade immune stimulation when introduced unto cells by mechanical means, even *in vivo* (Heidel *et al.*, 2004, *Nat Biotechnol* 22: 1579-1582). However, lipid based delivery methods are convenient, effective, and widely used. Some general strategy

to prevent immune responses is needed, especially for *in vivo* application where all cell types are present and the risk of generating an immune response is highest. Use of chemically modified RNAs may solve most or even all of these problems.

In certain embodiments, modifications can be included in the anti-AR DsiRNA agents of the present invention so long as the modification does not prevent the DsiRNA agent from possessing AR inhibitory activity. In one embodiment, one or more modifications are made that enhance Dicer processing of the DsiRNA agent (an assay for determining Dicer processing of a DsiRNA is described *supra*). In a second embodiment, one or more modifications are made that result in more effective AR inhibition (as described herein, AR inhibition/AR inhibitory activity of a DsiRNA can be assayed *via* art-recognized methods for determining RNA levels, or for determining AR polypeptide levels, should such levels be assessed in lieu of or in addition to assessment of, *e.g.*, AR mRNA levels). In a third embodiment, one or more modifications are made that support greater AR inhibitory activity (means of determining AR inhibitory activity are described *supra*). In a fourth embodiment, one or more modifications are made that result in greater potency of AR inhibitory activity per each DsiRNA agent molecule to be delivered to the cell (potency of AR inhibitory activity is described *supra*). Modifications can be incorporated in the 3'-terminal region, the 5'-terminal region, in both the 3'-terminal and 5'-terminal region or in some instances in various positions within the sequence. With the restrictions noted above in mind, numbers and combinations of modifications can be incorporated into the DsiRNA agent. Where multiple modifications are present, they may be the same or different. Modifications to bases, sugar moieties, the phosphate backbone, and their combinations are contemplated. Either 5'-terminus can be phosphorylated.

Examples of modifications contemplated for the phosphate backbone include phosphonates, including methylphosphonate, phosphorothioate, and phosphotriester modifications such as alkylphosphotriesters, and the like. Examples of modifications contemplated for the sugar moiety include 2'-alkyl pyrimidine, such as 2'-O-methyl, 2'-fluoro, amino, and deoxy modifications and the like (see, *e.g.*, Amarzguioui *et al.*, 2003, *Nucleic Acids Research* 31: 589-595). Examples of modifications contemplated for the base groups include abasic sugars, 2-O-alkyl modified pyrimidines, 4-thiouracil, 5-bromouracil, 5-iodouracil, and 5-(3-aminoallyl)-uracil and the like. Locked nucleic acids, or LNA's, could also be incorporated. Many other modifications are known and can be used so long as the above criteria are satisfied.

Examples of modifications are also disclosed in U.S. Pat. Nos. 5,684,143, 5,858,988 and 6,291,438 and in U.S. published patent application No. 2004/0203145 A1. Other modifications are disclosed in Herdewijn (2000, *Antisense Nucleic Acid Drug Dev* 10: 297-310), Eckstein (2000, *Antisense Nucleic Acid Drug Dev* 10: 117-21), Rusckowski *et al.* (2000, *Antisense Nucleic Acid Drug Dev* 10: 333-345), Stein *et al.* (2001, *Antisense Nucleic Acid Drug Dev* 11: 317-25); Vorobjev *et al.* (2001, *Antisense Nucleic Acid Drug Dev* 11: 77-85).

One or more modifications contemplated can be incorporated into either strand. The placement of the modifications in the DsiRNA agent can greatly affect the characteristics of the DsiRNA agent, including conferring greater potency and stability, reducing toxicity, enhance Dicer processing, and minimizing an immune response. In one embodiment, the antisense strand or the sense strand or both strands have one or more 2'-O-methyl modified nucleotides. In another embodiment, the antisense strand contains 2'-O-methyl modified nucleotides. In another embodiment, the antisense stand contains a 3' overhang that is comprised of 2'-O-methyl modified nucleotides. The antisense strand could also include additional 2'-O-methyl modified nucleotides.

In certain embodiments of the present invention, the anti-AR DsiRNA agent has one or more of the following properties: (i) the DsiRNA agent is asymmetric, *e.g.*, has a 3' overhang on the antisense strand and (ii) the DsiRNA agent has a modified 3' end on the sense strand to direct orientation of Dicer binding and processing of the dsRNA to an active siRNA. According to this embodiment, the longest strand in the dsRNA comprises 25-35 nucleotides (e.g., 25, 26, 27, 28, 29, 30, 31, 32, 33, 34 or 35 nucleotides). In certain such embodiments, the DsiRNA agent is asymmetric such that the sense strand comprises 25-34 nucleotides and the 3’ end of the sense strand forms a blunt end with the 5’ end of the antisense strand while the antisense strand comprises 26-35 nucleotides and forms an overhang on the 3’ end of the antisense strand. In one embodiment, the DsiRNA agent is asymmetric such that the sense strand comprises 25-28 nucleotides and the antisense strand comprises 25-30 nucleotides. Thus, the resulting dsRNA has an overhang on the 3' end of the antisense strand. The overhang is 1-4 nucleotides, for example 2 nucleotides. The sense strand may also have a 5' phosphate.

In other embodiments, the sense strand of the DsiRNA agent is modified for Dicer processing by suitable modifiers located at the 3' end of the sense strand, i.e.,

the DsiRNA agent is designed to direct orientation of Dicer binding and processing. Suitable modifiers include nucleotides such as deoxyribonucleotides, dideoxyribonucleotides, acyclonucleotides and the like and sterically hindered molecules, such as fluorescent molecules and the like. Acyclonucleotides substitute a 2-hydroxyethoxymethyl group for the 2'-deoxyribofuranosyl sugar normally present in dNMPs. Other nucleotides modifiers could include 3'-deoxyadenosine (cordycepin), 3'-azido-3'-deoxythymidine (AZT), 2',3'-dideoxyinosine (ddI), 2',3'-dideoxy-3'-thiacytidine (3TC), 2',3'-didehydro-2',3'-dideoxythymidine (d4T) and the monophosphate nucleotides of 3'-azido-3'-deoxythymidine (AZT), 2',3'-dideoxy-3'-thiacytidine (3TC) and 2',3'-didehydro-2',3'-dideoxythymidine (d4T). In one embodiment, deoxynucleotides are used as the modifiers. When nucleotide modifiers are utilized, 1-3 nucleotide modifiers, or 2 nucleotide modifiers are substituted for the ribonucleotides on the 3' end of the sense strand. When sterically hindered molecules are utilized, they are attached to the ribonucleotide at the 3' end of the antisense strand. Thus, the length of the strand does not change with the incorporation of the modifiers. In another embodiment, the invention contemplates substituting two DNA bases in the DsiRNA agent to direct the orientation of Dicer processing of the antisense strand. In a further embodiment of the present invention, two terminal DNA bases are substituted for two ribonucleotides on the 3'-end of the sense strand forming a blunt end of the duplex on the 3' end of the sense strand and the 5' end of the antisense strand, and a two-nucleotide RNA overhang is located on the 3'-end of the antisense strand. This is an asymmetric composition with DNA on the blunt end and RNA bases on the overhanging end.

The sense and antisense strands of a DsiRNA agent of the instant invention anneal under biological conditions, such as the conditions found in the cytoplasm of a cell. In addition, a region of one of the sequences, particularly of the antisense strand, of the DsiRNA agent has a sequence length of at least 15 (in certain embodiments, 19) nucleotides, wherein these nucleotides are adjacent to the 3' end of antisense strand (e.g., in the 21-nucleotide region adjacent to the 3' end of the antisense strand and are sufficiently complementary to a nucleotide sequence of the target AR RNA.

Additionally, the DsiRNA agent structure can be optimized to ensure that the oligonucleotide segment generated from Dicer's cleavage will be the portion of the oligonucleotide that is most effective in inhibiting gene expression. For example, in one embodiment of the invention, a 27-bp oligonucleotide of the DsiRNA agent

structure is synthesized wherein the anticipated 21 to 22-bp segment that will inhibit gene expression is located on the 3'-end of the antisense strand. The remaining bases located on the 5'-end of the antisense strand will be cleaved by Dicer and will be discarded. This cleaved portion can be homologous (*i.e.*, based on the sequence of the target sequence) or non-homologous and added to extend the nucleic acid strand.

The DsiRNA agent can also have one or more of the following additional properties: (a) the antisense strand has a right shift from the typical 21mer (*e.g.*, the DsiRNA comprises a length of antisense strand nucleotides that extends to the 5' of a projected Dicer cleavage site within the DsiRNA, with such antisense strand nucleotides base paired with corresponding nucleotides of the sense strand extending 3' of a projected Dicer cleavage site in the sense strand), (b) the strands may not be completely complementary, *i.e.*, the strands may contain simple mismatched base pairs (in certain embodiments, the DsiRNAs of the invention possess 1, 2, 3, 4 or even 5 or more mismatched base pairs, provided that AR inhibitory activity of the DsiRNA possessing mismatched base pairs is retained at sufficient levels (e.g., retains at least 50% AR inhibitory activity or more, at least 60% AR inhibitory activity or more, at least 70% AR inhibitory activity or more, at least 80% AR inhibitory activity or more, at least 90% AR inhibitory activity or more or at least 95% AR inhibitory activity or more as compared to a corresponding DsiRNA not possessing mismatched base pairs. In certain embodiments, mismatched base pairs exist between the antisense and sense strands of a DsiRNA. In some embodiments, mismatched base pairs exist (or are predicted to exist) between the antisense strand and the target RNA. In certain embodiments, the presence of a mismatched base pair(s) between an antisense strand residue and a corresponding residue within the target RNA that is located 3' in the target RNA sequence of a projected Ago2 cleavage site retains and may even enhance AR inhibitory activity of a DsiRNA of the invention) and (c) base modifications such as locked nucleic acid(s) may be included in the 5' end of the sense strand. A "typical" 21mer siRNA is designed using conventional techniques. In one technique, a variety of sites are commonly tested in parallel or pools containing several distinct siRNA duplexes specific to the same target with the hope that one of the reagents will be effective (Ji *et al.*, 2003, *FEBS Lett* 552: 247-252). Other techniques use design rules and algorithms to increase the likelihood of obtaining active RNAi effector molecules (Schwarz *et al.*, 2003, *Cell* 115: 199-208; Khvorova *et al.*, 2003, *Cell* 115: 209-216; Ui-Tei *et al.*, 2004, *Nucleic Acids Res* 32: 936-948; Reynolds *et al.*, 2004,

Nat Biotechnol 22: 326-330; Krol *et al.*, 2004, *J Biol Chem* 279: 42230-42239; Yuan *et al.*, 2004, *Nucl Acids Res* 32(Webserver issue):W130-134; Boese *et al.*, 2005, *Methods Enzymol* 392: 73-96). High throughput selection of siRNA has also been developed (U.S. published patent application No. 2005/0042641 A1). Potential target sites can also be analyzed by secondary structure predictions (Heale *et al.*, 2005, *Nucleic Acids Res* 33(3): e30). This 21mer is then used to design a right shift to include 3-9 additional nucleotides on the 5' end of the 21mer. The sequence of these additional nucleotides is not restricted. In one embodiment, the added ribonucleotides are based on the sequence of the target gene. Even in this embodiment, full complementarity between the target sequence and the antisense siRNA is not required.

The first and second oligonucleotides of a DsiRNA agent of the instant invention are not required to be completely complementary. They only need to be sufficiently complementary to anneal under biological conditions and to provide a substrate for Dicer that produces a siRNA sufficiently complementary to the target sequence. Locked nucleic acids, or LNA's, are well known to a skilled artisan (Elmen *et al.*, 2005, *Nucleic Acids Res* 33: 439-447; Kurreck *et al.*, 2002, *Nucleic Acids Res* 30: 1911-1918; Crinelli *et al.*, 2002, *Nucleic Acids Res* 30: 2435-2443; Braasch and Corey, 2001, *Chem Biol* 8: 1-7; Bondensgaard *et al.*, 2000, *Chemistry* 6: 2687-2695; Wahlestedt *et al.*, 2000, *Proc Natl Acad Sci USA* 97: 5633-5638). In one embodiment, an LNA is incorporated at the 5' terminus of the sense strand. In another embodiment, an LNA is incorporated at the 5' terminus of the sense strand in duplexes designed to include a 3' overhang on the antisense strand.

In certain embodiments, the DsiRNA agent of the instant invention has an asymmetric structure, with the sense strand having a 25-base pair length, and the antisense strand having a 27-base pair length with a 2 base 3'-overhang. In other embodiments, this DsiRNA agent having an asymmetric structure further contains 2 deoxynucleotides at the 3' end of the sense strand in place of two of the ribonucleotides.

Certain DsiRNA agent compositions containing two separate oligonucleotides can be linked by a third structure. The third structure will not block Dicer activity on the DsiRNA agent and will not interfere with the directed destruction of the RNA transcribed from the target gene. In one embodiment, the third structure may be a chemical linking group. Many suitable chemical linking groups are known in the art

and can be used. Alternatively, the third structure may be an oligonucleotide that links the two oligonucleotides of the DsiRNA agent in a manner such that a hairpin structure is produced upon annealing of the two oligonucleotides making up the dsRNA composition. The hairpin structure will not block Dicer activity on the DsiRNA agent and will not interfere with the directed destruction of the AR RNA.

In certain embodiments, the anti-AR DsiRNA agent of the invention has several properties which enhance its processing by Dicer. According to such embodiments, the DsiRNA agent has a length sufficient such that it is processed by Dicer to produce an siRNA and at least one of the following properties: (i) the DsiRNA agent is asymmetric, *e.g.*, has a 3' overhang on the sense strand and (ii) the DsiRNA agent has a modified 3' end on the antisense strand to direct orientation of Dicer binding and processing of the dsRNA to an active siRNA. According to these embodiments, the longest strand in the DsiRNA agent comprises 25-30 nucleotides. In one embodiment, the sense strand comprises 25-30 nucleotides and the antisense strand comprises 25-28 nucleotides. Thus, the resulting dsRNA has an overhang on the 3' end of the sense strand. The overhang is 1-4 nucleotides, such as 2 nucleotides. The antisense strand may also have a 5' phosphate.

In certain embodiments, the sense strand of a DsiRNA agent is modified for Dicer processing by suitable modifiers located at the 3' end of the sense strand, *i.e.*, the DsiRNA agent is designed to direct orientation of Dicer binding and processing. Suitable modifiers include nucleotides such as deoxyribonucleotides, dideoxyribonucleotides, acyclonucleotides and the like and sterically hindered molecules, such as fluorescent molecules and the like. Acyclonucleotides substitute a 2-hydroxyethoxymethyl group for the 2'-deoxyribofuranosyl sugar normally present in dNMPs. Other nucleotide modifiers could include 3'-deoxyadenosine (cordycepin), 3'-azido-3'-deoxythymidine (AZT), 2',3'-dideoxyinosine (ddI), 2',3'-dideoxy-3'-thiacytidine (3TC), 2',3'-didehydro-2',3'-dideoxythymidine (d4T) and the monophosphate nucleotides of 3'-azido-3'-deoxythymidine (AZT), 2',3'-dideoxy-3'-thiacytidine (3TC) and 2',3'-didehydro-2',3'-dideoxythymidine (d4T). In one embodiment, deoxynucleotides are used as the modifiers. When nucleotide modifiers are utilized, 1-3 nucleotide modifiers, or 2 nucleotide modifiers are substituted for the ribonucleotides on the 3' end of the sense strand. When sterically hindered molecules are utilized, they are attached to the ribonucleotide at the 3' end of the antisense strand. Thus, the length of the strand does not change with the incorporation of the

modifiers. In another embodiment, the invention contemplates substituting two DNA bases in the dsRNA to direct the orientation of Dicer processing. In a further invention, two terminal DNA bases are located on the 3' end of the sense strand in place of two ribonucleotides forming a blunt end of the duplex on the 5' end of the antisense strand and the 3' end of the sense strand, and a two-nucleotide RNA overhang is located on the 3'-end of the antisense strand. This is an asymmetric composition with DNA on the blunt end and RNA bases on the overhanging end.

In certain other embodiments, the antisense strand of a DsiRNA agent is modified for Dicer processing by suitable modifiers located at the 3' end of the antisense strand, *i.e.*, the DsiRNA agent is designed to direct orientation of Dicer binding and processing. Suitable modifiers include nucleotides such as deoxyribonucleotides, dideoxyribonucleotides, acyclonucleotides and the like and sterically hindered molecules, such as fluorescent molecules and the like. Acyclonucleotides substitute a 2-hydroxyethoxymethyl group for the 2'-deoxyribofuranosyl sugar normally present in dNMPs. Other nucleotide modifiers could include 3'-deoxyadenosine (cordycepin), 3'-azido-3'-deoxythymidine (AZT), 2',3'-dideoxyinosine (ddI), 2',3'-dideoxy-3'-thiacytidine (3TC), 2',3'-didehydro-2',3'-dideoxythymidine (d4T) and the monophosphate nucleotides of 3'-azido-3'-deoxythymidine (AZT), 2',3'-dideoxy-3'-thiacytidine (3TC) and 2',3'-didehydro-2',3'-dideoxythymidine (d4T). In one embodiment, deoxynucleotides are used as the modifiers. When nucleotide modifiers are utilized, 1-3 nucleotide modifiers, or 2 nucleotide modifiers are substituted for the ribonucleotides on the 3' end of the antisense strand. When sterically hindered molecules are utilized, they are attached to the ribonucleotide at the 3' end of the antisense strand. Thus, the length of the strand does not change with the incorporation of the modifiers. In another embodiment, the invention contemplates substituting two DNA bases in the dsRNA to direct the orientation of Dicer processing. In a further invention, two terminal DNA bases are located on the 3' end of the antisense strand in place of two ribonucleotides forming a blunt end of the duplex on the 5' end of the sense strand and the 3' end of the antisense strand, and a two-nucleotide RNA overhang is located on the 3'-end of the sense strand. This is also an asymmetric composition with DNA on the blunt end and RNA bases on the overhanging end.

The sense and antisense strands anneal under biological conditions, such as the conditions found in the cytoplasm of a cell. In addition, a region of one of the

sequences, particularly of the antisense strand, of the dsRNA has a sequence length of at least 19 nucleotides, wherein these nucleotides are adjacent to the 3' end of antisense strand and are sufficiently complementary to a nucleotide sequence of the target AR RNA.

Additionally, the DsiRNA agent structure can be optimized to ensure that the oligonucleotide segment generated from Dicer's cleavage will be the portion of the oligonucleotide that is most effective in inhibiting gene expression. For example, in one embodiment of the invention, a 27-bp oligonucleotide of the DsiRNA agent structure is synthesized wherein the anticipated 21 to 22-bp segment that will inhibit gene expression is located on the 3'-end of the antisense strand. The remaining bases located on the 5'-end of the antisense strand will be cleaved by Dicer and will be discarded. This cleaved portion can be homologous (*i.e.*, based on the sequence of the target sequence) or non-homologous and added to extend the nucleic acid strand.

US 2007/0265220 discloses that 27mer DsiRNAs show improved stability in serum over comparable 21mer siRNA compositions, even absent chemical modification. Modifications of DsiRNA agents, such as inclusion of 2'-O-methyl RNA in the antisense strand, in patterns such as detailed above, when coupled with addition of a 5' Phosphate, can improve stability of DsiRNA agents. Addition of 5'-phosphate to all strands in synthetic RNA duplexes may be an inexpensive and physiological method to confer some limited degree of nuclease stability.

The chemical modification patterns of the dsRNA agents of the instant invention are designed to enhance the efficacy of such agents. Accordingly, such modifications are designed to avoid reducing potency of dsRNA agents; to avoid interfering with Dicer processing of DsiRNA agents; to improve stability in biological fluids (reduce nuclease sensitivity) of dsRNA agents; or to block or evade detection by the innate immune system. Such modifications are also designed to avoid being toxic and to avoid increasing the cost or impact the ease of manufacturing the instant dsRNA agents of the invention.

AR Biology and Biochemistry

AR, also known as NR3C4 (nuclear receptor subfamily 3, group C, member 4), is a nuclear receptor (Wardell *et al.*, *Pharmacol. Rev.* 58 (4): 782–97) that is activated by cytoplasmic binding of androgenic hormones (testosterone or dihydrotestosterone; Roy *et al.*, *Vitam. Horm.* 55: 309–52), resulting in nuclear

translocation of AR. Among nuclear receptors, AR is most closely related to the progesterone receptor, and progestins in higher dosages have been shown to block AR (Bardin *et al.*, *Pharmacol. Ther.* 23 (3): 443–59; Raudrant and Rabe, *Drugs* 63 (5): 463–92). Androgen regulated genes are critical for the development and maintenance of the male sexual phenotype.

Two isoforms of the androgen receptor (A and B) have been identified (Wilson and McPhaul, *Proc. Natl. Acad. Sci. U.S.A.* 91 (4): 1234–8). AR-B is a 110 kDa full length form, while AR-A is an 87 kDa protein that results from in vitro proteolysis of the N-terminus of the full length form (accordingly, AR-A lacks the first 187 amino acids of the full length form, AR-B; Gregory *et al. J Mol Endocrinol* 27: 309-19).

Like other nuclear receptors, the androgen receptor is modular in structure and, from the N-terminus to the C-terminus, is composed of the following functional domains:

An N-terminal regulatory domain contains: activation function 1 (AF-1) between residues 101 and 370, required for full ligand activated transcriptional activity (Jenster *et al.*, *J. Biol. Chem.* 270: 7341–6); activation function 5 (AF-5) between residues 360-485, which is responsible for constitutive activity (activity without bound ligand); a dimerization surface involving residues 1-36 (containing an FXXLF motif where F = phenylalanine, L = leucine, and X = any amino acid residue) and 370-494, which both interact with the LBD in an intramolecular (Schaufele *et al. Proc. Natl. Acad. Sci. U.S.A.* 102: 9802–7; Klokk et al. *Mol. Cell. Biol.* 27 (5): 1823–43; van Royen et al. *J. Cell Biol.* 177 (1): 63–72) head-to-tail interaction (Langley *et al. J. Biol. Chem.* 270 (50): 29983–90; Berrevoets *et al. Mol. Endocrinol.* 12 (8): 1172–83; Dubbink *et al. Mol. Endocrinol.* 18 (9): 2132–50);

a DNA binding domain (DBD);

a hinge region, which is a flexible region that connects the DBD with the LBD; along with the DBD, this region contains a ligand dependent nuclear localization signal (Kaku *et al. Endocrinology* 149: 3960);

a ligand binding domain (LBD) containing: activation function 2 (AF-2), responsible for agonist induced activity (activity in the presence of bound agonist); AF-2, which binds either the N-terminal FXXFL motif intramolecularly or coactivator

proteins (containing the LXXLL or preferably FXXFL motifs; Dubbink *et al. Mol. Endocrinol.* **18** (9): 2132–50); and a ligand dependent nuclear export signal (Saporita et al. *J. Biol. Chem.* **278** (43): 41998–2005); and

a C-terminal domain.

Known human and mouse AR cDNA and polypeptide sequences include the following:

Human Wild-type AR sequence, long transcript (SEQ ID NO: 3766; Homo sapiens AR, transcript variant 1; GenBank Accession No. NM_000044.2):

CGAGATCCCGGGGAGCCAGCTTGCTGGGAGAGCGGGACGGTCCGGAGCA
AGCCCAGAGGCAGAGGAGGCGACAGAGGGAAAAAGGGCCGAGCTAGCC
GCTCCAGTGCTGTACAGGAGCCGAAGGGACGCACCACGCCAGCCCCAGCC
CGGCTCCAGCGACAGCCAACGCCTCTTGCAGCGCGGCGGCTTCGAAGCCG
CCGCCCGGAGCTGCCCTTTCCTCTTCGGTGAAGTTTTTAAAAGCTGCTAAA
GACTCGGAGGAAGCAAGGAAAGTGCCTGGTAGGACTGACGGCTGCCTTTG
TCCTCCTCCTCTCCACCCCGCCTCCCCCCACCCTGCCTTCCCCCCCTCCCCC
GTCTTCTCTCCCGCAGCTGCCTCAGTCGGCTACTCTCAGCCAACCCCCCTC
ACCACCCTTCTCCCCACCCGCCCCCCCCGCCCCCGTCGGCCCAGCGCTGCCA
GCCCGAGTTTGCAGAGAGGTAACTCCCTTTGGCTGCGAGCGGGCGAGCTA
GCTGCACATTGCAAAGAAGGCTCTTAGGAGCCAGGCGACTGGGGAGCGG
CTTCAGCACTGCAGCCACGACCCGCCTGGTTAGGCTGCACGCGGAGAGAA
CCCTCTGTTTTCCCCCACTCTCTCTCCACCTCCTCCTGCCTTCCCCACCCCG
AGTGCGGAGCCAGAGATCAAAAGATGAAAAGGCAGTCAGGTCTTCAGTA
GCCAAAAAACAAAACAAACAAAAACAAAAAAGCCGAAATAAAAGAAAA
AGATAATAACTCAGTTCTTATTTGCACCTACTTCAGTGGACACTGAATTTG
GAAGGTGGAGGATTTTGTTTTTTTCTTTTAAGATCTGGGCATCTTTTGAATC
TACCCTTCAAGTATTAAGAGACAGACTGTGAGCCTAGCAGGGCAGATCTT
GTCCACCGTGTGTCTTCTTCTGCACGAGACTTTGAGGCTGTCAGAGCGCTT
TTTGCGTGGTTGCTCCCGCAAGTTTCCTTCTCTGGAGCTTCCCGCAGGTGG
GCAGCTAGCTGCAGCGACTACCGCATCATCACAGCCTGTTGAACTCTTCTG
AGCAAGAGAAGGGGAGGCGGGGTAAGGGAAGTAGGTGGAAGATTCAGCC
AAGCTCAAGGATGGAAGTGCAGTTAGGGCTGGGAAGGGTCTACCCTCGGC
CGCCGTCCAAGACCTACCGAGGAGCTTTCCAGAATCTGTTCCAGAGCGTG

CGCGAAGTGATCCAGAACCCGGGCCCCAGGCACCCAGAGGCCGCGAGCG
CAGCACCTCCCGGCGCCAGTTTGCTGCTGCTGCAGCAGCAGCAGCAGCAG
CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC
AAGAGACTAGCCCCAGGCAGCAGCAGCAGCAGGGTGAGGATGGTTC
TCCCCAAGCCCATCGTAGAGGCCCCACAGGCTACCTGGTCCTGGATGAGG
AACAGCAACCTTCACAGCCGCAGTCGGCCCTGGAGTGCCACCCCGAGAGA
GGTTGCGTCCCAGAGCCTGGAGCCGCCGTGGCCGCCAGCAAGGGGCTGCC
GCAGCAGCTGCCAGCACCTCCGGACGAGGATGACTCAGCTGCCCCATCCA
CGTTGTCCCTGCTGGGCCCCACTTTCCCCGGCTTAAGCAGCTGCTCCGCTG
ACCTTAAAGACATCCTGAGCGAGGCCAGCACCATGCAACTCCTTCAGCAA
CAGCAGCAGGAAGCAGTATCCGAAGGCAGCAGCAGCGGGAGAGCGAGGG
AGGCCTCGGGGGCTCCCACTTCCTCCAAGGACAATTACTTAGGGGGCACT
TCGACCATTTCTGACAACGCCAAGGAGTTGTGTAAGGCAGTGTCGGTGTC
CATGGGCCTGGGTGTGGAGGCGTTGGAGCATCTGAGTCCAGGGGAACAGC
TTCGGGGGGATTGCATGTACGCCCCACTTTTGGGAGTTCCACCCGCTGTGC
GTCCCACTCCTTGTGCCCCATTGGCCGAATGCAAAGGTTCTCTGCTAGACG
ACAGCGCAGGCAAGAGCACTGAAGATACTGCTGAGTATTCCCCTTTCAAG
GGAGGTTACACCAAAGGGCTAGAAGGCGAGAGCCTAGGCTGCTCTGGCA
GCGCTGCAGCAGGGAGCTCCGGGACACTTGAACTGCCGTCTACCCTGTCT
CTCTACAAGTCCGGAGCACTGGACGAGGCAGCTGCGTACCAGAGTCGCGA
CTACTACAACTTTCCACTGGCTCTGGCCGGACCGCCGCCCCCTCCGCCGCC
TCCCCATCCCCCACGCTCGCATCAAGCTGGAGAACCCGCTGGACTACGGCA
GCGCCTGGGCGGCTGCGGCGGCGCAGTGCCGCTATGGGGACCTGGCGAGC
CTGCATGGCGCGGGTGCAGCGGGACCCGGTTCTGGGTCACCCTCAGCCGC
CGCTTCCTCATCCTGGCACACTCTCTTCACAGCCGAAGAAGGCCAGTTGTA
TGGACCGTGTGGTGGTGGTGGGGGTGGTGGCGGCGGCGGCGGCGGCGGC
GGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGAGGCGGGAGCTGTAGCCC
CCTACGGCTACACTCGGCCCCCTCAGGGGCTGGCGGGCCAGGAAAGCGAC
TTCACCGCACCTGATGTGTGGTACCCTGGCGGCATGGTGAGCAGAGTGCC
CTATCCCAGTCCCACTTGTGTCAAAAGCGAAATGGGCCCCTGGATGGATA
GCTACTCCGGACCTTACGGGGACATGCGTTTGGAGACTGCCAGGGACCAT
GTTTTGCCCATTGACTATTACTTTCCACCCCAGAAGACCTGCCTGATCTGT
GGAGATGAAGCTTCTGGGTGTCACTATGGAGCTCTCACATGTGGAAGCTG
CAAGGTCTTCTTCAAAAGAGCCGCTGAAGGGAAACAGAAGTACCTGTGCG

DEMANDE OU BREVET VOLUMINEUX

LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVET COMPREND PLUS D'UN TOME.

