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(54) Title: INFLUENZA TARGETS

(57) Abstract: The present invention relates to pharmaceutical compositions comprising modulators of kinases, kinase binding polypeptides or/and an inhibitor for influenza virus replication for the prevention or/and treatment of influenza.

Influenza Targets

Description

The present invention relates to a pharmaceutical composition comprising an inhibitor of influenza virus replication. In particular, the present invention relates to a pharmaceutical composition comprising a modulator of a kinase or/and a kinase binding polypeptide for the prevention or/and treatment of influenza. Further, the present invention concerns a screening method for identification of a modulator of a kinase or/and a kinase binding polypeptide, which modulator is suitable for prevention or/and treatment of influenza. Yet another aspect is a screening method for identification of new targets for the prevention, alleviation or/and treatment of influenza.

In view of the threatening influenza pandemic, there is an acute need to develop and make available lastingly effective drugs. In Germany alone the annual occurrence of influenza causes between 5,000 and 20,000 deaths a year (source: Robert-Koch Institute). The recurring big influenza pandemics are especially feared. The first big pandemic, the so-called "Spanish Flu", cost about 40 million lives in the years 1918-1919 including a high percentage of healthy, middle-aged people. A similar pandemic could be caused by the H5N1 influenza virus, which at the moment replicates mainly in birds, if acquired mutations enable the virus to be transmitted from person to person. The probability of a human pandemic has recently grown more acute with the spreading of bird flu (H5N1) worldwide and the infection of domestic animals. It is only a question of time until a highly pathogenic human influenza-recombinant emerges. The methods available at the moment for prophylaxis or therapy of an influenza infection, such as vaccination with viral surface proteins or the use of antiviral drugs (neuraminidase inhibitors or ion channel blockers), have various disadvantages. Already at this early stage resistance is appearing against one of our most effective preparations (Tamiflu), which may make it unsuitable to contain a pandemic. A central problem in the use of vaccines

and drugs against influenza is the variability of the pathogen. Up to now the development of effective vaccines has required accurate prediction of the pathogen variant. Drugs directed against viral components can rapidly lose their effectiveness because of mutations of the pathogen.

An area of research which has received little attention up to now is the identification of critical target structures in the host cell. Viruses are dependent on certain cellular proteins to be able to replicate within the host. The knowledge of such cellular factors that are essential for viral replication but dispensable (at least temporarily) for humans could lead to the development of novel drugs. Rough estimates predict about 500 genes in the human genome which are essential for viral multiplication. Of these, 10% at least are probably dispensable temporarily or even permanently for the human organism. Inhibition of these genes and their products, which in contrast to the viral targets are constant in their structure, would enable the development of a new generation of antiviral drugs in the shortest time. Inhibition of such gene products could overcome the development of viral escape mutants that are not longer sensitive to antiviral drugs. Amongst other gene families kinases that are important regulatory proteins within the cell are often hijacked by viruses to manipulate the constitution of the host cell.

It is the object of the present invention to provide a screening method for genes involved in influenza virus replication. Another object is a screening method for identification of modulators of such genes.

In the context of the present invention, it was surprisingly found that inhibition of particular genes or the modulation of kinases or/and kinase binding polypeptides leads to reduction of influenza virus replication.

Table 1a, 1b and 4 describe targets for the prevention, alleviation or/and treatment of an influenza virus infection.

Examples of genes which upon downregulation increase the influenza virus replication are described in Table 1a. Thus, by increasing expression or/and activity of these genes or/and gene products, the influenza virus replication can be reduced.

Examples of genes which upon downregulation decrease the influenza virus replication are described in Table 1b and 4. Thus, by decreasing expression or/and activity of these genes or/and gene products, the influenza virus replication can be reduced.

Subject of the present invention is thus a screening method covering different aspects related to influenza virus infection, in particular influenza virus replication.

In a first aspect the screening method is a screening method for identification of a compound suitable for modulation of a kinase or/and a kinase binding polypeptide, comprising the steps

(a) providing a kinase or/and a kinase binding polypeptide,
(b) contacting a compound with the kinase or/and a kinase binding polypeptide of (a),
(c) determining the activity of the kinase or/and the kinase binding polypeptide,
(d) selecting a compound which modulates the activity of the kinase or/and the kinase binding polypeptide.

The screening method of the present invention may comprise a cellular screening assay or/and a molecular screening assay. A cellular screening assay includes the determination of the activity or/and expression of a kinase or/and of a kinase binding polypeptide in a cell or/and in a non human organism. A molecular screening assay includes determination of the activity of an isolated kinase or/and of an isolated kinase binding polypeptide.

The screening assay in the screening method of the present invention may

be performed in vivo or/and in vitro.

In the screening method of the present invention the kinase or/and the kinase binding polypeptide may be provided in an isolated form. "Isolated" in the context of the present invention refers to any protein or polypeptide isolation procedure known by a person skilled in the art. "Isolated form" or "isolated kinase or/and isolated kinase binding polypeptide" includes essentially pure or crude preparations or formulations of the kinase or/and kinase binding polypeptide.

In the screening method of the present invention, the kinase or/and the kinase binding polypeptide may be provided by a cell or/and a non-human organism capable of expressing the kinase or/and the kinase binding polypeptide.

In yet another aspect the screening method is a screening method for identification of a kinase modulator suitable for prevention, alleviation or/and treatment of an influenza virus infection, comprising the steps

(I) providing a cell or/and a non-human organism capable of being infected with an influenza virus and capable of expressing a kinase or/and a kinase binding polypeptide,

(II)contacting the cell or/and the organism of (I) with an influenza virus and with a compound known to be capable of modulating the expression or/and activity of the kinase or/and kinase binding polypeptide,

(III)determining the amount of influenza virus produced by the cell or/and the organism, and

(IV)selecting a compound which reduces the amount of the influenza virus produced by the cell or/and the organism.

In a further aspect the screening method is a screening method for identification of compound suitable for the prevention, alleviation or/and treatment of an influenza virus infection, comprising the steps

(A) providing a cell or/and a non-human organism capable of being infected with an influenza virus and capable of expressing a gene, wherein the gene or/and gene product thereof is capable of modulating an influenza virus replication,

(B) contacting the cell or/and the organism of (A) with an influenza virus and with a compound known to be capable of modulating the expression or/and activity of the gene of (A) or/and the gene product thereof,

(C) determining the amount of influenza virus produced by the cell or/and the organism, and

(D) selecting a compound which reduces the amount of the influenza virus produced by the cell or/and the organism.

The gene of (A) is preferably selected from Table 1A, 1B and 4, in more preferred embodiments from one of the Tables 1A, 1B or 4. "Modulation" in (A) and (B) may be "activation" or "inhibition", in particular "inhibition".

In a further aspect, the screening method is a screening method for identification of a compound suitable for prevention, alleviation or/and treatment of an influenza virus infection, comprising the steps

(i) providing a cell or/and a non-human organism capable of expressing a kinase or/and a kinase binding polypeptide,

(ii) contacting a compound with the cell or/and the organism of (i),

(iii) determining the amount or/and the activity of kinase or/and a kinase binding polypeptide, and

(iv) selecting a compound which modulates the amount or/and the activity of the kinase or/and the kinase binding polypeptide.

In a further aspect, the screening method is a screening method for identification of a compound suitable for prevention, alleviation or/and treatment of an influenza virus infection, comprising the steps

i. providing a cell or/and a non-human organism capable of expressing a gene, wherein the gene or/and gene product thereof

is capable of modulating an influenza virus replication,

ii. contacting a compound with the cell or/and the organism of i.,

iii. determining the amount or/and the activity of gene product of the gene of (i), and

iv. selecting a compound which modulates the amount or/and the activity of the gene product of i.

The gene of (i) is preferably selected from table 1A, 1B and 4, in more preferred embodiments from one of the Tables 1A, 1B or 4. "Modulation" in i. and ii. may be "activation" or "inhibition", in particular "inhibition".

In yet another aspect of the present invention, the screening method is a screening method for identification of genes suitable as targets for the prevention, alleviation or/and prevention of an influenza virus infection, comprising the steps

(1) providing a cell or/and a transgenic non-human animal capable of expressing, particularly over- or underexpressing a gene,

(2) contacting the cell or/and the organism of (1) with an influenza virus,

(3) modulating the expression or/and activity of the gene and determining the amount of influenza virus produced by the cell or/and the organism, and

(4) selecting a gene the expression or/and activity of which is positively or negatively correlated with reduction of the amount of the influenza virus produced by the cell or/and the organism.

The at least one kinase or/and kinase binding polypeptide employed in the screening method of the present invention is preferably encoded by a nucleic acid or/and gene selected from Table 1A and Table 1B. Nucleic acids comprising at least one sequence of Tables 1a, 1b, 2 or/and 4 and fragments thereof may be employed in the screening method of the present invention.

In the context of the present invention, a "target" includes a nucleotide sequence in a gene or/and a genome, a nucleic acid, or/and a polypeptide

which is involved in regulation of influenza virus replication in a host cell. The target may be directly or indirectly involved in regulation of influenza virus replication. In particular, a target is suitable for reduction of influenza virus replication, either by activation of the target or by inhibition of the target.

Examples of targets are genes and partial sequence of genes, such as regulatory sequences. The term "target" also includes a gene product such as RNA, in particular mRNA, tRNA, rRNA, a polypeptide or/and a protein encoded by the target gene. Preferred gene products of a target gene are selected from mRNA, polypeptide(s) and protein(s) encoded by the target gene. The most preferred gene product is a polypeptide or protein encoded by the target gene. A target protein or a target polypeptide may be posttranslationally modified or not.

"Gene product" of a gene as used herein includes RNA (in particular mRNA, tRNA, rRNA), a polypeptide or/and a protein encoded by said gene.

In the context of the present invention, "activity" of the gene or/and gene product includes transcription, translation, posttranslational modification, modulation of the activity of the gene or/and gene product. The activity may be modulated by ligand binding, which ligand may be an activator or inhibitor.

A further subject of the present invention is a pharmaceutical composition comprising at least one inhibitor of influenza virus replication optionally together with pharmaceutically acceptable carriers, adjuvants, diluents or/and additives, for the prevention, alleviation or/and treatment of an influenza virus infection.

Yet another subject of the present invention is a pharmaceutical composition comprising at least one modulator of a kinase or/and at least one modulator of a kinase binding polypeptide optionally together with pharmaceutically acceptable carriers, adjuvants, diluents or/and additives, for the prevention,

alleviation or/and treatment of an influenza virus infection.

The influenza virus infection may be an influenza A virus infection. The influenza A virus may be selected from influenza A viruses isolated so far from avian and mammalian organisms. In particular, the influenza A virus may be selected from H1N1, H1N2, H1N3, H1N4, H1N5, H1N6, H1N7, H1N9, H2N1, H2N2, H2N3, H2N4, H2N5, H2N7, H2N8, H2N9, H3N1, H3N2, H3N3, H3N4, H3N5, H3N6, H3N8, H4N1, H4N2, H4N3, H4N4, H4N5, H4N6, H4N8, H4N9, H5N1, H5N2, H5N3, H5N6, H5N7, H5N8, H5N9, H6N1, H6N2, H6N3, H6N4, H6N5, H6N6, H6N7, H6N8, H6N9, H7N1, H7N2, H7N3, H7N4, H7N5, H7N7, H7N8, H7N9, H9N1, H9N2, H9N3, H9N5, H9N6, H9N7, H9N8, H10N1, H10N3, H10N4, H10N6, H10N7, H10N8, H10N9, H11N2, H11N3, H11N6, H11N9, H12N1, H12N4, H12N5, H12N9, H13N2, H13N6, H13N8, H13N9, H14N5, H15N2, H15N8, H15N9 and H16N3. More particularly, the influenza A virus is strain Puerto Rico/8/34 or the Avian Influenza virus isolate H5N1. The influenza virus as described herein may be employed in the screening method of the present invention.

The inhibitor of influenza virus replication or/and the modulator employed in the pharmaceutical compositions of the present invention is preferably selected from the group consisting of nucleic acids, nucleic acid analogues such as ribozymes, peptides, polypeptides, and antibodies. The modulator as described herein may also be employed in the screening method of the present invention.

The inhibitor of influenza virus replication or/and the modulator may also be a compound having a molecular weight smaller than 1000 Dalton.

The pharmaceutical composition of the present invention may comprise at least one inhibitor of influenza virus replication, wherein the at least one inhibitor of influenza virus replication modulates the expression of a gene selected from Table 1A, Table 1B, and Table 4, or/and a gene product thereof. In particular, the at least one inhibitor of influenza virus replication

inhibits the expression of a gene selected from Table 1B and Table 4 or/and a gene product thereof, or the at least one inhibitor of influenza virus replication activates the expression of a gene selected from Table 1A or/and a gene product thereof.

The pharmaceutical composition of the present invention may comprise a modulator of a kinase or/and a modulator of a kinase binding polypeptide, wherein the at least one kinase or/and kinase binding polypeptide is encoded by a nucleic acid or/and gene selected from Table 1A and Table 1B. Such a kinase or/and kinase binding polypeptide may thus be the target of the modulator.

The pharmaceutical composition of the present invention may comprise at least one modulator which is an activator. The pharmaceutical composition of the present invention may comprise at least one activator comprising

(a) a nucleotide sequence selected from Table 1A or/and a fragment thereof, or/and

(b) a fragment which is at least 70 %, preferably at least 80%, more preferably at least 90% identical to the sequence of (a),

or/and at least one activator capable of activating expression or/and gene product activity of a gene comprising sequence (a) or/and (b).

The pharmaceutical composition of the present invention may comprise at least one modulator which is an inhibitor. Suitable inhibitors are RNA molecules capable of RNA interference. The pharmaceutical composition of the present invention may comprise at least one inhibitor comprising

(a) a nucleotide sequence selected from Table 1B and 4 or/and a fragment thereof, or

(b) a sequence which is at least 70 %, preferably at least 80%, more preferably at least 90% identical to the sequence of (a),

or/and at least one inhibitor capable of inhibiting expression or/and gene product activity of a gene comprising sequence (a) or/and (b).

The activator or/and the inhibitor as described herein may also be employed in the screening methods of the present invention.

The pharmaceutical composition of the present invention preferably comprises a nucleic acid, wherein the nucleic acid comprises a nucleotide sequence selected from the sequences of Table 2 and Table 4 and fragments thereof. Preferably, the nucleic acid is RNA or DNA.

In a more preferred embodiment, the pharmaceutical composition of the present invention comprises

(i) an RNA molecule capable of RNA interference,
(ii) a precursor of the RNA molecule (i), or/and
(iii) a DNA molecule encoding the RNA molecule (i) or/and the precursor (ii).

RNA molecules capable of RNA interference are described in WO 02/44321 which is included herein by reference.

The RNA molecule of the present invention may be a double-stranded RNA molecule, preferably a double-stranded siRNA molecule with or without a single-stranded overhang alone at one end or at both ends. The RNA molecule may comprise at least one nucleotide analogue or/and deoxyribonucleotide.

The DNA molecule as employed in the present invention may be a vector.

The nucleic acid employed in the present invention may be an antisense nucleic acid or a DNA encoding the antisense nucleic acid.

The nucleic acid or/and nucleic acid fragment employed in the present invention may have a length of at least 15, preferably at least 17, more preferably at least 19, most preferably at least 21 nucleotides. The nucleic acid or/and the nucleic acid fragment may have a length of at the maximum

29, preferably at the maximum 27, more preferably at the maximum 25, especially more preferably at the maximum 23, most preferably at the maximum 21 nucleotides.

In another preferred embodiment, the pharmaceutical composition of the present invention comprises an antibody, wherein the antibody may be directed against a kinase or/and kinase binding polypeptide.

Preferably the antibody is directed against a kinase or/and kinase binding polypeptide comprising

(a) an amino acid sequence encoded by a nucleic acid or/and gene selected from Table 1A, and Table 1B, or/and

(b) an amino acid sequence which is at least 70%, preferably at least 80%, more preferably at least 90% identical to the sequence of (a).

In another preferred embodiment, the antibody is directed against a polypeptide comprising

(a) an amino acid sequence encoded by a nucleic acid or/and gene selected from Table 4, or/and

(b) an amino acid sequence which is at least 70%, preferably at least 80%, more preferably at least 90% identical to the sequence of (a).

The antibody of the present invention may be a monoclonal or polyclonal antibody, a chimeric antibody, a chimeric single chain antibody, a Fab fragment or a fragment produced by a Fab expression library.

Techniques of preparing antibodies of the present invention are known by a skilled person. Monoclonal antibodies may be prepared by the human B-cell hybridoma technique or by the EBV-hybridoma technique (Köhler et al., 1975, Nature 256:495-497, Kozbor et al., 1985, J. Immunol. Methods 81,31-42, Cote et al., PNAS, 80:2026-2030, Cole et al., 1984, Mol. Cell Biol. 62:109-120). Chimeric antibodies (mouse/human) may be prepared by carrying out the methods of Morrison et al. (1984, PNAS, 81:6851-6855),

Neuberger et al. (1984, 312:604-608) and Takeda et al. (1985, Nature 314:452-454). Single chain antibodies may be prepared by techniques known by a person skilled in the art.

Recombinant immunoglobulin libraries (Orlandi et al, 1989, PNAS 86:3833-3837, Winter et al., 1991, Nature 349:293-299) may be screened to obtain an antibody of the present invention. A random combinatory immunoglobulin library (Burton, 1991, PNAS, 88:11120-11123) may be used to generate an antibody with a related specifity having a different idiotypic composition.

Another strategy for antibody production is the in vivo stimulation of the lymphocyte population.

Furthermore, antibody fragments (containing $F(ab')_2$ fragments) of the present invention can be prepared by protease digestion of an antibody, e.g. by pepsin. Reducing the disulfide bonding of such $F(ab')_2$ fragments results in the Fab fragments. In another approach, the Fab fragment may be directly obtained from an Fab expression library (Huse et al., 1989, Science 254:1275-1281).

Polyclonal antibodies of the present invention may be prepared employing an amino acid sequence encoded by a nucleic acid or/and gene selected from Table 1A and Table 1B or immunogenic fragments thereof as antigen by standard immunization protocols of a host, e.g. a horse, a goat, a rabbit, a human, etc., which standard immunization protocols are known by a person skilled in the art.

The antibody may be an antibody specific for a gene product of a target gene, in particular an antibody specific for a polypeptide or protein encoded by a target gene.

The antibody as described herein may also be employed in the screening method of the present invention.

Fragments of polypeptides or/and peptides as employed in the present invention, in particular fragments of an amino acid sequence encoded by a nucleic acid or/and gene selected from Table 1A, Table 1B and Table 4 may have a length of at least 5 amino acid residues, preferably at least 10, more preferably at least 20 amino acid residues. The length of said fragments may be 200 amino acid residues at the maximum, preferably 100 amino acid residues at the maximum, more preferably 60 amino acid residues at the maximum, most preferably 40 amino acid residues at the maximum.

In the screening methods of the present invention, modulating the expression of a gene may be downregulation or upregulation, in particular of transcription or/and translation.

It can easily be determined by a skilled person if a gene is upregulated or downregulated. In the context of the present invention, upregulation of gene expression may be an upregulation by a factor of at least 2, preferably at least 4. Downregulation in the context of the present invention may be a reduction of gene expression by a factor of at least 2, preferably at least 4. Most preferred is essentially complete inhibition of gene expression, e.g. by RNA interference.

"Decrease (increase) of the amount" may be a downregulation (upregulation) of gene expression by a factor of at least 2, preferably at least 4. In the case of reduction, essentially complete inhibition of gene expression is most preferred, e.g. by RNA interference.

Modulation of the activity of a gene may be decreasing or increasing of the activity.

"Decrease (increase) of the activity" may be a decrease (increase) of activity of a gene or gene product by a factor of at least 2, preferably at least 4. In the case of activity reduction, essentially complete inhibition of activity is

most preferred.

Modulation may be performed by a single nucleic acid species or by a combination of nucleic acids comprising 2, 3 4, 5, 6 or even more different nucleic acid species, which may be selected from Tables 1a, 1b or/and 2 and fragments thereof. Preferred combinations are described in Table 3 (also referred herein as "pools"). Table 3 includes combinations of at least two kinase or/and kinase binding polypeptide genes. It is also preferred that the combination modulates one gene, for instance selected from Table 1a and 1b. A combination of two nucleic acid species is preferred. More preferred is a combination of two nucleic acids of Table 2. Most preferred is a combination of two nucleic acids of Table 2, which modulate one gene.

Modulation may be a knock-down performed by RNA interference. The nucleic acid or the combination of nucleic acid species may be an siRNA, which may comprise a sequence selected from the sequences of Table 2 and Table 4 and fragments thereof. It is preferred that the combination knocks down one gene, for instance selected from Table 1b and Table 4 . A combination of two siRNA species is preferred, which may be selected from those sequences of Table 2, which are derived from genes of Table 1b, and the sequences of Table 4, wherein the combination preferably knocks down one gene.

The gene employed in the various embodiments of the present invention may be selected from any of the Tables 1A, 1B, 2, or 4, or any combination thereof. A gene which when expressed or up-regulated is capable of modulating influenza virus replication may be selected from Tables 1A and 1B, from Tables 1A, 1B and 4, from Table 1A, 1B, 2 and 4. A gene which when expressed or up-regulated is capable of inhibiting influenza virus replication may be selected from Table 1B, from Tables 1B and 4, or from Tables 1B, 2 and 4. A gene which when expressed or up-regulated is capable of activating influenza virus replication may be selected from Table 1A, or from Tables 1A and 2.

The cell employed in any of the screening methods of the present invention may be any cell capable of being infected with in influenza virus. Preferably the cell is a mammalian cell or an avian cell. More preferably the cell is a human cell. Even more preferred is an epithelial cell. Most preferred is a lung epithelial cell. The cell may be a cell line. A suitable lung epithelial cell line is A594. Another suitable cell is the human embryonic kidney cell line 293T.

The modulator of a target gene or/and a gene product thereof as described herein may be used for the manufacture of a pharmaceutical composition for prevention, alleviation or/and prevention of an influenza virus infection.

Another subject of the present invention is the use of a inhibitor of influenza virus replication as described herein, for the prevention, alleviation or/and prevention of an influenza virus infection. Preferred is the use of an inhibitor capable of inhibiting the expression of a gene selected from Table 1b and 4, for the manufacture of a medicament for the prevention, alleviation or/and prevention of an influenza virus infection. Also preferred is the use of an inhibitor capable of inhibiting a gene product of a gene selected from Table 1b and 4, for the manufacture of a medicament for the prevention, alleviation or/and prevention of an influenza virus infection.

Yet another subject of the present invention is the use of a kinase modulator or/and a kinase binding protein modulator for the manufacture of a medicament for the prevention, alleviation or/and prevention of an influenza virus infection.

Yet another aspect of the present invention is the use of a nucleic acid comprising a gene sequence or/and a nucleotide sequence of Table 1a, 1b, 2 or/and 4 and fragments thereof in a method for screening for compounds or/and targets suitable for the prevention, alleviation or/and treatment of an influenza virus infection.

The invention is further illustrated by the following figures, tables and examples.

Figure and Table legends:

Figure 1: The experimental setting of the siRNA kinase screen of the example.

Figure 2: The effect of transfected (control)-siRNAs in regard to luminescence data. This diagram shows a typical screening result from one 96 well plate. During all experiments several controls were included in triplets, like uninfected, transfected with a siRNA against luciferase, mock treated and siRNAs against the viral nucleoprotein gene (NP) from influenza A viruses. The difference of the luminescence between cells treated with luciferase siRNAs and anti-NP siRNAs was set to 100 % inhibition per definition.

Figure 3: The inhibition of influenza virus replication shown for all siRNAs tested in the example.

Figure 4: The values "% inhibition" from all analyzed siRNAs were used to calculate the z-scores. Highly efficient siRNAs are labelled in pink showing more than 50% inhibition compared to the luciferase siRNA transfected control cells.

Figure 5: The experimental setup of the genome wide siRNA screen (see Example 4).

Table 1: Results of the siRNa kinase screen: **a:** activation ("negative" inhibition) of virus replication in %, normalized against the cell number, and the standard deviation calculated using four independent experiments. **b:** inhibition of virus replication in %, normalized against the cell number, and

the standard deviation calculated using four independent experiments. Pool X, wherein X denotes the number of the pool, refers to combinations described in Table 3.

Table 2: Oligonucleotide sequences employed in the siRNA kinase screen of example 1. Knock-down of a particular gene was performed (a) by a combination of two oligonucleotide sequences ("target 1" and "target 2") specific for said gene, or (b) by pooled oligonucleotides specific for different genes ("Pool X", wherein X denotes the number of the pool described in Table 3).

Table 3: Oligonucleotide pools employed in the siRNA kinase screen of the example.

Table 4: Oligonucleotide sequences employed in the siRNA screen of example 4. Up to four oligonucleotide sequences ("target sequence 1", "target sequence 2", "target sequence 3", and "target sequence 4") specific for a gene were employed (each in a separate test).

Example 1

Since kinases are one of the most promising candidates that can influence virus progeny we used siRNAs against this group of genes to identify the individual role of each kinase or kinase binding polypeptide in respect of a modified replication of influenza viruses. All siRNAs were tested in four independent experiments. Since siRNAs against kinases can influence the replication of cells or are even cytotoxic, the effect of each individual siRNA transfection in regard to the cell number was analysed by using an automatic microscope. The amount of replication competent influenza viruses was quantified with an influenza reporter plasmid that was constructed using a RNA polymerase I promoter/terminator cassette to express RNA transcripts encoding the firefly luciferase flanked by the untranslated regions of the

influenza A/WSN/33 nucleoprotein (NP) segment. Human embryonic kidney cells (293T) were transfected with this indicator plasmid one day before influenza infection. These cells were chosen, because they show a very strong amplification of the luciferase expression after influenza A virus infection. The cell based assay comprised the following steps (also Fig. 1 which describes the experimental setting of the siRNA kinase screen):

Day 1:	Seeding of A549 cells (lung epithelial cells) in 96-well plates
Day 2:	Transfection with siRNAs directed against kinases or kinase binding proteins
Day 3:	Infection with influenza A/WSN/33 + transfection of 293T cells with the influenza indicator plasmid
Day 4:	Infection of 293T cells with the supernatant of A549 cells + determination of cell number by the automatic microscope
Day 5:	Lysis of the indicator cells and performing the luciferase assay to quantify virus replication

For the identification of influenza relevant kinases the luminescence values were normalised against the cell number (measured after siRNA transfection and virus infection). Thereby unspecific effects due to the lower (or higher) cell numbers can be minimized.

Several controls were included to be able to demonstrate an accurate assay during the whole screening procedure (Fig. 2). The control siRNA against the viral nucleoprotein could nearly reduce the replication to levels of uninfected cells.

The illustration of the inhibition in percentage shows that some siRNAs can enhance the influenza virus replication, whereas others can inhibit the replication stronger (>113%) than the antiviral control siRNA against the influenza NP gene (Fig. 3). Thereby 47 siRNA decreased the replication more than 50%, 9 siRNAs showed more than 80 % inhibition. The list of the results is provided in Table 1a and 1b, showing the activation (Table 1a,

"negative" inhibition) and inhibition (Table 1b) of virus replication in %, normalized against the cell number, and the standard deviation calculated using four independent experiments.

Similar results were obtained using the calculation of z-scores. The z-score represents the distance between the raw score and the population mean in units of the standard deviation. The z-scores were calculated using the following equation:

$$z = \frac{X - \mu}{\sigma}.$$

where X is a raw score to be standardized, σ is the standard deviation of the population, and μ is the mean of the population.

Example 2

In a future experiment the antiviral effect will be validated in more detail by using individual siRNAs instead of pooled siRNAs. Furthermore new siRNAs (at least two additional siRNAs per identified gene) will be tested using the experimental setting of Example 1. Those confirmed genes that seem to be important for the replication of influenza viruses will then be knocked down in mice using intranasally administered siRNAs. For the evaluation of this antiviral therapy it is of highest importance to determine the efficiency of transportation of compounds to lung epithelial tissue. The success of a therapy depends on the combination of high efficient kinase inhibitors and adequate transport system. A potentially compatible and cost efficient agent is chitosan which we are applying for the delivery of siRNAs in *in vivo* studies successfully. We will apply the compounds either intranasally or administer them directly into the lung.

Efficient siRNAs should lead to a decreased viral titre within the lung tissue and due to this animals should be protected against an otherwise lethal influenza infection.

For testing the biological effect of the kinase inhibitors, we will divide the experiments in four parts:

1. Analysis of the kinase inhibitor distribution in the respiratory apparatus after intranasal application of compound/chitosan nano particles. Optimisation of the compound/chitosan concentration for best effectiveness. Further tests will only be performed in case of success.
2. In LD50 tests the absolute pathogenicity of the virus isolates Influenza A/Puerto Rico/8/34 and the Avian Influenza isolate (for test 4) will be estimated.
3. Test of antiviral effect of selected siRNAs after intranasal application and infection with Influenza A/Puerto Rico/8/34 by analyzing virus titre in lung tissue or survival rate (in certain cases).
4. Test of antiviral effect of selected siRNAs after intranasal application and infection with highly pathogenic Avian Influenza virus isolate (such as H5N1) by analyzing the virus titre in lung tissue or survival rate (in certain cases).

The used virus isolate is dependant on current development and spreading of the Avian Influenza. We aim at inhibiting the replication of the current prevalent strain in vivo efficiently

Kinase inhibitors against the confirmed genes will also be tested in mice regarding to an impaired virus replication.

The Max-Planck-Institut für Infektionsbiologie, Berlin, Germany, has genome-wide RNAi libraries that, in principle, enable the shutting-off of every single human gene in suitable cell cultures (A549 cells). So in the next level the screen will be expanded to a genome wide scale, because many additional cellular factors involved in the attachment, replication and budding of viruses are still unknown.

Example 3

Additional siRNAs (not only siRNAs against kinases or kinase binding proteins) will also be validated in regard to a decline of the replication of influenza A viruses. For the evaluation of these siRNAs the same experimental setting will be used as described in example 1, except that the cell number is quantified indirectly by using a commercial cell viability assay (instead of using an automated microscope) and that these siRNAs will be reverse transfected, i.e. cells will be added to the siRNA transfection mix already prepared in 384 well plates.

Example 4

Among the human genome hundreds of genes are presumably relevant for the replication of influenza viruses. Therefore the screening procedure of kinases and kinase binding factors (described in Example 1) was expanded to a genome wide scale analysing all known human genes by using about 59886 siRNAs.

The experimental setup was performed in a similar way as described in Example 1, except:

- The screen was extended to genome wide level using 59886 siRNAs
- Cells were seeded in 384 well plates.
- Because of the huge number of transfected cells, not all cell numbers could be analysed by automated microscopy.
- siRNAs were reversely transfected in freshly seeded A549 cells using the transfection reagent HiperFect (Qiagen, Hilden, Germany).
- Knock-down of a particular gene was independently performed by up to four siRNAs ("target sequence 1", "target sequence 2", "target sequence 3", and "target sequence 4" in Table 4) specific for a particular gene.
- Additional controls were included: "AllStars Negative Control siRNA" (Qiagen, Hilden, Germany, Order No. 1027280) as negative control,

siRNAs directed against PKMYT (GeneID: 9088, GenBank accessionnumber: NM_182687, target sequence: CTGGGAGGAACTTACCGTCTA) as positive control (cellular factor against influenza replication), siRNAs directed against PLK (GeneID: 5347, GenBank accessionnumber: BC014135, target sequence: CCGGATCAAGAAGAATGAATA) as transfection control (cytotoxic after transfection).

- The infection rate of transfected A549 cells in selected wells is measured by automated microscopy to be able to dissect the inhibitory effects to early or late events during the infection process.
- Results were analysed by the statistical R-package "cellHTS" software, developed by Michael Butros, Ligia Bras and Wolfgang Huber, using the B-score normalisation method (based on "Allstars Negative Control siRNA" transfected control wells).
- Read-out is inhibition of virus replication.

The siRNAs and corresponding genes that showed a strong antiviral activity (z-scores < -2.0) are listed in Table 4.

The cell based assay comprised the following steps (see also Fig. 5 which describes the experimental setup of the genome wide siRNA screen:

Day 1:	Seeding of A549 cells (lung epithelial cells) + reverse transfection of siRNAs
Day 3:	Infection with influenza A/WSN/33 + transfection of 293T cells zq with indicator plasmid
Day 4:	Infection of 293T cells with the supernatant of A549 cells + fixation of A549 cells with formaldehyde
Day 5:	Luciferase Assay to quantify virus replication in 293T cells
Day x:	Determination of infection rate by the automated microscope.

Claims

1. A pharmaceutical composition comprising at least one modulator of a kinase or/and at least one modulator of a kinase binding polypeptide optionally together with pharmaceutically acceptable carriers, adjuvants, diluents or/and additives, for the prevention, alleviation or/and treatment of an influenza virus infection.

2. The pharmaceutical composition as claimed in claim 1, wherein the influenza virus infection is an influenza A virus infection, more preferably with strain Puerto Rico/8/34 or an Avian Influenza virus isolate such as H5N1.

3. The pharmaceutical composition as claimed in any of the preceding claims, wherein the at least one modulator is selected from the group consisting of nucleic acids, nucleic acid analogues such as ribozymes, peptides, polypeptides, and antibodies.

4. The pharmaceutical composition as claimed in any of the claims 1 to 3, wherein the at least one kinase or/and kinase binding polypeptide is encoded by a nucleic acid or/and gene selected from Table 1A and Table 1B.

5. The pharmaceutical composition as claimed in any of the claims 1 to 4, wherein the at least one modulator is an activator.

6. The pharmaceutical composition as claimed in claim 5, wherein the at least one activator comprises
   (a) a nucleotide sequence selected from Table 1A or a fragment thereof, or/and
   (b) a fragment which is at least 70 %, preferably at least 80%, more preferably at least 90% identical to the sequence of (a),

or/and the at least one activator is capable of activating expression or/and gene product activity of a gene comprising sequence (a) or/and (b).

7. The pharmaceutical composition as claimed in any of the claims 1 to 4, wherein the at least one modulator is an inhibitor.

8. The pharmaceutical composition as claimed in claim 7, wherein the at least one inhibitor comprises
   (a) a nucleotide sequence selected from Table 1B or/and a fragment thereof, or
   (b) a sequence which is at least 70 %, preferably at least 80%, more preferably at least 90% identical to the sequence of (a),
   or/and the at least one inhibitor is capable of inhibiting expression or/and gene product activity of a gene comprising sequence (a) or/and (b).

9. The pharmaceutical composition as claimed in any of the claims 3 to 8, wherein the nucleic acid comprises a nucleotide sequence selected from the sequences of Table 2 and fragments thereof.

10. Pharmaceutical composition comprising at least one inhibitor of influenza virus replication optionally together with pharmaceutically acceptable carriers, adjuvants, diluents or/and additives, for the prevention, alleviation or/and treatment of an influenza virus infection.

11. The pharmaceutical composition as claimed in claim 10, wherein the at least one inhibitor comprises
   (a) a nucleotide sequence selected from Table 1B and 4 or/and a fragment thereof, or
   (b) a sequence which is at least 70 %, preferably at least 80%, more preferably at least 90% identical to the sequence of (a),
   or/and the at least one inhibitor is capable of inhibiting expression or/and gene product activity of a gene comprising sequence (a) or/and (b).

12. The pharmaceutical composition as claimed in claim 10 or 11, wherein the nucleic acid comprises a nucleotide sequence selected from the sequences of Table 4 and fragments thereof.

13. The pharmaceutical composition as claimed in any of the claims 3 to 12, wherein the nucleic acid is RNA or DNA.

14. The pharmaceutical composition as claimed in claim 7 to 13, wherein the nucleic acid is
    (i) an RNA molecule capable of RNA interference,
    (ii) a precursor of the RNA molecule (i), or/and
    (iii) a DNA molecule encoding the RNA molecule (i) or/and the precursor (ii).

15. The pharmaceutical composition as claimed in any of the claims 7 to 14, wherein the RNA molecule is a double-stranded RNA molecule, preferably a double-stranded siRNA molecule with or without a single-stranded overhang alone at one end or at both ends.

16. The pharmaceutical composition as claimed in any of the claims 13 to 15 wherein the RNA molecule comprises at least one nucleotide analogue or/and deoxyribonucleotide.

17. The pharmaceutical composition as claimed in any of the claims 3 to 13, wherein the nucleic acid is an antisense nucleic acid or a DNA encoding the antisense nucleic acid.

18. The pharmaceutical composition as claimed in any of the claims 3 to 17, wherein the nucleic acid has a length of at least 15, preferably at least 17, more preferably at least 19, most preferably at least 21 nucleotides.

19. The pharmaceutical composition as claimed in any of the claims 3 to 17,

wherein the nucleic acid has a length of at the maximum 29, preferably at the maximum 27, more preferably at the maximum 25, especially more preferably at the maximum 23, most preferably at the maximum 21 nucleotides.

20. The pharmaceutical composition as claimed in claim 3 or 4, wherein the antibody is directed against a kinase or/and kinase binding polypeptide.

21. The pharmaceutical composition as claimed in claim 20, wherein the antibody is directed against a kinase or/and kinase binding polypeptide comprising
    (a) an amino acid sequence encoded by a nucleic acid or/and gene selected from Table 1A and Table 1B, or/and
    (b) an amino acid sequence which is at least 70%, preferably at least 80%, more preferably at least 90% identical to the sequence of (a).

22. The pharmaceutical composition as claimed in claim 10 comprising an antibody, wherein the antibody is preferably directed against a polypeptide comprising
    (a) an amino acid sequence encoded by a nucleic acid or/and gene selected from Table 4, or/and
    (b) an amino acid sequence which is at least 70%, preferably at least 80%, more preferably at least 90% identical to the sequence of (a).

23. The pharmaceutical composition of any of the preceding claims further comprising an agent suitable of transportation of the at least one modulator of a kinase or/and a kinase binding polypeptide into a cell, in particular into a lung epithelial cell.

24. The pharmaceutical composition of claim 23, wherein the further agent is chitosan, which preferably is formulated in nanoparticles.

25. A screening method for identification of a compound suitable for

modulation of a kinase or/and a kinase binding polypeptide, comprising the steps

(a) providing a kinase or/and a kinase binding polypeptide,

(b) contacting a compound with the kinase or/and a kinase binding polypeptide of (a),

(c) determining the activity of the kinase or/and the kinase binding polypeptide,

(d) selecting a compound which modulates the activity of the kinase or/and the kinase binding polypeptide.

26. The method of claim 25 which comprises a cellular screening assay or/and a molecular screening assay.

27. The method of claim 25 or 26, wherein the kinase or/and the kinase binding polypeptide is provided by a cell or/and a non-human organism capable of expressing the kinase or/and the kinase binding polypeptide.

28. The method of claim 25 or 26, wherein the kinase or/and the kinase binding polypeptide is provided in an isolated form.

29. A screening method for identification of a kinase modulator suitable for prevention, alleviation or/and treatment of an influenza virus infection, comprising the steps

(I) providing a cell or/and a non-human organism capable of being infected with an influenza virus and capable of expressing a kinase or/and a kinase binding polypeptide,

(II) contacting the cell or/and the organism of (I) with an influenza virus and with a compound known to be capable of modulating the expression or/and activity of the kinase or/and kinase binding polypeptide,

(III) determining the amount of influenza virus produced by the cell or/and the organism, and

(IV) selecting a compound which reduces the amount of the influenza

virus produced by the cell or/and the organism.

30. A screening method for identification of compound suitable for the prevention, alleviation or/and treatment of an influenza virus infection, comprising the steps

(A) providing a cell or/and a non-human organism capable of being infected with an influenza virus and capable of expressing a gene, wherein the gene or/and gene product thereof is capable of modulating an influenza virus replication,

(B) contacting the cell or/and the organism of (A) with an influenza virus and with a compound known to be capable of modulating the expression or/and activity of the gene of (A) or/and the gene product thereof,

(C) determining the amount of influenza virus produced by the cell or/and the organism, and

(D) selecting a compound which reduces the amount of the influenza virus produced by the cell or/and the organism.

31. The method of claim 30, wherein the gene of (A) is selected from table 1A, 1B and 4.

32. A screening method for identification of a compound suitable for prevention, alleviation or/and treatment of an influenza virus infection, comprising the steps

(i) providing a cell or/and a non-human organism capable of expressing a kinase or/and a kinase binding polypeptide,

(ii) contacting a compound with the cell or/and the organism of (i),

(iii) determining the amount or/and the activity of kinase or/and a kinase binding polypeptide, and

(iv) selecting a compound which modulates the amount or/and the activity of the kinase or/and the kinase binding polypeptide.

33. The screening method as claimed in claim 32, wherein the kinase activity

in steps (iii) or/and (iv) is determined by measuring kinase expression.

34. A screening method for identification of a compound suitable for prevention, alleviation or/and treatment of an influenza virus infection, comprising the steps
    i. providing a cell or/and a non-human organism capable of expressing a gene, wherein the gene or/and gene product thereof is capable of modulating an influenza virus replication,
    ii. contacting a compound with the cell or/and the organism of i.,
    iii. determining the amount or/and the activity of gene product of the gene of (i), and
    iv. selecting a compound which modulates the amount or/and the activity of the gene product of i.

35. The method of claim 34, wherein the gene of i. is preferably selected from Table 1A, 1B and 4.

36. A screening method for identification of genes suitable as targets for the prevention, alleviation or/and prevention of an influenza virus infection, comprising the steps
    (1) providing a cell or/and a transgenic non-human animal capable of expressing, particularly over- or underexpressing a gene,
    (2) contacting the cell or/and the organism of (1) with an influenza virus,
    (3) modulating the expression or/and activity of the gene and determining the amount of influenza virus produced by the cell or/and the organism, and
    (4) selecting a gene the expression or/and activity of which is positively or negatively correlated with reduction of the amount of the influenza virus produced by the cell or/and the organism.

37. The method of claim 36, wherein modulating the expression of a gene is downregulation or upregulation.

38. The method of claim 36 or 37, wherein modulation of the activity of a gene is decreasing or increasing of the activity.

39. The screening method of any of the claims 25 to 38, wherein the influenza is selected from influenza A viruses, more preferably from strain Puerto Rico/8/34 and Avian Influenza virus isolates such as H5N1.

40. The screening method of any of the claims 25 to 39, wherein the cell is a mammalian cell.

41. Use of a kinase modulator or/and a kinase binding protein modulator for the manufacture of a medicament for the prevention, alleviation or/and prevention of an influenza virus infection.

42. Use of a inhibitor of influenza virus replication capable of inhibiting the expression of a gene selected from Table 1b and 4, or/and of inhibiting a gene product thereof, for the manufacture of a medicament for the prevention, alleviation or/and prevention of an influenza virus infection.

43. Use of a nucleic acid comprising a gene sequence or/and a nucleotide sequence selected from Table 1a, 1b, 2, or/and 4 and fragments thereof in a method for screening for compounds or/and targets suitable for the prevention, alleviation or/and treatment of an influenza virus infection.

44. Use of claim 43, wherein a combination of at least two nucleic acids is used.

45. Use of claims 43 to 44, wherein the nucleic acid or the combination is selected from Table 1b and 4.

46. Use of claim 45, wherein the combination of nucleic acids inhibits expression or/and activity of one gene.

Fig. 1

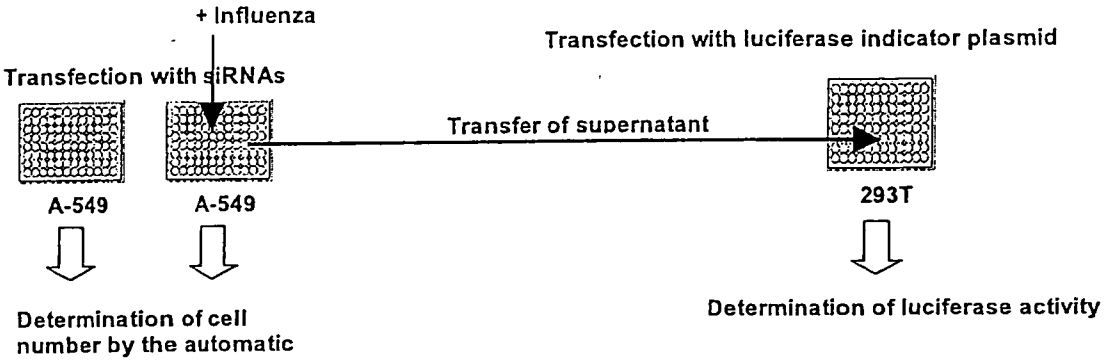

+ Influenza
Transfection with siRNAs
Transfection with luciferase indicator plasmid
Transfer of supernatant
A-549
A-549
293T
Determination of cell number by the automatic
Determination of luciferase activity

Fig. 2

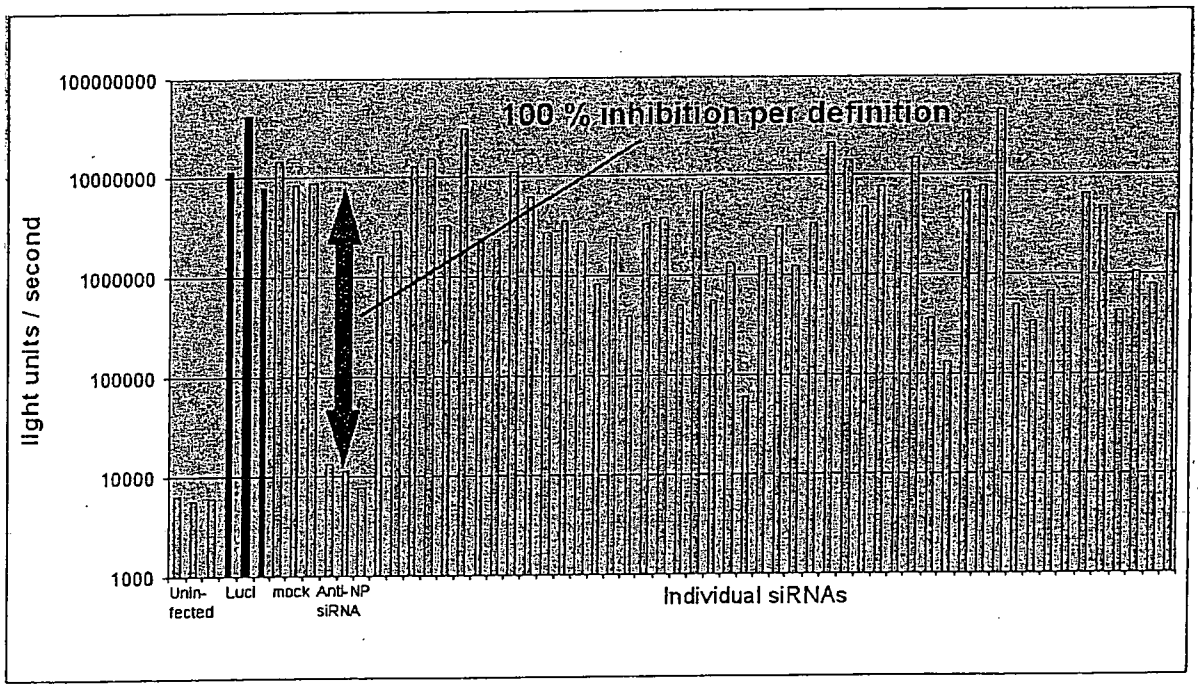

100000000
10000000
1000000
100000
10000
1000
light units / second
100 % inhibition per definition
Unin-fected
Lucl
mock
Anti-NP siRNA
Individual siRNAs

Fig. 3

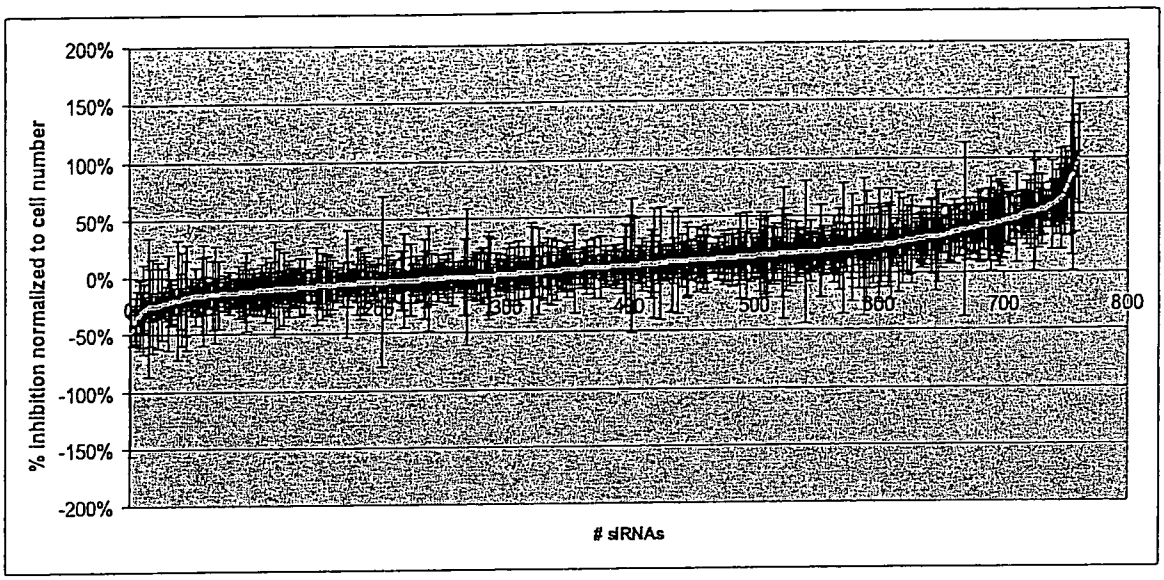

200%
150%
100%
50%
0%
-50%
-100%
-150%
-200%
% inhibition normalized to cell number
400
500
700
800
siRNAs

Fig. 4

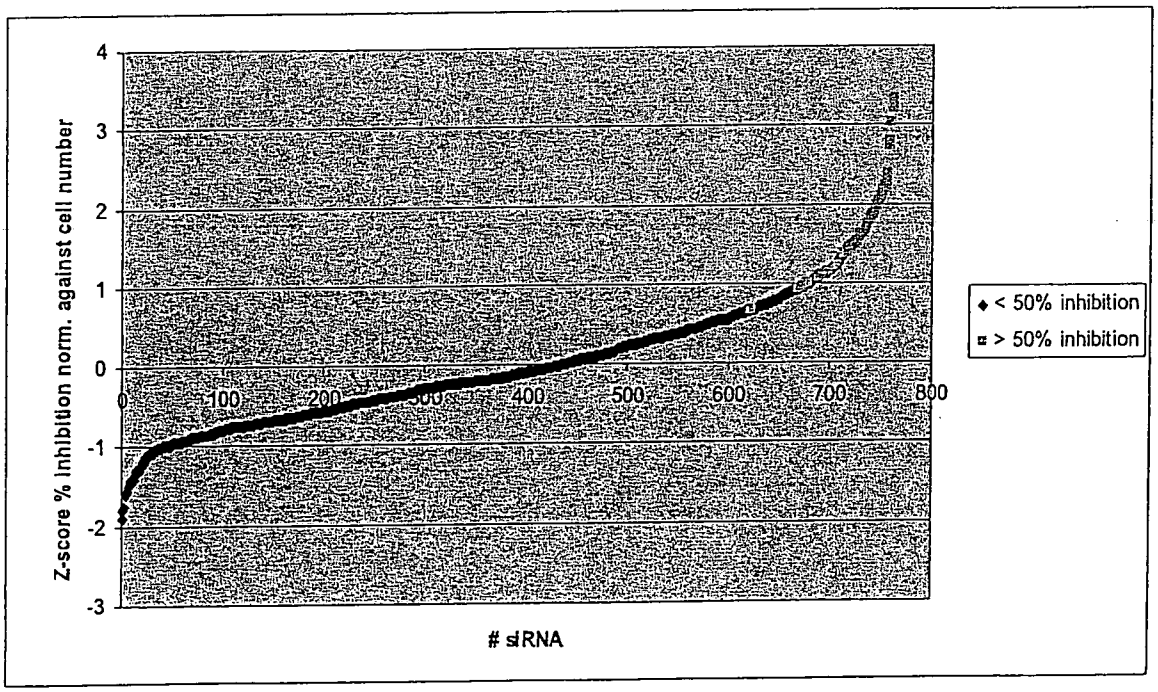

4
3
2
1
0
-1
-2
-3
Z-score % inhibition norm. against cell number
100
200
400
500
600
700
800
siRNA
< 50% inhibition
> 50% inhibition

Fig. 5

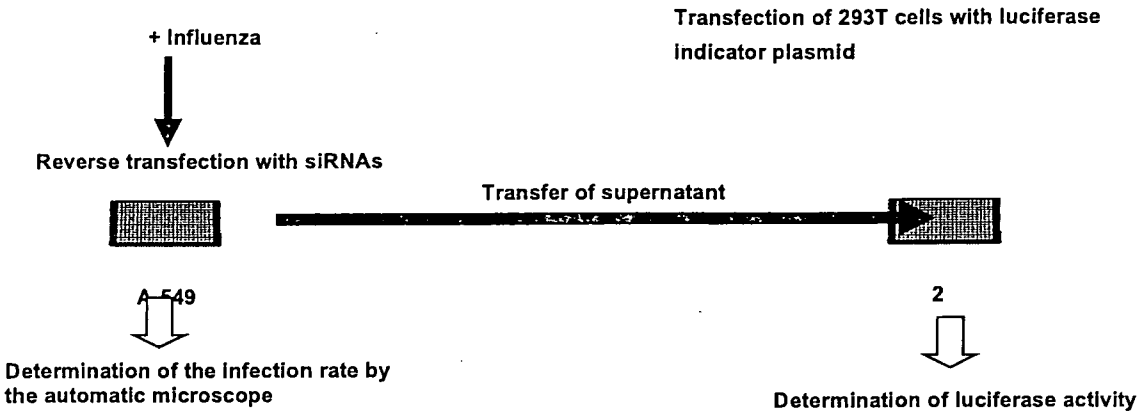

+ Influenza
Reverse transfection with siRNAs
A-549
Determination of the infection rate by the automatic microscope
Transfection of 293T cells with luciferase indicator plasmid
Transfer of supernatant
2
Determination of luciferase activity

Table 1a

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
Pool 19			-47%	109%
CKM	1158	NM_001824	-46%	14%
MAP3K3	4215	NM_002401	-45%	3%
SNARK	81788	NM_030952	-39%	16%
DDR1	780	NM_001954	-38%	21%
IHPK2	51447	NM_016291	-34%	23%
MARK3	4140	NM_002376	-33%	8%
Pool 31			-33%	30%
Pool 69			-31%	30%
AK7	122481	NM_152327	-30%	17%
Pool 46			-28%	17%
ARAF1	369	NM_001654	-28%	39%
Pool 75			-27%	22%
AKAP1	8165	NM_003488	-27%	10%
Pool 56			-27%	8%
IRAK2	3656	NM_001570	-26%	60%
ERK8	225689	NM_139021	-25%	34%
PANK3	79646	NM_024594	-25%	12%
AK5	26289	NM_174858	-25%	41%
PDK2	5164	NM_002611	-25%	6%
DGUOK	1716	NM_001929	-25%	12%
HGS	9146	NM_004712	-25%	10%
Pool 114			-24%	38%
Pool 33			-24%	9%
Pool 39			-23%	8%
Pool 43			-23%	31%
Pool 55			-23%	12%
MAPK8IP2	23542	NM_012324	-23%	10%
SKP2	6502	NM_005983	-22%	15%
Pool 45			-22%	7%
STK23	26576	NM_014370	-22%	41%
SRPK2	6733	NM_182692	-21%	20%
PKIG	11142	NM_181805	-21%	20%
PRKY	5616	NM_002760	-21%	16%
TESK1	7016	NM_006285	-21%	19%
NEK2	4751	NM_002497	-20%	11%
Pool 64			-20%	12%
PSKH1	5681	NM_006742	-20%	5%
PRKAR2B	5577	NM_002736	-20%	52%
TRAD	11139	NM_007064	-20%	11%
DYRK1A	1859	NM_001396	-20%	24%
LIMK1	3984	NM_002314	-19%	41%
WEE1	7465	NM_003390	-19%	10%
Pool 37			-18%	6%
ADRBK1	156	NM_001619	-18%	33%
TPK1	27010	NM_022445	-18%	46%
PHKB	5257	NM_000293	-17%	6%

Table 1a (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
PRKWNK4	65266	NM_032387	-17%	11%
Pool 82			-17%	16%
Pool 32			-17%	17%
PIK4CA	5297	NM_002650	-17%	17%
MK-STYX	51657	NM_016086	-17%	7%
Pool 103			-17%	26%
IRAK1BP1	134728	BX537762	-17%	13%
PRKCD	5580	NM_006254	-16%	17%
KIT	3815	NM_000222	-16%	9%
IRAK1	3654	NM_001569	-16%	14%
FGFR2	2263	NM_000141	-16%	8%
Pool 106			-16%	33%
Pool 111			-16%	44%
DGKH	160851	NM_178009	-16%	17%
Pool 113			-16%	35%
DAPK1	1612	NM_004938	-15%	11%
RAGE	5891	NM_014226	-15%	9%
KSR	8844	XM_290793	-15%	12%
TAO1	9344	NM_016151	-15%	3%
TAO1	9344	NM_004783	-15%	3%
Pool 30			-15%	31%
PAK2	5062	NM_002577	-15%	16%
AURKC	6795	NM_003160	-15%	42%
MARK2	2011	NM_004954	-15%	13%
MVK	4598	NM_000431	-15%	30%
MAPKBP1	23005	XM_031706	-15%	30%
PRKCE	5581	NM_005400	-14%	5%
EKI1	55500	NM_018638	-14%	7%
EPHA7	2045	NM_004440	-14%	10%
CDK4	1019	NM_000075	-14%	16%
AKAP12	9590	NM_005100	-14%	6%
Pool 29			-14%	16%
AURKB	9212	NM_004217	-14%	9%
PIK3C3	5289	NM_002647	-14%	18%
MAP2K6	5608	NM_002758	-14%	19%
ADCK4	79934	NM_024876	-14%	14%
MAPK8IP1	9479	NM_005456	-13%	5%
Pool 65			-13%	12%
PIK3CB	5291	NM_006219	-13%	10%
PIK3R3	8503	NM_003629	-13%	12%
PDK1	5163	NM_002610	-13%	11%
HRI	27102	NM_014413	-13%	23%
CSNK1G1	53944	NM_022048	-13%	17%
BMPR1A	657	NM_004329	-13%	12%
DAPK3	1613	NM_001348	-13%	20%
SIK2	23235	AB096248	-13%	10%
PDPK1	5170	NM_002613	-12%	27%
Pool 104			-12%	35%
CAMKK1	84254	NM_032294	-12%	10%

Table 1a (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
TK1	7083	NM_003258	-12%	20%
CSNK2B	1460	NM_001320	-12%	10%
MGC4796	83931	NM_032017	-12%	16%
DGKB	1607	NM_145695	-12%	16%
MET	4233	NM_000245	-12%	5%
ERBB4	2066	NM_005235	-12%	21%
PRKCDBP	112464	NM_145040	-12%	16%
BTK	695	NM_000061	-12%	11%
RPS6KB1	6198	NM_003161	-11%	13%
AKAP11	11215	NM_016248	-11%	9%
PRKAG1	5571	NM_002733	-11%	15%
PIK3C2A	5286	NM_002645	-11%	22%
CDK11	23097	NM_015076	-11%	16%
Pool 54			-11%	14%
MKNK2	2872	NM_017572	-11%	29%
PTK9	5756	NM_002822	-11%	11%
FLT3LG	2323	BF688722	-11%	13%
CDK8	1024	NM_001260	-11%	20%
ITPKA	3706	NM_002220	-11%	24%
CDK3	1018	NM_001258	-11%	14%
CDK7	1022	NM_001799	-11%	9%
PRKACA	5566	NM_002730	-11%	41%
Pool 3			-10%	11%
LAK	80216	NM_025144	-10%	16%
ITPKB	3707	NM_002221	-10%	35%
PI4KII	55361	NM_018425	-10%	12%
PRKCBP1	23613	NM_183048	-10%	16%
SH3KBP1	30011	NM_031892	-10%	5%
BRAF	673	NM_004333	-10%	13%
Pool 34			-10%	33%
KHK	3795	NM_000221	-10%	9%
DCAMKL1	9201	NM_004734	-10%	21%
CLK3	1198	NM_001292	-10%	13%
BCR	613	NM_004327	-10%	25%
STK16	8576	NM_003691	-10%	17%
MAPKAPK3	7867	NM_004635	-10%	18%
IKBKE	9641	XM_375834	-9%	12%
ATR	545	NM_001184	-9%	15%
STK17A	9263	NM_004760	-9%	16%
MOS	4342	NM_005372	-9%	16%
MAPK3	5595	NM_002746	-9%	9%
SMG1	23049	NM_014006	-9%	26%
FER	2241	NM_005246	-9%	17%
PFKP	5214	NM_002627	-9%	12%
CSK	1445	NM_004383	-9%	13%
BUB1	699	NM_004336	-9%	24%
AK3L1	50808	NM_016282	-9%	13%
GRK7	131890	NM_139209	-9%	3%
MAP3K6	9064	NM_004672	-9%	6%

Table 1a (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
ACVR2B	93	NM_001106	-9%	6%
IRAK4	51135	NM_016123	-8%	14%
EPHA5	2044	NM_004439	-8%	15%
PRKWNK3	65267	NM_020922	-8%	4%
RIOK1	83732	NM_031480	-8%	7%
MAK	4117	NM_005906	-8%	12%
CSNK2A2	1459	NM_001896	-8%	35%
Pool 60			-8%	17%
AXL	558	NM_001699	-8%	21%
IHPK1	9807	NM_153273	-8%	15%
Pool 98			-8%	29%
JAK2	3717	NM_004972	-8%	3%
Pool 61			-8%	17%
DDR2	4921	NM_006182	-8%	26%
ADCK5	203054	NM_174922	-8%	27%
EPHA1	2041	NM_005232	-7%	14%
Pool 77			-7%	25%
GKAP42	80318	NM_025211	-7%	12%
PIK3R4	30849	NM_014602	-7%	22%
ROCK1	6093	NM_005406	-7%	3%
Pool 22			-7%	13%
LCK	3932	NM_005356	-7%	8%
RPS6KA2	6196	NM_021135	-7%	13%
KIDINS220	57498	AB033076	-7%	15%
Pool 24			-7%	10%
SNF1LK	150094	NM_173354	-7%	6%
FGFR1	2260	NM_015850	-7%	10%
Pool 53			-7%	19%
PRKCI	5584	NM_002740	-7%	9%
HSPB8	26353	NM_014365	-6%	10%
JAK1	3716	NM_002227	-6%	47%
Pool 68			-6%	20%
CLK1	1195	NM_004071	-6%	13%
SAST	22983	AB023190	-6%	8%
PDGFRB	5159	NM_002609	-6%	11%
CLK2	1196	NM_001291	-6%	9%
VRK2	7444	NM_006296	-6%	12%
LOC91807	91807	NM_182493	-6%	17%
MELK	9833	NM_014791	-5%	29%
Pool 18			-5%	11%
CCRK	23552	NM_178432	-5%	31%
PRKAG3	53632	NM_017431	-5%	21%
SPEC2	56990	NM_020240	-5%	6%
Pool 44			-5%	27%
ACVR1B	91	NM_004302	-5%	10%
CHUK	1147	NM_001278	-5%	22%
FYN	2534	NM_002037	-5%	17%
DTYMK	1841	NM_012145	-5%	8%
SRMS	6725	NM_080823	-5%	19%

Table 1a (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
MAP3K9	4293	XM_027237	-5%	6%
ALK	238	NM_004304	-5%	13%
PAK6	56924	NM_020168	-5%	10%
Pool 8			-5%	15%
ILKAP	80895	NM_176799	-5%	16%
SPHK2	56848	NM_020126	-5%	4%
CDK2	1017	NM_001798	-5%	21%
NEK3	4752	NM_152720	-5%	7%
TESK2	10420	NM_007170	-5%	9%
AKT2	208	NM_001626	-5%	74%
PRKG1	5592	NM_006258	-5%	8%
KIP2	10518	NM_006383	-5%	8%
Pool 88			-4%	32%
MAPK14	1432	NM_001315	-4%	15%
CARKL	23729	NM_013276	-4%	23%
NME4	4833	NM_005009	-4%	5%
VRK1	7443	NM_003384	-4%	17%
TAO1	9344	NM_016151	-4%	11%
TAO1	9344	NM_004783	-4%	11%
NLK	51701	NM_016231	-4%	10%
NME1	4830	NM_000269	-4%	19%
Pool 12			-4%	18%
CALM3	808	NM_005184	-4%	10%
ADRBK2	157	NM_005160	-4%	8%
Pool 21			-4%	10%
PRKWNK2	65268	NM_006648	-4%	26%
Pool 97			-4%	20%
Pool 115			-4%	41%
RAF1	5894	NM_002880	-4%	7%
PACSIN3	29763	NM_016223	-4%	6%
PGK2	5232	NM_138733	-4%	9%
MAPK10	5602	NM_002753	-3%	7%
Pool 36			-3%	32%
PRKWNK1	65125	NM_018979	-3%	13%
ITPKC	80271	NM_025194	-3%	15%
FLJ13052	65220	NM_023018	-3%	8%
RPS6KA3	6197	NM_004586	-3%	21%
MAST2	23139	NM_015112	-3%	10%
STK25	10494	NM_006374	-3%	18%
LMTK2	22853	NM_014916	-3%	11%
MAPK1	5594	NM_002745	-3%	13%
MAGI-3	260425	NM_020965	-3%	8%
PFKFB1	5207	NM_002625	-3%	20%
Pool 71			-3%	35%
GRK6	2870	NM_002082	-3%	25%
STK6	6790	NM_003600	-3%	13%
Pool 101			-3%	46%
STK11IP	114790	NM_052902	-3%	10%
DOK1	1796	NM_001381	-2%	23%

Table 1a (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
PTK9L	11344	NM_007284	-2%	9%
CNK1	10256	NM_006314	-2%	9%
FLT3	2322	NM_004119	-2%	13%
ZAP70	7535	NM_001079	-2%	13%
MAPKAP1	79109	NM_024117	-2%	20%
AK1	203	NM_000476	-2%	9%
FGFR3	2261	NM_000142	-2%	6%
TXK	7294	NM_003328	-2%	10%
CDKN1C	1028	NM_000076	-2%	14%
Pool 7			-2%	17%
MUSK	4593	NM_005592	-2%	8%
ACVR1	90	NM_001105	-2%	22%
AKAP5	9495	NM_004857	-2%	11%
MKNK1	8569	NM_003684	-2%	11%
UGP2	7360	NM_006759	-2%	10%
RYK	6259	NM_002958	-2%	5%
Pool 107			-2%	25%
ITPK1	3705	NM_014216	-1%	13%
RPS6KL1	83694	NM_031464	-1%	8%
PIM1	5292	NM_002648	-1%	6%
CAMK2D	817	NM_001221	-1%	13%
CAMK2G	818	NM_172173	-1%	8%
TYK2	7297	NM_003331	-1%	13%
LIMK2	3985	NM_005569	-1%	10%
HK2	3099	NM_000189	-1%	14%
Pool 91			-1%	33%
DYRK1B	9149	NM_004714	-1%	17%
TTBK1	84630	XM_166453	-1%	59%
Pool 58			-1%	15%
Pool 41			-1%	8%
MAP3K5	4217	NM_005923	-1%	17%
CDKL2	8999	NM_003948	-1%	10%
LOC149420	149420	NM_152835	-1%	20%
EGFR	1956	NM_005228	-1%	15%
FRK	2444	NM_002031	-1%	22%
Pool 78			-1%	21%
CDKN2C	1031	NM_001262	-1%	14%
IRAK3	11213	NM_007199	-1%	4%

Table 1b

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
AKAP8	10270	NM_005858	1%	19%
Pool 2			1%	13%
HSA250839	55351	NM_018401	1%	14%
JAK3	3718	NM_000215	1%	18%
LYK5	92335	NM_153335	1%	8%
PIK3C2G	5288	NM_004570	1%	12%
EPHB4	2050	NM_004444	1%	14%
KIAA1804	84451	NM_032435	1%	11%
STK39	27347	NM_013233	1%	22%
ABL1	25	NM_005157	1%	10%
Pool 48			1%	16%
PRKR	5610	NM_002759	1%	27%
IKBKAP	8518	NM_003640	1%	17%
PRKCB1	5579	NM_002738	1%	6%
PLK4	10733	NM_014264	1%	13%
EPHA8	2046	NM_020526	1%	24%
PFKM	5213	NM_000289	2%	11%
EPHB6	2051	NM_004445	2%	11%
Pool 110			2%	28%
Pool 62			2%	14%
DYRK4	8798	NM_003845	2%	14%
MAPK7	5598	NM_002749	2%	10%
Pool 81			2%	23%
PRKCL2	5586	NM_006256	2%	10%
PACSIN1	29993	NM_020804	2%	14%
YES1	7525	NM_005433	2%	9%
MAP3K7IP1	10454	NM_006116	2%	13%
PSKH2	85481	NM_033126	2%	22%
Pool 108			3%	43%
Pool 74			3%	39%
MYLK2	85366	NM_033118	3%	22%
Pool 73			3%	14%
RIPK3	11035	NM_006871	3%	22%
PRKCM	5587	NM_002742	3%	2%
PHKG2	5261	NM_000294	3%	9%
SGK2	10110	NM_016276	3%	38%
STK17B	9262	NM_004226	3%	13%
Pool 6			3%	23%
PRPF4B	8899	NM_176800	3%	26%
DMPK	1760	NM_004409	3%	6%
PIK3AP1	118788	NM_152309	3%	6%
BMP2K	55589	NM_017593	3%	15%
Pool 52			3%	29%
CKMT2	1160	NM_001825	4%	16%
Pool 5			4%	21%
Pool 51			4%	29%
TK2	7084	NM_004614	4%	8%
CAMK1G	57172	NM_020439	4%	6%

Table 1b (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
CALM2	805	NM_001743	4%	14%
Pool 99			4%	26%
Pool 11			4%	19%
ITK	3702	NM_005546	4%	10%
PKM2	5315	NM_182471	4%	17%
Pool 17			4%	17%
MST4	51765	NM_016542	4%	16%
ROCK2	9475	NM_004850	4%	19%
OSR1	9943	NM_005109	4%	13%
PRKAR1A	5573	NM_002734	4%	18%
MARK4	57787	NM_031417	5%	25%
DGKZ	8525	NM_003646	5%	14%
MAPK6	5597	NM_002748	5%	20%
PRKAG2	51422	NM_016203	5%	13%
CaMKIINalpha	55450	NM_018584	5%	18%
EPHA3	2042	NM_005233	5%	8%
Pool 70			5%	38%
PGK1	5230	NM_000291	5%	9%
CAMK1	8536	NM_003656	5%	5%
MAP2K2	5605	NM_030662	5%	3%
PTK2B	2185	NM_173176	5%	14%
EPHB3	2049	NM_004443	5%	8%
TBK1	29110	NM_013254	5%	17%
GUK1	2987	NM_000858	6%	14%
LOC161635	161635	BC028192	6%	18%
ACVRL1	94	NM_000020	6%	24%
MERTK	10461	NM_006343	6%	15%
DGKQ	1609	NM_001347	6%	9%
SSTK	83983	NM_032037	6%	6%
HIPK3	10114	NM_005734	6%	19%
ROR1	4919	NM_005012	6%	10%
ARK5	9891	XM_374996	6%	18%
URKL1	54963	NM_017859	6%	27%
CDK9	1025	NM_001261	6%	10%
CDKN2B	1030	NM_004936	6%	10%
KIS	127933	NM_175866	6%	4%
TGFBR2	7048	NM_003242	6%	6%
BLK	640	NM_001715	6%	28%
TTK	7272	NM_003318	6%	12%
CDKL1	8814	NM_004196	6%	11%
CLK4	57396	NM_020666	7%	15%
PRKDC	5591	NM_006904	7%	18%
STK38L	23012	NM_015000	7%	15%
AKAP4	8852	NM_003886	7%	3%
STK11	6794	NM_000455	7%	5%
MAGI1	154043	NM_173515	7%	13%
SNRK	54861	NM_017719	7%	9%
CDC42BPA	8476	NM_003607	7%	17%

Table 1b (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
CERK	64781	NM_182661	7%	13%
RBKS	64080	NM_022128	7%	14%
ATM	472	NM_000051	7%	19%
MAPK8IP3	23162	NM_015133	7%	7%
HAK	115701	NM_052947	7%	16%
RIPK2	8767	NM_003821	7%	8%
GRK5	2869	NM_005308	7%	13%
AKAP6	9472	NM_004274	7%	13%
Pool 13			7%	25%
MATK	4145	NM_002378	8%	37%
Pool 1			8%	35%
GIT1	28964	NM_014030	8%	8%
CAMK1D	57118	NM_020397	8%	13%
Pool 87			8%	43%
KSR2	283455	NM_173598	8%	58%
SGK	6446	NM_005627	8%	12%
Pool 92			8%	41%
NEK4	6787	NM_003157	8%	5%
PIK3CD	5293	NM_005026	8%	9%
ASK	10926	NM_006716	8%	17%
TIE	7075	NM_005424	8%	16%
AKAP7	9465	NM_004842	8%	17%
XYLB	9942	NM_005108	8%	23%
MARK1	4139	NM_018650	8%	11%
FN3K	64122	NM_022158	8%	13%
NEK6	10783	NM_014397	9%	12%
RPS6KC1	26750	NM_012424	9%	20%
MAPKAPK5	8550	NM_003668	9%	3%
ICK	22858	NM_014920	9%	8%
Pool 23			9%	15%
PRKAB2	5565	NM_005399	9%	30%
HK3	3101	NM_002115	9%	25%
Pool 96			9%	48%
IBTK	25998	AB037838	9%	8%
PDK3	5165	NM_005391	9%	8%
SKIP	80309	XM_051221	9%	19%
PRKAA2	5563	NM_006252	9%	14%
HCK	3055	NM_002110	9%	50%
STK29	9024	NM_003957	10%	14%
DGKA	1606	NM_001345	10%	17%
GK	2710	NM_000167	10%	8%
DAPK2	23604	NM_014326	11%	15%
STK31	56164	NM_031414	11%	10%
Pool 59			11%	16%
PI4K2B	55300	NM_018323	11%	8%
MADD	8567	NM_003682	11%	8%
PRKCQ	5588	NM_006257	11%	12%
PDK4	5166	NM_002612	11%	44%

Table 1b (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
PRKRIR	5612	NM_004705	11%	19%
PFKFB4	5210	NM_004567	11%	15%
CAMK2A	815	NM_015981	11%	10%
Pool 83			11%	46%
DGKG	1608	NM_001346	11%	8%
APEG1	10290	NM_005876	11%	16%
Pool 80			11%	23%
CKS1B	1163	NM_001826	11%	15%
DYRK2	8445	NM_003583	11%	17%
PACSIN2	11252	NM_007229	11%	17%
LYN	4067	NM_002350	11%	33%
Pool 67			12%	30%
MAP4K3	8491	NM_003618	12%	13%
PNKP	11284	NM_007254	12%	17%
PMVK	10654	NM_006556	12%	18%
Pool 4			12%	10%
LATS2	26524	NM_014572	12%	13%
CKMT1	1159	NM_020990	12%	7%
HIPK1	204851	NM_181358	12%	29%
STK10	6793	NM_005990	12%	16%
STK22D	83942	NM_032028	12%	16%
TRIO	7204	NM_007118	12%	20%
GIT2	9815	NM_014776	12%	21%
AKAP28	158798	NM_178813	12%	15%
UMP-CMP	51727	NM_016308	13%	26%
Pool 14			13%	21%
LIM	10611	NM_006457	13%	20%
PIP5K2C	79837	NM_024779	13%	30%
PRKG2	5593	NM_006259	13%	6%
PCTK1	5127	NM_006201	13%	9%
Pool 35			13%	9%
PKLR	5313	NM_181871	13%	13%
LATS1	9113	NM_004690	13%	9%
ACVR2	92	NM_001616	13%	11%
STK24	8428	NM_003576	13%	8%
NJMU-R1	64149	NM_022344	13%	18%
PANK4	55229	NM_018216	13%	19%
CDKL3	51265	NM_016508	13%	12%
PHKG1	5260	NM_006213	13%	7%
ERN1	2081	NM_001433	13%	14%
MAP3K7IP2	23118	NM_015093	13%	24%
AK2	204	NM_001625	13%	21%
GRAF	23092	NM_015071	13%	21%
PRKD2	25865	NM_016457	14%	10%
PRKAA1	5562	NM_006251	14%	21%
TTBK2	146057	NM_173500	14%	8%
Pool 50			14%	20%
KDR	3791	NM_002253	14%	25%

Table 1b (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
NME6	10201	NM_005793	14%	20%
EIF2AK3	9451	NM_004836	14%	16%
CDK6	1021	NM_001259	14%	9%
FGFR4	2264	NM_002011	15%	17%
CDK5R2	8941	NM_003936	15%	24%
SYK	6850	NM_003177	15%	37%
DCK	1633	NM_000788	15%	21%
MAP4K4	9448	NM_004834	15%	12%
BUB1B	701	NM_001211	15%	21%
CHK	1119	NM_001277	15%	21%
Pool 38			15%	38%
FLJ11149	55312	NM_018339	15%	7%
DYRK3	8444	NM_003582	15%	8%
NRGN	4900	NM_006176	15%	23%
PIK3CA	5290	NM_006218	15%	20%
PAK1	5058	NM_002576	15%	16%
TYRO3	7301	NM_006293	15%	11%
TLK2	11011	NM_006852	15%	10%
NEK9	91754	NM_033116	15%	12%
ERBB3	2065	NM_001982	16%	20%
PFKFB3	5209	NM_004566	16%	14%
NEK1	4750	NM_012224	16%	32%
PKE	282974	NM_173575	16%	38%
PRKCG	5582	NM_002739	16%	21%
CDK5	1020	NM_004935	16%	34%
PCTK2	5128	NM_002595	16%	25%
ALS2CR7	65061	NM_139158	16%	38%
Pool 76			16%	34%
HIPK2	28996	NM_022740	16%	6%
CDC42BPB	9578	NM_006035	16%	14%
EPHB1	2047	NM_004441	16%	24%
BCKDK	10295	NM_005881	16%	23%
STK22C	81629	NM_052841	17%	26%
CSNK1G3	1456	NM_004384	17%	13%
AK3	205	NM_013410	17%	23%
EPHA2	1969	NM_004431	17%	10%
ANKRD3	54101	NM_020639	17%	14%
NEK11	79858	NM_024800	17%	7%
Pool 94			17%	39%
LTK	4058	NM_002344	17%	25%
Pool 100			17%	57%
MAP3K12	7786	NM_006301	17%	8%
Pool 66			18%	34%
MAP2K7	5609	BC005365	18%	21%
NUCKS	64710	NM_022731	18%	9%
PIK3CG	5294	NM_002649	18%	29%
TYROBP	7305	NM_003332	18%	8%
ROR2	4920	NM_004560	18%	9%

Table 1b (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
PFTK1	5218	NM_012395	18%	12%
MAP3K14	9020	NM_003954	18%	17%
PRKRA	8575	NM_003690	18%	27%
pknbeta	29941	NM_013355	18%	19%
SGKL	23678	NM_013257	18%	22%
PANK2	80025	NM_024960	18%	13%
CDC2L5	8621	NM_003718	18%	16%
MAP2K3	5606	NM_002756	18%	14%
PKIB	5570	NM_181795	18%	20%
MAP3K7	6885	NM_003188	18%	63%
PFKFB2	5208	NM_006212	19%	11%
CDKN1A	1026	NM_000389	19%	12%
CSNK2A1	1457	NM_177560	19%	17%
PIP5K2A	5305	NM_005028	19%	17%
STK36	27148	NM_015690	19%	27%
CINP	51550	NM_032630	19%	17%
TEK	7010	NM_000459	19%	15%
MAP4K2	5871	NM_004579	19%	7%
EEF2K	29904	NM_013302	19%	14%
Pool 72			19%	12%
TLK1	9874	NM_012290	19%	20%
ULK1	8408	NM_003565	19%	16%
Pool 79			19%	40%
CDKN2D	1032	NM_001800	19%	19%
NRBP	29959	NM_013392	19%	21%
CDK10	8558	NM_003674	19%	17%
NEK8	284086	NM_178170	19%	13%
NYD-SP25	89882	BC033792	20%	10%
NYD-SP25	89882	NM_033516	20%	10%
MAP2K5	5607	NM_002757	20%	8%
PRKACB	5567	NM_182948	20%	13%
NTRK2	4915	NM_006180	20%	21%
MAP3K13	9175	NM_004721	20%	16%
CSNK1D	1453	NM_001893	20%	29%
MAP2K1IP1	8649	NM_021970	20%	17%
PINK1	65018	NM_032409	20%	8%
Pool 25			20%	23%
ERBB2	2064	NM_004448	21%	12%
Pool 42			21%	36%
AKAP10	11216	NM_007202	21%	17%
PANK1	53354	NM_138316	21%	10%
Pool 47			21%	57%
MAPKAPK2	9261	NM_004759	21%	17%
Pool 15			21%	21%
PRKX	5613	NM_005044	21%	21%
TOPK	55872	NM_018492	21%	9%
TNIK	23043	XM_039796	21%	8%
Pool 27			22%	27%

Table 1b (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
FES	2242	NM_002005	22%	47%
Pool 84			22%	22%
PHKA2	5256	NM_000292	22%	7%
MAP3K4	4216	NM_005922	22%	9%
ULK2	9706	NM_014683	22%	15%
MAPK13	5603	NM_002754	22%	36%
Pool 10			22%	13%
Pool 49			22%	13%
NME2	4831	NM_002512	22%	27%
Pool 116			23%	59%
BMPR2	659	NM_001204	23%	19%
CASK	8573	NM_003688	23%	28%
HSMDPKIN	55561	XM_290516	23%	48%
AKT1	207	NM_005163	23%	13%
PXK	54899	NM_017771	23%	36%
RIPK1	8737	NM_003804	23%	15%
DGKD	8527	NM_003648	23%	14%
IHPK3	117283	NM_054111	23%	33%
RPS6KA5	9252	NM_182398	23%	10%
PKIA	5569	NM_181839	24%	27%
RPS6KB2	6199	NM_003952	24%	14%
Pool 95			24%	49%
CDKL5	6792	NM_003159	24%	36%
CDC2	983	NM_001786	24%	33%
MAP4K5	11183	NM_006575	24%	5%
Pool 85			25%	29%
VRK3	51231	NM_016440	25%	8%
EPHA4	2043	NM_004438	25%	12%
IKBKG	8517	NM_003639	25%	37%
PLK2	10769	NM_006622	25%	33%
CAMK4	814	NM_001744	25%	48%
PIK3R1	5295	NM_181504	25%	17%
Pool 16			25%	17%
EPHB2	2048	NM_017449	25%	5%
MGC45419	139728	NM_198452	25%	14%
T3JAM	80342	NM_025228	26%	21%
MAP3K8	1326	NM_005204	26%	11%
Pool 112			26%	43%
PHKA1	5255	NM_002637	27%	6%
TGFBR1	7046	NM_004612	27%	18%
AKAP9	10142	NM_005751	27%	37%
PAK7	57144	NM_177990	27%	26%
MINK	50488	NM_015716	27%	13%
CSNK1A1	1452	NM_001892	28%	30%
PIM2	11040	NM_006875	28%	31%
PIP5K1A	8394	NM_003557	28%	10%
PLK1	5347	NM_005030	29%	29%
PIP5K3	200576	NM_152671	29%	39%

Table 1b (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
PRKCABP	9463	NM_012407	29%	7%
MAP3K2	10746	NM_006609	29%	18%
TEC	7006	NM_003215	29%	14%
FLT4	2324	NM_182925	29%	18%
CDKN2A	1029	NM_000077	30%	12%
EIF2AK4	27104	BX640919	30%	21%
Pool 9			30%	20%
PTK2	5747	NM_005607	30%	26%
MARCKS	4082	NM_002356	30%	23%
AKAP13	11214	NM_006738	30%	26%
Pool 63			30%	17%
UCK1	83549	NM_031432	31%	25%
STK33	65975	NM_030906	31%	20%
SRC	6714	NM_005417	31%	16%
P101-PI3K	23533	NM_014308	31%	6%
MAP3K10	4294	NM_002446	31%	32%
PIP5K1C	23396	NM_012398	31%	33%
RET	5979	NM_020975	31%	13%
TNNI3K	51086	NM_015978	31%	21%
Pool 105			31%	48%
PRKCH	5583	NM_006255	31%	24%
Pool 89			31%	41%
ADK	132	NM_001123	32%	15%
MAP2K1	5604	NM_002755	32%	28%
FLT1	2321	NM_002019	32%	15%
MGC33182	122011	NM_145203	32%	9%
Pool 26			32%	15%
SKP1A	6500	NM_006930	33%	4%
AKIP	54998	NM_017900	33%	26%
CHEK1	1111	NM_001274	33%	23%
MAP3K11	4296	NM_002419	33%	25%
RPS6KA1	6195	NM_002953	34%	25%
STK38	11329	NM_007271	34%	21%
PIP5K1B	8395	NM_003558	34%	7%
PIK3R2	5296	NM_005027	35%	28%
SLK	9748	NM_014720	36%	22%
CAMKK2	10645	NM_006549	36%	10%
AKAP3	10566	NM_006422	36%	23%
GNE	10020	NM_005476	36%	22%
KIAA1446	57596	NM_020836	37%	7%
AATK	9625	AB014541	37%	15%
ADCK2	90956	NM_052853	37%	17%
Pool 28			37%	76%
PTK6	5753	NM_005975	37%	28%
MAPK12	6300	NM_002969	37%	22%
CRK7	51755	NM_016507	38%	7%
PASK	23178	NM_015148	38%	27%
TNK1	8711	NM_003985	38%	13%

Table 1b (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
PFKL	5211	NM_002626	38%	20%
MAP4K1	11184	NM_007181	38%	23%
MAPK9	5601	NM_002752	39%	20%
FUK	197258	NM_145059	39%	13%
LOC55971	55971	NM_018842	39%	13%
ZAK	51776	NM_016653	39%	30%
NTRK3	4916	NM_002530	40%	25%
NTRK1	4914	NM_002529	40%	32%
STK35	140901	NM_080836	41%	12%
CDK5R1	8851	NM_003885	41%	21%
PAK3	5063	NM_002578	41%	22%
CAMK2B	816	NM_001220	41%	4%
NME5	8382	NM_003551	41%	22%
Pool 90			41%	31%
GAK	2580	NM_005255	41%	32%
AKT3	10000	NM_181690	42%	41%
ADCK1	57143	NM_020421	42%	19%
STK4	6789	NM_006282	43%	26%
AKAP8L	26993	NM_014371	43%	29%
MAPK11	5600	NM_002751	43%	28%
UMPK	7371	NM_012474	43%	35%
CSNK1G2	1455	NM_001319	43%	24%
PIK3C2B	5287	NM_002646	43%	38%
C21orf124	85006	NM_003681	44%	31%
CKB	1152	NM_001823	44%	33%
CIB3	117286	NM_054113	45%	28%
ILK	3611	NM_004517	45%	19%
PRKACG	5568	NM_002732	45%	20%
SRPK1	6732	NM_003137	45%	5%
AAK1	22848	NM_014911	46%	21%
PCTK3	5129	AK126879	46%	23%
NEK7	140609	NM_133494	46%	22%
LOC375449	375449	NM_198828	46%	4%
ROS1	6098	NM_002944	47%	11%
PDGFRA	5156	NM_006206	47%	19%
CIT	11113	NM_007174	48%	12%
LOC388226	10595	XM_370946	48%	39%
CDKN1B	1027	NM_004064	48%	5%
NME7	29922	NM_197972	48%	8%
RPS6KA6	27330	NM_014496	49%	16%
Pool 57			49%	20%
PIK4CB	5298	NM_002651	51%	16%
Pool 20			51%	20%
MAP2K4	6416	NM_003010	51%	14%
CHEK2	11200	NM_007194	51%	28%
ALS2CR2	55437	NM_018571	52%	18%
GRK1	6011	NM_002929	52%	17%
Pool 93			52%	32%

Table 1b (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
MAPK4	5596	NM_002747	52%	24%
STK22B	23617	NM_053006	52%	15%
Pool 109			52%	51%
NYD-SP25	89882	BC033792	53%	44%
NYD-SP25	89882	NM_033516	53%	44%
ANKK1	255239	NM_178510	53%	7%
SPHK1	8877	NM_021972	53%	33%
PLK3	1263	NM_004073	53%	19%
GRK4	2868	NM_182982	54%	23%
PIP5K2B	8396	NM_003559	54%	30%
Pool 102			55%	22%
NIPA	51530	NM_016478	55%	11%
RPS6KA4	8986	NM_003942	55%	16%
IKBKB	3551	NM_001556	56%	10%
FGR	2268	NM_005248	57%	12%
PTK7	5754	NM_152883	58%	5%
RIOK2	55781	NM_018343	59%	20%
CSNK1E	1454	NM_001894	59%	39%
PRKCL1	5585	NM_002741	60%	21%
STK3	6788	NM_006281	60%	20%
GSK3A	2931	NM_019884	60%	28%
HK1	3098	NM_033498	61%	19%
PRKCZ	5590	NM_002744	62%	16%
RIOK3	8780	NM_003831	62%	19%
CKS2	1164	NM_001827	63%	31%
FASTK	10922	NM_006712	63%	44%
MST1R	4486	NM_002447	65%	24%
BMPR1B	658	NM_001203	66%	33%
PRKAR2A	5576	NM_004157	69%	39%
CDC2L1	984	NM_001787	73%	26%
PRKAB1	5564	NM_006253	74%	30%
PKMYT1	9088	NM_182687	78%	15%
PAK4	10298	NM_005884	81%	49%
CALM1	801	NM_006888	82%	68%
BMX	660	NM_001721	84%	83%
NME3	4832	NM_002513	85%	50%
JIK	51347	NM_016281	89%	27%
ACK1	10188	NM_005781	93%	11%
HUNK	30811	NM_014586	94%	35%
MAPK8	5599	NM_002750	98%	47%
DGKE	8526	NM_003647	113%	25%

