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(54) Title: METHODS OF MODULATING THE SEX OF AVIANS

(57) Abrégé/Abstract:
The present invention relates to nucleic acids and methods for modulating the sex of avians. In particular, the invention relates to the in ovo delivery of a dsRNA molecule, especially siRNAs, to increase the production of female birds.

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(54) **Title**: METHODS OF MODULATING THE SEX OF AVIANS

(57) **Abstract**: The present invention relates to nucleic acids and methods for modulating the sex of avians. In particular, the invention relates to the *in ovo* delivery of a dsRNA molecule, especially siRNAs, to increase the production of female birds.

METHODS OF MODULATING THE SEX OF AVIANS

FIELD OF THE INVENTION

The present invention relates to nucleic acids and methods for modulating the sex of avians. In particular, the invention relates to the *in ovo* delivery of a dsRNA molecule, especially siRNAs, to increase the production of female birds.

BACKGROUND OF THE INVENTION

Man has modified the phenotypic characteristics of domestic animals through selection of seed stock over many generations ever since animals were domesticated. This has led to improvements in quantitative production parameters such as body size and muscle mass. More recent innovations of modifying production traits of poultry and/or improving resistance to pathogens has focussed on transgenic approaches, however, many consumers have concerns about genetically modified organisms.

Chicken producers have been searching for an efficient, economical method of determining the sex of day old chicks. Vent sexing and feather sexing have been used by the various producers, but these methods have been found to have substantial economic disadvantages because of the substantial time required and labour costs in separating the male from the female chicks. The use of probes (US 5,508,165) is also an expensive procedure and not practical economically. Light sensing of anal areas of chicks (US 4,417,663) is another way of determining sex of chicks, but it is also expensive and time consuming as each chick must be handled and manipulated. The use of experts who could feather sex the chicks has been used, but such experts are costly and feathering is time consuming.

There is a need for nucleic acids and methods for modifying avian sex that do not result in transformation of the bird's genome, but are amenable to high throughout processing.

SUMMARY OF THE INVENTION

The present inventors have identified nucleic acid molecules, in particular dsRNA molecules, which can be used to modify the sex of avians *in ovo*.

Accordingly, in one aspect the present invention provides an isolated and/or exogenous nucleic acid molecule comprising a double-stranded region which reduces the level of at least one RNA molecule and/or protein when administered to an avian egg, wherein if the embryo of the egg is male the sex is altered to female following administration of the isolated and/or exogenous nucleic acid molecule, and wherein the

isolated and/or exogenous nucleic acid molecule does not comprise a sequence selected from:
CCAGUUGUCAAGAAGAGCA (SEQ ID NO:254)
GGAUGCUCAUUCAGGACAU (SEQ ID NO:369)
CCCUGUAUCCUUACUAUAA (SEQ ID NO:474)
GCCACUGAGUCUUCCUCAA (SEQ ID NO:530)
CCAGCAACAUACAUGUCAA (SEQ ID NO:605)
CCUGCGUCACACAGAUACU (SEQ ID NO:747)
GGAGUAGUUGUACAGGUUG (SEQ ID NO:3432)
GACUGGCUUGACAUGUAUG (SEQ ID NO:3433)
AUGGCGGUUCUCCAUCCCU (SEQ ID NO:3434) or a variant of any one thereof.

In another aspect, the present invention provides an isolated and/or exogenous nucleic acid molecule comprising one or more of the sequence of nucleotides provided as SEQ ID NO's 11 to 3431 or a variant of any one or more thereof, wherein the isolated and/or exogenous nucleic acid molecule does not comprise a sequence selected from:
CCAGUUGUCAAGAAGAGCA (SEQ ID NO:254)
GGAUGCUCAUUCAGGACAU (SEQ ID NO:369)
CCCUGUAUCCUUACUAUAA (SEQ ID NO:474)
GCCACUGAGUCUUCCUCAA (SEQ ID NO:530)
CCAGCAACAUACAUGUCAA (SEQ ID NO:605)
CCUGCGUCACACAGAUACU (SEQ ID NO:747)
GGAGUAGUUGUACAGGUUG (SEQ ID NO:3432)
GACUGGCUUGACAUGUAUG (SEQ ID NO:3433)
AUGGCGGUUCUCCAUCCCU (SEQ ID NO:3434) or a variant of any one thereof.

In a preferred embodiment, the nucleic acid molecule is dsRNA. More preferably, the dsRNA is a siRNA or a shRNA.

In a preferred embodiment, the nucleic acid molecule reduces the level of a protein encoded by a DMRT1 gene, ASW gene or r-spondin gene, in an avian egg.

In a preferred embodiment of the two above aspects, the nucleic acid does not comprise the full length open reading frame of the RNA molecule or the cDNA encoding therefor. In a related embodiment, preferably the nucleic acid does not comprise a sequence of nucleotides provided as SEQ ID NO's 2, 4 or 6, or a sequence of nucleotides provided as SEQ ID NO's 2, 4 or 6 where each T (thymine) is replaced with a U (uracil).

As the skilled addressee will appreciate, because the nucleic acid is double stranded it will also comprise the corresponding reverse complement of the relevant nucleotide sequence provided herewith.

Also provided is a vector encoding a nucleic acid molecule, or a single strand thereof, according to the invention. Such vectors can be used in a host cell or cell-free expression system to produce nucleic acid molecules useful for the method of the invention.

In another aspect, the present invention provides a host cell comprising an exogenous nucleic acid molecule, or a single strand thereof, of the invention and/or a vector of the invention.

In another aspect, the present invention provides a composition comprising a nucleic acid molecule, or a single strand thereof, of the invention, a vector of the invention, and/or a host cell of the invention.

In a further aspect, the present invention provides a method of modifying the sex of an avian, the method comprising administering to an avian egg at least one nucleic acid molecule of the invention.

Preferably, the nucleic acid is administered to a non-cellular site of the egg. More preferably, the non-cellular site is the air sac, yolk sac, amnionic cavity or chorion allantoic fluid.

In a further preferred embodiment, the egg is not electroporated.

Preferably, the nucleic acid is not delivered by administering a vector encoding the nucleic acid molecule.

Preferably, the nucleic acid molecule administered is dsRNA.

Preferably, the nucleic acid molecule is administered by injection.

Conveniently, the nucleic acid may be administered in a composition of the invention.

In a preferred embodiment, the method modifies the sex of the embryo of the egg from male to female.

The avian can be any species of the Class *Aves*. Examples include, but are not limited to, chickens, ducks, turkeys, geese, bantams and quails. In a particularly preferred embodiment, the avian is a chicken.

In a further aspect, the present invention provides an avian produced using a method of the invention.

In another aspect, the present invention provides a chicken produced using a method of the invention.

In a further aspect, the present invention provides an avian egg comprising a nucleic acid molecule, or a single strand thereof, of the invention, a vector of the invention, and/or a host cell of the invention.

In another aspect, the present invention provides a kit comprising a nucleic acid molecule, or a single strand thereof, of the invention, a vector of the invention, a host cell of the invention, and/or a composition of the invention.

As will be apparent, preferred features and characteristics of one aspect of the invention are applicable to many other aspects of the invention.

Throughout this specification the word "comprise", or variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated element, integer or step, or group of elements, integers or steps, but not the exclusion of any other element, integer or step, or group of elements, integers or steps.

The invention is hereinafter described by way of the following non-limiting Examples and with reference to the accompanying figures.

BRIEF DESCRIPTION OF THE ACCOMPANYING DRAWINGS

Figure 1 - Selected shRNAs for knockdown of EGFP-Dmrt1 gene fusion expression. Mean fluorescence intensity for each transfection condition expressed relative to pEGFP-Dmrt1. Error bars indicate standard error calculated on each individual experiment completed in triplicate.

Figure 2 – qPCR analysis of DMRT1 gene expression following silencing.

KEY TO THE SEQUENCE LISTING

SEQ ID NO:1 - Partial chicken DMRT1 protein sequence (Genbank AF123456).

SEQ ID NO:2 - Partial nucleotide sequence encoding chicken DMRT1 (Genbank AF123456).

SEQ ID NO:3 - Chicken WPKCI (ASW) (Genbank AF148455).

SEQ ID NO:4 - Nucleotide sequence encoding chicken WPKCI (ASW) (Genbank AF148455).

SEQ ID NO:5 - Chicken r-spondin (Genbank XM_417760).

SEQ ID NO:6 - Nucleotide sequence encoding chicken r-spondin (Genbank XM_417760).

SEQ ID NO:7 - Nucleotide sequence of chicken U6-1 promoter.

SEQ ID NO:8 - Nucleotide sequence of chicken U6-3 promoter.

SEQ ID NO:9 - Nucleotide sequence of chicken U6-4 promoter.

SEQ ID NO:10 - Nucleotide sequence of chicken 7SK promoter.
SEQ ID NO's 11 to 3430 – RNA sequences provided in Tables 1 to 3 for silencing the chicken DMRT1, ASW or r-spondin genes.
SEQ ID NO's 3431 to 3434 - RNA sequences suitable for silencing the chicken DMRT1 gene.
SEQ ID NO's 3435 to 3485 – Target regions of chicken DMRT1.
SEQ ID NO's 3486 to 3499 – Oligonucleotide primers and probes.

DETAILED DESCRIPTION OF THE INVENTION

General Techniques and Definitions

Unless specifically defined otherwise, all technical and scientific terms used herein shall be taken to have the same meaning as commonly understood by one of ordinary skill in the art (e.g., in cell culture, molecular genetics, avian biology, RNA interference, and biochemistry).

Unless otherwise indicated, the recombinant protein, cell culture, and immunological techniques utilized in the present invention are standard procedures, well known to those skilled in the art. Such techniques are described and explained throughout the literature in sources such as, J. Perbal, A Practical Guide to Molecular Cloning, John Wiley and Sons (1984), J. Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbour Laboratory Press (1989), T.A. Brown (editor), Essential Molecular Biology: A Practical Approach, Volumes 1 and 2, IRL Press (1991), D.M. Glover and B.D. Hames (editors), DNA Cloning: A Practical Approach, Volumes 1-4, IRL Press (1995 and 1996), and F.M. Ausubel et al. (editors), Current Protocols in Molecular Biology, Greene Pub. Associates and Wiley-Interscience (1988, including all updates until present), Ed Harlow and David Lane (editors).

The term "avian" as used herein refers to any species, subspecies or race of organism of the taxonomic Class *Aves*, such as, but not limited to, such organisms as chicken, turkey, duck, goose, quail, pheasants, parrots, finches, hawks, crows and ratites including ostrich, emu and cassowary. The term includes the various known strains of *Gallus gallus* (chickens), for example, White Leghorn, Brown Leghorn, Barred-Rock, Sussex, New Hampshire, Rhode Island, Australorp, Cornish, Minorca, Amrox, California Gray, Italian Partidge-coloured, as well as strains of turkeys, pheasants, quails, duck, ostriches and other poultry commonly bred in commercial quantities.

As used herein, the term "egg" refers to a fertilized ovum that has been laid by a bird. Typically, avian eggs consist of a hard, oval outer eggshell, the "egg white" or albumen, the egg yolk, and various thin membranes. Furthermore, "*in ovo*" refers to in an egg.

As used herein, the term "non-cellular site" refers a part of the egg other than the embryo.

The terms "reduces", "reduction" or variations thereof as used herein refers to a measurable decrease in the amount of a target RNA and/or target protein in the egg when compared to an egg from the same species of avian, more preferably strain or breed of avian, and even more preferably the same bird, that has not been administered with a nucleic acid as defined herein. The term also refers to a measurable reduction in the activity of a target protein. Preferably a reduction in the level of a target RNA and/or target protein is at least about 10%. More preferably, the reduction is at least about 20%, 30%, 40%, 50%, 60%, 80%, 90% and even more preferably, about 100%.

As used herein, the phrase "the nucleic acid molecule results in a reduction" or variations thereof refers to the presence of the nucleic acid molecule in the egg inducing degradation of homologous RNAs in the egg by the process known in the art as "RNA interference" or "gene silencing". Furthermore, the nucleic acid molecule directly results in the reduction, and is not transcribed *in ovo* to produce the desired effect.

The "at least one RNA molecule" can be any type of RNA present in, and/or produced by, an avian egg. Examples include, but are not limited to, mRNA, snRNA, microRNA and tRNA.

A "variant" of a nucleic acid molecule of the invention includes molecules of varying sizes of, and/or with one or more different nucleotides, but which are still capable of being used to silence the target gene. For example, variants may comprise additional nucleotides (such as 1, 2, 3, 4, or more), or less nucleotides. Furthermore, a few nucleotides may be substituted without influencing the ability of the nucleic acid to silence the target gene. In an embodiment, the variant includes additional 5' and/or 3' nucleotides which are homologous to the corresponding target RNA molecule and/or which enhance the stability of the nucleic acid molecule. In another embodiment, the nucleic acid molecules have no more than 4, more preferably no more than 3, more preferably no more than 2, and even more preferably no more than 1, nucleotide differences when compared to the sequences provided herein. In a further embodiment, the nucleic acid molecules have no more than 2, and more preferably no more than 1, internal additional and/or deletional nucleotides when compared to the sequences

provided herein. In an embodiment, a nucleic acid of the invention has one, preferably two, additional non-target nucleotides at the 5' and/or 3' end, for example an additional UU at the 3'end. Such additions can increase the half-life of the molecule *in ovo*.

By an "isolated nucleic acid molecule", we mean a nucleic acid molecule which is at least partially separated from the nucleic acid molecule with which it is associated or linked in its native state. Preferably, the isolated nucleic acid molecule is at least 60% free, preferably at least 75% free, and most preferably at least 90% free from other components with which they are naturally associated. Furthermore, the term "polynucleotide" is used interchangeably herein with the term "nucleic acid".

The term "exogenous" in the context of a nucleic acid molecule refers to the nucleic acid molecule when present in a cell, or in a cell-free expression system, in an altered amount. Preferably, the cell is a cell that does not naturally comprise the nucleic acid molecule. However, the cell may be a cell which comprises an exogenous nucleic acid molecule resulting in an increased amount of the nucleic acid molecule. An exogenous nucleic acid molecule of the invention includes nucleic acid molecules which have not been separated from other components of the recombinant cell, or cell-free expression system, in which it is present, and nucleic acid molecules produced in such cells or cell-free systems which are subsequently purified away from at least some other components.

Sex Determination

The present invention relates to the modulation of the sex of avians *in ovo*. Examples of genes which can be targeted to modulate avian sex include, but are not necessarily limited to, the DMRT1 gene, the ASW (WPKCI) gene, the R-spondin gene, the Fox9 gene and the β-catenin gene.

In a preferred embodiment, the nucleic acid molecule reduces the level of a protein encoded by a DMRT1 gene. DMRT1 was the first molecule implicated in sex determination that shows sequence conservation between phyla. The avian homologue of DMRT1 is found on the Z (sex) chromosome of chickens and is differentially expressed in the genital ridges of male and female chicken embryos (Raymond et al., 1999; Smith et al., 1999). DMRT1 is one of the few genes thus far implicated in mammalian sex determination that appears to have a strictly gonadal pattern of expression (Raymond et al., 1999).

Examples of nucleic acid molecules that can be used to reduce the level of chicken DMRT1 protein, and mRNA encoding therefor, include, but are not limited to, nucleic acids comprising one or more of the sequence of nucleotides provided in Table

1 (SEQ ID NO's 11 to 1644), or a variant of any one or more thereof, with the exception that the nucleic acid molecule does not comprise a sequence selected from:
CCAGUUGUCAAGAAGAGCA (SEQ ID NO:254)
GGAUGCUCAUUCAGGACAU (SEQ ID NO:369)
CCCUGUAUCCUUACUAUAA (SEQ ID NO:474)
GCCACUGAGUCUUCCUCAA (SEQ ID NO:530)
CCAGCAACAUACAUGUCAA (SEQ ID NO:605)
CCUGCGUCACACAGAUACU (SEQ ID NO:747)
GGAGUAGUUGUACAGGUUG (SEQ ID NO:3432) (reverse complement of SEQ ID NO:493)
GACUGGCUUGACAUGUAUG (SEQ ID NO:3433) (reverse complement of SEQ ID NO:612)
AUGGCGGUUCUCCAUCCCU (SEQ ID NO:3434) (reverse complement of SEQ ID NO:1520), or a variant of any one thereof.

In a particularly preferred embodiment, the nucleic acid molecule that can be used to reduce the level of chicken DMRT1 protein comprises a sequence selected from; GAGCCAGUUGUCAAGAAGA (SEQ ID NO:251), GACUGCCAGUGCAAGAAGU (SEQ ID NO:116), CUGUAUCCUUACUAUAACA (SEQ ID NO:476), and CUCCCAGCAACAUACAUGU (SEQ ID NO:602), or a variant of any one thereof. More preferably, the nucleic acid molecule that can be used to reduce the level of chicken DMRT1 protein comprises the sequence, GAGCCAGUUGUCAAGAAGA (SEQ ID NO:251), or a variant thereof such as GAGCCAGUUGUCAAGAAGAUU (SEQ ID NO:3431).

A further example of a gene that can be targeted to modify sex is the WPKCI gene. The avian gene WPKCI has been shown to be conserved widely on the avian W chromosome and expressed actively in the female chicken embryo before the onset of gonadal differentiation. It is suggested that WPKCI may play a role in the differentiation of the female gonad by interfering with the function of PKCI or by exhibiting its unique function in the nucleus (Hori et al., 2000). This gene has also been identified as ASW (avian sex-specific W-linked) (O'Neill et al., 2000).

Examples of nucleic acid molecules that can be used to reduce the level of chicken ASW (WPKCI) protein, and mRNA encoding therefor, include, but are not limited to, nucleic acids comprising one or more of the sequence of nucleotides provided in Table 2 (SEQ ID NO's 1645 to 2209), or a variant of any one or more thereof.

In yet another example of a gene that can be targeted to modify sex is the r-spondin gene. Examples of nucleic acid molecules that can be used to reduce the level of chicken r-spondin protein, and mRNA encoding therefor, include, but are not limited to, nucleic acids comprising one or more of the sequence of nucleotides provided in Table 3 (SEQ ID NO's 2210 to 3430), or a variant of any one or more thereof.

Gene Silencing

The terms "RNA interference", "RNAi" or "gene silencing" refers generally to a process in which a double-stranded RNA (dsRNA) molecule reduces the expression of a nucleic acid sequence with which the double-stranded RNA molecule shares substantial or total homology. However, it has more recently been shown that gene silencing can be achieved using non-RNA double stranded molecules (see, for example, US 20070004667).

RNA interference (RNAi) is particularly useful for specifically inhibiting the production of a particular RNA and/or protein. Although not wishing to be limited by theory, Waterhouse et al. (1998) have provided a model for the mechanism by which dsRNA (duplex RNA) can be used to reduce protein production. This technology relies on the presence of dsRNA molecules that contain a sequence that is essentially identical to the mRNA of the gene of interest or part thereof, in this case an mRNA encoding a polypeptide of interest. Conveniently, the dsRNA can be produced from a single promoter in a recombinant vector or host cell, where the sense and anti-sense sequences are flanked by an unrelated sequence which enables the sense and anti-sense sequences to hybridize to form the dsRNA molecule with the unrelated sequence forming a loop structure. The design and production of suitable dsRNA molecules for the present invention is well within the capacity of a person skilled in the art, particularly considering Waterhouse et al. (1998), Smith et al. (2000), WO 99/32619, WO 99/53050, WO 99/49029 and WO 01/34815.

The present invention includes nucleic acid molecules comprising and/or encoding double-stranded regions for gene silencing. The nucleic acid molecules are typically RNA but may comprise DNA, chemically-modified nucleotides and non-nucleotides.

Table 1. DsRNA molecules targeting mRNA encoding chicken DMRT1.

SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'
11	CCGGCGGCGGGCAAGAAGC	41	CCCAAGUGUGCCCGCUGCC	71	UACUCCUCGCCGCUGAAGG
12	CGGCGGCGGGCAAGAAGCU	42	CCAAGUGUGCCCGCUGCCG	72	ACUCCUCGCCGCUGAAGGG
13	GGCGGCGGGCAAGAAGCUG	43	CAAGUGUGCCCGCUGCCGC	73	CUCCUCGCCGCUGAAGGGG
14	GCGGCGGGCAAGAAGCUGC	44	AAGUGUGCCCGCUGCCGCA	74	UCCUCGCCGCUGAAGGGGC
15	CGGCGGGCAAGAAGCUGCC	45	AGUGUGCCCGCUGCCGCAA	75	CCUCGCCGCUGAAGGGGCA
16	GGCGGGCAAGAAGCUGCCG	46	GUGUGCCCGCUGCCGCAAC	76	CUCGCCGCUGAAGGGGCAC
17	GCGGGCAAGAAGCUGCCGC	47	UGUGCCCGCUGCCGCAACC	77	UCGCCGCUGAAGGGGCACA
18	CGGGCAAGAAGCUGCCGCG	48	GUGCCCGCUGCCGCAACCA	78	CGCCGCUGAAGGGGCACAA
19	GGGCAAGAAGCUGCCGCGU	49	UGCCCGCUGCCGCAACCAC	79	GCCGCUGAAGGGGCACAAG
20	GGCAAGAAGCUGCCGCGUC	50	GCCCGCUGCCGCAACCACG	80	CCGCUGAAGGGGCACAAGC
21	GCAAGAAGCUGCCGCGUCU	51	CCCGCUGCCGCAACCACGG	81	CGCUGAAGGGGCACAAGCG
22	CAAGAAGCUGCCGCGUCUG	52	CCGCUGCCGCAACCACGGC	82	GCUGAAGGGGCACAAGCGG
23	AAGAAGCUGCCGCGUCUGC	53	CGCUGCCGCAACCACGGCU	83	CUGAAGGGGCACAAGCGGU
24	AGAAGCUGCCGCGUCUGCC	54	GCUGCCGCAACCACGGCUA	84	UGAAGGGGCACAAGCGGUU
25	GAAGCUGCCGCGUCUGCCC	55	CUGCCGCAACCACGGCUAC	85	GAAGGGGCACAAGCGGUUC
26	AAGCUGCCGCGUCUGCCCA	56	UGCCGCAACCACGGCUACU	86	AAGGGGCACAAGCGGUUCU
27	AGCUGCCGCGUCUGCCCAA	57	GCCGCAACCACGGCUACUC	87	AGGGGCACAAGCGGUUCUG
28	GCUGCCGCGUCUGCCCAAG	58	CCGCAACCACGGCUACUCC	88	GGGGCACAAGCGGUUCUGC
29	CUGCCGCGUCUGCCCAAGU	59	CGCAACCACGGCUACUCCU	89	GGGCACAAGCGGUUCUGCA
30	UGCCGCGUCUGCCCAAGUG	60	GCAACCACGGCUACUCCUC	90	GGCACAAGCGGUUCUGCAU
31	GCCGCGUCUGCCCAAGUGU	61	CAACCACGGCUACUCCUCG	91	GCACAAGCGGUUCUGCAUG
32	CCGCGUCUGCCCAAGUGUG	62	AACCACGGCUACUCCUCGC	92	CACAAGCGGUUCUGCAUGU
33	CGCGUCUGCCCAAGUGUGC	63	ACCACGGCUACUCCUCGCC	93	ACAAGCGGUUCUGCAUGUG
34	GCGUCUGCCCAAGUGUGCC	64	CCACGGCUACUCCUCGCCG	94	CAAGCGGUUCUGCAUGUGG
35	CGUCUGCCCAAGUGUGCCC	65	CACGGCUACUCCUCGCCGC	95	AAGCGGUUCUGCAUGUGGC
36	GUCUGCCCAAGUGUGCCCG	66	ACGGCUACUCCUCGCCGCU	96	AGCGGUUCUGCAUGUGGCG
37	UCUGCCCAAGUGUGCCCGC	67	CGGCUACUCCUCGCCGCUG	97	GCGGUUCUGCAUGUGGCGG
38	CUGCCCAAGUGUGCCCGCU	68	GGCUACUCCUCGCCGCUGA	98	CGGUUCUGCAUGUGGCGGG
39	UGCCCAAGUGUGCCCGCUG	69	GCUACUCCUCGCCGCUGAA	99	GGUUCUGCAUGUGGCGGGA
40	GCCCAAGUGUGCCCGCUGC	70	CUACUCCUCGCCGCUGAAG	100	GUUCUGCAUGUGGCGGGAC

SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'
101	UUCUGCAUGUGGCGGGACU	131	AAGUGCAGCCUGAUCGCCG	161	GUGAUGGCCGUGCAGGUUG
102	UCUGCAUGUGGCGGGACUG	132	AGUGCAGCCUGAUCGCCGA	162	UGAUGGCCGUGCAGGUUGC
103	CUGCAUGUGGCGGGACUGC	133	GUGCAGCCUGAUCGCCGAG	163	GAUGGCCGUGCAGGUUGCA
104	UGCAUGUGGCGGGACUGCC	134	UGCAGCCUGAUCGCCGAGC	164	AUGGCCGUGCAGGUUGCAC
105	GCAUGUGGCGGGACUGCCA	135	GCAGCCUGAUCGCCGAGCG	165	UGGCCGUGCAGGUUGCACU
106	CAUGUGGCGGGACUGCCAG	136	CAGCCUGAUCGCCGAGCGG	166	GGCCGUGCAGGUUGCACUG
107	AUGUGGCGGGACUGCCAGU	137	AGCCUGAUCGCCGAGCGGC	167	GCCGUGCAGGUUGCACUGA
108	UGUGGCGGGACUGCCAGUG	138	GCCUGAUCGCCGAGCGGCA	168	CCGUGCAGGUUGCACUGAG
109	GUGGCGGGACUGCCAGUGC	139	CCUGAUCGCCGAGCGGCAG	169	CGUGCAGGUUGCACUGAGG
110	UGGCGGGACUGCCAGUGCA	140	CUGAUCGCCGAGCGGCAGC	170	GUGCAGGUUGCACUGAGGA
111	GGCGGGACUGCCAGUGCAA	141	UGAUCGCCGAGCGGCAGCG	171	UGCAGGUUGCACUGAGGAG
112	GCGGGACUGCCAGUGCAAG	142	GAUCGCCGAGCGGCAGCGG	172	GCAGGUUGCACUGAGGAGG
113	CGGGACUGCCAGUGCAAGA	143	AUCGCCGAGCGGCAGCGGG	173	CAGGUUGCACUGAGGAGGC
114	GGGACUGCCAGUGCAAGAA	144	UCGCCGAGCGGCAGCGGGU	174	AGGUUGCACUGAGGAGGCA
115	GGACUGCCAGUGCAAGAAG	145	CGCCGAGCGGCAGCGGGUG	175	GGUUGCACUGAGGAGGCAG
116	GACUGCCAGUGCAAGAAGU	146	GCCGAGCGGCAGCGGGUGA	176	GUUGCACUGAGGAGGCAGC
117	ACUGCCAGUGCAAGAAGUG	147	CCGAGCGGCAGCGGGUGAU	177	UUGCACUGAGGAGGCAGCA
118	CUGCCAGUGCAAGAAGUGC	148	CGAGCGGCAGCGGGUGAUG	178	UGCACUGAGGAGGCAGCAA
119	UGCCAGUGCAAGAAGUGCA	149	GAGCGGCAGCGGGUGAUGG	179	GCACUGAGGAGGCAGCAAG
120	GCCAGUGCAAGAAGUGCAG	150	AGCGGCAGCGGGUGAUGGC	180	CACUGAGGAGGCAGCAAGC
121	CCAGUGCAAGAAGUGCAGC	151	GCGGCAGCGGGUGAUGGCC	181	ACUGAGGAGGCAGCAAGCC
122	CAGUGCAAGAAGUGCAGCC	152	CGGCAGCGGGUGAUGGCCG	182	CUGAGGAGGCAGCAAGCCC
123	AGUGCAAGAAGUGCAGCCU	153	GGCAGCGGGUGAUGGCCGU	183	UGAGGAGGCAGCAAGCCCA
124	GUGCAAGAAGUGCAGCCUG	154	GCAGCGGGUGAUGGCCGUG	184	GAGGAGGCAGCAAGCCCAG
125	UGCAAGAAGUGCAGCCUGA	155	CAGCGGGUGAUGGCCGUGC	185	AGGAGGCAGCAAGCCCAGG
126	GCAAGAAGUGCAGCCUGAU	156	AGCGGGUGAUGGCCGUGCA	186	GGAGGCAGCAAGCCCAGGA
127	CAAGAAGUGCAGCCUGAUC	157	GCGGGUGAUGGCCGUGCAG	187	GAGGCAGCAAGCCCAGGAA
128	AAGAAGUGCAGCCUGAUCG	158	CGGGUGAUGGCCGUGCAGG	188	AGGCAGCAAGCCCAGGAAG
129	AGAAGUGCAGCCUGAUCGC	159	GGGUGAUGGCCGUGCAGGU	189	GGCAGCAAGCCCAGGAAGA
130	GAAGUGCAGCCUGAUCGCC	160	GGUGAUGGCCGUGCAGGUU	190	GCAGCAAGCCCAGGAAGAG

SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'
191	CAGCAAGCCCAGGAAGAGG	221	AGCCACCCUGUACCCCUGC	251	GAGCCAGUUGUCAAGAAGA
192	AGCAAGCCCAGGAAGAGGA	222	GCCACCCUGUACCCCUGCC	252	AGCCAGUUGUCAAGAAGAG
193	GCAAGCCCAGGAAGAGGAG	223	CCACCCUGUACCCCUGCCC	253	GCCAGUUGUCAAGAAGAGC
194	CAAGCCCAGGAAGAGGAGC	224	CACCCUGUACCCCUGCCCA	254	CCAGUUGUCAAGAAGAGCA
195	AAGCCCAGGAAGAGGAGCU	225	ACCCUGUACCCCUGCCCAG	255	CAGUUGUCAAGAAGAGCAG
196	AGCCCAGGAAGAGGAGCUG	226	CCCUGUACCCCUGCCCAGU	256	AGUUGUCAAGAAGAGCAGC
197	GCCCAGGAAGAGGAGCUGG	227	CCUGUACCCCUGCCCAGUG	257	GUUGUCAAGAAGAGCAGCA
198	CCCAGGAAGAGGAGCUGGG	228	CUGUACCCCUGCCCAGUGC	258	UUGUCAAGAAGAGCAGCAG
199	CCAGGAAGAGGAGCUGGGG	229	UGUACCCCUGCCCAGUGCC	259	UGUCAAGAAGAGCAGCAGC
200	CAGGAAGAGGAGCUGGGGA	230	GUACCCCUGCCCAGUGCCC	260	GUCAAGAAGAGCAGCAGCA
201	AGGAAGAGGAGCUGGGGAU	231	UACCCCUGCCCAGUGCCCC	261	UCAAGAAGAGCAGCAGCAG
202	GGAAGAGGAGCUGGGGAUC	232	ACCCCUGCCCAGUGCCCCU	262	CAAGAAGAGCAGCAGCAGC
203	GAAGAGGAGCUGGGGAUCA	233	CCCCUGCCCAGUGCCCCUG	263	AAGAAGAGCAGCAGCAGCA
204	AAGAGGAGCUGGGGAUCAG	234	CCCUGCCCAGUGCCCCUGA	264	AGAAGAGCAGCAGCAGCAG
205	AGAGGAGCUGGGGAUCAGC	235	CCUGCCCAGUGCCCCUGAG	265	GAAGAGCAGCAGCAGCAGC
206	GAGGAGCUGGGGAUCAGCC	236	CUGCCCAGUGCCCCUGAGC	266	AAGAGCAGCAGCAGCAGCU
207	AGGAGCUGGGGAUCAGCCA	237	UGCCCAGUGCCCCUGAGCC	267	AGAGCAGCAGCAGCAGCUC
208	GGAGCUGGGGAUCAGCCAC	238	GCCCAGUGCCCCUGAGCCA	268	GAGCAGCAGCAGCAGCUCC
209	GAGCUGGGGAUCAGCCACC	239	CCCAGUGCCCCUGAGCCAG	269	AGCAGCAGCAGCAGCUCCU
210	AGCUGGGGAUCAGCCACCC	240	CCAGUGCCCCUGAGCCAGU	270	GCAGCAGCAGCAGCUCCUG
211	GCUGGGGAUCAGCCACCCU	241	CAGUGCCCCUGAGCCAGUU	271	CAGCAGCAGCAGCUCCUGU
212	CUGGGGAUCAGCCACCCUG	242	AGUGCCCCUGAGCCAGUUG	272	AGCAGCAGCAGCUCCUGUC
213	UGGGGAUCAGCCACCCUGU	243	GUGCCCCUGAGCCAGUUGU	273	GCAGCAGCAGCUCCUGUCU
214	GGGGAUCAGCCACCCUGUA	244	UGCCCCUGAGCCAGUUGUC	274	CAGCAGCAGCUCCUGUCUC
215	GGGAUCAGCCACCCUGUAC	245	GCCCCUGAGCCAGUUGUCA	275	AGCAGCAGCUCCUGUCUCC
216	GGAUCAGCCACCCUGUACC	246	CCCCUGAGCCAGUUGUCAA	276	GCAGCAGCUCCUGUCUCCU
217	GAUCAGCCACCCUGUACCC	247	CCCUGAGCCAGUUGUCAAG	277	CAGCAGCUCCUGUCUCCUG
218	AUCAGCCACCCUGUACCCC	248	CCUGAGCCAGUUGUCAAGA	278	AGCAGCUCCUGUCUCCUGC
219	UCAGCCACCCUGUACCCCU	249	CUGAGCCAGUUGUCAAGAA	279	GCAGCUCCUGUCUCCUGCA
220	CAGCCACCCUGUACCCCUG	250	UGAGCCAGUUGUCAAGAAG	280	CAGCUCCUGUCUCCUGCAG

SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'
281	AGCUCCUGUCUCCUGCAGG	311	CCUGCUCACUCCACGAGCA	341	GCAGCAGCGAGCGCACCAC
282	GCUCCUGUCUCCUGCAGGA	312	CUGCUCACUCCACGAGCAC	342	CAGCAGCGAGCGCACCACC
283	CUCCUGUCUCCUGCAGGAC	313	UGCUCACUCCACGAGCACG	343	AGCAGCGAGCGCACCACCA
284	UCCUGUCUCCUGCAGGACA	314	GCUCACUCCACGAGCACGG	344	GCAGCGAGCGCACCACCAG
285	CCUGUCUCCUGCAGGACAG	315	CUCACUCCACGAGCACGGU	345	CAGCGAGCGCACCACCAGA
286	CUGUCUCCUGCAGGACAGC	316	UCACUCCACGAGCACGGUG	346	AGCGAGCGCACCACCAGAG
287	UGUCUCCUGCAGGACAGCA	317	CACUCCACGAGCACGGUGG	347	GCGAGCGCACCACCAGAGG
288	GUCUCCUGCAGGACAGCAG	318	ACUCCACGAGCACGGUGGC	348	CGAGCGCACCACCAGAGGG
289	UCUCCUGCAGGACAGCAGC	319	CUCCACGAGCACGGUGGCA	349	GAGCGCACCACCAGAGGGA
290	CUCCUGCAGGACAGCAGCA	320	UCCACGAGCACGGUGGCAG	350	AGCGCACCACCAGAGGGAC
291	UCCUGCAGGACAGCAGCAG	321	CCACGAGCACGGUGGCAGC	351	GCGCACCACCAGAGGGACG
292	CCUGCAGGACAGCAGCAGC	322	CACGAGCACGGUGGCAGCA	352	CGCACCACCAGAGGGACGG
293	CUGCAGGACAGCAGCAGCC	323	ACGAGCACGGUGGCAGCAG	353	GCACCACCAGAGGGACGGA
294	UGCAGGACAGCAGCAGCCC	324	CGAGCACGGUGGCAGCAGC	354	CACCACCAGAGGGACGGAU
295	GCAGGACAGCAGCAGCCCU	325	GAGCACGGUGGCAGCAGCA	355	ACCACCAGAGGGACGGAUG
296	CAGGACAGCAGCAGCCCUG	326	AGCACGGUGGCAGCAGCAG	356	CCACCAGAGGGACGGAUGC
297	AGGACAGCAGCAGCCCUGC	327	GCACGGUGGCAGCAGCAGC	357	CACCAGAGGGACGGAUGCU
298	GGACAGCAGCAGCCCUGCU	328	CACGGUGGCAGCAGCAGCA	358	ACCAGAGGGACGGAUGCUC
299	GACAGCAGCAGCCCUGCUC	329	ACGGUGGCAGCAGCAGCAG	359	CCAGAGGGACGGAUGCUCA
300	ACAGCAGCAGCCCUGCUCA	330	CGGUGGCAGCAGCAGCAGC	360	CAGAGGGACGGAUGCUCAU
301	CAGCAGCAGCCCUGCUCAC	331	GGUGGCAGCAGCAGCAGCG	361	AGAGGGACGGAUGCUCAUU
302	AGCAGCAGCCCUGCUCACU	332	GUGGCAGCAGCAGCAGCGA	362	GAGGGACGGAUGCUCAUUC
303	GCAGCAGCCCUGCUCACUC	333	UGGCAGCAGCAGCAGCGAG	363	AGGGACGGAUGCUCAUUCA
304	CAGCAGCCCUGCUCACUCC	334	GGCAGCAGCAGCAGCGAGC	364	GGGACGGAUGCUCAUUCAG
305	AGCAGCCCUGCUCACUCCA	335	GCAGCAGCAGCAGCGAGCG	365	GGACGGAUGCUCAUUCAGG
306	GCAGCCCUGCUCACUCCAC	336	CAGCAGCAGCAGCGAGCGC	366	GACGGAUGCUCAUUCAGGA
307	CAGCCCUGCUCACUCCACG	337	AGCAGCAGCAGCGAGCGCA	367	ACGGAUGCUCAUUCAGGAC
308	AGCCCUGCUCACUCCACGA	338	GCAGCAGCAGCGAGCGCAC	368	CGGAUGCUCAUUCAGGACA
309	GCCCUGCUCACUCCACGAG	339	CAGCAGCAGCGAGCGCACC	369	GGAUGCUCAUUCAGGACAU
310	CCCUGCUCACUCCACGAGC	340	AGCAGCAGCGAGCGCACCA	370	GAUGCUCAUUCAGGACAUC

SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'
371	AUGCUCAUUCAGGACAUCC	401	AGCAGAGGGCACUUGGAGA	431	UUGGUUGUGGACUCCACCU
372	UGCUCAUUCAGGACAUCCC	402	GCAGAGGGCACUUGGAGAG	432	UGGUUGUGGACUCCACCUA
373	GCUCAUUCAGGACAUCCCU	403	CAGAGGGCACUUGGAGAGC	433	GGUUGUGGACUCCACCUAC
374	CUCAUUCAGGACAUCCCUU	404	AGAGGGCACUUGGAGAGCA	434	GUUGUGGACUCCACCUACU
375	UCAUUCAGGACAUCCCUUC	405	GAGGGCACUUGGAGAGCAC	435	UUGUGGACUCCACCUACUA
376	CAUUCAGGACAUCCCUUCC	406	AGGGCACUUGGAGAGCACG	436	UGUGGACUCCACCUACUAC
377	AUUCAGGACAUCCCUUCCA	407	GGGCACUUGGAGAGCACGU	437	GUGGACUCCACCUACUACA
378	UUCAGGACAUCCCUUCCAU	408	GGCACUUGGAGAGCACGUC	438	UGGACUCCACCUACUACAG
379	UCAGGACAUCCCUUCCAUC	409	GCACUUGGAGAGCACGUCU	439	GGACUCCACCUACUACAGC
380	CAGGACAUCCCUUCCAUCC	410	CACUUGGAGAGCACGUCUG	440	GACUCCACCUACUACAGCA
381	AGGACAUCCCUUCCAUCCC	411	ACUUGGAGAGCACGUCUGA	441	ACUCCACCUACUACAGCAG
382	GGACAUCCCUUCCAUCCCC	412	CUUGGAGAGCACGUCUGAU	442	CUCCACCUACUACAGCAGU
383	GACAUCCCUUCCAUCCCCA	413	UUGGAGAGCACGUCUGAUU	443	UCCACCUACUACAGCAGUU
384	ACAUCCCUUCCAUCCCCAG	414	UGGAGAGCACGUCUGAUUU	444	CCACCUACUACAGCAGUUU
385	CAUCCCUUCCAUCCCCAGC	415	GGAGAGCACGUCUGAUUUG	445	CACCUACUACAGCAGUUUU
386	AUCCCUUCCAUCCCCAGCA	416	GAGAGCACGUCUGAUUUGG	446	ACCUACUACAGCAGUUUUU
387	UCCCUUCCAUCCCCAGCAG	417	AGAGCACGUCUGAUUUGGU	447	CCUACUACAGCAGUUUUUA
388	CCCUUCCAUCCCCAGCAGA	418	GAGCACGUCUGAUUUGGUU	448	CUACUACAGCAGUUUUUAC
389	CCUUCCAUCCCCAGCAGAG	419	AGCACGUCUGAUUUGGUUG	449	UACUACAGCAGUUUUUACC
390	CUUCCAUCCCCAGCAGAGG	420	GCACGUCUGAUUUGGUUGU	450	ACUACAGCAGUUUUUACCA
391	UUCCAUCCCCAGCAGAGGG	421	CACGUCUGAUUUGGUUGUG	451	CUACAGCAGUUUUUACCAG
392	UCCAUCCCCAGCAGAGGGC	422	ACGUCUGAUUUGGUUGUGG	452	UACAGCAGUUUUUACCAGC
393	CCAUCCCCAGCAGAGGGCA	423	CGUCUGAUUUGGUUGUGGA	453	ACAGCAGUUUUUACCAGCC
394	CAUCCCCAGCAGAGGGCAC	424	GUCUGAUUUGGUUGUGGAC	454	CAGCAGUUUUUACCAGCCA
395	AUCCCCAGCAGAGGGCACU	425	UCUGAUUUGGUUGUGGACU	455	AGCAGUUUUUACCAGCCAU
396	UCCCCAGCAGAGGGCACUU	426	CUGAUUUGGUUGUGGACUC	456	GCAGUUUUUACCAGCCAUC
397	CCCCAGCAGAGGGCACUUG	427	UGAUUUGGUUGUGGACUCC	457	CAGUUUUUACCAGCCAUCC
398	CCCAGCAGAGGGCACUUGG	428	GAUUUGGUUGUGGACUCCA	458	AGUUUUUACCAGCCAUCCC
399	CCAGCAGAGGGCACUUGGA	429	AUUUGGUUGUGGACUCCAC	459	GUUUUUACCAGCCAUCCCU
400	CAGCAGAGGGCACUUGGAG	430	UUUGGUUGUGGACUCCACC	460	UUUUUACCAGCCAUCCCUG

SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'
461	UUUUACCAGCCAUCCCUGU	491	AACAACCUGUACAACUACU	521	AUGGCAGUGGCCACUGAGU
462	UUUACCAGCCAUCCCUGUA	492	ACAACCUGUACAACUACUC	522	UGGCAGUGGCCACUGAGUC
463	UUACCAGCCAUCCCUGUAU	493	CAACCUGUACAACUACUCC	523	GGCAGUGGCCACUGAGUCU
464	UACCAGCCAUCCCUGUAUC	494	AACCUGUACAACUACUCCC	524	GCAGUGGCCACUGAGUCUU
465	ACCAGCCAUCCCUGUAUCC	495	ACCUGUACAACUACUCCCA	525	CAGUGGCCACUGAGUCUUC
466	CCAGCCAUCCCUGUAUCCU	496	CCUGUACAACUACUCCCAG	526	AGUGGCCACUGAGUCUUCC
467	CAGCCAUCCCUGUAUCCUU	497	CUGUACAACUACUCCCAGU	527	GUGGCCACUGAGUCUUCCU
468	AGCCAUCCCUGUAUCCUUA	498	UGUACAACUACUCCCAGUA	528	UGGCCACUGAGUCUUCCUC
469	GCCAUCCCUGUAUCCUUAC	499	GUACAACUACUCCCAGUAC	529	GGCCACUGAGUCUUCCUCA
470	CCAUCCCUGUAUCCUUACU	500	UACAACUACUCCCAGUACC	530	GCCACUGAGUCUUCCUCAA
471	CAUCCCUGUAUCCUUACUA	501	ACAACUACUCCCAGUACCA	531	CCACUGAGUCUUCCUCAAG
472	AUCCCUGUAUCCUUACUAU	502	CAACUACUCCCAGUACCAA	532	CACUGAGUCUUCCUCAAGU
473	UCCCUGUAUCCUUACUAUA	503	AACUACUCCCAGUACCAAA	533	ACUGAGUCUUCCUCAAGUG
474	CCCUGUAUCCUUACUAUAA	504	ACUACUCCCAGUACCAAAU	534	CUGAGUCUUCCUCAAGUGA
475	CCUGUAUCCUUACUAUAAC	505	CUACUCCCAGUACCAAAUG	535	UGAGUCUUCCUCAAGUGAG
476	CUGUAUCCUUACUAUAACA	506	UACUCCCAGUACCAAAUGG	536	GAGUCUUCCUCAAGUGAGA
477	UGUAUCCUUACUAUAACAA	507	ACUCCCAGUACCAAAUGGC	537	AGUCUUCCUCAAGUGAGAC
478	GUAUCCUUACUAUAACAAC	508	CUCCCAGUACCAAAUGGCA	538	GUCUUCCUCAAGUGAGACA
479	UAUCCUUACUAUAACAACC	509	UCCCAGUACCAAAUGGCAG	539	UCUUCCUCAAGUGAGACAG
480	AUCCUUACUAUAACAACCU	510	CCCAGUACCAAAUGGCAGU	540	CUUCCUCAAGUGAGACAGG
481	UCCUUACUAUAACAACCUG	511	CCAGUACCAAAUGGCAGUG	541	UUCCUCAAGUGAGACAGGG
482	CCUUACUAUAACAACCUGU	512	CAGUACCAAAUGGCAGUGG	542	UCCUCAAGUGAGACAGGGG
483	CUUACUAUAACAACCUGUA	513	AGUACCAAAUGGCAGUGGC	543	CCUCAAGUGAGACAGGGGG
484	UUACUAUAACAACCUGUAC	514	GUACCAAAUGGCAGUGGCC	544	CUCAAGUGAGACAGGGGGU
485	UACUAUAACAACCUGUACA	515	UACCAAAUGGCAGUGGCCA	545	UCAAGUGAGACAGGGGGUA
486	ACUAUAACAACCUGUACAA	516	ACCAAAUGGCAGUGGCCAC	546	CAAGUGAGACAGGGGGUAC
487	CUAUAACAACCUGUACAAC	517	CCAAAUGGCAGUGGCCACU	547	AAGUGAGACAGGGGGUACG
488	UAUAACAACCUGUACAACU	518	CAAAUGGCAGUGGCCACUG	548	AGUGAGACAGGGGGUACGU
489	AUAACAACCUGUACAACUA	519	AAAUGGCAGUGGCCACUGA	549	GUGAGACAGGGGGUACGUU
490	UAACAACCUGUACAACUAC	520	AAUGGCAGUGGCCACUGAG	550	UGAGACAGGGGGUACGUUU

SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'
551	GAGACAGGGGGUACGUUUG	581	AUGAAAAACAGCCUUCGAA	611	ACAUACAUGUCAAGCCAGU
552	AGACAGGGGGUACGUUUGU	582	UGAAAAACAGCCUUCGAAG	612	CAUACAUGUCAAGCCAGUC
553	GACAGGGGGUACGUUUGUA	583	GAAAAACAGCCUUCGAAGC	613	AUACAUGUCAAGCCAGUCA
554	ACAGGGGGUACGUUUGUAG	584	AAAAACAGCCUUCGAAGCC	614	UACAUGUCAAGCCAGUCAG
555	CAGGGGGUACGUUUGUAGG	585	AAAACAGCCUUCGAAGCCU	615	ACAUGUCAAGCCAGUCAGG
556	AGGGGGUACGUUUGUAGGG	586	AAACAGCCUUCGAAGCCUC	616	CAUGUCAAGCCAGUCAGGA
557	GGGGGUACGUUUGUAGGGU	587	AACAGCCUUCGAAGCCUCC	617	AUGUCAAGCCAGUCAGGAA
558	GGGGUACGUUUGUAGGGUC	588	ACAGCCUUCGAAGCCUCCC	618	UGUCAAGCCAGUCAGGAAA
559	GGGUACGUUUGUAGGGUCA	589	CAGCCUUCGAAGCCUCCCA	619	GUCAAGCCAGUCAGGAAAA
560	GGUACGUUUGUAGGGUCAG	590	AGCCUUCGAAGCCUCCCAG	620	UCAAGCCAGUCAGGAAAAC
561	GUACGUUUGUAGGGUCAGC	591	GCCUUCGAAGCCUCCCAGC	621	CAAGCCAGUCAGGAAAACA
562	UACGUUUGUAGGGUCAGCC	592	CCUUCGAAGCCUCCCAGCA	622	AAGCCAGUCAGGAAAACAG
563	ACGUUUGUAGGGUCAGCCA	593	CUUCGAAGCCUCCCAGCAA	623	AGCCAGUCAGGAAAACAGU
564	CGUUUGUAGGGUCAGCCAU	594	UUCGAAGCCUCCCAGCAAC	624	GCCAGUCAGGAAAACAGUG
565	GUUUGUAGGGUCAGCCAUG	595	UCGAAGCCUCCCAGCAACA	625	CCAGUCAGGAAAACAGUGG
566	UUUGUAGGGUCAGCCAUGA	596	CGAAGCCUCCCAGCAACAU	626	CAGUCAGGAAAACAGUGGC
567	UUGUAGGGUCAGCCAUGAA	597	GAAGCCUCCCAGCAACAUA	627	AGUCAGGAAAACAGUGGCA
568	UGUAGGGUCAGCCAUGAAA	598	AAGCCUCCCAGCAACAUAC	628	GUCAGGAAAACAGUGGCAG
569	GUAGGGUCAGCCAUGAAAA	599	AGCCUCCCAGCAACAUACA	629	UCAGGAAAACAGUGGCAGA
570	UAGGGUCAGCCAUGAAAAA	600	GCCUCCCAGCAACAUACAU	630	CAGGAAAACAGUGGCAGAU
571	AGGGUCAGCCAUGAAAAAC	601	CCUCCCAGCAACAUACAUG	631	AGGAAAACAGUGGCAGAUG
572	GGGUCAGCCAUGAAAAACA	602	CUCCCAGCAACAUACAUGU	632	GGAAAACAGUGGCAGAUGA
573	GGUCAGCCAUGAAAAACAG	603	UCCCAGCAACAUACAUGUC	633	GAAAACAGUGGCAGAUGAA
574	GUCAGCCAUGAAAAACAGC	604	CCCAGCAACAUACAUGUCA	634	AAAACAGUGGCAGAUGAAG
575	UCAGCCAUGAAAAACAGCC	605	CCAGCAACAUACAUGUCAA	635	AAACAGUGGCAGAUGAAGG
576	CAGCCAUGAAAAACAGCCU	606	CAGCAACAUACAUGUCAAG	636	AACAGUGGCAGAUGAAGGG
577	AGCCAUGAAAAACAGCCUU	607	AGCAACAUACAUGUCAAGC	637	ACAGUGGCAGAUGAAGGGA
578	GCCAUGAAAAACAGCCUUC	608	GCAACAUACAUGUCAAGCC	638	CAGUGGCAGAUGAAGGGAA
579	CCAUGAAAAACAGCCUUCG	609	CAACAUACAUGUCAAGCCA	639	AGUGGCAGAUGAAGGGAAU
580	CAUGAAAAACAGCCUUCGA	610	AACAUACAUGUCAAGCCAG	640	GUGGCAGAUGAAGGGAAUG

SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'
641	UGGCAGAUGAAGGGAAUGG	671	GCCAUGAGCUCCCAGUACC	701	UACUACCCGCCCACCUCAU
642	GGCAGAUGAAGGGAAUGGA	672	CCAUGAGCUCCCAGUACCG	702	ACUACCCGCCCACCUCAUA
643	GCAGAUGAAGGGAAUGGAG	673	CAUGAGCUCCCAGUACCGG	703	CUACCCGCCCACCUCAUAC
644	CAGAUGAAGGGAAUGGAGA	674	AUGAGCUCCCAGUACCGGA	704	UACCCGCCCACCUCAUACC
645	AGAUGAAGGGAAUGGAGAA	675	UGAGCUCCCAGUACCGGAU	705	ACCCGCCCACCUCAUACCU
646	GAUGAAGGGAAUGGAGAAC	676	GAGCUCCCAGUACCGGAUG	706	CCCGCCCACCUCAUACCUG
647	AUGAAGGGAAUGGAGAACC	677	AGCUCCCAGUACCGGAUGU	707	CCGCCCACCUCAUACCUGG
648	UGAAGGGAAUGGAGAACCG	678	GCUCCCAGUACCGGAUGUG	708	CGCCCACCUCAUACCUGGG
649	GAAGGGAAUGGAGAACCGC	679	CUCCCAGUACCGGAUGUGC	709	GCCCACCUCAUACCUGGGC
650	AAGGGAAUGGAGAACCGCC	680	UCCCAGUACCGGAUGUGCU	710	CCCACCUCAUACCUGGGCC
651	AGGGAAUGGAGAACCGCCA	681	CCCAGUACCGGAUGUGCUC	711	CCACCUCAUACCUGGGCCA
652	GGGAAUGGAGAACCGCCAU	682	CCAGUACCGGAUGUGCUCC	712	CACCUCAUACCUGGGCCAG
653	GGAAUGGAGAACCGCCAUG	683	CAGUACCGGAUGUGCUCCU	713	ACCUCAUACCUGGGCCAGG
654	GAAUGGAGAACCGCCAUGC	684	AGUACCGGAUGUGCUCCUA	714	CCUCAUACCUGGGCCAGGG
655	AAUGGAGAACCGCCAUGCC	685	GUACCGGAUGUGCUCCUAC	715	CUCAUACCUGGGCCAGGGG
656	AUGGAGAACCGCCAUGCCA	686	UACCGGAUGUGCUCCUACU	716	UCAUACCUGGGCCAGGGGG
657	UGGAGAACCGCCAUGCCAU	687	ACCGGAUGUGCUCCUACUA	717	CAUACCUGGGCCAGGGGGU
658	GGAGAACCGCCAUGCCAUG	688	CCGGAUGUGCUCCUACUAC	718	AUACCUGGGCCAGGGGGUU
659	GAGAACCGCCAUGCCAUGA	689	CGGAUGUGCUCCUACUACC	719	UACCUGGGCCAGGGGGUUG
660	AGAACCGCCAUGCCAUGAG	690	GGAUGUGCUCCUACUACCC	720	ACCUGGGCCAGGGGGUUGG
661	GAACCGCCAUGCCAUGAGC	691	GAUGUGCUCCUACUACCCG	721	CCUGGGCCAGGGGGUUGGC
662	AACCGCCAUGCCAUGAGCU	692	AUGUGCUCCUACUACCCGC	722	CUGGGCCAGGGGGUUGGCA
663	ACCGCCAUGCCAUGAGCUC	693	UGUGCUCCUACUACCCGCC	723	UGGGCCAGGGGGUUGGCAG
664	CCGCCAUGCCAUGAGCUCC	694	GUGCUCCUACUACCCGCCC	724	GGGCCAGGGGGUUGGCAGU
665	CGCCAUGCCAUGAGCUCCC	695	UGCUCCUACUACCCGCCCA	725	GGCCAGGGGGUUGGCAGUC
666	GCCAUGCCAUGAGCUCCCA	696	GCUCCUACUACCCGCCCAC	726	GCCAGGGGGUUGGCAGUCC
667	CCAUGCCAUGAGCUCCCAG	697	CUCCUACUACCCGCCCACC	727	CCAGGGGGUUGGCAGUCCC
668	CAUGCCAUGAGCUCCCAGU	698	UCCUACUACCCGCCCACCU	728	CAGGGGGUUGGCAGUCCCA
669	AUGCCAUGAGCUCCCAGUA	699	CCUACUACCCGCCCACCUC	729	AGGGGGUUGGCAGUCCCAC
670	UGCCAUGAGCUCCCAGUAC	700	CUACUACCCGCCCACCUCA	730	GGGGGUUGGCAGUCCCACC

SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'
731	GGGGUUGGCAGUCCCACCU	761	AUACUGGCCUCGGAGGACA	791	UCAGAGUCGAAAGCGAGAG
732	GGGUUGGCAGUCCCACCUG	762	UACUGGCCUCGGAGGACAC	792	CAGAGUCGAAAGCGAGAGU
733	GGUUGGCAGUCCCACCUGC	763	ACUGGCCUCGGAGGACACC	793	AGAGUCGAAAGCGAGAGUG
734	GUUGGCAGUCCCACCUGCG	764	CUGGCCUCGGAGGACACCC	794	GAGUCGAAAGCGAGAGUGU
735	UUGGCAGUCCCACCUGCGU	765	UGGCCUCGGAGGACACCCC	795	AGUCGAAAGCGAGAGUGUU
736	UGGCAGUCCCACCUGCGUC	766	GGCCUCGGAGGACACCCCC	796	GUCGAAAGCGAGAGUGUUU
737	GGCAGUCCCACCUGCGUCA	767	GCCUCGGAGGACACCCCCU	797	UCGAAAGCGAGAGUGUUUU
738	GCAGUCCCACCUGCGUCAC	768	CCUCGGAGGACACCCCCUC	798	CGAAAGCGAGAGUGUUUUC
739	CAGUCCCACCUGCGUCACA	769	CUCGGAGGACACCCCCUCC	799	GAAAGCGAGAGUGUUUUCG
740	AGUCCCACCUGCGUCACAC	770	UCGGAGGACACCCCCUCCU	800	AAAGCGAGAGUGUUUUCGC
741	GUCCCACCUGCGUCACACA	771	CGGAGGACACCCCCUCCUA	801	AAGCGAGAGUGUUUUCGCC
742	UCCCACCUGCGUCACACAG	772	GGAGGACACCCCCUCCUAC	802	AGCGAGAGUGUUUUCGCCG
743	CCCACCUGCGUCACACAGA	773	GAGGACACCCCCUCCUACU	803	GCGAGAGUGUUUUCGCCGC
744	CCACCUGCGUCACACAGAU	774	AGGACACCCCCUCCUACUC	804	CGAGAGUGUUUUCGCCGCC
745	CACCUGCGUCACACAGAUA	775	GGACACCCCCUCCUACUCA	805	GAGAGUGUUUUCGCCGCCC
746	ACCUGCGUCACACAGAUAC	776	GACACCCCCUCCUACUCAG	806	AGAGUGUUUUCGCCGCCCA
747	CCUGCGUCACACAGAUACU	777	ACACCCCCUCCUACUCAGA	807	GAGUGUUUUCGCCGCCCAG
748	CUGCGUCACACAGAUACUG	778	CACCCCCUCCUACUCAGAG	808	AGUGUUUUCGCCGCCCAGC
749	UGCGUCACACAGAUACUGG	779	ACCCCCUCCUACUCAGAGU	809	GUGUUUUCGCCGCCCAGCA
750	GCGUCACACAGAUACUGGC	780	CCCCCUCCUACUCAGAGUC	810	UGUUUUCGCCGCCCAGCAG
751	CGUCACACAGAUACUGGCC	781	CCCCUCCUACUCAGAGUCG	811	GUUUUCGCCGCCCAGCAGC
752	GUCACACAGAUACUGGCCU	782	CCCUCCUACUCAGAGUCGA	812	UUUUCGCCGCCCAGCAGCC
753	UCACACAGAUACUGGCCUC	783	CCUCCUACUCAGAGUCGAA	813	UUUCGCCGCCCAGCAGCCA
754	CACACAGAUACUGGCCUCG	784	CUCCUACUCAGAGUCGAAA	814	UUCGCCGCCCAGCAGCCAG
755	ACACAGAUACUGGCCUCGG	785	UCCUACUCAGAGUCGAAAG	815	UCGCCGCCCAGCAGCCAGG
756	CACAGAUACUGGCCUCGGA	786	CCUACUCAGAGUCGAAAGC	816	CGCCGCCCAGCAGCCAGGA
757	ACAGAUACUGGCCUCGGAG	787	CUACUCAGAGUCGAAAGCG	817	GCCGCCCAGCAGCCAGGAC
758	CAGAUACUGGCCUCGGAGG	788	UACUCAGAGUCGAAAGCGA	818	CCGCCCAGCAGCCAGGACU
759	AGAUACUGGCCUCGGAGGA	789	ACUCAGAGUCGAAAGCGAG	819	CGCCCAGCAGCCAGGACUC
760	GAUACUGGCCUCGGAGGAC	790	CUCAGAGUCGAAAGCGAGA	820	GCCCAGCAGCCAGGACUCG

SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'
821	CCCAGCAGCCAGGACUCGG	851	CUGUCGAGCAGCGAGAGCA	881	CUGGAGUGCGAGCCCCACC
822	CCAGCAGCCAGGACUCGGG	852	UGUCGAGCAGCGAGAGCAC	882	UGGAGUGCGAGCCCCACCA
823	CAGCAGCCAGGACUCGGGC	853	GUCGAGCAGCGAGAGCACC	883	GGAGUGCGAGCCCCACCAA
824	AGCAGCCAGGACUCGGGCC	854	UCGAGCAGCGAGAGCACCA	884	GAGUGCGAGCCCCACCAAG
825	GCAGCCAGGACUCGGGCCU	855	CGAGCAGCGAGAGCACCAA	885	AGUGCGAGCCCCACCAAGA
826	CAGCCAGGACUCGGGCCUG	856	GAGCAGCGAGAGCACCAAG	886	GUGCGAGCCCCACCAAGAG
827	AGCCAGGACUCGGGCCUGG	857	AGCAGCGAGAGCACCAAGG	887	UGCGAGCCCCACCAAGAGC
828	GCCAGGACUCGGGCCUGGG	858	GCAGCGAGAGCACCAAGGG	888	GCGAGCCCCACCAAGAGCC
829	CCAGGACUCGGGCCUGGGG	859	CAGCGAGAGCACCAAGGGA	889	CGAGCCCCACCAAGAGCCC
830	CAGGACUCGGGCCUGGGGU	860	AGCGAGAGCACCAAGGGAG	890	GAGCCCCACCAAGAGCCCG
831	AGGACUCGGGCCUGGGGUG	861	GCGAGAGCACCAAGGGAGA	891	AGCCCCACCAAGAGCCCGG
832	GGACUCGGGCCUGGGGUGC	862	CGAGAGCACCAAGGGAGAC	892	GCCCCACCAAGAGCCCGGC
833	GACUCGGGCCUGGGGUGCC	863	GAGAGCACCAAGGGAGACC	893	CCCCACCAAGAGCCCGGCG
834	ACUCGGGCCUGGGGUGCCU	864	AGAGCACCAAGGGAGACCU	894	CCCACCAAGAGCCCGGCGC
835	CUCGGGCCUGGGGUGCCUG	865	GAGCACCAAGGGAGACCUG	895	CCACCAAGAGCCCGGCGCC
836	UCGGGCCUGGGGUGCCUGU	866	AGCACCAAGGGAGACCUGG	896	CACCAAGAGCCCGGCGCCU
837	CGGGCCUGGGGUGCCUGUC	867	GCACCAAGGGAGACCUGGA	897	ACCAAGAGCCCGGCGCCUU
838	GGGCCUGGGGUGCCUGUCG	868	CACCAAGGGAGACCUGGAG	898	CCAAGAGCCCGGCGCCUUC
839	GGCCUGGGGUGCCUGUCGA	869	ACCAAGGGAGACCUGGAGU	899	CAAGAGCCCGGCGCCUUCG
840	GCCUGGGGUGCCUGUCGAG	870	CCAAGGGAGACCUGGAGUG	900	AAGAGCCCGGCGCCUUCGC
841	CCUGGGGUGCCUGUCGAGC	871	CAAGGGAGACCUGGAGUGC	901	AGAGCCCGGCGCCUUCGCG
842	CUGGGGUGCCUGUCGAGCA	872	AAGGGAGACCUGGAGUGCG	902	GAGCCCGGCGCCUUCGCGG
843	UGGGGUGCCUGUCGAGCAG	873	AGGGAGACCUGGAGUGCGA	903	AGCCCGGCGCCUUCGCGGU
844	GGGGUGCCUGUCGAGCAGC	874	GGGAGACCUGGAGUGCGAG	904	GCCCGGCGCCUUCGCGGUG
845	GGGUGCCUGUCGAGCAGCG	875	GGAGACCUGGAGUGCGAGC	905	CCCGGCGCCUUCGCGGUGA
846	GGUGCCUGUCGAGCAGCGA	876	GAGACCUGGAGUGCGAGCC	906	CCGGCGCCUUCGCGGUGAG
847	GUGCCUGUCGAGCAGCGAG	877	AGACCUGGAGUGCGAGCCC	907	CGGCGCCUUCGCGGUGAGC
848	UGCCUGUCGAGCAGCGAGA	878	GACCUGGAGUGCGAGCCCC	908	GGCGCCUUCGCGGUGAGCC
849	GCCUGUCGAGCAGCGAGAG	879	ACCUGGAGUGCGAGCCCCA	909	GCGCCUUCGCGGUGAGCCC
850	CCUGUCGAGCAGCGAGAGC	880	CCUGGAGUGCGAGCCCCAC	910	CGCCUUCGCGGUGAGCCCG

SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'
911	GCCUUCGCGGUGAGCCCGG	941	GAGUAGGCGCGGCGUCGGG	971	CGGCGUUCACUGUUGCCUU
912	CCUUCGCGGUGAGCCCGGU	942	AGUAGGCGCGGCGUCGGGC	972	GGCGUUCACUGUUGCCUUG
913	CUUCGCGGUGAGCCCGGUU	943	GUAGGCGCGGCGUCGGGCG	973	GCGUUCACUGUUGCCUUGU
914	UUCGCGGUGAGCCCGGUUC	944	UAGGCGCGGCGUCGGGCGG	974	CGUUCACUGUUGCCUUGUU
915	UCGCGGUGAGCCCGGUUCU	945	AGGCGCGGCGUCGGGCGGC	975	GUUCACUGUUGCCUUGUUC
916	CGCGGUGAGCCCGGUUCUU	946	GGCGCGGCGUCGGGCGGCU	976	UUCACUGUUGCCUUGUUCU
917	GCGGUGAGCCCGGUUCUUG	947	GCGCGGCGUCGGGCGGCUG	977	UCACUGUUGCCUUGUUCUG
918	CGGUGAGCCCGGUUCUUGA	948	CGCGGCGUCGGGCGGCUGC	978	CACUGUUGCCUUGUUCUGU
919	GGUGAGCCCGGUUCUUGAG	949	GCGGCGUCGGGCGGCUGCU	979	ACUGUUGCCUUGUUCUGUU
920	GUGAGCCCGGUUCUUGAGG	950	CGGCGUCGGGCGGCUGCUG	980	CUGUUGCCUUGUUCUGUUG
921	UGAGCCCGGUUCUUGAGGG	951	GGCGUCGGGCGGCUGCUGC	981	UGUUGCCUUGUUCUGUUGG
922	GAGCCCGGUUCUUGAGGGC	952	GCGUCGGGCGGCUGCUGCG	982	GUUGCCUUGUUCUGUUGGG
923	AGCCCGGUUCUUGAGGGCG	953	CGUCGGGCGGCUGCUGCGC	983	UUGCCUUGUUCUGUUGGGG
924	GCCCGGUUCUUGAGGGCGA	954	GUCGGGCGGCUGCUGCGCG	984	UGCCUUGUUCUGUUGGGGU
925	CCCGGUUCUUGAGGGCGAG	955	UCGGGCGGCUGCUGCGCGG	985	GCCUUGUUCUGUUGGGGUU
926	CCGGUUCUUGAGGGCGAGU	956	CGGGCGGCUGCUGCGCGGC	986	CCUUGUUCUGUUGGGGUUG
927	CGGUUCUUGAGGGCGAGUA	957	GGGCGGCUGCUGCGCGGCG	987	CUUGUUCUGUUGGGGUUGC
928	GGUUCUUGAGGGCGAGUAG	958	GGCGGCUGCUGCGCGGCGU	988	UUGUUCUGUUGGGGUUGCG
929	GUUCUUGAGGGCGAGUAGG	959	GCGGCUGCUGCGCGGCGUU	989	UGUUCUGUUGGGGUUGCGG
930	UUCUUGAGGGCGAGUAGGC	960	CGGCUGCUGCGCGGCGUUC	990	GUUCUGUUGGGGUUGCGGG
931	UCUUGAGGGCGAGUAGGCG	961	GGCUGCUGCGCGGCGUUCA	991	UUCUGUUGGGGUUGCGGGG
932	CUUGAGGGCGAGUAGGCGC	962	GCUGCUGCGCGGCGUUCAC	992	UCUGUUGGGGUUGCGGGGG
933	UUGAGGGCGAGUAGGCGCG	963	CUGCUGCGCGGCGUUCACU	993	CUGUUGGGGUUGCGGGGGG
934	UGAGGGCGAGUAGGCGCGG	964	UGCUGCGCGGCGUUCACUG	994	UGUUGGGGUUGCGGGGGGG
935	GAGGGCGAGUAGGCGCGGC	965	GCUGCGCGGCGUUCACUGU	995	GUUGGGGUUGCGGGGGGGC
936	AGGGCGAGUAGGCGCGGCG	966	CUGCGCGGCGUUCACUGUU	996	UUGGGGUUGCGGGGGGGCG
937	GGGCGAGUAGGCGCGGCGU	967	UGCGCGGCGUUCACUGUUG	997	UGGGGUUGCGGGGGGGCGU
938	GGCGAGUAGGCGCGGCGUC	968	GCGCGGCGUUCACUGUUGC	998	GGGGUUGCGGGGGGGCGUU
939	GCGAGUAGGCGCGGCGUCG	969	CGCGGCGUUCACUGUUGCC	999	GGGUUGCGGGGGGGCGUUG
940	CGAGUAGGCGCGGCGUCGG	970	GCGGCGUUCACUGUUGCCU	1000	GGUUGCGGGGGGGCGUUGG

SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'
1001	GUUGCGGGGGGGCGUUGGG	1031	CGGGGCGGGGGGGGCACGG	1061	CCGGGCCGGCGGGGCGGGG
1002	UUGCGGGGGGGCGUUGGGU	1032	GGGGCGGGGGGGGCACGGC	1062	CGGGCCGGCGGGGCGGGGC
1003	UGCGGGGGGGCGUUGGGUU	1033	GGGCGGGGGGGGCACGGCG	1063	GGGCCGGCGGGGCGGGGCG
1004	GCGGGGGGGCGUUGGGUUU	1034	GGCGGGGGGGGCACGGCGG	1064	GGCCGGCGGGGCGGGGCGG
1005	CGGGGGGGCGUUGGGUUUC	1035	GCGGGGGGGGCACGGCGGG	1065	GCCGGCGGGGCGGGGCGGG
1006	GGGGGGGCGUUGGGUUUCU	1036	CGGGGGGGGCACGGCGGGG	1066	CCGGCGGGGCGGGGCGGGG
1007	GGGGGGCGUUGGGUUUCUU	1037	GGGGGGGGCACGGCGGGGC	1067	CGGCGGGGCGGGGCGGGGC
1008	GGGGGCGUUGGGUUUCUUC	1038	GGGGGGGCACGGCGGGGCC	1068	GGCGGGGCGGGGCGGGGCG
1009	GGGGCGUUGGGUUUCUUCU	1039	GGGGGGCACGGCGGGGCCG	1069	GCGGGGCGGGGCGGGGCGG
1010	GGGCGUUGGGUUUCUUCUU	1040	GGGGGCACGGCGGGGCCGC	1070	CGGGGCGGGGCGGGGCGGG
1011	GGCGUUGGGUUUCUUCUUU	1041	GGGGCACGGCGGGGCCGCG	1071	GGGGCGGGGCGGGGCGGGA
1012	GCGUUGGGUUUCUUCUUUC	1042	GGGCACGGCGGGGCCGCGG	1072	GGGCGGGGCGGGGCGGGAC
1013	CGUUGGGUUUCUUCUUUCC	1043	GGCACGGCGGGGCCGCGGC	1073	GGCGGGGCGGGGCGGGACG
1014	GUUGGGUUUCUUCUUUCCG	1044	GCACGGCGGGGCCGCGGCC	1074	GCGGGGCGGGGCGGGACGG
1015	UUGGGUUUCUUCUUUCCGG	1045	CACGGCGGGGCCGCGGCCG	1075	CGGGGCGGGGCGGGACGGG
1016	UGGGUUUCUUCUUUCCGGG	1046	ACGGCGGGGCCGCGGCCGG	1076	GGGGCGGGGCGGGACGGGG
1017	GGGUUUCUUCUUUCCGGGG	1047	CGGCGGGGCCGCGGCCGGG	1077	GGGCGGGGCGGGACGGGGC
1018	GGUUUCUUCUUUCCGGGGC	1048	GGCGGGGCCGCGGCCGGGC	1078	GGCGGGGCGGGACGGGGCG
1019	GUUUCUUCUUUCCGGGGCG	1049	GCGGGGCCGCGGCCGGGCC	1079	GCGGGGCGGGACGGGGCGG
1020	UUUCUUCUUUCCGGGGCGG	1050	CGGGGCCGCGGCCGGGCCG	1080	CGGGGCGGGACGGGGCGGG
1021	UUCUUCUUUCCGGGGCGGG	1051	GGGGCCGCGGCCGGGCCGG	1081	GGGGCGGGACGGGGCGGGG
1022	UCUUCUUUCCGGGGCGGGG	1052	GGGCCGCGGCCGGGCCGGC	1082	GGGCGGGACGGGGCGGGGC
1023	CUUCUUUCCGGGGCGGGGG	1053	GGCCGCGGCCGGGCCGGCG	1083	GGCGGGACGGGGCGGGGCG
1024	UUCUUUCCGGGGCGGGGGG	1054	GCCGCGGCCGGGCCGGCGG	1084	GCGGGACGGGGCGGGGCGG
1025	UCUUUCCGGGGCGGGGGGG	1055	CCGCGGCCGGGCCGGCGGG	1085	CGGGACGGGGCGGGGCGGA
1026	CUUUCCGGGGCGGGGGGGG	1056	CGCGGCCGGGCCGGCGGGG	1086	GGGACGGGGCGGGGCGGAG
1027	UUUCCGGGGCGGGGGGGGC	1057	GCGGCCGGGCCGGCGGGGC	1087	GGACGGGGCGGGGCGGAGC
1028	UUCCGGGGCGGGGGGGGCA	1058	CGGCCGGGCCGGCGGGGCG	1088	GACGGGGCGGGGCGGAGCC
1029	UCCGGGGCGGGGGGGGCAC	1059	GGCCGGGCCGGCGGGGCGG	1089	ACGGGGCGGGGCGGAGCCG
1030	CCGGGGCGGGGGGGGCACG	1060	GCCGGGCCGGCGGGGCGGG	1090	CGGGGCGGGGCGGAGCCGC

SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'
1091	GGGGCGGGGCGGAGCCGCG	1121	GUCCGGGCCGGGGCCGCCG	1151	CCCGCUCCCGUCGGGGCGG
1092	GGGCGGGGCGGAGCCGCGC	1122	UCCGGGCCGGGGCCGCCGU	1152	CCGCUCCCGUCGGGGCGGA
1093	GGCGGGGCGGAGCCGCGCG	1123	CCGGGCCGGGGCCGCCGUC	1153	CGCUCCCGUCGGGGCGGAG
1094	GCGGGGCGGAGCCGCGCGG	1124	CGGGCCGGGGCCGCCGUCG	1154	GCUCCCGUCGGGGCGGAGC
1095	CGGGGCGGAGCCGCGCGGG	1125	GGGCCGGGGCCGCCGUCGG	1155	CUCCCGUCGGGGCGGAGCG
1096	GGGGCGGAGCCGCGCGGGG	1126	GGCCGGGGCCGCCGUCGGG	1156	UCCCGUCGGGGCGGAGCGU
1097	GGGCGGAGCCGCGCGGGGG	1127	GCCGGGGCCGCCGUCGGGU	1157	CCCGUCGGGGCGGAGCGUC
1098	GGCGGAGCCGCGCGGGGGC	1128	CCGGGGCCGCCGUCGGGUC	1158	CCGUCGGGGCGGAGCGUCC
1099	GCGGAGCCGCGCGGGGGCC	1129	CGGGGCCGCCGUCGGGUCU	1159	CGUCGGGGCGGAGCGUCCG
1100	CGGAGCCGCGCGGGGGCCG	1130	GGGGCCGCCGUCGGGUCUC	1160	GUCGGGGCGGAGCGUCCGA
1101	GGAGCCGCGCGGGGGCCGC	1131	GGGCCGCCGUCGGGUCUCG	1161	UCGGGGCGGAGCGUCCGAC
1102	GAGCCGCGCGGGGGCCGCA	1132	GGCCGCCGUCGGGUCUCGG	1162	CGGGGCGGAGCGUCCGACG
1103	AGCCGCGCGGGGGCCGCAG	1133	GCCGCCGUCGGGUCUCGGC	1163	GGGGCGGAGCGUCCGACGA
1104	GCCGCGCGGGGGCCGCAGU	1134	CCGCCGUCGGGUCUCGGCC	1164	GGGCGGAGCGUCCGACGAU
1105	CCGCGCGGGGGCCGCAGUC	1135	CGCCGUCGGGUCUCGGCCC	1165	GGCGGAGCGUCCGACGAUC
1106	CGCGCGGGGGCCGCAGUCC	1136	GCCGUCGGGUCUCGGCCCG	1166	GCGGAGCGUCCGACGAUCG
1107	GCGCGGGGGCCGCAGUCCG	1137	CCGUCGGGUCUCGGCCCGC	1167	CGGAGCGUCCGACGAUCGG
1108	CGCGGGGGCCGCAGUCCGG	1138	CGUCGGGUCUCGGCCCGCU	1168	GGAGCGUCCGACGAUCGGC
1109	GCGGGGGCCGCAGUCCGGG	1139	GUCGGGUCUCGGCCCGCUC	1169	GAGCGUCCGACGAUCGGCC
1110	CGGGGGCCGCAGUCCGGGC	1140	UCGGGUCUCGGCCCGCUCC	1170	AGCGUCCGACGAUCGGCCU
1111	GGGGGCCGCAGUCCGGGCC	1141	CGGGUCUCGGCCCGCUCCC	1171	GCGUCCGACGAUCGGCCUC
1112	GGGGCCGCAGUCCGGGCCG	1142	GGGUCUCGGCCCGCUCCCG	1172	CGUCCGACGAUCGGCCUCC
1113	GGGCCGCAGUCCGGGCCGG	1143	GGUCUCGGCCCGCUCCCGU	1173	GUCCGACGAUCGGCCUCCA
1114	GGCCGCAGUCCGGGCCGGG	1144	GUCUCGGCCCGCUCCCGUC	1174	UCCGACGAUCGGCCUCCAC
1115	GCCGCAGUCCGGGCCGGGG	1145	UCUCGGCCCGCUCCCGUCG	1175	CCGACGAUCGGCCUCCACG
1116	CCGCAGUCCGGGCCGGGGC	1146	CUCGGCCCGCUCCCGUCGG	1176	CGACGAUCGGCCUCCACGA
1117	CGCAGUCCGGGCCGGGGCC	1147	UCGGCCCGCUCCCGUCGGG	1177	GACGAUCGGCCUCCACGAA
1118	GCAGUCCGGGCCGGGGCCG	1148	CGGCCCGCUCCCGUCGGGG	1178	ACGAUCGGCCUCCACGAAA
1119	CAGUCCGGGCCGGGGCCGC	1149	GGCCCGCUCCCGUCGGGGC	1179	CGAUCGGCCUCCACGAAAC
1120	AGUCCGGGCCGGGGCCGCC	1150	GCCCGCUCCCGUCGGGGCG	1180	GAUCGGCCUCCACGAAACG

SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'
1181	AUCGGCCUCCACGAAACGC	1211	GUGUUUGUAGUGGUUCCUC	1241	ACGUUUUCUCCUCGUAUCG
1182	UCGGCCUCCACGAAACGCG	1212	UGUUUGUAGUGGUUCCUCG	1242	CGUUUUCUCCUCGUAUCGC
1183	CGGCCUCCACGAAACGCGG	1213	GUUUGUAGUGGUUCCUCGU	1243	GUUUUCUCCUCGUAUCGCC
1184	GGCCUCCACGAAACGCGGU	1214	UUUGUAGUGGUUCCUCGUA	1244	UUUUCUCCUCGUAUCGCCA
1185	GCCUCCACGAAACGCGGUG	1215	UUGUAGUGGUUCCUCGUAG	1245	UUUCUCCUCGUAUCGCCAA
1186	CCUCCACGAAACGCGGUGC	1216	UGUAGUGGUUCCUCGUAGG	1246	UUCUCCUCGUAUCGCCAAA
1187	CUCCACGAAACGCGGUGCC	1217	GUAGUGGUUCCUCGUAGGC	1247	UCUCCUCGUAUCGCCAAAU
1188	UCCACGAAACGCGGUGCCG	1218	UAGUGGUUCCUCGUAGGCU	1248	CUCCUCGUAUCGCCAAAUU
1189	CCACGAAACGCGGUGCCGU	1219	AGUGGUUCCUCGUAGGCUC	1249	UCCUCGUAUCGCCAAAUUA
1190	CACGAAACGCGGUGCCGUG	1220	GUGGUUCCUCGUAGGCUCC	1250	CCUCGUAUCGCCAAAUUAA
1191	ACGAAACGCGGUGCCGUGA	1221	UGGUUCCUCGUAGGCUCCA	1251	CUCGUAUCGCCAAAUUAAC
1192	CGAAACGCGGUGCCGUGAU	1222	GGUUCCUCGUAGGCUCCAG	1252	UCGUAUCGCCAAAUUAACG
1193	GAAACGCGGUGCCGUGAUG	1223	GUUCCUCGUAGGCUCCAGA	1253	CGUAUCGCCAAAUUAACGC
1194	AAACGCGGUGCCGUGAUGU	1224	UUCCUCGUAGGCUCCAGAC	1254	GUAUCGCCAAAUUAACGCG
1195	AACGCGGUGCCGUGAUGUG	1225	UCCUCGUAGGCUCCAGACG	1255	UAUCGCCAAAUUAACGCGU
1196	ACGCGGUGCCGUGAUGUGU	1226	CCUCGUAGGCUCCAGACGU	1256	AUCGCCAAAUUAACGCGUU
1197	CGCGGUGCCGUGAUGUGUU	1227	CUCGUAGGCUCCAGACGUU	1257	UCGCCAAAUUAACGCGUUU
1198	GCGGUGCCGUGAUGUGUUU	1228	UCGUAGGCUCCAGACGUUU	1258	CGCCAAAUUAACGCGUUUU
1199	CGGUGCCGUGAUGUGUUUG	1229	CGUAGGCUCCAGACGUUUU	1259	GCCAAAUUAACGCGUUUUG
1200	GGUGCCGUGAUGUGUUUGU	1230	GUAGGCUCCAGACGUUUUC	1260	CCAAAUUAACGCGUUUUGC
1201	GUGCCGUGAUGUGUUUGUA	1231	UAGGCUCCAGACGUUUUCU	1261	CAAAUUAACGCGUUUUGCA
1202	UGCCGUGAUGUGUUUGUAG	1232	AGGCUCCAGACGUUUUCUC	1262	AAAUUAACGCGUUUUGCAU
1203	GCCGUGAUGUGUUUGUAGU	1233	GGCUCCAGACGUUUUCUCC	1263	AAUUAACGCGUUUUGCAUA
1204	CCGUGAUGUGUUUGUAGUG	1234	GCUCCAGACGUUUUCUCCU	1264	AUUAACGCGUUUUGCAUAU
1205	CGUGAUGUGUUUGUAGUGG	1235	CUCCAGACGUUUUCUCCUC	1265	UUAACGCGUUUUGCAUAUU
1206	GUGAUGUGUUUGUAGUGGU	1236	UCCAGACGUUUUCUCCUCG	1266	UAACGCGUUUUGCAUAUUA
1207	UGAUGUGUUUGUAGUGGUU	1237	CCAGACGUUUUCUCCUCGU	1267	AACGCGUUUUGCAUAUUAC
1208	GAUGUGUUUGUAGUGGUUC	1238	CAGACGUUUUCUCCUCGUA	1268	ACGCGUUUUGCAUAUUACA
1209	AUGUGUUUGUAGUGGUUCC	1239	AGACGUUUUCUCCUCGUAU	1269	CGCGUUUUGCAUAUUACAG
1210	UGUGUUUGUAGUGGUUCCU	1240	GACGUUUUCUCCUCGUAUC	1270	GCGUUUUGCAUAUUACAGU

SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'
1271	CGUUUUGCAUAUUACAGUU	1301	CUUAGAUUGCAAUAUAAGC	1331	AAGUCUCAAAAAAAAGUUA
1272	GUUUUGCAUAUUACAGUUG	1302	UUAGAUUGCAAUAUAAGCG	1332	AGUCUCAAAAAAAAGUUAC
1273	UUUUGCAUAUUACAGUUGA	1303	UAGAUUGCAAUAUAAGCGG	1333	GUCUCAAAAAAAAGUUACG
1274	UUUGCAUAUUACAGUUGAG	1304	AGAUUGCAAUAUAAGCGGC	1334	UCUCAAAAAAAAGUUACGU
1275	UUGCAUAUUACAGUUGAGU	1305	GAUUGCAAUAUAAGCGGCC	1335	CUCAAAAAAAAGUUACGUG
1276	UGCAUAUUACAGUUGAGUG	1306	AUUGCAAUAUAAGCGGCCA	1336	UCAAAAAAAAGUUACGUGC
1277	GCAUAUUACAGUUGAGUGC	1307	UUGCAAUAUAAGCGGCCAG	1337	CAAAAAAAAGUUACGUGCG
1278	CAUAUUACAGUUGAGUGCC	1308	UGCAAUAUAAGCGGCCAGC	1338	AAAAAAAAGUUACGUGCGU
1279	AUAUUACAGUUGAGUGCCU	1309	GCAAUAUAAGCGGCCAGCA	1339	AAAAAAAGUUACGUGCGUU
1280	UAUUACAGUUGAGUGCCUC	1310	CAAUAUAAGCGGCCAGCAA	1340	AAAAAAGUUACGUGCGUUU
1281	AUUACAGUUGAGUGCCUCG	1311	AAUAUAAGCGGCCAGCAAA	1341	AAAAAGUUACGUGCGUUUC
1282	UUACAGUUGAGUGCCUCGA	1312	AUAUAAGCGGCCAGCAAAC	1342	AAAAGUUACGUGCGUUUCU
1283	UACAGUUGAGUGCCUCGAC	1313	UAUAAGCGGCCAGCAAACA	1343	AAAGUUACGUGCGUUUCUG
1284	ACAGUUGAGUGCCUCGACU	1314	AUAAGCGGCCAGCAAACAA	1344	AAGUUACGUGCGUUUCUGC
1285	CAGUUGAGUGCCUCGACUU	1315	UAAGCGGCCAGCAAACAAG	1345	AGUUACGUGCGUUUCUGCG
1286	AGUUGAGUGCCUCGACUUA	1316	AAGCGGCCAGCAAACAAGU	1346	GUUACGUGCGUUUCUGCGA
1287	GUUGAGUGCCUCGACUUAG	1317	AGCGGCCAGCAAACAAGUC	1347	UUACGUGCGUUUCUGCGAG
1288	UUGAGUGCCUCGACUUAGA	1318	GCGGCCAGCAAACAAGUCU	1348	UACGUGCGUUUCUGCGAGU
1289	UGAGUGCCUCGACUUAGAU	1319	CGGCCAGCAAACAAGUCUC	1349	ACGUGCGUUUCUGCGAGUG
1290	GAGUGCCUCGACUUAGAUU	1320	GGCCAGCAAACAAGUCUCA	1350	CGUGCGUUUCUGCGAGUGU
1291	AGUGCCUCGACUUAGAUUG	1321	GCCAGCAAACAAGUCUCAA	1351	GUGCGUUUCUGCGAGUGUU
1292	GUGCCUCGACUUAGAUUGC	1322	CCAGCAAACAAGUCUCAAA	1352	UGCGUUUCUGCGAGUGUUA
1293	UGCCUCGACUUAGAUUGCA	1323	CAGCAAACAAGUCUCAAAA	1353	GCGUUUCUGCGAGUGUUAU
1294	GCCUCGACUUAGAUUGCAA	1324	AGCAAACAAGUCUCAAAAA	1354	CGUUUCUGCGAGUGUUAUU
1295	CCUCGACUUAGAUUGCAAU	1325	GCAAACAAGUCUCAAAAAA	1355	GUUUCUGCGAGUGUUAUUU
1296	CUCGACUUAGAUUGCAAUA	1326	CAAACAAGUCUCAAAAAAA	1356	UUUCUGCGAGUGUUAUUUU
1297	UCGACUUAGAUUGCAAUAU	1327	AAACAAGUCUCAAAAAAAA	1357	UUCUGCGAGUGUUAUUUUG
1298	CGACUUAGAUUGCAAUAUA	1328	AACAAGUCUCAAAAAAAAG	1358	UCUGCGAGUGUUAUUUUGU
1299	GACUUAGAUUGCAAUAUAA	1329	ACAAGUCUCAAAAAAAAGU	1359	CUGCGAGUGUUAUUUUGUU
1300	ACUUAGAUUGCAAUAUAAG	1330	CAAGUCUCAAAAAAAAGUU	1360	UGCGAGUGUUAUUUUGUUA

SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'
1361	GCGAGUGUUAUUUUGUUAA	1391	AGUGUCCUCUUCCUGUGUU	1421	CCUGAAAUGAAACUAGUCU
1362	CGAGUGUUAUUUUGUUAAG	1392	GUGUCCUCUUCCUGUGUUA	1422	CUGAAAUGAAACUAGUCUG
1363	GAGUGUUAUUUUGUUAAGA	1393	UGUCCUCUUCCUGUGUUAC	1423	UGAAAUGAAACUAGUCUGG
1364	AGUGUUAUUUUGUUAAGAA	1394	GUCCUCUUCCUGUGUUACA	1424	GAAAUGAAACUAGUCUGGA
1365	GUGUUAUUUUGUUAAGAAC	1395	UCCUCUUCCUGUGUUACAG	1425	AAAUGAAACUAGUCUGGAA
1366	UGUUAUUUUGUUAAGAACG	1396	CCUCUUCCUGUGUUACAGA	1426	AAUGAAACUAGUCUGGAAA
1367	GUUAUUUUGUUAAGAACGG	1397	CUCUUCCUGUGUUACAGAA	1427	AUGAAACUAGUCUGGAAAA
1368	UUAUUUUGUUAAGAACGGC	1398	UCUUCCUGUGUUACAGAAG	1428	UGAAACUAGUCUGGAAAAA
1369	UAUUUUGUUAAGAACGGCU	1399	CUUCCUGUGUUACAGAAGC	1429	GAAACUAGUCUGGAAAAAU
1370	AUUUUGUUAAGAACGGCUC	1400	UUCCUGUGUUACAGAAGCC	1430	AAACUAGUCUGGAAAAAUU
1371	UUUUGUUAAGAACGGCUCA	1401	UCCUGUGUUACAGAAGCCA	1431	AACUAGUCUGGAAAAAUUC
1372	UUUGUUAAGAACGGCUCAC	1402	CCUGUGUUACAGAAGCCAA	1432	ACUAGUCUGGAAAAAUUCA
1373	UUGUUAAGAACGGCUCACA	1403	CUGUGUUACAGAAGCCAAC	1433	CUAGUCUGGAAAAAUUCAU
1374	UGUUAAGAACGGCUCACAG	1404	UGUGUUACAGAAGCCAACC	1434	UAGUCUGGAAAAAUUCAUU
1375	GUUAAGAACGGCUCACAGU	1405	GUGUUACAGAAGCCAACCU	1435	AGUCUGGAAAAAUUCAUUG
1376	UUAAGAACGGCUCACAGUG	1406	UGUUACAGAAGCCAACCUG	1436	GUCUGGAAAAAUUCAUUGU
1377	UAAGAACGGCUCACAGUGU	1407	GUUACAGAAGCCAACCUGA	1437	UCUGGAAAAAUUCAUUGUU
1378	AAGAACGGCUCACAGUGUC	1408	UUACAGAAGCCAACCUGAA	1438	CUGGAAAAAUUCAUUGUUC
1379	AGAACGGCUCACAGUGUCC	1409	UACAGAAGCCAACCUGAAA	1439	UGGAAAAAUUCAUUGUUCU
1380	GAACGGCUCACAGUGUCCU	1410	ACAGAAGCCAACCUGAAAU	1440	GGAAAAAUUCAUUGUUCUC
1381	AACGGCUCACAGUGUCCUC	1411	CAGAAGCCAACCUGAAAUG	1441	GAAAAAUUCAUUGUUCUCU
1382	ACGGCUCACAGUGUCCUCU	1412	AGAAGCCAACCUGAAAUGA	1442	AAAAAUUCAUUGUUCUCUG
1383	CGGCUCACAGUGUCCUCUU	1413	GAAGCCAACCUGAAAUGAA	1443	AAAAUUCAUUGUUCUCUGU
1384	GGCUCACAGUGUCCUCUUC	1414	AAGCCAACCUGAAAUGAAA	1444	AAAUUCAUUGUUCUCUGUA
1385	GCUCACAGUGUCCUCUUCC	1415	AGCCAACCUGAAAUGAAAC	1445	AAUUCAUUGUUCUCUGUAG
1386	CUCACAGUGUCCUCUUCCU	1416	GCCAACCUGAAAUGAAACU	1446	AUUCAUUGUUCUCUGUAGU
1387	UCACAGUGUCCUCUUCCUG	1417	CCAACCUGAAAUGAAACUA	1447	UUCAUUGUUCUCUGUAGUU
1388	CACAGUGUCCUCUUCCUGU	1418	CAACCUGAAAUGAAACUAG	1448	UCAUUGUUCUCUGUAGUUG
1389	ACAGUGUCCUCUUCCUGUG	1419	AACCUGAAAUGAAACUAGU	1449	CAUUGUUCUCUGUAGUUGC
1390	CAGUGUCCUCUUCCUGUGU	1420	ACCUGAAAUGAAACUAGUC	1450	AUUGUUCUCUGUAGUUGCA

SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'
1451	UUGUUCUCUGUAGUUGCAG	1481	AUAAAAAUGUUAUUGAUGA	1511	GCAGAUGAAAGGGAUGGAG
1452	UGUUCUCUGUAGUUGCAGC	1482	UAAAAAUGUUAUUGAUGAC	1512	CAGAUGAAAGGGAUGGAGA
1453	GUUCUCUGUAGUUGCAGCU	1483	AAAAAUGUUAUUGAUGACU	1513	AGAUGAAAGGGAUGGAGAA
1454	UUCUCUGUAGUUGCAGCUG	1484	AAAAUGUUAUUGAUGACUG	1514	GAUGAAAGGGAUGGAGAAC
1455	UCUCUGUAGUUGCAGCUGU	1485	AAAUGUUAUUGAUGACUGA	1515	AUGAAAGGGAUGGAGAACC
1456	CUCUGUAGUUGCAGCUGUA	1486	AAUGUUAUUGAUGACUGAA	1516	UGAAAGGGAUGGAGAACCG
1457	UCUGUAGUUGCAGCUGUAC	1487	AUGUUAUUGAUGACUGAAA	1517	GAAAGGGAUGGAGAACCGC
1458	CUGUAGUUGCAGCUGUACC	1488	UGUUAUUGAUGACUGAAAA	1518	AAAGGGAUGGAGAACCGCC
1459	UGUAGUUGCAGCUGUACCU	1489	GUUAUUGAUGACUGAAAAA	1519	AAGGGAUGGAGAACCGCCA
1460	GUAGUUGCAGCUGUACCUG	1490	UUAUUGAUGACUGAAAAAA	1520	AGGGAUGGAGAACCGCCAU
1461	UAGUUGCAGCUGUACCUGA	1491	UAUUGAUGACUGAAAAAAA	1521	GGGAUGGAGAACCGCCAUG
1462	AGUUGCAGCUGUACCUGAA	1492	AUUGAUGACUGAAAAAAAA	1522	GGAUGGAGAACCGCCAUGC
1463	GUUGCAGCUGUACCUGAAA	1493	UUGAUGACUGAAAAAAAA	1523	GAUGGAGAACCGCCAUGCC
1464	UUGCAGCUGUACCUGAAAU	1494	UGAUGACUGAAAAAAAAA	1524	AUGCCCGGUGACUCCCCGG
1465	UGCAGCUGUACCUGAAAUA	1495	GAUGACUGAAAAAAAAAA	1525	UGCCCGGUGACUCCCCGGC
1466	GCAGCUGUACCUGAAAUAA	1496	AUGACUGAAAAAAAAAAA	1526	GCCCGGUGACUCCCCGGCC
1467	CAGCUGUACCUGAAAUAAA	1497	UGACUGAAAAAAAAAAAA	1527	CCCGGUGACUCCCCGGCCG
1468	AGCUGUACCUGAAAUAAAA	1498	GACUGAAAAAAAAAAAAA	1528	CCGGUGACUCCCCGGCCGU
1469	GCUGUACCUGAAAUAAAAA	1499	ACUGAAAAAAAAAAAAAA	1529	CGGUGACUCCCCGGCCGUC
1470	CUGUACCUGAAAUAAAAAU	1500	CUGAAAAAAAAAAAAAAA	1530	GGUGACUCCCCGGCCGUCA
1471	UGUACCUGAAAUAAAAAUG	1501	UGAAAAAAAAAAAAAAAA	1531	GUGACUCCCCGGCCGUCAG
1472	GUACCUGAAAUAAAAAUGU	1502	AAAACAGUGGCAGAUGAAA	1532	UGACUCCCCGGCCGUCAGC
1473	UACCUGAAAUAAAAAUGUU	1503	AAACAGUGGCAGAUGAAAG	1533	GACUCCCCGGCCGUCAGCA
1474	ACCUGAAAUAAAAAUGUUA	1504	AACAGUGGCAGAUGAAAGG	1534	ACUCCCCGGCCGUCAGCAA
1475	CCUGAAAUAAAAAUGUUAU	1505	ACAGUGGCAGAUGAAAGGG	1535	CUCCCCGGCCGUCAGCAAG
1476	CUGAAAUAAAAAUGUUAUU	1506	CAGUGGCAGAUGAAAGGGA	1536	UCCCCGGCCGUCAGCAAGC
1477	UGAAAUAAAAAUGUUAUUG	1507	AGUGGCAGAUGAAAGGGAU	1537	CCCCGGCCGUCAGCAAGCC
1478	GAAAUAAAAAUGUUAUUGA	1508	GUGGCAGAUGAAAGGGAUG	1538	CCCGGCCGUCAGCAAGCCC
1479	AAAUAAAAAUGUUAUUGAU	1509	UGGCAGAUGAAAGGGAUGG	1539	CCGGCCGUCAGCAAGCCCC
1480	AAUAAAAAUGUUAUUGAUG	1510	GGCAGAUGAAAGGGAUGGA	1540	CGGCCGUCAGCAAGCCCCC

SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'
1541	GGCCGUCAGCAAGCCCCCG	1571	GCCGGGGGACAAGGCGGGC	1601	GGCGGCGGCCCAAAUGGCG
1542	GCCGUCAGCAAGCCCCCGG	1572	CCGGGGGACAAGGCGGGCG	1602	GCGGCGGCCCAAAUGGCGG
1543	CCGUCAGCAAGCCCCCGGA	1573	CGGGGGACAAGGCGGGCGG	1603	CGGCGGCCCAAAUGGCGGC
1544	CGUCAGCAAGCCCCCGGAC	1574	GGGGGACAAGGCGGGCGGC	1604	GGCGGCCCAAAUGGCGGCC
1545	GUCAGCAAGCCCCCGGACG	1575	GGGGACAAGGCGGGCGGCC	1605	GCGGCCCAAAUGGCGGCCG
1546	UCAGCAAGCCCCCGGACGG	1576	GGGACAAGGCGGGCGGCCU	1606	CGGCCCAAAUGGCGGCCGC
1547	CAGCAAGCCCCCGGACGGC	1577	GGACAAGGCGGGCGGCCUC	1607	GGCCCAAAUGGCGGCCGCC
1548	AGCAAGCCCCCGGACGGCG	1578	GACAAGGCGGGCGGCCUCG	1608	GCCCAAAUGGCGGCCGCCC
1549	GCAAGCCCCCGGACGGCGC	1579	ACAAGGCGGGCGGCCUCGG	1609	CCCAAAUGGCGGCCGCCCC
1550	CAAGCCCCCGGACGGCGCC	1580	CAAGGCGGGCGGCCUCGGC	1610	CCAAAUGGCGGCCGCCCCG
1551	AAGCCCCCGGACGGCGCCG	1581	AAGGCGGGCGGCCUCGGCA	1611	CAAAUGGCGGCCGCCCCGG
1552	AGCCCCCGGACGGCGCCGG	1582	AGGCGGGCGGCCUCGGCAA	1612	AAAUGGCGGCCGCCCCGGC
1553	GCCCCCGGACGGCGCCGGG	1583	GGCGGGCGGCCUCGGCAAG	1613	AAUGGCGGCCGCCCCGGCG
1554	CCCCCGGACGGCGCCGGGC	1584	GCGGGCGGCCUCGGCAAGG	1614	AUGGCGGCCGCCCCGGCGG
1555	CCCCGGACGGCGCCGGGCC	1585	CGGGCGGCCUCGGCAAGGC	1615	UGGCGGCCGCCCCGGCGGC
1556	CCCGGACGGCGCCGGGCCG	1586	GGGCGGCCUCGGCAAGGCG	1616	GGCGGCCGCCCCGGCGGCG
1557	CCGGACGGCGCCGGGCCGG	1587	GGCGGCCUCGGCAAGGCGG	1617	GCGGCCGCCCCGGCGGCGG
1558	CGGACGGCGCCGGGCCGGG	1588	GCGGCCUCGGCAAGGCGGC	1618	CGGCCGCCCCGGCGGCGGG
1559	GGACGGCGCCGGGCCGGGG	1589	CGGCCUCGGCAAGGCGGCG	1619	GGCCGCCCCGGCGGCGGGC
1560	GACGGCGCCGGGCCGGGGG	1590	GGCCUCGGCAAGGCGGCGG	1620	GCCGCCCCGGCGGCGGGCA
1561	ACGGCGCCGGGCCGGGGGA	1591	GCCUCGGCAAGGCGGCGGC	1621	CCGCCCCGGCGGCGGGCAA
1562	CGGCGCCGGGCCGGGGGAC	1592	CCUCGGCAAGGCGGCGGCC	1622	CGCCCCGGCGGCGGGCAAG
1563	GGCGCCGGGCCGGGGGACA	1593	CUCGGCAAGGCGGCGGCCC	1623	GCCCCGGCGGCGGGCAAGA
1564	GCGCCGGGCCGGGGGACAA	1594	UCGGCAAGGCGGCGGCCCA	1624	CCCCGGCGGCGGGCAAGAA
1565	CGCCGGGCCGGGGGACAAG	1595	CGGCAAGGCGGCGGCCCAA	1625	CCCGGCGGCGGGCAAGAAG
1566	GCCGGGCCGGGGGACAAGG	1596	GGCAAGGCGGCGGCCCAAA	1626	GGCAGCGGGUGAUGGCCGC
1567	CCGGGCCGGGGGACAAGGC	1597	GCAAGGCGGCGGCCCAAAU	1627	GCAGCGGGUGAUGGCCGCG
1568	CGGGCCGGGGGACAAGGCG	1598	CAAGGCGGCGGCCCAAAUG	1628	CAGCGGGUGAUGGCCGCGC
1569	GGGCCGGGGGACAAGGCGG	1599	AAGGCGGCGGCCCAAAUGG	1629	AGCGGGUGAUGGCCGCGCA
1570	GGCCGGGGGACAAGGCGGG	1600	AGGCGGCGGCCCAAAUGGC	1630	GCGGGUGAUGGCCGCGCAG

SEQ ID NO	Sequence 5'-3'
1631	CGGGUGAUGGCCGCGCAGG
1632	GGGUGAUGGCCGCGCAGGU
1633	GGUGAUGGCCGCGCAGGUU
1634	GUGAUGGCCGCGCAGGUUG
1635	UGAUGGCCGCGCAGGUUGC
1636	GAUGGCCGCGCAGGUUGCA
1637	AUGGCCGCGCAGGUUGCAC
1638	UGGCCGCGCAGGUUGCACU
1639	GGCCGCGCAGGUUGCACUG
1640	GCCGCGCAGGUUGCACUGA
1641	CCGCGCAGGUUGCACUGAG
1642	CGCGCAGGUUGCACUGAGG
1643	GCGCAGGUUGCACUGAGGA
1644	CGCAGGUUGCACUGAGGAG

Table 2. DsRNA molecules targeting mRNA encoding chicken ASW (WPKCI).

SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'
1645	CGUCUGCGGGUGCCUUGCG	1675	UGGCUGACGAGAUCCGCAA	1705	CGCGCCCUGGUGGGGACAC
1646	GUCUGCGGGUGCCUUGCGA	1676	GGCUGACGAGAUCCGCAAG	1706	GCGCCCUGGUGGGGACACC
1647	UCUGCGGGUGCCUUGCGAU	1677	GCUGACGAGAUCCGCAAGG	1707	CGCCCUGGUGGGGACACCA
1648	CUGCGGGUGCCUUGCGAUA	1678	CUGACGAGAUCCGCAAGGC	1708	GCCCUGGUGGGGACACCAU
1649	UGCGGGUGCCUUGCGAUAC	1679	UGACGAGAUCCGCAAGGCG	1709	CCCUGGUGGGGACACCAUC
1650	GCGGGUGCCUUGCGAUACG	1680	GACGAGAUCCGCAAGGCGC	1710	CCUGGUGGGGACACCAUCU
1651	CGGGUGCCUUGCGAUACGU	1681	ACGAGAUCCGCAAGGCGCA	1711	CUGGUGGGGACACCAUCUU
1652	GGGUGCCUUGCGAUACGUC	1682	CGAGAUCCGCAAGGCGCAG	1712	UGGUGGGGACACCAUCUUC
1653	GGUGCCUUGCGAUACGUCG	1683	GAGAUCCGCAAGGCGCAGG	1713	GGUGGGGACACCAUCUUCG
1654	GUGCCUUGCGAUACGUCGG	1684	AGAUCCGCAAGGCGCAGGC	1714	GUGGGGACACCAUCUUCGG
1655	UGCCUUGCGAUACGUCGGC	1685	GAUCCGCAAGGCGCAGGCC	1715	UGGGGACACCAUCUUCGGG
1656	GCCUUGCGAUACGUCGGCA	1686	AUCCGCAAGGCGCAGGCCG	1716	GGGGACACCAUCUUCGGGA
1657	CCUUGCGAUACGUCGGCAU	1687	UCCGCAAGGCGCAGGCCGC	1717	GGGACACCAUCUUCGGGAA
1658	CUUGCGAUACGUCGGCAUG	1688	CCGCAAGGCGCAGGCCGCG	1718	GGACACCAUCUUCGGGAAG
1659	UUGCGAUACGUCGGCAUGG	1689	CGCAAGGCGCAGGCCGCGC	1719	GACACCAUCUUCGGGAAGA
1660	UGCGAUACGUCGGCAUGGC	1690	GCAAGGCGCAGGCCGCGCG	1720	ACACCAUCUUCGGGAAGAU
1661	GCGAUACGUCGGCAUGGCU	1691	CAAGGCGCAGGCCGCGCGC	1721	CACCAUCUUCGGGAAGAUU
1662	CGAUACGUCGGCAUGGCUG	1692	AAGGCGCAGGCCGCGCGCC	1722	ACCAUCUUCGGGAAGAUUA
1663	GAUACGUCGGCAUGGCUGA	1693	AGGCGCAGGCCGCGCGCCC	1723	CCAUCUUCGGGAAGAUUAU
1664	AUACGUCGGCAUGGCUGAC	1694	GGCGCAGGCCGCGCGCCCU	1724	CAUCUUCGGGAAGAUUAUC
1665	UACGUCGGCAUGGCUGACG	1695	GCGCAGGCCGCGCGCCCUG	1725	AUCUUCGGGAAGAUUAUCC
1666	ACGUCGGCAUGGCUGACGA	1696	CGCAGGCCGCGCGCCCUGG	1726	UCUUCGGGAAGAUUAUCCG
1667	CGUCGGCAUGGCUGACGAG	1697	GCAGGCCGCGCGCCCUGGU	1727	CUUCGGGAAGAUUAUCCGC
1668	GUCGGCAUGGCUGACGAGA	1698	CAGGCCGCGCGCCCUGGUG	1728	UUCGGGAAGAUUAUCCGCA
1669	UCGGCAUGGCUGACGAGAU	1699	AGGCCGCGCGCCCUGGUGG	1729	UCGGGAAGAUUAUCCGCAA
1670	CGGCAUGGCUGACGAGAUC	1700	GGCCGCGCGCCCUGGUGGG	1730	CGGGAAGAUUAUCCGCAAG
1671	GGCAUGGCUGACGAGAUCC	1701	GCCGCGCGCCCUGGUGGGG	1731	GGGAAGAUUAUCCGCAAGG
1672	GCAUGGCUGACGAGAUCCG	1702	CCGCGCGCCCUGGUGGGGA	1732	GGAAGAUUAUCCGCAAGGA
1673	CAUGGCUGACGAGAUCCGC	1703	CGCGCGCCCUGGUGGGGAC	1733	GAAGAUUAUCCGCAAGGAG
1674	AUGGCUGACGAGAUCCGCA	1704	GCGCGCCCUGGUGGGGACA	1734	AAGAUUAUCCGCAAGGAGA

SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'
1735	AGAUUAUCCGCAAGGAGAU	1765	UAAUCUACGAGGACGAGCA	1795	UCCAUGAUAUCUCACCCCA
1736	GAUUAUCCGCAAGGAGAUU	1766	AAUCUACGAGGACGAGCAG	1796	CCAUGAUAUCUCACCCCAA
1737	AUUAUCCGCAAGGAGAUUC	1767	AUCUACGAGGACGAGCAGU	1797	CAUGAUAUCUCACCCCAAG
1738	UUAUCCGCAAGGAGAUUCC	1768	UCUACGAGGACGAGCAGUG	1798	AUGAUAUCUCACCCCAAGC
1739	UAUCCGCAAGGAGAUUCCC	1769	CUACGAGGACGAGCAGUGC	1799	UGAUAUCUCACCCCAAGCU
1740	AUCCGCAAGGAGAUUCCCG	1770	UACGAGGACGAGCAGUGCC	1800	GAUAUCUCACCCCAAGCUC
1741	UCCGCAAGGAGAUUCCCGC	1771	ACGAGGACGAGCAGUGCCU	1801	AUAUCUCACCCCAAGCUCC
1742	CCGCAAGGAGAUUCCCGCC	1772	CGAGGACGAGCAGUGCCUU	1802	UAUCUCACCCCAAGCUCCA
1743	CGCAAGGAGAUUCCCGCCA	1773	GAGGACGAGCAGUGCCUUG	1803	AUCUCACCCCAAGCUCCAA
1744	GCAAGGAGAUUCCCGCCAA	1774	AGGACGAGCAGUGCCUUGC	1804	UCUCACCCCAAGCUCCAAC
1745	CAAGGAGAUUCCCGCCAAC	1775	GGACGAGCAGUGCCUUGCG	1805	CUCACCCCAAGCUCCAACG
1746	AAGGAGAUUCCCGCCAACA	1776	GACGAGCAGUGCCUUGCGU	1806	UCACCCCAAGCUCCAACGC
1747	AGGAGAUUCCCGCCAACAU	1777	ACGAGCAGUGCCUUGCGUU	1807	CACCCCAAGCUCCAACGCA
1748	GGAGAUUCCCGCCAACAUA	1778	CGAGCAGUGCCUUGCGUUC	1808	ACCCCAAGCUCCAACGCAU
1749	GAGAUUCCCGCCAACAUAA	1779	GAGCAGUGCCUUGCGUUCC	1809	CCCCAAGCUCCAACGCAUU
1750	AGAUUCCCGCCAACAUAAU	1780	AGCAGUGCCUUGCGUUCCA	1810	CCCAAGCUCCAACGCAUUU
1751	GAUUCCCGCCAACAUAAUC	1781	GCAGUGCCUUGCGUUCCAU	1811	CCAAGCUCCAACGCAUUUU
1752	AUUCCCGCCAACAUAAUCU	1782	CAGUGCCUUGCGUUCCAUG	1812	CAAGCUCCAACGCAUUUUC
1753	UUCCCGCCAACAUAAUCUA	1783	AGUGCCUUGCGUUCCAUGA	1813	AAGCUCCAACGCAUUUUCU
1754	UCCCGCCAACAUAAUCUAC	1784	GUGCCUUGCGUUCCAUGAU	1814	AGCUCCAACGCAUUUUCUA
1755	CCCGCCAACAUAAUCUACG	1785	UGCCUUGCGUUCCAUGAUA	1815	GCUCCAACGCAUUUUCUAG
1756	CCGCCAACAUAAUCUACGA	1786	GCCUUGCGUUCCAUGAUAU	1816	CUCCAACGCAUUUUCUAGU
1757	CGCCAACAUAAUCUACGAG	1787	CCUUGCGUUCCAUGAUAUC	1817	UCCAACGCAUUUUCUAGUG
1758	GCCAACAUAAUCUACGAGG	1788	CUUGCGUUCCAUGAUAUCU	1818	CCAACGCAUUUUCUAGUGA
1759	CCAACAUAAUCUACGAGGA	1789	UUGCGUUCCAUGAUAUCUC	1819	CAACGCAUUUUCUAGUGAU
1760	CAACAUAAUCUACGAGGAC	1790	UGCGUUCCAUGAUAUCUCA	1820	AACGCAUUUUCUAGUGAUU
1761	AACAUAAUCUACGAGGACG	1791	GCGUUCCAUGAUAUCUCAC	1821	ACGCAUUUUCUAGUGAUUC
1762	ACAUAAUCUACGAGGACGA	1792	CGUUCCAUGAUAUCUCACC	1822	CGCAUUUUCUAGUGAUUCC
1763	CAUAAUCUACGAGGACGAG	1793	GUUCCAUGAUAUCUCACCC	1823	GCAUUUUCUAGUGAUUCCU
1764	AUAAUCUACGAGGACGAGC	1794	UUCCAUGAUAUCUCACCCC	1824	CAUUUUCUAGUGAUUCCUA

SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'
1825	AUUUUCUAGUGAUUCCUAA	1855	UCAGGUUAUCUGAAGCAGA	1885	AAUCUCUUCUGGGGCAUUU
1826	UUUUCUAGUGAUUCCUAAG	1856	CAGGUUAUCUGAAGCAGAA	1886	AUCUCUUCUGGGGCAUUUA
1827	UUUCUAGUGAUUCCUAAGA	1857	AGGUUAUCUGAAGCAGAAG	1887	UCUCUUCUGGGGCAUUUAA
1828	UUCUAGUGAUUCCUAAGAA	1858	GGUUAUCUGAAGCAGAAGA	1888	CUCUUCUGGGGCAUUUAAU
1829	UCUAGUGAUUCCUAAGAAG	1859	GUUAUCUGAAGCAGAAGAU	1889	UCUUCUGGGGCAUUUAAUG
1830	CUAGUGAUUCCUAAGAAGC	1860	UUAUCUGAAGCAGAAGAUU	1890	CUUCUGGGGCAUUUAAUGA
1831	UAGUGAUUCCUAAGAAGCC	1861	UAUCUGAAGCAGAAGAUUC	1891	UUCUGGGGCAUUUAAUGAU
1832	AGUGAUUCCUAAGAAGCCA	1862	AUCUGAAGCAGAAGAUUCU	1892	UCUGGGGCAUUUAAUGAUU
1833	GUGAUUCCUAAGAAGCCAA	1863	UCUGAAGCAGAAGAUUCUG	1893	CUGGGGCAUUUAAUGAUUG
1834	UGAUUCCUAAGAAGCCAAU	1864	CUGAAGCAGAAGAUUCUGA	1894	UGGGGCAUUUAAUGAUUGU
1835	GAUUCCUAAGAAGCCAAUU	1865	UGAAGCAGAAGAUUCUGAU	1895	GGGGCAUUUAAUGAUUGUU
1836	AUUCCUAAGAAGCCAAUUG	1866	GAAGCAGAAGAUUCUGAUG	1896	GGGCAUUUAAUGAUUGUUG
1837	UUCCUAAGAAGCCAAUUGU	1867	AAGCAGAAGAUUCUGAUGA	1897	GGCAUUUAAUGAUUGUUGG
1838	UCCUAAGAAGCCAAUUGUC	1868	AGCAGAAGAUUCUGAUGAA	1898	GCAUUUAAUGAUUGUUGGC
1839	CCUAAGAAGCCAAUUGUCA	1869	GCAGAAGAUUCUGAUGAAU	1899	CAUUUAAUGAUUGUUGGCA
1840	CUAAGAAGCCAAUUGUCAG	1870	CAGAAGAUUCUGAUGAAUC	1900	AUUUAAUGAUUGUUGGCAA
1841	UAAGAAGCCAAUUGUCAGG	1871	AGAAGAUUCUGAUGAAUCU	1901	UUUAAUGAUUGUUGGCAAG
1842	AAGAAGCCAAUUGUCAGGU	1872	GAAGAUUCUGAUGAAUCUC	1902	UUAAUGAUUGUUGGCAAGA
1843	AGAAGCCAAUUGUCAGGUU	1873	AAGAUUCUGAUGAAUCUCU	1903	UAAUGAUUGUUGGCAAGAA
1844	GAAGCCAAUUGUCAGGUUA	1874	AGAUUCUGAUGAAUCUCUU	1904	AAUGAUUGUUGGCAAGAAG
1845	AAGCCAAUUGUCAGGUUAU	1875	GAUUCUGAUGAAUCUCUUC	1905	AUGAUUGUUGGCAAGAAGU
1846	AGCCAAUUGUCAGGUUAUC	1876	AUUCUGAUGAAUCUCUUCU	1906	UGAUUGUUGGCAAGAAGUG
1847	GCCAAUUGUCAGGUUAUCU	1877	UUCUGAUGAAUCUCUUCUG	1907	GAUUGUUGGCAAGAAGUGU
1848	CCAAUUGUCAGGUUAUCUG	1878	UCUGAUGAAUCUCUUCUGG	1908	AUUGUUGGCAAGAAGUGUG
1849	CAAUUGUCAGGUUAUCUGA	1879	CUGAUGAAUCUCUUCUGGG	1909	UUGUUGGCAAGAAGUGUGC
1850	AAUUGUCAGGUUAUCUGAA	1880	UGAUGAAUCUCUUCUGGGG	1910	UGUUGGCAAGAAGUGUGCU
1851	AUUGUCAGGUUAUCUGAAG	1881	GAUGAAUCUCUUCUGGGGC	1911	GUUGGCAAGAAGUGUGCUG
1852	UUGUCAGGUUAUCUGAAGC	1882	AUGAAUCUCUUCUGGGGCA	1912	UUGGCAAGAAGUGUGCUGC
1853	UGUCAGGUUAUCUGAAGCA	1883	UGAAUCUCUUCUGGGGCAU	1913	UGGCAAGAAGUGUGCUGCU
1854	GUCAGGUUAUCUGAAGCAG	1884	GAAUCUCUUCUGGGGCAUU	1914	GGCAAGAAGUGUGCUGCUA

SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'
1915	GCAAGAAGUGUGCUGCUAA	1945	CCAAUGGAUUCCGGAUGGU	1975	GGCCUGAGGGUGGGCAGUC
1916	CAAGAAGUGUGCUGCUAAC	1946	CAAUGGAUUCCGGAUGGUU	1976	GCCUGAGGGUGGGCAGUCU
1917	AAGAAGUGUGCUGCUAACC	1947	AAUGGAUUCCGGAUGGUUU	1977	CCUGAGGGUGGGCAGUCUG
1918	AGAAGUGUGCUGCUAACCU	1948	AUGGAUUCCGGAUGGUUUU	1978	CUGAGGGUGGGCAGUCUGU
1919	GAAGUGUGCUGCUAACCUG	1949	UGGAUUCCGGAUGGUUUUG	1979	UGAGGGUGGGCAGUCUGUC
1920	AAGUGUGCUGCUAACCUGG	1950	GGAUUCCGGAUGGUUUUGA	1980	GAGGGUGGGCAGUCUGUCU
1921	AGUGUGCUGCUAACCUGGG	1951	GAUUCCGGAUGGUUUUGAA	1981	AGGGUGGGCAGUCUGUCUA
1922	GUGUGCUGCUAACCUGGGC	1952	AUUCCGGAUGGUUUUGAAU	1982	GGGUGGGCAGUCUGUCUAU
1923	UGUGCUGCUAACCUGGGCC	1953	UUCCGGAUGGUUUUGAAUG	1983	GGUGGGCAGUCUGUCUAUC
1924	GUGCUGCUAACCUGGGCCU	1954	UCCGGAUGGUUUUGAAUGA	1984	GUGGGCAGUCUGUCUAUCA
1925	UGCUGCUAACCUGGGCCUG	1955	CCGGAUGGUUUUGAAUGAA	1985	UGGGCAGUCUGUCUAUCAU
1926	GCUGCUAACCUGGGCCUGA	1956	CGGAUGGUUUUGAAUGAAG	1986	GGGCAGUCUGUCUAUCAUG
1927	CUGCUAACCUGGGCCUGAC	1957	GGAUGGUUUUGAAUGAAGG	1987	GGCAGUCUGUCUAUCAUGU
1928	UGCUAACCUGGGCCUGACC	1958	GAUGGUUUUGAAUGAAGGG	1988	GCAGUCUGUCUAUCAUGUA
1929	GCUAACCUGGGCCUGACCA	1959	AUGGUUUUGAAUGAAGGGC	1989	CAGUCUGUCUAUCAUGUAC
1930	CUAACCUGGGCCUGACCAA	1960	UGGUUUUGAAUGAAGGGCC	1990	AGUCUGUCUAUCAUGUACA
1931	UAACCUGGGCCUGACCAAU	1961	GGUUUUGAAUGAAGGGCCU	1991	GUCUGUCUAUCAUGUACAU
1932	AACCUGGGCCUGACCAAUG	1962	GUUUUGAAUGAAGGGCCUG	1992	UCUGUCUAUCAUGUACAUC
1933	ACCUGGGCCUGACCAAUGG	1963	UUUUGAAUGAAGGGCCUGA	1993	CUGUCUAUCAUGUACAUCU
1934	CCUGGGCCUGACCAAUGGA	1964	UUUGAAUGAAGGGCCUGAG	1994	UGUCUAUCAUGUACAUCUC
1935	CUGGGCCUGACCAAUGGAU	1965	UUGAAUGAAGGGCCUGAGG	1995	GUCUAUCAUGUACAUCUCC
1936	UGGGCCUGACCAAUGGAUU	1966	UGAAUGAAGGGCCUGAGGG	1996	UCUAUCAUGUACAUCUCCA
1937	GGGCCUGACCAAUGGAUUC	1967	GAAUGAAGGGCCUGAGGGU	1997	CUAUCAUGUACAUCUCCAU
1938	GGCCUGACCAAUGGAUUCC	1968	AAUGAAGGGCCUGAGGGUG	1998	UAUCAUGUACAUCUCCAUA
1939	GCCUGACCAAUGGAUUCCG	1969	AUGAAGGGCCUGAGGGUGG	1999	AUCAUGUACAUCUCCAUAU
1940	CCUGACCAAUGGAUUCCGG	1970	UGAAGGGCCUGAGGGUGGG	2000	UCAUGUACAUCUCCAUAUU
1941	CUGACCAAUGGAUUCCGGA	1971	GAAGGGCCUGAGGGUGGGC	2001	CAUGUACAUCUCCAUAUUC
1942	UGACCAAUGGAUUCCGGAU	1972	AAGGGCCUGAGGGUGGGCA	2002	AUGUACAUCUCCAUAUUCU
1943	GACCAAUGGAUUCCGGAUG	1973	AGGGCCUGAGGGUGGGCAG	2003	UGUACAUCUCCAUAUUCUG
1944	ACCAAUGGAUUCCGGAUGG	1974	GGGCCUGAGGGUGGGCAGU	2004	GUACAUCUCCAUAUUCUGG

SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'
2005	UACAUCUCCAUAUUCUGGG	2035	UGGGCUGGCCUCCUGGCUA	2065	CCACAAGAGAUGCUGCAUG
2006	ACAUCUCCAUAUUCUGGGA	2036	GGGCUGGCCUCCUGGCUAA	2066	CACAAGAGAUGCUGCAUGU
2007	CAUCUCCAUAUUCUGGGAG	2037	GGCUGGCCUCCUGGCUAAG	2067	ACAAGAGAUGCUGCAUGUG
2008	AUCUCCAUAUUCUGGGAGG	2038	GCUGGCCUCCUGGCUAAGA	2068	CAAGAGAUGCUGCAUGUGU
2009	UCUCCAUAUUCUGGGAGGU	2039	CUGGCCUCCUGGCUAAGAU	2069	AAGAGAUGCUGCAUGUGUA
2010	CUCCAUAUUCUGGGAGGUC	2040	UGGCCUCCUGGCUAAGAUU	2070	AGAGAUGCUGCAUGUGUAC
2011	UCCAUAUUCUGGGAGGUCG	2041	GGCCUCCUGGCUAAGAUUU	2071	GAGAUGCUGCAUGUGUACA
2012	CCAUAUUCUGGGAGGUCGU	2042	GCCUCCUGGCUAAGAUUUU	2072	AGAUGCUGCAUGUGUACAA
2013	CAUAUUCUGGGAGGUCGUC	2043	CCUCCUGGCUAAGAUUUUU	2073	GAUGCUGCAUGUGUACAAA
2014	AUAUUCUGGGAGGUCGUCA	2044	CUCCUGGCUAAGAUUUUUG	2074	AUGCUGCAUGUGUACAAAU
2015	UAUUCUGGGAGGUCGUCAG	2045	UCCUGGCUAAGAUUUUUGC	2075	UGCUGCAUGUGUACAAAUC
2016	AUUCUGGGAGGUCGUCAGU	2046	CCUGGCUAAGAUUUUUGCA	2076	GCUGCAUGUGUACAAAUCA
2017	UUCUGGGAGGUCGUCAGUU	2047	CUGGCUAAGAUUUUUGCAC	2077	CUGCAUGUGUACAAAUCAC
2018	UCUGGGAGGUCGUCAGUUG	2048	UGGCUAAGAUUUUUGCACC	2078	UGCAUGUGUACAAAUCACU
2019	CUGGGAGGUCGUCAGUUGG	2049	GGCUAAGAUUUUUGCACCA	2079	GCAUGUGUACAAAUCACUA
2020	UGGGAGGUCGUCAGUUGGG	2050	GCUAAGAUUUUUGCACCAC	2080	CAUGUGUACAAAUCACUAG
2021	GGGAGGUCGUCAGUUGGGC	2051	CUAAGAUUUUUGCACCACA	2081	AUGUGUACAAAUCACUAGC
2022	GGAGGUCGUCAGUUGGGCU	2052	UAAGAUUUUUGCACCACAA	2082	UGUGUACAAAUCACUAGCA
2023	GAGGUCGUCAGUUGGGCUG	2053	AAGAUUUUUGCACCACAAG	2083	GUGUACAAAUCACUAGCAA
2024	AGGUCGUCAGUUGGGCUGG	2054	AGAUUUUUGCACCACAAGA	2084	UGUACAAAUCACUAGCAAA
2025	GGUCGUCAGUUGGGCUGGC	2055	GAUUUUUGCACCACAAGAG	2085	GUACAAAUCACUAGCAAAU
2026	GUCGUCAGUUGGGCUGGCC	2056	AUUUUUGCACCACAAGAGA	2086	UACAAAUCACUAGCAAAUA
2027	UCGUCAGUUGGGCUGGCCU	2057	UUUUUGCACCACAAGAGAU	2087	ACAAAUCACUAGCAAAUAG
2028	CGUCAGUUGGGCUGGCCUC	2058	UUUUGCACCACAAGAGAUG	2088	CAAAUCACUAGCAAAUAGA
2029	GUCAGUUGGGCUGGCCUCC	2059	UUUGCACCACAAGAGAUGC	2089	AAAUCACUAGCAAAUAGAU
2030	UCAGUUGGGCUGGCCUCCU	2060	UUGCACCACAAGAGAUGCU	2090	AAUCACUAGCAAAUAGAUU
2031	CAGUUGGGCUGGCCUCCUG	2061	UGCACCACAAGAGAUGCUG	2091	AUCACUAGCAAAUAGAUUU
2032	AGUUGGGCUGGCCUCCUGG	2062	GCACCACAAGAGAUGCUGC	2092	UCACUAGCAAAUAGAUUUG
2033	GUUGGGCUGGCCUCCUGGC	2063	CACCACAAGAGAUGCUGCA	2093	CACUAGCAAAUAGAUUUGU
2034	UUGGGCUGGCCUCCUGGCU	2064	ACCACAAGAGAUGCUGCAU	2094	ACUAGCAAAUAGAUUUGUU

SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'
2095	CUAGCAAAUAGAUUUGUUU	2125	AGCCACUGUUAAUGUAAAU	2155	AUGUGUCUUUGGAGGGCAA
2096	UAGCAAAUAGAUUUGUUUC	2126	GCCACUGUUAAUGUAAAUU	2156	UGUGUCUUUGGAGGGCAAU
2097	AGCAAAUAGAUUUGUUUCC	2127	CCACUGUUAAUGUAAAUUG	2157	GUGUCUUUGGAGGGCAAUA
2098	GCAAAUAGAUUUGUUUCCC	2128	CACUGUUAAUGUAAAUUGU	2158	UGUCUUUGGAGGGCAAUAA
2099	CAAAUAGAUUUGUUUCCCA	2129	ACUGUUAAUGUAAAUUGUU	2159	GUCUUUGGAGGGCAAUAAA
2100	AAAUAGAUUUGUUUCCCAU	2130	CUGUUAAUGUAAAUUGUUC	2160	UCUUUGGAGGGCAAUAAAU
2101	AAUAGAUUUGUUUCCCAUC	2131	UGUUAAUGUAAAUUGUUCU	2161	CUUUGGAGGGCAAUAAAUG
2102	AUAGAUUUGUUUCCCAUCA	2132	GUUAAUGUAAAUUGUUCUU	2162	UUUGGAGGGCAAUAAAUGC
2103	UAGAUUUGUUUCCCAUCAA	2133	UUAAUGUAAAUUGUUCUUG	2163	UUGGAGGGCAAUAAAUGCU
2104	AGAUUUGUUUCCCAUCAAC	2134	UAAUGUAAAUUGUUCUUGG	2164	UGGAGGGCAAUAAAUGCUC
2105	GAUUUGUUUCCCAUCAACU	2135	AAUGUAAAUUGUUCUUGGA	2165	GGAGGGCAAUAAAUGCUCU
2106	AUUUGUUUCCCAUCAACUU	2136	AUGUAAAUUGUUCUUGGAU	2166	GAGGGCAAUAAAUGCUCUG
2107	UUUGUUUCCCAUCAACUUA	2137	UGUAAAUUGUUCUUGGAUA	2167	AGGGCAAUAAAUGCUCUGA
2108	UUGUUUCCCAUCAACUUAG	2138	GUAAAUUGUUCUUGGAUAU	2168	GGGCAAUAAAUGCUCUGAA
2109	UGUUUCCCAUCAACUUAGC	2139	UAAAUUGUUCUUGGAUAUG	2169	GGCAAUAAAUGCUCUGAAC
2110	GUUUCCCAUCAACUUAGCC	2140	AAAUUGUUCUUGGAUAUGU	2170	GCAAUAAAUGCUCUGAACA
2111	UUUCCCAUCAACUUAGCCA	2141	AAUUGUUCUUGGAUAUGUG	2171	CAAUAAAUGCUCUGAACAG
2112	UUCCCAUCAACUUAGCCAC	2142	AUUGUUCUUGGAUAUGUGU	2172	AAUAAAUGCUCUGAACAGC
2113	UCCCAUCAACUUAGCCACU	2143	UUGUUCUUGGAUAUGUGUC	2173	AUAAAUGCUCUGAACAGCA
2114	CCCAUCAACUUAGCCACUG	2144	UGUUCUUGGAUAUGUGUCU	2174	UAAAUGCUCUGAACAGCAC
2115	CCAUCAACUUAGCCACUGU	2145	GUUCUUGGAUAUGUGUCUU	2175	AAAUGCUCUGAACAGCACU
2116	CAUCAACUUAGCCACUGUU	2146	UUCUUGGAUAUGUGUCUUU	2176	AAUGCUCUGAACAGCACUU
2117	AUCAACUUAGCCACUGUUA	2147	UCUUGGAUAUGUGUCUUUG	2177	AUGCUCUGAACAGCACUUG
2118	UCAACUUAGCCACUGUUAA	2148	CUUGGAUAUGUGUCUUUGG	2178	UGCUCUGAACAGCACUUGC
2119	CAACUUAGCCACUGUUAAU	2149	UUGGAUAUGUGUCUUUGGA	2179	GCUCUGAACAGCACUUGCA
2120	AACUUAGCCACUGUUAAUG	2150	UGGAUAUGUGUCUUUGGAG	2180	CUCUGAACAGCACUUGCAC
2121	ACUUAGCCACUGUUAAUGU	2151	GGAUAUGUGUCUUUGGAGG	2181	UCUGAACAGCACUUGCACA
2122	CUUAGCCACUGUUAAUGUA	2152	GAUAUGUGUCUUUGGAGGG	2182	CUGAACAGCACUUGCACAA
2123	UUAGCCACUGUUAAUGUAA	2153	AUAUGUGUCUUUGGAGGGC	2183	UGAACAGCACUUGCACAAU
2124	UAGCCACUGUUAAUGUAAA	2154	UAUGUGUCUUUGGAGGGCA	2184	GAACAGCACUUGCACAAUA

2185	CACUUGCACAAUAAAGAUA
2186	ACUUGCACAAUAAAGAUAC
2187	CUUGCACAAUAAAGAUACA
2188	UUGCACAAUAAAGAUACAG
2189	UGCACAAUAAAGAUACAGC
2190	GCACAAUAAAGAUACAGCA
2191	CACAAUAAAGAUACAGCAU
2192	ACAAUAAAGAUACAGCAUG
2193	CAAUAAAGAUACAGCAUGU
2194	AAUAAAGAUACAGCAUGUG
2195	AUAAAGAUACAGCAUGUGG
2196	UAAAGAUACAGCAUGUGGA
2197	AAAGAUACAGCAUGUGGAA
2198	AAGAUACAGCAUGUGGAAA
2199	AGAUACAGCAUGUGGAAAA
2200	GAUACAGCAUGUGGAAAAA
2201	AUACAGCAUGUGGAAAAAA
2202	UACAGCAUGUGGAAAAAAA
2203	ACAGCAUGUGGAAAAAAAA
2204	CAGCAUGUGGAAAAAAAAA
2205	AGCAUGUGGAAAAAAAAAA
2206	GCAUGUGGAAAAAAAAAAA
2207	CAUGUGGAAAAAAAAAAAA
2208	AUGUGGAAAAAAAAAAAAA
2209	UGUGGAAAAAAAAAAAAAA

Table 3. DsRNA molecules targeting mRNA encoding chicken r-spondin.

SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'
2210	AUGGAUCUAACAGGCGGCA	2240	AAGGGCAAGAGGCAAAGGC	2270	GAGCUGAGCCAGGGCUGUG
2211	UGGAUCUAACAGGCGGCAG	2241	AGGGCAAGAGGCAAAGGCG	2271	AGCUGAGCCAGGGCUGUGC
2212	GGAUCUAACAGGCGGCAGC	2242	GGGCAAGAGGCAAAGGCGA	2272	GCUGAGCCAGGGCUGUGCC
2213	GAUCUAACAGGCGGCAGCA	2243	GGCAAGAGGCAAAGGCGAA	2273	CUGAGCCAGGGCUGUGCCA
2214	AUCUAACAGGCGGCAGCAA	2244	GCAAGAGGCAAAGGCGAAU	2274	UGAGCCAGGGCUGUGCCAG
2215	UCUAACAGGCGGCAGCAAA	2245	CAAGAGGCAAAGGCGAAUU	2275	GAGCCAGGGCUGUGCCAGG
2216	CUAACAGGCGGCAGCAAAG	2246	AAGAGGCAAAGGCGAAUUA	2276	AGCCAGGGCUGUGCCAGGG
2217	UAACAGGCGGCAGCAAAGU	2247	AGAGGCAAAGGCGAAUUAG	2277	GCCAGGGCUGUGCCAGGGG
2218	AACAGGCGGCAGCAAAGUG	2248	GAGGCAAAGGCGAAUUAGC	2278	CCAGGGCUGUGCCAGGGGC
2219	ACAGGCGGCAGCAAAGUGG	2249	AGGCAAAGGCGAAUUAGCA	2279	CAGGGCUGUGCCAGGGGCU
2220	CAGGCGGCAGCAAAGUGGU	2250	GGCAAAGGCGAAUUAGCAC	2280	AGGGCUGUGCCAGGGGCUG
2221	AGGCGGCAGCAAAGUGGUG	2251	GCAAAGGCGAAUUAGCACU	2281	GGGCUGUGCCAGGGGCUGC
2222	GGCGGCAGCAAAGUGGUGA	2252	CAAAGGCGAAUUAGCACUG	2282	GGCUGUGCCAGGGGCUGCG
2223	GCGGCAGCAAAGUGGUGAA	2253	AAAGGCGAAUUAGCACUGA	2283	GCUGUGCCAGGGGCUGCGA
2224	CGGCAGCAAAGUGGUGAAG	2254	AAGGCGAAUUAGCACUGAG	2284	CUGUGCCAGGGGCUGCGAC
2225	GGCAGCAAAGUGGUGAAGG	2255	AGGCGAAUUAGCACUGAGC	2285	UGUGCCAGGGGCUGCGACC
2226	GCAGCAAAGUGGUGAAGGG	2256	GGCGAAUUAGCACUGAGCU	2286	GUGCCAGGGGCUGCGACCU
2227	CAGCAAAGUGGUGAAGGGC	2257	GCGAAUUAGCACUGAGCUG	2287	UGCCAGGGGCUGCGACCUG
2228	AGCAAAGUGGUGAAGGGCA	2258	CGAAUUAGCACUGAGCUGA	2288	GCCAGGGGCUGCGACCUGU
2229	GCAAAGUGGUGAAGGGCAA	2259	GAAUUAGCACUGAGCUGAG	2289	CCAGGGGCUGCGACCUGUG
2230	CAAAGUGGUGAAGGGCAAG	2260	AAUUAGCACUGAGCUGAGC	2290	CAGGGGCUGCGACCUGUGC
2231	AAAGUGGUGAAGGGCAAGA	2261	AUUAGCACUGAGCUGAGCC	2291	AGGGGCUGCGACCUGUGCU
2232	AAGUGGUGAAGGGCAAGAG	2262	UUAGCACUGAGCUGAGCCA	2292	GGGGCUGCGACCUGUGCUC
2233	AGUGGUGAAGGGCAAGAGG	2263	UAGCACUGAGCUGAGCCAG	2293	GGGCUGCGACCUGUGCUCU
2234	GUGGUGAAGGGCAAGAGGC	2264	AGCACUGAGCUGAGCCAGG	2294	GGCUGCGACCUGUGCUCUG
2235	UGGUGAAGGGCAAGAGGCA	2265	GCACUGAGCUGAGCCAGGG	2295	GCUGCGACCUGUGCUCUGA
2236	GGUGAAGGGCAAGAGGCAA	2266	CACUGAGCUGAGCCAGGGC	2296	CUGCGACCUGUGCUCUGAG
2237	GUGAAGGGCAAGAGGCAAA	2267	ACUGAGCUGAGCCAGGGCU	2297	UGCGACCUGUGCUCUGAGU
2238	UGAAGGGCAAGAGGCAAAG	2268	CUGAGCUGAGCCAGGGCUG	2298	GCGACCUGUGCUCUGAGUU
2239	GAAGGGCAAGAGGCAAAGG	2269	UGAGCUGAGCCAGGGCUGU	2299	CGACCUGUGCUCUGAGUUC

SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'
2300	GACCUGUGCUCUGAGUUCA	2330	AGAUGUUCCCCCAAGCUCU	2360	GAGAGGAACGAUAUCCGGC
2301	ACCUGUGCUCUGAGUUCAA	2331	GAUGUUCCCCCAAGCUCUU	2361	AGAGGAACGAUAUCCGGCA
2302	CCUGUGCUCUGAGUUCAAC	2332	AUGUUCCCCCAAGCUCUUC	2362	GAGGAACGAUAUCCGGCAA
2303	CUGUGCUCUGAGUUCAACG	2333	UGUUCCCCCAAGCUCUUCA	2363	AGGAACGAUAUCCGGCAAA
2304	UGUGCUCUGAGUUCAACGG	2334	GUUCCCCCAAGCUCUUCAU	2364	GGAACGAUAUCCGGCAAAU
2305	GUGCUCUGAGUUCAACGGG	2335	UUCCCCCAAGCUCUUCAUC	2365	GAACGAUAUCCGGCAAAUU
2306	UGCUCUGAGUUCAACGGGU	2336	UCCCCCAAGCUCUUCAUCC	2366	AACGAUAUCCGGCAAAUUG
2307	GCUCUGAGUUCAACGGGUG	2337	CCCCCAAGCUCUUCAUCCU	2367	ACGAUAUCCGGCAAAUUGG
2308	CUCUGAGUUCAACGGGUGC	2338	CCCCAAGCUCUUCAUCCUU	2368	CGAUAUCCGGCAAAUUGGG
2309	UCUGAGUUCAACGGGUGCC	2339	CCCAAGCUCUUCAUCCUUC	2369	GAUAUCCGGCAAAUUGGGA
2310	CUGAGUUCAACGGGUGCCU	2340	CCAAGCUCUUCAUCCUUCU	2370	AUAUCCGGCAAAUUGGGAU
2311	UGAGUUCAACGGGUGCCUG	2341	CAAGCUCUUCAUCCUUCUG	2371	UAUCCGGCAAAUUGGGAUC
2312	GAGUUCAACGGGUGCCUGA	2342	AAGCUCUUCAUCCUUCUGG	2372	AUCCGGCAAAUUGGGAUCU
2313	AGUUCAACGGGUGCCUGAG	2343	AGCUCUUCAUCCUUCUGGA	2373	UCCGGCAAAUUGGGAUCUG
2314	GUUCAACGGGUGCCUGAGA	2344	GCUCUUCAUCCUUCUGGAG	2374	CCGGCAAAUUGGGAUCUGC
2315	UUCAACGGGUGCCUGAGAU	2345	CUCUUCAUCCUUCUGGAGA	2375	CGGCAAAUUGGGAUCUGCC
2316	UCAACGGGUGCCUGAGAUG	2346	UCUUCAUCCUUCUGGAGAG	2376	GGCAAAUUGGGAUCUGCCU
2317	CAACGGGUGCCUGAGAUGU	2347	CUUCAUCCUUCUGGAGAGG	2377	GCAAAUUGGGAUCUGCCUC
2318	AACGGGUGCCUGAGAUGUU	2348	UUCAUCCUUCUGGAGAGGA	2378	CAAAUUGGGAUCUGCCUCC
2319	ACGGGUGCCUGAGAUGUUC	2349	UCAUCCUUCUGGAGAGGAA	2379	AAAUUGGGAUCUGCCUCCC
2320	CGGGUGCCUGAGAUGUUCC	2350	CAUCCUUCUGGAGAGGAAC	2380	AAUUGGGAUCUGCCUCCCA
2321	GGGUGCCUGAGAUGUUCCC	2351	AUCCUUCUGGAGAGGAACG	2381	AUUGGGAUCUGCCUCCCAU
2322	GGUGCCUGAGAUGUUCCCC	2352	UCCUUCUGGAGAGGAACGA	2382	UUGGGAUCUGCCUCCCAUC
2323	GUGCCUGAGAUGUUCCCCC	2353	CCUUCUGGAGAGGAACGAU	2383	UGGGAUCUGCCUCCCAUCC
2324	UGCCUGAGAUGUUCCCCCA	2354	CUUCUGGAGAGGAACGAUA	2384	GGGAUCUGCCUCCCAUCCU
2325	GCCUGAGAUGUUCCCCCAA	2355	UUCUGGAGAGGAACGAUAU	2385	GGAUCUGCCUCCCAUCCUG
2326	CCUGAGAUGUUCCCCCAAG	2356	UCUGGAGAGGAACGAUAUC	2386	GAUCUGCCUCCCAUCCUGU
2327	CUGAGAUGUUCCCCCAAGC	2357	CUGGAGAGGAACGAUAUCC	2387	AUCUGCCUCCCAUCCUGUC
2328	UGAGAUGUUCCCCCAAGCU	2358	UGGAGAGGAACGAUAUCCG	2388	UCUGCCUCCCAUCCUGUCC
2329	GAGAUGUUCCCCCAAGCUC	2359	GGAGAGGAACGAUAUCCGG	2389	CUGCCUCCCAUCCUGUCCA

SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'
2390	UGCCUCCCAUCCUGUCCAC	2420	GGCCUUCGCAAUACAGACA	2450	AUCAAAUGCAAAAUCGAGA
2391	GCCUCCCAUCCUGUCCACU	2421	GCCUUCGCAAUACAGACAU	2451	UCAAAUGCAAAAUCGAGAA
2392	CCUCCCAUCCUGUCCACUG	2422	CCUUCGCAAUACAGACAUG	2452	CAAAUGCAAAAUCGAGAAC
2393	CUCCCAUCCUGUCCACUGG	2423	CUUCGCAAUACAGACAUGA	2453	AAAUGCAAAAUCGAGAACU
2394	UCCCAUCCUGUCCACUGGG	2424	UUCGCAAUACAGACAUGAA	2454	AAUGCAAAAUCGAGAACUG
2395	CCCAUCCUGUCCACUGGGA	2425	UCGCAAUACAGACAUGAAC	2455	AUGCAAAAUCGAGAACUGU
2396	CCAUCCUGUCCACUGGGAU	2426	CGCAAUACAGACAUGAACA	2456	UGCAAAAUCGAGAACUGUG
2397	CAUCCUGUCCACUGGGAUA	2427	GCAAUACAGACAUGAACAA	2457	GCAAAAUCGAGAACUGUGA
2398	AUCCUGUCCACUGGGAUAC	2428	CAAUACAGACAUGAACAAG	2458	CAAAAUCGAGAACUGUGAG
2399	UCCUGUCCACUGGGAUACU	2429	AAUACAGACAUGAACAAGU	2459	AAAAUCGAGAACUGUGAGU
2400	CCUGUCCACUGGGAUACUU	2430	AUACAGACAUGAACAAGUG	2460	AAAUCGAGAACUGUGAGUC
2401	CUGUCCACUGGGAUACUUU	2431	UACAGACAUGAACAAGUGC	2461	AAUCGAGAACUGUGAGUCC
2402	UGUCCACUGGGAUACUUUG	2432	ACAGACAUGAACAAGUGCA	2462	AUCGAGAACUGUGAGUCCU
2403	GUCCACUGGGAUACUUUGG	2433	CAGACAUGAACAAGUGCAU	2463	UCGAGAACUGUGAGUCCUG
2404	UCCACUGGGAUACUUUGGC	2434	AGACAUGAACAAGUGCAUC	2464	CGAGAACUGUGAGUCCUGC
2405	CCACUGGGAUACUUUGGCC	2435	GACAUGAACAAGUGCAUCA	2465	GAGAACUGUGAGUCCUGCU
2406	CACUGGGAUACUUUGGCCU	2436	ACAUGAACAAGUGCAUCAA	2466	AGAACUGUGAGUCCUGCUU
2407	ACUGGGAUACUUUGGCCUU	2437	CAUGAACAAGUGCAUCAAA	2467	GAACUGUGAGUCCUGCUUC
2408	CUGGGAUACUUUGGCCUUC	2438	AUGAACAAGUGCAUCAAAU	2468	AACUGUGAGUCCUGCUUCA
2409	UGGGAUACUUUGGCCUUCG	2439	UGAACAAGUGCAUCAAAUG	2469	ACUGUGAGUCCUGCUUCAG
2410	GGGAUACUUUGGCCUUCGC	2440	GAACAAGUGCAUCAAAUGC	2470	CUGUGAGUCCUGCUUCAGC
2411	GGAUACUUUGGCCUUCGCA	2441	AACAAGUGCAUCAAAUGCA	2471	UGUGAGUCCUGCUUCAGCC
2412	GAUACUUUGGCCUUCGCAA	2442	ACAAGUGCAUCAAAUGCAA	2472	GUGAGUCCUGCUUCAGCCG
2413	AUACUUUGGCCUUCGCAAU	2443	CAAGUGCAUCAAAUGCAAA	2473	UGAGUCCUGCUUCAGCCGA
2414	UACUUUGGCCUUCGCAAUA	2444	AAGUGCAUCAAAUGCAAAA	2474	GAGUCCUGCUUCAGCCGAA
2415	ACUUUGGCCUUCGCAAUAC	2445	AGUGCAUCAAAUGCAAAAU	2475	AGUCCUGCUUCAGCCGAAA
2416	CUUUGGCCUUCGCAAUACA	2446	GUGCAUCAAAUGCAAAAUC	2476	GUCCUGCUUCAGCCGAAAC
2417	UUUGGCCUUCGCAAUACAG	2447	UGCAUCAAAUGCAAAAUCG	2477	UCCUGCUUCAGCCGAAACU
2418	UUGGCCUUCGCAAUACAGA	2448	GCAUCAAAUGCAAAAUCGA	2478	CCUGCUUCAGCCGAAACUU
2419	UGGCCUUCGCAAUACAGAC	2449	CAUCAAAUGCAAAAUCGAG	2479	CUGCUUCAGCCGAAACUUU

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2481	GCUUCAGCCGAAACUUUUG	2511	AGGAAGGUUUGUAUUUGCA	2541	GUUACGUCACGUGCCCCGA
2482	CUUCAGCCGAAACUUUUGC	2512	GGAAGGUUUGUAUUUGCAC	2542	UUACGUCACGUGCCCCGAA
2483	UUCAGCCGAAACUUUUGCA	2513	GAAGGUUUGUAUUUGCACA	2543	UACGUCACGUGCCCCGAAG
2484	UCAGCCGAAACUUUUGCAC	2514	AAGGUUUGUAUUUGCACAA	2544	ACGUCACGUGCCCCGAAGG
2485	CAGCCGAAACUUUUGCACA	2515	AGGUUUGUAUUUGCACAAA	2545	CGUCACGUGCCCCGAAGGC
2486	AGCCGAAACUUUUGCACAA	2516	GGUUUGUAUUUGCACAAAG	2546	GUCACGUGCCCCGAAGGCU
2487	GCCGAAACUUUUGCACAAA	2517	GUUUGUAUUUGCACAAAGG	2547	UCACGUGCCCCGAAGGCUA
2488	CCGAAACUUUUGCACAAAA	2518	UUUGUAUUUGCACAAAGGG	2548	CACGUGCCCCGAAGGCUAC
2489	CGAAACUUUUGCACAAAAU	2519	UUGUAUUUGCACAAAGGGA	2549	ACGUGCCCCGAAGGCUACU
2490	GAAACUUUUGCACAAAAUG	2520	UGUAUUUGCACAAAGGGAG	2550	CGUGCCCCGAAGGCUACUC
2491	AAACUUUUGCACAAAAUGU	2521	GUAUUUGCACAAAGGGAGA	2551	GUGCCCCGAAGGCUACUCU
2492	AACUUUUGCACAAAAUGUA	2522	UAUUUGCACAAAGGGAGAU	2552	UGCCCCGAAGGCUACUCUG
2493	ACUUUUGCACAAAAUGUAA	2523	AUUUGCACAAAGGGAGAUG	2553	GCCCCGAAGGCUACUCUGC
2494	CUUUUGCACAAAAUGUAAG	2524	UUUGCACAAAGGGAGAUGU	2554	CCCCGAAGGCUACUCUGCU
2495	UUUUGCACAAAAUGUAAGG	2525	UUGCACAAAGGGAGAUGUU	2555	CCCGAAGGCUACUCUGCUG
2496	UUUGCACAAAAUGUAAGGA	2526	UGCACAAAGGGAGAUGUUA	2556	CCGAAGGCUACUCUGCUGC
2497	UUGCACAAAAUGUAAGGAA	2527	GCACAAAGGGAGAUGUUAC	2557	CGAAGGCUACUCUGCUGCC
2498	UGCACAAAAUGUAAGGAAG	2528	CACAAAGGGAGAUGUUACG	2558	GAAGGCUACUCUGCUGCCA
2499	GCACAAAAUGUAAGGAAGG	2529	ACAAAGGGAGAUGUUACGU	2559	AAGGCUACUCUGCUGCCAA
2500	CACAAAAUGUAAGGAAGGU	2530	CAAAGGGAGAUGUUACGUC	2560	AGGCUACUCUGCUGCCAAU
2501	ACAAAAUGUAAGGAAGGUU	2531	AAAGGGAGAUGUUACGUCA	2561	GGCUACUCUGCUGCCAAUG
2502	CAAAAUGUAAGGAAGGUUU	2532	AAGGGAGAUGUUACGUCAC	2562	GCUACUCUGCUGCCAAUGG
2503	AAAAUGUAAGGAAGGUUUG	2533	AGGGAGAUGUUACGUCACG	2563	CUACUCUGCUGCCAAUGGC
2504	AAAUGUAAGGAAGGUUUGU	2534	GGGAGAUGUUACGUCACGU	2564	UACUCUGCUGCCAAUGGCA
2505	AAUGUAAGGAAGGUUUGUA	2535	GGAGAUGUUACGUCACGUG	2565	ACUCUGCUGCCAAUGGCAC
2506	AUGUAAGGAAGGUUUGUAU	2536	GAGAUGUUACGUCACGUGC	2566	CUCUGCUGCCAAUGGCACC
2507	UGUAAGGAAGGUUUGUAUU	2537	AGAUGUUACGUCACGUGCC	2567	UCUGCUGCCAAUGGCACCA
2508	GUAAGGAAGGUUUGUAUUU	2538	GAUGUUACGUCACGUGCCC	2568	CUGCUGCCAAUGGCACCAU
2509	UAAGGAAGGUUUGUAUUUG	2539	AUGUUACGUCACGUGCCCC	2569	UGCUGCCAAUGGCACCAUG