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CLAIMS

We claim:

1. An isolated double stranded ribonucleic acid (dsRNA) comprising first and second nucleic acid strands, wherein said first strand is 15-35 nucleotides in length and said second strand of said dsRNA is 19-35 nucleotides in length, wherein said second oligonucleotide strand is sufficiently complementary to a target AR cDNA sequence selected from Table 13 along at least 19 nucleotides of said second oligonucleotide strand length to reduce AR target gene expression when said double stranded nucleic acid is introduced into a mammalian cell.

2. The isolated dsRNA of claim 1 comprising a duplex region of at least 25 base pairs.

3. The isolated dsRNA of claim 1, wherein said second oligonucleotide strand comprises 1-5 single-stranded nucleotides at its 3' terminus.

4. The isolated dsRNA of claim 1, wherein said first strand is 25-35 nucleotides in length.

5. The isolated dsRNA of claim 1, wherein said second strand is 25-35 nucleotides in length.

6. The isolated dsRNA of claim 1, wherein said second oligonucleotide strand is complementary to a target AR cDNA sequence selected from the group consisting of GenBank Accession Nos. NM_000044.2 and NM_001011645.1 along at most 27 nucleotides of said second oligonucleotide strand length.

7. The isolated dsRNA of claim 1, wherein starting from the first nucleotide (position 1) at the 3' terminus of the first oligonucleotide strand, position 1, 2 and/or 3 is substituted with a modified nucleotide.

8. The isolated dsRNA of claim 1, wherein said 3' terminus of said first strand and said 5' terminus of said second strand form a blunt end.

9. The isolated dsRNA of claim 1, wherein said first strand is 25 nucleotides in length and said second strand is 27 nucleotides in length.

10. The isolated dsRNA of claim 1, wherein said second strand comprises a sequence selected from the group consisting of SEQ ID NOs: 164, 166, 174, 177, 179, 1975, 1984, 1986, 1987, 1992, 1994, 1998, 224, 2074, 1283, 2136, 246, 2204, 2220, 2227, 2230, 2235 and 2239.

11. The isolated dsRNA of claim 1, wherein said first strand comprises a sequence selected from the group consisting of SEQ ID NOs: 11, 13, 21, 24, 26, 1570, 1579, 1581, 1582, 1587, 1589, 1593, 71, 1669, 1220, 1731, 93, 1799, 1815, 1822, 1825, 1830 and 1834 .

12. The isolated dsRNA of claim 1 comprising a pair of first strand/second strand sequences selected from the group consisting of DsiRNA agents shown in Tables 2, 3, 5, 7, 9 and 11.

13. The isolated dsRNA of claim 1, wherein each of said first and said second strands has a length which is at least 26 nucleotides.

14. The isolated dsRNA of claim 7, wherein said modified nucleotide residue of said 3' terminus of said first strand is selected from the group consisting of a deoxyribonucleotide, an acyclonucleotide and a fluorescent molecule.

15. The isolated dsRNA of claim 7, wherein position 1 of said 3' terminus of the first oligonucleotide strand is a deoxyribonucleotide.

16. The isolated dsRNA of claim 1, wherein said nucleotides of said 3' overhang comprise a modified nucleotide.

17. The isolated dsRNA of claim 16, wherein said modified nucleotide of said 3' overhang is a 2'-O-methyl ribonucleotide.

18. The isolated dsRNA of claim 1, wherein all nucleotides of said 3' overhang are modified nucleotides.

19. The isolated dsRNA of claim 1, wherein one or both of the first and second oligonucleotide strands comprises a 5' phosphate.

20. The isolated dsRNA of claim 1 wherein said modified nucleotide residues are selected from the group consisting of 2'-O-methyl, 2'-methoxyethoxy, 2'-fluoro, 2'-allyl, 2'-O-[2-(methylamino)-2-oxoethyl], 4'-thio, 4'-CH2-O-2'-bridge, 4'-(CH2)2-O-2'-bridge, 2'-LNA, 2'-amino and 2'-O-(N-methlycarbamate).

21. The isolated dsRNA of claim 1, wherein said 3' overhang is 1-3 nucleotides in length.

22. The isolated dsRNA of claim 1, wherein said 3' overhang is 1-2 nucleotides in length.

23. The isolated dsRNA of claim 1, wherein said 3' overhang is two nucleotides in length and wherein said modified nucleotide of said 3' overhang is a 2'-O-methyl modified ribonucleotide.

24. The isolated dsRNA of claim 1, wherein said second oligonucleotide strand, starting from the nucleotide residue of said second strand that is complementary to the 5' terminal nucleotide residue of said first oligonucleotide strand, comprises alternating modified and unmodified nucleotide residues.

25. The isolated dsRNA of claim 1, wherein said second oligonucleotide strand, starting from the nucleotide residue of said second strand that is complementary to the 5' terminal nucleotide residue of said first oligonucleotide strand, comprises unmodified nucleotide residues at all positions from position 18 to the 5' terminus of said second oligonucleotide strand.

26. The isolated dsRNA of claim 1, wherein each of said first and said second strands has a length which is at least 26 and at most 30 nucleotides.

27. The isolated dsRNA of claim 1, wherein said dsRNA is cleaved endogenously in said cell by Dicer.

28. The isolated dsRNA of claim 1, wherein the amount of said isolated double stranded nucleic acid sufficient to reduce expression of the target gene is selected from the group consisting of 1 nanomolar or less, 200 picomolar or less, 100 picomolar or less, 50 picomolar or less, 20 picomolar or less, 10 picomolar or less, 5 picomolar or less, 2, picomolar or less and 1 picomolar or less in the environment of said cell.

29. The isolated dsRNA of claim 1, wherein said isolated dsRNA possesses greater potency than isolated 21mer siRNAs directed to the identical at least 19 nucleotides of said target AR cDNA in reducing target AR gene expression when assayed *in vitro* in a mammalian cell at an effective concentration in the environment of a cell of 1 nanomolar or less.

30. The isolated dsRNA of claim 1, wherein said isolated dsRNA possesses greater potency than isolated 21mer siRNAs directed to the identical at least 19 nucleotides of said target AR cDNA in reducing target AR gene expression when assayed *in vitro* in a mammalian cell at an effective concentration in the environment of a cell selected from the group consisting of 200 picomolar or less, 100 picomolar or less, 50 picomolar or less, 20 picomolar or less, 10 picomolar or less, 5 picomolar or less, 2, picomolar or less and 1 picomolar or less in the environment of said cell.

31. The isolated dsRNA of claim 1, wherein said isolated dsRNA is sufficiently complementary to the target AR cDNA sequence to reduce AR target gene expression by an amount (expressed by %) selected from the group consisting of at least 10%, at least 50%, at least 80-90%, at least 95%, at least 98%, and at least 99% when said double stranded nucleic acid is introduced into a mammalian cell.

32. The isolated dsRNA of claim 1, wherein the first and second strands are joined by a chemical linker.

33. The isolated double stranded nucleic acid of claim 1, wherein said 3' terminus of said first strand and said 5' terminus of said second strand are joined by a chemical linker.

34. The isolated double stranded nucleic acid of claim 1, wherein a nucleotide of said second or first strand is substituted with a modified nucleotide that directs the orientation of Dicer cleavage.

35. The isolated double stranded nucleic acid of claim 1 comprising a modified nucleotide selected from the group consisting of a deoxyribonucleotide, a dideoxyribonucleotide, an acyclonucleotide, a 3'-deoxyadenosine (cordycepin), a 3'-azido-3'-deoxythymidine (AZT), a 2',3'-dideoxyinosine (ddI), a 2',3'-dideoxy-3'-thiacytidine (3TC), a 2',3'-didehydro-2',3'-dideoxythymidine (d4T), a monophosphate nucleotide of 3'-azido-3'-deoxythymidine (AZT), a 2',3'-dideoxy-3'-thiacytidine (3TC) and a monophosphate nucleotide of 2',3'-didehydro-2',3'-dideoxythymidine (d4T), a 4-thiouracil, a 5-bromouracil, a 5-iodouracil, a 5-(3-aminoallyl)-uracil, a 2'-O-alkyl ribonucleotide, a 2'-O-methyl ribonucleotide, a 2'-amino ribonucleotide, a 2'-fluoro ribonucleotide, and a locked nucleic acid.

36. The isolated double stranded nucleic acid of claim 1 comprising a phosphate backbone modification selected from the group consisting of a phosphonate, a phosphorothioate and a phosphotriester.

37. The isolated double stranded nucleic acid of claim 1 comprising a modification selected from the group consisting of a morpholino nucleic acid and a peptide nucleic acid (PNA).

38. A method for reducing expression of a target AR gene in a mammalian cell comprising contacting a mammalian cell *in vitro* with an isolated dsRNA of claim 1 in an amount sufficient to reduce expression of a target AR gene in said cell.

39. The method of claim 38, wherein target AR gene expression is reduced by an amount (expressed by %) selected from the group consisting of at least 10%, at least 50% and at least 80-90%.

40. The method of claim 38, wherein AR mRNA levels are reduced by an amount (expressed by %) of at least 90% at least 8 days after said cell is contacted with said dsRNA.

41. The method of claim 38, wherein AR mRNA levels are reduced by an amount (expressed by %) of at least 70% at least 10 days after said cell is contacted with said dsRNA.

42. A method for reducing expression of a target AR gene in a mammal comprising administering an isolated dsRNA of claim 1 to a mammal in an amount sufficient to reduce expression of a target AR gene in the mammal.

43. The method of claim 42, wherein said isolated dsRNA is administered at a dosage selected from the group consisting of 1 microgram to 5 milligrams per kilogram of said mammal per day, 100 micrograms to 0.5 milligrams per kilogram, 0.001 to 0.25 milligrams per kilogram, 0.01 to 20 micrograms per kilogram, 0.01 to 10 micrograms per kilogram, 0.10 to 5 micrograms per kilogram, and 0.1 to 2.5 micrograms per kilogram.

44. The method of claim 42, wherein said isolated dsRNA possesses greater potency than isolated 21mer siRNAs directed to the identical at least 19 nucleotides of said target AR cDNA in reducing target AR gene expression when assayed *in vitro* in a mammalian cell at an effective concentration in the environment of a cell of 1 nanomolar or less.

45. The method of claim 42, wherein said administering step comprises a mode selected from the group consisting of intravenous injection, intramuscular injection, intraperitoneal injection, infusion, subcutaneous injection, transdermal, aerosol, rectal, vaginal, topical, oral and inhaled delivery.

46. A method for selectively inhibiting the growth of a cell comprising contacting a cell with an amount of an isolated dsRNA of claim 1 sufficient to inhibit the growth of the cell.

47. The method of claim 46, wherein said cell is a tumor cell of a subject.

48. The method of claim 46, wherein said cell is a tumor cell *in vitro*.

49. The method of claim 46, wherein said cell is a prostate cancer cell.

50. The method of claim 49, wherein said cell is a prostate cancer cell selected from the group consisting of 22Rv1 and VCaP.

51. The method of claim 49, wherein said cell is an A549 adenocarcenomic human alveolar cancer cell.

52. The method of claim 46, wherein said cell is a mammalian prostate cell.

53. The method of claim 46, wherein said cell is a human cell.

54. A formulation comprising the isolated dsRNA of claim 71, wherein said dsRNA is present in an amount effective to reduce target AR RNA levels when said dsRNA is introduced into a mammalian cell *in vitro* by an amount (expressed by %) selected from the group consisting of at least 10%, at least 50% and at least 80-90%, and wherein said dsRNA possesses greater potency than isolated 21mer siRNAs directed to the identical at least 19 nucleotides of said target AR cDNA in reducing target AR RNA levels when assayed *in vitro* in a mammalian cell at an effective concentration in the environment of a cell of 1 nanomolar or less.

55. The formulation of claim 54, wherein said effective amount is selected from the group consisting of 1 nanomolar or less, 200 picomolar or less, 100 picomolar or less, 50 picomolar or less, 20 picomolar or less, 10 picomolar or less, 5 picomolar or less, 2, picomolar or less and 1 picomolar or less in the environment of said cell.

56. A formulation comprising the isolated dsRNA of claim 2, wherein said dsRNA is present in an amount effective to reduce target AR RNA levels when said dsRNA is introduced into a cell of a mammalian subject by an amount (expressed by

%) selected from the group consisting of at least 10%, at least 50% and at least 80-90%, and wherein said dsRNA possesses greater potency than isolated 21mer siRNAs directed to the identical at least 19 nucleotides of said target AR cDNA in reducing target AR RNA levels when assayed *in vitro* in a mammalian cell at an effective concentration in the environment of a cell of 1 nanomolar or less.

57. The formulation of claim 56, wherein said effective amount is a dosage selected from the group consisting of 1 microgram to 5 milligrams per kilogram of said subject per day, 100 micrograms to 0.5 milligrams per kilogram, 0.001 to 0.25 milligrams per kilogram, 0.01 to 20 micrograms per kilogram, 0.01 to 10 micrograms per kilogram, 0.10 to 5 micrograms per kilogram, and 0.1 to 2.5 micrograms per kilogram.

58. A mammalian cell containing the isolated dsRNA of claim 1.

59. A pharmaceutical composition comprising the isolated dsRNA of claim 1 and a pharmaceutically acceptable carrier.

60. A kit comprising the isolated dsRNA of claim 1 and instructions for its use.

61. A composition possessing AR inhibitory activity consisiting essentially of an isolated double stranded ribonucleic acid (dsRNA) comprising first and second nucleic acid strands, wherein said first strand is 15-35 nucleotides in length and said second strand of said dsRNA is 19-35 nucleotides in length, wherein said second oligonucleotide strand is sufficiently complementary to a target AR cDNA sequence selected from Table 13 along at least 19 nucleotides of said second oligonucleotide strand length to reduce AR target gene expression when said double stranded nucleic acid is introduced into a mammalian cell.

62. An isolated dsRNA of claim 61 comprising a duplex region of at least 25 base pairs.

63. The isolated dsRNA of claim 61, wherein said second oligonucleotide strand comprises 1-5 single-stranded nucleotides at its 3' terminus.

64. The isolated dsRNA of claim 61, wherein said first strand is 25-35 nucleotides in length.

65. The isolated dsRNA of claim 61, wherein said second strand is 25-35 nucleotides in length.

66. The composition of claim 65, wherein said second oligonucleotide strand of said dsRNA is complementary to a target AR cDNA sequence selected from the group consisting of GenBank Accession Nos. NM_000044.2 and NM_001011645.1 along at most 27 nucleotides of said second oligonucleotide strand length.

67. A method for treating or preventing an AR-associated disease or disorder in a subject comprising administering the isolated dsRNA of claim 1 and a pharmaceutically acceptable carrier to the subject in an amount sufficient to treat or prevent said AR-associated disease or disorder in said subject, thereby treating or preventing said AR-associated disease or disorder in said subject.

68. The method of claim 67, wherein said AR-associated disease or disorder is selected from the group consisting of prostate cancer and adenocarcinoma.

69. An isolated double stranded ribonucleic acid (dsRNA) comprising first and second nucleic acid strands, wherein said dsRNA comprises blunt ends, wherein each of said first and second oligonucleotide strands consists of the same number of nucleotide residues and is at most 35 nucleotides in length, wherein said second oligonucleotide strand is sufficiently complementary to a target AR cDNA sequence selected from Table 13 along at least 19 nucleotides of said second oligonucleotide strand length to reduce AR target gene expression when said double stranded nucleic acid is introduced into a mammalian cell.

70. An isolated dsRNA of claim 69 comprising a duplex region of at least 25 base pairs.

71. The isolated dsRNA of claim 69, wherein each of said first strand and said second strand is 25-35 nucleotides in length.

72. The isolated dsRNA of claim 69, wherein said dsRNA is capable of reducing target gene expression at a concentration of less than 1 nanomolar in the environment of a cell.

73. The isolated dsRNA of claim 69, wherein each of said first and said second strands has a length which is at least 26 nucleotides.

74. The isolated dsRNA of claim 69, wherein each of said first and said second strands has a length which is 26-30 nucleotides.

75. The isolated dsRNA of claim 69, wherein each of said first and said second strands has a length which is 27 nucleotides.

76. The isolated dsRNA of claim 69, wherein said second strand comprises a sequence selected from the group consisting of SEQ ID NOs: 164, 166, 174, 177, 179, 1975, 1984, 1986, 1987, 1992, 1994, 1998, 224, 2074, 1283, 2136, 246, 2204, 2220, 2227, 2230, 2235 and 2239.

77. The isolated dsRNA of claim 69, wherein said first strand comprises a sequence selected from the group consisting of SEQ ID NOs: 4517, 4519, 4527, 4530, 4532, 4876, 4885, 4887, 4888, 4893, 4895, 4899, 4577, 4975, 4778, 5037, 4599, 5105, 5121, 5128, 5131, 5136 and 5140.

78. The isolated dsRNA of claim 69 comprising a pair of first strand/second strand sequences selected from the group consisting of DsiRNA agents shown in Tables 2, 3, 5, 7, 9 and 11.

79. An isolated double stranded ribonucleic acid (dsRNA) comprising first and second nucleic acid strands, wherein said dsRNA comprises a blunt end, wherein each of said first and second oligonucleotide strands consists of the same number of nucleotide residues and is at most 35 nucleotides in length, wherein the ultimate and

penultimate residues of said 3' terminus of said first strand and the ultimate and penultimate residues of said 5' terminus of said second strand form one or two mismatched based pairs, wherein said second oligonucleotide strand is sufficiently complementary to a target AR cDNA sequence selected from Table 13 along at least 19 nucleotides of said second oligonucleotide strand length to reduce AR target gene expression when said double stranded nucleic acid is introduced into a mammalian cell.

80. An isolated dsRNA of claim 79 comprising a duplex region of at least 25 base pairs.

81. The isolated dsRNA of claim 79, wherein each of said first strand and said second strand is 25-35 nucleotides in length.

82. The isolated dsRNA of claim 79, wherein said first strand comprises a sequence selected from the group consisting of SEQ ID NOs: 3794, 3796, 3804, 3807, 3809, 4153, 4162, 4164, 4165, 4170, 4172, 4176, 3854, 4252, 4055, 4314, 3876, 4382, 4398, 4405, 4408, 4413 and 4417.

83. A composition possessing AR inhibitory activity consisting essentially of an isolated double stranded ribonucleic acid (dsRNA) comprising first and second nucleic acid strands, wherein said dsRNA comprises a blunt end, wherein each of said first and second oligonucleotide strands consists of the same number of nucleotide residues and is at most 35 nucleotides in length, wherein the ultimate and penultimate residues of said 3' terminus of said first strand and the ultimate and penultimate residues of said 5' terminus of said second strand form one or two mismatched based pairs, wherein said second oligonucleotide strand is sufficiently complementary to a target AR cDNA sequence selected from Table 13 along at least 19 nucleotides of said second oligonucleotide strand length to reduce AR target gene expression when said double stranded nucleic acid is introduced into a mammalian cell.

84. An isolated dsRNA of claim 83 comprising a duplex region of at least 25 base pairs.

85. The isolated dsRNA of claim 83, wherein each of said first strand and said second strand is 25-35 nucleotides in length.

86. An isolated dsRNA molecule, consisting of: (a) a sense region and an antisense region, wherein said sense region and said antisense region together form a duplex region consisting of 15-35 base pairs and said antisense region comprises a sequence that is the complement of a sequence selected from Table 13; and (b) from zero to two 3' overhang regions, wherein each overhang region is six or fewer nucleotides in length.

87. The isolated dsRNA molecule of claim 86, wherein said duplex region consists of 19-35 base pairs.

88. The isolated dsRNA molecule of claim 86, wherein said duplex region consists of 25-35 base pairs.

89. The isolated dsRNA molecule of claim 86, wherein said duplex region consists of 25-30 base pairs.

90. An siRNA molecule, consisting of: (a) a sense region and an antisense region, wherein said sense region and said antisense region together form a duplex region consisting of 19-23 base pairs and said antisense region comprises a sequence that is the complement of a sequence selected from Table 13; and (b) from zero to four overhang regions, wherein each overhang region is six or fewer nucleotides in length.

91. An isolated double stranded ribonucleic acid (dsRNA) comprising first and second nucleic acid strands and a duplex region of at least 25 base pairs, wherein said first strand is 25-34 nucleotides in length and said second strand of said dsRNA is 26-35 nucleotides in length and comprises 1-5 single-stranded nucleotides at its 3' terminus, wherein said second oligonucleotide strand is sufficiently complementary to a target AR cDNA sequence selected from the group consisting of SEQ ID NOs: 307-459, 826-915, 1024-1077, 1312-1374, 2311-2715 and 3622-3669 along at least 19 nucleotides of said second oligonucleotide strand length to reduce AR target gene

expression when said double stranded nucleic acid is introduced into a mammalian cell.

92. The isolated dsRNA of claim 91, wherein said second oligonucleotide strand is complementary to a target AR cDNA sequence selected from the group consisting of SEQ ID NOs: 3766, 3768 and 3770 along at most 27 nucleotides of said second oligonucleotide strand length.

93. The isolated dsRNA of claim 91, wherein starting from the first nucleotide (position 1) at the 3' terminus of the first oligonucleotide strand, position 1, 2 and/or 3 is substituted with a modified nucleotide.

94. The isolated dsRNA of claim 91, wherein said 3' terminus of said first strand and said 5' terminus of said second strand form a blunt end.

95. The isolated dsRNA of claim 91, wherein said first strand is 25 nucleotides in length and said second strand is 27 nucleotides in length.

96. The isolated dsRNA of claim 91, wherein said second strand comprises a sequence selected from the group consisting of SEQ ID NOs: 154-306, 796-825, 970-1023, 1249-1311, 1906-2310 and 3574-3621.

97. The isolated dsRNA of claim 91, wherein said first strand comprises a sequence selected from the group consisting of SEQ ID NOs: 1-153, 766-795, 916-969, 1186-1248, 1501-1905 and 3526-3573.

98. The isolated dsRNA of claim 91 comprising a pair of first strand/second strand sequences selected from the group consisting of DsiRNA agents shown in Table 9.

99. The isolated dsRNA of claim 91, wherein each of said first and said second strands has a length which is at least 26 nucleotides.

100. The isolated dsRNA of claim 93, wherein said modified nucleotide residue of said 3' terminus of said first strand is selected from the group consisting of a deoxyribonucleotide, an acyclonucleotide and a fluorescent molecule.

101. The isolated dsRNA of claim 93, wherein position 1 of said 3' terminus of the first oligonucleotide strand is a deoxyribonucleotide.

102. The isolated dsRNA of claim 91, wherein said nucleotides of said 3' overhang comprise a modified nucleotide.

103. The isolated dsRNA of claim 102, wherein said modified nucleotide of said 3' overhang is a 2'-O-methyl ribonucleotide.

104. The isolated dsRNA of claim 91, wherein all nucleotides of said 3' overhang are modified nucleotides.

105. The isolated dsRNA of claim 91, wherein one or both of the first and second oligonucleotide strands comprises a 5' phosphate.

106. The isolated dsRNA of claim 91 wherein said modified nucleotide residues are selected from the group consisting of 2'-O-methyl, 2'-methoxyethoxy, 2'-fluoro, 2'-allyl, 2'-O-[2-(methylamino)-2-oxoethyl], 4'-thio, 4'-CH2-O-2'-bridge, 4'-(CH2)2-O-2'-bridge, 2'-LNA, 2'-amino and 2'-O-(N-methlycarbamate).

107. The isolated dsRNA of claim 91, wherein said 3' overhang is 1-3 nucleotides in length.

108. The isolated dsRNA of claim 91, wherein said 3' overhang is 1-2 nucleotides in length.

109. The isolated dsRNA of claim 91, wherein said 3' overhang is two nucleotides in length and wherein said modified nucleotide of said 3' overhang is a 2'-O-methyl modified ribonucleotide.

110. The isolated dsRNA of claim 91, wherein said second oligonucleotide strand, starting from the nucleotide residue of said second strand that is complementary to the 5' terminal nucleotide residue of said first oligonucleotide strand, comprises alternating modified and unmodified nucleotide residues.

111. The isolated dsRNA of claim 91, wherein said second oligonucleotide strand, starting from the nucleotide residue of said second strand that is complementary to the 5' terminal nucleotide residue of said first oligonucleotide strand, comprises unmodified nucleotide residues at all positions from position 18 to the 5' terminus of said second oligonucleotide strand.

112. The isolated dsRNA of claim 91, wherein each of said first and said second strands has a length which is at least 26 and at most 30 nucleotides.

113. The isolated dsRNA of claim 91, wherein said dsRNA is cleaved endogenously in said cell by Dicer.

114. The isolated dsRNA of claim 91, wherein the amount of said isolated double stranded nucleic acid sufficient to reduce expression of the target gene is selected from the group consisting of 1 nanomolar or less, 200 picomolar or less, 100 picomolar or less, 50 picomolar or less, 20 picomolar or less, 10 picomolar or less, 5 picomolar or less, 2, picomolar or less and 1 picomolar or less in the environment of said cell.

115. The isolated dsRNA of claim 91, wherein said isolated dsRNA possesses greater potency than isolated 21mer siRNAs directed to the identical at least 19 nucleotides of said target AR cDNA in reducing target AR gene expression when assayed *in vitro* in a mammalian cell at an effective concentration in the environment of a cell of 1 nanomolar or less.

116. The isolated dsRNA of claim 91, wherein said isolated dsRNA possesses greater potency than isolated 21mer siRNAs directed to the identical at least 19 nucleotides of said target AR cDNA in reducing target AR gene expression when assayed *in vitro* in a mammalian cell at an effective concentration in the environment

of a cell selected from the group consisting of 200 picomolar or less, 100 picomolar or less, 50 picomolar or less, 20 picomolar or less, 10 picomolar or less, 5 picomolar or less, 2, picomolar or less and 1 picomolar or less in the environment of said cell.

117. The isolated dsRNA of claim 91, wherein said isolated dsRNA is sufficiently complementary to the target AR cDNA sequence to reduce AR target gene expression by an amount (expressed by %) selected from the group consisting of at least 10%, at least 50%, at least 80-90%, at least 95%, at least 98%, and at least 99% when said double stranded nucleic acid is introduced into a mammalian cell.

118. The isolated dsRNA of claim 91, wherein the first and second strands are joined by a chemical linker.

119. The isolated double stranded nucleic acid of claim 91, wherein said 3' terminus of said first strand and said 5' terminus of said second strand are joined by a chemical linker.

120. The isolated double stranded nucleic acid of claim 91, wherein a nucleotide of said second or first strand is substituted with a modified nucleotide that directs the orientation of Dicer cleavage.

121. The isolated double stranded nucleic acid of claim 91 comprising a modified nucleotide selected from the group consisting of a deoxyribonucleotide, a dideoxyribonucleotide, an acyclonucleotide, a 3'-deoxyadenosine (cordycepin), a 3'-azido-3'-deoxythymidine (AZT), a 2',3'-dideoxyinosine (ddI), a 2',3'-dideoxy-3'-thiacytidine (3TC), a 2',3'-didehydro-2',3'-dideoxythymidine (d4T), a monophosphate nucleotide of 3'-azido-3'-deoxythymidine (AZT), a 2',3'-dideoxy-3'-thiacytidine (3TC) and a monophosphate nucleotide of 2',3'-didehydro-2',3'-dideoxythymidine (d4T), a 4-thiouracil, a 5-bromouracil, a 5-iodouracil, a 5-(3-aminoallyl)-uracil, a 2'-O-alkyl ribonucleotide, a 2'-O-methyl ribonucleotide, a 2'-amino ribonucleotide, a 2'-fluoro ribonucleotide, and a locked nucleic acid.

122. The isolated double stranded nucleic acid of claim 91 comprising a phosphate backbone modification selected from the group consisting of a phosphonate, a phosphorothioate and a phosphotriester.

123. A method for reducing expression of a target AR gene in a mammalian cell comprising contacting a mammalian cell *in vitro* with an isolated dsRNA of claim 91 in an amount sufficient to reduce expression of a target AR gene in said cell.

124. The method of claim 123, wherein target AR gene expression is reduced by an amount (expressed by %) selected from the group consisting of at least 10%, at least 50% and at least 80-90%.

125. The method of claim 123, wherein AR mRNA levels are reduced by an amount (expressed by %) of at least 90% at least 8 days after said cell is contacted with said dsRNA.

126. The method of claim 123, wherein AR mRNA levels are reduced by an amount (expressed by %) of at least 70% at least 10 days after said cell is contacted with said dsRNA.

127. A method for reducing expression of a target AR gene in a mammal comprising administering an isolated dsRNA of claim 91 to a mammal in an amount sufficient to reduce expression of a target AR gene in the mammal.

128. The method of claim 127, wherein said isolated dsRNA is administered at a dosage selected from the group consisting of 1 microgram to 5 milligrams per kilogram of said mammal per day, 100 micrograms to 0.5 milligrams per kilogram, 0.001 to 0.25 milligrams per kilogram, 0.01 to 20 micrograms per kilogram, 0.01 to 10 micrograms per kilogram, 0.10 to 5 micrograms per kilogram, and 0.1 to 2.5 micrograms per kilogram.

129. The method of claim 127, wherein said isolated dsRNA possesses greater potency than isolated 21mer siRNAs directed to the identical at least 19 nucleotides of said target AR cDNA in reducing target AR gene expression when assayed *in vitro* in

a mammalian cell at an effective concentration in the environment of a cell of 1 nanomolar or less.

130. The method of claim 127, wherein said administering step comprises a mode selected from the group consisting of intravenous injection, intramuscular injection, intraperitoneal injection, infusion, subcutaneous injection, transdermal, aerosol, rectal, vaginal, topical, oral and inhaled delivery.