Table 2

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
AB014541	9625	AATK	apoptosis-associated tyrosine kinase	CTCCAACGTGTCAGCCAACAA	TCCGCTGAGATCAGAAGGCAA
AB023190	22983	SAST	syntrophin associated serine/threonine kinase	CAGCCTCCGTATACATATGTA	CCCGAGGTCATCCTGCGTCAA
AB033076	57498	KIDINS220	likely homolog of rat kinase D-interacting substance of 220 kDa	CAGGCGAGACTCCTTATAATA	TCGCAGATGCGCTATTATCTA
AB037838	25998	IBTK	inhibitor of Bruton agammaglobulinemia tyrosine kinase	CAGATTGAGGAGCATGCCATA	TAGAAGAGTCATTACACCATA
AB096248	23235	SIK2	salt-inducible serine/threonine kinase 2	AAGGGCAAGATTATTTGCTTA	CCGAAGGATGTTGGTCCTAGA
NM_004935	1020	CDK5	cyclin-dependent kinase 5	CCCTTTGTGGACTTTATTTAA	CCGGGAGATCTGCCTACTCAA
AK126879	5129	PCTK3	PCTAIRE protein kinase 3	AACCCGTTACTTAGCTGTGTA	CAGGTTGGATACGGATGGCAT
BC028192	161635	LOC161635	similar to casein kinase I alpha	TCCATCGATCTGGAATTTATA	TTGGTCGTGTGAATTATTAAA
BC033792	89882	NYD-SP25	protein kinase NYD-SP25	ATCATATACTTCAGACATCAA	CACGTTAAATCAAGGAAGGAA
BF688722	2323	FLT3LG	Fms-related tyrosine kinase 3 ligand	GCGGGATTTGTTGAAGAGAAA	TAGTATAGTTGAAATAAGAAA
BX537762	134728	IRAK1BP1	interleukin-1 receptor-associated kinase 1 binding protein 1/DKFZp779F0411	AACCTGGAGTATCATATTATA	ACCAAGATACTTGAGTGATTA
BX640919	27104	EIF2AK4	eukaryotic translation initiation factor 2 alpha kinase 4	CTGCAGGAATTTAGTAACATT	TCCGATAATCTTGCAGTGCAA
NM_000020	94	ACVRL1	activin A receptor type II-like 1	CACCGAGTTCGTCAACCACTA	CAGGAAGACGCTGGAATAAGA
NM_000051	472	ATM	ataxia telangiectasia mutated (includes complementation groups A, C and D)	AACCATGAGTCTAGTACTTAA	TTGGCTTATACGCGCAGTGTA
NM_000061	695	BTK	Bruton agammaglobulinemia tyrosine kinase	CAGCTCGAAACTGTTTGGTAA	CCCTTTATGATTACATGCCAA
NM_000075	1019	CDK4	cyclin-dependent kinase 4	AAGGTAATCCGGAGTGAGCAA	CCGAACTGACCGGGAGATCAA
NM_000076	1028	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	AAGCTTTAAGAGTCATTTATA	TACACTGGTCCCAAAGTGTAA
NM_000077	1029	CDKN2A	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	CACGCCCTAAGCGCACATTCA	CAGGTGTGCCACATTCGCTAA
NM_000141	2263	FGFR2	fibroblast growth factor receptor 2	CCGAATGAAGAACACGACCAA	CGGAGGAGCGTTGCCATTCAA
NM_000142	2261	FGFR3	fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)	ACCCTACGTTACCGTGCTCAA	CCGATGTTATTAGATGTTACA
NM_000167	2710	GK	glycerol kinase	CCACCACTTAAGTGACATAAA	CTGAGGGTAGCCCATTTATAA
NM_000189	3099	HK2	hexokinase 2	CCGGCCGTGCTACAATAGGTA	CGGCCGTGCTACAATAGGTAA
NM_000215	3718	JAK3	Janus kinase 3 (a protein tyrosine kinase, leukocyte)	CGGGAGATTCAGATCCTCAAA	TCCGGGAGGCGCAGACACTTA
NM_000221	3795	KHK	ketohexokinase (fructokinase)	TAGCCGCACCATCCTATACTA	TAGGGTGGGTAAGGCCTTATA
NM_000222	3815	KIT	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	CACGGTTGAATGTAAGGCTTA	CTCGCACCTTTCCAAAGTTAA
NM_000245	4233	MET	met proto-oncogene (hepatocyte growth factor receptor)	ACCGAGGGAATCATCATGAAA	CGCGCCGTGATGAATATCGAA
NM_000269	4830	NME1	non-metastatic cells 1, protein (NM23A) expressed in	TAGGATTCATTGAGTTGGTTA	TTCCGCCTTGTTGGTCTGAAA
NM_000289	5213	PFKM	phosphofructokinase, muscle	AACAGATCAGTGCCAATATAA	AAGGACTTTCGGGAACGAGAA
NM_000291	5230	PGK1	phosphoglycerate kinase 1	CACAATTATAGATTAGATCAA	GAGGAACGGATCAGATGTCTA
NM_000292	5256	PHKA2	phosphorylase kinase, alpha 2 (liver)	CCGCCTAACAAGGTAGATGAA	CCGGATTCTTAGTCACATATA
NM_000293	5257	PHKB	phosphorylase kinase, beta	AGGGCTGTTCGTGGTCAGTTA	TCGATGGGTCTTTGAATAGAA
NM_000294	5261	PHKG2	phosphorylase kinase, gamma 2 (testis)	CTGCATGCACTGCATATGAAA	TACGGGCACTGGGTAAAGAAA
NM_000389	1026	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	CAGTTTGTGTGTCTTAATTAT	CTGGCATTAGAATTATTTAAA
NM_000431	4598	MVK	mevalonate kinase (mevalonic aciduria)	CCGCTTGGCGATGCCAGCCAA	GCGGTGGGCCTGGTTAAATAA
NM_000455	6794	STK11	serine/threonine kinase 11 (Peutz-Jeghers syndrome)	CAGGAGTGTGCGGTCAATATT	GAGGGCCGTCAAGATCCTCAA
NM_000459	7010	TEK	TEK tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal)	ACGGGCCAGATTGTAAGCTTA	TCGGTGCTACTTAACAACTTA
NM_000476	203	AK1	adenylate kinase 1	CCGGGATGCCATGGTGGCCAA	GCGGCTGGAGACCTATTACAA
NM_000788	1633	DCK	deoxycytidine kinase	AAGTTGCAAAGTGGAATTAAA	TTGGTATAAATTAATTTGTTA
NM_000858	2987	GUK1	guanylate kinase 1	CAGGGCTGACATCCTAATAAA	CCCGGCGAGGAGAACGGCAAA
NM_001079	7535	ZAP70	zeta-chain (TCR) associated protein kinase 70kDa	CCGCAACGTCCTGCTGGTTAA	GGCGTAGATCACCAGAATAAA
NM_001105	90	ACVR1	activin A receptor, type I	CGGATGGTGAGCAATGGTATA	CTGGTCTGTCTTTGGATAATA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_001106	93	ACVR2B	activin A receptor, type IIB	CAGCTCATGAATGACTTTGTA	TACGGTCATGTGGACATCCAT
NM_001123	132	ADK	adenosine kinase	AAGGGTATGGTAATGCTTGTA	TAGTTTGATAGTGCCACTTAA
NM_001184	545	ATR	ataxia telangiectasia and Rad3 related	CAGGCACTAATTGTTCTTCAA	GCCGCTAATCTTCTAACATTA
NM_001203	658	BMPR1B	bone morphogenetic protein receptor, type IB	AACGAATGTAATAAAGACCTA	ACGGATATTGTTTCACGATGA
NM_001204	659	BMPR2	bone morphogenetic protein receptor, type II (serine/threonine kinase)	AAGCACCGAAGCGAAACTTAA	CTCGTAAGTATGTAAAGGAAA
NM_001211	701	BUB1B	BUB1 budding uninhibited by benzimidazoles 1 homolog beta (yeast)	ACGAGAATACCTAATATGTGA	CAGATTTAGCACATTTACTAT
NM_001220	816	CAMK2B	calcium/calmodulin-dependent protein kinase (CaM kinase) II beta	CAAGAGTTTACTCAACAAGAA	CCGGAAGCAGGAGATCATTAA
NM_001221	817	CAMK2D	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	CCGCCTGCATAGCATATATTA	GTGCGACTTCATGATAGCATA
NM_001258	1018	CDK3	cyclin-dependent kinase 3	ATGGATATGTTCCAGAAGGTA	CAGACTGGATTTGGAGATGGA
NM_001259	1021	CDK6	cyclin-dependent kinase 6	AAGACTCAAGGTGGTCAGTAA	TCTGAAGTGTTTGACATTTAA
NM_001260	1024	CDK8	cyclin-dependent kinase 8	CCAGCTGGACAGAATATTCAA	TTCGAGAGCTTAAGCATCCAA
NM_001261	1025	CDK9	cyclin-dependent kinase 9 (CDC2-related kinase)	TAGGGACATGAAGGCTGCTAA	TGGGCACAGTTTGGTCCGTTA
NM_001262	1031	CDKN2C	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	CAGGCTTATGAATATATTTAA	TGCCTCTACTTTATCAATTAA
NM_001274	1111	CHEK1	CHK1 checkpoint homolog (S. pombe)	AAGAAAGAGATCTGTATCAAT	CCCGCACAGGTCTTTCCTTAT
NM_001277	1119	CHK	choline kinase	AGCCGGCGATTAGATACTGAA	CCGGCCCTTACCAAACCTGAT
NM_001278	1147	CHUK	conserved helix-loop-helix ubiquitous kinase	CAGGAGAAGTTCGGTTTAGTA	TTCCATAAGCTTGGTGACAAA
NM_001291	1196	CLK2	CDC-like kinase 2	CAGCTACAGACGCAACGATTA	TCGCCTGGATTGGGATGAGAA
NM_001292	1198	CLK3	CDC-like kinase 3	CACGAAGATCTCGGTCCAGAA	CTGCATTCTCTTTGAGTACTA
NM_001315	1432	MAPK14	mitogen-activated protein kinase 14	CAGAGAACTGCGGTTACTTAA	CTCAGTGATACGTACAGCCAA
NM_001319	1455	CSNK1G2	casein kinase 1, gamma 2	AAGAATCTCTATACAAATGAA	TAGGAAAGAATCTCTATACAA
NM_001320	1460	CSNK2B	casein kinase 2, beta polypeptide	CAGGTCCCTCACTACCGACAA	GTGGTGGGAATATGAAATAAA
NM_001345	1606	DGKA	diacylglycerol kinase, alpha 80kDa	ATCCATCTTCTCAACATGCAA	CACGACCAGTGTGCCATGAAA
NM_001346	1608	DGKG	diacylglycerol kinase, gamma 90kDa	ACCGCAAATGTGAATTATCAA	TAGCCACTCACATAAAGTTTA
NM_001347	1609	DGKQ	diacylglycerol kinase, theta 110kDa	CAGCGACACCAGGTTTGAGAA	CCGGAAGGTGACGCTCACCAA
NM_001348	1613	DAPK3	death-associated protein kinase 3	CCCAGAGATTGTGAACTATGA	CCGGCAGAAGGGCACGGGCAA
NM_001381	1796	DOK1	docking protein 1, 62kDa (downstream of tyrosine kinase 1)	AGGGATCAAAGAAGATGGTTA	CCGCCTGGACTGCAAAGTGAT
NM_001396	1859	DYRK1A	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A	CAAGAATGGGTTGCCATTAAA	TACGGTCGCTGACTACTTGAA
NM_001433	2081	ERN1	ER to nucleus signalling 1	CAGCACGGACGTCAAGTTTGA	CAGGACGTGAGCGACAGAATA
NM_001569	3654	IRAK1	interleukin-1 receptor-associated kinase 1	CCGGGCAATTCAGTTTCTACA	TCCCATCGCCATGCAGATCTA
NM_001570	3656	IRAK2	interleukin-1 receptor-associated kinase 2	CAGCAACGTCAAGAGCTCTAA	CCAGATCATCCTGAACTGGAA
NM_001616	92	ACVR2	activin A receptor, type II	GAGGTATTAGAGGGTGCTATA	TCCACGGTTGCTAAATTATAA
NM_001619	156	ADRBK1	adrenergic, beta, receptor kinase 1	CCGGGAGATCTTCGACTCATA	CGGCTGGAGGCTCGCAAGAAA
NM_001625	204	AK2	adenylate kinase 2	ATGGGTGGGAATGATAGGACA	CCACATGTAAAGACTTGGTTA
NM_001626	208	AKT2	v-akt murine thymoma viral oncogene homolog 2	ACGGGCTAAAGTGACCATGAA	CAAGCGTGGTGAATACATCAA
NM_001654	369	ARAF1	v-raf murine sarcoma 3611 viral oncogene homolog 1	CCGACTCATCAAGGGACGAAA	CCGGGATGGCATGAGTGTCTA
NM_001699	558	AXL	AXL receptor tyrosine kinase	CCGGTGTTCTAAGATGTGATA	TCCAAGATTCTAGATGATTAA
NM_001715	640	BLK	B lymphoid tyrosine kinase	CAGCCGTGCTGTTAAACCAAA	CTGGTAAGCGACTGTCATCAA
NM_001721	660	BMX	BMX non-receptor tyrosine kinase	CCCAATATGACAACGAATCAA	CGGAACAAAGTTTCCAGTCAA
NM_001743	805	CALM2	calmodulin 2 (phosphorylase kinase, delta)	ACAAAGGAATTGGGAACTGTA	CAAAGGAATTGGGAACTGTAA
NM_001744	814	CAMK4	calcium/calmodulin-dependent protein kinase IV	CAGAAGCCTTATGCTCTCAAA	TTGCAAGTTAACACAACGTAA
NM_001786	983	CDC2	cell division cycle 2, G1 to S and G2 to M	TCGGGAAATTTCTCTATTAAA	TTGACTAACTATGGAAGATTA
NM_001787	984	CDC2L1	cell division cycle 2-like 1 (PITSLRE proteins)	CAAGATCTACATCGTGATGAA	CAGGATAAAGCTCGCCGGGAA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_001798	1017	CDK2	cyclin-dependent kinase 2	CACGTACGGAGTTGTGTACAA	CAGGTTATATCCAATAGTAGA
NM_001799	1022	CDK7	cyclin-dependent kinase 7 (MO15 homolog, Xenopus laevis, cdk-activating kinase)	CCGGATGGCTCTGGACGTGAA	GAGGCTTTAAGGTAGCTTTAA
NM_001800	1032	CDKN2D	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)	ACCCAAGGGCAGAGCATTTAA	ATGAGTTATGAGTTATTCATA
NM_001823	1152	CKB	creatine kinase, brain	CCAGATTGAAACTCTCTTCAA	CCGGCCTCACCCAGATTGAAA
NM_001824	1158	CKM	creatine kinase, muscle	GACGGGCGAGTTCAAAGGGAA	TCCACGCAAAGCGATAAATAA
NM_001825	1160	CKMT2	creatine kinase, mitochondrial 2 (sarcomeric)	CCTGCCTATCTTTACAATAAA	GAGGTTGAGCTTGTTCAGATA
NM_001826	1163	CKS1B	CDC28 protein kinase regulatory subunit 1B	AACATCTTTCTGATAACATTA	AAGAAATCTGTTCATGTTAAA
NM_001827	1164	CKS2	CDC28 protein kinase regulatory subunit 2	CTGTAAGATGTTTAAGATAAA	TCGGACAAGTACTTCGACGAA
NM_001892	1452	CSNK1A1	casein kinase 1, alpha 1	AGGGCTAAAGGCTGCAACAAA	CAAGAGTAACATGAAAGGTTT
NM_001893	1453	CSNK1D	casein kinase 1, delta	CCGGTCTAGGATCGAAATGTT	CTCCCTGACGATTCCACTGTA
NM_001894	1454	CSNK1E	casein kinase 1, epsilon	GAGCTTTATCGTGGTTGTTAA	GTGGTTGTTAATTTGAAGTAA
NM_001896	1459	CSNK2A2	casein kinase 2, alpha prime polypeptide	CAGGAGTACAATGTTCGTGTA	CTGGGACAACATTCACGGAAA
NM_001929	1716	DGUOK	deoxyguanosine kinase	CACCTTTGTAAAGAATCTGTA	CAGCACGATGGTCCTACACAT
NM_001954	780	DDR1	discoidin domain receptor family, member 1	ACGGTGTGAATCACACATCCA	CAGGAATGATTTCCTGAAAGA
NM_001982	2065	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	ACCGGCGATGCTGAGAACCAA	CCAGAGCTTCAAGACTGTTTA
NM_002005	2242	FES	feline sarcoma oncogene	AAGGCCAAGTTTCTACAGGAA	CAGCCTGAGGCTGAGTACCAA
NM_002011	2264	FGFR4	fibroblast growth factor receptor 4	CACATTGACTACTATAAGAAA	CCGCCTGACCTTCGGACCCTA
NM_002019	2321	FLT1	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)	ACCGCATATGGTATCCCTCAA	CACTACAGTATTAGCAAGCAA
NM_002031	2444	FRK	fyn-related kinase	CAGGACAGTCAAGGTGATATA	CTGGGAGTACCTAGAACCCTA
NM_002037	2534	FYN	FYN oncogene related to SRC, FGR, YES	AAGAAGCAGGATGCTGATCTA	AAGACATGTGGTGTATATAAA
NM_002082	2870	GRK6	G protein-coupled receptor kinase 6	AAGGATGTTCTGGACATTGAA	AGGCATGTGGGCGGCACGTAA
NM_002093	2932	GSK3B	glycogen synthase kinase 3 beta	AACACTGGTCACGTTTGGAAA	CTGCATTTATCGTTAACCTAA
NM_002110	3055	HCK	hemopoietic cell kinase	AACGACGGGCTCTGCCAGAAA	CGGGAGCACATCAGAGGCTTA
NM_002115	3101	HK3	hexokinase 3 (white cell)	CACTCAGGTTAGCAATATATA	CCGGAATGCGATGTCTCCTTA
NM_002220	3706	ITPKA	inositol 1,4,5-trisphosphate 3-kinase A	CACCAGCGGGCTGATCCTGAA	CCGGTCTAACGTCTCACACCA
NM_002221	3707	ITPKB	inositol 1,4,5-trisphosphate 3-kinase B	AAGGCCATTCGAACCACTCTA	GACGTAAAGATTCTATGAATA
NM_002227	3716	JAK1	Janus kinase 1 (a protein tyrosine kinase)	ACCGGATGAGGTTCTATTTCA	CACGGATAACATCAGCTTCAT
NM_002253	3791	KDR	kinase insert domain receptor (a type III receptor tyrosine kinase)	AACGCTGACATGTACGGTCTA	AAGGCTAATACAACTCTTCAA
NM_002314	3984	LIMK1	LIM domain kinase 1	CTGCCTGGTCCGCGAGAACAA	GAGCATCTAGGAAGTATTAAA
NM_002344	4058	LTK	leukocyte tyrosine kinase	ACAGATCTTTGGAGTGCCTAA	CCTGCAGATGCTTCTAATAAA
NM_002350	4067	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	CCCGGACGACTTGTCTTTCAA	CGGGAAATATGGGATGTATAA
NM_002356	4082	MARCKS	myristoylated alanine-rich protein kinase C substrate	CTCCTTCAAGAAGAACAAGAA	TTGAGTTTCTTTGTTGAAGAA
NM_002376	4140	MARK3	MAP/microtubule affinity-regulating kinase 3	AACGGCGAACCGCAACATATA	CCCGGGAACGGCGAACCGCAA
NM_002378	4145	MATK	megakaryocyte-associated tyrosine kinase	ACGGATTCTAAGGACTCTAAA	GACGGATTCTAAGGACTCTAA
NM_002401	4215	MAP3K3	mitogen-activated protein kinase kinase kinase 3	CAGGAATACTCAGATCGGGAA	CCACGTGTCTGTGCACCACAA
NM_002419	4296	MAP3K11	mitogen-activated protein kinase kinase kinase 11	CCCGACGTCTGGAGGACTCAA	CCGGAGGAGAAACGTCTTCGA
NM_002446	4294	MAP3K10	mitogen-activated protein kinase kinase kinase 10	AAGCGGCTTGAAGTCATCGAA	CAGGATGTTCACTCTATTTAT
NM_002447	4486	MST1R	macrophage stimulating 1 receptor (c-met-related tyrosine kinase)	ATGGAGCATCCTTCTCCGATA	TGCCATTAAGTTTGAGTATAT
NM_002497	4751	NEK2	NIMA (never in mitosis gene a)-related kinase 2	TACGAGGATGTTAAACTTAAA	TTACGAGGATGTTAAACTTAA
NM_002512	4831	NME2	non-metastatic cells 2, protein (NM23B) expressed in	ATAGAGCATATTTGCCAATAA	TAGAGCATATTTGCCAATAAA
NM_002513	4832	NME3	non-metastatic cells 3, protein expressed in	ACGCACCTTCCTGGCCGTGAA	CTGCATCGAGGTTGGCAAGAA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_002529	4914	NTRK1	neurotrophic tyrosine kinase, receptor, type 1	CACATCATCGAGAACCCACAA	CGAGAGCATCCTGTACCGTAA
NM_002530	4916	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	CACGGATAACTTTATCTTGTT	CTGGTTGGAGCGAATCTGCTA
NM_002576	5058	PAK1	p21/Cdc42/Rac1-activated kinase 1 (STE20 homolog, yeast)	TCCACTGATTGCTGCAGCTAA	TTGAAGAGAACTGCAACTGAA
NM_002577	5062	PAK2	p21 (CDKN1A)-activated kinase 2	CCGCGACCGGATCATACGAAA	CCGGATCATACGAAATCAATT
NM_002578	5063	PAK3	p21 (CDKN1A)-activated kinase 3	CAAGAAGGAATTAATTATTAA	TTCCAGTACTTTGTACAGGAA
NM_002595	5128	PCTK2	PCTAIRE protein kinase 2	AGGCTTAATTCTTGCGTATAA	TAGGCTTAATTCTTGCGTATA
NM_002609	5159	PDGFRB	platelet-derived growth factor receptor, beta polypeptide	CCGAGCAACTTTGATCAACGA	CTGCCGAGCAACTTTGATCAA
NM_002610	5163	PDK1	pyruvate dehydrogenase kinase, isoenzyme 1	CCCGAACTAGAACTTGAAGAA	TCGGGTTTCTATAGGAAACTA
NM_002611	5164	PDK2	pyruvate dehydrogenase kinase, isoenzyme 2	AAGAACCTTGTTAGACCGAGA	TAGGTCTGTGATGGTCCCTAA
NM_002612	5166	PDK4	pyruvate dehydrogenase kinase, isoenzyme 4	ACCCGTGTCAATTAACATTTA	AGGCCTCTTGTTCACATCAAA
NM_002613	5170	PDPK1	3-phosphoinositide dependent protein kinase-1	AAGCGGTTAGGCTGTGAGGAA	CACGCCTAACAGGACGTATTA
NM_002625	5207	PFKFB1	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1	CTCCACAAAGCTCACACGATA	CTGCGAGACCAAGATAAATAT
NM_002626	5211	PFKL	phosphofructokinase, liver	CACGATGGCTTCGAAGGCCTA	CCGGACCTACTCGCACCTGAA
NM_002627	5214	PFKP	phosphofructokinase, platelet	CAGCACTTTATGCACGTATTA	CCGCCTGAAGGCTGCTTGCAA
NM_002637	5255	PHKA1	phosphorylase kinase, alpha 1 (muscle)	ATGGGAGTGCTTGGAACTTCA	CCCAATCGTCTGTACTATGAA
NM_002645	5286	PIK3C2A	phosphoinositide-3-kinase, class 2, alpha polypeptide	CAAGATGGTCGAATCAAGGAA	TACCCACTAATTGCATTGGAA
NM_002646	5287	PIK3C2B	phosphoinositide-3-kinase, class 2, beta polypeptide	AAGGGTTGTCTTCCTCGCCAA	CAGGGTGGTCCAGTCCGTCAA
NM_002647	5289	PIK3C3	phosphoinositide-3-kinase, class 3	AACGCGAAAGTGGAAATCGTA	TCGGTTGGTGCATCTAATGAA
NM_002648	5292	PIM1	pim-1 oncogene	AAACATCCTTATCGACCTCAA	AAAGATTGTAGTGGATCTAAT
NM_002649	5294	PIK3CG	phosphoinositide-3-kinase, catalytic, gamma polypeptide	ATCGAAGTTTGCAGAGACAAA	CACCTTTACTCTATAACTCAA
NM_002650	5297	PIK4CA	phosphatidylinositol 4-kinase, catalytic, alpha polypeptide	CATCTGGAACATGAAGACTAA	CCAGTTCATCTGGAACATGAA
NM_002651	5298	PIK4CB	phosphatidylinositol 4-kinase, catalytic, beta polypeptide	CCGAGAGTATTGATAATTCAT	TCGGCTGATAGTGGCATGATT
NM_002730	5566	PRKACA	protein kinase, cAMP-dependent, catalytic, alpha	CAAGGACAACTCAAACTTATA	CAGAAGGTGGTGAAACTGAAA
NM_002732	5568	PRKACG	protein kinase, cAMP-dependent, catalytic, gamma	AACCAGCTGGATCGCCATCTA	CTGGATCGCCATCTATGAGAA
NM_002733	5571	PRKAG1	protein kinase, AMP-activated, gamma 1 non-catalytic subunit	CCCTAAGATAATAGCACAACA	TTGGCCCTGATTCAACCCTAA
NM_002734	5573	PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	CAGCTAGTGCCAAATAATTGA	CTGGACCGACCTAGATTTGAA
NM_002736	5577	PRKAR2B	protein kinase, cAMP-dependent, regulatory, type II, beta	ACGAACATGGATATTGTTGAA	CACGCCATTGGGACTGTCAAA
NM_002737	5578	PRKCA	protein kinase C, alpha	CGCAGTGGAATGAGTCCTTTA	TACAAGTTGCTTAACCAAGAA
NM_002738	5579	PRKCB1	protein kinase C, beta 1	CAAGAGCTAAGTAGATGTGTA	CCGGATGAAACTGACCGATTT
NM_002739	5582	PRKCG	protein kinase C, gamma	AACGGTGAAAGCCACGCTAAA	GACCTTTGTGTTCAACCTGAA
NM_002740	5584	PRKCI	protein kinase C, iota	CACCCAATATCTTCTCTTGTA	TACCACGTTCTATGTCTGTAA
NM_002741	5585	PRKCL1	protein kinase C-like 1	CAGGACAGTAAGACCAAGATT	CCGCAAGGAGCTGAAGCTGAA
NM_002742	5587	PRKCM	protein kinase C, mu	CAGGAAGGCGATCTTATTGAA	CCTCAGTATATTTAAACTCAA
NM_002744	5590	PRKCZ	protein kinase C, zeta	CGGAAGCATGACAGCATTAAA	GACCAAATTTACGCCATGAAA
NM_002745	5594	MAPK1	mitogen-activated protein kinase 1	AACACTTGTCAAGAAGCGTTA	ATCATGGTAGTCACTAACATA
NM_002746	5595	MAPK3	mitogen-activated protein kinase 3	CCCGTCTAATATATAAATATA	CTCCCTGACCCGTCTAATATA
NM_002747	5596	MAPK4	mitogen-activated protein kinase 4	AAGGATCGTTGATCAGCATTA	CGCCTTAAATCTAATCAGCAA
NM_002748	5597	MAPK6	mitogen-activated protein kinase 6	CAAGTTCAATTTGAAAGGAAA	CAGGCTTCCTGTTGAAATAAA
NM_002749	5598	MAPK7	mitogen-activated protein kinase 7	CAGACCCACCTTTCAGCCTTA	TACGAGATCATCGAGACCATA
NM_002750	5599	MAPK8	mitogen-activated protein kinase 8	AAGCCCAGTAATATAGTAGTA	TCGGGACTTAAAGCCCAGTAA
NM_002751	5600	MAPK11	mitogen-activated protein kinase 11	CAGGATGGAGCTGATCCAGTA	CTGAGCGACGAGCACGTTCAA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_002752	5601	MAPK9	mitogen-activated protein kinase 9	AAAGTCGATTTATGTGTATTA	ATCGTGAACTTGTCCTCTTAA
NM_002753	5602	MAPK10	mitogen-activated protein kinase 10	CCGCATGTGTCTGTATTCATA	TCCGAGCACAATAAACTCAAA
NM_002754	5603	MAPK13	mitogen-activated protein kinase 13	CCGGAGTGGCATGAAGCTGTA	CGGGATGAGCCTCATCCGGAA
NM_002755	5604	MAP2K1	mitogen-activated protein kinase kinase 1	CTGGAAGAATTCCTGAACAAA	CTGGATCAAGTCCTGAAGAAA
NM_002756	5606	MAP2K3	mitogen-activated protein kinase kinase 3	ACGGATATCCTGCATGTCCAA	CCGGGCCACCGTGAACTCACA
NM_002757	5607	MAP2K5	mitogen-activated protein kinase kinase 5	AAGACGTATGTTGGAACAAAT	CAAGACGTATGTTGGAACAAA
NM_002758	5608	MAP2K6	mitogen-activated protein kinase kinase 6	AAGGCTTGCATTTCTATTGGA	TAGACCTATGATAAATAACCA
NM_002759	5610	PRKR	protein kinase, interferon-inducible double stranded RNA dependent	ACGGAAAGACTTACGTTATTA	CGGAAAGACTTACGTTATTAA
NM_002760	5616	PRKY	protein kinase, Y-linked	CCAGAGTTCGCCTACAGATAA	TTGGGATACAGTAAGAGAATA
NM_002822	5756	PTK9	PTK9 protein tyrosine kinase 9	ACCGGCATCCAAGCAAGTGAA	TCCAAGCAAGTGAAGATGTTA
NM_002880	5894	RAF1	v-raf-1 murine leukemia viral oncogene homolog 1	CAGATCTTAGTAAGCTATATA	TGGGAAATAGAAGCCAGTGAA
NM_002929	6011	GRK1	G protein-coupled receptor kinase 1	CCAGATGAAGGCGACCGGCAA	CTGGAAAGACATCGAGGACTA
NM_002944	6098	ROS1	v-ros UR2 sarcoma virus oncogene homolog 1 (avian)	AAGGTAATTGCTCTAACTTTA	ACCGAGAAGGGTTAAACTATA
NM_002953	6195	RPS6KA1	ribosomal protein S6 kinase, 90kDa, polypeptide 1	CCCAACATCATCACTCTGAAA	TGCCACGTACTCCGCACTCAA
NM_002958	6259	RYK	RYK receptor-like tyrosine kinase	CGGTCTTGATGCAGAACTTTA	CTGATCGGTCTTGATGCAGAA
NM_002969	6300	MAPK12	mitogen-activated protein kinase 12	CTGGACGTATTCACTCCTGAT	TGGAAGCGTGTTACTTACAAA
NM_003010	6416	MAP2K4	mitogen-activated protein kinase kinase 4	AGGGAGAATGGTGCTGTTTAA	AGGGTGTATAGTGTTCACAAA
NM_003137	6732	SRPK1	SFRS protein kinase 1	CAGACTCTTGTACACCTATAA	TACCATGTGATCCGAAAGTTA
NM_003157	6787	NEK4	NIMA (never in mitosis gene a)-related kinase 4	CACAATCAGTAGCGTAAATAT	CAGACATATATAATGGGTGAA
NM_003159	6792	CDKL5	cyclin-dependent kinase-like 5	AAGATAGACGCTTCATGTTAA	AAGGCAATAATGCTAATTACA
NM_003160	6795	AURKC	aurora kinase C	AAGATGTAAGATGCTAATTAA	CCGGGTGTACCTGATTCTGGA
NM_003161	6198	RPS6KB1	ribosomal protein S6 kinase, 70kDa, polypeptide 1	AAGAAGGGTATCCTTTCATTA	CAGAGAGTCAATGTCATTACA
NM_003177	6850	SYK	spleen tyrosine kinase	CCCGCTCTTAAAGATGAGTTA	TCCGGAATGCATCAACTACTA
NM_003188	6885	MAP3K7	mitogen-activated protein kinase kinase kinase 7	CAAGAATATATGAAAGTTCAA	CCCGTGTGAACCATCCTAATA
NM_003215	7006	TEC	tec protein tyrosine kinase	CAGTACAAAGTCGCAATCAAA	CCGCAGCTAATCAGAATCAGA
NM_003242	7048	TGFBR2	transforming growth factor, beta receptor II (70/80kDa)	CTCCAATATCCTCGTGAAGAA	TCGGTTAATAACGACATGATA
NM_003258	7083	TK1	thymidine kinase 1, soluble	CGGGCCGATGTTCTCAGGAAA	TCGGCTCTGCTACTTCAAGAA
NM_003318	7272	TTK	TTK protein kinase	CAGCAATACCTTGGATGATTA	TCCGACTTTATGATTATGAAA
NM_003328	7294	TXK	TXK tyrosine kinase	CAGCTGGGTTTAGCTACGAAA	CCCGGTGACATTCTATTTCCA
NM_003331	7297	TYK2	tyrosine kinase 2	CACCATCTGGTAATAAACTCA	CTGATGCTATATTTCCGCATA
NM_003332	7305	TYROBP	TYRO protein tyrosine kinase binding protein	CCGAATCATGACAGTCAGCAA	CTGGATCCAGCCATTCCTGAA
NM_003384	7443	VRK1	vaccinia related kinase 1	CAGGTTATACTCCTTAAGTTA	CCAGGTGTACTTGGTAGATTA
NM_003390	7465	WEE1	WEE1 homolog (S. pombe)	CAGGGTAGATTACCTCGGATA	TTGACTAATAATACTGGCTAA
NM_003488	8165	AKAP1	A kinase (PRKA) anchor protein 1	AGCGCTGAACTTGATTGGGAA	CACGCAGAGATGACAGTACAA
NM_003551	8382	NME5	non-metastatic cells 5, protein expressed in (nucleoside-diphosphate kinase)	ATGATATTAGCTAGACATAAA	CATGATATTAGCTAGACATAA
NM_003557	8394	PIP5K1A	phosphatidylinositol-4-phosphate 5-kinase, type I, alpha	CAGCCTCTTGATGTCAATCCA	CCCTGCCTTGATAATATGTTA
NM_003558	8395	PIP5K1B	phosphatidylinositol-4-phosphate 5-kinase, type I, beta	AAGGCTCAACGTATAAGCGAA	CAGGCCTACACTCTATTCAAA
NM_003559	8396	PIP5K2B	phosphatidylinositol-4-phosphate 5-kinase, type II, beta	CACGCCATACGATACAAAGAA	CCGCTTTAAGTTTAAGGAGTA
NM_003565	8408	ULK1	unc-51-like kinase 1 (C. elegans)	CGCGCGGTACCTCCAGAGCAA	TGCCCTTTGCGTTATATTGTA
NM_003576	8428	STK24	serine/threonine kinase 24 (STE20 homolog, yeast)	CCCACCGACGTTGGAAGGAAA	CTGGAGGGAGCACGAACCTAA
NM_003582	8444	DYRK3	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	AGCCAATAAGCTTAAAGCTAA	TCGACAGTACGTGGCCCTAAA
NM_003583	8445	DYRK2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	TAGAAGCGGTATTAAAGTAAT	TGCACAGAGATTATTGTATTA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_003600	6790	STK6	serine/threonine kinase 6	CACCTTCGGCATCCTAATATT	CACGTGCTCTACCTCCATTTA
NM_003607	8476	CDC42BPA	CDC42 binding protein kinase alpha (DMPK-like)	CAGACTTTCCGTAGCAGCTTA	CAGATAATAGTCGGAAACAAA
NM_003618	8491	MAP4K3	mitogen-activated protein kinase kinase kinase kinase 3	GAGGTGGTTCTTTACAGGATA	TCGAGCTGTTGGATAAAGTAA
NM_003629	8503	PIK3R3	phosphoinositide-3-kinase, regulatory subunit, polypeptide 3 (p55, gamma)	AGGGAGGCAATAATAAGTTAA	GAGGATATCAATCGAGTACAA
NM_003639	8517	IKBKG	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma	CTCCTCTAGTTCAGAGACATA	TTCGGAAATGCCTCACATATA
NM_003640	8518	IKBKAP	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein	CAGCGGTTTACTATAGACAAA	GCGGTTTACTATAGACAAATA
NM_003646	8525	DGKZ	diacylglycerol kinase, zeta 104kDa	CAAGAGGAACGACTTCTGTAA	CTGGAGCGAGTCAGCGACATA
NM_003647	8526	DGKE	diacylglycerol kinase, epsilon 64kDa	ATCGATGGAAAGTTCAAGTAA	CTGGAAGTCGTTGGAGTATAT
NM_003648	8527	DGKD	diacylglycerol kinase, delta 130kDa	CAGCAGATTCTCTTCTATGAA	CCGCCTCGTGACCAAGTTTAA
NM_003656	8536	CAMK1	calcium/calmodulin-dependent protein kinase I	CAGGTGCTGGATGCTGTGAAA	CTGCATGACCTGGGCATTGTA
NM_003668	8550	MAPKAPK5	mitogen-activated protein kinase-activated protein kinase 5	ACCGACCTTTCTGATTAGTAA	CCGACCTTTCTGATTAGTAAA
NM_003674	8558	CDK10	cyclin-dependent kinase (CDC2-like) 10	CCGTCTGAAGTGTATTCGTAA	CTGATGCTGAGCGAAGCTATA
NM_003681	85006	C21orf124	chromosome 21 open reading frame 124	CACAGGTTATACGAGGGACAA	GAGGCTGAACAACATGAATAA
NM_003682	8567	MADD	MAP-kinase activating death domain	CAGACCCACTACTATAGTAAA	CAGGAGGGCGTTAGTGGATCA
NM_003684	8569	MKNK1	MAP kinase-interacting serine/threonine kinase 1	CCAGCAAAGATGATACCTTAA	TAGATAGTGCTCTGTGCCTAA
NM_003688	8573	CASK	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	AACCAATGGGAATCACTTTAA	AAGGACGACAGATCTATGTAA
NM_003690	8575	PRKRA	protein kinase, interferon-inducible double stranded RNA dependent activator	ATGATTGATTGTTAAATTTCA	TAAGTATGATTGATTGTTAAA
NM_003691	8576	STK16	serine/threonine kinase 16	CACATAGTGTTCTGACTCCAA	CAGGAGAATGTGTAACAAGAA
NM_003718	8621	CDC2L5	cell division cycle 2-like 5 (cholinesterase-related cell division controller)	AACGACGTAGTTTCATTGGAA	TCAGAGTATTATCAATATGAA
NM_003804	8737	RIPK1	receptor (TNFRSF)-interacting serine-threonine kinase 1	CCGACATTTCCTGGCATTGAA	TACCACTAGTCTGACGGATAA
NM_003821	8767	RIPK2	receptor-interacting serine-threonine kinase 2	ACGTATGATCTCTCTAATAGA	CACAAGGACATCGACCTGTTA
NM_003831	8780	RIOK3	RIO kinase 3 (yeast)	ATGCGGCAGTTATATCATGAA	CTGGCTGTATTAGTACAGGAA
NM_003845	8798	DYRK4	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4	CTCCATATGAACAAAGTGAAA	CTGCATCACGGCGGAGTTGTA
NM_003885	8851	CDK5R1	cyclin-dependent kinase 5, regulatory subunit 1 (p35)	CCGGAAGGCCACGCTGTTTGA	TGAGCTGGTTTGACTCATTAA
NM_003886	8852	AKAP4	A kinase (PRKA) anchor protein 4	GTCGGTGAACACATTCTCAAA	TACAGTGTCTATGCCGATCAA
NM_003936	8941	CDK5R2	cyclin-dependent kinase 5, regulatory subunit 2 (p39)	CAGCAAGAAGGTGACACCCAA	CCGCGAGAACCTTCTCCGCAA
NM_003942	8986	RPS6KA4	ribosomal protein S6 kinase, 90kDa, polypeptide 4	CAGGCTGTGCCTTTGACTTTA	CGCCACCTTCATGGCATTCAA
NM_003948	8999	CDKL2	cyclin-dependent kinase-like 2 (CDC2-related kinase)	ATGATGTGTTTAGGTAATCTA	TTCTACGGACTTTAAATTAAA
NM_003952	6199	RPS6KB2	ribosomal protein S6 kinase, 70kDa, polypeptide 2	ACCGCAGAGAACCGGAAGAAA	CGGGCTGAGCGGAACATTCTA
NM_003954	9020	MAP3K14	mitogen-activated protein kinase kinase kinase 14	CACATGCATGTGACTCCTCAA	TACCTAGTGCATGCTCTGCAA
NM_003957	9024	STK29	serine/threonine kinase 29	CCCGACTGCCAGAGTCTGCTA	GCGAGCTACTGTAAACTTTAA
NM_003985	8711	TNK1	tyrosine kinase, non-receptor, 1	AAGGATCTAGTCTGCCCACTA	ATCGGTCATGATGAACTTGGA
NM_004064	1027	CDKN1B	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	AAAGCGTTGGATGTAGCATTA	ACCGACGATTCTTCTACTCAA
NM_004071	1195	CLK1	CDC-like kinase 1	AAAGCCGGTATCAGAACCATA	AACGTGATGAACGCACCTTAA
NM_004073	1263	PLK3	polo-like kinase 3 (Drosophila)	CAGAAAGACTGTGCACTACAA	CTGCATCAAGCAGGTTCACTA
NM_004119	2322	FLT3	fms-related tyrosine kinase 3	CCGGCTTGAGTGAATTGTGTA	TACGTTGATTTCAGAGAATAT
NM_004157	5576	PRKAR2A	protein kinase, cAMP-dependent, regulatory, type II, alpha	AACGGCATGTCTCTCCAACAA	AACTTGAAAGTCAGCACTAAA
NM_004196	8814	CDKL1	cyclin-dependent kinase-like 1 (CDC2-related kinase)	CTGGACCGAGTGACTACTATA	TCGGGAAATCCGAATGCTCAA
NM_004197	8859	STK19	serine/threonine kinase 19	CCCGGAGACCTTTGGAGTTAA	CTGTTATTACTCTGTCTTGAA
NM_004217	9212	AURKB	aurora kinase B	AACGCGGCACTTCACAATTGA	ACGCGGCACTTCACAATTGAT
NM_004226	9262	STK17B	serine/threonine kinase 17b (apoptosis-inducing)	AGCATATATGTTGTTAACTCA	CATGTTAATGAAATAATTCAA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_004274	9472	AKAP6	A kinase (PRKA) anchor protein 6	AAGCATGTGGATGTACATCTA	CACGTTTGTCACTGCCGTTTA
NM_004302	91	ACVR1B	activin A receptor, type IB	CCGTTCTTACGTCGCCATAAA	CTGTGATTACCTCTCAATCTA
NM_004304	238	ALK	anaplastic lymphoma kinase (Ki-1)	CACCTACGTATTTAAGATGAA	CTGGGCCTGTATACCGGATAA
NM_004327	613	BCR	breakpoint cluster region	ACGGCAGTCCATGACGGTGAA	CAGCATTCCGCTGACCATCAA
NM_004329	657	BMPR1A	bone morphogenetic protein receptor, type IA	CAGCTACGCCGGACAATAGAA	GCGGCAGACATTAAAGGTACA
NM_004333	673	BRAF	v-raf murine sarcoma viral oncogene homolog B1	ACACGACATGTGAATATCCTA	TTGCTTATATGTTAAATTGAA
NM_004336	699	BUB1	BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)	CAGCTTGTGATAAAGAGTCAA	TGGCACTTACATGAAAGTGAA
NM_004383	1445	CSK	c-src tyrosine kinase	CCGGTACAGAATGTATTGCCA	TACGCGCCTCATTAAACCAAA
NM_004384	1456	CSNK1G3	casein kinase 1, gamma 3	CAACATATCTTCGTTATGTAA	TACCGCAAACTTGATATGGAA
NM_004409	1760	DMPK	dystrophia myotonica-protein kinase	AACCAGAACTTCGCCAGTCAA	GAGCCTGAGGGCTAAATTTAA
NM_004431	1969	EPHA2	EphA2	CAGCGCCAAGTAAACAGGGTA	TCGGACAGACATATAGGATAT
NM_004438	2043	EPHA4	EphA4	CCCGCGAATGAAGTTACCTTA	CCGCCAGGACATTTCCTATAA
NM_004439	2044	EPHA5	EphA5	ACCAGTTGGATCTCCAATGAA	CCCGGCAGTATGTGTCTGTAA
NM_004440	2045	EPHA7	EphA7	ACCAGTCATGATAGTAATAGA	CAGGCTGCGAAGGAAGTACTA
NM_004441	2047	EPHB1	EphB1	ATGGCCCTGGATTATCTACTA	GCGGGATGATGTGACCTACAA
NM_004443	2049	EPHB3	EphB3	CCGCAGCTGACCGCCAGATTA	GCGGGTCTACGTGGAGCTCAA
NM_004444	2050	EPHB4	EphB4	CCCAGCCAATAGCCACTCTAA	TCGGACAAACACGGACAGTAT
NM_004445	2051	EPHB6	EphB6	AACCGCCAATCTCTAGATCAA	CTGGAGCTTTGGGATACTCAT
NM_004448	2064	ERBB2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	AACAAAGAAATCTTAGACGAA	CACGTTTGAGTCCATGCCCAA
NM_004517	3611	ILK	integrin-linked kinase	AAGGAAGAGCAGGGACTTCAA	TAGCCGTAGTGTAATGATTGA
NM_004560	4920	ROR2	receptor tyrosine kinase-like orphan receptor 2	CCGGTTTGGGAAAGTCTACAA	CTGGTGCTTTACGCAGAATAA
NM_004566	5209	PFKFB3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	CAGGGACTTGTCGCTGATCAA	CTCCAATATCATGGAAGTTAA
NM_004567	5210	PFKFB4	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	ACGGAGAGCGACCATCTTTAA	CAGAAAGTGTCTGGACTTGTA
NM_004570	5288	PIK3C2G	phosphoinositide-3-kinase, class 2, gamma polypeptide	CCAGATCAAGAAATTCGTAAA	CCCGTAGAAATGATAACTCCA
NM_004579	5871	MAP4K2	mitogen-activated protein kinase kinase kinase kinase 2	CTGGCTCTACTGCGTGAACAA	TCGGTCAGCCTCAGAATTCCA
NM_004586	6197	RPS6KA3	ribosomal protein S6 kinase, 90kDa, polypeptide 3	AGCGCTGAGAATGGACAGCAA	TCCAAACATTATCACTCTAAA
NM_004612	7046	TGFBR1	transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kDa)	TCCATTGGTGGAATTCATGAA	TGGGATTGTACTATACCAGTA
NM_004614	7084	TK2	thymidine kinase 2, mitochondrial	ATGCCAGAAGTGGACTATGTA	CGGGATCGAATATTAACTCCA
NM_004635	7867	MAPKAPK3	mitogen-activated protein kinase-activated protein kinase 3	CAGGCTTTCACTGAGAGAGAA	CCAGATAGTAATAAACACCAT
NM_004672	9064	MAP3K6	mitogen-activated protein kinase kinase kinase 6	CACCATCCAAATGCTGTTGAA	TCAGAGGAGCTGAGTAATGAA
NM_004690	9113	LATS1	LATS, large tumor suppressor, homolog 1 (Drosophila)	CCCATGAATCCTCCTAATCAA	CGCGATCTAGTATATGTTTAA
NM_004705	5612	PRKRIR	protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor)	AAGGTGTATGTAGACCACTTA	CTGGACAGTTACAAGAAATTA
NM_004712	9146	HGS	hepatocyte growth factor-regulated tyrosine kinase substrate	CCGGAACGAGCCCAAGTACAA	GCACGTCTTTCCAGAATTCAA
NM_004714	9149	DYRK1B	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1B	CACGGAGATGAAGTACTATAT	CCGGACCTACCGCTACAGCAA
NM_004721	9175	MAP3K13	mitogen-activated protein kinase kinase kinase 13	CAGACTCAATATGCACGGACA	GCGAATAATTTATACATGGAA
NM_004734	9201	DCAMKL1	doublecortin and CaM kinase-like 1	CAGGTTTATAACTTCGACACA	CCGGAAGTGATAACACGCAAA
NM_004759	9261	MAPKAPK2	mitogen-activated protein kinase-activated protein kinase 2	CGCCATCATCGATGACTACAA	CTACGAGCAGATCAAGATAAA
NM_004760	9263	STK17A	serine/threonine kinase 17a (apoptosis-inducing)	AACCAGGATATTTAACAGGTA	TCCATTGTAACCGAAGAGTTA
NM_004783	9344	TAO1	thousand and one amino acid protein kinase	CACGCCCAAAGCTCAGCACAA	GCCCAAGAGCCTCAAATCTAA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_004834	9448	MAP4K4	mitogen-activated protein kinase kinase kinase kinase 4	AGGCAAGATCCTACCCGGAAA	TCGGAGCTGCACCGAGGGCAA
NM_004836	9451	EIF2AK3	eukaryotic translation initiation factor 2-alpha kinase 3	CACAAACTGTATAACGGTTTA	CGGCAGGTCATTAGTAATTAT
NM_004842	9465	AKAP7	A kinase (PRKA) anchor protein 7	AACGATGGGTCTGAAGTCCAA	CCCGATGACGCTGAACTAGTA
NM_004850	9475	ROCK2	Rho-associated, coiled-coil containing protein kinase 2	AAGCTACATATGGAGCTTAAA	ATGCACTTGTATAAAGCCATA
NM_004857	9495	AKAP5	A kinase (PRKA) anchor protein 5	AGGGCTTTCATCAAGAAATTA	ATCAGGTTGATCTTTAAATAA
NM_004936	1030	CDKN2B	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	CTGCTTACTTATGCCATAGAA	GAGAGCAATTGTAACGGTTAA
NM_004938	1612	DAPK1	death-associated protein kinase 1	AAGCATGTAATGTTAATGTTA	CGGCTATTACTCTGTGGCCAA
NM_004954	2011	MARK2	MAP/microtubule affinity-regulating kinase 2	CACCTCTAATTCTTACTCTAA	CCACCTCTAATTCTTACTCTA
NM_004972	3717	JAK2	Janus kinase 2 (a protein tyrosine kinase)	AGCCATCATACGAGATCTTAA	CTGCCTTACGATGACAGAAAT
NM_005009	4833	NME4	non-metastatic cells 4, protein expressed in	ACCAACTACCTCCGTCAGCAA	CAGCACATGGGTGGTACACTA
NM_005012	4919	ROR1	receptor tyrosine kinase-like orphan receptor 1	CCCAGTGAGTAATCTCAGTAA	CCGTACTGCGATGAAACTTCA
NM_005026	5293	PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide	CCGGTCACGCATGAAGGCAAA	CGCCGTGATCGAGAAAGCCAA
NM_005027	5296	PIK3R2	phosphoinositide-3-kinase, regulatory subunit, polypeptide 2 (p85 beta)	CCGCGAGTATGACCAGCTTTA	TTGGTACGTGGGCAAGATCAA
NM_005028	5305	PIP5K2A	phosphatidylinositol-4-phosphate 5-kinase, type II, alpha	ATGGAATTAAGTGCCATGAAA	CTGCCCGATGGTCTTCCGTAA
NM_005030	5347	PLK1	polo-like kinase 1 (Drosophila)	CCGGATCAAGAAGAATGAATA	CGCGGGCAAGATTGTGCCTAA
NM_005044	5613	PRKX	protein kinase, X-linked	CGGATGGGATTCACTTAAGAA	TTGGAATACTCTAAGAGAATA
NM_005100	9590	AKAP12	A kinase (PRKA) anchor protein (gravin) 12	ACGGATGTAGTGTTGAAAGTA	CCCGAAATAATCGAACAGATT
NM_005108	9942	XYLB	xylulokinase homolog (H. influenzae)	CTGAAATTATTGGACGTCATA	TCAGGACTCCAGCTAAATCAA
NM_005109	9943	OSR1	oxidative-stress responsive 1	CTGGAGTAGGGACTAACTATA	TAGGGACTAACTATAGCACAA
NM_005157	25	ABL1	v-abl Abelson murine leukemia viral oncogene homolog 1	ACGCACGGACATCACCATGAA	CCAGTGGAGATAACACTCTAA
NM_005158	27	ABL2	v-abl Abelson murine leukemia viral oncogene homolog 2 (arg, Abelson-related gene)	ATCAAGCATCCTAATCTGGTA	CCCAAGTGTAATAAGCCTACA
NM_005160	157	ADRBK2	adrenergic, beta, receptor kinase 2	AAGATGTTCAGTGTTGGGTAA	CAAGTGTATGGGATTAACTAA
NM_005163	207	AKT1	v-akt murine thymoma viral oncogene homolog 1	ACGCTACTTCCTCCTCAAGAA	CACGCTTGGTCCCGAGGCCAA
NM_005184	808	CALM3	calmodulin 3 (phosphorylase kinase, delta)	CACCAATTGATTGACTGAGAA	CCGCAGAGCTGCGTCACGTAA
NM_005204	1326	MAP3K8	mitogen-activated protein kinase kinase kinase 8	AAGAAAGTGATCCATCATGAT	AGAGATTGATTTATTAATTAA
NM_005228	1956	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	CCCATCCAATTTATCAAGGAA	CCCGTCGCTATCAAGGAATTA
NM_005232	2041	EPHA1	EphA1	CAGATGGGATCCCGTATCGAA	TACCTCAGTAATCACAATTAT
NM_005233	2042	EPHA3	EphA3	TCGGATATGATTGTTTCTCAA	TTGGATAGTTTCCTACGTAAA
NM_005235	2066	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	CTACGTGTTAGTGGCTCTTAA	TCGGGATTTGGCAGCCCGTAA
NM_005246	2241	FER	fer (fps/fes related) tyrosine kinase (phosphoprotein NCP94)	CAGAACAACTTAGTAGGATAA	CAGATAGATCCTAGTACAGAA
NM_005248	2268	FGR	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog	CACGTGGAACGGCAGCACTAA	CAGACCTTGTCTAGTTATTTA
NM_005255	2580	GAK	cyclin G associated kinase	ACGCGTGTGACATTCAAGAAA	CCCGTGGTTGTCTGTACAGAA
NM_005308	2869	GRK5	G protein-coupled receptor kinase 5	AGCGTCATAACTAGAACTGAA	CAGGAACAACGCGGTAGGCAA
NM_005356	3932	LCK	lymphocyte-specific protein tyrosine kinase	AAGGGCCAGGACTTTATCTAA	CGCCATTACACCAATGCTTCA
NM_005372	4342	MOS	v-mos Moloney murine sarcoma viral oncogene homolog	CGCGAACATCTTGATCAGTGA	CTCGGTGTACAAGGCGACTTA
NM_005391	5165	PDK3	pyruvate dehydrogenase kinase, isoenzyme 3	AACGTTGTAGGTTGAAACTGA	TTCATTAGCACTAACATCCAA
NM_005399	5565	PRKAB2	protein kinase, AMP-activated, beta 2 non-catalytic subunit	ACCCAAAGTACTACTCATTTA	TCCAATATTAGTTGGAGTTAA
NM_005400	5581	PRKCE	protein kinase C, epsilon	CACGGAAACACCCGTACCTTA	CCCGACCATGGTAGTGTTCAA
NM_005406	6093	ROCK1	Rho-associated, coiled-coil containing protein kinase 1	AACGGTTAGAACAAGAGGTAA	CAAGCTCGAATTACATCTTTA
NM_005417	6714	SRC	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	AAGCAGTGCCTGCCTATGAAA	CGGCTTGTGGGTGATGTTTGA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_005424	7075	TIE	tyrosine kinase with immunoglobulin and epidermal growth factor homology domains	CCCAGTGAGAACGTGACGTTA	GCGCTTCAAGGTCAATGTGAA
NM_005433	7525	YES1	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	CCAGCCTACATTCACTTCTAA	GAGGCTCCTGCTTATTTATAA
NM_005456	9479	MAPK8IP1	mitogen-activated protein kinase 8 interacting protein 1	CTGGAGGAGTTTGAGGATGAA	TGGCATCAGCTTACAGTGCAA
NM_005476	10020	GNE	glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase	ATGGAAATACATATCGAATGA	CCCGATCATGTTTGGCATTAA
NM_005546	3702	ITK	IL2-inducible T-cell kinase	CAGGACTTTAGTAGAGACTGA	CTGGTGAGTTAAGTAAGATTA
NM_005569	3985	LIMK2	LIM domain kinase 2	CAGGAGGAATCTGTTACTCGA	CAGGGTGAACCTGCCTGTGAA
NM_005592	4593	MUSK	muscle, skeletal, receptor tyrosine kinase	ACGGCCTGGAATGAACTGAAA	CCCACCAATGACGTCCTCAAA
NM_005607	5747	PTK2	PTK2 protein tyrosine kinase 2	CACCTGGGTACTGGTATGGAA	CCGGTCGAATGATAAGGTGTA
NM_005627	6446	SGK	serum/glucocorticoid regulated kinase	CACAGCTGAAATGTACGACAA	CTGGGCTGTGATGACGAATAT
NM_005734	10114	HIPK3	homeodomain interacting protein kinase 3	CACGTTTGGCCAGGTAGTTAA	CTCATTCTGGTTGGAGATTAA
NM_005751	10142	AKAP9	A kinase (PRKA) anchor protein (yotiao) 9	CAGCCTATCAGTGAACATCAA	CAGCTTCAAAGGGATATACAA
NM_005781	10188	ACK1	activated Cdc42-associated kinase 1	ACGCAAGTCGTGGATGAGTAA	CGGCAGTCAGATCCTGCATAA
NM_005793	10201	NME6	non-metastatic cells 6, protein expressed in (nucleoside-diphosphate kinase)	CAGACTTCTCCTAGACATCTA	CAGGATCTAGCCTTCTATCTA
NM_005813	23683	PRKCN	protein kinase C, nu	CACGATATGTCAGTACTGCAA	CGGGAGAGTGTTACCATTGAA
NM_005858	10270	AKAP8	A kinase (PRKA) anchor protein 8	CAAGGTTAGCACGCAACAGAA	GAGGCCGGTAGTGATCCTCAA
NM_005876	10290	APEG1	aortic preferentially expressed protein 1	AACACCTATTTCTTAACTCAA	CAGCTGGAATAACAAGCCCAA
NM_005881	10295	BCKDK	branched chain alpha-ketoacid dehydrogenase kinase	AACGCCCACCATGATGCTCTA	CAGAACTTGGAGAGCAGGGAA
NM_005884	10298	PAK4	p21(CDKN1A)-activated kinase 4	CGGCGCCGAGCCGATGAGTAA	CTGGACAACTTCATCAAGATT
NM_005906	4117	MAK	male germ cell-associated kinase	CACAGTGTTGATATATGGGTA	CCGGATATAATCGATCAGGTT
NM_005922	4216	MAP3K4	mitogen-activated protein kinase kinase kinase 4	CACCAATCCCTGAAAGATTAA	CTCAAGCATCGCATAGTTTAA
NM_005923	4217	MAP3K5	mitogen-activated protein kinase kinase kinase 5	CAGCGAGTAGATAATATCGAA	CCGGGAATCTATACTCAATGA
NM_005965	4638	MYLK	myosin, light polypeptide kinase	AACCTGAAATCCGCTAGCAAA	CAGCATCCATGGCTAATGAAA
NM_005975	5753	PTK6	PTK6 protein tyrosine kinase 6	CCGGGTCCAGGTGGCCATTAA	CGGGTTAGCCAGGCTTATCAA
NM_005983	6502	SKP2	S-phase kinase-associated protein 2 (p45)	AAGTGATAGTGTCATGCTAAA	ACCCTTCAACTGTTAAAGGAA
NM_005990	6793	STK10	serine/threonine kinase 10	CACGGAATTAGAGAACCTGGA	CAGCTCAAACTGATGAAGAAA
NM_006035	9578	CDC42BPB	CDC42 binding protein kinase beta (DMPK-like)	CGCCGAGATATTCCATGTATA	TAGGACCTTAAGAGAATAGTA
NM_006116	10454	MAP3K7IP1	mitogen-activated protein kinase kinase kinase 7 interacting protein 1	CACCTTGGACAAGCCACACAA	CTGCAGGTGAGAGGATTTAAA
NM_006176	4900	NRGN	neurogranin (protein kinase C substrate, RC3)	AAGCCGGACGACGACATTCTA	TGGGTTGGAATGTGAACAATA
NM_006180	4915	NTRK2	neurotrophic tyrosine kinase, receptor, type 2	ACCACGAACAGAAGTAATGAA	CTGACGAGTTTGTCTAGGAAA
NM_006182	4921	DDR2	discoidin domain receptor family, member 2	ACGCACTGTCAGTTACACCAA	CCGGTTCATTCCAGTCACCGA
NM_006201	5127	PCTK1	PCTAIRE protein kinase 1	CACCATAATCGCTGTATGAAA	CACGCCAACATCGTTACGCTA
NM_006206	5156	PDGFRA	platelet-derived growth factor receptor, alpha polypeptide	ACGCAGGAAGCCTACTATTTA	CGCAGGAAGCCTACTATTTAA
NM_006212	5208	PFKFB2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	CCAGAGCAAGATAGTCTACTA	CCGTGACAAGCCAACTAACAA
NM_006213	5260	PHKG1	phosphorylase kinase, gamma 1 (muscle)	CAAGAGCCTGCAAGCACTTAA	CCGGGAGATCGTCATCCGAGA
NM_006218	5290	PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	CTGAGTCAGTATAAGTATATA	TGCGAAATTCTCACACTATTA
NM_006219	5291	PIK3CB	phosphoinositide-3-kinase, catalytic, beta polypeptide	CCCTTCGATAAGATTATTGAA	TCGGGAAGCTACCATTTCTTA
NM_006251	5562	PRKAA1	protein kinase, AMP-activated, alpha 1 catalytic subunit	CCCACGATATTCTGTACACAA	TCGGGATCAGTTAGCAACTAT
NM_006252	5563	PRKAA2	protein kinase, AMP-activated, alpha 2 catalytic subunit	ACGACTAAGCCCAAATCTTTA	CCGATTTCGGATTATCTAATA
NM_006253	5564	PRKAB1	protein kinase, AMP-activated, beta 1 non-catalytic subunit	CACGTCTAGAAGTCACATGAA	CTGGCTATGGAACTAAATACA
NM_006254	5580	PRKCD	protein kinase C, delta	CCGCTTCAAGGTTCACAACTA	CCGGGACACTATATTCCAGAA
NM_006255	5583	PRKCH	protein kinase C, eta	CGCCGTGTGCTCATCACTGAA	GACCAGATTTGTGGCTTATAA
NM_006256	5586	PRKCL2	protein kinase C-like 2	AAAGTATGATATCTACGCAAA	CACGTCAAAGTATGATATCTA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_006257	5588	PRKCQ	protein kinase C, theta	CCGCAGACAAGTAATCACTAA	CGGGCAGATGTATATCCAGAA
NM_006258	5592	PRKG1	protein kinase, cGMP-dependent, type I	CCGGTGTATATACCATACAAA	GAGGTTCGTTTGAAGATTCTA
NM_006259	5593	PRKG2	protein kinase, cGMP-dependent, type II	GACCTACAATTTGATTCTCAA	TTGAGTACTACTAACGTTTAA
NM_006281	6788	STK3	serine/threonine kinase 3 (STE20 homolog, yeast)	CCGGCGCCTAAGAGTAAACTA	CGGCGCCTAAGAGTAAACTAA
NM_006282	6789	STK4	serine/threonine kinase 4	AGGATTCATAGCATCACTATA	CACCATTTGCTGTGCGAATTA
NM_006285	7016	TESK1	testis-specific kinase 1	CAGGACCGCCCTGACACACAA	CTGCGGTACCTGCACTCCAAA
NM_006293	7301	TYRO3	TYRO3 protein tyrosine kinase	AACGGTGACCTTTAGTGCCAA	CGGACTGACCAAATCACCCAA
NM_006296	7444	VRK2	vaccinia related kinase 2	CACACAATAGGTTAATCGAAA	CTGGAGGATTTGGATTGATAT
NM_006301	7786	MAP3K12	mitogen-activated protein kinase kinase kinase 12	CAGGGAGCACTATGAAAGGAA	CTCGTATTCCTTGTACATAGA
NM_006314	10256	CNK1	connector enhancer of KSR-like (Drosophila kinase suppressor of ras)	CCGCCGCTGGTTTGTGCTCAA	CGGACTCAGCTTAGTGCTGAA
NM_006343	10461	MERTK	c-mer proto-oncogene tyrosine kinase	CAGATGAATGTTGTTAAGGAA	TTGCCTGACGTTCGGAACCAA
NM_006374	10494	STK25	serine/threonine kinase 25 (STE20 homolog, yeast)	AAGGGCATCGATAACCACACA	CACCAAGCTATGGATCATCAT
NM_006383	10518	KIP2	DNA-dependent protein kinase catalytic subunit-interacting protein 2	CACCGAAGAGCAGCTAGACAA	CTGCACCTTCTTCAATAAGAA
NM_006422	10566	AKAP3	A kinase (PRKA) anchor protein 3	AGGGATCATGACCTATGCTAA	ATCAAGCTATCCATAATGAAA
NM_006457	10611	LIM	LIM protein (similar to rat protein kinase C-binding enigma)	CAGCAGGGAAACGAACTCCGA	TCCGATGTGCGCCCATTGTAA
NM_006549	10645	CAMKK2	calcium/calmodulin-dependent protein kinase kinase 2, beta	CCGCAAGATCTTCTCTGGGAA	CTAGCTGATTGTTGTGGTCAA
NM_006556	10654	PMVK	phosphomevalonate kinase	CCCAGTGTGGATACTAATAAA	TTGGCTGTGCTTGAAGGCGAA
NM_006575	11183	MAP4K5	mitogen-activated protein kinase kinase kinase kinase 5	CTTGCCTATTTGCATACTAAA	TCCGCTTATTAGGATCAGACA
NM_006609	10746	MAP3K2	mitogen-activated protein kinase kinase kinase 2	CACAGTAATATGATTGTCCTA	CAGAATGATGTCCGAGTCAAA
NM_006622	10769	PLK2	polo-like kinase 2 (Drosophila)	CAGATGCTCCTGAGCAATTTA	CAGATTGTGTCTGGACTGAAA
NM_006648	65268	PRKWNK2	protein kinase, lysine deficient 2	AACGTTCATCGAGCAGATGAA	ACCTATAAGTCTAGTAGCAAA
NM_006712	10922	FASTK	FAST kinase	CAGCAGCAAGGTGGTACAGAA	CTGGTGGTTCAGGAAACGCAA
NM_006716	10926	ASK	activator of S phase kinase	CAGTATCAAGTTGTTGATGAT	CATGAATCTATTGTCACTAAA
NM_006738	11214	AKAP13	A kinase (PRKA) anchor protein 13	CCGCCTGTTTGGGTTAACAAA	CTCGGTGTTTCAGGCACTAAA
NM_006742	5681	PSKH1	protein serine kinase H1	CCCGATTAGGGTCGAGTGTCA	CCGCTCCACACGCTCCAATAA
NM_006759	7360	UGP2	UDP-glucose pyrophosphorylase 2	CCCAAAGTTAGTTACTCTTAA	CGAGTTCAAGTCTGTATCAAA
NM_006852	11011	TLK2	tousled-like kinase 2	AAGGTTCATCTGTCCATGCAA	CAAGAGAATACGATTCTTAAA
NM_006871	11035	RIPK3	receptor-interacting serine-threonine kinase 3	ACCGCTCGTTAACATATACAA	CAGCCTGATGTCGTGCGTCAA
NM_006875	11040	PIM2	pim-2 oncogene	CCGGGATTGTCCAATTACTAA	CGGGATTGTCCAATTACTAAA
NM_006888	801	CALM1	calmodulin 1 (phosphorylase kinase, delta)	CGGCAACTTACACACATTGAA	CTGGTTGTATCTTATTAGCAA
NM_006904	5591	PRKDC	protein kinase, DNA-activated, catalytic polypeptide	CTCGTGTATTACAGAAGGAAA	TTCGGCTAACTCGCCAGTTTA
NM_006930	6500	SKP1A	S-phase kinase-associated protein 1A (p19A)	AGGGTACTTTAGAGCAACTTA	TAGGAAAGACTACTCAAGTTA
NM_007064	11139	TRAD	serine/threonine kinase with Dbl- and pleckstrin homology domains	CAGGACATCAATCAAGTCTTA	CCCATTGAGTATCAACGGAAA
NM_007118	7204	TRIO	triple functional domain (PTPRF interacting)	ACCGTTGTTCTTAGATGTCGA	CCGGGAATGTATGGATACGTA
NM_007170	10420	TESK2	testis-specific kinase 2	CCGGGAAGAATCGCTATCTGA	CGAGATGAGCCCTATAATGAA
NM_007174	11113	CIT	citron (rho-interacting, serine/threonine kinase 21)	ATGGAAGGCACTATTTCTCAA	CAGGATATACCGTAACACGAA
NM_007181	11184	MAP4K1	mitogen-activated protein kinase kinase kinase kinase 1	CTGACTAAGAGTCCCAAGAAA	TACGTGGGTGTACTCCATCAA
NM_007194	11200	CHEK2	CHK2 checkpoint homolog (S. pombe)	ACGCCGTCCTTTGAATAACAA	AGGACTGTCTTATAAAGATTA
NM_007199	11213	IRAK3	interleukin-1 receptor-associated kinase 3	CACATTCGAATCGGTATATTA	CTGGATGTTCGTCATATTGAA
NM_007202	11216	AKAP10	A kinase (PRKA) anchor protein 10	CAGATAAGCATAGAACTGATA	TAGCAGGACAGCCACACTTAA
NM_007229	11252	PACSIN2	protein kinase C and casein kinase substrate in neurons 2	CACCCTTAATGTCCCGAGCAA	GAAGCTTTACATAGAACCTTA
NM_007254	11284	PNKP	polynucleotide kinase 3'-phosphatase	CACGTGAACAGGGACACGCTA	CACGTGTGAGACAGCCCTGAA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_007271	11329	STK38	serine/threonine kinase 38	AACCTTATCGCTCAACATGAA	TACGTCGGCCATAAACAGCTA
NM_007284	11344	PTK9L	PTK9L protein tyrosine kinase 9-like (A6-related protein)	AAGACAGAGATCAGTGTGGAA	TTGGGATGGTTGAATGCTGTA
NM_012145	1841	DTYMK	deoxythymidylate kinase (thymidylate kinase)	ATCAGTTGGAATTCTCCTAAA	TCCCGGAAAGATCAACTGAAA
NM_012290	9874	TLK1	tousled-like kinase 1	CAGAGAGTATAGAATACACAA	CCGGAGAAGAAACAATCGGAA
NM_012324	23542	MAPK8IP2	mitogen-activated protein kinase 8 interacting protein 2	ACAGGTAATGTCGGCTTCCAA	CTGGAAGAATTTGACGACGAA
NM_012395	5218	PFTK1	PFTAIRE protein kinase 1	AAGGGACACCTTTCACAGCTA	CTGGGTCTTGTCAACATCTAA
NM_012398	23396	PIP5K1C	phosphatidylinositol-4-phosphate 5-kinase, type I, gamma	CCGCGTCGTGGTCATGAACAA	CGGCAAGACCTATTTATAATA
NM_012407	9463	PRKCABP	protein kinase C, alpha binding protein	CCGGTGTCAATGGCAGGTCAA	TCGCCTCACCATCAAGAAGTA
NM_012424	26750	RPS6KC1	ribosomal protein S6 kinase, 52kDa, polypeptide 1	CAGGATTGGTTTATATGATTA	CCGGGTTGTTTCACGAAGAAA
NM_012474	7371	UMPK	uridine monophosphate kinase	CCGGATGCCTTTGACAATGAA	TCAGTACATTACGTTCGTCAA
NM_013233	27347	STK39	serine threonine kinase 39 (STE20/SPS1 homolog, yeast)	TGGAATAGTCTCAGATCTAAA	TTGGAGTATTTGTAACTTCTA
NM_013254	29110	TBK1	TANK-binding kinase 1	CAGAACGTAGATTAGCTTATA	CTGACTTGACACGTTTGTAAA
NM_013257	23678	SGKL	serum/glucocorticoid regulated kinase-like	ACCAACTAACTTACATGCTTA	CCACAGCGAGACCCTAGTTAA
NM_013276	23729	CARKL	carbohydrate kinase-like	ATGAAACATATTGTCTCTTTA	CAGGTAGTTTATTCAAAGAGA
NM_013302	29904	EEF2K	elongation factor-2 kinase	CAGACACTACATGAACACGAA	CGGGATGGCGCTCTTCTTCTA
NM_013355	29941	pknbeta	protein kinase PKNbeta	AGGGAAATACTACGCCATCAA	CCCGGGAAGTTTCAAGTTTGA
NM_013392	29959	NRBP	nuclear receptor binding protein	CCGGTTGACTTCTCTGCTAGA	TCGGTGGAGGAGGGAGTCAAA
NM_013410	205	AK3	adenylate kinase 3	CAGGAAGATGTGGTCATTCAT	CCTGGTAACAGTGAAATTGAA
XM_375834	9641	IKBKE	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon	ACGGCGGAACAAGGAGATCAT	CCGCATCATCGAACGGCTAAA
NM_014006	23049	SMG1	PI-3-kinase-related kinase SMG-1	ATCGATGTTGCCAGACTACTA	CACCATGGTATTACAGGTTCA
NM_014030	28964	GIT1	G protein-coupled receptor kinase-interactor 1	CAGCCTTGACTTATCCGAATT	GCCGCTGAGGATGTCCCGAAA
NM_014216	3705	ITPK1	inositol 1,3,4-triphosphate 5/6 kinase	CACGCCGTCATTGACATCAAT	CCGATTAATGTCTGTACGTCA
NM_014226	5891	RAGE	renal tumor antigen	AAAGAATAAGCTGTCGTTAAA	CCGGCTGTGTGTTCTACGAGA
NM_014264	10733	PLK4	polo-like kinase 4 (Drosophila)	CACCAAATGGTCAAACAACTA	CTGGTAGTACTAGTTCACCTA
NM_014308	23533	P101-PI3K	phosphoinositide-3-kinase, regulatory subunit, polypeptide p101	ACCGGTGCTGCTGCAACTCTA	ATCGCAGATCAAAGTGGACAA
NM_014326	23604	DAPK2	death-associated protein kinase 2	CGGAATTTGTTGCTCCAGAAA	CTGGTTAAAGAGACCCGGAAA
NM_014365	26353	HSPB8	heat shock 27kDa protein 8	CCGCATGGTTTGGTTAATGAA	CGCATGGTTTGGTTAATGAAA
NM_014370	26576	STK23	serine/threonine kinase 23	AAGATGAGGCGCAAACGGAAA	AAGCGCTTTGTGGCCCTCAAA
NM_014371	26993	AKAP8L	A kinase (PRKA) anchor protein 8-like	AAGGAACACTTTAAGTACGTA	CAGGATAACACCACCAACTAT
NM_014397	10783	NEK6	NIMA (never in mitosis gene a)-related kinase 6	ACCACGGAAGTCGAGAATTAA	ACCGGAGAGGATCCATGAGAA
NM_014413	27102	HRI	heme-regulated initiation factor 2-alpha kinase	CCCGAATATGACGAATCTGAT	CTGATTAAGGGTGCAACTAAA
NM_014496	27330	RPS6KA6	ribosomal protein S6 kinase, 90kDa, polypeptide 6	CAGCGGTATACTGCTGAACAA	GGCGAGGTAAATGGTCTTAAA
NM_014572	26524	LATS2	LATS, large tumor suppressor, homolog 2 (Drosophila)	CACACTCACCTCGCCCAATAA	CAGGACCTTCACTGCATTAAA
NM_014586	30811	HUNK	hormonally upregulated Neu-associated kinase	CACGGGCAAAGTGCCCTGTAA	TCGGACCAAGATCAAACCAAA
NM_014602	30849	PIK3R4	phosphoinositide-3-kinase, regulatory subunit 4, p150	AAGCAGAATTCTAGATCAGAA	TAGAGGCAGAAGATTACTTAA
NM_014683	9706	ULK2	unc-51-like kinase 2 (C. elegans)	ACCGGGAAGTTATCAGATCAA	ATCGGTACAGTTATTCTTAAA
NM_014720	9748	SLK	SNF1 sucrose nonfermenting like kinase (yeast)	CCAGATCAGGACCGTGATAAA	TAGCATCTTGTGATCACCCAA
NM_014776	9815	GIT2	G protein-coupled receptor kinase-interactor 2	AAGCATCGTGCAATAAGTGAA	CTGCCTATGGCTGAAACTATA
NM_014791	9833	MELK	maternal embryonic leucine zipper kinase	CGGGTTGTCTTCCGTCAGATA	CTGGATCATGCAAGATTACAA
XM_374996	9891	ARK5	AMP-activated protein kinase family member 5	CTTGAGTTGATGATCAATTAA	TAGGGATTTACTGGCATGGTA
NM_014911	22848	AAK1	AP2 associated kinase 1	AACGTGAGTAGCGGTGATGTA	CCAGGTGGTAAACCTGATGAA
NM_014916	22853	LMTK2	lemur tyrosine kinase 2	CACCTCCGACTTAAATGTGAA	CAGATCAGACTAAGTATAGTA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_014920	22858	ICK	intestinal cell (MAK-like) kinase	ACCTAATGACTTGGTAAATTA	CTCAGTAATCTAGCTTATATA
NM_015000	23012	STK38L	serine/threonine kinase 38 like	AGGGAGATGTACTGTATTATA	TACAACCATGATAACCATTAT
NM_015071	23092	GRAF	GTPase regulator associated with focal adhesion kinase pp125(FAK)	ACCGTATGGCCTATAGTTTAA	AGGGAGTATACTAGTAGGTTA
NM_015076	23097	CDK11	cyclin-dependent kinase (CDC2-like) 11	CACTGTCGTCAGGAAGATATA	GAGGATTTGTTTGAGTACGAA
NM_015093	23118	MAP3K7IP2	mitogen-activated protein kinase kinase kinase 7 interacting protein 2	CAGTCAATAGCCAGACCTTAA	TGGCTGGGTATCTCAGTTTAA
NM_015112	23139	MAST2	microtubule associated serine/threonine kinase 2	CAGGAGTGTGCTGTCTGGCAA	CAGTGAAATAATAATGATGAA
NM_015133	23162	MAPK8IP3	mitogen-activated protein kinase 8 interacting protein 3	CAGCCGCAACATGGAAGTACA	GACGAGTGGTCTGATGTTCAA
NM_015148	23178	PASK	PAS domain containing serine/threonine kinase	ATCCTGGTTGCTAACGACAAA	CGCGCTGACACTGTTTGGTTA
NM_015690	27148	STK36	serine/threonine kinase 36 (fused homolog, Drosophila)	ATGGATGCTGACCTCCTTATA	CCAGTTGGTGTCAGCCCTGTA
NM_015716	50488	MINK	misshapen/NIK-related kinase	CACGTACGGGCGCATCATTAA	CGCAGACTTTGTGTTGCTGAA
NM_015850	2260	FGFR1	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)	CAGAGATTTACCCATCGGGTA	CCGGCCTCTATGCTTGCGTAA
NM_015978	51086	TNNI3K	TNNI3 interacting kinase	CAGCATTCGGCGTATACCTAA	GGAGCTAATGTCAATATTCAA
NM_015981	815	CAMK2A	calcium/calmodulin-dependent protein kinase (CaM kinase) II alpha	CAGGAACTTCTCCGGAGGGAA	CCAGGATTTCATCTCACCATA
NM_016086	51657	MK-STYX	map kinase phosphatase-like protein MK-STYX	AAGCTTCTGCACATCCGGATA	CAAGATTCAGAAGGACTTGAA
NM_016123	51135	IRAK4	interleukin-1 receptor-associated kinase 4	ATCCTATTAGTCATATATTTA	TTGCAGGACAGTGGTTATTAA
NM_016151	9344	TAO1	thousand and one amino acid protein kinase	AACGGAAACCACCGCTCTTTA	ATCGAGCTGGCTGAACGGAAA
NM_016203	51422	PRKAG2	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	AAGCACGAGCCTGAACGGTTA	CCGGAAAGCATTCCTCTCGAA
NM_016223	29763	PACSIN3	protein kinase C and casein kinase substrate in neurons 3	AAGGATATGCTGCTCACCTTA	CAGAGGACAATCAGCCGGAAA
NM_016231	51701	NLK	nemo like kinase	CCGGATAGACCTATTGGATAT	TTGGTGTTGTCTGGTCAGTAA
NM_016248	11215	AKAP11	A kinase (PRKA) anchor protein 11	ACCGGTTATCTAAATCTATTA	CTGACCGGTTATCTAAATCTA
NM_016276	10110	SGK2	serum/glucocorticoid regulated kinase 2	CAGGGCCAATGGGAACATCAA	TGGGTACGTGACTATCCCTAA
NM_016281	51347	JIK	STE20-like kinase	CAAACAGTATAAAGCACTCAA	CAGCTCCTCCGTCGTGCATAA
NM_016282	50808	AK3L1	adenylate kinase 3 like 1	CCCGTGGCACTATGTAAATAA	CCGTGGCACTATGTAAATAAA
NM_016291	51447	IHPK2	inositol hexaphosphate kinase 2	AAGCATCGGAACCAGTACAAA	TCGGAACCAGTACAAATTTAT
NM_016308	51727	UMP-CMP	UMP-CMP kinase	AAGTATTGCTAAGTACTATAA	CGCGTATATATCCCTCTAGTA
NM_016440	51231	VRK3	vaccinia related kinase 3	AACCAGGGCATTCTCTATGAA	CTCACTCAAACTGGATGCCAA
NM_016457	25865	PRKD2	protein kinase D2	CACGACCAACAGATACTATAA	TTGGGTGGTTCATTACAGCAA
NM_016478	51530	NIPA	nuclear interacting partner of anaplastic lymphoma kinase (ALK)	AGGGAGAATGGTGGAACTGAA	CCGCTTGAGGCTCTCTATGAA
NM_016507	51755	CRK7	CDC2-related protein kinase 7	ACCGGATATCGGGAAGTTCAA	ATCGGGATATTAAGTGTTCTA
NM_016508	51265	CDKL3	cyclin-dependent kinase-like 3	CAACATTATTGTCATGGACTA	TGGGCAGATAGTGGCCATTAA
NM_016542	51765	MST4	Mst3 and SOK1-related kinase	CAGCAAGTCGTTGCTATTAAA	CCAAACCTACGTCAAGATTAA
NM_016653	51776	ZAK	sterile alpha motif and leucine zipper containing kinase AZK	ACGTGGTAGTATATCACTCAA	TCGGGTAGCAACAAACTTATT
NM_017431	53632	PRKAG3	protein kinase, AMP-activated, gamma 3 non-catalytic subunit	CAGATCTATGAGATTGAACAA	TAGCCTGTTTGAAGCTGTCTA
NM_017449	2048	EPHB2	EphB2	CACGCTTTCTAGAGGACGATA	CCGAGAGGACCTCGTCTACAA
NM_017567	55577	NAGK	N-acetylglucosamine kinase	ACCTGAGTGAAAGCTACTTAA	CCCGGTCTTGTTCCAGGGCAA
NM_017572	2872	MKNK2	MAP kinase-interacting serine/threonine kinase 2	CCGCTTCTACCTGGTGTTTGA	TTGGACTTTCTGCATAACAAA
NM_017593	55589	BMP2K	BMP2 inducible kinase	AGGCATCACCTGAATATCTTA	TCCGATGTGCATTGAAGCGAA
NM_017719	54861	SNRK	SNF-1 related kinase	ACCACTGAATTGGAACGGATA	CACCACTGAATTGGAACGGAT
NM_017771	54899	PXK	PX domain containing serine/threonine kinase	CTGGCAGATTGTTAGAAGATA	TAAGATCCCTACAAAGTTAAA
NM_017859	54963	URKL1	uridine kinase-like 1	ACCCAGGACTGTTGAATACAA	TACAATGAACACGGCACGCAA
NM_017900	54998	AKIP	aurora-A kinase interacting protein	ATCCGTAGTAATAAATTCTCA	CTGCTGTGATCCGTAGTAATA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_018216	55229	PANK4	pantothenate kinase 4	CTGGGAGACGTTCATATTGGA	TCGACATAGGCGGGTCGTTAA
NM_018323	55300	PI4K2B	phosphatidylinositol 4-kinase type-II beta	ATGAACTTTGTGCAAGATTTA	CAGAGTACTGGCCTTGTTCAA
NM_018339	55312	FLJ11149	riboflavin kinase	ACGATGTAATTTAATGCTAAA	CACGATGTAATTTAATGCTAA
NM_018343	55781	RIOK2	RIO kinase 2 (yeast)	AACGCGATTATCATAAACATA	CGCGGTTGAAATGGGCATGAA
NM_018401	55351	HSA250839	gene for serine/threonine protein kinase	CTGGGACGCGGTGTTCAAGAA	TTGGGCTGAGTTCACGAATTA
NM_018425	55361	PI4KII	phosphatidylinositol 4-kinase type II	ACGCAAATGTATGAATAACAA	CCGCATCGGGCTACCACCAAA
NM_018492	55872	TOPK	T-LAK cell-originated protein kinase	AAGTGTGGCTTGCGTAAATAA	TCAGTAGTTATTAGACTCTAA
NM_018571	55437	ALS2CR2	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 2	CAGGAACACTGGTAACTATAA	CCAGTGGAACTCACACAGTAA
NM_018584	55450	CaMKIINalpha	calcium/calmodulin-dependent protein kinase II	AGCAAGCGGGTTGTTATTGAA	CGGGTTGTTATTGAAGATGAT
NM_018638	55500	EKI1	ethanolamine kinase	CCGTATGTGGTGGATTAGAAA	TCCGTATGTGGTGGATTAGAA
NM_018650	4139	MARK1	MAP/microtubule affinity-regulating kinase 1	CCCGGTGTAGAAACTCCATTA	CCGGCCCAGTAGTGACTTAAA
NM_018842	55971	LOC55971	insulin receptor tyrosine kinase substrate	CACGGAGAGCACCTACCGGAA	CTCAACGAGAGTCTTGATGAA
NM_018979	65125	PRKWNK1	protein kinase, lysine deficient 1	CTAGAGGATCTTGATGCTCAA	CTGCGACGACTACGAGATAAA
NM_019884	2931	GSK3A	glycogen synthase kinase 3 alpha	CAGGGAACTAGTCGCCATCAA	CCGGGTGTAAATAGATTGTTA
NM_020126	56848	SPHK2	sphingosine kinase 2	CAGGATTGCGCTCGCTTTCAT	CCGAGGGTAGTGCCTGATCAA
NM_020168	56924	PAK6	p21(CDKN1A)-activated kinase 6	CGGAAGGACCATGTTCCGCAA	CTGTGTTACCTTTCAAGTTTA
NM_020240	56990	SPEC2	non-kinase Cdc42 effector protein SPEC2	AAGGGAGGTTATGGAGGTGGA	CAGGAGACCTGTTCAGTGGAA
NM_020397	57118	CAMK1D	calcium/calmodulin-dependent protein kinase ID	CAGGCGCTTTCTATACTTAAT	CCAGGCGCTTTCTATACTTAA
NM_020421	57143	ADCK1	aarF domain containing kinase 1	TAACAAGTACTTGGACCCTAA	TACGACGGCTGTCATCAGTTA
NM_020439	57172	CAMK1G	calcium/calmodulin-dependent protein kinase IG	AACAGGCCGCCTGAAACTCAA	CAGGTCTTGTCGGCAGTGAAA
NM_020526	2046	EPHA8	EphA8	ACGGCCCACCAGGGTATGTAA	GAGCGTGTGCTTATCCGTTAA
NM_020639	54101	ANKRD3	ankyrin repeat domain 3	AAGCCTGATGACGAAGTGAAA	CACACGCAGTATGAAGATAAA
NM_020666	57396	CLK4	CDC-like kinase 4	AAGTCTGACTATGTAGTCAAA	TCGAAGAATGTTAGAATATGA
NM_020804	29993	PACSIN1	protein kinase C and casein kinase substrate in neurons 1	CAGCAGCTACATCCATGTGTA	CGCCATAGAGTTCCAGACATA
NM_020836	57596	KIAA1446	brain-enriched guanylate kinase-associated protein	CGGGCGGACCATGTCACCGTA	CTGCAGCTTCTCTGAACGCTA
NM_020922	65267	PRKWNK3	protein kinase, lysine deficient 3	AAGATTGGTGATCTAGGATTA	CCGGGTGACGCCAATAAAGAA
NM_020965	260425	MAGI-3	membrane-associated guanylate kinase-related (MAGI-3)	CCCTATGATGTTGTCTTGCAA	CGGGATGTCGAAGACGCTGAA
NM_020975	5979	RET	ret proto-oncogene (multiple endocrine neoplasia and medullary thyroid carcinoma 1, Hirschsprung disease)	CCGCTGGTGGACTGTAATAAT	TAGGCTGGTTCTCAACCGGAA
NM_020990	1159	CKMT1	creatine kinase, mitochondrial 1 (ubiquitous)	ACGGATCTAGATGCCAGTAAA	CTGGACGTTACTATAGGCTCA
NM_021135	6196	RPS6KA2	ribosomal protein S6 kinase, 90kDa, polypeptide 2	CCGAGTGAGATCGAAGATGGA	CCGGAGGTCCTGAAGCGTCAA
NM_021733	60385	TSKS	testis-specific kinase substrate	AACCAACGTCTTGAAGCAGAA	CACCAACGTGTCACTGCTCAA
NM_021970	8649	MAP2K1IP1	mitogen-activated protein kinase kinase 1 interacting protein 1	ATGCCCAGGCTTGCAGAATAA	TAGCATATAGATGTAATTTAT
NM_021972	8877	SPHK1	sphingosine kinase 1	CACGAACCAAATCCAAATAAA	CCGGCTGCTGTCACCCATGAA
NM_022048	53944	CSNK1G1	casein kinase 1, gamma 1	ATGGACCATCCTAGTAGGGAA	CCGGCAGACCAATACCTCATA
NM_022128	64080	RBKS	ribokinase	AACACAGTCATCTTACCCTTA	CAGGTGGTAATCATTACCTTA
NM_022158	64122	FN3K	fructosamine-3-kinase	CCAGCTGTTTAACTACCTGAA	CCCAGTGTTCGTCAAAGTCAA
NM_022344	64149	NJMU-R1	protein kinase Njmu-R1	TTGAGTTACACTCCTGTTGAA	TTGGCAGATACTAATCTACCA
NM_022445	27010	TPK1	thiamin pyrophosphokinase 1	AACCTGGTGCATCGAAATGTA	CAGGTTGTCTGTAGAGAATGA
NM_022731	64710	NUCKS	nuclear ubiquitous casein kinase and cyclin-dependent kinase substrate	AAGGTGTACCACGGTTGTAAA	ACCCTAGAATTTAATCAACAA
NM_022740	28996	HIPK2	homeodomain interacting protein kinase 2	AACCAGTACCCTTACATATAA	TCCCGAAGTCTCCATACTAAA
NM_023018	65220	FLJ13052	NAD kinase	AAAGAGCGTCCTTGTCATCAA	CCAGGAGAACATGATCGTGTA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_024117	79109	MAPKAP1	mitogen-activated protein kinase associated protein 1	CTAGGTATCTCTGGAGACAAA	GACCCTGTTACGAATCAGAAA
NM_024594	79646	PANK3	pantothenate kinase 3	AAGCGAGAATCTGTTAGTAAA	TCCAAAGGTGATAGCACACAA
NM_024779	79837	PIP5K2C	phosphatidylinositol-4-phosphate 5-kinase, type II, gamma	CCGGAGCAGTATGCTAAGCGA	TTGATGTGTGATAATCTCATA
NM_024800	79858	NEK11	NIMA (never in mitosis gene a)- related kinase 11	CTGCCTATGCTTGGAGTCATA	TGAGATAAGCTTATAGATCAA
NM_024876	79934	ADCK4	aarF domain containing kinase 4	CAGATGCTGAGAGTTCTTGAA	CCGGGTCCCAGCCGTGGTTAA
NM_024960	80025	PANK2	pantothenate kinase 2 (Hallervorden-Spatz syndrome)	CAGAGCGACTTTGATCACCAT	CTGTGTGTGAACTTACTGTAA
NM_025144	80216	LAK	lymphocyte alpha-kinase	CAGCCCTTGGTCCTATCTGAA	CAGGCCCTACATTTAAAGCTA
NM_025194	80271	ITPKC	inositol 1,4,5-trisphosphate 3-kinase C	CCGGAAGGACATGTATGAGAA	TCGGCCGAAGCCCGAACCGAA
NM_025211	80318	GKAP42	protein kinase anchoring protein GKAP42	AACGCTCAACATGATCTTCCA	CATGCTGTTTGTAACGCTCAA
NM_025228	80342	T3JAM	TRAF3-interacting Jun N-terminal kinase (JNK)-activating modulator	CAGACTTGGCACCAACATTAA	TAGCAGGGACTTACAGATGAA
NM_030662	5605	MAP2K2	mitogen-activated protein kinase kinase 2	CAGCATTTGCATGGAACACAT	CCGGCCTGCCATGGCCATCTT
NM_030906	65975	STK33	serine/threonine kinase 33	ATGTGTCTAGTGCATCCTTAA	CAGGATGGTAATAGGTTAAGA
NM_030952	81788	SNARK	likely ortholog of rat SNF1/AMP-activated protein kinase	CCGGTGGCTGTTGATGGTGAA	CTGAACGAAGAGGATACTAAA
NM_031414	56164	STK31	serine/threonine kinase 31	CACAGTACAAGCTAAGTACAA	CCCAGTGTGGATCACTTGCTA
NM_031417	57787	MARK4	MAP/microtubule affinity-regulating kinase 4	CCGCATCATGAAGGGCCTAAA	CTGCAGCCTGTTGCCCAATAA
NM_031432	83549	UCK1	uridine-cytidine kinase 1	AACGGTGGAGGTGCCGACCTA	TGCGGTTTAAAGATCCCTCTA
NM_031464	83694	RPS6KL1	ribosomal protein S6 kinase-like 1	CGCGATGTTAGTGAGGACTAT	CTGAATTTGATTGGAAAGGAA
NM_031480	83732	RIOK1	RIO kinase 1 (yeast)	GCCCAACAAGATAATATTCTA	TACCATGTCCAGAACCAATAA
NM_031892	30011	SH3KBP1	SH3-domain kinase binding protein 1	CTCTGAGATCTCAATGCGAAA	TAGCTTATATATGACGGTATA
NM_032017	83931	MGC4796	Ser/Thr-like kinase	CAGCGCTACCTGCGGAAATAA	CCGGATGGTTAAGAAGATGAA
NM_032028	83942	STK22D	serine/threonine kinase 22D (spermiogenesis associated)	CCAGCTTTCCTTGGCCATCAA	TAGAAGCTGATTTAACACCAA
NM_032037	83963	SSTK	serine/threonine protein kinase SSTK	ATCGAGGTGTGCAACGGGAAA	CCGGTTGGAACCTGCAATAAA
NM_032294	84254	CAMKK1	calcium/calmodulin-dependent protein kinase kinase 1, alpha	AGCGATGAGCAAACTCTATAA	CGGCGTTATCTGGAAAGTGGA
NM_032387	65266	PRKWNK4	protein kinase, lysine deficient 4	CAGCTTGTTGGGCGTTTCCAA	CAGGAGGAGCCAGCACCATTA
NM_032409	65018	PINK1	PTEN induced putative kinase 1	CCGGACGCTGTTCCTCGTTAT	GACGCTGTTCCTCGTTATGAA
NM_032435	84451	KIAA1804	mixed lineage kinase 4	ACGGACCATGTCTGATGGAAA	CGGGAACTTAACATTCTGATA
NM_032630	51550	CINP	cyclin-dependent kinase 2-interacting protein	CGGCTGATTGGCACAATTTAA	GCGGCTGATTGGCACAATTTA
NM_033116	91754	NEK9	NIMA (never in mitosis gene a)- related kinase 9	CACGAACCAGTGAAGTCTATA	TACACTTGGGTGAACATGCAA
NM_033118	85366	MYLK2	myosin light chain kinase 2, skeletal muscle	AACGCTGTAACCGACGCCTTA	CGGGATCCTCTTCATGCACAA
NM_033126	85481	PSKH2	serine/threonine kinase PSKH2	AAGGACTTTATAGACAAACTA	GAGGATCAAGTTTACATGGTA
NM_033214	2712	GK2	glycerol kinase 2	CTCGGGTGTGCCATAATAATA	TACGTTAGAAGAGCACTGTAA
XM_370946	10595	LOC388226	similar to protein kinase/ribonuclease IRE1 beta	AAGGATGAAACTGGCTTCTAT	CACCTGCATTCTTTACACATA
NM_033498	3098	HK1	hexokinase 1	CACGATGTAGTCACCTTACTA	CCGTGTCGTATGACCTAGTAA
NM_033516	89882	NYD-SP25	protein kinase NYD-SP25	ATGGACCTAACTATACATCTT	TAGACGAAATGTGCCATTATA
NM_052841	81629	STK22C	serine/threonine kinase 22C (spermiogenesis associated)	ATGGCAAGTGCTCTCCAATAA	TGGCAAGTGCTCTCCAATAAA
NM_052853	90956	ADCK2	aarF domain containing kinase 2	CAGATTGACCTGCGTTACGAA	CCGGAATGTGAAAGCCGTCAA
NM_052902	114790	STK11IP	serine/threonine kinase 11 interacting protein	AAAGTTGTTTCCAACTCATAA	CTCTGCGTTTCTTGAACCTAA
NM_052947	115701	HAK	heart alpha-kinase	AGCGAAGACCTTGGCATTTAT	CGGCCTCATGCCTGTCTTCAA
NM_053006	23617	STK22B	serine/threonine kinase 22B (spermiogenesis associated)	CAAGTTCAATGTGGCTGTCAA	GTCGGCCTTCACGTAAACTAA
NM_054111	117283	IHPK3	inositol hexaphosphate kinase 3	AAGACTGGTGGACAAGTGTAA	CTGAGATACGTTACCCAATTA
NM_054113	117286	CIB3	calcium and integrin binding family member 3	CACGAGCAGCTGGAAGCGTAT	CTGGAGCAGACGGTGACCAAA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_080823	6725	SRMS	src-related kinase lacking C-terminal regulatory tyrosine and N-terminal myristylation sites	CAGACCAACCCTGGTACTTTA	CCGGGTCTCCATGGCAGCTGA
NM_080836	140901	STK35	serine/threonine kinase 35	CTCGGCTGTTAGGGATCTGAA	TTGGGTTGGTATGATACATTA
NM_133494	140609	NEK7	NIMA (never in mitosis gene a)-related kinase 7	ACGACCGGATATGGGCTATAA	CCGGATATGGGCTATAATACA
NM_138316	53354	PANK1	pantothenate kinase 1	AACGCTGGTTAAATTGGTGTA	CCGAAGGATATTACAGCCGAA
NM_138733	5232	PGK2	phosphoglycerate kinase 2	CAGCAACATGTAGTTAATATA	CAGGCCATCAGGAACTCTTAA
NM_139021	225689	ERK8	extracellular signal-regulated kinase 8	CCCACTGACTTCCTCCAATAA	CCCAGAGAACATTCCGGGAAA
NM_139158	65061	ALS2CR7	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 7	CTGGACATAAACTAAGTCTAA	CTGGCGTACATCCACCACCAA
NM_139209	131890	GRK7	G protein-coupled receptor kinase 7	ATCCATGACATCTGTGAATTA	TCGGCTGACATAATCCTCGAA
NM_145040	112464	PRKCDBP	protein kinase C, delta binding protein	AAGGAGCGAATCCTACATCCA	CACGCCCTAATAAGGAGCGAA
NM_145059	197258	FUK	fucokinase	CCGAAGGGAGTTGATTGGACA	TGGCTTAGAGTTGTAGACTTA
NM_145203	122011	MGC33182	casein kinase I alpha S-like	CAAGAATAATGTGAAAGATAA	CAGATTATCTTTAGAATTCCA
BC005365	5609	MAP2K7	mitogen-activated protein kinase kinase 7	ATGGATCTCTCTCAACAACTA	CCGGCGGAGGATCGACCTCAA
NM_145695	1607	DGKB	diacylglycerol kinase, beta 90kDa	CCCGAACTACTTCTCCTGCAA	CTCATTCTAGTCCAATGGTAA
NM_152309	118788	PIK3AP1	phosphoinositide-3-kinase adaptor protein 1	ATGCTCAAGAGTCACATTAAA	CAGCAGGGTATTTAAGTGCTA
NM_152327	122481	AK7	adenylate kinase 7	CAAGATTGTCTTGACCATTTA	GACGATCAATATATAATTAGA
NM_152671	200576	PIP5K3	na	ACCCAGTAACATAATATTTCA	TTGCCGTTACCCAGTAACATA
NM_152720	4752	NEK3	NIMA (never in mitosis gene a)-related kinase 3	ACGATAGAGGTGGTTCTGTAA	CAGAGATATCAAGTCCAAGAA
NM_152835	149420	LOC149420	casein kinase	AAGCTAGACTCTACCCTCTAA	CAGCCAAAGTACGATCTAATA
NM_152883	5754	PTK7	PTK7 protein tyrosine kinase 7	ACGGTTCGAGGTCTTCAAGAA	ATGGGACATGGTACCGTTGTA
NM_153273	9807	IHPK1	inositol hexaphosphate kinase 1	AAGGTGGATGTCCGCATGATT	CCGGCAGATGCGGAAATGCGA
NM_153835	92335	LYK5	protein kinase LYK5	CACCCAGATGCTGCTAGAGAA	CTGGTTCTAGTTCTGGTTCTA
NM_172173	818	CAMK2G	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	CCGATGAGAAACCTCGTGTTA	GAGGAAGAGATCTATACCCTA
NM_173176	2185	PTK2B	PTK2B protein tyrosine kinase 2 beta	AAGCTGATCGGCATCATTGAA	CAGGAGAACTTAAAGCCCAAA
NM_173354	150094	SNF1LK	SNF1-like kinase	AGCGAAATAAGCAATACGTTA	CACAATTGATTCCAACACAAA
NM_173500	146057	TTBK2	tau tubulin kinase 2	ACGGCCCAGGTTAAATGGAAA	CACATTGGTCATGACATGTTA
NM_173515	154043	MAGI1	membrane associated guanylate kinase interacting protein-like 1	CCGGAGTTGTGTTACTGCTTA	CGGAGTTGTGTTACTGCTTAA
NM_173575	282974	PKE	PKE protein kinase	CCGGGCTTCGTGCCCAACAAA	TCCGAGAATGACTATCTTCAA
NM_173598	283455	KSR2	kinase suppressor of Ras-2	ATCCGGTGACCTCGAATCCAA	TCCGTTGTGAGGGATGCCAAA
NM_174858	26289	AK5	adenylate kinase 5	CAGAGCTAGTCAGTACATGAA	CAGCATGGCAGTTGACAACAA
NM_174922	203054	ADCK5	aarF domain containing kinase 5	AAGGCCTTTGCTGAGCAGATA	CCGCTACTTCCTTATGGCTAA
NM_175866	127933	KIS	kinase interacting with leukemia-associated gene (stathmin)	AAGCAGTACTGTAGTACTGAA	CCACATATGAATGCAGGACTA
NM_176799	80895	ILKAP	integrin-linked kinase-associated serine/threonine phosphatase 2C	ATGGAGGAATTCGAGCCTCAA	TTCGGTGATCTTTGGTCTGAA
NM_176800	8899	PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	GAGCCGATCCTTAGAAAGAAA	TCGTCTGATGATAACCTTGAA
NM_177560	1457	CSNK2A1	casein kinase 2, alpha 1 polypeptide	ACCGTTGCTTGTGGATTTATA	CTGGTCGCTTACATCACTTTA
NM_177990	57144	PAK7	p21(CDKN1A)-activated kinase 7	ATGATCTGGATCCGTATTATA	ATGGTGTGCACGTTTCATTAA
NM_178009	160851	DGKH	diacylglycerol kinase, eta	CAGGTGGAGTATAATGACATA	CCGGATCTAGATTCCGTAGAT
NM_178170	284086	NEK8	NIMA (never in mitosis gene a)- related kinase 8	ACGGACAGTTGGGCACCAATA	CCAGAAGCTGGTGATCATCAA
NM_178432	23552	CCRK	cell cycle related kinase	AAGGAGAAGTGCAGAGAGTAA	TGGCGAGATAGTTGCCCTCAA
NM_178510	255239	ANKK1	ankyrin repeat and kinase domain containing 1	AGGAGCCGAGATGGAAATTTA	GCGGACGGAGTACGCCATCAA
NM_178813	158798	AKAP28	A-kinase anchoring protein 28	CCCATTGTCGTTTCTTATGTA	TACGAGGATGAATTGACTCAA
NM_181358	204851	HIPK1	homeodomain interacting protein kinase 1	AGGGAAGCTGTACACCACTAA	CTGAGCTATGTTTGTAATGCA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_181504	5295	PIK3R1	phosphoinositide-3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)	CAGCATTAAACCAGACCTTAT	TAGCTGGTTATGAACTAGTAA
NM_181690	10000	AKT3	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	AACTGTTGGCTTTGGATTAAA	CAGCAGGCACGTTAACTCGAA
NM_181795	5570	PKIB	protein kinase (cAMP-dependent, catalytic) inhibitor beta	CAGCATGTGTATATTAGATAA	CCGGAATGCCTTACCAGACAT
NM_181805	11142	PKIG	protein kinase (cAMP-dependent, catalytic) inhibitor gamma	CCACAAGATGTTATTTATTGA	GAGCTCCATGTCCCAGATAAA
NM_181839	5569	PKIA	protein kinase (cAMP-dependent, catalytic) inhibitor alpha	ATGATTATCATTAGAAGCTAA	TCACTTGATCATATGACGAAA
NM_181871	5313	PKLR	pyruvate kinase, liver and RBC	CGGGTGCAATTTGGCATTGAA	GAGGCCTATCTGAGACTATAA
NM_182398	9252	RPS6KA5	ribosomal protein S6 kinase, 90kDa, polypeptide 5	AAGCCAGTCATTCGAGATGAA	CTGGATCTCTTACGTAATTCA
NM_182471	5315	PKM2	pyruvate kinase, muscle	AACATCAAGATTATCAGCAAA	CCCGATCAGTGGAGACGTTGA
NM_182493	91807	LOC91807	myosin light chain kinase (MLCK)	ACGGAGGACAATGACCTTGCA	GACCATGAATTTCATTGTAAA
NM_182661	64781	CERK	ceramide kinase	ATGGCATTATTTGATCTGAAA	CGGCTTAAACTTTGATCTGTA
NM_182687	9088	PKMYT1	membrane-associated tyrosine- and threonine-specific cdc2-inhibitory kinase	CCGGCCAGAGTCCTTCTTCCA	CTGGGAGGAACTTACCGTCTA
NM_182692	6733	SRPK2	SFRS protein kinase 2	AACGGTGACTCTCATTCTTTA	CCGGTATCATGTTATTAGAAA
NM_182925	2324	FLT4	fms-related tyrosine kinase 4	CACCGTGTGGGCTGAGTTTAA	CACGCTCTTGGTCAACAGGAA
NM_182948	5567	PRKACB	protein kinase, cAMP-dependent, catalytic, beta	CAGCCTGTGTAGTGTGACAAA	CTGACCAATCAAGTACACTAA
NM_182982	2868	GRK4	G protein-coupled receptor kinase 4	CAGGATGTTACTCACCAAGAA	CCGGGTGTTTCAAAGACATCA
NM_183048	23613	PRKCBP1	protein kinase C binding protein 1	AGCGAACTTGTCATAGATTTA	CACCATTGAACAGTTATCCTA
NM_197972	29922	NME7	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase)	CCCGGCATTTACGCCCTGGAA	TTCATGTAGATCACCAGTCAA
NM_198452	139728	MGC45419	Similar to calcium/calmodulin-dependent protein kinase 1, beta	CTCGAAGATCATGGTCTCTGA	TCCGTGTGTCACAGCCCGAAA
NM_198828	375449	LOC375449	similar to microtubule associated testis specific serine/threonine protein kinase	ATGAATTGCCACCACATTAAA	GAGGAGCTTGACCACATATTA
XM_027237	4293	MAP3K9	mitogen-activated protein kinase kinase kinase 9	AGCGATGAAATTGTCGTGTAT	CAGCGATGAAATTGTCGTGTA
XM_031706	23005	MAPKBP1	likely ortholog of mouse mitogen activated protein kinase binding proten 1	CAGGACCGAAATATTCGGATA	CCCGTTTGTACTGATGTATGA
NM_001556	3551	IKBKB	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta	CAGACCGACATTGTGGACTTA	CAGGACACTGTGAGGGAACAA
XM_039796	23043	TNIK	TRAF2 and NCK interacting kinase	AAGGACCATATTGATAGAACA	CTGGAATATAAGCGCAAACAA
XM_042066	4214	MAP3K1	mitogen-activated protein kinase kinase kinase 1	CACGCATGTCAAATTCTCATA	CTCCGGGTGTTTCAACTAGAA
XM_051221	80309	SKIP	SPHK1 (sphingosine kinase type 1) interacting protein	CTGAAATTCTGGACACCTTAA	GGCAAGTATGCTACAAATTTA
XM_166453	84630	TTBK1	tau tubulin kinase 1	CAGGAACGAGAAGTTTAACTA	TGGCAGGAACGAGAAGTTTAA
XM_290516	55561	HSMDPKIN	myotonic dystrophy protein kinase like protein	CGCCGGTGGCTTTGCACTCTA	CTCGCCGCCTACCAACTTCAA
XM_290793	8844	KSR	kinase suppressor of ras	AAGGGCGAAGCTGGTCCGTTA	CTGGAAGTCAGCTGACATTAA
NM_012224	4750	NEK1	NIMA (never in mitosis gene a)-related kinase 1	ACCGTAGGAGATGTTCGTCAA	TAGGGATAGACCATCAGTCAA

Table3

Pool No.	Accession #	LocusLink	Symbol	Gene Name
1	NM_005734	10114	HIPK3	homeodomain interacting protein kinase 3
	NM_181358	204851	HIPK1	homeodomain interacting protein kinase 1
2	NM_000269	4830	NME1	non-metastatic cells 1, protein (NM23A) expressed in
	NM_002512	4831	NME2	non-metastatic cells 2, protein (NM23B) expressed in
	NM_002513	4832	NME3	non-metastatic cells 3, protein expressed in
	NM_003551	8382	NME5	non-metastatic cells 5, protein expressed in (nucleoside-diphosphate kinase)
	NM_005009	4833	NME4	non-metastatic cells 4, protein expressed in
	NM_005793	10201	NME6	non-metastatic cells 6, protein expressed in (nucleoside-diphosphate kinase)
	NM_197972	29922	NME7	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase)
3	NM_000291	5230	PGK1	phosphoglycerate kinase 1
	NM_138733	5232	PGK2	phosphoglycerate kinase 2
4	NM_182471	5315	PKM2	pyruvate kinase, muscle
	NM_181871	5313	PKLR	pyruvate kinase, liver and RBC
5	NM_018323	55300	PI4K2B	phosphatidylinositol 4-kinase type-II beta
	NM_018425	55361	PI4KII	phosphatidylinositol 4-kinase type II
6	NM_000289	5213	PFKM	phosphofructokinase, muscle
	NM_002626	5211	PFKL	phosphofructokinase, liver
	NM_002627	5214	PFKP	phosphofructokinase, platelet
7	NM_002733	5571	PRKAG1	protein kinase, AMP-activated, gamma 1 non-catalytic subunit
	NM_016203	51422	PRKAG2	protein kinase, AMP-activated, gamma 2 non-catalytic subunit
	NM_017431	53632	PRKAG3	protein kinase, AMP-activated, gamma 3 non-catalytic subunit
8	NM_025144	80216	LAK	lymphocyte alpha-kinase
	NM_052947	115701	HAK	heart alpha-kinase
9	NM_000189	3099	HK2	hexokinase 2
	NM_002115	3101	HK3	hexokinase 3 (white cell)
	NM_033498	3098	HK1	hexokinase 1
10	NM_002742	5587	PRKCM	protein kinase C, mu

Table3 (continued)

	NM_005813	23683	PRKCN	protein kinase C, nu
	NM_016457	25865	PRKD2	protein kinase D2
11	NM_002648	5292	PIM1	pim-1 oncogene
	NM_006875	11040	PIM2	pim-2 oncogene
12	NM_003936	8941	CDK5R2	cyclin-dependent kinase 5, regulatory subunit 2 (p39)
	NM_003885	8851	CDK5R1	cyclin-dependent kinase 5, regulatory subunit 1 (p35)
13	NM_013410	205	AK3	adenylate kinase 3
	NM_016282	50808	AK3L1	adenylate kinase 3 like 1
14	NM_000476	203	AK1	adenylate kinase 1
	NM_174858	26289	AK5	adenylate kinase 5
15	NM_004721	9175	MAP3K13	mitogen-activated protein kinase kinase kinase 13
	NM_006301	7786	MAP3K12	mitogen-activated protein kinase kinase kinase 12
16	NM_173598	283455	KSR2	kinase suppressor of Ras-2
	XM_290793	8844	KSR	kinase suppressor of ras
17	NM_002314	3984	LIMK1	LIM domain kinase 1
	NM_005569	3985	LIMK2	LIM domain kinase 2
18	NM_000142	2261	FGFR3	fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)
	NM_015850	2260	FGFR1	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndron
19	NM_004438	2043	EPHA4	EphA4
	NM_005233	2042	EPHA3	EphA3
	NM_020526	2046	EPHA8	EphA8
20	NM_004441	2047	EPHB1	EphB1
	NM_004443	2049	EPHB3	EphB3
	NM_017449	2048	EPHB2	EphB2
21	NM_002645	5286	PIK3C2A	phosphoinositide-3-kinase, class 2, alpha polypeptide
	NM_002646	5287	PIK3C2B	phosphoinositide-3-kinase, class 2, beta polypeptide
	NM_004570	5288	PIK3C2G	phosphoinositide-3-kinase, class 2, gamma polypeptide
22	NM_005026	5293	PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide
	NM_006219	5291	PIK3CB	phosphoinositide-3-kinase, catalytic, beta polypeptide
	NM_006218	5290	PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide

Table3 (continued)

23	NM_003629	8503	PIK3R3	phosphoinositide-3-kinase, regulatory subunit, polypeptide 3 (p55, gamma)
	NM_005027	5296	PIK3R2	phosphoinositide-3-kinase, regulatory subunit, polypeptide 2 (p85 beta)
	NM_181504	5295	PIK3R1	phosphoinositide-3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)
24	NM_000167	2710	GK	glycerol kinase
	NM_033214	2712	GK2	glycerol kinase 2
25	NM_012474	7371	UMPK	uridine monophosphate kinase
	NM_017859	54963	URKL1	uridine kinase-like 1
	NM_031432	83549	UCK1	uridine-cytidine kinase 1
26	NM_005399	5565	PRKAB2	protein kinase, AMP-activated, beta 2 non-catalytic subunit
	NM_006253	5564	PRKAB1	protein kinase, AMP-activated, beta 1 non-catalytic subunit
27	NM_020421	57143	ADCK1	aarF domain containing kinase 1
	NM_024876	79934	ADCK4	aarF domain containing kinase 4
	NM_052853	90956	ADCK2	aarF domain containing kinase 2
	NM_174922	203054	ADCK5	aarF domain containing kinase 5
28	NM_000292	5256	PHKA2	phosphorylase kinase, alpha 2 (liver)
	NM_002637	5255	PHKA1	phosphorylase kinase, alpha 1 (muscle)
29	NM_007229	11252	PACSIN2	protein kinase C and casein kinase substrate in neurons 2
	NM_016223	29763	PACSIN3	protein kinase C and casein kinase substrate in neurons 3
	NM_020804	29993	PACSIN1	protein kinase C and casein kinase substrate in neurons 1
30	NM_080836	140901	STK35	serine/threonine kinase 35
	NM_152835	149420	LOC149420	casein kinase
31	NM_001184	545	ATR	ataxia telangiectasia and Rad3 related
	NM_006904	5591	PRKDC	protein kinase, DNA-activated, catalytic polypeptide
32	NM_003648	8527	DGKD	diacylglycerol kinase, delta 130kDa
	NM_178009	160851	DGKH	diacylglycerol kinase, eta
33	NM_001345	1606	DGKA	diacylglycerol kinase, alpha 80kDa
	NM_001346	1608	DGKG	diacylglycerol kinase, gamma 90kDa
	NM_145695	1607	DGKB	diacylglycerol kinase, beta 90kDa
34	NM_001258	1018	CDK3	cyclin-dependent kinase 3
	NM_001786	983	CDC2	cell division cycle 2, G1 to S and G2 to M

Table3 (continued)

35	NM_003583	8445	DYRK2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2
	NM_003582	8444	DYRK3	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3
	NM_003845	8798	DYRK4	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4
36	NM_001396	1859	DYRK1A	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A
	NM_004714	9149	DYRK1B	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1B
37	NM_003137	6732	SRPK1	SFRS protein kinase 1
	NM_014370	26576	STK23	serine/threonine kinase 23
	NM_182692	6733	SRPK2	SFRS protein kinase 2
38	NM_004071	1195	CLK1	CDC-like kinase 1
	NM_020666	57396	CLK4	CDC-like kinase 4
39	NM_005906	4117	MAK	male germ cell-associated kinase
	NM_014920	22858	ICK	intestinal cell (MAK-like) kinase
40	NM_002093	2932	GSK3B	glycogen synthase kinase 3 beta
	NM_019884	2931	GSK3A	glycogen synthase kinase 3 alpha
41	NM_001315	1432	MAPK14	mitogen-activated protein kinase 14
	NM_002751	5600	MAPK11	mitogen-activated protein kinase 11
	NM_002969	6300	MAPK12	mitogen-activated protein kinase 12
	NM_002754	5603	MAPK13	mitogen-activated protein kinase 13
42	NM_002752	5601	MAPK9	mitogen-activated protein kinase 9
	NM_002753	5602	MAPK10	mitogen-activated protein kinase 10
	NM_002750	5599	MAPK8	mitogen-activated protein kinase 8
43	NM_002745	5594	MAPK1	mitogen-activated protein kinase 1
	NM_002746	5595	MAPK3	mitogen-activated protein kinase 3
44	NM_003718	8621	CDC2L5	cell division cycle 2-like 5 (cholinesterase-related cell division controller)
	NM_016507	51755	CRK7	CDC2-related protein kinase 7
45	NM_000075	1019	CDK4	cyclin-dependent kinase 4
	NM_001259	1021	CDK6	cyclin-dependent kinase 6
46	NM_001260	1024	CDK8	cyclin-dependent kinase 8
	NM_015076	23097	CDK11	cyclin-dependent kinase (CDC2-like) 11
47	NM_001787	984	CDC2L1	cell division cycle 2-like 1 (PITSLRE proteins)

Table3 (continued)

	NM_003674	8558	CDK10	cyclin-dependent kinase (CDC2-like) 10
48	NM_001825	1160	CKMT2	creatine kinase, mitochondrial 2 (sarcomeric)
	NM_001823	1152	CKB	creatine kinase, brain
	NM_001824	1158	CKM	creatine kinase, muscle
	NM_020990	1159	CKMT1	creatine kinase, mitochondrial 1 (ubiquitous)
49	NM_002736	5577	PRKAR2B	protein kinase, cAMP-dependent, regulatory, type II, beta
	NM_004157	5576	PRKAR2A	protein kinase, cAMP-dependent, regulatory, type II, alpha
50	NM_003384	7443	VRK1	vaccinia related kinase 1
	NM_006296	7444	VRK2	vaccinia related kinase 2
	NM_016440	51231	VRK3	vaccinia related kinase 3
51	NM_001319	1455	CSNK1G2	casein kinase 1, gamma 2
	NM_001893	1453	CSNK1D	casein kinase 1, delta
	NM_001894	1454	CSNK1E	casein kinase 1, epsilon
	NM_001892	1452	CSNK1A1	casein kinase 1, alpha 1
	NM_004384	1456	CSNK1G3	casein kinase 1, gamma 3
	NM_022048	53944	CSNK1G1	casein kinase 1, gamma 1
	NM_145203	122011	MGC33182	casein kinase I alpha S-like
52	NM_002610	5163	PDK1	pyruvate dehydrogenase kinase, isoenzyme 1
	NM_002611	5164	PDK2	pyruvate dehydrogenase kinase, isoenzyme 2
	NM_002612	5166	PDK4	pyruvate dehydrogenase kinase, isoenzyme 4
	NM_005391	5165	PDK3	pyruvate dehydrogenase kinase, isoenzyme 3
53	NM_024594	79646	PANK3	pantothenate kinase 3
	NM_024960	80025	PANK2	pantothenate kinase 2 (Hallervorden-Spatz syndrome)
	NM_138316	53354	PANK1	pantothenate kinase 1
54	NM_016291	51447	IHPK2	inositol hexaphosphate kinase 2
	NM_054111	117283	IHPK3	inositol hexaphosphate kinase 3
	NM_153273	9807	IHPK1	inositol hexaphosphate kinase 1
55	NM_002220	3706	ITPKA	inositol 1,4,5-trisphosphate 3-kinase A
	NM_025194	80271	ITPKC	inositol 1,4,5-trisphosphate 3-kinase C
56	NM_018979	65125	PRKWNK1	protein kinase, lysine deficient 1

Table3 (continued)

	NM_020922	65267	PRKWNK3	protein kinase, lysine deficient 3
	NM_032387	65266	PRKWNK4	protein kinase, lysine deficient 4
57	NM_001433	2081	ERN1	ER to nucleus signalling 1
	XM_370946	10595	LOC388226	similar to protein kinase/ribonuclease IRE1 beta
58	NM_001262	1031	CDKN2C	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)
	NM_001800	1032	CDKN2D	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)
	NM_004936	1030	CDKN2B	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)
59	NM_020639	54101	ANKRD3	ankyrin repeat domain 3
	NM_178510	255239	ANKK1	ankyrin repeat and kinase domain containing 1
60	NM_001348	1613	DAPK3	death-associated protein kinase 3
	NM_004938	1612	DAPK1	death-associated protein kinase 1
	NM_014326	23604	DAPK2	death-associated protein kinase 2
61	NM_012290	9874	TLK1	tousled-like kinase 1
	NM_006852	11011	TLK2	tousled-like kinase 2
62	NM_004073	1263	PLK3	polo-like kinase 3 (Drosophila)
	NM_005030	5347	PLK1	polo-like kinase 1 (Drosophila)
	NM_006622	10769	PLK2	polo-like kinase 2 (Drosophila)
63	NM_000294	5261	PHKG2	phosphorylase kinase, gamma 2 (testis)
	NM_006213	5260	PHKG1	phosphorylase kinase, gamma 1 (muscle)
64	NM_004226	9262	STK17B	serine/threonine kinase 17b (apoptosis-inducing)
	NM_004760	9263	STK17A	serine/threonine kinase 17a (apoptosis-inducing)
65	NM_033118	85366	MYLK2	myosin light chain kinase 2, skeletal muscle
	NM_182493	91807	LOC91807	myosin light chain kinase (MLCK)
66	NM_003684	8569	MKNK1	MAP kinase-interacting serine/threonine kinase 1
	NM_017572	2872	MKNK2	MAP kinase-interacting serine/threonine kinase 2
67	NM_003668	8550	MAPKAPK5	mitogen-activated protein kinase-activated protein kinase 5
	NM_004635	7867	MAPKAPK3	mitogen-activated protein kinase-activated protein kinase 3
	NM_004759	9261	MAPKAPK2	mitogen-activated protein kinase-activated protein kinase 2
68	NM_001220	816	CAMK2B	calcium/calmodulin-dependent protein kinase (CaM kinase) II beta
	NM_001221	817	CAMK2D	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta

Table3 (continued)

	NM_015981	815	CAMK2A	calcium/calmodulin-dependent protein kinase (CaM kinase) II alpha
	NM_172173	818	CAMK2G	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma
69	NM_006742	5681	PSKH1	protein serine kinase H1
	NM_033126	85481	PSKH2	serine/threonine kinase PSKH2
70	NM_003656	8536	CAMK1	calcium/calmodulin-dependent protein kinase I
	NM_020397	57118	CAMK1D	calcium/calmodulin-dependent protein kinase ID
	NM_020439	57172	CAMK1G	calcium/calmodulin-dependent protein kinase IG
	NM_198452	139728	MGC45419	Similar to calcium/calmodulin-dependent protein kinase 1, beta
71	NM_003565	8408	ULK1	unc-51-like kinase 1 (C. elegans)
	NM_014683	9706	ULK2	unc-51-like kinase 2 (C. elegans)
72	NM_006549	10645	CAMKK2	calcium/calmodulin-dependent protein kinase kinase 2, beta
	NM_032294	84254	CAMKK1	calcium/calmodulin-dependent protein kinase kinase 1, alpha
73	NM_032037	83983	SSTK	serine/threonine protein kinase SSTK
	NM_052841	81629	STK22C	serine/threonine kinase 22C (spermiogenesis associated)
	NM_032028	83942	STK22D	serine/threonine kinase 22D (spermiogenesis associated)
	NM_053006	23617	STK22B	serine/threonine kinase 22B (spermiogenesis associated)
74	NM_003160	6795	AURKC	aurora kinase C
	NM_003600	6790	STK6	serine/threonine kinase 6
	NM_004217	9212	AURKB	aurora kinase B
75	XM_374996	9891	ARK5	AMP-activated protein kinase family member 5
	NM_030952	81788	SNARK	likely ortholog of rat SNF1/AMP-activated protein kinase
76	NM_004954	2011	MARK2	MAP/microtubule affinity-regulating kinase 2
	NM_018650	4139	MARK1	MAP/microtubule affinity-regulating kinase 1
	NM_031417	57787	MARK4	MAP/microtubule affinity-regulating kinase 4
77	NM_006251	5562	PRKAA1	protein kinase, AMP-activated, alpha 1 catalytic subunit
	NM_006252	5563	PRKAA2	protein kinase, AMP-activated, alpha 2 catalytic subunit
78	NM_018401	55351	HSA250839	gene for serine/threonine protein kinase
	NM_173575	282974	PKE	PKE protein kinase
79	NM_004690	9113	LATS1	LATS, large tumor suppressor, homolog 1 (Drosophila)
	NM_014572	26524	LATS2	LATS, large tumor suppressor, homolog 2 (Drosophila)

Table3 (continued)

80	NM_007271	11329	STK38	serine/threonine kinase 38
	NM_015000	23012	STK38L	serine/threonine kinase 38 like
81	NM_006258	5592	PRKG1	protein kinase, cGMP-dependent, type I
	NM_006259	5593	PRKG2	protein kinase, cGMP-dependent, type II
82	AB023190	22983	SAST	syntrophin associated serine/threonine kinase
	NM_015112	23139	MAST2	microtubule associated serine/threonine kinase 2
83	NM_001619	156	ADRBK1	adrenergic, beta, receptor kinase 1
	NM_005160	157	ADRBK2	adrenergic, beta, receptor kinase 2
84	NM_002741	5585	PRKCL1	protein kinase C-like 1
	NM_006256	5586	PRKCL2	protein kinase C-like 2
	NM_013355	29941	pknbeta	protein kinase PKNbeta
85	NM_002744	5590	PRKCZ	protein kinase C, zeta
	NM_002740	5584	PRKCI	protein kinase C, iota
86	NM_002737	5578	PRKCA	protein kinase C, alpha
	NM_002738	5579	PRKCB1	protein kinase C, beta 1
	NM_002739	5582	PRKCG	protein kinase C, gamma
	NM_005400	5581	PRKCE	protein kinase C, epsilon
	NM_006254	5580	PRKCD	protein kinase C, delta
	NM_006255	5583	PRKCH	protein kinase C, eta
	NM_006257	5588	PRKCQ	protein kinase C, theta
87	NM_002730	5566	PRKACA	protein kinase, cAMP-dependent, catalytic, alpha
	NM_002732	5568	PRKACG	protein kinase, cAMP-dependent, catalytic, gamma
	NM_002760	5616	PRKY	protein kinase, Y-linked
	NM_005044	5613	PRKX	protein kinase, X-linked
	NM_182948	5567	PRKACB	protein kinase, cAMP-dependent, catalytic, beta
88	NM_002953	6195	RPS6KA1	ribosomal protein S6 kinase, 90kDa, polypeptide 1
	NM_004586	6197	RPS6KA3	ribosomal protein S6 kinase, 90kDa, polypeptide 3
	NM_014496	27330	RPS6KA6	ribosomal protein S6 kinase, 90kDa, polypeptide 6
	NM_021135	6196	RPS6KA2	ribosomal protein S6 kinase, 90kDa, polypeptide 2
89	NM_001626	208	AKT2	v-akt murine thymoma viral oncogene homolog 2

Table3 (continued)

	NM_005163	207	AKT1	v-akt murine thymoma viral oncogene homolog 1
	NM_181690	10000	AKT3	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)
90	NM_005627	6446	SGK	serum/glucocorticoid regulated kinase
	NM_013257	23678	SGKL	serum/glucocorticoid regulated kinase-like
	NM_016276	10110	SGK2	serum/glucocorticoid regulated kinase 2
91	NM_003161	6198	RPS6KB1	ribosomal protein S6 kinase, 70kDa, polypeptide 1
	NM_003952	6199	RPS6KB2	ribosomal protein S6 kinase, 70kDa, polypeptide 2
92	NM_002082	2870	GRK6	G protein-coupled receptor kinase 6
	NM_005308	2869	GRK5	G protein-coupled receptor kinase 5
	NM_182982	2868	GRK4	G protein-coupled receptor kinase 4
93	NM_003942	8986	RPS6KA4	ribosomal protein S6 kinase, 90kDa, polypeptide 4
	NM_182398	9252	RPS6KA5	ribosomal protein S6 kinase, 90kDa, polypeptide 5
94	NM_002497	4751	NEK2	NIMA (never in mitosis gene a)-related kinase 2
	NM_003157	6787	NEK4	NIMA (never in mitosis gene a)-related kinase 4
	NM_014397	10783	NEK6	NIMA (never in mitosis gene a)-related kinase 6
	NM_024800	79858	NEK11	NIMA (never in mitosis gene a)- related kinase 11
	NM_033116	91754	NEK9	NIMA (never in mitosis gene a)- related kinase 9
	NM_133494	140609	NEK7	NIMA (never in mitosis gene a)-related kinase 7
	NM_152720	4752	NEK3	NIMA (never in mitosis gene a)-related kinase 3
	NM_178170	284086	NEK8	NIMA (never in mitosis gene a)- related kinase 8
	NM_012224	4750	NEK1	NIMA (never in mitosis gene a)-related kinase 1
95	NM_004783	9344	TAO1	thousand and one amino acid protein kinase
	NM_016151	9344	TAO1	thousand and one amino acid protein kinase
	NM_016281	51347	JIK	STE20-like kinase
96	NM_002756	5606	MAP2K3	mitogen-activated protein kinase kinase 3
	NM_002758	5608	MAP2K6	mitogen-activated protein kinase kinase 6
97	NM_002401	4215	MAP3K3	mitogen-activated protein kinase kinase kinase 3
	NM_006609	10746	MAP3K2	mitogen-activated protein kinase kinase kinase 2
98	NM_005109	9943	OSR1	oxidative-stress responsive 1
	NM_013233	27347	STK39	serine threonine kinase 39 (STE20/SPS1 homolog, yeast)

Table3 (continued)

99	NM_003618	8491	MAP4K3	mitogen-activated protein kinase kinase kinase kinase 3
	NM_006575	11183	MAP4K5	mitogen-activated protein kinase kinase kinase kinase 5
100	NM_004834	9448	MAP4K4	mitogen-activated protein kinase kinase kinase kinase 4
	NM_015716	50488	MINK	misshapen/NIK-related kinase
101	NM_002576	5058	PAK1	p21/Cdc42/Rac1-activated kinase 1 (STE20 homolog, yeast)
	NM_002577	5062	PAK2	p21 (CDKN1A)-activated kinase 2
	NM_002578	5063	PAK3	p21 (CDKN1A)-activated kinase 3
	NM_005884	10298	PAK4	p21(CDKN1A)-activated kinase 4
	NM_020168	56924	PAK6	p21(CDKN1A)-activated kinase 6
	NM_177990	57144	PAK7	p21(CDKN1A)-activated kinase 7
102	NM_006281	6788	STK3	serine/threonine kinase 3 (STE20 homolog, yeast)
	NM_006282	6789	STK4	serine/threonine kinase 4
103	NM_006374	10494	STK25	serine/threonine kinase 25 (STE20 homolog, yeast)
	NM_016542	51765	MST4	Mst3 and SOK1-related kinase
104	NM_003607	8476	CDC42BPA	CDC42 binding protein kinase alpha (DMPK-like)
	NM_006035	9578	CDC42BPB	CDC42 binding protein kinase beta (DMPK-like)
105	NM_004850	9475	ROCK2	Rho-associated, coiled-coil containing protein kinase 2
	NM_005406	6093	ROCK1	Rho-associated, coiled-coil containing protein kinase 1
106	NM_001743	805	CALM2	calmodulin 2 (phosphorylase kinase, delta)
	NM_005184	808	CALM3	calmodulin 3 (phosphorylase kinase, delta)
	NM_006888	801	CALM1	calmodulin 1 (phosphorylase kinase, delta)
107	NM_006383	10518	KIP2	DNA-dependent protein kinase catalytic subunit-interacting protein 2
	NM_054113	117286	CIB3	calcium and integrin binding family member 3
108	NM_003559	8396	PIP5K2B	phosphatidylinositol-4-phosphate 5-kinase, type II, beta
	NM_005028	5305	PIP5K2A	phosphatidylinositol-4-phosphate 5-kinase, type II, alpha
	NM_024779	79837	PIP5K2C	phosphatidylinositol-4-phosphate 5-kinase, type II, gamma
109	NM_003557	8394	PIP5K1A	phosphatidylinositol-4-phosphate 5-kinase, type I, alpha
	NM_003558	8395	PIP5K1B	phosphatidylinositol-4-phosphate 5-kinase, type I, beta
	NM_012398	23396	PIP5K1C	phosphatidylinositol-4-phosphate 5-kinase, type I, gamma
110	NM_001616	92	ACVR2	activin A receptor, type II

Table3 (continued)

	NM_001106	93	ACVR2B	activin A receptor, type IIB
111	NM_000020	94	ACVRL1	activin A receptor type II-like 1
	NM_001105	90	ACVR1	activin A receptor, type I
	NM_001203	658	BMPR1B	bone morphogenetic protein receptor, type IB
	NM_004329	657	BMPR1A	bone morphogenetic protein receptor, type IA
	NM_004302	91	ACVR1B	activin A receptor, type IB
	NM_004612	7046	TGFBR1	transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 5
112	NM_002005	2242	FES	feline sarcoma oncogene
	NM_005246	2241	FER	fer (fps/fes related) tyrosine kinase (phosphoprotein NCP94)
113	NM_000061	695	BTK	Bruton agammaglobulinemia tyrosine kinase
	NM_001721	660	BMX	BMX non-receptor tyrosine kinase
	NM_003215	7006	TEC	tec protein tyrosine kinase
	NM_003328	7294	TXK	TXK tyrosine kinase
114	NM_005157	25	ABL1	v-abl Abelson murine leukemia viral oncogene homolog 1
	NM_005158	27	ABL2	v-abl Abelson murine leukemia viral oncogene homolog 2 (arg, Abelson-related g
115	NM_001715	640	BLK	B lymphoid tyrosine kinase
	NM_002110	3055	HCK	hemopoietic cell kinase
	NM_002350	4067	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog
	NM_002037	2534	FYN	FYN oncogene related to SRC, FGR, YES
	NM_005356	3932	LCK	lymphocyte-specific protein tyrosine kinase
	NM_005433	7525	YES1	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1
	NM_005248	2268	FGR	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog
	NM_005417	6714	SRC	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)
116	NM_002344	4058	LTK	leukocyte tyrosine kinase
	NM_004304	238	ALK	anaplastic lymphoma kinase (Ki-1)

Table 4

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
2	A2M	NM_000014	CTCAAAGATTCGTAAACCCAA	CACCAACTCAAAGATTCGTAA	CACGGAGACCGTACGAAAGTA	ACGGATGAGCATGGCCTTGTA
12	SERPINA3	NM_001085	AAGGTTCTACTTGAGCAAGAA	AAGGCTGTGCTTGATGTATTT	CCCAAGATACTCATCAGTCAA	AAGGACCATTGTGCGTTTCAA
14	AAMP	NM_001087	CAGGGAAGCCCTATCCATGTA	GAGGAAGAGATACTAGTTAAA		
20	ABCA2	NM_001606	CCGCAGAGAGATGGACAAGAT	CTGGGTCAGTCCCGTATTTAT	CAGCATGCCCACCTACCTCAA	CTGGAAGAACGTGACGCTCAA
21	ABCA3	NM_001089	CACGGAGAAATTACATGTGGA	CCAAGTTTATCTCATCCTTTA	TACGTTGTGACCATCCAGAAA	CCGCTTGAAGATTCAGTCGGA
25	ABL1	NM_005157	CTGGGCGAATGTCTTATTTAA	CCAGTGGAGATAACACTCTAA	ACGCACGGACATCACCATGAA	AACACTCTAAGCATAACTAAA
29	ABR	NM_001092	CACGGACGTGATTGAGATGAA	CAGCGAAGAGATCTACATTAA		
30	ACAA1	NM_001607	CACGCTGCTCAATGAGCTGAA	AAGGCCATGGTTAATTCTTAA		
31	ACACA	NM_000664	TCCGTAGGTGGTCTTATGAAA	TCGCATCACAATTGGCAATAA	AACGCAGGCATCAGAAGATTA	CTGGATAATCTGGTCAATGTA
34	ACADM	NM_000016	AAGGAGATGAGTATATTATTA	AAGGTACTTCACAAATTCAAA	CTGGCTGAAATGGCAATGAAA	CAACTTGACAGTAACTTTGTA
38	ACAT1	NM_000019	CGGGCTAACTGATGTCTACAA	CCAGATGTAGTGGTGAAAGAA	AAGCTGAATATTGCACGAAAT	TAGTCTGGTTGTACTAGCAAA
54	ACP5	NM_001611	CACTGGTGTGCAAGACATCAA	ACGGCGCTGCTCATCCTGCAA	CTGGTACGTGCTAGCCGGAAA	CTCGGGCAAGTCCCTCTTTAA
55	ACPP	NM_001099	ATGAACAGGTTTATATTCGAA	CTCTATTACCATTATGGATAA	CCGGACTTTGATGAGTGCTAT	ACAGATGGCGCTAGATGTTTA
56	ACRV1	NM_001612	TCCATAGATCATCAAACTTCA	ATGGAACGAGGATGCAAATTA	CCAGCAGTGCATGTTAAAGAA	CAGGCACAATATTAAATTGCT
72	ACTG2	NM_001615	CCGCTGGAATTCATGAGACAA	CAGGAAGTGCTTCTAAAGTCA		
94	ACVRL1	NM_000020	CCGGGAGACTGAGATCTATAA	CACGGACTGCTTTGAGTCCTA	CAGGAAGACGCTGGAATAAGA	CACCGAGTTCGTCAACCACTA
101	ADAM8	NM_001109	CCGGCTACACAGAGACCTATA	AGGCATCATCGTCTACCGCAA	CAAGCTATATCAGAAACTCAA	CCCAGCTTTGTGTGTGTTTAA
102	ADAM10	NM_001110	ATGGTGTTGCTGAGAGTGTTA	ACCAAACTTCACAGACTGTAA	ATGGTAAGAAGAAGTCCTTAA	ATGGGACACATGAGACGCTAA
112	ADCY6	NM_015270	AAGTGCTTAGGTAATGAGCTA	CAGCCTGAGTCTAGCATGTTT	CAGCCCGGATGCTGAATTTAA	ACCATGTATTTCAGTGAAATA
123	ADFP	NM_001122	AAGAATGTGTATAGTGCCAAT	TCCGTTGCAGTTGATCCACAA	CTGGTTCAGAAGCCAAGTTAT	CTGCAGGATAGACCAGTTAAA
125	ADH1B	NM_000668	AACCAATCCATTACAGCTTAA	AAGCCTCAATTACTAATTGTA	AAGGAGGTAGCTGTCTCCAAA	AAGACCTTAGACATAAAGTAA
126	ADH1C	NM_000669	ATGCATTAATAACAAATATTT	GGGAAATTATTTGTCAAGCAA	CTGCTCTTCAGAGATGTTAAA	ACTGGATGCATTAATAACAAA
131	ADH7	NM_000673	CACCAGTACATTTACCGAGTA	CAGATATAGCGTATAAAGATA	CTGGGAATTAGTATAATAACA	AACGATTAAGAATCATCATTA
132	ADK	NM_001123	TCCACTGATGGAAGAGCTGAA	AAGTTGTACCACAATATTCAA	TAGTTTGATAGTGCCACTTAA	AAGGGTATGGTAATGCTTGTA
133	ADM	NM_001124	AGAGGTAACTATCAATATTTA	ACCGAGTCTCTGTATAATCTA	GAGGTAACTATCAATATTTAA	CTGTATAATCTATTTACATAA
135	ADORA2A	NM_000675	CCACACCAATTCGGTTGTGAA	AAGGGCTTGGGTTCTGAGGAA	CAGGAGTGTCCTGATGATTCA	CAGCATGAGGCCCAGCAAGAA
140	ADORA3	NM_000677	CAACTGCATCATCTACTTTAA	CCCTATCGTCTATGCCTATAA	TCGGAACAAACTCAGTCTGAA	AAGCGTCAACTCGTGCAAGAA
141	ADPRH	NM_001125	CTGGTCTACCTCCTAAATATA	CAGAGTTATGTTTACGAATAA		
142	PARP1	NM_001618	CTTGAAATATGTAGTATTAAA	CCCGGTGGCTGTGGTATGAAT	CCGAGAAATCTCTTACCTCAA	ACGGTGATCGGTAGCAACAAA
147	ADRA1B	NM_000679	GGCGGTCATTCTAGTCATGTA	CAGGAGTTCCATAGCTGTCAA	GAGGGCGGACTCTAAGATGAA	CCGTGTCTATATAGTGGCCAA
150	ADRA2A	NM_000681	CCCGCTGTAAATATACACTAT	GTGGATCAAGACATAAGTAAA	CTCCCGCCGCTTAGAAATAAA	CAAGGCTTGGTGCGAGATCTA
156	ADRBK1	NM_001619	CAGGCCCTTGGTGGAATTCTA	CGGCTGGAGGCTCGCAAGAAA	CGGCTGGAGGCTCGCAAGAAA	CCGGGAGATCTTCGACTCATA
157	ADRBK2	NM_005160	AAGCTACTTGATTGCGACCAA	TGGGATTAACTAATCATTGAA	CAAGTGTATGGGATTAACTAA	AAGATGTTCAGTGTTGGGTAA
166	AES	NM_198970	TAGCTGTGCCTTTCCAATAAA	CGGCTTGAACATCGAGATGCA	CTGACATGTGAGGCAAGCTAA	CAGGCCCACCTCTCCAAGGAA
177	AGER	NM_172197	TAGCTCCTGGTGGAACCGTAA	CACGGCTGGTGTTCCCAATAA	CTGTATAATCTCTCTCCTGTA	AAGGGAGTATCTGTGAAGGAA
181	AGRP	NM_007316	CTGAAGAAGACAACTGCAGAA	CAGCCGCACCTAGCTGGCCAA	AAGCTGGGTACTGCCATGAAT	CAAGCTGGGTACTGCCATGAA

WO 2008/043561 PCT/EP2007/008852

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
183	AGT	NM_000029	ACCGACCAGCTTGTTTGTGAA	CTGTTTGAATGCGGAACAATA	CTCCGTGTAGTGTCTGTAATA	CAGAGTCTACCCAACAGCTTA
185	AGTR1	NM_000685	ATCCAAGATGATTGTCCCAAA	CTGGATGTATTGATTCAACTA	CGCGGGTTTGATATTTGACAA	ACGCACAATGCTTGTAGCCAA
187	AGTRL1	NM_005161	CACCTGCATCAGCTACGTCAA	CACCATCATGCTGACCTGTTA	CACTGTGGTTCATCAAATAAA	CACCACTAAGGTGCAGTGCTA
189	AGXT	NM_000030	CCGAGTGCACCCGATGACCAA	CTGGAGAGACATCGTCAGCTA	CCAGGATGTACCATCACACAA	CTCCCGGGAATGTTTAATAAA
190	NR0B1	NM_000475	ACGGCAGGGCAGCATCCTCTA	ATGGATGATATGATGCTGGAA	ATCGAACTTAATAGTACCCTT	ATGCTCTGTACAAAGATATAA
197	AHSG	NM_001622	CCAGGGCTGATTTATAGACAA	CTGAAAGACCTTCCTTAATAA	AAGCTTATATGTGCCTGTTAA	CACATGCGATCTACATTAATA
199	AIF1	NM_004847	CCCAGATATCATGTCCCTGAA	CAGAGTCAACAAATTAAATAA	AAGCCAGAGTCAACAAATTAA	CACCTAGCAGTTGGTTGGCAA
207	AKT1	NM_005163	CAGGGTTTACCCAGTGGGACA	AAGGTTTAAATTTGTTATTGT	CACGCTTGGTCCCGAGGCCAA	ACGCTACTTCCTCCTCAAGAA
210	ALAD	NM_000031	CAGGGTATCGGTGATGAGCTA	AAGGGTGAGCCATCAAGCTAA	CCCAAGAACTAGAACTTTAAA	CTCCCAATAATCAACAGCAAA
215	ABCD1	NM_000033	CCGCACCTTCCTGTCGGTGTA	CCACCTCTTTCTACAGCCTAA	CTCGGAGGAGATCGCCTTCTA	CTCTTTCTACAGCCTAATTTA
217	ALDH2	NM_000690	CAGGCATACACTGAAGTGAAA	CACAGTCAAAGTGCCTCAGAA	AAGCTATTGTTTACAATTATA	CAGCCATTGATGGAAAGTTCA
219	ALDH1B1	NM_000692	CTTGGATTACTCAGCCATAAA	TTGAACTAGGTGGATACTAAA	CTCAGAGTTCTACCTATCTAA	CAGCACGTGGATGTTGACAAA
220	ALDH1A3	NM_000693	TTGGGAAAGGATTCACAGTAA	ACCAGTGTGTGTATAACGAAA	AACGGTCTGGATCAACTGCTA	AACCTTGATAGTGATACGTTA
222	ALDH3B2	NM_000695	CTCCGGCCTGGAGAAATTAAA	CACGGCCGTCTCCACCAGAAA	CAGGCCTGGATGAAGGATGAA	CCCACCCTATACCGACTGGAA
225	ABCD2	NM_005164	CAGTGACACATTGGCAATTAA	CAGCATTGATGTCGAAGGAAA	CACTCGAGAATTATAGCCAAT	TCGCCTAGTAGACCACGCCTA
226	ALDOA	NM_000034	CTGTCTCTGCTTCGAGATCAA	TCCGGCACACTGCCAAATAAA	CACGTCAACGATTCTATTTGA	GCCAAATAAACAGCTATTTAA
239	ALOX12	NM_000697	CAAGCCCAAAGCTGTGCTAAA	CCCAAAGCTGTGCTAAACCAA	CTGGCCCTATGAATATCTGAA	CTGGTATGCCTGGGTCCCTAA
248	ALPI	NM_001631	CCGGGCTACGTGTTCAACTCA	CCAGACAATAAAGGGACCAAA	TCCATTCTCCTAGGAGACAAA	CACGTCCATCCTGTACGGCAA
258	AMBN	NM_016519	CACCATCAGATAAGCCACCAA	TACCAGCATGACACTATTATA		
262	AMD1	NM_001634	CGGGAGAAGAGGTTTAATTTA	CTGGGCTTAATATTCTTTAAA	TGGGTTTATATACTAATTCTA	AAGGTGGACCTTGTTGCTAAA
265	AMELX	NM_001142	ATCCCTGAGTTTCAAACAGAA	CAAACAGAAACTTGCACTGAA	TCCCTGAGTTTCAAACAGAAA	CAGGAGTGACACAAGAACACA
268	AMH	NM_000479	CCAATAAAGACCAGCAAGCAA	CCACGTGGTGCTGCTGCTGAA	CAGGCCATCCGCGGAACTCGA	CGCGTGGCTGCTGAACTGCAA
269	AMHR2	NM_020547	CACGACCACATTGTCCGATTT	ATGGCCAATATAAACCAGGTA	CTGGCAGAATGGCCAATATAA	CAGAATGTGCTCATTCGGGAA
270	AMPD1	NM_000036	AACCTGGGCTATCACCTCAAA	CGCCATGTCACCACTAAGTAA	CACCTTCTTAGACGATATGAA	TTGCTGAGGGTCTTAAATCAA
271	AMPD2	NM_004037	CAAGTTTAATGCCAAATACAA	CGGCTTCTCGCACAAGGTAAA	CCGGAACTGCATCTCTTCTTA	CCGGACCAATGTGCCAGACAT
283	ANG	NM_001145	CCGGGATGACAGATACTGTGA	CAGCATCAAGGCCATCTGTGA	CGGGATGACAGATACTGTGAA	AACGTTGTTGTTGCTTGTGAA
287	ANK2	NM_001148	AAGCTTGGTTACACACCTTTA	CAGGACCCTTCTAAACATAAA	ATCAAGCTATTTGCAACTTAA	ACCGTGCAAACGGGTGATATA
288	ANK3	NM_001149	CAGGATTATCACGAAAGATTT	CGCATCCTTAGCTTTACGTAA	AAGGATCTTAACCTCAATTAA	CTAGTCGATTATTTAAGCATA
290	ANPEP	NM_001150	CACCACCTTGGACCAAAGTAA	CCGGGTGAACTACGACGAAGA	AACGATCTCTTCAGCACATCA	CCGAAATGCCACACTGGTCAA
291	SLC25A4	NM_001151	CTGTATCATCAAGATCTTCAA	CAGATCCATTGTGTGGTTTAA	TACAGTGAACTTGATCTACAA	CTGAATGTGAAACATCAATAA
292	SLC25A5	NM_001152	CAGGCATGTTGTATTCTATAA	CGGAAGATTGCTCGTGATGAA	CACAATCTTGAGCATTCTTGA	ATGTTGTATTCTATAACACAA
310	ANXA7	NM_001156	CAGAAATTCTTCGTAAGGCAA	CTGTGTAATAATATTGAATAA		
312	ANXA13	NM_001003954	CAGGCCAAGCTGTGTAAGTTA	CAAGAGCACATTCCAAATCAA		
317	APAF1	NM_001160	TAGGCAGAGTATAAAGTATTA	CAGTGAAGGTATGGAATATTA	CCGCATTCTGATGCTTCGCAA	AAGGGCAATGGAGATAAATTA
320	APBA1	NM_001163	CAGGATCAAGATGGCCCAGAA	CAGGAAGAGAAGAATCCACAA		
324	APC	NM_000038	CAGAGACTAATGAAAGTTCTA	CCGGTGATTGACAGTGTTTCA	TCCATCTAACATCATAATTAA	CAGACTAAGCATTGAGCATAA