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2570	GCUGCCAAUGGCACCAUGG	2600	CCUGCGCAAUGUGAAAUGA	2630	CCCUGGGGGCCCUGCUCCA
2571	CUGCCAAUGGCACCAUGGA	2601	CUGCGCAAUGUGAAAUGAG	2631	CCUGGGGGCCCUGCUCCAA
2572	UGCCAAUGGCACCAUGGAG	2602	UGCGCAAUGUGAAAUGAGU	2632	CUGGGGGCCCUGCUCCAAG
2573	GCCAAUGGCACCAUGGAGU	2603	GCGCAAUGUGAAAUGAGUG	2633	UGGGGGCCCUGCUCCAAGA
2574	CCAAUGGCACCAUGGAGUG	2604	CGCAAUGUGAAAUGAGUGA	2634	GGGGGCCCUGCUCCAAGAA
2575	CAAUGGCACCAUGGAGUGC	2605	GCAAUGUGAAAUGAGUGAG	2635	GGGGCCCUGCUCCAAGAAG
2576	AAUGGCACCAUGGAGUGCA	2606	CAAUGUGAAAUGAGUGAGU	2636	GGGCCCUGCUCCAAGAAGA
2577	AUGGCACCAUGGAGUGCAG	2607	AAUGUGAAAUGAGUGAGUG	2637	GGCCCUGCUCCAAGAAGAG
2578	UGGCACCAUGGAGUGCAGC	2608	AUGUGAAAUGAGUGAGUGG	2638	GCCCUGCUCCAAGAAGAGG
2579	GGCACCAUGGAGUGCAGCA	2609	UGUGAAAUGAGUGAGUGGG	2639	CCCUGCUCCAAGAAGAGGA
2580	GCACCAUGGAGUGCAGCAG	2610	GUGAAAUGAGUGAGUGGGG	2640	CCUGCUCCAAGAAGAGGAA
2581	CACCAUGGAGUGCAGCAGU	2611	UGAAAUGAGUGAGUGGGGG	2641	CUGCUCCAAGAAGAGGAAG
2582	ACCAUGGAGUGCAGCAGUC	2612	GAAAUGAGUGAGUGGGGGC	2642	UGCUCCAAGAAGAGGAAGC
2583	CCAUGGAGUGCAGCAGUCC	2613	AAAUGAGUGAGUGGGGGCC	2643	GCUCCAAGAAGAGGAAGCU
2584	CAUGGAGUGCAGCAGUCCU	2614	AAUGAGUGAGUGGGGGCCC	2644	CUCCAAGAAGAGGAAGCUG
2585	AUGGAGUGCAGCAGUCCUG	2615	AUGAGUGAGUGGGGGCCCU	2645	UCCAAGAAGAGGAAGCUGU
2586	UGGAGUGCAGCAGUCCUGC	2616	UGAGUGAGUGGGGGCCCUG	2646	CCAAGAAGAGGAAGCUGUG
2587	GGAGUGCAGCAGUCCUGCG	2617	GAGUGAGUGGGGGCCCUGG	2647	CAAGAAGAGGAAGCUGUGU
2588	GAGUGCAGCAGUCCUGCGC	2618	AGUGAGUGGGGGCCCUGGG	2648	AAGAAGAGGAAGCUGUGUG
2589	AGUGCAGCAGUCCUGCGCA	2619	GUGAGUGGGGGCCCUGGGG	2649	AGAAGAGGAAGCUGUGUGG
2590	GUGCAGCAGUCCUGCGCAA	2620	UGAGUGGGGGCCCUGGGGG	2650	GAAGAGGAAGCUGUGUGGC
2591	UGCAGCAGUCCUGCGCAAU	2621	GAGUGGGGGCCCUGGGGGC	2651	AAGAGGAAGCUGUGUGGCU
2592	GCAGCAGUCCUGCGCAAUG	2622	AGUGGGGGCCCUGGGGGCC	2652	AGAGGAAGCUGUGUGGCUU
2593	CAGCAGUCCUGCGCAAUGU	2623	GUGGGGGCCCUGGGGGCCC	2653	GAGGAAGCUGUGUGGCUUC
2594	AGCAGUCCUGCGCAAUGUG	2624	UGGGGGCCCUGGGGGCCCU	2654	AGGAAGCUGUGUGGCUUCA
2595	GCAGUCCUGCGCAAUGUGA	2625	GGGGGCCCUGGGGGCCCUG	2655	GGAAGCUGUGUGGCUUCAA
2596	CAGUCCUGCGCAAUGUGAA	2626	GGGGCCCUGGGGGCCCUGC	2656	GAAGCUGUGUGGCUUCAAG
2597	AGUCCUGCGCAAUGUGAAA	2627	GGGCCCUGGGGGCCCUGCU	2657	AAGCUGUGUGGCUUCAAGA
2598	GUCCUGCGCAAUGUGAAAU	2628	GGCCCUGGGGGCCCUGCUC	2658	AGCUGUGUGGCUUCAAGAA
2599	UCCUGCGCAAUGUGAAAUG	2629	GCCCUGGGGGCCCUGCUCC	2659	GCUGUGUGGCUUCAAGAAG

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2660	CUGUGUGGCUUCAAGAAGG	2690	CGAACGCGGCGGAUCCUGC	2720	GGGGACGUGUCCCUGUGCC
2661	UGUGUGGCUUCAAGAAGGG	2691	GAACGCGGCGGAUCCUGCA	2721	GGGACGUGUCCCUGUGCCC
2662	GUGUGGCUUCAAGAAGGGG	2692	AACGCGGCGGAUCCUGCAG	2722	GGACGUGUCCCUGUGCCCC
2663	UGUGGCUUCAAGAAGGGGA	2693	ACGCGGCGGAUCCUGCAGG	2723	GACGUGUCCCUGUGCCCCG
2664	GUGGCUUCAAGAAGGGGAA	2694	CGCGGCGGAUCCUGCAGGC	2724	ACGUGUCCCUGUGCCCCGC
2665	UGGCUUCAAGAAGGGGAAC	2695	GCGGCGGAUCCUGCAGGCU	2725	CGUGUCCCUGUGCCCCGCC
2666	GGCUUCAAGAAGGGGAACG	2696	CGGCGGAUCCUGCAGGCUC	2726	GUGUCCCUGUGCCCCGCCA
2667	GCUUCAAGAAGGGGAACGA	2697	GGCGGAUCCUGCAGGCUCC	2727	UGUCCCUGUGCCCCGCCAC
2668	CUUCAAGAAGGGGAACGAG	2698	GCGGAUCCUGCAGGCUCCC	2728	GUCCCUGUGCCCCGCCACC
2669	UUCAAGAAGGGGAACGAGG	2699	CGGAUCCUGCAGGCUCCCU	2729	UCCCUGUGCCCCGCCACCA
2670	UCAAGAAGGGGAACGAGGA	2700	GGAUCCUGCAGGCUCCCUC	2730	CCCUGUGCCCCGCCACCAC
2671	CAAGAAGGGGAACGAGGAC	2701	GAUCCUGCAGGCUCCCUCU	2731	CCUGUGCCCCGCCACCACG
2672	AAGAAGGGGAACGAGGACC	2702	AUCCUGCAGGCUCCCUCUG	2732	CUGUGCCCCGCCACCACGG
2673	AGAAGGGGAACGAGGACCG	2703	UCCUGCAGGCUCCCUCUGG	2733	UGUGCCCCGCCACCACGGA
2674	GAAGGGGAACGAGGACCGA	2704	CCUGCAGGCUCCCUCUGGG	2734	GUGCCCCGCCACCACGGAG
2675	AAGGGGAACGAGGACCGAA	2705	CUGCAGGCUCCCUCUGGGG	2735	UGCCCCGCCACCACGGAGG
2676	AGGGGAACGAGGACCGAAC	2706	UGCAGGCUCCCUCUGGGGA	2736	GCCCCGCCACCACGGAGGU
2677	GGGGAACGAGGACCGAACG	2707	GCAGGCUCCCUCUGGGGAC	2737	CCCCGCCACCACGGAGGUG
2678	GGGAACGAGGACCGAACGC	2708	CAGGCUCCCUCUGGGGACG	2738	CCCGCCACCACGGAGGUGC
2679	GGAACGAGGACCGAACGCG	2709	AGGCUCCCUCUGGGGACGU	2739	CCGCCACCACGGAGGUGCG
2680	GAACGAGGACCGAACGCGG	2710	GGCUCCCUCUGGGGACGUG	2740	CGCCACCACGGAGGUGCGC
2681	AACGAGGACCGAACGCGGC	2711	GCUCCCUCUGGGGACGUGU	2741	GCCACCACGGAGGUGCGCA
2682	ACGAGGACCGAACGCGGCG	2712	CUCCCUCUGGGGACGUGUC	2742	CCACCACGGAGGUGCGCAG
2683	CGAGGACCGAACGCGGCGG	2713	UCCCUCUGGGGACGUGUCC	2743	CACCACGGAGGUGCGCAGA
2684	GAGGACCGAACGCGGCGGA	2714	CCCUCUGGGGACGUGUCCC	2744	ACCACGGAGGUGCGCAGAU
2685	AGGACCGAACGCGGCGGAU	2715	CCUCUGGGGACGUGUCCCU	2745	CCACGGAGGUGCGCAGAUG
2686	GGACCGAACGCGGCGGAUC	2716	CUCUGGGGACGUGUCCCUG	2746	CACGGAGGUGCGCAGAUGC
2687	GACCGAACGCGGCGGAUCC	2717	UCUGGGGACGUGUCCCUGU	2747	ACGGAGGUGCGCAGAUGCA
2688	ACCGAACGCGGCGGAUCCU	2718	CUGGGGACGUGUCCCUGUG	2748	CGGAGGUGCGCAGAUGCAC
2689	CCGAACGCGGCGGAUCCUG	2719	UGGGGACGUGUCCCUGUGC	2749	GGAGGUGCGCAGAUGCACU

SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'
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2751	AGGUGCGCAGAUGCACUGU	2781	AAUGCCCCGAAGGGAAAAG	2811	ACGAGCAAGGAAAGCAAGA
2752	GGUGCGCAGAUGCACUGUG	2782	AUGCCCCGAAGGGAAAAGG	2812	CGAGCAAGGAAAGCAAGAU
2753	GUGCGCAGAUGCACUGUGC	2783	UGCCCCGAAGGGAAAAGGA	2813	GAGCAAGGAAAGCAAGAUA
2754	UGCGCAGAUGCACUGUGCA	2784	GCCCCGAAGGGAAAAGGAA	2814	AGCAAGGAAAGCAAGAUAA
2755	GCGCAGAUGCACUGUGCAG	2785	CCCCGAAGGGAAAAGGAAG	2815	GCAAGGAAAGCAAGAUAAU
2756	CGCAGAUGCACUGUGCAGA	2786	CCCGAAGGGAAAAGGAAGA	2816	CAAGGAAAGCAAGAUAAUA
2757	GCAGAUGCACUGUGCAGAA	2787	CCGAAGGGAAAAGGAAGAA	2817	AAGGAAAGCAAGAUAAUAC
2758	CAGAUGCACUGUGCAGAAG	2788	CGAAGGGAAAAGGAAGAAA	2818	AGGAAAGCAAGAUAAUACA
2759	AGAUGCACUGUGCAGAAGA	2789	GAAGGGAAAAGGAAGAAAA	2819	GGAAAGCAAGAUAAUACAA
2760	GAUGCACUGUGCAGAAGAG	2790	AAGGGAAAAGGAAGAAAAA	2820	GAAAGCAAGAUAAUACAAA
2761	AUGCACUGUGCAGAAGAGC	2791	AGGGAAAAGGAAGAAAAAG	2821	AAAGCAAGAUAAUACAAAC
2762	UGCACUGUGCAGAAGAGCC	2792	GGGAAAAGGAAGAAAAAGG	2822	AAGCAAGAUAAUACAAACG
2763	GCACUGUGCAGAAGAGCCA	2793	GGAAAAGGAAGAAAAAGGA	2823	AGCAAGAUAAUACAAACGG
2764	CACUGUGCAGAAGAGCCAA	2794	GAAAAGGAAGAAAAAGGAC	2824	GCAAGAUAAUACAAACGGG
2765	ACUGUGCAGAAGAGCCAAU	2795	AAAAGGAAGAAAAAGGACG	2825	CAAGAUAAUACAAACGGGA
2766	CUGUGCAGAAGAGCCAAUG	2796	AAAGGAAGAAAAAGGACGA	2826	AAGAUAAUACAAACGGGAA
2767	UGUGCAGAAGAGCCAAUGC	2797	AAGGAAGAAAAAGGACGAG	2827	AGAUAAUACAAACGGGAAC
2768	GUGCAGAAGAGCCAAUGCC	2798	AGGAAGAAAAAGGACGAGC	2828	GAUAAUACAAACGGGAACA
2769	UGCAGAAGAGCCAAUGCCC	2799	GGAAGAAAAAGGACGAGCA	2829	AUAAUACAAACGGGAACAG
2770	GCAGAAGAGCCAAUGCCCC	2800	GAAGAAAAAGGACGAGCAA	2830	UAAUACAAACGGGAACAGA
2771	CAGAAGAGCCAAUGCCCCG	2801	AAGAAAAAGGACGAGCAAG	2831	AAUACAAACGGGAACAGAA
2772	AGAAGAGCCAAUGCCCCGA	2802	AGAAAAAGGACGAGCAAGG	2832	AUACAAACGGGAACAGAAA
2773	GAAGAGCCAAUGCCCCGAA	2803	GAAAAAGGACGAGCAAGGA	2833	UACAAACGGGAACAGAAAU
2774	AAGAGCCAAUGCCCCGAAG	2804	AAAAAGGACGAGCAAGGAA	2834	ACAAACGGGAACAGAAAUC
2775	AGAGCCAAUGCCCCGAAGG	2805	AAAAGGACGAGCAAGGAAA	2835	CAAACGGGAACAGAAAUCG
2776	GAGCCAAUGCCCCGAAGGG	2806	AAAGGACGAGCAAGGAAAG	2836	AAACGGGAACAGAAAUCGG
2777	AGCCAAUGCCCCGAAGGGA	2807	AAGGACGAGCAAGGAAAGC	2837	AACGGGAACAGAAAUCGGA
2778	GCCAAUGCCCCGAAGGGAA	2808	AGGACGAGCAAGGAAAGCA	2838	ACGGGAACAGAAAUCGGAA
2779	CCAAUGCCCCGAAGGGAAA	2809	GGACGAGCAAGGAAAGCAA	2839	CGGGAACAGAAAUCGGAAA

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2841	GGAACAGAAAUCGGAAAGA	2871	CAAAGUCUGGCACCAAGAA	2901	AACAGAGGGGGGCUGUGGC
2842	GAACAGAAAUCGGAAAGAC	2872	AAAGUCUGGCACCAAGAAG	2902	ACAGAGGGGGGCUGUGGCC
2843	AACAGAAAUCGGAAAGACA	2873	AAGUCUGGCACCAAGAAGA	2903	CAGAGGGGGGCUGUGGCCC
2844	ACAGAAAUCGGAAAGACAC	2874	AGUCUGGCACCAAGAAGAG	2904	AGAGGGGGGCUGUGGCCCC
2845	CAGAAAUCGGAAAGACACC	2875	GUCUGGCACCAAGAAGAGG	2905	GAGGGGGGCUGUGGCCCCC
2846	AGAAAUCGGAAAGACACCA	2876	UCUGGCACCAAGAAGAGGA	2906	AGGGGGGCUGUGGCCCCCA
2847	GAAAUCGGAAAGACACCAA	2877	CUGGCACCAAGAAGAGGAA	2907	GGGGGGCUGUGGCCCCCAC
2848	AAAUCGGAAAGACACCAAA	2878	UGGCACCAAGAAGAGGAAG	2908	GGGGGCUGUGGCCCCCACC
2849	AAUCGGAAAGACACCAAAG	2879	GGCACCAAGAAGAGGAAGA	2909	GGGGCUGUGGCCCCCACCA
2850	AUCGGAAAGACACCAAAGA	2880	GCACCAAGAAGAGGAAGAG	2910	GGGCUGUGGCCCCCACCAC
2851	UCGGAAAGACACCAAAGAU	2881	CACCAAGAAGAGGAAGAGC	2911	GGCUGUGGCCCCCACCACA
2852	CGGAAAGACACCAAAGAUG	2882	ACCAAGAAGAGGAAGAGCA	2912	GCUGUGGCCCCCACCACAU
2853	GGAAAGACACCAAAGAUGC	2883	CCAAGAAGAGGAAGAGCAA	2913	CUGUGGCCCCCACCACAUC
2854	GAAAGACACCAAAGAUGCA	2884	CAAGAAGAGGAAGAGCAAA	2914	UGUGGCCCCCACCACAUCC
2855	AAAGACACCAAAGAUGCAA	2885	AAGAAGAGGAAGAGCAAAC	2915	GUGGCCCCCACCACAUCCG
2856	AAGACACCAAAGAUGCAAA	2886	AGAAGAGGAAGAGCAAACA	2916	UGGCCCCCACCACAUCCGC
2857	AGACACCAAAGAUGCAAAG	2887	GAAGAGGAAGAGCAAACAG	2917	GGCCCCCACCACAUCCGCC
2858	GACACCAAAGAUGCAAAGU	2888	AAGAGGAAGAGCAAACAGA	2918	GCCCCCACCACAUCCGCCA
2859	ACACCAAAGAUGCAAAGUC	2889	AGAGGAAGAGCAAACAGAG	2919	CCCCCACCACAUCCGCCAG
2860	CACCAAAGAUGCAAAGUCU	2890	GAGGAAGAGCAAACAGAGG	2920	CCCCACCACAUCCGCCAGC
2861	ACCAAAGAUGCAAAGUCUG	2891	AGGAAGAGCAAACAGAGGG	2921	CCCACCACAUCCGCCAGCC
2862	CCAAAGAUGCAAAGUCUGG	2892	GGAAGAGCAAACAGAGGGG	2922	CCACCACAUCCGCCAGCCC
2863	CAAAGAUGCAAAGUCUGGC	2893	GAAGAGCAAACAGAGGGGG	2923	CACCACAUCCGCCAGCCCU
2864	AAAGAUGCAAAGUCUGGCA	2894	AAGAGCAAACAGAGGGGGG	2924	ACCACAUCCGCCAGCCCUG
2865	AAGAUGCAAAGUCUGGCAC	2895	AGAGCAAACAGAGGGGGGC	2925	CCACAUCCGCCAGCCCUGC
2866	AGAUGCAAAGUCUGGCACC	2896	GAGCAAACAGAGGGGGGCU	2926	CACAUCCGCCAGCCCUGCC
2867	GAUGCAAAGUCUGGCACCA	2897	AGCAAACAGAGGGGGGCUG	2927	ACAUCCGCCAGCCCUGCCC
2868	AUGCAAAGUCUGGCACCAA	2898	GCAAACAGAGGGGGGCUGU	2928	CAUCCGCCAGCCCUGCCCA
2869	UGCAAAGUCUGGCACCAAG	2899	CAAACAGAGGGGGGCUGUG	2929	AUCCGCCAGCCCUGCCCAA

SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'
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2931	CCGCCAGCCCUGCCCAAUA	2961	ACGUCACCUGACGGCAAGA	2991	CUAUGUAUAUGAAAGCUUU
2932	CGCCAGCCCUGCCCAAUAG	2962	CGUCACCUGACGGCAAGAC	2992	UAUGUAUAUGAAAGCUUUA
2933	GCCAGCCCUGCCCAAUAGC	2963	GUCACCUGACGGCAAGACU	2993	AUGUAUAUGAAAGCUUUAU
2934	CCAGCCCUGCCCAAUAGCU	2964	UCACCUGACGGCAAGACUU	2994	UGUAUAUGAAAGCUUUAUU
2935	CAGCCCUGCCCAAUAGCUG	2965	CACCUGACGGCAAGACUUC	2995	GUAUAUGAAAGCUUUAUUG
2936	AGCCCUGCCCAAUAGCUGC	2966	ACCUGACGGCAAGACUUCA	2996	UAUAUGAAAGCUUUAUUGA
2937	GCCCUGCCCAAUAGCUGCC	2967	CCUGACGGCAAGACUUCAU	2997	AUAUGAAAGCUUUAUUGAA
2938	CCCUGCCCAAUAGCUGCCC	2968	CUGACGGCAAGACUUCAUU	2998	UAUGAAAGCUUUAUUGAAC
2939	CCUGCCCAAUAGCUGCCCC	2969	UGACGGCAAGACUUCAUUG	2999	AUGAAAGCUUUAUUGAACC
2940	CUGCCCAAUAGCUGCCCCU	2970	GACGGCAAGACUUCAUUGC	3000	UGAAAGCUUUAUUGAACCA
2941	UGCCCAAUAGCUGCCCCUU	2971	ACGGCAAGACUUCAUUGCU	3001	GAAAGCUUUAUUGAACCAG
2942	GCCCAAUAGCUGCCCCUUU	2972	CGGCAAGACUUCAUUGCUG	3002	AAAGCUUUAUUGAACCAGA
2943	CCCAAUAGCUGCCCCUUUA	2973	GGCAAGACUUCAUUGCUGC	3003	AAGCUUUAUUGAACCAGAG
2944	CCAAUAGCUGCCCCUUUAC	2974	GCAAGACUUCAUUGCUGCU	3004	AGCUUUAUUGAACCAGAGC
2945	CAAUAGCUGCCCCUUUACG	2975	CAAGACUUCAUUGCUGCUA	3005	GCUUUAUUGAACCAGAGCA
2946	AAUAGCUGCCCCUUUACGU	2976	AAGACUUCAUUGCUGCUAU	3006	CUUUAUUGAACCAGAGCAC
2947	AUAGCUGCCCCUUUACGUC	2977	AGACUUCAUUGCUGCUAUG	3007	UUUAUUGAACCAGAGCACU
2948	UAGCUGCCCCUUUACGUCA	2978	GACUUCAUUGCUGCUAUGU	3008	UUAUUGAACCAGAGCACUG
2949	AGCUGCCCCUUUACGUCAC	2979	ACUUCAUUGCUGCUAUGUA	3009	UAUUGAACCAGAGCACUGC
2950	GCUGCCCCUUUACGUCACC	2980	CUUCAUUGCUGCUAUGUAU	3010	AUUGAACCAGAGCACUGCU
2951	CUGCCCCUUUACGUCACCU	2981	UUCAUUGCUGCUAUGUAUA	3011	UUGAACCAGAGCACUGCUA
2952	UGCCCCUUUACGUCACCUG	2982	UCAUUGCUGCUAUGUAUAU	3012	UGAACCAGAGCACUGCUAC
2953	GCCCCUUUACGUCACCUGA	2983	CAUUGCUGCUAUGUAUAUG	3013	GAACCAGAGCACUGCUACA
2954	CCCCUUUACGUCACCUGAC	2984	AUUGCUGCUAUGUAUAUGA	3014	AACCAGAGCACUGCUACAC
2955	CCCUUUACGUCACCUGACG	2985	UUGCUGCUAUGUAUAUGAA	3015	ACCAGAGCACUGCUACACA
2956	CCUUUACGUCACCUGACGG	2986	UGCUGCUAUGUAUAUGAAA	3016	CCAGAGCACUGCUACACAA
2957	CUUUACGUCACCUGACGGC	2987	GCUGCUAUGUAUAUGAAAG	3017	CAGAGCACUGCUACACAAC
2958	UUUACGUCACCUGACGGCA	2988	CUGCUAUGUAUAUGAAAGC	3018	AGAGCACUGCUACACAACA
2959	UUACGUCACCUGACGGCAA	2989	UGCUAUGUAUAUGAAAGCU	3019	GAGCACUGCUACACAACAU

SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'
3020	AGCACUGCUACACAACAUU	3050	AAAGACAGAGCUAUACUCC	3080	GAAGCCACAUCCACAACAC
3021	GCACUGCUACACAACAUUA	3051	AAGACAGAGCUAUACUCCU	3081	AAGCCACAUCCACAACACU
3022	CACUGCUACACAACAUUAC	3052	AGACAGAGCUAUACUCCUA	3082	AGCCACAUCCACAACACUU
3023	ACUGCUACACAACAUUACA	3053	GACAGAGCUAUACUCCUAG	3083	GCCACAUCCACAACACUUA
3024	CUGCUACACAACAUUACAC	3054	ACAGAGCUAUACUCCUAGA	3084	CCACAUCCACAACACUUAA
3025	UGCUACACAACAUUACACA	3055	CAGAGCUAUACUCCUAGAC	3085	CACAUCCACAACACUUAAG
3026	GCUACACAACAUUACACAU	3056	AGAGCUAUACUCCUAGACU	3086	ACAUCCACAACACUUAAGG
3027	CUACACAACAUUACACAUG	3057	GAGCUAUACUCCUAGACUC	3087	CAUCCACAACACUUAAGGA
3028	UACACAACAUUACACAUGU	3058	AGCUAUACUCCUAGACUCG	3088	AUCCACAACACUUAAGGAG
3029	ACACAACAUUACACAUGUC	3059	GCUAUACUCCUAGACUCGA	3089	UCCACAACACUUAAGGAGG
3030	CACAACAUUACACAUGUCA	3060	CUAUACUCCUAGACUCGAC	3090	CCACAACACUUAAGGAGGC
3031	ACAACAUUACACAUGUCAG	3061	UAUACUCCUAGACUCGACA	3091	CACAACACUUAAGGAGGCG
3032	CAACAUUACACAUGUCAGA	3062	AUACUCCUAGACUCGACAG	3092	ACAACACUUAAGGAGGCGG
3033	AACAUUACACAUGUCAGAA	3063	UACUCCUAGACUCGACAGA	3093	CAACACUUAAGGAGGCGGU
3034	ACAUUACACAUGUCAGAAA	3064	ACUCCUAGACUCGACAGAA	3094	AACACUUAAGGAGGCGGUA
3035	CAUUACACAUGUCAGAAAG	3065	CUCCUAGACUCGACAGAAG	3095	ACACUUAAGGAGGCGGUAC
3036	AUUACACAUGUCAGAAAGA	3066	UCCUAGACUCGACAGAAGC	3096	CACUUAAGGAGGCGGUACC
3037	UUACACAUGUCAGAAAGAC	3067	CCUAGACUCGACAGAAGCC	3097	ACUUAAGGAGGCGGUACCC
3038	UACACAUGUCAGAAAGACA	3068	CUAGACUCGACAGAAGCCA	3098	CUUAAGGAGGCGGUACCCC
3039	ACACAUGUCAGAAAGACAG	3069	UAGACUCGACAGAAGCCAC	3099	UUAAGGAGGCGGUACCCCC
3040	CACAUGUCAGAAAGACAGA	3070	AGACUCGACAGAAGCCACA	3100	UAAGGAGGCGGUACCCCCG
3041	ACAUGUCAGAAAGACAGAG	3071	GACUCGACAGAAGCCACAU	3101	AAGGAGGCGGUACCCCCGG
3042	CAUGUCAGAAAGACAGAGC	3072	ACUCGACAGAAGCCACAUC	3102	AGGAGGCGGUACCCCCGGC
3043	AUGUCAGAAAGACAGAGCU	3073	CUCGACAGAAGCCACAUCC	3103	GGAGGCGGUACCCCCGGCA
3044	UGUCAGAAAGACAGAGCUA	3074	UCGACAGAAGCCACAUCCA	3104	GAGGCGGUACCCCCGGCAC
3045	GUCAGAAAGACAGAGCUAU	3075	CGACAGAAGCCACAUCCAC	3105	AGGCGGUACCCCCGGCACC
3046	UCAGAAAGACAGAGCUAUA	3076	GACAGAAGCCACAUCCACA	3106	GGCGGUACCCCCGGCACCA
3047	CAGAAAGACAGAGCUAUAC	3077	ACAGAAGCCACAUCCACAA	3107	GCGGUACCCCCGGCACCAU
3048	AGAAAGACAGAGCUAUACU	3078	CAGAAGCCACAUCCACAAC	3108	CGGUACCCCCGGCACCAUG
3049	GAAAGACAGAGCUAUACUC	3079	AGAAGCCACAUCCACAACA	3109	GGUACCCCCGGCACCAUGA

SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'
3110	GUACCCCCGGCACCAUGAA	3140	GGGGCAGUGGGACACUGCA	3170	GAGGAUGAACCAAGGAUGG
3111	UACCCCCGGCACCAUGAAU	3141	GGGCAGUGGGACACUGCAG	3171	AGGAUGAACCAAGGAUGGG
3112	ACCCCCGGCACCAUGAAUG	3142	GGCAGUGGGACACUGCAGG	3172	GGAUGAACCAAGGAUGGGG
3113	CCCCCGGCACCAUGAAUGG	3143	GCAGUGGGACACUGCAGGA	3173	GAUGAACCAAGGAUGGGGG
3114	CCCCGGCACCAUGAAUGGC	3144	CAGUGGGACACUGCAGGAC	3174	AUGAACCAAGGAUGGGGGC
3115	CCCGGCACCAUGAAUGGCA	3145	AGUGGGACACUGCAGGACC	3175	UGAACCAAGGAUGGGGGCA
3116	CCGGCACCAUGAAUGGCAU	3146	GUGGGACACUGCAGGACCA	3176	GAACCAAGGAUGGGGGCAU
3117	CGGCACCAUGAAUGGCAUC	3147	UGGGACACUGCAGGACCAG	3177	AACCAAGGAUGGGGGCAUG
3118	GGCACCAUGAAUGGCAUCC	3148	GGGACACUGCAGGACCAGA	3178	ACCAAGGAUGGGGGCAUGG
3119	GCACCAUGAAUGGCAUCCA	3149	GGACACUGCAGGACCAGAG	3179	CCAAGGAUGGGGGCAUGGG
3120	CACCAUGAAUGGCAUCCAU	3150	GACACUGCAGGACCAGAGG	3180	CAAGGAUGGGGGCAUGGGG
3121	ACCAUGAAUGGCAUCCAUU	3151	ACACUGCAGGACCAGAGGU	3181	AAGGAUGGGGGCAUGGGGC
3122	CCAUGAAUGGCAUCCAUUG	3152	CACUGCAGGACCAGAGGUG	3182	AGGAUGGGGGCAUGGGGCC
3123	CAUGAAUGGCAUCCAUUGG	3153	ACUGCAGGACCAGAGGUGA	3183	GGAUGGGGGCAUGGGGCCU
3124	AUGAAUGGCAUCCAUUGGG	3154	CUGCAGGACCAGAGGUGAG	3184	GAUGGGGGCAUGGGGCCUU
3125	UGAAUGGCAUCCAUUGGGG	3155	UGCAGGACCAGAGGUGAGG	3185	AUGGGGGCAUGGGGCCUUG
3126	GAAUGGCAUCCAUUGGGGC	3156	GCAGGACCAGAGGUGAGGA	3186	UGGGGGCAUGGGGCCUUGG
3127	AAUGGCAUCCAUUGGGGCA	3157	CAGGACCAGAGGUGAGGAU	3187	GGGGGCAUGGGGCCUUGGG
3128	AUGGCAUCCAUUGGGGCAG	3158	AGGACCAGAGGUGAGGAUG	3188	GGGGCAUGGGGCCUUGGGA
3129	UGGCAUCCAUUGGGGCAGU	3159	GGACCAGAGGUGAGGAUGA	3189	GGGCAUGGGGCCUUGGGAC
3130	GGCAUCCAUUGGGGCAGUG	3160	GACCAGAGGUGAGGAUGAA	3190	GGCAUGGGGCCUUGGGACA
3131	GCAUCCAUUGGGGCAGUGG	3161	ACCAGAGGUGAGGAUGAAC	3191	GCAUGGGGCCUUGGGACAC
3132	CAUCCAUUGGGGCAGUGGG	3162	CCAGAGGUGAGGAUGAACC	3192	CAUGGGGCCUUGGGACACU
3133	AUCCAUUGGGGCAGUGGGA	3163	CAGAGGUGAGGAUGAACCA	3193	AUGGGGCCUUGGGACACUU
3134	UCCAUUGGGGCAGUGGGAC	3164	AGAGGUGAGGAUGAACCAA	3194	UGGGGCCUUGGGACACUUG
3135	CCAUUGGGGCAGUGGGACA	3165	GAGGUGAGGAUGAACCAAG	3195	GGGGCCUUGGGACACUUGC
3136	CAUUGGGGCAGUGGGACAC	3166	AGGUGAGGAUGAACCAAGG	3196	GGGCCUUGGGACACUUGCC
3137	AUUGGGGCAGUGGGACACU	3167	GGUGAGGAUGAACCAAGGA	3197	GGCCUUGGGACACUUGCCU
3138	UUGGGGCAGUGGGACACUG	3168	GUGAGGAUGAACCAAGGAU	3198	GCCUUGGGACACUUGCCUU
3139	UGGGGCAGUGGGACACUGC	3169	UGAGGAUGAACCAAGGAUG	3199	CCUUGGGACACUUGCCUUG

SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'
3200	CUUGGGACACUUGCCUUGU	3230	CACGUGGACUGGAUUUCUG	3260	CGGGGAACUGGACUCACAU
3201	UUGGGACACUUGCCUUGUG	3231	ACGUGGACUGGAUUUCUGC	3261	GGGGAACUGGACUCACAUA
3202	UGGGACACUUGCCUUGUGC	3232	CGUGGACUGGAUUUCUGCU	3262	GGGAACUGGACUCACAUAA
3203	GGGACACUUGCCUUGUGCC	3233	GUGGACUGGAUUUCUGCUC	3263	GGAACUGGACUCACAUAAA
3204	GGACACUUGCCUUGUGCCC	3234	UGGACUGGAUUUCUGCUCU	3264	GAACUGGACUCACAUAAAG
3205	GACACUUGCCUUGUGCCCA	3235	GGACUGGAUUUCUGCUCUU	3265	AACUGGACUCACAUAAAGG
3206	ACACUUGCCUUGUGCCCAG	3236	GACUGGAUUUCUGCUCUUC	3266	ACUGGACUCACAUAAAGGC
3207	CACUUGCCUUGUGCCCAGC	3237	ACUGGAUUUCUGCUCUUCC	3267	CUGGACUCACAUAAAGGCA
3208	ACUUGCCUUGUGCCCAGCC	3238	CUGGAUUUCUGCUCUUCCA	3268	UGGACUCACAUAAAGGCAA
3209	CUUGCCUUGUGCCCAGCCA	3239	UGGAUUUCUGCUCUUCCAG	3269	GGACUCACAUAAAGGCAAU
3210	UUGCCUUGUGCCCAGCCAG	3240	GGAUUUCUGCUCUUCCAGA	3270	GACUCACAUAAAGGCAAUG
3211	UGCCUUGUGCCCAGCCAGC	3241	GAUUUCUGCUCUUCCAGAC	3271	ACUCACAUAAAGGCAAUGU
3212	GCCUUGUGCCCAGCCAGCC	3242	AUUUCUGCUCUUCCAGACC	3272	CUCACAUAAAGGCAAUGUC
3213	CCUUGUGCCCAGCCAGCCA	3243	UUUCUGCUCUUCCAGACCG	3273	UCACAUAAAGGCAAUGUCC
3214	CUUGUGCCCAGCCAGCCAC	3244	UUCUGCUCUUCCAGACCGG	3274	CACAUAAAGGCAAUGUCCU
3215	UUGUGCCCAGCCAGCCACG	3245	UCUGCUCUUCCAGACCGGG	3275	ACAUAAAGGCAAUGUCCUC
3216	UGUGCCCAGCCAGCCACGU	3246	CUGCUCUUCCAGACCGGGG	3276	CAUAAAGGCAAUGUCCUCU
3217	GUGCCCAGCCAGCCACGUG	3247	UGCUCUUCCAGACCGGGGA	3277	AUAAAGGCAAUGUCCUCUU
3218	UGCCCAGCCAGCCACGUGG	3248	GCUCUUCCAGACCGGGGAA	3278	UAAAGGCAAUGUCCUCUUU
3219	GCCCAGCCAGCCACGUGGA	3249	CUCUUCCAGACCGGGGAAC	3279	AAAGGCAAUGUCCUCUUUC
3220	CCCAGCCAGCCACGUGGAC	3250	UCUUCCAGACCGGGGAACU	3280	AAGGCAAUGUCCUCUUUCU
3221	CCAGCCAGCCACGUGGACU	3251	CUUCCAGACCGGGGAACUG	3281	AGGCAAUGUCCUCUUUCUC
3222	CAGCCAGCCACGUGGACUG	3252	UUCCAGACCGGGGAACUGG	3282	GGCAAUGUCCUCUUUCUCU
3223	AGCCAGCCACGUGGACUGG	3253	UCCAGACCGGGGAACUGGA	3283	GCAAUGUCCUCUUUCUCUU
3224	GCCAGCCACGUGGACUGGA	3254	CCAGACCGGGGAACUGGAC	3284	CAAUGUCCUCUUUCUCUUC
3225	CCAGCCACGUGGACUGGAU	3255	CAGACCGGGGAACUGGACU	3285	AAUGUCCUCUUUCUCUUCC
3226	CAGCCACGUGGACUGGAUU	3256	AGACCGGGGAACUGGACUC	3286	AUGUCCUCUUUCUCUUCCC
3227	AGCCACGUGGACUGGAUUU	3257	GACCGGGGAACUGGACUCA	3287	UGUCCUCUUUCUCUUCCCC
3228	GCCACGUGGACUGGAUUUC	3258	ACCGGGGAACUGGACUCAC	3288	GUCCUCUUUCUCUUCCCCC
3229	CCACGUGGACUGGAUUUCU	3259	CCGGGGAACUGGACUCACA	3289	UCCUCUUUCUCUUCCCCCC

SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'
3290	CCUCUUUCUCUUCCCCCCA	3320	UGUGUUUUAAGCUGUAUGA	3350	AGAAUAAUACAUGUUAAAC
3291	CUCUUUCUCUUCCCCCCAA	3321	GUGUUUUAAGCUGUAUGAC	3351	GAAUAAUACAUGUUAAACG
3292	UCUUUCUCUUCCCCCCAAC	3322	UGUUUUAAGCUGUAUGACU	3352	AAUAAUACAUGUUAAACGU
3293	CUUUCUCUUCCCCCCAACC	3323	GUUUUAAGCUGUAUGACUU	3353	AUAAUACAUGUUAAACGUU
3294	UUUCUCUUCCCCCCAACCC	3324	UUUUAAGCUGUAUGACUUU	3354	UAAUACAUGUUAAACGUUU
3295	UUCUCUUCCCCCCAACCCU	3325	UUUAAGCUGUAUGACUUUA	3355	AAUACAUGUUAAACGUUUG
3296	UCUCUUCCCCCCAACCCUU	3326	UUAAGCUGUAUGACUUUAU	3356	AUACAUGUUAAACGUUUGU
3297	CUCUUCCCCCCAACCCUUU	3327	UAAGCUGUAUGACUUUAUC	3357	UACAUGUUAAACGUUUGUG
3298	UCUUCCCCCCAACCCUUUA	3328	AAGCUGUAUGACUUUAUCA	3358	ACAUGUUAAACGUUUGUGG
3299	CUUCCCCCCAACCCUUUAU	3329	AGCUGUAUGACUUUAUCAC	3359	CAUGUUAAACGUUUGUGGU
3300	UUCCCCCCAACCCUUUAUU	3330	GCUGUAUGACUUUAUCACU	3360	AUGUUAAACGUUUGUGGUA
3301	UCCCCCCAACCCUUUAUUU	3331	CUGUAUGACUUUAUCACUG	3361	UGUUAAACGUUUGUGGUAA
3302	CCCCCCAACCCUUUAUUUU	3332	UGUAUGACUUUAUCACUGA	3362	GUUAAACGUUUGUGGUAAG
3303	CCCCCAACCCUUUAUUUUG	3333	GUAUGACUUUAUCACUGAG	3363	UUAAACGUUUGUGGUAAGA
3304	CCCCAACCCUUUAUUUUGU	3334	UAUGACUUUAUCACUGAGA	3364	UAAACGUUUGUGGUAAGAG
3305	CCCAACCCUUUAUUUUGUG	3335	AUGACUUUAUCACUGAGAA	3365	AAACGUUUGUGGUAAGAGG
3306	CCAACCCUUUAUUUUGUGU	3336	UGACUUUAUCACUGAGAAU	3366	AACGUUUGUGGUAAGAGGU
3307	CAACCCUUUAUUUUGUGUU	3337	GACUUUAUCACUGAGAAUA	3367	ACGUUUGUGGUAAGAGGUC
3308	AACCCUUUAUUUUGUGUUU	3338	ACUUUAUCACUGAGAAUAA	3368	CGUUUGUGGUAAGAGGUCA
3309	ACCCUUUAUUUUGUGUUUU	3339	CUUUAUCACUGAGAAUAAU	3369	GUUUGUGGUAAGAGGUCAG
3310	CCCUUUAUUUUGUGUUUUA	3340	UUUAUCACUGAGAAUAAUA	3370	UUUGUGGUAAGAGGUCAGU
3311	CCUUUAUUUUGUGUUUUAA	3341	UUAUCACUGAGAAUAAUAC	3371	UUGUGGUAAGAGGUCAGUG
3312	CUUUAUUUUGUGUUUUAAG	3342	UAUCACUGAGAAUAAUACA	3372	UGUGGUAAGAGGUCAGUGG
3313	UUUAUUUUGUGUUUUAAGC	3343	AUCACUGAGAAUAAUACAU	3373	GUGGUAAGAGGUCAGUGGU
3314	UUAUUUUGUGUUUUAAGCU	3344	UCACUGAGAAUAAUACAUG	3374	UGGUAAGAGGUCAGUGGUA
3315	UAUUUUGUGUUUUAAGCUG	3345	CACUGAGAAUAAUACAUGU	3375	GGUAAGAGGUCAGUGGUAU
3316	AUUUUGUGUUUUAAGCUGU	3346	ACUGAGAAUAAUACAUGUU	3376	GUAAGAGGUCAGUGGUAUC
3317	UUUUGUGUUUUAAGCUGUA	3347	CUGAGAAUAAUACAUGUUA	3377	UAAGAGGUCAGUGGUAUCU
3318	UUUGUGUUUUAAGCUGUAU	3348	UGAGAAUAAUACAUGUUAA	3378	AAGAGGUCAGUGGUAUCUG
3319	UUGUGUUUUAAGCUGUAUG	3349	GAGAAUAAUACAUGUUAAA	3379	AGAGGUCAGUGGUAUCUGC

SEQ ID NO	Sequence 5'-3'	SEQ ID NO	Sequence 5'-3'
3380	GAGGUCAGUGGUAUCUGCC	3410	UCAAAGAGUUAUUUCAAAU
3381	AGGUCAGUGGUAUCUGCCC	3411	CAAAGAGUUAUUUCAAAUU
3382	GGUCAGUGGUAUCUGCCCU	3412	AAAGAGUUAUUUCAAAUUA
3383	GUCAGUGGUAUCUGCCCUG	3413	AAGAGUUAUUUCAAAUUAA
3384	UCAGUGGUAUCUGCCCUGA	3414	AGAGUUAUUUCAAAUUAAA
3385	CAGUGGUAUCUGCCCUGAA	3415	GAGUUAUUUCAAAUUAAAA
3386	AGUGGUAUCUGCCCUGAAU	3416	AGUUAUUUCAAAUUAAAAG
3387	GUGGUAUCUGCCCUGAAUC	3417	GUUAUUUCAAAUUAAAAGC
3388	UGGUAUCUGCCCUGAAUCU	3418	UUAUUUCAAAUUAAAAGCA
3389	GGUAUCUGCCCUGAAUCUG	3419	UAUUUCAAAUUAAAAGCAA
3390	GUAUCUGCCCUGAAUCUGC	3420	AUUUCAAAUUAAAAGCAAA
3391	UAUCUGCCCUGAAUCUGCU	3421	UUUCAAAUUAAAAGCAAAA
3392	AUCUGCCCUGAAUCUGCUU	3422	UUCAAAUUAAAAGCAAAAC
3393	UCUGCCCUGAAUCUGCUUC	3423	UCAAAUUAAAAGCAAAACA
3394	CUGCCCUGAAUCUGCUUCA	3424	CAAAUUAAAAGCAAAACAA
3395	UGCCCUGAAUCUGCUUCAA	3425	AAAUUAAAAGCAAAACAAA
3396	GCCCUGAAUCUGCUUCAAA	3426	AAUUAAAAGCAAAACAAAA
3397	CCCUGAAUCUGCUUCAAAG	3427	AUUAAAAGCAAAACAAAAC
3398	CCUGAAUCUGCUUCAAAGA	3428	UUAAAAGCAAAACAAAACA
3399	CUGAAUCUGCUUCAAAGAG	3429	UAAAAGCAAAACAAAACAA
3400	UGAAUCUGCUUCAAAGAGU	3430	AAAAGCAAAACAAAACAAA
3401	GAAUCUGCUUCAAAGAGUU		
3402	AAUCUGCUUCAAAGAGUUA		
3403	AUCUGCUUCAAAGAGUUAU		
3404	UCUGCUUCAAAGAGUUAUU		
3405	CUGCUUCAAAGAGUUAUUU		
3406	UGCUUCAAAGAGUUAUUUC		
3407	GCUUCAAAGAGUUAUUUCA		
3408	CUUCAAAGAGUUAUUUCAA		
3409	UUCAAAGAGUUAUUUCAAA		

The double-stranded regions should be at least 19 contiguous nucleotides, for example about 19 to 23 nucleotides, or may be longer, for example 30 or 50 nucleotides, or 100 nucleotides or more. The full-length sequence corresponding to the entire gene transcript may be used. Preferably, they are about 19 to about 100 nucleotides in length, more preferably about 19 to about 50 nucleotides in length, and even more preferably about 19 to about 23 nucleotides in length.

The degree of identity of a double-stranded region of a nucleic acid molecule to the targeted transcript should be at least 90% and more preferably 95-100%. The % identity of a nucleic acid molecule is determined by GAP (Needleman and Wunsch, 1970) analysis (GCG program) with a gap creation penalty=5, and a gap extension penalty=0.3. Preferably, the two sequences are aligned over their entire length.

The nucleic acid molecule may of course comprise sequences unrelated to the target which may function to stabilize the molecule.

The term "short interfering RNA" or "siRNA" as used herein refers to a nucleic acid molecule which comprises ribonucleotides capable of inhibiting or down regulating gene expression, for example by mediating RNAi in a sequence-specific manner, wherein the double stranded portion is less than 50 nucleotides in length, preferably about 19 to about 23 nucleotides in length. For example, the siRNA can be a nucleic acid molecule comprising self-complementary sense and antisense regions, wherein the antisense region comprises a nucleotide sequence that is complementary to nucleotide sequence in a target nucleic acid molecule or a portion thereof and the sense region having nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof. The siRNA can be assembled from two separate oligonucleotides, where one strand is the sense strand and the other is the antisense strand, wherein the antisense and sense strands are self-complementary.

As used herein, the term siRNA is equivalent to other terms used to describe nucleic acid molecules that are capable of mediating sequence specific RNAi, for example micro-RNA (miRNA), short hairpin RNA (shRNA), short interfering oligonucleotide, short interfering nucleic acid (siNA), short interfering modified oligonucleotide, chemically-modified siRNA, and others. In addition, as used herein, the term RNAi is equivalent to other terms used to describe sequence specific RNA interference, such as post transcriptional gene silencing, translational inhibition, or epigenetics. For example, siRNA molecules of the invention can be used to epigenetically silence genes at both the post-transcriptional level or the pre-transcriptional level. In a non-limiting example, epigenetic regulation of gene

expression by siRNA molecules of the invention can result from siRNA mediated modification of chromatin structure to alter gene expression.

Preferred siRNA molecules comprise a nucleotide sequence that is identical to about 19 to 23 contiguous nucleotides of the target mRNA. In an embodiment, the target mRNA sequence commences with the dinucleotide AA, comprises a GC-content of about 30-70% (preferably, 30-60%, more preferably 40-60% and more preferably about 45%-55%), and does not have a high percentage identity to any nucleotide sequence other than the target in the genome of the avain (preferably chickens) in which it is to be introduced, e.g., as determined by standard BLAST search.

By "shRNA" or "short-hairpin RNA" is meant an siRNA molecule where less than about 50 nucleotides, preferably about 19 to about 23 nucleotides, is base paired with a complementary sequence located on the same RNA molecule, and where said sequence and complementary sequence are separated by an unpaired region of at least about 4 to 15 nucleotides which forms a single-stranded loop above the stem structure created by the two regions of base complementarity. Examples of sequences of a single-stranded loops are 5' UUCAAGAGA 3' and 5' UUUGUGUAG 3'.

Included shRNAs are dual or bi-finger and multi-finger hairpin dsRNAs, in which the RNA molecule comprises two or more of such stem-loop structures separated by single-stranded spacer regions.

siRNAs can be generated *in vitro* by using a recombinant enzyme, such as T7 RNA polymerase, and DNA oligonucleotide templates, or can be prepared *in vivo*, for example, in cultured cells. In a preferred embodiment, the nucleic acid molecule is produced synthetically.

Strategies have been described for producing a hairpin siRNA from vectors containing, for example, a RNA polymerase III promoter. Various vectors have been constructed for generating hairpin siRNAs in host cells using either an H1-RNA or an snU6 RNA promoter (see SEQ ID NO's 7 to 9). A RNA molecule as described above (e.g., a first portion, a linking sequence, and a second portion) can be operably linked to such a promoter. When transcribed by RNA polymerase III, the first and second portions form a duplexed stem of a hairpin and the linking sequence forms a loop. The pSuper vector (OligoEngines Ltd., Seattle, Wash.) can also be used to generate siRNA.

Modifications or analogs of nucleotides can be introduced to improve the properties of the nucleic acid molecules of the invention. Improved properties include increased nuclease resistance and/or increased ability to permeate cell membranes. Accordingly, the terms "nucleic acid molecule" and "double-stranded RNA molecule" includes synthetically modified bases such as, but not limited to, inosine, xanthine,

hypoxanthine, 2-aminoadenine, 6-methyl-, 2-propyl- and other alkyl- adenines, 5-halo uracil, 5-halo cytosine, 6-aza cytosine and 6-aza thymine, pseudo uracil, 4-thiuracil, 8-halo adenine, 8-aminoadenine, 8-thiol adenine, 8-thiolalkyl adenines, 8-hydroxyl adenine and other 8-substituted adenines, 8-halo guanines, 8-amino guanine, 8-thiol guanine, 8-thioalkyl guanines, 8-hydroxyl guanine and other substituted guanines, other aza and deaza adenines, other aza and deaza guanines, 5-trifluoromethyl uracil and 5-trifluoro cytosine.

Vectors and Host Cells

The present invention also provides a vector encoding a nucleic acid molecule comprising a double-stranded region, or single strand thereof, of the present invention. Preferably, the vector is an expression vector capable of expressing the open reading frame(s) encoding a dsRNA in a host cell and/or cell free system. The host cell can be any cell type such as, not limited to, bacterial, fungal, plant or animal cells, preferably an avian cell.

Typically, a vector of the invention comprises a promoter operably linked to an open reading frame encoding a nucleic acid molecule of the invention, or a strand thereof.

As used herein, the term “promoter” refers to a nucleic acid sequence which is able to direct transcription of an operably linked nucleic acid molecule and includes, for example, RNA polymerase II and RNA polymerase III promoters. Also included in this definition are those transcriptional regulatory elements (e.g., enhancers) that are sufficient to render promoter-dependent gene expression controllable in a cell type-specific, tissue-specific, or temporal-specific manner, or that are inducible by external agents or signals.

"Operably linked" as used herein refers to a functional relationship between two or more nucleic acid (e.g., DNA) segments. Typically, it refers to the functional relationship of a transcriptional regulatory element to a transcribed sequence. For example, a promoter is operably linked to a coding sequence, such as an open reading frame encoding a double-stranded RNA molecule defined herein, if it stimulates or modulates the transcription of the coding sequence in an appropriate cell. Generally, promoter transcriptional regulatory elements that are operably linked to a transcribed sequence are physically contiguous to the transcribed sequence, i.e., they are *cis*-acting. However, some transcriptional regulatory elements, such as enhancers, need not be physically contiguous or located in close proximity to the coding sequences whose transcription they enhance.

By "RNA polymerase III promoter" or "RNA pol III promoter" or "polymerase III promoter" or "pol III promoter" is meant any invertebrate, vertebrate, or mammalian promoter, e.g., chicken, human, murine, porcine, bovine, primate, simian, etc. that, in its native context in a cell, associates or interacts with RNA polymerase III to transcribe its operably linked gene, or any variant thereof, natural or engineered, that will interact in a selected host cell with an RNA polymerase III to transcribe an operably linked nucleic acid sequence. By U6 promoter (e.g., chicken U6, human U6, murine U6), H1 promoter, or 7SK promoter is meant any invertebrate, vertebrate, or mammalian promoter or polymorphic variant or mutant found in nature to interact with RNA polymerase III to transcribe its cognate RNA product, i.e., U6 RNA, H1 RNA, or 7SK RNA, respectively. Examples of suitable promoters include cU6-1 (SEQ ID NO:7), cU6-3 (SEQ ID NO:8), cU6-4 (SEQ ID NO:9) and c7SK (SEQ ID NO:10).

When *E. coli* is used as a host cell, there is no limitation other than that the vector should have an "ori" to amplify and mass-produce the vector in *E. coli* (e.g., JM109. DH5α, HB101, or XL1Blue), and a marker gene for selecting the transformed *E. coli* (e.g., a drug-resistance gene selected by a drug such as ampicillin, tetracycline, kanamycin, or chloramphenicol). For example, M13-series vectors, pUC-series vectors, pBR322, pBluescript, pCR-Script, and such can be used. pGEM-T, pDIRECT, pT7, and so on can also be used for subcloning and excision of the gene encoding the dsRNA as well as the vectors described above.

With regard to expression vectors for use in *E. coli*, such vectors include JM109, DH5α, HB101, or XL1 Blue, the vector should have a promoter such as lacZ promoter, araB promoter, or T7 promoter that can efficiently promote the expression of the desired gene in *E. coli*. Other examples of the vectors are "QIAexpress system" (Qiagen), pEGFP, and pET (for this vector, BL21, a strain expressing T7 RNA polymerase, is preferably used as the host).

In addition to the vectors for *E. coli*, for example, the vector may be a mammal-derived expression vector (e.g., pcDNA3 (Invitrogen), pEGF-BOS, pEF, and pCDM8), an insect cell-derived expression vector (e.g., "Bac-to-BAC baculovairus expression system" (GibcoBRL) and pBacPAK8), a plant-derived expression vector (e.g., pMH1 and pMH2), an animal virus-derived expression vector (e.g., pHSV, pMV, and pAdexLcw), a retrovirus-derived expression vector (e.g., pZIPneo), a yeast-derived expression vector (e.g., "Pichia Expression Kit" (Invitrogen), pNV11, and SP-Q01), or a *Bacillus subtilis*-derived expression vector (e.g., pPL608 and pKTH50).

In order to express nucleic acid molecules in animal cells, such as CHO, COS, Vero and NIH3T3 cells, the vector should have a promoter necessary for expression in

such cells, e.g., SV40 promoter, MMLV-LTR promoter, EF1α promoter, CMV promoter, etc., and more preferably it has a marker gene for selecting transformants (for example, a drug resistance gene selected by a drug (e.g., neomycin, G418, etc.). Examples of vectors with these characteristics include pMAM, pDR2, pBK-RSV, pBK-CMV, pOPRSV and pOP13.

Nucleic acid molecules comprising a double-stranded region of the present invention can be expressed in animals such as avians by, for example, inserting an open reading frame(s) encoding the nucleic acid into an appropriate vector and introducing the vector by the retrovirus method, liposome method, cationic liposome method, adenovirus method, and so on. The vectors used include, but are not limited to, adenoviral vectors (e.g., pAdexlcw) and retroviral vectors (e.g., pZIPneo). General techniques for gene manipulation, such as insertion of nucleic acids of the invention into a vector, can be performed according to conventional methods.

The present invention also provides a host cell into which an exogenous nucleic acid molecule, typically in a vector of the present invention, has been introduced. The host cell of this invention can be used as, for example, a production system for producing or expressing the nucleic acid molecule. For *in vitro* production, eukaryotic cells or prokaryotic cells can be used.

Useful eukaryotic host cells may be animal, plant, or fungi cells. As animal cells, mammalian cells such as CHO, COS, 3T3, myeloma, baby hamster kidney (BHK), HeLa, or Vero cells MDCK cells, DF1 cells, amphibian cells such as *Xenopus* oocytes, or insect cells such as Sf9, Sf21, or Tn5 cells can be used. CHO cells lacking DHFR gene (dhfr-CHO) or CHO K-1 may also be used. The vector can be introduced into the host cell by, for example, the calcium phosphate method, the DEAE-dextran method, cationic liposome DOTAP (Boehringer Mannheim) method, electroporation, lipofection, etc.

Useful prokaryotic cells include bacterial cells, such as *E. coli*, for example, JM109, DH5a, and HB101, or *Bacillus subtilis*.

Culture medium such as DMEM, MEM, RPMI-1640, or IMDM may be used for animal cells. The culture medium can be used with or without serum supplement such as fetal calf serum (FCS). The pH of the culture medium is preferably between about 6 and 8. Cells are typically cultured at about 30 to 40° C for about 15 to 200 hr, and the culture medium may be replaced, aerated, or stirred if necessary.

Compositions

The present invention also provides compositions comprising a nucleic acid molecule comprising a double-stranded region that can be administered to an avian egg. A composition comprising a nucleic acid molecule comprising a double-stranded region may contain a pharmaceutically acceptable carrier to render the composition suitable for administration.

Suitable pharmaceutical carriers, excipients and/or diluents include, but are not limited to, lactose, sucrose, starch powder, talc powder, cellulose esters of alkonoic acids, magnesium stearate, magnesium oxide, crystalline cellulose, methyl cellulose, carboxymethyl cellulose, gelatin, glycerin, sodium alginate, antibacterial agents, antifungal agents, gum arabic, acacia gum, sodium and calcium salts of phosphoric and sulfuric acids, polyvinylpyrrolidone and/or polyvinyl alcohol, saline, and water. In an embodiment, the carrier, excipient and/or diluent is phosphate buffered saline or water.

In an embodiment, the composition may also comprise a transfection promoting agent. Transfection promoting agents used to facilitate the uptake of nucleic acids into a living cell are well known within the art. Reagents enhancing transfection include chemical families of the types; polycations, dendrimers, DEAE Dextran, block copolymers and cationic lipids. Preferably, the transfection-promoting agent is a lipid-containing compound (or formulation), providing a positively charged hydrophilic region and a fatty acyl hydrophobic region enabling self-assembly in aqueous solution into vesicles generally known as micelles or liposomes, as well as lipopolyamines.

In another embodiment, the composition comprises a polymeric biomaterial such as chitosan.

It is understood that any conventional media or agent may be used so long as it is not incompatible with the compositions or methods of the invention.

Administration

Administration of a nucleic acid molecule comprising a double-stranded region (including a composition comprising a nucleic acid molecule comprising a double-stranded region) is conveniently achieved by injection into the egg, and generally injection into the chorion allantoic fluid. Notwithstanding that the air sac is the preferred route of *in ovo* administration, other regions such as the yolk sac, air sac or amnionic cavity (amnion) may also be inoculated by injection. The hatchability rate might decrease slightly when the air sac is not the target for the administration although not necessarily at commercially unacceptable levels. The mechanism of injection is not critical to the practice of the present invention, although it is preferred that the needle

does not cause undue damage to the egg or to the tissues and organs of the developing embryo or the extra-embryonic membranes surrounding the embryo.

Preferably, the nucleic acid molecule is administered within four days of the egg having been laid.

Generally, a hypodermic syringe fitted with an approximately 22 gauge needle is suitable. The method of the present invention is particularly well adapted for use with an automated injection system, such as those described in US 4,903,635, US 5,056,464, US 5,136,979 and US 20060075973.

The nucleic acid molecule is administered in an effective amount sufficient to modify sex in at least some of the eggs which have been administered. The modification can be detected by comparing a suitable number of samples subjected to the method of the invention to a similar number that have not. Statistically significant variation in the sex of the birds between the two groups will be indicative that an effective amount has been administered. Other means of determining an effective amount for sex are well within the capacity of those skilled in the art.

Preferably, about 1ng to 100µg, more preferably about 100ng to 1µg, of nucleic acid is administered to the egg. Furthermore, it is preferred that the nucleic acid to be administered is in a volume of about 1µl to 1ml, more preferably about 10µl to 500 µl.

EXAMPLES

Example 1 - Identification of shRNA molecules for down-regulating DMRT1 protein production in chickens

Selection of shRNA sequences targeting DMRT1

The present inventors identified 51 predicted shRNA sequences to target chicken Dmrt1 (Table 4).

There are several algorithms available to select potential siRNA sequences for specific target genes. Taxman et al. (2006) have specifically designed an algorithm to predict effective shRNA molecules and the present inventors have made their own modification to the algorithm to improve shRNA prediction. There are four criteria for shRNA selection using the Taxman algorithm. Three of the criteria are scored for out of a maximum number of 4 points. These criteria are: 1) C or G on the 5' end of the sequence = 1 point, A or T on 5' end = -1 point; 2) A or T on the 3' end = 1 point, C or G on the 3' end = -1 point; 3) 5 or more A or T in the seven 3' bases = 2 points, 4 A or T in the seven 3' bases = 1 point. shRNA sequences with the highest scores are preferred. The fourth criteria is based on a calculation for the free-energy of the 6 central bases of the shRNA sequence (bases 6-11 of the sense strand hybridised to

bases 9-14 of the antisense strand). shRNAs with a central duplex $\Delta G > -12.9$ kcal/mol are preferred.

The shRNA designer website uses this algorithm to provide a score for each shRNA target. Based on the algorithm and their calculated ΔG value, the present inventors chose 4 of the shRNA target finder shRNA sequences as potentially effective shRNAs to test for their ability to knockdown Dmrt1 gene expression. The selected sequences are shown in their 5' – 3' sequence in Table 5. These 4 sequences were used to construct ddRNAi plasmids for the expression of the 6 shRNAs.

Construction of ddRNAi plasmids for expression of selected shRNAs

To construct the Dmrt1 shRNA expression constructs, two oligonucleotides complementary to each other were designed to contain the sense, loop, antisense and termination signal, followed by a spacer sequence (GGAA) and a BamHI restriction site for screening. In addition, the "bottom oligo (B)" or reverse oligonucleotide contained a SalI overhang at the 5' end for insertion into the expression vector containing the chicken polymerase III promoter cU6-4 (DQ531570). Table 6 lists the shRNA targets to their corresponding oligonucleotides. The complementary oligonucleotides for each target shRNA, were annealed together and ligated into the PmeI-SalI digested pU6-4 vector. Full length clones were positive if linearised by *BamHI* digestion. All shRNA expression vectors were sequence confirmed. The four constructs were referred to as 105sh, 240sh, 465sh and 591sh as shown in Figure 1. The non-silencing control shRNA construct (NSsh) was designed in the same way. However, the sequence used was that of an irrelevant target (ie. NP gene of influenza).