131. A method for selectively inhibiting the growth of a cell comprising contacting a cell with an amount of an isolated dsRNA of claim 91 sufficient to inhibit the growth of the cell.

132. The method of claim 131, wherein said cell is a tumor cell of a subject.

133. The method of claim 131, wherein said cell is a tumor cell *in vitro*.

134. The method of claim 131, wherein said cell is a human cell.

135. A formulation comprising the isolated dsRNA of claim 91, wherein said dsRNA is present in an amount effective to reduce target AR RNA levels when said dsRNA is introduced into a mammalian cell *in vitro* by an amount (expressed by %) selected from the group consisting of at least 10%, at least 50% and at least 80-90%, and wherein said dsRNA possesses greater potency than isolated 21mer siRNAs directed to the identical at least 19 nucleotides of said target AR cDNA in reducing target AR RNA levels when assayed *in vitro* in a mammalian cell at an effective concentration in the environment of a cell of 1 nanomolar or less.

136. The formulation of claim 135, wherein said effective amount is selected from the group consisting of 1 nanomolar or less, 200 picomolar or less, 100 picomolar or less, 50 picomolar or less, 20 picomolar or less, 10 picomolar or less, 5 picomolar or less, 2, picomolar or less and 1 picomolar or less in the environment of said cell.

137. A formulation comprising the isolated dsRNA of claim 91, wherein said dsRNA is present in an amount effective to reduce target RNA levels when said

dsRNA is introduced into a cell of a mammalian subject by an amount (expressed by %) selected from the group consisting of at least 10%, at least 50% and at least 80-90%, and wherein said dsRNA possesses greater potency than isolated 21mer siRNAs directed to the identical at least 19 nucleotides of said target AR cDNA in reducing target AR RNA levels when assayed *in vitro* in a mammalian cell at an effective concentration in the environment of a cell of 1 nanomolar or less.

138. The formulation of claim 137, wherein said effective amount is a dosage selected from the group consisting of 1 microgram to 5 milligrams per kilogram of said subject per day, 100 micrograms to 0.5 milligrams per kilogram, 0.001 to 0.25 milligrams per kilogram, 0.01 to 20 micrograms per kilogram, 0.01 to 10 micrograms per kilogram, 0.10 to 5 micrograms per kilogram, and 0.1 to 2.5 micrograms per kilogram.

139. A mammalian cell containing the isolated dsRNA of claim 91.

140. A pharmaceutical composition comprising the isolated dsRNA of claim 91 and a pharmaceutically acceptable carrier.

141. A kit comprising the isolated dsRNA of claim 91 and instructions for its use.

142. A composition possessing AR inhibitory activity consisiting essentially of an isolated double stranded ribonucleic acid (dsRNA) comprising first and second nucleic acid strands and a duplex region of at least 25 base pairs, wherein said first strand is 25-34 nucleotides in length and said second strand of said dsRNA is 26-35 nucleotides in length and comprises 1-5 single-stranded nucleotides at its 3' terminus, wherein said second oligonucleotide strand is sufficiently complementary to a target AR cDNA sequence selected from the group consisting of SEQ ID NOs: 307-459, 826-915, 1024-1077, 1312-1374, 2311-2715 and 3622-3669 along at least 19 nucleotides of said second oligonucleotide strand length to reduce AR target gene expression when said double stranded nucleic acid is introduced into a mammalian cell.

143. The composition of claim 142, wherein said second oligonucleotide strand of said dsRNA is complementary to a target AR cDNA sequence selected from the group consisting of SEQ ID NOs: 3766, 3768 and 3770 along at most 27 nucleotides of said second oligonucleotide strand length.

144. A method for treating or preventing an AR-associated disease or disorder in a subject comprising administering the isolated dsRNA of claim 91 and a pharmaceutically acceptable carrier to the subject in an amount sufficient to treat or prevent said AR-associated disease or disorder in said subject, thereby treating or preventing said AR-associated disease or disorder in said subject.

145. The method of claim 144, wherein said AR-associated disease or disorder is prostate cancer.

146. An isolated double stranded ribonucleic acid (dsRNA) comprising first and second nucleic acid strands and a duplex region of at least 25 base pairs, wherein said dsRNA comprises blunt ends, wherein each of said first and second oligonucleotide strands consists of the same number of nucleotide residues and is at most 35 nucleotides in length, wherein said second oligonucleotide strand is sufficiently complementary to a target AR cDNA sequence selected from the group consisting of SEQ ID NOs: 307-459, 826-915, 1024-1077, 1312-1374, 2311-2715 and 3622-3669 along at least 19 nucleotides of said second oligonucleotide strand length to reduce AR target gene expression when said double stranded nucleic acid is introduced into a mammalian cell.

147. The isolated dsRNA of claim 146, wherein said dsRNA is capable of reducing target gene expression at a concentration of less than 1 nanomolar in the environment of a cell.

148. The isolated dsRNA of claim 146, wherein each of said first and said second strands has a length which is at least 26 nucleotides.

149. The isolated dsRNA of claim 146, wherein each of said first and said second strands has a length which is 26-30 nucleotides.

150. The isolated dsRNA of claim 146, wherein each of said first and said second strands has a length which is 27 nucleotides.

151. The isolated dsRNA of claim 146, wherein said second strand comprises a sequence selected from the group consisting of SEQ ID NOs: 154-306, 796-825, 970-1023, 1249-1311, 1906-2310 and 3574-3621.

152. The isolated dsRNA of claim 146, wherein said first strand comprises a sequence selected from the group consisting of SEQ ID NOs: 3784-5229.

153. The isolated dsRNA of claim 146 comprising a pair of first strand/second strand sequences selected from the group consisting of DsiRNA agents shown in Table 5.

154. An isolated double stranded ribonucleic acid (dsRNA) comprising first and second nucleic acid strands and a duplex region of at least 25 base pairs, wherein said dsRNA comprises a blunt end, wherein each of said first and second oligonucleotide strands consists of the same number of nucleotide residues and is at most 35 nucleotides in length, wherein the ultimate and penultimate residues of said 3' terminus of said first strand and the ultimate and penultimate residues of said 5' terminus of said second strand form one or two mismatched based pairs. wherein said second oligonucleotide strand is sufficiently complementary to a target AR cDNA sequence selected from the group consisting of SEQ ID NOs: 307-459, 826-915, 1024-1077, 1312-1374, 2311-2715 and 3622-3669 along at least 19 nucleotides of said second oligonucleotide strand length to reduce AR target gene expression when said double stranded nucleic acid is introduced into a mammalian cell.

155. The isolated dsRNA of claim 154, wherein said first strand comprises a sequence selected from the group consisting of SEQ ID NOs: 3784-4506.

156. A composition possessing AR inhibitory activity consisting essentially of an isolated double stranded ribonucleic acid (dsRNA) comprising first and second nucleic acid strands and a duplex region of at least 25 base pairs, wherein said dsRNA

comprises a blunt end, wherein each of said first and second oligonucleotide strands consists of the same number of nucleotide residues and is at most 35 nucleotides in length, wherein the ultimate and penultimate residues of said 3' terminus of said first strand and the ultimate and penultimate residues of said 5' terminus of said second strand form one or two mismatched based pairs. wherein said second oligonucleotide strand is sufficiently complementary to a target AR cDNA sequence selected from the group consisting of SEQ ID NOs: 307-459, 826-915, 1024-1077, 1312-1374, 2311-2715 and 3622-3669 along at least 19 nucleotides of said second oligonucleotide strand length to reduce AR target gene expression when said double stranded nucleic acid is introduced into a mammalian cell.

157. An isolated dsRNA molecule, consisting of: (a) a sense region and an antisense region, wherein said sense region and said antisense region together form a duplex region consisting of 19-35 base pairs and said antisense region comprises a sequence that is the complement of a sequence selected from the group consisting of SEQ ID NOs 613-765, 886-915, 1132-1185, 1438-1500 and 3121-3765; and (b) from zero to two 3' overhang regions, wherein each overhang region is six or fewer nucleotides in length.

158. The isolated dsRNA molecule of claim 157, wherein said duplex region consists of 25-35 base pairs.

159. An siRNA molecule, consisting of: (a) a sense region and an antisense region, wherein said sense region and said antisense region together form a duplex region consisting of 19-23 base pairs and said antisense region comprises a sequence that is the complement of a sequence selected from the group consisting of SEQ ID NOs 613-765, 886-915, 1132-1185, 1438-1500 and 3121-3765; and (b) from zero to four overhang regions, wherein each overhang region is six or fewer nucleotides in length.

Figure 1

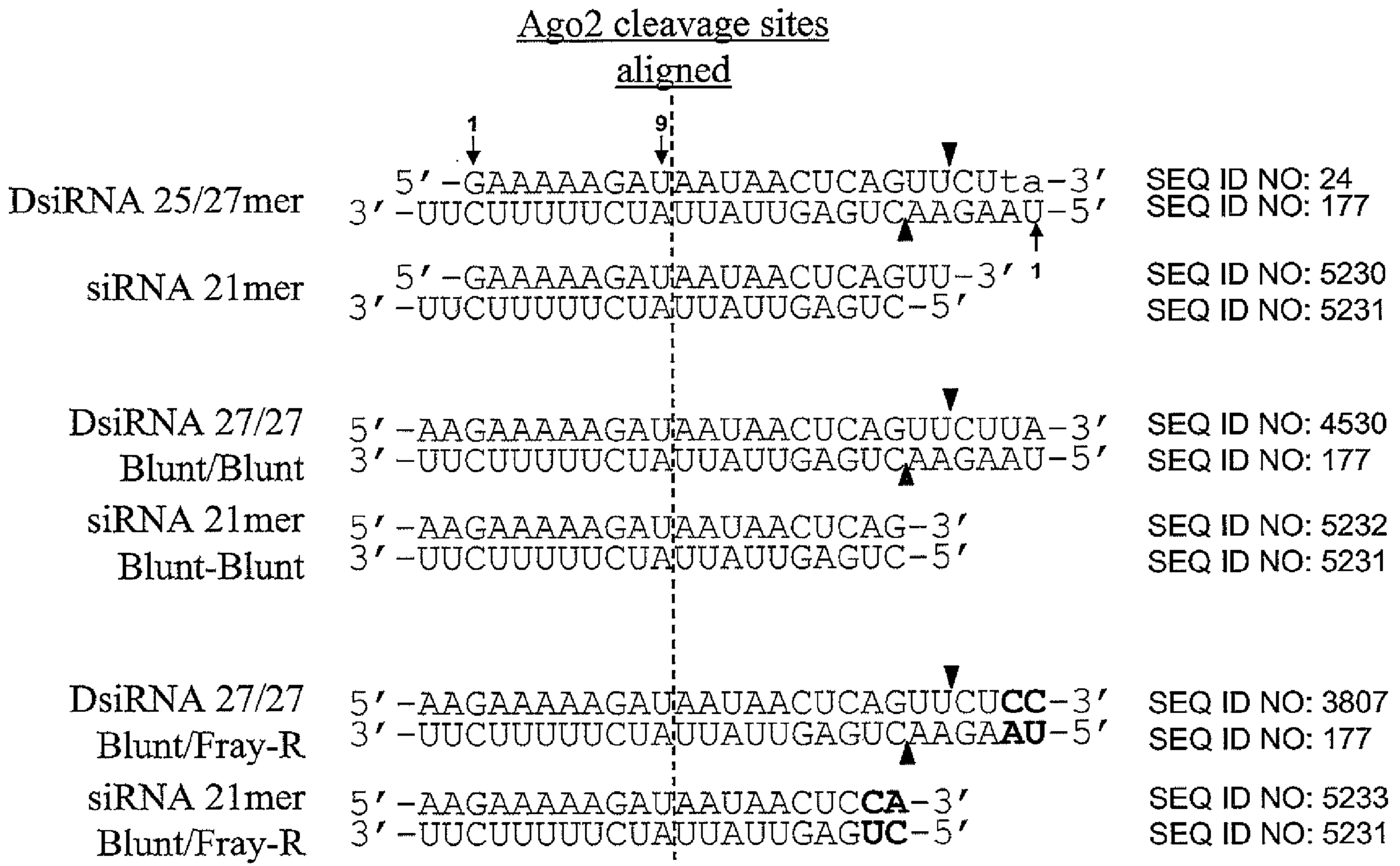

Ago2 cleavage sites aligned
1
9
DsiRNA 25/27mer
5′-GAAAAAGAUAAUAACUCAGUUCUta-3′
3′-UUCUUUUUCUAUUAUUGAGUCAAGAAU-5′
SEQ ID NO: 24
SEQ ID NO: 177
siRNA 21mer
5′-GAAAAAGAUAAUAACUCAGUU-3′
3′-UUCUUUUUCUAUUAUUGAGUC-5′
1
SEQ ID NO: 5230
SEQ ID NO: 5231
DsiRNA 27/27 Blunt/Blunt
5′-AAGAAAAAGAUAAUAACUCAGUUCUUA-3′
3′-UUCUUUUUCUAUUAUUGAGUCAAGAAU-5′
SEQ ID NO: 4530
SEQ ID NO: 177
siRNA 21mer Blunt-Blunt
5′-AAGAAAAAGAUAAUAACUCAG-3′
3′-UUCUUUUUCUAUUAUUGAGUC-5′
SEQ ID NO: 5232
SEQ ID NO: 5231
DsiRNA 27/27 Blunt/Fray-R
5′-AAGAAAAAGAUAAUAACUCAGUUCUCC-3′
3′-UUCUUUUUCUAUUAUUGAGUCAAGAAU-5′
SEQ ID NO: 3807
SEQ ID NO: 177
siRNA 21mer Blunt/Fray-R
5′-AAGAAAAAGAUAAUAACUCCA-3′
3′-UUCUUUUUCUAUUAUUGAGUC-5′
SEQ ID NO: 5233
SEQ ID NO: 5231

Figure 2

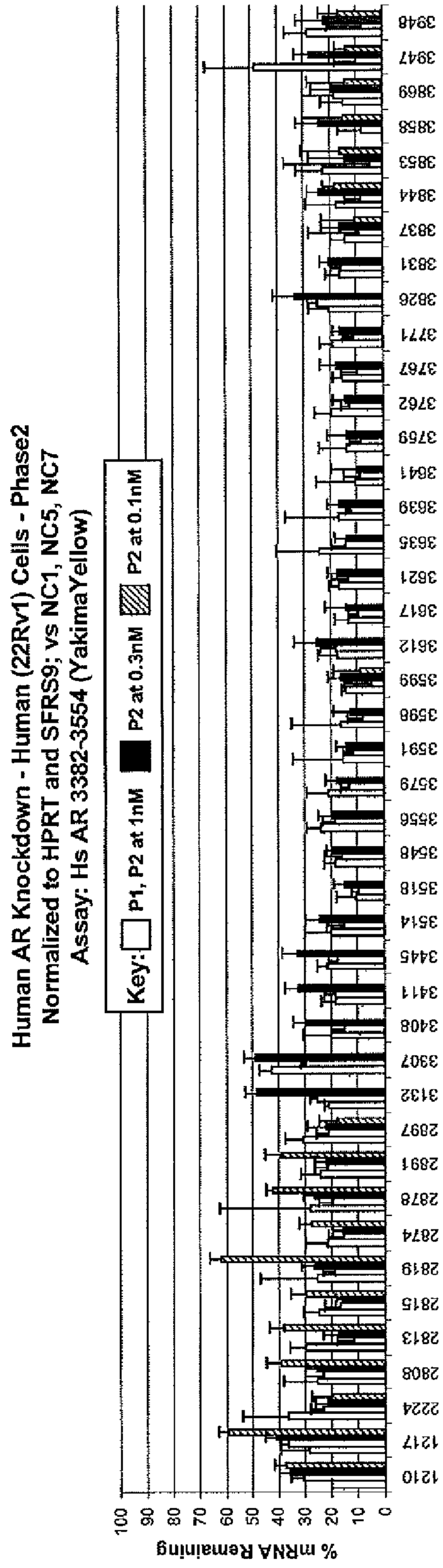

Human AR Knockdown - Human (22Rv1) Cells - Phase2
Normalized to HPRT and SFRS9; vs NC1, NC5, NC7
Assay: Hs AR 3382-3554 (YakimaYellow)
Key: P1, P2 at 1nM P2 at 0.3nM P2 at 0.1nM
% mRNA Remaining
100 90 80 70 60 50 40 30 20 10 0
Human DsiRNA Location (NM_000044.2)
1210 1217 2224 2808 2813 2815 2819 2874 2878 2891 2897 3132 3307 3408 3411 3445 3514 3518 3548 3556 3579 3591 3598 3599 3612 3617 3621 3635 3639 3641 3759 3762 3767 3771 3826 3831 3837 3844 3853 3858 3869 3947 3948

Figure 3

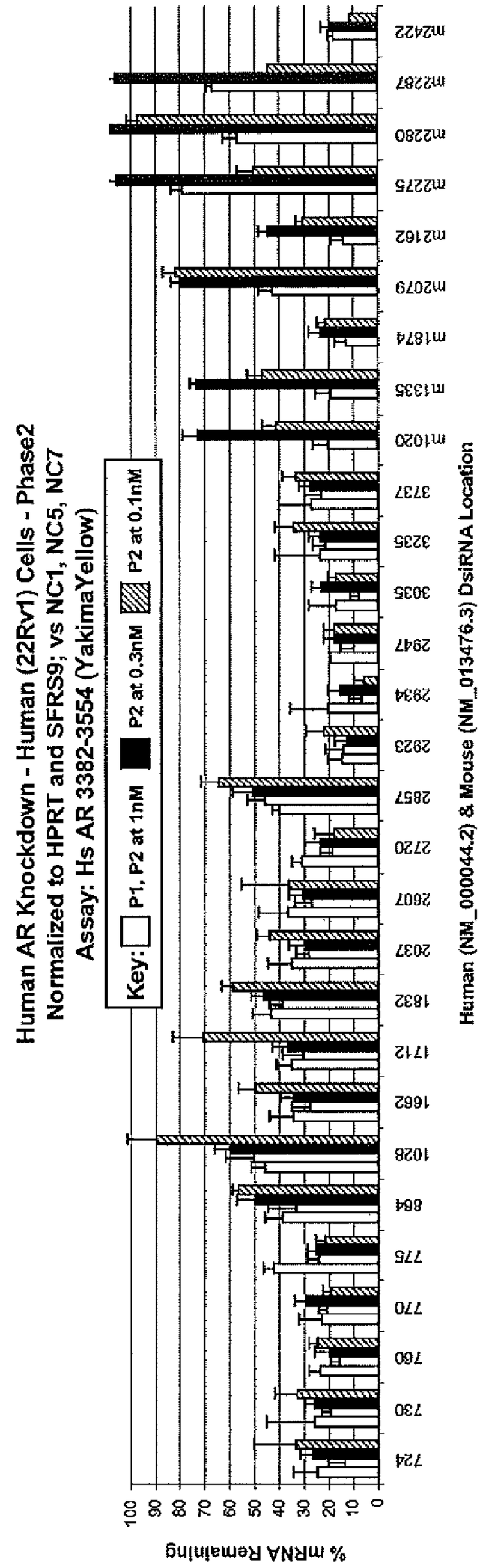
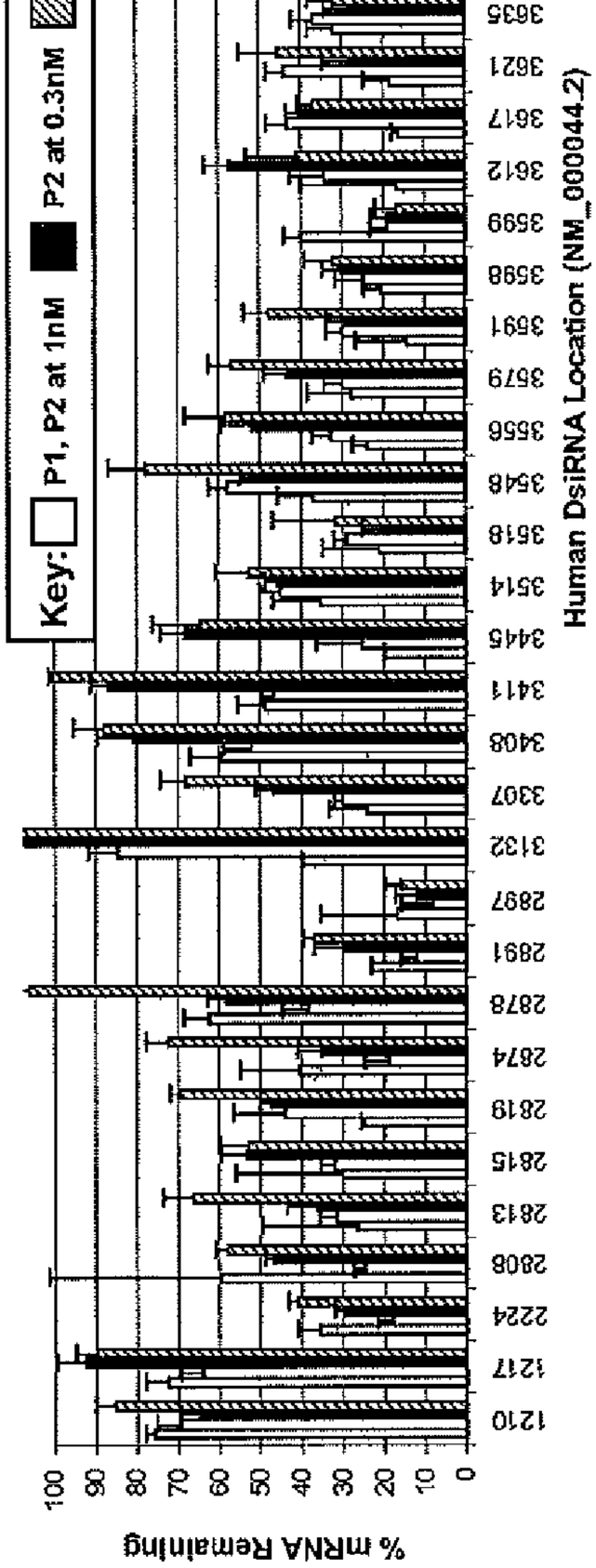

Human AR Knockdown - Human (22Rv1) Cells - Phase2
Normalized to HPRT and SFRS9; vs NC1, NC5, NC7
Assay: Hs AR 3382-3554 (YakimaYellow)
Key: P1, P2 at 1nM P2 at 0.3nM P2 at 0.1nM
% mRNA Remaining
100 90 80 70 60 50 40 30 20 10 0
Human (NM_000044.2) & Mouse (NM_013476.3) DsiRNA Location
724 730 760 770 775 664 1028 1662 1712 1832 2037 2607 2720 2857 2923 2934 2947 3035 3235 3737 m1020 m1335 m1874 m2079 m2162 m2275 m2422 m2280 m2287

Figure 4

Mouse AR Knockdown - Mouse (LMTK-) Cells - Phase2
Normalized to HPRT and Rpl23; vs NC1, NC5, NC7



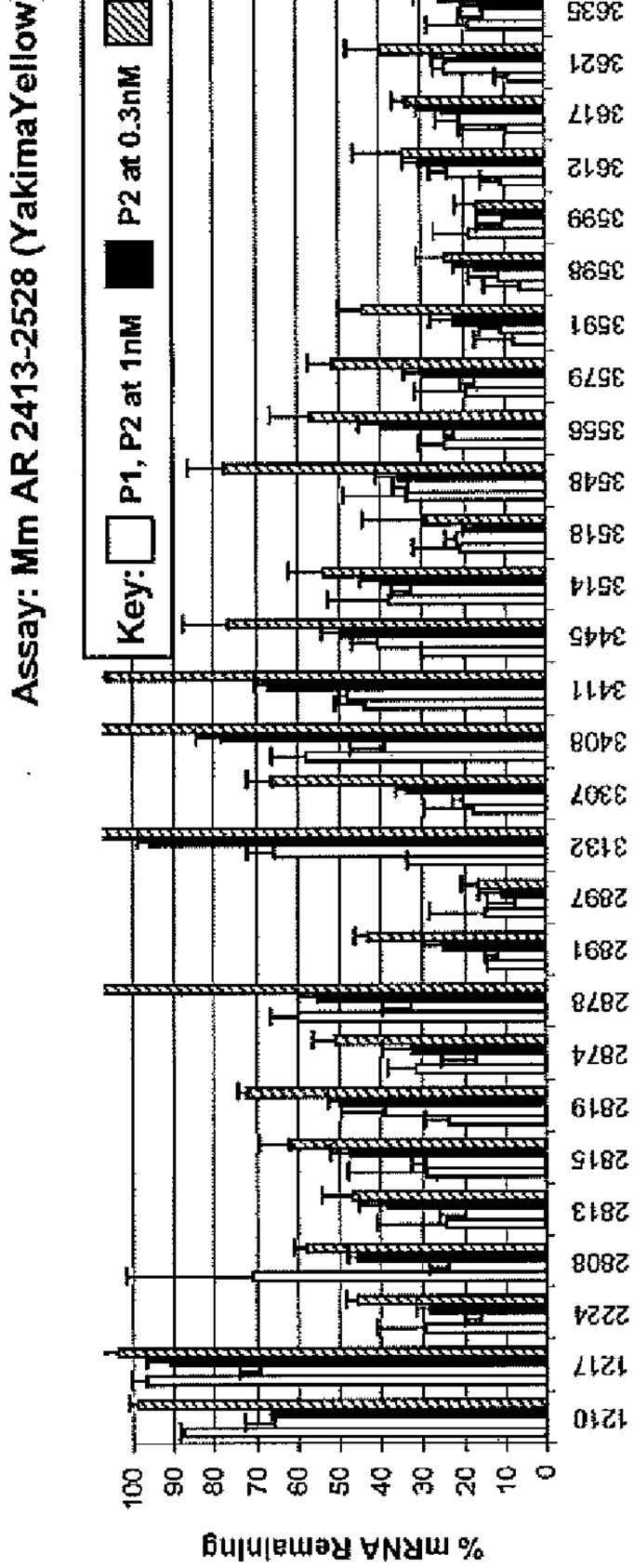


Figure 5

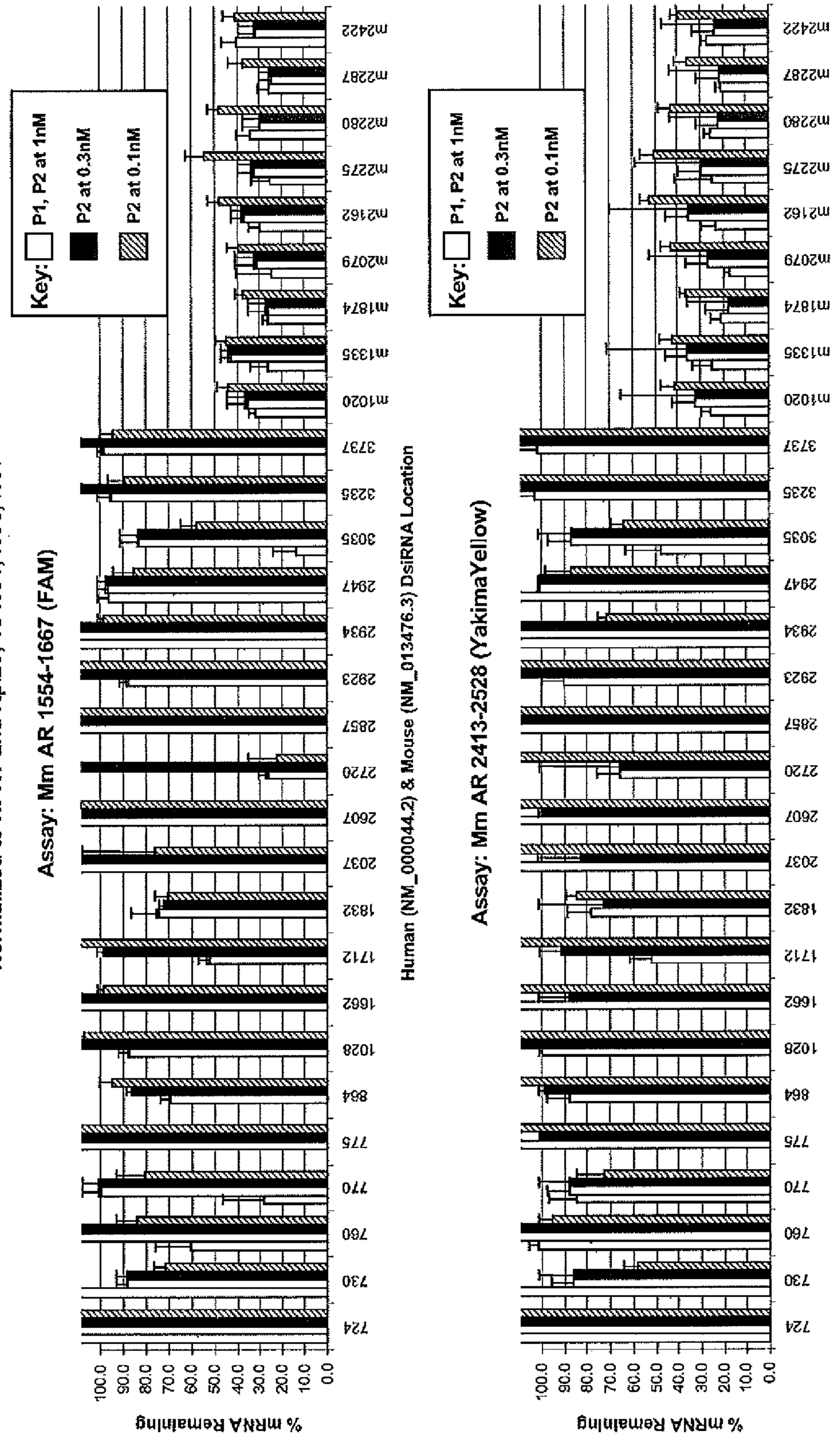
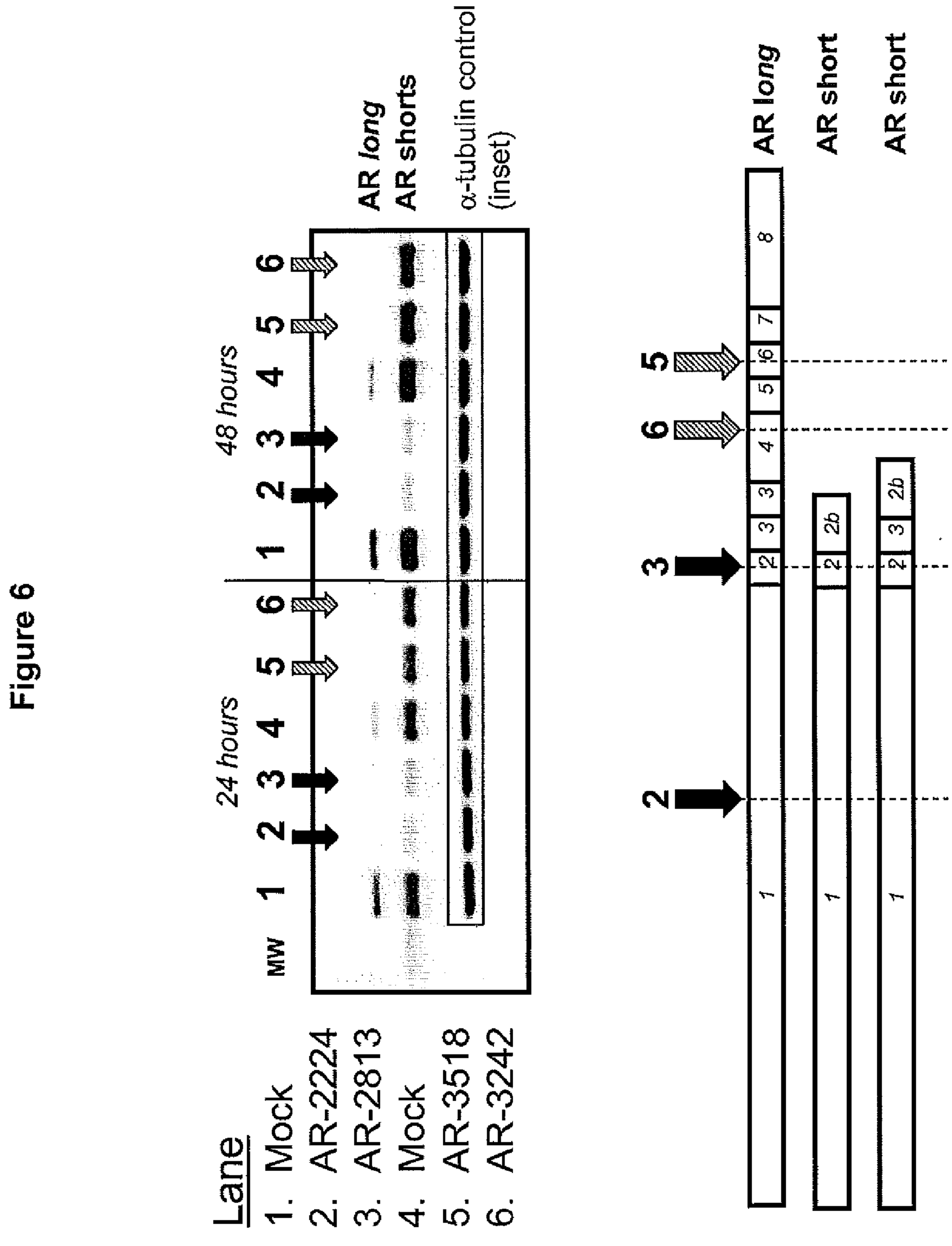