WO 2008/043561 PCT/EP2007/008852

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
327	APEH	NM_001640	CCGCCAATACCTGGTGTTCCA	CAGGAGGAACACTTTGATGCA	CTGGAAGTTGCTCACAATTGA	CAGAGGAATGTGGGCTATGTA
329	BIRC2	NM_001166	CAGGGCTTTAAGTTAGTATTA	TCCCAGGTCCCTCGTATCAAA	TCGAAACTTTATAAAGGGATA	TAGGCGTTTCTGATAACACTA
336	APOA2	NM_001643	ATCAAGAAGGCTGGAACGGAA	CCCACTCTTTGCTACAATAAA	TACAATAAATGCTGAATGAAT	AGGCCAAGTCTTACTTTGAAA
339	APOBEC1	NM_001644	CACCAATCACGTGGAAGTTAA	CACCCTGTTTAAAGATTTCAA		
345	APOC3	NM_000040	AAGACTACTGGAGCACCGTTA	CTGGAGCACCGTTAAGGACAA	CAGGAACAGAGGTGCCATGCA	CCCAATAAAGCTGGACAAGAA
350	APOH	NM_000042	ACACATGGAAATTGGACTAAA	CTGGATGGCCCGGAAGAAATA	CACATGGAAATTGGACTAAAT	CAAGTTGTAAAGCATCTTGTA
351	APP	NM_000484	CTGGTCTTCAATTACCAAGAA	ACCCAATTAAGTCCTACTTTA	CAGACTGAACATGCACATGAA	AAGGATGACTACAGACATTAA
353	APRT	NM_000485	CACACTGAACCCAATTACACA	CTGTGTTTCAGCCACACTGAA	CAGCTGGATCCCAGGGAAATA	CAGCCACACTGAACCCAATTA
355	FAS	NM_000043	TCAGTGTATGTTAGTACAAAT	CACATTGATTAAAGATCTCAA	CAGAATTTAAATAAGGCTCTA	AAGGACATTACTAGTGACTCA
366	AQP9	NM_020980	CAGCCTCTAATTGGAACGGCA	CAACCAAACCCTAAATTGAAA	AACCGTCTTTGGCATTTACTA	ACGACTGTGCTTGTCCATTAT
367	AR	NM_000044	AAGAAACTTGGTAATCTGAAA	CACGGGAAGTTTAGAGAGCTA	CAGGAATTCCTGTGCATGAAA	AAGGAACTCGATCGTATCATT
368	ABCC6	NM_001171	CTGAGGGAATCCACACTTCAA	ACGGTTGACGTGGACATTCCA	CACCCATTGGTCACCTGCTAA	CACGTGTGCTGTGCTGAGCAA
372	ARCN1	NM_001655	AAGGCAAATTCTTTAATCAAA	CCCACTTGTGTCAATATTAAA		
375	ARF1	NM_001658	AAGCTGGAGCTGTTAAATTTA	CACGATCCTCTACAAGCTTAA		
382	ARF6	NM_001663	CTCAGTATGTTAAACAGGTAA	ATGGTTAACCTCTAACTACAA		
388	RHOB	NM_004040	CCTGCTGATCGTGTTCAGTAA	CCCAGTGGTACTTCTACTAAA	AGCTAAGATGGTGTTATTTAA	CACAATTGTTTCATTGTTTGA
389	RHOC	NM_175744	CAGGAGAGAGCTGGCCAAGAT	CCCTACTGTCTTTGAGAACTA	CCGGATCAGTGCCTTTGGCTA	CACCATGGCTGCAATCCGAAA
391	RHOG	NM_001665	CAACAGGATGGTGTCAAGGAA	CGGGCGCACAGTGAACCTGAA		
397	ARHGDIB	NM_001175	AAAGGAAACCATTGTGTTAAA	CACTGAATAAATAGATCAGAA	AAGGAAGGTTCTGAATATAGA	CACAGCTGGGTCCCTCTTCAA
401	PHOX2A	NM_005169	CCAGCAGAGCGGAGTTCTTTA	CAGAGGGATTCTCTTTCCCTA		
403	ARL3	NM_004311	CAGACCTGTAAGGACTTGCAA	ACCGATATTCTTATATATGTA	ATCTGACATGAAAGTCATTAA	AGGGAACAACACGGTTTAGAA
405	ARNT	NM_001668	AACCCGAGACTTGGCCATAAA	ACGGAACAAGATGACAGCCTA	CCCAGCCAATATACAACTGTA	CAGCCAATATACAACTGTAAA
406	ARNTL	NM_001178	TACGTTTGGACCCAAGCTTAA	TAGGCACATCGTGTTATGAAT	TCGGCACGCGATAGATGGAAA	TCGATGGTTCAGTTTCATGAA
410	ARSA	NM_000487	CTGGGTCTGCGGTATCGGAAA	CAGGGCTTCCATCGATTTCTA	CCCGGTTCGGATGGGCATGTA	TCGGCAGTCTCTCTTCTTCTA
411	ARSB	NM_000046	AAGGGTATGGTCTCTAGGCAA	CACATTTCTTACGCAAATGAA	ATGGGTGTACACTACGCATAA	AACCAACTTTATAGTACATAA
414	ARSD	NM_001669	ATGGAGGACATTTAGAGGCAA	AAGGTTCTTAATGCCATCGAA	AACAGCGAGTCTTATGCTAAA	TCGGTTGCTACGGGAACAATA
415	ARSE	NM_000047	CCGCTGGGAACTCTCAGAGAA	CACGAGTTCCTGATGCATTAT	CCCTCTTATCACTATGGAGAA	AGGGAAGATGACCCACAATAA
416	ARSF	NM_004042	CGCGTTCTTGACGGGAAGATA	CTGAACGAGCTGGATCCATTA	CAGGTATGGTTTCTAGTGGTA	ACGGAGGGCATTTGGAAGCTA
421	ARVCF	NM_001670	CACGGAGAGCCGGAACTTCAA	CCGGAAGGACACTGACAACAA		
427	ASAH1	NM_004315	CACGGATGGCACGAAAGCCAA	CACGTTCTGTTAATTTAGTAA	ATGGTATGTGGTACAAACAAA	CACGATTAACTGTGAAATGTA
430	ASCL2	NM_005170	CACGCTTTGGGCCTTACAGAA	GAGGGTTATCTATACATTTAA	AAGGAAGGAGGGCGTGAGAAA	AGGGAGCGTGAACTTTATAAA
432	ASGR1	NM_001671	CTCCTTTAATTTATTTCTTCA	TCCGAAGGTGAGGAGCTTGAA	CAGGAGCCACCTCTCCTTTAA	CAGGTTATCATTGTGAACTTT
433	ASGR2	NM_080914	CTGTAATTCATTGTAATTATT	GAGCAGAAATTCATTGTACAA	CAGACTATAGGCACAACTACA	CACGAGCTGGGTGGAAGTGAA
443	ASPA	NM_000049	AACCGGAGTATTTCTGGTTAA	CTGCGCCATTGAGGTCTATAA	TACGTTTATCTGATTGAGCAT	TACATCTTACACGGTGTCTTA
472	ATM	NM_000051	TTGGCTTATACGCGCAGTGTA	CACTTATTCATTAGTAATTTA	CACCTGTTTGTTAGTTTATTA	AACCATGAGTCTAGTACTTAA
473	RERE	NM_012102	CAAGAGAGAGTGAGAATTCAA	CAGGAAGATTATTACAGTCGA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
477	ATP1A2	NM_000702	ACCCATAGCAATGGAGATTGA	CCGATTAATTGGAGATTACTA	AACAATCAGATTAGACACTAT	CAGATTAGACACTATGTGTTA
480	ATP1A4	NM_144699	CTGGTTTATGCTGGCCCGAAT	CTCAATGAACGATGAAATGAA	AAAGGGAGACGTACTACTAAA	CCGGGCTGACTTTAAGGCTAA
483	ATP1B3	NM_001679	CCGCATTGGAATATACATTCA	CAGACTGTGGACTGTAATAAA		
486	FXYD2	NM_001680	CACCAGCCTCTCCAAGCTCAA	CCCGTTCTACTATGACTATGA	CCACCTCATGCTTATAATAAA	ATCAATGAAGATGAGCCGTAA
487	ATP2A1	NM_004320	CCCGTGTCATGTGTCTGTTTA	CCCGATAGTGACACATCTTCA	CACCAACATTGCAGCCGGCAA	TCGGAACTACCTAGAGGGATA
492	ATP2B3	NM_021949	CCCTCTTTATAAAGCATTATA	CCGGAAGACAAGCTTTACAAA	TTCCCTGATGTCCTTGTTTAA	CACAGATACGTAATAATTTAA
501	ALDH7A1	NM_001182	CGGGAGAAGATCCAAGTACTA	TCCGATTCTCTATGTCTTTAA	AAGGATGATTGGAGGACCTAT	AAGGTCTACTTGTACTATCAA
506	ATP5B	NM_001686	AACAGTATTTAAGGTTTCCAA	AAGAATTACCACTACCAAGAA	ATCTGGTGTTATCAACTTAAA	ACCCGTGAAGGCAATGATTTA
509	ATP5C1	NM_001001973	CAGGTCTGTCATCTCCTATAA	CAGCAAGATATTTGTAAATTA		
523	ATP6V1A	NM_001690	TAAGGTAGAGTCAATTATGAA	ACCCAAATTGTGATAGCATAA	GAGCTTGAATTTGAAGGTGTA	ATGGAGGTTGATGGTAAGGTA
527	ATP6V0C	NM_001694	CTGGATGTTTATTTATAAAGA	CAGCCACAGAATATTATGTAA		
533	ATP6V0B	NM_004047	CAGCTGGAGCTGTGTCCCTTA	TCCTAGTGTTTGTGAAATAAA		
535	ATP6V0A1	NM_005177	AAGGTTCAGTTTCGTGACTTA	ACGGCCGATGTTTACTTATAA		
537	ATP6AP1	NM_001183	CACAGTGACATTCAAGTTCAT	CAGGGAAGTCCTCACAGGCAA		
538	ATP7A	NM_000052	CAGCAAGTCACTTAGATCATA	CAGCCAGTTATTCTTCCATTA	CTGGACCGGATTGTTAATTAT	TAGCAGCTTGTAGTATTGAAA
545	ATR	NM_001184	AAGGACATGTGCATTACCTTA	GCCGCTAATCTTCTAACATTA	CCGCTAATCTTCTAACATTAA	CAGGCACTAATTGTTCTTCAA
546	ATRX	NM_000489	ACCGGTGGTGAACATAAGAAA	CCGACAGAAACTAACCCTGTA	CCGGTGGTGAACATAAGAAAT	AGGCGACGTATTAAGGTTCAA
547	KIF1A	NM_004321	TCGGATCAACGACACGACCAA	CAGCCCGATCGTTTCCAAGAA	TCGGGTCATGCCACTGTCCAA	CAACTCGGAAATTAACTATAA
552	AVPR1A	NM_000706	CAGAAATACAACAGAAGTTAT	CACTTTATTAATATAACCATA	TCGCAAACATAGGGTAATAAA	ATGAACGGACTGGATAGTAAA
567	B2M	NM_004048	CAGGTTTACTCACGTCATCCA	TCCGACATTGAAGTTGACTTA	CTGGGTTTCATCCATCCGACA	AAGTGGGATCGAGACATGTAA
570	BAAT	NM_001701	TTGGCTTACCATAACTATGAA	ATGGCTATTTACCTAAAGCAA		
576	BAI2	NM_001703	CCCACTGCATATAAATATATA	CGAGGTCTTGCTCATCAACAA	CTCTCTGATTGTCACAGATAA	CCCGAACGAAAGGATACGGTA
577	BAI3	NM_001704	TTCGGGATATACCAAATACAA	GAGATCCATAATACTAATTAA	TTGGATGATAATGCAGGACTA	ATGGACTAAGGTAGAGACAAA
578	BAK1	NM_001188	CTCTGAGTGTTTGGAAATAAA	CAGGATTCAGCTATTCTGGAA	CTGGACTTAAGCGAAGTCTTT	AACCCATTCACTACAGGTGAA
580	BARD1	NM_000465	TCCGATGAATTCATTAGTCTT	GACCATCAATACAGTCGCATA	TGCAGTAATTCTTAAGGCTAA	CTGAATATTATACCAGATGAA
581	BAX	NM_004324	CCGAGTGGCAGCTGACATGTT	CAGCTCTGAGCAGATCATGAA	CAGGGTTTCATCCAGGATCGA	ATCATCAGATGTGGTCTATAA
587	BCAT2	NM_001190	CCGGCTCATCGAAGTGGACAA	CACCTGAAGTGCAATACGAAA	AACCATGAACATCTTTGTCTA	CTGAAGTGCAATACGAAATAA
594	BCKDHB	NM_000056	CAGGCCGAAGTCATACAGGAA	CTGGAAGATTATGACTAGATA		
595	CCND1	NM_053056	ATGCATGTAGTCACTTTATAA	CTCCTACGATACGCTACTATA	AGGGTTATCTTAGATGTTTCA	AAGGCCAGTATGATTTATAAA
596	BCL2	NM_000633	GTGGATGACTGAGTACCTGAA	CCGGGAGATAGTGATGAAGTA	CTGTGGCATTATTGCATTATA	CAGGCTTAAGATTTGGAATAA
598	BCL2L1	NM_001191	CAAGCTTTCCCAGAAAGGATA	AAGGCGGATTTGAATCTCTTT	CTGCTTGGGATAAAGATGCAA	AAAGTGCAGTTCAGTAATAAA
602	BCL3	NM_005178	CTCGACATCTACAACAACCTA	CACGATGTAAATTATTAAGCA	CAACGTGAACGCGCAAATGTA	ACGGATCACGATGTAAATTAT
605	BCL7A	NM_020993	TACGATGCTGATCATCATTGA	CTGCACTTCGAGAAGAATCAA	CAGCACCTTCCTACAACCCTA	TGGAATGTTCATTATCGCCAA
611	OPN1SW	NM_001708	TTGGCCTGTTTGCAACAGCTA	GCGCTACATTGTCATCTGTAA	CGCCATGTACATGGTCAACAA	CAAGAGTGCTTGCATCTACAA
613	BCR	NM_004327	CAGCCGCAACGGCAAGAGTTA	TGAACTTAACTTAGAGTCTAA	CAGCATTCCGCTGACCATCAA	ACGGCAGTCCATGACGGTGAA
622	BDH	NM_004051	TGGCTGCTTGATGAAGGACAA	CAGCAGCGAAGAGGTGGAGAA	CTCAATGTCTGCAGCAGCGAA	CAAGCAGGTGGCAGAAGTGAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
624	BDKRB2	NM_000623	ATGAGTTGATGTCTCCGGTAA	GCCCTGGGTTTCTTTAATCTA	CTGGCAGGTTAGAACCTAGAA	CTGCACGGTGGCAGAGATCTA
638	BIK	NM_001197	GAGGAGAAATGTCTGAAGTAA	TCGGCAAAGAATCTACTGGAA	CCACACTTAAGGAGAACATAA	CCGAGGAGCAGGAGTGCTCAA
640	BLK	NM_001715	AAGGTGGTTCTTTAGATCACA	CAACATGAAGGTGGCCATTAA	CTGGTAAGCGACTGTCATCAA	CAGCCGTGCTGTTAAACCAAA
641	BLM	NM_000057	GACGCTAGACAGATAAGTTTA	CTGACCATCTGTGACTATAAA	ATGCTCGGAAATAAAGCCCAA	CCGAATCTCAATGTACATAGA
643	BLR1	NM_001716	AACGCTGGAAATGGACCTCGA	ACGGAGAAAGGTGGACTGGAA	CCCGCTAACGCTGGAAATGGA	CAGCCATGAACTACCCGCTAA
644	BLVRA	NM_000712	TCCAGAAATATTGCTGTTCAA	ACCATTATCTCTATTCTTAAA		
649	BMP1	NM_001199	AAAGGGCTTCTTTGCAGTCTA	CAGCTATATTGTGTTCACCTA	CTGGCTCAAGTTCGTCTCTGA	AAGGACTATGGCCACATTCAA
651	BMP3	NM_001201	CCCAGCTGGTTTGGAGTTCAA	CCGCCATTTCTGAGCCAGAAA	CTGTCTAAAGATATCACTCAA	CAGGAGATACCTCAAGGTAGA
654	BMP6	NM_001718	CCCGGACGACCATGAGAGATA	CAGCATTTATCAAGTCTTACA	CCGGACGACCATGAGAGATAA	ACCGTGCTGTGCGCCAACTAA
656	BMP8B	NM_001720	CAGGTAGACATGTGGAGTCAA	TAGGAAAGACATGTAAGAGCA	CTGAGTGAACAGCATGATTTA	ACAGATATGATGTAAAGTGAA
657	BMPR1A	NM_004329	ACCAATTTATGTAACCAGTAT	CACTGAATGATAGTCATTTAA	GCGGCAGACATTAAAGGTACA	CAGCTACGCCGGACAATAGAA
659	BMPR2	NM_001204	CCATATGAGCATTGTAATTAA	AAGCTCTAAATTGATGTGCTA	CTCGTAAGTATGTAAAGGAAA	AAGCACCGAAGCGAAACTTAA
671	BPI	NM_001725	CCCAGGGTTAACGAGAAACTA	CAGACGTTGTCTATAAATGAA	CAGGGTTAACGAGAAACTACA	AGGAATCGTGTTTCAATTGTA
675	BRCA2	NM_000059	TACGTACTCCAGAACATTTAA	TTGGAGGAATATCGTAGGTAA	CAGCGTTTGTGTATCGGGCAA	CAGGACACAATTACAACTAAA
686	BTD	NM_000060	AACCAGAACCTTGACATCTAT	CACAAATGTCGTGTTCAGCAA	CAGATTATAGTGTTTCCAGAA	ATGCGATTGGTCTCAAGCTAA
708	C1QBP	NM_001212	CAGGCTTTGGCCAGTGAACAA	CACGGTCACTTTCAACATTAA		
710	SERPING1	NM_000062	CGCCAACTTGGAGCTCATCAA	AACCTGAAACATCGTCTTGAA	CTGGGTGGCCAAGAACACCAA	TCACCAGACTCTATAAATAAA
712	C1QA	NM_015991	ACGGTCATCACCAACCAGGAA	CCCGGGAATTAAAGGCACCAA		
713	C1QB	NM_000491	CAGAAGTGCCATGCTCAGAAA	CACCAACATGAACAACAATTA		
717	C2	NM_000063	CCGGGATATGACTGAGGTGAT	ACCCTGGCATGTCACTATTAA	CAGAGAGATCCTGAACATCAA	CCCAGTTATGAAATTAATAAA
718	C3	NM_000064	CCGAGCCGTTCTCTACAATTA	CACGGAGAAGCGAATGGACAA	CACGGTCATCGCTGTGCATTA	TAGGAACACCCTCATCATCTA
720	C4A	NM_007293	AACCCTGTACGACTACTACAA	TCCAGTGTTAGACAGGAGCAT		
721	C4B	NM_000592	AACCTGGGAAAGAATATTTGA	AACCCTGTACGACTACTACAA		
726	CAPN5	NM_004055	CCCGGGAGTCGCTGTGGCAAA	CCGCGTGATCAACACATCCCA	CCGGTACTTCACGGACATCAT	CTGGTGTTCTCCCACCTTGAA
730	C7	NM_000587	CACGCAGTTATACTTCACATA	AAGGATTAGAACACTCATTAA	ACCCTGGTAAATATATTTCAA	CCGAAGATTAATCGACCAGTA
757	C21orf4	NM_006134	AAGGGATAATACATGATCAAA	AAGCTGGGATACAGCATTTAA	CACCTGGTATGCTTACATTAA	ATGGAGTAGATTGTACATTAA
762	CA4	NM_000717	ATGCACATAGTACATGAGAAA	CTGGCTACGATAAGAAGCAAA	TGGGACTTTAGGCATGATTAA	CTGGTCCGACTTGCCATATAA
773	CACNA1A	NM_000068	CACCGTCGTACAAGTGAACAA	CCGGGTGCTACGACCTCTTAA	TCGGAACAACGTGCTGCGATA	CGGGTGCTACGACCTCTTAAA
774	CACNA1B	NM_000718	CCCAGGAACAACGCTCTGAAA	CCGGCAGTCGTTCCAGTATAA	CCCGAACACTATTGTACATAT	TCGAATTGGCTCTGACCCTTA
778	CACNA1F	NM_005183	CACCATCATGTCTTCACCAAT	CTGGCCTGCACTGCTATACAA	CACCACACTTCTGCAATTTAT	CCGGACATCCCTGAAGATCAA
780	DDR1	NM_001954	CAAGATCTGGTTAGTCTTGAT	CACTAGGCAGGTAATAATAAA	CAGGAATGATTTCCTGAAAGA	ACGGTGTGAATCACACATCCA
781	CACNA2D1	NM_000722	ATCGGGCATTATGGTAAGCAA	TTCGATAACGACAGTAAATCA	TCGGCCGTCACTATCAAATCA	CCGCCTGTTATGACCTTCTAA
784	CACNB3	NM_000725	CCGGCGTGAAGTAGAGAGCCA	CCGCTTGTTAGGTTAGGGTTA	CTGGAGAGCATCCGGCTCAAA	CTCACTGTCATCACTAATAAA
797	CALCB	NM_000728	AAGGAATGAAACTGAATGCAA	CCCACCAATGTGGGTTCCAAA	ACCTTTGTCACTTGAAAGGAA	AACCTTGGTGATGCATTACAA
801	CALM1	NM_006888	TTCCTGAACAACGAATGTAAA	CTGGTTGTATCTTATTAGCAA	CGGCAACTTACACACATTGAA	ATGCCCGTGTATGTTGGTTTA
813	CALU	NM_001219	CAGGGTTTCAGTCCTTATCAA	AAGCCTGAGATCAATAAGAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
816	CAMK2B	NM_001220	CAGGATCTCTGACATCCTGAA	CCCGGAAGCAGGAGATCATTA	CCGGAAGCAGGAGATCATTAA	CAAGAGTTTACTCAACAAGAA
823	CAPN1	NM_005186	TCCCACGGAACTGCTGTCAAA	CCGGACCATCCGCAAATGGAA	TAGGATCATCAGCAAACACAA	CAGGGACTTGTGTACTGGTTA
824	CAPN2	NM_001748	CTGGAACACTATAGACCCAGA	AACGGATGCTATGAAGCTCTA	AACATGGTATATCATGAAGTA	CCCGAGAATACTGGAACAATA
834	CASP1	NM_001223	TCGGCAGAGATTTATCCAATA	CTCATTGAACATATGCAAGAA	TACCTCTTCCCAGGACATTAA	CCCAGATATACTACAACTCAA
839	CASP6	NM_001226	ACCCAAGATATTTATCATTCA	CTCAGGAAATTAGATAAATAA	GCGCAGATAGAGACAATCTTA	CAGGAATTAAATCATCCCTTA
841	CASP8	NM_001228	GACAAAGTTTACCAAATGAAA	AAGATAATCAACGACTATGAA	CGGAGGGTCGATCATCTATTA	AAGAGTCTGTGCCCAAATCAA
845	CASQ2	NM_001232	CGGCATATTTGGGAACGAGAA	TAGCCTAAGCTGGGATCTGAA	GAGGTTGATTTGCTCTCTAAA	TAGTGTTAAGTGTGCAGTATA
857	CAV1	NM_001753	TCCAGTCTTCCTGACACTTTA	CTGGTCAACCGCGACCCTAAA	TCCTGACACTTTAATTACCAA	CAGCCGTGTCTATTCCATCTA
860	RUNX2	NM_004348	CACCTTGACCATAACCGTCTT	CAGCAGCACTCCATATCTCTA	CAGAAGCTTGATGACTCTAAA	CAGCACGCTATTAAATCCAAA
861	RUNX1	NM_001754	CAGGTCGTTCTTATCTAGAGA	CTCCCTTTCATGTTAATCAAA	TTGGCGATAGGTCTCACGCAA	CAGGAAAGTTAAGGTATCAAT
868	CBLB	NM_170662	ACGGGCAATAAGACTCTTTAA	TCGGTTGGCAAACGTCCGAAA	TCCGGTTAAGTTGCACTCGAT	CACAGCGAGTTCAAATGTCAA
871	SERPINH1	NM_001235	CTCAATCAGTATTCATATTTA	CCCAACCTCTCCCAACTATAA	CAGCCCTCTTCTGACACTAAA	CAAGAACTTATTTGTACATTT
883	CCBL1	NM_004059	CAAGTGGATGATCAAGAACAA	CACAGACATCTCAGACTTCAA		
885	CCK	NM_000729	ATCTATTTATTAAGTTCTCAA	ACCAGAATTGTGCAAATGGAA	TGGACGAATGTCCATCGTTAA	ACGAATGTCCATCGTTAAGAA
887	CCKBR	NM_176875	CACAGCGTCCCTAGCAGTGAA	CCCAAACTGTTCAAGAAATAA	CCGCCGGGTCGAGCTGAGTAA	CCCGTGTACACTGTCGTGCAA
896	CCND3	NM_001760	TGGGACAGAATTGGATACATA	GACCATCATCCTACTGTAATA	CACAACTTTAAGAGGACATAA	CAGGAACCACACCACATCTAA
899	CCNF	NM_001761	CACAGATGGCGTCAATGTGAA	CCGGTTTATCAGTAAAGAGAT	AACCCAAGCGTTGGAACTGTA	CACGGACAACACTTACAAGTA
901	CCNG2	NM_004354	GGGACAGTGGATAATCCTTAA	CTGGAGAGAGTTGGTTTCTAA	AAGGCAGAAATAATTAGGCTA	AAGAGTGAGTATGCTCTTAAA
905	CCNT2	NM_001241	CTCGATGTAAGGGATCATTAT	AAGGGCTTTCTTGGTAATTTA	TCCACATATGATAGTGTTATA	AAGCAAGAATATACTCATAAA
910	CD1B	NM_001764	AAAGCAGATCTGCAAAGACAA	CTTGGTCTAAAGGTAACTTTA	CACAGAAATTCTGTGCACTAA	CTGAGTGTCAAGAATGCTTCA
914	CD2	NM_001767	AACCTGTATCAAGATGGGAAA	TAAGATGAGCTTTCCATGTAA	CCCAACAAATTCCAGCTTCAA	CCCGAATTAAACCTGTATCAA
915	CD3D	NM_000732	CTCACTTATTAATTCTAGTAA	CACGAGGAATATATAGGTGTA	TGGCACGATATGTTAAACCAA	CAGGCTATATATGGTATTAAA
919	CD3Z	NM_000734	CAGGAAGGCCTGTACAATGAA	CACGCTTTCAGCGAATGACAA	TTGGTTATATTTAGCTCCAAA	ACCCAACACATGGGACCTATA
923	CD6	NM_006725	CAGCACTACTGCGGCCACAAA	CTGGCGGTTCAACAACTCCAA	CCGGCAGGATGTACTACTCAT	CAGGGAGGATGCTGCCTCCAA
926	CD8B1	NM_172100	TAGCACTAAATTCGAGAAGCA	CAAATACAATAGAGCCACTAA	TAGCTGTGTTTCGGGATGCAA	ACCCGGCAACATCAGTTTAAA
928	CD9	NM_001769	CAAAGAGGTCTTCGACAATAA	ACAAATGTCTATCAACTTTAA	CCGCGAGATGGTCTAGAGTCA	AAAGAGGTCTTCGACAATAAA
929	CD14	NM_000591	CCCGAGGTGGATAACCTGACA	CTCAGAGGTTCGGAAGACTTA	CAGAATAATGAATGGACTCAA	CAGCCTAGACCTGTCTGACAA
931	MS4A1	NM_021950	GAGCAACTTTCTTACACTGAA	TTCAATCATGGACATACTTAA	CACACACCATATATTAACATA	CACCATATATTAACATATACA
939	TNFRSF7	NM_001242	AACGAAGGAAATATAGATCAA	ACCGAGTGTGATCCTCTTCCA	AGGAAATATAGATCAAACAAA	AAGGTTGGCTTGCCACCTGAA
940	CD28	NM_006139	TGGGTTAAGCATGCCAATTTA	CAGGGATGAGGTGCTATAATA	CTCGAGTGACTAGACCAAATA	ATGATGGTTCTTCAACTATAA
961	CD47	NM_198793	TACCATTCCTATAGTACTTTA	CACTACTGAAGTATACGTAAA	TACAGCTGTGTTACCGTTAAA	CACGATAAGTTTACTCCTCCA
962	CD48	NM_001778	CTGGCGAGTCTGTAAACTACA	CTGCAAGTGCTTGACCCTGTA	CACCCTTATGCCACATAATTA	CAGAAGCATGCTGCTGAATTA
965	CD58	NM_001779	TCCAATTGATTGGTAACAGAA	TAGCAGTAATTACAACATGTA	ATGCATGATACCAGAGCATTA	AGCAATGTAAACGTAACTCAA
967	CD63	NM_001780	CTGGCTATGTGTTTAGAGATA	CAGATGGAGAATTACCCGAAA	TGGGATTAATTTCAACGAGAA	CAACGAGAAGGCGATCCATAA
970	TNFSF7	NM_001252	CTGCGTCTCAGCTTCCACCAA	CAGCTACGTATCCATCGTGAT		
975	CD81	NM_004356	AAGGAACATCAGGCATGCTAA	CCGCCTGTGTATATAACGTTT	CGCCTTCAACTGTAATCACAA	CACCTTCTATGTAGGCATCTA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
983	CDC2	NM_001786	AAGCCTAGCATCCCATGTCAA	TTGACTAACTATGGAAGATTA	TCGGGAAATTTCTCTATTAAA	CAGGTTATATCTCATCTTTGA
987	LRBA	NM_006726	CACGATGGAAACAGATGATAA	CAAGGGTACATTTAAATTCAA		
988	CDC5L	NM_001253	ACGCAGATTTCAGGAAATTAA	TCGAGACAAGTTAAACATTAA		
995	CDC25C	NM_001790	GAGCTGCAATCTAGTTAACTA	CCAGGGAGCCTTAAACTTATA	CCAGAGCTATATATCCTTAAA	CAGGAAGGGCTTATGTTTAAA
1002	CDH4	NM_001794	CCAGAATATGTTCACCATCAA	CACGTCCATCATCAAAGTCAA		
1010	CDH12	NM_004061	CAAAGTCAATATACTGATTAA	CTCCACCTTCTTCTAATTCAA		
1012	CDH13	NM_001257	CAGGATATATTTAAATTTGCA	CTGGAAGATCTCCAAGATCAA		
1019	CDK4	NM_000075	CAAGGTAACCCTGGTGTTTGA	CCGAACTGACCGGGAGATCAA	ACCCTGGTGTTTGAGCATGTA	AAGGTAATCCGGAGTGAGCAA
1022	CDK7	NM_001799	CTCTTGAAATGTAGAATTGAA	TTGGACATAGATCAGAAGCTA	GAGGCTTTAAGGTAGCTTTAA	CCGGATGGCTCTGGACGTGAA
1024	CDK8	NM_001260	CAGGGCAATAACCACACTAAT	TTCGAGAGCTTAAGCATCCAA	CCAGCTGGACAGAATATTCAA	CAGAAGAAATACGTATACCAA
1025	CDK9	NM_001261	CGGCCAGAAGGTGGCTCTGAA	TGGGCACAGTTTGGTCCGTTA	TAGGGACATGAAGGCTGCTAA	AACCGCTGCAAGGGTAGTATA
1027	CDKN1B	NM_004064	CTGTAAGTAACTTCACATTAA	CACGCATTTGGTGGACCCAAA	ACCGACGATTCTTCTACTCAA	AAAGCGTTGGATGTAGCATTA
1029	CDKN2A	NM_000077	TACCGTAAATGTCCATTTATA	CAGGTGTGCCACATTCGCTAA	CAGAACCAAAGCTCAAATAAA	CACGCCCTAAGCGCACATTCA
1043	CDW52	NM_001803	GAGAATAAAGTTACCCTTGTA	CTGGTTATGGTACAGATACAA		
1046	CDX4	NM_005193	CACCGGCTTTCTCGCACTATA	CAAGGAGAGAAAGATGATCAA	GTAGTTTACACTGATCATCAA	CAGGTTATAGTCTCCGAATGA
1047	CLGN	NM_004362	CTGGATTATATTGCAGCATAT	AAGAAAGTAATCAATCAAATA		
1050	CEBPA	NM_004364	CAAGAAGTCGGTGGACAAGAA	CTCAGCCTTGTTTGTACTGTA	CCGAGTCACACCAGAAAGCTA	CAGCCGATATCAACACTTGTA
1056	CEL	NM_001807	CAGCCACATCCTGGCTGGCAA	AGCCCTGACGCTGGCCTATAA	CCCGTTATGATCTGGATCTAT	TCCCATGAGCCTTGGTATCAA
1059	CENPB	NM_001810	CCGGGAGAAGTCACGGATCAT	TTCGAGGTCTTGGACATCAAA	CACGCTGAGCACGATCCTGAA	CGCCTTGAGAAGCACAGTTTA
1069	CETN2	NM_004344	AAGCTCTTTGATGATGATGAA	GCGAATTACCCTAATTCTCAA	AAGCACATGTAACTAGATTTA	CAGAACGACTTTAGACAAGCA
1070	CETN3	NM_004365	CTGGTGACATTTAAAGAATTA	TCGAGCTATGATAGAAGAATT	TAGCTTTGTATTTATAATAGA	CAGTTACCATCTTATATTCTA
1072	CFL1	NM_005507	CAAGGTGTTCAACGACATGAA	CTGACAGGGATCAAGCATGAA	CAGTAAGGGACCTTCGATTAA	CAAGCATGAATTGCAAGCAAA
1082	CGB	NM_000737	CACCACCATCTGTGCCGGCTA	CCCACAATAAAGGCTTCTCAA	CCAGGACTCCTCTTCCTCAAA	CCCGAGGTATAAAGCCAGGTA
1084	CEACAM3	NM_001815	CAGTTCCATGTATACCAAGAA	CAGGACAGCAGCTTCCATCTA		
1088	CEACAM8	NM_001816	TTGCTTCTTCTTCAAGATTTA	CAGGCATGCAATGCTAGATAA		
1103	CHAT	NM_020549	CAGGACGGTCCTCGTGAAAGA	CCCGAGATGTTCATGGATGAA	CCGGAAATTCAAGGCCACTTA	CACGGAGATGTTCTGCTGCTA
1109	AKR1C4	NM_001818	CTGGGAACCCAACGACATAAA	GAGGGTGTTGCACGACATCTA	ATGGACCATCCTGATTATCCA	CCAGAAAGCAAACATAATAAA
1112	CHES1	NM_005197	CTGGACTTGGTTTATATTGCA	TCGAAGGAGCCTTCACGTAAA	CACGGCCAAATTAATTTACGA	CCGGTCCTGTTTGAATAACAT
1113	CHGA	NM_001275	TACCGAGGTGATGAAATGCAT	TCCAAGGATGTTATGGAGAAA	AAGGAGTGGGAGGACTCCAAA	TATGAACTTTATCTAAAGAAA
1116	CHI3L1	NM_001276	CAGCTGCTCAATAAAGTACAA	AAGGCCGAATTTATAAAGGAA		
1119	CHKA	NM_001277	TACCACAGAGATTGTACTATA	CACAGAGATTGTACTATACAA	CCGGCCCTTACCAAACCTGAT	AGCCGGCGATTAGATACTGAA
1121	CHM	NM_000390	TCGGAGTTTGATGTGATCGTA	CCGGAGAGTTCTGCATGTTGA	CGGAGTTTGATGTGATCGTAA	CTCCAATATATTGTCATGCAT
1128	CHRM1	NM_000738	TGGCTCCGAAGTGGTGATCAA	CAGCAAGACAATGACACTGGA	TACAGTCAAGAGGCCGACTAA	CCGGCTTGGCTAGTCACATAT
1130	LYST	NM_000081	CACATCATTGTCAACACCTAA	CACGCCGACCTGATTACCTAA	TCCGAGTATGCCATAAGTTAA	CAAGGTGTTATTAAACTATTA
1135	CHRNA2	NM_000742	CAGCCTCTGTTTGACCATGAA	CACGGGCACCTACAACAGCAA	CAGGAGTGGAGCGACTACAAA	AAGGGCTTTGAACAATGTTTA
1136	CHRNA3	NM_000743	GCGGCTGTTTGAAGATTACAA	AACTGTCTTAGTACACCATAA	TACCGATAAATGAACATTTAA	CCCACCTTCTATCTAAGACAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
1138	CHRNA5	NM_000745	CTGAACCTTCTTCTATTGCAA	CTGAAGTATACATTTAGTTAA	ATCGTTCTTCCTCAACACATA	CTGAGTAACAGCTAATCTTTA
1142	CHRNB3	NM_000749	CCACCACAGGTTTCAACTCAA	CGGAGAATGGGAAATACTGAA	ACGCTGGAATCCTGATGATTA	CAGGTAGTACAAGACTGGAAA
1143	CHRNB4	NM_000750	CCCAGGGAGAAGGACAGTGAA	CAGCAAGTCATGCGTGACCAA	CAGCTACGTGGACGTGACTTA	CACATGAAGAATGACGATGAA
1144	CHRND	NM_000751	CCGGCACCTGTTTCAAGAGAA	CCGCCAGGACATCACCTTCTA	CGGCTGAAGTGGAATGCTGAA	AACAATTACAATGAGGAGAAA
1146	CHRNG	NM_005199	CACCAATGTCTGGATAGAGAT	CTGCTCTATCTCAGTCACCTA	CACCAACCTCATCTCCCTGAA	CCACCAGAAGGTGGTGTTCTA
1147	CHUK	NM_001278	CAGCGTGCCATTGATCTATAT	CAGGGCAATAGTATGATGAAT	TTCCATAAGCTTGGTGACAAA	CAGGAGAAGTTCGGTTTAGTA
1163	CKS1B	NM_001826	CCAAGAAACCAAAGAAATGAA	GCGATCATGTCGCACAAACAA	AAGAAATCTGTTCATGTTAAA	AACATCTTTCTGATAACATTA
1164	CKS2	NM_001827	TAGGTTACTGTAAGATGTTTA	TCGGACAAGTACTTCGACGAA	CTGTAAGATGTTTAAGATAAA	AAGTTTGTATGTTGCATTTAA
1173	AP2M1	NM_004068	ACGTGTGACTTCGTCCAGTTA	TGCCATCGTGTGGAAGATCAA	TTGGAGGCTTATTCATCTATA	TGGAGGCTTATTCATCTATAA
1178	CLC	NM_001828	CACCTTTGACCATAGAATCAA	CAGGATGGCCAAGAATTTGAA		
1181	CLCN2	NM_004366	ACCGGGATGAAGAGACTATTA	CCGAATCAAGAAACTGCCCTA	CAGATGGAATTCATACGGACA	CTCATTGGAATCGTTACTCTA
1184	CLCN5	NM_000084	CACCGAGAGATTACCAATAAA	AAGGATGTGTTAAAGCATATA	TAAGTGGACTCTGGTTATCAA	ATCCTTGTTCCTGTTACAATA
1185	CLCN6	NM_001286	AAGATGTGAATTCAAGTATCA	TCAGATTTACGTCTACCCTAA	CACCAGAAACATAAAGGATTA	CCGGTGAATGTTATTGGAATT
1186	CLCN7	NM_001287	AGCGTGGAGCTGGATGATGAA	CTGGCTGACCATGTTTCGAAT	CCAGATCAAGTGCTTCCTCAA	CCAGCTCATCGTTCTCCTAAA
1187	CLCNKA	NM_004070	ACTGGCCATCACATTAATGAA	CTGAGTGTGAGAAGATGGAAA	CAGCTCCATTCTTTGGCATAA	TTGGCATAACAGGCAACTCTA
1192	CLIC1	NM_001288	TTCCTGCTGTATGGCACTGAA	AAGGTGTCTCTCAGAGGAAGT	CTGGTGGTTTCCACATTGCTA	AAACCCAGCACTCAATGACAA
1193	CLIC2	NM_001289	AAGCTAGACGGTCTTCTTAAA	CACAATGCCTATGCCCGTGAA	CTGGCTGATTGTAGCTTGTTA	CCCGTGAAGAATTTACCCACA
1195	CLK1	NM_004071	CCGTATTTCCAACACACGATA	CACGATAGTAAGGAGCATTTA	AACGTGATGAACGCACCTTAA	AAAGCCGGTATCAGAACCATA
1198	CLK3	NM_001292	CTGCAAACCTCTGAAGAGTTA	ACCCAAGCTATTTATATGTTA	CTGCATTCTCTTTGAGTACTA	CACGAAGATCTCGGTCCAGAA
1212	CLTB	NM_001834	CTCGGTGCTCATGTCCCTGAA	CAGCGCCAGAGTGAACAAGTA		
1230	CCR1	NM_001295	AAGCACGGGCCATATGAATAA	CAGCGATTAATAACAGGCAAA	GACGGAAGAGTTGAGACCTAA	CTGGATCGACTACAAGTTGAA
1234	CCR5	NM_000579	AGGCAACATATAGGTTGTAAA	AAGGGACATATTCATTTGGAA	TAGGTGAGGATTGATTACCTA	AAGATGGATTATCAAGTGTCA
1238	CCBP2	NM_001296	CACCAGATTACAACAAATTTA	CTCAATTAGCGTTATTGGCAA	CTGCATGAGCCTGGACAAGTA	CTCAGTGACTGTGTTGCTAAA
1244	ABCC2	NM_000392	CTGATCCAATACAGCAGACAA	CTGGAGTACCTACAAGCAATA	CTGGTGGATAGCAACAATATT	CCGTATCAGGTTTGCCAGTTA
1258	CNGB1	NM_001297	CACAAATAGCGCCATCATCAA	CGCCATCGACGTGAACTACAA	CATGGCCTTCTTCGAGTTTAA	CAGAAGTTACTCCGGAAGAAA
1260	CNGA2	NM_005140	CAGGGCTGAGATAGCCATCAA	TGGCGAGATCAGTATCCTTAA	TAGAGGCACCTATGAGTTAAA	AGCACCGACTATAGACATTTA
1261	CNGA3	NM_001298	CCACCTGATAATGGGTATATA	AAGGTTGGAATGGTGTACTAA	CACCTGATAATGGGTATATAA	TCCCTTGGAATTGCATCCCAA
1263	PLK3	NM_004073	GTGGGTTGACTACTCCAATAA	CTGCATCAAGCAGGTTCACTA	CCCGAAATCGTAGTGCTTGTA	CAGAAAGACTGTGCACTACAA
1272	CNTN1	NM_001843	CAGCCTAGTAGCAGTCATTAA	AAGGGTGATAATTGAATGCAA		
1281	COL3A1	NM_000090	TCCGTTCTCTGCGATGACATA	ACCGATGAGATTATGACTTCA	CGCGGTGAGGCTGGTATTCCA	CTCAAGTCTGTTAATGGACAA
1284	COL4A2	NM_001846	CACACCATTCATCGAATGCAA	CACGTTGTCCCTGAGATTTAA		
1285	COL4A3	NM_031366	CTGCTTGTATCCAAGCATATA	TCCCAAGGTTACTTAATTCAA	TACATTCCCAAGGTTACTTAA	AGCGGATATAGAGCTAGCTAA
1287	COL4A5	NM_000495	AAGGGTGATGATGGAATTCCA	CCGGGTCTCAATGGAATGAAA		
1290	COL5A2	NM_000393	CCGGGTCTACGTGGTGAAAGA	TAGGTTTAAGATGACCAATGA	CCGCACGTGTGATGACCTAAA	CACACTAGTATATACCATTTA
1297	COL9A1	NM_001851	CACCGACAGATCAGCACATTA	CAGCATGATTACAATGTATTA	AACGGTTTGCCAGGAGCTATA	CACCTCCCTTGAACAAATTTA
1299	COL9A3	NM_001853	CAGGGTGACAGAGGAGACAAA	CAGGCTCTCGAAGCTCATAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
1300	COL10A1	NM_000493	TACGGAAGTCCTGGACTCCAA	AGCAATCTTAAGGCTCTTTAA	CCCAGCTGGCATAGCAACTAA	AAGCCTGTTTCTAACTATGAA
1307	COL16A1	NM_001856	AAGGGTATTTCCCTCCTTAAA	CAGGAAGGACTCAAATTGGAA		
1314	COPA	NM_004371	CTGGATTTCAACAGCTCCAAA	TCCCACTGAGTTCAAATTCAA		
1315	COPB	NM_016451	CAAGGATTGGTTATAATATAA	CAGGATCACACTATCAAGAAA		
1347	COX7A2	NM_001865	ATCAATATTTATTGACTTGTA	GACCAGTAATCTGATAAATAA		
1349	COX7B	NM_001866	CAGCTCATAATTGATGCCAAA	TGGCATTATTGAAGAAATAAA		
1352	COX10	NM_001303	ACCATAGTCCTTCTAACAATA	AAAGGGATTGTAGGTAGATAA	AAGGGTAGCCCTGGACTTAAT	TAGGTAGATAACATCCAATCA
1359	CPA3	NM_001870	CCCAATAGAATCAACAATTTA	CAGTAGCACCATAACGAAGTA	ATCCTCAAGCATACTTCCTAA	AACGAAGTAGCTTTAAGTGAA
1363	CPE	NM_001873	TACCTGGAAACTATAAACTTA	CTCGGAGTTGTGAGCACTCTA	CAGGCTATCTGGCAATAACAA	TAGTCCGTTAACACTACTTAA
1365	CLDN3	NM_001306	CACCGGCCAGATGCAGTGCAA	CACCATTATCCGGGACTTCTA	CACCACCACCACCACCACCAA	CACGGCCACCAAGGTCGTCTA
1366	CLDN7	NM_001307	GCCGTTGGTGGGAGAGACAAA	CCGCTCTTACCCTAAGTCCAA		
1369	CPN1	NM_001308	CCGCAACTTCCCTGATCTCAA	CAAGGGAATGCAAGACTTTAA	CCGGTGGATGCACTCCTTCAA	AAGACTTTAATTATCTCCATA
1378	CR1	NM_000573	CAGTCCTACGATCCCAATTAA	CTGCATGGTGAGCATACCCTA	TCGGTGTATTTCTACTAATAA	CTGGAGCCAATTGGATCATTA
1385	CREB1	NM_004379	CAGCCACAGATTGCCACATTA	CCGCATGCATAAAGTAAGTAA	CAGCCGGGTACTACCATTCTA	AGGGCAGTTGTTGCTTCTTAA
1393	CRHBP	NM_001882	CTGCAGCTTCTCCATAATTTA	CAGGAAATGGATTCACATTAA		
1394	CRHR1	NM_004382	CAGGACTGCAGTGCAACGCAT	CCGCTACAATACCACAAACAA	GCGGGTGGCTGGTATAAATAA	CAGGTTGGTGACAGCCGCCTA
1395	CRHR2	NM_001883	CTGCAGCTCGTTGACCATGAA	AAGCTCTACTATGAGAATGAA	CACGGCCATTGTCATGACCTA	ACGGATCAGCTTCCACAGCAT
1397	CRIP2	NM_001312	CTGGCACAAGTTCTGCCTCAA	GAGCCTTGTGCTGTCAATAAA		
1398	CRK	NM_005206	TACACTATTTGGACACTACAA	CAGGATGTACCGAGCACTTTA	CTGAGTATAGTTCAACAGTTT	CAGCAGCTAACTAGAGTCCTA
1401	CRP	NM_000567	AAGCGCTGATCTTCTATTTAA	AAGGAGAAATGATGTTATAAA		
1407	CRY1	NM_004075	GAGGATCTTGATGCCAATCTA	AAGGAATGGAACATTACTAAA	CTGTTTGTGATTCGTGGACAA	ATCAGCAGCTTTCACGATATA
1409	CRYAA	NM_000394	CCCGGAGGACCTCACCGTGAA	CCGGGACAAGTTCGTCATCTT		
1421	CRYGD	NM_006891	TCCTCCTTTGTTGTTTCTTAA	TTGTTGTTTCTTAATTTGGAA	CAGCGGCTGCTGGATGCTCTA	ACCGCTTCCGCTTCAATGAAA
1427	CRYGS	NM_017541	AAGATTCAGATCTTTGAGAAA	CCAAATAGGCATCATCAATAA		
1428	CRYM	NM_001888	CACCAAGTTGGTCACCTTCTA	CTGGATGATGAGCTCATGAAA		
1436	CSF1R	NM_005211	CTGGAAGATCATCGAGAGCTA	ATGAGCCAAGTGGCAGCTAAA	ATGGAAATGGACTGACTTTAT	ACCCTCAACCTCGATCAAGTA
1441	CSF3R	NM_172313	TCCTATAACTTCAGTATTGTA	CCAGGCGATCTGCATACTTTA	CTCCTGCATCATCAAGCAGAA	CAGGCGATCTGCATACTTTAA
1444	CSHL1	NM_001318	CCTCAGGAGTACCTTCACCAA	CAGGAGTACCTTCACCAACAA		
1445	CSK	NM_004383	AGGGAACAAAGTCGCCGTCAA	CCCAACTGGTACAAAGCCAAA	TACGCGCCTCATTAAACCAAA	CCGGTACAGAATGTATTGCCA
1447	CSN2	NM_001891	CAGAGTGATGCCTGTCCTTAA	ATGGAAGTCCCTAAAGCTAAA		
1452	CSNK1A1	NM_001892	AAGAACTTAATTTCAGTATAA	CACAGTTGTGATGGTTGTTAA	CAAGAGTAACATGAAAGGTTT	AGGGCTAAAGGCTGCAACAAA
1453	CSNK1D	NM_001893	AACACGCACCTTGGAATTGAA	CGGTCTAGGATCGAAATGTTA	CTCCCTGACGATTCCACTGTA	CCGGTCTAGGATCGAAATGTT
1454	CSNK1E	NM_001894	TCCCTCCGAATTCTCAACATA	CTGGCTCTGAGTTATAAATTA	GTGGTTGTTAATTTGAAGTAA	GAGCTTTATCGTGGTTGTTAA
1455	CSNK1G2	NM_001319	ATGTAAGACTTTGGCCGAAAT	GCACACCAAGAGCCTAATCTA	TAGGAAAGAATCTCTATACAA	AAGAATCTCTATACAAATGAA
1456	CSNK1G3	NM_004384	CAGGTTGTAAGTTCTACAAAT	AAGAGCATAATCAAACAGGAA	TACCGCAAACTTGATATGGAA	CAACATATCTTCGTTATGTAA
1465	CSRP1	NM_004078	CAGGATGTTGTTTGATCTTCT	TGGGAGGATCCTAATGAAATA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
1466	CSRP2	NM_001321	CAGGCCTACAACAAATCCAAA	CAGATAATCTTTAACACTAAA		
1475	CSTA	NM_005213	CAGGAGATTGTTGATAAGGTT	CTGGAACAAATTACTACATTA		
1486	CTBS	NM_004388	CTCCCTATAATCAGACATTAA	AACGATCATGAAGCAAATAAA		
1489	CTF1	NM_001330	CCCGTTCTCTTAACTCTTGGA	CAGCAGATCTGTGGAGACAAA		
1493	CTLA4	NM_005214	AAGAAGAGAGTCCATATTTCA	AAGCATCACTTGGGATTAATA	CCCAAATTACGTGTACTACAA	CAGCATTATGATGTGGGTCAA
1495	CTNNA1	NM_001903	ACAGACTTTACCCGAGGTAAA	GCGAATTGTGGCAGAGTGTAA	CAGTCACTGTTCGTCACTCAA	CACCCTGATGTCGCAGCCTAT
1496	CTNNA2	NM_004389	CAGCATGTAAGCAGGATTTAT	TACCATTGTATTCACTAACTA	ACAGGCTTTAAGTGAATTCAA	CCCATGAATTGAACAATTTAA
1497	CTNS	NM_004937	CTCGCTAGGCGCCCTAAGCAA	CGCCATTAGCATCATAAACCA	CAGCGCCATTAGCATCATAAA	CACCTACTTGAGACTCACCAA
1511	CTSG	NM_001911	CAGACGGAATCGAAACGTGAA	CACAGTGTTGCCAGAGCCTTA	CAGCCTTTCAGGAAAGATGCA	CCACAGAGTATAAATAACCAA
1512	CTSH	NM_004390	GTCCTTCTTAACAGACTCAAA	CACCCGTGTCTATGACGCAAA	CGAGTATATCCTGTACAACAA	ATGGATGTCTAAGCACCGTAA
1513	CTSK	NM_000396	CCCGATGGAATAAATCTAGCA	AGGGCTGATGCTGTACAGGTA	CCGCAGTAATGACACCCTTTA	CACGGGACTAGTTAGCTTTAA
1520	CTSS	NM_004079	CTGCCACATGTTCAAAGTACA	TGGGATAATGTCATTAATATA	AAGGATATATTCGGATGGCAA	AGGAATCTAATTATATCGAAA
1521	CTSW	NM_001335	CCCAGCATGGGCAGAGAAATA	CGCGTTCATAACTGTCCTCAA	CGGCGCCATCTCACCCATCAA	CACCGTGACCATCAACATGAA
1524	CX3CR1	NM_001337	AACTCAGACTAGTTTAGTTAA	CAGACTAGTTTAGTTAAATGA	TCAGATGTGGTAACTGTTAAA	TAGAGTTGCAATCGTAATGTA
1525	CXADR	NM_001338	CTCCATCAATTCTGTATTCCA	CAGGTAATAGGGACTTAGCAA	TTGGTTATATCGAAATAGTTA	CAGGAACTGTACGGAATATAT
1536	CYBB	NM_000397	CACGCTGTGCCTCATATTAAT	CCAGATCATTAGGACATAATA	ACCCTTCGCATCCATTCTCAA	CAGGCTAAGGATACTAACCAA
1538	CYLC1	XM_088636	CAGGTAGAGTTCCTCCATCAA	AAGGAATTACTCACAGAATAA		
1548	CYP2A6	NM_000762	CAACACGGAGTTCTACTTGAA	CACCTTCGACTGGGTCTTCAA	CCGCTTTGACTATAAGGACAA	TCGGGATTTCTTCCTCCCTAA
1549	CYP2A7	NM_000764	ATGCAAATATTCCAAACTCTT	CCTGATGATGAGCACGTTGAA	CCCAAGCTAGGTGGCATTCAT	CAGCTTCTTCTCCAACCCTCA
1558	CYP2C8	NM_000770	CCGGCGTTTCTCCCTCACAAA	ACGAAGTTACATTAGGGAGAA	AACTCACAACAAAGTGCTTAA	AAGTCAGAATTCAATATTGAA
1572	CYP2F1	NM_000774	CAGCATAAGCACAGCCATCTT	CACCATTATCCGCCTTATCAA	CAGCGGGTACCAAGCTGTGAA	TCGCGGCTTCCTGATACCCAA
1579	CYP4A11	NM_000778	CCCTGACGCACCATAATCTAA	ATCAATTGTATCTTGAGTTAA	TCCTATATTAGTTTCCTATTA	CAGCTGTAAATTGTGTGCTTA
1584	CYP11B1	NM_000497	CTGGGACTGCATCTTCCAGTA	CAGGTGGAGACACTAACCCAA	CAGGACAGTGCTGCCCTTTGA	CACCTTCAGAGCCATCAACTA
1585	CYP11B2	NM_000498	CAGGGAGGCTGCAGTTCCCTA	CAGAGATGGCTTCCTTGTTTA	AAGGCGGAACTGTCACTAGAA	CACTAGATCATGGGATCCTAA
1586	CYP17A1	NM_000102	CAGACATGGCCATATGCATAA	CCGGAGTGACTCTATCACCAA	TGAGTTGAATGTCATACAGAA	CAGGCTGAGGGTAGCACCTAA
1591	CYP24A1	NM_000782	CTCGGACTCTTGACAAGGCAA	AAGTTAGAGATCTGTTATATA	TAGGGTAAAGATGAAGCAATA	TGCAATACTTATAAGACTTAA
1593	CYP27A1	NM_000784	CAGCGGAAGCAGCGCTCTATA	CACGCTGACATGGGCCCTGTA	CTCGAAGATATGGAGGCCCAA	CCGCATTGTCCTGGTTCCCAA
1595	CYP51A1	NM_000786	TCCGTTACAAACGAAGATCAA	TAGGGAATAATCGAACATCTA	TAGGTAATTGGCAGATTCTAA	AAGGTCCTTGGGAGTAATAAA
1600	DAB1	NM_021080	AAGGATAAGCAGTGTGAACAA	AAGGATTAAGTAGGATGTCAA		
1601	DAB2	NM_001343	TGGGAGGTTATGTTTATTTGA	TAGAGCATGAACATCCAGTAA	ACGAAGTAGAAACAAGTGCAA	AAGGTTGGCCTTAGTAGTCAA
1603	DAD1	NM_001344	CAACTTTCTAACAAACATTTA	TTGCCTGAGAATACAGATCAA	CAGCCTCTGCCTTTCATTAAA	CAGATTTGACACTTACTGCTA
1605	DAG1	NM_004393	CAAGAAGATTGCCTTGGTAAA	AAGGGTGTGCATTACATTTCA	AAGAACCATATTGACAGGGTA	CCGGTGGTGAATAACAGACTA
1608	DGKG	NM_001346	CAGCATGTACGGAGGCACCAA	CAGCCATGTTGCACGATTAAA	TAGCCACTCACATAAAGTTTA	ACCGCAAATGTGAATTATCAA
1610	DAO	NM_001917	CTGGAGGGAAAGAACTATCTA	ATGGAGGATAATTGAGGCTAA	CAAGAATTATTGGTGAACGAA	CAAGTTGTACTAACATATTAA
1611	DAP	NM_004394	CTGCTGGGAAATCTAAGGCAA	CACCAAAGAAGAGAAAGACAA		
1613	DAPK3	NM_001348	CGCAGCCAAGTTCATCAAGAA	CACCAACATCTCAGCCGTGAA	CCGGCAGAAGGGCACGGGCAA	CCCAGAGATTGTGAACTATGA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
1622	DBI	NM_020548	CTGGATTTGGTTACTGTGCCA	CCAGTTAAACCAGCTACTCAA	AAAGTGTATTTGTTACTTTAA	CAACAAAGTAGAAGAGCTAAA
1627	DBN1	NM_004395	AAAGTTGATAGGAGACTTGTA	CTCATGTCTGTTAATAAAGAA		
1629	DBT	NM_001918	ATGACTGTTCCTATACTAGTA	ACGATTTGTATCGTATGATTA	AACGATTTGTATCGTATGATT	TAGCCATATACAGACAGTATA
1630	DCC	NM_005215	CCGAGGAGTTCCAGTGATCAA	CAGCATACCAATTACCCATAA	TCACTGCAATGTCAAAGTTTA	CACCTGTGTCCAAGAACTCTA
1633	DCK	NM_000788	AGGCAGCCTGCTATAAAGTTA	TGGACTCATCTTAGTTCTGTA	TTGGTATAAATTAATTTGTTA	AAGTTGCAAAGTGGAATTAAA
1636	ACE	NM_000789	CTCCTGTTACCCGAAACGAAA	CACCACAGAGGCTATGCTAAA	CCCGAAATACGTGGAACTCAT	CAGCGACGAGCATGACATCAA
1641	DCX	NM_000555	AAGGGTTTGATGAATAGCACA	ACCCTGCACATTTGATTCTAA	ATGGACTTTAGTATTAGCCTA	CTGAATAGACAGTCCATATAA
1645	AKR1C1	NM_001353	CACGTGGGAGGCCGTGGAGAA	AATTGTTCTGGTTGCCTATAG	CTTGGTGATTTCAGCAAGCTA	AAGGTGGAATGTCATCCTTAC
1649	DDIT3	NM_004083	AGGGAGAACCAGGAAACGGAA	CAGCTTGTATATAGAGATTGT	CAGCTAGCTGAAGAGAATGAA	AAGGAAGTGTATCTTCATACA
1650	DDOST	NM_005216	CCAGTTTAAAGTGGATTACAA	CAGCCTGTCTCTCATAAAGTA		
1652	DDT	NM_001355	AACATTCCTGTGATCACATAA	TCCTCATATGAAATAAATGAA		
1653	DDX1	NM_004939	ATGAAAGTCTGTAGTCTTAAA	CCGGATGGTTACATTGTCAAA	CCGGGCAATCAAGGAACATAA	CACGGTGTTCCTTATGTTATA
1660	DHX9	NM_001357	TTGGTTGTTGAAGTAACCAAA	CTGTGGTTCATTGTAGTTTAA		
1665	DHX15	NM_001358	CCGGACATGTACAGACATCAA	AGGGACTATTATATTAATATA		
1673	DEFB4	NM_004942	TGCCTTAAGAGTGGAGCCATA	GCCCTAGAAGGTATAAACAAA	GCGACATGTAAACCAAATTAA	GACGTGCGACATGTAAACCAA
1676	DFFA	NM_004401	TGCCTTGAACTGGGACATAAA	CCGGAGCATCTCAGCAAGCAA		
1687	DFNA5	NM_004403	CTGATAAGTTACAGCTTCTAA	TAGAAAGAGTCTGACCCTTTA	AACATACTAATTCTATGTCTA	GCGGTCCTATTTGATGATGAA
1716	DGUOK	NM_001929	AAGGCTCTCCATCGAAGGCAA	CCGCCTGAAAGTACAGCTGGA	CAGCACGATGGTCCTACACAT	CACCTTTGTAAAGAATCTGTA
1723	DHODH	NM_001361	CAGGTATGGATTTAACAGTCA	CTCCGGGATTTATCAACTCAA	CAGGGCTTTGGCGGAGTCACA	CAGGAACTTGACTGTCTTTCA
1733	DIO1	NM_000792	TTGGGAGTTTATGCAAGGTAA	CCCAATCAAGACAAATTGTTA	CACAGTTAATCTGGACAGATA	AAGAGGAGAGTACTCACTTTA
1737	DLAT	NM_001931	CACAGCGATTAATGCAATCAA	TTGGTTTATCATCGATGGGAA	TACCTCATTATTACCTTTCTA	CTCCAGCATCGTCTCATGTAA
1739	DLG1	NM_004087	CGGGTCAATGACTGTATATTA	ACGGGTTATTAACATATTTCA	ATGACTGTATATTACAAGTAA	AACAGTGAAATTCAATTCTAA
1740	DLG2	NM_001364	CCGGACTAACGTGAAGAAGTA	TACGCTCGATTTGAGGCCAAA	CTCGGCTGTATGTGCGTAGAA	CTCGACTAACCCACGAAGTAA
1749	DLX5	NM_005221	ATGTAAGTTATTGCATTTCAA	CTGTATATTCTGGATAAATAA		
1756	DMD	NM_004014	CTGCTTCCAATTTGCTAATAA	CAGGAGTCTAAAGCACTTTAA		
1760	DMPK	NM_004409	CAGCGAGGTAGCGGTAGTGAA	CTGGGTGTATTCGCCTATGAA	GAGCCTGAGGGCTAAATTTAA	AACCAGAACTTCGCCAGTCAA
1761	DMRT1	NM_021951	CTGCATGATTTAAGTGCTTTA	TTGGTAAAGGGTGTAATTTAA	AAGCCATTTGTGTGCCTCTAA	ATGGAGTACTTTGTTATATAA
1774	DNASE1L1	NM_006730	AAGGAAAGTTACTGAGAACAA	CAGGGAGAAACAGACATCAAA		
1777	DNASE2	NM_001375	AAGGGCCACCACGTTAGCCAA	GACCTTGATTGTGTGCCTTAA	CAGCAGAGCTTATAAGATCTA	AAGGGCCACCACGTTAGCCAA
1778	DNCH1	NM_001376	AAGGAGGTTCTTAGCAAATTT	CAGGAGGTAATTGCAGACAAA	CCCGTGATTGATGCAGATAAA	CAGGTGGGTGTACATTACGAA
1788	DNMT3A	NM_022552	TTGATTAATTGGCGTAACTTA	CAGAACAAGCCCATGATTGAA	CTCAGTGGTGTGTGTTGAGAA	AACACCGGGATCTATGTTTAA
1791	DNTT	NM_004088	ACCGGTGGAAATGACAGGAAA	CTGGGATTGGATTATATTGAA		
1796	DOK1	NM_001381	CCGGCAGAAGGCCCAGGGAAA	AAGGATCCCAATTCTGGGTAA	CCGCCTGGACTGCAAAGTGAT	AGGGATCAAAGAAGATGGTTA
1803	DPP4	NM_001935	ACACTCTAACTGATTACTTAA	CAGTAAAGAGGCGAAGTATTA	AACAATGACATTTATGTTAAA	ATCGGGAAGTGGCGTGTTCAA
1804	DPP6	NM_001936	TACTGTCTTAATAGAAGGCAA	TCCCTACACGTTATTGGCTTA	ATGGTTAACCTGATAGAATTA	ACGCTAATGGTTAACCTGATA
1806	DPYD	NM_000110	CTGAGGATAGTAGTTAAATAA	TCGGTGAATGATGGAAAGCAA	CCCACGGAAGGTTATAGTAAA	TCGAGAGTATCCTGGCTTTAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
1807	DPYS	NM_001385	AACACCCGACTTCCTCATGAA	TGGGAAGTTTATTCCTCGAAA	CTCCCTAGGATCCTTTAGAAA	CGGCAGGAGATGGGAAGTTTA
1808	DPYSL2	NM_001386	TACCATGGAACGCCTAATAAA	CAGGCTTGCGTTATTGGCCTA	ACGGATTGCCAGATTTATGAA	CTCGTGTTTATTATTCCTTAA
1809	DPYSL3	NM_001387	CTCAGCTTATATGAAAGTCAA	AAGGATTGTAGTCATCCTGAA		
1810	DR1	NM_001938	AAGATAGTATTAAGTAATTAA	CAGCCGTATATGGAACATAAA		
1812	DRD1	NM_000794	ATCGGTCATATTGGACTATGA	CACAATTAACTCCGTTTCCAA	GACGGTGAGTATCAATAACAA	ACGGTGAGTATCAATAACAAT
1820	ARID3A	NM_005224	CAGCATGTCGGTGGAGATCAA	AAGGATATCTATATATCTATA		
1830	DSG3	NM_001944	AAGGCTCTAGATTATGAACAA	CTCACTGGTGATGATACTAAA		
1832	DSP	NM_004415	CAGAAGAATGACTATGACCAA	CCGACATGAATCAGTAAGTAA	CAGGGAGATCATGTGGATCAA	AAGGGCCACGGTATTCGCTTA
1834	DSPP	NM_014208	GAGGATGTCGCTGTTGTCCAA	CATGATAGTAGCATAGGTCAA	AACGAGGGTAATACAAGTGAA	TCGGATAGTAAAGAATATTAT
1837	DTNA	NM_001390	CAGCCATAGAATTTAGTGTAA	TGCGACCTATTCAATACATTA	CAGCATTCAAATTATATAGAA	CCCGTTGTCATAGCTATTTCA
1838	DTNB	NM_021907	CAGCTTATTGCAGAACTGGAA	CCACTTGACCTTGCACATATA		
1840	DTX1	NM_004416	CCGGGAAGAAGTTCACCGCAA	GTGGGAGTCAGCCAAGATTTA	CACTGTGGGTGGAGAAATAAA	GACCAAGAAGAAGCACCTTAA
1844	DUSP2	NM_004418	CGCGGGAAAGACCGAAAGGAA	AAACTTAGCACTTTATATTTA	CTGGTCCACCACCATGTTGAA	CAGCCTGAGAGCTCCAAGGAA
1856	DVL2	NM_004422	CTGGCTGGTGTCCTCAGATAA	CACGCTAAACATGGAGAAGTA	CCGGATACGAGAGCTCCTCTA	CTGGGAGATTTGGGCCATGTA
1857	DVL3	NM_004423	CCCGGCTAAATGGAACTGCGA	CTCCTGGTTACTTCATCACAA	CAGCATATCATATCCATTTCA	ACCAAGTATGTTCCTCCTGAA
1869	E2F1	NM_005225	CTCACTGAATCTGACCACCAA	CAGATGGTTATGGTGATCAAA	CAGGACCTTCGTAGCATTGCA	ACGCTATGAGACCTCACTGAA
1870	E2F2	NM_004091	TCCGTGCTGTTGGCAACTTTA	TAGGGACCAGGTAGACTTTAA	ACCCATTGGGAATGAGTTTAA	TTGAGACGAGGGATTATTTCA
1874	E2F4	NM_001950	GCGGATTTACGACATTACCAA	AACGAATGGATTCCTATATAA	ACCCGGGAGATTGCTGACAAA	AGGTATCGGGCTAATCGAGAA
1893	ECM1	NM_004425	CTGAACACTCATTACACTAAA	CCGGGACATCTTGACCATTGA		
1908	EDN3	NM_000114	CTGGACGTCAGCAGTAATTCA	TAGACACAGATCATAGCTCTA	CAGAAGCATGCGACTTTCATA	TTGCAGGAAGCCGACTGTAAA
1912	PHC2	NM_004427	CTGGTTCACAAAGAGCATTAA	CCGGGTGGACTTTGCCTATAA		
1915	EEF1A1	NM_001402	CAACGTTACAACGGAAGTAAA	AAGCTGGAAGATGGCCCTAAA	CTGGGTCTTGGATAAACTGAA	CTGGTTAATGATAACAATGCA
1933	EEF1B2	NM_001959	CTGGATCATGGCATTTAAATA	ATCCTGGATCATGGCATTTAA		
1936	EEF1D	NM_001960	CTGGTTCGACAAGTTCAAATA	CCGGCTGAACGTGCTGGAGAA		
1937	EEF1G	NM_001404	CACCCTGTTGTGGCTCTATAA	ATGGCCCAGTTTGATGCTAAA		
1938	EEF2	NM_001961	TGCCGTTTCTTTCAATATTTA	CCGCGCCATCATGGACAAGAA		
1942	EFNA1	NM_004428	CACCATACATGTGCAGCTGAA	TACAATGTTCTTTGTCTCAAA	CCCGGAGAAGCTGTCTGAGAA	CACGTGTATAGTATCTGTATA
1945	EFNA4	NM_005227	CTGGAGAGACTTACTACTACA	CTGGGATTTGGTATGATCAAA		
1947	EFNB1	NM_004429	AGCGACATCATCATTCCCTTA	ACGGACTACAGAGAACAACTA	CTACATTACCTCAACATCCAA	CTCACGGTAATTAATGTCTTA
1952	CELSR2	NM_001408	CCCACTATACAGTGAATGTTA	CCGGGAGGAAGTTGATTTCTA	CACGTGGTGGTCTTCAACGTA	ACGACAACAATCCAACCTTTA
1953	EGFL3	NM_001409	CCCGTATTTATGTAAAGGTAT	CAGGACCTGCCTGGCCATTAA		
1955	EGFL5	XM_376905	TTGGAAGATGATGGCAATGAA	CCCAGGTAAATTGACCATTAA		
1956	EGFR	NM_005228	TACGAATATTAAACACTTCAA	CCCGTCGCTATCAAGGAATTA	CCCATCCAATTTATCAAGGAA	CAGGAACTGGATATTCTGAAA
1964	EIF1AX	NM_001412	CACGTAGAATGTATATTTGTA	AAGTCTGTTTGTCATATTTAA		
1969	EPHA2	NM_004431	CAGCCTTCGGACAGACATATA	TTGCAGATGATTCAAACCGAA	TCGGACAGACATATAGGATAT	CAGCGCCAAGTAAACAGGGTA
1973	EIF4A1	NM_001416	AAGGATCATGTCTGCGAGCCA	CCCGATGGGATGGAGCCCGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
1979	EIF4EBP2	NM_004096	CAGGAATAAGCTGGATCTCCA	CACCTTAATTGAAGACTCCAA		
1993	ELAVL2	NM_004432	CTGAATGGATTGAGACTTCAA	CAAGACCAACTTAATAGTCAA		
1995	ELAVL3	NM_001420	CTGGTGCATCTTCGTGTACAA	CCCGACTTTAGCTATAGTTAA		
1996	ELAVL4	NM_021952	ATGGTCCGACATCCAATACAA	AAAGGTGATTCGTGACTTCAA	TTGGAGCAGTGAACAACGTAA	CCAGTGTTGCCTAAGTATTAA
1997	ELF1	NM_172373	CAGAACTTAAATAGAAGGCAA	CAGAGTGAATTTGTATTTAAA		
1998	ELF2	NM_006874	AAGCATCAGTTCACAGCAGTA	AACAACTGAACCCATCAATAA	CACCAGATAGCCATGAACCAA	TACGATATCAAGTTACACTAA
2009	EML1	NM_001008707	CAGGCCGTGCTTAACAGGAAA	CAGATTGAAATTTATTGTTTA		
2012	EMP1	NM_001423	TAGTATGTTATTCCTGGTTAA	CTCTATGTTTATTCTAGTTAA		
2020	EN2	NM_001427	CCCGCTCTTTCGGATCGCTAA	TACGTTGTACATAATAGTGTA	CACCAAGTACCTATATATGTA	CCCACGGTAAACAATATGGAA
2021	ENDOG	NM_004435	CCGCACCTACGTGATGCCCAA	CTGGAACAACCTGGAGAAATA	CTGATGGGAAATCCTACGTAA	CCCGGGCGAGCTGGCCAAGTA
2022	ENG	NM_000118	AAGGGAGAACTTGAAACAGAT	CGCCATGACCCTGGTACTAAA	ACCAATAAATCAGACCATGAA	CAGCAATGAGGCGGTGGTCAA
2027	ENO3	NM_001976	CCAGACCTGCTTCCTGAAATA	TAAGAGCTTTATCAAGAACTA		
2029	ENSA	NM_004436	TTGGGAGAAATATCAATGAAA	TCAGTATTCGAAATAAACAAA	CTAGTTGAGAACTCAACATTA	TAGTTGAGAACTCAACATTAA
2030	SLC29A1	NM_004955	CCGCCTGGAATTCTACCGCTA	CAGCCTCAGGACAGATACAAA		
2033	EP300	NM_001429	CAGGGAATGAATGTAACAAAT	CACCGATAACTCAGACTTGAA	CCGTTTGTGGTTTAAAGCAAA	TTGGACTACCCTATCAAGTAA
2035	EPB41	NM_004437	ACCGAGCAGCTAAGAAATTAT	CACGGCCTAGTGAATGGGATA	GAGGATTTAGACAAGAGTCAA	TAGGATATCAGAATTGTTCAA
2037	EPB41L2	NM_001431	CAGGTCTTAGATAAAGAGGAA	ACGCAGTAACTTCTACATTAA		
2039	EPB49	NM_001978	CAGAAGATCTATCCCTATGAA	CCGCCCAGATTCCAACATCTA		
2040	STOM	NM_004099	CCCATTCATTACATAGTATAA	TTGGTGATTTATATAAGGTAA		
2043	EPHA4	NM_004438	AGGGTGTATATTGAGATTAAA	CCAGTACTGAATAAACTCAAA	CCGCCAGGACATTTCCTATAA	CCCGCGAATGAAGTTACCTTA
2044	EPHA5	NM_004439	ACCAGCTACACGATTATCAAA	AACGGAATGGTGCCATTGTAA	CCCGGCAGTATGTGTCTGTAA	ACCAGTTGGATCTCCAATGAA
2045	EPHA7	NM_004440	CCCAATGGAGTCATCACAGAA	TACGAGAAAGATCAAAGGGAA	CAGGCTGCGAAGGAAGTACTA	ACCAGTCATGATAGTAATAGA
2047	EPHB1	NM_004441	GAGATGTACCTTCAATTGAAA	ATGATACTGACTGATTAATTA	GCGGGATGATGTGACCTACAA	ATGGCCCTGGATTATCTACTA
2048	EPHB2	NM_017449	CCCGGATCATTCACTGTGATA	TAGGCCTCACTCAACAACCAA	CCGAGAGGACCTCGTCTACAA	CACGCTTTCTAGAGGACGATA
2051	EPHB6	NM_004445	CGCCAATCTCTAGATCAACAA	CCGGGAGACCTTCACCCTTTA	CTGGAGCTTTGGGATACTCAT	AACCGCCAATCTCTAGATCAA
2052	EPHX1	NM_000120	CCACTATGGCTTCAACTCCAA	TTCCAGGAATTCTACATTCAA	CAACAGATACCCTCACTTCAA	CAACATGGCTTTGATGATAAA
2058	EPRS	NM_004446	AAGCATGAAGAGCTAATGCTA	CAGGAGGAGACTATACAACTA	AAGGAGGTGGGCTCTCATCAA	AAGGCGATTACTCAGTGTTAA
2059	EPS8	NM_004447	CGCCATATAGATAGAAATTAT	TTGGATATTGTGAGACCTCCA	CAGGTGGATGTTAGAAGTCGA	TCGGTTCTAAAGGATGATATT
2065	ERBB3	NM_001982	AACACTGGTGCTGATCGGCAA	CTTCGTCATGTTGAACTATAA	CCAGAGCTTCAAGACTGTTTA	ACCGGCGATGCTGAGAACCAA
2066	ERBB4	NM_005235	CACCGGAATACTGTGGTGTAA	TCGGGATTTGGCAGCCCGTAA	CTGGAGAATTTACGCATTATT	CTACGTGTTAGTGGCTCTTAA
2067	ERCC1	NM_001983	CACCGTGAAGTCAGTCAACAA	CACCGTGAAGTCAGTCAACAA	CCCGGGTGACTGAATGTCTGA	ACCGTGAAGTCAGTCAACAAA
2068	ERCC2	NM_000400	CCGGGAGGATATTGCTGTGAT	CCGATTCTATGAGGAATTTGA	TCGAAAGTTGCTCAACTTCTA	CCCGCTCACCCTCCTTGCTAA
2070	EYA4	NM_004100	CTGGGTCAGTAATTACAAGTA	CAGCTTTAGCAAAGAACTCTT	AGCGTATATGACATCGAATAA	CAGTCCTATTTAGACATGTAA
2071	ERCC3	NM_000122	ACCCATGTGCATGAGTACAAA	CCGGGAATATGTGGCAATCAA	CCGGTTCACCTCCGATGCCAA	ACCGTTCTGAATAAACAGAAT
2103	ESRRB	NM_004452	CAGCTGCGGCTCCTTCATCAA	ACGCAGGTACAAGAAGCTCAA	CCGCTTCATGAAATGCCTCAA	CAGCACTTCTATAGCGTCAAA
2113	ETS1	NM_005238	CTCGGATTACTTCATTAGCTA	CCGACGAGTGATGGCACTGAA	TCGGATTACTTCATTAGCTAT	ATGCATGTCGTTCCAAACTAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
2114	ETS2	NM_005239	CCCGGTCAAGTTGGTTTCAAA	CTGTGATGAGTCAAGCCTTAA	CTCATTGTATGTGAGGTTGAA	AGGGATTTATGTAGCAGCTAT
2118	ETV4	NM_001986	ATGGGCTATGGCTATGAGAAA	CAGCAGAGCTTTAAGCAAGAA	ACCGGAGTCATTGGGAAGGAA	CCGGAGTCATTGGGAAGGAAA
2119	ETV5	NM_004454	CAGAAATTACTCAATGCTGAA	CAGGATCTCAGTCAACTTCAA		
2121	EVC	NM_014556	CAGCTAATCGATAATATGGAA	AAGAAGCAACTTGTAGTTTAA		
2122	EVI1	NM_005241	CTGAACTAGCAGATCACCAAA	CCAGTGCTATCCAGTCCATAA	GAGCTGTGAATGATTCTATAA	CAGCACTACGTCTTCCTTAAA
2123	EVI2A	NM_014210	AACCCTATAACTCCTGAAGTA	CATGGTAGACCTTGCAATTTA	ATGGCTATGCTAATTTGCTTA	GAGCTAAACTGTGTAATTTAA
2124	EVI2B	NM_006495	CAGGATTTATCTTAGATACTA	CAGGTATTGGCTAATTCTCAA		
2130	EWSR1	NM_005243	CAGAGTAGCTATGGTCAACAA	CTGCATTGACTACCAGATTTA	TCCGGGTTGTGGAAACCAGAA	CAAGAGGGCCTCTTAACTGTA
2134	EXTL1	NM_004455	CCCGACTGCATCAACCAGATA	TAGATGGATGGCAGACATTAA		
2138	EYA1	NM_000503	CCCAATGGCACCGAAGTTAAA	CAGGAAATAATTCACTCACAA	TCGGTATAAATATGTAGATAA	AACTCGGTAACTCTCATATAA
2151	F2RL2	NM_004101	TCAGTTAGGATACATCACTAA	AAGGCTAACTTGCTAATCACA	CAGTTAGGATACATCACTAAA	CAGGAGCCACGATTACTGTAA
2153	F5	NM_000130	TTGGATAATTTCTCAAACCAA	CCCATTCAAGACCCTGATCAA	TAGGAATTAGGTCATTCCGAA	CGCCATTAATGGGATGATCTA
2155	F7	NM_000131	CAGTTGAATATCCATGTGGAA	TCGAACTGTCCTGGCACCAAA	CAGGGTCTCCCAGTACATCGA	CTGGTTCTTATCCATTATCAT
2162	F13A1	NM_000129	CACGAGCGTTCACCTGTTCAA	AGCGTTGACATTCTATTGGAA	CAAGGAGAGATGGGACACTAA	TACAATGTAATAGAAGCTTAA
2177	FANCD2	NM_033084	CGGCTTCTCGGAAGTAATTTA	TTGGAGGAGATTGATGGTCTA	CAGAGTTTGCTTCACTCTCTA	ACGGGAGAGAGTCAGAATCAA
2178	FANCE	NM_021922	TCGAATCTGGATGATGCTAAA	TAGCCTGAGGATAAAGGCTGA	CTGACTTGAATAATTTATCAA	AACGCCGAGGAGAGCTTGTAA
2182	ACSL4	NM_004458	ATGCATCATAGCAATTTGATA	TTGGAGCGATTTGAAATTCCA	CAGATTATAGATCGTAAGAAA	AAGGGCAGAGTTACTTGATAA
2189	FANCG	NM_004629	CCGGCTCGTTCGACAGGCCAA	CCGCGGGAACTAACTCTTCAA	CTCATTGAGGTAGAATTACTA	CCCAGGTAATCGAGACACTTA
2192	FBLN1	NM_001996	CAGGTCATGTGAAGACATCAA	CAGGATGTGTGTCGATGTCAA		
2197	FAU	NM_001997	GGCCGCATGCTTGGAGGTAAA	CCGCCGTTCAGTCGCCAATAT	ACAGGAGAAGAAGAAGAAGAA	AAGCCACTTAGTTCAGTCAAA
2204	FCAR	NM_002000	TGGAACTAAGTTATTCGGCAA	GAGCTTATTGTCGTAAGAATA		
2205	FCER1A	NM_002001	TCCATGGAATAGAATATTTAA	CACATTTCTCTTGAAGATTAA		
2212	FCGR2A	NM_021642	CCCAATGTCCAGCCTCTTTAA	AACCTCTAACAACAAATTAAA		
2214	FCGR3A	NM_000569	TTCGCTGAGTTAAGTTATGAA	CAGACTGAGAAGTCAGATGAA		
2220	FCN2	NM_004108	CAGCTTTGCAAATGGCATCAA	AAGGATACAATTATAGCTACA	CCGGGACTGGGCCACGTACAA	CTGCCATGTGTCAAACCTGAA
2232	FDXR	NM_004110	CAGGTTGGGAACATGCTGGAA	TGGGAACATGCTGGAAATAAA	CACGTGGACATCTACGAGAAA	AAGCGTGCCCTTTGACTCCAA
2235	FECH	NM_000140	CTGGAATATTAATGCTAAACA	CCGACTGGTGTGGCAATCCAA	ACCCATATCCTCAGGAGGTAA	CCCAAGGGTAATAAACGTGTA
2237	FEN1	NM_004111	CACAATGATGAGTGCAAACAT	TAAGTCCATTGTTACATGAAA	CTGACTGCCAGTGAAGCCAAA	CAAGAGCTACTTTGGCCGTAA
2239	GPC4	NM_001448	ATGGCCATTTATACATGCAAA	TACCAAATGATAGCTCATAAA	CAGATTGTATTCAAAGCATCA	TAGGTAGAGCTGAGAATACTA
2243	FGA	NM_000508	AGGGTTGATTGATGAAGTCAA	AGGGCTTTAGCTCGTGAAGTA	CAGCCAATAACCGTGATAATA	ACGCGTCGTTCATGCTCTAAA
2244	FGB	NM_005141	ACCGTATAGAGTATACTGTGA	CAGGAAATGGGATCCATATAA	TAGAGTATACTGTGACATGAA	CAGCACGTATGACAGAGACAA
2246	FGF1	NM_000800	GCCCATTTCGAAGATATACAA	GAGAATGATAGTAATAGGATA	AAAGTAGGAACTCTTAAGCAA	CTGATACTTATTTACCTATAA
2247	FGF2	NM_002006	TGCCTTGTGGATATCAAGAAA	ATGCTAAACTTTACTGATGTA	TAGCACTAGTCTTAAATTGTA	AACAATATTAGTCGTATCCAA
2248	FGF3	NM_005247	CGGGCGGTACCTGGCCATGAA	TTGTGTCATCACAACATTAAA	CAGGGTCCAGTGGGAACTGAA	TTGCTCCTGGGTGGAAATTAA
2252	FGF7	NM_002009	CACAAGAGTCTAGATCAGTTA	TAGTTTGTAGCTACAGTAGAA	AGCCTTTACATTTGTACACAA	CACCCGGAGCACTACACTATA
2253	FGF8	NM_006119	GCGCTTCGAGTTCCTCAACTA	CAAGAGCAACGGCAAAGGCAA	CACGGAGATTGTGCTGGAGAA	CTACATCTGCATGAACAAGAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
2254	FGF9	NM_002010	TTGGATATACCTCGCCTAATA	GCGATACTATGTTGCATTAAA	TACGTACTCGTCAAACCTATA	ATCGCAGTGAACTTAAAGCAA
2259	FGF14	NM_004115	CAGGAAGTAAGCTAATGCTTA	AGGGTTGTATATAGCCATGAA		
2262	GPC5	NM_004466	AAGAATTTAGTGTATCTGTAA	CAGCTTTGTGCTAATGAATTA		
2264	FGFR4	NM_002011	CAGGAGGTTCTGGGCCTCTGA	CCGCCTGACCTTCGGACCCTA	CAGGCTCTTCCGGCAAGTCAA	CACATTGACTACTATAAGAAA
2268	FGR	NM_005248	CAGCACTAAGGTGGCGGTGAA	TTGATTCTGTAAATAAGTAAA	CAGACCTTGTCTAGTTATTTA	CACGTGGAACGGCAGCACTAA
2271	FH	NM_000143	GAGATCTACGATGAACTTTAA	CAGGAATTTAGTGGTTATGTT	CCCAACGATCATGTTAATAAA	TAGGATGTGCTAGGTCTAAGA
2272	FHIT	NM_002012	TCCACTGAGAACAGTCTGTAA	TTCGCTCTTGTGAATAGGAAA		
2274	FHL2	NM_001450	ACCCTTTAGTGCTTTGTGATA	CTCCCGTTGCGTCAAGTCTAA	AAGGTAATGACCAGTTGTTAT	ATCGAGTAAGGCACACCCAAA
2281	FKBP1B	NM_004116	CACTGCCTTACCTTCACTTAA	CAGAGGGACTTGAGCCAGTTA	CACAAGGTGCTCAGACATGAA	AACAATGTCCTCTTTGAGAAA
2288	FKBP4	NM_002014	CACGCTTGTATTTGAGGTGGA	AGGGATGAGGTCTGATAAGAA	TTGAGTGAATTAGACCTTTAT	AGCAATAAAGTGGAAACAATA
2289	FKBP5	NM_004117	GCGACAGGTTCTCTACTTAAA	TCGGCTGGCAGTCTCCCTAAA	AACGCCGATGATTGGAGACAA	ACGGGTAAACAGATTGAGCAT
2296	FOXC1	NM_001453	CCGCCACAACCTCTCGCTCAA	AACGGGAATAGTAGCTGTCAA	CTCCAGTGAACGGGAATAGTA	ACGGGAATAGTAGCTGTCAAA
2298	FOXD4	NM_207305	AAGACCATCATCCCTGGACTA	TCCACCACACATGGTCTTGAA		
2301	FOXE3	NM_012186	CACCAGGGCTCCTGACTGAAA	TAGGACTTATTGGGTTATTAT		
2305	FOXM1	NM_021953	CCAAATTATCCTCTAATTATA	CCGCCGGAACATGACCATCAA		
2306	FOXD2	NM_004474	CCGAGTGAGCCTTAACATCCA	CACTGGGTGTGCATTGATTTA	CCGGCGGGTCGTGCCCTGGAA	CCCATTGGTGTCAATTGAATA
2313	FLI1	NM_002017	ACCTTTGTATTTGTTCTTTAA	CAGGACATATGTGGCCTTGAA		
2316	FLNA	NM_001456	CACAGGCAACATGGTGAAGAA	CCGCTTCACCATCGACACCAA		
2321	FLT1	NM_002019	CCCGAATCTATCTTTGACAAA	TCGCCGGAAGTTGTATGGTTA	CACTACAGTATTAGCAAGCAA	ACCGCATATGGTATCCCTCAA
2322	FLT3	NM_004119	ACCAATTCAAGTGAAGATTAT	CAGGTTTAAAGCCTACCCACA	TACGTTGATTTCAGAGAATAT	CCGGCTTGAGTGAATTGTGTA
2323	FLT3LG	BF688722	TAGTATAGTTGAAATAAGAAA	GCGGGATTTGTTGAAGAGAAA	GCGCGTGAACACGGAGATACA	CTCCTCCGACTTCGCTGTCAA
2324	FLT4	NM_002020	CCGCCGATTATTCCTTGGTAA	CGCGCTGATGTCGGAGCTCAA	CACGCTCTTGGTCAACAGGAA	CACCGTGTGGGCTGAGTTTAA
2326	FMO1	NM_002021	CAGTACTTTCATAGCCGGCAA	AGGCCTCACTGTACAAGTATA	ATCATGCAAATTACGGCTTAA	CCGAACATTCAAGGTCATCAA
2328	FMO3	NM_006894	CCGGACATCATGTGTATCCCA	AAGAATCATGTCATGATCTTA	CCCGCTGGGCAGCACAAGTAA	AACTATGTTCTTTATATCTAA
2329	FMO4	NM_002022	ACGAAGATTATCCTAATTTCA	ATCGGCCTTATCGGCCTTAAA	AAAGAAGATATTTCTATACAA	CACGATGGGTCACAAGAGTAT
2330	FMO5	NM_001461	AAGGCGGACAGGCGACACTAA	AACCAAAGGTTTGACCATGAA	CTGAGTCAGCATCCAACCTTA	CTGGGCCACTCAGGTATTTAA
2334	FMR2	NM_002025	CACGTGATAGTCATAACCCTA	CTGGGTAAGACTACTCAGTAA	TAGGAACTAATTAAACATGGA	CGGCCTTATTCTCATAATTAA
2348	FOLR1	NM_000802	CTGGACTTCAGGGTTTAACAA	CACATGTGTCTTGAGAATTAT	CCCACTGTTCTGTGCAATGAA	TAAGGATGTTTCCTACCTATA
2353	FOS	NM_005252	TAGAGGGTTCCTGTAGACCTA	TGGGTTCATTATTGGAATTAA	ATGGATTCTCAGATATTTATA	GACCAATATTATACTAAGAAA
2356	FPGS	NM_004957	CTGGAGTGAATTAAAGCCTTT	CCGCACTGTCCCAGTAGCCAA		
2357	FPR1	NM_002029	ACGACCCTAAAGAGAGGATAA	TTGCAAGGCATGTACAAAGAA	CACCGTGAGCCTGGCCAAGAA	AACCAGTGACACAGCTACCAA
2475	FRAP1	NM_004958	CCGGAGTGTTAGAATATGCCA	CCGGCACAATGCAGCCAACAA	ACCAATTATACCCGTTCTTTA	CAGGCCTATGGTCGAGATTTA
2488	FSHB	NM_000510	CAACATCACCATTGCAATAGA	TCGTTTCTGCATAAGCATCAA	AAGAATGTCGTTTCTGCATAA	CACCAGGGATCTGGTGTATAA
2515	ADAM2	NM_001464	CGGGCTGCGGATGGACAGTAA	TGCTATAATGGTGAAAGTTAA	CTGTTGGTTAGTAGACACTAA	AACCATATACTGTGAATTTAA
2516	NR5A1	NM_004959	ACGCAGGTGCATGGTCTTCAA	AAGGATAACCGAGTTTGCTAA	CAGGGAGAAGTTGAGCAGGTA	CTGGAATAAATTTCGCAATTA
2517	FUCA1	NM_000147	CCGGAAGAGGAACATCCGCTA	TACGACCTTGTTAACAGCTAT	TCCACTCTATCTACTTGATAA	TTCGCTATGTTTACAGTGATA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
2521	FUS	NM_004960	ACAGGATAATTCAGACAACAA	CAAGCAGATTGGTATTATTAA	CTGGGTGAGAATGTTACAATT	ACAGCCCATGATTAATTTGTA
2524	FUT2	NM_000511	CAGCGGCTAGCGAAGATTCAA	CACGGGCGGAGACACCATCTA	CAGTGCTAGCCTCAACATCAA	CACCATCTACCTGGCCAATTA
2531	FVT1	NM_002035	CAGGCAAAGAAAGAAATTGAA	TAGACTCAAATGCTTAGGGAA	CAGGAATGTGGCTGCAAGCAA	AAGAATTTACAGTTCCTTCAA
2532	FY	NM_002036	CTGGACACCCTTGGAAGCAAA	CACCTGTCAACCTGAATTAAA	CAGCTGGACTTCGAAGATGTA	ACCAGTGTCCTGGGTATCCTA
2535	FZD2	NM_001466	CACGGTGAGACCACCGTGTGA	CACCATGGTGTCGGTGGCCTA	CACGTACTTGGTAGACATGCA	CACGGTCTACATGATCAAATA
2537	G1P3	NM_002038	CAGCAGCGTCGTCATAGGTAA	CAGAATAAACTTCACCCAGAA		
2538	G6PC	NM_000151	TAGCAGAGCAATCACCACCAA	CTGGCTTATTCCCATGTGTGA	TGGGATCCAGTCAACACATTA	CAGCAGGTGTATACTACGTGA
2539	G6PD	NM_000402	ATCGGGTGACCTGGCCAAGAA	CACCAAGATGATGACCAAGAA	CTGCGTTATCCTCACCTTCAA	CAGCCTCTCTGCTATAAGAAA
2542	SLC37A4	NM_001467	TTGGATATAGGTGGGAAGAAA	CCGGGTGGCGCTGGAAGTTAT		
2547	G22P1	NM_001469	CAGGTTAAAGCTGAAGCTCAA	GAGGGTTAGCGTTAGCCTTAA	GAGGATCATGCTGTTCACCAA	CGCCTAGTGAGCAGTAGCCAA
2556	GABRA3	NM_000808	TACAATGAGGTTAACAATTCA	CCCGACTGAGACCAAGACCTA	CAGAGATAATCCGGTCTAGTA	CCCTCAATTCATATTTATGAA
2561	GABRB2	NM_000813	TCCTATAATGTAATACCTTTA	TACCTATTTCCTGAACGATAA	CAGAAGCACAATGCTAGCCTA	ATCCCTCAGCTTTAAGCTTAA
2563	GABRD	NM_000815	CCGCGGCACCAGAGCGATGAA	ATCGGAGGACATCGTCTACTA	CACCTTCATCGTGAACGCCAA	CACGGAGCTGATGAACTTCAA
2564	GABRE	NM_004961	CCGCATCTACAAGGATGGCAA	CAGGCATTACTCGCCATTGAT	CAGCAGACCATTTCAAATTAT	CACTCTAACCATCACAATCAA
2566	GABRG2	NM_000816	CACCATCAGATCATAAGCATA	CACCCTAAGGTTGACAATTGA	TAGGAGTGAAGCCAACGTTAA	TAGATTCATAATGCAATTAGA
2568	GABRP	NM_014211	TAGATTGGTCTTACAGTTTGA	AAGTGGCTTAGCTTAAGTAAA	GAGCCCAAGATTACAAATGTA	CAGAAATAAACCAAGGCTCTA
2569	GABRR1	NM_002042	CAGGGTTACAGTAACTGCAAT	CACCACCAAACTGGCTTTCTA	ACGTGCTCTCTTGAAATTGAA	CAGAAATAACTGTATAATGAA
2572	GAD2	NM_000818	ACGGGCGGCATCGGAAACAAA	CGCCTTGGACAAGATTTATAA	AAGTTTCGATAGATCAACCAA	CAACCTGTTCTTCCTACCAAA
2580	GAK	NM_005255	CACGCAGTACACGGTCTTCCA	AAGGCCTAACTATGCCTCGAA	CCCGTGGTTGTCTGTACAGAA	ACGCGTGTGACATTCAAGAAA
2581	GALC	NM_000153	TTCAAGGTGGTTGATGTTATA	TACACTCACGTTAACTATTAA	CAGTATTATAGGAGACTACAA	TAGGAATTTATAAGAGTCTAA
2585	GALK2	NM_002044	TCCTAGGTTACTGAAGCTAAA	CTGGAGGAACTCCGAACCCAA	TGCGCGAGTGCTCCAGTTTAA	AAAGCTCTCTATGCTTCATAA
2615	GARP	NM_005512	CTGGAGTTTGAGACTATGGAA	AACCAACAGTATAAAGCCTAA		
2622	GAS8	NM_001481	CACCGACATTAAGAACTACTA	ATGCATAAGTATATTTGTTTA		
2628	GATM	NM_001482	TAGAATGTACACAGATCCAAA	CAGGTCAATTATCAAAGACTA	CCACTAATAATTAACCATCTA	ACCGAGCGTACAGGTCAATTA
2629	GBA	NM_000157	CCGGAATTACTTGCAGGGCTA	CCAGAACAGAAGTTCCAGAAA	CAGGGCTAACCTAGTGCCTAT	AAGAAGGAATCGGATATAACA
2642	GCGR	NM_000160	CCGCAATGCCATCCACGCGAA	CAGCTCCGTGCTGGTCATTGA	CTCCAACAATAAAGAGCTCAA	CAACAGAACCTTCGACAAGTA
2645	GCK	NM_000162	CTGGACAAGCATCAGATGAAA	CACGATGATCTCCTGCTACTA	CAGCTGTATGAGAAGCTCATA	CAGGACTTTGATGCATTTCCA
2661	GDF9	NM_005260	ATCAGTGGAACTGCTATTTAA	CAAGTCAGTCTTGCTGTACAA	TACCGTTGAACACTTACTCAA	CAGCTGGTATTCCCTTCACTA
2662	GDF10	NM_004962	AGCGCTCGAGGTGCTATGCAA	AACAGGATAATCGTGGTGTAA	CACGGAAAGAACTCTGTTTAA	TAGTAACGTGGGAATACTAAA
2664	GDI1	NM_001493	ATCCACTGACCAAATCCTTAA	ACCCTTATCTTGCAAAGTGAA	CTCTAGTGTATTTCACAGAAA	CCGCATCAAGTTGTACAGTGA
2668	GDNF	NM_000514	CGGGACTTTAAGATGAAGTTA	CTGGAGTTAATGTCCAACCTA	CTGGTTTACCATATTCTAAGA	CGCGCTGAGCAGTGACTCAAA
2671	GFER	NM_005262	ATGGCCCAGTTCATACATTTA	CCGGGCCTGCGTCGACTTCAA		
2677	GGCX	NM_000821	CCGCCTGCTTCCCAAGTATAA	CAGACCTTTCTTAGACGCCAA	TACGTCTATGTCAACACTACA	CAGGAAGAGGTTAGACGCAAT
2702	GJA5	NM_005266	CTCCCTCTACTCAGCCTTAAA	CTCAATGACGTTGCTCATTAA		
2705	GJB1	NM_000166	CTGCACAGACATGAGACCATA	TGCCTGAAATGTTACACATTA	TGGCATCTGCATCATCCTCAA	GCCTGAAATGTTACACATTAA
2720	GLB1	NM_000404	CCAGAGGATGTTTGAAATTGA	ACCACTGATGGAGCACATAAA	CAGAATGGAGGGCCAGTTATA	CACCAAAGTTTGCATATGGAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
2740	GLP1R	NM_002062	CAGGAACTCCAACATGAACTA	CAGACTCAAACTCAAGGTCAA	CCAGACAGAGCCGCAAATCAA	CAGGCTCGTTCGTGAATGTCA
2741	GLRA1	NM_000171	CTGGAGTTTAACAAACAGCAA	TCGGATTTCCTGGATAAGCTA	CCCATAACTCGTGGACTACAA	CCGCTTTAACTTCTCTGCCTA
2746	GLUD1	NM_005271	CAAGCCTAACCTTGACTCAAA	CCTATAGAAATAATAAATGAA	CAGTGAATGCCTATAGAAATA	CAGAATTTGCTTACCATAATT
2768	GNA12	NM_007353	TAGCTATACTGTGTACACATA	GAGGTAGTTGTGCCTCAATTA	GTCCGTTTAACTCGATAGAAA	CCGGATCGGCCAGCTGAATTA
2769	GNA15	NM_002068	CTCCGTGCGGGCTGAAATTAA	CCGGTTTGCGGACGAGAGAAA	GAGGTTCATCCTGGACATGTA	TCCGTGCGGGCTGAAATTAAA
2779	GNAT1	NM_000172	CACCGACACGCAGAACGTCAA	CAGCATCTGTTTCCCGGACTA	ACGCACAGACTCAGCAATAAA	ACGCGCCATGACCACACTCAA
2780	GNAT2	NM_005272	TAGGGAGTCTCAGTCAATGTA	AACCAATTAGAACGAATTACA	ACGGCAAATATGGGAAGTGGA	TGGGATAGCTATTGCAGCTTA
2783	GNB2	NM_005273	CGCCTGTGATGCCTCTATCAA	CGGCCATGAATCCGACATCAA		
2784	GNB3	NM_002075	CAGATTGCAGATGCCAGGAAA	TCCGGGTGCCATTCCCACTAA	CAACATGTGTTCCATCTACAA	TCCCTTAATGAGCAAGGACAA
2785	GNG3	NM_012202	CTCGGTGACCTGCTCAGACAA	GTGGAACAGCTTAAGATTGAA	CTGGAGCTACTGGGAGGGTAA	CAAGATGGTGGAACAGCTTAA
2788	GNG7	NM_052847	CAGGGCATCATTCAGTAATTA	ACGGCTAAACTCGGATTGTGA	ATGGTTGAACCCGTCGCTAAA	ACGCATCCATCTCCAAGTTAA
2794	GNL1	NM_005275	TCGGCTTTCCACTAAGGTCAA	CCAGGCTACAGTGAACAGAAA		
2798	GNRHR	NM_000406	ACCAGTATTGATGAATAACTA	CAGGTTGTCAGACCCAGTAAA	ACGGTTGCATTTGCCACTTCA	AAGCATGGATTGGATCAGTAA
2799	GNS	NM_002076	CGGCGGCATGACACCGCTAAA	AAGCAAGATGCTGGTTGCCAA	CTGGTTAATTAGGCAAGCCAA	ATCAGTCAACTTCCACATTAA
2802	GOLGA3	NM_005895	CGGAAACTTTAGAGAAGTTAA	CTGGCCGATTACAGAACTGAA		
2813	GP2	NM_001502	TTGATGGGACCTTGAAAGCAA	CCAGAACTACACGAATCCTTA	CACAGGCTTGGTATTAACAGA	CAGGACCTCAATAGTTCTGAT
2817	GPC1	NM_002081	TTGAGTCCTTGTATGAATAAA	TACAACACAGACGATATTTAA	CAGGGACACGCTCACGGCCAA	CCGCCAGATCTACGGAGCCAA
2825	GPR1	NM_005279	CCGGGACACTGTGGAGTTCAA	CTCAGTTGCTGAGATACTCAA	CCGACTCCACTTTCATAGTTA	AAGCCTTAAGTCTTAATATTA
2838	GPR15	NM_005290	CCCAGAAGAAACTTCAGTTTA	CAGCTATTCTTCAGCTTGGTA	TTGCGGCAAGAACACTATTTA	TTCAGTTTATTTGGATTATTA
2846	GPR23	NM_005296	TAGGTTGGGCCTATAAATATA	TTGGGAAACTAGGTTCTATAA	GGGCCTATAAATATAGAACAA	AGGAAGTGAGTGATCAAACAA
2848	GPR25	NM_005298	GCGCATCATCTTCGCCATCGA	CAGGGACGACAGTTCCGTGTT	CTGCGCCAACCCGCTCATCTA	CCGGAGGAACTCGCTGCGCAT
2857	GPR34	NM_005300	CTGAATAGATTCAGTCATTAT	AAGGAGGGCATAATTCCACAA	TGCGACTATTACCAAATAGAA	TCAGGCGAACCTGAACTTTAA
2859	GPR35	NM_005301	CAGGCAGATCCCAGGAGAGAA	CAGGACCATGAATGGCACCTA	CGCCCTGTACATAACCAGCAA	CCGGCACAATTTCAACTCCAT
2868	GRK4	NM_182982	AAGCCTTTGAGGAATGTACTA	CACCGCAGATGAAGACTTCTA	CCGGGTGTTTCAAAGACATCA	CAGGATGTTACTCACCAAGAA
2870	GRK6	NM_002082	CCGGAGGTGGTGAAGAATGAA	CAGAGACTCTTCAGTCGCCAA	AGGCATGTGGGCGGCACGTAA	AAGGATGTTCTGGACATTGAA
2876	GPX1	Y00433	CAGGAGAACGCCAAGAACGAA	GAGGAACACCTTGATCTTACA	CCGGGACTACACCCAGATGAA	AACACCTTGATCTTACAGAAA
2886	GRB7	NM_005310	CGGGAGTGGATCTGAAATAAA	CCCAACAAGCTTCGAAATGGA	CGCCAAGTACGAACTGTTCAA	CACACTGGTATATCCCATGAA
2888	GRB14	NM_004490	CAGCGATTGATTATTCAGCAA	CAGAAGTGACTTATTAAACTA		
2889	RAPGEF1	NM_005312	GCAGGTCTTGTTGCCAATTTA	CAGGGTTACATTGTAATATAT	CCGGGTTTAGGACGTGGTCAA	CAGGAAAGATTTGGTGTTGTA
2890	GRIA1	NM_000827	CAGGTGCGATTTGAAGGTTTA	CAGCATCCGAAAGATTGGTTA	CTCCACGTGATTGAAATGAAA	CACCATGAAGGTGGGAGGTAA
2895	GRID2	NM_001510	AAGCAATGGATCGGAGAACAA	CACGATTACAAATGGGATCAA	AACGATGTGGACGTACAGGAA	CTGGCAGAAATTCATTATATT
2897	GRIK1	NM_000830	CCAGCATTAACAGAAACCGAA	TGGGCATATCACCTTTAATAA	ACAGGTCTAATTCGTCTACAA	ACGGATTTAGAATGTGGTAAA
2900	GRIK4	NM_014619	CCGGCAATTCCTTATCTCCAA	CGCGTTCATATGGGACGCAAA	TGGGATGGTGTCAGCCTATTA	CAGGGTGTTGAATTCCAACTA
2902	GRIN1	NM_000832	GACGCGTTCGGTCCTATTAAA	CAAGGAGGAGTTCACAGTCAA	CAGACTGAAGATTGTGACGAT	CACGCTGGACTCGTTCATGCA
2903	GRIN2A	NM_000833	TACGATAACATTGTCGACAAA	CACAGTGGCCATTGTAGTTTA	ACCAGATAGGTGAGTCCTTAA	AGGGTTGTATAGTATCTGTTA
2909	GRLF1	NM_004491	CACCACCGAAGAGGTGTTTAA	CAGGATGTTCTGGGAGAGGAA	CAAGGTTTCCATCGTGAGCAA	CAGCCTAAGGAGGAACACTAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
2912	GRM2	NM_000839	CCGCTACAACATCTTCACCTA	CTGCACGCTTTATGCCTTCAA	CTACAAGGACTTTGTGCTCAA	CACCATCGAGCTGGCCTCCTA
2913	GRM3	NM_000840	CACGGCTCCATTCAACCCAAA	TAGGTCCTTGTTGTAACTAAT	TACGGTGGCAATATTATGTAA	GTCCTTGTTGTAACTAATTTA
2917	GRM7	NM_000844	AAGGGTTTGATGCCTACTTTA	CACGCTTACAATCTCCATGAA	TCGGATTTATCGCATATTTGA	CCCAGATTAGTTATGCATCAA
2931	GSK3A	NM_019884	CGGGTGTAAATAGATTGTTAT	CAATAAATTATTGGCATGAAA	CCGGGTGTAAATAGATTGTTA	CAGGGAACTAGTCGCCATCAA
2932	GSK3B	NM_002093	CACGTTTGGAAAGAATATTAA	CTGCATTTATCGTTAACCTAA	CACTCAAGAACTGTCAAGTAA	AACACTGGTCACGTTTGGAAA
2944	GSTM1	X08020	CCACCGTATATTTGAGCCCAA	TCCAGAATTTGAGAAACTGAA	CAGACTCAAGCTATGAGGAAA	CTGCTACAATCCAGAATTTGA
2947	GSTM3	NM_000849	AACGGAAGAAGTTACCCTTAA	ATGGCTGGATGTGAAATTCAA		
2950	GSTP1	NM_000852	CCTCATCTACACCAACTATGA	TCCTTTCTCCAGGACCAATAA	GCCGCCCTACACCGTGGTCTA	CCAGATCTCCTTCGCTGACTA
2954	GSTZ1	NM_001513	TACCATCAGCTCCATCAACAA	ACGGTGCCCATCAATCTCATA	CTGAAATTTGGCGTGAATTAA	CGCGCTGAAATTTGGCGTGAA
2956	MSH6	NM_000179	CAGCAGGGCTATAATGTATGA	CCGAAGTTGTAGAGCTTCTAA	AAGCCTATTGTGTGCTTGTTA	ATCGCCATTGTTCGAGATTTA
2957	GTF2A1	NM_015859	CAGCTTCTACTGCAAGTTCAA	CAGGAACTCTTTGACACAGAA		
2959	GTF2B	NM_001514	TTGCCTGTTGTACATAGCCTA	TTGACGAATTTGGCAATTCTA	CCAGTGTGGATTTGATTACAA	ACGTCAAATTCTTGAATACAA
2965	GTF2H1	NM_005316	AAGGCAAAGATAGATTTACAA	CCCAGAGCTGATGCTATTGTA	TCGGCTGAATACAGGGTCAAA	ATGGCACAGGGTAGACCTTAA
2974	GUCY1B2	NM_004129	CAGCATCCGCAGATTTATCAA	CAGTGTGCACGCAGTCTATAA	CGCAGATTTATCAACAGTCAA	CCGATGTTCAGAGGCATCCAA
2975	GTF3C1	NM_001520	CAGGAAAGAGGATGAACTTAA	CAGGCCTATCTCAACTATAAA		
2983	GUCY1B3	NM_000857	CAGTTTCTTGTCAGAATAATA	CAAGACTTTCTTCTAGATATA	AAGGGTCAAATGATCTACTTA	ACCTAACATGGTGATCTGCAA
2986	GUCY2F	NM_001522	CAGGCAGACAGAATTCGCATA	ACCGTTGTTTGGAACCATCTA	CTGGAGTTCGATCAAGTTTCA	AAGGCAGTTGGTGAGAAACAA
2997	GYS1	NM_002103	CTGGGCGAGGAGCGTAACTAA	CCGCTATGAGTTCTCCAACAA		
3024	HIST1H1A	NM_005325	ACCCAAGAAAGCGGCACCCAA	CAGGTTTATACCACTTTATTT		
3029	HAGH	NM_005326	CTGGTCCGTGCGGGAAATTCA	ATCGGACATTCTAATGCATAT	TCAGTCTTGATTTAACCTTAA	ACAAGTATTTATTCCCATAAA
3037	HAS2	NM_005328	GTGGAAGATTGGTACAATCAA	CAGCTCGATCTAAGTGCCTTA	CCAGCTAGTAGGTCTCATAAA	AACGCAATTGGTCTTGTCCAA
3038	HAS3	NM_005329	CACCTTCTCGTGCATCATGCA	TACCAGTTCATCCACACGGAA		
3053	SERPIND1	NM_000185	CAACGCCAAGTTCGCTTTCAA	CCCAAGGAGGGTACACAACTA	TGGCATCATTTACGTAGTTTA	TGGGCTAATGTTAGGGCTTAA
3055	HCK	NM_002110	CCGGGATAGCGAGACCACTAA	CGGCAGGGAGATACCGTGAAA	CGGGAGCACATCAGAGGCTTA	AACGACGGGCTCTGCCAGAAA
3059	HCLS1	NM_005335	CAGCCAGTGATAGCTATGGAA	AAGGAGAAGTGGAGAAGCATA		
3062	HCRTR2	NM_001526	CCCGTGATGTCCGGCACCAAA	CCGGAAGTCCTTGACCACTCA	CCGGTGCAACATCGCCTGTAA	ACCGACTATGACGACGAGGAA
3066	HDAC2	NM_001527	GACCCATAACTTGCTGTTAAA	CTGGGTTGTTTCAATCTAACA	TCCCAATGAGTTGCCATATAA	ACGGTCAATAAGACCAGATAA
3067	HDC	NM_002112	TGCCGACTCCTTCACCTTTAA	CCACAATAGGATACAAACGAA	CTGGGTCAAGGACAAGTACAA	CAGCTTGTGACATGATATATA
3068	HDGF	NM_004494	CCAGCTTATAGTCATATATAT	GAGGGAGCAATTGAATTTCAA		
3074	HEXB	NM_000521	TTCGACGATATCATGGCTATA	TGGATATTATTGCAACCATAA	CCAGACATTATCTGCCAGTTA	CCGGGCACAATAGTTGAAGTA
3092	HIP1	NM_005338	CAGGTTAGGGTGCTAGAGCTA	CACAACAATGGGTATCCTTAA	CAGGAACTTGCCACAAGCCAA	ATGGCTTAGGATCGACAAGAA
3097	HIVEP2	NM_006734	CTGGGTTATCTTTGTGCTATA	ACCGTAAAGCATTAAAGTAAA		
3098	HK1	NM_000188	AACGGTGGAAATGCACAACAA	CAGATCGAGAGTGACCGATTA	CCGTGTCGTATGACCTAGTAA	CACGATGTAGTCACCTTACTA
3107	HLA-C	NM_002117	ACCGGGAGACACAGAAGTACA	AAGCGTTGATGGATTAATTAA		
3118	HLA-DQA2	NM_020056	ATGGTTATAGCAGAAATACAA	CAGGGCTGACTGAGAGCATAA		
3119	HLA-DQB1	NM_002123	CCGGAGGCCTTCGGGCAGCAA	ATCCATCACAGGAGTCAGAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
3120	HLA-DQB2	NM_182549	AAGGATTTCTTGGTCCAGTTT	CAAGAGAAGCATGACAAACAA		
3122	HLA-DRA	NM_019111	CAACCTGGAAATCATGACAAA	CTGAAGAAACTTCTGCTTTAA		
3135	HLA-G	NM_002127	ATAACTTACTTCTGTATTAAA	ATGAGGTTTCTTTGACTTCAA		
3142	HLX1	NM_021958	AAGGTTTGAGATTCAGAAGTA	CGCCTTAAATTTGTAAATAAA		
3159	HMGA1	NM_002131	CAGCCAGCCCTTGGCCTCCAA	CTGGACAAGGCTAACATCCCA	CAGCGAAGTGCCAACACCTAA	CACCACAACTCCAGGAAGGAA
3162	HMOX1	NM_002133	CACCAAGTTCAAGCAGCTCTA	CGGGCCAGCAACAAAGTGCAA	CAGGCAGAGGGTGATAGAAGA	CAGGCAATGGCCTAAACTTCA
3174	HNF4G	NM_004133	AAGCACTGACATAAACGTTAA	CACCGGATGGATTCTGATGAA	ACCGATAAGCAGCGAGTGTAA	ACCCTGTAATTTATTCGTGTA
3175	ONECUT1	NM_004498	ATGGAAGAGATCAATACCAAA	AAGGAAGAACCACAAACTAAA		
3176	HNMT	NM_006895	CGGGAAATATGTTGAATCTTT	TGCAGGCTCAACATAACATAA	TGGGACTTTATTCATATGATT	CAACATAACATAAGCTAGAAA
3187	HNRPH1	NM_005520	AAGCAGTTGAATTATGTTAAA	CAGGTATATTGAAATCTTTAA		
3198	HOXA1	NM_005522	CAGGATAATATATTTGCAGAT	TAGGATGTCTGTAATAAATAA	CACACTGAGTTCTATCAGTTA	CAGCTCCTTTATTATAATCAA
3201	HOXA4	NM_002141	AAGCCATGTGCTAAGAATAAA	CTGGACCATAATAGACACCAA		
3225	HOXC9	NM_006897	CACGACAATGAAGACCTCCTA	CCGAAATAAATGACACATACA		
3236	HOXD10	NM_002148	GTGCATCCTTATATACCTCAA	CCCTATGAGTATATATATATA	CTCCTTCACCACCAACATTAA	CAGGGTAACTATTATTGCGCA
3240	HP	NM_005143	TGGAGTGTACACCTTAAACAA	AAGGTGTCTGTTAATGAGAGA	CAAACAGAAGGTGTCTGTTAA	CTGACCAAGACCAATGCATAA
3242	HPD	NM_002150	AGGAGGTTTGACTAAGATCAA	CCAGGAATATGTGGACTATAA	ATCCATTGTGGTGGCCAACTA	CTGGTGGACTACGACGAGAAA
3248	HPGD	NM_000860	CAGCCGGTTTATTGTGCTTCA	CAAGAGCTTCTTAGAGTAGTA	CAAGACTATGATACAACTCCA	CTGGCAGTGACTAATCAGTAA
3249	HPN	NM_002151	GTGGATCTTCCAGGCCATAAA	CAGCCAGGGAATCATTAACAA	TGGGATGCTCTTTAAATAATA	GGGATGCTCTTTAAATAATAA
3250	HPR	NM_020995	CTGCATTGCTGAGTCAATCAA	CTGACCAATACGATTGCATAA	AAGCAAGATTTCAGCCTGGAA	AAGGTGCTTGTTAATGAGAGA
3251	HPRT1	NM_000194	TCCTATTGACATCGCCAGTAA	CACTATTGAGTGAAACATTGA	AACATTGAACTCATATCTGTA	ATGGGAGGCCATCACATTGTA
3280	HES1	NM_005524	CTGGTGCTGATAACAGCGGAA	AAAGACGAAGAGCAAGAATAA	CACGACACCGGATAAACCAAA	ACCATGCACTATATTTGTATA
3292	HSD17B1	NM_000413	AACCATGGTCATGTGAGTTAT	ATCCCAGAGCTTCAAAGTGTA	CTGGACGAAACCAACACATAT	CAGCTGTGGGTGGCTAATTAA
3299	HSF4	NM_001538	AAGGGCGAGAATGGACCCTGA	CAGAGCCGTTTCGCCAAGGAA	CCGGGTCATTGGCAAGCTGAT	CCGACTATCCCTGCACATAAA
3300	DNAJB2	NM_006736	AAAGAGTTTGCTGAGAAGAAA	TTCGCTCTGTTTCTACATCTA		
3308	HSPA4	NM_198431	ATGGACATTGATTGATTCCAA	CAGGTATAAAGGTGACATATA	CCAGGTAATTTCTAATGCAAA	CAGACTATTATAAAGCTTTAA
3309	HSPA5	NM_005347	AACTGTTACAATCAAGGTCTA	TGGGATAAGGAAACACTTCTA	CAAGCCCAATACAGCCATTAA	TAGGGTGTGTGTTCACCTTCA
3313	HSPA9B	NM_004134	AACCAAGATGGAAGAATTCAA	TAGGATGAATTGATCATTATA		
3321	IGSF3	NM_001007237	CAGGGTGATTTGGCCGTCAAA	CAGGAGCGGCTCAGTCATGAA		
3324	HSPCAL3	XM_084514	ACCAGCCTTCTTCCTAGTCAT	CTGGAGATAAATCCTGATGAT		
3326	HSPCB	NM_007355	AAGCTCATGAAAGAAATCTTA	CAAGAATGATAAGGCAGTTAA	AAGGCTGAGGCCGACAAGAAT	CCGCATCTATCGCATGATCAA
3338	DNAJC4	NM_005528	TAGGGAGTGGCAGGTGCTCAA	CAGGAGGGTGGGTGAATTCCA		
3339	HSPG2	NM_005529	CGGGAAGTGCAGGCCCGTCAA	CACCCGAGCCATGGATTTCAA	ACGGTGGGAAGTTGCGATACA	ACGCCTGGACGTGGAGTTCAA
3359	HTR3A	NM_000869	CACCGTATCCATTGACGTCAT	ATCCATTGACGTCATTGTCTA	TACGTGTATATTCGGCATCAA	CAAGCTGCTATTCCACATTTA
3361	HTR5A	NM_024012	TGGATTTACCAGTGAACCTAA	TACGGCTTTCAACAAGAACTA	CTCGGTCTTCGGAGTGCTTAT	CCTGATCTATACGGCTTTCAA
3362	HTR6	NM_000871	CTGCAGCGCCTCCATCCTCAA	CAGGGCCGCTGCCGCCGTCAA	CGCCGTCAATTTCTTCAACAT	CAGGAGGCTGCAAGTCTCCTA
3363	HTR7	NM_000872	TCCAGTCATCAGCTAATACAA	ATGGCACTATGTAGTAATTAA	CTGAAGTGACCGTATATATTA	CGGCGCGATGATGGACGTTAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
3371	TNC	NM_002160	AAGGACCTTCAGGTTTCTGAA	CTGGGATGCCCTCAAACTCAA	CCGAACGTACCAGGGACTTAA	CCGGGCATCAGTCACCGGTTA
3375	IAPP	NM_000415	ACAGCTAATAATGAAGTTATT	TTAGAGGACAATGTAACTCTA	ATGCAGGGTATTGCGAAACAA	CTGGTACTAAGAGGCTATTTA
3431	SP110	NM_004509	TCCCAATCTGGTGACGATTTA	AAGGAAAGGCTGATTACGGAA	ATGGAACTTGGTTAACACCAA	CCCAGACACTTCATAGGATTA
3441	IFNA4	NM_021068	CTGGTTCAACATGGAAATGAT	ACAGAGCAAAGTCTTCAGAAA	ATCTATTTATTTAAATATTTA	AACCTAGAGGCCGAAGTTCAA
3442	IFNA5	NM_002169	ACAGGAGGACTTTGATGATAA	ATGCAGGAGGTTGGAGTGGAA	CAGGAGGACTTTGATGATAAT	ATCCTTCTCTTTATCAGCAAA
3443	IFNA6	NM_021002	CAGCAGCTGAATGACCTGGAA	ATCCTTCTCTTCATCAAGAAA	CTAGACAAACTCTATACTGAA	CATCAAGAAACTTGCAAGAAA
3444	IFNA7	NM_021057	TCCACTGAACTTTACCAGCAA	CTGGTTCATCATGGAAATGAT	CAGCAACTGAATGACCTGGAA	TAGCCTAGTGATATTTGCAAA
3446	IFNA10	NM_002171	GTCGCTTTACATTGTGGTTAA	CTGGTTCAACATGGCAATGAT	TCCACTGAACTTTACCAGCAA	CAGCAACTGAATGACCTGGAA
3455	IFNAR2	NM_000874	AGGCGAGAGCTGCAAAGTTTA	CACAGTGATGAGCAAGCAGTA	CAAGTTAATTCCAAACACGAA	AAGCACCATAGTGACACTGAA
3456	IFNB1	NM_002176	CAGGTAGTAGGCGACACTGTT	CAGAGTGGAAATCCTAAGGAA	CAAGGACAGGATGAACTTTGA	CAGGTTACCTCCGAAACTGAA
3460	IFNGR2	NM_005534	ACCAAGTGCAGTTTAAATACA	TCGGGCATTTAAGCAACATAT	AAGGCTTCTCTTAAACACTAA	AGGCTTCCCAATGGATTTCAA
3467	IFNW1	NM_002177	AGGGCCTGACTTCCTACATAA	AACCATGTGTTTCCTATTAAA	TAGATTGTTGTCATCCTCTTA	AAGACTCTTATTTCGGCTTTA
3468	IFNWP2	XM_378052	CACAGGTAGGCAGGCCAACAA	ACAGGAAAGATTGAGAAGTAA		
3479	IGF1	M27544	CCGGAGCTGAATTACCTTTCA	ATCAATAATGTTCTATAGAAA	CCAGAAGGAAGTACATTTGAA	ACGGTAATACGTGAAAGCAAA
3483	IGFALS	NM_004970	CACCAACGTGGCGGTCATGAA	CCGACTCTTCCTCAAGGACAA	CCGCCTGGAGGCATTGCCCAA	CAGCTTGAGGTGCTCACGCTA
3484	IGFBP1	NM_000596	CATACATAACTTGATATAGAA	AAGGAGGACGGTTAACTTGTA	TACATGTGTAGGGAAAGTTAA	TACACTGGATATGTTGTTAAA
3491	CYR61	NM_001554	TCCCTTCTACAGGCTGTTCAA	AAGGTATTTCGAAACTGCCAA	AGGGCACACCTAGACAAACAA	AGGCAGCTATCTGCACTCTAA
3508	IGHMBP2	NM_002180	CAGGAGAACATCTCTCTGAAA	CAGAGGGATATAAATTATTTA		
3512	IGJ	NM_144646	AAGAAGTGAAGTCAAGATGAA	CAGAGCAATATCTGTGATGAA		
3547	IGSF1	NM_001555	CTGGAGGAGCTCACTGGAGAA	AAGCAAGTTCCTGCTGCTGAA		
3549	IHH	XM_050846	CTGGGTGTATTACGAGTCAAA	CGGCTTTGACTGGGTGTATTA	CCGCCTGAACTCGCTGGCTAT	CTGGGTGTATTACGAGTCAAA
3550	IK	NM_006083	AACCCGTAACAAGAAGCTTAA	CAGCGAGTATATGAACAACAA	GAGGAGGTGGATTATAGCAAA	CAGGCGCTTCAAGGAAACCAA
3551	IKBKB	NM_001556	TAGGGAGCTATTCATGTTTCA	CAGGACACTGTGAGGGAACAA	CAGACCGACATTGTGGACTTA	CACACTGGAGGTCCTCCATTA
3552	IL1A	NM_000575	TCGAGTTGAATGAACATAGAA	CTGAGGTGATTTATGCCTTAA	AAGGCAAAGCACGAAATGTTA	CACGCCTACTTAAGACAATTA
3557	IL1RN	NM_000577	AAGGAATAAATTGCTCCTTGA	CAGCGAATGAATGCTGTATAT	CTGGATACTTGCAAGGACCAA	CCAAATGTCAATTTAGAAGAA
3559	IL2RA	NM_000417	CCCGTTCACGTTGCCTAATAA	CTCCACCCTATATGTAGTATA	CAGAGAATCATACTTAGCAAA	CCACCCTATATGTAGTATAAA
3560	IL2RB	NM_000878	CCAGTTCACATGCTTCTACAA	ATGGCTGAAGAAGGTCCTGAA	TGGCTTCATCATCTTAGTGTA	CCCGGATGCCTTGGAGATAGA
3561	IL2RG	NM_000206	CACGACAATTCTGACGCCCAA	CTGAACAATCAGTGGATTATA	AAGAACTCGGATAATGATAAA	CTAGAGGATCTTGTTACTGAA
3566	IL4R	NM_000418	CCCGGCAGATTTCAGAATCTA	CCGCCTCGTGGCTATAATAAT	CAGAATCTATAACGTGACCTA	CACATACATGAGGGTCTCTTA
3577	IL8RA	NM_000634	CCGGTGCTTCAGTTAGATCAA	CAGGCAGATGTTCCTAATAAA	TCCGCCAGGCTTACCATCCAA	CCCGTTGAACGTCACATCTTT
3578	IL9	NM_000590	GAGGCAAGATATGAAGATGAA	TACCACCATGCAAACAAGATA	ATCCTATTTATTAAATTTAAA	ATCAGTTGAAGTACTAAAGAA
3581	IL9R	NM_002186	CCAGAGATAGTTGGGTGACAA	AAGGACAAGGGCCAAGGTCTA	CAGAGATAGTTGGGTGACAAA	CAGCTATGAGCTGGCCTTCAA
3596	IL13	NM_002188	CAGCATGGTATGGAGCATCAA	AACAAGTTGTTTCATTGACTA	CAGCTCTCAGCCAACGAGTAA	TTCATTGACTATCAAACTGAA
3597	IL13RA1	NM_001560	CCAAATAATGGTCAAGGATAA	CTCAGTGATGGAGATAATTTA	ACCATGTTTGTGGCTATTAAA	AACCATGTTTGTGGCTATTAA
3608	ILF2	NM_004515	CAGACAGCCTTTGGCCCTAAA	CTCCATAGAAGTGTCATTCCA	TTGAAATGTTGTGAAATGTTA	CAGGCCCTTTGTACCACATAT
3609	ILF3	NM_153464	CAAGCTGCACGTGGCCGTTAA	CTGGTTTAGCTAGAGAGTGAA	CAAGAGTTGAAGTATTGATAA	AACGATTTCACCACATCTGAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
3612	IMPA1	NM_005536	CCAGATTTGGTGACTCATCAA	TAGAAAGTTAACTGTTTGGAA	CCGGAAGAGACGAGTGCGGTA	ACGAAGAGTAATTGCTGCAAA
3614	IMPDH1	NM_183243	CCCAGGATTCATAGACTTCAT	CAGCAGCAGCCAGAAACGATA	CCGCACCGACCTGAAGAAGAA	ATGGCCTGCACTCTTACGAAA
3617	IMPG1	NM_001563	CTCCAAGTTCAAGGAACCAAA	CCGTAGAATATGAAGAATTTA	AAGGGCGAAGTTGTACTATAT	TCGGATCTTTCTGGATCGCAT
3623	INHA	NM_002191	CGGATGGAGGTTACTCTTTCA	AAGGCAGAGTTGGGAAATAGA	CAAGTATGAGACAGTGCCCAA	CAGCACTGTGCTTGTATCTAA
3624	INHBA	NM_002192	CAGGAAGACGCTGCACTTCGA	AAGGAAGATGTGGAAATCTTA	ACCCATGTCCATGTTGTACTA	CTGCAGTAGTGTGGACTAGAA
3625	INHBB	NM_002193	CAGCCTGTGGCTTTACCTGAA	CCACGTGAACTATGCAATTTA	CAGGTGGAACATGGTGGAGAA	CACGTGAACTATGCAATTTAA
3627	CXCL10	NM_001565	TTAGTTTGCAGTTACACTAAA	CAGGAAGGTAGAAATATCTGA	TGCATCAGCATTAGTAATCAA	CTGACTCTAAGTGGCATTCAA
3635	INPP5D	NM_005541	TCGGAATTGCGTTTACACTTA	CCCGGGACTGTTGACAGCCAA	TCCCATCAACATGGTGTCCAA	CAGGTGCTATGCCACATTGAA
3641	INSL4	NM_002195	AGCAGCAAGTCTCTAAAGAAA	CTGAGCCAACTCCTTAGAGAA	TAGGTACGACATCAGAATTCA	ATCCATTCTGTTGTGAAGTAA
3643	INSR	NM_000208	TCGAACGATGTTGGACTCATA	TAGGAAGACGTTTGAGGATTA	CAACGGGAGTCTGATCATCAA	ACCGCTTTACGCTTCTTCAAA
3646	EIF3S6	NM_001568	CAGGAGTCTTACACATATAAA	AAGGAATTATTACAAGGTAAA		
3656	IRAK2	NM_001570	GAGAATATGTGTTGTTATTTA	CCGGTTTACCTGAAGGACTTA	CCAGATCATCCTGAACTGGAA	CAGCAACGTCAAGAGCTCTAA
3660	IRF2	NM_002199	CCCTATCAGAACGGCCTTCTA	ACGGTGAACATCATAGTTGTA	CGGTCCTGACTTCAACTATAA	CACCTTATCTTAAAGCACTTA
3663	IRF5	NM_002200	CGGAGATAACACCATCTTCAA	CCGCATGGTGGAGCAATTCAA		
3667	IRS1	NM_005544	CCGCCTTTGCCTGACCAGCAA	CCGGTATCGTTTCGCATGGAA	ACAATAGGCCATGTTAATTAA	CCGGGTGAACCTCAGTCCTAA
3670	ISL1	NM_002202	TACGGTGGTCTTTGAATTATA	CCGGCTTAAATTGGACTCCTA		
3672	ITGA1	NM_181501	CCCTCGAAACACAACCTTTAA	CTGCATGTCGCCACCACTGAA	CCCTAGATTCACTAAGACAAA	ACTGAGGACATTGGAAATGAA
3673	ITGA2	NM_002203	TCGGAGCAATTCAATATGCAA	TCGCTAGTATTCCAACAGAAA	CCGGTTGATGGGACAGAAGTA	CCCGAGCACATCATTTATATA
3675	ITGA3	NM_002204	CAGCTACATGATTCAGCGCAA	CTGGATTGACTTTGCTGTCAA	CTCGCTTAGCATGGTAAATCA	CACCATCAACATGGAGAACAA
3679	ITGA7	NM_002206	GACCAGGGAGCTGATATGCAA	CACAGTGAAGTCCTCCATAAA	CCCTTTGATGGTGATGGGAAA	CCCAGTGATGGTATACTTGGA
3680	ITGA9	NM_002207	ACAGGTCACTGTCTACATCAA	CACATGCTAATGTGTGCTAAA	CCGAAGGTACAAAGAAATTAT	ACCGAAGATCAGGCACCTTAA
3683	ITGAL	NM_002209	AACGTGTGACCAGAACACCTA	CCCTGTTTAATGATTGACGTA	CTCGGTTGAATTGCACGCCAA	CAGGGCGTGGGACATCTAGTA
3684	ITGAM	NM_000632	CGCAATGACCTTCCAAGAGAA	CTCGTTTGACTGGTACATCAA	TCGGGTCATGCAGCATCAATA	TCAGACATCGGTTCATATTAA
3685	ITGAV	NM_002210	AGCAACTTTATTATAGATTTA	CACATACATGATACCATCCAA	TAGCATGATGTTACAGGAATA	ATGTAGTAGTTTGATGAATAA
3688	ITGB1	NM_002211	CTGCGAGTGTGATAATTTCAA	ACAGATGAAGTTAACAGTGAA	TACGTATTCAGTGAATGGGAA	AAGAGGGATAATACAAATGAA
3690	ITGB3	NM_000212	CAAGCTGAACCTAATAGCCAT	CCGCTTCAATGAGGAAGTGAA	CTCTCCTGATGTAGCACTTAA	CACGTGTGGCCTGTTCTTCTA
3692	ITGB4BP	NM_002212	CCGAGCTTCGTTCGAGAACAA	AAGCTACTGTGTCTTCAGCAA	CAGGGAGACAGAAGAAATTCT	CTGGATCTATCATTACTGCAA
3693	ITGB5	NM_002213	CTCGGTGTGATCTGAGGGCAA	CCGCTATGAAATGGCTTCAAA	ATGGGTGGACACCATCGTGAA	CAAGATTGTTTGGGATTGGAA
3700	ITIH4	NM_002218	CACATCTATGGTAGTCACCAA	ATGGATCGAAGTGACCTTCAA		
3704	ITPA	NM_033453	CAGGAGGCAGTTCGCCAGGTA	GAGGAGGTCGTTCAGATTCTA	CTGGATGAGACTTGTTTCCAA	CTGGAGAAGTTAAAGCCTGAA
3706	ITPKA	NM_002220	CTCCTGCAGCACCGACTTCAA	CCCAGCGTTCCCAGAGCCAAA	CCGGTCTAACGTCTCACACCA	CACCAGCGGGCTGATCCTGAA
3710	ITPR3	NM_002224	CAGGTGTTCCTGCGAACTACA	CCGCAGCATGCCGCTGATCTA	AAGCCGGTGAAGCGCATTCAA	TCAGTTTACCTTAATGCCTTA
3714	JAG2	NM_002226	CCAGAGGTTGTGCACTGTTTA	CTACGTTTCTTTAACCTTGTA	CACTCTGTATATTTGATTGAA	CTGCGTCGTCACCAAATCGTA
3725	JUN	NM_002228	TTCGTTAACATTGACCAAGAA	CGCGCGCGAGTCGACAAGTAA	CTGCCCAGTGTTGTTTGTAAA	AAGAAGTGTCCGAGAACTAAA
3730	KAL1	NM_000216	ATGCATGTCTATATAATTATA	AAGCGTAAATCTAATCAATAA		
3741	KCNA5	NM_002234	ACCAGGGAACCCATTTCTCTA	CAGAGGGATAACCCAAACAAA	CGCAGAGTATTTGAAGTCACA	AGGAATACTTCTGATAATTTA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
3742	KCNA6	NM_002235	TACAATGACCACGGTAGGTTA	CTGGTGTTCGGTCTACATTTA	CAGGACCAAATACCTGGACTA	CTCGATCTTGCCATAACTTTA
3744	KCNA10	NM_005549	CTAGTTATTAGTTTATGCAAA	CACCGGGAGACTGAGAATGAA	CCGGGAGGATAGGGAGCTAAA	CAGCACAGACTCTCTTAATAA
3745	KCNB1	NM_004975	CCGGAGCATTGAGATGATGGA	TCGGTATTTCATAGTACCTGA	AACCACTTGTCTCCTAACAAA	CACGCTTTCTTTACATCACTA
3753	KCNE1	NM_000219	GCCCAGGATGATCCTGTCTAA	AAGAGAAGGACAAGGCCTATG	AACCATCTGGCCATAGAACAA	AACTGGGATTCTTCGGCTTCT
3756	KCNH1	NM_002238	ATCAGCGATGTGAAACGTGAA	CTGAGATACTCAGGATATTAA	TACAGCCATCTTGGTCCCTTA	TCGGCGGTCCAATGATACTAA
3758	KCNJ1	NM_000220	CAGGGTGTTGACAGAAAGTAT	CTCCCATAGTATCCAAGACAA	CAGTCTATACTTGGAGTTATA	TACGTTTAGACAGAGGCTAAA
3759	KCNJ2	NM_000891	CAGGAGCCGCTTTGTGAAGAA	CGAGATGGTGATGTACTCTTA	AGGGTCAATGAGAGCCATAAA	CAACTCTCTTATGGTATTATA
3760	KCNJ3	NM_002239	ACCAGCCATAACTAACAGCAA	AAGGCTACTGGCATTAATTAT	ATGGACTAGATGATATTACTA	CTGTGTGAAGTTACACAATTA
3764	KCNJ8	NM_004982	CAGGACGATGTTGGCCAGAAA	AAGGTGCAATTTATGACTCCA	GAGGTGGTTCCTATTCACCAA	CCAGATCGCTGTGTTACTAAT
3765	KCNJ9	NM_004983	TGGGAAGATGGTAGCAGATAA	AGGGATAATTCAAACTGACAA	GTGAATGACCTTAGTCCGCAA	CAGGCCCGACAGAGAGATGAA
3769	KCNJ13	NM_002242	AACCTACAAACTAGACTTGTA	ATCGCCTTACTTGCCATACAA	CAAACTAGACTTGTAGATTAA	CACATGGATGGCAAACCTAAT
3770	KCNJ14	NM_013348	CGCGGTCGCTTCGTCAAGAAA	CTGGATTCACCTAAGATTCAA	CAGGGTGAGAAGCCAATGGTA	AAGACTGAAGTGACAGATTAA
3773	KCNJ16	NM_018658	CAGACTGGCACTTTATCTCAA	CCGGTAACTATTGTCCATGAA	CAGCAGCTATCATATTATCAA	AAGCTTAATATTAGAGACCCA
3776	KCNK2	NM_014217	CACGACCATTAATGTTATGAA	TCGCATCATCTCAACAATCAT	AGGGATTATACCGTTAGGAAA	AGCCTAGATATGGACCATTTA
3778	KCNMA1	NM_002247	ACCGAGAGAGCCGTATATTAA	ACGGGATGTTACGTCAACCAT	AACCATCTTAAGATCCAAGAA	TAGGCAGAGCAAGTTTATTTA
3780	KCNN1	NM_002248	CAGGGAGACGTGGCTCATCTA	ACCGTCATGTACGACCTTGTA	CACGCTTACCGACCTAGCCAA	CCGGCCTAGCCTAGAATCCTA
3785	KCNQ2	NM_004518	CAGCCAGGGCGTGTGGTTTAA	CCCGCCCTCCTGAGCTATGAA	AACGGTCACCGTGCCCATGTA	CCCATTGACACAAACCCTCAA
3788	KCNS2	NM_020697	CCCATAAAGTTAAATCCCTTA	CACCAAGTGAACTCAGTTTAA	CACCTTATGGTTATGGTGTAA	AGGGACTATTATGCCCATAAA
3792	KEL	NM_000420	CTGGTAAATGGACTTCCTTAA	CCCGACAAGAATACAACGATA	ACCCGAAGTGCTGCCATGAAA	CAGCACAGAAATATCGACCAA
3796	KIF2	NM_004520	AAGAACCAAGATTGTTCTAAA	CAGCAAGCAAATCAACCCGAA	CCAAACCAGATTGATGACTTA	ACCATATAACATGTGATTATA
3806	KIR2DS1	NM_014512	ATCATAGGTCTATATGAGAAA	AACAGCGAGGATTCTGATGAA		
3808	KIR2DS3	NM_012313	CACGTTCTGATTGGGACCTCA	CACCATGTCGCTCATGGTCAT		
3809	KIR2DS4	NM_012314	AGCGAGGATTCTGATGAACAA	CAGCTCCATCTATCCAGGGAA		
3810	KIR2DS5	NM_014513	AACAGGGAGGATTCTGATGAA	TACCTGCGGCTGGAATCTGAA		
3814	KISS1	NM_002256	CAGGACTGAGGCAAGCCTCAA	CCAGGTGGTCTCGTCACCTCA	AAGAAATGTTGCGTAACTCAA	CACCCTCTGGACATTCACCCA
3817	KLK2	NM_005551	CAGCATATAATTCTCCCTGCA	TACTTGAATAATTGACCTGAA	GACGAGTATGGAGTACTTGAA	CTGAGGTTCCCTAGAGTTCAA
3818	KLKB1	NM_000892	CAGCAAGTTCAATCAATGACA	AACGTGGAATCTGGATTCTCA	CGCTATAAAGGTGCTGAGTAA	ATGGTCTGTGCTGGCTATAAA
3827	KNG1	NM_000893	CCGCATAACTGAAGCCACTAA	CTCGGCTGTGTGCATCCTATA	TCCCTCTTCATGCTTAATGAA	ACCGGTGAATGTACAGATAAT
3832	KIF11	NM_004523	CTCGGGAAGCTGGAAATATAA	GCCGATAAGATAGAAGATCAA	CTAGATGGCTTTCTCAGTATA	ACGGAGGAGATAGAACGTTTA
3833	KIFC1	XM_371813	TCGGGAAACACAGGCCATTAA	TGGGACTTAAAGGGTCAGTTA	CAGGGCTATCAAATAAAGAAT	TCGGGAAACACAGGCCATTAA
3835	KIF22	NM_007317	CCACAGTATCCTTATTGCCAA	CAGGACATCTATGCAGGTTCA	ACAGATGGAGTCCTTCCTGAA	ATCCACATCCTGAAGAATAAA
3849	KRT2A	NM_000423	AAGCAGCACCATTTCATCAAA	CTGGTGGAAGCCGGAGATCAA		
3856	KRT8	NM_002273	CCAGGAGCTGATGAACGTCAA	CAGGGTGACCCAGAAGTCCTA	CAGGGCCGTGGTTGTGAAGAA	CAGCATCATTGCTGAGGTCAA
3860	KRT13	NM_002274	CGCCAAGAGTGCAGAGCTGAA	CTGCCTTTCTGCAAACATAAA		
3861	KRT14	NM_000526	CTGGCAATCAATACAGCTTCA	CAAGTATGAGACAGAGTTGAA		
3884	KRTHA3B	NM_002279	ATGGTCTGGAAGGAGAACAAA	CCGAGGCATCACCACAAATCA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
3887	KRTHB1	NM_002281	CAATAAATTAATGTAGCCAAA	CAGCAGCTGCCGGAAATGTTA		
3891	KRTHB5	NM_002283	CAGCCCTTCACTTAACTCCTA	CAGGTCTTGCTATTCAGTGAA		
3912	LAMB1	NM_002291	CCGAAACAGCAACGCCTGTAA	TACCAAGATCCTGTTACTTTA	AGGGAATTTGTGACAGCTATA	TCCGTTCACTCCTAAAGGATA
3913	LAMB2	NM_002292	CGGGTGAACCTGACTCGTCTA	CCAGGCCACCTTTGAACGCTA	CAGGTACTTGATATTTCCTAA	GCGAGATAGGCTTGCACTTAA
3914	LAMB3	NM_000228	ACAGTTACACTTGACAGACAA	ACCGGTTGGGTCAGAGTTCCA	TTGGCATGCCATTGAAACTAA	AAGAGGGATTTGAGAGAATAA
3916	LAMP1	NM_005561	CACGTAATGCATTGCCTGTAA	CACGAGAAATGCAACACGTTA		
3920	LAMP2	NM_002294	CAGTACGCTATGAAACTACAA	CTGGAGCATTTCAGATAAATA	CTGGAACCTATTCAGTTAATA	TAAGGACTATAGTGATTTAAA
3930	LBR	NM_002296	AAGACTCAAGTATAGATTAAA	TAGCAATTAAATTCTAGTGAA	CAGAAGACAGTCTTAATATAA	TAAGGTAGCTTTAGCAATTAA
3931	LCAT	NM_000229	CTGGCTGGATCTCAACATGTT	AACCAGATGTGGTGAACTGGA	CAGCATCAAGCTGAAAGAGGA	AACAGCATCTCAACATGGTCT
3932	LCK	NM_005356	CTACGGGACATTCACCATCAA	CGCCATTACACCAATGCTTCA	AGGCATCAAGTTGACCATCAA	AAGGGCCAGGACTTTATCTAA
3939	LDHA	NM_005566	AAGGATCAGCTGATTTATAAT	CAGATTTGGCAGAGAGTATAA	CAGCTGATTTATAATCTTCTA	AAGTCCAATATGGCAACTCTA
3956	LGALS1	NM_002305	CGCCAACACCATCGTGTGCAA	CGCCAGCAACCTGAATCTCAA	GACGGTGACTTCAAGATCAAA	CACCATCGTGTGCAACAGCAA
3957	LGALS2	NM_006498	CAAGCTGAACCTGCATTTCAA	CACTGATGGCTTTGTAATTAA		
3959	LGALS3BP	NM_005567	CACGGTCATCCTGACTGCCAA	CTGAGGCTCAGCTTCAAGAAA	CAGCTTCCTCTTCCAGGACAA	CAGCTTCAAGAAATTACTGGA
3965	LGALS9	NM_002308	CTCCTTTCCCAGTGTCCTTAA	CCCACCATCAACAGACTGGAA		
3977	LIFR	NM_002310	CAAGACCATTATCAACTCCTA	TTGGAAGCCTTTACCCATTAA	TGGGTCGATCACAATCAACAA	TGCAGATTCGATATTAGTAAA
3980	LIG3	NM_002311	CAGCTGGTTGAAGGTCAACAA	CTGGGAAGAGCTGGAAGATAA	CACCCGAATCCGAGATGATAA	CTGGAAGATAATGAGAAGGAA
3984	LIMK1	NM_002314	CAGAGGTTTCTGGGAGACCTA	GAGCATCTAGGAAGTATTAAA	CTGCCTGGTCCGCGAGAACAA	CACCATGGACTTTGGCCTCAA
3988	LIPA	NM_000235	TACCTGGTCTCGGAAACATAA	CACGTTTGCACTCATGTCATA	CTGACTTAAGCGAGGTATAAA	CCCGCTACTGTCGTTATTGAT
3990	LIPC	NM_000236	AAGTTTATCATTACCAGTTAA	CTGAAGACGATCAGAGTCAAA	AAAGGAATTGCTAGTAATAAA	CAGGAGAAACCCAGCAAAGAA
3992	FADS1	NM_013402	TCGGAATGTTACAATGGTAAA	CAGGAAGAGATTTAACACTAA		
4000	LMNA	NM_005572	AAGCGCCAGAATGGAGATGAT	CCCACCAAAGTTCACCCTGAA	CCGGCTGCGCAACAAGTCCAA	CCAGGAGCTTCTGGACATCAA
4010	LMX1B	NM_002316	CCGCTTCCTGATGCGAGTCAA	CAGCAGATCGTGGCCATGGAA		
4012	LNPEP	NM_005575	CAGGGCACAATTATACGTTGA	CCGCTTTATCAAATATGCCTA	TCCAATGGAACTCAAAGCCTA	CACGTAAATGCCAACCATCTA
4015	LOX	NM_002317	AAGCTGGCTACTCGACATCTA	CTGCACAATTTCACCGTATTA	AACTACTACGATACTTATGAA	CTGGAACTTTAGTGAAACATA
4016	LOXL1	NM_005576	CAAGGTGCACGTGAACCCAAA	TCGCTACGTTTCTGCAACAAA		
4017	LOXL2	NM_002318	CTCGAGATTCCGGAAAGCATA	CCGGAGTTGCCTGCTCAGAAA	CAGGCAATGAGAAGTCCATTA	CCAGTCTATTATAGTCACATA
4033	LRMP	NM_006152	CTGGGAAAGTATAGCATGAAA	CAGATTATCTTTGGGATTTAA		
4034	LRCH4	NM_002319	CCGCCTGGATTTCTCCTGTAA	CAGCGTTGATAGTGGCAGCAA	TTGGCTCCATTCAGAGACCAA	GCTGGTTGTGTTGACAATAAA
4038	LRP4	XM_035037	CAGCGTGTTGACAAATACTCA	CCGCAAAGTACTGATCAACAA	CCGCGCGGTGCTCATCAACAA	CAGGAAATCATTCGCAACAAA
4041	LRP5	NM_002335	CTGGACGGACTCAGAGACCAA	CCCGTTCGGTCTGACGCAGTA	CTGGATGGGCAAGAACCTCTA	CAGGGCTGGGAGAACTTTGTA
4043	LRPAP1	NM_002337	CTGGAAGAAACTAAAGCTTGA	TACCATGCACAGAGTCCTTAA	CAAGTATGGTCTGGACGGAAA	CGGGAGTTCCTGCATCACAAA
4046	LSP1	NM_002339	CCGCTCCATAGAGAAGAGTAA	CAAGGAGAAACTGCAGGTCAA		
4049	LTA	NM_000595	CAGGTGGTCTTCTCTGGGAAA	CCGGAGCTTTCAAAGAAGGAA	CAAGGCTGACCAAGAGAGAAA	ACCCTCGATGAAGCCCAATAA
4052	LTBP1	NM_000627	CCCAATATATCTACCATTGTA	TTGATTAAATTTGGCATTTAA	CTGGGTATGAATGCTACTGTA	TACCGGGTTATAAGCGGGTTA
4054	LTBP3	NM_021070	CCGCTACTGCGTGGATGTGAA	CCGGGACAGATCTCAGCAGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
4055	LTBR	NM_002342	TACATCTACAATGGACCAGTA	CCGGCGGGTCTATGACTATCA	AAAGGGAGTCATTAACAACTA	CCGCCACACGGTCACCTGCAA
4057	LTF	NM_002343	ACCCTTGATGGTGGTTTCATA	CAGCCACGAACTCACTATTAT	CAGAGAGAGCACAGTGTTTGA	AAGCAGTGACCCTGATCCTAA
4058	LTK	NM_002344	CAGGGATATTGCCGCCCGGAA	CCGGGCCTTGCTCCCAGTCAA	CCTGCAGATGCTTCTAATAAA	ACAGATCTTTGGAGTGCCTAA
4067	LYN	NM_002350	CTCCGAGTCACTAATGTGCAA	CCCAATAATTGCAGAACTAAA	CGGGAAATATGGGATGTATAA	CCCGGACGACTTGTCTTTCAA
4070	TACSTD2	NM_002353	TCGGCGCAAAGGAGACGTTTA	TTGCGACATTGTGAAGGCTTA	CCCGGGATCGTTTGCAAGTAA	CTCGAAATAAGTGGTACTATT
4071	TM4SF1	NM_014220	TTCACTTGTATTCATTTGTAA	TCACAGGATGTCAGTGTTTAA		
4084	MAD	NM_002357	CAGTAGCAGATCAACTCACAA	TACGTTGAGTTTATTAACAAA	CCGAATCAAGTCGACACACTA	AGCCAAATTGCACATAAAGAA
4085	MAD2L1	NM_002358	AAGAGTCGGGACCACAGTTTA	CTGAAAGTAACTCATAATCTA	TCCGCCTTCGTTCATTTACTA	ATGGATATTTGTACTGTTTAA
4086	SMAD1	NM_005900	TTGGAAGTTAAGAATTGATTA	CACACACACCTTGGTAACATA	AACCGGAATTCCACTATTGAA	CAGGACTTTGTGTACAGTTAA
4088	SMAD3	NM_005902	CCGCTGTTCCAGTGTGTCTTA	ATCAAGGGATTTCCTATGGAA	AAGAGATTCGAATGACGGTAA	AAGGAGCACCTTGACAGACTT
4093	SMAD9	NM_005905	CAGCCTCAAGGTCTTCAACAA	TTGGACTTCTTTCTAATGTAA		
4099	MAG	NM_080600	CACTCGCTGTACAGAATGATA	CCCGGTGATTGTGGAGATGAA	CTCGCTGTACAGAATGATATT	ATCGCGCAATGTGACCGTGAA
4101	MAGEA2	NM_005361	TCGACAGATGCAGTGGTTCTA	CAGGGAGTTGATGACCTTGTT		
4109	MAGEA10	NM_021048	CCCAGAAGTGAGATAGATGAA	AAGAAGATCTTCAATCCCAAA		
4118	MAL	NM_002371	TCAGATGGAAGTCTTCATAAA	ACCCTGTGAAATACTTTATAA		
4123	MAN2C1	NM_006715	CACCCAGAAATTGAGCTGGAA	CTCGCTCTTGCGGGCGCCTAA	CAGCCTGTGTTCGTAGTGCAA	CAGGATGCTGGCGTTATCCAA
4125	MAN2B1	NM_000528	GCGCCTTGATTATCAAGATAA	CGCCAAGGAGCTGGTCGATTA	TCGACCCACCTGGAAACTGAA	GCGGAGTATCGGAGCCACTAA
4128	MAOA	NM_000240	TTGCATATTTGGATTACAATA	ACCCTGGTGTGAGGACATAAA	ACGCTGAACCATGAACATTAT	CAGATGTGCCTAGACACGAAA
4137	MAPT	NM_016835	CGGGAAGGTGCAGATAATTAA	TTAGGCAACATCCATCATAAA	CAGTGTGCAAATAGTCTACAA	CCGCCAGGAGTTCGAAGTGAT
4141	MARS	NM_004990	CAGCGAGGGATTCACGGCGAA	TAGGAGCTGAGGATAACTATA	CTGCATAACCCGAGACCTCAA	CTCGACATGGCAACCAATATA
4142	MAS1	NM_002377	CCCATATGCATGAGATACTAA	GAGATACTAATTAATGATGAA	ACAGTTGAGACTGTCGTCTAA	AAGTATCTCCTAAATGTGATA
4144	MAT2A	NM_005911	CAGCAGGATCCTGATGCCAAA	CAACAGTTTAATGAAGATCTA		
4148	MATN3	NM_002381	CACCACTGTGAGTGTAGCCAA	CACCTTGAATGCCGACAAGAA	AAGGTCAGCTCGTATCTTCAA	TTGGTAGGAAATAGAATGAAA
4150	MAZ	NM_002383	CCGCGACGTCTACCACCTGAA	CGCGTCTGCCTTGGAGAAGAA		
4152	MBD1	NM_002384	AAGAGAGTTCCGGGAAACATA	CCGGGAACAGAGAATGTTTAA	CCTGAGGATAACTCAATATAA	AAGGATGATTCTGCCTCCAAA
4153	MBL2	NM_000242	TAGGGTTCCCTTATATTAATA	TACGATGTTTAGTAACCTCAA	CAAGTCAAGATTTCCATATAA	CACATTGAGTCTATCAATCAA
4155	MBP	NM_002385	CACGGCCGGACCCAAGATGAA	CAGTTAAATGAGAACATGAAA		
4157	MC1R	NM_002386	CCAGGAAAGTCTGGTAATAAA	CAGGAAAGTCTGGTAATAAAT	CACGCTCTTCATCGCCTACTA	CACCAGGGCTTTGGCCTTAAA
4161	MC5R	NM_005913	CACCATCTACCTACTCAACAA	TCGCTTCATGTCTCACTTCAA	CTGGGAGACCATCACCATCTA	CGGCATTGTCTTCATCCTGTA
4162	MCAM	NM_006500	CAGCTGGTTAAAGAAGACAAA	TACACACATTATGGCTGTAAA	CCGAACTTGTAGTTGAAGTTA	AAGACCGAACTTGTAGTTGAA
4168	MCF2	NM_005369	TAGAATGTCATCGGCAAATAA	CACGTACTAAATGAACTGATA	TGGCTATATTGGAAACTTAAA	AGGGACTATAGCTCAAGTAAA
4172	MCM3	NM_002388	CAGGGAATTTATCAGAGCAAA	CGGCAGGTATGACCAGTATAA	ATCCAGGTTGAAGGCATTCAA	CACGATTTGACTTGCTCTTCA
4193	MDM2	NM_002392	GCCCAGTATGTAGACAACCAA	CCGGATCTTGATGCTGGTGTA	CAGGCAAATGTGCAATACCAA	AACCTGAAATTTATTCACATA
4201	MEA	NM_014623	CACAGTGAGAGCTGCCTTATA	TGGGAAGATGTGGTACAGAAA		
4222	MEOX1	NM_004527	CAGGCTTGACTGGGTGGACAA	CTCAATTCACTTTGTAAGAAA		
4224	MEP1A	NM_005588	AAGGACGGACCGGGATGATTA	GACACCTATGATGATAGCTTA	CCGGGATGATTATGTGAACAT	GAGGCTGAACCGAATGTACAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
4234	METTL1	NM_005371	CGCGCATGGCTGCGTCATTAA	CACGTGGATTTGGTAGAGAAA	CAGAATATGCCTACGTGCTAA	CTGGTGTATACCATAACCGAT
4239	MFAP4	NM_002404	CTGGACTGTGACGACATCTAT	CCGCGGCTGGAATGACTACAA	CAGAAGAGATTCAATGGCTCA	AACTGGCTTCATACACACAAA
4242	MFNG	NM_002405	ATGCTTATTTGTTTAAGTCAA	CTGGCTAATGTCTCTCAGTCA	CTGGCCGTTGGCCCTGGCTAA	CAAGACAATCATCCACAGCTA
4254	KITLG	NM_000899	AAGCGAGATGGTAGTACAATT	CAGAAATGTCTAAATGCTGAA	TACTGTGAAACTGGCACTGAA	CACTGAATTAATCATCTATAA
4255	MGMT	NM_002412	AAGCTGCTGAAGGTTGTGAAA	CCGGCTCTTCACCATCCCGTT	AAGGTTGTGAAATTCGGAGAA	CACCAGACAGGTGTTATGGAA
4259	MGST3	NM_004528	CAAGATGGCTGTCCTCTCTAA	CTGGTGCTGCCAGCTTTATAA	ATGGCTGTCCTCTCTAAGGAA	CCAGAACACGTTGGAAGTGTA
4283	CXCL9	NM_002416	ACCAATAAGTATTCTGTGTTA	CCACCCGAACGTCTTATCTAA	CCGGTGGAGATCCCACCCGAA	CAGGTAGACAGTATATAACTA
4284	MIP	NM_012064	CCGCTGTGCTGTATAGCGTTA	CCGAGGAAACCTAGCACTCAA	CCGGCTCAAGAGTATTTCTGA	CCCGATGTCTCCAATGGACAA
4286	MITF	NM_000248	ATCGATGACATCATTAGCCTA	CAGCCTACAACTGAATAGCAA	TAGCCTAGAATCAAGTTATAA	CATGATGGTATCTATAGTCAA
4287	ATXN3	NM_004993	CAACATTGCCTGAATAACTTA	TGCGTCGGTTGTAGGACTAAA	TCGGAAGAGACGAGAAGCCTA	TACGATGGGATCATTATTTCA
4291	MLF1	NM_022443.1	GAGGGAGAGCTCATAATCGTA	CAGGAGTTCATCAATATGAAT	GACCGAGCTCATGTCATTAAA	GACCAATCTCTTGCTGTTAAA
4295	MLN	NM_002418	CAGCAAATAAAGCATGAAATA	AAGGAACGGAATAAAGGGCAA	CCAGCTGGGCTTGGAAGGAAA	CTCCAAGATGGTATCCCGTAA
4296	MAP3K11	NM_002419	CAAGGCCTCCACCTTCTCTAA	CCGGCCTTGACCGGAGGAGAA	CCGGAGGAGAAACGTCTTCGA	CCCGACGTCTGGAGGACTCAA
4301	MLLT4	NM_005936	TAGCTCTACAGTCCACTTTAA	CAGCAGTTGGGCCATATTGAA	CTCTATAATAATTCAACTCAA	ATGCCGGTATGTATTGTCCAA
4306	NR3C2	NM_000901	CCAGACCTAGTCTTTAATGAA	CAGCAATTAATTAGATCAACA	CCACGAGGAAGCAGCAATTAA	CAACATTACCTTGTCTTTCAA
4308	TRPM1	NM_002420	AACGGGAATGTATCTTTGTAA	CAAGATTATACAATCTCTTTA	TTCAGTTGCAGTAGTATCAAA	CACCATTAGGTCACTTAAGAA
4317	MMP8	NM_002424	AACGCACTAACTTGACCTACA	ATGGACCAACACCTCCGCAAA	CCGAAGAAACATGGACCAACA	TCCCAAGGATATATCAAACTA
4319	MMP10	NM_002425	GACAGTAATCTCATTGTTAAA	CAGGATGGTGACACACATATT	GAGCCTAAGGTTGATGCTGTA	GACACACATATTAAAGAGTAA
4324	MMP15	NM_002428	CCGGAGCGCTGAGCCAGACAA	CACCAAATACTGGAAATTCGA	CTGGCTCTTTCGAGAAGCGAA	TACATTTATTTCTGTAAATAA
4326	MMP17	NM_016155	CACAAGATCGTCTTCTTTAAA	AAGGACAATAACGTAGAGGAA	CTGGGTGTTCAAGGACAATAA	ATGACAGGACTTATTTCTTTA
4328	MMPL1	NM_004142	ATCGGTGTGTAAGGTGGCCTA	CTCCATTATGAGGCCCTTCTA	CAGGCTGGAGTGCAATGACAT	CAGGGATGATGGAGAGTTCAT
4329	ALDH6A1	NM_005589	CAGGTCTTGCTCCGCTATCAA	CAGCTTTGTGGGATCCAACAA	TGCGATCATCCGGACATCAAA	AACCATCATCTCGAATGTCAA
4355	MPP2	NM_005374	CTAGCGATTGACAAGCAATAA	AACGGCCGAGTTTGTCCCTTA	ACGGCGCAGCCTGAAGAACAA	CCAGTTCTTCCAAGTGTCTAA
4357	MPST	NM_021126	CAAGACCTACGAGGACATCAA	CACCAAGAGAGTGTTTCTTCA	CAGGAATTCCGTTGACTTGTT	AACCAAGTGCTAAATCTTGTA
4361	MRE11A	NM_005590	TGCGATTCAGTTCACCGCTAA	CACATCTTTATTGAACTTGAA	CCCGACATTTCTTCATAGGTA	AAGGGTTATTTGAGCAAGTAA
4435	CITED1	NM_004143	CAGAAACTTAATAGCCAGTAT	ACCAATTCTGTTGTAAATAAA		
4436	MSH2	NM_000251	CAAGGATATGATATCATGGAA	TCCAGGCATGCTTGTGTTGAA	TTGATAAGCTATTGTCTGTAA	CCCATGGGCTATCAACTTAAT
4438	MSH4	NM_002440	AACCATTAACATGAGATTAGA	TCGCTCATATTAATTGATGAA	ATCAATTGTCTTGGATGCCAA	ATGCAGTGAGGTCTAACATAA
4439	MSH5	NM_002441	TTGCCAGACATTAGTGGATAA	TAGGAAGACTCCCGGATTCTA	CACCTTCATGATCGACCTCAA	AAGAAAGATATTGTTTCTTTA
4482	MSRA	NM_012331	ACCCTTCTTGGTAGAAGCTAA	AAGGAAATTCTGGGTCTTGAA		
4486	MST1R	NM_002447	CAGGTCTGCGTAGATGGTGAA	AGGGAGTACTATAGTGTTCAA	TGCCATTAAGTTTGAGTATAT	ATGGAGCATCCTTCTCCGATA
4493	MT1E	NM_175617	CTGCAAGTGCAAAGAGTGCAA	CTGGGCTTTCTTTGCCCTCAT	AAATATGTGACTGACAATAAA	CTCCAGGCTTTCTGCCCTAAA
4499	MT1K	NM_176870	GCCTAGCAGTCGCTCCATTTA	CACGCCGTCCGGGTGGGCCTA		
4520	MTF1	NM_005955	CAGCACAAATAGGCAGCTTAA	ATGAAAGGTCATGATAACAAA		
4521	NUDT1	NM_002452	CCGCGAGGTGGACACGGTCTA	CCGGGTTTCATCTGGAATTAA		
4522	MTHFD1	NM_005956	GAGGTAGAATTATATGGTGAA	ACAGGTGAATGGATTATTCTA	CAGATCACCATCCATCTTCAA	ATCGTTTGGTGCCATCAGTAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
4524	MTHFR	NM_005957	AAGCGCCGAGAGGAAGATGTA	CTCGGGAGAACCAAACCGGAA	AACCTAGTACTCTCTGCTCTA	TGCCCTGTAACTTATCTAGAA
4544	MTNR1B	NM_005959	CGGCCTCGCTGTGGCCATCAA	CTGCCTGAATGCCATTGTCTA	CACTAGCTACTTACTGGCTTA	AACCCACGGCACTGCATTCAA
4580	MTX1	NM_002455	TTGGATAGACACCAAGAACTA	CAGGGCCCGCTCCAAACATAA		
4583	MUC2	NM_002457	CCGGTTTGGCAACAACACCAA	CCCGCTGGGATTCGAAGTGAA		
4586	MUC5AC	XM_495860	CCAGTCTGTTGCATAAATACA	ACCCTTCAAGATGTGCCTCAA	CTGGACAGTGTGCAGCATCAA	CACCCGGAGGTGAACATTGAA
4587	MUC5B	XM_039877	CACCTATGATGAGAAACTCTA	CCCGATGGGTTTCCTAAATTT		
4591	TRIM37	NM_015294	TTGGACTTACTCGCAAATGAA	CTCGAAGGTGGTCCTACTACA	CTAGAGCTTAGTTGTGTTTAA	CTGTAGATTAGTGAACAGAAA
4594	MUT	NM_000255	AAGAGAGATACTATGGACTTA	CTGGGCTCACTTAATAGAGAA	CTGGAGCTGGCCTATACTTTA	AGGGAATACCTAAACTTCGAA
4595	MUTYH	NM_012222	CACATCAAGCTGACATATCAA	CAGGAGGAATTTCACACCGCA	GAGAATCCTGTTGTTAGTAAA	CAAGCTGACATATCAAGTATA
4598	MVK	NM_000431	AAGGGAAGATTTCATCCTTAA	CTGTGGCATCACACTCCTCAA	GCGGTGGGCCTGGTTAAATAA	CCGCTTGGCGATGCCAGCCAA
4599	MX1	NM_002462	TAGAGCTTACTTTGCAAAGAA	TCCGTTAGCCGTGGTGATTTA	CTGAAGAAACTTGTGAACGAA	TAAGATCAAGACACTCATCAA
4606	MYBPC2	NM_004533	CCGCCTCGAGGTCAAAGCCAA	TCCCAAGTTCCTGATAACCAA		
4607	MYBPC3	NM_000256	CAAGGTCAAGTTCGACCTCAA	TAGCACGGAGCTCTTTGTGAA	CCGCATAAAGGTGTCCCACAT	CAGGATGTCGGCAACACGGAA
4609	MYC	NM_002467	TAGCAGTTACACAGAATTTCA	CTCGGTGCAGCCGTATTTCTA	CCCAAGGTAGTTATCCTTAAA	AACGTTTATAGCAGTTACACA
4610	MYCL1	NM_005376	CAGCACTATTTCTACGACTAT	TGGCTAGTGACAAATAAATTA	CTGTGGCTAGTGACAAATAAA	CTCCAGTTGGCTTTACTTTAA
4615	MYD88	NM_002468	TCCGGCAACTGGAACAGACAA	CTCTGGCATATTCATCAAGTA	CAGAGAGTAGCTGTGTTTGAA	CATCCTGAGTTTATAATAATA
4618	MYF6	NM_002469	CTCGTGATAACGGCTAAGGAA	AAGTGGGAAAGTTGCATTTAA	TGCGAGGATCCTGGTATTGTA	TCCTGGTATTGTAATATTAAA
4619	MYH1	NM_005963	AAGCGCATCCATGAACTGGAA	CTGGGCTTTACTTCAGATGAA		
4625	MYH7	NM_000257	CAGAGAGAGATTATCACATTT	CAGACGGAGGAGGACAGGAAA		
4628	MYH10	NM_005964	CTCGTTCATCGCATCAATAAA	AAGCGGTTCAAAGCAAATCTA	CCCATGTTGCTTCTTCACATA	CAGGACTAATCTATACTTATT
4636	MYL5	NM_002477	CAAGGAGGCATTCACACTCAT	CTCATCCAATGTCTTCTCCAA		
4653	MYOC	NM_000261	CCCATTCAAGAACCGCTATAA	GGCGTAGACAATTTCATATAA	CAGCATTTATGGGATGTTTAA	CAGCATCGAATATAAGTAAGA
4654	MYOD1	NM_002478	CCGCCTGAGCAAAGTAAATGA	CCGCCTGAGCAAAGTAAATGA	CTGCACGTCGAGCAATCCAAA	TACAGGGAATTTGTACGTTTA
4656	MYOG	NM_002479	CAGGCTCAAGAAGGTGAATGA	CCCAGATGAAACCATGCCCAA	CCAACTGAGATTGTCTTCCAA	CTGCCCTGAATTGAGAGAGAA
4670	HNRPM	NM_005968	TGGCATCTTGTTGACATCGAA	CCCACCCAGTATCCTAAATAA	CCCGCAGGAATGGGAATGGAA	CCGGATGATGAATGGCATGAA
4671	BIRC1	NM_004536	ATCCTCAATCTAAGTACTTAA	CTCAATCTAAGTACTTAACTA	TCGAAATTCATGATACTACTA	CGTGGTGAACTTTGTGAATTA
4684	NCAM1	NM_000615	CCGATTCATAGTCCTGTCCAA	TCCATGTACCTTGAAGTGCAA	CCGAAACAACGTACGCCGTAA	CAGCGCGGCCTCCGAGTTCAA
4686	NCBP1	NM_002486	CAGGTATGGACTGCTGATAAA	CTGGAAGAAGCTAAAGAGAAA		
4688	NCF2	NM_000433	CAGAAGCATTAACCGAGACAA	CAAGAAGGATTACCTAGGCAA	CAAGTACACGGTAGTCATGAA	CAGTTTGGAAGTGTTAACTAT
4691	NCL	NM_005381	ACGGTGAAATTGATGGAAATA	TCCGTCTAGTTAACATTTCAA	TTGACTGGATATTCATATAAA	ATCCGTCTAGTTAACATTTCA
4692	NDN	NM_002487	CCGCGAAATCACCAAGATGCA	CAGTGCAGTATTCACGTGTAA	CCCACCGTGAGTCAACTTTAA	CCACCGTGAGTCAACTTTAAA
4696	NDUFA3	NM_004542	CAGCCTGGAGTGGCTGAAGAA	CAAGTACTCCGTCATGATCAA		
4704	NDUFA9	NM_005002	TCCGGAAGCCATTATCGTAAA	AAGAGAGGATAGATTCCTTAA		
4705	NDUFA10	NM_004544	AAGCAGGACAATCGCACTTTA	CTGGATGTTTGGAACCCTTTA		
4709	NDUFB3	NM_002491	CAGATTGAGGATGCACATATA	CAGAATATTAGTAAAGATTTA		
4716	NDUFB10	NM_004548	CAGCAGAACTGTATCAAGGAA	ATGACTGTTGCTGAAATATAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
4717	NDUFC1	NM_002494	CTCATCAAACAACACAATGAA	CACCATCTGTTGAGTTGTAAA		
4718	NDUFC2	NM_004549	CTGTAGGTATTAAGTCATTAA	CTGGTCTATATGTGATTTCAA		
4719	NDUFS1	NM_005006	CCGCAGATAATTAATGGACAA	TTGGCTTATCTTCATAAATAA		
4722	NDUFS3	NM_004551	CCGGAGAGTCTCAAGCTTGAA	TTGAGTGTCCGTGTAAATAAA		
4736	RPL10A	NM_007104	CAGCGCCTATATTAAGGCACA	CACATTTGAATAAATTCTATT		
4739	NEDD9	NM_006403	CGCTGCCGAAATGAAGTATAA	CACCCAAGAACAAGAGGTATA		
4741	NEF3	NM_005382	CCCAATCACAATATCCAGTAA	CAGCAGTACTTGCTCAATAAA		
4745	NELL1	NM_006157	TGCGAGAAAGATATTGATGAA	CTCATGTGAGTGAGAAATTAA		
4750	NEK1	NM_012224	ATGGCTCTCTCTACATAGTAA	CAGAATAAAGCTCGAGCCGAA	TAGGGATAGACCATCAGTCAA	ACCGTAGGAGATGTTCGTCAA
4760	NEUROD1	NM_002500	CACGAATTTGGTGTGGCTGTA	CAGATCGTATTAATTATCTGA	CAAGCTTGTATATACATATTA	CCCATGGTGGGTTGTCATATA
4761	NEUROD2	NM_006160	CAATGGCAACTTCTCACTCAA	CCCGCTCTGTCTCAATGGCAA	CTCGGAGAATCTCTTGTCTTA	CAAGACAATTTGTAACTAGAA
4762	NEUROG1	NM_006161	CCCAGGCTGTTGGGAACGTAA	CCGGCTGACAATACAATGAAA	CAGGGCTGGAGAGTACTTTAA	CAGACGCTTCATGTAAATAAA
4779	NFE2L1	NM_003204	AAGGGTAGAGTGAACAGGAAA	AAGGAGATTCCCAATATTCAA		
4781	NFIB	NM_005596	CTGGACAATCAGGAAGTCCAA	TACAATCACTAATTCCCTTAA	AAGGTTAAACTGTAATGACAT	ACAGAGGGCAAGTGCAATTTA
4784	NFIX	NM_002501	CTGGTGCTTCTTACATTATAA	CCGGACAATCAGATAGTTCAA		
4796	NFKBIL2	NM_013432	CCCATCCGGGTTCGAGTTCAA	CGGGAGCTCAGTGTAGCTGAA		
4804	NGFR	NM_002507	ATGGCAATTCTTTGACCTCAA	CTCCTGAAACTTACACACAAA	ACGTTAAGTGATGAACATTAA	AACGTTAAGTGATGAACATTA
4814	NINJ1	NM_004148	CAGGACATTCCAGAAGGACAA	CACGCTCTTTGTCAGGCTCAA		
4818	NKG7	NM_005601	AACCTTGTGAGCAGAAGGCAA	CTCCTTCTCTCTGAGATTCAA		
4824	NKX3-1	NM_006167	ACGCTATAAGACTAAGCGAAA	CAGGCTATCATATATACTGTA	AACTGTGTTTATTGCCTATAA	CCGGAGTACTAGCCAGCACAA
4825	NKX6-1	NM_006168	CCCGCTGTACCCTGCCGCGTA	CTGGAGAAGACTTTCGAACAA		
4832	NME3	NM_002513	CCGGCAGATGCGCGTCACAGA	ACGGCCGCCTTGTCAAGTATA	CTGCATCGAGGTTGGCAAGAA	ACGCACCTTCCTGGCCGTGAA
4833	NME4	NM_005009	ACGCCTTTATGCAAGTTGTAA	TTGTAAGGAGTTGAACAGTAA	CAGCACATGGGTGGTACACTA	ACCAACTACCTCCGTCAGCAA
4838	NODAL	NM_018055	GTGCTCCTAGATCACCATAAA	CTGGATGTTCTCTTTACTGAA	AAGATTAAGGATCACTGTATA	AAGGATCACTGTATAGATTAA
4849	CNOT3	NM_014516	ACGGCTGAGGGACCAAATCAA	CTCGGACACTGTGGAATTCTA		
4853	NOTCH2	NM_024408	TACCAGCATGTTATAGGGCAA	TTAGATGATAATGGACAACTA	AAGGGAAGGTAAGATGGATAA	CTGACTAAACGTAGTAAGGAA
4858	NOVA2	NM_002516	GAGGTGGTCAACATCCTTCAA	CAGGTCTGTGTGATATCTGTA		
4861	NPAS1	NM_002517	TGGCTTTGTGTTCGCCTTGAA	CGCCTTGAACCAGGAAGGAAA	CAGCGTCTTCGACTACATTCA	GCCCGTAGCCCTGAGAATTAA
4868	NPHS1	NM_004646	CAAGGCCTCATTCACCGTGAA	CAGCAGCAATCCGCCGGTCAA	TCGGACCAAACCAACATTCAA	CTGGTTAGGTGAGCTCCATAA
4879	NPPB	NM_002521	CACCTGCTTCTGATTCCACAA	CTGAGGCGGCATTAAGAGGAA	AAGATGGTTTCTTACCTTTGA	TCCACGGTGAAATAAAGTCAA
4880	NPPC	NM_024409	CAAGGGCTGCTTCGGCCTCAA	CCCAACGCGCGCAAATACAAA		
4881	NPR1	NM_000906	CCGGTACTCACTCACCAATGA	CCTGACGTTGCGCAAATTTAA	ACGCATTGAGCTGACACGAAA	AACGCATTGAGCTGACACGAA
4882	NPR2	NM_000907	CCCGGGAGGATGGACTTCGAA	ACCCAACTGAATGAAGAGCTA	CAGGACAATCGCACCCGGGAA	AAGGATGCCCTAGATGAGCTA
4885	NPTX2	NM_002523	TTCGATTAAAGTGCACTGAAA	CTGGACTGTCTTCATCAAGTA		
4889	NPY5R	NM_006174	CCCTTAGTTTGTCTTACTGTA	TAGGCATTTCAAGTTGGTGTA	TTGGGCTCTATACATTTGTAA	CACAGTCTTGTGGAACTTCAA
4899	NRF1	NM_005011	CAGGCAGATGAATGTCTTGAA	CAGAGGTGCAATCAAATGGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
4901	NRL	NM_006177	CCGAATTTAGATGCTGGTCAT	CAAGATTTCAATATCCAACAA	ATCCAACAACTAGATAGATTA	CTAGATAGATTAGGACCTCTA
4905	NSF	NM_006178	AAGGAATGCAATAAAGAGTAA	CAGGTACACATTTACACTGAA		
4913	NTHL1	NM_002528	CAGGCTGAGGTGGACCAAGAA	GAGCAAGGTGAAATACATCAA	CTGGAGGAGCAAGGTGAAATA	CACGCTGGGCAAGCTCATCTA
4915	NTRK2	NM_006180	CTGCATAGACAAAGGCCTTAA	ATGGCTTAAGCCTGTGTATAA	CTGACGAGTTTGTCTAGGAAA	ACCACGAACAGAAGTAATGAA
4916	NTRK3	NM_002530	CGCGATGGTTTCAGACGCTGA	CAGAGAGCACGGATAACTTTA	CTGGTTGGAGCGAATCTGCTA	CACGGATAACTTTATCTTGTT
4919	ROR1	NM_005012	CAGCAATGGATGGAATTTCAA	CCCAATATTGTCTGCCTTCTA	CCGTACTGCGATGAAACTTCA	CCCAGTGAGTAATCTCAGTAA
4928	NUP98	NM_005387	CGGGATTTCTTTGTAAAGCAT	CTGGAGTTAGCACTAACATAA	CAGTGTATTACTGCTATGAAA	TGGGACTACTATTAAATTTAA
4935	GPR143	NM_000273	CTGAGGCTGGCTGTAAAGTAA	CTGGCTGTAAAGTAAGTGTAA	TCGGATATGAACCACACGGAA	CAGCTAGAGCTTCTTCCCGAA
4948	OCA2	NM_000275	CCGCGGAAGTGTAGAAACCCA	CTGGCTGTGATTGGCGATAGA	TGGAATAGACCTTGACACTAA	GACCTTGACACTAACACTCTA
4967	OGDH	NM_002541	CAGGATCAATCGTGTCACCGA	CTGCAATTGGGTTGTTGTCAA	CACTCTTTCTTTCTCCTTTAA	TTGGCTTGACCCATAAACTAA
4975	OMP	NM_006189	AAGGAGGACTCGGATGCCATA	CCGGGCAAGGTCACCATCACA	CTCGGATGCCATAGATTGGAA	CTGGAATGTCGTGCTGGACAA
4978	OPCML	NM_002545	CACGTGTAGGATAATCATTCA	ATGCATGAAACCCAACACTAA	TAGGCCAAAGTAGCAAGCTAA	CTGGGACACTATCCTACTATA
4985	OPRD1	NM_000911	CACGCTCACCATGATGAGTGT	CTCCATCGACTACTACAATAT	CGGCATCGTCCGGTACACTAA	CAGCATCTTCACGCTCACCAT
4986	OPRK1	NM_000912	CAGGGAAGACGTCGATGTCAT	ATCGATGGGATGAATAAACCA	TAGGTTTAACTCAGATCACTA	CAGATGCTTTAGTTACTACAA
4987	OPRL1	NM_000913	CTGCCTTGTCATGTACGTCAT	CAGCGGTGCAATGAACTATCA	CTGGCTGGGTATTCTTCGTAA	ATGGGACAGGTCAAAGCATTA
4988	OPRM1	NM_000914	CCGTAGTAACACATAAAGTAA	AGGGAAGAGATTAGCATGAAA	TTCACCGTAGTAACACATAAA	TCCAGAGTGTGAATTACCTAA
4992	OR1F1	NM_012360	CCCACTCAGCTGAGAAAGACA	CTGAGAAAGACACTATGGCTA	CAGCACCATCATTGCTGTGTA	ATGGGTGGTTGCCAACCTGAA
4993	OR2C1	NM_012368	TCAGCTATGGTGGCTGCATAA	CCCAAATGCTGATCAATTTAT	CAAGTTCATTTCCCTGTTCTA	AAGCATCATCGTGATCTCCTA
4994	OR3A1	NM_002550	CTGGGTTCAACCAAGCTTTCA	TTCAGGTATCTTTAACTATAT	CAAGCTTTCAGACAAGGATAA	AAGCTTTCAGACAAGGATAAA
4995	OR3A2	NM_002551	AGGGTGCTCTGTGGCAAATAT	ATGGACAAACTCCAAGGCAAA	CACGTGGCAGCTGCAGTTCTA	AAGAGGTATCTTCAACTACAT
5003	SLC22A1LS	NM_007105	CTGCAGCAACATAGAGTACAA	CTCAGCCAGTCTTAAAGGCAA		
5004	ORM1	NM_000607	TCGAAACGAGGAGTACAATAA	TTCCCTCACTTGCATCAATAA	CAGCACGAGAAGGAGAGGAAA	CACGATCTTTCTCAGAGAGTA
5008	OSM	NM_020530	CAAGGCCTGGATGTTCCTAAA	CGGGCTCAGGAACAACATCTA	CTGACGTAAGGTGGATATTAA	TGGAGGGACATGACTAATTTA
5009	OTC	NM_000531	AGCGGTGGAGCTTGGCATAAA	AGGGCATAGAATCGTCCTTTA	AGCATCCATCCCAATTATCAA	TACGTGCTTAACTTTGCTTAA
5025	P2RX4	NM_002560	CTCCGTTACGACCAAGGTCAA	AGGCAGGTGCGTAGCTTTCAA	TCGTGCATTTATGATGCTAAA	CGGGACGTTGAGCACAACGTA
5030	P2RY4	NM_002565	CTGGGATGCAACGGCCACCTA	CAGAGGTGAGGGAACCCAATA	CCCAATAGTGATACCTGGTAA	CAGATAGATTGTAACACGGGA
5033	P4HA1	NM_000917	CAGAGAAGTTAGATCGGCTAA	TGGCAACAAATGGGTATCCAA	CGAAATCATCATATTGCATAA	CAGGGTGGTAATATTGGCATT
5034	P4HB	NM_000918	GAGGAAGACGATGATCAGAAA	CTATTTCACAATCGAATTGAA	CAGGACGGTCATTGATTACAA	AAGATGAACTGTAATACGCAA
5051	PAFAH2	NM_000437	CAGCGGGTAAGCGAGTGTTTA	ACGGGTGTTGAAGATCCTGCA	CCCGAGGACCTGTGTTCTTTA	GAGAAGTAGTTTGGTCAGCTA
5062	PAK2	NM_002577	TGCAGTAGTATAAATCATGAA	CCGGATCATACGAAATCAATT	CCGCGACCGGATCATACGAAA	ACGAGTAATTGTGAAGCATAA
5069	PAPPA	NM_002581	TGGGCAGTTCATGAAGCTCTA	CCGACAAGAAGTCTCCTTCAA	CTGGCCAATGCTTAAATACTA	CAGGGAGTGCTTGTTTGATAT
5101	PCDH9	NM_020403	ACGGTTCACCATCAATTTAAA	ACCGTCTAATACTTCCTTTAA	ACCGACGTGGGTTATACTTAA	AAGGCGGTATATGACAACCAA
5104	SERPINA5	NM_000624	CTCCGTTTCCTCATAGAACAA	TACACAGGTTTAGTTGACTAA	CACCAGCATGGTAGTGGCAAA	AAGGTGGAAATGGCCCATTTA
5108	PCM1	NM_006197	CGGATAAACTTCAGTGATTTA	CAGTATCACATCTGAACTAAA	ACCGTGATTCACTTAGATCAA	CAGGCTTTAACTAATTATGGA
5110	PCMT1	NM_005389	CAGGCGCTAATAGATCAGTTA	TTGGAGCAGTATGACAAGCTA	CTACAAGATGGCAGCATCAAA	TACGTGCCTTTAACAGATAAA
5111	PCNA	M15796	TGCGGATATGGGACACTTAAA	TACACTAAGGGCCGAAGATAA	ATGGATTTAGATGTTGAACAA	AAGGATCTTAGGCATTCTTAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
5121	PCP4	NM_006198	ATCATCTGTCAAGAAATTAAA	ATGGAATTGTGAGTAGCTTAA		
5129	PCTK3	NM_002596	CCGGCGGAATGAGAACTTGCA	CCGGGTATAAGGAGCAAAGGA	CAGGTTGGATACGGATGGCAT	AACCCGTTACTTAGCTGTGTA
5133	PDCD1	NM_005018	CTGGTTGGAGATGGCCTTGGA	CCCTGTGGTTCTATTATATTA	CCCATTCCTGAAATTATTTAA	ATCGGAGAGCTTCGTGCTAAA
5134	PDCD2	NM_002598	CAGATCATCTGGACCATATAA	CCAGATCATCTGGACCATATA		
5138	PDE2A	NM_002599	TCCGACGATGAGTATACCAAA	CATGAATTTCATCAACAACTA	ATCGCGGAGCTGATCTACAAA	ACCGCTTTGTACATGAGAATA
5140	PDE3B	NM_000922	TACGGAGTATTAGTAGCTTAA	TGGGATCGTAATAATGGCAAA	CACAGAGTGAACAGCAAACAA	CAGGTTATGTATACCTTATTT
5141	PDE4A	NM_006202	CAGGGCTGGCGGGCCATGTAA	CTGCTGTATTATACAACTGTA	ATGGGAAGTCGTGTCATCCTA	TTCGATCTTGTCTCCAATTAA
5146	PDE6C	NM_006204	AAGGTCGTCCTTTCTGAACAA	CTGGTGGGCCCTGACAAAGAA	CACGGTTAGATCATATCTGAA	ACGGATTGATTAAATGTGGAA
5150	PDE7A	NM_002603	CAGATAGGTGCTCTGATACTA	TCGGACGTGGGAATTAAGCAA	CCCGAACATACAGCAATATGA	CCGAACATACAGCAATATGAA
5152	PDE9A	NM_002606	ATGGACGCATTCAGAAGGTAA	CCGGAGGGAAGGAGCATTTGA	CGCGTGGAATTGGAAGGACTA	AACGGATATCCTGATCCTAAT
5156	PDGFRA	NM_006206	CTGAGCCAGATTGGCCAATTA	CGCAGGAAGCCTACTATTTAA	CCCGAGACTCCTGTAACCTTA	ACGCAGGAAGCCTACTATTTA
5157	PDGFRL	NM_006207	CCAGGAGAGAATAGAATCAAA	CTGCGTATCTGGACACCTTTA	CTGGAGGATGTTACTGGCCAA	ACGCAGTCTATCATGATGCAA
5158	PDE6B	NM_000283	GCCCACCACATTTGACATCTA	CTGAAGCCAACTGTGAATAAA	CACGCTGCTCATGACCGGCAA	CCGGGAAATTGTCTTCTACAA
5166	PDK4	NM_002612	CAGGACACTTTACGGGATCAA	CTAGACAGTGACATTTCTTAA	AGGCCTCTTGTTCACATCAAA	ACCCGTGTCAATTAACATTTA
5178	PEG3	NM_006210	AAGGATGACCCTGATGACAAA	CCGGATGTCATCATAGGAGAA		
5184	PEPD	NM_000285	CACCGTGGAGCCGGGCATCTA	CAGGCTGTGACAAGGCCTTTA	TCGGCATTTGATCAGACCAAA	CTGTCCTTTAGTAGCAAGTAA
5189	PEX1	NM_000466	CAGTAGCAAGTTTATGGACTA	CAGAGTATATCCACCAGAGAA	CTCATGGATACTATCCAGTTA	AAGGCAGATACCGGAGCCAAA
5190	PEX6	NM_000287	CCAGAGAGTTACACATCGAAA	CACACGCAAATTCAAGCTAGA	CCAGAGCTCATTAACATGTAT	CAGGATGTGTTTGTGATTGGA
5191	PEX7	NM_000288	CGGGCTGTGGAACCCTACTAA	CAGGAGGTGTATAGTGTTGAT	AAGCCTGACTCTCTTCTTGAA	TAGGTTATACGTATATAGATA
5204	PFDN5	NM_002624	ACAGGCCGTCATGGAAATGAT	CAACATGGCGCAGTCTATTAA		
5205	ATP8B1	NM_005603	CTGGATATCTTTGCAAATGAA	CTGGTTCTTGGTTGAATGAAA		
5208	PFKFB2	NM_006212	CAGAACAACAACAGCTATGAA	GCCCTTGTCACTAATCACCAA	CCGTGACAAGCCAACTAACAA	CCAGAGCAAGATAGTCTACTA
5209	PFKFB3	NM_004566	CTCCTAGTTGCTGAAAGTTAA	CTGGGATATAAAGCTATGCTA	CTCCAATATCATGGAAGTTAA	CAGGGACTTGTCGCTGATCAA
5210	PFKFB4	NM_004567	CCCACGGGAATTGACACAGAA	TACGAGGAAATTCAGGATAAT	CAGAAAGTGTCTGGACTTGTA	ACGGAGAGCGACCATCTTTAA
5214	PFKP	NM_002627	TCGGAGAACCGTGCCCGGAAA	TGCGGGCAACCTGAACACCTA	CCGCCTGAAGGCTGCTTGCAA	CAGCACTTTATGCACGTATTA
5216	PFN1	NM_005022	TCAACAAGAAATGTTATGAAA	CCACGGTGGTTTGATCAACAA	TAGCATGGATCTTCGTACCAA	CGGGTGGAACGCCTACATCGA
5228	PGF	NM_002632	CAGGCTCTGCACAGTCAAGCA	AAGAGCTGCCTGGATGAGAAA	TGCCCTCTATTTATTAGCCAA	ACCCGGCTCGTGTATTTATTA
5236	PGM1	NM_002633	CAGGTACAGTTTACACTACAA	CAGCAAGACAATTGAAGAATA		
5243	ABCB1	NM_000927	GAGGTCGGAATGGATCTTGAA	GACAGAAAGCTTAGTACCAAA	CACGGAAGGCCTAATGCCGAA	ATCGAGTCACTGCCTAATAAA
5253	PHF2	NM_005392	CTGGATTTGTTTCTCAGGCAA	AAGATGAATCTTCAACTTTAA		
5256	PHKA2	NM_000292	CTGGTGAAATCGATCCCTTAA	CACCACATCGTTCTACACATA	CCGGATTCTTAGTCACATATA	CCGCCTAACAAGGTAGATGAA
5265	SERPINA1	NM_000295	AAGGCTGACACTCACGATGAA	TACGTGGAGAAGGGTACTCAA	CACCCACGATATCATCACCAA	CCCGAGGTCAAGTTCAACAAA
5271	SERPINB8	NM_002640	CTCAATCAAGGCGGACGTGAA	AGGGCAAACCCTATAGAGTAA	ACCACTGAGTCCTCTAACTAA	TTAGACAGTTTGAGTAATTAA
5281	PIGF	NM_002643	CACCATGAAAGATAACGATAT	AAGAAGTTCATTATCACACAA		
5283	PIGH	NM_004569	CAGGAAGAAATGTCCTACAAA	CAGGTTTACTTTGTTGATGTT		
5288	PIK3C2G	NM_004570	CTGGTGTGTGGTAACATTCAT	CCGGGCCTCTGAATCACATAA	CCCGTAGAAATGATAACTCCA	CCAGATCAAGAAATTCGTAAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
5295	PIK3R1	NM_181504	ACGGCTGAATATGAATAGATA	CACCCAGTGTAGCATCCTAAA	TAGCTGGTTATGAACTAGTAA	CAGCATTAAACCAGACCTTAT
5296	PIK3R2	NM_005027	CAGGGCCAGACTCAAGAGAAA	CGGCGTGAGGGCAACGAGAAA	TTGGTACGTGGGCAAGATCAA	CCGCGAGTATGACCAGCTTTA
5298	PIK4CB	NM_002651	TGGCGACATGTTCAACTACTA	CGACATGTTCAACTACTATAA	TCGGCTGATAGTGGCATGATT	CCGAGAGTATTGATAATTCAT
5300	PIN1	NM_006221	CGGCTACATCCAGAAGATCAA	CAGGCCGAGTGTACTACTTCA	GACCGCCAGATTCTCCCTTAA	CAGTATTTATTGTTCCCACAA
5303	PIN4	NM_006223	CACACTATTCACACAACTGAA	CAGCATTTGCCTTGCCTGTAA		
5310	PKD1	NM_000296	CCGCGTGAACAGGGCGCATTA	CCGAGCCATTTACCACCCATA	CTGGGTCTCAGCCACGTACAA	CCCGTCCATTGTGGGTAGCAA
5313	PKLR	NM_000298	CTGAAAGTCTGTGTCCAATTA	AAGCATGTCGATCCAGGAGAA	GAGGCCTATCTGAGACTATAA	CGGGTGCAATTTGGCATTGAA
5314	PKHD1	NM_170724	TTGCAGCTAGATATAAATTAT	CTGATGAGTATTGAAGTACTA	CACGAGATAGCTGTACTTTCA	CACCGGCATATTGGAAGTGTA
5315	PKM2	NM_182471	CTGGATAACGCCTACATGGAA	CCGGGTGAACTTTGCCATGAA	CCCGATCAGTGGAGACGTTGA	AACATCAAGATTATCAGCAAA
5317	PKP1	NM_000299	CAGGATGAATCTGCCAAGCAA	AAGCATAACCACAAACTGCAA	TCCCGAGGGCCTTATGAGAAA	CTGGTGTTAGAGAGGAATTAA
5318	PKP2	NM_001005242	CAGGAGATACTTTACCTATAA	CAGAATGGAAATGACAAGAAA		
5324	PLAG1	NM_002655	AAGGGTCAGTTGGGACATTAA	AACCAACATAATCTTCTTAAA		
5325	PLAGL1	NM_002656	CAGCATTGTGATTAGAATGAA	CAGGAACATATTTGCATGTTA		
5326	PLAGL2	NM_002657	AAGGATATTTATGTAATAAGA	TCCAGATTATTTAAAGAGAAA		
5328	PLAU	NM_002658	CTGCCTGCCCTCGATGTATAA	CACGAGAGTCTCACACTTCTT	GAGCTGGTGTCTGATTGTTAA	CCGCATGACTTTGACTGGAAT
5330	PLCB2	NM_004573	CTCGGTGCAGTTTGTGGACTA	CCGGCCGGACAAGCAGTTCAA	CTCCATCAATCCTGTCTGGAA	GCGGCTTGCCTGGAACAGATA
5332	PLCB4	NM_000933	ACCAATAATAACTCATGGAAA	CAGGTCAATTCTTATCAGATA	CTGCAGATTCCGGATATTATA	AACCCGGTAGTCTAGAACTAA
5334	PLCL1	NM_006226	CTCGATGTAAGTGATGGTTCA	TCGAAGGATGTCGGTAGATTA	AAGGATGTCGGTAGATTACAA	CTCAGGAATATCGGTCTTAAA
5336	PLCG2	NM_002661	GACGCGGACTACCAAGATCAA	TAGGGTCTCTTTGCAGAGGAA	GACGACGGTTGTGAATGATAA	CACGTGGAAGATTGACAGCAA
5338	PLD2	NM_002663	CCACAGGTCCTTGATTCTCAA	CCGGCCTTTCGAAGATTTCAT	CAGCCTGCTGACAGACACTAA	CGGGACCTCCTGAGACACAAA
5340	PLG	NM_000301	CTGGGAGCAGGAAGTATAGAA	CTGCCGCAATCCTGACGGAAA	CACCACCACCACAGGAAAGAA	CAGGAAAGAAGTGTCAGTCTT
5341	PLEK	NM_002664	CTGGATGATGGGTTAATACAA	CTGTGACAAATCAACGGGAAA	GAGCATTTCTCTAACGTTTAT	ACCATTGACTTAGGTGCCTTA
5346	PLIN	NM_002666	ACGCCTTATTTGATTTAACTA	ACCCTAGTCTTCGAAATGTTA	GCGGGTTTCTCTAACAAATAA	TGGCTTGTTTATGAACATTAA
5347	PLK1	NM_005030	CAACGGCAGCGTGCAGATCAA	CGCGGGCAAGATTGTGCCTAA	CCGGATCAAGAAGAATGAATA	CACCATATGAATTGTACAGAA
5356	PLRG1	NM_002669	ACGGATTCATATGTTCATAAA	CGGCATTATCATGGACATTTA		
5357	PLS1	NM_002670	TAGGATGTTATTAGAGAGATA	ATAGAATATATTCATAATCAA		
5364	PLXNB1	NM_002673	ATGCTGGACCAGCTTTATAAA	ATCCTAGGTCTAAGAGTTGAA	CCGGGTGGAATTTATCCTTGA	AACGCGGACAGTTCAAGTATA
5371	PML	NM_002675	TGCGGTGAACCGGGAAAGCAA	CTCCAAGATCTAAACCGAGAA	CAGGGTTGTCCGCTCTGATTA	CAGGAGCAGGATAGTGCCTTT
5376	PMP22	NM_000304	CAGCCTCGTGTTGAGCCTTAA	TAGGCTGCTATTATTACTATA		
5407	PNLIPRP1	NM_006229	CCGCTTCCTGCTGTACACCAA	CCGGGACTTTGTGGCTTGCAA	CAAGTATTACTTGGAAAGCAT	CCCGATGGGTTTGCTGCATAT
5408	PNLIPRP2	NM_005396	CTAGTTGGAGATATAAGGTAT	TCAGGATTGCTTTGTATGGAA	CTGGAACAAACGTGGGATAAA	TGCGGCTATTGCGGTAATAAA
5412	UBL3	NM_007106	TGGGTGTATATCAAACGGCAA	CCCGGCGGATATGATAAATTT	AAGGACGATTTCTACATGGAA	CGCGTAGTATATAGAACAATA
5413	NA	NM_002688	AACAATGTTGGTGAACGTCAA	CCGGACGGTCACAGCACCCAA		
5423	POLB	NM_002690	CCGGAGCGAATGAGGCCTGTA	CCCAATAGGAGTCTTAATTTA	TACGAGTTCATCCATCAATTT	CAAGATATTGTACTAAATGAA
5426	POLE	NM_006231	CCAGATTATGATGATTTCCTA	CTGGATGGATCCATCTAACTA	CCGCCTCTCCATTGACCTGAA	CCGCATCATCCTCTGTACAAA
5428	POLG	NM_002693	CTCACTGACAATAGTGCCATA	CTCCAAGGCAGTGGAAATAAA	CAGATGCGGGTCACACCTAAA	CACGAGCAAATCTTCGGGCAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
5429	POLH	NM_006502	CAGCCAAATGCCCATTCGCAA	GAGGCAGTGTCATAAAGTAAA	CTGGTTGTGAGCATTCGTGTA	ATCCATTTAGGTGCTGAGTTA
5430	POLR2A	NM_000937	CTCGGGAAGAACAAAGCTAAA	CACCACAGTCTCCAACCTATA		
5434	POLR2E	NM_002695	CTGGAGGAGTTCAAAGCCCAA	ACGAAATAAATTTGCTTGATA		
5435	POLR2F	NM_021974	TCACTTTATATGTGTAAATAA	CACACCATACATGACCAAGTA		
5436	POLR2G	NM_002696	CTGGTGCTTCTTGTAGCTTAA	CAGGGAAGTATGGCTTTGTAA		
5437	POLR2H	NM_006232	CAGAGTTTATCTCCTGATGAA	ATGGATCTAATCTTAGATGTA		
5439	POLR2J	NM_006234	CAGCGGTGACTTCGCAAGCAA	CAGGGATGAATTCATTCTGGA		
5440	POLR2K	NM_005034	CAAGAGATTAATAATAATGTA	AACAATGATAACATACTATAA		
5441	POLR2L	NM_021128	AAGGTCTTTCAGAACCACTAA	CTGGAAGGAACCATCCAGTAA		
5452	POU2F2	NM_002698	TCCAGAAATAAGAATGTCTAA	AAGAAATGGACCAGACACTAA		
5464	PP	NM_021129	CTGGAAAGTCATTGCCATTAA	TAGCACATGCTTAAATATCAA		
5467	PPARD	NM_006238	CCCGTGGAGCAGTGATCTCTA	CAGTGATATCATTGAGCCTAA	CACAGACTGACGAAACTTTAA	ACTGACGAAACTTTAAATAAA
5468	PPARG	NM_005037	GAGGGCGATCTTGACAGGAAA	CAGACAAATCACCATTCGTTA	CCGGAGAACAATCAGATTGAA	CAGCGACTTGGCAATATTTAT
5475	PPEF1	NM_006240	CTGGGAAACCCTCTTCAATAA	ATCGAATATGCTGATGAACAA	CCCAATCGGTACAATCGTTGA	CAGCATTAGTACCTACATATT
5476	PPGB	NM_000308	CCGGAGTACAAGAACAACAAA	TGCAACTTTCTGGTAAACTTA	ATACCAGATCCTATTATATAA	CCGGCCCTGGTTAGTGAAGTA
5496	PPM1G	NM_002707	GAAGTTGTAGATTTCATTCAA	TACTCTGTGAACTTTATTTAA	CCAGAGGATGAAGTAGAACTA	CAGGACCTGAGGACTCAACTA
5498	PPOX	NM_000309	CAGCGGCTTGGCCGCCAGTTA	CACGTTATTAGTGCCATTCCA	CAGGAAGCAGCTGCTACACAA	CTGCTTGGTCCATCTACACAA
5501	PPP1CC	NM_002710	GAGGAGTAAGTGTACAATTGA	CTGCGGTGAAGTTGAGGCTTA	CTGGTTATAACAGCAAATGAA	AACATCGACAGCATTATCCAA
5509	PPP1R3D	NM_006242	TCAGGTGACTAGAGAATTTCA	AAGGATAGCTTTCTTCGGTAT	CTGAGTTAGGCAATCACTTAA	CAGGTACCCACCAACTTTATA
5511	PPP1R8	NM_002713	AACCCTGAAGCTGTAAATGAA	CTGCTGAAGTTTCTTATTTAA	TACAAATAAAGATGCCCTAAA	CAGGCCCAGGAACTGAAGAAA
5514	PPP1R10	NM_002714	CAGCAACATCTAAGCCCTTGA	CACAGGATCAGCTGCACTTAA	CCGAAGGACCGTCACTACATA	CCCAGCCTGCTGAGAAAGATA
5516	PPP2CB	NM_004156	CACCGGATACAAACTACTTAT	ATGGAATTAGATGACACTTTA	TGGGATCTGTCTTGGCATTAA	CCGACAAATTACCCAAGTATA
5519	PPP2R1B	NM_002716	TGGACCAATTCTAGATACCAA	CTGACGTTCGTTTGAATATCA	CAGGAAATAACTACTAAGCAA	CAGAAGTTAGGTCAAGATGAA
5520	PPP2R2A	NM_002717	AAGCGAGACATAACCCTAGAA	CTCGCCGTGTCTGGCACTGAA	CTGCAGATGATTTGCGGATTA	ATGGAAGGTATAGAGATCCTA
5521	PPP2R2B	NM_004576	CGGCTACAAATAACCTATATA	CCGGAAGATCCAAGCAACAGA	CAGGGACTACTTGACCGTCAA	CAGGAAATGATTGGAATAGAA
5524	PPP2R4	NM_178003	CGGATTCATCCTTACCCTCAA	CCGCTCCCTAAGGGTAACCTA	CTGAGGTGGCTGTTTACCTAA	CTCCGGGTGGATGACCAAATA
5527	PPP2R5C	NM_002719	CTGGAAATATTGGGAAGTATA	CTGCTACTTCAGTAAGAATAA	CCCATTGGAACAAGTAAGAAA	AACGAGCTGCTTTAAGTGAAA
5528	PPP2R5D	NM_006245	GAAGTTGTTTATGGAAATGAA	CAGGAGATTATTCTCACCAAA		
5532	PPP3CB	NM_021132	CAGCCCGGAAAGAAATCATAA	TAGTTTATTGTGAGTACTCAA	TAGGAGATTAGATAGATTCAA	AAGGGTTTGGATAGGATCAAT
5534	PPP3R1	NM_000945	GAGCCTCATGAAGCCAACTAA	TCCCTTTATAGTTTCTCTATA	GCCCATATAATTGGTAATGGA	ATCCTTTAGTACAGCGAGTAA
5544	PRB3	NM_006249	TCCCTCCGTAATATCAGGAAA	CCGGGAAAGCCAGAAGGACAA	CAAGAAGGTAACAAACCTCAA	AAGAAGGTGGTCATAGCTCTA
5549	PRELP	NM_002725	CAGGTCAAGAATAACACTTCA	AAAGATTATACTCTTAAGAAA		
5551	PRF1	NM_005041	GAGCACCGTGTGGGACAATAA	ACCATGTACATAGCTTGATAA	CACGGTGGAGTGCCGCTTCTA	CACCGTGTGGGACAATAACAA
5554	PRH1	NM_006250	TCAGCTCAGGATTTAAATGAA	TAACTTCAGTATACCAATAAA	CAGGAAGTGAATAAGAAGATA	TGGCATCATGCTCTAACTTCA
5562	PRKAA1	NM_006251	CAGCAATAAGCATGCATAATA	ACCAGAGTATATTTAAGTATA	TCGGGATCAGTTAGCAACTAT	CCCACGATATTCTGTACACAA
5567	PRKACB	NM_182948	ACCAATGTGTTCTATATGTAA	GGCATTAGGAGTGCTAATCTA	CTGACCAATCAAGTACACTAA	CAGCCTGTGTAGTGTGACAAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
5569	PKIA	NM_181839	CAGCAATGAATTAGCCTTGAA	CTCAAGTGTTCACCCAGTAAA	TCACTTGATCATATGACGAAA	ATGATTATCATTAGAAGCTAA
5573	PRKAR1A	NM_002734	CTGGACCGACCTAGATTTGAA	CAGCTAGTGCCAAATAATTGA	CAAATATTGGTTAGTATTTAA	ATGAAATAATTTAAATTCTTA
5576	PRKAR2A	NM_004157	AGCAGATTTAATAGACGAGTA	CTGCAGAAACCTGTTGTATAA	AACTTGAAAGTCAGCACTAAA	AACGGCATGTCTCTCCAACAA
5577	PRKAR2B	NM_002736	CTGGCCTTAATGTACAATACA	AAGGATGTTATCATAGGCTAT	CACGCCATTGGGACTGTCAAA	ACGAACATGGATATTGTTGAA
5578	PRKCA	NM_002737	TACAAGTTGCTTAACCAAGAA	CGCAGTGGAATGAGTCCTTTA	CAGCTGGTTATTGCTAACATA	CAAGACGTCTTTGGAATCCAA
5581	PRKCE	NM_005400	TACAATGACGTTAAGTCTTAA	GCCCATCATATTCATGTGTAA	CCCGACCATGGTAGTGTTCAA	CACGGAAACACCCGTACCTTA
5583	PRKCH	NM_006255	AGGGACATCTTCCAATGATTA	CAGGATGAGTTTAGAAACTTT	GACCAGATTTGTGGCTTATAA	CGCCGTGTGCTCATCACTGAA
5585	PKN1	NM_002741	CCGGAGCAGCCTCAAAGCAGA	CAGCCTCAAAGCAGAAGCCGA	CCGCAAGGAGCTGAAGCTGAA	CAGGACAGTAAGACCAAGATT
5587	PRKD1	NM_002742	AACAAAGCTGTTAAACTGTTA	TCGATTATTTCCAGTGTTCTA	CCTCAGTATATTTAAACTCAA	CAGGAAGGCGATCTTATTGAA
5589	PRKCSH	NM_002743	CAGCCTTCAAAGATGGGTAAA	CACCACCAACGAATACGTCTA	CTGCACCAACACTGGCTATAA	ACCTGTGACCTCAATACAATA
5592	PRKG1	NM_006258	AAACACTTCAATGTAGTATAA	TAGATTACTATGGTACAGAAA	GAGGTTCGTTTGAAGATTCTA	CCGGTGTATATACCATACAAA
5593	PRKG2	NM_006259	CTGGTTATAGATCGAGAAACA	CACGACGACCTGAGGATTTGA	TTGAGTACTACTAACGTTTAA	GACCTACAATTTGATTCTCAA
5599	MAPK8	NM_002750	TCGGGACTTAAAGCCCAGTAA	CTGGTAATAGATGCATCTAAA	AAGCCCAGTAATATAGTAGTA	AAGCAGTTAGATGAAAGGGAA
5603	MAPK13	NM_002754	CAGAAGGGTCCTTCTCCTTAT	TAGGGATGCTCTAACGAATTA	CGGGATGAGCCTCATCCGGAA	CCGGAGTGGCATGAAGCTGTA
5604	MAP2K1	NM_002755	AACAACGTGTATAGTGCCTAA	CTAGATGTTTAACAAATCTAA	CTGGATCAAGTCCTGAAGAAA	CTGGAAGAATTCCTGAACAAA
5605	MAP2K2	NM_030662	CACAAACCACACCTTCATCAA	TTCCAGGAGTTTGTCAATAAA	CCGGCCTGCCATGGCCATCTT	CAGCATTTGCATGGAACACAT
5606	MAP2K3	NM_002756	CTGGATGCCATCCAAGTTGTA	CTCCAATGTCCTTATCAACAA	CCGGGCCACCGTGAACTCACA	ACGGATATCCTGCATGTCCAA
5610	EIF2AK2	NM_002759	CTCCACATGATAGGAGGTTTA	TACGTGTGAGTCCCAAAGCAA	CGGAAAGACTTACGTTATTAA	ACGGAAAGACTTACGTTATTA
5617	PRL	NM_000948	CAGCGAATTCGATAAACGGTA	TGCAACGATCACGAACATGAA	CAGCATATTGCGATCCTGGAA	CCCGGAGGCTATCCTATCCAA
5619	PRM1	NM_002761	CCGAGATGTAGAAGACACTAA	CCGCCTGTCAATAAATGTTGA		
5631	PRPS1	NM_002764	CCCAAGGTCTATGCTAAATTA	CACCATCTGCTTGACTATGTA	AACATGCTTCCTGCTATGTAA	TTGATTAATTTAAGTATTTAA
5639	PRRG2	NM_000951	CCCAGTGAGGAGACAGACCAA	TTGGGAGAGCTACATCTACAA		
5653	KLK6	NM_002774	CTGACCCTGATGCTTAATAAA	CACGTTTGATTTCTTCCTGCA	CTGCAGATTTCTCACCTGTAA	CACCATGCACTCAATAAAGAA
5654	PRSS11	NM_002775	CCGGGTCAAAGTTGAGCTGAA	CGGTGAAGTGATTGGAATTAA	AGCGTATATAATTGAAGTAAT	CGACGTCATAATCAGCATCAA
5660	PSAP	NM_002778	CCGACATATGCAAGAACTATA	AAGAACTATATCAGCCAGTAT	CAAGCTGATTGACAACAACAA	CTGCCTGAATGTAACCTGCTA
5663	PSEN1	NM_000021	CTCAGGTTCCAAATTCAGTAA	CTGAGGTTGCTTTATCCTAAA	CAGGCATATCTCATTATGATT	CAGCTCTCATTTACTCCTCAA
5676	PSG7	NM_002783	CCCATGGAACCTCAAAGAGCA	ATCCTTGTACCTGATGTCTGA		
5682	PSMA1	NM_002786	CTGCCTGTGTCTCGTCTTGTA	TCCATTGGAATTGTTGGTAAA	CACAGTTGGTCTGAAATCAAA	ATGGAGTGTAATTTAAATGAA
5683	PSMA2	NM_002787	ATGCAAGAATATACTCAGTCA	ATGAGGGACGACCATATTTAT	AAGGATTACTTGGCTGCCATA	GAGATACATTATGTAAATAAA
5687	PSMA6	NM_002791	CAGGGTGGCCTTACATCAGTA	CACAGTGACTCACTTATTCAA	ACCGAAGTGGTTAGGACTCTA	CCAGGGATTGTGTTTAAAGTA
5688	PSMA7	NM_002792	AACAGATGATCTGACCATTAA	GACCATTAAGCTGGTGATCAA	ATGGATGAGTCTCGATGTGTA	CACACTGAGTGTCCTACAATA
5689	PSMB1	NM_002793	CCGGATCTGCATAGTGACCAA	ATCGGTGGACTTGATGAAGAA		
5690	PSMB2	NM_002794	CGCACTCTTGATAAATGGTTA	AAGATGCGAAATGGATATGAA	CAGCAATATTGTCCAGATGAA	GTGACTATGGATATAATTGAA
5692	PSMB4	NM_002796	TCGCATTATGCGAGTCAACAA	ATGCTTGGTGTAGCCTATGAA	ACCATTGTCTACAGAGACCAA	CACATGATCAGTGGCTTTGAA
5694	PSMB6	NM_002798	CGCCTGAATCCTGGGATTCTA	TGGGATTCTAGTATGCAATAA	CTGGGATTCTAGTATGCAATA	CTCCGGGAGCTCCTACATCTA
5698	PSMB9	NM_002800	CTGCAAATGTGGTGAGAAATA	GTGAGAAATATCAGCTATAAA	AAGGAGGTCAGGTATATGGAA	CAGCACCTTTATCTATGGTTA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
5699	PSMB10	NM_002801	CCCAGACAGTGAAGCCACTAA	CAGGCTATGGAGGTGGAGTAA	CACACGGATGGTGGCGTCCAA	CTGCGAGAAGATCCACTTCAT
5705	PSMC5	NM_002805	CAAGGTTATCATGGCTACTAA	CCGGGTGGCTCTAAGGAATGA	AAGGTACATCCTGAAGGTAAA	TTGGTCAAGGTACATCCTGAA
5706	PSMC6	NM_002806	CTGAGAAATGTTTGTACTGAA	AAGGAGTTAAGGGAACAATTA		
5707	PSMD1	NM_002807	CAGGCTGTGAGTGATATCTTA	TTGGAAGGCATCGTAAATAAA		
5708	PSMD2	NM_002808	TAGCGAACACTTTGACTCCAA	CAGGGTTCCAGACGCATACAA	CTCCGGAGGGCTGTACCTTTA	TGGGTGTGTTCCGAAAGTTTA
5718	PSMD12	NM_002816	ATGGGTTTAAATTTAACATAA	AAGGATTACATTCGAACACAA		
5723	PSPH	NM_004577	CAGAGACTCATAGCAGAGCAA	TAGGCTGAAATTCTACTTTAA	TGCCAATAGGCTGAAATTCTA	CCGGCATAAGGGAGCTGGTAA
5727	PTCH	NM_000264	ACCAAGCTTCATTAGTCTTAA	CCCGTCATTAGTGCTCTTTCA	TCGCACAGAACTCCACTCAAA	ACAGCATACCTCCTAGGTAAA
5729	PTGDR	NM_000953	AAGCATAATTTCTTACCCTAT	TCCAGTATCTGAGATAATATA	CCGGTGCAGCAATTCCACTAA	CCAGTATCTGAGATAATATAA
5733	PTGER3	NM_000957	AACAAATATCGCTAAACCTTA	CCGCTATAGAGTATTCCATAA	AAGGACCGATTTGAGCACTAA	ATCGATACCATTATTCAAATA
5739	PTGIR	NM_000960	TCGGGCGACAGGAGCCAGAAA	CAGAAAGAATGGTTCTCTCAA	CCCATCCATCTCATTGTCTAA	CCCAGGGTCCTGAATAAATAA
5743	PTGS2	NM_000963	TCGTATTGCTGCTGAATTTAA	TAGGGTAGAATCACCTGTAAA	CCCGCAGTACAGAAAGTATCA	ACGCTTTATGCTGAAGCCCTA
5745	PTHR1	NM_000316	AGGGAAGCCCAGGAAAGATAA	CTCCATTGTGCTCAACTTCAT	CGCCGTGAGCATCTTCGTCAA	CAGCATAATGGAATCAGACAA
5746	PTHR2	NM_005048	AACGCCTCTATGTAATGTATA	CTGAATACGGTTAGAGTTCTA	TGGCATGTGGGATCAATTAAA	AAGGTGTTACTTAATAATAGT
5747	PTK2	NM_005607	CCGGTCGAATGATAAGGTGTA	CCCAGGTTTACTGAACTTAAA	CACCTGGGTACTGGTATGGAA	AACAATTTATGTTCACATTAA
5754	PTK7	NM_152883	ACGCCACAGCACAAGTGATAA	CCGAGAGAAGCCCACTATTAA	ATGGGACATGGTACCGTTGTA	ACGGTTCGAGGTCTTCAAGAA
5764	PTN	NM_002825	CTGGAGCTGAGTGCAAGCAAA	ACCGTAGGCTTTGTATTCAAA	TACCGTAGGCTTTGTATTCAA	TACATGATAAATGATAGACAA
5771	PTPN2	NM_002828	CACAAAGGAGTTACATCTTAA	TCGATTGAATTGTACTGGATA	CCGCTGTACTTGGAAATTCGA	AACTGTATTCATACATGTCAA
5774	PTPN3	NM_002829	CCGCTCATTTGCTGACTTCAA	CCGAGAAATGCTGGTCACAAA	CCGGGTATTATTGCAGGGAAA	CAGGTTATTCAGCGATAGTTA
5775	PTPN4	NM_002830	AGCACGTACCTTAGAACTCTA	CTCCGTCATCAACACAAGCTA	TCCGTCATCAACACAAGCTAA	CTCCGAACAAATAGTAAATAA
5777	PTPN6	NM_002831	CCAGTTCATTGAAACCACTAA	CCGCACCTCGTCCAAACACAA	TAGGCCCTGATGAGAACGCTA	CCGGAACAAATGCGTCCCATA
5781	PTPN11	NM_002834	GCCGCTCATGACTATACGCTA	GCGGTCCAGCATTATATTGAA	CCGCTCATGACTATACGCTAA	CAGAAGCACAGTACCGATTTA
5782	PTPN12	NM_002835	GTGGATCATGATAACACTTCA	CTGCTTGTAGACATGTTAATA	TTGCAGGTTATCAGAGATCAA	AAGCTTAATGAGGAAATATCA
5787	PTPRB	NM_002837	CCAGTATTAGTGGAGACTTAA	TCGGGTGTATCAGACTAATTA	CCGGTCGACTTTATCAAGTTA	CCCGGAGATGTGGATAACTAT
5789	PTPRD	NM_002839	ATGGCATTATCACCAAGTATA	CGCCTTGTTAATATTATGCCA	CTGGGTGTCATTGAAGCAATA	ACGGCCAGTCCCGAACAGTAA
5794	PTPRH	NM_002842	TCGAAGCACAGCACACACTAA	CAGGTACTGACATCACCCTAA	CCGGGTCATTGTATACGTGTT	CCGGGACGTTGTACAATTTCA
5795	PTPRJ	NM_002843	ACCCGTATCTTCTACAATCAA	ACGAGTCGTCATCTAACTATA	TCGGGTAGAAATAACCACCAA	TCCGAGTATGTCTACCATTTA
5796	PTPRK	NM_002844	CAGGATTTGTATCGCTGTGTA	CCGGCGAGTCAAGTTATCAAA	CTGGAGATTAGTGTATGATTA	CCGGGTTAAATGCTATAAATA
5798	PTPRN	NM_002846	CTGGTGAAGTCTGAACTGGAA	CAGGAAGGTGAACAAGTGCTA	CAGGTCTGGCTTGGCACCCAA	CACCCTTCACTGAGTTACGAA
5800	PTPRO	NM_002848	CAGCTTCAAAGTAGAGTAGAA	CCGGGAAGACTTAGCCTTAAA		
5801	PTPRR	NM_002849	AACCCTTTGTGTCTATACCAA	TAGGTTTATCACACAGCCTAA	TCGCCTCATTGGAAAGAAGAA	CGCCACCAGATTGTCAATTCA
5803	PTPRZ1	NM_002851	CAGACTAATTACACTGAGATA	CCGCCAAATTTATATCATTAA	TAGCCATATACCAATACCTAA	ACGCTGGAATTTGGTAGTGAA
5810	RAD1	NM_002853	TCGAATGTGTTACCAAGGTTA	CTGCAGCACCAATGTTATTAA	CAGTATATGATTAGAAATGAA	CAGCACCAATGTTATTAATAA
5818	PVRL1	NM_203286	CAGGTGGAGGTCAATATCACA	CAGGTGAACGACTCCATGTAT	AGGGCTGTTGTCAGAATTCTA	ACAGATCAGTCTGTCAATAAA
5819	PVRL2	NM_002856	CCCGTGACACTCAGGAGTTAA	CAGAGTCATAGCCAAGCCCAA	CTGGACGACACTGGAGTGGAA	CAGGTCATCTTTGTCCGAGAA
5830	PEX5	NM_000319	ACCGATCGCTGGTATGATGAA	CCAGTTCACAAGACCAGTAAA	TACGTCAGCTACCTATGATAA	CAGCTTCCTTGGGCAGTGTAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
5837	PYGM	NM_005609	CACACTCGTAAAGGACCGCAA	CTACCTGTCTTTAGAGTTCTA	TCGGGATGTGGCCAAAGTGAA	CAAGTTGAAGTTTGCTGCCTA
5870	RAB6A	NM_002869	CAGATGGGTCATATTCTTTAT	ATGGGTGTGATTGTCTTCCTA	TACGGTCTTCTTTGAGGTCAA	CCCACTTATTGTCACCTTGTA
5871	MAP4K2	NM_004579	ACGGTATTTAAGAGAGAACTA	GAGAACTATATTGGTATTAAA	TCGGTCAGCCTCAGAATTCCA	CTGGCTCTACTGCGTGAACAA
5876	RABGGTB	NM_004582	AAGGATGTTATTATCAAGTCA	TACGCTGTATGACAGTATTAA	ACGCTGTATGACAGTATTAAT	CCGGAGAAGTTACCAGATGTA
5878	RAB5C	NM_004583	GAACAAGATCTGTCAATTTAA	CAGCCGATCGATCGACCTCAA	CCCGACTGGAATCCACTCTAA	CACCATGATTTCTCCATATAA
5879	RAC1	NM_006908	TACATTGTACAAGGAATGAAA	GGGCATTTAATTCATCTTTAA	ACGATGTTCTGTACAACTTAA	AAGGTTGGTATTATCAGGAAA
5881	RAC3	NM_005052	GACATGCTTGCTGATCAGCTA	CAACGTGATGGTGGACGGGAA	CGCGCCCATGCAGGCCATCAA	CCGGGAGATTGGCTCTGTGAA
5892	RAD51L3	NM_002878	CCCAGTAACGCCTGCTGTTTA	CTCACTCTCTGTAAGCATATA	CTGGGTGGAAATAAGCTTATA	CTGGAAGAGGTAGCTCAGAAA
5893	RAD52	NM_002879	TCGGGTAATTAATCTGGCCAA	CAGCTGAAGGATGGTTCATAT	CAGGAGTGACTCAAGAATTAA	AAGGAAGGAAATAATCATCTA
5901	RAN	NM_006325	CAGCAGTATTCTATTTGGTTA	TAGTGTGAAGTTGATACGCAA	TTGGGAATTCTTGCTGTTAAA	ATGTGGTTTGTACATATCAAA
5902	RANBP1	NM_002882	CTCGGTGAAGGAGGAGACCAA	CGGCGCCAGACGCGGAGGGAA		
5905	RANGAP1	NM_002883	ACGGAAGATTCTGGACCCTAA	AGGCAAGAGCCTCAAACTCAA		
5908	RAP1B	NM_015646	AATGGTGTACTGTATACTTTA	TAGCATCAGTAGTTCAATAAA	GACGAGTACTGTGGATGTGAA	CAGTATAATGTCTTAGATTAA
5909	RAP1GA1	NM_002885	CCGGCTCATCGTCACCTTTGA	CCACCTTGTCTTCTCACTCAA		
5911	RAP2A	NM_021033	AAGGCATAGTCCATCGATCTA	ACCAGTGTATTCCGTCAAGTA	CCAGTGTATTCCGTCAAGTAA	CAGAGATAATTGCCTATACTA
5912	RAP2B	NM_002886	AAGGTGGTCTTAGTAATATAA	TAGAATAGAGGCAAAGCCTAA	TACGGTTCTTTCGTAGAACAA	CTCACTTAAGTTTGATATCAA
5919	RARRES2	NM_002889	CTGCCGGAAGAGGGACTGGAA	CCCAATGGGAGGAAACGGAAA	CAGGGAGAGGAACCCGTTCTA	CTGGAAGAAACCCGAGTGCAA
5924	RASGRF2	NM_006909	AAGGTGAAAGATGGCTATTTA	AAGAAGGAACACCAAACTTTA		
5926	ARID4A	NM_002892	CTCGAGATGTAAATTCTATTA	ATGGCTTATCTAAGACAGCAA	CTGGTTTGACATTGCTAAGTA	ACGATTGAAGTTGATAGTATT
5927	JARID1A	NM_005056	CGGCAAGTAAAGAATCTGCTA	GCGGACGTTTCTTAAGAAGAA	CAGATGCTTAATTGAGCTCTA	AAGGAATGGTATCACAGTCTA
5930	RBBP6	NM_006910	GACGCTATCATTCACGATCAA	CCAGGTCTAAATCTCCCTATA	ATAGTGGTTCTTCGTATTCAA	CCCAGTTAAGTCATTCCTCTA
5933	RBL1	NM_002895	CTGGATGTTTCAAATGAGTTA	CTCCAGGTTTCTGCAAACAAA	CACCAAGTGACCAACTTATAA	ACAGGCTAATGTGGAGTATAA
5935	RBM3	NM_006743	CAGGAGGAAATTACAGAGACA	CCAAATGGCTGTATTTATAAA		
5950	RBP4	NM_006744	CTGGTACGCCATGGCCAAGAA	CCAGATGAGCGCCACAGCCAA	CCCTGCCAAGTTCAAGATGAA	CTGGATCGTCGACACAGACTA
5961	RDS	NM_000322	CAGCACCACACCATCCCTAAA	CACGGTGAAAGTGCTGCTCTA	GAGGAGCGATGTGATGAATAA	CACGGATTTAGTCCCACCCTA
5967	REG1A	NM_002909	CCCAGTCTTTGGAACCCTAAA	CAGCAATTACAACGGAGTCAA		
5968	REG1B	NM_006507	CTGCAATTACTATGAAGTCAA	CTCAGTCTCTAGAGCCCTGAA		
5971	RELB	NM_006509	CACAGATGAATTGGAGATCAT	CAGCTACGGCGTGGACAAGAA	GCGGATTTGCCGAATTAACAA	CCAGATTGCCATTGTGTTCAA
5976	RENT1	NM_002911	ATCAAGGTCCCTGATAATTAT	CACCATGAGCGTGGAGGCGTA	CATCTTATTCTGGGTAATAAA	ACGGAGCGCTGCACACCGAAA
5977	DPF2	NM_006268	ATCCATCTTGCCTCCAATTTA	CTGTATTCTAAACATTAGTAA	CTGGATGACCTCGATGATGAA	CTGGACCTGTTGAAAGAGAAA
5992	RFX4	NM_002920	CAGGCATTACCTGACAGCTTA	CTGGAGGAACGTGGACCTGAA		
6000	RGS7	NM_002924	TTGATAAAGAACTTAACTATA	TGCCTGGATGTGTAAATACAA	AAGTATATATCAATAAGTATA	ACGGATCATCTTGTAGCATGA
6003	RGS13	NM_144766	CCAGATTTCTAAAGTCAGAAA	CAGAATTTCTAGGGCAAAGAA	CACAGTGACGAGAATATTCAA	CCAGAGTGCCATCGAAGGTAA
6015	RING1	NM_002931	CCGAAAGAAGCTGGTGTCCAA	CAGGGTCAGATCAGACCACAA	CTGGAGCTGGTGAATGAGAAA	CAGCCAATAAGAGGACACAAA
6039	RNASE6	NM_005615	CCCTGTGTTCACAGCAATAAA	CACTTAGATAGTATTCTCTAA		
6041	RNASEL	NM_021133	GCCAATGTTAATTTCCAGGAA	CCCGAAATGTCCTGTCATCTA	CCAGACTACACTAGTCCATAA	CACCTGGACATGTCAATTAAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
6051	RNPEP	NM_020216	CACGCCTGCTGTTAAATACAA	CCGAAGCATCTTAGCCGATGA	CTGGACATGAAGGCCATTGAA	CACCAGGAAGATTTCTGGAAA
6059	ABCE1	NM_002940	ACCCATAAATACATGTTGTAA	ATGGCTAGAAAGTATGGTTTA	CCAGTTGGGTTCTAAATTGTA	CTGATTGACATTTGATAAATA
6097	RORC	NM_005060	TAGGATGTGCCGGGCCTACAA	CCGGGCCTACAATGCTGACAA	AAGGAGCTCTTCAGCACTGAA	CGGGTTCATCTGAGTAAACAT
6100	RP9	NM_203288	TCTGTTGTTGAGAATAATAAA	AAGGAAGATGAGACTAAGCCA		
6103	RPGR	NM_000328	CCCGGTAAATTCTGGTTTAAA	TCCGAAGGGCAAATTGGTTTA	CACAGCTTTGATAACAGATAT	ATGAGCCTGAATTCCAATGAA
6122	RPL3	NM_000967	CGGCAAGCTGATCAAGAACAA	TGGCGTGATGTCTCACAGAAA		
6125	RPL5	NM_000969	TTCGTGTGACAAACAGAGATA	AAACTTATGAACAGCAACTAA		
6128	RPL6	NM_000970	CAGCGCAAGATTGATCAGAAA	GACCGGAAGCCGGGACCTTAA		
6129	RPL7	NM_000971	CTGGTTGGTTAATAAACAGTA	ACGCTTCAAAGAGGCAAATAA		
6130	RPL7A	NM_000972	CACCTTGGTGGAGAACAAGAA	ACAGGTGAACTCGGAAGACAA	CACCACCTTGGTGGAGAACAA	CAGGTGAACTCGGAAGACAAA
6132	RPL8	NM_000973	CTCAATAAAGTTTGTGTTTAT	CCGGGCGTACCACAAATATAA		
6133	RPL9	NM_000661	CAGGCTGATGAATAAGATCTA	CGGACTATTTGTAGTCATGTA		
6134	RPL10	NM_006013	CCCGTTGTTACCGGTATTGTA	CAGCAAAGCCTTGCAATCCCA	TGGCCTTATGTCAGTTGTCTA	CAGAAACAGGTTGACAACTCA
6136	RPL12	NM_000976	ATCCGGGTTCATCCGACACCA	AACATTTCAATAAAGGATCAT		
6144	RPL21	NM_000982	CCACATATATGCGAATCTATA	CTGGAAGAGTCTACAATGTTA		
6152	RPL24	NM_000986	AAGAGGAATCAGAAACCTGAA	AAGGCTAAGCAAGCATCTAAA		
6154	RPL26	NM_000987	CAGGTTGTACGTGGACACTAT	CAGGAATAAAGTAATCTTATA		
6156	RPL30	NM_000989	CAGGAAGATGGTGGCCGCAAA	CTGAAATAGAGTACTATGCTA		
6157	RPL27A	NM_000990	AGGGAGTTTCATTAAATGCTA	CCGGATCAACTTCGACAAATA		
6160	RPL31	NM_000993	CAGATCAAATAAAGTTATAAA	ATCGCTGATCGTCAGATCAAA		
6164	RPL34	NM_000995	AAGCACAGAGTCAGAAAGCTA	CAGTATATGATCACTAATATA		
6165	RPL35A	NM_000996	CCGAGATGAAACAGAATTCTA	GCGCTTATGTATATAAAGCAA		
6170	RPL39	NM_001000	CTGAAGGTCACGATCATGTTA	TTGGTTGGCTGGATTCAGTAA		
6173	RPL36A	NM_021029	CTGGTTGAGTTCACATCATAT	AAGCTAGAGCCATCAATACAA		
6176	RPLP1	NM_001003	CTGCATCTACTCGGCCCTCAT	AAGAAAGTGGAAGCAAAGAAA		
6181	RPLP2	NM_001004	CAGCGTGGGTATCGAGGCGGA	CAGCGCCAAGGACATCAAGAA	AAGGAGGAGTCTGAAGAGTCA	CAAGGTTATCAGTGAGCTGAA
6187	RPS2	NM_002952	CACCTTTGATGCCATTTCTAA	CCGCTTGGTCAAGGACATGAA		
6188	RPS3	NM_001005	CGGCAAGATGGCAGTGCAAAT	GAGGTTGTGGTGTCTGGGAAA		
6189	RPS3A	NM_001006	CCGGAAGAAGATGATGGAAAT	CACCTGCTATGTTCAATATAA		
6191	RPS4X	NM_001007	CAGATCTTTGTACGTAATTAA	AAGAATTGGTGTGATCACCAA		
6193	RPS5	NM_001009	CACCGATGATGTGCAGATCAA	CTCGAACTCCTATGCCATTAA		
6194	RPS6	NM_001010	ATCCAGTCAGAAATAAGATTT	TTGAGTAACAAATAAATAAGA		
6196	RPS6KA2	NM_021135	CTGGAACACGCTGTACCGGAA	CTCGATATCTGACGCAGCTAA	CCGGAGGTCCTGAAGCGTCAA	CCGAGTGAGATCGAAGATGGA
6202	RPS8	NM_001012	TTGGAGTTCTATCTTAGGAAA	TCAGAGTGTTGTACTCGTAAA		
6203	RPS9	NM_001013	ACGGCGTCTGTTCGAAGGCAA	CCCGCGGAGACCCTTCGAGAA		
6204	RPS10	NM_001014	CGCAGAGATGTTGATGCCTAA	ACCGCGCATGCTCCTTCCTTT		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
6205	RPS11	NM_001015	CCCTGCGTAATCGATAAGGAA	CGGGAAGATGGCGGACATTCA		
6206	RPS12	NM_001016	AAGGTTGATGACAACAAGAAA	AAGATTCAACTTCACCCGTAA		
6208	RPS14	NM_005617	CAGGAGGAAATAGGACCAAGA	CCGAGATGAATCCTCACCATA		
6217	RPS16	NM_001020	TACCAGAAATCCTACCGATAA	CCCTCGTCGCTGCGAGTCCAA		
6218	RPS17	NM_001021	CCGCAACAAGATAGCAGGTTA	AAGCGAATTCAGAGAGGCCCA		
6223	RPS19	NM_001022	TGGCTCCATGACCAAGATCTA	AAGAAGCATTAGAACAAACCA	CTGGGTTAATAAATTGCCTCA	AACAAGAAGCATTAGAACAAA
6227	RPS21	NM_001024	TGGAATATTTGTCATAAATAA	CGGCGAGTTCGTGGACCTGTA		
6229	RPS24	NM_001026	CGCAAGAACATTAATAAACTA	CAAGAACATTAATAAACTAAA		
6233	RPS27A	NM_002954	TTGTCTGACTACAATATTCAA	CTGGCTGTCCTGAAATATTAT	CTGACTTACTGTTTCAACAAA	AAGGTGGATGAGAATGGCAAA
6234	RPS28	NM_001031	AGCGTTTGTGTTTCAAGTTAA	CTGAGATGCTCCTTTAAATAA		
6235	RPS29	NM_001032	ATGATAATTCTTTGTATATAA	CCGGCACGGTCTGATCCGGAA		
6240	RRM1	NM_001033	CCGAGATTTCTCTTACAATTA	CTGAGAGTATATAACAACACA	AACGGATATATTGAGAATCAA	CTGGTGGGTCTCTAGAAGCAA
6272	SORT1	NM_002959	CAAGGACAGGGTACAAACTTA	CTGGGTTTGGCACAATCTTTA	CCCACGTCAGTTACACATTAA	CAGCAGAGAATTGACTAGATA
6284	S100A13	XM_371380	CTGAAGATCAGGAAGAAGTAA	ACCGCACTCTTCCCAAATAAA	CAGGAAGAAGAAAGACCTGAA	AACCGCACTCTTCCCAAATAA
6286	S100P	NM_005980	CAGGAGGAAGGTGGGTCTGAA	TAGGCTGAGCCTGCTCATGTA		
6289	SAA2	NM_030754	TAGGCATCTAATAAATGCTTA	GCCGATCAGGCTGCCAATAAA	ATGGCATATAATAGGCATCTA	AAGCTGAGATATGGCATATAA
6293	VPS52	NM_022553	TCCATTCGGGATTATATTCAA	CCGGGTCAAGGCAGTGACGAA		
6294	SAFB	NM_002967	CCGAAGATGACTCGGATACAA	AAGGTGGTAATCCTGACGAAA	CTGCCATATTGTAGCTCAATA	ACGGACTGTAGTAATGGATAA
6296	SAH	NM_005622	CCCTCAGAATTTCTCCAACTA	CAGAAGCCTGTTCCCTACAAA	CAAGCTGATTGTATCAGAGAA	ATGCTTGTACAGAATGATATA
6297	SALL2	NM_005407	TAGGAAGTAGGGAGAAATGAA	CGGCCTGAGGGTCACAATAAT	CCCGGGAATGTCTCGGCGAAA	AAGCTGGGCACTGCTTACCAA
6300	MAPK12	NM_002969	CGGCGCTAAGGTGGCCATCAA	CACAGGCAAGACGCTGTTCAA	TGGAAGCGTGTTACTTACAAA	CTGGACGTATTCACTCCTGAT
6301	SARS	NM_006513	CCAGTTTGATGAAGAACTTTA	CTGATGAAACCATGTAATAAA		
6304	SATB1	NM_002971	TGGGTACGCGATGAACTGAAA	CACTCTTATTGTTGTATGCAA	ACCGAATATACCAGGACGAAA	TCCAAGCAATTCATACTATAA
6305	SBF1	NM_002972	GACGCCTGTGTTCCACAATTA	TCCGGTCGTTACCGACCACTA	CCGCGTGGTGTGGCCCTGTTA	CAGCGCCGAGCTCTTCCGTAA
6311	ATXN2	NM_002973	ATGGATCAACTACTAAACAAA	CTGACGGATTATTATTTATAA		
6317	SERPINB3	NM_006919	AAGGTAATATTGGCAGCAATA	CTCGTGCTATCTGGAGTCCTA	TAGGATTCGGATCATCACCTA	TCGGATCATCACCTACTTCAA
6324	SCN1B	NM_001037	CCACATTGAGGTAGTGGACAA	CACATTGAGGTAGTGGACAAA	CAGAGATGATTTACTGCTACA	ACCGCCATGCATGATGGGTAA
6328	SCN3A	NM_006922	CAGCGTAATTTCAGATGTTAT	AAAGCTGATAGTCTATGTCAA	TTGGATTTATGTGAGGTCAAA	CTCCCATAATAAATTATATAA
6329	SCN4A	NM_000334	GACGCCTACATCAGTGATGAA	AACGCTGAACATGCTCATCAA	CAAGATTGCCTTGGACTGCAA	CTGGCTCAATGTCAAGGTCAA
6331	SCN5A	NM_000335	CCCGCTGTGGATGTCCATCAA	CTGGAGCACTACAACATGACA	CTGGACCAAGGTGAAAGTCAA	TCCTGTAAGAGTATTAACAAA
6332	SCN7A	NM_002976	TCCAATGAGTAAACAAACTAA	CCCAGCATTATTGAACATCAT	AGAGATGTTCATGCTACTAAA	CCGATGGTAATTAAGCTTGTA
6336	SCN10A	NM_006514	CGGGCTCTTTCTCGATTTGAA	TCCCGGGAGGTCAACATGCAA	CACAGGCGAATGTGTCATGAA	CCGCTCCATGGCACTCTCTAA
6337	SCNN1A	NM_001038	CTGCACCTTTGGCATGATGTA	CAGCCTCAACATCAACCTCAA	TACAGGTACCCGGAAATTAAA	CCCGATGTATGGAAACTGCTA
6338	SCNN1B	NM_000336	CCGGAACTTCACGTCCATCTT	CACGTCCATCTTCTACCCTCA	TCGGCCAACCCTGGAACTGAA	CTGCAATGACACCCAGTACAA
6339	SCNN1D	NM_002978	CTGCAGGGAGTCTGCATTCAA	CCGCAATGGCTGAGCACCGAA	CTGCAGGGAGGCAGAAGGCAA	CACACTTGGGCTGCTCTGAAA
6340	SCNN1G	NM_001039	CGGCGGTAGCATCATTCACAA	AAGAGTGGACACTAACCACAA	CAAGGCCGGCAAGTAAACAAA	ATCCCGGGACCTGAACTATTA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
6343	SCT	NM_021920	CAGCGAGCAGGACGCAGAGAA	CTGGCGCTGCTGCAGAAGGAA	ACCAATAAAGGAGGAATCAGA	GTGGTACTTGGCACCAATAAA
6344	SCTR	NM_002980	CACAGGATGGCTGGTCAGAAA	CAGAAAGGGACAGGGAAATAA	CTCCTTCTTCTCTGAAAGAAA	CCGGATGCTCACCAGCAGAAA
6354	CCL7	NM_006273	TTGGGATTAATACTTCAACTA	TTGGATGTATATGTCATCTCA	TGGAAGCATATTGTTATTATA	AAGATTTGCTTTAATTGTTAA
6367	CCL22	NM_002990	CTGGGTGAAGATGATTCTCAA	TACCTTTGACTTGGTATTATA	TAAGCTGGAGTTATATATGTA	CAGGTAAAGGACATAAATGTT
6368	CCL23	NM_145898	GACAGAGTTCATGATGTCAAA	TAGAGCAATTCATCTAATAAA	CAGGAAGAATTGAACTTGTCA	CTCCTGGAGAGTTACTTTGAA
6369	CCL24	NM_002991	CTGCATGTTCTTTGTTTCCAA	CAGGCCTGATGACCATAGTAA	CAGAGATATCCTGGCAACCAA	AGGAGTGATCTTCACCACCAA
6376	CX3CL1	NM_002996	CCACGGTGTGACGAAATGCAA	CAGCAAGATGACATCAAAGAT	CGGAGCTGTGGTAGTAATTCA	CACCATCAAGCCACCAACATA
6382	SDC1	NM_002997	TCCGACTGCTTTGGACCTAAA	GCCGCAAATTGTGGCTACTAA	CAGGGCCTCCTGGACAGGAAA	CAGGAGGAATTCTATGCCTGA
6383	SDC2	NM_002998	GACGCTGAATATACAGAACAA	CCGTTTAGTCATATCTATCTA	ATGAATAGACATAAATTGTAA	AAGGTACGAGTAGAGGTTTAA
6386	SDCBP	NM_005625	AGAGATTGTGATGATTCTTAA	GAGATTGTGATGATTCTTAAA	TTGACTCTTAAGATTATGTAA	TGGGATGGTCTTAGAATATTT
6396	SEC13L1	NM_030673	CAGATTGATCATCTGCCTTAA	TCGGAGATGCTTTGTAATCTA		
6400	SEL1L	NM_005065	CTGCAAATTGGGCGTCGTCTA	AAGAGTGAACATGTACACAAA	CAGGATATTCACCTTGCGAAA	ACGGCACAAGGAAGCATTGAA
6401	SELE	NM_000450	CATGGTAGAATTGGAGAGTAA	ACCAGTGTGGTTTGTGTTTGA	CGGAAAGTATTTCAAGCCTAA	CAGGTTGAATGCACCACTCAA
6404	SELPLG	NM_003006	TCCATGGAACCTACTACCAAA	CAGCAATTTGTCCGTCAACTA	ATGGAGATACAGACCACTCAA	ACGGAGGCACAGACCACTCAA
6406	SEMG1	NM_003007	AGGGTAGTTATACACCATAAA	CAGGGTAGTTATACACCATAA		
6423	SFRP2	NM_003013	TAGCATGATTTCTTCAAGTAA	TACATAGTAGTTTACCTTTAA		
6425	SFRP5	NM_003015	ACGAATGTTGTTACTGGCACA	TAGGCTAAGCTATTTGGGAAA	CTGCGAGGAGTACGACTACTA	CCGCTGGGACAAGAAGAATAA
6428	SFRS3	NM_003017	CACAATATGGTTCAAATGTAA	CAGACTGATAATAAACCTCTA		
6434	SFRS10	NM_004593	TCGGGCAAATCCTGATCCTAA	CCCAATTTCACTCAAATGTTT	CGGGACTACTATAGCAGATCA	CCCGATCTGAATCTAGGTCTA
6435	SFTPA1	NM_005411	CACAGCAGGGATGAGGACAGA	ACAGATGGTGTGAGTCAGTGA		
6439	SFTPB	NM_000542	AACATGGAAGTCAACGTTTAT	CCCACCATCTCTGGTCTACAA	ACGGCTTGCACCATTCAGCTA	AAGGGACGAGATCGTTAGCTA
6441	SFTPD	NM_003019	TGCTGCCAATATCCTAATAAA	TAGGATTAGGATTGTTGTGAA	CTACCTGGAAGCAGAAATGAA	AGGAGTTTGGCCAGAAGTCAA
6443	SGCB	NM_000232	CTGCTTCGATTTAAGCAAGTA	ATGGGTGGTAATATGGAGTTA	ATGCAGATTTCTAGTGCATTA	CACTTTGAATTGTGCACATAA
6452	SH3BP2	NM_003023	CCCACGGACAATGAAGACTAT	AACCTCTAACAAAGTGAGGAA	TAGCACCTTATGTCAGGGAAA	TAGGAAGTAAACGATCTGCAA
6455	SH3GL1	NM_003025	AAGGTGCTCTTAGAAACACTA	CCGCCTGGACTTTGACTACAA	ACGGTCCAGGGCAAACTGAAA	ACGCCCTAAGCGGGAGTATAA
6468	SHFM3	NM_022039	CCGGGAAGGAGGCACAAGGAA	ACGAGTGAAGGTGTCTCAGAA	TGGGAAGATTGGCATTCATAA	CAGCACCTTCACTGTCAAGTA
6472	SHMT2	NM_005412	CAGCAAATTCAATTTGTTAAA	CCGGAGAGTTGTGGACTTTAT		
6487	SIAT6	NM_006279	CACAATATCCAGCGAGAGAAA	TCGGTTGGGCTTCCTCCTGAA		
6489	SIAT8A	NM_003034	CTGGCTTAATAATATTAATAA	CAGAAAGACATTTGTGGACAA		
6492	SIM1	NM_005068	CACAGAAAGATCGGAATCTGA	ATCCAGTTTGATCCTAGCTAA	CACACTAAACTTCTTAACGAA	TCACCTGGTATCCATTATAAA
6493	SIM2	NM_005069	CACGGGCAACAGTATTTATGA	TAGCAGCTCGTCTCCAGCTAA	CCGGCAAATGCGCACGACCTA	CCGTGATTCTTGAAAGGTGTA
6497	SKI	NM_003036	CTGGACGACGTGAAGGAGAAA	AACCAGTAAGGAGACTTGAAA	GCGAGTGTTTGTAACCATGTA	CCGACTTTATAGAGCAGTCAA
6502	SKP2	NM_005983	AGGCCAACTATTGGCAACAAA	CTCAAATTTAGTGCGACTTAA	ACCCTTCAACTGTTAAAGGAA	AAGTGATAGTGTCATGCTAAA
6503	SLA	NM_006748	AAGGAACTTCGTGACACTAAA	CTGGCTGGATCGGGTAGGTAA	CTGGATCGGGTAGGTAAGAAT	CCCGGTACTTTATTCTAAGAA
6504	SLAMF1	NM_003037	CTCCGGCAGTTGGGAAGCAAA	CAGGACCCTTGCACCACCATA	CAGAGTCTGTCCAGGAAACAA	AACAAATTCCATCACAGTCTA
6510	SLC1A5	NM_005628	CTGGATTATGAGGAATGGATA	CCGGTCCTGTACCGTCCTCAA	CAGCCTTTCGCTCATACTCTA	CACGCTGCCGCTGATGATGAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
6512	SLC1A7	NM_006671	CCGGAACATGTTCCCAGCCAA	CACGTTAAGGTCAAGACACTA		
6514	SLC2A2	NM_000340	TGGGTTATCAGTTAACATTAA	ATGGTGTGTTCCTAACATAAA	CAGACTTTAGCTTACAGTCAA	CAGGGTGCTAACGTATCTCTA
6517	SLC2A4	NM_001042	CAGGATCGGTTCTTTCATCTT	AAGGGCCATGCTGGTCAACAA	ACGCTGCTGCCTCCTATGAAA	CACCTTGGACTCCTCCCACAA
6523	SLC5A1	NM_000343	AACCATAGTGTCTGATGGCAA	TTGGGATTTCACGTATGATTA	AAGGAGACCATTGAAATAGAA	GAGGACAGTGTTGAACGTCAA
6525	SMTN	NM_006932	CACATTCACCATCGAGATCAA	CAGCACCATGATGCAAACCAA		
6528	SLC5A5	NM_000453	CGGAATTATCTGCACCTTCTA	ACCCAGGAAACTCGTGATTAT	CAGCTTCTATGCCATCTCCTA	CTGGATTGCCTTGTATGCAAA
6529	SLC6A1	NM_003042	CAGCAAGGAGGCCTACATCTA	ATCCTTAATAACTATGGTAAA	CACGTAAGGTCTCATTTGATA	CGGGCGTTATGTAAGTTTCTA
6534	SLC6A7	NM_014228	CCCGCTCTCCAAGATGAAGAA	TTGGTTCATTGTTAATAAATA	CCTGGTGTATAGCATCGTCAA	CACGTTTCACCAGAACATCTA
6541	SLC7A1	NM_003045	CAGCACCCAATAGACTATTTA	ACGGATCTGGATATACACTAT	ACGCTTATGACTCCTAATGTA	GAGGGTTGGTTTATTATCAAA
6543	SLC8A2	NM_015063	CACGGTGGATAAACTCATCAA	CTGGAATGAGACGGTGTCCAA		
6550	SLC9A3	NM_004174	CAGCACCGACAACGTGGTCAA	CCCGTTCATCTGGACCTGGAA	TGCGCAGAATTTCACCATCAA	CACCACCATCATCGTAGTGTT
6554	SLC10A1	NM_003049	ACGGAGTCAGCCGGAGAACAA	CACCATAGGGATCGTCCTCAA	AGGGATCGTCCTCAAATCCAA	CACAAGTGCTGTAGAATTAAA
6558	SLC12A2	NM_001046	CAGGATTGTCTACTTCAGCAA	AACGTTAATGACACTATCGTA	CAGGATTTACACCACTAATTT	CAGAGTATTCATTGGTGGAAA
6559	SLC12A3	NM_000339	ATCGCTGAGCTCAACACCATA	CCCGGCCACAGTGGAAGACTA	CAAGAAGACCATAGACATCTA	CAGGATGGACCAGGAGAGAAA
6560	SLC12A4	NM_005072	CCGGGAGCTGGTGCACATTAA	CCGGCATGATCTACAAATACA		
6570	SLC18A1	NM_003053	CCGGATGTATGCAACCCAGAA	CAGCATTGTCTTGCTGCCAAA		
6572	SLC18A3	NM_003055	CACGTCTGGCATAGCCATGAT	CACCATTGCCACGTGGATGAA	CTGCTTGATGAGCCACCGCAA	TACGGAGAGCGAAGACGTGAA
6573	SLC19A1	NM_003056	CAAGCGCAGCCTCTTCTTCAA	CCGCAAGCAGTTCCAGTTATA		
6578	SLCO2A1	NM_005630	AAGGAGGTCATTCATCAACAA	AACCTTTATTCTATTATATTA		
6581	SLC22A3	NM_021977	AAGGAACTTATGGGCATATTA	ATCAATTATATCCATGCTTAA		
6591	SNAI2	NM_003068	GAGGGAAAGATTAGCTTTGAA	TACCACAAATGCAATAATACA	CCGAAGCCAAATGACAAATAA	CACACTGAGTGACGCAATCAA
6601	SMARCC2	NM_003075	AAGAAGTATATACAAGCTGAA	CCGAAAGAAGATTTCAGCCAA		
6602	SMARCD1	NM_003076	AAGCACTGTGGCAATATATTA	TCCAAATATGATGCCACTAAA		
6604	SMARCD3	NM_003078	GTGGCAGTATGTGAAGACCAA	CAGGACTCCCATGACAAGGAA	CTCAAGGTGATGACAGATGTA	CAGTCGCTACTTCTACTGCAA
6610	SMPD2	NM_003080	CCGCATTGACTACGTGCTTTA	CAGGAGGTCAATGGCTTATAT		
6616	SNAP25	NM_003081	AAGATGCTGGGAAGTGGTTAA	CAGAGCTCACGTTGCATTGAA	AAGATTAAGTTATACCAGCAA	AAGGTTGTACATAGTGGTCAT
6623	SNCG	NM_003087	ACCCACCATGGATGTCTTCAA	AAGACCAAGGAGAATGTTGTA		
6624	FSCN1	NM_003088	AACTGGAAATAGCGAAATAAA	CACGGGCACCCTGGACGCCAA		
6625	SNRP70	NM_003089	CGAGAGTGAATTATGACACAA	CTCCGGAGAATGGGTATTTGA	CCGGAGAGAGTTTGAGGTGTA	AAGATTGAGCGGCGACAGCAA
6627	SNRPA1	NM_003090	TAGCCTTGTTTGTGTTAGCAA	TCCACTCACTATGCTACCAAA	CAGCATTGTTGAAATGCTTAA	AGCCTTGTTTGTGTTAGCAAA
6628	SNRPB	NM_003091	ATGAAACTGGTTTATAATAAA	CTGGTTTATAATAAACTCTTA		
6632	SNRPD1	NM_006938	AACGCTGAGTATTCGAGGAAA	ACAGTTCTATGTACTGAGAAA	TAGGCTAAACTTAACAATATA	CAGAGCTGTCTATTTAGTATA
6633	SNRPD2	NM_004597	AACGGAGAGCGTAGTGACCAT	CGCGGAGGAAACGGGAGTGAA		
6634	SNRPD3	NM_004175	CAAGAGGAAGAGGACGTGGAA	CAGCTCAGCTTTAACAACACA	ACCCATGTTAAAGAGCATGAA	AAGGACTTTGTGTTCATTTGA
6636	SNRPF	NM_003095	GCCAGTGATGGTGAAACTTAA	AAGGTGTAATAATGTCCTTTA		
6638	SNRPN	NM_003097	CAGAAAGATCAAGCCAAAGAA	TTGGATTTGGTGGAACAGCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
6640	SNTA1	NM_003098	CACCGTATTTCAAGAACTCTA	CCGGAACTTCAGCGAGGCCAA		
6641	SNTB1	NM_021021	CAGGAATTAAATAAAGCATCA	TAGACTGAATGCTATAATCAA		
6643	SNX2	NM_003100	AACCATCTAAATAAACCACTA	AGGGAAGAGATTGAAGAAGAA		
6649	SOD3	NM_003102	CTGGAATGGATGAGCACCCAA	AAGGGCTGCTATGATTGAGAA	CTCCTTCATCTCTTTAATAAT	AACCTTTGTGTTACAGATTAA
6651	SON	NM_003103	ATGATGTTGATTTATCTTTAA	CAGAATCTTCAATTACGTTAA		
6653	SORL1	NM_003105	CAAGACGGTCATTGTCAGTAA	CACGTCCTTTCTTGACCTCTA	CTGGGATTTATCGGAGCAATA	TACGGACAGGTTAGTCTGAAT
6654	SOS1	NM_005633	TACGGCATTATGAAATTACAA	CATGAACTTAGTGTAAAGTTA	TGGGTTGAATCCATCACTAAA	ACGAGTAGAATCAGATATCAA
6656	SOX1	NM_005986	CAACGTTAAGATGAAATTATA	TTGGGTTGGTTTGTTAATTTA		
6659	SOX4	NM_003107	CCGCGAGAAACTTGCATTGGA	TCCTTTCTACTTGTCGCTAAA	CACGGTCAAACTGAAATGGAT	AAGGACAGACGAAGAGTTTAA
6662	SOX9	NM_000346	ACCGAAGAAAGAGAGGACCAA	TCGTGTGATCAGTGTGCTAAA	ATGGGAGTAAACAATAGTCTA	CAGCCCACTGACAGACCTTAA
6675	UAP1	NM_003115	AAAGGTTTCTATGGTACTAAA	TTAGAGCATTATGAACATTAA		
6683	SPG4	NM_014946	CACGATGCTAGTAGACGCCTA	TGCCCTTAGTTTACTGGTTAA	AACGTTATTGATACTTGGATA	TCAGGTTAATACTATCTTAAA
6693	SPN	NM_003123	TTCAATAACAAGTGACCCTAA	ATGGTTCATATAGGACACACA	AAGGGTGTTTGTAGAGTTGTT	CCCAATGGCCTTTATCATCTA
6697	SPR	NM_003124	CAGGAAAGGCTGCTCGTGATA	CACGTGGACTTCTATGACAAA	AACTGCTGAGCTTACTGGAAA	AAGGAAAGGCTGCTCGTGATA
6699	SPRR1B	NM_003125	GAGACTTAAGATGAAAGCAAA	AAGGTCTTAGTACCAGAGCTA		
6700	SPRR2A	NM_005988	ATGATGATCCCTGACAGCAAA	ACCAAGAAAGGATAAGGATAT		
6710	SPTB	NM_000347	CTGCCGCATCACCGATCTCTA	ACGGCCCGCAAGGACAATATA	CACTCTCTGGATCAACGACAA	CAGGATGTCTCCTATGATGAA
6712	SPTBN2	NM_006946	CCGGCTCATCTCGGACATCAA	CAGCGTCAACATCCTGCTCAA		
6715	SRD5A1	NM_001047	CTCCGGAAATTTGAAGAGTAT	CGGGCATCGGTGCTTAATTTA	ATCCATTCAGATCATATCCTA	GAGGCTTATTTGAATACGTAA
6717	SRI	NM_003130	CAAAGAATACTCCACACATAA	TACATTATAAGCTTAACTATA	CAGGCTGTGAATTCAATTGCA	AGGATTCACCTTAGAAGTTTA
6718	AKR1D1	NM_005989	CAGGGTCCTCCAGCTAGATTA	ATGGCAAATGGTTATATCACA	CTGGGTAGTAGCGTTGGTAAT	TAGTGTTACTTGGATAGCTTA
6729	SRP54	NM_003136	ATGGGATTCAATAATATGTAA	ATGGATAGTATGAATGATCAA		
6732	SRPK1	NM_003137	CACCCTTGGCTTAACTCCTAA	AAGCAATAGACTAGAACTGAA	TACCATGTGATCCGAAAGTTA	CAGACTCTTGTACACCTATAA
6737	TRIM21	NM_003141	CAGCGTTGAGTTGCCCTGTAA	AGCGTTGAGTTGCCCTGTAAA	CCGGCAGCGCTTTCTGCTCAA	CAGAGCATACCTGGAAATGAA
6738	SSA2	NM_004600	CAGGATGGATATGTATGGCAA	CTGAGGGAGTATCGAAAGAAA		
6746	SSR2	NM_003145	CAGGTGCTTTCCAGACTCCAA	CCCAGTGTCTATTCTGGGTTA	CACCTCGGCAACAATTACTTA	CAAAGGGTATCTTAAATGCAA
6750	SST	NM_001048	TGCAGAGATCTGCTAACTCAA	CAGCGAGACCCTTGCATTAGA	CCCTTGCATTAGAAACTGAAA	ACGGAGAATGATGCCCTGGAA
6751	SSTR1	NM_001049	CTGGTGGTGCCTATTAATCAT	TGGGAACTCTATGGTCATCTA	CGCGCTGGTGGTGCCTATTAA	CACGAACTCATTAACAACTCA
6755	SSTR5	NM_001053	CACCGTCAACATCGTCAACCT	ACGGGCTTATGCAGACCAGCA	CGGGCTTATGCAGACCAGCAA	CGGGAACACGCTGGTCATCTA
6757	SSX2	NM_003147	CCACCTTTCATGTGTAATAAA	AGGGCAGTTCTGAGTGTTTAA	CCCGAAGATCATGCCCAAGAA	TTGGTCGATTCAGTTTGTCAA
6775	STAT4	NM_003151	TGGAATCAAGTCCAACAGTTA	TCAGAGGCCGTTGGTACTTAA	TTGGTACAACGTGTCAACCAA	CAGCCTCGATTTCAAGAGAAA
6778	STAT6	NM_003153	CACCCTTGAGAGCATATATCA	AACCAAGACAACAATGCCAAA	CAGGATGGCTCTCCACAGATA	ACGGATAGGCAGGAACATACA
6788	STK3	NM_006281	CAGACCATGATTGAACATAAT	CAGCTGCATACCAGTAATAAA	CGGCGCCTAAGAGTAAACTAA	CCGGCGCCTAAGAGTAAACTA
6790	STK6	NM_003600	TAGCATGTGTGTAAACTTTAA	GAGGGTTTAACTCCTATTTAA	CACGTGCTCTACCTCCATTTA	CACCTTCGGCATCCTAATATT
6793	STK10	NM_005990	TGCAGAATGTATATAACGCAA	CAGAATGTATATAACGCAATA	CAGCTCAAACTGATGAAGAAA	CACGGAATTAGAGAACCTGGA
6794	STK11	NM_000455	AACGTGAAGAAGGAAATTCAA	CCGCCCAAATTTGGCAATAAA	GAGGGCCGTCAAGATCCTCAA	CAGGAGTGTGCGGTCAATATT