Each ddRNAi plasmid was constructed so that the start of each shRNA sequence was at the +1 position of the native U6 snRNA transcripts. All final shRNA expression vectors consisted of either one of the full length chicken U6 promoters, a shRNA sense sequence, a loop sequence, a shRNA antisense sequence, a termination sequence and a *BamHI* site. The loop sequence used in all shRNAs was 5' UUCAAGAGA 3'.

Table 4. Algorithm selection of shRNA sequences targeting Dmrt1.

Target Sequence	Start Position	SEQ ID NO	Score
GGCACAAGCGGTTCTGCAT	79	3435	3
GACTGCCAGTGCAAGAAGT	105	3436	3
CTGAGCCAGTTGTCAAGAA	238	3437	3
GAGCCAGTTGTCAAGAAGA	240	3438	3
GACGGATGCTCATTCAGGA	355	3439	3
GCACGTCTGATTTGGTTGT	409	3440	3
GTGGACTCCACCTACTACA	426	3441	3
CCAGCCATCCCTGTATCCT	455	3442	3
CCATCCCTGTATCCTTACT	459	3443	3
CATCCCTGTATCCTTACTA	460	3444	3
CCCTGTATCCTTACTATAA	463	3445	4
CTGTATCCTTACTATAACA	465	3446	4
CTTACTATAACAACCTGTA	472	3447	3
CTCCCAGTACCAAATGGCA	497	3448	3
GCCACTGAGTCTTCCTCAA	519	3449	3
CTGAGTCTTCCTCAAGTGA	523	3450	3
GAGTCTTCCTCAAGTGAGA	525	3451	3
CTCCCAGCAACATACATGT	591	3452	4
CCCAGCAACATACATGTCA	593	3453	3
CCAGCAACATACATGTCAA	594	3454	3
CAGATGAAGGGAATGGAGA	633	3455	3
CCACCTGCGTCACACAGAT	733	3456	3
CACCTGCGTCACACAGATA	734	3457	3
CCTGCGTCACACAGATACT	736	3458	3
CTCCTACTCAGAGTCGAAA	773	3459	3
CACTGTTGCCTTGTTCTGT	967	3460	3
GGTGCCGTGATGTGTTTGT	1189	3461	3
GTGCCGTGATGTGTTTGTA	1190	3462	4
GCCGTGATGTGTTTGTAGT	1192	3463	4
CCTCGTATCGCCAAATTAA	1239	3464	4
GCCTCGACTTAGATTGCAA	1283	3465	3
CCTCGACTTAGATTGCAAT	1284	3466	4
CTCGACTTAGATTGCAATA	1285	3467	4
CGACTTAGATTGCAATATA	1287	3468	4
GACTTAGATTGCAATATAA	1288	3469	4
GCGGCCAGCAAACAAGTCT	1307	3470	3
GGCCAGCAAACAAGTCTCA	1309	3471	3
GCCAGCAAACAAGTCTCAA	1310	3472	3
CCAGCAAACAAGTCTCAAA	1311	3473	3
GCGTTTCTGCGAGTGTTAT	1342	3474	4
GTGTCCTCTTCCTGTGTTA	1381	3475	3
GTCCTCTTCCTGTGTTACA	1383	3476	3
CCTCTTCCTGTGTTACAGA	1385	3477	3
CTCTTCCTGTGTTACAGAA	1386	3478	4
GAAGCCAACCTGAAATGAA	1402	3479	4
GCCAACCTGAAATGAAACT	1405	3480	4
CCAACCTGAAATGAAACTA	1406	3481	4
CCTGAAATGAAACTAGTCT	1410	3482	3
GTTGCAGCTGTACCTGAAA	1452	3483	3
GCAGCTGTACCTGAAATAA	1455	3484	4
CAGCTGTACCTGAAATAAA	1456	3485	4

Table 5. Sequence of Dmrt1 shRNAs.

Target Number	Position	Target Sequence	Score	ΔG
1	105 bp	GACTGCCAGTGCAAGAAGT (SEQ ID NO:3436)	3	-17.1
2	240 bp	GAGCCAGTTGTCAAGAAGA (SEQ ID NO:3438)	3	-12.7
3	465 bp	CTGTATCCTTACTATAACA (SEQ ID NO:3446)	4	-11.9
4	591 bp	CTCCCAGCAACATACATGT (SEQ ID NO:3452)	4	-14.0

Testing selected shRNAs for knockdown of Dmrt1 gene expression

A reporter gene expression assay was used to test shRNAs for silencing of Dmrt1. The reporter gene was a transcriptional gene fusion of Dmrt1 inserted downstream of the 3' end of the Enhanced Green Fluorescent Protein (EGFP) gene in pEGFP-C (Clontech). The reporter plasmid was constructed as follows: cDNA of Dmrt1 was reverse transcribed from total RNA isolated from 4 day old embryo's and cloned into the multiple cloning site of pCMV-Script (Stratagene). The Dmrt1 insert was removed from the cloning vector as a NotI – EcoRI fragment and cloned downstream of the EGFP gene in pEGFP-C (Clontech). The resulting plasmid was named pEGFP-Dmrt1. This plasmid was transfected into chicken DF-1 cells and expression of the transcriptional gene fusion was confirmed by measuring EGFP fluorescence using flow cytometry as described below.

Dmrt1 gene silencing assays were conducted by co-transfecting DF-1 cells with the pEGFP-Dmrt1 reporter plasmid and each of the ddRNAi plasmids expressing the Dmrt1 specific and control shRNAs. The co-transfection experiments were performed as follows: DF-1 cells (ATCC CRL-12203, chicken fibroblast) were maintained in a humidified atmosphere containing 5% CO_2 at 37°C in Dulbecco's Modified Eagle's Medium (DMEM) containing 4.5g/l glucose, 1.5g/l sodium bicarbonate, 10% foetal calf serum (FCS), 2mM L-glutamine supplemented with penicillin (100 U/ml) and streptomycin (100 µg/ml). DF1 cells were passaged as required using 0.25% (w/v) trypsin-ethylenediaminetetraacetic acid (EDTA).

Table 6. Sequence and details of primers used.

Target Number	Position	Target Sequence	Score	ΔG
1	105 bp	GACTGCCAGTGCAAGAAGT (SEQ ID NO:3436)	3	-17.1
DMRT1-105T-U6.4 GACTGCCAGTGCAAGAAGTTTCAAGAGAACTTCTTGCACTGGCAGTCTTTTT**G** **GAA***GGATCC* (SEQ ID NO:3486) DMRT1-105B-U6.4 TCGA*GGATCC***TTC**CAAAAAGACTGCCAGTGCAAGAAGTTCTCTTGAAACTTC TTGCACTGGCAGTC (SEQ ID NO:3487)				
Target Number	**Position**	**Target Sequence**	**Score**	**ΔG**
2	240 bp	GAGCCAGTTGTCAAGAAGA (SEQ ID NO:3438)	3	-12.7
DMRT1-240T-U6.4 GAGCCAGTTGTCAAGAAGATTCAAGAGATCTTCTTGACAACTGGCTCTTTTT**G** **GAA***GGATCC* (SEQ ID NO:3488) DMRT1-240B-U6.4 TCGA*GGATCC***TTC**CAAAAAGAGCCAGTTGTCAAGAAGATCTCTTGAATCTTCT TGACAACTGGCTC (SEQ ID NO:3489)				
Target Number	**Position**	**Target Sequence**	**Score**	**ΔG**
3	465 bp	CTGTATCCTTACTATAACA (SEQ ID NO:3446)	4	-11.9
DMRT1-465T-U6.4 CTGTATCCTTACTATAACATTCAAGAGATGTTATAGTAAGGATACAGTTTTT**G** **GAA***GGATCC* (SEQ ID NO:3490) DMRT1-465B-U6.4 TCGA*GGATCC***TTC**CAAAAACTGTATCCTTACTATAACATCTCTTGAATGTTAT AGTAAGGATACAG (SEQ ID NO:3491)				
Target Number	**Position**	**Target Sequence**	**Score**	**ΔG**
4	591 bp	CTCCCAGCAACATACATGT (SEQ ID NO:3452)	4	-14.0
DMRT1-591T-U6.4 CTCCCAGCAACATACATGTTTCAAGAGAACATGTATGTTGCTGGGAGTTTTT**G** **GAA***GGATCC* (SEQ ID NO:3492) DMRT1-591B-U6.4 TCGA*GGATCC***TTC**CAAAAACTCCCAGCAACATACATGTTCTCTTGAAACATGT ATGTTGCTGGGAG (SEQ ID NO:3493)				

Bold = spacer sequence; *Italics = BamHI restriction site*; Underline = SalI overhang

Co-transfection of pEGFP-Dmrt1 and ddRNAi plasmids for EGFP-Dmrt1 fusion silencing assays was conducted in DF-1 cells grown to 80-90% confluence, in 24 well culture plates (Nunc) for flow cytometry analysis. Cells were transfected with a total of 1μg of plasmid DNA, per well, using Lipofectamine™2000 transfection reagent (Invitrogen). EGFP expression was analysed in transfected DF-1 cells at 60 hours post-transfection using flow cytometry analysis of transfections performed in triplicate. Cells were trypsinised using 100 μl of 0.25% trypsin-EDTA, pelleted at 2000 rpm for 5 minutes, washed once in 1 ml of cold phosphate buffered saline-A (PBSA) (Oxoid), twice in 1 ml of FACS-wash solution (PBSA + 1% FCS) and resuspended in 250 μl of FACS-wash solution. Flow cytometry sampling was performed using a FACScalibur (Becton Dickinson) fluorescence activated cell sorter. Data acquisition and calculation of mean fluorescence intensity (MFI) values for triplicate co-transfection samples, was performed using CELLQuest software (Becton Dickinson). The results of the gene silencing assay are shown in Figure 1. Compared to the negative control irrelevant shRNA expressed from NSsh, the Dmrt1 specific shRNAs were observed to knockdown expression of the reporter gene to varying levels. Dmrt1 shRNA 240sh induced the greatest level of gene silencing of approximately 60%.

Example 2 - *In ovo* modulation of *DMRT1* gene expression in chickens

An siRNA targeted to a conserved exon of the chicken *DMRT1* gene was designed using the Ambion siRNA Target Finder tool (www.ambion.com). The chosen siRNA was designated *DMRT1*-343-siRNA (5'-GAGCCAGUUGUCAAGAAGAUU-3') (SEQ ID NO:3431). The siRNA was synthesized and obtained from Qiagen.

For *in ovo* delivery, the siRNA was formulated with lipoefectamine 2000 (Invitrogen) according to the manufacturer's instructions. The now complexed siRNA was then delivered *in ovo* at a dose of either 100 pmol or 200 pmol. The siRNA was injected into embryonated eggs via an intravenous (I.V.) route or directly into the amnion at embryonic day 4.5 (E4.5). For both I.V. and amnion delivery, a small opening (1cm x 1cm) was created at the top of the blunt end of the egg so as to avoid the membrane, veins and arteries, and 100 pmol or 200 pmol in a 4 μl volume was then injected directly into a vein or into the amnionic cavity using a micro-capillary pipette. Micro-capillaries of 1 mm diameter were used for injections, and their tips were pulled to a diameter of 40 microns with bevelled tip of 22.5°. After injection, the holes in the eggs were sealed with appropriate sized parafilm squares using a heated scalpel blade.

In total, 286 embryonated eggs (E4.5) were used in this experiment;

Group 1: 48 eggs were used as controls and were not injected with the *DMRT1*-343-siRNA formulation;

Group 2: 51 eggs were injected I.V. with 100 pmol of siRNA;

Group 3: 53 eggs were injected I.V. with 200 pmol of siRNA;

Group 4: 81 eggs were injected into the amnion with 100 pmol of siRNA and;

Group 5: 53 eggs were injected into the amnion with 200 pmol of siRNA.

All embryos were incubated until day E10. At E10, all embryos were assessed for viability and then removed from the egg. Control Group 1 had an embryo viability of 100%; Group 2 had a viability of 76%; Group 3 had a viability of 94%; Group 4 had a viability of 40% and; Group 5 had a viability of 75%. A single limb bud from each embryo was removed and used in a sex determination PCR test to determine if the embryos were of male or female genotype. Lower limb buds from each embryo were collected into 50 µl of PCR digestion buffer (50 mM KCl; 10 mM Tris-HCl, pH8.3; 0.1 mg/ml gelatine; 0.45% Nonidet P-40; 0.45% Tween-20; 0.2 mg/ml proteinase K; stock stored at -20°C) at room temperature and digested at 55°C for a minimum of 1 h, then at 95°C for 10 min to release genomic DNA.

Sexing was carried out by PCR using the method of Clinton et al. (2001). The PCR mix consisted of 1 µl of digestion mix, 10 X RedTaq reaction buffer (Sigma-Aldrich), $MgCl_2$ to 1.5 mM (Promega), 1 unit of RedTaq DNA polymerase (Sigma-Aldrich) and Milli-Q water (Millipore) to a total volume of 20 µl. Reactions were carried out in a Master cycler S (Eppendorf) PCR machine. Products were run on a 1.5% 1 X Tris-borate (TBE) agarose gels.

Once the sex PCR test was complete and analysed, the embryos were definitively labelled as either being genotypically male or female. The embryos were then opened via dissection and the gonads exposed for macroscopic analysis of gonadal development. The gonadal development of all control embryos was normal as expected. Control female embryo's showed typical asymmetric development that was characterised by a large left ovary and smaller regressing right gonad. Control male embryos all had typical bilateral testes. All female embryos from the siRNA knockdown groups (Groups 2-5) had normal gonadal development. In contrast, some male embryos from the siRNA knockdown groups showed varying degrees of female-like asymmetry at the macroscopic level of the gonads. The feminisation effect of the *DMRT1*-343-siRNA was characterised by an average or small-sized right testis and a larger feminised left gonad (Table 7). Feminisation was observed in a number of male embryos in Groups 2, 3 and 5 and resulted in an increase in the ratio of embryos with female-like gonads in these groups.

Table 7. *DMRT1* embryo injection results.

siRNA dose and injection route	No. embryos injected	No. viable at E10	% Male :Female Genotype (PCR sex test)	% Male:Female Macroscopic Gonad phenotype
Group 1 No injection control	48	48 (100%)	60:40	60:40
Group 2 I.V. – 100 pmol	51	39 (76%)	59:41	54:46
Group 3 I.V. – 200 pmol	53	50 (94%)	54:46	46:54
Group 4 Amnion – 100 pmol	81	33 (40%)	48:52	48:52
Group 5 Amnion – 200 pmol	53	40 (75%)	33:67	28:72

Gonads from both male and female embryos in each treatment groups were assessed for *DMRT1* gene expression using quantitative RT-PCR analysis. Both the female and male gonads were pooled separately from each group and RNA was extracted for cDNA synthesis and qPCR analysis. The pooled gonads were added to 1 ml of Trizol and homogenised well by pipetting and vortexing at room temperature until all gonad tissue had dissolved. 200 µl of chloroform was added and mixed well by inverting the sample for 15 sec. The sample was then incubated at room temperature for 3 min and then centrifuged at 12000 g for 15 min at 4°C. The aqueous phase of the sample was then transferred to a new tube and then 500 l of isopropanol was added and mixed well by inversion. The mix was then incubated at room temperature for 10 min and then centrifuged at 12000 g for 10 min at 4°C. The supernatant was removed from the tube carefully, so as not to disturb the RNA pellet, and the pellet was then washed with 1 ml of 70% ethanol. The tube was then centrifuged at 7500 g for 5 min at 4°C and the supernatant again was carefully removed and the RNA pellet was air dried at room temperature for 10 min. The RNA pellet was then resuspended in 25 µl of RNase-free water and the final concentration of RNA was determined using a NanoDrop ND-1000 Spectrophotometer (Thermo Scientific). RNA was reverse transcribed to complimentary DNA (cDNA) using the Promega Reverse

Transcription kit (Promega). The reaction mix contained 1 µg of RNA, random hexamers (1 µl), dNTPs (2 µl), AMV reverse transcriptase (Promega) (0.5 µl) and nuclease free water added to a total reaction volume of 20 µl. The mix was incubated at 42°C for 1 hour, followed by a 10 min incubation at 95°C for enzyme inactivation.

cDNA was then used to quantify relative *DMRT1* gene expression levels in the pooled male and female gonad samples from each treatment group. qPCR primers and probes were designed using Primer Express (Applied Biosystems) software and sequences are shown in Table 8. PCR's were set up in 20 µl reaction volumes that contained 2 X TaqMan qRT PCR mastermix (Applied Biosystems), 1 µl of primer/probe mix, 1 µl of cDNA sample and made up to final volume with Nuclease free water (Promega). PCR cycling was performed at 95°C for 1 min, followed by 40 cycles of 95°C for 15 sec; 61°C for 30 sec and; 68°C for 30 sec. Ct values were obtained at a standard threshold value of 0.2 for all reactions. This threshold value corresponded to the midway point of the logarithmic phase of all amplification plots. Ct values were exported to Microsoft Excel for analysing relative gene expression using the comparative Ct method.

Table 8. Primer and probe sequences.

Sequence Name	**Sequence 5' – 3'**
DMRT1 TaqMan MGB probe	CCATCCCTTTCATCTGCC (SEQ ID NO:3494)
DMRT1 Forward primer	TCAAGCCAGTCAGGAAAACAGT (SEQ ID NO:3495)
DMRT1 Reverse primer	TCATGGCATGGCGGTTCT (SEQ ID NO:3496)
18S rRNA TaqMan MGB probe	TGCTGGCACCAGACTTGCCCTC (SEQ ID NO:3497)
18S rRNA Forward primer	CGGCTACCACATCCAAGGAA (SEQ ID NO:3498)
18S rRNA Reverse primer	GCTGGAATTACCGCGGCT (SEQ ID NO:3499)

Relative levels of *DMRT1* mRNA were compared with the chicken house keeping 18S rRNA species across all cDNA samples (Figure 2). Quantitative RT-PCR analysis confirmed that *DMRT1* mRNA expression was specifically reduced in all pooled groups of male embryos when compare to control Group 1. Almost 40% of

DMRT1 gene expression knockdown was observed for Group 3 male embryos treated with the *DMRT1*-343-siRNA. It is interesting to note that Group 3 was also the group that resulted in the greatest degree of observed feminisation of male gonads at the macroscopic level.

It will be appreciated by persons skilled in the art that numerous variations and/or modifications may be made to the invention as shown in the specific embodiments without departing from the spirit or scope of the invention as broadly described. The present embodiments are, therefore, to be considered in all respects as illustrative and not restrictive.

All publications discussed and/or referenced herein are incorporated herein in their entirety.

The present application claims priority from US 61/138,235 filed 17 December 2008, the entire contents of which are incorporated by reference.

Any discussion of documents, acts, materials, devices, articles or the like which has been included in the present specification is solely for the purpose of providing a context for the present invention. It is not to be taken as an admission that any or all of these matters form part of the prior art base or were common general knowledge in the field relevant to the present invention as it existed before the priority date of each claim of this application.

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CLAIMS

1. An isolated and/or exogenous nucleic acid molecule comprising a double-stranded region which reduces the level of at least one RNA molecule and/or protein when administered to an avian egg, wherein if the embryo of the egg is male the sex is altered to female following administration of the isolated and/or exogenous nucleic acid molecule, and wherein the isolated and/or exogenous nucleic acid molecule does not comprise a sequence selected from:
CCAGUUGUCAAGAAGAGCA (SEQ ID NO:254)
GGAUGCUCAUUCAGGACAU (SEQ ID NO:369)
CCCUGUAUCCUUACUAUAA (SEQ ID NO:474)
GCCACUGAGUCUUCCUCAA (SEQ ID NO:530)
CCAGCAACAUACAUGUCAA (SEQ ID NO:605)
CCUGCGUCACACAGAUACU (SEQ ID NO:747)
GGAGUAGUUGUACAGGUUG (SEQ ID NO:3432)
GACUGGCUUGACAUGUAUG (SEQ ID NO:3433)
AUGGCGGUUCUCCAUCCCU (SEQ ID NO:3434) or a variant of any one thereof.

2. An isolated and/or exogenous nucleic acid molecule comprising one or more of the sequence of nucleotides provided as SEQ ID NO's 11 to 3431 or a variant of any one or more thereof, wherein the isolated and/or exogenous nucleic acid molecule does not comprise a sequence selected from:
CCAGUUGUCAAGAAGAGCA (SEQ ID NO:254)
GGAUGCUCAUUCAGGACAU (SEQ ID NO:369)
CCCUGUAUCCUUACUAUAA (SEQ ID NO:474)
GCCACUGAGUCUUCCUCAA (SEQ ID NO:530)
CCAGCAACAUACAUGUCAA (SEQ ID NO:605)
CCUGCGUCACACAGAUACU (SEQ ID NO:747)
GGAGUAGUUGUACAGGUUG (SEQ ID NO:3432)
GACUGGCUUGACAUGUAUG (SEQ ID NO:3433)
AUGGCGGUUCUCCAUCCCU (SEQ ID NO:3434) or a variant of any one thereof.

3. The nucleic acid molecule of claim 1 or claim 2 which is a dsRNA molecule.

4. The nucleic acid molecule of claim 3, wherein the dsRNA is a siRNA or a shRNA.

5. The nucleic acid molecule according to any one of claim 1 to 4 which reduces the level of a protein encoded by a DMRT1 gene, ASW gene or R-spondin gene, in an avian egg.

6. A vector encoding a nucleic acid molecule, or a single strand thereof, according to any one of claims 1 to 5.

7. A host cell comprising an exogenous nucleic acid molecule, or a single strand thereof, according to any one of claims 1 to 5 and/or a vector of claim 6.

8. A composition comprising a nucleic acid molecule, or a single strand thereof, according to any one of claims 1 to 5, a vector of claim 6, and/or a host cell of claim 7.

9. A method of modifying the sex of an avian, the method comprising administering to an avian egg at least one nucleic acid molecule according to any one of claims 1 to 5.

10. The method of claim 9, wherein the nucleic acid is administered to a non-cellular site of the egg.

11. The method of claim 10, wherein the non-cellular site is the air sac, yolk sac, amnionic cavity or chorion allantoic fluid.

12. The method according to any one of claims 9 to 11, wherein the egg is not electroporated.

13. The method according to any one of claims 9 to 12, wherein the nucleic acid is not delivered by administering a vector encoding the nucleic acid molecule.

14. The method according to any one of claims 9 to 13, wherein the nucleic acid molecule administered is dsRNA.

15. The method according to any one of claims 9 to 14, wherein the nucleic acid molecule is administered by injection.

16. The method according to any one of claims 9 to 16, wherein the avian is selected from chickens, ducks, turkeys, geese, bantams and quails.

17. An avian produced using a method according to any one of claims 9 to 16.

18. A chicken produced using a method according to any one of claims 9 to 16.

19. An avian egg comprising a nucleic acid molecule, or a single strand thereof, according to any one of claims 1 to 5, a vector of claim 6, and/or a host cell of claim 7.

20. A kit comprising a nucleic acid molecule, or a single strand thereof, according to any one of claims 1 to 5, a vector of claim 6, a host cell of claim 7, and/or a composition of claim 8.

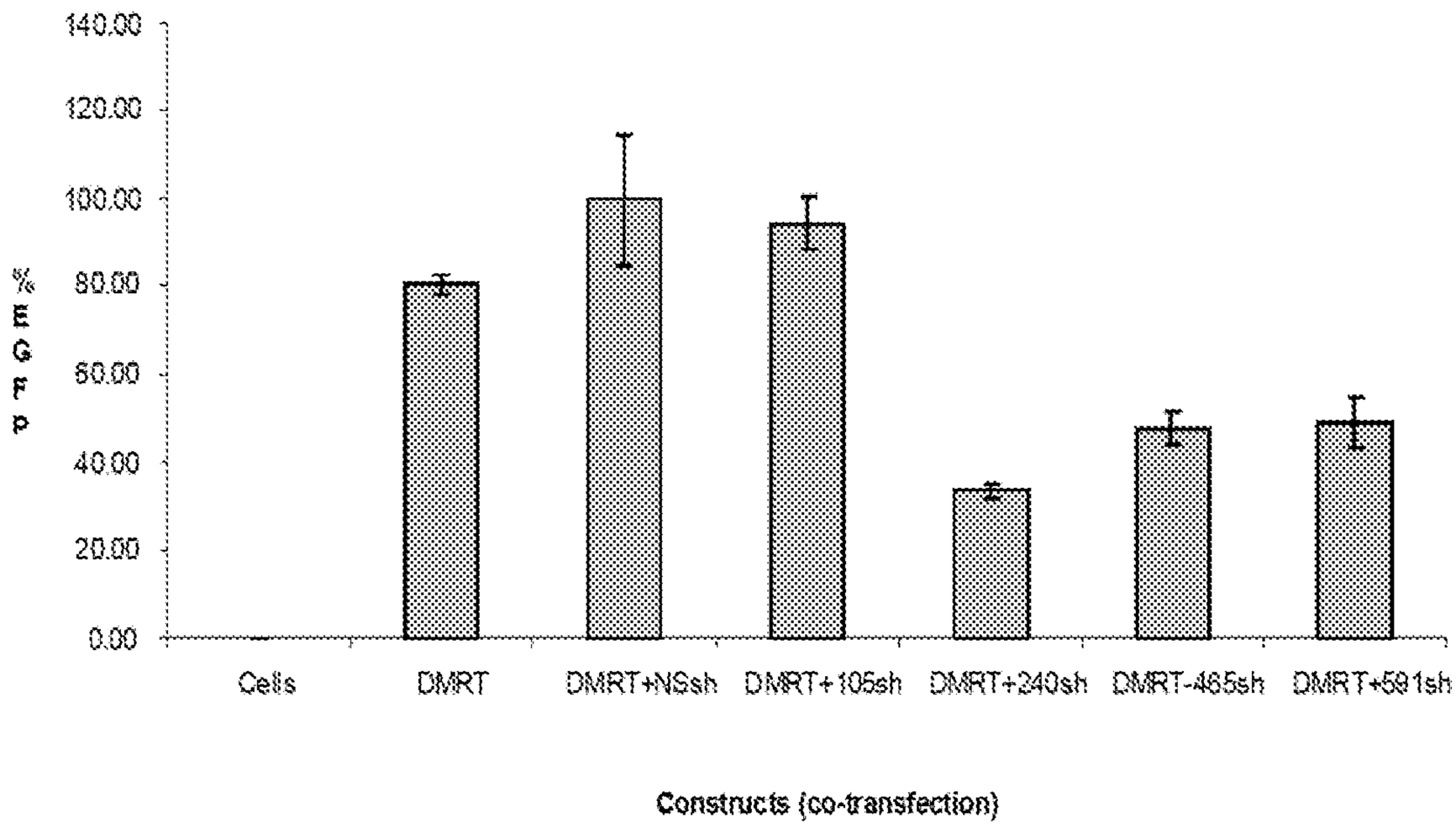
140.00
120.00
100.00
80.00
60.00
40.00
20.00
0.00
% EGFP
Cells
DMRT
DMRT+NSsh
DMRT+105sh
DMRT+240sh
DMRT-465sh
DMRT+591sh
Constructs (co-transfection)

Figure 1

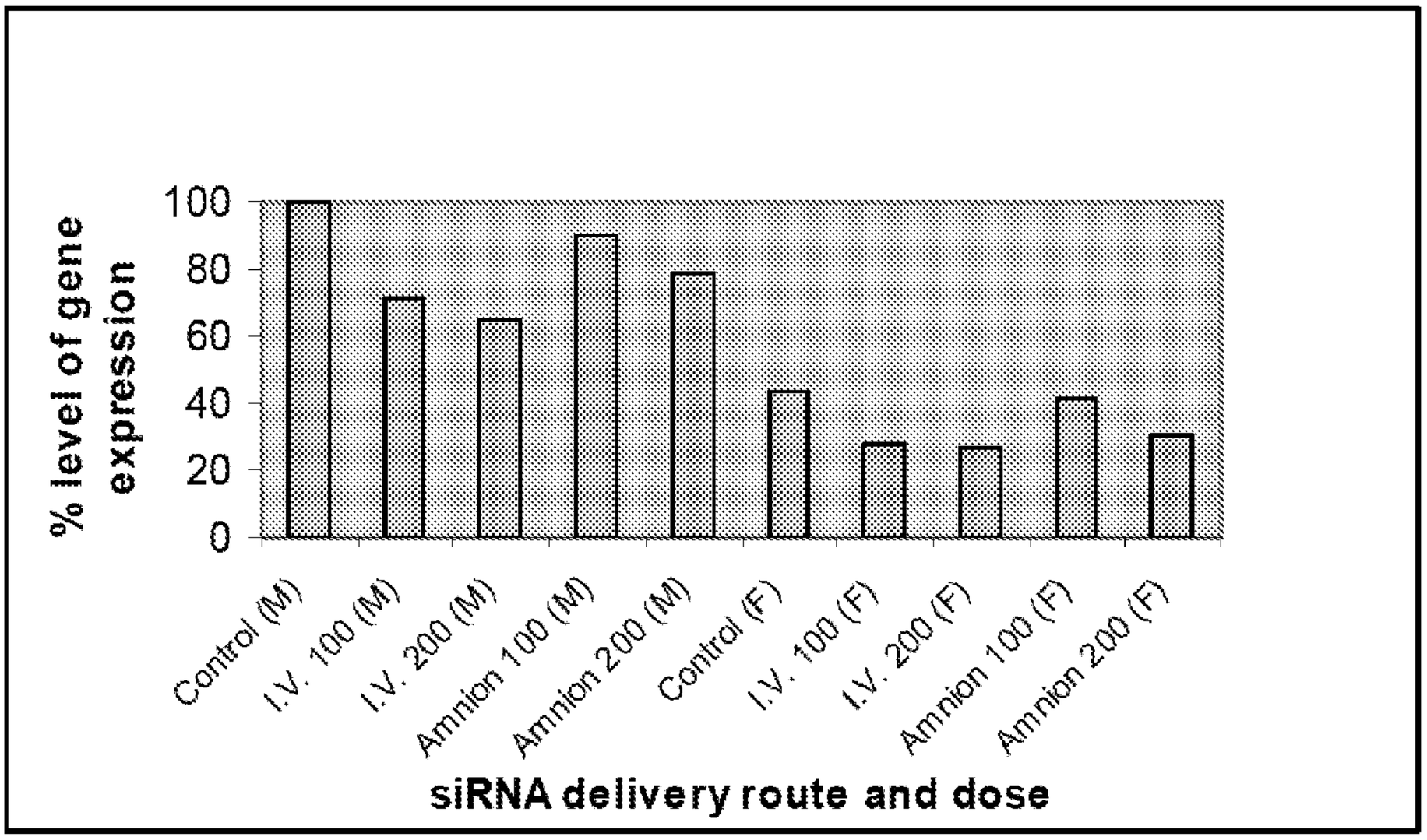
% level of gene expression
100
80
60
40
20
0
Control (M)
I.V. 100 (M)
I.V. 200 (M)
Amnion 100 (M)
Amnion 200 (M)
Control (F)
I.V. 100 (F)
I.V. 200 (F)
Amnion 100 (F)
Amnion 200 (F)
siRNA delivery route and dose

Figure 2