Mouse AR Knockdown - Mouse (LMTK-) Cells - Phase2
Normalized to HPRT and Rpl23; vs NC1, NC5, NC7
Assay: Mm AR 1554-1667 (FAM)
Human (NM_000044.2) & Mouse (NM_013476.3) DsiRNA Location
% mRNA Remaining
Key: P1, P2 at 1nM
P2 at 0.3nM
P2 at 0.1nM
m2422
m2287
m2280
m2275
m2162
m2079
m1874
m1335
m1020
3737
3235
3035
2947
2934
2923
2857
2720
2607
2037
1832
1712
1662
1028
864
775
770
760
730
724
100.0
90.0
80.0
70.0
60.0
50.0
40.0
30.0
20.0
10.0
0.0
Assay: Mm AR 2413-2528 (YakimaYellow)

Figure 6



Lane
1. Mock
2. AR-2224
3. AR-2813
4. Mock
5. AR-3518
6. AR-3242

Figure 7-1

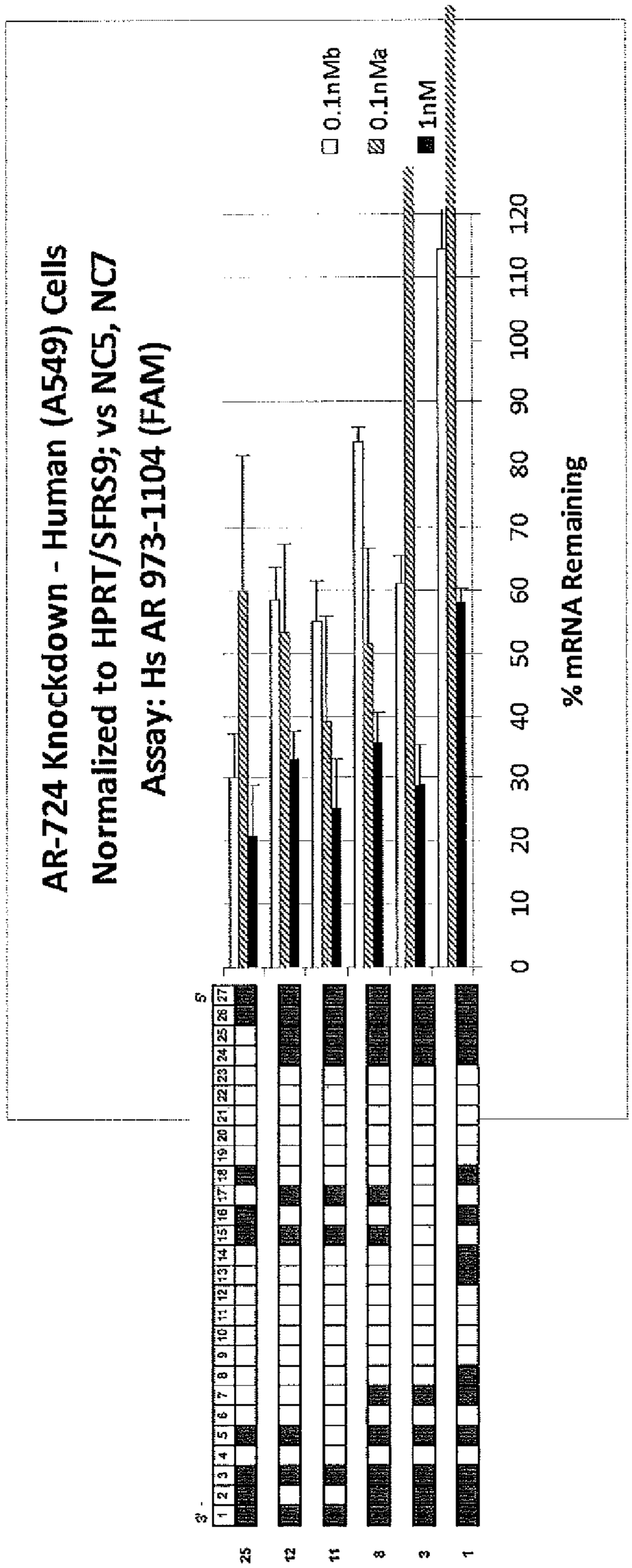

AR-724 Knockdown - Human (A549) Cells
Normalized to HPRT/SFRS9; vs NC5, NC7
Assay: Hs AR 973-1104 (FAM)
0.1nMb
0.1nMa
1nM
0
10
20
30
40
50
60
70
80
90
100
110
120
% mRNA Remaining
5'
3'
25
12
11
9
3
1

Figure 7-2

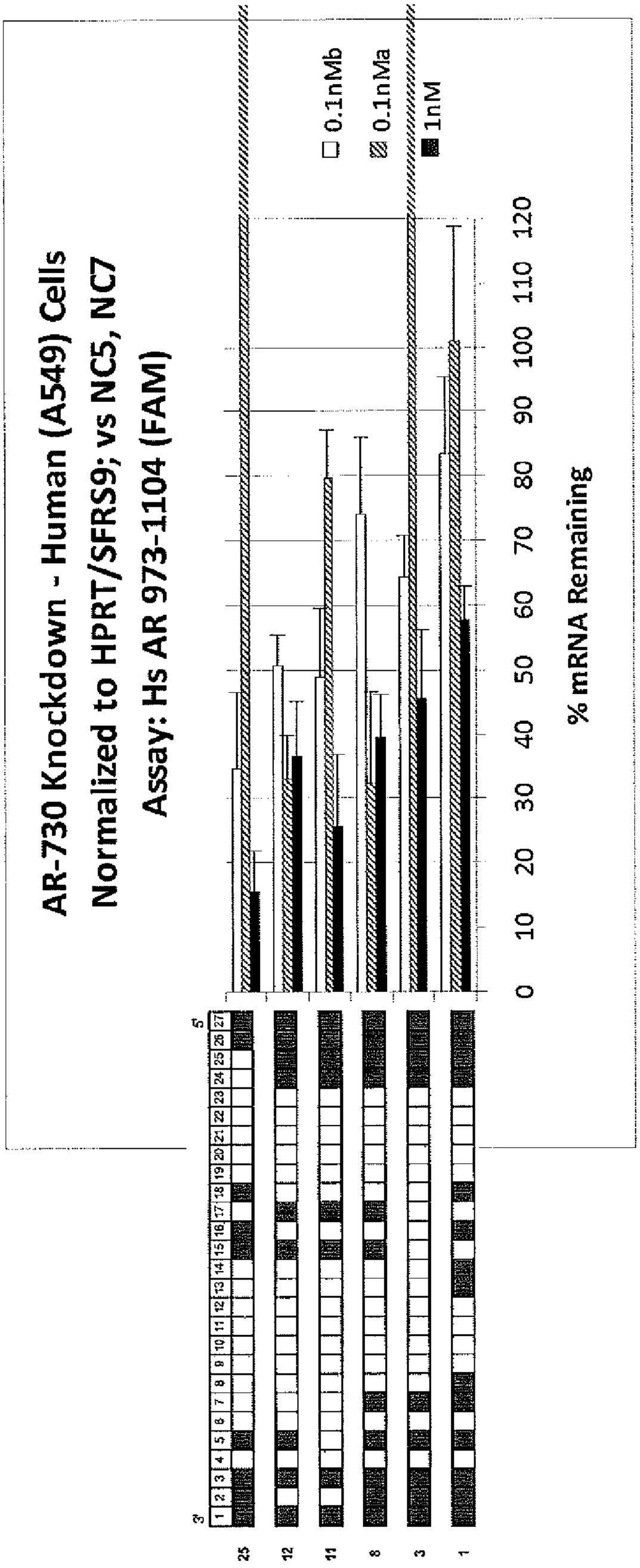

AR-730 Knockdown - Human (A549) Cells
Normalized to HPRT/SFRS9; vs NC5, NC7
Assay: Hs AR 973-1104 (FAM)
0.1nMb
0.1nMa
1nM
0
10
20
30
40
50
60
70
80
90
100
110
120
% mRNA Remaining
5'
3'
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
25
12
11
8
3
1

Figure 7-3

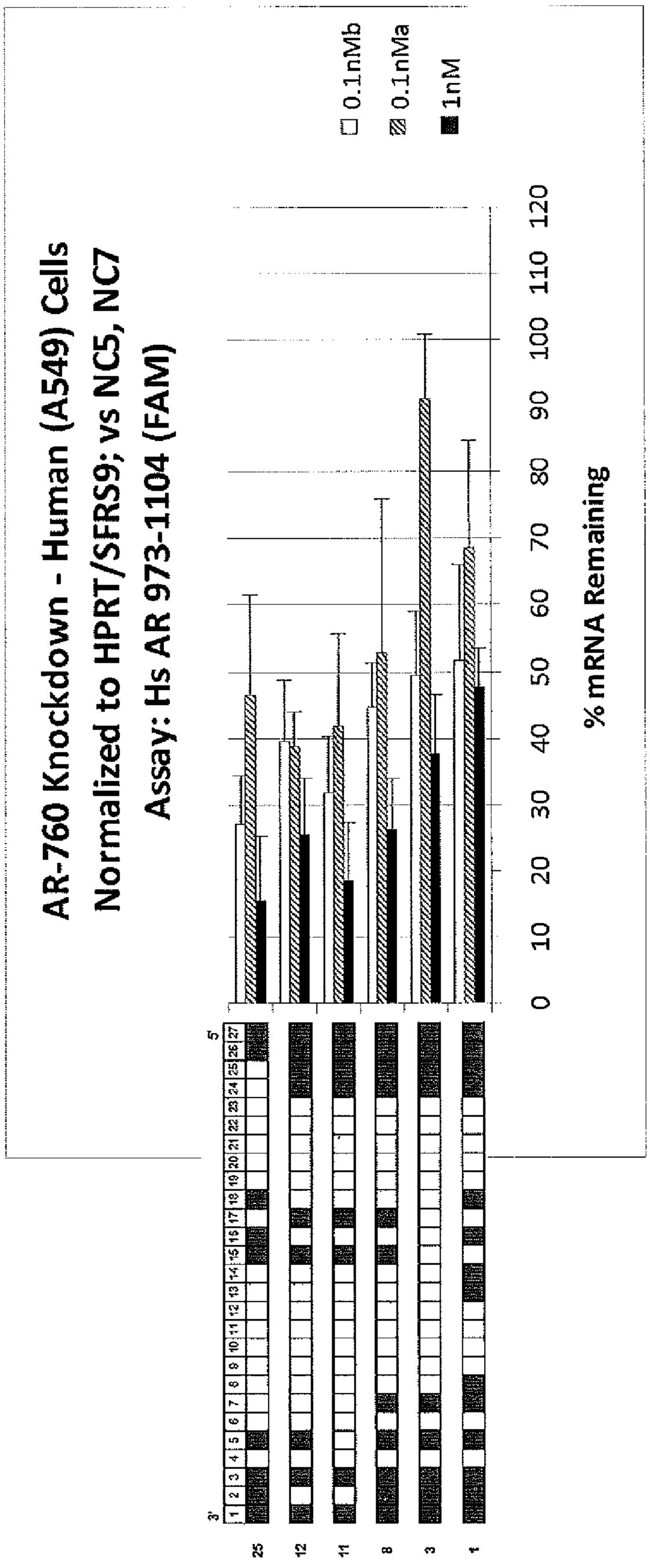

AR-760 Knockdown - Human (A549) Cells
Normalized to HPRT/SFRS9; vs NC5, NC7
Assay: Hs AR 973-1104 (FAM)
0.1nMb
0.1nMa
1nM
% mRNA Remaining
0
10
20
30
40
50
60
70
80
90
100
110
120
5'
3'
25
12
11
8
3
1

Figure 7-4

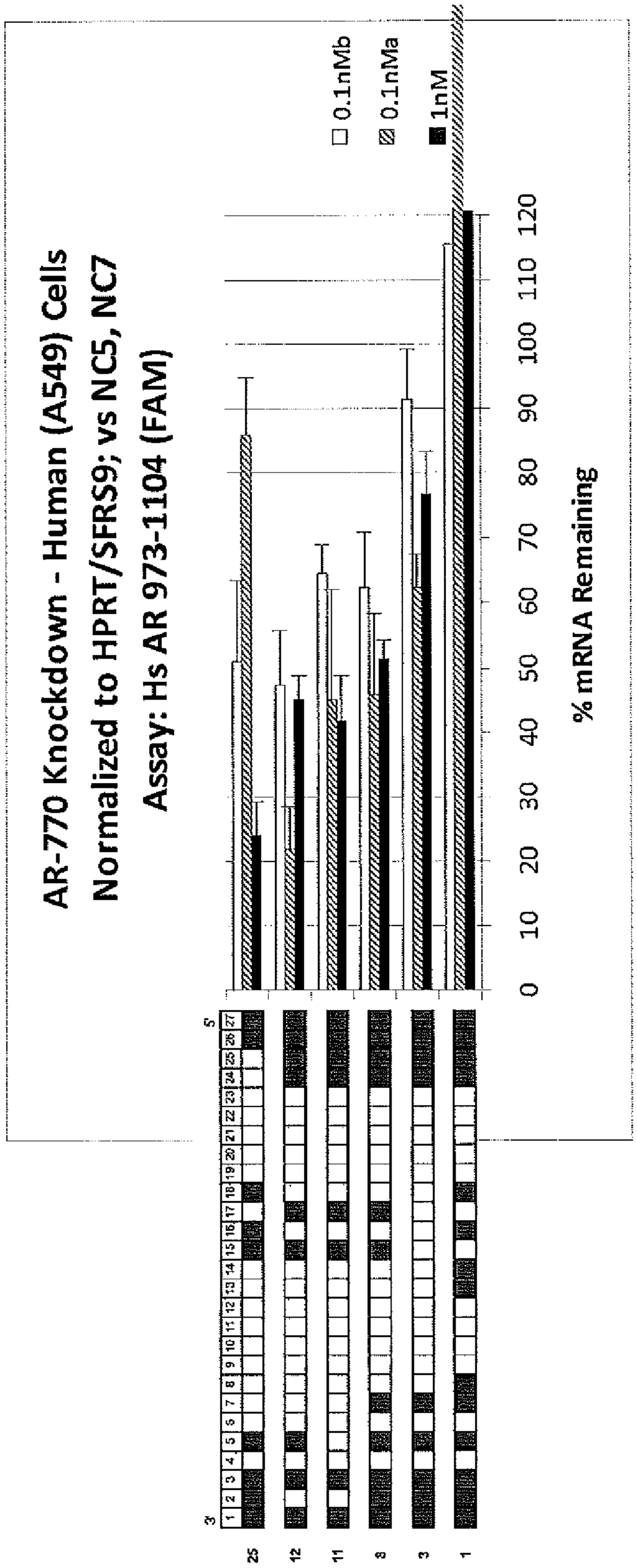

AR-770 Knockdown - Human (A549) Cells
Normalized to HPRT/SFRS9; vs NC5, NC7
Assay: Hs AR 973-1104 (FAM)
0.1nMb
0.1nMa
1nM
% mRNA Remaining
0
10
20
30
40
50
60
70
80
90
100
110
120
5'
3'
25
12
11
9
3
1

Figure 7-5

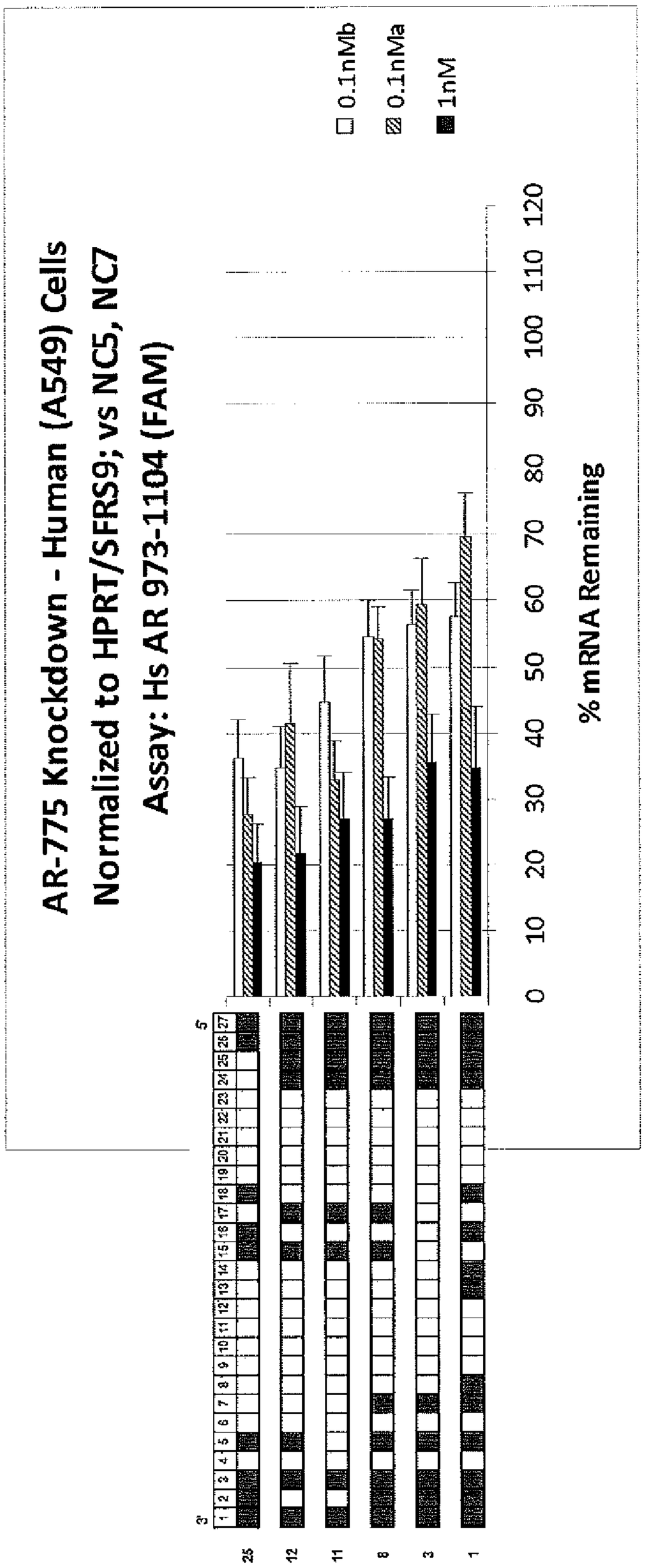
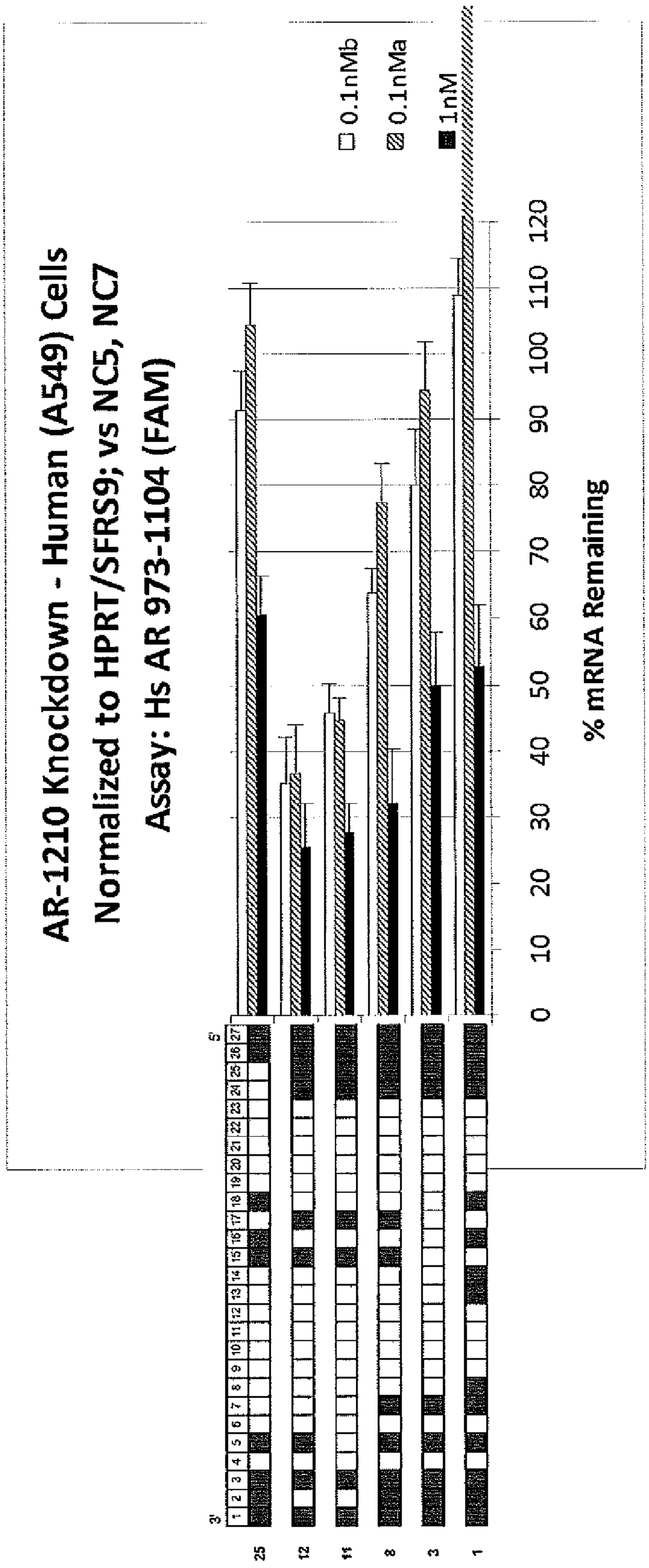

AR-775 Knockdown - Human (A549) Cells
Normalized to HPRT/SFRS9; vs NC5, NC7
Assay: Hs AR 973-1104 (FAM)
0.1nMb
0.1nMa
1nM
% mRNA Remaining
0
10
20
30
40
50
60
70
80
90
100
110
120
5'
3'
25
12
11
8
3
1

Figure 7-6


AR-1210 Knockdown - Human (A549) Cells
Normalized to HPRT/SFRS9; vs NC5, NC7
Assay: Hs AR 973-1104 (FAM)
0.1nMb
0.1nMa
1nM
% mRNA Remaining
0
10
20
30
40
50
60
70
80
90
100
110
120
5'
3'
25
12
11
8
3
1

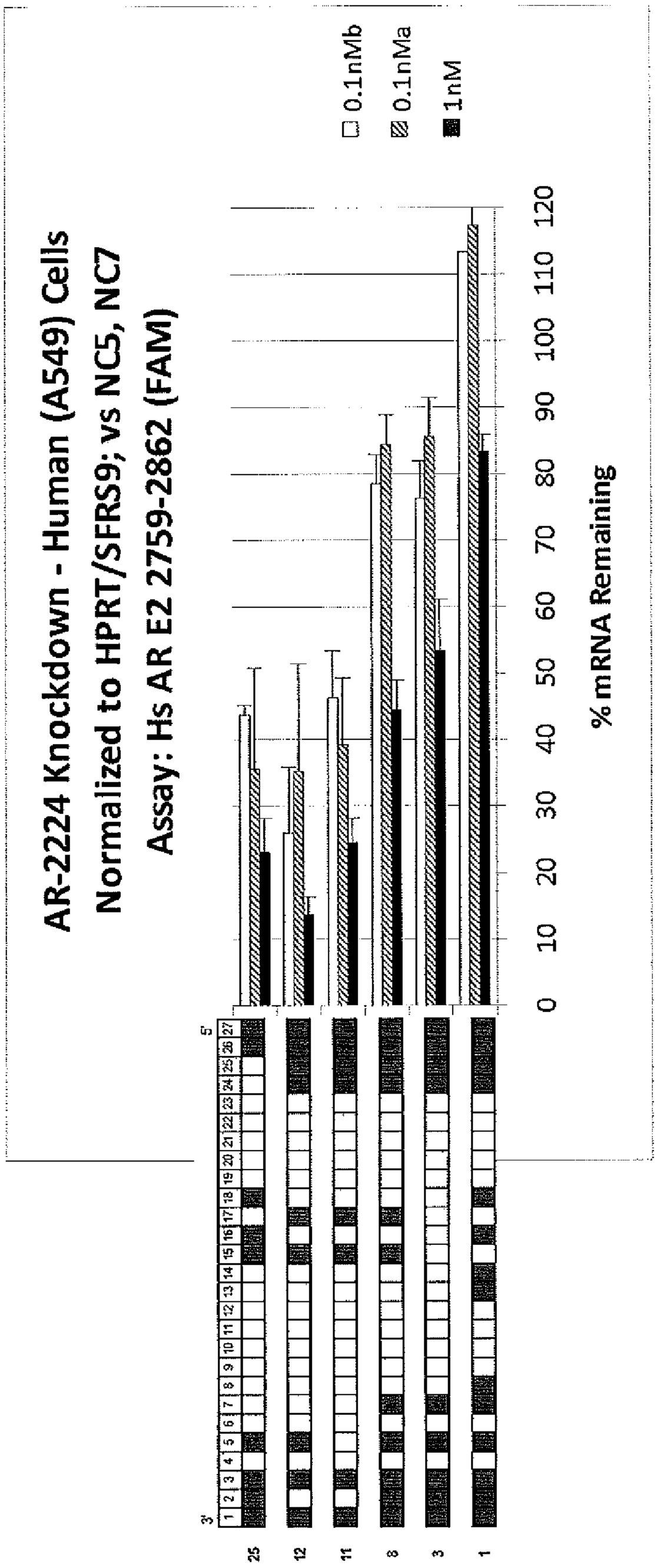

0.1nMb
0.1nMa
1nM
AR-2224 Knockdown - Human (A549) Cells
Normalized to HPRT/SFRS9; vs NC5, NC7
Assay: Hs AR E2 2759-2862 (FAM)
% mRNA Remaining
0 10 20 30 40 50 60 70 80 90 100 110 120
5'
3'
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27
25 12 11 8 3 1