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
6799	SULT1A2	NM_001054	CACGTCGTTCAAGGAGATGAA	AAGAGGCTCCAGAATAAAGTA		
6810	STX4A	NM_004604	AGGAAGCTGATGAGAACTATA	CAGCTCGGACGAAGAGGACAA	TCCGGACAATTCGGCAGACTA	AAGCGAGGTGTTTGTGTCCAA
6811	STX5A	NM_003164	CAGTGGAAATTGAAGAGCTAA	CAGCAAGACTGTCAGCCTCAA	AAGTCCCTCTTTGATGATAAA	ATCAATAGCCTCAACAAACAA
6829	SUPT5H	NM_003169	CCGGAAGGGCTTTCTGTTCAA	CAGAACAACATCCATGTGAAA		
6830	SUPT6H	NM_003170	TAGGAGCATCTTTGAAATGTA	CAGCACAATTCAGAAGATCAA		
6840	SVIL	NM_003174	CACATCGAAGCCATGATTTAA	ACCGGTTGTAAACAAACAGTA	CAGGACTGATGTCAAGGCATA	CCGAGTATTTATCCCGCTATA
6844	VAMP2	NM_014232	ATAGTTTACTTCAGCTCTTAA	CAGCTGTTATTTATACATATA	TCCCTTCATTTGCATCTGCTA	CCCATTAGTTCTTGTATCACA
6853	SYN1	NM_006950	CCAGATGGTTCGACTGCATAA	ATGGTTCGACTGCATAAGAAA		
6854	SYN2	NM_003178	CCAGCTGGTCGCTATCTATAA	CTCACTGGAATCCATATACAA		
6860	SYT4	NM_020783	CAGGGAGATCTTAATACCTAA	CTGCACTGTATTAAACATGTA		
6873	TAF2	NM_003184	AAGCATAAGCATGACAGTAAA	TAGAATCAAGTTGAACAGCAA		
6884	TAF13	XM_496381	TAGGGTGATATTGGTGCATGT	GCCCTTGTAAGCTATACTGTA		
6887	TAL2	NM_005421	GACCAGGAAGATCTTCACAAA	CAGAACTCTGCTTGAGAACTA	CCCACTCACCCTCCAGACAAA	AAACGCTTCGCCTGGCAATGA
6891	TAP2	NM_000544	CAGGACCAGGTGAACAACAAA	CCTGCTTTCCTTTATGATCTA	TAGCGACATTGGTAACAGCTA	CCCTATGAGGTTGGTTATTAT
6898	TAT	NM_000353	TTCGCTAGTGATGGACCCATA	CTCGGGCAAATATAATGGCTA	TCGGGCAAATATAATGGCTAT	CAAGCTATTGACCTTTGTTTA
6900	CNTN2	NM_005076	ACGATAGTTACTCACAAGTAA	CAGCCACAAACAAGTACTTTA		
6906	SERPINA7	NM_000354	CACTATGGTCTTAGTGAACTA	CACCCTATTATCCAAATTGAT	ACCCTATTATCCAAATTGATA	TAGGGAAAGTTGTGAACCCAA
6910	TBX5	NM_000192	AAGGCGGATGTTTCCCAGTTA	GCCGACGATCACAGATACAAA	CCACAAGATCACGCAATTAAA	TACCATTGTACCAAGAGGAAA
6916	TBXAS1	NM_001061	CCCAATAAGAACCGAGACGAA	CCGGAGACCTTCAACCCTGAA	ACCGCTGCAGCTAGAATCCAA	CCGCTGCAGCTAGAATCCAAA
6921	TCEB1	NM_005648	CCGAGATTCCTGAATTCCCAA	AAAGTTGAAATTTGTTTGCTA	TACCTGTAGTTCAGTTAGTAA	TGCGAACTTCTTAGATTGTTA
6924	TCEB3	NM_003198	TAGCATCTTTGTAAACTATAA	TACAATCATGTATTAATTGAA		
6926	TBX3	NM_005996	GCGAATGTTTCCTCCATTTAA	GTGCACTTTGTCGGATATAAA	TCGGGACAAGTGAACACATTA	CTGCCTATAGAGATATATTCA
6927	TCF1	NM_000545	CAGCCGAGCCATGGTTTCTAA	CAGGAGTAGCTGAGCTCACAA	CAGGACAAGCATGGTCCCACA	GCGAGTGGCACGTTTATTTAA
6928	TCF2	NM_006481	CACGGATCTTATCTGGTTTAA	CTGGGATATGCTAGTGATGTA	GCGGTGTAATAAGATCCTATA	TAAGGTTATAACTGTGGCTAA
6929	TCF3	NM_003200	CTCGGTCATCCTGAACTTGGA	CTGGATGATTGGGACTTTAAA	CCGGGCACATGTGAAAGGTAT	CCCGGATCACTCAAGCAATAA
6932	TCF7	NM_003202	TACGAACATTTCAACAGCCCA	ATGAGCTGGTTTGTCAAACAA	AACAGAAATAATCTGACACTA	CTGGGCAGCTTGAGAGGGCAA
6939	TCF15	NM_004609	AGAGAGAATTGGTGAGTTTAA	TCTGATATGGTTGGTAAAGAA	ATGGTTGGTAAAGAAATCTTA	TGGTTGGTAAAGAAATCTTAA
6943	TCF21	NM_003206	CAGATCCTGGCTAACGACAAA	CTGGTCCAAGTGCAATATGTA	CAAGTGCAATATGTAATTATA	ATCTTTCTTTATATTGCTAAA
6949	TCOF1	NM_000356	TACGTTGGTCTCAGAAACTGA	CAGCGAGGAATCGGACAGTGA	CAAGCAGTGAGGAATCAGATA	ACGGTTGAAGGTGGAGATCAA
6975	TECTB	NM_058222	CAGGGCAACCTTCCAATTCAA	TAGGTTTAAAGTGGTCTTGAA		
6988	TCTA	NM_022171	CCGGAGTCACTCATCCCTTAA	TAGGATGGTACCAAGCATTTA		
6992	PPP1R11	NM_021959	TGGCTTGAGATTGGTCACTTA	CAGAGATCAGTCAAATCCATA	CGCCCTAACTTTGCTTGCTAA	AACATGAGTAGCGAACACTTA
6993	TCTEL1	NM_006519	AACGCTTATCAACACAGCAAA	ATGTAGTAGAACAAACTTTAA		
6997	TDGF1	NM_003212	CCCGCTTCTCTTACAGTGTGA	AACCAAGTGATCAAACTACAT	CTGCCTTTCTATACAAAGCTA	TTGAATTATATGTTCAGATTA
7005	TEAD3	NM_003214	ATGGGTTATATCATAAATGCA	AACCAGCACAATAGCGTCCAA		
7006	TEC	NM_003215	CACGTGCATTTGGCCTATGTA	TCAGGTGACCTTCGCAACAAA	CCGCAGCTAATCAGAATCAGA	CAGTACAAAGTCGCAATCAAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
7010	TEK	NM_000459	CAGCACGTTGATGTGAAGATA	TGGAATGACATCAAATTTCAA	TCGGTGCTACTTAACAACTTA	ACGGGCCAGATTGTAAGCTTA
7019	TFAM	NM_003201	AAGGAATTATATATTCAGCAT	AGGACGAAACTCGTTATCATA	CACAATAAAGAAACAACGAAA	AAGATTGAGATGTGTTCACAA
7026	NR2F2	NM_021005	CTGGCCGTATATGGCAATTCA	TAGGTGAAGTCGAGCACTCTA	GTGGAATTTATTGGCAGCCAA	CCGCTTAGTTCTTGAATTGTT
7029	TFDP2	NM_006286	CTGGTACAGAGAAATCGACAA	AGGGACTACTTCTGAACTCTA	CGCTACTTCTTAAGTACTTAA	AAGGCAGAAATGAACATGAAA
7030	TFE3	NM_006521	TCCGGGATTGTTGCTGACATA	AAGGAGATTGATGATGTCATT	TCGCAGGCGATTCAACATTAA	CAGCTCCGAATTCAGGAACTA
7036	TFR2	NM_003227	CACGGAGTGGCTAGAAGGCTA	CAGGCACATCGGGAACCTCAA	GACGGTCATACTGTCGGTTAA	TGGAGTTTCAATATCAATAAA
7040	TGFB1	NM_000660	CTAGGTTATTTCCGTGGGATA	CACACTGCAAGTGGACATCAA	CAGCATATATATGTTCTTCAA	CACGTGGAGCTGTACCAGAAA
7043	TGFB3	NM_003239	CCGAGTCGGAATACTATGCCA	CCGGGTCTTGCGGGTGCCCAA	ACGCATAGACTGAGGTATAAA	AAGTATGAATATTACTCTCAA
7045	TGFBI	NM_000358	CGGGAAGGCGATCATCTCCAA	AAGGCGATCATCTCCAATAAA	CCGCACCATAATGAGATGTGA	TGGAGAAATGGCATCATTATA
7046	TGFBR1	NM_004612	CTGTAATGTTACGTCATGAAA	TGGGATTGTACTATACCAGTA	TCCATTGGTGGAATTCATGAA	CTGCCTTATTATGATCTTGTA
7048	TGFBR2	NM_003242	TACCATGACTTTATTCTGGAA	TCGGTTAATAACGACATGATA	TCGCTTTGCTGAGGTCTATAA	CTCCAATATCCTCGTGAAGAA
7049	TGFBR3	NM_003243	GACAATGGCTATAGTCCAATA	CACCTTCAACATGGAGCTATA	CCCGCAAGCTGACATGGATAA	ACCTGAAATCGTGGTGTTTAA
7050	TGIF	NM_003244	TACCACTGTGACTGCATTGAA	TACCCAGAGGACACTTGTAAA	TCCAAGAACTATAAACTTAAA	CACATACTGTCTAATTAATAA
7052	TGM2	NM_004613	CACCTTGATCCCAATCCTTAT	ATGGCCCAGCCTTGTAAATAA	CCGCAAGGAGCAAACACTGAA	CCGCGTCGTGACCAACTACAA
7058	THBS2	NM_003247	TGCATAAGCCATTATGATAAA	ATGACATAAGCTACCGATTAA	CAAGAGAGTGTCGAATGATAA	AGCGTTGGGATACTTCATTAA
7059	THBS3	NM_007112	CACGCCGTGAACCTACAGCAA	CCGCCTGGGTTTCCTGGGCAA	CTGCATGGAAGTGTACGAGTA	ATCGATGGCTACCCAGACCAA
7064	THOP1	NM_003249	CAAGTTGAAGGTCACCCTCAA	TGCGGTGATTCTGGAGCTGAA	CAAGTTCTACCTGGACCTGTA	CAGCAAGGTTGGCATGGATTA
7067	THRA	NM_003250	CAGCGAGTTTACCAAGATCAT	CTGGCCCAAGCTGCTGATGAA	CTGGATGGAATTGAAGTGAAT	CCCGATGACATTGGCCAGTCA
7072	TIA1	NM_022173	CGGAAGATAATGGGTAAGGAA	CACAACAAATTGGCCAGTATA	CTGGGCTAACAGAACAACTAA	AACGATTTGGGAGGTAGTGAA
7074	TIAM1	NM_003253	CGCCTGAAATTTCTAATAGAA	AACGGAAATGGTAGAGTTTCA	CTGGTTCTGTCTGCCCAATAA	ACGGCGAGCTTTAAGAAGAAA
7075	TIE1	NM_005424	CCAGTGAGAACGTGACGTTAA	TACTTGTATATCGCTATTGAA	GCGCTTCAAGGTCAATGTGAA	CCCAGTGAGAACGTGACGTTA
7077	TIMP2	NM_003255	CAGGCACATTATGTAAACATA	CTCAAATACCTTCACAATAAA	CTCGCTGGACGTTGGAGGAAA	CTCGACATCGAGGACCCATAA
7078	TIMP3	NM_000362	CAGGTGAAAGACTGAGATGAA	CCCTGCGGAGTCGATAAATTA	CGGCGGCATTATTCCCTATAA	CACGCTGGTCTACACCATCAA
7080	TITF1	NM_003317	CCCACTTGTCACTGACACAAA	TGGCTTAAATATAGTTCCTAA	TACCTTGTCATCAGCATGTAA	CTCCGTTACGTGTACATCCAA
7084	TK2	NM_004614	AAGGTGTTCAATTAATCTGCA	CTCCCGATAAAGAACAGGAAA	CGGGATCGAATATTAACTCCA	ATGCCAGAAGTGGACTATGTA
7087	ICAM5	NM_003259	CCGGGAGAACGTGACCATCTA	CAGGAGGAAACTTCACGTTGA		
7088	TLE1	NM_005077	AAGGTTAAACATTTGTATAAA	TCGAATTTATAGAAATAGAAA		
7089	TLE2	NM_003260	CTGCATTGATATTTCCGATTA	CAGCGAGAAGACGGAAATGCA		
7090	TLE3	NM_005078	CAGGATCAAAGACGAATTCCA	CACAGTTTATGAGGTCATCTA		
7092	TLL1	NM_012464	GAGGCGTTATTCCTTATGTTA	CAGATCGAGATAACCACGTAA	TAGAATCAATCTCGACCTATA	CAGCATTACAAGGATATTTGA
7096	TLR1	NM_003263	CACCATTTATATGTGGTATTA	CTGGTTTGGCATACAACTGTA	CCGCAAAGTTATATCTATGAA	CAGGGTCTTCATGAACACTAA
7097	TLR2	NM_003264	CTGGGCAGTCTTGAACATTTA	AACATTTAGACTTATCCTATA	CAGGTAAAGTGGAAACGTTAA	CCGCAACTCAAAGAACTTTAT
7101	NR2E1	NM_003269	CCGGTTGATGCTAACACTCTA	TACGTTATGTTGGAGCATTTA	TCCCGTTAACATAGTGCTGAA	CTCTATACTTATGGAAATGTA
7102	TM4SF2	NM_004615	CACGGACGCTATGCAGACTTA	AAGGGTTGTTATGATCTGGTA	CCGGTTCATCACGGCCAATCA	CAGGCTGCCTAAGACATGTAA
7104	TM4SF4	NM_004617	AAGGAAGAAAGCACATTTAAA	CAGGTCAGGGAGAATGTATAA		
7108	TM7SF2	NM_003273	CCGCATCATGCCCTACATCTA	CACCATGGATATCACACATGA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
7112	TMPO	NM_003276	ACCCATCAAATTACAGTATAA	GAGGAGAAGTATGCAAAGTAA		
7124	TNF	NM_000594	AACCCAAGCTTAGAACTTTAA	CAAGCTTAGAACTTTAAGCAA	TAGGGTCGGAACCCAAGCTTA	CCGACTCAGCGCTGAGATCAA
7126	TNFAIP1	NM_021137	CTCACATACGGTAAAGCCAAA	TGCCCTCTTGAGGTCCTTTAA	CAGGAGGTGAGTTCCTCTTTA	ACCCATGTCTTTCTACCCTAA
7127	TNFAIP2	NM_006291	CTGGCTGTGTAACCTAACATA	TAGGAGTTAGCGTGTTTGATA	CCGGATGTCCATGGAGCAGAA	CAGGGTGATGCTGAAGATGAT
7128	TNFAIP3	NM_006290	CTCGGCTATGACAGCCATCAT	CAGATGTATGGCTAACCGGAA	CCGAGCTGTTCCACTTGTTAA	CAGCCTTTACTCATACTATTA
7130	TNFAIP6	NM_007115	CTGGCACATTAGACTCAAGTA	CCCACTGCATAGAAATAACAA	TGGCGTCTTTACAGATCCAAA	AAGGCGGTGTGTGAATTTGAA
7139	TNNT2	NM_000364	CAGGCAGCTCCTGTTTGGAAA	CCACTCCACACCAGTAATAAA	CCGAAACAGGATCAACGATAA	CAGGATCAACGATAACCAGAA
7140	TNNT3	NM_006757	AAGCGTCAGAACAAAGACCTA	GAGGAGCAGTACGAAGAAGAA		
7142	TNP2	NM_005425	CAGAAAGAACTTGGAAGGCAA	CAGGATGGAAATCCAACTAAT		
7151	TOP1P1	M55632	CTCACAATTCACACCAATAAA	TTGGGACATCATGAAAGTTTA	TGCCTTCATATTAATATATAA	GTGGAAGTTTACTGACAGGAA
7153	TOP2A	NM_001067	CCCATTGTAAAGGTATCTAAA	CAGACTATAGGGAATACCATA	CACGTAGGCTGTTTAAAGAAA	ACGAATAACCATAGAAATGAA
7155	TOP2B	NM_001068	GTGGATTATGTGGTAGATCAA	CTGATTGAAGTAGTTAAGAAA	CAGCCGAAAGACCTAAATACA	TCGGGCTAGGAAAGAAGTAAA
7158	TP53BP1	NM_005657	AAGCAGTAACACCTCTTACAA	CTCCAGAACTACCGTAATTAT	TTGTTTGACCAGAGCAATAAA	CAGGACAGTCTTTCCACGAAT
7161	TP73	NM_005427	CCCGCTCTTGAAGAAACTCTA	CCGGGCCATGCCTGTTTACAA	CCCGGGATGCTCAACAACCAT	ATCGAGTATTTCACCTCCCAA
7164	TPD52L1	NM_001003395	CAGCTAGAAGACGAAATTACA	CAGCAATAGGATGATTTACTA		
7166	TPH1	NM_004179	AAAGACAATGTCTACCGTAAA	CGGGAGGATAATATCCCACAA	TCCATTTGGAGTGAAGTATAA	CGGAGTATTCAGATCCTGAAA
7167	TPI1	NM_000365	CCGAGGATGGCTGAAGTCCAA	ATGGAAGGCGTGGTGGGATTT		
7168	TPM1	NM_000366	CACACTGTGCTTTCTATTGTA	CTCAAGGGCACCGAAGATGAA	TGCGGAGAGGTCAGTAACTAA	AACGATATGACTTCCATGTAA
7171	TPM4	NM_003290	AGCGTTTGCTTTCGCCTGTAA	ATAGTAATTAATAGATGGTAA		
7172	TPMT	NM_000367	ACCGAAATTCCTGGAACCAAA	AGGGTTCAAGGTGGTCCCAAA	CACCGGTTGAATGGACAACTA	ACCGGTTGAATGGACAACTAA
7175	TPR	NM_003292	CTGAAGGAAGATCTAAATAAA	CAGGAGGTTTCTAGAGAACAA		
7177	TPSAB1	NM_003293	CTGAGTGCTGGACCTCATTAA	CTGCCTGGGACCGGACGTCAA	CTGGACCTCATTAAAGTGCAT	CAGGATCATCGTGCACCCACA
7187	TRAF3	NM_003300	CTGGAAGATTCGCGACTACAA	ACACTTCACTCTGAAGAATTA	TCCGATGATCGCGCTGCAGAA	AGAGAGCATCGTTAAAGATAA
7188	TRAF5	NM_004619	AAGGTAGGCTGTTCCAGTTAA	AAGCATTTCTTTAGCCCACAA	CTGGAGGGTACTTGCTATAAT	AGGGTACTTGCTATAATGGAA
7189	TRAF6	NM_004620	CAGGAAACTATTCACCAGTTA	CAGCGCTGTGCAAACTATATA	CAGGGATGAGTTTAAACCCTA	AGGGATGAGTTTAAACCCTAA
7224	TRPC5	NM_012471	CAGAGCTATCGATGAGCCTAA	GAGGCCTGTTCTCAAAGTGAA	CACACTAAGTCCATCTTACAA	ACCAGCTATCAGATAAGGCAA
7252	TSHB	NM_000549	GAGAGTGTGCTTATTGCCTAA	CCCAGGATGTTTGCACATATA	CTGCATACATGAAGCCATCAA	AAGACAAACTACTGTACCAAA
7253	TSHR	NM_000369	TCCAGAATCTACGTATCTATA	CAGAATCTACGTATCTATAGA	TACGCAGACTCTGAAGCTTAT	AGCACTGATATTCAGGTTCAA
7262	PHLDA2	NM_003311	CACTGTGCCCATTGCAAATAA	CGGCTTTGAATGAATAAATGA	CTGGTTCTTTGTAGTCACATA	CGCGCTCGGCACGACATGAAA
7266	DNAJC7	NM_003315	AAGCTTATAATTATTATACAA	AAGGAAGGAAATTACAAACTA		
7270	TTF1	NM_007344	AAGGAGATACTGAGAAGTTAA	CAGTTTGATTATATTTATATA		
7272	TTK	NM_003318	ATCCGACTTTATGATTATGAA	TTGGACTGTTATACTCTTGAA	TCCGACTTTATGATTATGAAA	CAGCAATACCTTGGATGATTA
7273	TTN	NM_003319	TGCGGCGAGTATACATGCAAA	TCGGGACGGTCAAACCTATAA	CGCATTCTAGCTCGAGTCAAA	ATCGACTATTACATCGTAGAA
7280	TUBB2	NM_001069	CAGATCAATCGTGCATCCTTA	CATGGTCTTTCTACTTGTAAA	CTGTGAAGGTATCTATACTAA	GAAGGTATCTATACTAATAAA
7297	TYK2	NM_003331	ACGAAATTCCTTGAGCTCATA	CTGATGCTATATTTCCGCATA	CGGGTCTGTGCTGAATGTGTA	CACCATCTGGTAATAAACTCA
7299	TYR	NM_000372	ACCCATGTTTAACGACATCAA	AAGGATTTGCTAGTCCACTTA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
7314	UBB	NM_018955	GAGGCTCATCTTTGCAGGCAA	CCAACTTAAGTTTAGAAATTA	ATGGCATTACTCTGCACTATA	CAGGATCCTGGTATCCGCTAA
7316	UBC	NM_021009	TTGCACTTTCCTTTCAATAAA	AACGTCAAAGCAAAGATCCAA	GAGGTTGATCTTTGCTGGGAA	GAGGTTGATCTTTGCCGGAAA
7317	UBE1	NM_003334	CCCGCTCACCTTTGATGTCAA	CTGGGATGTCACGAAGTTAAA		
7318	UBE1L	NM_003335	TTGGAGTTTGACACCAACCAA	CGGCCGGATGGTCACCTGAAA	CAGCAGAAGGAACTGAACAAA	ATGCTTGTTAAAGGAAGGCAA
7320	UBE2B	NM_003337	CTCATTAGAAAGGCTAACAAA	TTGGATTACAGTATGGCAATA	CCCAGTATTAGCAATGAATTA	ACCTCTCATTAGAAAGGCTAA
7325	UBE2E2	NM_152653	TCCGATGGAGATCAACGTGAA	CCGCTGCTAAATTGTCAACTA		
7334	UBE2N	NM_003348	ACCTTGTCTCTTGCAGTTTAA	AAGATGAAGAATTAACTATTA	TAGCCAGTCATAAATACATAA	CAGATTTGTGTTAAGATAGTA
7335	UBE2V1	NM_021988	ATCCATGCGAGTAAACATTTA	TTGGATGTAACGGCTTGGTAA	CACGGGAATTATTATTGTCAA	AAGGAAGACTTGAACCTAGAA
7343	UBTF	NM_014233	CCGGAGAAGAAGAAGATGAAA	CAGGACTTCCAGAGAGAGAAA		
7350	UCP1	NM_021833	TCCAGTGTTATTAGGTATAAA	CAGAATAATAGCAACAACCGA	TGCAATGAAAGTGTTCACTAA	AACGAGAACTGTCAAAGTCAA
7358	UGDH	NM_003359	TACAATCATGTTTGAAATTAA	ACGGTTGTTGATGTCAATGAA		
7363	UGT2B4	NM_021139	CTGGGAAACCCAATAAATGAA	CCCAATAAATGAACTCCTTTA	ATGAGGTTATATTGAAATGTA	AGGAAGCTAATAAATAATTAA
7367	UGT2B17	NM_001077	CACATTGTATTTGAACACAAA	TTGGGAATATTCTGACTATAA		
7376	NR1H2	NM_007121	CAGGGCAACAGGAGTAGTTCA	CCGGAAGAAGAAGATTCGGAA	ATCGTGGACTTCGCTAAGCAA	CTGGGCGAGCCTGTAGACCTA
7378	UPP1	NM_003364	CAGGAAACTAATTTCCTGATA	CACACTTTACACAAGAATCTA		
7380	UPK3A	NM_006953	CACGGAGTACAGGTTCAAGTA	CAGTGTGACTTTCGCCACCAA		
7384	UQCRC1	NM_003365	CCGGGAGCACACAGCTTACTA	CGCCACCGTGATGATGCTCTA	CCGGACAATGTGGCCTTGCAA	CCACAGGTGACCACCAATAAA
7385	UQCRC2	NM_003366	TACATCCAGTCTGACGACAAA	CCAGAATTTCGTCGTTGGGAA	ATCAAGGCTGCCTATAATCAA	AAGGCTGCCTATAATCAAGTA
7392	USF2	NM_003367	CCGGGAGTTGCGCCAGACCAA	CAGCAAGACGGGAGCGAGTAA	AAGACTGTAACGCAGACAACA	AAGAGCCCAGCACAACGAAGT
7399	USH2A	NM_007123	CAGGTACAATTTGACCATTGA	CAGAGGGAAACTTGACTTTAA		
7407	VARS2	NM_006295	CCGGATTTACCACCAGTTGAA	CTGTTTCACCATGGACCCTAA	CACGAGGAAGGCATCATCTAT	CCGGTTTGGATTATGTGCCTA
7414	VCL	NM_003373	CGGATTAGAACCAACCTCTTA	AAGAGAGTAATGGGTTTCATA	TAGGTGTTTGTTCATCTGTAA	CTGATATAAATGCAATATTAA
7415	VCP	NM_007126	CACAAGCAGTTTCTAAACCAA	CCCATTGATGACACAGTGGAA		
7422	VEGF	AF022375	GAGGGTTTCAATATACATCTA	CTGGAATTTGATATTCATTGA	ATAGAGAATTCTACATACTAA	AAGAAAGATAGAGCAAGACAA
7423	VEGFB	NM_003377	CAGGACAGAGTTGGAAGAGGA	CCGGATGCAGATCCTCATGAT	CAGTGTGAATGCAGACCTAAA	AAGACCCAAACCTCTGCATAA
7425	VGF	NM_003378	CCGGAGGAAGAAGCAGCTGAA	CGGCAGCCTCTTGGTCATGAA		
7434	VIPR2	NM_003382	CACCGGTTGCTGGGATACAAA	CTCCAGCATTTAGATAATCTT	CCCGCTGTTCGGCGTCCACTA	AACGGAGACCTCGGTCATCTA
7436	VLDLR	NM_003383	CCCTGAAAGAGTGTCATATAA	ATCCAACTAGTTGAACAGCTA	CAAGGTTGGTAGACATGTTAA	CAAGATCGTAGGATAGTACTA
7441	VPREB1	NM_007128	AGGCTATGTATTACTGTGCTA	CTGCTGAGATATTTCTCACAA	TCCCAGGTTCCTGCTGAGATA	AGACTGCATTAGGGAATTAAA
7442	TRPV1	NM_018727	CAAGTGGGACAGATTCGTCAA	CAGAACCACATCCCAAAGGTA	CTCAATTGCTGTGCAGGTTAA	CCCGAGGAAGTTTATCTGCGA
7447	VSNL1	NM_003385	TAAGCGTTTACCCGAATTAAA	CGGCTTAAGCGTTTACCCGAA	CAGAGACGGCTTAAGCGTTTA	AGCGTTTACCCGAATTAAATA
7450	VWF	NM_000552	AAGGGACGAGATCGTTAGCTA	AACATGGAAGTCAACGTTTAT	CCCACCATCTCTGGTCTACAA	ACGGCTTGCACCATTCAGCTA
7453	WARS	NM_004184	CAGAAGGGAAACTGAAAGAAA	AAAGAGCTAATAAACCGAATA	CAGGTTCTTGATGCCTATGAA	AGGGTTCCAAGTATACTCTTA
7455	ZAN	NM_173059	TGCGATCTTAATAAACCCTCA	CCGTGTGCTAATCAACAGCAA	CCCGGCTATGTGCTGAGTGAA	CAGCTTAAGAATGGCCAGTAT
7461	CYLN2	NM_003388	CACCTTCTGAACCTTCTTCAA	CAGGACAAAGCTCAGAAACAA		
7462	WBSCR5	NM_014146	AAGCTTGTACAGTTAACTTAT	AAGGACCATTTCCCAGAGCTA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
7472	WNT2	NM_003391	AAGGCATTTATTGCCATATTA	CTGGAGAAGAATGGCTTTCAA		
7474	WNT5A	NM_003392	CAGAGTAAATACTCTGAATAA	CCGGATAACCTTGTAACATAT	CCGGGTCTGCAGAGAATGAAA	CACACAAACTTTACACTTTAA
7480	WNT10B	NM_003394	AAACCTGAAGCGGAAATGCAA	CAGGCACTGTTTGGAGCCATA	CAGGATCGGCTGAGGGCCAAA	ACGAATGCGAATCCACAACAA
7483	WNT9A	NM_003395	CCGGCTGAAGCTGGAGCGGAA	CCGTGTGGACTTCCACAACAA		
7484	WNT9B	NM_003396	CAGCACCAAGTTTCTGAGCAA	AAGCAAAGCCTCCTCCCTTAA		
7498	XDH	NM_000379	GACAGTCTTTGCGAAGGATAA	CTGCACCATTGCTGTTCCAAA	CCGGATTGTGGTTCGAGTGAA	ACAGGTAATAACGTGAAGGAA
7499	XG	NM_175569	CAGCCAGTTATTTCAAACTAA	ACGGTGGAGATCACCATTCAA		
7511	XPNPEP1	NM_020383	AAGGAGAACCTCGTTGACAAA	ATGAGATTGCGTGGCTATTTA	CCCGACTGGAACCAAAGGTCA	CCCGACTTCTTTGGCCAGTGA
7514	XPO1	NM_003400	TACATGTTACTCCCTAATCAA	CTGTGTCAGTTTGTAATGGAA	CCCATTGTAAAGCGACTTCAA	CAGCAAAGAATGGCTCAAGAA
7516	XRCC2	NM_005431	CACGATGTATACTTCCCAAAT	AGGGTACTACGCAAGCCTTAA	TTGCAACGACACAAACTATAA	CAGGGTACTACGCAAGCCTTA
7517	XRCC3	NM_005432	AAGCCAAACTGAAATCGGTAA	CCGCTGTGAATTTGACAGCCA	GAGACACTTAAGGGAAATTAA	CAGAATTATTGCTGCAATTAA
7520	XRCC5	NM_021141	GACGATTTATTGGACATGATA	ACCCTCATAAGTCGTCACTAA	AAGCGAGTAACCAGCTCATAA	AAGCATAACTATGAGTGTTTA
7525	YES1	NM_005433	GAGGCTCCTGCTTATTTATAA	CCAGCCTACATTCACTTCTAA	AAGTATAATGCAGTACATTAA	AACAGTCAGTATGCAATCTTA
7529	YWHAB	NM_003404	AAGGTTTAATCTGATATCAAA	CTGCCGTTGTTCGGGACTTAA	CTGGATAATACCTTTAAGAAT	CAGCAATATGTTCACTATGTT
7533	YWHAH	NM_003405	ATCAAGATGGGTGATTATGAA	ATGGGTGATTATGAAATGCCA	TTCCATCAGCTTTATAATAAA	CAGGCTACAGTTGATATTTAA
7555	ZNF9	NM_003418	CAGCAAGACAAGTGAAGTCAA	AAGAGTTGAGTCAGACCAGTA	CTGACCTCAGTAGCTATTAAA	CACATAGATGGTGATGGCAAA
7559	ZNF12	NM_006956	CAGCAATGGATTATAGTTTAA	CTCGCAGAAGTCAGCACTTAA		
7567	ZNF19	NM_006961	CAGGCTATTGTAGCTATTATA	CACCAGTGAATCCATTCTCAA		
7579	ZNF31	NM_145238	CAGGGAAGTTATCTTGGTATA	ACCAGGTAATTTGGAAGTGAA		
7592	ZNF41	NM_007130	CAGCATATCCTGGGACATAAA	CACAGTGTATATGCAATTCTA		
7593	ZNF42	NM_003422	CCGCAGGTCCAGGTAGTGTAA	CTGGCGATTACATAAGTATAA		
7596	ZNF45	NM_003425	AACGAGATGATTTGCACTATA	CACCAAGATCAATGTATACAA		
7617	ZNF66	NM_001009883	CAGGATCAAATTCTCACATAA	CAGCATATAAACAGAACCAAA		
7620	ZNF69	NM_021915	AAGAAAGTCAATGAAATTAAA	CAGGCTGAACTTCCAGGAGAA		
7629	ZNF76	NM_003427	CCGCTCCTTCACCACATCTAA	CATGGATGAATGAGTATTTAA		
7634	ZNF80	NM_007136	CAGGGTTATATGCAATGTTCA	CTGGAGGAAGATGAGCCCTAA		
7675	ZNF121	NM_001008727	CACATTTGAATTCACACTGAA	TAGGAATTTCTCATACCATAA		
7681	MKRN3	NM_005664	CCAGTGGGACTTGCTTCATTA	TCCTGTTTAGCTTGACATGAA	AAGCCAGTAATTAGCATCTAA	GAGGACTTACAAAGCACTATA
7695	ZNF136	NM_003437	ATGCTTAATCTCACAAAGAAA	ATGGAAGGACCAGAACATTAA		
7705	ZNF146	NM_007145	CACGAATGAGGTTAACTTTAA	CTGGATTCATTTCCAATTAAA		
7707	ZNF148	NM_021964	CAGGAATGAATTCTCCACTAA	TCGGATGGCATAAGTGATTAA		
7712	ZNF157	NM_003446	CCGAATGAAGATGACTCTCAA	CAGGGTGAACATGCCAGCTAA		
7730	ZNF177	NM_003451	CCTGAGTACATTTATATTTAA	CTGGGTATAAGTAAGCAAGAA		
7739	ZNF185	NM_007150	CGCAATTATAATAAATGCTAA	CTCCCTGAACTTCACACATAA		
7743	ZNF189	NM_003452	AACACTAACATTATCCGTAAA	CTGCCAAGTATTGGAAATGAA		
7748	ZNF195	NM_007152	AAGACCTTTCATGAAATATAA	CACAAGAGTATTTCTTCTGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
7750	ZNF198	NM_003453	ACGGGCGAGATATGAACTTAA	CGCCATGAAGTCAGCTTTAAA	CACGCTGGGTATTACCATGTA	ACGCTGGGTATTACCATGTAA
7756	ZNF207	NM_003457	CAGGTACATAAAGAAACAATA	CAGGAACTATTGGACATTTAT		
7780	SLC30A2	NM_001004434	AAGGGCTGTATTTGGGCCTAA	GAGAGGCTTCTTACTAGGTAA		
7799	PRDM2	NM_015866	CTGGCACTAATTTATAACTAT	CTACACGTAAGTATAAATGAA	CCCGGGTGATTGAGATCCAAA	CAGATGTATGTCTACACGTAA
7804	LRP8	NM_017522	TTGCGGAAAGGTAACCACAAA	CTGGACTGACTCGGGCAATAA	CCGGATGGTGTATGACTGGAT	CAGTACCTTACTCATCATTTA
7809	BSND	NM_057176	CTCGGTGTTTAGGCTGAACTA	CCAGATGAAAGTCATGAGCTA	CTGGACATGGACTCCAGTGAA	TGGGATGATATGGAGGTTCAA
7818	DAP3	NM_033657	CCCGAGGAATTAGCACTTGTT	CGGCACTGTGCCTACCTCTAA	TTGGCTCTGGACCTGCATTAA	TCGCTTTGTGATGCAGGTGAA
7837	D2S448	XM_056455	TACCTGCACTTTAATCAGATA	ACGGAACAAGTTACCACTACA	AACAACCGGATTACACATTTA	CAGGAGTGGAATGTACATATT
7857	SCG2	NM_003469	ATGACTGTGTTTAATAGTATA	CTGGATGAGAATAATACTCGA		
7862	BRPF1	NM_004634	CCGAAAGGTCTACAAGAGTTA	TCCCAAGTCAGGCAAACATAA	AAGGGAGACGATCAAGGTTCA	CAGCAACTGCCTCAAGTATAA
7866	IFRD2	NM_006764	CCGGATCTACGCTGCCTTCAA	ACGCTTTGAGAAGCACCTGTA		
7874	USP7	NM_003470	ATGGAGTTGCGTGGGATTCAA	CCCAAATTATTCCGCGGCAAA	CGGGCCGACACCAGTACATAA	CGAGTATGAAGTAAATTTGAA
7879	RAB7	NM_004637	AACGTTGATTTGCATAATACA	TCCCGTTAGATCAGCATTCTA	TAGATCAGCATTCTACTACAA	CACGTAGGCCTTCAACACAAT
7884	SLBP	NM_006527	TACGATCGTTATATTAAAGAA	ATCAGTTAATTTACCATGTAA		
7903	SIAT8D	NM_005668	ACGAGATGTGTCAGTGGTCAA	CACAATGTAGAAGGTTGGAAA		
7915	ALDH5A1	NM_001080	AAGAAAGACTCCGTAATCTTA	ACCCTCTTTCAAAGACAATAA	TTCGGAAGTGGTACAATTTAA	AAGGAGACTTATCTACATATA
7917	BAT3	NM_004639	CAGCGGTTGATCAACTTGGTA	ATGATGCACATGAACATTCAA	CCGGTTGCTGGAGTTGTGTAA	CAGCTCCGGTCTGATATACAA
7919	BAT1	NM_004640	CCAGGTGGTGATCTTTGTGAA	CTCAACCTCAAACACATTAAA		
7940	LST1	NM_007161	ATGGCTCACCCTTCCACCCAA	TTCAAATTGATCATCATCAAA		
7942	TFEB	NM_007162	CAGCAGCCACCTGAATGTGTA	GAGACGAAGGTTCAACATCAA	CCGCCTGGAGATGACCAACAA	AAGCAGGAGCTGCCTAGCGAA
7979	SHFM1	NM_006304	CCGGTAGACTTAGGTCTGTTA	AAGAAGTGTTGAAGTAACCTA		
7988	ZNF212	NM_012256	CAGAAACGTGATGGAGAGTAA	TAAGTAGAAGAAATAATTTAA		
7991	TUSC3	NM_006765	ACGGATGTTCATATTCGGGTT	CACGGCTATCCTTATAGTGAT	CAGGATTGAAATAAATGACAA	ATGGTAGCATTTAGTAATCTA
7993	D8S2298E	NM_005671	CGGGTGAAGCCTGGAAATTAA	AAGGATTGCTTTCTATATATA		
7994	MYST3	NM_006766	CGGCGCTATACTAATCCAATA	AAGTTGTTTCTTGACCACAAA	CTGGACTTCCGTAGTGACCAA	CAGCTGAATTTGCGACCTGTA
8000	PSCA	NM_005672	CCCAGCATTCTCCACCCTTAA	CCCAGTAAAGGCTGAGATGAA		
8021	NUP214	NM_005085	CCCGGAGATGATCCCAACAAA	CAGAGATATTTGTGAACTTTA		
8022	LHX3	NM_014564	CCCACAGATGTCTGTTGCCAA	CTGGCCTGTGTGTAAGTCAAA	CAGCTCTTTCCAAGACTTCAA	CTGCTATTTCTAGACATGAAA
8029	CUBN	NM_001081	CGGAACCATCTCTCACATTAA	CACCTATGTCATAGAGGCTAA	CAGCTGCAATTTGAAGATCGA	CCGGTTAGAATCCATGGACAA
8031	NCOA4	NM_005437	AAGAGAAGTGGTTATATCGAA	CCCACGTTAGTTCTACATTAT	CTGGTCAATAGTGATTACCAA	ACCGACTAAGCAAATAGGCAA
8048	CSRP3	NM_003476	ATGGGAGAGGCAATAAATAAA	AACGAGTTGCAGAGCATATAA		
8061	FOSL1	NM_005438	CTGGACAGTATCCCACATCCA	CACAATTTGCACTAAATCAGA	CCGAGTAAGGCGCGAGCGGAA	CCCACCTAGAACACTAACTCA
8065	CUL5	NM_003478	CTGGAGGACTTGATACCGGAA	CCAGCTGATTCAGTTAATATA	CAGGTTTGAATCAGTCACCTA	CAGCTGGTTATTGGAGTAAGA
8073	PTP4A2	NM_003479	AGGGACTGTGTTGCTTGTGAA	ATGCAACAATAGATTCCATTA	CAGAGAATGCTGGTAGCTTAA	AACAGCATACCTGCTAAGCTA
8085	MLL2	NM_003482	CTCGGAGTGGTTTGAGAACTA	CCCGTTGAGTCCCATAGGGAA	CGGCCGGAGTTTGTAATCAAA	CACCAGCATGTCTAAGGCATA
8111	GPR68	NM_003485	TAGAGCTTGAACCACCTTCTA	CAGGATGGCGGTGGAGAGACA	CCGCGTGTGCTTTGAGCACTA	CAGCGTGGTCATCTGGGCCAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
8131	C16orf35	NM_012075	CCCGGCGTCCCAGACAAGTAA	CAGACATGGGTTGATCACCTA		
8139	GAN	NM_022041	AACGTTGGCAATGAAAGATAT	CACCATAACATAGCTCCGAAA	ATCATGATGAATTGAAATGAA	CCGCACAGTCATGTAATTCAA
8153	ARHN	NM_005440	CAGGTTCCTCTTACTATGATA	CAGCTATTCTCACACATCTAA		
8175	SF3A2	NM_007165	CCCGGGCTACAAAGTGACCAA	CTGCCTGACACTTCACAACAA		
8178	ELL	NM_006532	CCGAAGTGCCATTGTCATCAA	AAGGAATTATGAAGCTAAGAA		
8190	MIA	NM_006533	CTCCTTGGGTTTATGCAAATA	CAGGGAGATTACTATGGAGAT		
8192	CLPP	NM_006012	CCGGGTGGCGTCATGCAGGTA	GCCCATCCACATGTACATCAA	CACGATGCAGTACATCCTCAA	GCCCAGGAGTTTGGCATCTTA
8200	GDF5	NM_000557	CACTATGGGACTGGATACAAA	CAGCTCCTTCCTGCTGAAGAA	CTGTTAGACTGTTAGATTTAA	TAGATTTAAATGTATATTGAT
8204	NRIP1	NM_003489	GCGGAGAAGAATGAGTATGAA	ATGGTTGACAGTGTCCGTAAA	AAGCGTGCTAACGATAAAGAA	AACCAACCCAATACTATATTA
8209	C21orf33	NM_004649	ACCACATTTATGGACCATGAA	CAGGAAGAAAGGGAAATTGCA		
8214	DGCR6	NM_005675	CAGAGAAATAAAGATGCCTCA	TGGCTTCTACGTGACCACCAA	CTGGGCAGAGTTCATCTTCTT	ACCCTAGGATAGTCTCATAAA
8237	USP11	NM_004651	CCCATTGAACGCAAGGTCATA	AAGGTCGAAGTGTACCCAGTA	ACCGATTCTATTGGCCTAGTA	CTGCGTCGGGTACGTGATGAA
8241	RBM10	NM_005676	CAGGACTATCGGACCGAGCAA	CCAGAAGGTGTCGATGCACTA	CTCCAACGTGCGCGTCATAAA	ACCACTCACTATCGACGGCAA
8243	SMC1L1	NM_006306	TCGGAAGTGAATGACAAGAAT	ATGGAGGAGATTCGTAAGAAA	CGGCGTATTGATGAAATCAAT	CACCATCACACTTTAATTCCA
8260	ARD1	NM_003491	CCGGGCCGCCCTGCACCTCTA	ACGAGCTTTCACAATAAATTT	CACAGAGAGCACAGATGTCAA	CCGCCCTGCACCTCTATTCCA
8266	UBL4	NM_014235	TCCCTTCTGTTCAGTAAACAA	CTGTTCAGTAAACAAACTGAA	CAGGGACACACTCGTGAGCAT	TAGGCTGTTTCTGATATCCAA
8270	DXS9879E	NM_006014	CTGGTTCTTAAATGTTTGTTA	CCGAATTTCCGTCATCAACTT		
8273	SLC10A3	NM_019848	CAGGGACAGCCCTGCCATCAA	ATCAAGAACGTGAGTGCTATA	GCGGAGAGACTTCTGCATCAA	CATGGTGTTAATGCAGGACAA
8284	SMCY	NM_004653	CTGACGATTGCTTAGCATTAA	CGCGTCCAAAGGCTAAATGAA	CCCAGAGACGTTGGATCTCAA	CAGGGTAGAAACGTTGAGAAT
8291	DYSF	NM_003494	CACCGTCAAGGTCATCGATAA	CCGGGATGAGCCCAACATGAA		
8292	COLQ	NM_005677	TCCAATGACTTTGGGAATTTA	AACAGCGTTCTTCCAATCTCA	AAGAAGCGTGGTGGCCACAAA	AAGGACAAATTCCTGCTACTA
8309	ACOX2	NM_003500	ATGGCATATATGCAACATTAA	CTGCCTATGAGGAATATATAA		
8312	AXIN1	NM_003502	CGGGAAAGGTGTTGGCATTAA	CTGGATACCTGCCGACCTTAA	CAGCATCGTTGTGGCGTACTA	CAGCTACAGATACTACTTCAA
8318	CDC45L	NM_003504	ACGGATCTCCTTTGAGTATGA	ATTGAAGAGTCTGCAAATAAA	TAGGCCAGTCAATGTCGTCAA	TACGAGCAGTATGAATATCAT
8322	FZD4	NM_012193	ATGGTGCTTAATGAATCTCCA	CTGGAGAGAGTTGCTATTCCA	TAGGTGATCGATACTTGTCAA	CAGAATGATAGTGCCTTTAAA
8339	HIST1H2BG	NM_003518	CTCCAAGTAAATGTGTGCTTA	GCCACTCAAGTCTCACATAAA		
8340	HIST1H2BL	NM_003519	TTGCCACTATTGTTTCATTAT	CAAGCTCTTGTCCAACCCAAA		
8341	HIST1H2BN	NM_003520	CAAGGCCATGGGCATCATGAA	TTCGGTCAGTCTCGGCCCACA		
8347	HIST1H2BC	NM_003526	TAACGACATATTTGAGCGCAT	CCAAGTAAACATTCCAAGTAA		
8356	HIST1H3J	NM_003535	CTGCTCTATCTTGGGTTTCTT	ATCCGTGGCGAGCGAGCATAA		
8370	HIST2H4	NM_003548	CCGCAAGGTCTTGAGAGACAA	GCGGATCTCTGGCCTCATTTA		
8379	MAD1L1	NM_003550	CAGCTGGACCTGCAACACAAA	CAGGACCAAAGTGCTGCACAT	CAGGCGACTGCTCATCTTCAA	CAGCGATTGTGAAGAACATGA
8382	NME5	NM_003551	GAGGAGATACAAGATATTATT	CTCGAAAGAACAAATCATGAA	CATGATATTAGCTAGACATAA	ATGATATTAGCTAGACATAAA
8392	OR3A3	NM_012373	CAGGTGTCTTCAGCTACATGA	TGGAATCTTCAGACAAGGATA	CTGGGTTCAGTGGAATCTTCA	CAGGGCGCTCTGTGTCAGCTA
8396	PIP5K2B	NM_003559	CACGCGTTTCCTCACCACCTA	CCCATTTGACACCCAGGTTAA	CCGCTTTAAGTTTAAGGAGTA	CACGCCATACGATACAAAGAA
8417	STX7	NM_003569	CAGCAGATTATCAGCGCAAAT	TTGCTGTAGATTGCCTAGTAA	CAGCAGTATACTAACCAGCTT	TCTGATGAAATTAGCGAATAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
8419	BFSP2	NM_003571	CAGGGTGTGAGCTGGAACAAA	CAGGCTGAGACAGAATCCTTA		
8425	LTBP4	NM_003573	AACCGGCTTTGAAAGAGTTAA	ACACGTGATCTCAGAGGCCAA	GCGGCTGGAGTGCATCGATAA	TACGAGTACGGCCCAGACTTA
8435	SOAT2	NM_003578	CAGGTTAGGTTCCTGATGAAA	CAGGTGGAATTATGTGGCCAA		
8438	RAD54L	NM_003579	CGCGCGCTTTGGGAACAGGAA	CTCGCTAAAGAAGCTTTGTAA	ATGGAGGATCTAAGGATGAAA	AAGCATTTATTCGAAGCATTT
8440	NCK2	NM_001004720	ATCTCACAATTATGTATTTAA	GACACTAATACAGATGATTAA	TAGCCGTTTGTTGACACTAAT	TCGGCTTGTTTGAATCTCACA
8446	DUSP11	NM_003584	ATGATGCAATTGAATTATTCA	CACAATAAGCCTGTTAAACAA	CCCTTATGTATTCAAGCTTAA	CAGAAACTGTTCCTTACTTAA
8448	DOC2A	NM_003586	CACGAGTGTGTTGCACGTTTA	GCGGAGTTCTATATTCACATA		
8456	FOXN1	NM_003593	TCCCGTCAGCGAGATCTACAA	CAGCGTTTGCCTGGTCTGGAA	CGGGCTCACCTTAAAGGTCAA	CACACAAATTATTCAGATGTA
8459	TPST2	NM_001008566	CAGATTTGCCATCCTCCTTAA	AAGCATATTGCTTGCTATTAA		
8460	TPST1	NM_003596	AAGATATGCCTTTAATATTTA	GAGGCTGGTGTTACTGATGAA		
8468	FKBP6	NM_003602	CAGGCTTTGATCATTGACCAA	CAGGTTTCTGTTCAAACCGAA		
8476	CDC42BPA	NM_003607	ACGGCTTTCATTACCAAATAA	TCGGAAAGATATACCCTGTAT	CAGATAATAGTCGGAAACAAA	CAGACTTTCCGTAGCAGCTTA
8481	OFD1	NM_003611	CCGCCCGGGCTGGGCACTAAA	CTCAGACAAGTTCGACATTTA	CCCAGTCTTTGGCAATAACAA	TACCATCGGAGAGTCATTAAA
8493	PPM1D	NM_003620	TACATGGAGGACGTTACTCAA	ATGGCCAAGGGTGAATTCTAA	CTCGGCGTCGTCGAAGATAAA	ACGGGTCTTCCTAGCACATCA
8498	RANBP3	NM_003624	AACGAACTATTTCCTCCAGTA	CAGAGTTAAGCTGATAAATGA		
8499	PPFIA2	NM_003625	ACCGATGAAACTAGTCAAATA	TCCAATGAACGCCTACAACTA	TACCAGCTGGATTTAGGTTAA	AACGTTTGGGTGACTCATGAA
8504	PEX3	NM_003630	GCGGGTCCAGTTAAACATAAT	CGAGACATTACCACTATTAAA	TGGGTAAATCACCTATACTTA	ATGGTGAATTCCAACAACTAT
8507	ENC1	NM_003633	AAAGGCATTGTCCAAAGTTTA	CACCTTAGTACTTTAGACTAA	CAGCGGCTCCATTAACATCTA	ACGGCATGTATCACAGATGTA
8511	MMP23A	NM_004659	CGGCCAGAAGATCCTCCACAA	CCAGAAGATCCTCCACAAGAA	CCGGGCGCTCATGCACCTGAA	CAGAAGATCCTCCACAAGAAA
8513	LIPF	NM_004190	CAGCTTTGATGAAATGGCTAA	CACAATCGACTTCATTGTAAA	CAGCAATGCCTTATTTATAAT	CAGGCTGTTAAGTCTGGGAAA
8517	IKBKG	NM_003639	GAGGAGCTTCTGCATTTCCAA	ACCATAAATAATGGCATAGTA	TTCGGAAATGCCTCACATATA	CTCCTCTAGTTCAGAGACATA
8518	IKBKAP	NM_003640	ACTGGATATTATAGAAACCAA	AGCATGGTAACTTATATTGAA	GCGGTTTACTATAGACAAATA	CAGCGGTTTACTATAGACAAA
8520	HAT1	NM_003642	CACGCTAGAAGGGTTTATGAA	AAGACTAATTAGCCCATATAA	CCCTTCTTAAACAGTATAATA	TACCGGCGTGTTATTGAACGA
8526	DGKE	NM_003647	ATCCATTAATCAGATGCGTAA	CTAGATCGATGGAAAGTTCAA	CTGGAAGTCGTTGGAGTATAT	ATCGATGGAAAGTTCAAGTAA
8532	CPZ	NM_003652	CGCGCAGAACCTGGATCTGAA	CCCGGAGACAAAGGCAATCAT	CCGGATCTCAGTCAAAGGCAT	TACGCCAAAGTCATCAAGAAA
8535	CBX4	NM_003655	CAGCCCGAGGTCATCCTGCTA	CTGCCTCACCGTTACTTTCAA	GAGGCTGGTCGCCCAAATATA	AAGCCCTTCTTTGGGAATATA
8536	CAMK1	NM_003656	CAGCCTGGATGAAGACTCCAA	CAGGAGATACAGCTCTAGATA	CTGCATGACCTGGGCATTGTA	CAGGTGCTGGATGCTGTGAAA
8539	API5	NM_006595	CTCGAGTGGCAGATATACTAA	CCGACCTAGAACAGACCTTCA	CAAGTTTGCTATTCAAATCAA	AAGAGTAATGGTCAATCTTAA
8541	PPFIA3	NM_003660	CTGGTGGACGCTCGAATGTTA	TCGAATGTTAGATCACCTTAA	CACGGGTAAAGAGAACTGTTT	ACGGCTCAACTATGACCGGAA
8542	APOL1	NM_003661	CTGGACAACCTTGCAAGACAA	CAGGTGGAGAGGGTTAATGAA		
8543	LMO4	NM_006769	ATGGTGTATTTAAATAATAAA	ATGACTGAATATGAACATTAA		
8555	CDC14B	NM_003671	CCAAATAATGTCGGCTTACAA	CAGAATTGATGTGCTGCTAAA	CCGTACAGTGATGATGACGAA	CAAGATCAGCAAGAACCCGAA
8559	PRPF18	NM_003675	AACGGATATTATTAAATTCAT	CAGAATGATCTGAAAGTTCAT		
8564	KMO	NM_003679	TAGTGTTCTGCTTATAATTAA	CAGAGTTACCCTCTAAAGATA	AAGGCTATTAATATCATACTA	TGGGTACAACATCGAATAATA
8566	PDXK	NM_003681	CCCTGTATTAAGCAAGAATTA	CCCGGGCATGTTCGTCTCTCA	TCGAGTGACTTTCTAACCCAA	CCGGAGCTTCATCTAGTGATT
8567	MADD	NM_003682	CCAGGAAATGATCGACAGGTA	CTCAACAAGTTCTATACTAAA	CAGGAGGGCGTTAGTGGATCA	CAGACCCACTACTATAGTAAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
8568	D21S2056E	NM_003683	CAGGGAATTCAGCTCCAGTAA	TCCGAGCAGTGTGGTGGTTTA		
8600	TNFSF11	NM_003701	ATCCATGCTCTTGACCTTGTA	CAGCGTCGCCCTGTTCTTCTA	CAGATGGATCCTAATAGAATA	ACGGGTTGACCTTATGAGAAA
8601	RGS20	NM_003702	TAGCATGTTGTCAGTGGCCAA	TCGGTTTGAATACGTCACTTA	CACATATTCGATGATGCTCAA	CTGCTATATATTCACCATGTA
8612	PPAP2C	NM_177543	CATGGTGTTCTTGGCGCTGTA	ACCCGCGTGTCTGATTACAAA	TCGCTCGGACTTCAACAACTA	CCGGGTCAACTGCTCGGTCTA
8620	NPFF	NM_003717	TTGGGAAGAAGTGACATGTCA	TCCGCGGAGGAAGACAGCGAA	CCCAGAGGTTTGGCAGAAATA	CAGGGATCCTGGAGGAATGAA
8635	RNASET2	NM_003730	CCGGATTACTGGACAATACAT	CAGGATGAGGAAGTACAGACA		
8638	OASL	NM_003733	GCGGGTGCTGAAGGTAGTCAA	CAAGTACTACACACTCCACAA	CAGGTGCTCCTTAGCCAAATA	CAGCTGGAATTCCAAGGCCAA
8642	DCHS1	NM_003737	CACGGTATTGCTACCACCAAA	CTGGTGTTGCTTGAACCTCTA		
8644	AKR1C3	NM_003739	TAGAATGTCATCCGTATTTCA	CCGGAGTAAATTGCTAGATTT	CTGGGATCTCAACGAGACAAA	CACCCTAATTATCCATATTCA
8649	MAP2K1IP1	NM_021970	AAGAGCTAGCATATAGATGTA	TTGCATTGAGTGAGGAACATA	TAGCATATAGATGTAATTTAT	ATGCCCAGGCTTGCAGAATAA
8651	SOCS1	NM_003745	CTGTAGGATGGTAGCACACAA	TAGGATGGTAGCACACAACCA	CCCGCCGTGCACGCAGCATTA	CTGGTTGTTGTAGCAGCTTAA
8654	PDE5A	NM_001083	TCGGTTCAATGCAGAAGTTGA	AACAACAATCATTAGAAGTAA	TCGGATGTTTACTGACCTCAA	CAGAGATGGTGTGTTCTGCAA
8659	ALDH4A1	NM_003748	CCGGAAAGAGTGGGACCTGAA	CAGGGTAAGACCGTGATCCAA	CAACTTCTACATCAACGACAA	CAGGGTAAAGTGTAACTCAGA
8661	EIF3S10	NM_003750	GAGGATCTAGATAATATTCAA	CAGGAACATGAACAAATCAAA		
8663	EIF3S8	NM_003752	ACCGTGATTTCGAGTCCCATA	GGGCGTCATTGTCAAGATCAA	AACGAATGGATGAAGAATTTA	CCGCCGACGCATGATCAGCAA
8664	EIF3S7	NM_003753	TCGGAACATGTTGCAGTTCAA	CCGCCAAGTTTCAGTGATGAA		
8665	EIF3S5	NM_003754	CGGAGTTGACCTGATCATGAA	CACAATGAGTCAGAAGATGAA	CCGCATGAGCATCAAAGCCTA	TACGCGTACTACGACACTGAA
8666	EIF3S4	NM_003755	CACGCAGAACAAGACAGGGAA	GAGGTCATCAACGGAAACATA		
8668	EIF3S2	NM_003757	CAGATTAAGTATAACCGCGAA	AAGAAATAAATTGGTTTGGTA		
8673	VAMP8	NM_003761	CTGGTGCCTTCTCTTAAGTAA	AAGACCTTTCAGTATCCCTAA		
8675	STX16	NM_001001433	CTGGGATCAGTTATAATATAT	TCCAACGTAATTGGTCAGATA	ACCATCATTGATGTTAATTAA	CCGGATTAAGCAGAAGATGAA
8685	MARCO	NM_006770	CAGGACTTTGGCCATCTATAA	CCCAGGGATGTTCAGAATCAA	CAGGATTGTCGGCAGTAGTAA	CTGAAGTTTACTACAGTGGTA
8688	KRTHA7	NM_003770	CTGCATTAAATGGTCAATAAA	CCAGTGTTTCAGAATCTCCAA		
8692	HYAL2	NM_003773	TCCCTTGCCCTAGATAGTTTA	AAGGGCTCTCTTAGGCATGTA	CTGCCAGTACCTCAAAGATTA	AAAGATGTGTATCGCCGGTTA
8697	CDC23	NM_004661	CTGCAATAGCAAGAAAGCCTA	TAGGGACAGCTTGTATAATTA	TACGAGAAACTCAATCAACTA	ACCCATCTTAATTAAGCCTTA
8698	EDG6	NM_003775	TTGAAGTTCGATCATGGTAAA	CCGGCTCATTGTTCTGCACTA	CCGGAGCTTCCACCACCGACA	CAGCCGGCTCATTGTTCTGCA
8701	DNAH11	NM_003777	CACCGTCAAATGAAAGGATAA	CAGGTGGCTGTTAACATCTTA	GAGCTTGTTAACCATAATTAA	TACGTTGTACACGCTTTGCAA
8702	B4GALT4	NM_003778	CACAGTGAACTTGGGAATGAA	TACATATTAACTAATAATAAA		
8704	B4GALT2	NM_001005417	CCCATGGATGACCGCAACCTA	CAGAGGTTTACCAAGATTCAA		
8707	B3GALT2	NM_003783	ATGGAAGTATTTACAATGAAA	AACCGTGGATTTCATATTATA		
8708	B3GALT1	NM_020981	CAGAGTTAAGAGGAAGATTTA	CACACTGGATGTGATTATTAA		
8711	TNK1	NM_003985	AAAGAGCTACTATACATCATA	CCCTATTACATACATCTTTCA	ATCGGTCATGATGAACTTGGA	AAGGATCTAGTCTGCCCACTA
8717	TRADD	NM_003789	CAGGGTCAGCCTGTAGTGAAT	CCGAATGTTAAGCAATGATAA	CCCGAATGTTAAGCAATGATA	AGCAATGATAATAAAGTATAA
8718	TNFRSF25	NM_003790	GAGAACCACCATAATTCTGAA	CACAAGAAGATTGGTCTGTTT	CACCGTCCAGTTGGTGGGTAA	CGCGGTATTAAATCTGTGAAA
8720	MBTPS1	NM_003791	CACAGGAAGAATTGTAGATAA	CAGAACGGAGACAACATTGAA	CAGAACAGACTTCAACAGTAA	CAGGGATAATTTAAGGATGAA
8721	EDF1	NM_003792	CGGACGGGCCATACCCAATAA	CTAGGGCGAAATGAACACAAA	CAGAAGGACCTGGCCACGAAA	CACGGTGACGGTGCTGCGCAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
8722	CTSF	NM_003793	CCTGTCCGTCTTTGTCAATAA	CGGACATATGAGTCAAAGGAA	CACCTTTGTTGAATTGTGGTA	CCCAATCTCCGTGGCCATCAA
8723	SNX4	NM_003794	AACATTATGCAGATCAGTTAA	TACCTAGTATACATAAACATA	CCCATCCTTTGTAGAGACAAA	CTCGTTATTTCTAATGATGTA
8724	SNX3	NM_003795	ACCCTTCACATGGAAGATTAA	CAAGATGAAATAATAGATAAA		
8725	C19orf2	NM_003796	AAAGAGGGTTTCAAAGTTTAA	CTGGAAAGAATACCACTTTAA		
8726	EED	NM_003797	AAGGAATCTTATGATTATAAT	AAGCAACAGAGTTACCTTGTA	AGGCATAATTAGGATAATAAA	CTGAACGCCCTGATACACCTA
8727	CTNNAL1	NM_003798	CTGCAGAGGGTTTAAAGCTTA	CGGATGGGTCTCAGTTACAAA	ACGCTTATTAATCATAAAGAT	AAGCTTGGGAATCCCAAATTA
8729	GBF1	NM_004193	AAGAATATTTACATCATTCAA	ACGGGAACTAATTGAAATTAA		
8731	RNMT	NM_003799	CTGGTCTTAATTAACAGGTAA	CAGGGTGACTCTCCAAAGAAA		
8736	MYOM1	NM_003803	CACCAACTAATGACACTTTAA	CAGGTCTTTCACTCATATAAA		
8739	HRK	NM_003806	AGCGAGCAACAGGTTGGTGAA	ATACAGCTCTATATATATAAA	CGAGAAGGAAGTGGAGAGTAA	AGCGATCGTAGAAACACAGAA
8747	ADAM21	NM_003813	TACCACAAACATTGTCATTAA	CAGGAATATGTCGTCCACCTA		
8767	RIPK2	NM_003821	CAGGGACTTGATCATGAAAGA	CCAGGCTTAATTGCCCTACAA	CACAAGGACATCGACCTGTTA	ACGTATGATCTCTCTAATAGA
8772	FADD	NM_003824	TCCTAAGGTAATCCTATTAAA	CAGGACGAATTGAGATAATAT	CAGCGGGATCTCGTATCTTTA	AGCGGGATCTCGTATCTTTAA
8773	SNAP23	NM_003825	AAGAGGTTGTTACCTCAGTAA	TACCACATGAATTCAGATTTA	CAGGCCTATTAACATCATACA	CTGGCAAGGCTTATAAGACAA
8775	NAPA	NM_003827	CCGGGAATGCAAGTTGATGAA	CACCGAGTCGGTGAAGGAATA		
8778	SIGLEC5	NM_003830	TTGTGGCAATGTTAACATTAA	CTCGGAGATCAAGACAAGCAA	AAAGGTTGTTGTGAACATTAA	CAGGAACGGCATAGCCCTAGA
8784	TNFRSF18	NM_004195	CAGCAGAAGTGGGTGCAGGAA	CCCTGGGAACAAGACCCACAA	TCGGGATTCTCAGGTCATGAA	CAGGAGGGAGAGAGAGACACA
8787	RGS9	NM_003835	AAGCTATTGACCCTCAGGAAA	AACGATGGGCCTTCAACTTCA	CAAATAGGTGTTTGAACTGTA	CTGACACCAGTTTCAAATTTA
8792	TNFRSF11A	NM_003839	CCCAGTGTGTGTTCATTGTAA	TAAGTTTGTGTCGTTCCTTAA	CCCGCTAGGTGGTTAATTTAT	ACCCGCTAGGTGGTTAATTTA
8797	TNFRSF10A	NM_003844	CAGGAACTTTCCGGAATGACA	CAGGCAATGGACATAATATAT	CCGGGTCCACAAGACCTTCAA	ATCAAACTTCATGATCAATCA
8798	DYRK4	NM_003845	ACACGGCTCCTGAGAAATTTA	CAGATGCTTTCGGTAGAGAAA	CTGCATCACGGCGGAGTTGTA	CTCCATATGAACAAAGTGAAA
8802	SUCLG1	NM_003849	CAACATCTCTATGTTGATAAA	ATGGATCACGTAGACATGTAA		
8807	IL18RAP	NM_003853	AGCGGTAACCTGGTACAAGAA	ATCGTAGTGGATGAAGTTTAT	CCCAGTATCTTTGAACTACAA	CCCAGCCTAAGGAATGGTGAA
8808	IL1RL2	NM_003854	CAGGAGTCTACCAATGTGTTA	TAGGTGGTTTACCAAATTTAT	TGGGTCCAATAAAGTGGTATA	AAGGACTGTAACGAGATTAAA
8809	IL18R1	NM_003855	CGAGAAGAGATGAAACATTAA	CCGAGTCTTAATCTTCAGAAA	AAGAGTGAGATTGTCAGTGTA	TTGCTATTGCATAGTCTCTAA
8811	GALR2	NM_003857	CTGCACCTTCGTCTTCAGCTA	GACGGTTGATGTGGCCTGAAA	TACCAACCTGTTCATCCTTAA	CCCGCTCACGCGCGCCACTTA
8812	CCNK	NM_003858	CAGCCATATTGGCTCAATAAA	CTCAATAAATAGCTTCGGTAA	ATCCTGGATCTTTACTCACAA	AAGCAACTCAAAGGTGATAAA
8816	WDR22	NM_003861	CTGGTTAACTTGAGAAGCCAA	TAGAATTACTTTGGATTTGTA		
8818	DPM2	NM_003863	TAGCCTGATCATCTTCACCTA	CAGCATGTCATCCACAAGTAT		
8821	INPP4B	NM_003866	CTCCATAGATTTGAAACAGAA	ATCGATGTCAGTGACACTTGA	CCCGGAAAGTGTGAGCGGAAA	AACGATTTGCCGCAAACTGAA
8822	FGF17	NM_003867	CTGGAGGTGGCTGTCCTCAAA	CTGCTGATTCTCTGCTGTCAA		
8828	NRP2	NM_003872	CGCAAGTACTGTGGACAAGAA	CTGGTCTGTCATAAGACAGAA	CTCGTGATATTTGTAGGATAA	CAGGCTCTGAAGATTGCTCAA
8831	SYNGAP1	NM_006772	CAGAGCAGTGGTACCCTGTAA	ACGAACGAAGTCACAACCCAA	CCCGGCTGATGCAAAGCTTTA	ACGCTTGCCACTAAAGCCATA
8832	CD84	NM_003874	CTGGGACTTCAAGCTATGAAA	ACCCACAGAAATTATTATGAA	CTCAGAAATCTTCACAGTGAA	CAGAATGTGGGCTGCATATAA
8836	GGH	NM_003878	ATGCCGTAATAAAGTCATGAA	AAGCATTGATTTATCAGTTCA	TCAGTCCAATTTATACTGGAA	CTGGCTCTGATTCTTCATTAT
8848	TGFB1I4	NM_006022	AACTTTCAATAAAGCATATAA	CTCACTTTGTGTAATCTGAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
8851	CDK5R1	NM_003885	CACATGCACTACTGAAATTTA	CTGGTCATCAGTATTGTGTAA	TGAGCTGGTTTGACTCATTAA	CCGGAAGGCCACGCTGTTTGA
8852	AKAP4	NM_003886	CTGCCTTATCATGGCTAAGTA	CAAGACTCTCTTGGACATGAA	TACAGTGTCTATGCCGATCAA	GTCGGTGAACACATTCTCAAA
8875	VNN2	NM_004665	TGGGCGTTTGGTAAACAAGAA	ATGGCTACTTTCAATACAATA	AGGAGCTTTGCTGTCATTTAA	CAGCAATAACTTACCTGCTAA
8881	CDC16	NM_003903	AAAGAACTTCTTGAATCACTA	TAGAATATGGTTTGACCAATA	CCCATGCACTTCGGTCACGAA	ATAGTGGAATAAAGAAGGTAA
8882	ZNF259	NM_003904	GAGGAAGATCTCAGAAATGAA	CTGGAGGACATGAACAGAGAA		
8883	APPBP1	NM_003905	CAGGTATTGGTTCGTTTACAA	ATGGATTGTGATCATAGCTAA		
8888	MCM3AP	NM_003906	CAGGAGCATTTACGGATTTAA	CTGAGTGAAGATGGTCAGATA		
8893	EIF2B5	NM_003907	CTTGTATATGTTAATATTAAA	CAAAGTGAAGATGAAAGGTTA		
8896	G10	NM_003910	ATGAGAGAAGCTGAAACAGAA	CAGCAGAGAACTCTATGAATA		
8900	CCNA1	NM_003914	CAAGCAAGGGTTTGACATCTA	AAGCAATTAGGGAGAAGTACA	TTCGAAATATGAAGAGATATA	CACCGATGATACATACACAAA
8905	AP1S2	NM_003916	ATGGCATTAGATGGCTCTATA	ATGGCACATCATATACATGTA	AAGGGAACTTTAGTTAATTAA	CAGGCAGTATACATTTATTAA
8906	AP1G2	NM_003917	CCGCCAGGTGGTGTCCATCTA	CCCACAAATAAAGCCCAATAA		
8910	SGCE	NM_003919	CAGGTAAATGGTATCCCTGAA	TAACATTTAATACAAATTTAA		
8914	TIMELESS	NM_003920	CCGGCTCATGGGATCAGTAAA	CAGCCGCATCATCAAGAACAA		
8926	SNURF	NM_005678	GAGGTGGAAGTCCAAGTCAAA	CAAGAGGTGGTTAAAGCCATA		
8932	MBD2	NM_003927	ACCCTTCAGGTGTTACTAGAA	CTCGCGAGTGTAACTTTCATA	TGGAAAGATGATGCCTAGTAA	AAGATGATGCCTAGTAAATTA
8936	WASF1	NM_003931	TACACTCAGAAAGTACATTTA	TTGCTTGCCTATAGGAGTTAA	GCCCTATAACCGATTAATTAA	CAAGAACGTGTGGACCGTTTA
8938	BAIAP3	NM_003933	CTCGCCTGACTCCATCCAGAA	CAGCCAGAGGACCCAGGTGAA	GTCGACCTTGCTGGACATTAA	TGGGATCATGACGACGATGTA
8940	TOP3B	NM_003935	CACGGAGAAGAAAGAAGCTAA	CACGGACACAGACATCTGTAA		
8942	KYNU	NM_003937	CCACATGTAACTAACAATAAA	CAGATTTAAGATGGATAACAA		
8945	BTRC	NM_003939	CTGGTTTCAGGTGGAACTTAA	CTGGAGGCAGATGACATCTAA	CTGGGCTAGAATAAATGTAAA	CAGGATGAGCAACAACAGTAA
8972	MGAM	NM_004668	TCGGCATGATATGAATTGGAA	CTGGCCCATATTTAACAGAGA	CCCAATGGAAACGGAACTAAT	TGGGAGGAATAATATACCTAA
8976	WASL	NM_003941	ATGCTACATATGAATGTTGAA	CACATTGAGTAATATGCATAA	CAGATACGACAGGGTATCCAA	AACCTTAATGTAATTTACTTA
8986	RPS6KA4	NM_003942	CGGCCAGGAGTTCGCAGTCAA	AAGGAGATAGGTGGCTCCTAA	CGCCACCTTCATGGCATTCAA	CAGGCTGTGCCTTTGACTTTA
8989	TRPA1	NM_007332	CAGTAGACAGTTGCACATTAA	CCACGAATTCATATCTAATAA	CACGAATTCATATCTAATAAA	CTGGTTCTAACTTTCAATTTA
8992	ATP6V0E	NM_003945	AACGTTAACAGCACATTTGAA	AACCCTCTCTTTGGACCGCAA		
8993	PGLYRP1	NM_005091	CTGGTGCGACGTGGGCTACAA	CAGCTTCATGGGCAACTACAT	TGGCATCAGCTTCATGGGCAA	GAGGTCCAACTATGTGCTCAA
8996	NOL3	NM_003946	CCCAGTACCGCTGGAAGTGAA	ACCCTGGAGATCCCAAACCTA		
8999	CDKL2	NM_003948	TGCGAGAAATCAAGTTACTAA	TCAGGCATTTATAACATTAAT	TTCTACGGACTTTAAATTAAA	ATGATGTGTTTAGGTAATCTA
9002	F2RL3	NM_003950	CAGGCTGGTGCCCGCCCTCTA	ACGCGTGAAACACAGAAGAAA	CACATTCACGATACTGTGCAA	AAGGCTGTACTGGGTCGAACA
9015	TAF1A	NM_005681	AAGCAAGATCACCAAATCTTA	CCGGATGCACTAAGAATATAA		
9019	MPZL1	NM_024569	CTGGTTGCAGATAACGAACTA	CCAGTCATATATGCACAGTTA	CACCTTCTTTATAAAGCGTCA	AAGGCATTACTTAGAGATTGA
9025	RNF8	NM_003958	CAGCCTGTGATAGGCATTCAA	ATGGACAATTATGGACAACAA		
9026	HIP1R	NM_003959	CTCCGACATGCTGTACTTCAA	AAGTGTTCTGTTGGCAATAAA		
9028	RHBDL1	NM_003961	CCGCTGGTACTTCTACCGTCA	TGGGATGAGATGTCCCTACAA		
9038	PNR	NM_003967	CAGGCTCAGCAGATTACCACA	CCCACTGGTCTTTGACATCTT	CTGCCTCATTATGATCAGCTT	CACCATAGACACGATGGTCGA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
9045	RPL14	NM_003973	CAGATTGATAGTAGGATTATA	CACCAGAAGTATGTCCGACAA		
9046	DOK2	NM_201349	TGGGTGAGTCACCATCCCAAA	GACAATGTTGTACTAAAGAAA	CAGCAGACGTTTGGAAAGAAA	CAGATTTCTTGGTGGCATTAA
9048	ARTN	NM_057090	CTGGTGTTGATAGAGATGGAA	CCGGTGGGTGATGGATATCAT	CCCGAACAGGTGAAGGGACAA	CAGCATTTGAAGGACACATAT
9050	PSTPIP2	NM_024430	ACGAATAAACTTCTTCCGGAA	CTCAGTGGTGCAAGATTTAAA	CCGGCTAGTGCTTCTGTGATA	CCACGTTATGTCAGCAATGAA
9053	MAP7	NM_003980	AAGCTGTTGTACGGCGCACAA	AAGGGCTGTATCTCCATCTAA	GTGCTCCTTCTTAGCAATCAA	CAGGCATATGGTCTTTAGTAA
9056	SLC7A7	NM_003982	CCCTTCTTGCTTAAATCCATA	ATCAGATATTTGGAATATTTA	TAGAGAGACATGAAACTATCA	CAGGTGCTGGATGACAATAAA
9064	MAP3K6	NM_004672	CAGGAACTGAATGTGGATTCA	TACCAGACAAAGCGTATTAAA	TCAGAGGAGCTGAGTAATGAA	CACCATCCAAATGCTGTTGAA
9068	ANGPTL1	NM_004673	GAGGCGGGTCATACTCCTTAA	CAGAAAGTTTGGACAGCTTTA	CTCGTGTTACTCAACTCTATA	CGGGAGATAGATGTTCTGCAA
9075	CLDN2	NM_020384	AAGGCTAAGGGCTATAGACAA	CCAGACTAATTTGTGCATGAA		
9081	PRY	NM_004676	AAGGACTCAGAGAGACATGAA	AAGAAGGATCTTAAAGACTCA		
9086	EIF1AY	NM_004681	TTGGCTTTCATGAACAAGTAA	ACCATAATATTTGCTGTTAAA		
9088	PKMYT1	NM_004203	CTCCTACGGAGAGGTCTTCAA	CTGCCTGGCCGTGTCTAATAA	CTGGGAGGAACTTACCGTCTA	CCGGCCAGAGTCCTTCTTCCA
9091	PIGQ	NM_004204	ACGCTGCTGTGTGCTCCTGAA	CAGGTGTTGCTGTCACAGCTA		
9092	SART1	NM_005146	CTCAACCTTCATATTAAATAA	CCCGTGTACAGTGACCCAGAA		
9096	TBX18	XM_496819	TCGCCTGAAGATAGATAGGAA	CAGCAATGCCTTCGCCACTAA		
9101	USP8	NM_005154	CACGGAAAGAAGCACTTGTAA	AAGGCTCGTATTCATGCAGAA	CAGGTTCAGGCAAGCCATTTA	CAGGGTCAATTCAAATCTACA
9110	MTMR4	NM_004687	CCGGCTGCATATCAAATTCAA	AAGAGTGGCTCTCACGGCTAA	TTGCCATAGATGTAACCTAAA	TCGGCACTGGAGAGTACCAAA
9114	ATP6V0D1	NM_004691	CACTTTCATGTTCCTCCCTAA	CCGCGCCTTCATCATCACCAT		
9118	INA	NM_032727	CAGCTAAATAATCTTACTCTA	CAGCCTATTCCTGAACTATAA		
9126	CSPG6	NM_005445	AACCGGTTACCAATCGATAAA	TACCCAGGAACTGTAAATTTA	GAGGACTAAGTTGGAGCTTAA	ATGGAGGATATCGAACGCCAA
9132	KCNQ4	NM_004700	GACGATTACATTGACAACCAT	CTGGTACTACTATGACAGTAT	CGGGCATCTCTGAGACTCAAA	CCGCTCCATCAGGATTCTCAA
9136	RNU3IP2	NM_004704	CTGGAGGAAACTGCACAGGAA	CACTCTTATCCTCCTTATTTA		
9138	ARHGEF1	NM_004706	CAGCAGCTCTGAGAACGGCAA	TCGGAAAGTGCTGTCCCTGAA		
9140	APG12L	NM_004707	ATGGTATGTAGTAGAATTCAA	CAGCTTCGATTTGAATGACTA		
9141	PDCD5	NM_004708	CAGAACAAGGTTTAATAGAAA	CAAGTCTAGGACAGAAGTTAA		
9146	HGS	NM_004712	TACGAGCAGCTGAACAGGAAA	CACGTCCGGAGTAACACTACA	GCACGTCTTTCCAGAATTCAA	CCGGAACGAGCCCAAGTACAA
9149	DYRK1B	NM_004714	ACGGAGATGAAGTACTATATA	CTCGCTGAACCTGACCCGGAA	CCGGACCTACCGCTACAGCAA	CACGGAGATGAAGTACTATAT
9150	CTDP1	NM_004715	CCGAATATTATCAAGGGATGA	CCCGACAAACTTCCCGATAGA	CTCCATGGTTTGCATTATTGA	CCGGCTGTACGCACACACCAT
9156	EXO1	NM_003686	GAACGAGTGATTAGTACTAAA	AGGGTTAAATCTCCCAAGGAA	CAGATGTAGCACGTAATTCAA	ATGGATGTACTTTACCTTCTA
9159	PCSK7	NM_004716	CAAGCGCAGCGTCCACTTCAA	TAGCTATGACCTCAACTCTAA	ATGCCTTTCTATGCAGAAGAA	TCGGAGCATTGTGACCACTGA
9169	SFRS2IP	NM_004719	CACGAGGAAATGATCGGTACA	ATGGTTCTCAGCTACCTATAA	CTGGACAGGATTCTAGCCTAA	AAGGAGGTGATCCATTGGAAA
9170	EDG4	NM_004720	CTACCTGAGTCTGATTCTTTA	AAACCTTTCTTTACACTCTAA	GACCATCGGCTTCTTCTATAA	CCCGCGAGTCTGTCCACTATA
9181	ARHGEF2	NM_004723	CTGCAATGTGACTATCCACAA	CCGGCGGGACCGAGTGCTTTA	CAGCGATTGGTCAATCTCTAT	CAGCACCCTACTGCCCTTTAA
9183	ZW10	NM_004724	CTCGCCTATCAGACTTTACTA	GCCAGTGAATATATATTGCAA	TACCACGAAGTGATGAATTTA	ACCGGTGAATTTACAGACTTA
9187	SLC24A1	NM_004727	CACTGACTTACTACACCTCAA	CAGTGACATTACAGCAACCTA	CACAATGGGCATGGATCAGAA	ACTGCAGATTATGATGGTAAA
9196	KCNAB3	NM_004732	AACCCTAGGGAACATCCTCAA	AGGGAACATCCTCAAGAGCAA	CCGAGCGAGGTTTAAGCCGAA	TCGAGTAGTGATACGCATGAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
9200	PTPLA	NM_014241	AAGTGAGTTCAAGAATCTTTA	CTGGTGAACTTCTTACAATAT	CACTGTTTAATTGGAATTGTA	ACCACTTGCCATACTTCATTA
9201	DCAMKL1	NM_004734	CACCTTTAGGTTACCTATATA	CAGTGGAATGTGACCAGTCAA	CCGGAAGTGATAACACGCAAA	CAGGTTTATAACTTCGACACA
9211	LGI1	NM_005097	GCCGTGTGTACTTGTACCAAA	TCCCAGCGTCCTGTAATTTAT	AAGCAACACAATTATTCACTA	AAGATTCATTGGTGATTCCAA
9214	TOSO	NM_005449	TACCGTGGTATCCACCACCAA	CAGGTAAGCTGTAGGCATGTA	CCGAGTTACTCTGAAGCAATA	CAGGGTTGGGTCTTACACAAA
9215	LARGE	NM_004737	CACGGCCAAGAACCTACATTA	ACGGCCAAGAACCTACATTAA	AAGGGTTATCATCTTACTGCA	ACCAGCGAAAGCTGCATTTAA
9219	MTA2	NM_004739	TAGACGGATTGAGGAGCTCAA	ACGGCCTTATGCTCCTATCAA	CAGCCAAGCGTCAGAAACTAA	ACGCCAGTTCTCAGAAATAAA
9220	TIAF1	NM_004740	CAGATTCTTATGCACGCTTGA	CACGCTTGAGTCCGAGACTCA	TACCCGATGTATGGAAATAAA	AGGAGTGTCATTTGTCCCTAA
9228	DLGAP2	NM_004745	CAGGATGGAATTTCACAGGAA	CTCATTATTACTCAAAGTAAA		
9229	DLGAP1	NM_001003809	CACGAGGTAAAGATGATGAAA	CAGGAAGAAGGACCACTTTAA		
9244	CRLF1	NM_004750	CTGCTGGTCCAAGAACATGAA	CTCAAGGATTTCCTCTTTCAA	AACGCTGGATATCCTGGATGT	AACACCAACTACTCCCTCAAG
9247	GCM2	NM_004752	ATGGATTACCATTGTACTAAA	ACCCTGGTTATACAAATTCAA		
9256	BZRAP1	NM_004758	CCGCCGTCTGGTGGTCCTCAA	CAGGTCTTCCTAGCACGTTAT	CAGAGCTAAATGGCTCCTTAA	CACAGTGAGTATGTAACTTGA
9263	STK17A	NM_004760	TGCCTAAATACTAGTAACATA	TACTAGTAACATATCAGTGAA	TCCATTGTAACCGAAGAGTTA	AACCAGGATATTTAACAGGTA
9267	PSCD1	NM_004762	AAGGATGAGATAGCAGAAGTA	CAAGTTCTTGTTGGGCTTTAA		
9276	COPB2	NM_004766	CAGTACGTATTTGGCATTCAA	CCCAGTCAGGTTTCAAGGGTA	CAGGTTTCAAGGGTAGTGAAA	ACGATTCTTCAGAGTATGCAA
9278	ZNF297	NM_005453	CCCGCCCATTCTACTACTCAA	CAAGGTATTTCCAGAACTAAA		
9282	CRSP2	NM_004229	CGGGTTGGGACTTAACTTTAA	CGGGTGAAGTTTCGTGTTGAA	CACGTTTACCTGACATATGAA	CACGACAAGGTGAATGCACAA
9287	GPR58	NM_014626	CTGCCCAGTGATGTTCAACAA	CACCTTGTTTATGGCAGGTTT	CAGGATCCATATTCATCACAA	CACATGTAATCCGTTAATATA
9289	GPR56	NM_005682	AACCGACATGCTGGGAGATTA	CACCATCAAGGTGCACATGAA	TCGGCCGCCCATCATGGTTAA	GAGGGTCTGGCACATCCTTAA
9290	GPR55	NM_005683	CCGAGAGTTTGGACCCACATA	TTGATTAATCTGATTCGCCAA	CTGAGAGGACCTGATCATGTA	CCGGTTCTTGGCCATCCGTTA
9293	GPR52	NM_005684	CAGGAAGCACAAGAACCCAAA	AACGGGCTAATTCTTGCTCCA	CAGGTGTCCACGAGTCATTAA	AACCTGGCTTGCAGTAAGTAA
9294	EDG5	NM_004230	TCCAGGAACACTATAATTATA	AGGCGTGGCCTTCGTAGCCAA	CACCCTGAATTCCCTGCTCAA	ACCCACGTTTCTGGAGGGCAA
9296	ATP6V1F	NM_004231	CAGTGTCATTGTTGATGTTAA	CCGGCAATTTCTAAACCGGGA		
9311	ACCN3	NM_004769	CACCCGGATGGGAAAGTGCTA	TGGGAAAGTGCTACACATTTA	CTGGGCAGCCATCGAACCCAA	CCCAAATAAAGTCCTAATGCA
9312	KCNB2	NM_004770	CTGCGGCTTTGTCCAGTTCAA	CCCAATTATTGTGAACAATTT	CCCAGTTGACATAACTGTGAA	GCGGTTAATAATGCCTGTGAA
9319	TRIP13	NM_004237	ACCCAAATTGATCAGATTAAA	CAAGACTATTTAATGGATGTA	TTGACACAGAATTAAAGGTTA	GAGGATTCACATTAATATAAT
9322	TRIP10	NM_004240	TTGGAAGAACGCAGTCGTGAA	CACCATTGATGTACATACTCA	ACGGCTGAAATTGGAAGTGCA	ACGGCTAGACCAGGATATCAA
9329	GTF3C4	NM_012204	CAGGTCAAGCATAACAACGAA	CAGGTAGATTTAATAGACCTA		
9332	CD163	NM_004244	CCCGCCCAGAAGGAACTTGTA	CACATGGGAGATTGTCCTGTA	TCGCATTATTCTTCTTGACTA	CGCATTATTCTTCTTGACTAA
9333	TGM5	NM_004245	CAGGAGTATGTCATGAATGAT	CTGCCTGAAGCTGCTAGACAA	CTCCCAGTTCAAGGACCTCAA	CAGATCCAAGCTAATATGAGA
9337	CNOT8	NM_004779	ATGGCTTTCTTTAGGATGAAA	ATGCTTGTAAATACTATTTAT		
9343	U5-116KD	NM_004247	CTGATTGAAGGTGTTGATCAA	AACGCCTAATAAGAAGAACAA		
9349	RPL23	NM_000978	TGCGAAATTCCGGATTTCCTT	TTGCATGATTCTCCAGTATAT		
9356	SLC22A6	NM_004790	CACCAGAACCACATCATTAAA	CCGGAAGGTACTCATCTTGAA		
9360	PPIG	NM_004792	CAGGAAAGGAGTAGAAGTAAA	CTGGATAATTTGTACTGCTAA		
9361	PRSS15	NM_004793	CCCGCGCTTTATCAAGATTAT	CAGCCTTATGTCGGCGTCTTT	CCGGGACATCATTGCCTTGAA	TAGAAGCTATTTAATGATTAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
9364	RAB28	NM_004249	TTGGGAAACAGTACAAACAAA	ACCCTTCAAATTTGGGATATA	CAGGGCAGAAATAGTGAAGTA	CAGCGTATTGTCAGGGCAGAA
9368	SLC9A3R1	NM_004252	CAGGGCATCTGTTATCCTGAA	CAGAAGGAGAACAGTCGTGAA	CACCAGAAACGCAGCAGCAAA	AGCGAGGAGCTGAATTCCCAA
9369	NRXN3	NM_138970	CTGGAGGGTCATATATACAAT	CATGGCTTACTTGTTCCATAA	CAGGATTATAAAGAGATATCA	ACCAGTGTGCGTGTAACTTTA
9371	KIF3B	NM_004798	CAGAAATGCATGGGTAAGGTA	TTAGGGAAATAGCTTCTTTAA	CAGAGAATTCACCGAATCCTA	AACGCTAAGGTGGGTAGCCTA
9373	PLAA	NM_004253	TAGGTGTTGATTCTCAAATAA	AAGAGTGTGAACACAAATTTA		
9392	TGFBRAP1	NM_004257	CCGCCGATCGTCAAGAGGATA	CAGGTACATAGTAATCCAAGA	CACCCACTTAGCTGTGCTGTA	CACAGAGGTAGCAAATGGCTA
9394	HS6ST1	NM_004807	CCCGTACAACCTGGCCAACAA	CCGCGCGGCAGGACCATGGTT		
9404	LPXN	NM_004811	ATGGAAGAGTTAGATGCCTTA	CAGCTCGTGTATACTACCAAT	CTGCTTAATAGTCTTATAGAA	ATGACTAGGCTGATAATCTTA
9409	PEX16	NM_004813	CCGGACCATCCTGCTGCTCTA	CCGCGGAAGTTAAGCAACCAA		
9424	KCNK6	NM_004823	TCCGTCTGTGTCTCTCAATTA	CCGTCTGTGTCTCTCAATTAA	CTGGTTGAGCTCAAATCCCAA	ATCATCATAATACAACTTCAA
9427	ECEL1	NM_004826	CAGCATCCAGCTCTCAGTTAA	CCGGCTCAAGTACACACATGA	CAGGTGCTGACTGACAAGCAT	CTGCAAAGTCTGGTCAATAAA
9429	ABCG2	NM_004827	ACGGATTAACAGGGTCATTGA	ACCGAGCTCTATTAAGCTGAA	CTGGCGAAGAATATTTGGTAA	CTGGTCTAATTTATTAATCTA
9435	CHST2	NM_004267	ATCGTAGTGTGTTTAAATAAA	CCCTGTGGTGATACCTATAAA		
9436	NCR2	NM_004828	CAGGCTCTCAGGCACAATCCA	CAGGACATTACTGGTGTAGAA	CACGGGCAGTCTCTACGAGAA	ACACACTTTGTGAATAATAAA
9437	NCR1	NM_004829	TCGGTTCATCCTGGACCCGAA	CTGGATCTGGTGGTAACAGAA	ATGGTTGTATATTCCTAATAA	AAGCATGTTCTTACTGCTCAA
9440	CRSP6	NM_004268	TCAGTTCGTAATGGACCTGAA	GTCCAAATTCCTAGTGATTTA	CAGGTACATGCAGTTCAGCAA	CAGCCTACTCTAAATTATTGA
9443	CRSP9	NM_004270	TTGGAAAGTCAGGGCATCGAA	TAGCATCATATATTAGTTCAT	ATCAAGGAATATACGGATGAA	AGGCAGTAATTTCGCTGTATA
9446	GSTO1	NM_004832	GCCCTGCTTACTAGTGAGAAA	CAGGCATGAAGTCATCAATAT	CAGGAGTCAGCAATAAAGCTA	CAGCAATAAAGCTATGTCTGA
9448	MAP4K4	NM_004834	TCGGAGCTGCACCGAGGGCAA	CAGGACTTTAGTTAGAATTAA	AGGCAAGATCCTACCCGGAAA	AACCATTAATGTTTAATTTAA
9453	GGPS1	NM_004837	AGGGATGATTATGCTAATCTA	TACACTCGTAATACCCTTAAA		
9455	HOMER2	NM_004839	CGGAGCCAAGGTGATCATAAA	CAGCACAATCACACCGAATAT	CAGAACTAGGTCTACCTTCAA	ACCGAATATGACCTTCACCAA
9468	PCYT1B	NM_004845	AAGAGCCATGATCTAATTCAA	CACCATAATACTCCTCTGAAA		
9469	CHST3	NM_004273	CAGGTTGACTTAATTTATTTA	CAGCTGTATATTCTAGTCCAA		
9472	AKAP6	NM_004274	CTGCGGATGATTGCAAGTCAA	CCGGGAGACTTGCAATCTGAA	CACGTTTGTCACTGCCGTTTA	AAGCATGTGGATGTACATCTA
9479	MAPK8IP1	NM_005456	ATGCAGTTTATTGTAATATAT	CCGGCTCACCGTGCACTTTAA	TGGCATCAGCTTACAGTGCAA	CTGGAGGAGTTTGAGGATGAA
9493	KIF23	NM_004856	CAGAATAAACTCTGGGTTAAA	CACCTTTGCCGTCATGCGAAA	CAGAAGTTGAAGTGAAATCTA	AAGGCTGAAGATTATGAAGAA
9498	SLC4A8	NM_004858	TGGGACCAGTACAATTCTCAA	AAGCATCATCATCAGAATGAA	AGCCGTCATTATTAACAGGAA	GACGGCTATCTTAAAGTTTAT
9508	ADAMTS3	NM_014243	CAGGAAGCTTGGGTACCTTAA	CCGCTCTAGCCTGACATATAA	AACAATGTGATACGTAAATTA	TAGGCAAATTCCAGATAGTAA
9509	ADAMTS2	NM_014244	GACAGGCAAGTTCATCTTAAA	CCGGGTCTCACTGACGTACAA	CCGCCGGAGGCTGGACCACAA	CAGGCGAATGGGAGCCATGTA
9510	ADAMTS1	NM_006988	CGGCAGTGGTCTAAAGCATTA	TAGGATAGTTAGTGAGGATTA	CTGAGCAGTGATATAGCATAA	CAGCAACGTGAAATAACGCAA
9516	LITAF	NM_004862	CAAGGTCGTAAATGCATGCTA	CTGGGCCTGAACATAATTTCA	TGCCAATGTAGTCTCACTTAA	GCCAATGTAGTCTCACTTAAA
9520	NPEPPS	NM_006310	CAGACCAATGGGTGAAGTTAA	CATGGTGATGGCACTACTTTA	GAGGGATTTGCAGTTGATAAA	CTGGGAATGGTTAAACACAAA
9522	SCAMP1	NM_004866	AACACTGTTGTTAACATCTAA	CACCACATTTCTTATATTAAA		
9524	GPSN2	NM_004868	GTGGATGGCCTATTACATCAA	CTGGATCGGTTTCGCCATCAT		
9542	NRG2	NM_013982	TTGTCTTATAATACTAGCTAA	AGGGAAACTATTTATATGTAA	CCGAGACATTCGCATCAAATA	ACCCGTGGTGGTGGAGGGCAA
9554	SEC22L1	NM_004892	TAGGACATTCTCAAATTTCAA	CCACAATTTGCTAACATTTAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
9555	H2AFY	NM_004893	CTGGCTGTGGCCAATGATGAA	AAGGCTTTGGTTTCCAGTTTA		
9559	VPS26	NM_004896	CTGCATAATGTTGATTATAAA	CACCAAGGAATTAGAATTGAA		
9562	MINPP1	NM_004897	ATGAAATTCTTCCTACTTATA	AAGTCGGAAAGTACAATGAAA	CCGAGTGCAGATGTTATTAAA	CACGGTCAAACAGATCCGCAA
9570	GOSR2	NM_004287	TTGGGAGTGATTGTGGTCTAA	CAGGACAAGTACTTTATGATA	CAGCATTCCCACAGCCTGCAA	AACGAAATCCAAGCAAGCATA
9575	CLOCK	NM_004898	AAGGAGCCATCTACCTATGAA	GACACGCATGATAGAAGCAAA	ATCGGCAACAAGAAGAACTAA	ATCCAGCAACTTGCACCTATA
9580	SOX13	NM_005686	AAGGAACTCTATGGAAGCCAA	CACCATCAAGTCAGAGGAGAA		
9586	CREB5	NM_004904	TAGCTTTAAATACATCATTAA	CAGCAATAAACTTACAAGTAA		
9589	WTAP	NM_004906	AAGGTTCGATTGAGTGAAACA	GGGCAAGTACACAGATCTTAA	CAGACTAAAGACAAACTGGAA	ATGCAAGAGTGTACTACTCAA
9598	CSAG2	NM_004909	CAGCTGTGTGGTCAAACAGTA	CTACCACAAGACTAACATAAA		
9605	C16orf7	NM_004913	CTGGGTGTATCTCAGAGATAA	CGCCGTGTATACTCCGATGAA		
9609	RAB36	NM_004914	AAGACAGTACAAAGCATATAA	GTGGCCATTCTTGTAGTTATA	CAGCTCAGCGATTGCCAAATA	AGGCACTGTGGTGATCCCATA
9611	NCOR1	NM_006311	CCCGGTGGTTTCCTAGAAACA	CCCGCTCACCAGGGAGTATAA	AGGCAATTCAGTGGACTATAA	ACCGCAGTATTGTCCAAATTA
9620	CELSR1	NM_014246	CACCATGATGGAGCTGGACTA	TGGCGTTTCCTAAGTACGAAA	CGGGATCCTGGATGTGATCAA	CGCCAACAGTGTGATTACCTA
9625	AATK	AB014541	CCGGTTCCGCTGAGATCAGAA	CTGACTCAGCTAGACCCGTAA	TCCGCTGAGATCAGAAGGCAA	CTCCAACGTGTCAGCCAACAA
9629	CLCA3	NM_004921	CAGAGTACTTTCGGTTCTGAA	CCCAGCGAAGAAATGGATAAA	GAGAGCTACATTATAAGAATA	TAGGCCCGAAATGACTAGCAA
9636	G1P2	NM_005101	CAGGATCAAGGGCCGGAAATA	CCGGAAATAAAGGCTGTTGTA	AAGCACCGTGTTCATGAATCT	AATGCGACGAACCTCTGAGCA
9638	FEZ1	NM_005103	CACAGATAAACTCATCCTGAA	ATGGAGGACCTCGTAAATGAA		
9640	ZNF592	NM_014630	TCAGACTATATTTCAAATAAA	CCCACTAAAGAGAGTTCTAAA		
9648	GCC2	NM_014635	ACGGGAAGACTTAGAGTTTAA	ATGGATAATTTCCATAAGAAA		
9673	KIAA0446	NM_014655	AGGGTGATGTGTGTATAATTA	CCCGTGGTGGGCACAGTTCTA	CACCATGGAGGACAAACGCAA	CCGGAAGTTTGTAGCTGACTA
9674	KIAA0040	NM_014656	ACCCTGTGAATCATAATTTAA	CCGAGTGATCTTCTCTTCTAA		
9679	FAM53B	NM_014661	ATGGCGAGACCTGGACAGGAA	GACAAGAAGGTCGGTGTTAAA	CGGGAGATGCTTCCTTCTGTA	TACTTGTACTGTGTAAATAAA
9688	NUP93	NM_014669	TCGAAGTTTCCTGAACATTAA	AGGGATGAGAAAGATAGTCAA		
9706	ULK2	NM_014683	CAGCCTGAGATACGTGCCTTA	TAGGATAATCGGTACAGTTAT	ATCGGTACAGTTATTCTTAAA	ACCGGGAAGTTATCAGATCAA
9716	AQR	NM_014691	ACGATTGGAATTAGAATTAAA	CAGGATGGATTTAGCCGACTA		
9717	KIAA0420	XM_032693	ACGGTCCACCCTGAGAATGAA	CAGGCGGAAGTTCCTCATCTA		
9719	ADAMTSL2	NM_014694	CCAGGAGTTCTTCTCGGCTAA	CACCCTCAATGAGACTGTGAA		
9720	KIAA0565	XM_113947	TAGTCTTGTAGTATGTTTGAA	TAGCGTTACAATAGAATAGTA		
9722	CAPON	NM_014697	ACGGTATGAGTTTAAAGCCAA	CAGCAATATCTTCAGGTGTAA		
9726	ZNF646	NM_014699	AACAATTTATTTAAGTTTAAA	CGGGAGCTAGAAGACAATGAA		
9727	RAB11FIP3	NM_014700	CACATGAAATATATATATATA	CCCGTCCATCCTGGAGGTCAA		
9728	KIAA0256	NM_014701	AAGGATGAGAATATTCAACAA	CCACATAAGTTTATAATTTAA		
9730	VprBP	NM_014703	CAGAGTGAACTCAACAACCAA	CAGGGTGTTACTCCTCACCAA		
9733	SART3	NM_014706	CAGCAGCTGGAGAAATATAAA	ATGGAGTTGATCATCAAGTAA		
9735	KNTC1	NM_014708	CAGCACATTAAAGCTCACGAA	CAGGCAGTATATCCAGTTAGA	TGCTCTTAATTTCGAAATTAA	TCCCGTGGATCTAGAATATCA
9737	GPRASP1	NM_014710	TGGGTCTATAGATGTAATTAA	GGGTCTATAGATGTAATTAAA	CTAGCAGTAAATCCAGACCAA	ACGCCCTAAGAGTAAGGCCAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
9744	CENTB1	NM_014716	CACCGTGAGCCTGAACCACAA	ACGGGCCAGCAACGCATTTAA		
9746	CLSTN3	NM_014718	CCCAGTCAAGTTCCTCTGGAA	CAGGTGAAGCCCACCTGTAAA		
9748	SLK	NM_014720	GACCATTAACTGAGTCCCAAA	TCGAATGGCCATGTTTAAGAA	TAGCATCTTGTGATCACCCAA	CCAGATCAGGACCGTGATAAA
9751	SNPH	NM_014723	CACGATGTTCATCCAGGCCAA	ATGAGGGTTCCTAAACCTTAA		
9761	KIAA0152	NM_014730	AAAGATATAATTAACGATCAA	CAGGATTGTGCTGGCAGCCAA		
9767	PHF16	NM_014735	TCGGTGGGCCTTAGTCTGCAA	CACGCTAGCTGTGGACTTTAT	CACCAATAGGTGGGTGAAGAA	ACCATGATTATCAGACACTAA
9775	DDX48	NM_014740	CCGGAAGGGTGTGGCCATTAA	CCCATAAACTCTATACTTCTA	CCGCATCTTGGTGAAACGTGA	AAAGAGCAGATTTACGATGTA
9780	FAM38A	NM_014745	CTGCGTCATCATCGTGTGTAA	CAGCCTTGTATGCACCGTCAA		
9781	RNF144	NM_014746	TGCGATGACCACAACAAGGTA	AAGGATTAGAAACCGCAATTA	GTGGAGAAAGTGTATTCTTTA	CAGGAATAACTGTCCAAATTA
9783	RIMS3	NM_014747	CTCCAGTATCCTGACATGTAA	CAGGGAAGAATCATCTCCAAA		
9784	SNX17	NM_014748	ACGGAAGTTGCAAGAGTTTGA	CTCCGCCTACGTGGCCTATAA	CAGCGAGACTTTCAACAGTTT	CTGGCCCTCGATGCCAAATTA
9797	TATDN2	XM_376203	ACAGTTCTAAAGGGCTTTATA	CAGCCATGTGTGGATCTTGAA		
9806	SPOCK2	NM_014767	CACATGCATAAAGGAAATCAA	CACGTTTGTGTGTCCTTGTAA		
9810	RNF40	NM_014771	CAGCTTAACTCTGGCTACTAT	CACGCTGGCCCAGGTACGCAA	GCGCATCGAGTTTGAGCAGAA	AAGCGGAAGCTTCGAGAAGTA
9811	KIAA0427	NM_014772	CCCGGATTAGTGGGAGATCAA	CAGAACGAGACTGGCAAATTA		
9815	GIT2	NM_014776	CCCGTTGATTATGCAAGGCAA	CAGCGTTGAGAGTCAAGACAA	CTGCCTATGGCTGAAACTATA	AAGCATCGTGCAATAAGTGAA
9818	NUPL1	NM_001008564	AAGGTACAAGAAGATATTAAA	AAGCAAATAATTCACATATAA		
9819	KIAA0669	NM_014779	CAGGATTGCATTTAATAGATA	CTGGCATATTTCTAACACTAA		
9825	SPATA2	NM_006038	CACAATGTTAAGGGATTTATA	CCCAGTTCAATGGATACTAAA		
9826	ARHGEF11	NM_014784	CACTTGTATCTCCTTAGTTAA	AAGCGATTCAATCCTGATCAA	CTGGAGGATCAGCAAGGATAA	CACAACGACTCTCGACCGGAA
9830	TRIM14	NM_014788	CACCGAGAAGCTCAAGGCTAA	GCGCCTCACCTTAGCATTCAA	CAGGTGCCTATCACTGAGTAA	AAGCAGAGCTGCGTAAAGTTA
9832	KIAA0555	NM_014790	CTGCATTTAATGAAACATGTA	CACCTGCTTGAAAGAAATTAA		
9833	MELK	NM_014791	CACCTCGATGATGATTGCGTA	AAGACTAAAGCTTCACTATAA	CTGGATCATGCAAGATTACAA	CGGGTTGTCTTCCGTCAGATA
9834	KIAA0125	NM_014792	CAGCATGGTGACTATAGTTAA	CAGGAACAGTTCTGAAGTCAA		
9836	LCMT2	NM_014793	TAGATTTATAAGTGTCAATAA	ATGGCCATTAATGTTACACAA	ACCCACTAAAGTAGACAATAA	CAGAGGCATTTCCTCGCGTAA
9837	KIAA0186	XM_375911	ACAATTGATGTTGAACTTGTA	TTGGGAGAATTGACATCTTAA		
9842	PLEKHM1	NM_014798	CCCATTCATATTTCAACAGAA	CAGGCAGCCTCTGGAACTCAA		
9846	GAB2	NM_012296	CAGACCAGACGTTTCATTCTA	CACTAAGGACACAAGAATCAA	CACCAATTCTGAAGACAACTA	AACCTCAAACCTGATCGGAAA
9848	MFAP3L	NM_001009554	CCGAAACTGCAGAACCTTCTA	CACCATCGTCATGGTCCTCAA		
9851	KIAA0753	NM_014804	CAGAGAAAGGAAGAAACTTAA	CTGGCTCAGTTTGGTGATGAA		
9853	RUSC2	NM_014806	ATGTATTTATTTATTTATTTA	CCCGATCAAGACCTAGGACAA		
9854	TMEM24	NM_014807	TAAAGTCAAATTGGAGTTTAA	CACAATTGAGGAACTGATCAA		
9855	FARP2	NM_014808	CAGGAACATGCGCCAGTTAAA	CAGGTTTGGACACAACTACAA		
9860	LRIG2	NM_014813	AGGGATGTCATTGTAAATATA	CTGGAATATACTAGTATCTTA		
9863	AIP1	NM_012301	AACCCATTCATCGTAAACAAA	CAGACCTAAACTGATCCTAAA	TTGGATGTCATCCAAACTTTA	ACGCAGTGACTACGCAACCTA
9871	SEC24D	NM_014822	CAGCTGCTTAATTAATTGAAA	AAGGTACAATTGTACCATAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
9877	KIAA0663	NM_014827	AAGATTGATAGTGAAATTAAA	CAGCTAATGATTACAGTTTAA		
9880	KIAA0352	NM_014830	AAGCTTAACATCAGAATGAAA	CTGGGTGGTCTGTGTACTTAA		
9890	LPPR4	NM_014839	AAGGAGTTGTTTACAGATGAA	CACATTGTTAAGGACATATAA		
9894	KIAA0683	NM_016111	CCAGTTTGTGATGACCCAGAA	CCGGGAGACGCTGCTGGGCAA		
9896	KIAA0274	NM_014845	GAGGGTGATGTTGCAAATGAA	AAGAAATTCCACAAATATGAA		
9899	SV2B	NM_014848	CTGGTTGATTTGAGAGATAAA	AAGATGGATCTTGTAAATTTA		
9901	SRGAP3	NM_014850	AACCAGCAAGTTGTTCATTTA	AACCTAGTTAGTAGTCTTCAA		
9908	G3BP2	NM_012297	ACCAGCGTGTGTACACATAAA	CAGCCAAGAGTCGAAGCTAAA	TTCAGTGAATGTCATACTAAA	CCGAGTGGCTCCTGAATTTAA
9914	KIAA0703	NM_014861	ACGGACCTCTTGGTGGATGAA	CAGGCTGAAGAGACACCTAAA	ATGGACTTAAGTGATATTAAA	CCGAGAGTTGGCGTGAAGGAA
9915	ARNT2	NM_014862	CAGAATAACCACCATGAGGAA	TAGCTTTAGCCGAGAAAGAAA	CCGGAACAGCTCTAGGAATAA	GTGGACAGTTTAAGTACTTAA
9921	RNF10	NM_014868	TCCAAGCGTTATAATCGCAAA	CCGGGTAGTTCTGGAGGAGAA	TTCGATGAAGAAACCACGGAA	CAGGATTGAGATAGAGGAGAA
9936	DCL-1	NM_014880	CAGAATTATGTGCATACCAAT	ATGGCGTATTATGTGAACTAA	GAGGCTATTTAAGTAAATTTA	TAGCTAGTAATAACAATATAA
9940	DLEC1	NM_005106	ACAGCCTGACATGGAATTTAA	CAGGTTCTGCATTATGCCCAA		
9941	ENDOGL1	NM_005107	CTCGGGCAAGATGGCTATCAA	CAGAGGCAAGGTGTTACACTA	AAGAAGCTAGAAGAACTCAAA	AACAGTGGAATCCTAAATTTA
9949	AMMECR1	NM_015365	CCCACTGTTTGTAACATGGAA	CACACTTACCAGTGCCCTTAA	CTGACCAGGTATCGTAGTGAA	CGCCAGCATCATCATTTCCAA
9950	GOLGA5	NM_005113	CTGGACCTAAATCTACGTATA	AAGCAGGAGTTCCACTATATA	AAGAAGATCTTTATCGAACAA	CACGACCAACCATATGGCAAA
9951	HS3ST4	NM_006040	CCGTGTTGTTATAAAGCTTAA	CAGAGGATAAATAGTTGTCAA		
9958	USP15	NM_006313	ATGAATAATGTTGTAACTCGA	GACACAATAGATACAATTGAA	AAGATGATACCAGGCATATAA	TATGTCGGAATTCTTAATTAA
9965	FGF19	NM_005117	TTGTCTGATCATAACATTGTA	AAGAAACATCTAGAAGTTGTA	CAACATGATATTTATGAGTAA	CCGTAAGGCGCTACTATATAA
9970	NR1I3	NM_005122	AAGCCACAGGCTACCACTTTA	TTGAACAGTTTGTGCAGTTTA	CACACACTTCGCAGACATCAA	AACACTTTCATGGTACTGCAA
9976	CLECSF2	NM_005127	AAGCAGTAATGTCCTAAAGAA	CCCAGTTGAGAAAGTAAGAAA	CAGCTAGATGTTACACCGAAA	ACGTGTCAGGCTACACATAAA
9978	RBX1	NM_014248	CACATTATGGATCTTTGCATA	TTGCATAGAATGTCAAGCTAA	CTGCTGTTACCTAATTACAAA	AAGAAGCGCTTTGAAGTGAAA
9985	REC8L1	NM_005132	CCGGAGAAATTCCAGGAACAA	CAGAGGGACAATGTTCTACTA		
9988	DMTF1	NM_021145	ATGGATAAGCATAGTAACAAA	CAGATTATTGTTCATGCTTTA		
9989	PPP4R1	NM_005134	CAGCTAGTAATGAGAATGATA	AACCTGGTAACTACAAATCTA	TGGGAGTGCTGCAGTCTTTAA	CAGGCGTTGTTAGATCAGTAT
9993	DGCR2	NM_005137	TCGCTGGGAGGTGGCATTCAA	CTCCCTCAATACTGTGGTGTA	AAGCCCAGTTGTGAATATCAA	GAGGTGGGATTTGATACTGTA
9994	CASP8AP2	NM_012115	CAGCTGATGTGCGGAAGTCAA	CAGTATTCAAATAGTCAGAAA	CAGTCTGATCTCAATAAGGAA	AACGAAGTTTCGAGATTCTTA
10001	MED6	NM_005466	TCCCACTAGCTGATTACTATA	CACCCAAATTTGTGCAGCTAA	AAGGGTATTGGTGGCACTTCA	ACCCAAATTTGTGCAGCTAAA
10002	NR2E3	NM_014249	CAGGCAAGACTAATTGACAAT	AGGGAATACTCCAATGGAGAA	CACGGAGTTTGCCTGCATGAA	CACAAATGTATTCATACGTAA
10003	NAALAD2	NM_005467	CAGCAAGTATCTATAATCTAT	TCGATTGTGGATGAACATGAA	AAGAAACATGATCAACAATTA	ACGGTGGAAACTGGTATCCGA
10004	NAALADL1	NM_005468	CACAGAAGAGTTCTTCAACAA	ACGCATATCAACACTGCAGAA	TCCCTTTACTCCGGTGCTTTA	CTCCGGTGCTTTATATTTACA
10019	LNK	NM_005475	CAGCTTTACAGTGATAGTTAA	CAGCACATTGTGATAACATAA		
10020	GNE	NM_005476	CTGCTTACTAATGTATTAATA	ATGAAGGTTTCTACAACATAT	CCCGATCATGTTTGGCATTAA	ATGGAAATACATATCGAATGA
10025	THRAP5	NM_005481	CACCCGGATCCTGGCCATGAA	CAAGGTCATGATCAACCTCAA	TGGGAAGGACAGGTCCAATAA	CACGTGCAGCCCAGTATGGTA
10039	PARP3	NM_005485	CCAGACCAACATCGAGAACAA	CCCAGTGAGGACTGTGACTAA	CACGCAGAAGCTCATCACTAA	CAGCAAGGAGATGTTCAAGAA
10044	SH2D3C	NM_005489	CCAGAGAAACTCCACAAGGAA	CAACCAGGCCTTGCACTTCAA	CAGGCGAGAGCTACACACACA	CCACACCAATGCTGAAGTCAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
10046	CXorf6	NM_005491	AAGAATAAATTTGCAGGTCAA	CCGTCTAACATTACTCATGTA		
10048	RANBP9	NM_005493	CAGTGCAATATTAGAAACCCA	ACGGTGTGGTTATGACCTTTA	CAGGTTGGGATAAGCATTCAT	AAGCAATGAGTGAACAGCTAA
10050	SLC17A4	NM_005495	ACGCTAGTTATTTAACTGCAA	GAGCAAGATAGTACACTTTAA		
10053	AP1M2	NM_005498	CTCCGAGGGTATCAAGTATAA	CTGGATTGAGTCTGTCATTGA		
10054	UBA2	NM_005499	AAGAGTAGATTTGATATCAAA	CTGGGTATCTTGGACAAGTAA		
10055	SAE1	NM_005500	TACCAAGTCTTTGGATGTTAA	TCCAGGGATGTCATAGTTAAA		
10060	ABCC9	NM_005691	AACAGAGGACATTGCAATAAA	CAGCCAGATATTGACTTATTA	CTGCATCTATAGCATCCATTA	CCCAAATTTGTTCGCCCACAA
10062	NR1H3	NM_005693	CCCACAGAGATCCGTCCACAA	CAGGAGTGTCGGCTTCGCAAA	GAGATAGTTGACTTTGCTAAA	CATGAATGAGCTGCAACTCAA
10063	COX17	NM_005694	CTGAAGAATGAAGAAGATTAA	AAGGAATGCATGAGAGCCCTA		
10068	IL18BP	NM_005699	CTGCTTCGGATCCACACTGTA	TCCCATGTCTCTGCTCATTTA	CAGGATGTGGACGGACTGGTA	ACCGATCAAGTCAACTCAGTA
10077	PHEMX	NM_005705	CAGCAATGGTGCATTGAGCAA	TCAAATATACATCACATCAAA		
10086	HHLA1	NM_005712	CCCAAGTGGGCTACATTTGAA	CTGGAGGGTCTCTCTGGGAAA	AAGCATGTTAATGTTACCATT	CTCCAGCTAGATCATCAGTTA
10092	ARPC5	NM_005717	CAGCCTCTGAATGAAATGCTA	CAGGGTAGTTGGGATCTCAAA		
10094	ARPC3	NM_005719	GCGCTTAATAAGAATAAGTAA	CTCATGGATCCTGATACCAAA		
10095	ARPC1B	NM_005720	AAGCACTATGCTGGTCATGAA	TCGTGTGATCTCCATCTGTTA		
10102	TSFM	NM_005726	CAGGAAGGAAACACAACTGTA	CAGCAAGGAGCTCCTCATGAA		
10105	PPIF	NM_005729	CTGTGTGTTAAAGAAATTCAA	ATGGATTTGTGTTCACCTTAA		
10107	TRIM10	NM_006778	ACGGACATCAGAAGCACTCTA	TTAGTTTGTGTTAACTATGAA	TCCAATAATGTTAGAGTTCAT	CAGTTGTATGACTTTAAACAA
10111	RAD50	NM_005732	TAAGATTGAATTGAATCGTAA	CACGAGTAAGATTAAGAGCAA	CAGGAACAGATTCAACATCTA	CAGAAAGTGTATAATAAGAAA
10131	TRAP1	NM_016292	CCCGGTCCCTGTACTCAGAAA	AAGGATGTCGGTGAGTGGCAA	CCGCTACACCCTGCACTATAA	CGCGCTCATCAAGAAGCTGAA
10134	BCAP31	NM_005745	CTGCACGTTGACTGTGGGAAA	CACCTTCTTTGTGGTTCTCAT	CAAGAAGTACATGGAGGAGAA	AAAGGTGAACCTCCAGAACAA
10136	ELA3A	NM_005747	CACATCCTGAATAAAGAATAA	TGGCTGCAACTTCATCTGGAA	CTGGCTTTGGCTGCAACTTCA	AAGAATAAAGATCTCTCGGAA
10139	ARFRP1	NM_003224	CCGATTTAACAAGAACTACAA	CACCACCACCGTGGGCCTAAA		
10140	TOB1	NM_005749	CAGCCTGTTATGGCTAACTAA	AGCCTGTTATGGCTAACTAAA	CCAGCCTGTTATGGCTAACTA	CAGATATGGCCTCTTACAGTA
10142	AKAP9	NM_005751	CAGGTTCGTGAATATATGGAA	ACAGATTATATCACTCGGCTA	CAGCTTCAAAGGGATATACAA	CAGCCTATCAGTGAACATCAA
10154	PLXNC1	NM_005761	TTGGTGAGAATTTGACTTCAA	CCCAACCAGAGCAACCTACAA	TCGAGGGAAGCACAAGTTCAA	GACGTCGTACATATTTGGAAA
10158	MAP17	NM_005764	CCCTAATTTCTGTGAAATAAA	CCGGCCCTACCCGCCCTTGAA		
10165	SLC25A13	NM_014251	CAGACCAAAGATGGATTAATA	CTCAGAAATTTGGTCAGGTTA	TAGCAGATTTATATGAGCCAA	CAGTATCTACCTCAAAGGCTA
10166	SLC25A15	NM_014252	AGCCTTATGCACCTAATTCAA	CACCAGCAGGGTATCTCCCAA	ATAGGCCTGGATCGAAGTAAA	AGGCCGTCCATTAGAGATTTA
10168	ZNF197	NM_006991	TCAGGCCTAATTATACATCTA	CACCAATGAGTCCAAGATTGA	TCCCAACTTTCAAGTCTACAA	CACCTACACTTTAGACAATTA
10178	ODZ1	NM_014253	CCCAGTCATATCAACCATAAT	CCGACCTGCCTTTACCTTTAA	AAGGCTATAATCCGGCCTTAA	CTCTATGATTTCCTTACTAAA
10180	RBM6	NM_005777	CAAGCAAGAATTAATAACCTA	CAGACTGGTCTTCAGATACAA		
10188	TNK2	NM_005781	TGGCCTTACCATGGACTTGAA	CAGGATCTTGTGCCTGGAAAT	CGGCAGTCAGATCCTGCATAA	ACGCAAGTCGTGGATGAGTAA
10189	THOC4	NM_005782	CAGGAACTCTTTGCTGAATTT	CCAGTTAAACAGACCAGCAAA		
10194	SDCCAG33	NM_005786	CACGGGCAAGGTCAACATCAA	ACCGCGGAACATTGCACTAAA		
10202	DHRS2	NM_005794	CAGCACCGGGATAGACAGGAA	CTGGAAGAACTTCAAGGAACA	TAGATTTGGCTGATCCAATTA	CTCTCTGTAATTTGTGCTTTA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
10206	RFP2	NM_001007278	CAGAATTTGTGTGCAAATATA	AAGGAGATCATAAGAAATTAA		
10208	C13orf22	NM_005800	CAGCCTCAGTTTCACAGTTAA	CTGAATGAAGTTAGAGATGAA		
10213	PSMD14	NM_005805	TAGGACATGAACCAAGACAAA	CAGGCATTAATTCATGGACTA	ACAGACATTATTACTCCATTA	TTGGATACTGTCGTATTTAAA
10218	ANGPTL7	NM_021146	TCGGGCTTGGAAGGAAAGCTA	CCGCATCTCTGGAGTGTATAA	ACCGCCTGGGTGAGCACAATA	CTGAAGGTAGATGGTGTTATA
10220	GDF11	NM_005811	AAGGTGATGTTCACAAAGGTA	TTGGCAGAGCATCGACTTCAA	CAGAGCATCGACTTCAAGCAA	CTGAAATGGAGTAATAAATGA
10228	STX6	NM_005819	CAGGCTGAAGCTAAATAGAGA	TCCCAGGTTTCTTAAGAATAA	CTGAAGCTAAATAGAGAACAA	AACCTAGTCATTAATGAGTAA
10231	DSCR1L1	NM_005822	ATGGATTACTTTAGATGCAAA	CTCAAAGAGCTTAGACTTCAA		
10234	LRRC17	NM_005824	AGCGTAATAATTACTATAGTA	ATGCAGGGTAATCCAGCTAAA	AAGGAACAATTGGACCCGAAA	CCCGTGTGACGTGTACACATA
10244	RAB9P40	NM_005833	TAGGTGAAGAAACTAATGCAA	AAAGAGGATTCAGCTGACAAA	ATTGATATAAGTGACATGAAA	AAGCAACATGGTACACCTTGA
10245	TIMM17B	NM_005834	CAGCACTTCCTCCAGCTCCAA	GGCACCCTGATGAGTATTTAA		
10250	SRRM1	NM_005839	CAGAATAAATTTCTAAATTTA	TAGGTTGAAGTTCAACATGTA		
10257	ABCC4	NM_005845	TTGGCTATACTGCATCACTTA	TACAACCAATAGGAACAACAA	CTCCTAGTACTTAGAAATACA	GAGGTTAAAGACAGTCATATA
10261	IGSF6	NM_005849	CAGAATGTAAGGAAACTATAA	CAGGAAATTGCTCAAGAACTA		
10262	SF3B4	NM_005850	CTGGATGAGAAGGTTAGTGAA	CACAGGCAACTCCAAAGGTTA		
10267	RAMP1	NM_005855	CACCTGGCACATGGCGGAGAA	CCCGCCCGGCAGCATCCTCTA	CAGGTTCTTCCTGGCAGTGCA	CAGGGACGTGACCTTGACTTA
10276	NET1	NM_005863	ACGGAAAGAGACTTTGGTGTA	GAGCATCATAGGGTTACTTTA	TCGGTGTGGATTGATTGGAAA	CTGGAGGATGCTATATTGATA
10279	PRSS16	NM_005865	TCCGAGTATAATGACGTGGTA	ACGTGGTATCCCGAAGCCTAA	CAGAGAGTTATGGAAATATAA	CTGTTCTTTCCTAAAGATCAA
10280	OPRS1	NM_005866	CAGCGTCTTCCATTCCAGAAA	TGGGAACAAATGAGACACATA	CCGGCTTGAGCTCACCACCTA	AGGGATATCCATGCTTATGTA
10282	BET1	NM_005868	TCAGATTAAATAGCATTATAA	ATCATTTATTGGATTATTAAA	CAGAATAAATTATTAGCTGAA	CACTGATGTCGTGGCGCTTTA
10284	SAP18	NM_005870	AAGCCACGGGATTGTATGAAA	TCCCTTTAGTTTGTTACAGTA	AACGGCCTATAGGATTGTTAA	AGCCACGGGATTGTATGAAAT
10290	APEG1	NM_005876	CCCGAGGACACCACCACCGAA	CAAGTGTATCATCACTGCCAA	CAGCTGGAATAACAAGCCCAA	AACACCTATTTCTTAACTCAA
10291	SF3A1	NM_005877	CAGGTGTGTTACCGAGTGGAA	CGCAAGGATTATGATCCCAAA	CAGGATAAGACGGAATGGAAA	CAGCATGTAGGTAGCGTCCTA
10293	TRIP	NM_005879	CCGGCTCAGGAGCAAGATGAA	AAGGAAATCATGAGCCTGAAA	CGGGACCAGCCTGAGGTGTAA	CCGTGATGATATTGATCTCAA
10300	KATNB1	NM_005886	CTGCTGTAATTTATAAGGCAA	CAGGGAGGAGAGGCTGCATAA		
10322	SMYD5	NM_006062	CTCGAGGAGCTGGGCTAGATA	TTGGATGCTATGGGAATTACA	CTGGCCTTATGGAGTATGGAA	AACATTGAAGTCTTCCAGAAA
10328	NOC4	NM_006067	CTGGACAAACCCAGAGATCAA	TGCAAGATTGTTCCTATTAAA		
10329	TMEM5	NM_014254	CAGCCTCAGGAAACAAATGAA	TCCCTTTATCTTTATCAAGAA		
10344	CCL26	NM_006072	AACAATTGTGACTCAGCTGAA	TCCCAGAGTTACTTTAATAAA	AAGCTATGAATTCACCAGTAA	CAGGGCCGTCTCAGTCTCATA
10352	WARS2	NM_015836	CCGGCATTCAACCTACAGGAA	CTACCTCGATTACAACATTTA	GCCAATGGATGCGAACTTAAA	AAGGTAGATCTATCAAGCCAA
10360	NPM3	NM_006993	TTGGATAAAGGTTGAAATAAA	CACCCGCTCCTTCACCTTTAA		
10361	NPM2	NM_182795	CAGGAACGTTATGAAGCATCA	CAGGCGAGCGTGGCTAAGAAA		
10363	HMG20A	NM_018200	AAGGAAGATAACGGACTGTAA	CAGGAATGCATGAGATTTCAA		
10369	CACNG2	NM_006078	CCGTGTGATCTTTATAATTTA	ATACATATATCCATTATATTA	ATCCATTATATTAGTAGTGGA	TCGGTTGGGTGTTTATATAAT
10370	CITED2	NM_006079	TGGAAACAAAGTAAACTATAA	CTCCCTTATGTAGTTGAAATA	CAGATTTACGAGTGAAAGGAA	TGGAATGTCGTCAGTGGCAAA
10381	TUBB3	NM_006086	CACGGTGGTGGAGCCCTACAA	CCAGCAGATGTTCGATGCCAA	GCGGATCAGCGTCTACTACAA	TTGCTGTCAGATACCCTTAAA
10385	BTN2A2	NM_006995	AACTCCAAACATCGCGATTAA	CTCATTGAAATCAAGGCCCAA	TACGTCAGCATTCAGGTTCAA	AACGATTAATGTTTCATTATT