Figure 7-7

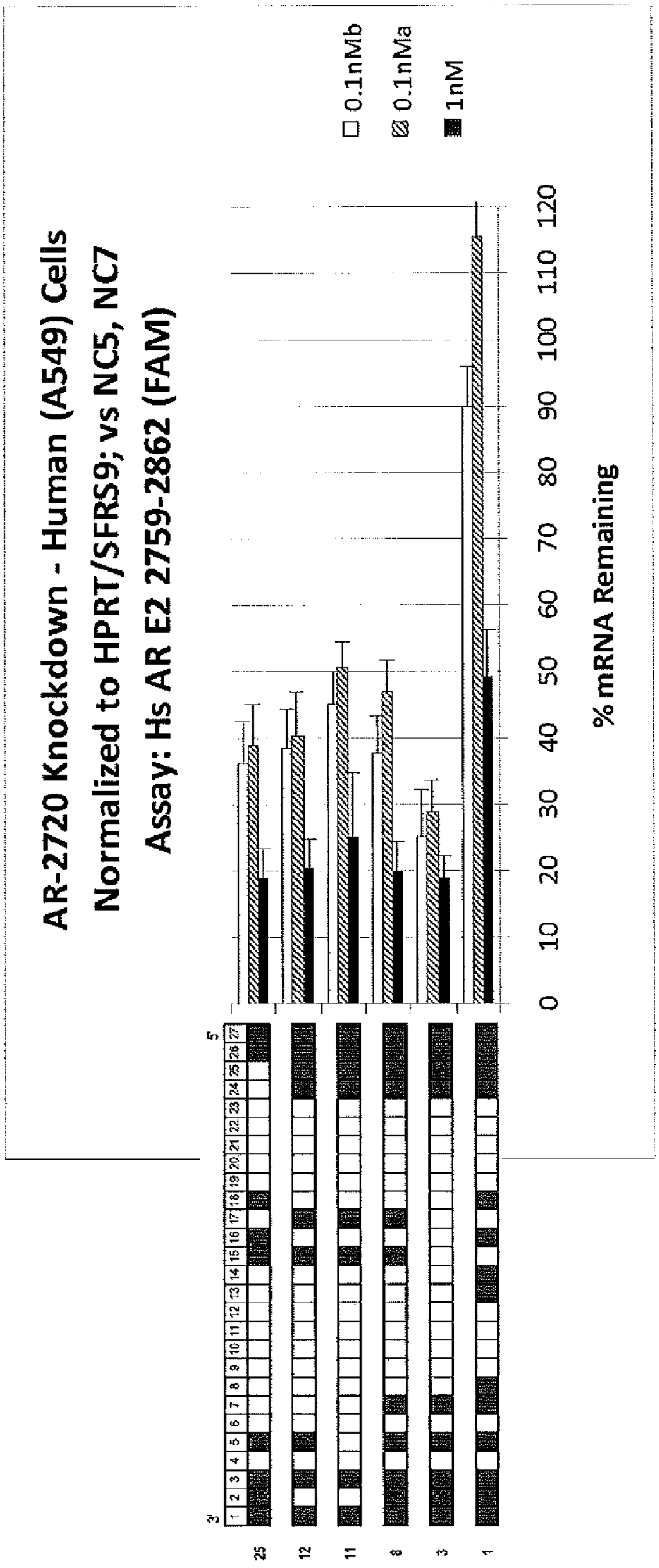

AR-2720 Knockdown - Human (A549) Cells
Normalized to HPRT/SFRS9; vs NC5, NC7
Assay: Hs AR E2 2759-2862 (FAM)
0.1nMb
0.1nMa
1nM
% mRNA Remaining
0
10
20
30
40
50
60
70
80
90
100
110
120
5'
3'
25
12
11
8
3
1

Figure 7-8

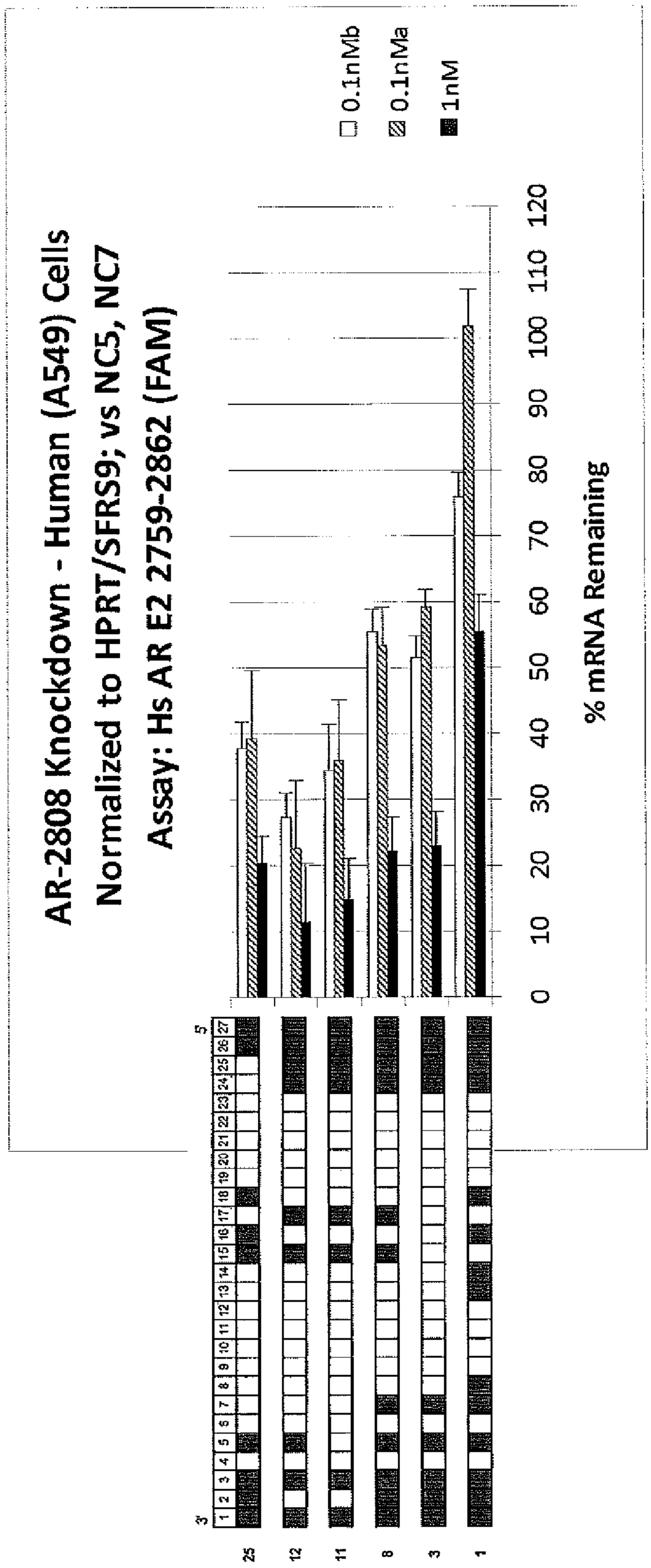

0.1nMb
0.1nMa
1nM
AR-2808 Knockdown - Human (A549) Cells
Normalized to HPRT/SFRS9; vs NC5, NC7
Assay: Hs AR E2 2759-2862 (FAM)
% mRNA Remaining
0
10
20
30
40
50
60
70
80
90
100
110
120
5'
3'
25
12
11
8
3
1

Figure 7-9

Figure 7-10

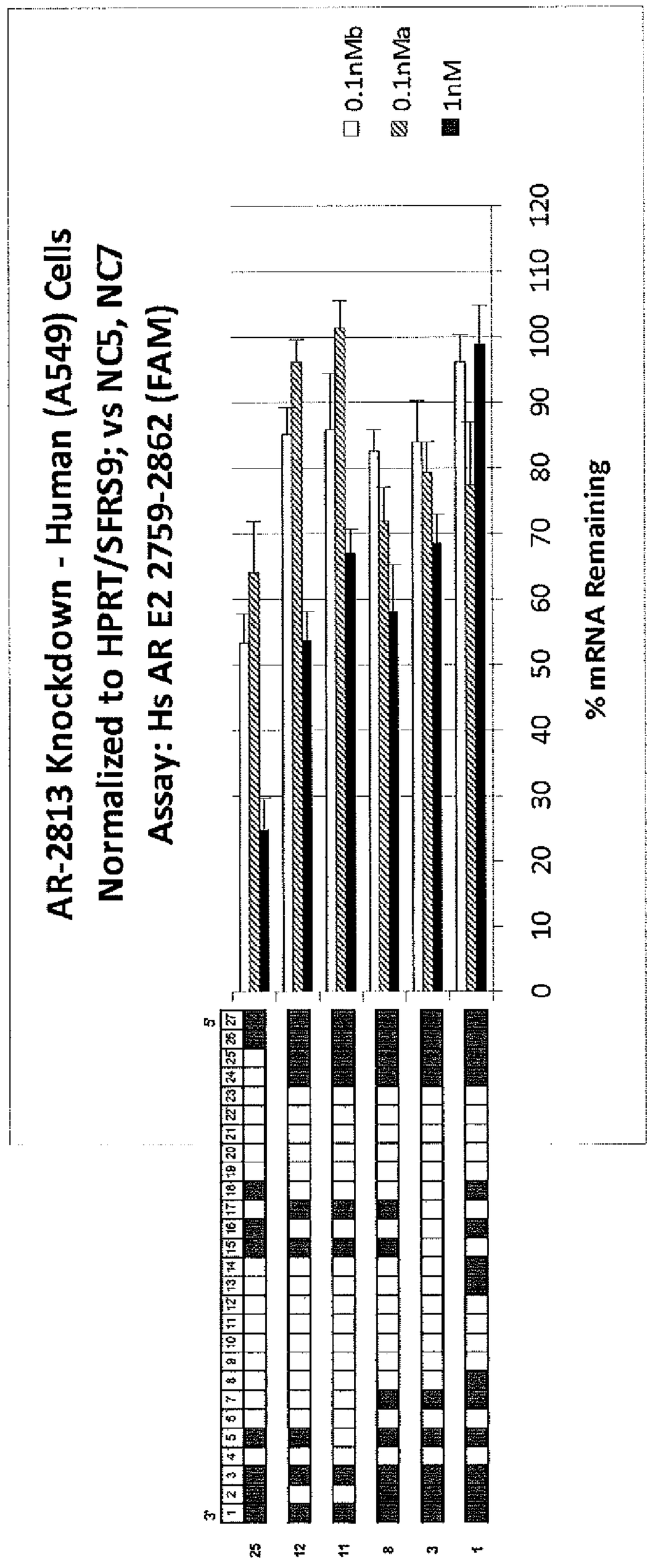
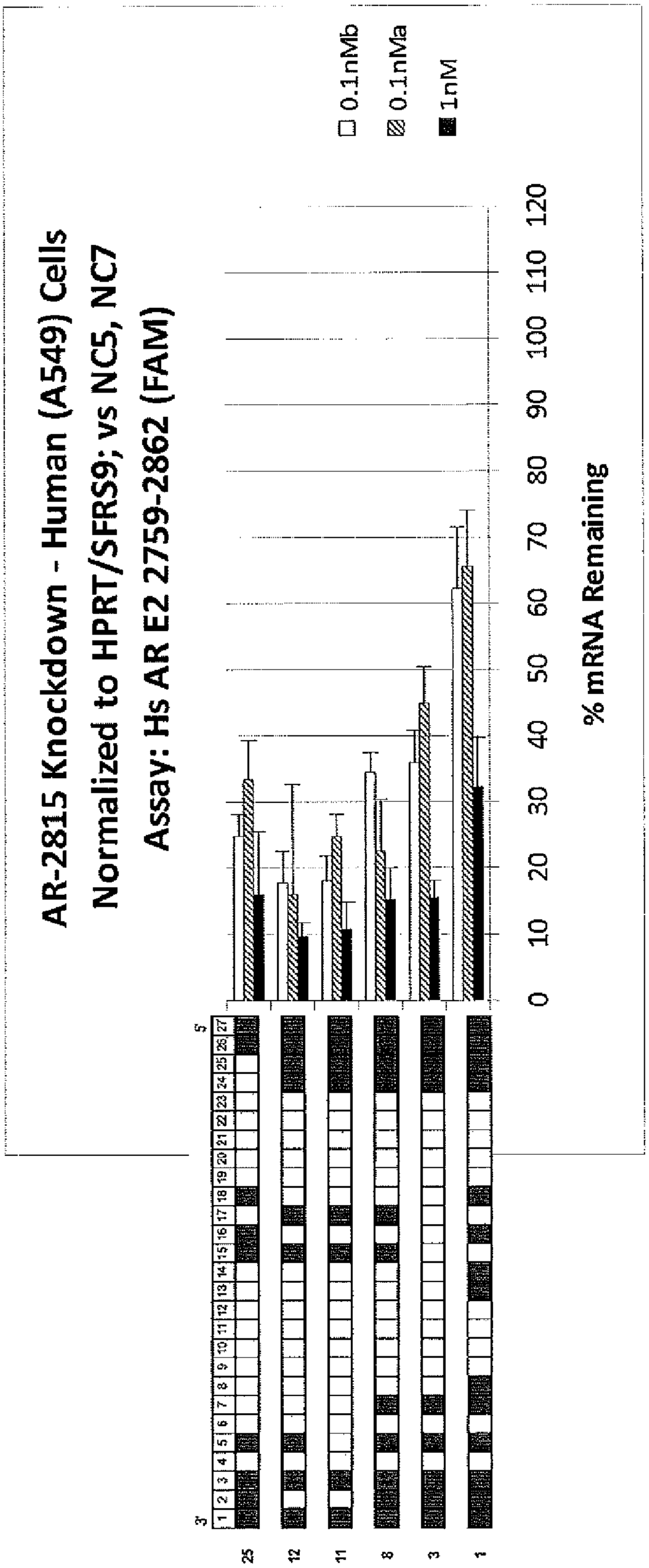

AR-2813 Knockdown - Human (A549) Cells
Normalized to HPRT/SFRS9; vs NC5, NC7
Assay: Hs AR E2 2759-2862 (FAM)
0.1nMb
0.1nMa
1nM
% mRNA Remaining
0
10
20
30
40
50
60
70
80
90
100
110
120
5'
3'
25
12
11
8
3
1

Figure 7-11


AR-2815 Knockdown - Human (A549) Cells
Normalized to HPRT/SFRS9; vs NC5, NC7
Assay: Hs AR E2 2759-2862 (FAM)
0.1nMb
0.1nMa
1nM
% mRNA Remaining
0
10
20
30
40
50
60
70
80
90
100
110
120
5'
3'
1
2
3
4
5
6
7
8
9
10
11
12
13
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25
12
11
8
3
1

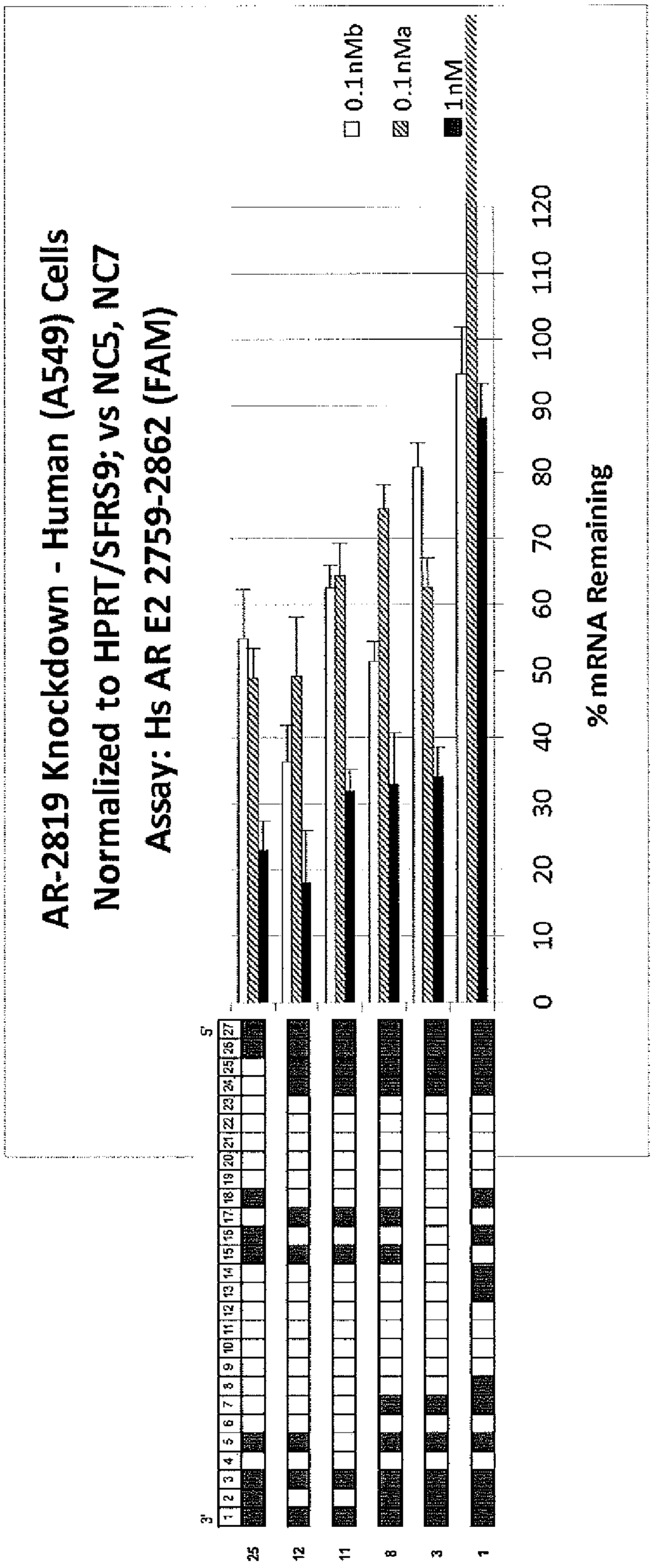

AR-2819 Knockdown - Human (A549) Cells
Normalized to HPRT/SFRS9; vs NC5, NC7
Assay: Hs AR E2 2759-2862 (FAM)
0.1nMb
0.1nMa
1nM
% mRNA Remaining
0
10
20
30
40
50
60
70
80
90
100
110
120
5'
3'
25
12
11
8
3
1

Figure 7-12

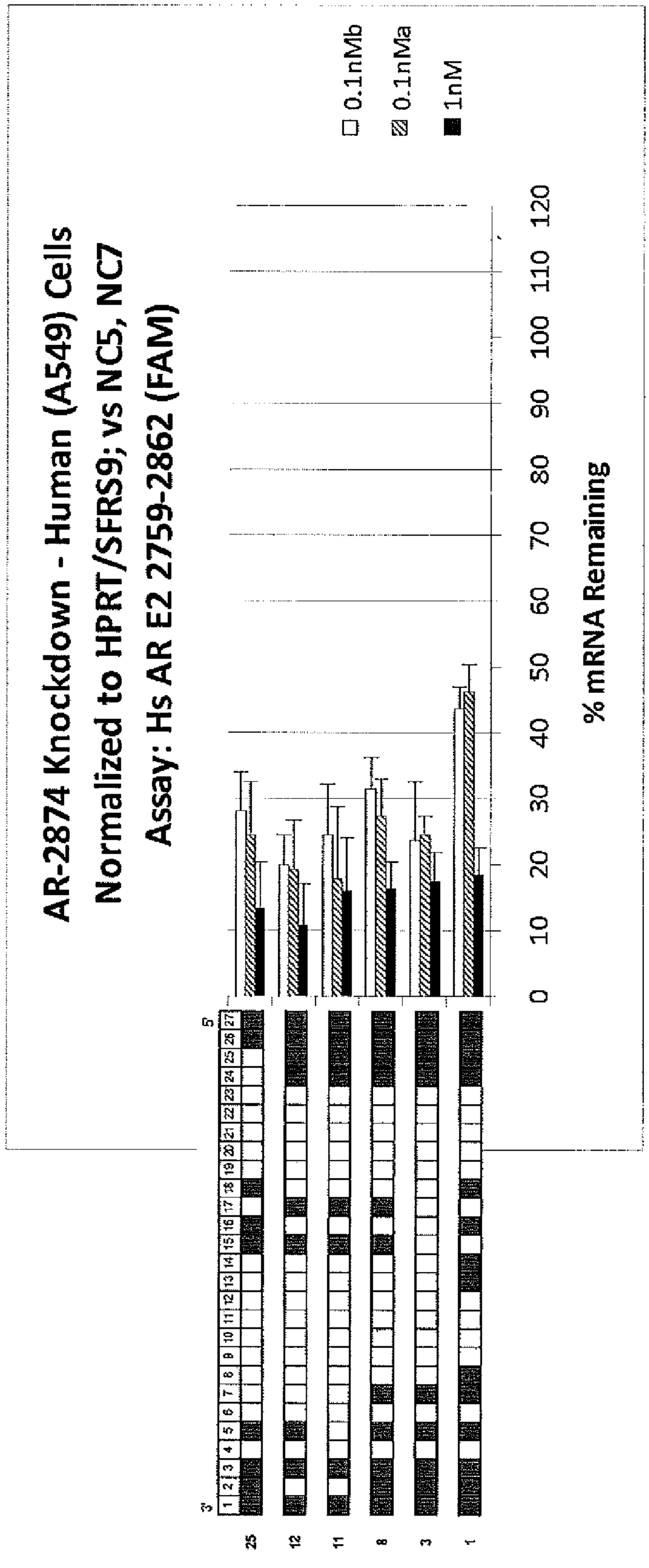
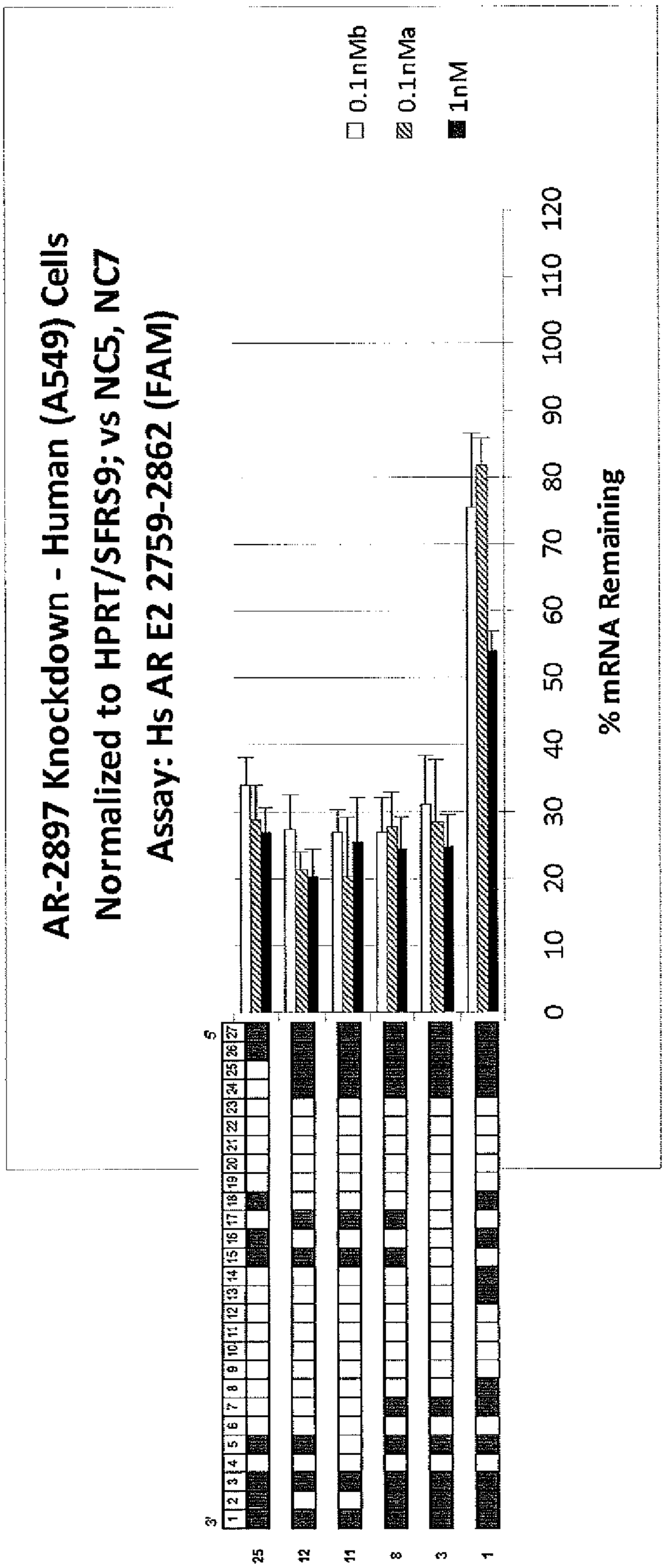

0.1nMb
0.1nMa
1nM
AR-2874 Knockdown - Human (A549) Cells
Normalized to HPRT/SFRS9; vs NC5, NC7
Assay: Hs AR E2 2759-2862 (FAM)
% mRNA Remaining
0
10
20
30
40
50
60
70
80
90
100
110
120
5'
3'
25
12
11
8
3
1

Figure 7-13

Figure 7-14


AR-2897 Knockdown - Human (A549) Cells
Normalized to HPRT/SFRS9; vs NC5, NC7
Assay: Hs AR E2 2759-2862 (FAM)
0.1nMb
0.1nMa
1nM
% mRNA Remaining
0
10
20
30
40
50
60
70
80
90
100
110
120
5'
3'
25
12
11
8
3
1

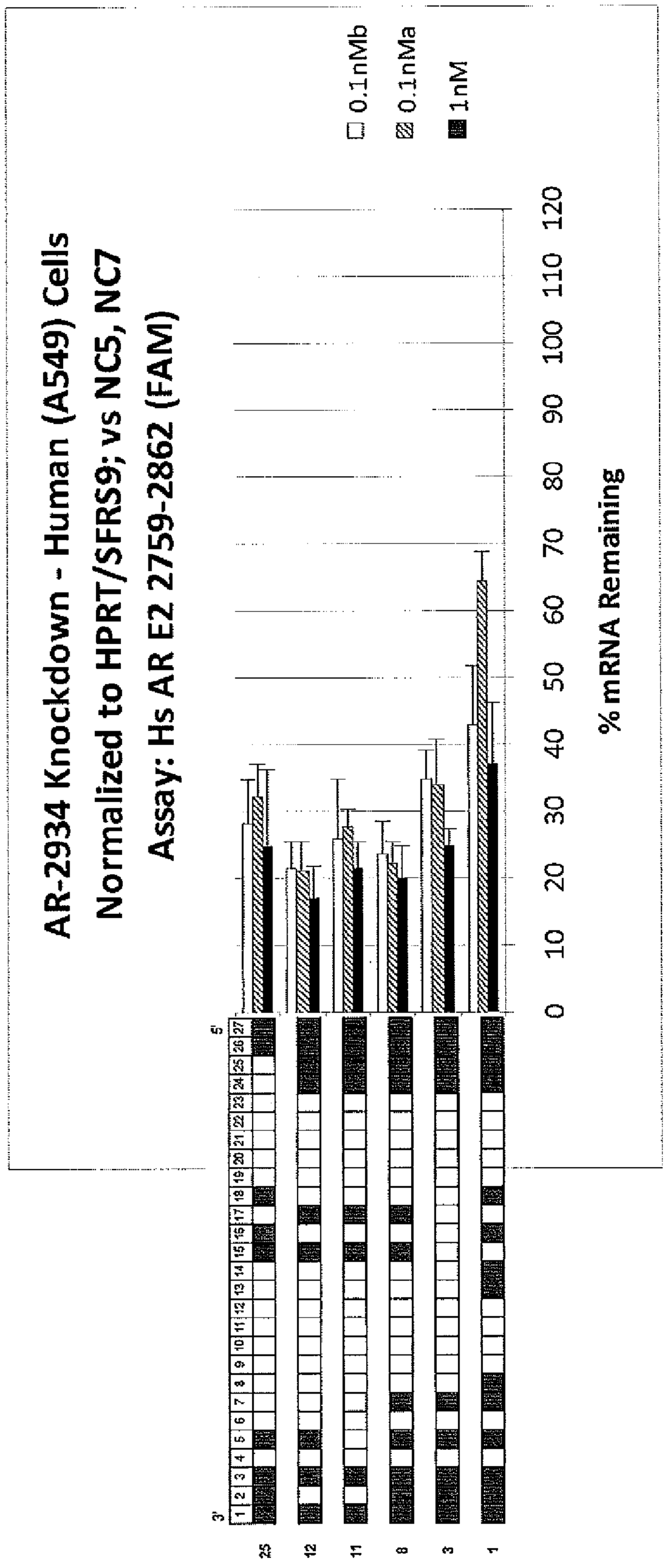
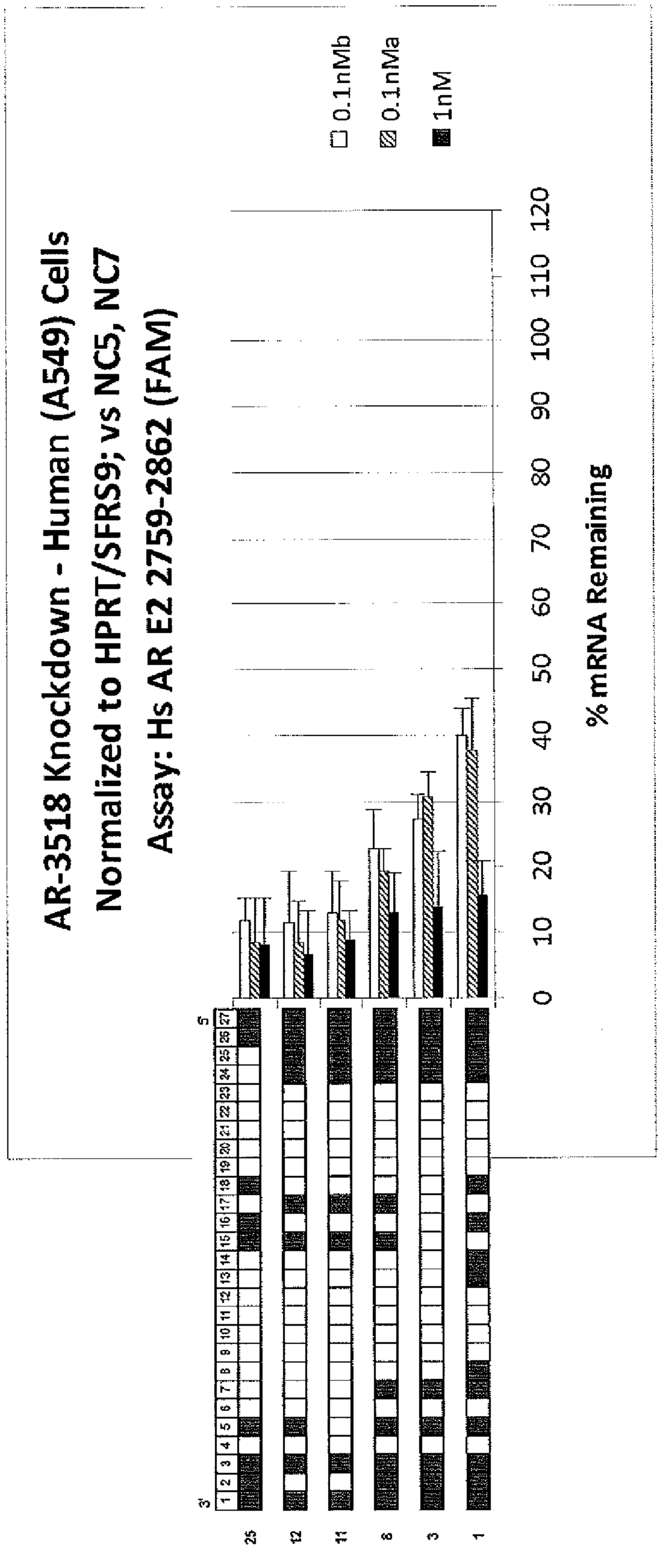