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
10395	DLC1	NM_006094	CAGCTTGATCAGGACATAGAA	AAGGTATTTCAGAGAAGGAAA		
10396	ATP8A1	NM_006095	GAGGATAAATTACAAGATCAA	ATGCAATGTAATGCAGTTTAA		
10398	MYL9	NM_006097	GAGGCACCCATTGATAAGAAA	ACCCATTGATAAGAAAGGCAA		
10403	KNTC2	NM_006101	CACAATTAGCAGAGTATCACA	TCCAAAGGTTATGACTTTGAA	TCCCTGGGTCGTGTCAGGAAA	CCGAGACCACTTAATGACAAA
10407	SPAG11	NM_016512	ATGGCAGATCTGGGATCTAAA	TTGAATGAATTTAGCACCAAA		
10412	TINP1	NM_014886	AAGAGATTTATTAAATTGTAA	AAGGCTAAGCTTTACCATAAA		
10423	CDIPT	NM_006319	CACCATGTGCCTGTTGGTCAA	CCGGATTGTCTTCGCCATCAT		
10424	PGRMC2	NM_006320	CCCTAAATCAAATCAATATTA	CACATCAATTTGAGTTGTTCA	CCGGCGGGTCCATATGGAATA	CAAGATAAATTAATCTCACTA
10426	TUBGCP3	NM_006322	TCGCATGGACTTTAACTGCAA	CCACTACCTAAGAGTATTTAA	TACGACTTTGTATCAGCATAA	TACCGCGAATGCATCAGCTAA
10431	TIMM23	NM_006327	CAGGCATGTTGTATAAATGTA	CCCGCTGTTATTGAGGAGTAA		
10436	C2F	NM_006331	CAGAAGAATGTTCTGATTGAA	AAGGTAATTAAGAATCCAGTA		
10450	PPIE	NM_006112	CAGATTCCTCTGGATTATGAA	AAGACGCTTGAAGAGAATAAA		
10454	MAP3K7IP1	NM_006116	ACGCCTTGGCTGAGAAGGCAA	CACGAGGACATGACCCTGCTA	CTGCAGGTGAGAGGATTTAAA	CACCTTGGACAAGCCACACAA
10457	GPNMB	NM_002510	CCGTGAGAATTCAGCATGGAA	ATCGAAATTCATCCGACGAAA	CTACTATTGATTAGAGCCTAA	TCCATGTAACTGTATGCATAA
10458	BAIAP2	NM_006340	AAGAAATACCAGACTGAGCAA	CACGGGCAACCTCCTGGACAA	CAGCAAGAATCCTCAGAAGTA	CTGCTTCTCCTGCCTAATAAA
10460	TACC3	NM_006342	CAGGAAGTTCTGAGAACCAAA	AAGGAACTTTCCAAAGCTGAA		
10465	PPIH	NM_006347	CAGGGTCATAAAGGATTTCAT	CCGCATGAAGATCGAGCTCTT		
10469	TIMM44	NM_006351	AAGAAATGAAAGAAAGTATAA	CTAGATAATGTCAAACAAGAA		
10474	TADA3L	NM_006354	ACCGACTGGCAGGATAAGAAA	CTGACCGAACTGGACACTAAA		
10478	SLC25A17	NM_006358	CTCCTGGAGATCATTAAAGAA	CTCATTGCTGTTGGTCTTCAA	CTGGACCTGTTGTCACCTTAA	ACCCAAATGATTCTCTTATAA
10480	GA17	NM_006360	ATGGATAAGAATACTCCTGTA	TTCGTGCTTATCTGAAATCTA		
10482	NXF1	NM_006362	CAGAACAAGTAGAACAGCTAA	AACGCGTTAATTTCCCTCAAA		
10489	MUF1	NM_006369	CCCAGGCTTTAGAGAAGTATA	CCGGCGTAAGAGTGAAGCCAA		
10490	VTI1B	NM_006370	AAGCAACAGGAAGCAAATGAA	ATGATATACCAAGGTAATAAA	AAGGTAATAAATGCTGTTTAT	CAGTATGATATACCAAGGTAA
10491	CRTAP	NM_006371	CAGCATGTCAGTGGCATTTAA	CAGGGAGATCAAGGACTTCAA		
10494	STK25	NM_006374	CCGGCCGAGTCCACACAGCAA	AAGACCTGACTTGGAGACAAA	CACCAAGCTATGGATCATCAT	AAGGGCATCGATAACCACACA
10499	NCOA2	NM_006540	CAGTCTAGTGCCAAAGATTAA	CCAGGAATGATGGGTAATCAA	AAGGATTGGCATTCAGTCAAA	AGGGCTGTTAACATTAGCAAA
10500	SEMA6C	NM_030913	CGCCCTGGAACCCAAATTCAA	CCGCGTAGCCCGAGTATGTAA		
10516	FBLN5	NM_006329	CAGATCTGCATCAATACTGAA	CAGATGGATGAAAGCAACCAA		
10517	FBXW10	NM_031456	CCGGTGTATATCCGAAATGAA	AAGGAAGGTCTTGAATTTCAA		
10521	DDX17	NM_006386	CACGTAAATGAAACCACTCAA	CTGGGACATTGTAATCATAAA		
10522	DEAF1	NM_021008	CAAGTCATTAACACACTTTAA	CAGCGGCACTCTGTACAAGAA		
10525	HYOU1	NM_006389	ACGCAAAGTCATCACCTTTAA	CAGCAAAGCCTTTAAAGTGAA		
10536	LEPREL2	NM_014262	GAGGCTGATGCTTTAAATGAA	CAGGAGTGGATAGAAGCCAAA		
10537	UBD	NM_006398	AAAGCATTCTTTGTCTATTAA	CTGGACAAACACAGCAATCCA	ATGGGATTTAATGACCTTTGA	AACCCATATGACAGCGTGAAA
10539	TXNL2	NM_006541	AACGAAGTTATGGCAGAGTTA	AGCGCTAATGAACATCTTAAA	TTCGATATATTGGAGGATGAA	TACCCTCAGCTGTATGTGAAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
10561	IFI44	NM_006417	CTGGGATATCTGAGAAGTATA	TCAGATGATAGTAAAGATCAA		
10562	OLFM4	NM_006418	CTCATTGTCCACCTTACTAAA	CGGGAATATTGCCAGAGTTAA	TAGGGATTCTTTGTACAGGAA	CAGAGTTAACCTGACCACCAA
10563	CXCL13	NM_006419	CTGAATGGATACAAAGAATGA	CGCTTCATTGATCGAATTCAA	AAGGGTGATGTACACATGTAT	ACGGAGGAGAATTAAGTCCTA
10569	SLU7	NM_006425	CTGGCTTTAATAAATATTTCA	CAGGCAGATCCTACAAAGCTA		
10571	SMA3	NM_006780	AAACTCATTCAAGGAGGTGAA	CAGCCGGGATGCACTAGGCAA		
10573	MRPL28	NM_006428	CAAGTTTGGGATGGACCTGAA	CAGTGAGATCCTGGACAAGAA		
10575	CCT4	NM_006430	CTCGATAATCTGGATAACTGA	TTGCCTGAAGTTGTATTGAAA	TTGCTCATATTGACCAATTTA	TAGAGTTGGCCCTACGATTAA
10577	NPC2	NM_006432	CCCGAGCTTGGAACTTCGTTA	GTGGATGGAGTTATAAAGGAA	AAGGACAGTCTTACAGCGTCA	CAGATCGTTTCTCATCTCTAA
10578	GNLY	NM_006433	CAGAAATTTCATGAGGAGGTA	CAGGGTGACCTGTTGACCAAA		
10580	SORBS1	NM_006434	TCCGGAACACTGAGAGATCAA	CTGAACAGAGATGATGATTCA	CAGGATTCCAGTCCTCTACTA	ACCCGGCAACACGAAAGCAAA
10581	IFITM2	NM_006435	ACCATGAACCACATTGTGCAA	CCAGGACCTCCACACCATTAA		
10594	PRPF8	NM_006445	ACGGGCATGTATCGATACAAA	CAACGTCGTCATCAACTATAA	CCGAAAGTCATATAAGATGAA	ATGGCTTGTCATCCTGAATAA
10595	ERN2	NM_033266	CAGCCACTCGACGACCCTGAA	CAGGGATTAATGAAACTGCCA	CACCTGCATTCTTTACACATA	AAGGATGAAACTGGCTTCTAT
10606	PAICS	NM_006452	CACGTGGAAATCTCCGTTATT	GCCCAAGGACTTCTAACAATA	CTCGACTAACAGGGACTATAA	CCCAAGGACTTCTAACAATAA
10613	SPFH1	NM_006459	CACTGGAATGTTAAACACTAA	CCCGGAATATCTGGAGCTCAA		
10615	SPAG5	NM_006461	TCGACATGACTTGGAAGATAA	CCCGAGTAGCATCAATGGTTT	TCCCGACAACTCACAGAGAAA	CCAAATTAGCTCTACTCCTAA
10623	POLR3C	NM_006468	CAGCTTGATAGGGAAAGGTAA	CCCACACTTGTCATTAATGAA		
10628	TXNIP	NM_006472	TAGAGGGCAGGTGTTCATAAA	TAGAGCTGATTTGATGGACAA	AAGAATACCTTAATTCCTTAA	AAGAGCCAATTTAACAAACTA
10630	T1A-2	NM_001006624	CGGGAAGGTACTCGCCCTAAA	CTCAAGTGTGTTTGAAACCAA	CAGGAAGTCGATAGTCTCAAA	ATCGAGGATCTGCCAACTTCA
10631	POSTN	NM_006475	ACGGATCTTGTGGCCCAATTA	CACGAGAAGAACGAATCATTA	ACCAGATTCATTACAATTCAA	CTGCTTATTGTTAACCCTATA
10634	GAS2L1	NM_006478	CTGGGACACGCTGGAGCATTA	CAGCAGAGCCTCTGACAGTAA		
10651	MTX2	NM_001006635	CTGCAGAACCTTGGCCTGAAA	AACCTCAAATTATATAATGTA		
10653	SPINT2	NM_021102	CAGCGATATGTTCAACTATGA	AAGGAGGAGTGCCTCAAGAAA		
10658	CUGBP1	NM_006560	TTCTAGAACTTCATAAGATAA	CGGCTTAAAGTGCAGCTCAAA	CGGGAACTCTTCGAACAGTAT	CAGGGTCCTCACCTAGCTCTA
10659	CUGBP2	NM_006561	CTGAAATTTATTATTAGACAA	CAGGAGAAAGGTTACTGTAAA		
10663	CXCR6	NM_006564	CTGCTATTCAGTCATAATCAA	CACCAGCATGTTCCAGTTATA	TCGTTTCATTGTAGTGGTTAA	CAGGTCATGTGCAAGAGCCTA
10668	CGRRF1	NM_006568	CTGATAGGACTTATAAACTAT	TCCATCTGTGTTGATACATAA	CGGGAAATTTATGATATTATT	CCGGGAAATTTATGATATTAT
10670	RRAGA	NM_006570	CCGGTTTGAGAAGATCAGCAA	TTGGTATGGTGTAACACTAAA		
10673	TNFSF13B	NM_006573	CACGCAGGACATCAACAAACA	CAGACAGTGAAACACCAACTA	CGGAGGGTAAATGCCAGCAAA	CACGCCTTACTTCTTGCCTTA
10683	DLL3	NM_016941	CCCGGTGAATGCCGATGCCTA	CCGGATGCACTCAACAACCTA	CCTGAAGATGTAGACCCTCAA	AAGGCTATTATTGTGATCAAA
10692	RRH	NM_006583	CTGGAAGAATCTGAAATAAGA	CACTGTACTGATGACCTTTAA	CAGACATGGATCATTGTCCTA	CACAAATGCAATTATTATTAA
10693	CCT6B	NM_006584	CAGGAGATGGTACTACTTCAA	TAGAACATCATTACAAACTAA		
10694	CCT8	NM_006585	AACCTTCGAGATATTGATGAA	CTGGACTTGAACAGTATGCTA	GAGGCTGTGTATAGAAACATA	AAGGCTGTATTTGTAGTAGTA
10713	USP39	NM_006590	GTGGCTGATGATGGTAAATAA	AAGAGGCGAGATAATGATGAA		
10716	TBR1	NM_006593	TCCCATTATCTCGACCACTGA	CTGGTTTGTGACGCCGGCCAA	ATGGCCGTCTGCAGCGAATAA	AAGTCTCGGCCTCCACATTAA
10717	AP4B1	NM_006594	TGGAACAATTGAAGAAATAAA	GAGGAAATTCTGAAACAGGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
10724	MGEA5	NM_012215	CTGGTACAAATCAAACATGAA	CAGGGAGAGAGTCTTCAATAA		
10726	NUDC	NM_006600	TGGCCTACTGTTACACATTAA	CACCAAGAAGATTAACCCTGA		
10730	YME1L1	NM_014263	TTCCAGATTGACCATGAATAA	GAGGCATTAGATAATGCCTTA	TCGGCATTTATGGACTTCTAA	TCCGTTGATCCAGAAATTATA
10735	STAG2	NM_006603	CAGAAATATATTGAAAGTTTA	TTGCTTGTCCTTTAAGATAAA		
10748	KLRA1	NM_006611	CTGGAATTAATTCTACAATAA	TCGGATTATCATATGATGAAA		
10749	KIF1C	NM_006612	ACCTCCATCATCAATCCTAAA	CCGGCTGATTAGAGAGCTGCA	CACGGTCCAGACCATTGTCAA	CTGGAGAATCAGTACCGGAAA
10753	CAPN9	NM_006615	CCCGAGAACTTCTATGAGATT	AAGGAGTTCATTCATCTCAAT	GAGGAGTGTAGTTTCCTTGTA	GAGAACTTCTATGAGATTCTA
10761	PLAC1	NM_021796	CCGGTTCAGGACAAAGTCCAA	AAGGATTTGTATAAAGAGTGA		
10765	JARID1B	NM_006618	TAGGGTTGTGTGATTAATCAT	CAGGAATGTAGTAAGCCACAA	ACGCACCAAGCCGAAAGTAAA	TCGTCCTAACATAACACTAAA
10768	AHCYL1	NM_006621	CAGGGTGGTAAAGCTAAATGA	AAACAGTTGTATCGTATGCAA	CTGATAGAACTCTATAATGCA	CCCACTTGGATTTATAGTATA
10771	ZMYND11	NM_006624	CCGGATGAAGTCGGACCACAA	ACCAGTGGGTATATGATTGAA	CACCTCATGTATCGTAAGTTA	TAGGAATGGATCGATAGTTGA
10773	ZNF482	NM_006626	AACGTTTGTATTATTCTATTA	TACAGGGTTAATAATCCTTAA		
10776	ARPP-19	NM_006628	CACATGAAAGATTAATCTGAA	CACTCTGTCATTGTTAATCTA	CGGCATGTTTGTAGCATACAA	CCCGGCCGGCTTATGATTTAA
10780	ZNF234	NM_006630	AAGGGTTTCATTTACAGTTCA	CAGGACTATATACAACTCACA		
10781	ZNF266	NM_006631	CTCGCCTTAGTGAACATACAA	TTGCTATTTCTTCAAATCTTA		
10783	NEK6	NM_014397	AAGGGATAAAGTGGAAATCAT	ATGCAAGTTAGCTAATACAAA	ACCGGAGAGGATCCATGAGAA	ACCACGGAAGTCGAGAATTAA
10785	WDR4	NM_018669	CAACGTGACCTCCTACCTGAA	CAGCTTCAGCAGTCTCTACAA		
10791	VAMP5	NM_006634	CTGCAGCAGCGTTCAGACCAA	GACGGAAATTATGCGTAACAA		
10797	MTHFD2	NM_006636	AGCGAGAAGTGCTGAAGTCTA	AGCCATTAACCTAGTGATTAA	TAGGATTATTCCTTGCTATTA	CTCGCGGCAGTTCGAAATGAA
10803	CCR9	NM_006641	TTGGAAGAAATGAGAAATACA	CCCACTTTATTCTGAGGAATA	CAGTCTTGTTATCCTTGTCTA	AAGGGATGAATCTGAACTATA
10811	NOXA1	NM_006647	CAGGTGGAGCAAGTTGGCAAA	CAGCAGGGAGATCAGCCCTAA		
10815	CPLX1	NM_006651	AGCCATAACGTTAGACTGCAA	CCGTGTTCACTTCTAAACTAA	AACGTTAGACTGCAATACTAA	CACGGCCGTGTTCACTTCTAA
10844	TUBGCP2	NM_006659	CCCGGTGGCTAAAGAGATCAT	AAAGAGATCATCTACACGTTA	CCAGGAGGATTACAACGACAA	CAGCGTCTGGATCAGCAACAA
10846	PDE10A	NM_006661	ATGCAGGGAGTTGTATATGAA	AACCCTTTGCATAAAGAACAA	TAGACTCTCATTCACAATGAA	CAGTATTACTATACAATGTAA
10849	ASE-1	NM_012099	CCGGGAAACTGAGGAACTAAA	AAGGAGCTGTTTCCTGGGTAA		
10858	CYP46A1	NM_006668	CACGAGTCCTGAGTCGGTTAA	CCTGATGTCAACCAAGTACAA	AGGCTTGGTGTCCGAATGCAA	GCGGATGGACACATACTTTGA
10859	LILRB1	NM_006669	CAGAAAGTGCATTAAACTGAA	ATGAATGAATTAGGAAAGAAA		
10863	ADAM28	NM_014265	TCGGATAATTTGCCCTGGAAA	CACCTAAGGACTCAAATCCAA	AAGAAATATCTCCGAAGTTAA	CACACTAATCTTGGAGGAATA
10869	USP19	XM_496642	CGGCCTTAGCTAGAAGTCGAA	GACCCGCATTATAAACATTAT	CCGGGCTGTGGAGAAGGATAA	ACCCGCATTATAAACATTATA
10874	NMU	NM_006681	CCAATATTACCTCAAGGATTA	CAAAGTCCCTTTGCAAGTCAA	CAGAGTGGACGAAGAATTCCA	GAGCAATGCTATGGAATACAA
10881	ACTL7A	NM_006687	CTGCTCGGAGATGTTCTTCAA	CACAAGAACCTACTGAATCAA		
10886	GPR74	NM_004885	CAGCTTGTCCAGGAATCTACA	CTACTACGCATTATATATTTA	CTGGCCATAAGTGATTTACTA	CCGGGAAGACTGGCCAAATCA
10890	RAB10	NM_016131	AAGGGACAAACTAGTAGGTTT	AAGCACTGATGTAACTTGCTA	CTGATGTAACTTGCTAGGTAA	CAAATTCGGTTTCATATTCTA
10897	YIF1	NM_020470	CACGAAGGCCTTCATTACTTA	CTGGCCTACAGTGGCTACAAA		
10901	DHRS4	NM_021004	CAGGATGCTCTGGATGGACAA	AACCCTTTCTTTGGAAGCATA	AAGGAGCAGAGTTGCAAATTA	TTGCGCGGCTTTGAATCCAAA
10906	FLN29	NM_006700	TACTGTTATAATAATTATTAA	CAGGAAAGGAATAGAGGCCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
10907	TXNL4A	NM_006701	TGGCAACAACAACAAGATTAA	CAGCATCGCCGAGAAGGTTAA	TGGCCTAATCTTAACTAATTA	AAGGTTTACTCTGGTTATAAA
10908	NTE	NM_006702	CCGGCGGTCTACAGACCTTAA	ACGCATGAGGAAGAAACTGAA		
10933	MORF4L1	NM_006791	CAGAAACAGCGAGAACTTCAA	TCCGGAGAGCAGAGTACTCAA		
10934	MORF4	NM_006792	GGGCACCCAGCTACTCAACAA	GCCGAAATTCTTGCAGATTGT		
10936	GPR75	NM_006794	CTCGGATTGAACCTTACTACA	ATGCATTATCACACCACTAAT	CCAGCTCGTATCAGCCATCAA	ATGGACTTTATTCTAACTTGA
10939	AFG3L2	NM_006796	CCGGCACCAATCGACCAGATA	GAGCGAGTGATTGGTGGCTTA	CATGGTATTGGAGAAACCTTA	ATGATGAAGTACGAATACTTA
10945	KDELR1	NM_006801	CCGCACGCTCTATCTCTTCAA	TAGCAAGTTCAAAGCTACTTA	CCACTGGTTGCCAAACACTAA	CACGTGTATGAAGGTGGTCTA
10946	SF3A3	NM_006802	AAGGAAGAATGCAGAGTATAA	CAGAGACTATTCAGTACCAAA		
10947	AP3M2	NM_006803	CCCAGTGTATGTCAAACATAA	CACAATTAACCTGCAGTTTAA		
10956	OS-9	NM_006812	ACCCACCATGTTCTTGAACAA	AACAATCAGGTTTCTAAATAA		
10957	PNRC1	NM_006813	TTGTATATATACAATGGATAA	TTGCCTTGTTGCAACATACAA	TACACTTGTATGAGCAACCAA	CAGATTTCAGTATGTGTGTAA
10966	RAB40B	NM_006822	AACGGTGATATTGGAGTGATT	ACGGTGATATTGGAGTGATTA	TCGGCGAATGCTGCTTGCGAA	CCGTCGGACTTCGAATTTCTA
10982	MAPRE2	NM_014268	AACGCAGGTCATACAGCTTAA	TCCCAATATCTTCTAGAATAA	GACCTTATTAATAGGAGCATA	CAGCAGGTGCAGCTAAATCAA
10983	CCNI	NM_006835	AAGGCTGTAGAAGGAAATATA	CAGCGTTATTTAAGCACATAA		
10985	GCN1L1	NM_006836	CTGGAAGATTGTTGTCTCCAA	CAGGTTCAGCTGGAATGTGAA		
11001	SLC27A2	NM_003645	CAGCCACTTGATATAATCCAA	CTGAGAGATGTCTTTAAGAAA		
11012	KLK11	NM_006853	CCAGGAGACGATGAAGAACAA	ACAGGAGATGCTGTCACTTAA	ATGCTGTCACTTAATAATCAA	CAGCTCCTGGCCATATATCAA
11016	ATF7	NM_006856	CGGGCTGTGGACAGAGATTTA	CAGCTACTGTTAGCTCATAAA		
11017	RY1	NM_006857	ATGACTTGCCATTATAATTAA	ATGGTTCTCTCCGCAAGTATA		
11027	LILRA2	NM_006866	CAGGCTGAGGAGTACCATCTA	GAGGCTCTGGAGGACAATCTA		
11031	RAB31	NM_006868	CGGGCACATTAGGCAGTTGAA	CACACACTGATTCATACTAAT	CAGGATTCACATAAACATTGT	AAGGAATACGCTGAATCCATA
11033	CENTA1	NM_006869	CACCCGTAACATCTTCATCTA	CGCAGTGGAGGCGCACTTCAA	CCGGAAGTTTGTGCTGACAGA	GAGGCGCACTTCAAGCATAAA
11035	RIPK3	NM_006871	ATGGCAAGTCTGGATAACGAA	CACAGGGTTGGTATAATCATA	CAGCCTGATGTCGTGCGTCAA	ACCGCTCGTTAACATATACAA
11041	B3GNT6	NM_006876	ACCGATGACAATGTGTAAATA	AAGTCTGAATACTTAATGAAA		
11045	UPK1A	NM_007000	AAGCATATACTAGATAGTCAA	CAAGCAGATGCTGACCTTCTA		
11054	OGFR	NM_007346	CACGGTGGGCCGAGCACAGAA	CAGGAGTGAACTGGCATGCCA	CACGCCAAACCTGAGTTTCTA	CAGAATGACAGGGTCCAGAAA
11068	CYB561D2	NM_007022	CACAAAGAGCAGCTTGGCAAA	CAGCTCATACTTGTACTGTAT	CAGGTGAGCAATGCCTACCTA	CACCAGCTTGGTCATTATGAA
11072	DUSP14	NM_007026	TAGCTGTTAAGTAACTATAAT	CCCAGGATTATATTAGCATTA	ACCCTTATTATTTAGCTGTTA	AAGGGAATGCATACATTGCTA
11073	TOPBP1	NM_007027	CAGCAATATTTCCAACATAAA	AACGAAGTTTGGAAACAGAAA		
11079	RER1	NM_007033	CACGATGAAGAGGCAAATCAA	CGGAATTATAAATATATATTA		
11092	C9orf9	NM_018956	CAGCATCGAGCAGAAGTACAA	CAGGTGCAGAGCTACATGGAA		
11098	PRSS23	NM_007173	ATGGTAGTCTTTGAACAGTAA	CACATATTAAACTATACCTTA	AACAGTTGTGGCCACACTAAA	CTGCATTGTAGCAATTTGTAA
11099	PTPN21	NM_007039	CCCACCGCAGTTGCACTATAA	AAGCACCTCCTTACCGGGCAA	GTGCATAGATTTCTATCTTAA	GAGGAGACCATTCAATTTCAA
11113	CIT	NM_007174	CCGGAAGCTCCAAGAAATCAA	AGGAATTTAGTCGGCGTCTTA	CAGGATATACCGTAACACGAA	ATGGAAGGCACTATTTCTCAA
11119	BTN3A1	NM_194441	TCAGCCTATAATGAATGGAAA	CTGGAGGAACTCAGATGGAGA	CAGATGGAGAAGTATCCAGTA	AAGACTCAGTTCAGAAAGAAA
11126	CD160	NM_007053	CTCAGTTGATGTTCACCATAA	ATGACCTCTTGTCATAGTTAA	AAGGAACGCGACTAAACTTAA	AAGAGATGCTAAATATACCAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
11127	KIF3A	NM_007054	GCCGATCAATAAATCAGAGAA	CCCAATTCATTTGCTCACATA	CTGGTTCAGAAAGACAGGCAA	GTGCCTTATCGTAACTCTAAA
11128	POLR3A	NM_007055	ACCAAGAAAGTCAGCATGTAA	ACGGCTGTAAAGACAGCTGAA		
11131	CAPN11	NM_007058	CAGGATGGCCATCAAATTCAA	CCCAAGAATACTGGCCATATT	CACATTCTTTCTAACCATGGA	ATGCGCCTGGTTATTGAGAAA
11132	CAPN10	NM_023083	CAGCAGGAACTTTGCCTCATA	CAGGATTGACAGGCCATCCAT	CTCCGTCATGGCAGTGATGAA	CAGATCTTCTTTATAACTATT
11135	CDC42EP1	NM_007061	GCCCAGCACAGTGCAAGCAAA	CTGGGAGAGACGAGCCATGAA		
11141	IL1RAPL1	NM_014271	GCGGGATACTTGTGAAATATA	ATCGGGCACTTTGAGAACTAA	ACGCATTGTGATGACCAGCAA	ATGCAACAAGTTGAACTCCAA
11146	GLMN	NM_007070	TAGCTATGCTTCAGCTGTATA	TAGCATCGAAACTAGGAGAAA	GAGGAACTTCAGTCTATAATA	AAGGCATATTCAATTGGATTA
11154	AP4S1	NM_007077	ATGCTCTTTCATTGAATATAA	CTGGTCCTTATCAGGAACCAA		
11157	LSM6	NM_007080	CTGGATGGCTACATGAATATA	CTGACATGTGAGTAAGATAAA		
11163	NUDT4	NM_019094	CAAATTCATGTTAGTGAAGTA	ATGAAACTGGTACCAATTTAA	CAGGTACTATTTGTCACATAA	AACATTTGTTCTACAAATTAA
11166	SOX21	NM_007084	CCGGTTTGTATGTACATAGAA	TTGAGCGAATATCAAAGTTAA		
11176	BAZ2A	NM_013449	CACTGAGAAGGCTAAGACTAA	CACCACTACAGAGATATCATA	CCCGCAGTGACGGCCAGTAAA	CTCGGTAGCTTTGAATCTTAA
11177	BAZ1A	NM_013448	CAGCTAGACCAGCTTATTGAA	AACGAGGAAGACCACAAGTTA	CACAAGTTAGATTGCCAGTTA	AACCCTCGTAACACAAGTGAA
11181	TREH	NM_007180	CAGGCCTGAGTCCTACAGCAA	CTCGCAGAAGTCAGCCATGTA		
11194	ABCB8	NM_007188	CACGATGCTGGTGCATTTATT	CACCTTCTTTGACGCCAATAA	AGGAATTTAAGTCATCCTTCA	AAGCTGGAAGCTTCCGATGAA
11197	WIF1	NM_007191	CACAAGGCATCAGTTGTTCAA	CCCTGTCGAAATGGAGGTAAA	TTGCATTGGCTTGAAGCAATA	AAGCAATATAATATATTGTAA
11211	FZD10	NM_007197	CAGGTGTGCAGCCGTAGGTTA	ACCTCACATTTGTGAACTCAA	CCCGATTATGGAGCAGTTCAA	CAGCCGTAGGTTAAAGAAGAA
11212	PROSC	NM_007198	AAGGTTCTCCTGAAAGGTTAA	ATGGCTCAGGTTAATTCTCAA		
11218	DDX20	NM_007204	CAGGGCATGGCAAGAATATTA	CCAGATGAAGACAAGACTTAA	CTGGACTATCAGTCAAATCAA	GGGCTCGATTTAATTGTTCAA
11221	DUSP10	NM_007207	CCGAAGATACTACACACTTTA	CAGGGCAGCTTAAGTGGTCTA	CAGGTTCATAGACCGAAGATA	ATGAGAATACAGGCTCTCTAA
11222	MRPL3	NM_007208	GCCGCCGAAACAGACAGTTAA	AGGGCATAAATATATCATTCA	CCGCCGAAACAGACAGTTAAA	CACATTAAATATATGAGTTAA
11224	RPL35	NM_007209	CGAGGAGAACCTGAAGACCAA	CAGGAAATTCTACAAGGGCAA	TGCAGCAATGGCCAAGATCAA	CCGTGTTCTCACAGTTATTAA
11226	GALNT6	NM_007210	CAGCGTGATCATTGTGTTCCA	CACCTTCTATGGTGCCATCAA		
11232	POLG2	NM_007215	CAGATACGAAATGGTGTTAAA	AAGGAACAAACTTTACTACAA		
11240	PADI2	NM_007365	CAGCAAGCGAATCACCATCAA	CAGCCTTGACTCATTTGGAAA		
11243	PMF1	NM_007221	AAGGATCTGCACAGTGTTATA	GAGGAAATCTCTGACATCAAA		
11248	NXPH3	NM_007225	CAGCGTCCACTTCCAACACAA	CGACTTCTACTCCAACATCAA		
11259	DOC1	NM_014890	AAGACTGAAACTGAAGCTAAA	GAGGATTTAACTAAACTGAAA		
11279	KLF8	NM_007250	CTCAGTCAGTCTGCCAAATAA	CTGAGATAGAATACAGAAGTA		
11283	CYP4F8	NM_007253	CAAGGACATAGTCTTCTACAA	TGCCCTTGTAGTGAAACGGAA	AGGGAATGTCTGTAACATCAA	CAGAGTCTAAGTAAAGACTTT
11284	PNKP	NM_007254	CAAGCTGGTGATCTTCACCAA	CGGGAAGTCCACCTTTCTCAA	CACGTGTGAGACAGCCCTGAA	CACGTGAACAGGGACACGCTA
11316	COPE	NM_007263	CAGAGCTGTCAGGACCATGAA	CCGGAAGGAGCTGAAGAGAAT		
11317	RBPSUHL	NM_014276	TCCCTTGTCCTTACACATACA	CTCAAAGGTCTCCCTCTTCAA	CCCATGATCATCCGTAAAGTA	CAGGTCCTTCCTGGAATATTA
11326	VSIG4	NM_007268	CAGACTCCTGATGGCAACCAA	CTGGTGCTCAATAAATATCTA		
11328	FKBP9	NM_007270	CAGCGGCGACTTCGTGCGCTA	AAGCTTGCCTACGGAAATGAA	TCGAGTCACAATCGCATGAAA	CTGGTGTTTGATGTTGCATTA
11329	STK38	NM_007271	AAGGCGTTGACTGGGAACATA	CCATAGTACTAAGGAAATAAA	TACGTCGGCCATAAACAGCTA	AACCTTATCGCTCAACATGAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
11331	PHB2	NM_007273	TCGCCACATCACAGAATCGTA	CAGAATCGTATCTATCTCACA	CACAGCTGCTGTAGAAGCCAA	AACCCAGGAATTCTCAATAAA
11334	TUSC2	NM_007275	AAGGCTGGTGCCAGTAGTTAT	CCAGTAGTTATGAGTAGCCTA	CCGCGGCTCTATGTTCTATGA	CAAGCTGAGGCGAGTGCATAA
11336	SEC6L1	NM_007277	CTGGAGCAACATCTGAATGAA	CACGCTCACTTCAAACATCAT		
11340	EXOSC8	NM_181503	CAGGAGATTTCTGAAAGAGAA	CAGAATTTGCAGCACCATCAA		
11343	MGLL	NM_007283	CCCGATTTGCCTGGTTCTGAT	AAGACAGAGGTCGACATTTAT	CTGGACCTACCTTAATGGTTA	TCAGAGCTTGATGCTACTGTA
11344	PTK9L	NM_007284	AAGGAATTCTTTGCCAAGGCA	CCAGATGAAGCTGGACCTAGA	TTGGGATGGTTGAATGCTGTA	AAGACAGAGATCAGTGTGGAA
22795	NID2	NM_007361	CCCACAGAAAGTAAAGTATCA	CTGGAATAGAGAAGCTCCTAA	AAAGCACATGTGATCAATATA	CACGTATAATGCTGCCAACAA
22803	XRN2	NM_012255	ATGGATTACATTAGAAGGCAA	AAGGAGGTTCAGGGCATCAAA		
22818	COPZ1	NM_016057	AGCGATTTAAATTGTATTGAA	TTGGCTGTGGATGAAATTGTA		
22820	COPG	NM_016128	CAGGAAAGGGACATTGTAAAT	AGGCCCGTGTATTTAATGAAA	CACCGACTCCACTATGTTGAA	CCGAGCCACCTTCTACCTAAA
22827	SIAHBP1	NM_014281	CTGGGACTCCGTCACCATGAA	CTCCGTCACCATGAAGCACAA		
22828	RBM16	NM_014892	CACGGTCGTATTCAAGTGAAA	CAGAATGATCCTGAACTTTAT		
22838	RNF44	NM_014901	CAGAGGGATATTCACTAATAA	CAGGTGACGTTTCTATATTTA		
22841	RAB11FIP2	NM_014904	TTGGAAGTATTTAATATGCAA	CTCGTTATAAACACTACTAAA		
22843	PPM1E	NM_014906	CCGCCTAATCATGTGTTTATA	TTGGTTCTATAAACTAGATAA	GAGGCGGTTTATAGTCAGAAA	CCCATTTAGGTCTGTACTAAA
22848	AAK1	NM_014911	CTCCTCGGACCTCTCAACAAA	CCCGAGAAGCTTGGAGGCTCA	CCAGGTGGTAAACCTGATGAA	AACGTGAGTAGCGGTGATGTA
22850	KIAA0863	NM_014913	AAGCAATTTCTTAAAGATTAT	CAGGAGAGAAATACTTTCATA		
22853	LMTK2	NM_014916	AGCGACTATTATATCCAGTTA	ACGGCTCTTAGCTGCGTTCAA	CAGATCAGACTAAGTATAGTA	CACCTCCGACTTAAATGTGAA
22871	NLGN1	NM_014932	CCGCCTCAACACAATGCCTTA	CGGAGGTATATTCTACCATTA	GAGGAATATTATGTGAATATA	AAGAAACATGACTGTCTCAAA
22882	ZHX2	NM_014943	ACGGCAGATCTTCCAAATCAA	CAGTACTATTGTGACATTAAA		
22888	UBOX5	NM_014948	CAGACAGTAACTTTGGTGTAA	TCCCTACAACTTGGTACTCTA	CCGGCACATTCCTTTCCTTTA	TCCGGTGTGCTTGTGTTCTTA
22901	KIAA1001	NM_014960	TCGCAATGGAGTCACACGCAA	CACAGGGTGATGGACCATCAA	AAGGACAAAGTTGACCACACA	CTGGAAGACGATACCGCAGAA
22902	RIPX	NM_014961	TTGGTATAAGTTCCTAATTAA	AACATTGTAAATAATCCTATA		
22913	RALY	NM_007367	CGGGCAGACCCTGGACATCAA	CTCAGCCAAGATCAAGTTAAA		
22915	MMRN1	NM_007351	CACAACTTACTTAGAAATGAA	TCCCTGTATATAAATATATAA		
22920	KIFAP3	NM_014970	TCGAGTTAGCTACAAACATAA	CCACATCTTGATGCTAAGTAA	CACAAGAGACGTCATAATCAA	CAGCATGATGGACCAACTAAA
22925	PLA2R1	NM_001007267	ATGCGTGGAAATATTATGCTA	ACGGTGTAAATACATCTGATA	AAGGTTTGGCTCATAGAGAAA	AAGGAGGTACGCTGTTAAGTA
22927	HABP4	NM_014282	AAGCGAGAATTTGAAAGATAT	CAGACCAAAGCCTGAGTTTAA		
22936	ELL2	NM_012081	CTGGGATTTATACAAGATAAA	CAGAAAGATGGTGTCAATCAA		
22937	SCAP	NM_012235	CCCGGTAGACCTGGAGGTGAA	CACCTGCTTAATTGACACCAA	CCTGACTGTAATAATATTAAA	CTGGCCGACGCTCTTCAGCTA
22938	SKIIP	NM_012245	CACAGGTCTCTCCAAAGTGAA	TCGGATGGTAGAAATGCAGAA	CTGGATATGGGACGAAAGAAA	CCCGATGAAGAAGCTATTAAA
22943	DKK1	NM_012242	CAGTAAATTACTGTATTGTAA	CCCTGTGATTGCAGTAAATTA	CACACTTGTCAGAGACACTAA	ATGTACTATCTTAATGCTTAA
22947	DUX4	NM_033178	GAGCTCTGCGGCACCCGGAAA	AGAGAGGAACGGGAGAGACTA		
22949	LTB4DH	NM_012212	CGCGCCGGAGGGAATAGGAAA	CACTGTTATCGGCCAGATGAA	CCGCATTTATGGGAATGCTGA	GGCCATTTAGATGATTAGTTA
22954	TRIM32	NM_012210	CTGGGTAGTTCTAGAACTTTA	CAGCAGGAATTTGACCCTCTA		
22977	AKR7A3	NM_012067	CTGGGCAGAGATGTACAGGAA	AAGGCTCTTCTGTAACATCTT	AACTGGAAGGAGCACCACTTT	AAGCGACTGCAGAGTGAAAAT