0.1nMb
0.1nMa
1nM
AR-2934 Knockdown - Human (A549) Cells
Normalized to HPRT/SFRS9; vs NC5, NC7
Assay: Hs AR E2 2759-2862 (FAM)
% mRNA Remaining
0
10
20
30
40
50
60
70
80
90
100
110
120
5'
3'
25
12
11
8
3
1

Figure 7-15

Figure 7-16


AR-3518 Knockdown - Human (A549) Cells
Normalized to HPRT/SFRS9; vs NC5, NC7
Assay: Hs AR E2 2759-2862 (FAM)
0.1nMb
0.1nMa
1nM
% mRNA Remaining
0 10 20 30 40 50 60 70 80 90 100 110 120
5'
3'
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27
25 12 11 8 3 1

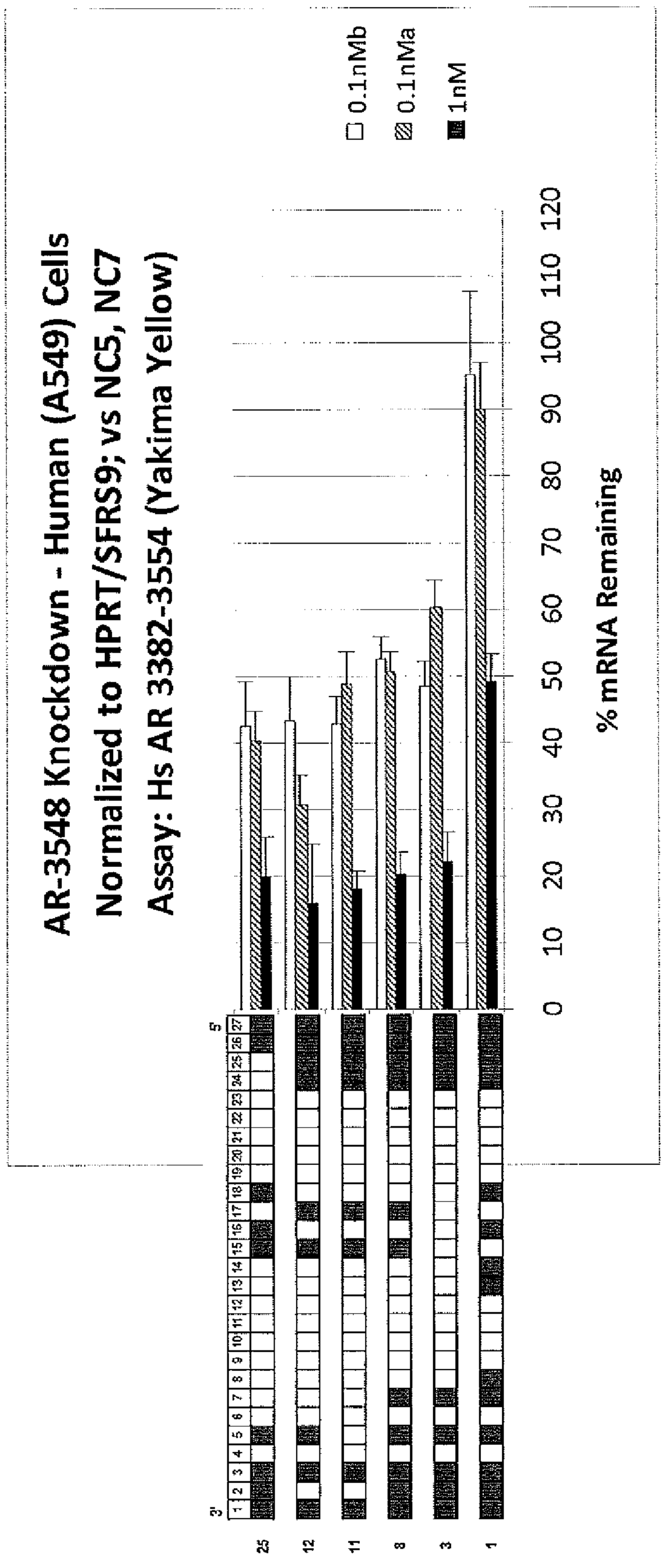

AR-3548 KD8 Knockdown - Human (A549) Cells
Normalized to HPRT/SFRS9; vs NC5, NC7
Assay: Hs AR 3382-3554 (Yakima Yellow)
0.1nMb
0.1nMa
1nM
% mRNA Remaining
0
10
20
30
40
50
60
70
80
90
100
110
120
5'
3'
25
12
11
8
3
1

Figure 7-17

Figure 7-18

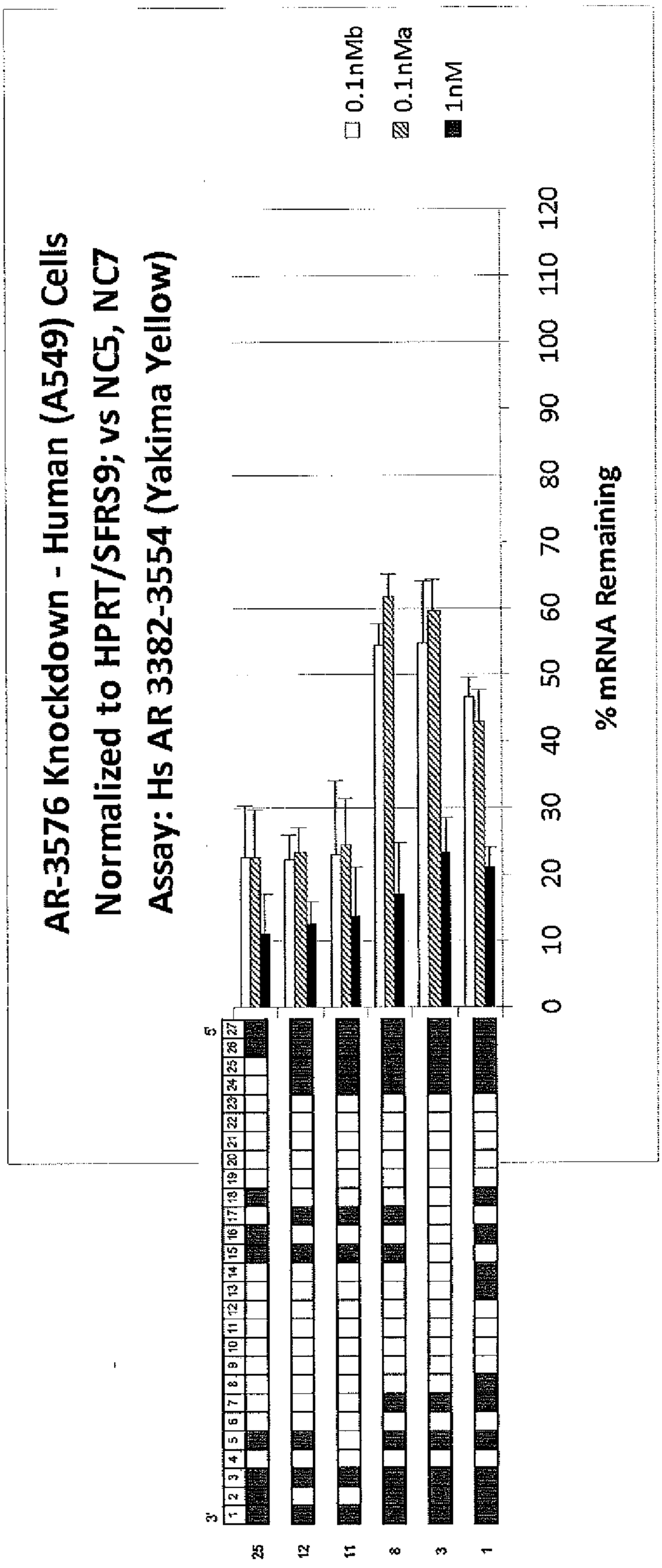
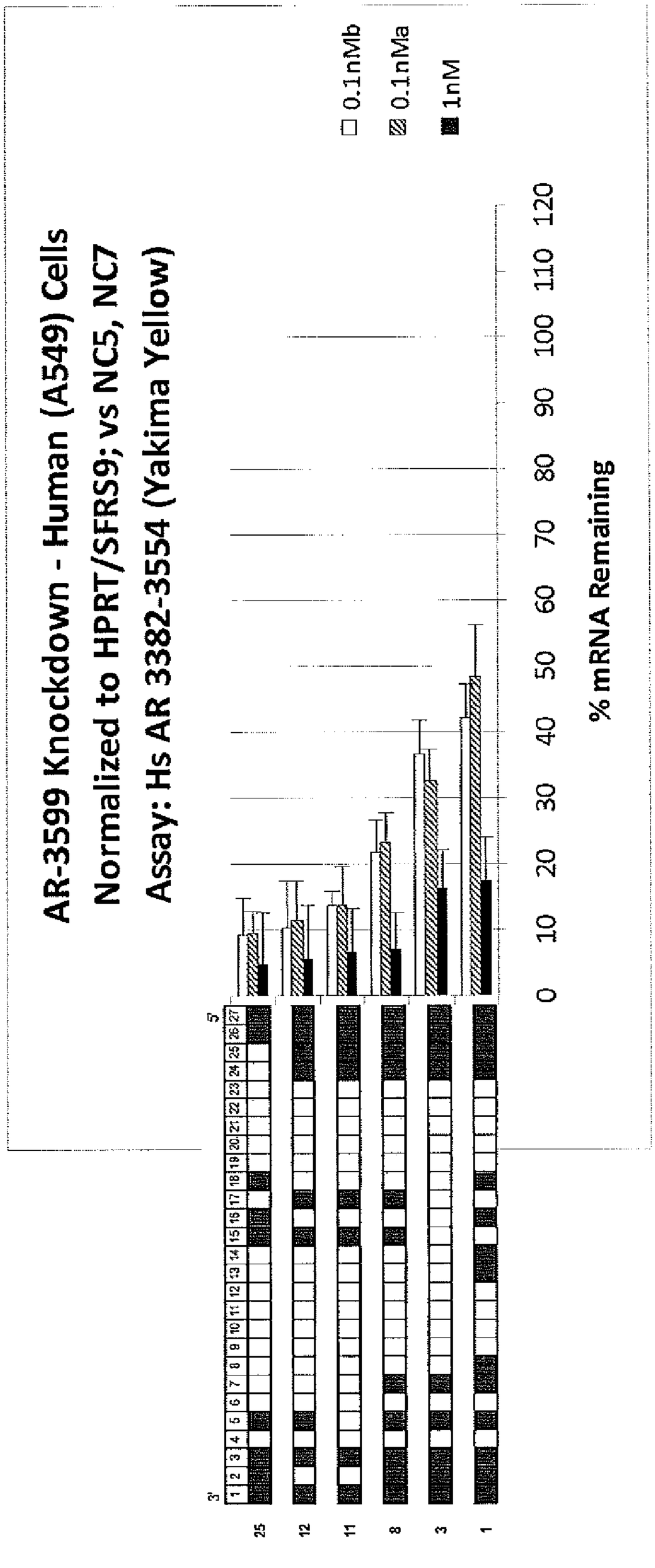

AR-3576 Knockdown - Human (A549) Cells
Normalized to HPRT/SFRS9; vs NC5, NC7
Assay: Hs AR 3382-3554 (Yakima Yellow)
0.1nMb
0.1nMa
1nM
% mRNA Remaining
0 10 20 30 40 50 60 70 80 90 100 110 120
5'
3'
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27
25 12 11 8 3 1

Figure 7-19


AR-3599 Knockdown - Human (A549) Cells
Normalized to HPRT/SFRS9; vs NC5, NC7
Assay: Hs AR 3382-3554 (Yakima Yellow)
0.1nMb
0.1nMa
1nM
% mRNA Remaining
0 10 20 30 40 50 60 70 80 90 100 110 120
5'
3'
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27
25 12 11 8 3 1

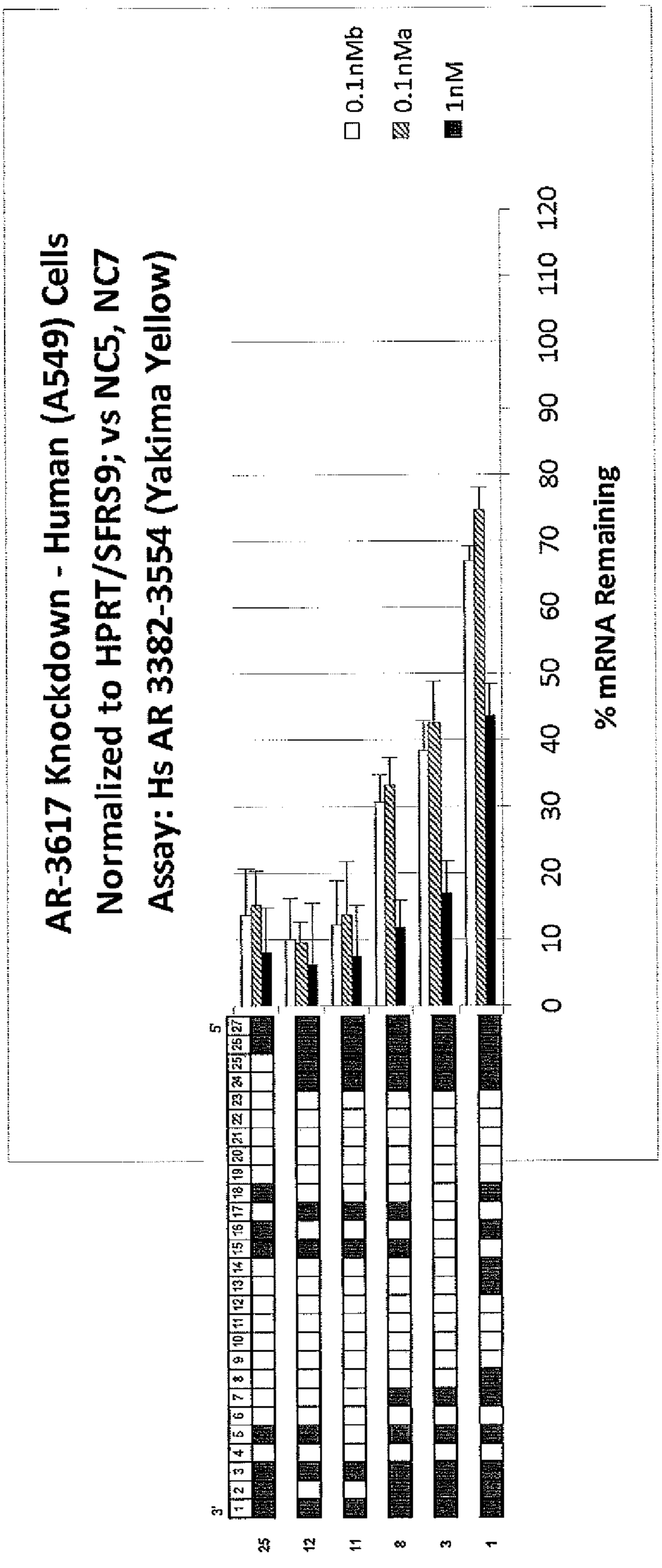

0.1nMb
0.1nMa
1nM
AR-3617 Knockdown - Human (A549) Cells
Normalized to HPRT/SFRS9; vs NC5, NC7
Assay: Hs AR 3382-3554 (Yakima Yellow)
% mRNA Remaining
0
10
20
30
40
50
60
70
80
90
100
110
120
5'
3'
25
12
11
8
3
1

Figure 7-20

Figure 7-21

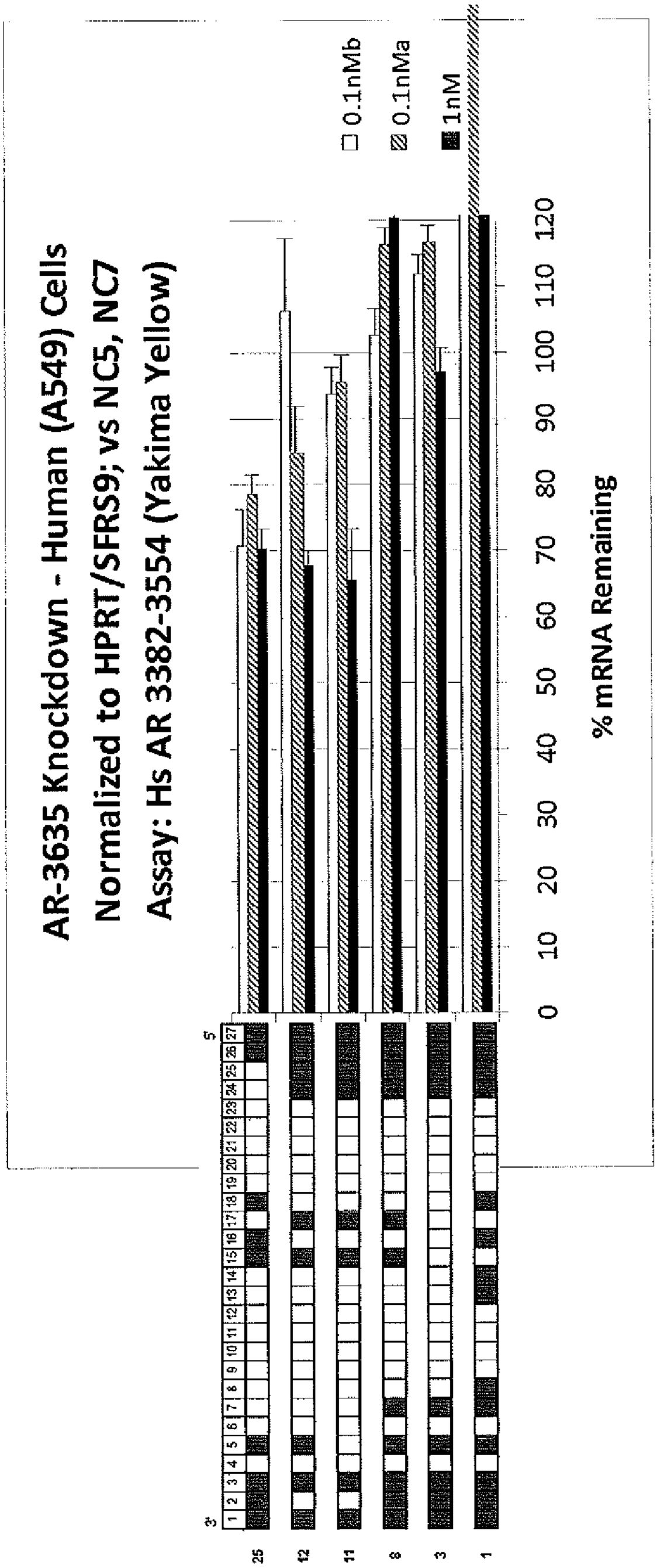

AR-3635 Knockdown - Human (A549) Cells
Normalized to HPRT/SFRS9; vs NC5, NC7
Assay: Hs AR 3382-3554 (Yakima Yellow)
0.1nMb
0.1nMa
1nM
% mRNA Remaining
0
10
20
30
40
50
60
70
80
90
100
110
120
5'
3'
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
25
12
11
8
3
1

Figure 7-22

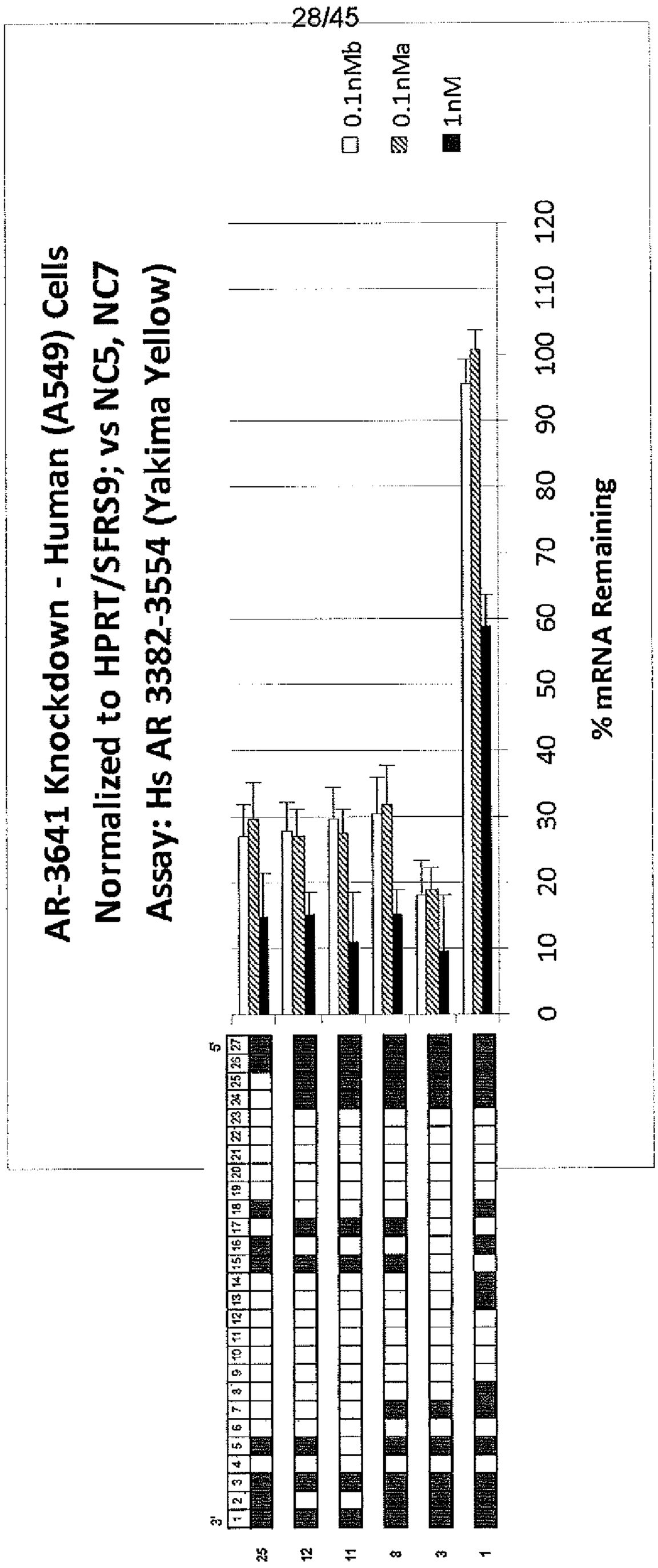
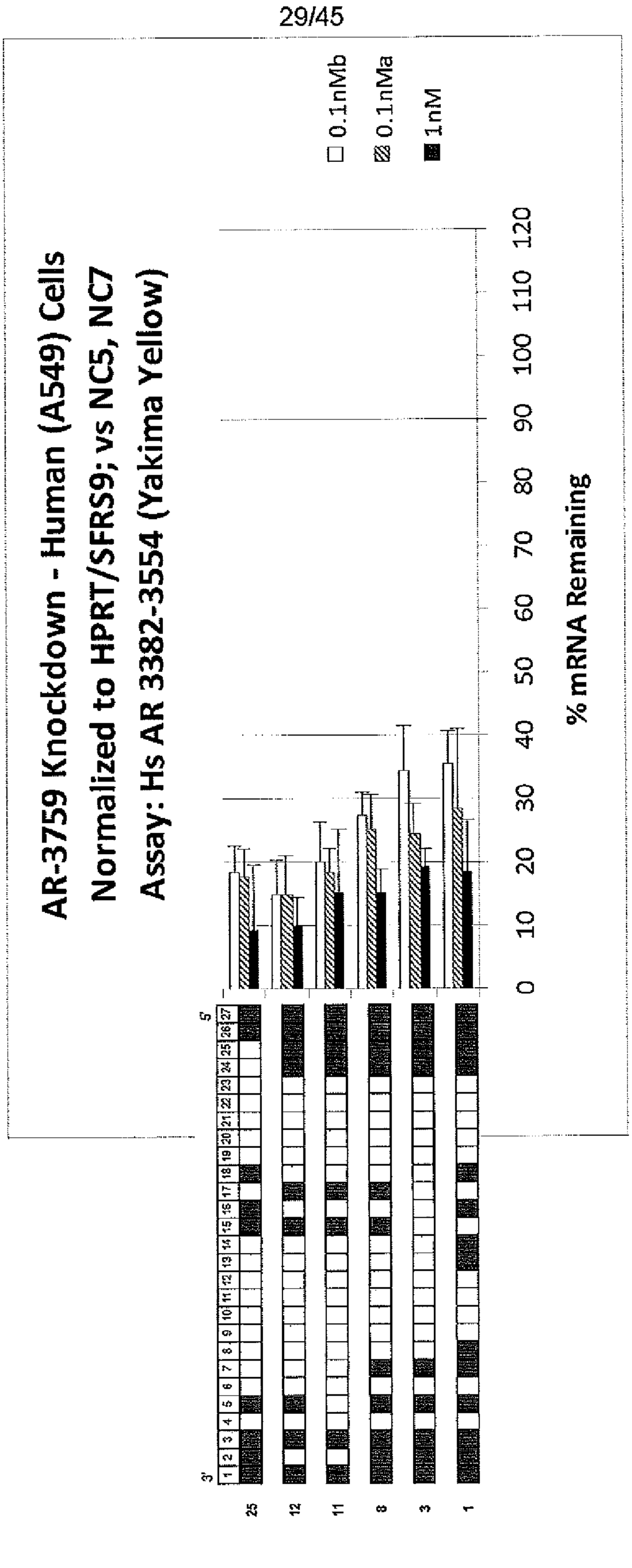

AR-3641 Knockdown - Human (A549) Cells
Normalized to HPRT/SFRS9; vs NC5, NC7
Assay: Hs AR 3382-3554 (Yakima Yellow)
0.1nMb
0.1nMa
1nM
% mRNA Remaining
0 10 20 30 40 50 60 70 80 90 100 110 120
5'
3'
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27
25 12 11 8 3 1

Figure 7-23


AR-3759 Knockdown - Human (A549) Cells
Normalized to HPRT/SFRS9; vs NC5, NC7
Assay: Hs AR 3382-3554 (Yakima Yellow)
0.1nMb
0.1nMa
1nM
% mRNA Remaining
0
10
20
30
40
50
60
70
80
90
100
110
120
5'
3'
25
12
11
8
3
1

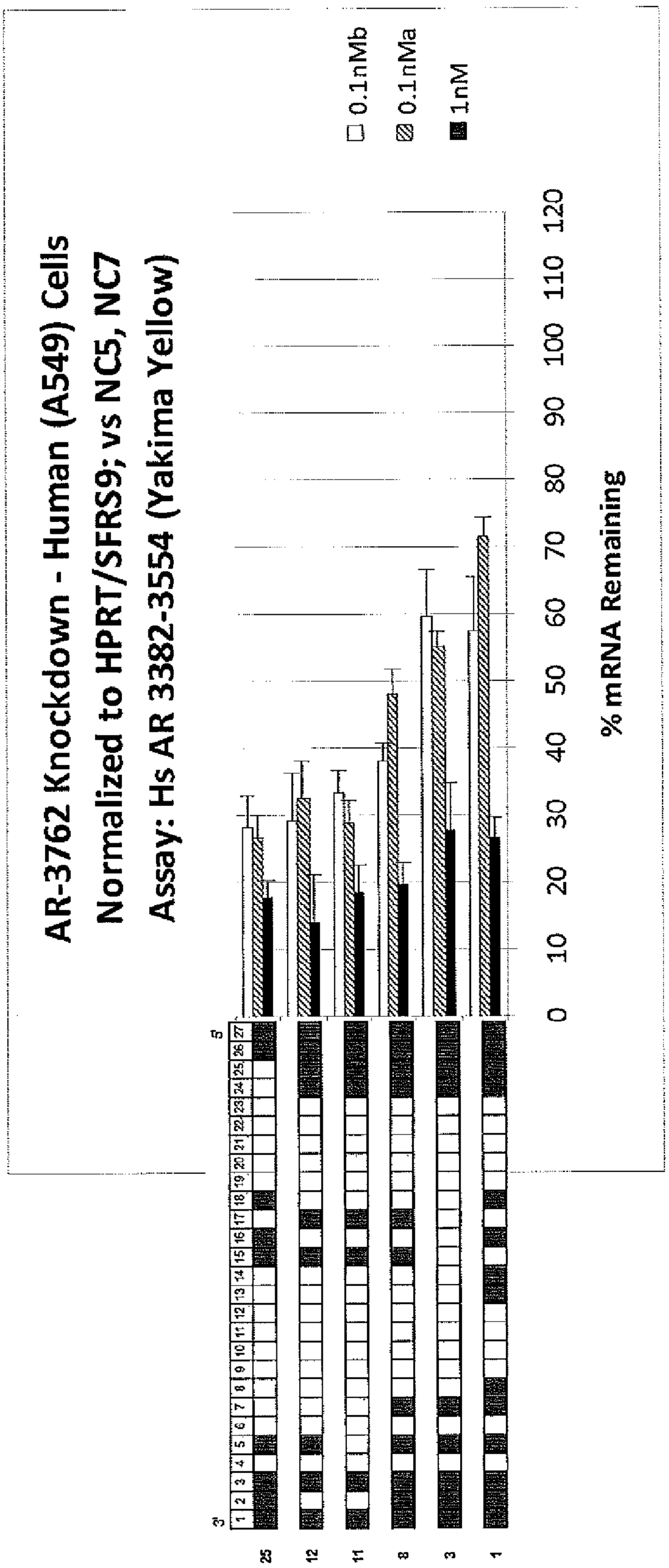

0.1nMb
0.1nMa
1nM
AR-3762 Knockdown - Human (A549) Cells
Normalized to HPRT/SFRS9; vs NC5, NC7
Assay: Hs AR 3382-3554 (Yakima Yellow)
% mRNA Remaining
0 10 20 30 40 50 60 70 80 90 100 110 120
5'
3'
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27
25 12 11 8 3 1

Figure 7-24

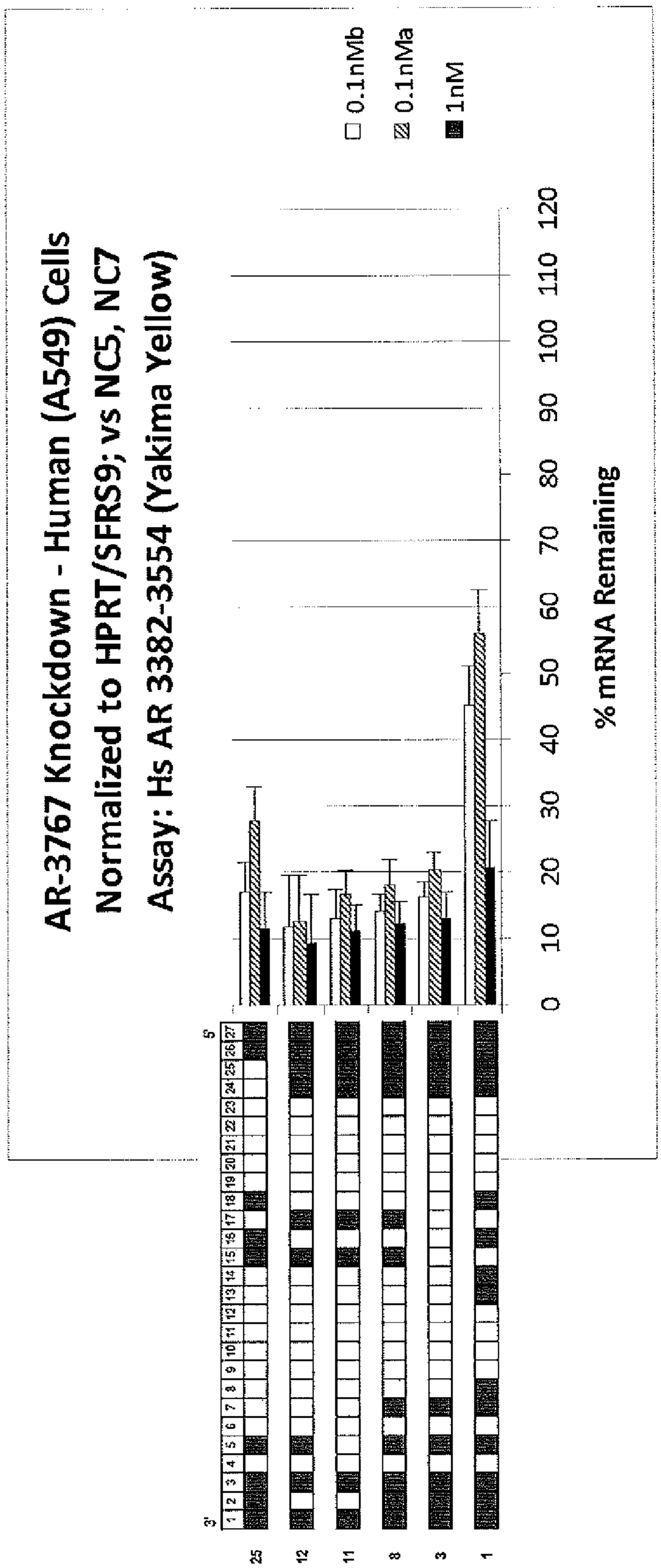

AR-3767 Knockdown - Human (A549) Cells
Normalized to HPRT/SFRS9; vs NC5, NC7
Assay: Hs AR 3382-3554 (Yakima Yellow)
0.1nMb
0.1nMa
1nM
% mRNA Remaining
0 10 20 30 40 50 60 70 80 90 100 110 120
5'
3'
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27
25 12 11 8 3 1

Figure 7-25

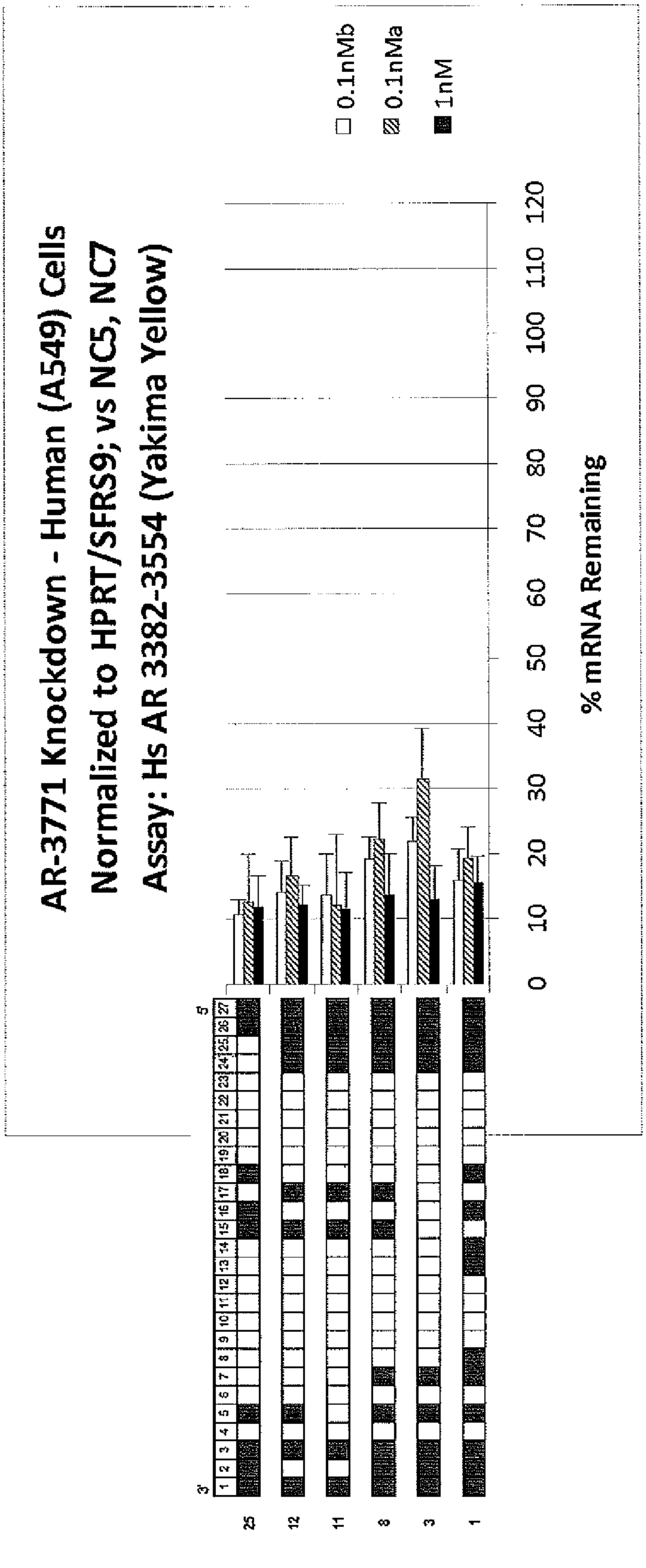

0.1nMb
0.1nMa
1nM
AR-3771 Knockdown - Human (A549) Cells
Normalized to HPRT/SFRS9; vs NC5, NC7
Assay: Hs AR 3382-3554 (Yakima Yellow)
% mRNA Remaining
0
10
20
30
40
50
60
70
80
90
100
110
120
5'
3'
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27
25
12
11
8
3
1

Figure 7-26

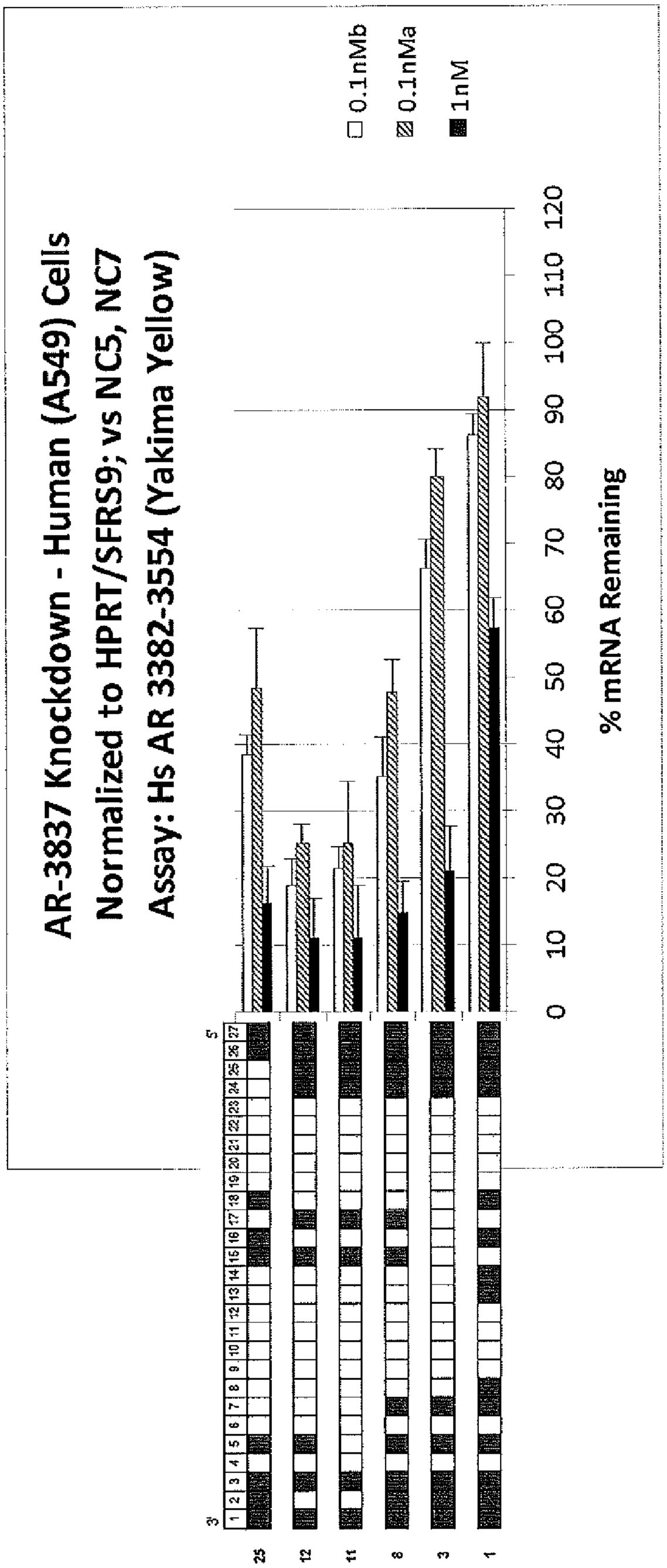

AR-3837 Knockdown - Human (A549) Cells
Normalized to HPRT/SFRS9; vs NC5, NC7
Assay: Hs AR 3382-3554 (Yakima Yellow)
0.1nMb
0.1nMa
1nM
% mRNA Remaining
0
10
20
30
40
50
60
70
80
90
100
110
120
5'
3'
25
12
11
8
3
1

Figure 7-27

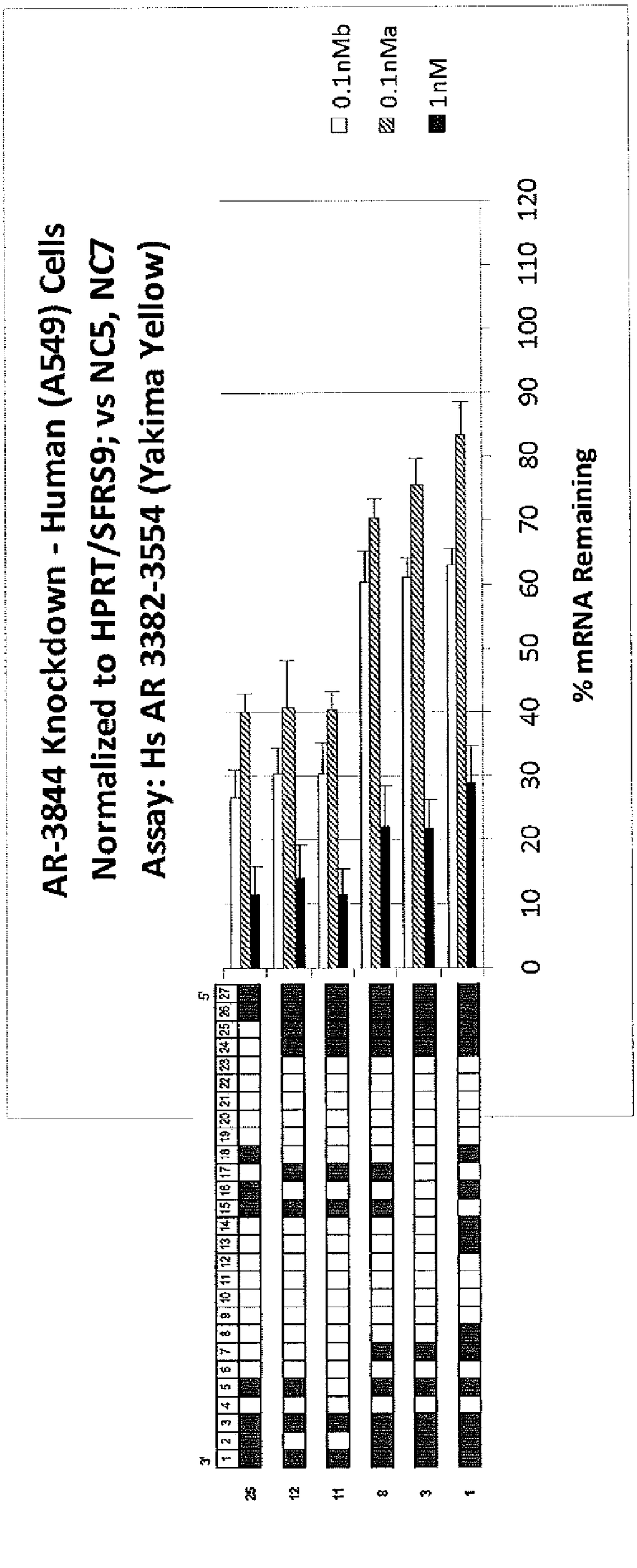

0.1nMb
0.1nMa
1nM
AR-3844 Knockdown - Human (A549) Cells
Normalized to HPRT/SFRS9; vs NC5, NC7
Assay: Hs AR 3382-3554 (Yakima Yellow)
% mRNA Remaining
0 10 20 30 40 50 60 70 80 90 100 110 120
5'
3'
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27
25 12 11 8 3 1

Figure 7-28

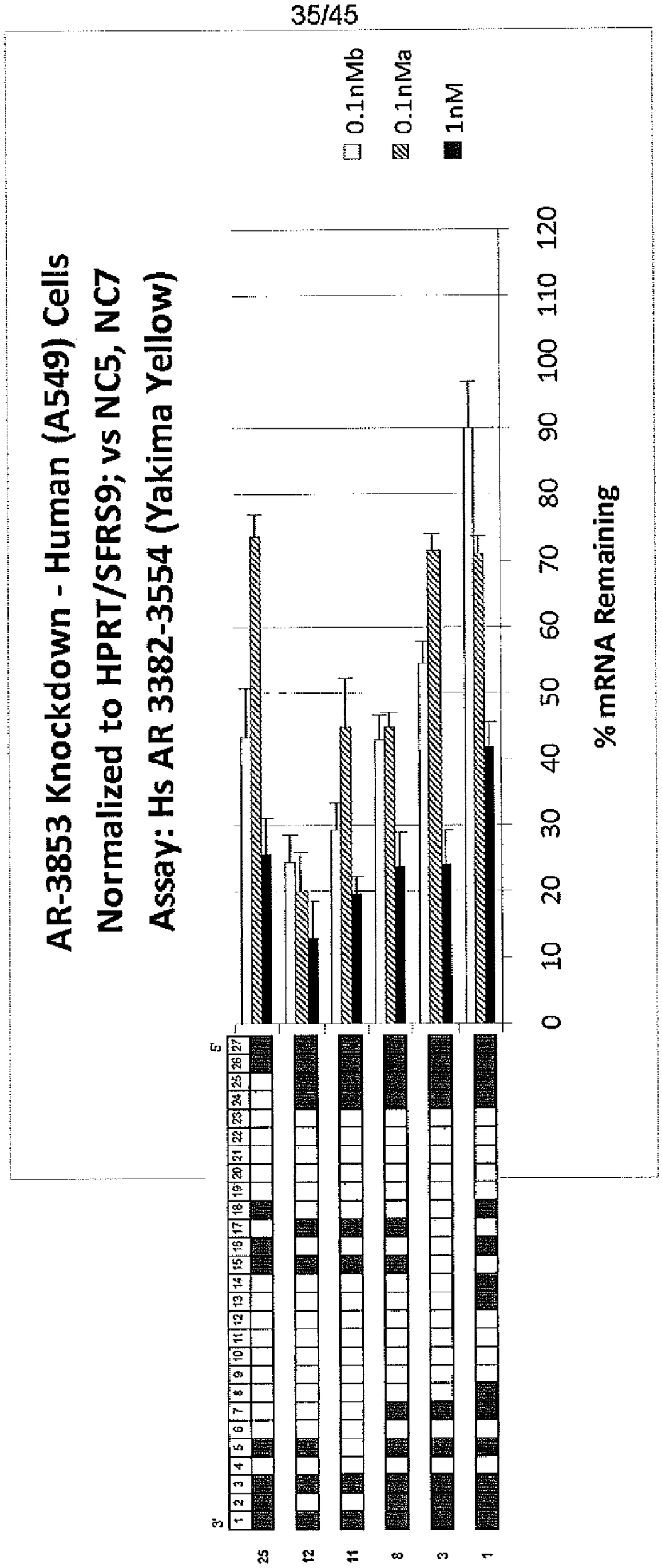
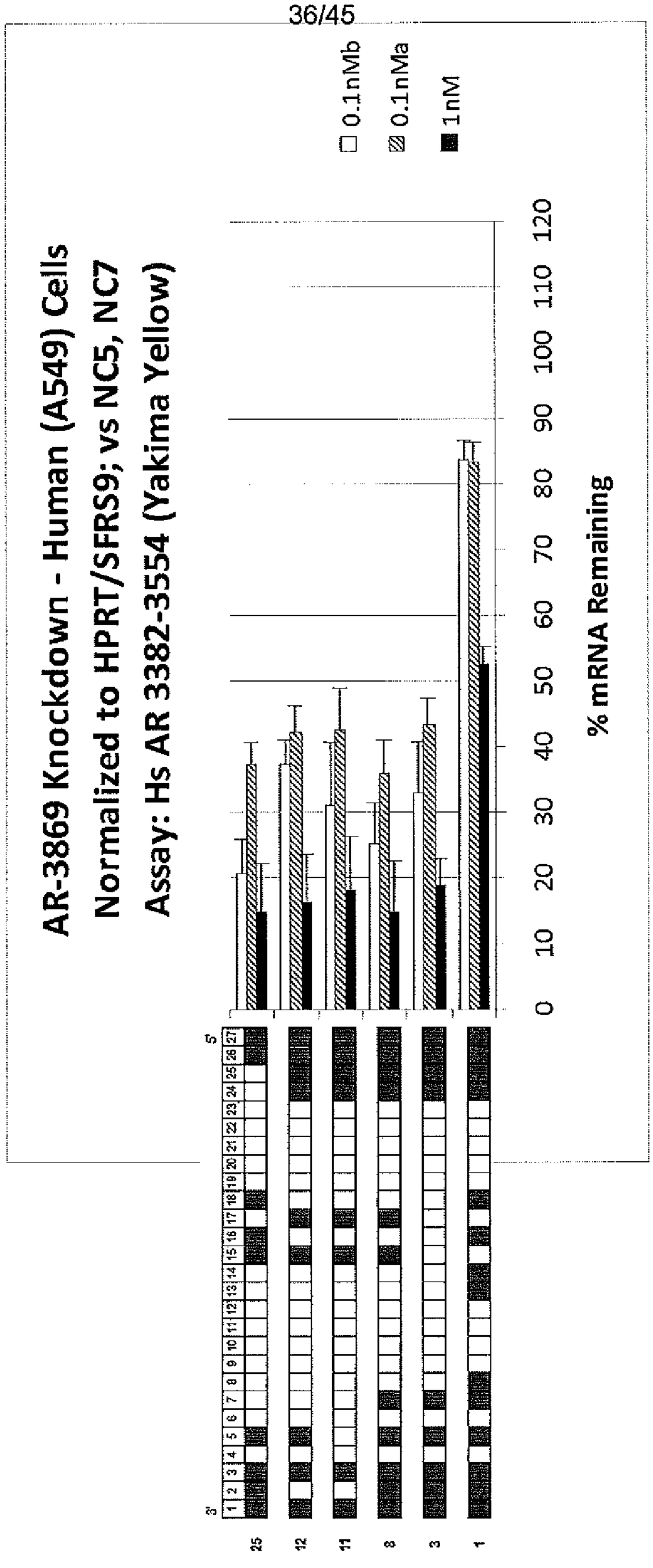

0.1nMb
0.1nMa
1nM
AR-3853 Knockdown - Human (A549) Cells
Normalized to HPRT/SFRS9; vs NC5, NC7
Assay: Hs AR 3382-3554 (Yakima Yellow)
% mRNA Remaining
0
10
20
30
40
50
60
70
80
90
100
110
120
5'
3'
25
12
11
8
3
1

Figure 7-29

Figure 7-30


AR-3869 K9 Knockdown - Human (A549) Cells
Normalized to HPRT/SFRS9; vs NC5, NC7
Assay: Hs AR 3382-3554 (Yakima Yellow)
0.1nMb
0.1nMa
1nM
% mRNA Remaining
0
10
20
30
40
50
60
70
80
90
100
110
120
5'
3'
25
12
11
8
3
1

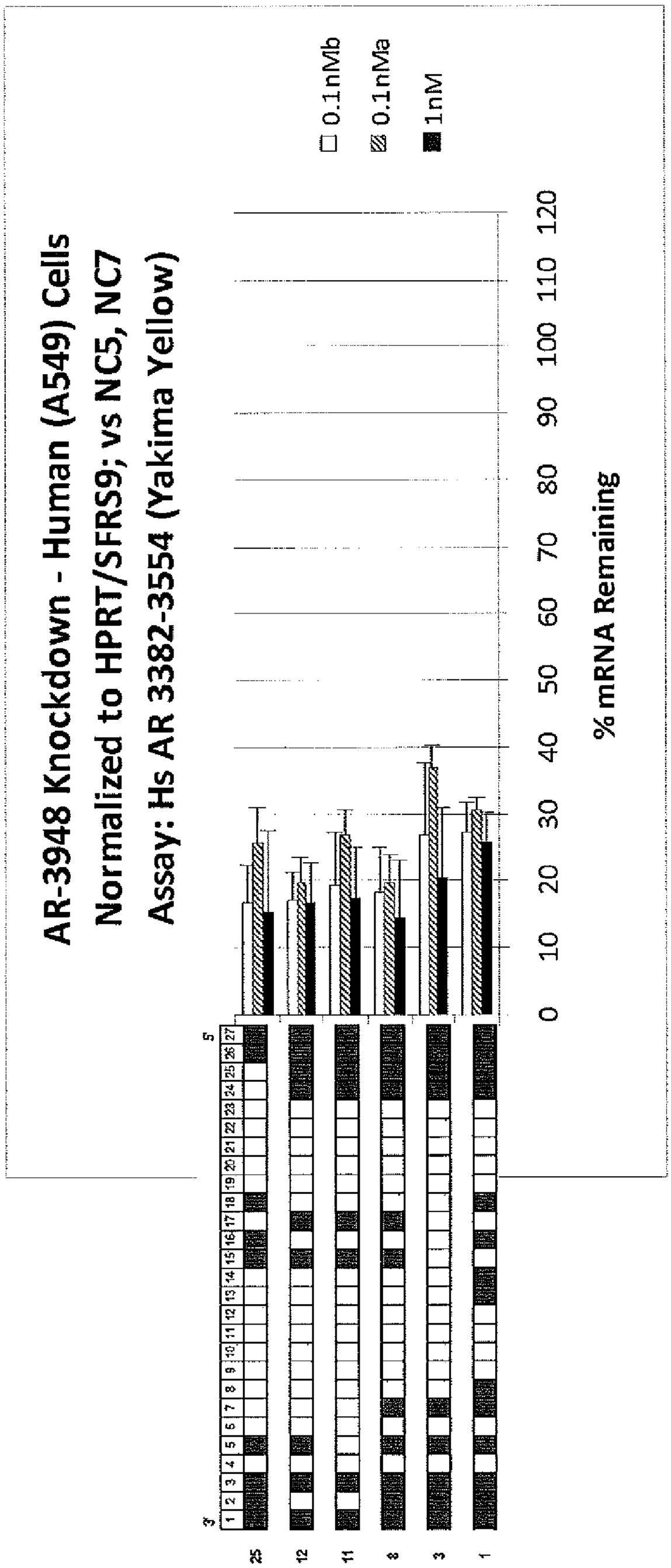

AR-3948 Knockdown - Human (A549) Cells
Normalized to HPRT/SFRS9; vs NC5, NC7
Assay: Hs AR 3382-3554 (Yakima Yellow)
0.1nMb
0.1nMa
1nM
% mRNA Remaining
0 10 20 30 40 50 60 70 80 90 100 110 120
5'
3'
25 12 11 8 3 1

Figure 7-31

Figure 7-32

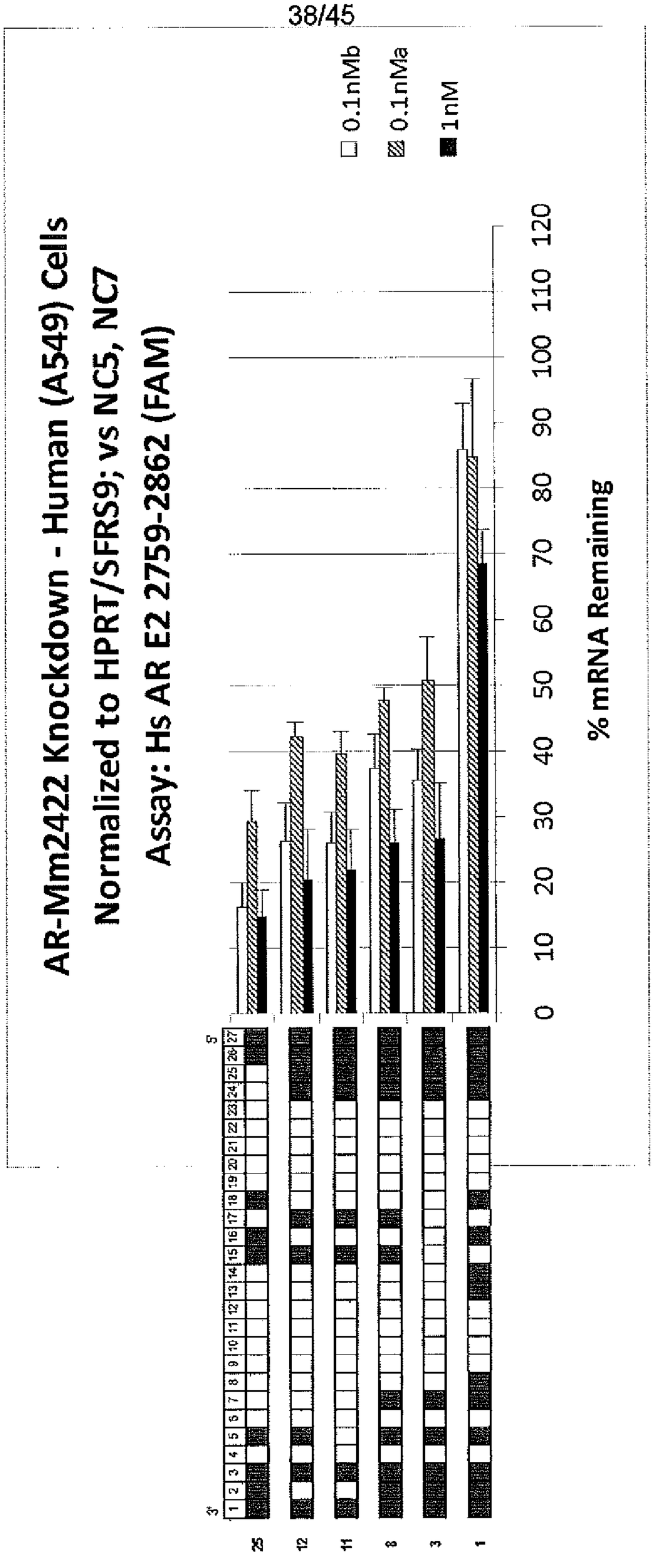

AR-Mm2422 Knockdown - Human (A549) Cells
Normalized to HPRT/SFRS9; vs NC5, NC7
Assay: Hs AR E2 2759-2862 (FAM)
0.1nMb
0.1nMa
1nM
% mRNA Remaining
0 10 20 30 40 50 60 70 80 90 100 110 120
5'
3'
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27
25 12 11 8 3 1