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
22979	KIAA0953	XM_039733	CTCAAGGATATCAGAAGCCAA	CAGCATTTGCGGAATTAACAA		
22980	KIAA1049	NM_014972	CCGGTCACTGTTGCCAAACTA	CCGCTTCGAGCTGATAAACAT		
22986	SORCS3	NM_014978	CAGGCTATTCTGAGCTCAGAA	ATGGAGGAGGGTGATCTACAA	AAGGCAGTCAGTGGATCTTAA	CACAACTTCCTTAAAGTCAAA
22987	SV2C	XM_043493	CCAGATTTAGCTGGAGATTAA	CTGCTCCTAATTTAACATTAA		
22992	FBXL11	NM_012308	AAGCCAGACTGAATCAACAAA	AGCGCTATGTGTACTGCATAA	CTCACTGGAGTTCCTATAGTA	ACCCATTTCGTTGCTACCCAA
23001	WDFY3	NM_014991	CGGCATTAATACTTTAATTTA	AACATGAAACTTCAAACTAAA		
23015	GOLGIN-67	NM_015003	CTGAAAGACAAGAGCATTTAA	ACCGGTCATCGTACAAAGAAA		
23030	JMJD2B	NM_015015	CCCGGCCACATTACCCTCCAA	CAAATTGAAGATGGAGATCAA	AAGCAATGTTTATATTATAAA	CACCTGACAAATCCTAGCGAA
23032	USP33	NM_015017	AAGAATTCCTTCGATGTTTAA	AAGAAGATCCGCAAACCATAA	CTGCAAGTAGTGGACACTATA	CCGGTTGTTCATGTTGATCCA
23033	KIAA1117	NM_015018	AAGGAGGGATATGTCTCTGAA	AACGAGAGATCTCCATATAAA	CCGGATTTCTGTTATGGGCAA	CCGGAGTTCTATGTACATAGA
23040	MYT1L	NM_015025	ACGGAAATGTATACAAATCAA	CAGGACTGAGTCAGAAATGAA		
23043	TNIK	XM_039796	CCGGAATATTGCTACATACTA	ATGGCGTTATTTCTAATTTAA	CTGGAATATAAGCGCAAACAA	AAGGACCATATTGATAGAACA
23045	KIAA0826	XM_093839	ATGCAAATTAATAGACATCAA	ACGCATTGGTACCAAATTTAA		
23049	SMG1	NM_014006	TTCGTTTGCATCACAGTTTAA	ATGGGTCAGGTTCGAAGTCAA	CACCATGGTATTACAGGTTCA	ATCGATGTTGCCAGACTACTA
23052	KIAA0830	XM_290546	AAGATCTATATGTTAAGCTAA	CAGCCAAACTATTATTTGATA	CCGCCCAGGATCAATCAGAAA	AACGAATGGTACAATCTCAAA
23053	KIAA0913	NM_015037	CTGGTATTTATTTGGCATTTA	CACGGGCAAGAGACTCCAATA		
23063	KIAA0261	NM_015045	CTGGATCATATTGTAGATAAA	AAGGAGATAAATCAAAGGAAA		
23081	JMJD2C	NM_015061	CAGATATTAATGGGAGCATAT	TCCCAGAAGTTCGATTCACTA	CCCAGAAGTTCGATTCACTAA	AGCGGGTAGGGCGATAATTTA
23082	PPRC1	NM_015062	AAGGAGCGTGCAATAGAAGAA	CAGGCTTTCATCAGTGAGATT	CAGACTAATAAACATCAACTA	AAGGGTGGTCTTCATTGGAAA
23085	RAB6IP2	NM_015064	CTGAAGTTATATAGCCTTGAA	AACGGGCTTTAACATGTTTAA	TAGAAGTAAATTAAAGTTGTA	CAGGAACTTAACCCAAATCTA
23086	SLAC2-B	NM_015065	AAGGAAGATTATGGAAACCAA	CAGGAGAATAAGAGATATGAA		
23090	ZNF423	NM_015069	CAGCAAGAAGTATAACTGTAA	CAGAGAGAAATGCTTAGTCAA		
23091	KIAA0853	NM_015070	CTGGCATATAGTAATACCCAA	AAGAAGCGCTATAGAAATGAA		
23098	SARM1	NM_015077	CTGGTGGTTAAGGGTAGCAAA	CAGGATCGGGATTACAGGCAA	CTGCTATTAAATCCACATTAA	AGCGGTGTTGGCGACTAACAA
23108	GARNL4	NM_015085	CACATTGTATTTGTTAATGTA	CAGGGAGTTTCTGCTCACCAA		
23116	KIAA0423	NM_015091	AAGGCGTATTTGGAAGTTTAA	CTGGAGCTATTTCACAGTATA		
23118	MAP3K7IP2	NM_015093	ATCCTAGGTAATTAAACCATA	CTGGGTAAACTATCTTTGTAA	TGGCTGGGTATCTCAGTTTAA	CAGTCAATAGCCAGACCTTAA
23126	POGZ	NM_015100	CAGGGATTTCCTGTAAGGAAT	CCGGGTGTAAGGTCCCTTTAA		
23129	PLXND1	NM_015103	CAGCCGCACTGCACAAGTGTA	CATGACAGTCATGGTCTATAA	CACGAGTACCGGGTCAAGATA	CACGCTCTGCAAGGTTCTCAA
23144	ZC3HDC3	NM_015117	AACGTGGTCATCAAAGTTAAA	CAGCGACTTCCTCAAAGGCTA		
23148	KIAA0363	XM_166571	CCGGGTGAGGCTGGAGTGCAA	ACGATCAGATCTGTCCTGCGA		
23149	FCHO1	NM_015122	CAGGAAGTTTGCAGAGAGTAA	CAAGTTCTATGTGCACATCAA		
23158	KIAA0882	NM_015130	CTGCAAGATAATGTAACTGAA	CTGAATGGATGTGGAAATGAA		
23163	GGA3	NM_014001	CTGGAGTCCTGGCTCAATAAA	AAGGAATAAATCCAAGAGCTT	CACGTTAGAGGAAGTTAACAA	CAGGGTGTCTGAGAAAGTGAA
23165	NUP205	NM_015135	CTGCGTCAGTTTAAATTTCAA	CTGACAGGAATTATAAGTAAA		
23166	STAB1	NM_015136	CACCTCGTGCGCGGCCATCAA	CACGAAATACTCCTACAAGTA	CACGCCAACTGTAGCCAGGTA	TAGGAACAATGGTCACTTGTA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
23170	KIAA0153	NM_015140	CGGCCACATCTTCAAGGTCTA	ACCCAGAACCTTCACCAGCAA		
23177	KIAA0582	NM_015147	CGGCAATTTAAGAAAGATATA	CACCCTCAAATCACCTACTAA		
23180	RAFTLIN	NM_015150	CAGGCAGATGAGGAAATCAAA	CTGAAATTCGTTGGTGTTATA		
23191	CYFIP1	NM_014608	TCGAAAGGTTATAGAAATAAA	CCAGCCAAATTTCAACACTAA		
23203	PMPCA	NM_015160	CAGAATAAGTTTGGACAGTTT	CAGGATCGAGATATGAAGCGA	CTCACCGAGATGATTCATGAA	TCGAGAAATGGTAGAAATCAT
23213	SULF1	NM_015170	AGCATGGATTTGATTATGCAA	AAGAGGCAAATTTCTACGTAA	TCCGTCGAATTTGAAGGTGAA	CTGGTGTTTGCGTACAGTTAA
23218	KIAA0540	XM_291064	CTCGGGAGAGACGGAATACAA	CACACAGAATGTATACTTCTA		
23231	KIAA0746	NM_015187	TAGAAGATTCTTAGTACTTAA	CCGGGAGGATTTCCATTATAA		
23235	SNF1LK2	NM_015191	CGGGTATGTCCTGGTGAATTA	ATCTACCGAGAAGTACAAATA	CCGAAGGATGTTGGTCCTAGA	AAGGGCAAGATTATTTGCTTA
23236	PLCB1	NM_015192	AAGCGAGTTGAAACTGCTTTA	CACACTACCAAGTATAATGAA	CAGAGATGATCCGGTCATATA	TCGAGATTACATGGATGTTAA
23258	RAB6IP1	NM_015213	CCGATTTGTCACTGCAATCAA	ACCATTGAGAAGAACATTCAA		
23259	DDHD2	NM_015214	CAGGATGAGTATGGACCTTAA	AAGAAAGAAGATATTAAACTA		
23268	DNMBP	NM_015221	TCCGAGGTTCCTCAAAGTTAA	CCAGCTCTTCACAAACTTTAA		
23277	KIAA0664	NM_015229	CAGCCCGACCTTCAAGAAGAA	CCGAGAAAGGGCCATATTCAA	AAGGGCCATATTCAAGGTGCA	CTCGGCCAAGCACATCTTCAA
23283	CSTF2T	NM_015235	CAGGATAAGGTTACACTTGTA	CAGCCATTTAGTCCTAATATA		
23284	LPHN3	NM_015236	CAAGCGTACAATGACAGGTTA	AAGTATGGGAGTAAAGCTAAA	CAGGAACTATAGGTGTATCAA	AAGCTAAACATTGCATATCAA
23303	KIF13B	NM_015254	AAGGTTATTCTTAATCCTGTA	ACGGGAAGCATTAGCAAGAAT	CCCACTAATGTCTTAACCTAA	ATGTCTTAACCTAAACCATAA
23304	UBR2	NM_015255	ATGGATCCAATTACACGTCAA	CCAGATTTATTACTACCATAA	CAGAACAATACTCTAATAGAA	CAGGTAAATGCTACAGATGAA
23309	SIN3B	NM_015260	CACATTAAAGTTAATAATTGA	CAGCTATGTGAATAAGATTAA		
23313	C22orf9	NM_001009880	CTCGCCCTTTGTAATAACCTA	AAGAATGTACCTGCACTCAAA		
23315	SLC9A8	NM_015266	CACCCTGGTTGTCACGACGAA	CTGGATGCCTATTTAGAAATA	CAGAGTCGCCTTAGTCCAGAA	TTGGCTCACCTTGGTAACAAA
23316	CUTL2	NM_015267	AACATTCTCATAAACATTTAA	AGGGAGGAACTCAACCATCAA		
23324	MAN2B2	NM_015274	GTCCAATATCAGAACTATTAA	CCGGACGTTCTTTATTCACTT	CACGGGTTTCTCTATGAAACA	CGGGCTTTCTTTGGAAGATGA
23326	USP22	XM_042698	AAGGTGAATTTCATAAATGTA	CTGAGTTTATACAGAAATTTA		
23332	CLASP1	NM_015282	CAGGATTAGAAACACACTTAA	AAGCGTAATGTTACACTTTAA		
23347	KIAA0650	XM_113962	AAGGATCTTAACAGTCAATTA	CAGGGATAAAGTAATTCCTAA	AGGACCAATTATCTCAGTCTA	CCCGTTCGTCTCAATGTTAAA
23352	RBAF600	NM_020765	CTGCGTGAAGGTGAAAGTCAA	CAGCAGGGTTATGCCCTTAAA		
23367	LARP	NM_015315	CAGGCTGAAGTGATTCATTCA	CACCTAATCCACAGAAAGTAA		
23378	KIAA0409	NM_015324	AAGGGTAGTACTACAAATGAT	AAGGGAAGAAGAAATGTCAAA		
23379	KIAA0947	XM_029101	CTGGCAGTTTATTGCTCTTAA	CCGCATCATTCAGAACATAAA		
23385	NCSTN	NM_015331	CCCGAATGGCTGAGCCCTGAA	CAGTGCCAGGATCCAAGTAAA	AAGGTTTAATGTCAGGGTCAA	TCAGATTGGGATTAACATAAA
23386	KIAA1068	NM_015332	AGGCAGGAACTTGAAGAGAAA	CCCTGCTTTAATAAACAGCAA		
23396	PIP5K1C	NM_012398	CGGCGAAACCACCTACAAGAA	GACGGCGAGAGCGACACATAA	CGGCAAGACCTATTTATAATA	CCGCGTCGTGGTCATGAACAA
23398	KIAA0073	NM_015342	AAGGTTGATGCTGTAAGATTA	ATGGGAGACATTCACACCAAA		
23403	FBXO46	XM_371179	CAAGATCACATGTGACTTATA	CCCGCCTTCTGCGGCCCTCAA	CAGCGATAGCTCCAAGGCCAA	CTAGATGGTTTGCCTATTAAA
23404	EXOSC2	NM_014285	CTGGTAAAGTTGGAAGAATAA	CTCCATTCCTATATCCTTTAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
23411	SIRT1	NM_012238	CAAGCGATGTTTGATATTGAA	TTGGGTCTTCCCTCAAAGTAA	CAGGATTATTGTATTTACGTT	ATAGCTGTTCTTTATGCATAA
23413	FREQ	NM_014286	CTGCGTGGCTAGGATGATTAA	CCCGGGCTGGTTGGTCTTGAA	GCGGAATAAACCCAATGGTTA	CGGAATAAACCCAATGGTTAA
23416	KCNH3	NM_012284	CCGGCGGGAGCAGGTGGTAAA	AGGGTAGTAGATGGCATTGAA	CCGTACCACATTCGTGTCCAA	CAAGGACATCAGCGAAACCAA
23417	MLYCD	NM_012213	CCCGGGTTCCTGAACCTAGAA	CAAGGTGTGTGTAGTAAGTTA	AAGTTGGATAATAGGCTTTAA	TAGGCTTTAAATGATCAGGGA
23428	SLC7A8	NM_012244	CTCCCAATATATTTACACGAA	TGGTGAGAAATTGTAAACAAA	CAGGCGGTTGAGGAACATATT	CCCGAATTCTGTCTGCTTAAA
23451	SF3B1	NM_001005526	AAGACTCACGAAGATATTGAA	CAGGTTATTATGACCAGGAAA		
23456	ABCB10	NM_012089	ACCCTGCTTCTGGAACTATTA	CCCAGTGTGGCTGAGATCCAA	CTAGGTATTATTAAGAATGAA	TAGACCCTAAGAAGTAATTAA
23457	ABCB9	NM_019624	CTCCCTAGCCTCCTAAGCAAA	TTGAGAGAACCCGGTCAATAA	CTGCGTGACCACGGCCATCTA	CCCGGTCAATAAAGTGTACTA
23463	ICMT	NM_012405	CAGAAATATGACTTATTTCTA	CAGAGTGTAAGTAAAGGATAA		
23468	CBX5	NM_012117	CAGGGAGAAGTCAGAAAGTAA	GCCGATGACATCAAATCTAAA		
23471	TRAM1	NM_014294	CCGGAACAATTGTGTGCTTTA	CTGGCATTATACTGAACTATA	ATGGTGTGAATGGAACATTAA	CAGGGTAACATGGAAATACTA
23474	ETHE1	NM_014297	TCCCTGGAGCTCCCTAAATAA	CAGCTGTGAGGAGTTTGTCAA		
23480	SEC61G	NM_014302	CAGCAATAGGATTTGCTATAA	CTAAATTAAAGTAATTTCAAA		
23484	LEPROTL1	NM_015344	TCCCAATGTTATGCAGACATA	CACAGTCATCTTTGCAACTAT	CAGAGACTTGCTGAAGGATTA	CAGACGGTTGGCATACGTTAT
23495	TNFRSF13B	NM_012452	CTGTAGGTCGTCATCACCTAA	CAGCGGAGTGGAGAAGTTGAA	AAAGGAGCAAGGCAAGTTCTA	AACCCTAAGCAATGTGCATAC
23506	KIAA0240	NM_015349	TTGGATATAGTCAACATATAA	CCCAATTAATATACAGCCAAA		
23507	TA-LRRP	NM_015350	AAGCATATTGGATTTATTTAA	CAGATCAACCTCAATAATGAA		
23511	NUP188	XM_497078	AACAATGTTATTCGGCTGAAA	AACAACCTCATTGCTGTTCTA		
23513	SCRIB	NM_015356	CTGGGAGGCAACGATCTGGAA	CAGGATGAAGTCATTGGAACA		
23524	SRRM2	NM_016333	CCCACTTGGTACAGAAATGAA	CTGGGTCATCTCCAGAAACAA		
23531	MMD	NM_012329	CGCCATTTGGAAATACCTTTA	ACGGACTTTATGCGGCATTTA	AACCATTTATGTATTTCTCTA	AACCACTAATATGTATGTAAA
23532	PRAME	NM_006115	AAGGAAGGTGCCTGTGATGAA	CAGGATGTGCATGCATCTTGA		
23533	PIK3R5	NM_014308	CAGGATCTATAAACTCTTCAA	TAGGATCCTTTCTAGAAGGAA	ATCGCAGATCAAAGTGGACAA	ACCGGTGCTGCTGCAACTCTA
23543	RBM9	NM_014309	TAAGAAGATGGTCACACCATA	TCCGTTTGGTTTATGGAGAAA	ACGGCTGCTTTGAAAGGTTTA	AACGGTATAAAGAGAGATCAA
23548	OSRF	NM_012382	CAGGAAGATACTATTGGTGTA	CCGCTTTATGTTAAAGATCTT		
23549	DNPEP	NM_012100	CACGAGGGTGATGAAGGCCTA	CAAGTACTTCATGACCAGGAA	GAGCTGAAGCTGGATTATTAA	AAGTGGATTGTCACTCAGAAA
23550	PSD4	NM_012455	CTGCCAGGAATTCATAACCAA	CACGGCCAAGGTGAAGCGCAA		
23551	RASD2	NM_014310	CTGGGAGGGATCCGACAGAAA	CTCCGTGTACACTATCAATAA	TCCGTGTACACTATCAATAAA	ATGGATCTCCGTGTACACTAT
23562	CLDN14	NM_012130	AACAAGTTTAATATAAAGTGA	ACGGCCGTGTCCTACCTGAAA	CGGGTACAGGCTGAACGACTA	CACGGCCGTGTCCTACCTGAA
23563	CHST5	NM_012126	CAGGGAGTAAGTTACTGCTAA	AGGGAGTAAGTTACTGCTAAA		
23564	DDAH2	NM_013974	CTGGATCTGGCCAAAGCTCAA	TAGGATAGTATAGGAAGTAGA		
23567	ZNF346	NM_012279	ATGGGCCAGACTACAACTTAA	GGGCCTCATGAAGGTCTTTAA	CGCAAAGAACTTAAAGCTGAA	ACGCAAAGAACTTAAAGCTGA
23584	VSIG2	NM_014312	CTGCCTGGTCAGGTTCCAGAA	CAGCACCGTGACGACCACCAA	CCCACCAGATTTCTACACCAA	ATCCAACTGGTTCTAAGTCAA
23586	DDX58	NM_014314	AAGGATAATACTGAACTGTAA	CAGGAATGTGAAGAAATTCTA		
23589	CARHSP1	NM_014316	CACCATCTGAAGAGCATTAAA	CTGCACATCTCTGATGTGGAA		
23590	TPRT	NM_014317	CTGGCACGAATTGGAAATACA	CAGAGTGATGGTGTGCAACAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
23604	DAPK2	NM_014326	ACGCCGGTGGACAACCAGCAA	AACCCTTGGTACCACAGAATA	CTGGTTAAAGAGACCCGGAAA	CGGAATTTGTTGCTCCAGAAA
23613	PRKCBP1	NM_183048	TTGACGCAAATAGCGAAAGTA	ATCGACACGTTCCGATCACAA	CACCATTGAACAGTTATCCTA	AGCGAACTTGTCATAGATTTA
23616	SH3BP1	NM_018957	CCCTGGAGACATCAACTTCAA	CAGCCCAGTCTCTTTGAGTAA		
23620	NTSR2	NM_012344	CAGCTTCGTGTGGTTCCACTA	CAGAGCCATCGTGGTCATGTA	TCGTATGGAAGAAGACCTTTA	CCGGACCTGAATGTAATGCAA
23624	CBLC	NM_012116	CAGACCATCCCTGCCAACAAA	CAAGATCTGTGCTGAGAGCAA	CTGGGAGGCCGTGAGTATCTA	CAGCCGAAAGTGAGACTCCTA
23626	SPO11	NM_012444	TACCTTCTACGATACAACTAA	ACAACTAATGTTAACGCATAA	TACATATATTATCTACATCAA	CAGAGTGTACTTACCTAACAA
23632	CA14	NM_012113	GTGGGTGAGACTAAGAATATA	TTGCATGAAGTCAGGCATAAA	AAGCAGGATCCTCGTATACCA	CGGGATCTCTCCTTAGGATAA
23633	KPNA6	NM_012316	CAGGTACTTATTATTGGCCAT	ACGCTTGGATTGAGTTATTTA	CTGGGTGGATTACATATGATA	AACCATTCTCTTACAGTTTAA
23636	NUP62	NM_016553	CTGGAGAGCCTGATCAACAAA	CCGCGAGGTGGAGAAGGTGAA	CGGCTTTGCCTTGAATTTAAA	ACCGGCTTTGCCTTGAATTTA
23645	PPP1R15A	NM_014330	CAGGATCAGCCGAGGATGAAA	GTGGGTTTATATAAGGAATAA	TGGGTTTATATAAGGAATAAA	CCAGTTGTTGATCTTATGCAA
23650	TRIM29	NM_012101	CTCCATGTACCTGACACCCAA	CCGGCCATTCTACGTCAACAA		
23673	STX12	NM_177424	AAGAATTTGATGAGCCAGCTA	CTATATTTAATTGGAAGGTAA	TCCTTCTGTTATTATACTTAA	CTGGGTTTAAAGTTTACTTCA
23678	SGKL	NM_013257	CCGAGATGTTGCTGAAATGTA	CATGGTATGATCGAAATGTAA	CCACAGCGAGACCCTAGTTAA	ACCAACTAACTTACATGCTTA
23682	RAB38	NM_022337	ACGAGGGTCTATTACCGAGAA	CAGCAAAGGCCTCAAGTCTTA	CTCCAAGTTAAGTCTCCCTAA	ATGATTTGGACTCCAAGTTAA
23683	PRKD3	NM_005813	CAGGCGGGAAACTGAATAATA	CTGAGCCTATTTCTAGTATAA	CGGGAGAGTGTTACCATTGAA	CACGATATGTCAGTACTGCAA
23704	KCNE4	NM_080671	CTCGGAGAACATCCATCAGAA	TCGGAGAACATCCATCAGAAT	CCCAGCCCATTTGCACACTAA	CCAGCCCATTTGCACACTAAA
23760	PITPNB	NM_012399	AACAAAGTAAATGAAATTTAA	CAGGATAAAGACTGATGTTTA		
23761	PISD	NM_014338	TTCCTTCTGCCTACAAATAAA	CAGCTTCGTGACGCACACCAA		
23765	IL17R	NM_014339	CAGGTTTGAGTTTCTGTCCAA	CAGGAAGGTCTGGATCATCTA	CGGCACCTACGTAGTCTGCTA	CAGCGGTCTGGTTATCGTCTA
23770	FKBP8	NM_012181	CTCCTACGACCTCGCCATCAA	CTGCCAGGAACTGACCACCTA	AAGACAACATCAAGGCTCTCT	AATCCCATGGAAGTGGCTGTT
23786	BCL2L13	NM_015367	CAGGCATTTCGGGAATGTACA	CTGGATGGTCCCTGTCTATAA	TTGGGCTTATAGAGCCAGTTA	CCGTGTCTTTCCAGCCCTAAA
24139	EML2	NM_012155	CAGCAGCTGCTTTGTCACCAA	CTGCGGGAAATCTCACATCTA		
24142	NAT6	NM_012191	CTGCTGGAGACACAATATCAA	CCGCCTGTCACGGGTGCTGAA		
25764	HYPK	NM_016400	CAGCAGAGTTACTGTACTCAA	CTGGATTAATTTATGGCAATA		
25776	PGEA1	NM_001002880	CGGCTGAAAGTGGACATCTTA	CTGGAAGAGAGTATCATATAA		
25777	UNC84B	NM_015374	CTGGGAGTGTGTATATATGTA	AAGGAGGATTTCCGCAGGGAA		
25778	RIPK5	NM_015375	CTGGTCCATTAGATTCCGAAA	CACCGCTTTATCGCCAGCTAA	TTGCTTCATCGTAAACCTAAA	TAGAGCTTGTTTGATGTTAAA
25788	RAD54B	NM_012415	CACGAACTTCGACCTACTGAA	CAAAGGCAGATCAGTAAGCAA	CTGGATCAAATTAAGAATATA	ACCCAAGAAATTATAAATAAA
25793	FBXO7	NM_012179	CCGATTTACAATTACATTGAA	CAGGATGAACAACCAAGTGAT	GACAATACTGTCAGAGTTCAA	CACAGATTGGAAAGAACTGTA
25796	PGLS	NM_012088	AAGCCAGGTGATCACCATTAA	CAGCGTGTGACCCTCACACTA		
25804	LSM4	NM_012321	ACGGATCTGCTCAGAAAGGAA	CGACAACTGGATGAACATTAA		
25822	DNAJB5	NM_012266	AACGAGGATGAGATCAAGAAA	CCGGAAGATGGCCTTGAAGTA		
25824	PRDX5	NM_012094	ATGGTGGTACAGGATGGCATA	CAGCCAGGAGGCGGAGTGGAA	CTGAGTGTTAATGATGCCTTT	CACCTGCAGCCTGGCACCCAA
25828	TXN2	NM_012473	CCCGGACAATATACACCACGA	CAGGATGGACCTGACTTTCAA	CGGGAAGGTGGTGATGGCCAA	CCCAAACTAGTGAGAGTAATA
25830	SULT4A1	NM_014351	AAGCAGATGCTTAATAGTAAA	CCGGAGGTTTATGAATGATAA		
25832	DJ328E19.C1.1	NM_015383	AACGATGACGATGAAGATGTT	AACGAGAGCTGACCCAGTTAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
25839	COG4	NM_015386	CAGGGATGTTCTGTGTAATAA	CAGGAGCTAATTGGCTTATAT		
25847	ANAPC13	NM_015391	CTGGAATTATTTGCCTGTTAA	ACGGTTTGTTTCAGTCTCCAA		
25853	WDR40A	NM_015397	CAGCATCAATGTGATTAGTAA	AACACTGATAATAGGAAGTAA		
25859	PART1	NM_016590	ATGAGATATTCTACACATTAA	AAGAAAGTCACTCATGAGTAA		
25865	PRKD2	NM_016457	CCGGCAGGGCCTGCAATGCAA	CAGCGGCACCTTCCCTTTCAA	TTGGGTGGTTCATTACAGCAA	CACGACCAACAGATACTATAA
25873	RPL36	NM_015414	CGGGAGGAGCTGAGCAACGTA	AAAGAACAGCTTGACAGGAAA	GCCCTCAAATTTATCAAGAAA	CTGCCCTCTCCCTGAAATAAA
25874	DKFZP564B167	NM_015415	AAGCTAAAGCACACAAATAAA	CAGGGTTTATTTGGTCAAGAT		
25886	DKFZP434C245	NM_015426	CCGGGCTCACACACAAATGAT	TAGAAATTGATTGCACATTGA	CTCCAGTGACTCAACCCTGAA	CCGGGAATGTGTCCACTCGTA
25903	OLFML2B	NM_015441	CAGGCTGCTGTTCGAGAATGA	TCGAGAATGAGTATTCCTATA	TTGTATAATATTGCAAATGTA	GCGGATTTACGTAACCAACTA
25911	DPCD	NM_015448	ATGGTCATATTTCCTGAGTAA	AAGGAAATGGCTGAAGAATAT		
25913	POT1	NM_015450	CAGGCTGAAGATTCAAGTATA	CAGGGTCTTGCCAGAAAGTAA		
25917	THUMPD3	NM_015453	AAGAGGATGTATCAACATTAA	CAGGAGAGAAACATTGCTTTA		
25926	DKFZP586L0724	NM_015462	CAGGACAGTCATCCTCTATAA	TTCGGGAGCTACAGAAATTAA		
25927	C2orf32	NM_015463	AAGGATGGTAACAAACTAGAA	CAAGGTTGAGGTGAAGATTAA		
25932	CLIC4	NM_013943	CACGAACATGCAGTTATTGAA	CTGGATATGTACTAACGAATA	TAGCAGTACAATGATTAGTAA	CAGGGAAGTTAGTCAAATGAA
25937	WWTR1	NM_015472	AGACATGAGATCCATCACTAA	CTGGCTGTAATCACTACCATT	CTGCGTTCTTGTGACAGATTA	ACAGTAGTACCAAATGCTTTA
25938	C14orf125	XM_113763	TCGATTTATGAGAAAGATGTA	TAGGTTCATATCTACATTGTA	CAGCCTTACAGTGCAACATAA	CTAGGCATAATATTAGCTAAA
25942	SIN3A	NM_015477	CAGAGGATATATGCTGATAAA	CAGATCCGCAGACATCCTACA	GAGCGTGTAAGCAAGCGTCTA	CTGGTCACTCGAGCACATCTA
25943	C20orf194	XM_045421	ACCGGGAAATTGAGAAGTATA	AAGGTAATTATCAGCATTGTA		
25959	ANKRD25	NM_015493	CAGGTTCATTAAAGAAGGCAA	AAGCTGATTGGAAACAATTAA		
25963	DKFZP564G202	NM_015497	AAGATTGTCATCAACACCATA	CAGAAGTTGTAGCTTATACAA	AGCGCTGATTGTTACAATGAA	CTGGCTTAATTTAAACAGTTA
25972	UNC50	NM_014044	CCGGCTGAAACTGCTTTCTTA	AAGAAAGAGCATTTAGTATAA		
25977	NECAP1	NM_015509	CGGGAACATTACAAACAAGAA	TAGCTTCTCCATCACATTCAA		
25979	DKFZp566O084	NM_015510	GAGGATGAAGTTGATTGACTA	CCGAGATGGAACAGTATGAAA	TTGCATTTGTTGAGACTTTAA	CAGATGTTATGTCACCTGAAA
25980	C20orf4	NM_015511	CAAGAGCATAATGTACATTAA	TAGGAGCTTAGGAAACAAGAA		
25981	XLHSRF-1	NM_015512	CAGGATGTACATCACCACCAA	CAGCCGTACATCGATAATGAA		
25988	MIZF	NM_015517	CCCAAGGACTTTCATGATTAT	CAGGGCATTATTCTAGAAACA		
25992	SNED1	XM_059482	AAACCTGTTCTTAGACTCCAA	CTCAGTGAAGCGAAACAGTAA	CAGGTAGTAAACACGATCTTA	CACCTAGGCTTCAGCCTTAAA
25998	IBTK	AB037838	AAGCATGGTGTTAGTCTGTAT	GAGGATTTAAATTATCCTAAA	TAGAAGAGTCATTACACCATA	CAGATTGAGGAGCATGCCATA
26009	ZZZ3	NM_015534	CAGCCTGATGGGAACACTAAA	TAGGAATTTACCTGAATATAA		
26015	RPAP1	NM_015540	AAGGAGGATAGCTGAAGCCAA	CAGCAACATCTGGTAAGAGAA		
26020	LRP10	NM_014045	TACAGAGAATCCTAATGATAA	CAGGGTGCCATCCCACCTGTA	ACCCTATGTAGCTGCTATAAA	CACCGGAATGCCAATTAACTA
26030	PLEKHG3	NM_015549	AGGAATGAAGCCAATAATTTA	CCGGTCTTCCTGCAAGAAGAA		
26031	OSBPL3	NM_015550	CTGCATTGTACTAATCTGTTA	AAGAACCAAGGTAGAATTTAA		
26033	ATRNL1	NM_207303	CAGGTTATTATGGAGATCCAA	CAGGGTGACAAGATATGTATA	CAGCTTTCCGCCTAACTAGAA	TTGGTCGTAGGTAAAGGTCAA
26038	CHD5	NM_015557	CCCACGGTACATGATCCTCAA	CAGCTACAAGATTGATTACAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
26040	SETBP1	NM_015559	ATGGAATGCCTTACACATCAA	CAGAGGGAAGTCTGAAGCTAA		
26043	KIAA0794	XM_087353	CAGCTTGAAAGGAGTGTTTAA	CAGCACGTGCATATTCATTTA		
26050	SLITRK5	NM_015567	TTGCATCTAAACAATAATAAA	CAGGCTAAACCTGAGGAGTAA		
26063	DECR2	NM_020664	CAGAATCGACATTCTCATTAA	CTGCACCACCTGTTTGCATAA	AAGATAATCTATTTACTGTAA	AAGAAAGAGGATTAAAGAGAA
26088	GGA1	NM_001001560	CAGAGGCCTACCAGATGCTAA	TCGGACATCGGAGAAGGTGAA	TCGGTGTGTCTCCTTCATTCA	CCGAAGAATGTGATCTTTGAA
26091	HERC4	NM_015601	TACGTTAGCGCTAAATGACAA	CAGAGTACCCAGAAATATTAA	TAGAAATACTACATAGGGTAA	GAGGGAATTATTGGATCCTAA
26127	FGFR1OP2	NM_015633	CCCGCCGGTGATGGCGTTGAA	TACGCTAAATTTCATCCTTAT	TAGACATATTTAGTAGGTTAA	ACGGAGGATTTGTACGCTAAA
26145	IRF2BP1	NM_015649	CTCCGATTTCGAGAAAGAGAA	CCCGTTCAATGTGCGCTTCAA	TTCAAGTACCTCGAATATGAA	ACCGCTGCCGCGGATAAATTA
26148	C10orf12	NM_015652	CAGAGGATTTATAATTATAAA	CAGGATTTAGAGGCAAATGAA		
26154	ABCA12	NM_015657	CACTCAGTTAATACCGATCAT	TTGCGACTCTTAATCAACGAA	AAGCCTAATGATCCGACTTTA	CAGGTGACTCCGATAATATAA
26155	DKFZP564C186	NM_015658	AAGGATGAGGACAGGAAGCAA	CACGGACAGTGCTGCATTCAA		
26165	C9orf36	NM_015667	GGGAAGAGAAAGAGTCCAGTA	CTCAGAAGCTCTCAGATCCTA		
26166	DKFZP434I092	NM_015668	CCCAGACTATATAAACTTCAA	TCGGACCAAATTGCTTATAAA		
26175	C14orf109	XM_058628	CAACATAGTGATGATTCAGAA	CTGGCCTTGGAACACATTCAA		
26190	FBXW2	NM_012164	CAGAGTGTATGCACTTTACTA	ACGGAATGGGTCACCAAGGTA	CCAGTGGGACTTTGCCAGTTA	CACGCAGTGCACAATCATTTA
26212	OR2B6	NM_012367	CCACAAATGCTAGTAAATTTA	CAGCATCATACAGGAGTTTAT		
26226	SHFM3P1	NM_012165	CCGGGAAGAGTACAAGGACAA	ACCGCTGGCTGTGGCACTTCA	CTGGCTGTGGCACTTCACCAA	CCCAGTGAAGGTGTCTCAGAA
26227	PHGDH	NM_006623	CTCGAGAATACTGCCCAGTTA	TGGGATGAAGACTATAGGGTA	CACGACAGGCTTGCTGAATGA	CAGCAATAACCGTCTAATAAA
26228	BRDG1	NM_012108	GAGGCTTCATTCTTACAGTAA	CACCTGAACACCAGAATTAGA	AAGGAACCAACTGAAGATTAT	CACCAGAATTAGAATTAAACA
26232	FBXO2	NM_012168	CACAAAGTGGGCTCTCAATAA	TCGAGGGTAGATAGGCCTTAA	AAGCTCACCGTTAAGCTACTG	AACGATGAGAGCGTCAAGAAG
26233	FBXL6	NM_012162	CCGGCTGACTCTAGCCAAGGA	CCCGGGCCTGCTCTACCTCAA		
26235	FBXL4	NM_012160	CACCGGTCTTTCCCATGTTAA	TTGGCTGGTGTACCAAATGTA	TCCGAATTAGTACGCCTTGAA	AACGACTTGTTCTCTATCGAA
26254	OPTC	NM_014359	CACCTGCAGAATAACCTGATA	CAGGGACAGCTTCTCTCCCAA		
26256	CABYR	NM_012189	ACCAGTGTAATGTATCAATAA	CCAGTGTAATGTATCAATAAA		
26261	FBXO24	NM_012172	CCACCACTCAATGACCTTCAA	CCGAATCTTCATGCAAGGAAA	CCCAAGGTGTGACACAGTTTA	CAGGCGAGTGACTGTCAAGAA
26273	FBXO3	NM_012175	CTGACGATTATCGATGTTCAT	CTGCCAGAACTTAGCTCTGTA	GTCGGGTATATGAATACACAA	TCGCTAAGACCTTGACTTTAA
26275	HIBCH	NM_014362	CAACTTAGGTATACAATATAA	CACGGGAGTCATAACACTAAA		
26276	VPS33B	NM_018668	CCGGAGAGGCATGGACATTAA	CAGCGTTGGATCAACACTGTA		
26292	MYCBP	NM_012333	AAGCAGGAGAATCCAAAGTAA	CAGGACAGAGGCAATATACAA		
26298	EHF	NM_012153	CAGCAATAATATGCAAATGAA	CTGGAAGTAAGAAGAATTAAA		
26330	GAPDS	NM_014364	CAGGCCAATGATAACCTTATA	CCCGGAATACATGGTGTACAT	CTCCATGAACATTGTGAGCAA	CCGAGACAAGTGAAACGGGAA
26338	OR5L2	XM_372387	CCGCTTTGTGGCCATCTGTAA	TTCACTCGTCCTTAGCTCTTA	CACCACTATCCTGAAGATACA	AACAGTGGAGATGTTGACAAA
26469	PTPN18	NM_014369	CCGGGTGTAAGTCTAACGCCA	GTGGGCCTGGATCAAAGTTAA	CCCAATGACTGTAGCATTCAA	CAGGCAGACATCAGTCCACAT
26507	CNNM1	NM_020348	CAGGTCTTAAGTGCAAATCAA	CAGGTGCAATTCCAAGCATAA		
26515	FXC1	NM_012192	CACCGAGAAGCTGAAACGGAA	CAAGTATTTGTTGGTTCATAA		
26523	EIF2C1	NM_012199	CCAGACCTCGACCATGATAAA	CAGCTACAACTTAGATCCCTA	CTCCAAGAATTGTGCAAGTAA	TAGGCTTAACATAAAGCCGAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
26533	OR10G3	NM_001005465	CTGCGTTTATCCTGACAGGAA	CTCATGATGAACTTCACTTTA		
26538	OR10H2	NM_013939	AGAACTGAAGGTTGCCATGAA	TGCCTCTGTCATCTACCTCAA	TTGGCCTGTGGAAATAATGTA	CACCCTGATGGCCACCACCTA
26539	OR10H1	NM_013940	CACCTTGATGGGCATCACCTA	TTCAGTAAACTCTACCCAGAA	GACCTTCTTCAGTAAACTCTA	AAGAAGACCTTCTTCAGTAAA
26578	OSTF1	NM_012383	CAGATGCAGTTCGAACATTAA	GAGGACTATCTCGATGATGAA		
26583	DUX2	NM_012147	AGCCAAAGCAAGGCCCTACAA	CTGAGGCAGCACTGGCATTAA		
26610	ELP4	NM_019040	AAGGAATTTGATGAAGATGTA	TTGGACCAGTATCATCTTCAA		
26658	OR7C2	NM_012377	CTGTGGAATCCTATTCTCTTA	CGCAGAGGACTCTGACATGCA	CTGGTGAATATCCAAACACAA	CTGCAGTTACACCACCTTCTA
26659	OR7A5	NM_017506	AAGATAATTTATTGGCTATAA	AACTGGTCTTGTAGAATTTAA	ACAGTCAGAGATGACCTTAAA	AAGCTTAGTGCCCATATATAA
26716	OR2H1	NM_030883	CTGCTAGACAACGTTTGATCA	TACGTAGGTCATGTAAGCAAA	TAGCTCCATAAGGCACACAAA	CCACATTAAAGTTGCAAATAA
26762	HAVCR1	NM_012206	AACGCTGATCCCATAATGCAT	TCGGAAGGACACACGCTATAA	GGCCTTTGGAATAACAATCAA	CACCATTGTACTCTTACACAA
26873	OPLAH	NM_017570	CTGCCTCATCATCGACAGTAA	CTGCTGCACATTGGCACCCAA		
26985	AP3M1	NM_012095	ACGGTCTTCCTGCATATTTAA	CTGGATTATGTAGAAGATTTA		
26993	AKAP8L	NM_014371	TAGCTCTGACACAAATGCAAA	CCGGCCAATGGCCTCAGGCTA	CAGGATAACACCACCAACTAT	AAGGAACACTTTAAGTACGTA
26995	TRUB2	NM_015679	AAGCTGTAACAGAAAGGTCAA	CTGCGGAAGTTGGTTCATGAA		
26998	FETUB	NM_014375	ACCGCTCAAGTCTGCCTTAAA	CAGCAGTATATATGTGCTGAA		
27012	KCNV1	NM_014379	CCGATATGTCCTGCACTACTA	AAGCTATGTACAATTAACTAA	CTGACACATTTGAGTGTCCAA	CTGTATCCCATTATTACTATA
27013	C2orf24	NM_015680	CTCCATGATGGTGGCCAGTAA	CTGGCTCTGGTGTACATTGAA		
27018	NGFRAP1	NM_014380	CTGCCATTTATCATGAGATTA	TGCCATTTATCATGAGATTAA	CTGGGAAAGAATCCCGGGAAA	ATGGCAAATATTCACCAGGAA
27020	SDFR1	NM_012428	TACATAAAGATGAGTAATATA	ACAGGTATATACAGCATATAA	CTGGTACATAAAGATGAGTAA	CAGGTATATACAGCATATAAA
27032	ATP2C1	NM_014382	AAGGTGCTTACGAACAAGTAA	AAGGGCAGACCTTGACACTTA	TAGGGTAACAGTGTCCATAAT	TACGTATTAAATGCACGTTAA
27034	ACAD8	NM_014384	CTGAATGTAAATCATGATAAA	AAGCTCTTTGCTACAGATGAA		
27036	SIGLEC7	NM_014385	CCGAATATAGTGAGATTGTAA	CAGGGAATGATATAAGCTGGA	TAGTGAGATTGTAACGTGAAA	CTGGAGGAGTCTGACCCTGTA
27040	LAT	NM_014387	CTACTCTGTGTAATAGAATAA	CCTCAGATAGTTTGTATCCAA	CCTCTTGTGGTTCTCAATAAA	CCCGTAACTTATTATCACTTT
27071	DAPP1	NM_014395	TCGGTCGTTCATCTTTAAATA	CTGGAAATTGGTCAAGGACAA	TAGGTAGTATAATAAAGGTAA	CTGGGCCTTATTAAAGAGCAA
27086	FOXP1	NM_032682	CAGGCGGTACTCAGACAAATA	CAAGACCTCCTTAATAATGAA		
27089	QP-C	NM_014402	CTGAAAGACCTTTCTCTGGAA	CCGCACGTCTTCACTAAAGGA		
27092	CACNG4	NM_014405	GACGACGAACAATGAACTAAA	CTAGGTGGTTACAAATCATAA	CAGGAGAGCAACTTACCTTCA	CCCTGTGTGTTTCGCCAGTTA
27098	CLUL1	NM_014410	CAGGTTGGTCAATGTATCCAA	CAGGAAAGTATGTTAGCTATA		
27099	NAG8	NM_014411	CAGGTTGTTATCTGTCTATTA	AGCCAGTATATTTAAAGGTAA		
27104	EIF2AK4	BX640919	CACCCATTATATTTCATTGAA	CAGGTATAATTACTAATTATA	TCCGATAATCTTGCAGTGCAA	CTGCAGGAATTTAGTAACATT
27120	DKKL1	NM_014419	CCGGGCTGTGGTCTAGCATAA	CAAGCACCATATGGAAATAAA		
27124	PIB5PA	NM_014422	ATGGGAATACCTACCAGGTAA	CTGGAGGTCATCCATTAGGAA	CTGGGACTGGATCGGCTTATA	CAGGTAACATTCAGTGAGGAA
27129	HSPB7	NM_014424	CAGGTGGACCATCCTCCCAAA	CAGAGGGAAGGTCACAGGCAA		
27148	STK36	NM_015690	CTCACCAGTTCTAGCGAGTAA	CTGGTCATGTCACCATAATAA	CCAGTTGGTGTCAGCCCTGTA	ATGGATGCTGACCTCCTTATA
27154	BRPF3	XM_166450	CCAGATTACCTGGAATTCATA	CCAGGATATCACCGAATGCAA	TACCAACTGCATGAAGTATAA	CCGGCTTGAGAAAGAGTCATA
27156	RTDR1	NM_014433	CTGCAGAGCTTCATTTGGAAA	CAGCATATCTCGAGAGGGCAA	CACAGTGATCACTGAAGGGAA	CAACAGTATGGTGCGCATAAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
27163	ASAHL	NM_014435	CCGGAGAACATCTGCCATCAA	CAGTGGATGTGCAATTCTTAA		
27177	IL1F8	NM_014438	CTGAGTGGAAATTCTTTAATA	CAAGCCTACTTTGCAGCTTAA	TTGGAATTCACACATGCATAA	AACGCTCTGTTTAGTATGTAT
27179	IL1F6	NM_014440	CCAGCCCACACTGCAGCTGAA	TCCAGTCACTATTGCCTTAAT	CTGGGCCTGAATGGACTCAAT	AAAGGATATAATGGATTTGTA
27190	IL17B	NM_014443	CGGAATGGACTGGCCTCACAA	TTGCACCTTTGTGCCAAGAAA	CTGCTGTTTCTTCTTACCATT	CCAGAGAAAGTGTGAGGTCAA
27199	OXGR1	NM_080818	TACATCGTTTCTAGACCATTA	CTCAATGGAACTCCTGGTAAA	CCGCTACTGTGTGATCATTCA	CACCAGTTCGGATGAACTCAA
27202	GPR77	NM_018485	TCGGGCCTGCCTGGTGGTCTA	TAGAGATATAGCAGTGACCAA	CAGCAAGAAATCCACCAGCCA	CACGTGCTGGACAAATCTTAA
27229	76P	NM_014444	CTGGATGTTACCACCAAGTAA	CAGGATCACCATCCATCTCAA		
27232	GNMT	NM_018960	AGGGAAGAACATCTACTATAA	AACATCAGTGCTGATAGTGAA	CAGACGGAAGGGTAAACAATA	GACGGAAGGGTAAACAATATA
27235	CL640	NM_015697	CTGGAGTTATGTGGACACTAA	TTGGAATAAATTTATCTCCAA		
27237	ARHGEF16	NM_014448	TACATTAAAGTTATTTCTTAA	CACCATTGTGGTCAAGAGCTA		
27239	GRCA	NM_014449	CCCGCCCAGTATGAAAGCTGA	TTGGACTTCCTTTGGGACTAA	CCGACTATGACTGGAACGAGA	ATCAATTGCAGGGATGCTTAA
27240	SIT	NM_014450	CAGACTGGAGTGGACCTGGAA	CCGGAGCTCTATGCCTCAGTA		
27247	HIRIP5	NM_001002755	CAGGTTATGGATGATGAATCA	AAGAAGCAAACTCACCTTAAA		
27254	PIPPIN	NM_014460	CAGGAGGTAGGTGGAGGGCAA	CACGTCAAACTCTCTTCCCAA		
27255	CNTN6	NM_014461	GTGGGTGTGTATAATAATGAA	CTGCAAAGGATTCATCTGTAA		
27257	LSM1	NM_014462	CAGCAAGTATCCATTGAAGAA	CCGCTGTGCATTGCAGCATTA		
27286	SRPX2	NM_014467	CCACTCGTTCTAGGAATGTTA	CTGGCTACTATCCGGATGAAA	CCCGATGGTGTTATACATTAA	GAAGATTAACGTCAACGTCAA
27291	C10orf28	NM_014472	AAGGAGCATAATTGTAGAGAA	CCCACATGTCATTGAAATTTA		
27292	HSA9761	NM_014473	CAGGTGTGCTATACTTATGTT	TTGGCACGTGTGGACCATCTA	TGGGATGGTCTAGTAAGGATA	CTGGTCCAATCTATTCATAAT
27295	PDLIM3	NM_014476	CGGGAACTACTTTGAACACAA	CAGGATTACACCAGGAAGCAA		
27302	BMP10	NM_014482	AAGGATGAGTTTCTTAAGACA	AGAGTACATGTTGGAACTCTA	TACGATGGAGTAGACCGGAAA	CCCGCTCTACATCGACTTCAA
27303	RBMS3	NM_001003792	CCGACAGCTGTTTCTATTGAA	ACCGTACAGTATTGCAACCAA		
27314	RAB30	NM_014488	CTGCGGGAGATAGAACAATAT	TAGGGCTTCGGTGGTAATCAT	TCGGTCCATTACCCAGAGTTA	AAGAGAGATTTCGGTCCATTA
27329	ANGPTL3	NM_014495	CAGTTGGGACATGGTCTTAAA	CTCAGAAGGACTAGTATTCAA	CAGGTAGTCCATGGACATTAA	ACCGTGGAAGACCAATATAAA
27330	RPS6KA6	NM_014496	TTGGATCATCTGCACCAATTA	CGGGAGGCTAGTGATATACTA	GGCGAGGTAAATGGTCTTAAA	CAGCGGTATACTGCTGAACAA
27334	P2RY10	NM_014499	CTGACGTGCATCAGTCTTCAA	TCAGAGTTTCGTGACCAACTA	CTCCCTATCATATTAACTTTA	AAGTTGAATAGTTTACCTTAA
27335	EIF3S12	NM_013234	AGCCAAGAAGAGAGCATTAAA	AAAGATGTGTTGACTCAGAAA		
27338	UBE2S	NM_014501	CCGCCTGCTCTTGGAGAACTA	CCGGCCGGCCGCAGCCATGAA	TCCCTCCAACTCTGTCTCTAA	CCCGATGGCATCAAGGTCTTT
27342	RABGEF1	NM_014504	ACGGAATTCTTTATCAATAAA	CAGGAAGAAGATGAGCCTTAA		
27345	KCNMB4	NM_014505	CCCGCGCTGCAGGATCTGCAA	AAGGAGGCTTGTAGAAAGCAA	CTGGAAGACTTGGAACCTCAA	ACCCTCAGTTTCCACTATTAA
27350	APOBEC3C	NM_014508	CAGCATAACCAAATCTTACTA	ACGCTGTAAGCAGGAAGAGAA		
27434	POLM	NM_013284	CTGAATGTCTCCAAGCAAATA	TAGGAGCTGGGAGGAAGATAA	CGGGAAGGACTGCGAACCTTA	CCCAGAATGCCCAGAAGAGAA
27436	EML4	NM_019063	CAGATGCAAATACCATAATTA	CGGCAATTCACTAACAAGAAA	CAGGAATCGATCGGATTGTAA	TCGGATTGTAAGGACATTGAT
28231	SLCO4A1	NM_016354	CTGCAGGGAAATGCACTTCAA	TGGATTGTAGTTAGAATACTA		
28232	SLCO3A1	NM_013272	TAGGACAAAGTTTATCTATAA	TCGGATGGCCATGCTCGTCAA		
28234	SLCO1B3	NM_019844	ATGGATAAGTCTATGCATCTA	CTAGAATATAAGGGAGGTAAA	TAGCTATGCCTTTATGGTTAA	TTCATCTATGTTGCAATTCAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
28951	TRIB2	NM_021643	TCGAAGAGTTGTCGTCTATAA	TACCCTTTCCATGACATTGAA	CAGGTTGTCCCACATGTATAA	CACGTGGACTCTAGTATGTAA
28952	CXorf37	NM_014008	CAGGAAGGAGGAGGTCTATAA	CAGAAGGAAATCAACTCCCTA		
28955	DEXI	NM_014015	ATGAGTGTTGTGCCTACTTAA	AAGCAATACTTAGGAGGCTTA		
28956	MAPBPIP	NM_014017	TAGAAGAACCTTCTTAGACAA	CACCGCTGCCATAGCCAGTAA		
28959	LR8	NM_014020	CCGGGCAAACTTGCTGGCTAT	CACAATGCTGATTAAACATAA	CTGATTAAACATAATAAACAA	GAGGAAGTTGTTCACAGCAAT
28964	GIT1	NM_014030	ATGGCTGACAGCCTTGACTTA	CACCTTGATCATCGACATTCT	GCCGCTGAGGATGTCCCGAAA	CAGCCTTGACTTATCCGAATT
28965	SLC27A6	NM_014031	TAGACAGATTTGGAAATATAA	AGGGAACTTTATGATCAAATA		
28977	MRPL42	NM_014050	CAGTAATATATAGTAAAGTAA	TAGCTTATGTATGATCCTTAA		
28988	DBNL	NM_014063	TGGGCTCTCTTTACCTATGAA	ATCCGTGTCTCTGAAGAACAA		
28989	AD-003	NM_014064	AAGGCCCGAACAAGACAGGAA	GAGGTGGATATGGTCGACATA	ACGGAGGACTTCCTGGTTCAA	CTCCAGCAGCATCGACATCAA
28990	HT001	NM_014065	AAGCAACTTTATGAATATCTA	GTGGAAGATCATAGTAATGAA		
28996	HIPK2	NM_022740	CCGAGTCAGTATCCAGCCCAA	ACGGGTCGGGACACCAGTGAA	TCCCGAAGTCTCCATACTAAA	AACCAGTACCCTTACATATAA
28998	MRPL13	NM_014078	CAGGTGGATTTAGACAAGTAA	CAGGAAGGTATAGTCCTTCAA		
29028	ATAD2	NM_014109	CTGGTACTTAGGCACCATAAA	AAGAATAATTAGCAGCGTTAA	CCGGATAAAGAAGAACGGACA	AAGGCATTTATAAAGATCGAA
29068	HSPC063	NM_014155	CAGGAAATGCTTGGAAAGCTA	CCGCAGGACATTTCTGATTTA		
29085	PHPT1	NM_014172	TAGCCTGGCCACAGAATTAAA	CCGATTCCACGTTTCCTTTAA	TCGGGCGACATGCAGAAGCAA	CACGCCATTTCAACTGAGAAA
29087	THY28	NM_014174	TCAGTTGATCCTAATTAGCAA	AGCAAATTACTTCATCATCTA		
29095	ORMDL2	NM_014182	TCCGGCTATATGGGCAACAAA	TCAGCTATAGCTGCAGTTTAA		
29097	HSPC163	NM_014184	CTGGTTCATCTTCCTTCTCAA	CTGCTTCTTCATGTATCTTTA		
29109	FHOD1	NM_013241	CACGGTCACCCTCATCAACAA	CAGCGAGAGGAGCATCTACAA		
29110	TBK1	NM_013254	CAGGATATCGACAGCAGATTA	CCCAATTTATCCAAGTTCTAA	CTGACTTGACACGTTTGTAAA	CAGAACGTAGATTAGCTTATA
29113	C6orf15	NM_014070	ATCGGTGTTGTGGAGGAGAAA	CTAGAGCACGATAGAGGGAAA		
29114	TAGLN3	NM_001008272	CTCTGTTTGATTATTTATTTA	ACCCAAGATCTCAGAGTCAAA		
29115	HCNGP	NM_013260	CTGGTCTGGATTCCACTTAAA	CAGCTCATTGTTTACAGGCAA		
29116	MYLIP	NM_013262	CCCAATTAATAGGATAGCTTA	TGCACTATTATAAACTATTAA	AAGTAAGTGCTTAAGTATTAA	ATCGGGTGCAATACTAGCTAA
29121	OCIL	NM_001004419	TCAGATATCTTGAGACAAGAA	CTCATAGAAACTGGAGGCAAA	TAGAAGCATATTGGAACTGAT	CAGGAGAGTGTGCCTATTTGA
29122	TSP50	NM_013270	CAAGCTCAAGCAGGAACTCAA	CACTCTGGTTCAGATCATCAA	CAGGGAGAAGTTCTGCTATGA	GAGGTGCTCAATTAAACATTA
29124	LGALS13	NM_013268	TACGTACATTACAATGAGTAT	TGGCAATCATGTGGTCATGAA		
29127	RACGAP1	NM_013277	CAGGTGGATGTAGAGATCAAA	CACCACAGACACCAGATATTA	CTGGTAGATAGAAGAGCTAAA	CTGAATGTATCTCCTAGCTAT
29775	CARD10	NM_014550	CACAGGGAGTGTGACACTTAA	CTGCACATTATGGAGCATTAA		
29798	C2orf27	NM_013310	ATGCTTCAGATTCAAGTGCTT	ATGATAGCAGAGTACCTTCAA		
29799	YPEL1	NM_013313	CAGGGTCTCTTTAGATAGCAA	CTGTCAGATATTAGAATTGAA		
29802	VPREB3	NM_013378	CTGCTGGTCTTCCCAGGCCAA	AATATTCAACATGTCAACAAA	TGGGTTAATAATATTCAACAT	AAATGGGTTAATAATATTCAA
29841	TFCP2L2	NM_014552	AGGGATGAAGAACGAAAGCAA	CTGCACTGTTTAACAAATGAA		
29851	ICOS	NM_012092	TGGGATTATGTTGTAGTTTAA	CCGGAATTGAAAGCAAATTTA		
29881	NPC1L1	NM_013389	AAGCACCTTGGTCATGGATTA	CAGCTTTGAAGGTTCTATCAA	AAGCCTCATGACACTCTCCAA	CCGAGTGATGGTGGACTCCAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
29882	ANAPC2	NM_013366	CAGCGGTGCAGTCCCGCCAAA	GAGAGTCTATATGCAGAGTAA	CTCACTGGATCGTATCTACAA	AAGGTTCTTCTACCGCATCTA
29894	CPSF1	NM_013291	CCGCGGCTTCCTGTACTTCAA	CAAGATGGTCATCTCCCTCAA		
29922	NME7	NM_013330	CGGCAAACACTGCTAAATTTA	CAGGTTGGGACATTTAGACAA	TTCATGTAGATCACCAGTCAA	CCCGGCATTTACGCCCTGGAA
29924	EPN1	NM_013333	AACTTTGGGAATAAATGGCAA	TCCCGCGACGCTCACCCTGAA		
29927	SEC61A1	NM_013336	CCGAGTGGACCTGCCAATCAA	AAGGTGAATAAGTGACAAATA		
29930	PCDHB1	NM_013340	CGCGCTGAGAACCATGGATTA	ACGTTTCAGATTGACCCTCAA	ACCAAGCATTCTAGAAAGGTA	CTCGGCCTTGTCCATATGAAA
29933	GPR132	NM_013345	CAGGATTGCCGGGTACTACTA	TACCAATTTCTCGTTCCTGAA	CTGGGTCACCATCGAGATCAA	ACGGACCATTCCCGCCAAGAA
29945	ANAPC4	NM_013367	TGGCTCGGAGTCTTTATTATA	CTGAGCTAGACTCCTAATCTA	CAAGGCTAGATGAACAGTGTA	CAAGCTGGTGCTGCCGCTTTA
29946	SERTAD3	NM_013368	CAGCCTGATCCAGTCTTCTTA	CAGGCATGTCCTCATCCATAA		
29947	DNMT3L	NM_013369	CCACTGCAAACCGGCACTGAA	AACTCACTTCCTCTTTATAAA	AAGCATGTGGTTGATGTCACA	AAGGCTAACCAGCGAAATATA
29948	OKL38	NM_013370	CCCGGTCATCATTGTGGGTAA	CAGAAGCAGGTCCCAAATAAA		
29953	TRHDE	NM_013381	CTGGAGATTATTAATTGATCA	CAGGAACAGAATACCACTAAA	CCGAATCTATAGAATAAAGTA	CACCACTGAATTCATGTAATA
29954	POMT2	NM_013382	ACCAACCATCATTAATGTTAA	AACCTGTGGATTATCAAGAAA		
29956	LASS2	NM_013384	AACGAAGAGAGTCTTTCTTAA	TTGGAGTAGAATGGCAACTAA		
29959	NRBP	NM_013392	AGGCGAGAAGAGGTGAATCAA	AACATGGATACTAGTGCCGTA	TCGGTGGAGGAGGGAGTCAAA	CCGGTTGACTTCTCTGCTAGA
29965	C16orf5	NM_013399	CACGTAGGACAGGGTCACAAA	CTGCCTCATCAATGACTTCAA		
29982	NRBF2	NM_030759	TTCGGTTTCTCCTGATACAAA	TTATGTGTAATTAATCTATAA	CACACTTTGCACTACTCATAA	CAAAGGGATAGCCATATGAAA
29984	RHOD	NM_014578	CCGGTGGTACCCAGAAGTGAA	AACCTGCAAGTGAAAGGCAAA		
29997	GLTSCR2	NM_015710	TCGAGAGAGAGCCAAGTTCAA	CAAGTTCAAACGCAAGTACAA	CTGACAAAGAAGAGAACCAAA	CCGGAGCTTCCTACAATCCAT
29998	GLTSCR1	NM_015711	CCCGCAGAACCTGACGTTCAT	CAGGCCATGCTCAATAAATAT	CGGGCTCAAGCTCAAGATCAA	CCGCATCGGGCTCAAGCTCAA
30000	TNPO2	NM_013433	CCCGAGCATCTCTCTCTGTAA	ATCGTGCAGGATAAACTCAAA		
30008	EFEMP2	NM_016938	CCTGGAGATGGTCACCATGAA	CCGCTCCTGTGTTGATGTGAA	CCGCTCCGCTGCCGTCATCAA	CACGGAATGCACAGATGGCTA
30009	TBX21	NM_013351	CCGCGTGAGGACTACGCGCTA	ACCTGTTGTGGTCCAAGTTTA	CCGCCTGGACCCAACTGTCAA	AACAAATACACGTATGTTATA
30010	NXPH1	NM_152745	AAGCAGCAAATCCACACTAAA	TAGGAGTATCTGCTTGTTAAA		
30062	RAX	NM_013435	CCGCACGACTTTCACCACGTA	CCGCGAGGAGCTGGCCGGCAA	CAGGCTGAAGCTCCTAAACTT	CCAGATAACCATAACAGGGAA
30811	HUNK	NM_014586	AACTAAGTACGTTGCAAATAA	TACGTTGCAAATAATAGTACA	TCGGACCAAGATCAAACCAAA	CACGGGCAAAGTGCCCTGTAA
30814	PLA2G2E	NM_014589	AAGCTGGGCTGTGAGCCCAAA	CTGGGCACCTACAACCGCAAA	CAAGTCCGCCCTGCAGTACAA	AACCGCAAATATGCCCATTAT
30817	EMR2	NM_013447	TAGGTCAGTGTAAGAATTAAA	TTGCTTGATATAGACTGCTAA	ACGGGTTTGATTATTTAGTCA	AAGCATGGTGATGATATAGGA
30818	CSEN	NM_013434	CCCGGCTGACCAACATTCAAA	TCCAGGAACATTCCCACATAA	CAGGAACATTCCCACATAATA	CCCACATAATACATTCCATCA
30836	ERBP	NM_014597	ACCACTGTGTTCCACCATATA	CCACTGGGAAGCAAAGTTTAA	CACGAACAGGCCAATGTTGAA	AAGAAGAAATTTCGCAATTAA
30837	SOCS7	NM_014598	CAGCTTTGAAGAACCAAATTA	CCCAAGTTGACAAGAACTCAA	CCGAAAGTTCTACTACTATGA	ACCAAATTAAGCTACCATGAA
30845	EHD3	NM_014600	CACTTTATATACATTATTCTA	CTGGTGGTGGATCCCAAGAAA		
30850	HUMPPA	NM_014603	CAGCGTCACCTTTGAAGTATA	CAGGCTGGTGCTGGAGAGTAA		
43849	KLK12	NM_019598	TCCCGGGAGAATCACGAGCAA	TCCCTGGAGTCTACACCTATA	TGGGAACTTCTTGGAACTTTA	TGCAATAGTCTGGAATAAATA
49861	CLDN20	NM_001001346	TACAAAGAAAGTAGAATGTAA	CTGCAGGAATCTCTAGTTTAA		
50484	RRM2B	NM_015713	AAGGGCTTATGGACTGAGAAA	AAGGAGCAGGCCATAACTTTA	GAGCAGTTCAGTGGTACATAA	AACCAGGAGGTTATCATGGTA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
50485	SMARCAL1	NM_014140	CCCGCAGAGCTGAGAAGTTAT	CAGAACAGCATCAGAGGACTA	TTGAGTTATGAGTTAGGTCAA	CAGCTTTGACCTTCTTAGCAA
50488	MINK1	NM_015716	CACATGTCTCATCAAGACTTA	CCGGAACAAGATTCTGCACAA	CGCAGACTTTGTGTTGCTGAA	CACGTACGGGCGCATCATTAA
50489	CD207	NM_015717	CTCGGTGACCTCAGAGAGTGA	CCAGGATGACTTTGCACGTTA	ACCCTGGATTCTGAAATTAAA	CAGGATGACTTTGCACGTTAA
50515	CHST11	NM_018413	CAGCATAGTGAGAATTATTTA	CCGCAACAAGTTCACCCAGAA		
50613	UBQLN3	NM_017481	CGAGGAGTCAGTAGCAATCAA	CTCCATATGCTGCAAGATTTA	CAAGATTTAGTTAGTACAAAT	TTGAGATGCAATTACACCCAA
50614	GALNT9	NM_021808	CCCGGAGATGAGGGTCTACAA	CACCAGGAAGCCCTACAACAA		
50615	IL21R	NM_021798	CCCGGTCATCTTTCAGACCCA	CTGCAAGAAGTCCATATTGTT	CCAGAGCAGACCCTCAATAAA	ACCTGTTGAAATGTGAATTAA
50616	IL22	NM_020525	CTGATAGGTTCCAGCCTTATA	CCTGCGTTAGTTACAAAGGAA	AAGGTAGACTTTCTAAGCATA	AACATGTTTATTTGACCTCAA
50628	GEMIN4	NM_015721	CCGCCATATGGAAGTGTGCTA	CAGCCAGAACGCGACGCTCTA	CACCGCAAGTTAGAACAGCTA	CAGCCTGGACTTTACAGTTAT
50649	ARHGEF4	NM_015320	AAGGTTGGCCTTGGCTCATAA	CAAGCCAGAAACCACATTTAA	CCGCGACGTGTTGTACTACAA	CACATTTAATTTCATAAATAA
50700	RDH8	NM_015725	CAGGGTGTCATCTTCAACGAT	AAGGATGAACAGACTCTTCAT	CAGCTGTCTCTGGGAAAGCAA	CACACCAGCAATGTATGTATA
50717	WDR42A	NM_015726	GAGGAATAAGTCATTAATCTA	CAGCTGAATTCTTGCCCTTAA		
50835	TAS2R9	NM_023917	CTCCCTAGTTAGACACACCAA	CCAGGTACTTTCAAACAGTTA	TGGATTCATTGTACTAGTTAA	CTGGCTGAAGCTAAAGATCAA
50846	DHH	NM_021044	ATGGCTCTCCTGACCAATCTA	TCGGTCAAAGCTGATAACTCA	ACCGAGTGGCCTCCACGCAAA	CCCAGGCATAGAAACCTCGAA
50852	TCRIM	NM_016388	AAGGTTGAGATGACAATGTTT	ATCAGTATTTCAAATAACTTA	AAGCATGAATGCGTTCTGGAA	AAGGATGGAGATGAGCAACTA
50861	STMN3	NM_015894	CACGTAGTAAAGTGAACTTAA	TTCAATCAAATGAACAATTAA		
50862	RNF141	NM_016422	ATCACGGATCATGAATTTATA	TTGGTGAGTAACACACATATA	CACTGATAAATTGTGCAATAA	CTCGATTTCCTTATATCTAAT
50939	IMPG2	NM_016247	GAGGATGGAGTCACAAGTATA	AAGGTTGGTAGTTATGTGGAA	TCAGGCATTCATCTAAATAAA	AAGGAAATTCGTGTACTTGAA
51015	CGI-111	NM_016048	TACCAACATCTTGAATATATA	AGGGATTCTAATATTTATTTA		
51020	C6orf74	NM_016063	AAGGCTAGGTTCATTGAATAA	CCAGATGAAATTGCTGCCTTA		
51031	C17orf25	NM_016080	CTGATGTAATTTAGAAATGAA	AACGATTTCTTCAGCCTGAAA		
51043	ZFP67	NM_015872	CAGAGGGTTCTGGAAGATGAA	CCCGGAAAGCTTTCCTGCAAA		
51056	LAP3	NM_015907	CCCAGTCTTCTTGGAAATTCA	ATGGGAGGAGCTGCAACTATA	AAAGCTTAATTTGCCCATTAA	AAGCTTAATTTGCCCATTAAT
51060	TLP19	NM_015913	CTACGTGATCTGCACCTTTAA	AAGGGAATATTGAGGAATCAT	AACAATTAAGCCGACCAGGAA	AAGTGTAAATCAGTTATTCTA
51062	SPG3A	NM_015915	ACGCCTCAAGGTCTCAGGGAA	TCCCGAGAGCCTAGATATTAA	CCCGAGAGCCTAGATATTAAA	ACAGCAGAAGCTAACAATTTA
51068	CGI-07	NM_015938	CAGCATGAAGATAATGGCTAA	CAGAATACACTTCGTATCAAA		
51070	NOSIP	NM_015953	CAGGATGACGCGGCATGGCAA	CCCGTGCACTTCACACCGCTA		
51076	CUTC	NM_015960	CAGGATGAAGGTAGAACTATA	CAGAATATTCCCTAAAGGTAA		
51077	C14orf111	NM_015962	AACCATAGATACAACATTGAA	AAGGAAGTATGCGACCATGAA		
51084	CRYL1	NM_015974	CAGCTTGATTGCATTTGACTA	CAGCCAGTGATTGTAGTTTCA		
51095	TRNT1	NM_016000	ACGCAGAGATCTCACTATAAA	AAGGATTTGGGTGGAACTGAA		
51097	CGI-49	NM_016002	CAGCTTATAAGTTGCTATCAA	AAGAAATGTATCAAATCTGAA		
51099	ABHD5	NM_016006	AAGGCCTGATTTCAAACGAAA	TACGTCTATATCACACCTTAA		
51101	CGI-62	NM_016010	CCAGGTGTGCTTACAAACAAA	CAGGTAAAGTGTCTTCAAGTA		
51105	PHF20L1	NM_016018	ATGGCTAAGTGGATAATTTAA	TCCGTTGATCTTAGTGGTGAA	CAGCTGAAGATTGGAATACTA	ACGGAAATTTAGGGTATTTAA
51112	TTC15	NM_016030	CAGGCTGGCACTACTAGTGAA	ATCCAGGGAGATGCAGTTAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
51116	MRPS2	NM_016034	CACGACATCATCGACCTGGAA	CACGCTCAACAACATCTTTGA		
51121	RPL26L1	NM_016093	AAAGAAGAACTTATTGAGAAA	GAGGGTCACCATGAAGTTCAA		
51130	ASB3	NM_016115	AACGCTTGGATTCTACAGCAA	ACCCATCTTTGTCGTTTGGAA	TACGGTCTGACAGTTATATTA	CTGAGGATGTATGAAGTTCCA
51131	PHF11	NM_016119	CACCGTGGGATGTGATTTAAA	ATGGAGTTCGAGGAATTTATA	GAGATCTTATGTCAAGTTCTA	ACAGCCCATGATAGCCTCTTA
51135	IRAK4	NM_016123	GTCCATTATTAGATTATGTTA	CAGCTTAGAAGAGTACTCCAA	TTGCAGGACAGTGGTTATTAA	ATCCTATTAGTCATATATTTA
51138	COPS4	NM_016129	CAGGAAGTACAAGCATTTAAA	CAGAATGAATCAACCAATGAA		
51162	EGFL7	NM_016215	AGGAGTGGACAGTGCAATGAA	CAGCACCTACCGAACCATCTA		
51167	NCB5OR	NM_016230	CAAGCTATGATTGGTTCCAAA	TTAAGGATTGTTTATATCTTA	AGGCTTCACACCAATGGTTAA	TCGATCATGTTTCCATGCAAA
51168	MYO15A	NM_016239	CAAGATTAGATTTGAACGGAA	CAGGATCGTGTTTCAGGCCAA		
51179	HAO2	NM_001005783	CCGGTCGGTCGCTGAGATCAA	CAGGAGGATCACAAACTCACA		
51182	HSPA14	NM_016299	CGCGAGCCATGATGAAATTAA	ATCCCTATTGGTGCAGCTATA	AATGGATTACGTGATATATTA	CTCTATTGAGATAGCATCTTA
51184	MGC14560	NM_016301	TTGGACCTAGATAACAAGTAA	CAGCCTCATGCCTGAATCAAA		
51187	C15orf15	NM_016304	CAGCATTTGTATAGTAACTAA	CCCTTTGTTAATGTTATAGAA		
51191	HERC5	NM_016323	CCGGACGCCGAAATGCATTAA	ACCATTTGAGTATGACAACTA	GAGGAGAATGGTAATGTTCAA	TGGAAGTAGCATAACTGTCAA
51194	IPO11	NM_016338	CAGCTACAACTTTGAAGTTAA	GAGGAGATTCTTGGAAATATA		
51195	RAPGEFL1	NM_016339	ACGGAGAAACTTCAATATTCA	CCCATTGCTCCTTCAAGCCAA	ACGGTGGAACTAAAGATTCCA	ACCCAAAGCTCTGGAATTGTA
51199	NIN	NM_016350	CTGGAAGAATATCGTGCACAA	CTGGAAGACCTAAGAAATGTA		
51205	ACP6	NM_016361	GAGGCCAAACTTGAAATACAA	GTGCCTTTATACAATGCCAAA	CCCGCTGGACATGTTCTTGAA	CCATGTCAGTTTATACCTTAA
51207	DUSP13	NM_016364	CAGGTGGACACAGGTGCCAAA	ACCCAATTCAGAGATTCTTTA	TCAGTCCATCTCTATAATAAA	ACCCTGAGATGTAAACAGCAA
51208	CLDN18	NM_001002026	AAGGATGAGCAGACAAGTCAA	CCCAACTTGGCTAGTAATAAA		
51214	IGF2AS	NM_016412	CAGGCGGTGGACGCTGCTGAA	CTCAATCTGCCCAAAGCCAAA		
51222	ZNF219	NM_016423	CCCAATAAACAGGTGTCTTAA	CAAGGGAGTCACAGTGCCTTA		
51234	LOC51234	NM_016454	CACAAAGAAACTATACCATAA	ATGGTTGAGAACAATGCATAA		
51237	PACAP	NM_016459	CAGGACTACGGAGTTCGAGAA	AAGGCAGAGACCAAACTTCAT		
51239	MGC41816	NM_016466	TGGACAGATGATCATATTCTA	CTGGGCCGAGTGAAGCATTTA		
51256	TBC1D7	NM_016495	CCGGGTGTGTTTGCACTACTA	ACGCTTTGTGAACCAATTAAA		
51258	MRPL51	NM_016497	AAGGGCCATGTTCGGAGTGTA	GACCTGCACAACCTTAATAAA		
51260	CXorf26	NM_016500	AAGGACATCTTTCTAGTCTAA	AACCGGGAAGGCTATAACAAA		
51265	CDKL3	NM_016508	CTAAAGCAATTTCATCACGAA	AGCTCCCGAATTAGTATTAAA	TGGGCAGATAGTGGCCATTAA	CAACATTATTGTCATGGACTA
51266	CLEC2	NM_016509	AAGGTGGACCAACTACCTTAA	ATACATCACCTTAAATATTAA	CTGACAGATACTGAAATTGTA	AGGGCTTTATTGTACAATAAA
51275	FLJ39616	NM_016534	CAGGATTGTATAGAATATATA	AGGATTGTATAGAATATATAA	GAGCATAAGTTAAGTAAGTAA	CTCCACCGATAACCTATCAAA
51276	ZNF571	NM_016536	CAGGGATTTCTGAATAATGTA	CTGAATTATATCCTTTATTAA		
51295	SITPEC	NM_016581	TACGAGTTTGACATCAATGAA	CCGCAACAAGTGTGTGTATTA		
51296	SLC15A3	NM_016582	CAGGAAGGGTAGGGCAAGAAA	CAAGGACTTTGGGAACATCAA		
51298	THEG	NM_016585	CCGGATCATCTCCCTGGCCAA	AAGGATGAGGAGGACAATAAT		
51301	C2GNT3	NM_016591	AAGGATGAAGTCAGGTATGAA	CAGCTTAGTTCCAGAGAGAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
51307	FAM53C	NM_016605	CAGGATGTTGGGTTTGCTCAA	CAGGTGCTGAGTGAAAGCGAA		
51312	MSCP	NM_016612	CACCAAGGAAACAGCCACCTA	CCGGACGGTGTACCAGCTCAA		
51317	BHC80	NM_016621	TACGGAAGAACCTGATAGTAA	ACGGAAGAACCTGATAGTAAA	ACCGGACAAGTTCCAAATACA	ACCATGCCAAGTGAAATAATA
51321	LOC51321	NM_016627	GACAACTATTATATTCCAGAA	ACCCATGAGATCGGACACATA	CAGCATTGTAGAAAGATACAA	CCCGTGGAAGCCTTTAAGGAA
51330	TNFRSF12A	NM_016639	CGCCCACTCATCATTCATTCA	CTCAGATGTCCTGAAATTCCA	CAGCTGACACTGACTAAGGAA	GAGGGAGAATTTATTAATAAA
51332	SPTBN5	NM_016642	CCGGCGTATGTTAGAAGAGCA	ACGGGCCACATTCGCAAGCTA		
51334	LOC51334	NM_016644	CCGGGAAAGATTCCTCACCAA	CTCAGCTATATATGTAATAAA		
51335	NEUGRIN	NM_016645	CTGGGCAAGTATTAATGTATA	CCCGGTTGCCCTTGCGATCAA		
51339	DACT1	NM_016651	CACAGAGACATTCACTATTAA	CCGCAGGAGAACAAAGTTGTA		
51343	FZR1	NM_016263	TCGCCAGATCGTCATCCAGAA	CAGGATTAACGAGAATGAGAA	TGCAGTGACGCTGTCATTAAA	CGGGTCGATCTTCCACATTCA
51347	TAOK3	NM_016281	CAGAGACTGTACTACGACAAA	ACGCAGCGAGAGAATAAAGAA	CAGCTCCTCCGTCGTGCATAA	CAAACAGTATAAAGCACTCAA
51352	WIT-1	NM_015855	CCCGGCCTCGAAGGTGCATAA	GCCTCTATTATTATACCGTAA	TAGGCCCATGAAATTGATGAA	CAGTCTGAGGTTACAATTAGA
51364	ZMYND10	NM_015896	CTGCAGGGAGTGCCAAGTCAA	CTGCAGGGTGGAGGACTTCAA		
51368	TEX264	NM_015926	CAGGACCCAGAATAAAGCCAA	CCGGGCCAGAGGAGAGGCATA		
51373	MRPS17	NM_015969	TGACATGTTTATGTTATGGAA	CTCTGTGGTGTTTATGAAATA	TCCCTATTTATTAAAGTATTT	CAGGCTTGTTCTGGATCCCTA
51374	C2orf28	NM_016085	ACCTCTTATATAGACAACCAA	AACCAAATCTGTCAAGGGCAA	CTGGAATACTATCACCTCTTA	AAGCCAAGACTTCATGAACTA
51382	ATP6V1D	NM_015994	AAAGAAGATAATAGAGACTAA	ATGGATGAAAGAGATCTGTAA		
51389	RWDD1	NM_001007464	AAGGGCCACGATGACAGATTA	CAGGAGAATATTCTTCTGATA		
51390	AIG1	NM_016108	CAGAGAGATGATATACCCGAA	CAGATGTTTCTCATTGCATAA		
51393	TRPV2	NM_016113	TCAGATAAGAGTCAACCTCAA	CTGGCTGAACCTGCTTTACTA	CAGAGGATCTTTCCAACCACA	CCAGTGAATTCTGGTGGCAAA
51400	PME-1	NM_016147	ACGGCAGCGATTATTAGTAGA	AGGAAGGAAGTGAGTCTATAA	AGGCGATACATCTGAGTTCAA	AACATCGAGCTCTGTTGTAAA
51409	HEMK1	NM_016173	CAGGGTGGCAACCAACTATAT	CAGTAAAGTATTGAGAGACTA	CAGGGATTGATTAGTCCTCCA	ATCCACGTTCATTTAACTGAA
51411	BIN2	NM_016293	CAGGGAAATGAGCAAGCTGAA	AACGATTTGAACAAAGCGCTA		
51412	ACTL6B	NM_016188	CACCTACAGCAAACACGTCAA	CACGGCCATTCCAGTACATGA	CTGGCATAACTACATGTGTAA	CAACAGCACCATGGAGCGCAA
51421	AMOTL2	NM_016201	AAGCATATTGCTCCAATTCAA	AAGGGTGTTAGTCTTGGAGAA		
51422	PRKAG2	NM_016203	AAGCGCGGTTATGGACACCAA	CGCGGTTATGGACACCAAGAA	CCGGAAAGCATTCCTCTCGAA	AAGCACGAGCCTGAACGGTTA
51426	POLK	NM_016218	AAGGATAAACCCATTGCTGTA	CAAGGATTTACCCATTAGAAA	TAGGATGGGACTTAATGATAA	CCGGGTGACGACGGGTAGAAA
51429	SNX9	NM_016224	ACAGATCTCAATGATGCAATA	CAGCCGCTTTCCAGTGATGTA	CCCATCATTGTTGGAGATTAT	TACCCAGTGTCAGATAATTAA
51435	SCARA3	NM_016240	CCCTGAGAAGTTCAACATTTA	ATAGTATTACTGACTCAGTAA	CCAGAGGAAGAGACCATGAAA	CACCATCTTCACCAACATCAA
51442	VGLL1	NM_016267	CTGCATATTGTTCCAGATAAA	CAGGTGATGGTCCAGAATTAA		
51449	PCYOX1	NM_016297	AAGCATCCAAATGGTAATTAA	CAGGATGGCTTATATGAGAAA		
51466	EVL	NM_016337	CACACAGTAATAAACGGTTTA	CGGCTTAAACTTTGCAAGTAA	CAGGTTGTGATCAATTATTCA	CCGGATCAACATCTACCACAA
51475	CABP2	NM_016366	CAGAAGCTGGAGGCAGCATAA	CAGCATGTTCCTTGAAGCCCA		
51490	C9orf114	NM_016390	AACGCTGCTAGGAGAATCGAA	TCGCAGGACCCTCGCACCAAA	TCGGGTGACTGTGCGACTGAA	CCGGCACACCTGAAAGTTCTA
51491	HSPC111	NM_016391	ACGAATAAATTGAGCCTTGTA	CAGGGTGGGTGATGTAAATAT	TCGGAGTAAGATCAACGTCTA	CGGGACCTCATTGACTATGTA
51496	HSPC129	NM_016396	CTCAGTTACAATCAATTTAAA	AAGTACAGTATTGGAAATTAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
51497	TH1L	NM_016397	CAGGAGGATGATTCTGGAGAA	AAGCGAGTGAGCATCAATAAA		
51513	ETV7	NM_016135	CAGATGTGAAGCTCAAATTAA	TGCGCCACTATTATAAGCTTA	GCGCCACTATTATAAGCTTAA	CCCGATATGAGCCCTACATCA
51524	HSPC196	NM_016464	CTAGCTGTGTTCAGCATTCAA	TAGAGAATAAATTGAATTCTT		
51526	C20orf111	NM_016470	CACAATGAAATCCGAAGCCAA	AAGGCTTGTCAAAGAGATTTA		
51531	C9orf156	NM_016481	CAGACTTTAATTTACAGAATA	AAGGTAGAAGGTGGAGCTATA		
51535	PPHLN1	NM_016488	CAGAATGAAGGAAATCCTGAA	AGGGACGATATGAATATGAAA		
51548	SIRT6	NM_016539	GTCGAGGATGTCGGTGAATTA	CACGGGAACATGTTTGTGGAA	CCGGCTCTGCACCGTGGCTAA	CTCCCTGGTCTCCAGCTTAAA
51550	CINP	NM_032630	ACGGATATCTGTGGACCTTAT	CAAGGGAATTTGTGAACTAGA	GCGGCTGATTGGCACAATTTA	CGGCTGATTGGCACAATTTAA
51552	RAB14	NM_016322	AGGAATCGAACTAACAATACA	AACGGTTCACGTCTAGCCAAA	TCCATTGATCCCGTATCTTAA	CACGTTAATAGAGGTAGTACA
51554	CCRL1	NM_016557	AACCCACTATGCTATAAGTTA	AAGAACGATTTCCCTGCATAA	TTCCATGGTAGTGGCAATTTA	CGCCGTGGTTGCAACTTATAA
51560	RAB6B	NM_016577	ATGGCCAGAGTGGGTCGTCAA	ATCCATGTTCTTAGAGCCTCA	CGGCTGTTACTTAAACAACTA	CAGGGATCACATCACTCTTAA
51561	IL23A	NM_016584	CGCGCTGAACAGAGAGAATCA	AACAGAGAGAATCAGGCTCAA	CCAGATTTGAGAAGAAGGCAA	CAGATTTGAGAAGAAGGCAAA
51574	HDCMA18P	NM_016648	TCAGGTGATTTAGTAAATAAA	CAGGAGAAAGTTAATGCAACA		
51582	OAZIN	NM_015878	CCGGATTTGCTTGTTCCAGTA	CGGATTTGCTTGTTCCAGTAA	CAGGTTAAGCTTGTCTGGTCA	ATCATAGTATTTGTTGACCTA
51592	TRIM33	NM_015906	CGCCAAGAATGCAGACAGATA	AAGGGTGCAATTGAGAATCTA	CTGGGCAAAGAATGTAGTCAA	TCCCGTAGTATCGGTACACAA
51596	C6orf82	NM_015921	TGAGGTGCTGATGATGATTAA	ACGTGTGGCCTTTGAGATCAA		
51599	LISCH7	NM_015925	CACGTCGTTTACGCTCATTAA	ACGTCGTTTACGCTCATTAAA	GAGGATTACCATCACCGGAAA	CGGGACGACCTCTATGACCAA
51606	ATP6V1H	NM_015941	CAAGAGATGCTTCAAACTGAA	CAGCAGAAGTACGATGATGAA		
51616	TAF9L	NM_015975	TAGGCTGAAGTCCTTAATTAA	ATCACTGATAGTAGCATTTAA		
51637	C14orf166	NM_016039	CTGGCATGTTTGGAAATCAAA	AAGATTCAAGATCGACAAGAA		
51639	SF3B14	NM_016047	TCGGATATTGTATATAAGAAA	AACATTCGACTTCCACCTGAA		
51645	PPIL1	NM_016059	CAGCTTCTAGATGACATAGAA	AAGGAAGTTAATACCTATGTA		
51659	Pfs2	NM_016095	CTGGGACATTCTTCAATTCCA	AAGCCTTAGGTAAATAAGTCA	CTGGCGATTAACCTGAAACAA	CTCCTGTTAAATCATGCTTCA
51660	BRP44L	NM_016098	CTGTAACTTAATGGCAATAAA	CAGTAATATGTATATCATCTA		
51661	FKBP7	NM_016105	CTGGCTAAAGACGGCTCGAAA	ACGGAGCATTGAGACATTTAA	CGGAGCATTGAGACATTTAAA	CACGATGAACTATAGCATATT
51667	NYREN18	NM_016118	AAGCAGTACTCTGACAGACTA	ACCGTACTTAGACATAGCTAA	TAGAGGCTTATGAGTATCTTA	ATCCTCAGATGTGGTGGTTAA
51676	ASB2	NM_016150	CCGAGAGACACCGCTCTACAA	CAAGTACGGTGCTGACATCAA	CGGCGCGAACATCGACGCCTA	CCCAGGCAGGCTGATTAGATA
51678	MPP6	NM_016447	TTGGTTGGTATACTCAAAGAA	ACGGATTCAGAGAGCATACAA	CTGATGATTCAGTAAGGTTAA	TGGAAGGTGTACTAATATATA
51684	SUFU	NM_016169	ATGGACGGCACTTTACATATA	TGGGACTGTTACAATACTTCA	GAGCGTACATCTGAAATTCAA	CCAGGTTACCGCTATCGTCAA
51700	CYB5R2	NM_016229	CCCTTGATTGAGAAAGAGAAA	CAGAGGCTTTGTGGACCTAAT	TCAGTATTTGGAGAACATGAA	CCAGGGAATCTTGGAATCAGA
51702	PADI3	NM_016233	TCGCTAATAAATCAACAGAAA	CACAGAAATGTTTGAGGTCTA		
51704	GPRC5B	NM_016235	CGCAAACTAAAGCAAAGCTAA	CTGCAGATACTCTAATCACTA	TCCGTTTAGAAGCAACGTGTA	CTCGCCCTGTTCCTACACTTA
51710	ZNF44	NM_016264	CACGCTGAATAGAAACTATAA	CAGGGATAGTCTACAAATGTA		
51715	RAB23	NM_016277	ATGATAAACTCTAGACATATA	TTCATTATTTGTACTAAACAA	CAGAATTTATATTGTTTATTA	AAGGTTAAAGTTAAGATTCTA
51716	CES4	NM_016280	CCACAGCAGAATCTAAAGAAA	CAAGCTTCTTGCTATAATGTA	ATGGAGGATTTCGGTAGATTT	ATCGATAGGAATCCAGACCTA
51720	RAP80	NM_016290	CAGATTGCTTAGTGGACTTTA	ACGACATGCCATGTACTGCAA	CACGTCGTGACTTAAATGAAT	CAGTATTGACTCGGAGACAAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
51727	UMP-CMPK	NM_016308	TCCGAGGTTCTTAATATGAGA	TACAGAGGTGGTTTAATCAAA	CGCGTATATATCCCTCTAGTA	AAGTATTGCTAAGTACTATAA
51738	GHRL	NM_016362	CACGACTGTTGTACAAGCTCA	CCGACAAGTGATCGCCCACAA	CAGGAGGCGAATAAATGTTCA	CGCCCGGAAGATGGAGGTCAA
51755	CRK7	NM_016507	CCGCTTGGTATCGAAGCACAA	AACGGCGACGTCAGCGACAAA	ATCGGGATATTAAGTGTTCTA	ACCGGATATCGGGAAGTTCAA
51759	C9orf78	NM_016482	ACGGTGTGATAATACTCTTTA	CAGGATGAGATCAGAAGGATA		
51760	LOC51760	NM_016524	CAGCTGGTGCATGGACTCAAA	CCGGAACGCAGGGAAAGGCAA		
51761	ATP8A2	NM_016529	CAGGAAGAAATAAGACATGAA	ATGCAATATCATGAACTTTAA		
51763	SKIP	NM_016532	ACGGTCGGAGTCCGGAAGAAA	CACGTTCGACTTGGAGCTGAA	CTGGAATTAGCCGCTTAAATA	CAGCCAAGTGTCGTCCACATA
51773	HBXAP	NM_016578	CCGGACGTCGGCAACGGAGAA	CAGCCAATTGGTCGAGACAAA	CACCGAGTCGTGTACCATGAA	ACGCACAAAGATTGAGTCCAA
51780	JMJD1B	NM_016604	AAGGAACTTTGTCACATCTAA	ACCCTGCATCAAAGAAATTAA		
51802	ACCN5	NM_017419	CAGTCTGATCACGATCATAGA	CACGATCATAGAAATTATTGA	ATCATAGAAATTATTGAATAT	AGGAGTGTTAATGGTCACTTA
51805	COQ3	NM_017421	CTCGGCGGTTTATGTGAAGAA	TCAGTGGGACTCTACAGATAA	AACCATATGGTTCAAATCCTA	CTGGAATCAAATGGTCTGTCA
53340	SPA17	NM_017425	ACCCTTGGATTTAGAATTATA	ATCCATCAACCTTCTTATTAA		
53342	IL17D	NM_138284	CTGGGCCTACAGAATCTCCTA	CAGCATCAACTCCAGCATCGA	TGGCTGGAAGCTGATGGGAAA	TGGGTGCTTGCCAAAGAGATA
53343	NUDT9	NM_024047	TTCGATTTAAGCATGGCTTAA	AAGATTAGTGCCACACTGAAA	ATGGATAATCTTATGCTAGAA	CACGCTGCAGATCCCATTATA
53347	UBASH3A	NM_001001895	CCCGCAGACGTCATCCGGGAA	CTGGGTGATTGGGATCTCACA	ACGGCCAAACTCATCCTGGAA	AACAGGTGTAATAGTCAATAA
53353	LRP1B	NM_018557	AACGTTTATACTGGACAGATA	CTGGATGGTGGTAATTTAGAA	CCCTACTATACTCGTTAGCAA	TAGATGATTCATGTAAGTTAA
53373	TPCN1	NM_017901	CGCACACAACTGGGAGATGAA	CCGAATGAACTACAGCCGCAA	TAACACAATAGTATTACTCTA	CGAGCTGTATTTCATCATGAA
53635	PTOV1	NM_017432	CCCAGTCCAGATCGTCAACAA	CAGATCGTCAACAACAAGTTT	CCGGCGTGTCATTGCCAACCA	CTGGAGCAGGAGCAACAGCAA
53826	FXYD6	NM_022003	CCCAGAAAGCAGAGAACTGAA	CAGGTGCAAGTGCAGTTTCAA		
53827	FXYD5	NM_014164	CACCAGAGGACAGACGTTGAA	CCCGGTTATGCCGGAATCGTT	GAGGACAGACGTTGAAAGATA	CTCAACTATCATGGACATTCA
53829	P2RY13	NM_023914	CAGGATGTTAATATGCTATAA	AAGGAGTAGTTAAGCTCTGTA	CAACTGTTTATTGCTAAAGAA	AAGACTGACTGTAGACTGCAA
53905	DUOX1	NM_017434	CCAACTAATCTTAGAAGGTAA	CCCGGGCAGATCCGTGTGGTA	TCGGCGGAGGTTTGGCAAGAA	CCAGTCTAACACCACAACTAA
53916	RAB4B	NM_016154	CTACATAAGAGTTATCTGTTA	AAGAGTTATCTGTTACTGTTA	CCGCACTATCCTCAACAAGAT	CAGGAGCTATAGTGGAGTGAA
53918	PELO	NM_015946	CATATTTGATTTAGAGGGTAA	AAGCAGTGGGATAGTGTGGTA	CTGAAGAGGATTAATGATTGA	ACGTACTACCATCTTGATTAA
53947	A4GALT	NM_017436	CAGGATCGCACTCATGTGGAA	CACGGACTTCATTGTTCTCAA	CACGTGCTGGTCCTGATGAAA	AGGAGAATAATCAATAGAATA
53981	CPSF2	NM_017437	CACATTTGGTTCAGAAATTAA	CTGCTTGACCTTTCTAAGAAA		
54039	PCBP3	NM_020528	CCGGCATGCAGTGGTAATTAT	ATGGATCTGCTCTAAACCTTA		
54058	C21orf58	NM_058180	CAAAGTCTAATTTAATAACTA	TAGGTGGAACTTGGGAAACTA		
54067	C21orf49	NM_001006116	TAGGTAATGTGTAGTTCTCAA	CACAGAAATGCTAGTTGGAAA		
54102	CLIC6	NM_053277	CCGAATCTAATTCCGCAGGAA	CACGCATATTCAGATGTTGCA	ACACACAATTTCATTCATATA	TGGTATGTGTTTGATGCTATA
54107	POLE3	NM_017443	AAGCTTTAGGAAACTACTAAA	AGGGATGAGGACAATGATGAA		
54112	GPR88	NM_022049	GGCGTTGAGTGTTATAGTGAA	CTCCTAGATGCTAGAACTTAT	TACCACGACATTTAACATCAA	ACCAGTATGAGTTGCCATTAA
54207	KCNK10	NM_021161	CGGGAGTCAGTCCAATAGGAA	TTGGCTGGAATTGGAGACCAA	CAGCGTGGAGATCCACGATAA	CTGGAATTTGTTGGAAGCAGA
54209	TREM2	NM_018965	CAGGGCTGAGAGACACGTGAA	AACACTTACAAATAAATCCAA	AAGGAAGATGATGGGAGGAAA	ATCCAAGACTGTCATATTTAA
54212	SNTG1	NM_018967	CTCACAAAGCACAATATTAAA	GAGGATTTGGATTAAGCATAA		
54329	GPR85	NM_018970	CTGTATGTCACTACATATGAA	TTGGAGCATAGTACCATAGAA	CAAGGGAACCTTACTGTGTTA	AAGCACAAACTAGGAAGACTA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
54332	GDAP1	NM_018972	ACGCATTCCTTCAGCTCTCAA	ACCCAGGTTAATGCCTGATAA	TCCCGGCTTATGCAACTACAA	CGAGCGTGTCTTGAAGAGAAA
54344	DPM3	NM_018973	CCCATTAAAGAGCCAGTTTAT	TCCCATTAAAGAGCCAGTTTA		
54361	WNT4	NM_030761	CAGGGAAGGCCGATAATTTAA	TTGGGTCCTCATGTTATTTAT	CTCATGTTATTTATTGCCGAA	CAGACCTAAGGTGGAGTAACA
54429	TAS2R5	NM_018980	TCAGCTCAATTCAGGAAGTTA	CCAAATTGGCTTAACATTCTA	TCGGTTTAATTGGAAATGGAA	GCCGTTGGCTTCGCTATCTTA
54431	DNAJC10	NM_018981	CTGGAGAACTGTGGTTTGTAA	CAGGGCCTATCCAACTGTTAA	CAGCTTAAGTTTGGTACACTA	CTCGACGGACTTATAATGTTT
54433	NOLA1	NM_018983	CTGCATGATCTGTTTCTACTA	ACCAGTTGACTTCTGCATTAA		
54439	RBM27	XM_291128	CAGGGAAAGATCGAAGTTTAA	AAGCAAGGAAATAACAATCAA		
54443	ANLN	NM_018685	CTCAATCTAAAGACAAATCTA	AAGGTTTCACTGAATGCGAAA	CTGATGCTTGCTACAAACCTA	CACCGTTTCCATCGTCTCGTA
54457	TAF7L	NM_024885	CTCCATAAGATTCAGAATAAA	CTGGTTGTTATTCACCAACTA		
54458	DKFZp564J157	NM_001005354	GAGCGGCCACATAATTACCAA	CGGCCACATAATTACCAATTA		
54461	FBXW5	NM_018998	CACCCAGTTCTCCCAGTTCAA	CTGGACCACGTCATAGACATA	CACGAGGATGTGGTCAACTCA	CCCGTTCAGGGCCCTGAATAA
54462	KIAA1128	NM_018999	GAGCATAATTATCTCAGGTAA	ACGAGTTGGCCTTATCCTTAA	ACCGTATATTTATGAAGCATA	CCGTATATTTATGAAGCATAA
54475	FLJ10458	NM_018096	ATGACCAAATAAGTAACTTAA	CAGCAGTGACAGCACACTGAA	AAGGACAAATGCCTCCGGATA	CCCAGGTTCTATGACCAAATA
54495	TXNDC10	NM_019022	TTCGAGGTTATCCAACAATTA	CAGATTGAAGTCAATTATTCA	ATGCTGTTAATTTAACAAGTA	TAGGATATTAAGACTATCAAT
54498	SMOX	NM_019025	CCAGTCAATGCTGAAAGTCAA	CACGTCATCCAGCTAGGGAAA	ACCGACAAGATCTTTCTGGAA	CCGGCACGATAAACCAGTCAA
54499	LOC54499	NM_019026	TTGGGTATGATTAGAGTGAAA	AAGAATAACAACAGAGATCTA		
54503	ZDHHC13	NM_001001483	TGGATACATATTGGACTTCAA	CAGCTCATTATTCATATGCTA		
54508	FLJ11235	XM_496773	CCGTAGCACAGTAGAAATGAA	CAGGATCAGCATAACCGCCAA		
54510	PCDH18	NM_019035	CTGAGTATAGTTTGACTGTAA	CCCGAAGCAACTGGTAAGCAA	CTGCGCCATAGTAGCAGGTAA	CCGGAGAATATTTCTCTCACA
54512	EXOSC4	NM_019037	CCCTAGTGAACTGTCAATATA	CAGGCAGATGGTGGGACCTAT		
54514	DDX4	NM_019039	CTGAATAACAACATTGCTAAA	AAGGTTTAAATGAAGAAGTAA		
54518	APBB1IP	NM_019043	AAGATTTAAATGAGTCCTTAA	CAGCATCTCTACAAGCATCAA		
54538	ROBO4	NM_019055	CCGGGCCTGTGAGTTAGGAAA	CCGGGAGGATTTCCAGATCCA	CACCTCAGGAAGTGACTCTAA	CTCCTGTAGATTACTCCTGAA
54540	FLJ10404	NM_019057	CCGAGAGGTGGAGTACTTTAA	CAGAAACTCAGAGCAACTAAA		
54554	WDR5B	NM_019069	AAGACTGTCCAGAAACTTTAA	AACCGTAACCTCACACATTAA	TAGCACAATAATTTAACTGAA	ATCAGAGTTACTAGTAGGGTA
54556	ING3	NM_019071	GAGGCGATCTTTGGAATTAGA	CGGCACTTATGACAACATTAA	AACCAAGATTGCCCTATAGAA	CTAGAGTACCTGGGTACATAA
54558	SPATA6	NM_019073	CAGGCTCATCAAAGACATTTA	CAGGATAAATTTATTTACCAT		
54575	UGT1A10	NM_019075	AAGCACAGGCACAAAGTATAT	CTGGAAGATCAGAACCGGGAA		
54579	UGT1A5	NM_019078	CACACTCAATCGTTCTTTGAA	CACCCTGGAGGTGAATATGTA		
54581	SCAND2	NM_022050	CTCCAAATAGTTAAACTGGAA	TAGAGTTAACTTTGTAATGTA		
54584	GNB1L	NM_053004	CCCGTCATGGACCTTGACTTT	CACGATCCGGCCAGATCGCAA	CAGCCTTGGCCTGAAACCTCA	CAGGTGCGTGGGACTCATGAA
54585	LZTFL1	NM_020347	AAGACGTATATTCAACATAAA	AAGCATTAAGATAAACAAATA		
54620	FBXL19	NM_019085	CCGCTGGATCGAGGATGTTAA	CACTCTTTCATCGTCATGGAA	CCGGGTCTGTACAATACGGTT	TACAATACGGTTTGCTATAAA
54658	UGT1A1	NM_000463	AAGGGAAGCTTTGTACCTTTA	CTGATGTTTCCTACAACTAAA	ATGGTTGCAATTGATCCTTAA	TTCCCACTTACTGCACAACAA
54662	TBC1D13	NM_018201	CCGGTGGAACACGTACTTCAA	CACAGAAATCTTGGAAACCAA		
54663	FLJ10439	NM_018093	AAGGTTTATCTCAAGTCTCAA	CACCGAGACTGGGATCTTGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
54716	SLC6A20	NM_020208	CGAGATGTTCCCGCAAATCAA	TGAGATGTTGTTAGCCTATAA	CCCGTGGATTCAATCTTCTTA	TCCAATTATATGGAAGAGTTA
54734	RAB39	NM_017516	TCAGTTCAGGATAAATACCAA	AAGGTTACAAACCCACACCAA	TAGCTTCACAACGTCAAGTTA	CAGGAGCGGTTCAGATCAATA
54737	HSMPP8	NM_017520	AAGGGTGAAATAAGAGATTTA	CTGGTGAACTTCTGTGCTTAA		
54741	LEPROT	NM_017526	ATGGCGTTTACTGGCCCTTAT	CTGGCCCTTATTCGTCCTGAT	CGGCCTTGTGTTGGCAGGCAA	AAGCATCATCATAGAGAAGTA
54752	DKFZp434H2215	NM_017559	ACGGGTGTCATCCCGAACAAA	GAGGATGATACCATCAACCTA		
54754	DKFZp434I1117	XM_030729	CCGGCCGGACGACTCCTGTAA	CCGCAGGAAGAGGACGGGATA		
54763	ROPN1	NM_017578	CTGGGATGGTGTGGTGAGCAA	CACACTAAGGATAGCAATTTA	AGGATAGCAATTTATCTCAAA	TACACACTAATAAACAATTAA
54790	FLJ20032	NM_017628	AAGGCCTTTCATATAAATTTA	CAGCTGTAGACTAACAATATA		
54795	TRPM4	NM_017636	CTGCACGACGTTCATAGTTGA	CAAGATCGTCATCGTGAGCAA	CGGGTTTACCTTTCTAAGGAA	AACGTGGGAATCGGTGCATAA
54801	FAM29A	NM_017645	CCGGAAGAAGTTGGTCATCTA	AAGGAACACTGTCAAACTATA		
54820	NDE1	NM_017668	ACGCAGCTGCAACAAATTGAA	CGCGCAGACCAAAGCCATTAA		
54828	BCAS3	NM_017679	CAGATTTAAATGATACATCAA	CTGGAAGAGATTGAACAAGAA		
54831	VMD2L1	NM_017682	CCGCGACAACAGCGCCCTTAA	TCGAGTTGTCATGAGGATGAA		
54836	BSPRY	NM_017688	CAGCTGATTCAGAAGGAGCAA	GTCGGAAATGTTAAACTTTAA	CTGGATGGTGAATGTCCAGAA	CCAGAACAGTTGTGCCTATAA
54841	BIVM	NM_017693	CTGCTGGAAATAATTCATCAA	GAGGTGGTTTAGACAAATTAA		
54843	SYTL2	NM_032379	AAGGGATTTAAATATAACAAA	CCGGTGGAATCTGATCTTGAA		
54847	SIDT1	NM_017699	CCGGACCAAGATGTTCCTTTA	CACATTCCTCTTAACAAGTAA		
54850	FBXL12	NM_017703	CTGGTGGATGTAACTACTCCA	CACCTTGAAGAGGGCAGATAA	TCGCGATTCAATGATCGATAT	AATGATCGATATGCTCATAAA
54855	FAM46C	NM_017709	TTGGAACATATTCCAATTCAA	CTGGTCATTCATGACCTTAAA		
54866	PPP1R14D	NM_017726	GAGCCTGAGATTGACCTGGAA	CAGGCCTGCCCTGAAACTCCA	CCGCCTGACAGTGAAGTATGA	CAGGAGCTCTTCCAGGATCAA
54873	PALMD	NM_017734	CTGGGTATTGGTGTAAATGAA	TAGGTTAAGGAAGGAGATAAA		
54901	CDKAL1	NM_017774	TAGCACATCCTTCAAATTAAA	CAGCGTACTCATGGAAATGAA		
54913	RPP25	NM_017793	TGGAGTCTTGTTTCCAATAAA	GACAGGTAGCATGGACCTTAA		
54918	CKLFSF6	NM_017801	AAGAATTATAAGAGAAATGAA	ATGGGAATTTAACATATTTAA		
54919	FLJ20397	NM_017802	CTGCAGCTGATTTGAAATTAA	GCCAAAGTGATTAGAAAGAAA		
54935	DUSP23	NM_017823	CAGGAGATGCCATTGCTGAAA	TTGGCTGAAGACACTGAAGTA	GAAGTGGACTAAAGTATTAAA	CAGTTCTACCAGCGAACGAAA
54937	FLJ20449	NM_017826	CAGAAACTATTTGCAAACATA	CTGAATTGTTCTTATATGTAA		
54938	SARS2	NM_017827	CACCTGGAAATTGGCGAGAAA	CTGGATATGCCCACCCAAGAA		
54939	COMMD4	NM_017828	ACCCTGGATGTTACATATAAA	AAGGAACCTATCGAAGAATAA		
54941	RNF125	NM_017831	CAGAAGTACATAGATAAGTAT	CTGGATCATTGTATTACTCAT	CTCGGTTTGCAAATTAGATAA	ATGGTTAGGCACGATAACTAA
54946	SLC41A3	NM_001008485	ACCCATCGTGAAGATCCTGAA	AAACCTCTATTTAGATTTCAA		
54955	FLJ20508	NM_017850	CAGGATATTGAGAGACATTAT	CCAGATAACTATTATTAATAA		
54957	TXNL4B	NM_017853	AAGGAAGTAGACCAGGCGATA	CCACCACTCTATTCAGGTAAA	CTCGTGGTGGTTATTGAAACA	TCGATATGCTAAGAAGAACAA
54958	FLJ20512	NM_017854	ATGGGTCGGGAAGCAGCATAT	CCCGAGGACTGGGACATTAAA		
54962	FLJ20516	NM_017858	ATGCTATTGCCAATACTTTAA	CAACAGCAACTTGATGCTACA	CTGAGTTAAGTAGAAGCCTAA	AAGCTTGGCGTTACTATGTAT
54973	FLJ20542	NM_017871	CCGCAAGATCGCCGTAGACAA	GAGGAACATGTTTGAGTTCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
54988	FLJ20581	NM_017888	TAAGATGATCACACAGCATTA	AAGAATATCATTGGCCCTGAT		
54989	FLJ20582	NM_014106	CAGGTAATAATGTTAACTATA	CAGGAGAATCACATGCTTTAA		
54998	AKIP	NM_017900	AAGCAGATCAAGTTCGAGAAA	CTCAGAGGACTCAGCCTTTAA	CTGCTGTGATCCGTAGTAATA	ATCCGTAGTAATAAATTCTCA
55002	C13orf11	NM_017905	CACGTGCAGATCACCACTTTA	CGGGCTCTTCATGGCCGTCAT	GAGGAGCAGCCAGTACATCAA	TAGTCAAATATTTGTTATTAA
55006	FLJ20628	NM_017910	CGGCGCCTTCGCGAAACACTA	CTGGCTAAGAAGAATTACAAA	GGCGTGATTCATGGAAATTAA	CAGGAGCAACCGAAGACATAA
55010	FLJ20641	NM_017915	TCCCAATTTGCTTGTACTTAT	ACAGAATAGATTGTACGGCAA	CCCAATTTGCTTGTACTTATA	CAGAATAGATTGTACGGCAAA
55011	FLJ20643	NM_017916	CAGGGAGGGCCTTGAGGACAA	TCCGGAATGGCGCATGATGAA	CCCGCTGCAGATCAACTCTCA	ACCGGAAGAGAAAGCAATTAA
55014	STX17	NM_017919	TTGAGGTTTGTTAGTGAGGAA	TTGCAATTTGGTCCAACTATA	CTCCTATAACCTCTAGGTAAA	ACCCTGAATTGGAGACCTTAA
55016	MARCH-I	NM_017923	TACCTTAACCAAGATGCCAAA	ACCAAGATGCCAAATTATCTA	AAGAACTTCTCATGTAATGTA	TAGGCAGTAATCAAAGATTAA
55049	FLJ20850	NM_017967	CCGCTCTTGTAGGGTAATTAA	CAGCTTCGCGGCAGCAGCTAA		
55066	PDPR	NM_017990	TTGGAGCAAGTATGTACTTAA	TAGCTACAAGATTCAGCTTTA	ATCTCTTATCTCCTTGATATA	ACCACATAGCCCAGTGATTAA
55072	RNF31	NM_017999	CTGGCGTGGTGTCAAGTTTAA	CCGAGATGTGCTGCGATTATA	ACGCATGAACGACCCAGAATA	CAGGACAATAACGTCATGTTT
55082	FLJ10154	NM_018011	CAGATTGTAGATGACAATATA	AAGGATGAAATTGAACGAGAA		
55083	FLJ10157	XM_371354	CAGCAAACACATTCCATACAA	CAAGCTCATAAACGAACGCAA	ATCAGTATTGCTTATGAATAA	AAGCACTTTGAGGAACCTTAA
55089	SLC38A4	NM_018018	CAGGACTGGATAAATAATTAA	ACCCAAATACTTTGTATTCAA		
55102	C14orf103	NM_018036	CTCCAACATGTTGACAGTGAA	CTGGGTGGCATGAGAAACCAA		
55104	FLJ10246	NM_018038	CAGGTTCATCTTTGACTTCAA	CAGGTTGTATCTCCAGATAAT		
55111	PLEKHJ1	NM_018049	CAGGGTGCTTGTTCTGTTCAA	CCCGTGCTGAATGAATGTACA		
55117	SLC6A15	NM_182767	TGGAATTACATAAGCCCTAAA	CACGCCTATTGTGGACACTTT	CCAGCAGATATTACTACTATA	CCCAATGGACGGTATGGAATA
55118	CRTAC1	NM_018058	CACCAGTCACTTAACTTGTTA	CCGGGACATCGCCTCACCCAA		
55122	C6orf166	NM_018064	CTGCAGCATCCTCACCATTAA	TTCACTGGTTGTGTAAATAAA		
55124	PIWIL2	NM_018068	AAGGATGTACATAAGATTGAA	AAGAAGCAAGTTTCTGAGTAA		
55128	TRIM68	NM_018073	TTCATGTATGTAGGAGTTAAA	ACGCATTCTGTCCACCATGAA	TAGGCCAAACTGGAGAAATAA	AAGAGAGATCCTGAAGACTTA
55129	FLJ10375	NM_018075	CAGACCCTTTATCAACATAAA	TAGACCATTGTTAAATAAATA		
55139	FLJ10415	NM_018089	CCGAAGGTTCATGGAGAAGAA	CAGGAGGAGCGTGAACGAGAA		
55148	C14orf130	NM_018108	AAGCCTCAACGCAGAATCAAA	CAAGGTTGCACTATTAGTATA	CACAATAGTACCGATCAGTTA	ATCAGTTAACTCAGCGCTGAA
55154	FLJ10504	NM_018116	AAGGAGCTAGTTTGCAATAAA	CTGATCCTTAGTAACATGTTA		
55166	C6orf139	NM_018132	TTGGATATTCTTCATAATTCA	ATGGAAGATTTAACTAATGTA		
55167	FLJ10546	NM_018133	CTGGCACGGGATATAATAGAA	CAAGGCGTTTACTGAGATTAA	CAGTGTCTTATGAAACATGTA	AGGGCCTTGATTGTTATGTAA
55170	HRMT1L6	NM_018137	CCGCCTGGGTATCCTTCGGAA	CCGCAGCGCTTTGCTCAGCTA	CACACCTTATCTAAGTCTGAA	ATAGCCTAACATTTATTGTAA
55174	FLJ10569	NM_018142	CTGGTTCTTCTTGAAGATGTA	CCAGTGTGAAATGTTACTAAA		
55180	WINS1	NM_018148	AACCCGGATATTGTCTGTCAA	AAGAAACTTCTTAGAGATTCA		
55182	FLJ10597	NM_018150	CAGGCAGCTCGCGAACACAAA	ACGGCAAGTCTTAGGAGGGAA	CCCAATCAGTATGCTGAATCA	CTCGGTGTTCAGTGGTGTATA
55183	RIF1	NM_018151	CTCATGGAAATTACAATTAAA	AAGGAAATGCATGTAAAGTAA		
55192	FLJ10634	NM_018163	ACCCAGAAACTTGATGAGAAA	AAGGAAGAAAGTGAAGCTTGA		
55193	PB1	NM_018165	CAAGGATGCAAATTCAATTAA	TCCCAGGTTTATAATGATGCA	CCGGAGTCTTTGATCTACAAA	CAGGCTTACATCGCACATACA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
55194	FLJ10647	NM_018166	CTCCGTTTACTTGATCTGCGA	GAGGTGAAGTGACCAAATGAA		
55200	FLJ10665	NM_018173	AAGGCAGAGGAGTATGTTCAA	CCCACAGAAAGTTGTGCATAA		
55206	SBNO1	NM_018183	CAGGTTCAACTTTGATAATAA	CTGGATGAACTTATCGATGAA		
55218	C14orf114	NM_018199	CAGAATCTCAGCAGAAGCCAA	GTGGGTAAATTTGGAAGGCAA		
55219	FLJ10747	NM_018202	ATCCTCTTTGTTTATATTGAA	CAGGCTGGAACAAGACATTAA		
55228	FLJ10781	NM_018215	CAGGTGTATGGTAGTAAGTAA	CACCATGACTAGTAAATGTAA		
55234	SMU1	NM_018225	CAGAATGTTCAAATACCTTTA	CAGGTTGTTCTGGAATTGATA		
55239	FLJ10826	NM_018233	CCGGATTGCCTTCATCCTGTA	TTGCCTGACAGTGTTCTTAAA		
55243	KIRREL	NM_018240	CTGGGAGGAAAGAGAGATAAA	CCGGGTCATGAAGGCCATCTA		
55247	FLJ10858	NM_018248	TCGGATATACAGCATATTCCA	AAGGATTATGCGACACAATAA	CCTGGATATTCTAACAGTGAA	ACGGATTCATTTCGGAATGAA
55256	MTCBP-1	NM_018269	AAGCCTTAAATGTTTAAGTAA	AACAGGAGTATTAGTACATAA		
55257	C20orf20	NM_018270	CTCGGATTAGCAAGCAATAAA	TCGTGTGACTGCGAACATTAA		
55265	KIF24	AK001795	AAGGTTATCAAATTCACTTAA	AAGGGCATGTAGTTTAATTAA	AACAAGTAATCCCTAGTACTA	TAGCGTAACATGATACATCTA
55274	PHF10	NM_018288	ACGAATTACAGACCATTATAA	CGGACAGTTCCAGGAATATTA	TCCAGGGAAGACAGAAATCAA	ATGGCAGTGTATGGAATGTAA
55275	FLJ10979	NM_018289	AAGGAGATTTAGATCAACCAA	ACCCGTGATATTAAGCAATTA		
55283	MCOLN3	NM_018298	TCAGTTAATCTTCGCAGTAAA	CAGACAGTTCGTCATCAAGAA	ATGACTTTACTCTGACTATAA	CTGATACATACGAAACAATTA
55284	FLJ11011	NM_001001481	AAGGTTAACAGCATGAATTAA	CTGGTTATAGTGGGAATATAA		
55295	FLJ11078	NM_018316	AAGAATTAACCTCCTATCTTA	CACGGGCATCGTACAGGTGTA		
55304	C20orf38	NM_018327	AAGCATCATATTTGAAGGAAA	CAGAGCTTCTTTAAAGCATAA		
55308	DDX19L	NM_018332	ATCAAGGAAGAGAAAGTCAAA	GGGAATTATGCTGTTCATTTA		
55314	FLJ11155	NM_018342	TAGGTTATCAGTAACAATTTA	ATCCTTTGTTTCATAAAGTAA		
55317	C20orf29	NM_018347	CACCGGAGTAAGAAACTACAA	CCCACAGTCATCGAAACACAA		
55324	ABCF3	NM_018358	CAGGGAAATAGCCAGGTGCTA	CCCAAGTGGCTGCTATGTAAA	TCGGTTGGAATCATCTGGCAA	CGAGGCTCGACTTAAGGCAAA
55342	STRBP	NM_018387	AAGGATGTATAGAGTCTCAAA	CTGGAAATTCTACAACTGAAA		
55359	STYK1	NM_018423	GCCCAAGAGTGTTATTCTCAA	CCGATTAGACTAAGGAGACTA	TTCACCTTAGGTATAGATAAA	CTGGGCTGCAAGATATCAATA
55361	PI4KII	NM_018425	TCCAAAGATATCGGACCCTAA	TCCGCACACAATCATAGAGAA	CCGCATCGGGCTACCACCAAA	ACGCAAATGTATGAATAACAA
55364	IMPACT	NM_018439	CAGGATGGATTCTGAAATATA	AAGAAGAGGAATGAACATTAA		
55366	LGR4	NM_018490	CACACTTGGGCCAATAACTAA	TCCAGCTAGATTGCAGTTTAA	TAGGTGTAGTAGAGCAATATA	TAGGATTTCATAGTAATTCTA
55437	ALS2CR2	NM_018571	CAGGATTTACATGGGTATAAT	ATGCTGTTACAGAAACTGAAA	CCAGTGGAACTCACACAGTAA	CAGGAACACTGGTAACTATAA
55503	TRPV6	NM_018646	CAGCAGAAGCTACTTCAGGAA	CAGGCCTGCATTACTCCTTCA	GAGGAGTAGCATGAACGCCAA	CTGCATGTCAGAGCACTTTAA
55511	SAGE1	NM_018666	AAGGGAGCTGTTTAAATTTAA	CTGGTATTTCATGCAGAAGTA		
55520	ELAC1	NM_018696	ATGAGTGGAATTACTAGGTAA	ATGAATTGGCTCAGTATTTAA		
55530	DKFZp761H039	NM_018711	CCCATGAAAGCCAGAGCTAAA	CCCGGCCAAACCCTCAGTGAA		
55534	MAML3	NM_018717	CTGACTTATGGCAACACTAAA	CAGCAGCTTTGGAGACACAAA		
55561	CDC42BPG	XM_290516	CACAGTCATTATATTGTTATT	CCGGCCCGTGTACACACTCAA	CTCGCCGCCTACCAACTTCAA	CGCCGGTGGCTTTGCACTCTA
55572	H17	NM_017547	CCCGCTAGTTGTCAACATGTA	CAGCTTTCTACGGAACATCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
55578	FAM48A	NM_017569	CTGAAGTTAAGCAGAAATTAA	AAAGATGATTATGTATTTGAA		
55600	ITLN1	NM_017625	CTCAGACAAGATTACAATGAA	CCCGGTGATCCCTGTGGTCTA	CTGCGGGATTTGTTCAGTTCA	ACCCAGTAGCTAGAATGTTAA
55601	FLJ20035	NM_017631	CCCAGTGTCAGTATTTATAAA	AAGGGTATTTGCTACCTTTAA		
55611	OTUB1	NM_017670	CAGCAGGACCGAATTCAGCAA	CAGGGCTTCACTGAATTCACA		
55621	FLJ20244	NM_017722	AAGGATCGTCTCTGTGGCTAA	CCAGGAGAGAAGGACACGCAA	ACGCCGGAATGTCCAGCTCAA	CAGCATCAGCGCTGACTTCTA
55622	FLJ20272	NM_017735	AAGCCATATTCTTAAATTCAA	CCGCAGGTGTATTTACGGTAA		
55626	FLJ20294	NM_017749	TGCGTAGAATTTAGAGTTATA	CTCCTAATGAATGCTAAATAA		
55627	FLJ20297	NM_017751	TAGGCTGTCGTCTGCCATCAA	CAGTGGTACTTAAGTATTCAA		
55629	PNRC2	NM_017761	CTGAAGGTTTAGTATATTAGA	AAGATGTAAACTCTTGCATAA	ACAAGTTTATGTAGTACTTAA	CCCAATGGCCCTGTTTATTAA
55632	KIAA1333	NM_017769	AACGACATTAAGTGATAAATA	CTCATTACATTGGACATTAAA	AAGGAATATTATAGCCACTTA	TAGATTAATCTGTATGGTCAA
55636	CHD7	NM_017780	CAGGGATTAGTTAACAATACA	TACCATTGGTATTATAATAAA		
55640	C14orf58	NM_017791	ATCAGATATTCTAAACTTAAA	AAAGGTATTAACAAATGTTTA		
55643	BTBD2	NM_017797	CCGCATCAGGTTCTCAGTCAA	CACGCTATACACCGCCAAGAA		
55644	OSGEP	NM_017807	CTGGACCACGGGAAAGAGATA	CTGGAGGGACTAATAAGATCA	TAGCAAAGCTATAGACTCCAA	CCAGGATGACTCAGCAATAAA
55652	FLJ20489	NM_017842	CTGGAGCTTCATTTCCTTCAA	GTGAGGAATCTTTGTACTTAA		
55662	HIF1AN	NM_017902	CACTGTGAACTTCTGGTATAA	CACCCACAAGTTCTTGTACTA	CAAGCTCAAGCCATACATAAA	AACACATAGGCTTGCGTCTTA
55663	FLJ20626	NM_017908	CCCAATGTCGATGGACAGGAA	AAATTCCACTTTCATAATAAA		
55667	C9orf55	NM_017925	CAGCACAATAATGTTCTTAAA	CAGCTTGAGATGGAAATTCAA		
55669	MFN1	NM_017927	ACCCAGCAAGAAATTATTGAA	AAGGCTTGTTATAGTCACTTA		
55680	RUFY2	NM_017987	AAGAATTATGTTGAAGAATTA	CAGGATGTAGAGAATGAGCTA		
55683	FLJ10081	NM_017991	CCGGATGCTTGTGTCATCCAA	CCGACCTGCCTTTATGATAAA		
55687	TRMT1	NM_001008568	CTGACAGAGATGGATCTGCTA	AACGAAAGAGTTTGTAAAGAA		
55690	PACS1	NM_018026	CCCGGAGGAAACTAACCTCAA	CCCGGTGCAGATGAACCTGTA		
55699	FLJ10326	NM_018060	CAGTCGTTCAATATATGTAAA	ACCGAATTATACAAACAATAT	ACCACTGAGCATATTGTTAAA	AAGAGTCTTCCTATAAAGTAA
55702	FLJ10374	NM_018074	CTGGAGCAGCTTCCAACACTA	TGCGAGGTGATCAGAAGGCAA		
55711	MLSTD1	NM_018099	CAGGTTGGGTTGATAATATAA	CAGGATGACAAAGCTCATGAA		
55718	POLR3E	NM_018119	CAGGAGGTGGATAAAGTACTA	CCGCGGAGAGATCGAGCTGAA		
55732	FLJ10706	NM_018186	CAGGATTTCTAAAGCACACCA	CAGGTAGCAGATCAACCTTAT	CAGCCTGGCTTTCAATGGAAA	CTGGGTTTGATGCTTTGTCAA
55734	ZFP64	NM_018197	AAGGACATGGAGCGGCATTTA	CAGCAGTTTAACAACCTGGAT		
55743	CHFR	NM_018223	AACAGTGATTAACAAGCTGAA	TCACCACGCCATGAAATTCAA	TCCCGTGGAGCGGATCTGTAA	AACCAGAGGTTTGACATGGAA
55754	TMEM30A	NM_018247	ATCGATGGCGATGAACTATAA	ACCGGATAACACGGCCTTCAA	CTCGAGATGATAGTCAACTAA	AACGATTTAAAGGTACAACAA
55760	DHX32	NM_018180	ATGGATCAGGTAACTACTTAA	ACGCCTTATCTTTGAAATTCA		
55769	ZNF83	NM_018300	ACGCAATTTAAATGTGATATA	AAGGAGAGTAATACAGGAGAA		
55779	FLJ11142	NM_018338	CTGAGATTAATAGAAATTGAA	AACTATCACTTTCAACATTAA		
55781	RIOK2	NM_018343	CTCATAAATGGTTATCCACTA	GAGCTATGAATCAGTATAGAA	CGCGGTTGAAATGGGCATGAA	AACGCGATTATCATAAACATA
55793	FLJ11280	NM_018379	TCCAGTTGTTTCAGAGCTTAA	TAGCACCATGACTAAGCATAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
55794	DDX28	NM_018380	CAGGGCAATGAGGAACAACTA	CACGTACTTGATCACTTTGTA		
55795	FLJ11305	NM_018386	AAGGATGATTCTGATCTATTT	AAAGCGTATTCTGAATTTATA		
55801	IL26	NM_018402	AACTTAATTTAAAGTATGTAA	AAGCAGCATGGCTCAAAGCAA	CAAGTACATTGTGTCAACTTA	CAGTGTGAACTTAGTACTTAA
55802	DCP1A	NM_018403	CAGGATACATTAATACATCTA	CTGGAGCAGAATAAGTCTAAA		
55805	DKFZp761O011	NM_018409	CTCAAAGATCTTAATGAGTAA	CCGCTAAACACTATTATTCTA		
55813	HCA66	NM_018428	CACGCATTGGATATTCATTTA	CTGGCCATTTATGAAGATGAA		
55814	BDP1	NM_018429	CAGAGCAAGGATAGAAATTAA	AAGGTTCTTAATGAATGTCTA		
55815	TSNAXIP1	NM_018430	CCGCACGCAGATGGAACTCAA	CAGGAGGGACTTTGAAATGCA		
55819	RNF130	NM_018434	CAGAATGATGTCGTCCGAATT	CTGTCCTATGTGCAAACTTAA	CAAGCTGTTAACCGAAGATCA	TCCGAGAACAGGAGAAATCAA
55829	SELS	NM_018445	AAGGAGATTTATGGACTTCAA	CTGGCGGATGAGGCTAAGAAT	AACCCTTAACCCTCGATTCAA	AGGCCTCTAGATGATTAGCAA
55830	GLT8D1	NM_018446	TACCGAGATCTCAAACATAAA	CAGACAGACTATAGACTATAA		
55836	C6orf35	NM_018452	TAGGCTCTAATTAGTCAGCAA	CTGCCTTTCATTTGTAACTAA		
55837	C14orf11	NM_018453	CCGGAGAAAGTGAATCATCTA	ATGAATTGTTCTATTAACAAA		
55844	PPP2R2D	BC047379	CCGCTCCATTAAGAACAGTGA	TTCATCCATATCCGATGTAAA	TAGGTGGTTACCACAACAGAA	CAGAGACTACCTGTCGGTGAA
55848	C9orf46	NM_018465	CTGCTTGGCTTCCACCTTTAA	AAAGGAGTTCATGCTTATGAA		
55850	MDS032	NM_018467	TCGAATCATGCCTAAACTCAA	ACCGGCCTCTGAGGTGATCAA		
55851	PEN2	NM_172341	CTCCCAGGACAGGCTCCTTAA	ACAGAACAGAGCCAAATCAAA	CTCGCCCAAAGAAGACTACAA	CACAGAACAGAGCCAAATCAA
55870	ASH1L	NM_018489	CAGGCTGTCGTATCAATGCAA	CCGAGATGATGGGAATATCAA	TCGACTGTTATCTCACATTAA	ACGGTAGTTCTTGCAATTATT
55872	PBK	NM_018492	AACGCTGTAAACTGTAACATT	TCAGTAGTTATTAGACTCTAA	CTCATTCTCCTTGGGCTGTAA	AAGTGTGGCTTGCGTAAATAA
55884	WSB2	NM_018639	CACGTTAATTCGGAAGCTAGA	CGGAAGCTAGAGGGCCATCAA	CACGGCTTCTTACGATACCAA	AAAGATGTCTTAATTGTGTAA
55889	GOLGA6	NM_018652	CAGGAGAGACTGTGTGAACAA	CGGACGGGACGGAGCAGTGGA		
55894	DEFB103A	NM_018661	TACCATTGGGTTCCTAATTAA	CAGGTCATGGAGGAATCATAA		
55897	MESP1	NM_018670	ACCCATAGGGCTAGACACTTT	CACGAGCTGCGCCGCTTTCTA	CTGCCTAATGTGAATTTATTT	GTGAATTTATTTATTTGTGAA
55908	LOC55908	NM_018687	CCGAGAATTTGAGGTCTTAAA	ACGGCTGACAAAGGCCAGGAA		
55914	ERBB2IP	NM_001006600	CTGCAGTAACTCGAAGTACAA	CAAGTTTGATTCAAATCATAA	CAAGATGTTATCAATTGGTTA	CCCGAAGAGCCAAATATAATA
55915	LANCL2	NM_018697	AAGGAAAGAATTTGAAGTCCA	CAGATGGGTTATTGCAGATTA	CTGGCAGTTCCAGAACATTTA	ACCCAGGTATATGTTACTAAA
55922	NKRF	NM_017544	TCGCTTATTTCTGGAATGTAA	CAAGATGTCAATTGAATACAA		
55929	DMAP1	NM_019100	GCGGATGTACGGGACATTCTA	CAGCTTTATCTCCACGATGAT		
55959	SULF2	NM_018837	CTCCATGGAGACGATTTACAA	TCGGTGCTACATCCTAGAGAA	TCGAAAGTGGCCAGAAATGAA	ATGACAGATTCTGGAGGATAA
55968	NSFL1C	NM_016143	CAGTAAATGCTTGACAAGTAA	CACCAGCATGTTGTACGGAAA		
55969	C20orf24	NM_018840	TGGATTCAGATGAAACATTAA	CTGGATTCAGATGAAACATTA		
55997	CFC1	NM_032545	CTGGAGTAAAGACACCTTCAA	TTCCTGGAAACTGATCTTCAA		
55998	NXF5	NM_032946	CAGGAAGCTAGTGAAATGACA	AAAGTATACTCTACCATTAAA		
56000	NXF3	NM_022052	CTGAATTTGATTCAGAATGAA	CCAGTTGAGTTTCACTATGAA		
56107	PCDHGA9	NM_018921	CAACGGATTTACCGAGTTAAA	ACGGAATAGAAATAGAAGTAA		
56108	PCDHGA7	NM_018920	AACATCCTGATGGAAGATAAA	AAGGATTAGATTATGAAGAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
56110	PCDHGA5	NM_018918	TCAGATTATAATATCACTTTA	CAGATTATAATATCACTTTAA		
56124	PCDHB12	NM_018932	AAGCTACACAATAAATCCGAA	CTCCAGGTCAAATAAGTTCAA		
56132	PCDHB3	NM_018937	CCGGAACTAGTACTGGATAAA	ATGGACACAAATATAGACTAA		
56143	PCDHA5	NM_018908	CACAATTGAGATACAGGTTAA	AAAGTCCAAATTTATAATTAA		
56156	TEX13B	NM_031273	CAGGAGAGACTCCGAACTCCA	CGGAGCTATTGTAGCAGGCAA		
56171	DNAH7	NM_018897	CAGGATAAATCGGCCAGCAAA	TTGGAGAGTTATGCTAAGCAA	TCGGAAGGCAATATATTAGAA	CGGGCTAATATCATTCGATCA
56172	ANKH	NM_054027	CACGCTCTGTTTCGTGATGTT	CACGGAGTTCGAAACCATCTA	ATCAATGAACATTGTACCTTA	TTGAATGTAAGGCTCAGTAAA
56204	FLJ10980	NM_019600	CAGCACCATAACCCAAATGAA	CACATTGTTGTGGAAGAATAA		
56241	SUSD2	NM_019601	CGGCACCAACTTCACATTCAA	CAGCCTGACCTGGCATGTCAA		
56255	DJ971N18.2	NM_021156	CTCCAATAACAGCCAGGTTTA	CAAGGTAGTCTTGTGAAGAAA	CTGGGTCTTGAACTACTTTAA	CTCCAGTACCTGAAAGTGAAA
56256	SERTAD4	NM_019605	AGGGAGTTATTTGGTAAGCAA	ATCCAAGATCACATACTTTAA		
56259	CTNNBL1	NM_030877	CAGGCATATCATCAAGGAGTA	TCGATTTGCTTCAGGAATTAA		
56265	CPXM	NM_019609	CCGGATTCGAGTCATCAAGAA	CTGGAGGACGGCGATCTATAT	CAACCAGAGCATCGATCTTAA	GAGCATCGATCTTAACCATAA
56270	WDR45L	NM_019613	AAGACTGTTATTGAAATAGAA	GCCGGTTTCTTTAGTTCTTTA		
56271	BEXL1	XM_043653	CTAATGGAAATTAGAATTCTA	AGGGCAGATGATGGAAATCAA		
56301	SLC7A10	NM_019849	TGGCTGGAACTTCCTCAACTA	CCCACTGGTGACCTTCGTGTA	CACGTTCACCAACATTGCCTA	CAGCTTCATCTCAGAGCCTAT
56311	ANKRD7	NM_019644	CCGGTTAAGTGAACTATGATA	AAGGATGGGTATACTCCACTA		
56341	HRMT1L4	NM_019854	CAGGCTCTTATGGGCATGAAA	CAACATCATCACCATATTTAA	CGCGTGTGCCTAGAATATATA	CAGATGTTAAGCAGCTATGAA
56479	KCNQ5	NM_019842	CGGGTTGCTGTTGTCGATATA	CAGAGTATTAAGAGCCGACAA	AAGGGCAAATCACATCAGATA	TCCAAGGTGCATCGACATTAA
56606	SLC2A9	NM_001001290	CACGTTGGACAATTATGTCAA	ACCCATTATTGGGAAGCTTAA		
56649	TMPRSS4	NM_019894	CAGGATCCTGACAGTGATCAA	CAAGGTGATTCTGGATAAATA	CAGGATCTGGATGTTGTTGAA	CTGGATGTTGTTGAAATCACA
56650	C3orf4	NM_019895	ACCGGAAAGAGTACACCTTAA	ACGGTGTATCACCATACCCAA		
56652	PEO1	NM_021830	CAGGCACCTAAGGCATTTCAA	CAGGATCGCAGCTCAAGACTA	TAGGATAGGCTGGAGCATAAA	CTGGCAGGCTAGTGTAGATAA
56659	KCNK13	NM_022054	ATCCTTATTCTTTAAGTCTAA	CCAGGCTTCCTTCAAAGCATA	TAACTAAAGAACATAGCTTAA	TGCAAAGATGATGACTATTTA
56660	KCNK12	NM_022055	TGGGACCATCCTGTTCTTCAA	CTGCATTTACTCGCTCTTCAA	CGCGCTGGGCATCATGAACAA	CTGGCGCTTTCTTAATCTTTA
56729	RETN	NM_020415	CAGCATTGGCCTGGAGTGCCA	CAGGAGGTCGCCGGCTCCCTA	CTCCATGGAAGAAGCCATCAA	CCCTAATATTTAGGGCAATAA
56848	SPHK2	NM_020126	CACGCTTTGCCCTCACCCTTA	CAGGTGGAGTATGGGCCGCTA	CCGAGGGTAGTGCCTGATCAA	CAGGATTGCGCTCGCTTTCAT
56851	C15orf24	NM_020154	TACATTATGTATATTAATTAA	CAGGTCCACCTTCTTACTTTA		
56888	KCMF1	NM_020122	CTCCTAATACTCCACATTCAA	CAAGAACATGTTACTTCTGAA		
56889	SMBP	NM_020123	CACGTCTTTCTGGGCATATAA	CAGATGTACATAGATGATTTA		
56893	UBQLN4	NM_020131	CACATGCTCAATAACCCTGAA	AGAGATGCTAATGGAATTTAA	CACACTGGCCTTTGTAAATAA	CCAGAGGAAATTCGTGTGAAA
56897	WRNIP1	NM_020135	ATGAATTAATGTTATAAGGAA	CGCCATGTTCATAGAGGATAA		
56900	AD-020	NM_020141	CTGGAAATTCTATTTACTTTA	AAGGTAATTTACAGCCAGAAA		
56904	SH3GLB2	NM_020145	CACCAAGAACTGGACAGAGAA	CAGACAGAGTTTGACCGGCAA		
56911	C21orf7	NM_020152	CTGAGAATTGTTGTAAAGTAA	AAGGTGTGGAATAACCCTTAA		
56915	EXOSC5	NM_020158	CCCAGCAAGGATAACATTCAA	ATGGAATGGATGAATCAATAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
56919	DHX33	NM_020162	ACGGTTCCTCTTAGCTATTTA	CTGGGTGAAGGTTGATTTGTA		
56922	MCCC1	NM_020166	CAACATTGACTTCTTACTCAA	TAGCATGCAGATTGAAGATAA	CATGGTTATGATCGCCATGAA	ATGCATTTGGGTCACTAATTA
56928	SPPL2B	NM_020172	CACGGTGAGGGCGGCGCTGTA	CAGGTTTGACATCCAGGTACA		
56930	LOC56930	XM_373790	CACCAACCCAGTTCTCAGTTA	TTGCCACGTGTTTCCTGTTAA		
56935	FN5	NM_020179	AAAGGAGATAATAGCCTTAAA	CTGGTCTTTGACTTGATTAAA		
56943	e(y)2	NM_020189	CGCGGTGATGGTGGTTAGCAA	AAGGAGCTCCTACAAAGAATA		
56949	XAB2	NM_020196	CCGGACCTTGTCTTCGAGGAA	CAGCTACGTTTGTACATCAAA	CCGCGTGTACAAGTCACTGAA	CACGTACAACACGCAGGTCAA
56950	SMYD2	NM_020197	AAGATAGAAATGACCGGTTAA	ACCGGTTAAGAGATTCTTATT	CCGGAGGGCCAAGCACTATAA	GAGGTTAGTCTGAATCTTGAA
56951	C5orf15	NM_020199	AAGGATATTTGTGTACAATTA	TAGGATAATGATATTGCTCAA		
56952	PRTFDC1	NM_020200	CAGGGTATGACTTGAATTTAT	TACCGGGAATGCAGCTATTAA	CCGGGAATGCAGCTATTAATA	CTCGAAACTAAGCAAGTATAA
56956	LHX9	NM_020204	CCGGCACTGCGACCACTTTAA	CAAAGTGTATTTGGATTTAAA	AACCAGATAATTAATTAGTTA	CCGGGCGTGTGTATATGGAAA
56961	SHD	NM_020209	CCAGGGCTTCCTGCATCTGAA	TCCGGAGACCTCCGCCCAGAA		
56967	C14orf132	NM_020215	CGCCATAAATTCTGAAATAAA	CAGCATGAAAGTGATGAGCTA		
56970	ATXN7L3	XM_375456	CAGCATCTATGATGACATCAA	CCACAAGAGTTTACAAATGAA		
56974	DKFZp547K054	XM_498167	CGGGTCGATGTGCAAATCCAA	CCGCATTAATGTCCTCTGGAA		
56981	PRDM11	NM_020229	CTGGCTGATTGTGGACAAGAA	CTGGATGAGGTACGTGGTCAT	CAGGTTCTGGATAACCCAGAA	ACGCCTACAGTCAGTGTGCAA
56988	C8orf17	NM_020237	AAGAGCAATAATACAATTCAA	ATCAAATTTCTTTATCTATAA		
56990	CDC42SE2	NM_020240	ACGGCGGATTGACAGAAGTAT	CCCACAAACTTTGTGCATACA	CAGGAGACCTGTTCAGTGGAA	AAGGGAGGTTATGGAGGTGGA
56992	KNSL7	NM_020242	CTCTATACACTCAGAATTCTA	CAGGATTCCTATGACAACTTA	TTGAGATTGACCAACTTTCAA	ACGCAATAACAAATTATCATT
56995	TULP4	NM_020245	CCGTTTCTTGATCACCACTTA	CTCGGTGCAGTAATCTATAAA	CACACTGTGTTGGACCAACAA	ATGCATTACTGTAAACATGAT
56996	SLC12A9	NM_020246	CAGCAGTACCCTGAAGGACAA	CACGATCGTCGCCGTCGCCTA	CCCACTGGTGTTGATCGGAAT	CTGGTGTTGATCGGAATCTAT
56998	CTNNBIP1	NM_020248	TCCCTTCAGACTGGCCCTTAA	CAGTATCGTTTGTTTATGAAA	TGCGTTTATAATTGGCTTAAA	CACCTGTTTGCCTGAAGTTAA
57007	CMKOR1	NM_020311	CACGCTCTCCTTCATTTACAT	CTGGGTGAATATCCAGGCCAA	CCGGAAGATCATCTTCTCCTA	CACTATTGGTGTACCTTATAA
57018	CCNL1	NM_020307	TTGGATATAAGGGATCTTGTA	CAGTGTGATGTATGGACTCAA	CTCCAAGAAGACACTATAATA	CCCTAGCAGTATCTAATTAAA
57019	CIAPIN1	NM_020313	CAGGTTGAACATGATGATCAA	CAAAGTGAAGACAGCATCTAA		
57026	PDXP	NM_020315	CAGGTTTCAGTCAGTAAATAA	CCAGTTTAGGTTCCTAAGTAA		
57048	PLSCR3	NM_020360	TAGCATCTGCTTGGCCAATTA	TACATTCATATAAACTTTGTA		
57060	PCBP4	NM_020418	AAGGGCGAGACTGTAAAGCGA	ACAGGAGTTCTTGGTTCCCAA		
57085	AGTRAP	NM_020350	TTGGGTCTTCTCAGGACCGTA	AACCTGAAGGTGATTCTCCTA	CTGCTTCGTCTACCACATGTA	CAGGGATTGCCTGAACCAAGA
57093	TRIM49	NM_020358	CAGGATCTCACATTTGCTTAA	TACGTATTGGTTCTTTATTAA	CAGGCCTTGTTTCTACCTCAA	ATGATATCTTTCTGTATGAAA
57105	CYSLTR2	NM_020377	CAGATTATGCCAGGCACTTTA	AAGGGTGGAGGTGATATGGCA	TGGGATCATATGGATCCTTAT	CAGGCTTTCTAAATTCTTCAA
57113	TRPC7	NM_020389	AACGGTGATGTGAACTTCCAA	CCGGATCAAACTCGCCATTAA	CGGATCAAACTCGCCATTAAA	CAGGCTTACGTCAACAGTCTA
57115	PGLYRP4	NM_020393	CCAGTGAATGTCCTTGTTATA	CAGGATGACTCTCCCAGCGAA	CAGCGAAGTATGGCATCATTA	TCAGCAGTGTCTGAAATTTAA
57117	LOC57117	NM_020395	CCAAGTTGTACTGAACGCCAA	AACCTGCTACTTCGTCAGCTA	TACGCCCACTGTACCTTTAAA	CAGGACCTAGTGGAAGTACTA
57118	CAMK1D	NM_020397	CTGAGAAAGATTAAGCATGAA	ATGGAGAAGGACCCGAATAAA	CCAGGCGCTTTCTATACTTAA	CAGGCGCTTTCTATACTTAAT
57122	NUP107	NM_020401	CAGCTTTAAGTGGGAATCTTA	CAGGTGAATATACTGAGTAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
57124	CD164L1	NM_020404	CAAGCGCATCACTGACTGCTA	CCAGCAGATGTGTGTCAACTA	CCCTATGATCTCAACCAAATA	CACGCTGGCTGTCGACGGCTA
57130	ATP13A1	NM_020410	CAGGAGCTGCACTTCATTGAA	CACCTTCGCCATCAATTACAA		
57140	RNPEPL1	NM_018226	CACCTACTCTGCCGTCGTCAA	CCTGATGAACCTGTTCACCTA	CCGAGCCTATGTGGAGAAGTA	CCGGGCAGGGCTGGAATTCGA
57144	PAK7	NM_177990	ACGCCTCTAGTAGCAAACCAT	AAGGTGGATTACGATCGAGCA	ATGGTGTGCACGTTTCATTAA	ATGATCTGGATCCGTATTATA
57146	LOC57146	NM_020422	AAGGTGTAGTTTCCACTGTAA	CAGATGGATGAAGACCACTAA		
57147	PACE-1	NM_020423	TGAGGAGTATTCAGTCAATAA	CAGGAGGTGGAATCACTGCTA	CAGGACAATTCCGGAAGTAAA	AAGCTCTATTATGAAATACAA
57148	KIAA1219	NM_020336	CCGGTACTTTGTCTTGGATAA	CCGGGCTGTTACTGTGAATAA		
57151	LYZL6	NM_020426	AAGCAAGTTCAACATATCAAA	CAGCAGCTTTCTTGCCCTAAA		
57152	SLURP1	NM_020427	CTGCTTCCGAGACCTCTGCAA	CAGCTCCTGTGTGGCCACCGA	CAGGGCGGAAGGTGCTCCTCA	CAGGACCATTACCCGCTGCAA
57153	CTL2	NM_020428	CCGGGACTTTGAGTACTATAA	CACAGTGAACACCCACGTTTA		
57161	PELI2	NM_021255	CAGAACTGTTTGGTTGATTAA	CAGGGTTAGGGTTTAAAGAAA	CACGTGATATAACTGGTTATA	CTCGGGTACAATGGTGCTTTA
57162	PELI1	NM_020651	CAGGACTACATTATAAATTTA	CAGGCTATATATTGTAGCTTA		
57167	SALL4	NM_020436	CCGAACCAACACATCCATTAA	CGCGGTGGATGTCAAACCCAA		
57172	CAMK1G	NM_020439	CTGGAAGAAACAGACCACCAA	TAGAAAGAAGTTCATGAGTAA	CAGGTCTTGTCGGCAGTGAAA	AACAGGCCGCCTGAAACTCAA
57176	VARS2L	XM_373419	CCGGAGGAACCGTGAAGCCAA	TAGTATTGTATGAAATCCCTA	CATGCAGGAATTGCTACACAA	CGCTTTATCCTCAATGCTTTA
57238	KIAA0492	XM_378914	CTGTGTTATAATGATACTTAA	TAGCAATTGAATAAACATAAA		
57325	CSRP2BP	NM_020536	CTGGAAGGAAGTGGACGTCAA	CAGGCGTGATTATGAAACAAA		
57404	CYP20A1	NM_020674	TAGAGAGACCCTCGTCCTTTA	ATCCTAGAAGACAGTATGATA	CAGAGTTGAGGTTTGCATATA	CCAGGGATTACTCCAACTGAA
57405	Spc25	NM_020675	CGGGACTAAGAGATACCTACA	ACGGTTTATAATTAACATACA	CTCGTCATTTCATTAGGTATA	CCACGGTTTATAATTAACATA
57407	HSCARG	NM_020677	CACCTTCATCGTGACCAATTA	AGGCACCAACATCTGAATAAA		
57413	AD026	NM_020683	CAGAGGAGCTATGATAGACCA	TGGGAAAGACCTATCAGGCAA	CTCGCGTGTCCTGACTCCAAA	CACGGCTTCTGCCATCTGCAA
57452	GALNTL1	XM_031104	AAGGATCCACATACCCATAGA	AGCAGCTAGGCGCGAGCGAAA		
57462	KIAA1161	NM_020702	CGCGGCCGCCATCAAAGTCAA	AGGACTCTCGTAGGAAATAAA	CAGGCCAGACTTCGTGCCTTA	CACCTCTATACCACCCATTAA
57472	KIAA1194	NM_015455	CCAGGATATATTGAACCTTTA	CAGAGGCAACTTATTCATGAA		
57484	RNF150	XM_371709	TCCAGAGGTTTCGATATGCAA	AACCCGGAACTTGCAGAAATA	CCGGAACGCGTTCCTGCAGAA	CAGAAGGACTGTTGCCTTGTA
57504	MTA3	NM_020744	AAGAAGGATAGAAGAACTCAA	ACGGCCGTTTGTTGCTATTAA		
57508	KIAA1287	NM_020748	CAGGTAAACCCTAATCATTAA	ATGAGTGTTAGTGGAATTTAA		
57510	XPO5	NM_020750	ATGGTACAGGCTACTGCTAAA	CACGGTTTGCTGTGTTTCAAA	CCAGATGTTTCGAACACTAAA	CTGTCTCGAATTGTAGTGGAA
57514	CDGAP	NM_020754	CAGGATGTCACCATAGATAAA	CTGGATCAGACTCCAAATCAA		
57520	HECW2	XM_038999	CTCCATCACTTGAGAAGTATA	ACGGTCTACTATCATCAGTAA	AAGGCTCTTCTCAGAATTCTA	CAGGATTGGTGCGCCTTTCAA
57529	RGAG1	NM_020769	CACCATCTCACTACATTCTTA	AAGCAATATCCTCACTGATAA	CAGGGCATATATGACTCCCTA	AAGGCCCATACCAACAAGTAA
57533	TBC1D14	NM_020773	CAGCAGGACTGTGTTCATGAA	AACACTGGAGTTGGCCTTAAA		
57538	ALPK3	NM_020778	CAGGTGGATGCTGGGACACAA	CAGGCAGATGGGAAGATACAA		
57558	USP35	XM_290527	GTGGATCATTGCACTGCTGAA	ATCGAGGTTTCGCTCACCAAA	CCCTTCTAACTTCTAACCGAA	ACCCATGTTCATAAATAAATA
57560	KIAA1374	NM_020800	AAGGAATGAAATTCTGATAAA	CCCAAAGTTATTACCACATAA		
57565	KLHL14	NM_020805	CCAAATTTAATCCATAATAAA	AAGCATTTATGAGAATTATAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
57572	DOCK6	NM_020812	CACGGTGAAGATGAAGGAACA	AAGACCAAGGATGAAATGGAA		
57579	KIAA1411	NM_020819	CAGCAATTACATTAAATTCAA	AAGGTGCTGAATAGCATTAAA		
57582	KCNT1	XM_029962	CTGGCTCTTTCCAAACTAGAA	AGCGCTGGAAACTTCTATTAA	CAGGTCATCGTGGCCATAATA	ACGAGGACGTAGCAAATTTAA
57585	CRAMP1L	NM_020825	CTGCATAATGATCCCATTTCA	CAGATCGTCAGTGGGATTGAA	CCCGACAACCTTGCCACCCAA	AAGGGCCACCACTGTACGTTA
57592	KIAA1441	NM_020832	CCGCCTGGTCTTCTTCAACAA	CAGGCTCTCAGGAATCCTTTA		
57593	KIAA1442	XM_044921	CAGGGAGAAGTGACCTGGAAA	CAAGTTCTTCCTCAAATGCAA		
57599	WDR48	NM_020839	CAAGTTTGTCATATAAAGTAA	AAGGGAGATCATAGTGAGTTA		
57605	PITPNM2	NM_020845	CTCCAAGATGATTATAAAGGA	CTCGTGCAAGCAGGAGAGAAA	CTCGAGTTTCTCAACTGTTCA	ACGGGAAGGCTTGGACTCCAA
57608	KIAA1462	XM_166132	CTGGAAGTAACTTTACTTATA	AAGGTAAATAATAGCCTATAA		
57609	KIAA1463	NM_173602	CCGGCATACATTGAGTATAAA	ATGGAATTAATTTACACGTAA		
57613	KIAA1467	XM_370682	GTGAATCTCTTAAGTATTTAA	CGGCGCAGTGATGGATGTTAA	CATGGTGTATTTGCAAACTAA	TTGGTTTAGTATAGAATTTGA
57617	VPS18	NM_020857	CCCGATTATCTCGCTGCATAA	ATGGAGGTGGAGAGCATTAAA		
57621	ZBTB2	NM_020861	AACGTTTAATTAAATGAGTAA	CAGGAGTACCTTTCACATCTA		
57633	LRRN1	NM_020873	AAGATTGATAACCCTCACATA	AACCTCTTCAATCCCACTAAA	CTGGTTTGATTCTACACCCAA	AAGACTTTGCTTGAATGTTTA
57636	ARHGAP23	XM_290799	CTCCTTCATCTCGGCCGTCAA	CTGGCTGAAAGCAGCACTGAA		
57642	KIAA1510	NM_020882	CCCGACCTTCACGCTCTTCAA	CTGGGAAGAGAGCAAGTTCAA		
57646	USP28	NM_020886	CTGGAACAGTTTGCAGATAAA	AAGGATTAGGTGGGCACATAA		
57647	DHX37	NM_032656	CCCAGTGACTGTGCATTTCAA	CCAGATCAACTTGGATCATTA		
57650	KIAA1524	NM_020890	ACCACTCTTATAGAACAACAA	CAGCTAGTAGACAGAGAACAT	CGGCACAATCTTTCTGTTCAA	CAGAAAGAGCGCAGAGTGATA
57654	KIAA1530	NM_020894	CACGGTGATCTCGAACTCCTA	ATCCAAGATCACAGAGATTTA		
57657	HCN3	NM_020897	CTGAGTGGGAACATACTTCTA	AGGGACAAGAGTAGTCCTTTA	CAGCTTTCTGCCAACATGTAA	CCCGCCTTGGATCGTCTTCAA
57661	KIAA1542	XM_290536	CACACGAACCATCTCCATCAA	CGAGCTCAATTTGGTGGTAAA	CGCGTCCTTGATAAATCTCTA	CCGGATCAATATTCCTGGAAA
57665	RDH14	NM_020905	TATAGTAAGTATAATGAATAA	ACAAGTCTTACTTGGAATAAA	CTGCCTGGTGTGTGCACACAA	CAAGCATGGATGACATATTAA
57666	KIAA1545	XM_495939	CCGAAGTTACAGATTATATTA	TAGTCTGTTGATATAAATATA		
57693	ZNF317	NM_020933	CCGCTGGAAGTCCAACTTTAA	CAGCTTGGCATTTAATGTCAA		
57703	KIAA1604	NM_020943	CAGGAACAGATTACAGATAAA	CAGCAAACAAATGATAGGAAA		
57707	KIAA1609	NM_020947	CAGGCAGTGCACTTAGAGAAA	CGCGTTGCAAACTATTATAAA		
57711	ZNF529	NM_020951	ATGGATTTAATAGGTAATCAA	AACCTTGTATACAGACATTAA		
57716	PRX	NM_020956	CAGGCTACTTCGAACCAGGAA	CCCGCTGCTCCTGAAGTTGTA	AGGGATGGAATTTGGCTTCAA	CCCGCCGTGGAAATTGAGGAA
57717	PCDHB16	NM_020957	ACAGCATTAAACAGTCAATAA	AACCTGATTTATAGTCCTGTA	AAGCAAGAGCTGAATATAATA	AACGGGTACGGTGATAATTAA
57722	NOPE	NM_020962	CCGGCTCAAGAAGAAAGTGAA	CCAGCCTATGATAACACTAAA		
57729	KIAA1639	XM_290923	TCGGAAGCACTGCTCAGTGAA	CACACAGAGGACCTACACATA	CACAAAGACCTTCGCATTCCA	CCGCACGGCATGTGTCAGCAA
57733	GBA3	NM_020973	AACCATGATTTGCAACTGTAA	CAGATAGACCTGGAAACATAA		
57758	SCUBE2	NM_020974	CAGGACAAGTGTAACCTTTAA	CAGGAACTCATTGAAGACATA		
57763	ANKRA2	NM_023039	CACAGTGTGATTGTTTACAAA	CTCGATTTGTGAAGTCCTTAA		
57787	MARK4	NM_031417	TAGGAGTTAGTTAGGCATTGA	CAGTAGGGCCTTGAAGGTTAT	CTGCAGCCTGTTGCCCAATAA	CCGCATCATGAAGGGCCTAAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
57801	HES4	NM_021170	CCGCCACTCGAAGCTGGAGAA	TGCCGAGACTGTAGCAGAGAA	CTCCAAGCCGGTCATGGAGAA	AAACGTATTTATTATTCCAAA
57804	POLD4	NM_021173	TTCACTAATGCTTATCAATAA	GAGGCTCAACTCCTCCATCTA		
57805	KIAA1967	NM_021174	CCACTTAACAACTAAATACAA	CCGGTTCCACTTAACAACTAA		
57820	CCNB1IP1	NM_021178	AAGATAATTTAGCTAACTTTA	TAGCAGGGCCTTCAAAGTAAA		
57823	SLAMF7	NM_021181	ATGTATTAATTGGCTCTATAA	CACCATGGGTCTGCAGAGCAA	AACAGATATTGTGAGATTCAA	CACTAATAGAACAATCCTAAA
57864	TSCOT	NM_033051	AAGGAAGAGGAGGTACATTAA	CACCTTGTACAACAAGATCTA		
58189	WFDC1	NM_021197	CCGGATGTGCTGAGGCCTAAA	CTCAAATGTTCCCAAGATAAA		
58190	CTDSP1	NM_021198	CAGCTCCTTCAAGCCAGTGAA	CTCCTTCAAGCCAGTGAACAA		
58475	MS4A7	NM_021201	TCGGAGTACTATTATCCAATA	CAGGAAGGATTTGACTATCAT	CACACTCATATTGCTTAAATA	CACGGTCTTGGATATAAGTAA
58480	RHOU	NM_021205	CACCTCTAATCTGGATGTTAA	TACCCAGTTACTTATGATTTA	CCCAGGTATTACACAAGCCAA	ACCCAGTTACTTATGATTTAA
58484	CARD12	NM_021209	AAGGTTCAAGCCAAAGTATAA	CCGGGATTTCAGCAAGTTGAA		
58490	C20orf77	NM_021215	AAGCTTAAATTTGTATATTAA	ATGGTTGGAAATAACCTTCTA		
58493	C9orf80	NM_021218	AAGTGACTTTGTAATATCAAA	TGCGTTTATAGTCAACATGTA		
58496	LY6G5B	NM_021221	CCGCATGTACTTGTTCCTCAA	CACCATCTATTATGATGTCAA		
58497	PRUNE	NM_021222	CTGGTATACTGTTCTCATAAA	ATGGCTGAATTTCTATTCTTA		
58499	ZNF462	NM_021224	CCCGGGATCCTTAAATTATAA	AAGAAGGGCAAGAATAATTAA		
58508	MLL3	NM_021230	ATCAGAGTTCACGACCATTAA	ACCAGTGATCACTTTACTAAA	CTAGAACAGATTCGTAAACAA	CCCAGTGAGCTTCCTCAACAA
58510	PRODH2	NM_021232	CAGGAGCTGCTCAGCCAAGAA	CAGGATGCTCCGGACCTGTTA		
58513	EPS15L1	NM_021235	AGCCTTGTTATTTAGCAACAA	CCGGATCCTTTCCAGACAGAA	AACCATCATCAAGTCCCTGAA	CAGAACCTTCTAGCACACATA
58533	SNX6	NM_021249	CCGAAACTTCCCAACAATTAT	GCCACTCTTATTTACCTTTAA	TCGCCAGTAGTTATATTACAA	CCGCGGACTTAAAGCAATAAA
58538	MPP4	NM_033066	CAGGCCACTAGTATCCTACTA	CAGGTGTTATCCTATGAGGTA	TCGAGGCACAATCATGTTCAA	TACGGTCAGAAGTTCTTTATA
59082	ICEBERG	NM_021571	CAGTGGGTGCAGGCACAATAA	AGCCAGGAAGACATGAACAAA	CCAAGTCTTGCTGCAAATTTA	AAGATATTCTCGTGAAAGAAA
59283	CACNG8	NM_031895	CACGCGCGCCCTCATCTGCAA	AGGCGTCTGCGTGAAGATCAA	CTGCGTGAAGATCAATCATTT	CACCAACACGCTCAACAGGAA
59286	UBL5	NM_024292	AACCTGGAGCTTTATTATCAA	TTGGAACAAGATTGTCCTGAA		
59341	TRPV4	NM_147204	CACCAAGTTTGTTACCAAGAT	CCCGGGCAAGAATGAGACCTA	CTGGAGTGAATTCTCTCTTCA	CTGGGATTTGCCGGTGCTCAA
59343	SENP2	NM_021627	ATGGTCGGAATCAGATTTGAA	CAGATTATATTTCTAGGGACA	CCACACAAGAACAAACGCTAA	AAGAACAAACGCTAACTAATA
59345	GNB4	NM_021629	TACCTTATATTTGCAGGTGAA	AAAGTAGGTAATAGCATATAA	TACGATGACTTTAATTGTAAT	CTGCTCTATATATAACTTAAA
59350	LGR7	NM_021634	CTGCAGTTACCTGCTTTGGAA	CAGGAGATGCCACCTGAGTTA	ACAGACTAGAATGGCTGATAA	AAAGGATGTTTAGACCTCTTA
60385	TSKS	NM_021733	GTGGAAGATGCTGAAATCAAA	AAGCTGTTCACCGGCATCGAA	CACCAACGTGTCACTGCTCAA	AACCAACGTCTTGAAGCAGAA
60386	SLC25A19	NM_021734	CTCCCTGTGATCAGTTACCAA	CTCGTATGAATTCTTCTGTAA	AACCTATTTAATAGACATTAA	ACCTATTTAATAGACATTAAA
60437	CDH26	NM_021810	CACAAGTTACACTTTCTTAAA	CACACTATTAGTTTGAATTAA		
60468	BACH2	NM_021813	CCGGGAAGATAACTCTAGCAA	CTGATGCAAGTGCACCTCTAA	CAGGTGATAATTATGTAGGAA	CACGAGGCATTGTGTGTTGAA
60490	MDS018	NM_021823	CCCGTATAACATGGTGGTTAA	ATGAAATAAACTATAACTAAA		
60526	FLJ21820	NM_021925	TTCGATATGTTCTCTATGTTA	AGGAGCATTTATGTAAGCTTA	CTGCACTAGACAGAGAATAAA	GAGATACTCACTGATACTAAA
60529	ALX4	NM_021926	CAGGTTCCCTGCTACGCTAAA	CAGCAGCTACCTGAGTGTCAA	CCGGACCACCTTCACCAGCTA	CAGCCTCAGCCCAGGCCTCAA
60592	SCOC	NM_032547	TAGGATTAGTAAGATATACAA	CTGGATGAGAACAGTTACAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
60673	FLJ11773	NM_021934	CACAGGCAAGTTCCACTACAA	CGGGAGAAGGTGGGTGAGAAA		
60675	PROK2	NM_021935	CAAGGCTCTTACCTTACTTTA	TCGCTCTGGAGTAGAAACCAA	TAGCCACATCTTACCTGTAAA	CGGTATTAAGTTGTAATTTAA
63027	C6orf85	NM_021945	ACGGAGTGAAATGTACATGAA	AAGGATATGCTAAGTGATGAA		
63891	RNF123	NM_022064	CACATGCGTGTACAAAGGGAA	CCGCAAGTTTCTGCTTAGCAA	CTGCGCTACTATTGGGATGAA	CAGGGCCACAGTGAGCATTAA
63892	THADA	NM_022065	CAGACTTCTATTGATGCTAAA	CACCTTGAGTTCACAGATTAA		
63925	ZNF335	NM_022095	CTGGAGGAGGATAGCGACTAT	CGGGCAGCGTTTCAACCGTAA	CAGGCGCTTCCTAGGCAAGAA	TGGCCTGTCAGTCTCAATAAA
63939	C20orf177	NM_022106	AAGCAAGATATTCTATACATA	AAGGGAAGTGTCTTTCAATAA		
63940	GPSM3	NM_022107	TTGGTTGTGTGAATAAATATA	CGGGCTGTGAATGGACCTTCA		
63971	KIF13A	NM_022113	CCGGCAGGCCGTCACAGTCAA	AACCTATGAAATAGTATCCAA	CCGCAACAACTTGGTAGGAAA	CTGGCGGGTAGCGAAAGAGTA
64061	TSPYL2	NM_022117	CAGACATATCTCCATGGGCTA	CAGCGAGAATCCTGACCACAA	CCAGAGGTTAGTTGACCCGAA	CACAAACATGGTGATTGTCAA
64072	CDH23	NM_022124	CCGGCTGCCCTTCTTCACCAA	CAGCGGAGTGCTGACCTTGAA		
64083	GOLPH3	NM_022130	CACCATTGGTTTCATAATGTA	CACAGTAAATACTTAATATAA		
64087	MCCC2	NM_022132	CCCGAGCACTTCACATATCAA	AACAATTACGGGCCCAAGAAA	ACCCTTACTATTCCAGCGCAA	CCCATAAAGCGGAGACAGTAA
64090	GAL3ST2	NM_022134	CACCAACATCATGTTCCTGAA	CACAGTCACCGAAGAAATGAA		
64100	ELSPBP1	NM_022142	AAGCTTAAATAACCACCTTTA	CAGCTGGTCCTTTGTGAAGAA		
64101	LRRC4	NM_022143	ACCACTATCTCTGAACCTTAT	AAGCCACAAGTTAACTTGCTA	CAGAAGGGATTTCTGGTATAA	AAGCTGTGAGATCCACAGTTA
64102	TNMD	NM_022144	CAGATTAAAGTGATTCCTGAA	TTGGAAGTACACGACTTTAAA		
64106	GPR147	NM_022146	CTACGGCTACTTCAACGAGAA	CACCAACATGTTCATCCTCAA	CTGTTTCATCGTGCTCAAGAA	CTGGTGGCCATTGCTGTGGAA
64109	CRLF2	NM_022148	AACCGTGCAGGTGACATGGAA	ACACACCACTGTCAAAGTCAA	CACATGAGTCTCTGTGTTCAA	CAGGATCCACGTTGACATTTA
64127	CARD15	NM_022162	CTGCCACATGCAAGAAGTATA	CAACATGGCCGTGAACTTTAT	TAGGCCGTTCCTTCAAAGCAA	CAGTTATGGATTGAAAGTTTA
64129	LCN7	NM_022164	AACGTACTGGGACAACTGTAA	CCCATCTTCCTCGGTCATGAA	CCGGCCTGGGATCCAGGCTAA	CAGCCCTGTATTCTTATTCTT
64131	XYLT1	NM_022166	CAGGGTGCTGACGAAATCCAA	CAGCAGGATCTCAACGGGAAA		
64132	XYLT2	NM_022167	CCGGGACAAGAATTTCCTCAA	CACACCCATTTCAGCCATCAA		
64145	ZFYVE20	NM_022340	CAGGATGGCAGCATCATTAAA	ATGGAGAAAGTTGACCAGAAA		
64146	PDF	NM_022341	CCGGTGGAGCGGGCGCAGCTA	CTGGTGCTGGGTCCTCCCGAA		
64147	KIF9	NM_182902	CCCGGACCTTATCAGAGGAAA	CACGCTCTGAAGGACTCGTTA	AACAGACAGACTGGTCGTTTA	CAGGACTTGGTTTATGAGACA
64149	NJMU-R1	NM_022344	AACTGTGGTAGTGGAGATATA	CACTGAGTCCTAGATAGATAA	TTGGCAGATACTAATCTACCA	TTGAGTTACACTCCTGTTGAA
64170	CARD9	NM_052813.1	CAGCGACAACACCGACACTGA	ATGCACTGTATTAGTGTTAGA	CCGCGTCTTCTCCATGATCAT	ACGTAAGGACTCCAAGATGTA
64174	DPEP2	NM_022355	CTCCATCTTACGTACCTTCTA	CTGGGCATGATGGTAGACTTA	CAAGGCTGTCATTGGATCCAA	CAGGCACAAATATTTCTTGAA
64211	LHX5	NM_022363	CAGGTACAAGCTAATACTCAA	GCCAATTTAGATATGCTATAA	TTAGATATGCTATAAATTTAA	AAGCAGCCTCCTGAAACCAAA
64223	GBL	NM_022372	CCAGGTGAACGCACCCATTAA	CAGCTACATGGCAGCTGTCAA		
64232	MS4A5	NM_023945	TAGACTGAAGTACCAACTAAA	CAGCATTATTGAATTATTCAT	AAGAACATGGTCTAGACTGAA	GAGGATTGTGATTGTGAACAA
64236	PDLIM2	NM_021630	AGACATAATCGTGGCCATCAA	CTGAGAGTCAGTCCTCCTTAA		
64328	XPO4	NM_022459	CAGAACTTTATGCTTAATTTA	AAGGAATGCCTTGGTAAGTAA		
64332	NFKBIZ	NM_001005474	ACCATTAAGTGCCTAATTCAA	TAGCTGCTGCTTATCATGTAA	CACTAAGTCTTTGTAGATAAA	TCCGACGTATCCTGAAGGGAA
64344	HIF3A	NM_022462	CAGACTCTTCACCTCCGGGAA	CTGTCGGAGAATGTCAGCAAA	CGGGCGCACCCTCAACCTCAA	ACCAATCTCTATACACCATAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
64359	NXN	NM_022463	AAGCTCAAACTTTGGAACAAA	CCGGGTCCTGGTGGAATCCTA	AACCGGCTGTACGGAATCCAA	AAGGTAATGGTTCATATCATA
64374	SIL1	NM_022464	CCGAAATAATTTGAAAGGCAA	AAGGCTGGATATCAACACCAA		
64375	ZNFN1A4	NM_022465	CAGACCATCACTGCACTTTAA	TTCCTTGAGATTCAAACCAAA		
64377	CHST8	NM_022467	TTGGATTAAGGTTCCAAATAA	CAGGAATAAAGTTCAACATCA		
64393	WIG1	NM_022470	CAGGCTCATTATCAGGGTAAA	CAGCATTTAGAGAGCAAGCAA		
64400	FTS	NM_022476	CTGCACTGTCTTACTGATTTA	AAGGTGAAGAGAAGACATTAA		
64409	WBSCR17	NM_022479	CTGGTTAGGGTGCACATATAA	CAGAAATGAGAAGATACAATA		
64419	FLJ22405	NM_022485	CAGCGTGATTCCAAACACGAA	CACGTTTGAGAGTACCGTACA	CTGCCCAGTAATCCTGTTCAA	AAGGTGAAGTTTGGCATGAAT
64421	DCLRE1C	NM_022487	AAGAAACGAATTATATCTATT	CCCAGTGGGAAGTATTCTTTA	CAGGTTCATGTGAATAAGCTA	AAGTACGGAGCCAAAGTATAA
64423	C14orf173	NM_022489	CAAGATCAGCACATTGCTGAA	CAGCGATGTCCTAACCACTGA	CCTGATTCTGATGATAATAAA	CCCGGCCTTGATGCTACAACA
64429	ZDHHC6	NM_022494	TAGAAGGTGTTTCAAGAATAA	TACGTTCTGTTCGGTTATCAA		
64446	DNAI2	NM_023036	CAGGGTAATGCTTAGCATATA	CCGGAAGAAAGTGGAGAAAGA		
64478	CSMD1	NM_033225	ACGGGCGAGCGCAATAGGATA	CCGGTTCAGTATGAAGATAAT	CAGGAAGTCGAATTCACCTAA	CAGGACTGATTCATAGCCATA
64582	GPR135	NM_022571	AAGACAATGTCCCTTCTTCAA	ACCAAGCATTGTGAACTGCTA	CAACAGGATGTCCTCTTCCAA	ACCAAACAGCCTAAATCCGAA
64601	VPS16	NM_022575	CTGCATGAAACAACATAACAA	CCGCACGGAGCTGGCCATCAA	CAGCATGGACTGGGACCTGAA	GAGGCCAGTGCTCGATATATA
64648	SPANXD	NM_032417	AAGCCTGCCGCTGACATTGAA	AACCTTGGGCAATGACAATAA		
64710	NUCKS	NM_022731	TACCACGGTTGTAAAGCAATA	CCCGACCTTATTTGAGGGTAT	ACCCTAGAATTTAATCAACAA	AAGGTGTACCACGGTTGTAAA
64711	HS3ST6	NM_001009606	CCGGCGCCTGCAGGAGTTCTA	TCGCCTGGTACCGGAGTCTGA		
64714	PDIP	NM_006849	CACTGTGGTTCTCTTCAAGAA	GCGCCTGGTCACGGAGTTCAA	CTGCGCTTGGTCAACCTTGAA	GAGCTGTGCATTGTGAATAAA
64747	FLJ14153	NM_022736	CAGGTGAAGTTATTAAATTAA	AACCTGGTGTTTGGACTTCAA		
64748	LPPR2	NM_022737	CCGCGTGGCCGAGTACCGAAA	CTGCGTTGTGCATAACTTTCA	CCGGGACAACTTCAGCCCTTA	CCCGTGTCTAAGCATGTGCAA
64759	TENS1	NM_022748	AAGGCGGATATTTCAAGAGAA	ACGGTCTCTACCCATGTTTAA	CGGTGTGATTGTGGACTACAA	CAGGACCTCGATATTATCGAT
64768	C9orf12	NM_022755	CACGCATGAGATGAAGCATAA	CAGCTTTGTTTAAAGATACAA		
64772	FLJ21865	NM_022759	CAGGCAATTAATTAGGAGTAA	CGGCTTCTTCACTAACTATAA		
64779	FLJ12998	NM_022764	CAGCCTTACATTTGCTCATTA	CAGGTCGTGGACATCCCTGAA		
64782	FLJ12484	NM_022767	AGGGTTGTAATGAGCACTAAA	AACCATTTGTTCTAGAATAAA		
64783	RBM15	NM_022768	AAGGTGATAGTTGGGCATATA	TTCGGTGATGTAAGTGTGAAA		
64785	FLJ13912	NM_022770	TAGGAGCTGGTTGACCTTGTA	AAGAATCACTGCCATATAATA		
64805	P2RY12	NM_022788	TCGGTCTAGTCTGGCATGAAA	TAGTCTGGCATGAAATAGTAA	CCGGAGTAAATCAAACTTTAT	CAGGGTCAGATTACAAGAGCA
64838	FNDC4	NM_022823	CTGGGACGTCCCAGAAGGCAA	CCAGGTGACATCACAGTGGAA		
64839	FBXL17	NM_022824	CTGTCTGAACTGGATCATAAA	AGGCATGATCGTCATAGCTAA	ACGAAAGTTAATTATACATTA	ACGAGAGGGTAGTCACATTAA
64840	PORCN	NM_022825	ACAGATGATTGTGGCCATGAA	CTGGATATCCTTCCACAGCTA		
64850	AGXT2L1	NM_031279	CACGACAACATTGTTGAGTAT	ACCAACTTGATAGGATTCTAA	CAGAATAAACCAAGTGATAAT	ATGTGTCAAATTAGAGAGCAA
64853	FLJ12806	NM_022831	CAGGTCATTAGCTTACTATAA	AAAGAATATTCTTACATATAA		
64854	USP46	NM_022832	CCGGGAGAATGTGTTGGCATA	CAGCACGGCATTGTTCCTTAT	TAGGGAAATGTTTGTACTATA	CAGTTATTTAATCGAAGTAAT
64856	WARP	NM_022834	CGGGACCGCACTGACAGGAAA	CACTAACATCCCAGACTTTAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
64924	SLC30A5	NM_022902	CTCACTCTTTGTGGACCACTA	TCGAATCATATGATCTCCTAA		
64926	FLJ21438	XM_029084	CACAACCTAACAAGCAATGAA	CAGTATGAAGTTGCCCAGTAA		
64943	FLJ12442	NM_022908	CCGCGTGGACTTCACCTTCTA	TAGGTCTTCAATCAAGGTTTA		
64951	MRPS24	NM_032014	CTCAAAGGTTGTGTATAAGTA	CAGTGAAACTTTGCTGTCCTA		
64965	MRPS9	NM_182640	AACAGTCATACTATTCATTAA	CCGCAGAAAGTTTACGTGGAA		
65009	NDRG4	NM_020465	AAGGGTCAGGTAGAAGAGAAA	CCGCAGAGACCTGGACATTAA		
65055	C2orf23	NM_022912	CTGAGCCGAAATATAAGAATA	CACCAATACCTAAATCTGTTA	AAGCCTGTAAGTGTACATGTA	CCCAGAATTATCAGAAACGAA
65083	NOL6	NM_022917	CACTACAGACCTGACAGTCAA	CACGCACACGGATGTCCTTAA	CCGGCCGCCCTTGGACATTTA	CAGGAGATCCATCCACCTATT
65084	FLJ22104	NM_022918	AAGATGTTGCTTAATAATTAA	AAGGTGTATTTCTACAATTTA		
65109	UPF3B	NM_023010	AAGGTGGTAATTCGAAGATTA	CAGAGCATACATCAACTTTAA		
65121	LOC65121	NM_023013	GACGGTTAGTTGCCAAATTCA	CCCACAGCACTCATTCCTGAA		
65123	FLJ21919	NM_023015	CTGCCTGATGATGGACATGAA	AAGGATAGCATTATGAACATA		
65217	PCDH15	NM_033056	ACCATAGTTGCTATTGATGAA	ACACGAGTCAATCTTAATGAA	ATCGCTATGTTCAGGAACAAA	ATGGATTTAGTAGTATGCTTA
65220	FLJ13052	NM_023018	CCAGACCATCATGCACATTCA	CACGCACCTCATGGAGGAGAA	CCAGGAGAACATGATCGTGTA	AAAGAGCGTCCTTGTCATCAA
65250	FLJ13231	NM_023073	AAGGCTCATCTTAAATTTGTA	ACCAGAGAATTCCATAATTAA		
65266	WNK4	NM_032387	CAAGGTCACTTCGGGCAGAAA	CACTAGTGTCTCAGACCAGAA	CAGGAGGAGCCAGCACCATTA	CAGCTTGTTGGGCGTTTCCAA
65268	WNK2	NM_006648	GACGCTGAAGACATACCTGAA	CACGTATATGGTGGAGCATGA	ACCTATAAGTCTAGTAGCAAA	AACGTTCATCGAGCAGATGAA
65975	STK33	NM_030906	TCCATAAGTGACTGTGCTAAA	CAGTGGTTAACAGGCAATAAA	CAGGATGGTAATAGGTTAAGA	ATGTGTCTAGTGCATCCTTAA
65977	PLEKHA3	NM_019091	CAGGGTGTATTGTAGCTTATA	CAGGAATTTGTTCACCATGAT		
65981	C1QDC1	NM_001002259	AAGCTTCGAACTATACTTCAA	CAGTACAGTATTGACAATAAA		
65983	NS3TP2	NM_023927	CTCGGTAACCCTAATAAAGAA	CAGGTTTGCTTCAAACAAGTA		
65987	KCTD14	NM_023930	CTGCCTGGAGATGGACATTAA	CAAGGTATTCTCCAAGTTCTA		
65989	EGFL9	NM_023932	AAGTTCTGTGACAAAGATGAA	CAGCCTCACACCAGAAATATT	AACCTGCCTTGACGGCATAAA	AAGACCTGTGAGCTTGTCTTA
65990	MGC2494	NM_023933	CTGAGTATTAGACACGATAAA	CAGGATCGTGCTGGCGGCCCA		
65999	MGC3036	NM_023942	CTGCAACTTAGTGGAAGGAAT	AAGGGCTGTGAGCAGGTGTAA		
66000	MGC3040	NM_023943	CAGGGAGATCCAGTCCCTTGA	CAGGACCAGATGATACCATGA	CACTGGGATGGTCCTTGTTAA	CCCTCTATTGCCAACTGTTAA
66002	CYP4F12	NM_023944	GTCCTATATAACGATCTTCAA	ACCTGCCTCATCGATATTATA	CCGCAGGAAGCTGGAATTGAT	TTGCAGATTGTCATGAATAAA
66036	MTMR9	NM_015458	TACGTTGGAATAGATCCTCTA	ATGCCTGAACCTGTTATCTAA	CAGGTCTAAGGATTAACTATA	CAGACCTAGTATTCTAAGTTA
78989	COLEC11	NM_024027	CCCAGAATTGCTCTTCCATAA	CCCAATGTCATTATGTAATTA		
78990	OTUB2	NM_023112	CAGGGAGATCTTCAAGTTCAA	CAGCCGATAAACATTGATTAA		
78994	MGC3121	NM_024031	ACCAATCAGGTTGAACAAGAA	CAGCCTCTGACTCGAGCATTA		
79000	MGC2603	NM_024037	CAAGACTAAATTGGAAAGAAA	CAGGAGGATGGGCCAACTCAA		
79012	MGC8407	NM_024046	TCGGAGGTGACTGACAGATAT	CTCGTGCTGCAAAGAGTGATA	AAGGTAGGGCAGTATGTTTAA	CTGCATGGCAATAACTCATAA
79016	PCIA1	NM_024050	CAGGAGCAAGTGGAGCTGGAA	CTGCGCTACCTGCATCAGCAA		
79018	C17orf39	NM_024052	GAGGGCAATACTAAACTTAAA	CTCCTCAATCCTGAAATTCAA		
79027	ZNF655	NM_024061	GTGCAGGACACCGACATGGAA	AGGAAGCAGCAGGGTCACCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
79048	SECISBP2	NM_024077	CTAGATTTGTTTGATAATCAA	CTGGAAATTGATCAGCATTAA		
79054	TRPM8	NM_024080	TCGAATGTTCTCACCTATTAA	CCGGGACGAGATGGACATAGA	CAGAATGTTATCATACTACAT	AAGGTTAGATTCCAATAAATA
79066	MGC3329	NM_024086	AAGGAGGAGCTTCGCATACAA	ATGGATGCTCTTAAAGAAGAA		
79068	FTO	XM_051200	AAGGAGATGTTAATAATTAAA	CAGGGTCATTACAGAGATTAA		
79073	MGC5508	NM_024092	CAGGTTTGATGTGGAATCACA	CACCGCCAGTGTCATACCAAA		
79075	DCC1	NM_024094	TTGGTTTAGATCAAAGTTCAA	AACGAGTTTATAATCCTATAA		
79080	MGC2574	NM_024098	CAGCCAGAGTACAGTCCTGAA	AGCGTCCAAGAAGTTGAATAA	CTCGGAGTTGGCCCAGAATAA	CCGAAAGGCCGCCGAAGACAA
79092	CARD14	NM_024110	ACGGACGGTTATAAGAGGCTA	ACCAGTGTGTTTACTTGTAAA	CCGCATCGTCAGTATGGACAA	CACCTGGATTATGAGCTCCTA
79094	MGC4504	NM_024111	TCCCATACTGTTACCCATAAA	CTGCTTGACACTGACTTACTA		
79095	C9orf16	NM_024112	CTGGCTTAGACACCTTCTCAA	GGCCTTGAGTGTCCACATTAA		
79097	TRIM48	NM_024114	CAGGCCCTGTTTCTACCTCAA	CTGGGAGAAGCTGTTAAAGAA	TTGCATTCTAATGTTATTAAA	AAGAATCAGAATGGCAATATA
79143	LENG4	NM_024298	AAGCATAAGCTTCCCATTTCA	TCCCAATAAAGTGTTGCACAA		
79153	MGC4171	NM_024307	CAGAGTGGTGGTGGTGTCACA	GACGCTATGACCGTAATGAAA	CCGGACCTCCTAAGTCCAGAA	ACCCATGAGCGTAGAGATCAA
79155	TNIP2	NM_024309	CCGGAAGTTAAAGCACACTTA	CGGGCTCAAAGTAGGATTCAA		
79169	C1orf35	NM_024319	TTGACTCTTTGTATTTCAATA	CTGGGAGGACGTGAAGACTGA		
79171	MGC10433	NM_024321	CCGCCCAATTATCGCGACCAA	CCGCTTCCCATCCTTCCTTAA		
79176	FBXL15	XM_370575	CAGCCTCTCTCTGGCCGTCAA	CTGAGGAAGAAGAGATAGCAA	CTGAGCTGTAGGGAAACTGAA	CACCCTGGAGCTTCAAATAAA
79178	THTPA	NM_024328	CAGGCTTTGCATCCTTGGGAA	ACGGAGTATAAGGAACTCACA		
79184	CXorf53	NM_024332	CAGCATTTGCAGGAATTACAA	CAGATTGAGATGAATTTGCAA	TACGATGTTGATTATAACATT	ATGGACCTACATACACACAAA
79187	FSD1	NM_024333	CAGAGGTACTCCATCTCCCAA	TCCGGCTATCATTGAAAGCGA	CACGGCCAAGCACGCCAACAA	AGGTCTCAAGTTTGACATGAA
79258	MELL1	NM_033467	CTCCCGAGAGTACTACTTCAA	CTGGACCGCATTGGTAGCCTA	CACGCACGGCTTTGACGACAA	TGGCCGGAACTTCGACAAGAA
79369	B3GNT4	NM_030765	CACCCTGTTAGCTCTGATTAA	CAGGAACACTAAGGTCAAATA		
79442	LRRC2	NM_024512	CAGGAGAGACTTGTAGGTACA	CCGCAAGATATAGACAGGCTA	AAGACCAAATACTGAAGTTAA	CTGGAGCTATATATAAATCTT
79573	TTC13	NM_024525	CAGGGTGATTTCTATAAATCA	TCCGATTATGAAGCAGTTTAA		
79574	EPS8L3	NM_024526	CAGCTTAGACACCTCCAAGAA	CAGGAAGAAGAAATTTGGGAA	AGCCATTTACTTGCACCGGAA	CCGGAAGGAGTACTCCCAGAA
79585	CORO7	NM_024535	CAGCCACATCACCAACCTCAA	CTGCAGCTTGATCGCCTTCAA		
79603	LASS4	NM_024552	CAGGTTCTGGTTACCACCCAA	AAGGACATTCGTAGTGATGTA		
79607	FLJ21103	NM_024556	CAGACAGTGTTTAACAAGTAA	CAGGAGGAAAGCAGTGACAAA		
79629	FLJ22709	NM_024578	TCCCAGTGAAATAAACATGTA	ATCCAGAAATTCGATGACCAA		
79631	EFTUD1	NM_024580	CACCAAATGAAAGAAGATCAA	CCCAACATACTAGTCAATAAA		
79635	FLJ13646	NM_024584	CTGGAATACCTGACTAACAAA	TCCCATTTAGTATAACTATAA		
79640	FLJ23584	NM_024588	CAGGGTCAGTTAGGAAATGAA	CAGAAACAATTAAGTCATGAA		
79642	FLJ23548	NM_024590	CTGATCTAACTTCTAGCTAAA	AGGCATATTGTTCATGTTTAA	CAGATTGATGAGGACATTCAA	CCGATCCATTATCAACATAAA
79654	FLJ21156	NM_024602	ACGGATCTACATCTACCCAGA	ACCACTGTACTGAGTGACCAA	TCGGGACATGTATGTACCCAA	CCCGAGGTATTTCACCTCTTA
79660	PPP1R3B	NM_024607	CTAGGATGACATGATGTTATA	CAGACAGTACTTTAAATGTTA	CCCGCTAGATATGCCATTCAA	CACCCAAGTTCTTATACGTTA
79671	NOD9	NM_024618	ACCTGACTTGCTGCTATTAAA	CTGCGGTTTCTCTGATACCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
79673	FLJ12586	NM_024620	CGGGAAATCCTTCAACAGAAA	TACCTGTGAATGAACAATGAA		
79679	B7-H4	NM_024626	ATCGTTCAAGAGAATGATTAA	CTCCAATATGAACAAGATAAA		
79684	FLJ23342	NM_024631	TACAGTTGTGTTGCCATTTAA	CTGGAAAGATGTTTACTACAA		
79686	C14orf139	NM_024633	AAGGAGGAATTTGTTTCTAAA	CAGGATGTTCAGGGCCTTAAA		
79692	ZNF322A	NM_024639	AGGGTTGGAAATACCAAGTAA	TACATATAATATGTATGAGAA		
79696	C14orf140	NM_024643	CAGGAGCAGAGTTAAAGGTAA	CTGGTAGCAAGCAATAATAAA		
79697	C14orf169	NM_024644	GAGGTCCAGGAAGATACGAAA	CAGATTCTAAGGATCCGCGAA	ACCCAAGTGCTTGGAAATATA	CTGCTTGAGACAGATATTAGA
79703	FLJ22531	NM_024650	CAGCTAGTGATTTCCATAGAA	CAGCATTATGTGAGACCAAAT		
79706	PRKRIP1	NM_024653	AACGATGATGATGAACACAGA	CAGCTGTGATTTCATCCCGAA		
79707	FLJ23323	NM_024654	CAGATTAAACCTGAATATTTA	ATGGAGTTTCATGGCCATGAA		
79714	FLJ12436	NM_024661	AAGGTTCATTTACATTAATTA	CAGCTTAGTCATTCCAGGCAA		
79718	TBL1XR1	NM_024665	TAGATACTAGATTGTATTGAA	AAGGAGCTATCTGTTTATGTA	ATCACAAATGATCATACTTAA	AAGCAAGATAACGGCATATAA
79724	FLJ23436	NM_024671	AGCCCAGAATTTGAAGCTCAA	AGGGAGCTAGAGGAACCTTTA		
79728	FLJ21816	NM_024675	CAGGAGGATTACCTATACAAA	CTCCTTGTAAATAAAGCTATA		
79733	FLJ23311	NM_024680	CGAGCAGATTATGATGATCAA	AAGACAAGTCTTTAAGGGTAA	CAGAGGATGTCCATTAATCAA	CACGTGGGAAACCAAACTTTA
79741	C10orf68	NM_024688	AAGCAATTTATAGAACATATA	ACCAAGAAACTTCAAGCTAAA		
79742	CXorf36	NM_024689	CTGGTTTGAAATGAAACCTTA	AACACCTAGATTAGCATTCAA		
79770	C5orf14	NM_024715	TACTATAAGGGTTATAGTAAA	AACTAGTATTGCAATAAGCAA	CTGCATGAACGTAATCCAGTA	CCGGCAGAATAGTGAGTAGAA
79784	MYH14	NM_024729	TCCCAGAATCGGGAAAGTGAA	CGCGGGCAAGGTCGACTACAA		
79794	FLJ21415	NM_024738	CCCGTGGAAAGTGCAGTTTAA	AACGTTGAGGCAATTCCTAAA		
79797	ZNF408	NM_024741	CAGCCTGGTGCTAATCCATAA	CCGAGACATCCTCGCTTTAAA		
79807	FLJ13273	NM_024751	CCAACTATACCTGTAGAAATA	TTGGTAATTATCAGCAGGAAA	AAGACTCAGAATCTTAAGGAA	GAGGTTTATAGGTTTAAGTAA
79811	FLJ13213	NM_024755	CAGCTTCGTTATGAACAAGAA	CAGAAGGTACTGTTACATTAA		
79815	FLJ13955	NM_024759	CACCTTTCAAGTACTAAGTTA	CTGCACAAGGCTGACACATAA		
79816	TLE6	NM_024760	CTGAATTATCAGGGCATTCTA	CACGATCTAGTCTGTGGTGTA		
79823	FLJ23451	NM_024766	CAGCCTTGTTGATGCAATAAA	CACGCCGAGGGAATACTTTAA		
79829	FLJ13848	NM_024771	CTGGATGTTGCTGCATTCTAA	AACGAATATGCAAACCATGTA		
79830	ZMYM1	NM_024772	CACCACTAATTTGAAGATAAA	CAGGAGTTGGTAAATAAACTA		
79836	RNF127	NM_024778	ATGGAGGAGCTCATAGCTAAA	CAGCGGGATGGCTACAACACA	TTCGCTCAAATTATCCCTAAA	CAGAGAGAAATTGAGTAGAAA
79837	PIP5K2C	NM_024779	TAGGATTCATTCTCCATGTAA	CTGTCCTGTCTTATACTGCAA	TTGATGTGTGATAATCTCATA	CCGGAGCAGTATGCTAAGCGA
79838	TMC5	NM_024780	CCGGGCTTATCGGAGATCCAA	TAGGGACACAGTGATGTACTA	CAGGAATGATTGGTTCTTAGA	CGCGATTATTGCTAATTGGAA
79841	FLJ23598	NM_024783	CAGCCTACCATCCAGAAGTAA	CAGCTTTGGAAACGCACCTAA	CCAATAGATATTCTCTCTAAA	CATGTATTACCCAGAATTTAA
79846	FLJ21062	NM_024788	CTGAAGTTAATTGTACTATAA	TTGGAGAAATATGGAATGAAA		
79852	ABHD9	NM_024794	ATGTATGTTAATTGAAATGAA	CTGGCATTTCTCCATCTACTA		
79864	FLJ23554	NM_024806	CAGGGCGCCAATAACAGGCAA	AAGACTTACATCGGATTTCAA		
79872	CBLL1	NM_024814	CGCGAACTCAAAGAACTATAA	CTCGATCGGTCAGTCAGGAAA	CCGCCTCAACATGGTGGTCCA	ACCATTATAATCCTAACTCAT