Figure 8

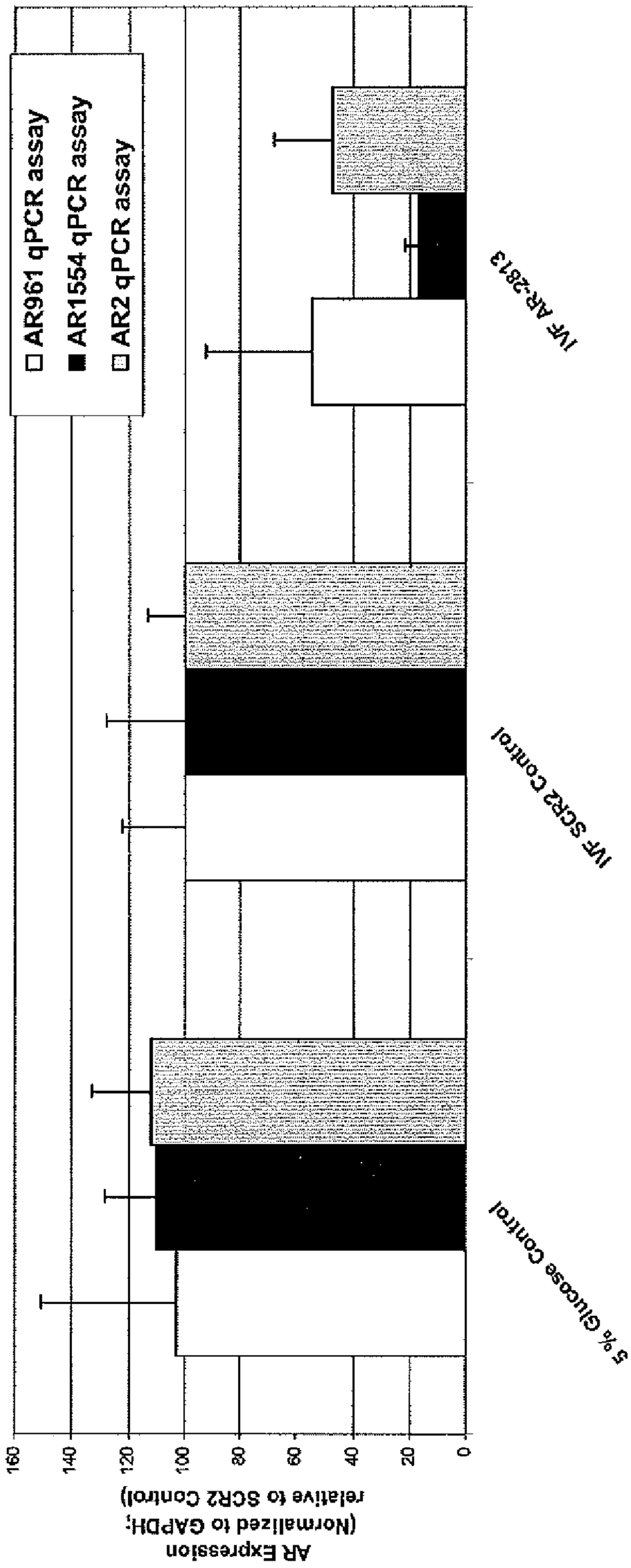
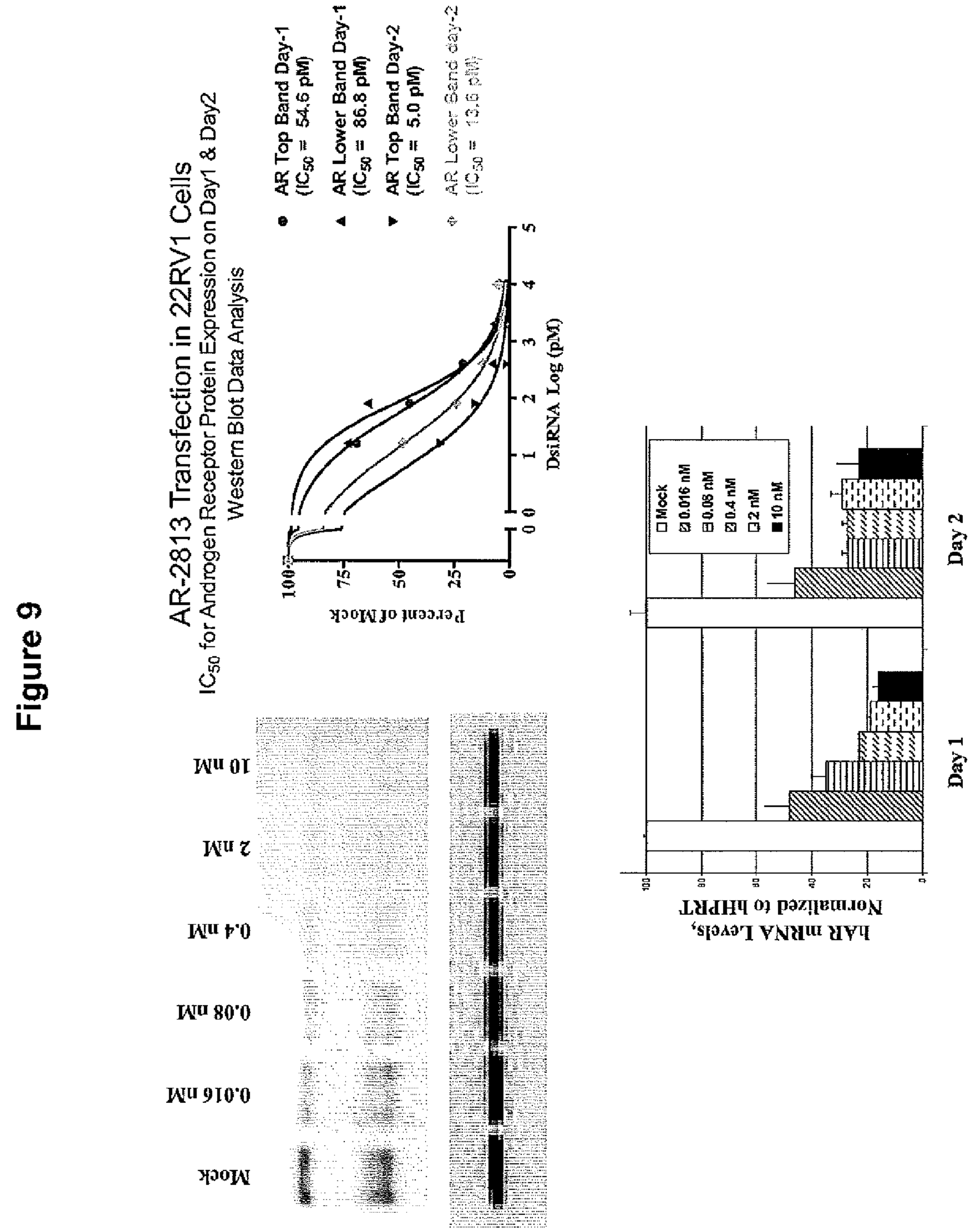

AR961 qPCR assay
AR1554 qPCR assay
AR2 qPCR assay
IVF AR-2813
IVF SCR2 Control
5 % Glucose Control
AR Expression
(Normalized to GAPDH;
relative to SCR2 Control)
160
140
120
100
80
60
40
20
0

Figure 9


AR-2813 Transfection in 22RV1 Cells
IC50 for Androgen Receptor Protein Expression on Day1 & Day2
Western Blot Data Analysis
AR Top Band Day-1 (IC50 = 54.6 pM)
AR Lower Band Day-1 (IC50 = 86.8 pM)
AR Top Band Day-2 (IC50 = 5.0 pM)
AR Lower Band day-2 (IC50 = 13.6 pM)
Percent of Mock
DsiRNA Log (pM)
Mock
0.016 nM
0.08 nM
0.4 nM
2 nM
10 nM
AR (Full length)
AR (Truncated)
α-Tubulin
hAR mRNA Levels, Normalized to hHPRT
Day 1
Day 2

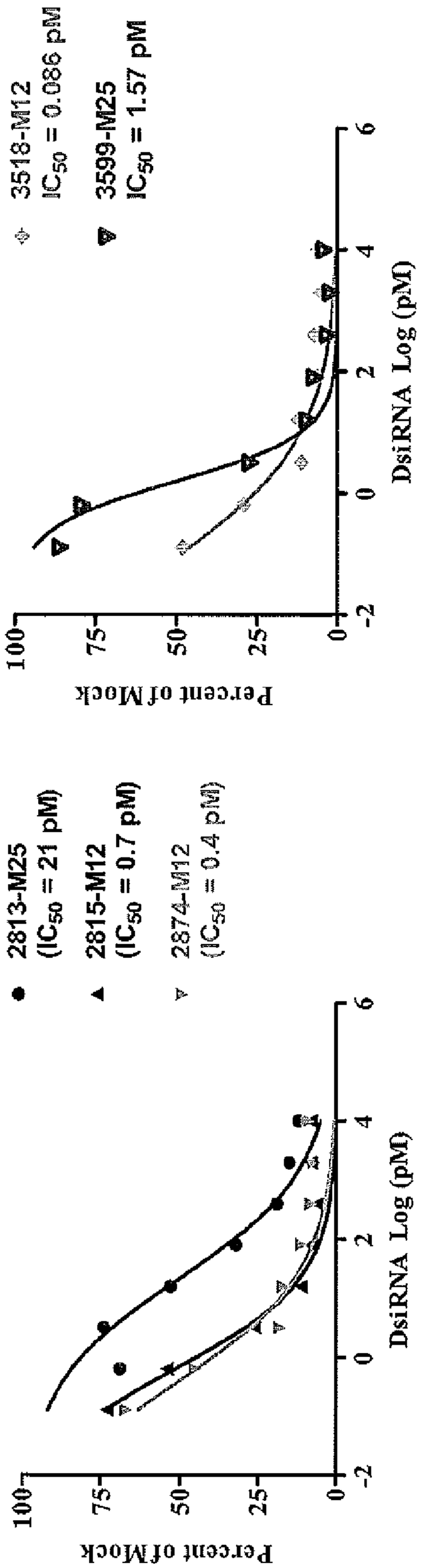

3518-M12
IC50 = 0.086 pM
3599-M25
IC50 = 1.57 pM
Percent of Mock
100
75
50
25
0
-2
0
2
4
6
DsiRNA Log (pM)

Figure 10

2813-M25
(IC50 = 21 pM)
2815-M12
(IC50 = 0.7 pM)
2874-M12
(IC50 = 0.4 pM)
Percent of Mock
100
75
50
25
0
-2
0
2
4
6
DsiRNA Log (pM)

Figure 11

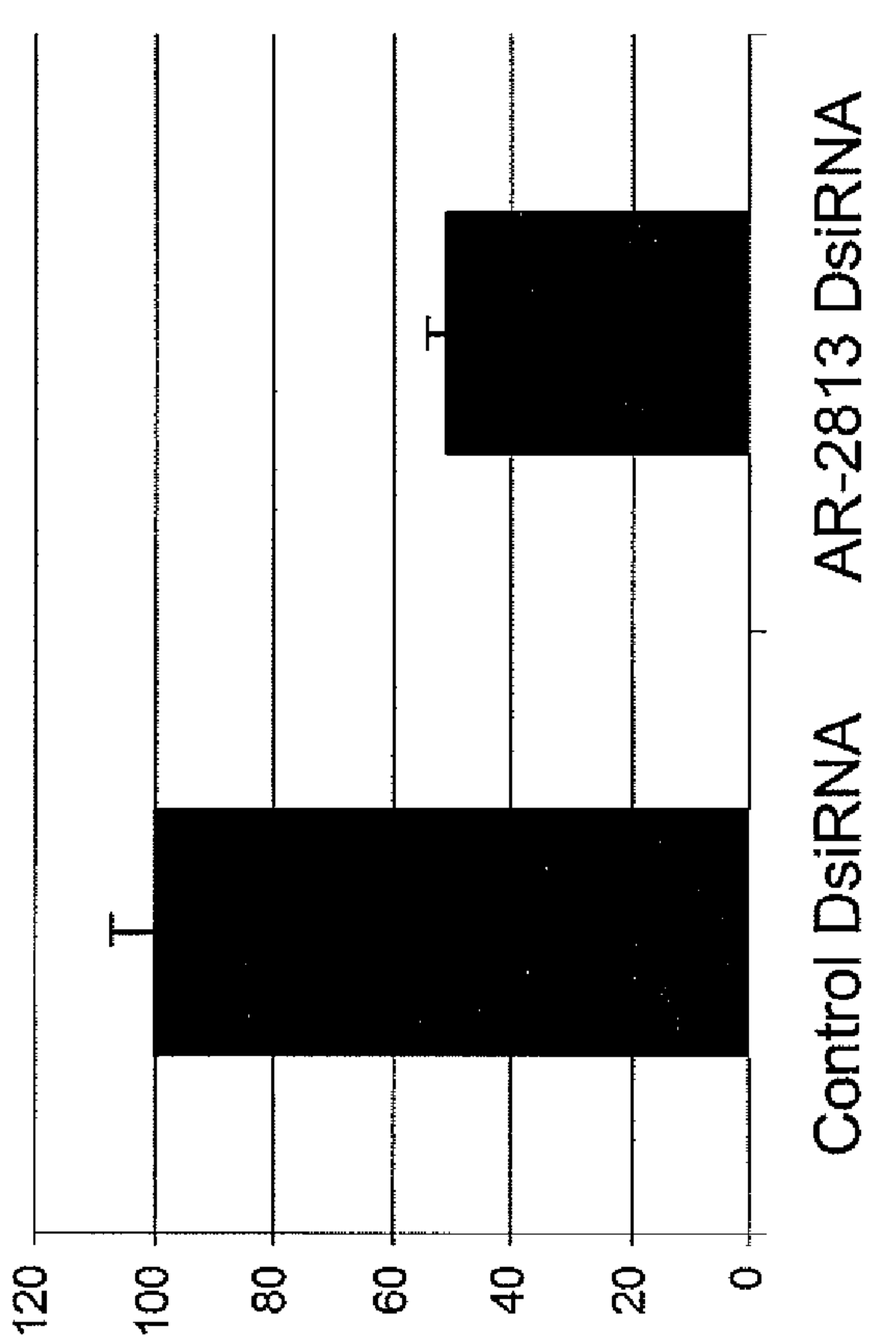
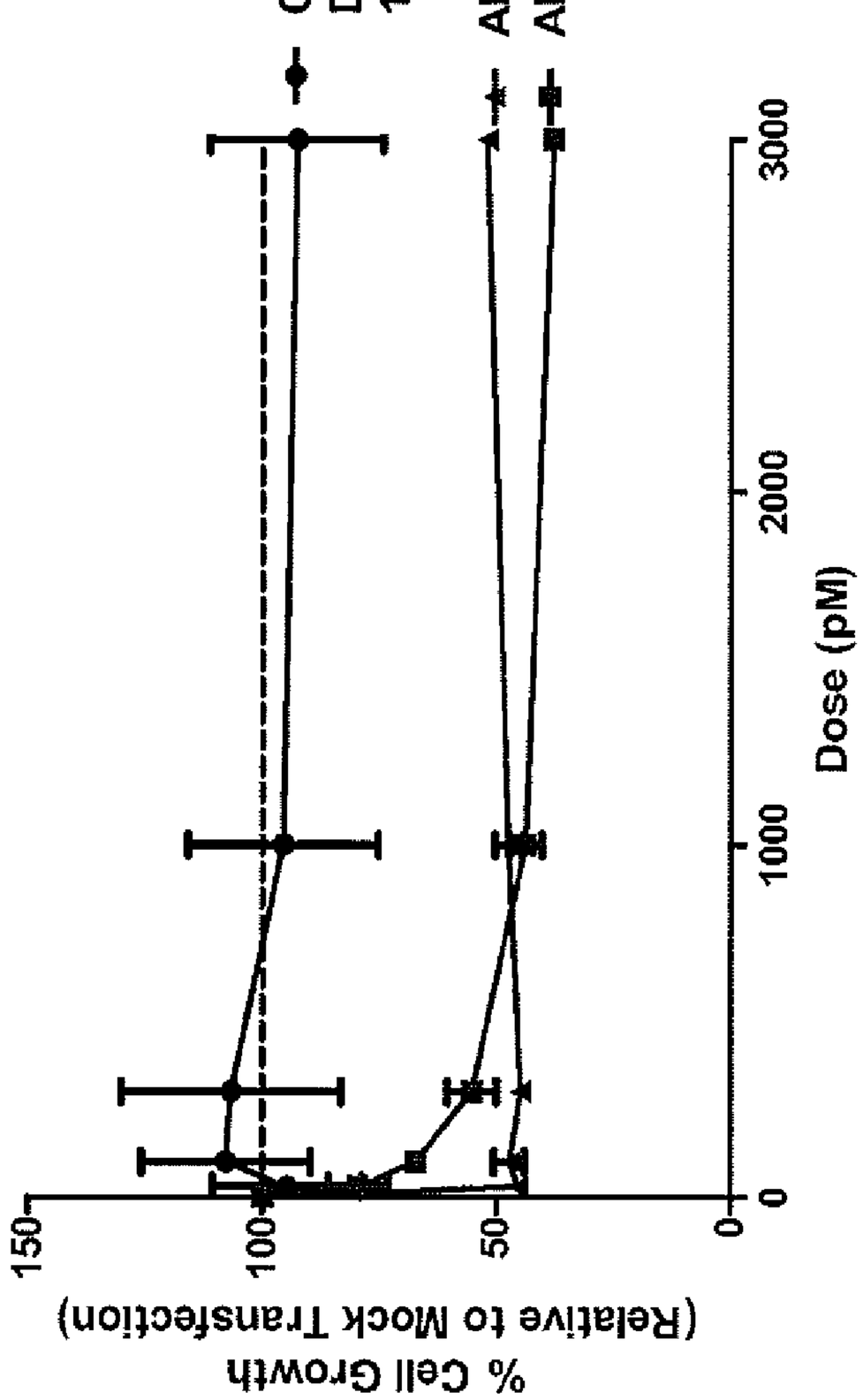

Cell Growth
(Relative to Control)
120
100
80
60
40
20
0
Control DsiRNA
AR-2813 DsiRNA

Figure 12


Control DsiRNAs 114 +121
AR-3599-M25
AR-2813-M25
3000
2000
1000
0
Dose (pM)
150
100
50
0
% Cell Growth
(Relative to Mock Transfection)

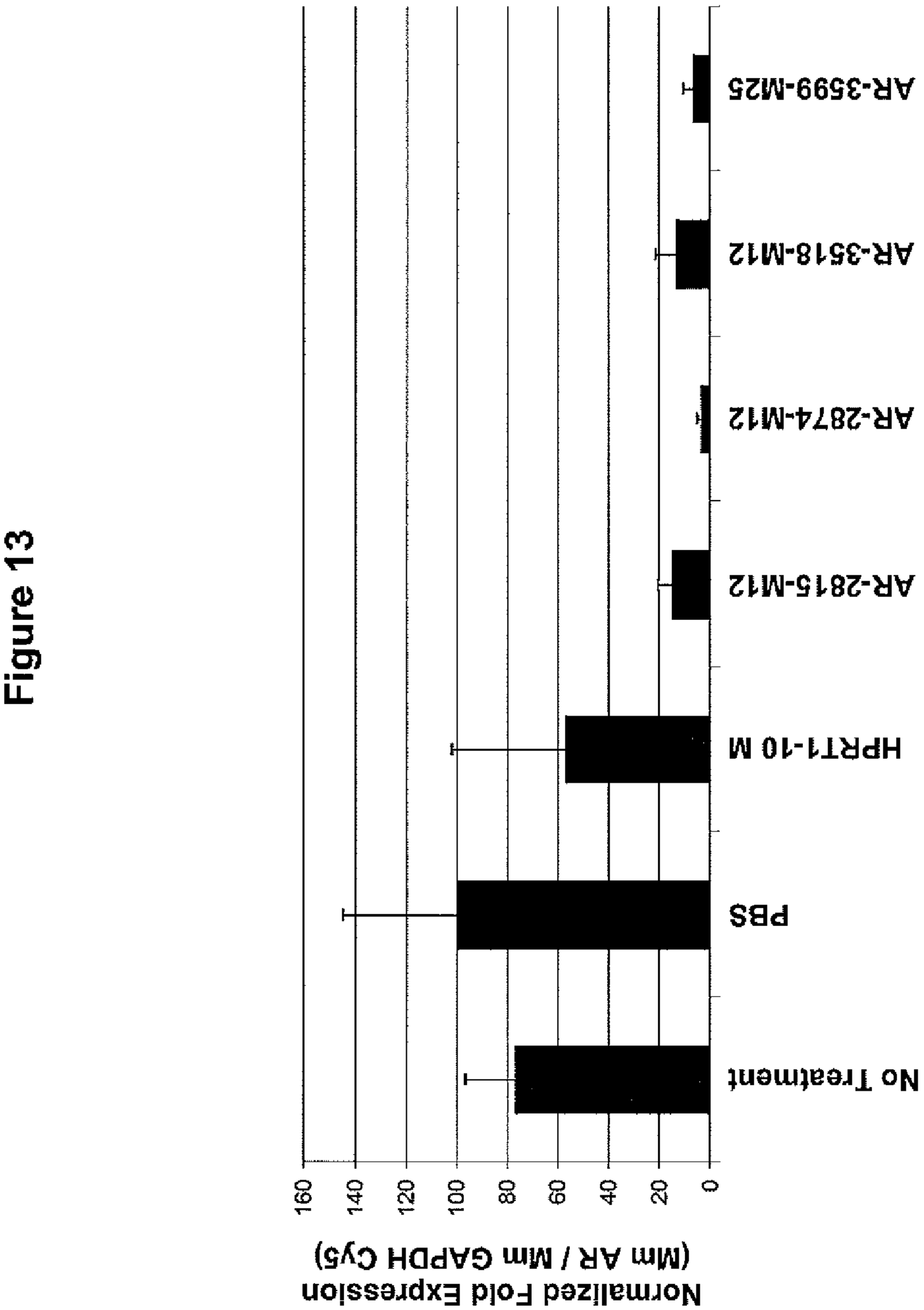

AR-3599-M25
AR-3518-M12
AR-2874-M12
AR-2815-M12
HPRT1-10 M
PBS
No Treatment
160
140
120
100
80
60
40
20
0
(Mm AR / Mm GAPDH Cy5)
Normalized Fold Expression

Figure 13

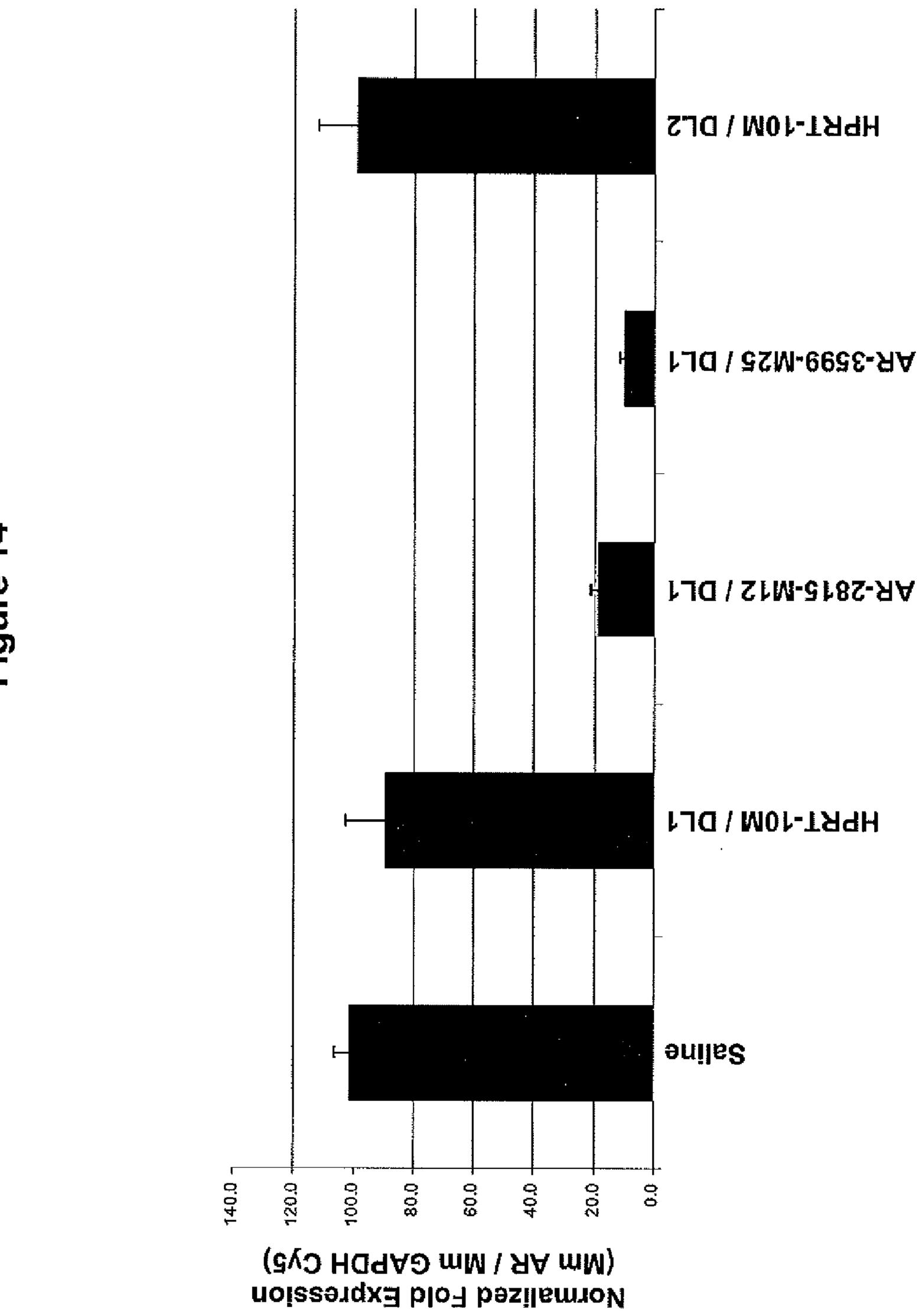

Normalized Fold Expression
(Mm AR / Mm GAPDH Cy5)
0
20
40
60
80
100
120
140
Saline
HPRT-10M / DL1
AR-2815-M12 / DL1
AR-3599-M25 / DL1
HPRT-10M / DL2

Figure 14

Figure 1

Ago2 cleavage sites
aligned
1
9
DsiRNA 25/27mer
5′-GAAAAAGAUAAUAACUCAGUUCUta-3′
3′-UUCUUUUUCUAUUAUUGAGUCAAGAAU-5′
SEQ ID NO: 24
SEQ ID NO: 177
siRNA 21mer
5′-GAAAAAGAUAAUAACUCAGUU-3′
3′-UUCUUUUUCUAUUAUUGAGUC-5′
1
SEQ ID NO: 5230
SEQ ID NO: 5231
DsiRNA 27/27
Blunt/Blunt
5′-AAGAAAAAAGAUAAUAACUCAGUUCUUA-3′
3′-UUCUUUUUCUAUUAUUGAGUCAAGAAU-5′
SEQ ID NO: 4530
SEQ ID NO: 177
siRNA 21mer
Blunt-Blunt
5′-AAGAAAAAAGAUAAUAACUCAG-3′
3′-UUCUUUUUCUAUUAUUGAGUC-5′
SEQ ID NO: 5232
SEQ ID NO: 5231
DsiRNA 27/27
Blunt/Fray-R
5′-AAGAAAAAAGAUAAUAACUCAGUUCUCC-3′
3′-UUCUUUUUCUAUUAUUGAGUCAAGAAU-5′
SEQ ID NO: 3807
SEQ ID NO: 177
siRNA 21mer
Blunt/Fray-R
5′-AAGAAAAAAGAUAAUAACUCCA-3′
3′-UUCUUUUUCUAUUAUUGAGUC-5′
SEQ ID NO: 5233
SEQ ID NO: 5231