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
79875	FLJ13710	NM_024817	CAGAAGAGAGAGAATCTTGTA	ATGAATATTGTGCTTTATTTA		
79884	FLJ21159	NM_024826	ATGGAATATCTTAAAGAGAAA	AAGGATGGACTAGAAGATAAA		
79896	THNSL1	NM_024838	CAGGATGTTGGTAATGAGCAA	CAGGCTTTAAAGATTAAAGAA		
79897	RPP21	NM_024839	CAAGCAGATTCCAAACCACTA	CTCAATGATCCCGGGCATTTA		
79908	BTNL8	NM_024850	GTGGACGGAGGACACAATAAA	CACGGGATATGTTGATAGAGA	CACAGTATCAAGGCAGGACAA	CAGGATTAGTTCCCAGTCTTA
79912	FLJ22028	NM_024854	CAGCGAGTTCAGGAGACTCTA	CTAGATCCAAATATTGATATA	TAGCAATATCTCGTTTGCTAA	AAGAATAATGATCATAGGGAA
79923	NANOG	NM_024865	ACCGAGTGTTTCGATGAGTAA	TTGGTTTAAGTTCAAATGAAT		
79924	ADM2	NM_024866	AAGGGCTCCTTCTGCTATTTA	CACTGAGCATTTAATTTACAA	CTGGTACGTCAAGGAGCCTAA	TAGCGAACACTGAGCATTTAA
79943	FLJ14129	NM_030895	CAGGCCTTTGTAAGTTGTCAA	CAGGTGCTAAAGAGAGCAGTA		
79953	C20orf39	NM_024893	CACCGCATTAGCAATATACAA	CCGGCCCAACATCATCCTCTA		
79958	FAM31C	NM_024898	CAGCTCAAACACACCAATAAA	TACCTTGGAGACGACCTTTAA		
79960	PHF17	NM_024900	ACTGACCAATGAAGAATTTAA	AAGCGGGAGCAGGATGTCTTA	CGCCCAGAGCAAGAAATGATA	ACCGATTAAATTCATTAGTGT
79962	FLJ13236	NM_024902	CAGGTGATAGTTGGCATCTAT	CAGCTTGAGGGTCTAAGGATA		
79963	FLJ14297	NM_024903	CACGAAGTAGAGGAACTCATA	CCCTAGGTGTCTGGAAATGAA		
79968	FLJ12973	NM_024908	AAGGGATTATCTAGCATTAAA	CAGGATGGAGACAGTGATGAA		
80006	FLJ13611	NM_024941	AAGCTTAGGCTGTTAAATAAA	CAAGAGCATATTTGCAACCAA		
80013	C10orf97	NM_024948	TCGCTCTCCTTCACTAAATTA	ATCACAGTTACTATTGATAAA	TTGAATGATTCCGGCTTGTAA	ACGTTATTTATTATGATCCTA
80028	FBXL18	NM_024963	CAGCACAGATCTGATTCTGAA	CCTGCAGCACATGAAATTCAA	CCGCGCGGCTTTGGCAAGAAA	CAGCCAGTTTCTGTTGTTTGA
80036	TRPM3	NM_020952	CAGACTAGAGGAATTGTACAA	ACGGCCTGAAACTCTTCATAA	ATCATCGTGTATAGACATCTA	CAAGGTAACAGTCATAGTTCA
80045	GPR157	NM_024980	CTAGATGATCTTGACTTTCCA	AAGACCTTACTTTGCGATTCA	CACCTGGGTGTCACACGGCAA	AAGGGCTTCTTTGATAAAGAA
80069	C6orf208	NM_025002	TTGGAGGTTGGCAGAATTCTA	CAGCAGGTGGATGAGACACAA		
80086	TUBA4	NM_025019	CCCAACCTACACCAACCTCAA	AAGGAGTTCATCGACCTGCTA	AGGCTTTAAGGTTGATATCAA	CTGTGTGTCTGTCCTACATAA
80094	FLJ14107	NM_025026	CACAAATTCCATTATTGTCAA	CCGCCACACCTTCCTCCATAA		
80099	FLJ21075	NM_025031	AAAGATAAATACGGTCCTGAA	TTCCACTTAATTTCACTATTA		
80110	ZNF614	NM_025040	CTGAGCTTAATTGTACATTAA	CACCACAAAGTCAGTACTCAA		
80115	FLJ22582	NM_025045	CAGGTCCACCATGGCCATCTA	TTGTAAATGATGAGAAATAAA		
80118	FLJ22684	NM_025048	AAAGAAATATTTAGTAAATTA	CTGGCCTAGGACCTTAAATAT	ATGGGCTAATTAGAATTATCA	AAAGCATATGAAAGAATTCAA
80122	FLJ23074	NM_025052	GTGGTACATCGCGATATCAAA	CGCGATATCAAAGGAAATAAT	CTGACCAGGTAAGAAACTGAA	ATGTCTAATTGGAGATTTCAA
80127	C14orf45	NM_025057	CACAAGCTGCTTTCAATTTAA	CAGGAGTGATGCATCCAGAAA		
80129	C6orf97	NM_025059	CCGATCCAAGATGCTTTCTAA	CACCAATGAACTGAAGATTAA	AAGCTCTAGCATGAAATTAAA	CAACCGTTCGTGAGTCATCAA
80139	FLJ14299	NM_025069	ACCGGACTGTGTATTTATTTA	CTGGGAATATAAGTGCATTAA		
80145	NIF3L1BP1	NM_025075	CAGACAGGCATGAGACATTAA	AAGCATGGAATCAGATCCTAA		
80146	UXS1	NM_025076	TAGAATTTGCTCAGTTAATTA	CTGGAGGAAGGTTTAAACAAA		
80161	CXYorf2	NM_025091	CACACTGGAAATCGTGCAGAA	TGCACTGATGATAACTTCAAA		
80167	FLJ21106	NM_025097	CAAGTGAATATTGAACCTTAA	ATGGATGAATGTACTCATGTA		
80184	Cep290	NM_025114	CCGGAAGAAATGAAGAATTAA	AACGATCATTATCAACTTCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
80194	FLJ21749	NM_025124	CTGCTCTGTGCCTTAACTTAT	CAGCATTGATGATGCCTTCGA		
80195	C10orf57	NM_025125	TAGAGGAGGTGCAGTAATTTA	CCAGTTGTTACTTAAGAAAGA	ACCCTGAAAGATTATGAACTA	AACCATAGAGTTAGGCATCAT
80207	OPA3	NM_025136	CCTGATCAGTGTTAACCTTTA	CTGAATCAATGTGTTATTGTT		
80209	C13orf23	NM_025138	CACCTGGGAAAGCGCCTTCAA	ACGGTGCAAGAGAATACTTGA	AAGGAAGACCTAGCCGCATAA	TACAAGTAAGACTTAGGATAA
80210	FLJ12584	NM_025139	CCAGATAGAATTCATCATCAA	TCGGATCTTCTTGGCCATGAA		
80213	BLP2	NM_025141	CTCAGCTTCAGTCATGTGTAA	TCGGGCGGTGAAAGTACTGAA	CTGAACTATGCTAATCTGGAA	CAGAATGTTTATGTCTAGTTA
80216	ALPK1	NM_025144	CACCCAATTCATCGTAATCAT	CCGCAGGTGGTTATTCGCCAA	CAGGCCCTACATTTAAAGCTA	CAGCCCTTGGTCCTATCTGAA
80217	C10orf79	NM_025145	AAGGACCAAATTGAAAGGCAA	CAGACTGAAGTTGAAAGATTA		
80222	TARSL1	NM_025150	CAGGCCGAACAGGTCCTTAAA	TCGCCAGTTGTTCAAGGATAA		
80223	RAB11FIP1	NM_001002233	ACAGAAGGAAACGATAAGCAA	AGGGCTTAATGTAGTTAATAA	CAGGTTAATGATTACAATTAA	CACAGAGTTCGGAATTCACAA
80233	FLJ22175	NM_025161	TAGGAGCAGAACGCTCATGAA	AAGCCTCAACGAGGCCATGAA		
80274	SCUBE1	NM_173050	CAAGCTCTGGATCCAGTTCAA	CAGGTGCTACAGGACAGCAAA	CACGTGTGGTTGCCACCAGAA	CCCGGCTTTGACCTTGCCCAA
80309	SKIP	XM_051221	CACCAACATGTTAATTCATGA	AAGAAGATGAGTCATATTGTA	GGCAAGTATGCTACAAATTTA	CTGAAATTCTGGACACCTTAA
80313	LRRC27	NM_030626	CTCCGGTACAATAGAATTAAA	CTGCTTTCTGATAGTGATCAA		
80318	GKAP1	NM_025211	CTGCAAGTTGATGAATCACAA	TAGCTCCCTAATGGTCTATAA	CATGCTGTTTGTAACGCTCAA	AACGCTCAACATGATCTTCCA
80329	ULBP1	NM_025218	AACCTGTATATGTACCTTGTA	ACCCTACAATTAAACACTGTA	TATGATGATAATTGTATAATA	TCGGGATATACCCACAGGAAA
80341	BPIL1	NM_025227	CTGCACATTGGGAGCCTTATA	CTGGTGCAGAAGCACATTAAA	CAGGCGAATTTCTCATTTCAA	ACCATACTTAGTCATCACCAA
80342	T3JAM	NM_025228	ACCCAGGACCTACAAGATCAA	CAGGACCTACAAGATCAACTA	TAGCAGGGACTTACAGATGAA	CAGACTTGGCACCAACATTAA
80343	C20orf50	XM_046437	AACGAAATCAAACAATATTTA	CAGGATTACTACAAAGCATTA		
80346	C8orf20	NM_025232	TCGGTTCCGTGCAACTTTCAA	CGCGTACATCGTGCAGGCCAA	CCCTTTCTACTATGAGATCAA	CAGGGATGCACCCACAATGTA
80347	COASY	NM_025233	CCGGGTGTTTGGGAATAAGAA	TCCGATTATGGGATAGGAGAA		
80381	B7H3	NM_025240	AAGAAGATGATGGACAAGAAA	CTGGCAGCTGACAGATACCAA	CTGAAACACTCTGACAGCAAA	CAGCATGACCCTGGAGCCCAA
80723	TMEM22	NM_025246	CAGGACTACCAGGAAATACTA	CTGATTATTATTGTCTCATTA		
80725	SNIP	NM_025248	CCGCAGTATTATCAAGATCTA	CTGGCCCAGATCCGAAGGCAA		
80736	C6orf29	NM_025257	CCCGGACAACAAGAAGAGGAA	CCGGGTCATCTTGGAGTATAT		
80740	LY6G6C	NM_025261	CAGGACAGCAATGCCTGACAA	TAAGCTGGGTCTGACATATAA		
80742	PRR3	NM_025263	ACCCATGACATGTCTTATAAA	AAGCTGGTCTCTTATCAAGAA		
80755	MGC2744	NM_025267	ACGGCAGTTGCTGACCATCTA	CTGGCTCATGTGGAACATTAT		
80759	C6orf148	NM_030568	CTCCTTCATTCCTACCGTCAA	TTGGCAAAGCAATCCAATAAA		
80761	UPK3B	NM_030570	CTCCTTCATGGGCAAGCGCTA	CTGGTTTCTCTCCCTCTCCAA		
80762	NDFIP1	NM_030571	TAGGATACAAATGAAGCTTAA	AAGTCTTTAATTGGTAAATAA		
80776	MGC4093	NM_030578	TCGCGGAAGTATCGCGGCTTA	CCAGCGGTTTCTCGGAAAGTA		
80789	KIAA1698	NM_030628	ACCCAGTTATATGCAGGGCTA	TCAGCAGGAAGTGATCTATAA	CTGGGTAATATGCATGAAGTA	CACGCGTACATTAATGGACAT
80824	DUSP16	NM_030640	AACCCAGTTGTTACTCTCTTA	CAGGACAAAGTGTTAATTACA	CCGGCCATTTGTGGAATACAA	AAGGTTGTAGTTTACGATCAA
80831	APOL5	NM_030642	GAGGAATAAATTGGTCTGAAA	TGGGAGAAGGTTGTAAAGAAA		
80832	APOL4	NM_030643	TTGCTCATATATAGTAGACAA	CAGCAATTGTTCAGGGAATAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
80834	TAS1R2	NM_152232	CACAATTTGCATCTCCTGTAT	GGCATTTATCACGGTACTCAA	CAGCGTGTACTCTGCGGTCTA	CACACTGAAGATGAATATGAA
80835	TAS1R1	NM_138697	CACTGTGGCGTTTAATGACAA	CTCCGGGCTGCCAATAAAGAA	CTCCATGAGTTCTGCCTACAA	CAAGGACACTGTGGCGTTTAA
80864	EGFL8	NM_030652	CAGCACTTACAGGACCATGTA	TCCCTCAGAGAGAGTCAGGGA		
81061	OR11H1	NM_001005239	CAACATATGCACTGACTATAA	ATCCTATACTCTTGTCCTGAA		
81127	OR4K15	NM_001005486	CAGCAGTTACTCAGTTGACAA	CCAGTTGGCATTCACTGTTAA		
81282	OR51G2	NM_001005238	CCCAGTTCTCTCACATTCTTA	CCGGGCAACTGCACAATTCTT		
81285	OR51E2	NM_030774	ATGGTTAGCTGTCACATACAA	ATGAGAGATAACCTTGCCCTA	TGGCTGGAATAGTAAACTAAA	ACGGGTGCTGGCTATGTTCAA
81300	OR4P4	NM_001004124	CACAACATTCTCAGAAGATAA	CCACTTGTAGTTCTCATGTAA		
81488	GRINL1A	NM_015532	CAGGGAGATACCGAGAAGTAA	CAGCAATTTGATTATGTATTA	CCGGGACTTAATTAAATACAA	ATATTTGAATATTGTGTTTAA
81494	CFHL5	NM_030787	AAGAATTTAATCATAATTCTA	AAGGGAAATTTGAATATCCTA		
81502	HM13	NM_030789	CAACCTCCTGCTGTCCATGTA	ATGCTTCAGACATGCCTGAAA		
81544	PP1665	NM_030792	CCGGGACGTCAGCATCATGAA	CAGGCCTGCCTCCATGCTTAA		
81553	FAM49A	NM_030797	CACCTAGACATTGAGAATGAA	AACAACATCTATAACGATAAA		
81554	WBSCR16	NM_030798	CTGGTGTTAAGGGTCACGCAA	CACAGGAGCCGGAAAGATAAA		
81557	MAGED4	NM_030801	AAGGATGTCATCAGAGAATAT	CCAGATGTTAGTCACCAGTAA		
81563	C1orf21	NM_030806	CACGTTCTTTATGAAAGGCAA	CCACGTGTATCTGAACATTAA		
81565	NDEL1	NM_030808	CAGGCTGAACAAAGAAATAGA	AAGACTTTGAACAAAGGCTAA		
81566	C12orf22	NM_030809	CTCCATCTTGATGATATATAA	CTGCGTAGTGCTGAACATTAA		
81577	MGC11335	NM_030819	CTGAGAAATGTTAATAAATAA	CACAGTGACACTCAACTTCAA		
81607	PVRL4	NM_030916	CTGCTTTGAATCCTTTACGAA	CTGCTTGACCTTTACCTCCAA	CCCTGATAGTCTCAAGGACAA	CAGAGCAGTATTAATGATGCA
81608	FIP1L1	NM_030917	ACCTGTAAATCTTAACATCAA	CAGGGAAGAACTGGAAACTCA		
81617	CAB39L	NM_030925	CTGAGAGATCCCAGAAGGTAA	GCCAATGTCTTTGGACTGTAA		
81620	CDT1	NM_030928	CCGGGCCAGAAGATAAAGAAA	CACCTGGTGGATTCACATTAA		
81622	UNC93B1	NM_030930	CTGCCCGACATCGACAGCAAA	CACCAGGATGGCGCAGAAGTA		
81693	AMN	NM_030943	CGCATTTGACCTGGAGCGGTA	CCAGGTGGTGCTGGTGGAGAA	CAGCCACAGTTACTTCGTCAA	CAGGGTGGCCTTACTCAGTAA
81706	PPP1R14C	NM_030949	CCGCAGAAGAAGAGTGTATGA	AACCCTTAATTTGAAGAACTA	TAAAGTTGTATGAACCCTTAA	AAGAGCTGCTTTCTCGGATAA
81787	DKFZP547L112	XM_375153	CAGGGCTGTACCCTGGACTGA	CTGCCAGGCCCTAGACCAAGA		
81792	ADAMTS12	NM_030955	CCCGGAGTGATCTATGATGTT	CCAGTGGAACGGGAACTATAA	CCGGAGAGTTCTGAAACCAAA	CAGGAAAGACGGCAAACCGTA
81794	ADAMTS10	NM_030957	CGGGCACACATTCGGCATGAA	CAGGACTTTGTGTACCCGACA	ACCGATTAATGCATCTCTCAT	CCGGAAGTTATTTATTGGGAA
81797	OR12D3	NM_030959	CCGGATAATGGCCATCATGTA	TACATTACTGTCCCTGCATTA	CCCAAATAACCAAACGCGTAA	CACAATCAAGCTAAACCTACA
81833	SPACA1	NM_030960	CTGGATAATAATGAAATAGTA	ATGAATGATGTTTGAATGATA		
81844	TRIM56	NM_030961	TTGGCTAAGATTAAGTATTAA	CAGCGACTTCCTGGCCTGTAA		
81858	Sharpin	NM_030974	CAGGAGGGCCTGGAACCCTCA	CCCGGAAGCCTCCACACTCAA	CAGGCTGCAGGTCACACTTGA	AGGCTGCAGGTCACACTTGAA
81875	FLJ12671	NM_030980	CAGGGCATACTGGGAAATGTA	CAGACTTAATACCCATTGAAA		
81930	KIF18A	NM_031217	CACATGAAGAGAAGTATTCAA	ATCCGTCTACAGTAACCTTAA	CAGGTGGAACTAATCTGGTTA	CAGGAGGACTTGGACTCTACA
81932	HDHD3	NM_031219	ATCGCTGAACAGCTTTATAAA	CAGTGTTATTACCTCCAGTAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
83259	PCDH11Y	NM_032971	CAGGAGATTATTTCACCTCAA	CAGGCAGATGATAATGATGAA		
83394	PITPNM3	NM_031220	CAGCAGTGGTCGCATCACATA	CTCGCGCATGATCCTGCGCAA	CACGAAGGACATCTCTGTCTA	CCGGGAGAAGTGGCTTCGTAA
83401	ELOVL3	NM_152310	CTGGGTCTTTCTTCTCAGCAA	ATCGATAATTCCACAGTCAAA		
83445	GSG1	NM_031289	AAGAGCAGTGTTAGGAGTTAA	CAGGATGGTGCTGGAGTTCAA		
83446	ZKFZP434K117	NM_031290	CCAGAAGAAACTAATGCACAA	CCGGCTGATAAGGAAGATGTT		
83449	PMFBP1	NM_031293	CAGGATGATCTCATTCAAGAA	AAGGGTGATCATTCAAAGGTA		
83468	GLT8D2	NM_031302	CCCGATGGTCCTCAAAGGGAA	CTGAGAGAAATAAACTTTAAA		
83479	ZKFZP564B102	NM_031306	AAGGTCAAACTAGGCCTTAAA	CAGGCCCATTATTGACTTTGA		
83482	SCRT1	NM_031309	TCGAATAATAATGACACATAT	CCCGGCTTTCTCCCAGCAATA		
83539	CHST9	NM_031422	CAGAATCTATGTAGAAGATAA	AAGGCATTATGTGATTTACAA		
83549	UCK1	NM_031432	TCCCTCTAGGTCACTGAGAAA	AAGGCTGGTTGTGGCCTACAA	TGCGGTTTAAAGATCCCTCTA	AACGGTGGAGGTGCCGACCTA
83552	MFRP	NM_031433	CAGGGAGTTTGTGGTCAGCGA	CGGACACAGCATAGAACTACA	CAGCATAGAACTACAGTTCCA	CTGCTCCTTCCTGTCCCTTTA
83650	AMAC1L2	NM_054028	CCGCACTCCAATGAGGTCACA	CAGGAGAGTTCCAGGGAAGAA		
83660	TLN2	NM_015059	CTCCTTGAATAACTGCGTAAA	CCAAGTGATAGGGAACCTCAA	CAGATGTTGTATGCAGCCAAA	CTGCATGATCGTGATGTCACA
83690	LOC83690	NM_031461	CTGGTGGATTTACATATTAAA	CTGCTGGTGGATAAACATTAA		
83698	CALN1	NM_031468	CCGGATGACCTTTGTAAGTTA	CAGACTCAGGTCATAAATCAA		
83706	URP2	NM_031471	CCAGCGAAAGTTCAAGGCCAA	CGGCCAGAAGTTCTGCATTAA		
83707	MGC11134	NM_031472	AAGGAGGAGGATCCAACAATA	CTGGCCATCCATCCTACTCAA		
83729	INHBE	NM_031479	AAGGGTTAGGGTGATGGTCCA	TGGCTTATACTTTCTTAATAA	AGGGCTGTTGAGGTACCTTAA	TAGGGTGATGGTCCAGAGCAA
83733	SLC25A18	NM_031481	CCCACTGTTTGCCAACCTTAA	CAGCACCTAGTTTGAGACCAA		
83743	GRWD1	NM_031485	TCCCAGGAGTTTCCAGGGTAA	GCGGATCTCATTAGGCGGAAA		
83844	USP26	NM_031907	TACCTATAATATAGAAATCAA	AAAGATTTGTATGAAGATAAA		
83849	SYT15	NM_031912	GCGGCGCTTCCTCCAATCCAA	CAGCCGCATGCTAGGACCCAA		
83855	KLF16	NM_031918	CTGCCTGGCCTCATCCTTGTA	TTGTATTTAATTAATTAAACA	TGGCCTCATCCTTGTATTTAA	TCCTTGTATTTAATTAATTAA
83861	RSHL2	NM_031924	CAGCGTGAGTATGAAGAACTA	AAGGCTATATTGTAATTCTAA		
83862	TMPIT	NM_031925	CTGGTGGGTGTTCCATCACTA	CTCGCCCTGAAGAAATGCAAA		
83872	FIBL-6	NM_031935	CTGCAGATTCTGAATACTCAA	CCGCCTGACATTACATGGCAT	TAGACTCTAAGCAATTGCCAA	CCGAGTATATGTTCCGCCAAA
83873	GPR61	NM_031936	TGGATTTATGAGGAAACTGAA	TACCCAGAACTGGGACTACAA	GTGGGATAGTCTCCCATTTAA	CCCATTTAAGCAGCTAATAAA
83876	MRO	NM_031939	CGGGATAACAATAGTAGGTAA	ATGGATGGTTAGAAATGTTAA		
83877	BLP1	NM_031940	TTGGTGGTTTGTTGACCTTAT	ATGGCCGTGGATTGTAATACA	CACTACTTCATAACCACTTTA	TGGATTGTAATACACACTGAA
83879	CDCA7	NM_031942	CAGAGTAAAGAAGAACTTAAA	CACAATAATAGTATTAACTAA		
83884	SLC25A2	NM_031947	TACAATTTGGTCTGTCGTGAA	GTCGTGAAGGGTATCCTTAAA	TACCCTAAATCTTAACTTTAT	CCCTATGTACCTAATCTGAAA
83886	MPN	NM_031948	ACCAGTGCCCTTCACCAATTA	CCCACCAGACTCATTTGTAAA	AACCCAAAACCATCAAGAATG	AAGTGCCCTTCACCAATTACA
83893	NYD-SP12	NM_031955	CAGGTAGAAATCACACTTGAA	CAGAATTGCTGCAGTCACTAA		
83899	KRTAP9-2	NM_031961	CCCTGGTAGCAGAAATCCTTA	ATCGATGATCTTTGCAATCTT		
83903	GSG2	NM_031965	TTCGGGCAGATGGGAAGAATA	CAGGCTCATGAAGAAGGAGAA	ACAGTCTGTTTAAGTAAGCTA	CAGTCTGTTTAAGTAAGCTAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
83933	HDAC10	NM_032019	CGGGTTCTGTGTGTTCAACAA	CCGTTAGTAAACATCGCTCAA	CGCCCTTGCGCCGTTAGTAAA	CAGGTGAACAGTGGTATAGCA
83938	C10orf11	NM_032024	CAGAAAGTAACCAGACAAGAA	TTGCCTTGAAATGAATGGAAA		
83941	BBP	NM_032027	ACGCTACGCAAGAACCAGTTA	AGCACCCAACATAACTTGTAA	AAGTAGTTACATTATAGATTA	ACGCAATTATATCCATAAATA
83954	FKSG83	NM_032030	TGGGCATGGCTCAAACTCAAA	AACGTGTGTCTTTCCACTTAT	AAGACTGTTTATATACTACCA	ACGTGTGTCTTTCCACTTATA
83956	FKSG42	NM_032032	AAGGAAACGAACTCCAATTTA	CAGATTTGGGAGCAAAGGCAA	CAGGTGGATGCAGACATCCAA	AAGGAAGGAAACGAACTCCAA
83959	SLC4A11	NM_032034	CCGAAAGTACCTGAAGTTAAA	CCGGGAAATCGAGATGAGCAA		
83983	SSTK	NM_032037	CGCAGTCACTTCACAAGGCAA	CAAGGGTACCGTGGCCATCAA	CCGGTTGGAACCTGCAATAAA	ATCGAGGTGTGCAACGGGAAA
83990	BRIP1	NM_032043	TAGCATGGCAACAATCTCTTA	CAGGCCCTTGGTAGATGTATT	AAGATAAACAGTCCACTTCAA	CCTGAACTTTACGATCCTGAA
84000	MSP	NM_032046	CTCAGTTGTTTCAGAAACATA	CAGCAACTGGAATGACTCCTA	CTGGAAATTACCTGGAGACAA	ACGGGAATGCATCTCCAGCAA
84034	EMILIN2	NM_032048	ACGGGTCATGATGGAATTAAA	CACCTGAAGGACAAAGTTCAA		
84058	FLJ12953	NM_032118	CCCTGTGGTATTCATAAAGTA	CAGGGCCAGAATTCACATTAT		
84062	DTNBP1	NM_032122	CTGCTGGATTAGAATTACTTA	CAACTGGAGAATTACAAGAAA	CACCCAGCAAATGAAGCTGAA	TTGGCTGTATGCGGAATTCCA
84066	DKFZP564J047	NM_032126	CTGAGGGAAGGTGAAGCTTAA	CCAGCTTGAAATGAGAGTAAA		
84083	ZRANB3	NM_032143	TTGCCAGTGTATGACACCTTA	TGCCAGTGTATGACACCTTAA	CCGGATTCACATCTATACTAA	TGGATAGTTCTATAGAATTAA
84106	PRAM-1	NM_032152	CCGGAAGAAGTTCAAGTTTGA	CCGAAGCCTGAGTTTGGTAAA	CCGCAAGTTCTCACAGCCTGA	CCGGAGCATCAAAGCAAAGTT
84108	PCGF6	NM_032154	TAGGAGAATTTGAGAAGTTTA	AAAGATTTCCATGAAATGTAA		
84109	GPR103	NM_198179	ATGCTTATTCTGTACAGTAAA	TTGTTATTGCATAGTAAATAA	ATGGAAATTCAGGAATTACAA	AGGAATTACAATGATGCGGAA
84132	USP42	XM_374396	CAGCCCGTGATGAATGGCAAA	CAGGACGAGGCGAAAGCCCAA	TTGGAGGATACCTAAGATCTA	CACGACAGAACTGCACTTGTA
84152	PPP1R1B	NM_181505	CTGAGTCTCACCTGCAGTCTA	CAGGGATTTGCCCTTCACAAT	CAGCTTGTTTGAAGCCCTTGA	ATAAATCTTTGTAAATAACAA
84162	KIAA1109	XM_371706	AAGGATGCAGCTTGACTTTAA	CAGGTGTGGAGTATAGATGAA	CTCGAAGAGATTCACTTTCAA	CACCTCTTAAGCGAATGGAAA
84168	ANTXR1	NM_018153	CAGCAGTGTTTGATACCGTAT	CTCCCATTATAGGGCAAACAA	CTGACAGAAGACAGAGAACAA	CCGAGGAACAACCTTAATGAA
84171	LOXL4	NM_032211	CCGGGTGGAAGTGCTCATGAA	CAGAGTCAGATTTCTCCAACA	CAGGATTGGTCTAAACTTCAA	CTCATTATGGACTGCTACAAA
84174	SLA2	NM_032214	CTCGTTGAGACCACCACCATA	TCGGACAGTCTAGGTCCTCAA	CATCAACAGGTTCTCAATTAA	CAGGTTCTCAATTAAAGATTT
84186	ZCCHC7	NM_032226	CAGGGAATTGAGCTTCAGCAA	ACAGATTTCCTAAACAAGTAA		
84196	USP48	NM_032236	CACAGTCTGGTGAATGGTATA	ATGGCTGAGATGCGTAAGCAA	CCGAAGTATGCGACATAGAAA	ACCAGATGCGTTGGTCCATAA
84197	FLJ23356	NM_032237	AACACTATGCTTACTGAATAT	ACGGGTCATGTGCGACTCCAA	CACGATGATCTCATGCCCTCA	AAGGTCTTGGATACACTTAGA
84203	TXNDC2	NM_032243	TAGCTTCTCATGTGTAAACTA	CACCTTGAAGCTCTCAAATAT	AGCAGTCATTGCAGAATTAAA	CAGAATTAAAGTAAACATGTA
84217	ZMYND12	NM_032257	CAGCATATTAAGGGAATATAA	CAGCTTGATGTCCATGAGCAA		
84220	RANBP2L1	NM_005054	CAGCATGAAATAAACACTCTA	CAGGCGTTCAGTGGAATTAAA	CAGCATGGTAATAATGTTCAA	CAGAATTATGATAATAAGCAA
84229	DKFZp434I099	NM_032269	CAGGACAATGACAGAGTACTA	CACACTGACCATCTCCATCTA		
84231	TRAF7	NM_032271	AAGGAGTGCGAGCACATCAAA	TCGGAGAAGATCGACCAGCTA	GCGGGACGCATCCATGTTAAA	CACGCTGGTCTCCTCACACAA
84233	DKFZp586C1924	NM_032273	CAGGTGATTTGGATTGTGAAA	ATCGGTTTATGTTGGATTAAA		
84259	MGC2714	NM_032299	AACATTTATTTCAGAACAATA	TCCCACGTGTATACAAGCTAA		
84263	HSDL2	NM_032303	AGGCACCTACCTTGCATCTAA	AAAGAGGTGACTTAAGTTCAA	ACCCAGTTCATGAATCGCTAA	CAGTTCATGAATCGCTAATAA
84265	MGC3200	NM_032305	AAGGGAGAAAGGAGAATTGAA	ATAGAGGATGATGACAGTTTA		
84266	SPATA11	NM_032306	CGGGACTCTGAGGGAAGTCAA	CAGGCGGGAGGTGGCGCCCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
84270	C9orf89	NM_032310	CAGGATCATCCTCCAGCTGAA	CAAGGTGCTGACCATATTAAA		
84279	C2orf7	NM_032319	CATGATTATTTGTACTTTCAA	CTGGCTAGAACCCGAAACAAA		
84284	MGC13186	NM_032324	AAAGATTTCTTGTTTATTTAA	AAAGATCAAATTAGCCTTAAT		
84288	MGC12458	NM_032328	AAAGATGATCGTAACACTTTA	AACGAGTAGCAGTGTAATGAA		
84289	ING5	NM_032329	CTGCGTGGACCTTACCACGAA	CCGGATCCGAGGAGCAAGTTA	AACCGTGAGGGATGTTAATTA	ACCGTGAGGGATGTTAATTAT
84291	MGC2408	NM_032331	CAGACACTATGCCCAAGCCTA	CAGCTCCAACTAGATCCAGAA	CTGGAGGCCGGTTTATCTCAA	TCCGGAGTTACCGGAGCGGAA
84292	MGC4238	NM_032332	CCGGCTCTATTGATTCCAGTA	ACGATTTAATGTGGATGGCAA		
84296	SLD5	NM_032336	CAGCACTTGATCCGATACAAA	TCGCCTCATGAAGATAGAGAA		
84298	MGC14817	NM_032338	CAAGCTCTACTGATACTTTAA	ATGAAAGATGTTCAAGAGATA		
84299	C17orf37	NM_032339	TGCCTTTGAGATAGAGATAAA	CCCAGGGTAAGTGCCCACGAA		
84302	C9orf125	NM_032342	CAGGGTTTAGCTGGCCTGTAA	CTGCAGGTATTTCACTGTTTA		
84310	MGC11257	NM_032350	CAGAGCGTGGATGCTCTGGAA	TGGCCTCACTTTCCATCATAA		
84311	MRPL45	NM_032351	AAGAAATAATTTATCCCTTAA	CACGCATATCATCTCTTTCAA		
84312	BRMS1L	NM_032352	CACAGCATTGATATTACCTCA	TAGGTAGTACTCTAAATAGAT	CCGCTGGCAACTTTACAGGAA	ATGCAAATTCGTACAAAGGTA
84318	MGC13183	NM_032358	AGGCTTTAAGACAGATATTAA	CACCAGAGAAATCAGAACAAA		
84321	THOC3	NM_032361	CAGCGTCTTCTTGCTGGAGAA	ACCAGCTTTGTTGGCATCCAA		
84324	CIP29	NM_033082	CAGGCATATCTTGAAGAACAT	CTCCTTCTTCTTGGTCACATA		
84327	ZBED3	NM_032367	CCTGGTGACTTTGAAAGGATA	CCCAGAATCCTTGGGAAATTA		
84329	MGC15619	NM_032369	CCCGGCCTTCTCCTTTAAGTA	TGGGAGCTCACTAAGAACAAA	CAGGTTCCAGGCCATCAGTAA	CAGCCCGACAAGAATAACTAT
84330	MGC15716	NM_032370	CACAGCAAACTGCACTACAAA	CACACAGTCCCTGGAAGGCAA		
84334	C14orf153	NM_032374	AAGGATTTGGAACAAGCTTAA	TCACAAATAAATTGTAATTAA		
84337	MGC4549	NM_032377	CCCGTGGATGTGTACAGTGAT	CTGGACAAGGGAAGCCCACTA		
84366	PRAC	NM_032391	CTGTCTCTATTTATACAATAA	TAGGCCGATGCTTGCTTGCAA		
84376	HOOK3	NM_032410	CTGCCAATAATTGATATACAA	CAGCATGAGAATAAGATGTTA		
84433	CARD11	NM_032415	CTGGATGATGACAGTCACGAA	CCCGTTGGACACATGCACCAA	CACAGTACTCGCAGTGCTTAA	CAACTCGAGATCGATCAGCTA
84435	GPR123	NM_032422	CCGACTTTCCTAGGCAACAAA	AAGCCGTGTTCTGATTATCAA	CTGCCCAAGGGTAAATTGCTA	CACTGTAAAGCTCTTCACCTA
84436	ZNF528	NM_032423	TAGGATTTACACAAGAAGTAA	AACGCAGATAATCCTTACAAA		
84439	KIAA1822	NM_032425	CAACAAGAACCTCAACTCAAA	GAGGATAATCCTGGAGGTCAA	CAGGAACACTTGATGAATAAA	GCGCATCGACGTGGACCGTAA
84441	MAML2	NM_032427	CCAGTCGAAAGTAATGGCTAA	CTCCAAATAAACAATGGACAA	CAGAGTTCAATTTCAGCTCAA	CAGGATACAGTATCCAATTTA
84450	ZNF512	NM_032434	CAGCACAGTTCCAGAAAGTAA	CAGCCAGGAAGTACTACATAA		
84465	MEGF11	NM_032445	AAGCAGCTATGTAGAAATGAA	CAGCAAGTTTACACTGCTTAA		
84498	KIAA1838	NM_032448	AACCCTGAAATTAAACAAGAA	CTGAAGTAAAGCAACAAGTAA		
84504	NKX6-2	NM_177400	CTCGGACGCCGAGAAGCTGAA	CGGCTGCTCAAGAAGCACAAA		
84520	C14orf142	NM_032490	CTGATTTATCATGTACCTTAA	AACAATCTGCATTGATTACAA		
84536	C21orf67	NM_058188	CAGAGGAAGATCAAAGATCAA	CAGAAGGACCACAGTAGAGAA		
84614	ZBTB37	NM_032522	CAGGGTTACACCAAATCTCAA	ATGCAGCATATTATAGACAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
84630	TTBK1	XM_166453	TGGCAGGAACGAGAAGTTTAA	AACGAGAAGTTTAACTATGTA	TGGCAGGAACGAGAAGTTTAA	CAGGAACGAGAAGTTTAACTA
84639	IL1F10	NM_032556	CCGGATAGCCTCAGTCAGGGA	CCATGGCAAGATACTACATAA	GCAAGATACTACATAATTAAA	AAGGCTCTATACACAAGAGAT
84641	FLJ14753	NM_032558	CACCAGTAAATGGACCATTAA	ACGAGTGAAGTTTATATCCAA		
84643	LOC84643	NM_032559	CACGGTAGAGTGGGTGGAGAA	AAGAGTCTTCTAGCCCTCAAA	CAGAGGGATGAATTTATTAAA	CTGGTGGAGTACACCATGATA
84645	C22orf23	NM_032561	AAGGGTCTTGCCACCACTTAA	CCGCCTTAGGCAAGTATTCAA		
84651	ECG2	NM_032566	CTCCATGGACATAGAGAGAAA	ATGGAGAAAGTTTCTGTGCTA		
84658	EMR3	NM_032571	CTCCGGGATGTGGAATCGAAA	AAGGAACGTGTCTCTCTCCAA	GTGGTTTAGAGAGATCGTAAA	AACGATAGTGTAGCTATTGAA
84659	RNASE7	NM_032572	CCACTTCATATTTGTATAGAA	CAGCACGAAGACCAAGCGCAA		
84675	TRIM55	NM_033058	TACAAACATATCACACATTAA	CAGAACATAAGTGTAACTTTA		
84676	TRIM63	NM_032588	AAGGAAGAAGGACACCAGTAA	AAGGAGCACGAAGATGAGAAA		
84678	FBXL10	NM_032590	CCGGCAAGACCGGGAAACAAA	CAGATCTAACAAAGTAGGCTA	TAGGAGTGGACTAGAAGTTTA	AGGAGTGGACTAGAAGTTTAA
84680	PHACS	NM_032592	CTGGGTTGACTTGAGAAAGTA	CAGCAGGTGCTTGCAGGCAAA		
84687	PPP1R9B	NM_032595	CCGGGAGGTGCGCAAGATTAA	CACTGAGGAATTCCAATTCTA	CCCGGGAGGTGCGCAAGATTA	CAACTCGAAGCTGGTCAGCAA
84691	NYD-SP18	NM_032599	CAGGTATGTGACCACTATCAA	CTGAGAAGATTTATTACCTAA		
84692	NYD-SP17	NM_032600	ACGGCTTTATTTGTTCCTTAA	CTGAAGAAACGTAACCATCAA		
84699	CREB3L3	NM_032607	CCCGAGAAGAGTCTCCAGGAA	ACGATGCAATCTCACCGTGAA		
84701	COX4I2	NM_032609	CTGGAGCTTGGTGCTGAGGAA	CCGCTGGGACTATGAGAAGAA		
84708	LNX	NM_032622	ATCATCCTCGATAGTACTCAA	CACGGTGCTTGTATAACTGTA	CTCGCTCAGAGAATTAATTAT	CACAGCTAACACAGCTCTTTA
84720	PIGO	NM_032634	CAGGTACTGGATGATCTGCAA	TAGGACTTCATTATTCTATAA		
84733	MGC10561	NM_032647	CACCTGCGGGTGCACCTTAAA	GCCGGCTGGATGTGACTCAAA		
84749	USP30	NM_032663	CAGAAATAACTCCCAAACAAA	CACACCAGTATTTATCCTTAA		
84750	FUT10	NM_032664	CAGCGCGAGAGTAGAAGTGAA	TAGGATCATTGCACAGTATAA		
84775	ZNF607	NM_032689	TAGGTTCATTTCTGTACTTAA	TAGGCTCAATTCATCCCTTAA		
84787	SUV420H2	NM_032701	AACCTTGTTATAAGCAGCAAA	CCGGCGCTATGGGCTGCCTTA	AAGAAGAATGAGCACTGTGAA	AATGACTTCAGCATCATGTAC
84816	RTN4IP1	NM_032730	TTCGAGCATTTCATATGCGAA	ATCATACACTATCCAAATGAA	CACGAGGAAAGACTGTAATTA	ACGAGGAAAGACTGTAATTAA
84833	USMG5	NM_032747	CAGCTGTGAAAGCAACATAAA	TACCAGTTCACTGGTATTAAA		
84836	MGC15429	NM_032750	CAGGTTACACACTAAAGTAAA	CTCAGGAATCAAGGAACATAA		
84844	PHF5A	NM_032758	ATGGCTAAACATCATCCTGAT	CTGGCACACCATATCGGAGAA		
84864	MINA	NM_032778	TTGGCTCGAATGTGTACATAA	CTGTTGCTACAAGACGATTAA	TACCTGCGTATCTACTAACAA	AACCAGTATTTAAGTCTATAA
84868	HAVCR2	NM_032782	AACCATCAGAATAGGCATCTA	CAGGCATAATGAATGATGAAA	CTGATATAAATCTAACACAAA	TTGACAGAGAGTGGTCCCTAA
84870	THSD2	NM_032784	ATGGAACTCGATATCCAGATA	ATGGAATACATCGGCAGCCAA	AAGGGAAGCATTACTGGGTTA	CTCGATATCCAGATATAAATA
84872	FLJ14451	NM_032786	CACCAAGAGTGGCAAGATAAA	CTGCCATGACTTCCAGAACAA		
84873	GPR128	NM_032787	CTCGATCAAAGTGCTGTGGAA	AAGAAGATTGTTAGCACATTA	CACAGCTCTATTACCTTCTAA	ACGCGAGTGGTTGGACAGATA
84875	PARP10	NM_032789	CAGGCAGATCATGAACTACAT	TTGAATAAACGTGAACGTGAA		
84888	SPPL2A	NM_032802	CAGCAATAATATTATGTGGAA	TGGGCTGTGTTTCGAAATGAA		
84893	FBXO18	NM_032807	CCCGCTGTTCATTCCTTGGAA	CTGCATAGCCGTGCTTCTCTA	TAGGGCGGAAGTACCAGTCAA	CACCGTCCTTACCATGAAGAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
84894	LRRN6A	NM_032808	CAGCGAGAACAAGATCGTTAT	CCGCTGGCGGCTCAACTTCAA	AAGGACTTCCCTGATGTGCTA	CAAGGGCAACACAAAGCACAA
84896	ATAD1	NM_032810	CTGGATTAATTTATCTGATAA	CAGGTGAACAATGGATAACAA		
84898	PLXDC2	NM_032812	TCCAGTGGATTTGATCGTCAT	CCAAGATAGCACTACATCTAA	CACAGTACATAGCACCTTTAA	ACAGACCACAATTACTATATA
84904	C9orf100	NM_032818	CTGGATTGTGGGAGAACTAAA	CCCAACTAAACCTCAAATGAA		
84918	LRP11	NM_032832	TACGTATTTCTAGACCATAAA	CAGAAACTTAGTTGAAGGCAA		
84925	DIRC2	NM_032839	ACAGATTATCACATTAATTTA	CACAGACTTGAAGGAGTTTAA		
84926	FLJ14800	NM_032840	CAGACCAGAGATGTTTATACA	CCCTACGATGTATGAAATGTA	CCAGTTTGGGTCAAAGTGCAA	CCGGTTTGTTCTCATGAACAA
84934	FLJ14827	NM_032848	ACCAAGGAAGAAGAACAAATA	CAGCTTTATAGGTGTGACCTA		
84938	APG4C	NM_032852	CACGTAATTGCAGGAAATGTA	ACAGATGAAGTTGACAAGCTA		
84948	TIGD5	NM_032862	CACAATCATCTCAGTGGCGAA	CCGCAAGGCCTACTCCATCAA		
84950	FLJ14936	NM_032284	AACCTGGATGTGAGGCATTAA	TCCGACGGAAATAGAATTGAA		
84959	STS-1	NM_032873	AAGAGAGTTGTTCTTAGGTTA	AACCAAATCATCAGTTATCAA	CCGGCTTATTTGAGTGGACAA	CCGCTTAAGGATGCTAACATT
84961	FBXL20	NM_032875	ATGGCAGTAACTGGCAGCGAA	CAGGACCCATTTACCCAATAT	GACCCATTTACCCAATATTAA	CTTGGCGAACTGAGTATTTAA
84972	MGC15912	NM_032886	ATGGATGAGGTCATCATGAAA	CTCGCTGGGTTTATATTTGAA		
84991	RBM17	NM_032905	TCCGCTGACTGAAATACTTAA	ATGGAGTATGTGGGTATAGAA		
85013	MGC13159	NM_032927	CAGCTTTAGTAATTACTATAA	TTGCATATGCATAAATTATTA		
85014	MGC14141	NM_032928	ATGGCTTATCCTTCTCTCCAA	CTGCATCTCCAACAAGTCCAA		
85015	USP45	XM_371838	AAGCATATATAATGTTATCAA	CAGAGAAAGCATGTTAAATTA	CGGGTGAAAGATCCAACTAAA	CAGGAAATTATCGGAACATAA
85236	HIST1H2BK	NM_080593	AAGAGAATCATTTACAAGTTA	AAGGAGGGACTTTCTCTGGAA		
85285	KRTAP4-10	NM_033060	AAGGGCATCCATCTACATTTA	TACATATTAACTGTTCTTCAA		
85300	ATCAY	NM_033064	CAGCGTCAAGTTCATCAACAA	CTCGCCTTTGTTTGCCAGTAA		
85315	C6orf33	NM_133367	TAGGAATTTAAGTCCATAGAA	AAAGCTAGAATTGCTTATCAA	AGGAAGCTTATTCTCATATAA	CTAGAATTGCTTATCAATCAA
85317	BAGE4	NM_181704	CCGAGGCAAGTCAAAGCTGAA	GAAGATCAAATTGAAGATAAA	CTGCAGATATTTCATCAAATA	ATGGCTGGAAATGCAAATGAA
85320	ABCC11	NM_032583	CCGGTGTATTTGAATAAACCA	CCGCTCATGATCCAAAGCTTA	CTCCTCCAGTTGGATCATCAA	AGGCTACTTGATGGCTCTCAA
85358	SHANK3	XM_037493	CAGGGATGTCCGCAACTACAA	CCGCAAGTTCATCGCCGTGAA		
85359	DGCR6L	NM_033257	AACCCTAGGATAGTCTCATAA	CCGCGCTCGGGATGTCGTGAA		
85360	7h3	NM_033025	CTCCATCTTTGTGGATAATAA	GCGCCTCTCCATAAAGATGAA		
85409	NKD2	NM_033120	CTCGTCTGTGTAACCCATAAA	CACGCTCTATGACTTTGACAA	CAGCCTCATGCACACCATCTA	CACGGAGCGCAGAAACCACTA
85411	C6orf114	NM_033069	TGGAATCAGAATTCAACTTAA	AACCTCCAATGTGGACATTTA		
85414	PCANAP6	NM_033102	CACAGGCATTTAAATATTTAA	CAGGCTCAGGGTTAACAGCTA		
85417	CCNB3	NM_033031	GTGCAGGATGTCAATATGGAA	TAAGGAGTCGTTAGCCTTTAA	AGGGCTAAGCATGCATGTTAA	AAGGCTGTGTATTACAAGTAT
85439	STN2	NM_033104	CAGATGTACCTTATAATTCAA	AAGCTGGATATTTCCTCTTTA		
85443	DCAMKL3	XM_047355	GAGGAAACTGTTTAACCTCAA	CTCGAGAATCACAGAGCGGAA	TCGAAGGAGCTCAGAGTTCAA	CCAGCTAATGAAGATAAACTA
85452	KIAA1751	XM_372193	CACCTTCAAGCCGATGATAAA	CAGGACTTTGATATTGGCAAA		
85455	DISP2	NM_033510	CCGGAACAGTCCGGACTACAA	CAAGAACTTCAGTGAGACTAA		
85459	KIAA1731	XM_374922	CAGCAGATACAGAAACATGAA	CAGCATGAACTTAGTGCTATA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
85464	SSH2	NM_033389	GAGGGTTTGCCTGGAAGTTAA	CAGGAGTCTTTGAGTATCATA	TTGAGGATGAATTAAACTTAA	CAGATTTAGTCTAGCATGAAA
85465	SELI	NM_033505	CAGGCATAGTTTCCACTTTAA	CACCACTGTGTTGATATGTAA		
85480	TSLP	NM_033035	GAGAAATTTCTTTGTCTATTA	TTGGTGGACTAGTATAGTATA	AGCACCTAAACTTACATTTAA	CTGGAACAAGTGTCACAATTA
85865	LOC85865	NM_033107	CAGCTTGGTGACTGTAATTAA	AAGCCTGAACTTGGAAAGATA		
89765	TSGA2	NM_080860	AACATGGTGAATATCGTTTAA	CCGAGAGGAGATCGTATCATA		
89777	SERPINB12	NM_080474	TAGGCAAAGATGATCGTCATA	TACGATCTTGGGTGGAGTTTA	ACGATCTTGGGTGGAGTTTAA	TTGGGTGGAGTTTAATGCCAA
89780	WNT3A	NM_033131	CAGGAACTACGTGGAGATCAT	GCCGCGCTACACCTACTTCAA	CCCGACTGTGCTGCTCGCGAA	ACCGCCATCCTCTGCCTCAAA
89792	GAL3ST3	NM_033036	CAGCCGCAAGGTGGACATTAT	CTCGAACTACCTGTTGCGCAA		
89796	NAV1	NM_020443	CGGGATCATCTAAGAAATGTA	TAGGTTGTCATTCAGACTTTA		
89797	NAV2	NM_145117	CACCTTTAACGTGGACCATAA	CAGCAAGAATGTGGACCTCAA		
89822	KCNK17	NM_031460	CCGGGATGTCGTCCAAGCATA	ATGGCTGGCCTTGATCATCAA	CAGCTCTAAGGAAGACTTCAA	CTGGGTGCAGCTATATGATTA
89832	CHRFAM7A	NM_139320	AACATTAAGATTACAAGTGGA	TCCATACAAATGCACAACATA	CACCGCAACATTAAGATTACA	ATCGGTTAAATTTGATGCAAA
89845	ABCC10	NM_033450	AGGAAGGGAGTTGATTCCTTA	ACGGCTGTGGAGGGCCTTGTA	CTGCTGGTACCCGTCAACAAA	AGCCCAGATTGTGGTAGATTA
89853	C9orf28	NM_001011703	AAGCCTTGCCAGAAACGTCAA	CTGGAAAGACGGCTTATTTAA		
89858	SIGLEC12	NM_033329	CAACAGGACATCAGAACTTAT	CAGGAAATGGAACTACATATA	CCGAGACTGATTCCTTTAGAA	ATGGAACTACATATATGACAA
89869	PLCZ1	NM_033123	CAGAAATACGAGCCTATCGAA	ATGGATTCACGTGAATGTCTA	CAGCAGACTCGTGTAATTAAA	TTAGCTATGCATCGCAATAAA
89870	TRIM15	NM_033229	CAGGAGTAAAGAACTGGCTTA	GAGGGATGAATATATCACAAA	CCGGCTTGGAGCCCAGGTCAA	ATCCGTGATTTCCACAGGAAA
89882	NYD-SP25	BC033792	AACAGGTATAGCCAAATTCAA	TAGACGAAATGTGCCATTATA	CACGTTAAATCAAGGAAGGAA	TTGAATGGACCTAACTATACA
89884	LHX4	NM_033343	CCGGACCACCATCACAGCCAA	CAGAACTTGGCCACACCAATA	CACCAATAGGATTTATGGCAA	TCGAAAGTACGCCAATGTGAA
89886	SLAMF9	NM_033438	CTGGCAATAAAGTCAAATTAA	CAGGCATGGATATGACCTACA	TCAGGGCTTTACCAAGCTCAA	CTGGCTGGCAATAAAGTCAAA
89890	KBTBD6	NM_152903	CAGTATTTATTTGATTATTTA	TAGGTTTGTATTGTTGATCTA		
89894	LOC89894	NM_138341	CTCGTGTTACCTTGATGGATA	CAGGGTCTACTCAACTGTGGA	ATGGCTACTCTGAGTGTTATA	CACCGTCAATTACATCTGGTA
89953	KNSL8	NM_201521	GACCAGAATAAGTATAAGGAA	CAGCTTCGCCGTTCTATGGAA	CAGCGGCTACAGCGCAGTGAA	AAGGTTGCGGACGTTGCACAA
90007	MIDN	XM_028067	CTGTCTTGGATACCTATTTAA	CCCTTTATGTGTTGAAAGTTA	ACCGGCTTCGGCAGACAGAAA	ACCGTTGTTCTCGTAGGTGAA
90024	LOC90024	XM_028217	TACGGTCGGAAGGAAAGTAGA	CCGACCAACTGCAGCACCCAA		
90025	C6orf157	NM_198920	ATGAATGATTATCAAATTAAA	CTGCGGTGAAGTCATAATAAA		
90102	PHLDB2	NM_145753	AAGCATGAAACTAAATTGAAA	CAGAATAACTTTATCACCCAA		
90133	LOC90133	XM_029323	TACCAGCGAATTCCCACCCTA	TACAAAGACTCAGATCTCCAA		
90231	MGC33867	NM_138346	CAGCCCAGGAGTGGAAATGAA	CCAGATGGAGTCGACGCTCAA		
90249	UNC5A	NM_133369	CACACCCATTGCCCACACTTA	CCGCATAGCCTATTTGCGCAA	CCGCATTAATGTCTCAAGGCA	CACCATGGAGGTCCGCATTAA
90316	TGIF2LX	NM_138960	AGGGCCCAGTGGTCCAGACAA	AAGGTCAAGGTTTCTGTCACA		
90378	SAMD1	NM_138352	CAGCTTTCCAAGAGCAGGAAA	CTCCATGGCAGCCATGAACAA		
90379	LOC90379	XM_373433	CTGCGTGGACATGGTCATGAA	CCGGGTGTGCGTGTCCCTCAA		
90390	THRAP6	NM_080651	ATGAAAGATTATTGTAATAAA	CTACAGGATAATCTTCGCCAA	CTGAGATTGGTATATGACAAA	CAGGAAGCTGAGATTGGTATA
90427	BMF	AK024472	GAGGTCTTCAGTACTATTGAA	CCAGAGGAACTCAGTTAAGAA	GACGCTAGAAACTAAATTATA	CAGACGCTAGAAACTAAATTA
90441	ZNF622	NM_033414	CAGGCACATATGAATGACAAA	CTCCTTGATGAGATACTACAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
90485	BC37295_3	NM_001005850	CTCGCTTATAGAGCACCAGAA	AACGCGATGAATTCAGCCGAA		
90507	SCRN2	NM_138355	CACAGGGTTACTGGAGCACTA	CAGGCTTATGCGTAAGCTTCA		
90529	LOC90529	NM_178122	AAGCTTTATGAAAGCTCTCAA	ACCCAGGTGATTCCAATGATA		
90594	ZNF439	NM_152262	TTGCTTTATGGAAGAAAGTAA	CTAGGATTCTTTGAATACAAA		
90637	LOC90637	NM_182491	GAGGGAGATGGTACTATAATA	CAAGATTTCTGTAAAGATCAT		
90736	CXorf44	NM_138362	TCCTGGATGAATAATATTGAA	CTGGGCTTCCTGGGTCAAGTA		
90737	PAGE-5	NM_130467	ATGCTGGAAATTTGACTGCTA	AACCAAGAATATTGTTCTTAT		
90780	PYGO2	NM_138300	AACATGAACTTTCCCAGCCAA	TCGGAGTGAGGTGAACGATGA	ACGTATCTTCTTCATACCAAA	CAGCCCATCTGTTGCACATTA
90835	LOC90835	XM_373675	CCCAGTCTCTCTCACATTCAT	CTGGAACATTCTGGAAACTTT		
90874	MGC45731	XM_371286	CACCAGGACTCAGAAGACAAA	CTGGCCTTGGTTTCTATGTAA		
90952	ESAM	NM_138961	CTGAAATTAGCTACTCACCAA	CAGAGGATAGGGAATCTCTTA	TCAGGTGTTGTCCTACATCAA	ATACATAATGTTTGTATGAAA
90987	ZNF251	XM_291262	CAGACTCGTGTTGGAGAGAAA	AAGCATAATTTATAAACAATA		
91050	DKFZp761B107	NM_173463	CAGGCTAATCTTGCACAACTA	AAGAAACTAATTATACTACAA		
91074	ANKRD30A	NM_052997	CTGCAGATATATGTGGAGTAA	AAGGCTAACTGCGGAATGAAA	CAGGAGATGCTTGTTTGCAAA	AACCGTATATATCAATATGAA
91151	TIGD7	NM_033208	CAGACGGAACTCATAAATTAA	AAGGTTCTAAGTAGAATTGAA		
91181	NUP210L	NM_207308	AAGGAGTACTTTGAAGAGCAA	CAGGATGAAGTACAGATTGAA		
91227	GGTL4	NM_080839	GAGGACAAGGCTGACAAGCAA	CACCAGCACCATCAACCTCTA		
91304	C19orf6	NM_033420	GCCCGATGACATGAACAACAA	CGAGTTCTTCGTGCTGCTCAA		
91316	LOC91316	XM_498877	CTGCTGTGGTCTCTGCTTCTA	ATCGTGGTATCCCAAGGGTTA		
91319	DERL3	NM_001002862	CACGGCCGACTTCGTCTTCAT	CTGGGAAGAGTCCCATGCTAA		
91351	FLJ31033	XM_037817	CTGGGTATTCCAGCATATTAA	TAAGAATAAGATAGTCATTAA		
91355	DKFZp434O0213	NM_182492	TTGGCTCTGTGCATCCTTGAA	AGCACTATAATATTTATTGTA	CACGTGCAGCCTATATGGGAA	CTGGAACAAATCAGTGAACAA
91368	MGC13017	NM_080656	CCCAGGAGTTATCACTGTAAA	TCCTGGTATTACCAACATAAA		
91369	MGC15396	NM_052855	CTGGGTGTTAATCCAGATCAA	AAGGATGTTGCTCGACTCCAA		
91404	SESTD1	NM_178123	CGCCAACAAATTGACTCGTTA	TCGGTTGATCCTGAAACAGTT	CAGCGTCGATTTAATGGCTCA	ATCCCGCATGTTGTCAACATA
91409	DKFZp434E2321	NM_207310	AAGCTCATAATGAATCAGACA	CTCCAAGAAATGCCTGCTTCT		
91445	FLJ38628	NM_152267	ACAGCCAAGGATGGCAAGCAA	CCTGAGTTTAATATTACAGAA	ACCACCATCCTCAGAAGCCAA	CTGAATCTTATTGAGGGACTA
91452	ACBD5	NM_145698	CAAAGTGATAATGATAAGAAA	ACCGTTAATGGTAAAGCTGAA		
91464	LOC91464	NM_001008494	ACGGGATACAGAGATAAACAA	CTGGATGAAAGGAGAAGGCTA		
91522	COL23A1	NM_173465	CAGGATCTTGGATGCCCTCAA	CAGGAAGGAGATGAAGGTAGA		
91561	LOC91561	XM_039218	CAGGGCCGCAGAGCTCGCGGA	CGGCTTCTCTCAAGGATGAGA		
91574	FLJ38663	NM_152269	CAGCATTATTATAGTGCTTCA	TTGGATGAGAATGAACTCGAA		
91584	DKFZp434G0625	NM_181775	CCGCATCGTCCAGACCTGCAA	CTGGCCTTTGTGGGCACCAAA	TACCTGGGAATTCTTCCTAAA	CAGCCGGAAACTGACCAAGAA
91607	FLJ34922	NM_152270	CCCGATAACCTTCACACTCAA	CAGATACAACTCAGCATTAAA		
91608	RASL10B	NM_033315	ACCAATTTAGAAATAACAATA	CAGGGCAAGCAGAGGCAGCAA		
91647	ATPAF2	NM_145691	CTCCGAGAGCACCACAGTCAA	GAGACATTAGTGGAACTTCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
91662	NALP12	NM_033297	CTCATGCAGATTGAGATCAAA	CCAGACCTTGACCGACCTTTA		
91664	LOC91664	XM_039908	AAGTATGATGATTGCAGCAAA	CGCTGCGAGTGTGGTGTTTAA	AACCTGGTGTCAAGATACAAA	ACCGCCGCTATTCTCCAGATA
91754	NEK9	NM_033116	CAGGTGTCATGTGGTGATGAT	TCGGGAATTATCAACCATGAA	TACACTTGGGTGAACATGCAA	CACGAACCAGTGAAGTCTATA
91833	WDR20	NM_144574	TGGGAACATGTACTTATATAA	CACGAGGAACCCTCTCCTTAA		
91860	CALML4	NM_033429	CACGGTGCTCTTAGCATTCAA	ATGGAATTTATGGTAACTTTA		
91862	MARVELD3	NM_052858	ACGAGAGGAGGTGGAATATTA	CTGGAATGCCACAAATGCAAA	CTGGGAGAGCCTGCTGCCAAA	CAGGCGCTGTACCAAAGCAAA
91942	LOC91942	NM_174889	CCAGTTCAAACTCAAATTAAA	CCCGCAGTACAAGAACTGGAG		
91966	CXorf40	NM_178124	ATACATTAGGTTAAATCTGAA	AGGGCCAGGTAAAGAAGCTAA		
91977	MYOZ3	NM_133371	CACTAAGGATATAACAGTTAA	CTCCAGGTGATTCCAGCATAA		
91978	C19orf20	NM_033513	GAGGGCCGCCTTCAACAACAA	CGGAGGTTACACCCTCAGCAA		
92002	MGC29729	NM_152274	CAGATTTGTAGGGAGAATGAA	TACAGGCATGACATCAATGAA		
92017	LOC92017	NM_001009607	CAGCGTCATGAACAAAGTCAT	ACGGAGAAAGCAGCTCCAGAA		
92106	MGC15763	NM_138381	ATCGTCTGCTTTAACGCCTTA	AACCAGCATAATGAAATCCAA	TACCAGCGAACTCCTGTTTAA	ATGCAGTTTGCATGTTACAAA
92181	DC-UbP	NM_152277	CTGCTCTAAATTCCCTATGAA	CAGGCTTTGAGACTCATGTAA	AAGGCAGTTAAGAAATAGATA	AGGCAGTTAAGAAATAGATAA
92211	PCDH21	NM_033100	AGGGCTGAGAATTGACGAGAA	AACCTGCTATCAGGAAATCTA	CAGGTTGGTAGCAAAGATCTT	CAGGTACAACTTCTATGTGAA
92235	LOC92235	XM_043739	ACCGTCTGTTGCAAGCATGAA	AAAGCTGGCCTCAGACAACAA	TCCGATATTCTTCCCGCAGTA	CAGAACTGGATTGCCAATGTA
92249	LOC92249	XM_499179	CTGCACTAAATTCCTTCATTA	AAGTTCCTATCTAATATTATA		
92255	DKFZp434H222(	NM_001007527	AAGGACTTTAAGAAAGATCAA	AAGATTAAGATTATACTTCAA		
92312	LOC92312	XM_044166	CCGCTCCAGGGCTTCTCTAAA	CAGGCCCAAATCGCCACCTCA	CAGGCAAGGCTGCAAGATTAA	ATCCTCGAGTACAACAATGAA
92369	SSB4	NM_080862	CTCGCTCAACGTCTTCGTCAA	CATGGCTGTCACAAAGCTTTA	AAGCTTTATTTGAGCAAATTA	ATGAAGAGCGTTTCTAATAAA
92454	MGC20460	NM_053043	CCCGGTGTAACCATTTATGAA	ATCGAGATCAATGAACCTTTA		
92579	G6PC3	NM_138387	CTGGGAAATGGCCAGAAGATA	CACATGTTCAGTGCCCAGGAA	GTGGCTCAACCTCATCTTCAA	CAGGTGCTGGCTGGCCTAATA
92609	TIMM50	NM_001001563	CCGGACATACAAATATTTCAA	CACCCTGGTCTCGGAATCTAA		
92610	TIFA	NM_052864	TAGGATTATTTACTTACCAAA	CAGAATAATGATTTCTCCTAA		
92714	ARRDC1	NM_152285	CACCAAGAAGTTCTCCTACAA	CCGGTCTTCATTGGCAATATT		
92715	C9orf112	NM_138778	CAGCCTTTCATACTTGTTTAA	CAAGGGTGGAATGGAAGTTAA		
92736	OTOP2	NM_178160	CAGGCAGGCCCTGGTCATCTA	AACGCTCTGGATCCTCTTCTA		
92799	SHKBP1	NM_138392	CAGGGCCTCCTTGGAATAAAT	CCAGCTAGTGTTCATCCAGAA		
92806	MGC16385	NM_145039	AAGCGAGTTCACAAATAGCTA	CGCCTTTAGACTTATCTTAAA	AAGGTGTAATCTCGACCTTGA	CTCGGTTGACTCGCCATCGAA
92815	HIST3H2A	NM_033445	CGGAAATGTCCGGTCGTGGTA	CCGCGGTGCTCGAGTACTTGA		
92822	ZFP276	NM_152287	CGGCATGAAGAAGCACATCAA	CAGGTTAGAAGACATACAGAA		
92999	ZNF651	NM_145166	CCCGAGTGATCTGAGGATTTA	GAGGCTAGCACTAATAGGAAA		
93010	B3GNT7	NM_145236	CAGGAAAGACAACAAATACTA	CTGGGACGTGACCACCACTAA		
93034	NT5C1B	NM_001002006	TTGGATGTTTGTAGATAACAA	TAGGATAAGTTTAGAACTTGA		
93082	LOC93082	NM_138397	CACGTGTATAATGGAAATGAT	CAGAGAGACCATGCATCTGAA		
93107	KCNG4	NM_172347	CCCGCTGAGCCGCCTGAGCAA	CAGCCAGGAGTTCTTCTTCGA	ATGAACGATGTCAATGACCTA	TTGCCTATCATGCACATGTAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
93134	ZNF561	NM_152289	CAGGCTGTGGACCGCAAATAA	CACGCCTAAGTAGACATGAAA		
93145	OLFM2	NM_058164	CGGAATAAACAGGACCTTTGA	CAACGGCTCCCTGTTCTATAA	CACGGACGTGCCCTTCCACAA	CAGGACCTTTGACATTTGAAA
93185	IGSF8	NM_052868	TGGGCCCAGATTGCAGAGAAA	CCGGCATTTATGAGTGCCACA		
94033	FTMT	NM_177478	CAGGTGAAGTCTATCAAAGAA	CCGGGATGACGTGGCCTTGAA		
94086	HSPB9	NM_033194	CAGAGACGGTTTCCAAATGAA	CCCGGAGGAACTGGTGGTGCA		
94097	SFXN5	NM_144579	CCCGCTCGCTGCGGTTGATTA	TAGGCCAGAGGTGAACATTCA	CAGCCGGACAGTGGTGTACAA	CAGGCTGGTAAATTTAGGATA
94104	C21orf66	NM_013329	CATGTTAAGGATACAAATCAA	CAGCATGAGAAACATCTGCAA		
94122	SYTL5	NM_138780	CAGAATTCAATGAAACACTAA	ATGGATTTGGCTGCTATTGAA		
94134	ARHGAP12	NM_018287	CACCATTGTATTGGACACTAA	CAGGGCGTTGCTATTACTATA		
94137	RP1L1	NM_178857	CCGGAGGATACTGCTGATTAA	TTGGATAAAGTTTGTTCTCAA		
94234	FOXQ1	NM_033260	CTCCATCAAACGTGCCTTAAA	CCGATGCTTCACTGTGCCAAA		
94235	GNG8	NM_033258	CTGGCTTTCTGCGAGACGCAT	CAAGATTGCCGAGGCCCGCAA	CAAGACGGTGGAACAGCTGAA	ACAGCTGAAGCTGGAGGTGAA
94241	TP53INP1	NM_033285	CAGAACGATGTTGACCTGTTA	AAGGGACATTTGGTTAGGTTA	CTGGGAGACACTAGTAGTATA	CCGCGTCAGTACAATTACTAA
96764	NCOA6IP	NM_024831	AAGGATCATAGTGAAATACTT	CCGGCCAAAGTGAACCACGTA	TCGCAATAATGCAGAAGTTTA	ATGGAAACTTACAGGACTTAA
112398	EGLN2	NM_017555	CCCTGTAGACAGAGAAACCAA	CCGCATGGCAGACAGCTTAAA	CAGGGAATTGTGTCTGCAGAA	CTGGCTAGGGTTACCCAGCAA
112479	MGC16943	NM_080663	TAGGTGCTTTCTAGAATCAAA	CCCAATATGAGTAAACAGGAA		
112597	MGC4677	NM_052871	CACCAGCCTCTCCTTGAATAA	AAGTTTCAAATTGACATTCCA		
112609	C6orf117	NM_138409	AAGCTGCACACTGGTATTAAA	ACCTATTGTTCTGGAAACTAA		
112616	CKLFSF7	NM_138410	CAGGCTGGTGGGCACCAGGAA	AAGCATATGGCTGTCCTATAA		
112724	RDH13	NM_138412	CCGCTTAAGGAAGGAAGGAAA	CTGGCAGACGAGGAAGTATAA	ACGAGGAAGTATAACACCAAA	AAGTACTTCGATGGACTCAAA
112770	MGC31963	NM_144580	CTGCAGAACCTGCTTCATATA	CAGCACTCCATCGACGATGAA		
112858	TP53RK	NM_033550	TTGGCTCGAATGCACGATGAA	CTAAGTAAAGGTGTTAAGATA	TAAGTTTATACCGCTAAACAA	AAGTATTGGCGTATAACATTA
112939	BTBD14B	NM_052876	CCGGCAGATCTGCAACATGTA	CCAAGTGAGATTGCACATTTA		
113026	PLCD3	NM_133373	GCGGATGAACTCAGCCAACTA	CCGGTTTGTGGTGGAAGATTA	AAGCAAGGGTACCGCCACATA	TAGGTTTGTAACTGTTTCATA
113177	C19orf36	NM_052878	CCCGAGGAGGTGGAACCTCAA	CCGCCACCATGTGAACTTCAA		
113178	SCAMP4	NM_079834	ACCCGTCAAATCTGTGCCTTA	CCGAGCCGACAGCTCCTTTAA		
113230	LOC113230	XM_053966	CCGCAGAAAGGTCTCGGAGAA	CAGGAGGAGCGCAAACCTTGA		
113246	GRCC10	NM_138425	CAGGAGGTTATCAAAGCCTAT	TCCGCTGAACCTAGAGCTTCA		
113451	ODC-p	NM_052998	TAAGCAAATTGCACAGATCAA	AAAGTTTGGAGTGTCACTGAA	CACCTCCAAGACCATCGTGTA	TAGTTCAAGTATGCAACATAA
113510	HEL308	NM_133636	TCGGTATGAGTGCAACATTAA	CAGCATTACTACCATAGGCAA		
113540	CKLFSF1	NM_052999	CCAGCCTAAATGTGACCATAA	CAGCCTAAATGTGACCATAAA		
113612	CYP2U1	NM_183075	CAGCGCTTTGATTACACTAAT	CAAGGGTATACCATTCCTAAA	CCGGAGGATTTCTACCCTAAT	CGGGTGTGTATGGGAGAACAA
113675	SDSL	NM_138432	TCCGACAACTCCGGCCAATAA	CTGCCAGGAGATGGCCAAGAA		
114026	ZIM3	NM_052882	CAGGAACTCTTAAACACTGAA	ATCAATCAACTTGCTAATTTA		
114041	C21orf88	NM_153754	CAGCCTTAATTCTACCTGCAA	TCCCGTCTCTTCCATTCTCTA		
114049	WBSCR22	NM_017528	CTGAGTGGAAGTTATCTGTCA	CCGAGCTGTCCTGCAGCTGTA	CCCTAACAGTGCCAAAGCAAA	CAGGGAGTCTGTGTTCACCAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
114131	UCN3	NM_053049	CCACAAGTTCTACAAAGCCAA	CAGAGGCACCCGGTACAGATA		
114294	LACTB	NM_032857	AAGCCAAATGCCGGAATTCAA	CTGGATCTTGATATTCCAGTA		
114548	CIAS1	NM_004895	AAGGCAGACCATGTGGATCTA	AAGCCAAGAATCCACAGTGTA	TTGATAATTTATATCTCTCAA	ACAGAACTAGTTGACTATATA
114625	ERMAP	NM_018538	AACTAGGTACAGCGACTTTAA	CACAAGACCATTGTACTGCAA	TTGGGAAAGGCTGATGAGTAA	TTGGAGAGTATTGATTTCAAA
114659	LOC114659	NM_052888	CTGAAGAAAGATCTAGCTGAA	TGGGTTCAAACTACAGATCTA		
114769	COPI	NM_052889	CAAACTGGAACTCATAAATTA	AAGGATCTCTATATCCTAGAA		
114771	PGLYRP3	NM_052891	CAGCCACTTCTTCTGAAAGAA	CTGCCAGACTGTCGTCCGAAA	CAGGATGGTGGCGTGTATGAA	CAGACTGTCGTCCGAAACATA
114783	LMTK3	XM_055866	GCCGCCTTTCTCGGAACTGAA	CCGGATGGGTAGACAACACGA	CCGGGAGACAGGACCCAGGAA	GCGGGAGGATGTGACAAGGAA
114788	CSMD3	NM_052900	CTGGTACACCCTTATATGGAA	CTGGCATTCCTCAATATGGTA	CAGGTGTATGATGGACCAAAT	CACGGTTTGCACAATGGTATA
114789	SLC25A25	NM_052901	CACGGTTGCACTTCCATTCCA	CAGGCCTGACTTCCCAACCTA	CAGAGTTATGTCCTAACTATT	GACGTTAGAAGTTGTCATTTA
114793	FMNL2	NM_001004417	CCGGTTTGTGAAAGCATATAA	ATGCAGTTTATTAATATTGTA		
114799	ESCO1	NM_052911	AAGCTACATGATAGAAATATA	TAGGCTGTTAACAAATCTCAA		
114804	RNF157	XM_290732	CAGGACGATCTCGCCTCTTGA	AAGCCTGGTCAATATCCGAAA	AAGCGTGAAAGCACTGGACAA	TCGGGTAGCCATCACCATCTA
114818	KBTBD9	XM_496546	CAGGACAGAATGGGAATTCAA	CCGGTTTGAGTTGTTATATAA		
114823	LENG8	NM_052925	TTGGAGAAGGGTGACCATGAA	CAACGTCTTCATGAAGGACAA		
114836	SLAMF6	NM_052931	CTCCAGTCCTTCGGACTTAAA	CTCCATTGTTTGAGCCAAGAA	CAGGGAATGTAGTTTCACAAA	CACAATTTACTCCACAATTAA
114881	OSBPL7	NM_017731	CGCATTGACCTTGACACTGAA	CTGGCAAGATATGAAGTGGAA		
114882	OSBPL8	NM_001003712	CAGAACTATAATGTGATTCAA	ATGGTTTAAATTAGTTAATTA		
114904	C1QTNF6	NM_031910	CAGCAACAAGTTAGTATTGCA	CAGGAAGACCTGTGCTATAAA		
114971	PLIP	XM_374879	CAGGAGTGGAAGAGACTAGGA	AACCTCCAGAAGGGAGTCCAA	CACCTTGGACAACCTCCAGAA	CAGCTGCGGCTCAGCACAGTA
115330	GPR146	NM_138445	CAGCATTCAGTTTGTCAATGA	CTGGTGTTAAATGGAGCTATT	CAGGGTTCTGAGAACATTTCA	AGCATTCAGTTTGTCAATGAA
115426	UHRF2	NM_152306	CACATACATAGTGTTACTAGA	AAGCGGTACTCTAGAAATGAA	CAGATATGATGGCATTTATAA	CACTATATTCCCTAAAGTATA
115548	FCHO2	XM_291142	AAACATATTAATAAAGTATAA	CGGGCGGGCGCGGACGCGGAA		
115557	GEFT	NM_133483	CAGGACCATATGAGAACTGGA	CTGGATATGTATACAAGAACA		
115650	TNFRSF13C	NM_052945	CCCATGGAGTTTGGTGTGCTT	ACGGCCGGCCCTGAGCAACAA	CTCCTGTTCCTGTGCCTTCAA	CCGGGAATCTCTGATGCCACA
115708	C14orf172	NM_152307	CACCATGAGCTTCGTGGCATA	CACGGTGGAGTTCCACCAGCA	CCGCAGCGGCACGCCCATGAA	CCAAGTGTGAGTGATGAGCAA
115827	RAB3C	NM_138453	AAGGACATTTGCCAACAATGA	GTGGCAAATATGTGATCTTAA	TACAAGATTGGTCAACTCAAA	ATGCAGTACAAGATTGGTCAA
115861	TXNL6	NM_138454	CCGCATCCTGATCCGCAACAA	CCGGCTGGTGCTGCTGTTCTT	AGCCCAGAGGTTCGAGATCAA	CTCAAGGACATGCCAAAGAAA
116068	LOC116068	XM_371760	TAGCAATTAGCTCATAATCAA	AAGGAGATACATTAAATGCAA		
116093	DIRC1	NM_052952	TTCGTTTGTACTCATACTCAA	CAGAGTTTCTCTTGCCCTTAA		
116115	ZNF526	NM_133444	CACGGAAGACTGAAGCAGAAA	CAGAGATGATGGAGATGTCAA		
116143	LOC116143	NM_138458	CACCGGCGTCATTCAGCTGTA	AAGGAGCACCTGAAATTGTGA	AAGGTGTGGGACCCAAGGCAA	ACGGTGGGAGACAAACATCAA
116166	LOC116166	XM_007651	ACCCATGATGCCATACCTACA	AAGCCGAAGCTCAGAGAGGAA		
116173	CKLFSF5	NM_138460	CTAAGTCATTCCCAAATTAAA	CAGGATGTGGCTTCTCATGAA		
116225	ZMYND19	NM_138462	ATGGGAAGGGTAGAAATTACA	ATCATTTGCTGTAATCCTTAA	CACGGGAGTTGTGTCCACAAA	CAGGACGGTTCTCATTATTTA
116285	BUCS1	NM_052956	CCGGAGGAATTTAACTTTGCA	AACATTGGCATCAGAATCAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
116362	RBP7	NM_052960	CAGGCTCACCTGTATCCAGAA	CAGCGACAACTTCGAGGGCTA		
116441	LOC116441	NM_138786	CTGGAGAATAATAACAACTAT	CAGCAATAAACTCACCAACTA		
116443	GRIN3A	NM_133445	CTGAAGAACGATCCAGAGAAA	CAGAGATTACACAGAGCAATA	ACCGACGGAAATACATCTTTA	CACCCAGGGAATAACAACTTA
116447	TOP1MT	NM_052963	AAGCCGGTGTACAAGAACTTA	AGCAGCTAAGATCTTATCCTA	CCAGACGAAGATCCAGGCAAA	GTGGAGAAGATCTACAGCAAA
116511	MAS1L	NM_052967	CCAACGGGCGTTAGCAGATAA	CAGGGTCGATGTGGAAACATA	CACGAATCCCTACATGGTATA	AGGGTCGATGTGGAAACATAA
116541	MRPL54	NM_172251	CAGGCCCTGGAGGCCAATAAA	CCGGATGCTGAGTACCCTGAA		
116841	IMAGE3451454	NM_053052	CTCCAGCATAGTTGAGATCAA	CAGCGGTTTATTGGAAAGCCA		
116844	LRG1	NM_052972	ACGGCTACATCTAGAAGGCAA	ACACCCTGGTATTGAAAGAAA		
117065	PRRXL1	XM_060970	CAGAGAAGAGCTCGCCATGAA	CCGGACGACGTTCACTCTTCA		
117194	MRGX2	NM_054030	CTGGTTAATGTTTAAGTTAAA	TACCAGATTTGAGTCACTAAA	CCGAAGAACTCGGAGCATTTA	ATCAATGTCAACACATATTTA
117248	GALNTL2	NM_054110	CTGGGAAATGATTATTACATA	CTCCAGGATACATAAATTCAA		
117283	IHPK3	NM_054111	CTGAGATACGTTACCCAATTA	AAGACTGGTGGACAAGTGTAA		
117285	DEFB118	NM_054112	CACCAATATGTAATTCTATTA	CAGCTGTGTAAAGAAGTCTAA		
117286	CIB3	NM_054113	TGGCAGCATGCCCGAGCTGAA	ACTCTGGTTTCTGAGAATAAA	CTGGAGCAGACGGTGACCAAA	CACGAGCAGCTGGAAGCGTAT
117289	TAGAP	NM_054114	CAGGAGAGCAGCCAACGAGAA	CTCACTATTCTATGCCTTAAA		
117579	RLN3	NM_080864	CAGGTACATGCTGCTGCTGCT	CCGGTGGAGACGATCAGACAT	CCCGGTGGAGACGATCAGACA	CCGGATGCAGATGCTGATGAA
117584	RFFL	NM_057178	TCGCAACTTTGTCAACTACAA	CCGGCTATACAAGGATCAGAA	ATCGGTTTCTTCAGTGCCTTA	TTGGTGAGAAATGAAATACAA
117854	TRIM6	NM_001003818	TTGAGATGTGCTCAATGTATA	CAGCTGTTGAGTGAGCTGCTA	CTACACTTTCTCTAAATATTA	TAGGAAGTTCTGATCTGTTAA
118425	GDEP	NM_058168	AAGAACTTAATGTGTAATTAA	AGCGATGTGCTGTGAAATCTA		
118426	LOH12CR1	NM_058169	CCCGATGTCATCAAGTTGCAA	ATGGATGATATTGTGGTTGTA		
118430	LOC118430	NM_058173	CTGCAATTGGTCACAACTATT	TCCTGTGATTTCATCCAACTA		
118442	GPR62	NM_080865	TAGGCTCCATTCTGCCATCTA	ATGGGCAGGTGTCACAAAGAA	CTGGACCAGTTTGGTATTAGA	CCCTAAGGGCTCACAACCAAA
118472	ZNF511	NM_145806	CCGGTTTGATAAGCCAAAGAA	CACGGAAATGTTTGCTCCTTT		
118670	FAM24A	XM_058332	CAAAGTAGCTAAGGCACTAAA	ATGAGCAATATTTCTTTCTTA		
118738	ZNF488	NM_153034	TGGCATATTGTTGGTGCATAA	CACATTGTGAGTATATGAATA		
118788	PIK3AP1	NM_152309	AAGTACGACTGTAGTTATCTA	TCCCATGGGATTATTCTCTAT	CAGCAGGGTATTTAAGTGCTA	ATGCTCAAGAGTCACATTAAA
118812	C10orf83	NM_178832	CAGCTGATAAGTATTGGGTAA	CAGGCTGTCTTCTTTCATCAA	CAGATTGTGGTGGAAGTTATA	AAAGGTGTTTATAAAGAATAA
118856	MMP21	NM_147191	ATGGTGAGATTTAGCACATAT	AAGGATCAGGCCCTCACAGAA	CCGCTTATTACTCCTATGCAT	CACACTGAACATGTAATAAGA
118945	LOC118945	XM_497242	ATCCATATGAAGGAAAGGTTA	ATGGACCAAGTGGAAGGCAAA	CAGGAATACAGCCAAGGGAAA	CAGCTTCACAATGGCCATGAA
119016	CTGLF1	NM_133446	CAGCATAGCCTCGGCCTAGGA	CAGCGGGAGTGCGTGGCCAAA		
119391	GSTO2	NM_183239	ACGGCTTGTCTTGGGAACCAA	CAGGAATTCAGCAACCTGGAA		
119764	OR4X2	NM_001004727	CAGGTGTGTACTGTCCTTGTA	CTGGCTGAAAGGAAAGTCATA		
119775	OR52P2P	XM_061677	ACCACCTTACTTGGCCATGAA	CTGCATGCTATCCACCATTGA	CGGCACATCCACATCCTTCTA	AAGCAGCTGTCTTATGGCATA
120105	LOC120105	XM_061864	GAAGATCTGTTTATAAACTAA	CACCCACAACATACTCTGTTA	TACGATGTGAGCATAAGTGAA	CCGATAGATGTGGAATACAAA
120114	FAT3	XM_061871	CACCATGCTCGGAACCTGTAA	TGCAAACTAAAGGAAACTTTA		
120318	LOC120318	XM_497316	GAGGCTAAAGAGAAGCATCAA	AACAGTGGGAACGACAAACAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
120793	OR56A4	NM_001005179	CACACTCTACTACGTCTAGAA	ATCCATTGAGATACCCGTCTA		
120796	OR56A1	NM_001001917	CTGTGATAATTTCACCCTTAA	AAGAGCTGTGCTTAGATTCAA		
120824	LOC120824	XM_062300	AGGGATTCAGAGTTTATCTTA	AAACCTGAATATGGCAACCAA		
120863	DEPDC4	NM_152317	CAGGATATGAAATGATTTCAA	CAGCATCTCTCTGAAACGAAA		
120872	LOC120872	XM_497349	GAGGAGTTAGCTGCATTTAAA	CAGGCTTATTAGAATGAACTA		
120939	FLJ31166	NM_153022	CAGCACAGCCATCGACATTAA	CCGCAGCACAGTGCTAATCTA		
121275	OR10AD1	NM_001004134	CTGGTTCTTTGGGCTGATCAA	CTCAGTTTAGTCTGTGGGCAA	CTGGTTCTTTGGGCTGATCAA	AGCTATGTTCTCTTACATGAA
121278	TPH2	NM_173353	AACGTGAAGCTGCTACCGAAA	ATGAAGTTGGTGGATTGGTAA	CTCAGTATACTTCAATCCCTA	CTGAAATAACGTATTATGTTT
121504	HIST4H4	NM_175054	CAGAATGTCTGGGCGAGGTAA	CAGCTTCTCTACAGACTCCAA		
121506	FLJ32115	NM_152321	AACAACCTGCATAATAAATAA	CTGGTGGACAGTGGTATGAAA		
121512	FGD4	NM_139241	CCGGTATGAGATGCTCCTTAA	CAGAGTCATTCTACCGATAAA		
121793	MGC35169	NM_152324	CAGCAGCAAGTTAGGGCTGAA	ATGATGTAACAGGGACAATAA		
122585	LOC122585	XM_063202	CACATATGTGTTCAGGGTGGA	CTGCGACTCGAGGCCACCCAA		
122664	C14orf8	NM_173846	CTGCGTTTGGAGAATCATCAA	ACGGGAAGAGATGACTGACAA		
122773	KLHDC1	NM_172193	CAGGCTTTATTTAAAGGATAA	CAAGTTATCTCTGAAATTTAA		
123624	FLJ32310	NM_152336	CCAGGTGATGTTATAAATAAA	AAGGAGGATCTTCTTGGCAAA		
123688	LOC123688	XM_058719	AAGACACTGCAGAGATTCCAT	CAGTAAAGATCTGTTGAATAA		
123803	NTAN1	NM_173474	TGGCATTGCTGTCAACATTAA	CAAGAAGATGACATTCACTTA		
123876	LOC123876	NM_001010845	TCCAGCATGACTAGAATATAA	CACCCTTAATCTGGGTAGGAA		
123879	MGC48972	NM_173475	CAGGAGTTATTTATTATCTTT	TAGGTTGAATTAACATTACAA		
124044	MGC26885	NM_152339	CAGGAAATGACCTGACCTCAA	AACACTCAGAGGGACGGTCAA		
124274	GPR139	XM_064062.4	CTCCATCTTCTTCATCTTGAA	CCGCATCATCATGATTCTTTA	ACCGTTAACCATTGACAGGTA	AAGAATTGTCGTGCACCTCAA
124402	LOC124402	NM_145253	AAGAACGAATTCCAAACCAAA	CACCATGTTCTCCCGTCTCAA		
124446	LOC124446	XM_378175	AGCCCTAGAATGGGTGAGGAA	TTTCTCAGGTGTGAATCAACT	TGAAGGCCTTGTGCTGACCAA	GGACAACTGGTCCTTATCACA
124460	SLIC1	NM_153337	CAGTACTGGCAGAACCAGAAA	CTGGCTGCATGGGACCCATAA		
124512	LOC124512	XM_497558	TCGGCAAAGCTGCCAAATGAA	CAGGAAGACATACAGTTGAAA		
124535	FLJ40311	XM_064190	TAGAAATATTACAGAGATCTA	TAGGAATATGAAACTAATTAA		
124538	OR4D2	NM_001004707	CCGGCTGGTTTGAGAGTGACA	CTCACCAATTTGCTTAAATTA	CTGGATGGCGTTATGATTTCA	ACCAATTTGCTTAAATTAGTA
124602	FLJ37300	NM_153209	CGGCCGGGCCAAGAACATTAA	CACCGAAGTCTCCACCATCAA	CCGGGAGAAGTCCTACCTGTT	CCGGGTCAAGAACATCTTGCA
124637	FLJ32499	NM_144607	CCGGAGCATCCGCATCATTAA	CAGGAAGATGGGATTTACAAA		
124641	OVCA2	NM_080822	CAAGGCCTTAATGGACATTGA	ACGATGGTGACTGCCACATAA		
124783	FLJ25414	NM_152343	CCGGAGTTTCACGGAGGAGAA	AACGAGGAGTCTGACTTTGAA		
124808	FLJ31795	NM_144609	AAGGAGCAGAAACATAATCAA	ACCACATTAAATTGTAAATAA		
124817	FLJ40137	NM_173478	CAGCAACATTACAGTCTTGAA	CAGCAAGTGCTTTCATCCAAA		
124930	FLJ25555	NM_152345	CCCAAGTAGACTGGACACAAA	CACCAAGACACAGAAGTTCAA		
124935	SLC43A2	NM_152346	TCGGTGCTAATTCCTTTGTAA	CCCGCTCTACCTGATCTGCTA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
125058	TBC1D16	NM_019020	CAGGGACATCTTTGCAAGCCA	GACGATAGAAACCTAAGGAAA		
125111	GJC1	NM_152219	CACAGCATCCTTGACAGCTAA	CCCGGTGCTGTTCGTCGTCTA		
125206	SLC5A10	NM_152351	ATGGGTGTTCGTGCCCATCTA	CAGCGGGCAACTCTTCATCTA		
125476	C18orf37	NM_194281	AAGGTGTTTGACAAGAAGATA	CTGGAAGAACCTGAAACAAAT		
125875	MGC33839	NM_152353	CACCGTGAAGAATGCGTGGAA	AAGTCTCAAGGTCTCCAGTAA		
125950	RAVER1	NM_133452	ACGGACCTTTGCTGAATTAAA	CCAGCACTCCATGAAGATAAA		
125958	OR7D4	NM_001005191	CTGTGTGGTCTCCTTGTTCTA	CTCAGATTGTCTCCTCCTTAA	CTGCTCTAACACCCTCCTCAA	ACAGATCGTGTAGAAGAGAAA
125963	OR1M1	NM_001004456	CAGGAAGCTGGTCAACAGAAA	CAGCGTCATAATCGCCATGAT		
125972	CALR3	NM_145046	CACGAACATTACTTCAATCAA	CTGGAACTTAACATCACTCAA		
126014	OSCAR	NM_130771	AAGGAGTAGCTGAAAGGAAGA	CCCGCTGTGCCCTGTGCTGTA	CCCAGCTTCATACCACCCTAA	AAGGTAGTAGTGAGACGTGAA
126037	LOC126037	XM_058967	AAGGCCAAGAAGCCTGCATTA	CTAGAAGGCCCTTTCATCAAT		
126074	FLJ35119	NM_175871	CCCAATCAATATGTTGTTTAT	CAGGGACATATGCAGATCCAA		
126119	SBBI54	NM_138334	CTACTACAACCTGGACTCCAA	ACCGGCAACTATGATGTCAAT	CTGGGAAAGGCCAGCACTTCA	CTGCCGCTGCTGCCTCAATAA
126133	MGC10204	NM_153329	AAGCCTGAACACAGAAATTCA	CAGGAGTCTGTGTGGGATGAA	CCGGCTGTCCTGCCTCTCCAA	CCCAATAAACTCTCTGACCAA
126205	NALP8	NM_176811	CAGGAAATGGGTGTTAGGTAA	CTGAGATACTTGGAAATACAA		
126353	C19orf21	NM_173481	CCCAAACTGCCCTGAAATAAA	TTCCGTTTCTATCTTCCTTTA		
126374	WTIP	XM_059037	CACCGTGGACGTGGAGAACAA	AAGGACAAGATTTGACTTAAA		
126402	FLJ40365	NM_173482	CACCTTGGTAGAAATGGCAAA	TTGGAGCTGAAGGAAAGATTA		
126410	FLJ39501	NM_173483	CGGGAGCTGGCCCTAAAGCAA	AAGGACCTGAGTGCAAGTAAT	CTGGACAACATGCACCATGTA	CAAGAGAAGATGAGTGATTAT
126526	FLJ36888	NM_178830	CTGGATCTCAATAAGGAGATA	CGAGGTCAAGGTCACCATTAA		
126537	LOC126537	XM_497611	CTGGTTCATGACTTCACAGAA	AAGGAGTTGTCTGATGAGGAA	CTCAGCCACCATTGCACCAAA	AAGCCGGAGGTCATAATGTAT
126626	MGC29891	NM_144618	AAGGAAATATACAGAAGACAA	CACCAATATATATGCCTTTAA		
126661	LOC126661	XM_059061	TTGGCAGTTGGAAGCTCTTAA	CCGCTAGGAGAGCAAGCACAA		
126792	B3GALT6	NM_080605	CCCGTCTCTCACGTACTTTAA	CCCGCTGCTGCCCGTGTTTAA		
126823	KARCA1	NM_001007255	ATGGAAGCATCTACACATTAA	CAAATGCTTATTAAATTTCAA		
126859	DKFZp686H1423	NM_144696	CCGGAGGACTATTTCAAATTA	CTCAAGATTATTAAACATTTA		
126868	FLJ38716	NM_152367	AACCAAGACATTAGATTTCAA	AAGGCATTGGATCAACACAAA		
127059	OR2M5	NM_001004690	CTCTATGGATGCAATCATTGA	ACTCAGGAAAGTGTTAGGAAA		
127247	ASB17	NM_080868	AACAATGAGTAAATCTACTAA	AACCTCGACTTCACTGAAATA	CTACTGCAATATGGAATCTTA	ACCATCAGGAATCAACTATTA
127281	MGC26818	NM_152371	CACCATTGCAGTGGCCATTTA	CCGGCAGCAACGAGCCATTAA		
127385	OR10J5	NM_001004469	AGGCCTGATATTTATCTCCTA	ATCAATGAGATAATAAATTAT		
127602	LOC127602	XM_059166	CAGGCTCATTTGGGAATTTAT	CCCAATTTAAACATAGAACAA		
127623	OR2B11	áNM_001004492	CAGGTGGTCCTGACGGTGCAA	CCCAAGAGCAGGGCAAATTTA	ACCGCTGTGAATGACACCATA	AAGCCTTATCCTCGGAAGTAA
127670	HE9	NM_172000	ATGGATCATGGTTATGTTTAA	TTGGCTTCATTTCAAACTTTA		
127733	UBXD3	NM_152376	CACCAGGACTTGAGCACATAA	CTGGTAAATAACCACAGTGTA		
128077	MGC46719	NM_153713	CCGATTCATGCTGGAATCCAA	AGCCATTTCAGTAGCACTAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
128136	LOC128136	XM_497739	TTGAGCCAAATGCAACTTTAA	TGGGATAATGCTGCAATCCAA		
128239	IQGAP3	NM_178229	CACACGGACCTGAGCAAGCTA	ATGGTAGGACATGGACCTTGA	GAGCACTAAGACCACCTTCTA	CTCCGTGGTTCCGTTGAAGAA
128312	HIST3H2BB	NM_175055	GCGCCCAAGAAGGGTTCTAAA	TTGGAGAGACTCAGCCATCAT		
128322	LOC128322	XM_060943	AAGAACATCAACGATGGCTTT	CAGGTTTGCCCTGCACAATTT		
128414	C20orf58	NM_152864	CAGCGTCAAGAGAGTTTGTAA	AAGTTGGTAAATAAACAGGAA		
128486	C20orf142	XM_371399	CTGGTAAGACTTGACCTTTAT	AAGCAAGATAGTTACAAGAAA		
128497	C20orf165	NM_080608	ACGGAAGGAATACAGCCGAAA	CTGCTTGTAGATGGATGAAAT		
128853	DUSP15	NM_177991	CCGAAATAAGATCACACACAT	CTGGAGGGTATTAAAGAGACA	CACCACGATTGTGACAGCGTA	ACGGGCCTGGAGGGTATTAAA
128859	BPIL3	NM_174897	CCCGGACTTTCTGGCCATGAA	CTGTAGCTTATCCCAAGTCAA	CCTGGTCAATGTGAAGACTAA	CTGGCTGAGCTGGACATAGTA
128939	LOC128939	XM_066243	CAGCAGGTGTTTGTTGGGCCA	CAACGAGTGCATGGATGGAAA		
128989	DKFZp761P1121	NM_152906	CTGGATGTGCTCAACAATAAA	CAGGAGTAGGCTTGTATTTAA		
129049	RUTBC2	XM_059318	ACGGACTTTGCTTAAATCCTA	CAGGTGAGAATTCTTGAGCAA		
129285	LOC129285	NM_152994	AAGGAAGTTCATGTCAATAAA	AAGGCTAAACTAGAAGTGAAA		
129530	LOC129530	NM_174898	CTCAAATGTTACACAGATAAA	CAGGTTTCCCAGACAACTGAA		
130063	LOC130063	XM_059396	CATGACTTTATTGTCTTTCAA	CAGCAGAACTGTGGACAGCAA		
130162	FLJ31438	NM_152385	CAGAATGGCTTTGACAAATTA	ACGGTTAGATTTAGTTACCAA		
130399	ACVR1C	NM_145259	AAGTGTGAAACTTGTGCCATA	CAGCAAATAGATATTCCTCTA	CACAGAGTAATGAATATTTAA	TACTTTGGTAAACGAGATTTA
130576	LOC130576	NM_177964	CACATTGGACCTCAAGGCGAA	CAGGTCAAACCCTCTTGTTTA	AAGACAAATGGTGTCCACAAA	AACGGTGAACTTTGGAGTGAA
130940	LOC130940	NM_138803	CTGAATGAAGTCAGATGTAAA	CACGAGAAATATTGTGACCAA		
131034	CPNE4	NM_130808	CCGAACTGAGGTTGTGATGAA	CAGCGTCAGAGGAAACTAACA	CACCAAGGAGGCATCGCAATA	AATGTTGATAGACGAAATATA
131096	KCNH8	NM_144633	TCGCACGTTATTTGCCATGTA	TTGGAGCAAATCTATCAATTA	CAGACTTTGGTAACAATCCAA	CAAGACTATCAAACAAATCTA
131118	TIM14	NM_145261	ATCAATGAAGCTAAAGATTTA	TAGAATTTATACACTAATAAA		
131601	GPR175	NM_016372	TACCCTGATGCCCATCTCTCA	CACCATGGTGGATGGACTGAA	TCGGAGGAGCTTCTACGTGTA	CAAGATCCTCTTCTCCTACAA
131616	TMEM42	NM_144638	AAAGCCAGTCATGTAACTCTA	ACGGACCAGCTGGAAAGATCA		
131973	LOC131973	XM_497912	CAGGAAGGTATCCTCCATGAA	CTCGGCCTGCTGCATGCACAA	CCCATCAGAGGCAGCACTCAA	CCGGAGTCCGCGGTTACTCAA
132001	MGC16471	NM_138807	CTGGAGTTTACTACAATTCAT	ATGGTGGTTGGAGAAGATAAA		
132320	FLJ30655	NM_144643	CAGCTGGAAATGGCAAATGAA	AAGGTTGCACAGTGAATTAAA		
132332	FLJ30834	NM_152399	AAGAATGGTATTTGGAATTAA	CAAGATTGTCTGAGAAATGTA		
132671	LOC132671	NM_145263	CAGCTTTGAGATAAATGTTAA	AAGGCTAAGTGTAGAAGATAA		
132789	GNPDA2	NM_138335	AAGCGTGTAATAAATAAGTTA	CTGGCTATTTATTATAAAGTA		
132946	ARL9	NM_206919	CTGGAGATTGGTGGCAGTAAA	CTGGGTAATAGTCAACTAATA		
133308	LOC133308	NM_178833	ACGTACAAAGACTGAGACAAA	GGGCTGTAGTTTGGTCAATTA	CAACGATAATGTGCAGATCAA	CTGCAGAAAGTTGAACATCAA
133396	IL31RA	NM_139017	CTGGACGATCCAGCAAGATAA	TTGGGTGTCTATGATTTCTTA	AAGAATAACGATCCCAGATAA	CGGGACCAGCATAAATTTCAA
133688	FLJ34658	NM_152404	CACACTGACACTTACAATGAA	CTCAATGTAGTTATTTGCTAA		
133746	JMY	NM_152405	TTGGATAACATTAGATCCAAA	ATGGCTGTACTGTCTATTCAA		
134145	LOC134145	NM_199133	CCAACTGTTTGTAGTATCCTA	CACATCTTTAACTAAACTTAT	CTGGGATAATGGTACACATAA	CACCTAGTCTTTGGTCCATAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
134391	GPR151	NM_194251	TGGAAATGGATGATAACCAAA	AGGGAAGGCTTGAAAGGTGTA	CTCCTTCACAATGCTTGGAAA	CCGAGCTACGGCGTACTCCAA
134466	LOC134466	XM_376436	CAGGGTCAGTTCAAGCCTTAA	CAGGCAAGTTGTAGTCATCAA		
134505	LOC134505	XM_068889	CCCAGCAGATCTTCATCTGTA	CCAGGGTATCAACAGGAACAA		
134860	TRAR3	NM_175057	CTGGCAGCGTTTGGAAACTTA	AAGCATCAGGCTAGGAAGATA	TAAGGACTGATTCGTCAACAA	CATGGTGTTTATATACAGTAA
135112	NCOA7	NM_181782	ATGGATATTGACTATATGTAA	CTCCATAGCACTGAAATTTAA	AACAATTATTATACTCCTTAA	CCGGAAATCGGCATCACTAGA
135295	SRrp35	NM_080743	CACAGTCAAGTTCACCTCAAA	AACTCTCATTATGTTAAATAA		
136242	LOC136242	XM_059830	CAGGAATTCCTTATGTGTGAA	ACGGTACTGAACAGACAATTA	ACCAATGTTTACAAATATGTA	CACCATGAAATATGTCTTCTA
136306	LOC136306	NM_174959	CCGCTGGAAGGTTAATCATAA	CGGGCCCTCCAGCAAATTAAA		
136371	ASB10	NM_080871	AGGGCTTGAGTGAAAGGAGAA	ATGGAGGGATTTCCGCTTCAA	CAGCGCCAACACCATGGACTA	CCGGGTGATGTCTGATGAAGA
137075	CLDN23	NM_194284	TAGCTACATATCATTGCATAA	CAGCAGCTTAATGGATTTCAT		
137362	MGC33309	NM_152413	CAGCTTGTTAAAGACCTACAA	CAGCTGTATCAATGCCAACAA		
138050	FLJ32731	XM_372038	ATGGATGTCTTTGGAACTTCA	CTGGACCAACTTGACCGTCTA		
138162	C9orf116	NM_144654	CTGCCATTTCACATCTAATAA	CTCCGTGTACAGGACCAGTAA		
138199	C9orf41	NM_152420	CCGGAAATGCATTGATCATAA	CACAATGTAATTGATTATATT		
138240	C9orf57	XM_059954	TACTGCATTAATTTAATTTAA	CACATTCAAGGTGGCATTCAA		
138428	C9orf115	NM_001002913	ACGGCGGCTTATGAACGCCAA	CCAGGCTGCCTGCGGATTAAA		
138429	PIP5KL1	NM_173492	ATGCTGGAACCAGGACTCAAA	ATCAAGATCATTCAGCAATAA	AAGATGGAACTGGATACCACC	AACGTCTCCACGAGGATGAGA
138639	PTPDC1	NM_152422	AACAGAGGGTTTCAAAGCATA	AGGCTATACATAAGTATTGTA	TACGTAGATACCAGAGGCCAA	CGGAATGTTGAGTGCCTTCAA
138724	MGC41945	NM_203299	CAGGAGAACCCTCAAACTCTA	CAGAAGCTACATGGAAGGATA		
138805	OR13F1	NM_001004485	CCGCTGTAGATTCACAGGAAA	TCAGTGGAAGGTCGAAGTAAA		
138864	LOC138864	XM_498304	TACCTGAGAATAAACCATCTA	TTGGGAGAGCATATCCCGAAA		
138883	OR1N1	NM_012363	CAGGAGTATTGTTTCCTCTTA	CTGCGTTGTTTGTGTGTTCTA		
139105	CXorf20	NM_153346	CAGCGAATTATCCAACTTTAA	AAGGTAGAGAAAGAAATTCAA		
139135	PASD1	NM_173493	ATGTTTGTAATTGTTTGTTAA	CAGCCTGTTTCTTGGAAGTTA		
139231	CXorf39	NM_207318	CAGGTGGAATATATTGAGTAT	TTGGTTATTAATAGAGCTCTA		
139411	PTCHD1	NM_173495	TCCGTGGAGTTTGGAGTGATA	CCCGTGTGGTTGACCAAATTA	AAGGATTTCACAAGAACTAAA	TCCCGGTTTGAGAGCTATTTA
139562	HSHIN6	NM_207320	CAAGACGACAGTAGCATTGAA	TGCGTATAACTTCACCACAAA		
139604	LOC139604	XM_498354	TGGGATCATGATGAAGGACAA	ACCCTTTGACACTGAAATAAA		
139760	GPR119	NM_178471	CAGTCTCTGCTTCACCTTGAA	CGGGCTGTGGTTAGTGTCTTA	CAGGAGTGTCACCTCTACCTA	CTCCCTCATCATTGCTACTAA
140432	ZNF183L1	NM_178861	ATCCCATGCCTGAGTATGTAA	CACTGCAGTATTATTTGCAAA	AACGGGAAGGAAATCCTCTTA	AAGGATCACATGCTACAACTA
140469	MYO3B	NM_138995	ATGGCCGTACACAGACTTCAA	CACCCATTTATTAAAGGAGTA	ACCCTGGTTGATAAATTTGAA	AACCAGTTAAATGGAACTCTA
140545	RNF32	NM_030936	CAGTATCAAACCCGAGTGATA	TGGGTTAAGTACTACAATGTA	CCGCTAATAGTCTGTCCTAAA	TTCAGTGGTATTCAACATCAA
140576	S100A16	NM_080388	CAGGGAGATGTCAGACTGCTA	CACCTGTTCAGTCTCATCTAA		
140609	NEK7	NM_133494	CGGACAATTTAGTGAAGTTTA	CCCATTTATGTCTGGTGTTAA	CCGGATATGGGCTATAATACA	ACGACCGGATATGGGCTATAA
140612	ZFP28	NM_020828	AAGGAAATTATTAAACTATAT	CCGGGCTTGGTGACTATCAAA		
140628	GATA5	NM_080473	CTGGGTTGGATGATACCTTAA	AAGGGCCTTGTTCTAGCTGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
140706	C20orf160	NM_080625	CACCATGGAATATGAAGTCAA	ACCATACTAAACAGTGTAGAA	CTGAGGGTTAAGACCTTAGAA	CACCCGATAAGAGCTCAATAA
140730	RIMS4	NM_182970	GTAGCTCATGTTGAAATTAAA	CAGAGTGGACAGAAAGCATTA		
140766	ADAMTS14	NM_080722	CAGCACCGACTTCTTCATTGA	CACCGGCAGCTTCATCCTCAA	CAGGAGTGTGTGTACACTGGA	CCGCTTGATCATGGTTGGCTA
140803	TRPM6	NM_017662	CACGAGCCTATTGCTCACTTA	AACCTGAAGTCAAACAATCAA	GAGCAGAATCCTGCACATTAA	TTGCCCAATTGCCAAACTAAA
140809	C20orf139	NM_080725	CACCTTCTATCAGAAAGTAAA	ATGGGTATTTATTTGGATAAA		
140823	C20orf52	NM_080748	AACCATGGTTGCCAACTACAT	CTGATGGGCGGCATTGGGAAA		
140862	C20orf82	XM_097736	CCGAGTCACTTCGGTTTCTAA	AAGCGAGTTCTTAAAGAAGTA		
140870	WFDC6	NM_080827	CAGCCTTACTTTATACCATAA	CAGGATTTGGCTCATAATCCA		
140873	C20orf173	NM_080828	CAGGAGGAAATTGTAAGATCA	TTGGATCAGAATAGCAAGGAA		
140876	C20orf175	NM_080829	CACGGAGTTGGGTACCATCAA	CAGGAAGGGCTCCTTGTACAA		
140880	CST11	NM_080830	TAGGCAATAAATGTTTGTCAA	CAGGATCTTCCGAGTCCTTAA		
140883	SUHW2	NM_080764	TCAAATGTTTAAGAAGCCTAA	CAGTGGATGTAGCATCCATAA	TAGCCGTTAGTGGAGAATGAA	CCCAACTTGAATCGAGATCAA
140885	PTPNS1	NM_080792	CCCGAGAAGAATGCCAGAGAA	ACGCCTGTAAATTACTGAGAA	CTCGCTGTGGACGCCTGTAAA	CGCCTGTAAATTACTGAGAAA
140901	STK35	NM_080836	CTACGTGTGAACAACTTTATA	GACTGAGGCTTTGTAAATTAA	TTGGGTTGGTATGATACATTA	CTCGGCTGTTAGGGATCTGAA
142679	DUSP19	NM_080876	AAGGTCATATATACTATACAA	TACGGTCCTCTTTCTCACATA	CAGAGTTAACCTAATGAGTCA	ATGGTCAGTATCACTGGATAA
142686	ASB14	NM_130387	CCGGTTAACTGCCTCCAGATA	AAGGCTGGACATCTACAGTTA	ACGACCTTTATGGACAAGGAA	CTCACTATATATTATAGTAAA
143187	VTI1A	NM_145206	TCCCATAAGAAGATAATTAAA	CAGAGCTTTATGATTCTGTAA		
143379	C10orf82	NM_144661	TTGCATGTCATTAATGATAAA	TCCCAAGGAGGTGAACTTTAA		
143458	LOC143458	NM_174902	CAGCACCTCTAGTTAGAGTTA	CTGCTGGGTAGTTACCTTATA	AAGGGACTATTTATATGTGTA	AACCTGTTTGACGCTAATTAA
143503	OR51E1	NM_152430	CTGGTTCAATTCCACTACCAT	GCCCTAGGTGTCAGTGATCAA	CTCATATCTGCTTATTCTTAA	CAGTTTGATGCTTGTCTGCTA
143872	FLJ32810	XM_370651	GTGGATCTATTCAAAGCTTAA	ACCGGAAATGTTTAAATTAAA		
144106	FAM10A5	NM_153291	CTCTAATTTGAGTGAAATAAA	ATAAAGCCCTGCTGAAGGAAA		
144195	SLC2A14	NM_153449	AGGGAGTCAATTCCTAGGATA	CAGAGAGATGGACAACAGACA		
144203	OVOS2	XM_495917	ATCCAGTGAGATCCAGTTTAA	TAGGCCTGATATTAATAGCAA		
144348	ZFOC1	NM_152437	AAGGAATGTTTAGAAGACCAA	CAGCGCATAAAGGAGATTTAA		
144360	FLJ32894	NM_144667	ACAGGATTTCATACTTATTAA	CTGCAGTAGCTAAGACTATAA		
144631	LOC144631	XM_096642	TTGGAGGCTAAAGGAAGTAAA	CAGCAGTTATTTGGGTGTGAA		
144742	LOC144742	XM_378388	TACGTTGTTGTGGGAGATTTA	CAGGGAATTCACAGCAAACTA		
144809	FLJ40919	NM_182508	CAGCATTATGAGGATTTACAA	CACAATGTCAATATACATTAT		
144962	LOC144962	XM_084990	TTGCAATATTATTAGATTAAA	CAGCAAGGGTATATTTATAAA		
145173	B3GTL	NM_194318	AACCATATTATTGATGATGAA	AAGGAATAATACTGTACATAA		
145389	SLC38A6	NM_153811	CCCATATACTGTGAACTTCAA	AAGGTTATAGTAAATACTTAT		
145414	LOC145414	XM_085138	CTTGGGATTTACAGCAATTAA	CTGCATGATGTCTCACAGAAA		
145501	THSD3	NM_182509	CAGCACCGACTTCTCACCTAA	CAAGAGCGACTTCCTAATCAA		
145645	MGC33951	NM_152448	TGGATGGTTTCTAATAATAAA	CAGAGCCTTGATTACATAGAA		
145660	LOC145660	XM_085200	CCAGCTCATTTGGTCACATAA	CCGGCTGAGGTGTTCAATAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
145773	MGC26690	NM_152450	CAGGAATACTTTAACAATTAA	TCCCAGTAGATTAGACTTCAA		
145790	UNC13C	XM_496070	ATGCAGTAGGAGAACAATGTA	CACTGCAAGCTAAATACATAA	ATGGGAATGTTTAGTTCACTA	CAAGCTGATCTAATACGTTAA
145846	LOC145846	XM_096883	AAGAAATTCATCAGCCTTCTA	CAGATCAGTGGCAATCATTTA		
145853	LOC145853	XM_096885	CCGCTTCTTCACGGCGCTCAA	AACCTCGGTATTCCAACTTTA		
145946	SPATA8	NM_173499	CCCACTGATTCAGAAGATAAA	ATGGTGTATTCTGGATGTCTA		
145978	FLJ31461	NM_152454	CCAGTAATGAATAATCATTAA	CACATGTGTCTTCACATTCAA		
146057	TTBK2	NM_173500	AGGCATCACCTCAAGATGAAA	AAGAGTAAGCCAGCCAGTAAA	CACATTGGTCATGACATGTTA	ACGGCCCAGGTTAAATGGAAA
146059	CDAN1	NM_138477	CAGCATGAGCCCAATGATGAA	CCGGAGGATGGTGACTGCCAA		
146110	LOC146110	XM_018432	CAGGGACTCAGTATGAACCTA	CAGCATTCTATGTGCAAGATA	CAGTATGAACCTACTGTCAAA	CTGCAGTCGTTCCGACACAAA
146167	LOC146167	XM_085347	CGGGCTGGTCATCCTGGGCTA	CGCTGTCTTCATCCTCATGAA		
146310	RNF151	XM_370927	CCGCCTGGAAGTCAAGTGCAA	CAGGGCCAACATACCTTGTAA	AAGGTTGTCCACATGAATAAA	TCCGGTGGCTAGCCAGACAAA
146378	FLJ25404	XM_375333	CCAGTTCTGCACCCACATAAA	GCCCAGTTTATTGGAGAGAAA		
146723	FLJ31882	NM_152460	CAGCACAATTTGCGATTGAAA	TCCAATCATAGTTGAGAACAA		
146849	FLJ32734	NM_144681	CCGCGCCATGAAGAAAGCCAA	CTGGGCGTTAAGGAAGCCCAA		
146880	MGC40489	XM_373742	CCGGAGCTGGCAGGTCTACAA	CTCACTGGTTATAGTGCTATA		
147011	PROCA1	NM_152465	CAGGACGACGCTCACAATTGA	CACAATTGAAAGATGGACTAA	CAGACGTGAGCCGATCATTAA	CAGGGTGGTCAGGGTGCAGAA
147179	WIRE	NM_133264	AAGCTTGGCAGGTATATTATA	CAGAGGATATATCCCAGCAAA	CAGGTATATTATATTTCATCA	CCCGCCTACAACAGAGAGAAA
147199	SCGB1C1	NM_145651	CACATGGAAATGTATCCTCAA	ATGGACTTCCTGCAAACACTA		
147339	C18orf25	NM_001008239	AAGAATCAGAATGTACCATAA	CAGTTTATTCTTGGCAATCAA		
147381	CBLN2	NM_182511	AAGGTCTTAAGGAGAAATGAA	CTGAATCATATAAGTTGGTAA		
147687	MGC34079	NM_152475	AACGTCATTCATCCACATTAA	CAAGAACTTTATGTTATCCAA		
147808	LOC147808	NM_203374	CCCATTGTGGTCCGTCCTTAA	TTCAGTTCTGTTCCTATTAAA		
147945	NALP4	NM_134444	AACAACAAGCTTGGAACATAA	AAGAAGCTAACTTTCATATTA		
147968	CAPN12	NM_144691	CACGCCCTGGGAAGAAAGCTA	GACAGACACAGGAGAAATAAA	CAAACCATCAATTAATATTAA	CAGGGCAGGGTTGCTGAGCAA
148003	LOC148003	XM_086001	TACGTGTGTCTCAATGAGTAT	AAGGTAAATGGTGAATACATT		
148022	TRIF	NM_014261	TACCACCTCTCCAAATACCAA	ATCGGAACAGAAATTCTATAA	CTCCCAGATCTTCGCCAGGAA	ATCATCGGAACAGAAATTCTA
148066	ZNRF4	NM_181710	CACGCGGTCATTCCAACTCAA	ACGGGCCGTGCTGGAAGACAA	CAGCTTTGACTCCACCACCTA	AAGAATAAAGTGGGTTTGAAA
148103	ZNF599	NM_001007247	AAGATTCATACCAGAGTTTAA	AAGAATTATATTAAAGATTCA		
148223	C19orf25	NM_152482	CAGGGTGTCCTGAGTCTCATA	CAGCACATAGACAGCGATGAA		
148252	DIRAS1	NM_145173	CTCGGCCAAGATGAACTACAA	CAGGGTTGTGTCCAACATACA		
148430	LOC148430	XM_042500	CCCTGGAGATCGCGGAGGCAA	CTCCGTGCTGGTGCACCTTAT		
148479	PHF13	NM_153812	CCCTGCCATTTAGGTGCCTAA	CAGCCTGTTAATGAACAGCCA	CAGCTGGTGGTTCTTAGGTTT	ATGGCCCGTGTTCATAACTCA
148523	LOC148523	NM_144697	CAGCTAGGACATCTAGCTTTA	CAGAAGTGTAAAGAACTCCAA		
148545	FLJ32833	NM_152488	ACCGCTGAGAGTGGACAAGCA	CAAGTGTGAAGAGTACAGGAA		
148870	FLJ32825	NM_152492	CAGAATGGAAACCGCACCAAA	CAGGAAGACGAGTGAACCCAA		
148898	LOC148898	NM_001008896	CCCTCCTTGTATATCCTTAAA	ACCCTCCTTGTATATCCTTAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
149041	KIAA2025	XM_086409	CAGCACCTTATCAGCAGGGTA	CTCCATATTCACCTCATCAAA	CTGCAAGCAATTCAGATTAAA	CAGCAAACTTGAACCGACTAA
149095	FLJ32785	NM_152494	AACAGACTCATGGACATTAAA	CACCGTGGAGCTGCAGATCAA	CAGAGACAGTGATGGAATCAA	TACAATGACCTATTGAAGAAA
149466	MGC52423	NM_182517	CCCGGCCAGCTTCTTAATGAA	CAGGCTCTGCACAGTACCCAA		
149478	LOC149478	XM_378860	CACCACAGGCTCGGCGAGAAA	CCCATTGACCTCCAGGACAAA		
149483	FLJ33084	NM_152500	CAGGAGATTCGAGAACTACAA	CCGGCGAGAGGCAGAACTTTA		
149620	LOC149620	XM_086604	AACATTCATAAGTAGGAAATA	CTGCAGAGTACAAGTTGCAAA		
149685	SMAF1	NM_174906	TAGCCACACATGCGCCATGAA	AGGGTGTGGGTCCATATTAAA		
149708	WFDC5	NM_145652	CCAGAGGCTAATTCTGATTTA	CAGAATGAATATTCTTGCAGA		
149709	LOC149709	XM_086637	CAAGAAGTGTTGCTACTACAA	CTGAGCTCTTCTAACACTAAA		
150051	LOC150051	XM_097792	CTGGGATGTATGTTCCTTACA	ACGCTGTGGAAGATAAACCTA		
150142	C21orf121	NM_198078	CCAGATCTCCGTGAAATTAAA	CCCACTGATGGTGGTTCACAA		
150147	C21orf128	NM_152507	CAGGCAAATGTTGGGAAGCAA	CACAAGTGAGTTAACATTTCA		
150159	LOC150159	NM_139173	CCTAATAATACTGCACATGAA	CATGCATACCACAGAATCAAA	TAAGAGGAGTATTGAATGTAA	CTCATTGATCCTAATAATACT
150209	FLJ30473	NM_144704	AACTAAGAAGGTCGTGTTCAA	CCGGGTGAAGTTCTACATGCA	CAGAAGATGCTCAACCCTCAA	AACATGTTAGACATTACCGTA
150244	FLJ31568	NM_152509	TCGCAGCCTGTCCTACAATAA	CTGGCATTTCTTTGATAACAT		
150248	C22orf15	NM_182520	CTGGCTGAGGATGGCAACCTA	CACCAACTCCACGCACATATA		
150291	FLJ35801	NM_153044	CACAGTGATACAAAGAATGAA	CAGGTTAGTGGTACAAAGTCA		
150353	DNAJB7	NM_145174	CCAAACATGTATCTCAATATA	CTGCGGACAATTAGTATTCAA	CAGGTTCAGACTACACAATTA	ACGACAGTCCGGGTAACATAA
150383	LOC150383	NM_001008917	CCGGGAGAACATCAATGCTTT	ATGCAGTTTATTCTACTCCAA		
150696	PROM2	NM_144707	CAGCATCATCTTTGCCGTCAA	CTGCATCTTATAAACCAGCAA		
150709	FLJ25415	XM_371586	ACGGGTATTGTGTATAGGAAA	CTCAATTACATGAACAATTTA		
151011	NA	NM_144710	CTCCAGGAAAGTAATGTTCAA	AAGGTGGATGTGAAACATGAA		
151121	LOC151121	XM_379133	TTGAATGAGTACAGTAATGAA	AAGCAACACATCTAACTTATA		
151242	PPP1R1C	XM_087137	AATGAGTTTAATTGACTTCAA	TAGGATTTATGTTATAGATAA	TTGGAACTGGTTAGTACCTAA	CTCGATCTGGAATTACAGCTA
151306	GPBAR1	NM_170699	CTACCTGTACCTCGAAGTCTA	TCGACCTGGACTTGAACTAAA	CAGGACCAAGATGACGCCCAA	AAGCCTCATCATCACCGCGAA
151313	DKFZp434N062	NM_199336	CCCGACATAGGATGAGGGCAT	CTAACAAGACGCAATGGGAAA		
151443	LOC151443	XM_087200	AAGCAAGGATTCTACATCAAA	ACGGCTTCTAATAGAGCTATA		
151449	GDF7	NM_182828	CCGGCCCTGGTCTCCACTCTA	CCACTTCATGATGTCGCTTTA	GCCGTTGCACGTGGACTTCAA	AACAACGTTGTCTACAAGCAA
151516	FLJ25084	NM_152792	TAGGAGCTCAGTACATGTAAA	AAGGTGGCCAATGGTGCTGAA	CAGGAGCTATCCCACTGAGAA	CAAGCTGCTGTTGATGACAAA
151531	UPP2	NM_173355	CAGAATAGGATTCGAGATTTA	CTCACACTAAATTAAATTCAA		
151636	DTX3L	NM_138287	CAGAGGGATATTTGCCTCCTA	AAGAGACAAGTCCTTACTATA	TGGAATGATATTCACCACAAA	TGGGCAAGCATTGGTAATAAA
151742	PPM1L	NM_139245	CTGTAGAGTCACATATATGAA	AAGCGTGAACCCATATTGATA	CTGGTGGTCTTAGGTCTATAA	CAGGACTACGAGAAAGACAAA
151760	LOC151760	XM_098117	CACCTTCAACACCACCACAAA	CCCACAGTAAACGCAAAGTAA		
151887	URB	NM_199511	TCCAGTAATATTGGCCACAAA	AAGGACCTTATTTGGCATATA		
151963	LOC151963	NM_178496	CTGCAAAGCCATCATCATTAA	AAGGGTAAGAAGGACAATGAA		
152028	MGC34923	NM_144717	CAGAATAATCCTTGAGAGAAA	CACCCAGCACTTGCAAGGCTA	CACGGACAAGGGATGAGAGAA	CTGGAGAAACAGTGTACTATT

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
152118	LOC152118	XM_098163	CAGAGAGAAGTGTAAATGACA	TAGTTGTTTGGTCACAAATAA		
152138	LOC152138	XM_093644	TTCTGCAGAGCTGGACTTCAA	CAGAACAATCTCCCTGGGAAA		
152404	IGSF11	NM_152538	CAAGAGCAGAATAGTACTTAA	AACCATTTCAGTATTGATAAA		
152485	LOC152485	NM_178835	AAGGAGAACACTGGTATGGAA	AACACAGATGGTGAAGATTAA		
152519	LOC152519	NM_207330	CAGAATTTCTACAAACTTTGA	CAGAAAGGTATAATCATGTAA		
152579	SCFD2	NM_152540	TACAAGTTCATTAGTTCTAAA	CAGGCTGTCTTTCACAATCCA		
153297	LOC153297	XM_098350	TCGGTCCTATTAAATAACATA	CTCATTTATAATAGTGCCAAA		
153571	CEI	NM_178569	CCCTGAGATTTGTGTTGTCAA	AACGGCATCGAGGCATTTCAA		
153745	MGC26988	NM_130899	ACGGAGATGATCGTCTTTGAA	AACGAAGAGAACCATGAGCAA		
154092	LOC154092	XM_379434	CCGGGTGTGCCCAGAAGTCAA	AAGCACTTAATCATACTTAAA		
154141	OACT1	XM_371801	TCGACTTGCTATCAAAGTGAA	CCGAATATACATCTTCCACTA		
154197	PNLDC1	NM_173516	AAGCAGAATATCCACAGCCTA	AAGGAGAGGCAAACAAGTATA		
154386	C6orf195	NM_152554	CACGGCCGACTTAGTAATTCA	CAGAGGGAGATTAGCAATGAA		
154810	AMOTL1	NM_130847	TAGGTTTGCAAACAAAGTTAA	CAGGAATGATTTGAACTGATA		
157724	SLC7A13	NM_138817	TACCATTGGTAAAGTCTCCAA	CCCAATCTATCTATACCTTAT	CGGGTTCATTATGGTCTATAT	AAGGTTAAACATATGATAGAA
157813	LOC157813	XM_098828	ACCCGCCATAGCAGTGACCAA	CCGAGAAGCCCTGGAGATAAA		
157869	RPESP	NM_153225	CACGGTGTGTGTGGATTGTCA	CAGAGGATGCTGGATACTGTA		
157983	C9orf66	NM_152569	CTGAGACACTAAATAAATATA	CGGCCTCAAACTCAAGATAAA		
158038	FLJ31810	NM_152570	CAGTAGGAGGATAATTAACAA	TGCGGGAATTATCATGATCAA	AAGGCGTTTCATCACCACCAA	ACCCAGGAGGTTCAACATGAA
158056	AEGP	NM_206920	ACGGCGCTGGCTGCAGAAGAA	CACGACCACACCACAGGCCAA	CAGGCTGCAGGTCTCAGGATA	CTCCACCTGGCTTATTATTTA
158228	C9orf122	XM_379636	CAGACCGAGTGAGCCCAGCTA	CACGCTCAGCCGAGCTCATCA		
158248	TTC16	NM_144965	CTGGTGGACTTCTATGCCTTA	CAGGACCTCACCTACTATGAA		
158399	ZNF483	NM_001007169	TAGAGTTGATTTCCCAGCTAA	CAGGATTTGGGTAAAGTCACA		
158511	CSAG1	NM_153478	CCGAACCAGGAACTCAATCAA	CAGCCAGTAATTCCCAGGCAA		
158835	DGAT2L4	NM_001002254	CAGCGATTATTTCCCTCTCAA	TTGGATGTGATTGAACTTTAT		
158880	USP51	NM_201286	AGGCCTGAGAGGGCTAATCAA	CCAGAGACTAGGAAACGTAAA	GAGGACTTACTCTACAGTGAA	CCCAGAGACTAGGAAACGTAA
159163	RBMY1F	NM_152585	TAGATGTAATATCTACCTTAA	CAGGCTCTTTGTCCTACTAAA		
159371	TMEM20	NM_153226	CTCCATTATTCTCTAAATGAA	ACGCTTTATGTTATACATTAA		
159491	C10orf64	NM_173524	CTGGGACATGCTGGAAAGGAA	AAGGCTGAAGACAGAAATGAA		
160065	PATE	NM_138294	CTGGATCACTTTCAATGAGAA	CTCCATCTTCTGCACACGAAA	AAGGAGGAAAGGGTAGTTTAA	AAGCCTGGAAAGAGTGATGAA
160287	LDHAL6A	NM_144972	AAGAATGTGTTTACTGTGTTA	CAGAAGGAGCTCAAGCTTTAA		
160760	TA-PP2C	NM_139283	CTCAATTCTCAGGGACTTTAA	CCCTCAAAGCCTAGAAATTTA	CACAAATTGTACGTAATGATA	AAAGGGATGGTACAAGTCTAA
160851	DGKH	NM_152910	TGGGAGTTCGATTATCAACAA	CTCCTAGTGCTTAGTGGTCAA	CCGGATCTAGATTCCGTAGAT	CAGGTGGAGTATAATGACATA
160897	ITR	NM_180989	CTCCCATTTAACTGAGTATAA	TCAGTTGACAATGACCATGAA	CCCAATCATAATTAAGCCGTA	ATGCCTCATCTTAATAGCTAA
161003	STOML3	NM_145286	CTCCAGATAATTTATAAGTAA	AAGGCATAGAATATAAATGAA		
161725	C15orf16	NM_130901	CTGGTTCTGGCCTATGATCAA	CAGGACGACATTGCCCAAGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
161823	LOC161823	XM_091156	CAGCTTACTAGTAGCCCTGAA	TCGAAGTTTCTCATCAGGAAA	TAGGTATTTGATAGCAGTTGA	TAAGATAGTTCTGAAAGGTAA
162073	LOC162073	XM_091331	TTCCTTGAAGGTGAACCGTAA	ACCCAAGAATTGGTTCAAATA		
162333	FLJ35757	NM_152598	AAGAGAGAGGTTGTCAAGAAA	AAGCAGAAGATACTACTTTAA		
162394	MGC19764	NM_144975	CAGAGTTAATTCACTATTAAA	TCCATTTAATTTAATAATCAA		
162466	PHOSPHO1	NM_178500	CCGTCCCTATCTATTCAGTTA	TACAACTATAAAGGAGGTGAA	TCGGGTCCGGACAGCCAGTAA	CGCCAACATGTGCAAGCACAA
162494	RHBDL4	NM_138328	CAAGTGGTACTATGACAGCTA	AGGCATGAAGTGCCAGTTCAA		
162605	KRT25D	NM_181535	CTGGGAATTCATCTAAAGATT	AAGACAGTGGTTGAAGAGCTA		
162835	LOC162835	XM_091830	CTGGAACACCTCATCATGCCT	CGCAAGGTGGTTGGCGCTGTA		
162993	LOC162993	XM_091914	CAGCACTTGCTAAACATCTAA	CAGGTATTCCACATACCTTAA		
162998	OR7D2	NM_175883	CCCATGCGTATACATTGTTTA	AACAATTAATCTCCAAGTAAT	ACCAATTACCTGAATAGTGAA	CAGCACGTTGATATACTTTAT
163259	FLJ37099	NM_198459	GTGGGTCTAGATATAAATGAA	AAGGAATAGACTCATCACATA		
163479	FLJ35838	NM_173532	CAGCACTTATCCCAAGACAAA	CAGGGCAACCTGAGATAACAA		
164091	MPRA	NM_178422	CCAGGGAGAGGGAAAGAGTTA	TGGCCTGGATGCAATAAAGTA	TCCTTGGAAGTCCAAACTCTA	CTGAATGGTCTTTGCTAAGAA
164118	LOC164118	XM_089384	CCCTAGCATCTTGGTACCCAA	CAGGCTGGCCAGAACCATGAA		
164153	LOC164153	NM_203412	CAGACCAAGAATAGCAGGAAA	CCCGATGTTCCTCACAGTCAA	GAGGCAGCAGCTGATCAGTAA	CTGCTTGTGCTTCCAGCTTAA
164395	LOC164395	NM_001008409	CTGCATGTTGTGGACATGGAA	CACAGGTTTATTTCAAGGCAA		
164656	TMPRSS6	NM_153609	CCGCCTGATGTTGTTACTCTT	CCGCCTGGGAACTTACTACAA	CACGCTGGGTTGTTACCGCTA	CACGGCCGGGATCACCATCAA
165140	OXER1	NM_148962	CAGGGCGAGGTCTCTCTGGAA	GTCCCTTCCAATATTAATAAA	CCGGGTGGAGGAGACAGGCAA	CCAGCTGATAGTGCCAATCAT
165257	C1QL2	NM_182528	AAGGCCACTCTCGATTCATAA	CCGCATGATCTGGGAACCTTA		
166614	DCAMKL2	NM_152619	CCGCACTATCTACACCATCGA	TACGTGTGTGCATCCAATGAA	CTGAGCTTGACCGTTGCATAA	ACAGATGCTCTGAATCATCAA
166647	GPR125	XM_291111.1	CAGCCTTACTTTGCTCTTATA	CAGGCTTGTATTTAATATAAT	CAGCTTGATAATAGTCTGACA	ATGGATTTGACGGGATCTGAA
166752	FREM3	XM_094074	AAGGAAGGGCTTTATGAGAAA	CTGGCTGATCGTTATGATGAA		
166979	FLJ37927	NM_152623	ACCGCTGAAAGTCATAACCCA	CACTGCTAGGTTGAACATCTA	CAAGGACAACCTATTACCAAA	AAGGAGATTGCAACTGGTCAA
167227	DCP2	NM_152624	TTGGAAATTGTCAAACATTTA	CTGGGTTATCAGAGTAATGAA		
167681	PRSS35	NM_153362	CCGAACCTTAACCAGGGTGAA	AAGGGAGTATCTGTTAGGAGA	TACGGCTAACAGAGACCTGAA	CCGTAGTGAGATCACTTCATA
167838	C6orf198	XM_371849	AAAGACTTCCACTGCAATATA	TGGGTTTCTCTCTCCCTTGTA		
168433	RNF133	NM_139175	CAGTGGAGTGATCATCTATAA	GTGGTTATGATTGGTAACTTA	ACCGGAGATGGCAGCGATTAA	AACGCTATAAGCCTAATGACA
168451	THAP5	NM_182529	TTGGAAGATGAGAAAGAAGTA	CACCATTTAAGATACGTGAAA		
168507	PKD1L1	NM_138295	CACCCTTATGGCATCATGGAA	CACGAATACAGGATGCATTAA	AACGAGTTTCATGGAACCGAA	CAGGTTGACCTCAAAGGTGTA
168544	ZNF467	NM_207336	GTGGATGATTCGGAAGGTGAA	CACCAGCTCATTCACGGCGAA	CCCGCTCTTCTTCTGAGCCTA	CAGGAAAGAGTGGTTATTTAT
169270	ZNF596	NM_173539	CCGCTCGGATTTGTCTTCTTA	CAGCTGTAGCGTTAACACTAA	TACCACTTTGCTCAACCTAAA	CAGCACTTCTATAATAGATCA
169436	C9orf96	NM_153710	CTCGGATCGAATAACGATAAA	CTGCCTGGTGATGGAGTTCAA		
169522	KCNV2	NM_133497	CACGTGATCCATCCTCCTAGA	ACGGAGAATGAGGGCAGCCAA	TACGAGGAGCAGACAGACGAA	CTGGACAGAGGGCAACTATAA
170082	MGC17403	XM_372198	CGGGAGCAAAGAGATGATTAA	CTGACCCATAATGGACATTAA		
170302	ARX	NM_139058	ACCACTCAAGACCAAATGGAA	GACGCCTGATATTGAAGTAAA		
170463	SSBP4	NM_032627	AAACATGTACACTATCATGAA	CCGCGAGAAGTTGGCGCTGTA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
170626	GAGED4	NM_130776	ACAGGCAACCACAGGTTTAAA	CCAGAAGGAGGTGACAGGCAA		
170692	ADAMTS18	NM_139054	AACCAGCATAAAGCAAATGAA	CAGGTTTAATAAGGACACGAA		
171568	POLR3H	NM_138338	CTGGTTCTGTTTGTTTCTCAA	CTGCACATTCATGATCAGAAA		
192669	EIF2C3	NM_024852	AAGGCTGTACAGATTCACCAA	CGGGATGAAATGGCTCATGTA	CTCCTATAGGAAGTATCGCAA	CTGACTGATTCTCATCGGGTA
196051	PPAPDC1	XM_113641	ATCCTTGAATTTGCAAGTGAA	AACAGACAAGACTGAAATTAA		
196264	LOC196264	NM_198275	CACAGTATCAATATTTCATTA	AACCACTTATTTATTGAATAA		
196335	OR56B4	NM_001005181	TACCATTTGCTGGGCATATTA	AGGGTTCATCATGCTCAGGAA	CTCATCATAATCACCATTCAA	ATGGCAGTAGACAGATACATA
196337	LOC196337	XM_113696	CCCATCTTTGATACCTTCATA	CACCTTCATCCTCTCAGATTA	AAGACACAATACGGACACTAA	CAGCTTATTTAAGATCCAGAA
196403	DTX3	NM_178502	TCAGATACAGTTCTCCCTTAA	CACCGTGTGTCTATCCTCATA	CGGCACCATTGTCATCCAGTA	ACCGAATGTCATCACCTGGAA
196463	LOC196463	NM_173542	CAGGCTGATGAGGTACAATGA	CTGGATGAACACGGTGGTGAA		
196743	PAOX	NM_207126	CTGGACACATAAAGCAAGTTA	CACGGAGATGCTGGACACATA	CCGGACTTGAGTCTGAGTTCA	CGGAGATGCTGGACACATAAA
196792	FAM24B	NM_152644	CTGGAGCAGAGGAGCCATTAT	TTGAATAAATGTACACTATTA		
196883	ADCY4	NM_139247	CCCGCCTTCAAATACTATGAA	CCGGCGCAACGAGGATCTCTA	CCCGTAGTAGCTGGAGTTATT	CTCGCCTTCTAAGAACCTCAA
197131	UBR1	NM_174916	CACGTCATATACAGCCTACAA	ATGCAGTAATATGTGACCTAA	AACCCACAATATGGACAGAAA	CAGGAATATTGGGATACTGTA
197187	MGC23284	XM_378628	AAGGCTTTGTGACTAACTCAA	CCCGCCCAGATATAAATATAA		
197258	FUK	NM_145059	CAGAATCATGGCGTCTACCTA	TCCCTATGGCTTAGAGTTGTA	TGGCTTAGAGTTGTAGACTTA	CCGAAGGGAGTTGATTGGACA
197322	LOC197322	NM_174917	CTGGCCTCCCTTAAACCTGAA	CCGGACCTCAGTGGACATCAT		
197358	NOD3	NM_178844	CTGGCTGGGAAGGGCAGTCAA	CAGCTTAGATTTACAGGAGAA	CTCCGGAGACTCAATCTTCAA	CAGGATGATCTCAGAGGCCAT
199692	ZNF627	NM_145295	ACGGTCTAATTTGTGTAGTAA	AACCATGTGCATACAACTTAA		
199897	LOC199897	XM_117152	CAGGACTACTTCATGAGCCAA	CCCACTGGGTTGTGAAATGAA		
199953	RP13-15M17.2	NM_001010866	CAGCAGTGGGTGAGCAGCCAA	CAGCCTCAGTTTGCCATCTAT		
199990	FLJ31031	NM_182533	ATGGATGTGCAAGACCTTGAA	ATCCTTCACTTTAATTTATAA		
200081	DKFZp451J0118	NM_175852	CGCGAGGAGCATATCGACAAA	CACATACTGTGTGGACAATAA	CTGGTGTATCCTTCACATCTA	CCGGACCTATGTGGCAAGGAA
200172	FLJ23878	NM_144990	ACCCATCTGTGTAGCCAAGAA	CTGGAACTTGTGACTGTCAAA		
200186	TORC2	NM_181715	CAGGACTTCATTCACCTCTCA	CCGGCCAATGAGTGACTTCAA		
200213	LOC200213	XM_114156	CCGCTTTAAGCAGGCCACCAA	CAGGGTTATTCTATGGAGTAT		
200312	LOC200312	XM_117224	ACCCACGAAAGTACAAGATCA	CCGCATCTGAAGTTACCCAAA		
200315	APOBEC3A	NM_145699	AAGCAGTATGCTCCCGATCAA	CAATGTATTAATGAAATGAAA		
200350	FOXD4L1	NM_012184	TAGCGTTCCTGCTTCTTGCAA	CCGGACGTTGTTGCAAAGGAG		
200407	CREG2	NM_153836	CAGCAAATCTCTAGAAATTTA	AAGGAGTAGCTTTGACATTAA		
200424	MGC22014	XM_371501	CCGGATCGAGAAGGTCATCTA	CCGGCTCTATGAAACCTTCAA		
200491	LOC200491	XM_117239	AAGACATGCAGTCTCATTGAA	TCCCTGGAGCTCAGAAGCCAA		
200539	ANKRD23	NM_144994	AAGAAGAAACTTGAAAGATTT	CCGGGAGAAGCTGAAATTGGA		
200624	LOC200624	XM_117257	AGCCACCATGCTGACAAGTAA	CAGGTAGTCTGTGGAGCATTA		
200728	TMEM17	NM_198276	ACCATGTTTCTTGACATGGAA	AAACAGTATATTAACCCTAAA		
201163	FLCN	NM_144606	CTCCTTTGCCTGGCTCCTGAA	CGGTCTTTGCTCCTTTACAAA	CAGGCCTGTTGCAGTCTCCAA	CCGGGATATATCAGCCATGAT

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
201175	LOC201175	XM_371057	AAGGGAGTTCCTTACTTACTA	AAGGGAGTTCCTTACTTACTA		
201516	ZSCAN4	NM_152677	AACCAATAAATTTCTGTTGAA	AAGGGATTTCTGAGTTCTCAA		
202018	FLJ90013	NM_153365	AGGGTACTTCCTTGAACATAA	TACCACCAGAATAACCCTTAA	CAGTGTTAACTTTAAGGTATA	TCCGCTTGAATTATTCTGTTA
202020	FLJ39653	NM_152684	CCGCATATAAATGGGCCTTGA	CGGAACCTTATTATTTATGAA		
203054	ADCK5	NM_174922	CTGGGTCCTCCAGGACCTGAA	CTGGGAGATGCTCAAGTTTGA	CCGCTACTTCCTTATGGCTAA	AAGGCCTTTGCTGAGCAGATA
203074	UNQ9391	NM_198464	CAGACCAATGCTGCTGACAAA	TAGCCCATCCATGGAAATAAA	CACCTCGTTGGTGAACTACAA	AGGGAAGAACTCGGTATTCCA
203076	LOC203076	XM_114621	CAGGTGGTCAAGTTCACAGAA	AAGGAAAGAAAGCGAAGGCAA		
203100	HTRA4	NM_153692	TACCTGAAACAATCAATTAAA	ACGATGTAATTGTCAACATAA	CCCGCTCAGGAGGAATTACAA	TAGGCAGTTCTTGGCAGAATA
203859	TMEM16E	NM_213599	TACGTTGATGACGTAAAGAAA	CAGGATCATGCTTGAACTTTA		
204219	LASS3	NM_178842	AACAGTAATGACTACAATAAA	CTGGAGATACCTGGAAATGAA		
204801	NALP11	NM_145007	CAACATAAGATTCGAGTTAAA	CAGCGATATCTGTCAATATAT	GCCAGGTTCAATAATACCTAA	CAGCCATGAGAACGTCAAATA
204851	HIPK1	NM_152696	CGGGCAGTGCTGCTACATCAA	CAGGAGTTCTCACGCAGGGAA	CTGAGCTATGTTTGTAATGCA	AGGGAAGCTGTACACCACTAA
205147	FLJ38377	NM_152698	TCCCAAGTGTTGAGAATCCAA	CAGGAGAGCCTAGGACTCAAA		
205564	SENP5	NM_152699	CACGATTGTGGTCACCTTGAA	CAAGGTTTGCAAGCTAAGAAA	GTGCCTGATTGCCACACTAAA	CAGAACATCGTTCTAATACCA
205655	LOC205655	XM_497917	CTGGTGCTCAGTTGTATGCAA	AATGATGAAGTTGGAAATGAA		
205860	FLJ25801	NM_173553	CACATGGTGTGTGGGATACAA	CAGGTGGCAAGTGGGCATATA	CAGCATGTTCAGAGTACTCCA	CGGGCAGATATCATTCTACAA
206426	MGC26597	NM_152700	AAAGTTGAGGTTATCCTGTAA	CTCTTAGTTTGTAATTTAATA	AGGGTACCACTTATTCTTCAA	ACGGACCCATATACTTTATAA
219402	MTIF3	NM_152912	GAGGAGATATTTCATCAAATA	AAGGCATATAAAGAAACTCAA		
219414	LOC219414	XM_169434	CTGAGTGGATTTGGAAACTGA	AAGGAGCTCGTTGAAATATCA		
219429	OR4C11	NM_001004700	CCGCTTGCACGTCTCACATAA	CTGGATAGGGTCTTTAATACA	CCCTATTTGATTGATCATTAT	TAGGGTCTTTAATACACTCTA
219445	OR7E5P	NM_153024	TTCAAAGTTGTTTACTTATAA	CAGTGACATCAATAACATATA	TAGCGTAAACATCACGACTGA	AACGTTGATGAGGAATAAATT
219464	OR5T2	NM_001004746	CAAGTTTGTTCTAGATTTCAA	CAGGTTATCAATAAAGTATAT		
219469	OR8H1	NM_001005199	CAGATGGCCCTCTTTATACTA	TACGACATTGAAATCATGATA		
219487	OR5M11	NM_001005245	CACCATCGTCTTGGTGTCCTA	AAGACTGTTGAGGAATCTAAA		
219537	CHASM	XM_166203	AAGGAGAAGGCTACTGATGAA	CAGGAGATGACTGGCAGGAAA		
219770	CX40.1	NM_153368	CAGGGTGTCAGGGCACACGAA	CAGGAGGATCGTTTGAGAATA		
219927	MRPL21	NM_181512	AAGGATCTTGTTCGAGTAGAA	CTGATCTTAATTGGAAATGAA		
219928	MRGPRF	NM_145015	GGCGGTGTTCTCCATCCTGAA	AAGGCATTATCAGTGAGCAAA	TAAGGCATTATCAGTGAGCAA	CAGGAGAAGAAAGATCTGTTT
219972	MPEG1	XM_166227	ATGGACGAAGTTGGAGTTCAA	CACCGTGAACTTCAAATTTGA		
219995	MGC35295	NM_152717	CAAGGCTACCACAGAAGGTTA	CCGGAATCCTCCAGAATGGAA	AAGGACAAGGCTACCACAGAA	CGCCTTCAGCGCAGACTTCAA
220001	FLJ32009	NM_152718	AAGCTGCTTGTTCCCACCCAA	CACAGGCAGAATCTTCTATAA		
220032	LOC220032	NM_182833	ATGGCTGAATACTCCAAATAA	AAGGAGTGACTGTGCATATAA		
220081	FLJ32682	XM_495949	CAGATGGAAACTGGTAATTAT	AGGCAAGTTATTCATCACAAA		
220158	GTSCR1	XM_496277	CAGGATAGAAAGACATCACTA	CTGGTTTATTGCTCCTATTTA		
220164	DOK6	NM_152721	ATCGTATGAACAGTTATTTAA	TACGCCAAACCTGGATATTTA	AACCATAATTTGGTGCATTAA	CTGAGCAACATGAAAGATTAA
220416	LOC220416	XM_166971	CCAGTAGAAGTTCAGAAGTTA	CTGACTGTTGATGGGAATGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
220441	RNF152	NM_173557	TAGGTTAGATATAGACACTAA	TAGGATTTATTTGGTATTAAT		
220717	LOC220717	XM_165448	AAACAAGGAAATAAAGGCTTA	CGGGAAGGTCGTGGTGCTGAT		
220972	MIR	NM_145021	CTGCTAGAGTCTACAGAAGTA	TCCAGCGGGATTGACACTCAA	TGGGAATTAGTGGATGCTAAA	TGGATGCTAAATGGCAATTAA
221044	C10orf49	NM_145314	TTGCTTATGGCTTACAAATAA	TACGAGGAACAAAGGAATGAA		
221060	C10orf111	NM_153244	AAGTACCTATGTAGAACCTAA	CAGGGAATCTTGAGCCCGAAA		
221078	NSUN6	NM_182543	CACCACGGATTCAGTTACTAA	CAAGACACTCGTCACTATTAA	CTCGTCACTATTAATTCGGAA	CAGAAGCAGTTTAATGGATTA
221120	DEPC-1	NM_139178	AAGAATCACTATGGAACCAAA	CACGCACATTTGAGATGAGAA	CAGAGAGGATATAACTTATCA	ATCGCTATCATCTTTAGGCAA
221178	SPATA13	NM_153023	CAGGGACATGCTGTACTACAA	CACGGTGATTACAGCAACATA		
221188	GPR114	NM_153837	CGGGCGTGTCTACAACATCTA	AAGCGGCTTTGTTTCAGCCTA	AGGCATGGGTCTCGAATCTTA	AGCGGCTTTGTTTCAGCCTAA
221223	FLJ31547	NM_145024	CTCAAGGTGCATTACCCGAAA	TTCCATTATCGGAGTCAATAA	CCCGCAATCATTAGCTTCTTT	CAACAAGATTTCTTCAATAAA
221241	C18orf20	NM_152728	CTCCTATTAAACATTTGTTTA	CTGGTTTATCAGCCACACTTA		
221261	C6orf184	XM_168053	ATGGAGGACCATTCCCAGTTA	CCCAGATACCCTAGAATATAA		
221357	GSTA5	NM_153699	CACAGAAGGTATAGTAGATTT	CACGACAGTGACAGAGTTTAA		
221391	OPN5	NM_181744	CAGCCTTTCACCATACTGGAA	CAGCCTTTCACCATACTGGAA	CACCGTAACCACAGTCAGGAA	CGCTGAAATAATGACTATCAA
221393	GPR115	NM_153838	CAGGTAAATGGTCTGGTGCTA	AGGCTCTCACTTTAACATTAA	TAGGCTCTCACTTTAACATTA	TAGGAGAATGTTCCCACTATA
221458	C6orf102	NM_145027	CAGCGTTACCATCGATGACAA	AGCGAGAAAGCTACAAATTTA	AAGATTGTCAAGAACCATTAA	ACGGTCCCAACTCCTCTCTAA
221527	ZBTB12	NM_181842	CGGCAAGTGCTTCACACAGAA	CAGCCAGTTCATTGAGCCCAA		
221656	AOF1	XM_173173	AACCTATTTCATCACTCTAAA	TTGGGTGATAGGACACTTTAA	AGGGACTAAATATGACTTTAA	ATCGATGCGGTATGAAACCAA
221662	RBM24	NM_153020	TAGTAGCTAATAAGAGAGTTA	TAGGAGCGTGGCAGTGGGTAA	AAGGTTAATGATAATGTGGTT	AACGATATATTGCTAGTTTCA
221785	ZNF498	NM_145115	AAGGTAAATGGTAATGACTAA	AAGGGTTTCATTTCTGTTTAA		
221830	TWISTNB	NM_001002926	CACATTCATCTTAACATTGAA	CTGGTTGAAGCTGGTAATCAA		
221895	JAZF1	NM_175061	ACGACCTATTAGAGTAATCTA	CAACAGCTAAACAGTCATAAA	ACGCAACTAGTTGGTGCATAA	ATGAGCCTTATTGACAATTAA
222171	LOC222171	NM_175887	CTGGTGGAAATCGCTCACCAA	CCCGAATCACTTGGCAAATAA		
222183	FLJ37078	NM_153043	TACATTTGACCCTGAGGTTAA	CAACATGGAATTTGCAAGTAA		
222229	DKFZp434K1815	NM_152892	AAGGACCAGGGACACAGCTAA	ATGGCAAGGATGCGTCCTCAA	CACAGCTAACTAACTTATTCA	GACGGTCAATGACAACCTGAA
222255	ATXN7L4	NM_152749	CAGGGAGGTTATGAGGCTTAA	CACGCAGAAGTCAGAATCAAA		
222389	C10orf30	NM_152751	CAGGTTGTACTCCATGAGAAT	AGGAAATTAATGCAAATTCAA		
222546	RFXDC1	NM_173560	CACGCAGATTGTGAAGGATAA	ACCCAGTTTAATAATGACAAA		
222584	C6orf143	XM_294139	CAGAATTATGGGTATGATGTA	TAAGATTAACTTGAAGTTCTA		
222642	BZRPL1	NM_001010873	AAGCACTTGGAGGAAGGCCTA	CAGCACTGATCTGGCATCCCA	CCCATTCTACAAAGTCTTATT	CAGAGGAGTGCTGTGGAGAAA
222658	C6orf69	NM_173562	CGGATGCTCATTAGAGGTTAA	AACATTCGCATTGGAATTGAA	TAGCATCACTGTGGAAATTAA	CCGGTCTGAAGTCATCTATAA
222698	C6orf194	NM_001007531	AAGCAGCAGTTCAGATTCCAA	AAAGAGAAAGATGACAAGTAA		
222699	LOC222699	XM_498063	CAGATGCTCTTTCTCCTCGGA	GGAGCTGGACATGAAGATCAA		
222967	LOC222967	NM_173565	CAGAACGAAGATGCCAGCCAA	CCGGACGGCAGCATGTATGAA	ACCGAGAACATTCGTCCAAAT	CTGGATGCTGAAAGACTTTAA
245934	DEFB121	NM_001011878	AAGAAAGTGAAGTATACTATA	CAGGTGCAGAACAACATGTAA		
246176	GAS2L2	NM_139285	CACAGTGTACCTCGTCAGGAA	CCCGTCCATCTACAAGCTGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
246181	AFAR3	NM_201252	AAGACGTGTTAAGTTAAAGAA	CAGACTATTATTCGGCCATTA	CACGTTGTATGATTTCGTTTA	CCCGCTTTGTCTAATTTAGAA
246721	POLR2J2	NM_032958	CACCATTAACAAGGACACCAA	TCCGGAAGAGGCCTCTTATTA		
246777	SPESP1	NM_145658	CAGGTGAAACTGCGATAGAAA	CAGAGGAACCTTATATTGAAA		
252839	TMEM9	NM_016456	CAAGGTCATCATTGTCATCTA	CCGGATGCATATACTGAGCAA		
252884	ZNF396	NM_145756	AGGGAAGAGACTCATAGTAAA	ATGGATGATCATCTTAATATA		
252983	STXBP4	NM_178509	AAGAACTGAACTATTATTAAA	CAGCAATTTATTGAACACTAA		
253143	MGC50372	NM_173566	CAGGCATGGAAGCTACATATA	AAGAAGGAGTTTAGTTTAGAA		
253150	MGC14276	NM_153248	AAGGAAATCGAGCTTAATGAA	CACCCAATTCAACTTAATAAA		
253558	LYCAT	NM_001002257	CAGATTAGATATAGCCCTAAA	CAGAATATTATTAAACAATCA		
253582	C6orf191	NM_001010876	CAGAAATAATGTTAAATAGAA	ATGGCTCAACATAAACTATAA		
253650	FLJ35740	NM_147195	ACGGAGAAACAGCGGATGAAA	TAGGTGCTCAAGGGAAGTTTA		
253738	DKFZp667B021C	NM_001005463	CACGTTTAGTATATTAAGACA	CCGGGTGATCCCGAAAGGTTA		
253769	MGC43690	NM_182552	ACAGAATTTGGTAAAGTTAAA	CTGGATGAATGTAGAGAGAAA		
253832	FLJ25952	NM_153251	CAGCATTGACTTAGAGCTACA	CAGAATGATGCCTTAATCTTA		
253962	LOC253962	XM_172968	CTGGCACAGCCGATTCCCAAA	CTGCGAGAAGAGGAAGCCTTA		
254102	EHBP1L1	XM_170658	CAGGGTTAGAAGCTGATACAA	ACCCGTAAGACAGAAATTATA		
254263	CNIH2	NM_182553	CGCGGGCACGCGAGCGTTTAA	CTGGTGCAAACTTGCCTTCTA		
254439	LOC254439	XM_170659	ACGGAGCTTGATGAAGCCAGA	CACGGTGTCCTGATGAAGGAA		
254786	OR6C3	NM_054104	CACATCCATCATGAACAGGAA	CAGGAATAAGACTATTTCCTA		
254950	KRTAP15-1	NM_181623	TTGGATCTCTTGGTTGTGGAA	CCCGCCAGACTAACTACATAA		
255061	TAC4	NM_170685	AAGCCAGTTCTTTGGGCTGAT	CTGGGTAATTGTGGCCTTGGA		
255187	LOC255187	XM_173160	TAGGATTGAGATACACAGTTT	CAGGCACCTTATATCCTCAAA		
255239	ANKK1	NM_178510	CAACATGATGATGATTATTAT	CTGAGTGTCATCAACCTCCTA	GCGGACGGAGTACGCCATCAA	AGGAGCCGAGATGGAAATTTA
255275	LOC255275	XM_171855	CACTGGAACATCATAAGGGAA	CAGCAGGATCCTGAAGCCCAT		
255324	LOC255324	XM_171078	CACCTAGATGGGCCTCTCTAA	CACAATGAAATGAGAAGATAA		
255620	LOC255620	XM_173132	GCCTTAGTTTACCACTTCTTA	CTGGGCTGTTCTGGACTTCAA		
255714	MGC87693	NM_207341	CAGGATCACACTGGCCAACAT	CCCAATAAACAATCATTTCAA		
255738	PCSK9	NM_174936	TCCCTGATTAATGGAGGCTTA	CAGGTCTGGAATGCAAAGTCA		
255743	LOC255743	NM_198278	CAGGCAAATAGTGTCATCGAT	ACGGCAGAATATATGGCTGTA	CTCATGTATATTGGAGGCAAA	CTGGCTTAGACTAGAGTATAA
255967	PAN3	NM_175854	ATGGCTAAAGACCTTAACCAA	AAGGCAAGTTTACATCACAAA	CCGGATACAGAAATCAAGTAA	TACCTATACTTTGATACTGAA
256006	ANKRD31	XM_293911	TCGGCATGTCATAGAGATTTA	CCCAGTAATCGGCAAATTAAA		
256051	ZNF549	NM_153263	AAGCCTTATGTGTGCAATATA	CAGAAGGTACATATAACAGAA		
256076	FLJ35880	NM_153264	AACAGTATACACCAAATGAAA	CAGCTTGGGAGAATACATAAA		
256112	ZNF37B	XM_497219	ATGGGAAATCTTATGCATGTA	CACCTGTGAAGCCAACTATAA		
256130	MGC42090	NM_152774	CAGAAACATTCTAGTACAATA	CTGCTTTGATGTATAGTTAAA		
256144	OR4C3	NM_001004702	CTCCTTGTCTTTATAGGCAAT	TGCAATTAGTTCTATTACTTA	CTCCTACATTGTCATCCTGTA	CTCAGTGACCTTGGAATCTAT

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
256236	NAPSB	XR_000169	CCCGCTGGATGTACTGGTGGA	TGGGACCAAGTTTGCCATTCA	CCGGTGCTCAGAAATCCCAAA	CAGGATTACGTCATCCAGTTT
256309	MGC33607	NM_152775	AAGCAAGTATTTATAAGAATA	AACGAGAATATTTAAGTTTAA		
256356	MGC40579	NM_152776	TCCCTGGATATGACCAGAATA	AACAGTGTTAGGGCAACTTAA	TACCATCTTGTACGAGCAATA	CAGCCAATGGGTGTAATTTCA
256453	LOC256453	XM_172917	ACCTCTTGCCTTTCATTTCAA	CAGGCAAATTCCACAAACATT		
256472	MGC33486	NM_153266	CAGGAGAAGAAGCTTCCAGAA	TTGGAGGAAGTGGAAGCCTAA		
256892	OR51F1	NM_001004752	CAGCGTGATCCTGTTTGTCAT	CACGTGAAATCAGTCTATATA		
257039	LOC257039	XM_172230	TCGACCTACAGTTGAGATAAA	AGGAATCAACAGAGAATGAAA		
257169	C9orf43	NM_152786	AAGAAAGAACTCGGCAGTGAA	CACGGAGAGACCAAAGATGAA		
257177	LOC257177	XM_170909	CCGGATCACTTCCATCGCTGA	CACCTTGTGTCAAGAAGGCAA		
257202	GPX6	NM_182701	AGGGCTAGCGACTGACAGAAA	AACGGCGAGGAGTACATCCAA	CAGACTATCCTGTGTCCCTAA	CCCGAGAAGTTGTGACATCTA
259249	MRGX1	NM_147199	CAGGAACGCCTTCTCCATCTA	CTGATTCTGCTTGGTGTCAAA	CGCCTTATATATTCCCTGTTA	CACGTGGACAGGGAAGTCTTA
259285	TAS2R39	NM_176881	AACATACTTGTCTGAGATCAA	ATGGCTATACATGCAGCTGAA		
260293	CYP4X1	NM_178033	AAGCCGAGTGTTGAATCAGTA	TGGGATGTATTTGCACCTGAA	CACCAATAGACTTTCATATAT	ATAGATGTGATCATTCCTATA
267012	DAOA	NM_172370	CAAGGAAATAACTTCTACCAA	TTGCAACTCTCTGGTCAGTAA	AGGCATTTACAGAGATCATTA	AAGAGAGACGGTAACAAGGAA
280636	C11orf31	NM_170746	AAGTATTTGAGTAATAGAGTA	CTGGTGATGTTGGAACATTAA		
282617	IL28B	NM_172139	CCGGGCCTGTATCCAGCCTCA	AGGGCCAAAGATGCCTTAGAA	CTGCCACATAGCCCAGTTCAA	CAGGCCTTTAAGAGGGCCAAA
282969	C10orf125	NM_198472	ACGGAGTACGAGTCCATCCTA	CTGCAGGGAGACGGCCCTCTA		
282973	C10orf39	NM_194303	CAGCAGAGAATTAAAGAGTTA	CAGCAGAATTCAAGTATTTAA		
283008	FAM22A	NM_001009610	CCCTATGAATGGAATATACAA	CAGATTTACATTGGTTTCTAA		
283092	OR4C13	NM_001001955	AAACAAGACTATCTTATTCAA	CAGCATGTTTGTAGCCTGCTA		
283117	LOC283117	XM_210184	CACCCTGCGAGTCTTCCAGAA	ATAGTTATTGATTCTGACAAA		
283130	LOC283130	NM_182556	TCCCGCCAGGGTTAAACATTA	CACGCCCTTAGACGTGATCAA	CCCGGCTGCCTTCACCTCTTA	GCGCTTCTTCAGAGTCATTAA
283135	FLJ90834	NM_173578	CCCGATTGTATGCTCCATCTA	CAGATGATCAATAAATACTAA		
283140	LOC283140	XM_498528	CGGCACCATCTAACACATTAA	CAGGCAGTCAGCACAAATTTA		
283149	BCL9L	NM_182557	CACCTACTTCTTATCAAAGAA	CAACATGAACATGAACATGAA		
283150	FOXR1	NM_181721	CCCTTCCTCTTTGATCTTTAA	CTGGATGTGGGTAAATCCCAA		
283155	LOC283155	XM_208545	CTCCTTTACAACCATACTTTA	CTGCATTTGATAGCAATGTAA	AAGAAATGTTATAAAGTAGAA	TTGGAACGGATGAAGCATTTA
283162	OR8B4	NM_001005196	CTGAATGACTTTGTTTCAGAA	CAGGGACATTCACCTACTTAA		
283177	LOC283177	XM_378327	CAGGAGCAAGGGTGTCATTTA	AAGGCGCTGTTTCTTAACCAA		
283189	OR9G4	NM_001005284	ACCCATTGCTTTATTCAGGTA	CACAGACTATACAACCACAAA		
283197	MGC39681	NM_174939	CACATTGTGTTGAAAGAAGAA	ATGGATGAATTTAAACAGTTT		
283202	LOC283202	XM_208563	CAGATCACTTGTCCTCCTCAA	AGGCTGTAAGGTCATCGTATA		
283209	PGM2L1	NM_173582	AAGGATTAATGCCAAACTAAA	CAGGTATTAATTTACAAATTA		
283212	FLJ33790	NM_173583	ATGGCTGATGCTAATAATAAT	CAGGGATAGTTTCCAGCTCAA		
283237	MGC29649	NM_173810	ATCCATCTGTTTATTTCTATA	CTGGGCATGTTTGGTTAACAA		
283238	MGC34821	NM_173586	CACCGTTGACTTATCAGGAAA	CACAATAAATTTATCTACATA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
283259	LOC283259	XM_208061	TTGAATTGCATTCTAATGTTA	CAGGCCCTGTTTCTACCTCAA	TTGCATTCTAATGTTATTAAA	ACGAATCAGAATGGCAATATA
283297	OR10A4	XM_208604.1	CACCTCTGTGTTTGAACTGGA	CACCATGGCATATGACCGCTA	CTCAAGGAATAAAGAAGTGAA	ACCATTTACTTGGTTACTTTA
283377	LOC283377	NM_207344	CAGGCCTTTCTCAGACTGTAT	CAGCTTTGTTTGAATTTATTA	AAAGCTAGGCATACAGCCAAA	TACCAGATGGCTGAAGAGTAA
283383	GPR133	NM_198827	TCCGGATGAGATCGCCATGTA	CAAGGAGGGCCTGAAAGTCTA	CAGCATGCACTACTACCTGAA	CAAGCACAGATTGACACGTAA
283389	LOC283389	XM_211009	TGGCAAAGGTTTGGTGAAATA	ATCAGGTTGCTCAGCAATGAA		
283440	LOC283440	XM_211040	TACAATGTTCAAGATAGAGAA	CCGGTACTCATAAACCTTCTA		
283455	KSR2	NM_173598	CAGGCTTACCGTGGACGCCTA	AAGGAAATCCATTACTTCAAA	TCCGTTGTGAGGGATGCCAAA	ATCCGGTGACCTCGAATCCAA
283483	LOC283483	XM_378431	CACACAAAGCTTTCTCTTAAA	AAGGTGGATTTGGAAGAACAA		
283551	LOC283551	XM_378455	CACCTTTGTCTTACAGTTTAT	CCAAATAAATACATAATACAA		
283553	LOC283553	XM_211086	CTCACTGGAGTTGACCATCAA	AAGCAGGAACTTAATTTAGAA		
283579	FLJ25976	NM_174943	CCGCAAGATGCTCACGCGAAA	CCGGAGGGTATGGGAAGAGAA		
283600	C14orf68	NM_207117	ACGCTGCACCTGCCACTTAAA	CAGGATCCAGACGGAGCCAAA	TTGGGAACTGTTGTCAATAAA	CACGGTGAAGGTCAGGATCCA
283601	C14orf70	NM_001007560	AAGGATGTGACTCTCCTAGAA	CCCAGGCAGATGAAAGCTTAA		
283659	FLJ25756	XM_370866	TAGGAAATGAAGAATCTTTAA	CAACAGTAAATTGGTAATTAA		
283677	LOC283677	XM_208778	CCCAGGGCAACTGAAAGTCAA	CTGGCGGGTTTGAGAAATTAA		
283685	FLJ36144	NM_182561	CACTGTGTGAATATAGTCTGA	TCCCTCCAAAGTTCTTTGTAA		
283694	OR4N4	NM_001005241	ATGTGCACCACTCGTGTCATT	CACCACTCGTGTCATTATTAT	TAAGCTGGCTTAAGAGATCAA	AAAGATGCTAACGGTAGCATA
283761	LOC283761	XM_378542	CCCACAGGGTTTGAACTGTAA	CCCAGTCAAGTTGACCTGTAA		
283777	FLJ39743	NM_182562	AAGGGTCCAATTGACTAGAAA	TAGGATGAATATGGACTTTGA		
283848	FLJ37464	NM_173815	CCCACTGAAAGTGGCCAAGAA	CCGTATGATGGACATAGTTCA	AAGAGTGGGCATGAAGCTCAA	CAGGTTGTGACATGGAGCAAA
283902	LOC283902	XM_211251	CCCATGCTAGTTGCAGAGAAA	CAGGACATTATCTCACCATAA		
283933	MGC46336	XM_290712	ACCGCATCTCTGTGAAATAAA	CTCCTTTCCCTTATACATTAA		
284029	FLJ34790	NM_173621	CCGCCCGTTATTGCTGCTCAA	CAGCGACACCATGATGATTTA		
284040	FLJ36674	NM_173622	TAAGAAATCAGTAAATATTAA	CAGGAAGGGAATACAAAGGTA		
284058	LOC284058	NM_015443	CAGAAGAATTGGAGAGATTTA	CAGGTTGAGAGGCATATACAA		
284067	LOC284067	XM_208990	ATCCAATATATCAATGATGAA	ATGCATGTGAATATACAATTA		
284069	MGC34829	XM_208993	CCGCCCTGGCTTCCTCACCAA	CCCGCAGGAGATCCTGATCAA		
284076	FLJ35808	NM_173623	CCAGTTGGTCTTCATCTCCAA	CTGGGAGAGTCCGAACACAAA		
284086	NEK8	NM_178170	CCAGTCGGGTGTGACCATCAA	CAGGAAGCTCAGCGAGTTGTA	CCAGAAGCTGGTGATCATCAA	ACGGACAGTTGGGCACCAATA
284111	SLC13A5	NM_177550	CAGGAGTCATAATGAACATAA	CAGACTGAGGAAGAAAGGAAA		
284114	FLJ36878	NM_178518	CACCCTTACTGCTTCCCATAA	CTGGACGGCACTGAACTGCAA		
284119	PTRF	NM_012232	CAACTTTAAAGTCATGATCTA	GAGGAAAGATTGAATCCTAAA		
284121	LOC284121	NM_001007533	CACGATGGACTGAGCCAGCTT	CGGGACCGGATACATTATTAA		
284131	FLJ35220	NM_173627	TTGGCCAAGGTTAGCGATTAT	TGGGTCTAGGATTCTCAGTAA	ATGGGTGAGAGTTGAAATGAA	AAGAGAGAGATTGGTGTTAAT
284134	LOC284134	XM_211345	TCCATCTGGACTAGCAATAAA	AAAGGTATTGAATGAATTGAA		
284185	FLJ39421	NM_178519	AGGGAGGGAGATGGACTCGAA	AAGGGCTATGGATCTAAATAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
284186	FLJ38792	NM_178520	CACACAAGAGTTCCCTTTCAA	CCCTGCGGGAATTCTATTAAA		
284207	METRNL	NM_001004431	AGGCCTGACCCTGGTACCGAA	AACAGGTGCTCTCATCGTTAA		
284222	C18orf58	XM_290817	GTGTCTTGCAGCAGACTTAAA	AAGTCTGCCAGTGCCTATTAA		
284230	LOC284230	XM_208185	AAGAGAATGCTGGCTATTAAA	CCCACCAGACTTTCTGTAAGA		
284266	CD33L3	NM_213602	CCCAGGAGTCCAATTATGAAA	ACGCATTAGCTTGAGCGTGAA		
284269	LOC284269	XM_209097	CAGGTTTGTGGTGGGAGAGAT	CAGCAGCTCTTCACAGTCTCA		
284273	ZADH2	NM_175907	ACCCGTAGGTACCGTCCTTAA	AACGCTTACATTCAATTCTTT	ACGCTTACATTCAATTCTTTA	TACGATGGTCTCAACACCTTT
284293	LOC284293	XM_209104	AAATGGCACATTTGCATTAAA	GTGGCAAATTCTACCAAGCAA	CAGCTAGACTTTGTGAATGAT	AACAACTATGCAAACATTAAA
284296	LOC284296	NM_175908	CAGGATTTCATTCAAACATGT	CAGAGACATCCTCTACTGAAA		
284312	ZSCAN1	NM_182572	CACACCAAAGGTGGTACCCAA	CCCTTGGAACCTAACAGATAA		
284352	LOC284352	XM_113978	CGCCACGGCCCTGAAGATGAA	CTCGACTGTCTGGACCTGAAA		
284353	NKPD1	NM_198478	AGCCGTGGACATAGCTTCCAA	CAGGGTATACATGCAATAAAT		
284361	LOC284361	NM_175063	CCGGGATGTGGCAGCCCTGAA	CTCCCTGTAAGTCTATTTAAA		
284393	LOC284393	XM_209178	CCGAATTTGTGCCAATAAGTA	ACCAAGTTCAATGCTGATGAA	CCGCACCAAGCTGCAGAACAA	CCCGTTGTTACCGGTATTGTA
284397	LOC284397	XM_209180	CAGGAGGATTAATAGGTGGAA	TCCCATGAGTATGTAGCCATA		
284427	MGC34725	NM_173637	AAGAATTACTTCTGTGGAATA	CTGGGTCAGAAGATTCCTGAA	ATGCATGACAACAACCTTGAA	AATGGTGAACATGTCACACAA
284475	LOC284475	XM_378886	TGGGATTTGGTGAGAATCTTA	AAGGGCAAACTTGAAACATAA		
284485	FLJ36032	XM_371311	AAGAAGTAGAGTGGCTCATAA	CAGACTCGGATTGCTAACGAA		
284498	DKFZp434E141C	XM_209234	CTGGCTTTACAGCAGAAACAA	CTCAGCTTTCTTATCTTTATA		
284593	FAM41C	XM_496333	GAGGACCTTGTGCATGAATAA	TGGAATGAAATGAATTCTCTA		
284610	KFZp434D177-like	XM_371388	CAGCTGAAATGGCACATTCTA	CAGGGCTGTCATCAGCATCAA		
284672	LOC284672	XM_208234	GCGGCAGTTGTGATAAATAAA	AAGCATTTAAATGAAATTGAT	CTGGAGAGAAGTGGACTCCAT	CAGCTTAGGGAAAGAGAGCTA
284988	LOC284988	XM_209429	CAGGGTCCCATTCGGCCTCTT	TTCCGGTTAATTGTTCTGGTA		
284992	FLJ39660	NM_173646	TACACTGAACTTTCACATAAA	AGGATTGTTGTTAATAATATA		
285033	LOC285033	XM_379111	ATGCCACATGATGAATACATA	CAGGTTTCAGATCCCAAGCTA		
285095	LOC285095	XM_211764	CCGGAGGGTCATGGAGAAGGA	CACAGGATCTTCATCATGGAA		
285188	LOC285188	XM_209505	CTGCCTGAACCTCGACTCCAA	AAGGAGCAACTGGACCAGGAA		
285189	PRGA	XM_376111	TGGAGGTTTCTTGAAGACCTA	AAGACCTAGAACATAGAAGAA	CAGAGAAGAATGTGCAGCAAA	ATGAAGATACGTGAAATTCAA
285195	SLC9A9	NM_173653	TACGATATGCTACAGCACCAA	TCGGCTCTTCAGAATGTGGTA	AAGGGAATGCCCAGCTATTTA	CCACTGTTTGTTAGGCCTTAA
285220	EPHA6	XM_114973	CACTGTTTATGTACTCATGTA	CACGTGAATTACACCTTTGAA	AAGGGTTATTTCCGAGCTGAA	CAGGTATGTAATGTAATGGAA
285248	LOC285248	XM_211816	CTCGCAGAAGTTATGGAGAAA	CAGGAAGTATTTATTGTGAAA		
285267	ZNF619	NM_173656	AAGGGAGGAGATAGCCAGGAA	CAGCTAAACATTTCTAAAGAA		
285268	ZNF621	NM_198484	CAGGCTGAACTGTCACTTTAA	CAGCATAAACTCTATGGTTAA		
285296	LOC285296	XM_208312	TGTGGGCAGCTCCCTGAACAA	CTGGGCTGTTCCGGACTTCAA		
285307	LOC285307	XM_211837	TGCCATCTAATCTAACTTCAA	CACGGAATCAAAGAGAACTAA		
285313	IGSF10	NM_178822	CACCAACAAACTATTATTAGA	AAGCAGAATCACAGTCCATAA	ACGCATCAATTTAGGATACAA	CAGGCGTATATCACTGTATAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
285326	LOC285326	XM_211843	CACAAGGACCAAACATATGAA	CAGATGGGATCTCAAAGCCAA		
285335	SLC9A10	NM_183061	AAGCCTCATCAGTTTAATTAA	AAGTTTGTTCCTAAACATAAA		
285362	SUMF1	NM_182760	TTGAGTGATACTAATCATGTA	CAAGTGAAGACCAATATTCAA		
285386	FLJ41238	NM_198485	AACAATGGGATAAGCATTTAA	AAGGATGACTTCCAAATTTAT		
285412	LOC285412	XM_208319	CAGCTGCTACTGTTGCTTCTA	AAGCAGAAATACCAGTGGTAA		
285453	LOC285453	XM_209616	CAGCTGCTTCAGACTACCAAA	ATGGATGAGGATGAATTGGAA	TGGCAGCTACTGCAAGGTTAA	GACATTCTTAATTACAGGTAA
285521	FLJ38991	NM_173827	AAGTATTAGAATAGAACCAAA	CTGGCAATTCCTAGTTAATAA		
285643	LOC285643	XM_209695	CTGCCTGGATCTATAAATGCA	CTGAGTGAGCACCGCCACAAA	AAGGAAGGTATTGCAGCTCGA	GCGGTAGAAGAAGAAGCTCAA
285671	LOC285671	NM_178532	CTGGATCATATGGTAAGTATA	AAGCAAGGAATTGATAACTAA		
285676	ZNF454	NM_182594	CAGGGATTTCAACCTAGCAAA	AAGAGTTCAACTCTTAATAAA		
285692	LOC285692	XM_498992	CAGGAACTCCTTCATAGATGA	CCCAGCCAAGTCAGCATATAA		
285703	LOC285703	XM_209728	ATGAGAGTGAATTCTGAAGAA	CTGGTTGAGCACTCTATACAT		
285733	LOC285733	XM_379432	CTGCACTTGATTACAATGAAA	CTGCAGCATCTTACTACATAA		
285741	LOC285741	XM_209741	CTGCGCTTGCTGCAAGCTTCA	CATGTTATGTATGTTGTCGAA		
285759	FLJ34503	NM_173673	ATTGATTGAATTAATGTTTAA	CAGACTATATTTCATCAGCAA		
285761	DCBLD1	NM_173674	CACAATGACATCTAAGAATTA	ACCGATTAATCTAGAGATAAA		
285770	LOC285770	XM_209753	AAGGTATTGGTGCCTATGAAA	CTCCTGCTATCTTTAAATCAA		
285830	FLJ35429	NM_001003807	ATCTATCATATTAGAAATCAA	AAGGAGAAGAATGACTATTTA		
285940	LOC285940	XM_376585	CTGCATCATCTTTGAGTACTA	CCCGGATGATCCGAAAGACAA	TACAGTCTTTGTGAAATGAAA	GTGAATATGTGAAACAGTAAA
285966	FLJ40722	NM_173678	CTCCTAATAAGTGTTCCATAA	CCCTGGTAACATCATCCTCAA		
285973	NOS3AS	NM_173681	CAGCTCTGGCACAGTCAAGAA	CAGCCTCACCTTTGCTCTCAA		
286094	LOC286094	XM_212170	AAGAATGGACTCTTCTATTAA	CAAGCTGTTTATAAACTATAA		
286122	FLJ37131	NM_173687	AACCATACTGTTAGTCTATTA	CTGGCTTTCCATGACTACCAA		
286183	FLJ39630	NM_173688	CACCGATCTAATGACATTCAA	CAAGTAGTTATTGAACTTCTA		
286187	LOC286187	XM_209936	AAGCATTCTGTTTCTGGAGAA	AAGCAATTCACTCATAAGTAA		
286204	CRB2	NM_173689	ACCGGAGGAGAGACTCATCTA	CAGGGTCAGTTTACTAAGTTA		
286207	C9orf117	XM_209941	CGGGACCAGCTTCCTTAGCAA	CAAGGAGATGAAGGAGTTCTA		
286238	LOC286238	XM_379684	CTCAATGAATATAGAAGGGAA	CAGCCAGGATTCAAACTATAA		
286262	C9orf75	NM_173691	CACAGTGGTGCCCAAGAGGAA	CTCCTCAAGAAAGAAGATGAA		
286327	LOC286327	XM_497054	ATCATTCTCATGAGTCGCAAA	CTGTATATCTGGAATGTTTAA		
286336	C9orf59	NM_033387	CAGCAGAATCCTTATTTATAA	AACCGCATAATTATTCATTAA		
286423	LOC286423	XM_210042	TAGGCAGATCTCCGTGAAGTT	TTGTACCAACGCAATGAACAA		
286453	dJ341D10.1	NM_001007535	TACAAAGACCAGTGAATTATA	TTGAATTCTATTAGTATGTAA		
286561	LOC286561	XM_210515	CTGGGCCAATGTTGTATCCTT	GAGGGAGGAGGCAACCTTGAA		
286749	SALF	NM_172311	TTGCTACAACATCCAGCCTAA	CAGTCTAGGTTCTACATCTTA		
286753	TUSC5	NM_172367	CAGCATTACCCTCATCATCAT	CAGGGAGAGGACAGAAATGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
286826	LIN9	NM_173083	TTCCTTTAGATGTCTCATAAA	TAGGCTTCCAACACCAAATAA	ACGAGTGGTTCTATTCAAATA	CCAGTAGAATTTCTTATCCAA
286828	CSN1S2A	XM_379270	CCCATTTAGAAGAACATGTAA	CAAGAAGAAACTGCAAATAAA		
317702	VN1R3	NM_174980	TAGCACAAAGACAAATGATTA	CCGATTTATGTGGATTGTCTT	CTGGCAAGTGGAACAGCATAA	CTCAGTGATATTGGATGCAAA
317781	DDX51	NM_175066	CAGGAGAGCCTCGTCCAGAAA	CTGGAGGAGTCTGTCAAGGAA		
326340	ZAR1	NM_175619	CAGCACTTTCAGCTTCAAATA	CACGATTTATACATTGCATAA		
337867	PHGDHL1	NM_177967	TCCGTTGTCCATCACAAACAA	CACGCTGGACATCCAGAGACA	TGCCATTACATTAGCATGTAT	GAGGGTAATGTTACTTCACAA
337976	KRTAP20-2	NM_181616	TACTATGGTGGTCTGCGTTAT	GTGCTACTACAGCAACTACTA		
338328	LOC338328	NM_178172	CTGCAGCTTCCTGCAGAGGAA	CCAGATGACTACGACGAGGAA	AAGTACAGAGTGAGACTTAAA	CACCAGTTCAACACTCCATTA
338382	RAB7B	NM_177403	CAAGGCTGGTGTAGAGAGAAA	AACGAGCAGACTAAGGAGTAA	TCGAGGTACCAGAGCATCTTA	CAGCATCCTCTCCAAGATTAT
338398	TAS2R60	NM_177437	AACTATTTAAGGAACCATCTA	TGGCGATAGCATACGGAGCTA	TCCGATGGCCTTCCCATACAA	CAGGCTGAGAGCTGTGCTGAA
338440	TP53I5	XM_374860	CACGGTGGTGTTCGCCATCTT	CTGCCTCAAGGGCTACGTCAA	GACCATCATCATCATGACCAA	CGGGAGCAGCCAGTTGATGAA
338611	LOC338611	XM_291745	CACAGCCATGTGCAGCCTATT	TCCAAGCAGTATATGAAGCTA		
338645	LOC338645	NM_001009909	CAGACCAATTATGATCCTTAA	AAGGAAATCTTTAATCAATAA		
338657	DLNB14	NM_198489	ATCATTGTCTTTCTTAGGAAA	CAGGACCATCTCTGACATTCA		
338661	LOC338661	XM_290501	AACATTTGTTGTTAATATAAT	AAGTATCCAGGATGACCTGAA		
338692	LOC338692	NM_207354	CACCGTGTTTGAAGTGCCCAA	CCGGAGGAGCTTCATCTTCAA		
338751	OR52L1	NM_001005173	CTGGTAGGGATTCCAGGTTTA	CACCGCTTTGGTCATCATGTA		
338879	RNASE10	XM_292225	AACGCTGGTGCTTAGCAACAA	CTGAATCTGGAGAGTGATCAA		
338949	LOC338949	XM_294751	AACAATGTTTAGAGTCATGAA	CAGAAATGGAATAAATATCAA		
339005	LOC339005	XM_370838	CAAAGTCACATCTTTGTGGCA	GCGAAGTTAGAGCCTAGTGTA		
339022	LOC339022	XM_294775	ATGGATTTATAGAGAACATCA	AGAGAATACATTTAAATTAAA		
339059	FLJ40448	NM_182605	AGGAGAATCACTTTCACTTAA	CACCATCTGGTTGCCTGGCAA		
339065	LOC339065	XM_294794	AAGCTACGATAGAGTCAGATA	CAGGGTAGTGATGACCTCACA		
339145	FLJ44299	NM_198491	CAGCTGAGTAGGGCAAATGAA	CAGAGTGGCTTAGAACAGTAA		
339201	DKFZp762C2414	NM_178542	CCCGGCTGATTGGATTCGTTA	CTCCATGAGGCTGGTCCTGAA		
339210	LOC339210	XM_378687	CTAATAAACATTGGTATTAAA	CTGCAAAGAAATACTTGATAA		
339324	LOC339324	XM_290838	AAACATCACAATATTCATACA	AAACATAATATGGAACAATTA		
339390	LSECtin	NM_198492	CTCCTGGAGCTGATTGCCAAA	AATAAATATTTGAGAAATGAA	CAGCCTGAGGAAGCATCAATA	CTGAGGAAGCATCAATAAATA
339398	LRRN6D	NM_001004432	CACCTTGAGGCTGTCTGGCAA	ATCATTAAACCTGCTGTCAAA	CACGGCTATAAGATTATTTCA	AGCGCTAGTCAGCTAGTCTAA
339403	RLN3R2	NM_181885	CCCGGGAGAGCCGCCCTTCTA	TTCAGACACCTTCGTCTTCAA	CAGGCGGTGGGTCGCAAGCAA	CCGATGCCTGTCAAATTCCTA
339451	KLHL17	NM_198317	CACGCTTGATGGGAACCTGTA	CAGCCTCAACTCCATCGAGAA		
339457	LOC339457	NM_001003808	CAGGCGAAGTTTGACACATTT	CAGGGTGTGGTCAGCCGCAAA		
339483	LOC339483	NM_178546	GCCGCTGACTGTAACATGTAA	TAGGGAGGTCTCAATAATAAA		
339488	TFAP2E	NM_178548	TATGTTGTAATTAAATTTGAA	CTCAAGGAACAAAGAAGATAA		
339512	MGC48998	NM_178550	CAGGGTGAAATGAGCCTTGAA	AAGGGATAATTTATACTTCAA		
339559	ZNF642	NM_198494	CCAGGAATTGTTGACTTTCAA	CAAGTGTAAATTGGTGATTTA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
339669	MGC35206	NM_178552	CTCCGTCTTCTCAGACTACTA	TAGAGGTGTCTTCTACTCAAA		
339766	LOC339766	XM_291007	CAGGATCTTCTTCGACAACGA	CCGGAGGAGATGAACCTGCAA		
339778	LOC339778	XM_496547	AAGGACTTTCTGTCCATCTAA	CACCATCATCCTTACTGATAA		
339788	LOC339788	XM_379074	TTGGTAGAATTTACCTTATAA	CTGAATGTTTGTACCCTCTAA		
339799	LOC339799	XM_290345	CGGAGTTGAGCTGATCATGAA	CACAATGAGTCAGAAGATGAA	TACGCATACTATGACACTGAA	CCGCATGAGCATCAAAGCCTA
339843	LOC339843	XM_290351	CTGGGTTGTGAGCTCCTTGAA	TACCATGGAATGGGTCAGAAA		
339862	LOC339862	XM_376212	CAGCTAAATAATTGCTAAATA	TAGGTTCAACTTCAGCATATA		
339879	LOC339879	XM_291054	CTGGGCGGCACGCACTCTCCA	TAGGCTGGTGACACGTCTCCA		
339983	FLJ37478	NM_178557	CAGCCTGAAACCAACACATTT	CACATTCAGCTTAGAAGTGGA		
339997	LOC339997	XM_295126	TACAGTACATTAGACATTCAA	CAGAGCCTATGTCAATGGCAA		
340024	SLC6A19	NM_001003841	CCAGAAGATCTCCTACCCGAA	CACGAACATCCTGACCCTCAT	CTCGGTGATTGTGTCCATCAT	CAGGTTCAATAAGGACATCGA
340074	LOC340074	XM_379355	CCGGCATACAGTCACCACCAA	ATGCATCTTAATCATTTACAA		
340094	LOC340094	XM_295155	AGGCAATAAACTTAAACAATA	AAAGGCCATTACAATATTTAA		
340096	LOC340096	XM_293943	CTCCGTGGAGAGGGTGCCGGA	CCTGGGAAACCTTGCACTCTA		
340113	LOC340113	XM_379324	CAGATGTTTGTTTCTGCTCTA	AAGGAGCAGAACATCTGTTAA		
340146	SLC35D3	NM_001008783	CAGGTATATGAAGAAGGATTA	CTGGAATATAATTCAGAATTA		
340156	LOC340156	XM_373109	ATCGGGATGCTAAGCAAATAA	AAGCTTCTGGGTAAACACATA	AAGAATAAACATGGACCTTAT	TTGGTGTTGATAAGAAATTAA
340168	LOC340168	XM_291161	AGAGCTAGAGTGATTCCTTAA	ACCAGTTTCCAGCCAATGCAA		
340265	GRID2IP	XM_294249	CAGGACTGTCCGAGTCTACAA	GCGCAGGACTGTCCGAGTCTA		
340267	LOC340267	XM_295195	CTGGTAGGTTGTGCTCAACTT	TACAGGATATCTTATTTGAAA		
340348	MGC50844	NM_178562	GCGGACATACTTAGATCCTAA	CAGCATTGTGCCAGAGTGATA		
340359	LOC340359	XM_294387	AAGGTATGACAGCATCTGCAA	CCGGGAGAAGAGTGAAGCCAA		
340393	LOC340393	XM_291270	CTGCCTGACTCAGATGCCTAA	CCGGAAACTCAACATCAACTA		
340485	ASAH3L	NM_001010887	TTGGGTCAGATGCTTGATGAA	CAACAAGAAATCATCAGTCAA		
340515	LOC340515	XM_379650	ACCAATGTATATGCACTTGTA	TAGGAAGAAGTGGTAAGCTAA		
340526	RGAG4	XM_291322	AAGGATGAAGAAGATGAAGAT	TGGGCAGTCGCTGTCGCATTT		
340542	LOC340542	XM_291335	AACATTGATATGATAGATGGA	AAAGTTAATAAAGCAATTTAA		
340595	FLJ46608	NM_001004308	CTGATTTATAACCTGCATTAA	CTGCAGTAGTTTCTAACTCTA		
340654	LIPL3	XM_291663	CAGCTTTACCACTCTGATGAA	CAGGCAGTGAATTCTGGTGAA	CAGGATACTCCCTCAAATCAA	CAGGACTAAATTGGCTGTTAA
340665	CYP26C1	NM_183374	GCGCTATGGGACAGTGTTCAA	CCGGGTGATGCCCTCGACCTA	CACCTTCGAGCTCGACGGCTA	CTGGAGCGTGATGTATAGCAT
340900	LOC340900	XM_291767	AACCTGGTATTGGAGATGTTA	CTGATTTATTAATTAGCTATA		
340913	LOC340913	XM_291770	AACAGCCATGTGGAAGTAATA	CTGAGTCATGTTTCTACCTAA		
341032	MGC50104	NM_198498	AAGGAGTGAGAGTGAAGCATA	CCGGGCAGACAAGTAACTCAA		
341356	LOC341356	XM_292023	AGGGTGGTGAGAAGAATTACA	ATGGAGTTGGTTTCAAGAAGA		
341418	OR6C4	NM_001005494	ATCCCTTCATATATACTTTAA	CAGCATGACAACAGGAAATAA		
341457	LOC341457	XM_292085	CAGGGAGAAATTTGATGACAA	CACCGTGTTCTTTGACACGGA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
341511	LOC341511	XM_292109	TAAGGACGTTAAAGCCAACAA	CAACATGCTTGTGTTCATTAA		
341784	LOC341784	XM_497370	ACCAACGTTCATGCTGAGGTA	CGGGATCATGAGGGAGTTTCA		
341883	FLJ46156	NM_198499	CTGAACCACAATACAATTAAA	CCGGTTGTTTGTAATATTTCA		
342346	LOC342346	XM_296817	CAGGAGTGCCCTGGCAGGCAA	AAGGACGTGAACACCAAGTTA		
342372	PKD1L3	NM_181536	CCGGTAGAAGACATCCTGGAA	CACCAGTTCTCGGAAATCAAA	ACGGAGATGCCCATTATGAAA	CAGCTGGATGATTTCAATTAT
342538	MGC71999	NM_199290	GAAGCTGTCGGAAACATTCAA	ACAGCATCTGATAGTGGTGAA		
342600	LOC342600	XM_292624	CCCGCTAGGCTTCCTGGGAAA	CTGGATTCTCTGAACACCCAA		
342618	LOC342618	XM_496207	AAGGACTTGTTTCACTGCAAA	CAGGAAGAGGTACAATTTAAA		
342669	LOC342669	XM_292674	CCAAGTGAACCTATCCGCAAA	CAGGGCATCTGCACTGGAGAA		
342853	LOC342853	XM_497574	CAGCATGTGGCACAAGAGACA	CATCAAGATCGCGGAGATCAA		
342931	LOC342931	XM_292796	GGCGCTGGTTTCCATCATCAA	AACGTTGTACTCTCTTCAGAA	GAGGGAAATACCAGTGCTTTA	AACGATCTCATCGTTTCTGAA
342933	LOC342933	XM_292723	AGCCGGGAAGGAGAAACTCAA	ACGTGTGCAATAAATCATTTA		
342934	LOC342934	XM_292724	CTGAATCTGAGAGGTCTCAAA	AAGGAATATCTTATGCAGGAA		
342945	HKR2	NM_181846	CCCGAGCAACCTCTCCAGTTA	CTCAGTATCTACAACACACAA	TAACCTAAAGCTTATCTGTAA	CAGGGTATAAGTATGCTGAGA
342969	LOC342969	XM_292824	CACTCATTCCTCACACCTAAA	ATCGGTTAAGATCGATGGCAA		
342970	LOC342970	XM_292810	AACATTGAAGATCAGTACAAA	CAGGAGGAGAAACCCTATGAA		
342977	NANOS3	XM_292819	ACGCCTGTGCTCTTTCTGCAA	CACCCGAAACTCGGCAGGCAA		
342979	LOC342979	XM_292820	ACCACTGGGCATAGAGAGAAA	ACGGAGGGAGATCTGAATCTA		
343035	C1orf36	NM_183059	TTGAGGGAAGGAAATAATTTA	AAGAGTTGATTGGCTTATTAA		
343169	OR6F1	NM_001005286	CACCTTTGTCTCCTATGTGTA	CTGGGCTTTCCTGGTTCTCAA		
343295	LOC343295	XM_497684	ATGATTGTAAGGGAACAGCAA	CCCATGGAATATGAGCATGAA	TGCCACATTGGTGATCCTCTA	ATGTATAACGATGACCTAGAA
343406	OR10R2	XM_372798	CCCAAGATGCTTATCAACTTA	ATGGAAGGTAGGGATAATGTA	TACAGGTAATTAGATGATTTA	CACAACTGTTATTCTGCCCAA
343413	LOC343413	NM_001004310	CAGGGATGGAAGAATACACCA	CACCAGAAAGGGAAAGATGAA	CAGACATTCACACAAACTTCA	CAGAGAGAGGAGTGAGCCCAA
343472	BARHL2	NM_020063	CACACAGAGTGCAACCAGTAA	CGCCTTATTTCTATCACCCAA		
343505	LOC343505	XM_291607	ACCAAGGAGCTTGATAAAGTA	TTGGCACTAGTTGAACAGAAA		
343563	OR2T29	NM_001004694	AACTGTGAGATTCGTCCTTTA	AACCCTTTAATCTATAGTCTT		
343629	LOC343629	XM_293121	CAGACCTGCATTCATATACAT	CAGAGGTTGAACATACCCTAA		
343990	MGC42367	NM_207362	ATGGAACTTGCCAGAAAGAAA	CACAAGGGTGATGGACATTAA		
344018	FIGLA	NM_001004311	CAGCAAAGTTGATATCCTTAA	TACCTTCTAGAGACAAATAAA		
344065	LOC344065	XM_292895	AAGCTCTTAGTGAGCATTTAA	AAGGATATTTCTGAAGAAGAA		
344165	LOC344165	XM_292957	AAGCCAGAGGATTGCAACCAA	CACGAAGACTGGAATCTGTAA		
344172	LOC344172	XM_497885	ACGGAACCAGTCGGTCAGGAA	CTGAATTCGAATCACTGTTTA		
344328	LOC344328	XM_497894	AAGAGTTAAGAAGGCATGAGA	CAGGATCCGAGCAAAGCTAAA		
344561	GPR148	NM_207364	GAGGATCTATGCAGAGGCCAA	CGCCATTGTGCTGCACACCTA	CCACTTATGACTAACTTCTTA	CAGCACAATATAATAGTGGAA
344709	LOC344709	XM_298233	CAGGACCAACTTCGCAGATCA	AAAGATTCACATGATGAATAA		
344805	TMPRSS7	XM_293599	TAACTATTCAATAACCAAGAA	CCCAGCGTTGTGATGGAGTAA	CCCGAGCTACTATCCTCCAAA	TCGGATTACTCGTCAACCATA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
344807	CD200R2	NM_001008784	AAGGATAGAAGCCACTCAGTA	CCAAGTCTGTTGATTGATTTA	CTGATCATTCTTTATGTGAAA	AGCGTTGTCCTTACTGATCAT
344838	PAQR9	NM_198504	AAGGCGTGTGTCATGATACAA	ATGCATGGAATGTGAACACAA	CAGGGCTTAACCTGCTAGAAA	CACACTCTTCGTGCACTTCTA
344892	RTP2	NM_001004312	CAGCGCTGCCTCTGAAGCCTA	CACATGATGTGGAGAATGCTA	CGGAATGAGAGGATTGCATTA	TAGGGTGTCGTACTTACCATA
345051	LOC345051	XM_293680	CAGAGGCTGGGCGATGTTGAA	CAGGATGATCCCAGCTTTGAT	CCAGCTTTGATTCACTGGAAA	CAGCTTCTTACCTCAGTCAAA
345079	LOC345079	XM_293687	AAGGCCAAGAGCAAGGAAATA	AAGCTGCTGAGAGTTGGTAAA		
345275	SCDR9	NM_178135	AAGAAAGAAGTGGGTGATGTA	TACCAAGACATTTGAGGTCAA	TCCATCGATGATGGAGAGAAA	CTCCCACTACATCAAGACTAA
345378	LOC345378	XM_293802	CTGCTGTTCTGTCTGAATTAA	ACCCTAGTAAATCATCTGCTA		
345537	LOC345537	XM_293868	TAGAATTTAGGTCCCTTGTTA	CTGGATGAGAGATCTTCCTAA		
346007	EGFL11	NM_198283	AACGATCCTGAAGATAATAAT	ATGTGGTAAATTGGACACTAA	GAGGAATAATGCTACATGTAA	AAGCTTGGAGCAAGACATATA
346305	LOC346305	XM_498257	CAGGGAGGCTTCTCAGACCTA	CACGGTGGAGACCATATTGTT		
346517	OR6V1	NM_001001667	CAGGATGCTCTCAGACCTGTT	CAGTAGTACCATCTTTCTGTA		
346702	LOC346702	XM_498271	CAGAAGGTCATTATTCACAAA	AGGCACCAATGGTATCTTCAA	AAGAGCCCTGCTCAAAGTTTA	CTCGTCATGGTTACCATTTCA
347051	SLC10A5	XM_376781	TAGAAATATCCTAATGCTTAT	CAGTGGGATTAGTGTTCTTAA	ATGCCTGTCAATTCTTATATA	ATCAATTGGAATAGTCATCAA
347088	GPR144	NM_182611	CAGCGAGTGGGCCAAGGCCAA	CTGCTGCAAATCTATGAAGTA	CCGAGTCAATGCCTTGGCCAA	CTGGCTCAATGTGCACACAAA
347292	LOC347292	XM_294581	TATGGCCATGGGCCTCTTCAA	AAGCGGCGTGCCATGGAGCTA		
347376	LOC347376	XM_293312	CTGAGTGTTGTGGGTGGGCTA	AACGTGTTTCAGAATACACCA		
347527	LOC347527	XM_293401	CACCGCTGGCTCAGGATCAAA	AAGCTCATTATGTGACTCCTA	GACGTTGGAATTGCATCCTTA	CAGCCATAAGAGAGCATCGTA
347549	LOC347549	XM_293416	CAAGAGGTGGCTGGGAAAGTT	CGCCATGGGCAGAGTGAGGAA		
347689	SOX2OT	XR_000282	CAGGACTTATCAGCTGGGATA	AGGAAGGTTGATTGGAAATAA	CAGGTGTAGATCACCTATTAT	TCCGGGTTCCCAAGAACTAAA
347731	LRRTM3	NM_178011	AAGGCTTGATTTATCAGGCAA	CAGAAATAATACATTAACCAA		
347732	CATSPER3	NM_178019	CCCAATGGTCTTGGATGATTT	CAGACAATGGTGACCATGATA	GCCCAACATTCAAGAAATTTA	CCGTTTCTTTAAGATAATTAT
347734	SLC35B2	NM_178148	CTCGCAGTTCCTGGTGCTAAT	CCCTGTCATGCTGATGGGAAA	CCCGATGTGGCAGGCCCTGAA	CAGCTTTATGGTACCTGGCTA
347918	FLJ33915	NM_182613	CTGGAGATGTGAATTCCATAA	AAGCATCTAAGAGGCAATGAA		
348035	MGC40069	NM_182615	CAACAGATGTTCATATTTCTA	TACCTTTGATAAGATGGCTAA	AACGGGATTATTCAGTAGGAA	CCCAGTCACCTGACAAATCTA
348094	LOC348094	NM_182703	CACACTGATGCCAGATGTTAA	ATGGACTTTAGTTAATAGTAA		
348174	LOC348174	NM_182619	GACACGGCCATCGGTCACTAA	CACTAATCTGCAGCACCGGAA		
348303	SELV	NM_182704	CAGCAATTTCCGAATCACCTA	ATCGATGAGGAAATCAAGAAA		
348327	ZNF530	NM_020880	CAGGTATCTGTCCTCATTCAA	CTGGATGAGTTCAAACCTTCA		
348487	FLJ36766	NM_182623	CTGTGTCATTGGCAAGGACAA	CCGGGCCCGCGGAGACATGAA		
349136	LOC349136	NM_198285	CAGCACAGATGGCACAGCCAA	CAGGATCCTGGTTGCCAACAA		
349236	LOC349236	NM_182635	ATGCATGACTGGGACAAGAAA	AAGGTGAGACTCCACATGGAA		
349565	NMNAT3	NM_178177	AAGGTCTAAATCACAAGGATA	AAGGGATAAATAATAAATTGA		
350383	GPR142	NM_181790	ATGGTGTCCCATGCACAGAAA	CAGGAGGCCCTCCTACTACTA	AACACTGGACGAGGTCCTCAA	CCGGGTCTTCGTCATGCTCTA
353145	LCE3E	NM_178435	CTGACGCATGCCTTCCCATAT	AGCGATCTTTGGAGGAAACAA		
353299	RGSL1	NM_181572	CAGGTCATTAGCCAGAATAAA	CCCGCTCTTACTTACAGTATA		
353376	TICAM2	NM_021649	CAGGAAGTATTTCTCATTTAG	CTCCGTTAACAGGCAGCATAA	TCGGGTACTATCACCCAGAAA	TTGCCTGAGATGAAACATATA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
353514	LIR9	NM_021250	ACGGCTGAGATTCGACAGGTT	CAGGAATACCGTCTGGTTAAA		
359948	IRF2BP2	NM_182972	CCTGATCTTAGTAGCAGACAA	CTCCGTCCTCTATGAACCAAA	CCCAATGATTACCCTTAATTA	CTGCTTGAATTGTATATATAT
360023	FRBZ1	NM_194314	AAGGCAGATAGTATATATATA	AAGCCTAATGTCTGTAATTAA		
360132	FKBP9L	NM_182827	GAGGACCGTGTATGAGAGAAA	CTGGAATATTCTGTCATAAGA		
373856	USP41	XM_036729	ATGCAAGCTACTGTGAATTAA	CAGCAGGATGACTATCCTTGA		
373863	DND1	NM_194249	GAGGGTGAATCCAGAGAACAA	CAGCCCTGTGTTCCTCACCAA		
374355	C10orf96	XM_495849	AAAGAGTGAATTGATACAAGA	AAACAGTACAGTGAAATTACA		
374383	)KFZp686O2416	NM_001009913	CTGGATCAAGTGGGCATGAAA	TAGGTTGTTAATACTCGTGAA		
374387	)KFZp779M065:	XM_374877	CCAGGAAAGATGAACATCCAA	ACCCTGGAAGGTAGCACATAA		
374618	TEX9	NM_198524	GAGGATGAAATTCAGAATTTA	ACGAAGATGATTACAGTTTAA		
374654	KIF7	NM_198525	TCCGTTACCCTTGACCTGGAA	AAAGAACTGGACCCTCATTTA	TACCCTCACTGGGATCAACAA	TTGGCCAAGAATCATCACGAA
374860	ANKRD30B	XM_371111	CACTTTGAGCCTGCCACTGAA	CAAGAGCTTGGCGATACAGAA		
374890	LOC374890	XM_373798	ATCCAGTTCTATGTCCTATAA	CCAGGCAGGACTGACAATAAA		
374920	LOC374920	NM_199341	CCCGCTGGAGTTCGCCTACTA	ACGGGTAGAGACGAAATGCAA		
374955	LOC374955	NM_198546	CTGGATATTCCTGAAATGCAT	TAGGAGAATACTGTTTACAAA		
375035	LOC375035	NM_199344	CTGAATTCCCATGAATACAAA	AAGCAACAATACATTCTCGAA		
375108	LOC375108	NM_198996	ATGCACTTGCTTGTGAATTAA	TCCAATGGTTTAGGCATTCAA	AAGGATTCCTTCAGAGATTTA	ACCATATAGCAGATTAGATTA
375189	PFN4	NM_199346	AAGAATGAATTAAGGGAGCAA	AAGGACTGTATTTCAAGGGAA		
375295	LOC375295	XM_374020	CCCGCTCAGTTCAATATTTCA	CAGGTTAGACCTGGCAGTAAA		
375298	CERKL	NM_201548	ACACTTGATCTTATTAATTTA	CAGCAGAGAAGTGGTACTTTA		
375318	AQP12	NM_198998	CTCCCAGTGGGCGCCTATGAA	CAGGCCGATGGCAGGTCTTAA		
375341	FLJ43654	NM_198562	AAGGATCTGCTTGATATGATT	ACCAAGTGAAGTATAGTATAA		
375347	FLJ44290	NM_198564	CTGGGTGGTATGGGAAGTGTA	AAGGATTCAACTATATTTATA		
375444	FLJ32363	NM_198566	CTGGTAATTTGTCAAACTGAA	CAACATATTATTAAAGTTTAA		
375484	FLJ44216	NM_198567	CACCAATATTATGTCATTCAA	CCGAAAGGACTTAATAATCAA		
375757	C9orf119	XM_372143	CTGCACCTTGACATTCAGAAA	CAGAAGGGTGTGGACATGATA		
376267	RAB15	NM_198686	CTGCACCAACCTCAACATTAA	AAGGACTATATTTGTACTGTA		
377630	DUB3	NM_201402	TCCGATGTCACAGGCAACAAA	CTGCTGGAGATCTCAAATCAA		
377677	CA13	NM_198584	AAGGGCAATGGGATAAAGCTA	ATGCACTATAAGTTAATATAA	CTCAGTGATGTTAGATGGAAA	CAGAGGGACACTAAGCATTAA
377841	UNQ2492	NM_198585	CACAGTTGAAGGGACAGGCAA	CAGCGTCTACACTCACAGCTA		
378832	C21orf123	NM_199175	CCGTGAAAGGATGGAAACAAA	CTGCAGGAGTGAGCAATTTAA		
379025	FLJ31306	XM_495990	CAGAGCTGTCAGAAAGAATAA	ATGAAACATACTCAAGATTTA		
386678	KRTAP10-11	NM_198692	GTCCAGCTGCTGAGTGCTCAA	AAGCAGGATTCTCCAGTCTCA		
387032	ZNF307	NM_019110	TTGGAAGAAGTCATTTGATAA	CGGAATAGAAGTCTTATTGAA		
387054	FOXD4L3	NM_199358	AAGCACCTGCTCCTCCATGAA	AAGATTAAGCCTAGTTATATA		
387082	SUMO4	NM_001002255	TCCGGTGTTCACCATGGCCAA	TCCGATTTGGTGGGCAACCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
387332	TBPL2	NM_199047	CAGAATATAGTTTCCACTGTA	TACAAGTACGTTACTTATTAA		
387357	C6orf190	NM_001010923	TACGCAGATAATGATCATTAA	AAGCCTGTTTATGAAATTCAA		
387509	GPR153	NM_207370	ACGGGCCTCGTGACCACCATA	CAGGACGTCGGGAGCAGGGAA	GACCACCATAGTCTTCATCTA	CAGCGTTGGCGCCAAGCAGAA
387601	LOC387601	NM_199352	AACGTCATAGTATACCATCAA	CTGCTAGTATTGGACATATAA		
387643	LOC387643	XM_370537	TTGAGTTGTCATGTAGATTAA	CAGGCAGTTTGTGAATATTAA		
387710	LOC387710	XM_373474	CCGGCTCTACTGAACTTCAGA	CTGCTCAGATGTGAGAAGTAA		
387715	LOC387715	XM_373477	CCGGGTGATAGGCATTAACTA	CAGCATCAATGTGAAGCCAAA		
387717	LOC387717	XM_373478	GAGGCAGGCCTCGCCATTTAA	CCCGGCTGGAATCCAGCTCAA		
387720	LOC387720	XM_370584	AACACAATGATTTGACAGGAA	AACAACTAATTTATGGAACAA		
387723	LOC387723	XM_370586	AAAGATAGACTTCTTCTTAAA	CTGAAGAATGAGGAACATAAA		
387748	OR56B1	NM_001005180	CACCAGTTCCTTAATCTTAAA	CACAGCGTGATTATTGCTCCA	ACCCTCTTCGCTATCCATCAA	AAGTCTTATTATACTGTCATA
387750	LOC387750	XM_370607	CAGCAGGCACTGAATATACAA	CAGGCCCATTTCTTTCATCTA		
387753	LOC387753	XM_370611	AAGAAAGACGCCAAAGAGAAA	AACCTATTTCCTATGAATTCA		
387758	LOC387758	NM_203371	AAGAAGATTAATGATCACTTA	CAGGTCTACATTATTTAATTA		
387763	LOC387763	XM_373497	ATGGCTGAAGGCATTTATTTA	AGGGAGAGACTTATACTTTAA		
387781	LOC387781	XM_370634	CACCTACTAAATACAAATAGA	CAGCCAGATATTTGTGGACAA		
387804	LOC387804	XM_370648	CAGCCTCATGTGGGTTTGTAA	CAGGGCCGTGCTGACACATAA		
387820	LOC387820	XM_370665	AACAGAAATGTTAAACTATAA	AAACAGGACATCTATGACAAA		
387823	LOC387823	XM_373519	CCGTGTGATCCTAAACATGTT	ACACCTCTTCCCATCATTTAA		
387825	LOC387825	XM_370668	CAAGGTTGTTAGAGACTTCAA	CAGAAACATGTTGCATGTTAA		
387836	UNQ5792	NM_207375	CAGAAATTGGACAGCCAGTAA	AAGGAGATTCTTGGAAATGGA		
387849	REP15	XM_370686	AAGGAGTACCTTGGATTTGAA	AAGAGAGATAATAAAGTCACA		
387851	AK3L2	NM_001002921	AAGCAGTTGCTGCCAGGCTAA	AAAGCCAGTCATTGAATTATA		
387856	LOC387856	XM_370691	AACCCGTGAATTGTGTAAATA	AACAATTTACCTGGAAATTAA		
387871	LOC387871	XM_373539	TAGGTATTTAATGTATTAATA	AAGGTACTTGAGAAACATTAA		
387873	LOC387873	XM_373541	CTGGGATTACAGAAAGAAGAA	CCCGGCCAAATGAGCTATTTA		
387880	LOC387880	XM_370704	GAGGGAATCATGGCAAGCCAA	CTCAATGGTGAACACCCGAAA		
387882	LOC387882	NM_207376	CACGACAATCTCATCATATTA	ACCAATGTATTTCAACAATTA		
387887	LOC387887	XM_373549	CACAGAGTCTTTCCAACTCAA	AACGCTGTTTCTAGTGCTTAA		
387895	LOC387895	XM_373553	ATGGACAATGAGAAACATGTA	CTCAGTAACAATAACAAGAAA		
387898	LOC387898	XM_373556	CGCGCAGATAATCTGGCATAA	CTCTTGGGACTCAGAAATCAA		
387911	LOC387911	NM_001007537	AAAGGCATCAAAGGTGATCAA	AAAGGAGATCGAGGAGAGAAA		
387917	LOC387917	XM_373562	ACAGGTGAAGAAACCCTTTAA	AAGGATGCTCTTGACGCCAAA		
387923	C13orf21	XM_370724	AAGGAACTGGCTGGCCCTGAA	ACCGGCAACTGAGATGTTTAA		
387930	LOC387930	XM_370727	CAACATTTCTGGCAATTTCTA	AGGCATCAACATTTCTGGCAA		
387937	LOC387937	XM_373569	CTGGACATCATTTAGCATATA	CAGGAAAGAGATTACTTGGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
387950	LOC387950	XM_373578	CCGGGCATTGGTGTTTGCAAA	AAGGAGGAAACGGATCACCAA		
387974	LOC387974	XM_373583	ATCGGATTCATCTGACATTTA	CTGGTTTAAATGCCACCTTTA		
387991	LOC387991	XM_370763	CCCAGAAACAAGGCAAATGAA	CAGATACATCAAATAAAGTTA		
387992	LOC387992	XM_373594	TAACAGATCTTTGAACACTAA	CACTTAAAGAAGAGAATTTAA		
388007	SERPINA13	NM_207378	CAACATAGACTTTGCCTTCAA	CCAAATGCTTTCTATCTCTTA	TCCGTGCATGATTGCTTTGAA	AAGGATAGTAATGGTGATCAA
388019	LOC388019	XM_373611	CAGCAATACAGTCACATTCCA	CAGGGTGTGTTTGCTGGATTA		
388021	FLJ42486	NM_207379	CTCAAATGAGAATCAGCTTAA	CACGCTCTTCTTCCTATGCAA		
388022	LOC388022	XM_370779	CTCCACAGAACTGCCAGTAAA	ACACGCTAAGTTTATGTTTAA		
388069	LOC388069	XM_370829	TTACAATGCAGTAAACTTTAA	AAGGAACCATGGAAATAACAA		
388076	LOC388076	XM_370833	AAGAAATATCATGAAAGGAAA	AACGATCATCGATGTTGTCTA		
388116	LOC388116	XM_370856	CAAAGCAGAAACGGAATTACA	CACCTGGTGAATGAAATCAAT		
388129	LOC388129	XM_373631	ACGGAGACCCAGGAAAGATAA	CAGCCGAGGGCGAGAAATGAA		
388142	LOC388142	XM_373638	CAGCCCTCACTAGACTACAAA	ACCATAAACCATGCAATACAA		
388143	LOC388143	XM_370879	TCCCTGCGCCATCTTCCAGTA	AACAGGTGTTAATAAATAAAT		
388159	FAM42B	XM_370893	ACAGTTGATCGCAAACTAGTA	CAGATTGACTATCCAGTTTAT		
388166	LOC388166	XM_370898	AAGAGGTTTCAGGCTGCCTTA	CTCCCTTAACATAGACATTGA		
388174	LOC388174	XM_370905	CAGCAATCTCTGCATGCCTTT	CCCAAGAGCTTGTGTATCTTT		
388177	LOC388177	XM_370909	AAGCCCTCTCAAAGACACTAA	ATGGGTGATAGTGGCTTTAAA		
388180	LOC388180	XM_373650	TGCAATCAGACTAGAAGGAAA	CCGGGCATGATTCTCAACTTT		
388205	LOC388205	XM_370930	CAGAACCGATTTGGATTTGGA	AGCCAGGATTCCAGTACAGAA		
388214	LOC388214	XM_373666	GCGGCTGGATCTGTAATGAAA	TAGGCTGATGTTAATAAATAA		
388227	LOC388227	XM_373670	TCCGATGACTTCTGTCCCTAA	CCCGCTGTTGGGAGTCCTTTA		
388231	LOC388231	XM_373671	CAGGAAGAACCTCATACCCAA	CAGCATGTTTCTGATCATATA		
388248	LOC388248	XM_370968	CAGGGATGGAAGTGAAGTGAT	CCAGGTCTTTAGGAGAAGAAA		
388255	LOC388255	XM_370973	CAGCATCTGAATTACACTTAT	CAGAGTTGTGTTCACGAAGAA		
388276	LOC388276	XM_373685	CAGAATGCCAAGCTCCAGTAA	CAGAAGGAGCTTGGGAATACA		
388295	LOC388295	XM_373693	CAGGCAGAATTAGTGACCGAT	CCCAATAAGGCTGCTGACTCA		
388298	LOC388298	XM_370992	CAGCAGGCTAGTGATGGTTAA	CTGGGTGTTTGAAAGAATCAA		
388300	LOC388300	XM_373695	TTGGGATTCATGCTAGATCAA	TTGGCTGTTTCTAGAAAGATA		
388325	UNQ5783	NM_207103	CTCACTGGTAAATAAAGTTAA	ATGGTTCTGAGTGATATTAAA		
388344	LOC388344	XM_371023	ACCGGTCATGCCCATCCGGAA	AAGGGAGACAGTTCTGCTGAA		
388364	UNQ9372	NM_206832	CAAGAGTAGATCTGAGTTTAA	CACCTGATTGTTAAAGATAAA		
388387	FLJ31222	NM_207388	CAGCCTCCAAATTTCTTTAAA	CCGGCTGAAATTGTATACTTT		
388394	LOC388394	NM_203400	CCGGCGCCGCGCGGCGATGAA	TGGAAAGAAATCTTGTAATAA		
388419	LOC388419	XM_371078	CAAGTTCATCAGGTACCTGTA	CGCCAAGTTCTTCGACGTCAA		
388420	LOC388420	XM_373749	TAGCCTTGTTTGGGATACAAA	CAGCTATTTGGCACATTTCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
388428	FLJ44861	NM_207389	CGGGTCCTTCAACTACCTCAA	CAGGTACATCCTGTCCATCAT		
388429	LOC388429	XM_373756	CTGGTGGAAGCTGCAGGAACA	ATGGGCGTCTCCTAACCGTAA		
388489	LOC388489	XM_373786	CACGGTCAGCGTGGCGAAGTA	TCAGATCATCTTCATGTTGAA	CAGGCTGTGCAGGTCCTGGAA	TAGCGTGTTCACCGAGTGGAA
388491	LOC388491	XM_371125	ATGCAGGCACTTGACATTTAT	CACCTTGAACATAACAGGAAA		
388494	LOC388494	XM_373788	CAGGAAGTATTTATCCAATGA	CAGAATCACAAGTGAAATAAA		
388514	LOC388514	XM_371145	ACCCTATATAAAGATCTTCAA	ATCTGCATCATCAACATTATA	CGGGACCCAGTTTATGGGAAA	CGCCTTCAGTACTTTCCACAA
388524	LOC388524	NM_001005472	ATGGAACAGTACATCTATAAA	AAGGAGGAATTTCAGGGTGAA	CACGGAGGCATCTTATGTTAA	CCCGTCGTAACTTAAAGGGAA
388531	FLJ45744	NM_207391	CAGGAGCTTTATTCCCTATTA	CAGCTTTAACTTGGGATTTAA		
388532	LOC388532	XM_371160	CTCACAAGTGTCACCATGGTA	CTGGGATAGCTTCCTGAAATA		
388533	UNQ467	NM_207392	CTGGGTGGTCCTGAGGAAGAA	CTGATTCTCAACCTACCATAA		
388536	MGC62100	NM_206894	CTGGTGGACTTGGAATGTTAA	CAGCGATCACATCTTATTAAA		
388538	LOC388538	XM_371165	AACCTTGGAGTGTACACTGAA	AAGGGCAGACATGGAGAAGAA		
388551	LOC388551	XM_371177	CCGCACAGGCTGCACCATCAA	CAGGCCCTAAAGAACGGCCAA		
388554	LOC388554	XM_371182	CTGGAGTGGGTCCAATATGAA	CACGGCCTTTGTGAAAGCCAA		
388564	LOC388564	XM_371196	CTCCCTCCTCACTTGGATAAA	CAGCGAGTGAGGCCCAGACAA		
388565	LOC388565	XM_371197	CAGCGCTTCGAGCCCATGGAA	CAGGGAGAGTCTGAAGCGCCA		
388566	FLJ26175	NM_001001668	AAGGCTTTCACTGATCACATA	AAGCATAGAGAGGATAAGTAA		
388579	LOC388579	XM_371207	AACAAATGTTCAACATTCAAA	ATGAGGGAGGTGGATGAACAA	CTGGTGTCTGAATATCAGCAA	CCAGCAGATGTTTGATGCTAA
388587	LOC388587	XM_373822	CCGGTTAGAAATGGCCGCGGA	CTGAGTGGATGTAGATGAGAA		
388605	HS6ST1P	XM_371230	CAGAGGTAGCTGCGTCCTGAA	ACCCATCTGTAGCTCCCTCAA		
388616	LOC388616	XM_373837	TACCATGGGATGGTTACTGTA	CCGTGTTATTTGGGAAACTCA		
388621	LOC388621	XM_371243	AAGCCGAGATAGCTTCCTGAA	AAAGAAAGAAGCCAAAGAGAA		
388624	LOC388624	XM_371244	CTGGCACTACTTCTCTCTCAA	AAGGATGTTACCAGTGCCTTA		
388630	LOC388630	XM_371250	AAGGGAGTGGATGTTAGGGAA	CAGGACATCCATGGCCAAATA		
388633	LOC388633	XM_371253	AAGCTTGTATAACACTGACAA	CACATCATTTCTGAATAGGAA		
388648	LOC388648	XM_373852	CCGCCAGCAGCCGGATTACAA	CAGGGATGTGCGGGTTCTCAA		
388652	LOC388652	XM_373854	CTGGCATTGTTTACTGGAGAA	AAGGGAAGTCGACGAAATAAA		
388662	SLC6A17	XM_371280	CACCCTCTCCGTGTCCTACAA	CAGCTACAATAAGCAGGACAA	GTGGTCGAGAATGCTGAGAAA	CTGGATTTATGGAACCAAGAA
388714	LOC388714	XM_371326	CAGGAATATATAAAGACATAT	CCGGATGATTACCCAAACTAT		
388720	LOC388720	XM_371330	CTGACTTACTGTTTCAACAAA	CGGATACAATAGATAATGTAA	AAGGTGGATGAGAATGGCAAA	TCGGATACAATAGATAATGTA
388730	LOC388730	NM_203376	TTGGTGGTGACTACACCTAAA	CTCCCACTTTGTGAAGTTTAA		
388818	LOC388818	NM_203405	CAGCTTCTTTGTTCCAGTGAA	CACCTTCTAGGGATAAATAAA		
388830	LOC388830	XM_371418	CAGGAGGGAAAGTCTAATGAA	AAGAATTGTGTTGGTCATGAA		
388882	LOC388882	NM_001006606	CACCTTGGTGAGAATCAGGAA	CCACAGATACAGATTATTAAA		
388885	LOC388885	XM_373949	ACCGTCAGCCACCTCAGTAGA	AGGCTACTACGTGAAGGAACA		
388900	LOC388900	XM_371466	CAGAGAAGAATTAATGTTGTA	CAGGAAGATGGAGGTCATCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
388903	LOC388903	XM_373962	CGGGAAGCACTTAACCAATGA	CAGCCAATCCTAGCTCGTTAA		
388907	LOC388907	XM_371470	CAGACAATAAACTTAGGGCCA	TTCGTGTAACTGACAGAGATA		
388917	LOC388917	XM_373970	CCATATGAAATTTGCAGTTAA	AGGGAGAATCTCAGACTACAA		
388922	LOC388922	XM_371476	AAGGATAGCAAGACAAATGAA	AAGGAAGTTGAAGGAAATCAA		
388927	LOC388927	XM_371478	CAGCTCCTTTCTCAAGCTTTA	CAGGGCTTTCAAGGTAATGAA		
388929	LOC388929	XM_371480	CCAGATTTATTACAACATAAA	CGCCATAATGTGATAAATAAA		
388931	LOC388931	XM_371481	CACGTTCTTCCAGGTGCCCTA	ACCCAATGTTCACACAAGTAA		
388939	LOC388939	XM_371488	AACCTCTTCATCCCAGCTGAA	AAAGAACAGCTGATTAAACTA		
388942	LOC388942	XM_373981	CAGGTTGACATCACATATGTA	CAGGACGAAGTCACACACTAA		
388954	LOC388954	XM_371495	ATGGAACAGTACATCTATAAA	AGGAGGAATTTCAGGACGGGA		
389002	ANKRD20B	XM_371535	AGAAGTAGTCACCGCCATGAA	GTTATTATTCATATTAATTTA		
389033	LOC389033	XM_374010	GCCAGGCAGCACCCTCTGATA	TCGGACTGAGAGCATTTCCTT		
389055	LOC389055	XM_374016	TAGCAGTGTGTGACACCATAA	CGGGAGTGCTCTGCAACTGAA		
389058	SP5	NM_001003845	CAGGGCGGTTCCAAACTCTAA	CAGCATGATATGTCTCTGTAA		
389067	LOC389067	XM_374021	CAACATTATTGTGACTATCAA	AAGAGTTATAATTACATTTCA		
389070	LOC389070	XM_374022	CAAGTTTCAGTGCTCAATATA	AAGAGATCAGTCATTACAATA		
389075	RESP18	NM_001007089	TAAGGAAGAAATTATCTATAA	CAGATTTGAATCATTAAAGTA		
389077	LOC389077	XM_374025	CACCTTACAGGCTGACCTTAA	TCCCACAAAGTTAGAAGCAAA		
389089	LOC389089	XM_374029	TACAGCATTCTCGACCTGTGA	TGGGAGGCTTGTGTTGAGTTA		
389090	OR6B2	NM_001005853	CCTGAGGAACAAGGAATTTAA	CACCGTGGTCACCGTCTTCTA	CACGCCAATAATTAACCCTTT	TTGGGTCAAACTTCACACTAA
389108	LOC389108	XM_374038	CAGGTTTCTGCCCGCCAAGAA	CACGTAGTTGCGAGAGCCCAA		
389118	LOC389118	NM_001007540	CAGCCTGCCCTGCTTTATAAA	CAGGCACAGCCTGAAGAGGAA		
389123	IQCF2	NM_203424	AAGCATTGAATGGAAGACATT	CAGGGCTAATGAACCATCTAA		
389127	LOC389127	XM_371645	CCCTGGAGACTCATTCCTACA	TCCCGAGGCTACAACACAGAA		
389145	LOC389145	XM_374048	GTGCATATTCCTGATCCTAGT	AGGCATGCCTGCCATCTTCAT		
389147	LOC389147	XM_371663	AAGGCCAGTAAGACCAGGGAA	CAGCACTGGCAAGGCCAGTAA	CACACAGTATTTGTTTCTTCA	AAGGAACAACTGTATCTTATA
389151	LOC389151	XM_371665	AAGGTATATTCTAGACCTCAT	AAATGTTAGTTTATTACTGTA		
389153	LOC389153	XM_374053	CCGGTCCTCTCTTGCCCACTA	TCGGGCTTGGATTTGGAGAAA		
389189	LOC389189	XM_374071	CCGGCTCTGGCTCCAAACAAA	CCGAGTGTGGTTTGCTATCAA		
389197	FLJ46481	NM_207405	CCGGGCTTCCCTTGATGTTAA	ACCGCTGGAGTTAGAAATGTA		
389233	LOC389233	XM_374091	CAGAAAGTCTGAGAAAGGATA	CAGGTTGTCATTGGAAGTCCA		
389239	LOC389239	XM_371714	AAGGATATCTGTCACAGATAT	CACAACTAAATGAAAGCCTAA		
389246	LOC389246	XM_371718	AGACATGAAATATGACATATA	CAGATTGGCTCAGAAACCATA	AAGCAACAGGAAGCAAATGAA	CACCAAGAGTAGACTGATAAA
389247	LOC389247	XM_374099	CAGGATAGAAATTGGAGGCTA	AGGGAATGATTTAGCAATAAA		
389253	LOC389253	XM_374104	CCGGGCAGCTGTCTCCCTCTA	CAGGCGGAATCCATCCAAGTA		
389288	LOC389288	XM_374120	TGGCACCTGAAGAAAGCATTA	AACGCCATTCATTTCTCTAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
389290	LOC389290	XM_374121	AAGGAACTAAGAGTTGCAGAA	CAGCTGAGAATACATACCAAA		
389293	LOC389293	XM_371741	TCCCAGAATAGCCCACATTAA	CACGGGAGAACTCATAATGAA		
389305	LOC389305	XM_371757	AAGAATGAACTAAGGTGTCTA	AACCTTTGTGAAGCTCAACAA		
389308	LOC389308	XM_371758	CAGAATGTCCGGCCTTATATA	CAGCGCCTATATTTGAATAAA		
389321	LOC389321	XM_371769	CAGAATCGAGGCATCTGTTGA	CAGCATCGAGAACAAGCTAAT		
389332	LOC389332	XM_374141	CGCGCTCAGAGCCGCCAGAAA	CGGGCTGTTGTAAAGCCGAAA		
389333	LOC389333	XM_374142	CCGGGACGCCTCACAGCCCAA	CAGGAAGCTCAGAATGGGTTA		
389338	LOC389338	XM_374145	CTCTCCGAATTGAAACACTAA	TAAGAAGATTGGCGAAATTTA		
389342	LOC389342	XM_371781	ACCAAGTTCAATGCTGATGAA	CCAATAAATTCTACTAACTCT		
389345	LOC389345	XM_374150	CACAGAGGCTACAACTAGAAA	CAGGCATTATCGGGACTATAA		
389352	LOC389352	XM_371791	CTGGGAGACAAGAGTCCGGAA	CCGGATGTCCAGAATGATGAA		
389383	UNQ3045	NM_207409	CAGCTTAGTATCTGCACATAA	CAGGGATTGCATCATATTCAT		
389389	LOC389389	XM_371820	TCCAACAAACTGTGTCTTTAA	TAGGATGGGAAACAAGGTTAA		
389390	LOC389390	XM_374167	TTGTTCCAGTTCAATGATTAA	ATGGAATCTGTCTCTCCTTAA		
389398	LOC389398	XM_374170	CAGCTATGATACTCAGAGAAA	CAGGAATATTTCACCCAAGTA		
389413	LOC389413	XM_374175	CTGCATCAACTGCCTCCCTTA	CTCACCTTACTTTCACCTTAA		
389415	LOC389415	XM_374177	CCAGCCCTTTGGAAGAGAGTA	CCAGGCCTTAGCCCTGAGCTA		
389425	LOC389425	XM_371843	AAGACTGATCTTTGCTGGAAA	CTGGCTGTCCTGAAATATTAT	CTGATCTTTGCTGGAAAGCAA	AAGGTGGATGAGAATGGCAAA
389427	LOC389427	XM_371845	GAGGATCAAATTATAGTTTCA	GCGGTTGAATCCAGTCATAAA		
389435	LOC389435	XM_371853	AAGAGCTGAGGAGAAGATTAA	CAAGCAGGCTGTCACCGTGCA		
389458	LOC389458	NM_203393	CCGGATGCTAACACCCAGGAA	CCCAGATGCATTTATTAGAAA		
389469	LOC389469	XM_374203	CAGGATAGTCAAGGACCTCTA	AAGAGAGAATGTAATACACAA		
389533	LOC389533	XM_374226	CCACCTTATATTATAGTCAAA	CAGGCACTCCTTGATGAAATA		
389541	LOC389541	NM_001008395	CGGCTGCACCGCGGCATGAAT	CTGTCTGTGGTCTTTGGAGAA		
389599	LOC389599	XM_372002	CGGGAACGCTGGTAACTACAA	CAGGATTTACATGGCTGGGTA		
389618	LOC389618	XM_372019	CTGGAATGCCTTTGTACATAT	CTTGCCTGAACTTCCCAAGAA		
389634	LOC389634	XM_374252	CAGGGATGGCAGTCCCAGGAT	CCCGCCGCTACCGGGCAGGAA		
389641	LOC389641	XM_374260	TTCAATCTATCTGAAGCTTTA	AAGAGTCTTGAAAGTCCTTAA		
389643	HMFN0672	XM_372035	AAGAGTCATCTTCAATACCTA	TAGAAAGAAATGAAATGATAA		
389674	LOC389674	XM_372050	AAGAATTGGATGCAGCTATGA	AAGCTTGTGTATCATCCATTA		
389676	LOC389676	XM_374276	GAGGATTTAGAGGGCAAGCAA	CAGGACTTTGACAGCATTCAT		
389727	LOC389727	XM_372092	CTGGCGGTGAATGACTTTGAA	CCGGGAGAAGTTCTATGCCAA	CCACGCAGAGATGACAGCCAA	CACGTACACACGGGAGCGCAA
389734	LOC389734	XM_372097	TAGCATTTACATGATGTTTAT	AAGGATTGGAATTAACTTTAT		
389753	LOC389753	XM_372112	CCCAATCTCCTTTGGATATAA	CTGATTTGTGGTCTTCATTTA		
389756	LOC389756	XM_497059	CCCGAGGTGGATGAGGGTGCT	CTGCCTCTTGCCTGCAGCGAT		
389757	LOC389757	XM_372114	CAAGTCCATCTTTGAACAATA	CGGGACCGAGGTGCAGCAGTT		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
389773	LOC389773	XM_374297	AAGAAATTGTAGCGCCAGTAA	AACCTAAATTTAATTAATAAA		
389777	LOC389777	XM_374300	AAGATGCTATGAATCCAGAAA	TCGCATCTGGATAATCCTTCA		
389792	IER5L	NM_203434	TCGAGCCATTGTCGCCTTCTA	CAGAAACAGCAGAAGCGTTAA		
389813	LOC389813	XM_372159	CAACGCCTGCCTCTACTTCAA	GACCGTGTACCAGGACATCAA		
389832	LOC389832	XM_372190	CAGGAGAACGCCAGCCCTTAT	CTACCATAACACTGAAATAAA		
389840	FLJ16518	XM_372199	ATCCCTCTATTCGGGAATTAA	CTGGATGTTCGCGATGGACAA	CTGATTGTTGCTGGACAACAA	GCCGATCAGCATAACATTAAA
389844	LOC389844	XM_372202	GTCCTTGATTCCAATCATGAA	CAGCTGCGAGGTCGCCATCAA		
389846	LOC389846	XM_374325	CAGGATTGGGTGGATAAATAT	CTGGATGCCAATCGAGATTTA		
389848	LOC389848	XM_372204	AAGGAGGAATTTCAGGGTGAA	TCCGGGAATACTGGCCAGGGA		
389878	CXorf35	XM_374333	ATGGGTGGCGATGTTGAAGAA	CAGCACCATACTGGAACTTCA		
389907	LOC389907	XM_372274	CCGCCTGCCAACCGCCTTCAA	CACGCTGGTCACCGTGGGTGA		
389932	tAKR	XM_372302	CAACGGCACTGTGAAGAGAAA	CTCAGCTTATACACACCTGAA	AAGATATATTCTATACCACAA	AAGGTTGCTATGAGTAATGTA
389950	LOC389950	XM_372307	TTGGTGTGTGATGTGGCTTAA	CTGGGTAGTCTGGACAATGCA		
389953	LOC389953	XM_372310	CAGCTAAGGAACACTGTGTAA	CAGGAATGGATTCTCCACATA		
389988	LOC389988	XM_372323	TACATCCAAAGTTGCCCATAA	CTCACTGAGACTGGAGTCGAA	CAGCCAGAGACAAGAAGAGTA	AAGGTTGTTATCTTTATTGAT
390003	LOC390003	XM_497249	CACAACTTATGATGTTTATAA	ATCCGTTACGTTGGTGACCAA	CTCAATGACGTGTACAGTTTA	CAGCATGAGATACACCAACAA
390020	LOC390020	XM_372337	TTCCAACATCATCACCATCAA	ACCCACCTTCTTTGAAATATA		
390036	OR52K1	NM_001005171	CCCAGTGATTGCCCATTGCTA	CCCATGGTCAATCCTATCATA		
390054	OR52A5	NM_001005160	CACAGGTTTGGTTCACACATA	TTAGTTATAATCAAATATGAA		
390058	OR51B6	NM_001004750	TCGGAGTGACATTGACCACAA	ACCCATTTATCTATAGCATTA		
390059	OR51M1	NM_001004756	CACAGATACCACCTTCAATAA	CCCAATCATATACAGCATTAA		
390063	OR51I1	NM_001005288	ATCCATGTTAACAACATTTAT	CAGGCATTCCTGGGATACAAA		
390067	OR52H1	NM_001005289	TCCCAAGATGCCTGCCAGAAA	TCCCAGGATGCCTTACACAAA	CAGATCAGAGATAAGGTTATA	TACCACCATCTTGACTCCCAA
390072	OR52N4	NM_001005175	ACCAGCTTCATTTATTCTGAA	TCCCTTTACTTTCCTCACCAA		
390083	OR56A3	NM_001003443	CCCAAGAAATTAAGCAGGGAA	CTGCGATGATGTCACCATCAA		
390144	OR5D16	NM_001005496	CTCCCTGATATCACTCTCTTA	TAGGCATTGGTATCCATTTAA		
390158	LOC390158	XM_372396	GCCCAAGACAGAAGTTATGAA	CTGGATGATAGTTCATGTAAT		
390167	OR5M10	NM_001004741	CAAGAACATTTGCATCTCTCT	TTACATGTATGGCTTCCTTAA		
390183	LOC390183	XM_495875	TTCCCAGCTTAACAGACTTAA	CAGGAGGGAATTTCTGTCTGA		
390190	OR5B2	NM_001005566	TGGGACAGTAATCTTCATCTA	AAGAAAGTGTTGAGAAGGCAA		
390205	LOC390205	XM_372416	CGGCCTCTGGCTCTACGGCAA	CTGCCTCTGGATCGAGGGCAA		
390212	GPR152	NM_206997	CCAGCCACAGGCAGACACTAA	CAGCTAGATTCTGAGGGTCCA	CAAATGGACACTACCATGGAA	CAGGACCATTCTGTCAGCCTA
390221	LOC390221	XM_497309	CCCACTGCTCTGTGCAGTGAA	CTGGACCTCAGGGTCTAACAA	CTCCTACACCTGCAAGAGCAA	CTGCCTGCAAACGGCACTTTA
390226	LOC390226	XM_495887	TACCAGGAGGCTGGCATTCCA	ACCAGGTTACCATATACTTCA		
390231	LOC390231	XM_372423	CTGGACAAAGAGGAATGACAT	AAGACTCTTGTAATTGGGTTA		
390233	LOC390233	XM_372424	AAGGAAGAGGATAATCACTAT	CTGAGCGAAGCAGACATGGAA	ACCCAGACTATGTGTCATTAA	CACTCTGATTACTCAATCTTA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
390234	LOC390234	XM_372425	AAGCTGAACCTCAACCAAATA	CAAGAGATTTGTTCAATGAAA		
390260	OR6X1	NM_001005188	CACAGTAATCACAGAATTCAT	AAGACTGGTCATGCAAAGTAA		
390264	OR10G4	NM_001004462	ATGGATGCCATGGATGGAGTT	GCACATCCTCAGAGGAAATAA		
390281	LOC390281	XM_497327	AAGCACCTATATGCCCTTCTA	CTGGAAGGACAGGTTGTTAAA		
390282	LOC390282	XM_372447	AAGCTGTTGAGAGAAAGGAAA	AAGGAAAGTTAAGGCCACCAA	CGAGATCATGCTCAACGGTAA	AACGTCAGAGTGAAATATGTA
390284	LOC390284	XM_372448	CCAGACAAACTCAGAGCTTCA	CTGGTGGTGGTCATCGAAGAA		
390335	LOC390335	XM_372466	AAGAAAGAAGCTGCCCAGAAA	CAGCTCTCATCTTGCAGTACA		
390349	LOC390349	XM_372472	CAGGTGTGCAGAGATACTTGA	CAGCACCAATGAAGACAGGAA		
390377	LOC390377	XM_372486	CACCCACCGTTTCATCACCAA	CAGAAGAGCTGGCGTCATGAA		
390387	LOC390387	XM_372490	CAGGGTCTCCATGGCCTGTCA	ATGACTCTGATTCCACATTAA		
390407	LOC390407	XM_497376	AGGTAGATGGTTTGACCTTAA	TCGAGACATCAGGACCTTCTA		
390421	LOC390421	XM_497382	CTGCCTGCATTTGTTCCTAAA	CAGGAGTGAGATCCCACCCAA		
390429	OR4N2	NM_001004723	AACAGTGATAAGAGAATTCAT	AAGGTGTTTAATAAGCACATA		
390442	OR11H4	NM_001004479	TTGGATTCCTTGGATACCCAA	TGGGACAGTCATGGTAATGTA		
390443	RNASE9	NM_001001673	AACGTATTCCTCATACTATAA	AAGGAGTGTATTGTAATTTAA		
390445	OR5AU1	NM_001004731	CAAGAGGAAAGTGATCTCTTA	CTCCTACTTCTTAATTCTCAA		
390529	LOC390529	XM_372542	GACCCTGGAGGAAGAAGCAAA	CAGGCGTTTGCTGCCTCCTTA		
390550	LOC390550	XM_374354	CCCACTCTCATGGATGCCTTA	ACACTCAGTATTGGTAGATAA		
390551	LOC390551	XM_372556	CTGAGGTGGGTCTGACTCAGA	AAGCAGGTAGGTGCGAATGAA		
390560	DNM1DN4-1	XM_497444	AGCAGTGTTTCTTCTCTATCA	CAGCTTCATCATCCTGGTTCA		
390564	LOC390564	XM_372562	ACCGATGGGTACAGAGGCCCA	CTCCCTACTCTTTGCGAGGAA	CAGGGTCAGCCGAATGCCAGA	ATGGACGACCTTCTGAACAAA
390570	LOC390570	XM_372566	CTGTCTCACCGAAGATGTTAA	CACGAATGTACCAGTGAACAA		
390577	LOC390577	XM_372569	CCGAGCTGGGTCGGAGCATGA	TGGCCCGGAGTTAGAGGCCAA		
390641	LOC390641	XM_497469	CAGGTGGACATGTAAAGAAGA	CAGCAGCTGAAGGACAGATAA		
390667	LOC390667	XM_372607	TTGCTCGTGGAGGAAGACCTT	CTGGAGGAACAGTTCCGGAGA		
390736	LOC390736	XM_372641	CGGCTCGATGTCTGCAGGCAA	GTGGAGGAAGATGGACAACTA		
390801	LOC390801	XM_372676	CACACTGAACTTCCAGAACTT	CACCACTGTGGACAACAACTA		
390842	LOC390842	XM_497583	CTGAGGAACCTGCAAGACTCA	ACCAATGACAGTATCCAGTAT		
390919	LOC390919	XM_497622	AAGGGCTTTCCTGCAGCGCAA	CAGAGAAAGTCTATACATCTA		
390975	LOC390975	XM_372749	CTGGTCCACGCAGATGTCAAA	CTGGTCACCCATCGTCAGAAA	CCCGGCAAACAGTCTGAGGAA	ATGAACTAGATCCAAATCCAA
390988	LOC390988	XM_372755	CCGCCTGGAGGAGACCCACAA	GACGGCCATGTTCGACTTCAA		
391039	LOC391039	XM_497673	CACCCTCTATGACACAACCTA	CAAGGACATGAAGATGCATAA		
391053	LOC391053	XM_497689	ATGATGGATAGTGACACCATA	ATGAACAACTCTACAACATAA		
391059	LOC391059	XM_372784	CACCTTTACATGACCCAAGAA	TCCTATAATTTCACAACCAAA	CAGATTGAAGTTACTTTGTCA	CTGAAGGTTCATGGTGCCTTA
391105	LOC391105	XM_497715	CAGCTCTGCTAAGGACTTGAA	TTCATCTGAGTTTGAGATTAA	CAGTTTCATTTGACTCCTCAA	CTGGATTTAACGGAAGTAATT
391109	OR10K1	NM_001004473	CACCCTAATATCTGTGTCATA	CCAAGACTAATTACACTTCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
391123	LOC391123	XM_372802	AAGGTCATTGTCACTGTCCAA	ATGAGGCTAGGTGGGAAGGAA		
391126	LOC391126	XM_497721	GTGACTTCCAACCAAATCAAA	CCACATTCACAGGAAGATTAT		
391137	LOC391137	XM_372805	TTCCTGCTTCACCACCCTCAA	AGGATTCTGCTCAGCCAGTAA		
391142	LOC391142	XM_496426	CCAGCAGAGACACTACAATCA	CAAGAGGGCACGGGAGGCCAA		
391192	OR2L3	NM_001004687	CTCCATATTCCTTATTGCCAA	CACCCTCACTCCAATGCTCAA	ATGGCTCTAATTGGAAACCTA	TAGGATTCTTCCCACCATCAA
391205	LOC391205	XM_372838	CTGGAGGAGCAGCGTCACGCA	CGACATCGTCTCTGCTCTGAA		
391209	LOC391209	XM_372840	CTGGTCGATCGCACTTGTACA	CACGGGCTGTGCTGAATGACA		
391253	C20orf137	XM_372869	CCGAAATAAAGACACAAGAAA	CCGGCTGTAATGGCAACCTTA		
391265	LOC391265	XM_497576	CCCAAGAAGGGCAGAGGAACA	CGGGACCAAGTCTGTCACTAA		
391340	LOC391340	XM_372908	ATCCCTATATTGAGGAGCAAA	CTGCCCATCATCTGTATCCTA		
391347	LOC391347	XM_372913	CAGGCCCTGCTGAGCTAGCAA	CAGATATGTGTTGTCCTGTTA		
391370	LOC391370	XM_372926	CAAAGGCTTTGGTGTGTTCAA	AAGATTGGGCTTCACCCATAA		
391429	LOC391429	XM_372954	CAGATGGCATAGAGCATCCAA	AAGATGGGATAGAGCATCCAA		
391599	LOC391599	XM_497949	CAGGGACTTCATCAGCTGCTA	CAGGACCTGTTTGGAGAACGA	CAGGAGATATTTAGGTACCAA	TCGGACAAGGATGGAAACTTT
391634	LOC391634	XM_496686	CCACATCTACTGCATGATCAA	AAGATTGGATGTTATATATTA		
391711	LOC391711	XM_373037	AAGAGAAGGATGATAAAGAAA	AAGAATTATAAGCACATTTCA		
391717	LOC391717	XM_496725	ATCAGGTGAGAGCGTGTGAAA	CTGGTGAATTTGAGAAGTGTA		
391722	LOC391722	XM_373042	CACCAGAACAGTGGTCATCTT	ACAGAGAAATGTGAATAAGAA		
391730	LOC391730	XM_497990	CTGGATGGAATTCCTTCCCAA	AAGAACTTGCTCCATCATTAA		
391733	LOC391733	XM_373053	GTCAGAGACGGAGAAAGATAA	CACCATCACGGCACACTCCAT		
391769	LOC391769	XM_373079	CACGCAGCTGCTCCTGCGCAA	CTCCGCAGAGAGGGTCCTTAA		
391773	LOC391773	XM_497999	CTCATCAACAATTACGGCCCA	CAGCGTCATGATAACGTGAAC		
391804	LOC391804	XM_498008	CACACTTTCTAGCCCGTACAA	CCGAAGGGCGTAGTCACAGAA		
391819	LOC391819	XM_498013	CTCAGTTTGGAGGAATTGGAA	CCAGGACATGGCGGTCAACAA		
391827	LOC391827	XM_498018	TGGGTTGATGGTGGAGGTAGA	CCCTGGAATCTCTACACTAAA		
391833	LOC391833	XM_498020	CCGGACTTCGCTGCTCCCGAA	CAGGCCAGCAGCATCCTTATA		
392169	LOC392169	XM_499232	ACGGGCGCGGTCAGTGCCTGA	ACGGTGAAGACCTGAGATTTA		
392222	LOC392222	XM_373253	ACGCACCAGTTTCTTGCTTTA	CTGAGTGATGAGGAAATGAAA		
392238	LOC392238	XM_374372	AAGGGAAGAATTACACAGGAA	CAGGTACACGTAAGAAAGAAA		
392262	LOC392262	XM_373263	CACCTATGACACAAATGTCAA	CTGCTGAAGAATCAAGTATAA		
392267	LOC392267	XM_496992	CACCTCAGCCCTTACCTGGAA	TGCCATGGTGTATTACGTCAA		
392281	LOC392281	XM_497005	TGGACCCAAATTGCTTACGAT	CAGGTACATTACTCCTCAGCA		
392309	OR13J1	NM_001004487	CAAGATCCTGGCAGTGCTGAA	CCCTCTGTGCTCAGCCATGTA		
392376	OR13C2	NM_001004481	AAGGGACTTTCTGGTCACCCA	AAGGATGTGAAAGAGGCAGTA		
392392	OR1K1	NM_080859	CCGTGTGGCCACTGTCATGTA	TGGGACAGTCATTGCAGTCTA		
392395	LOC392395	XM_373319	CAGCCAGGCCATCGCCAACTA	TGGGACAAAGAAAGAGACCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
392459	LOC392459	XM_373344	ATGGAGCACCATTTCCATGAA	CAGGCTAGCAACAAAGGTGAA		
392517	NCBP2L	XM_373362	CAGGCCTGTGATTAAGAGCAA	CCCAAGTGTTGTAGCCTTAAA		
392546	LOC392546	XM_373372	GCGGTCCGCATTACTCACATA	CACCCTCTTAACGATGATGGA		
392556	LOC392556	XM_498396	CACTCTATGGAGCCAATCTAA	CACGATTATAATGGAGGGCAA		
392583	LOC392583	XM_374379	CCGCCTTGTGAGCCAGAGCCA	CCAGCGGAGGTCCTCAGGAAA		
392702	LOC392702	XM_374730	CTCCTGGGCAGCGGAAACAAA	CTCCCGGAATCTGGTGGACAA		
392758	LOC392758	XM_374498	TCCAGTGGTCTTTGGAGAACA	CGGCTGCACCGCGGGCATGAA		
392895	LOC392895	XM_499284	AAGGTGCACCAGGTAAGATGA	CAGTGGGAAGAGGAATTTGAA		
399665	EEIG1	NM_203305	CAGGAAGGTTGGAGCAAGCAA	TGGAATCTTCTTGAAAGTTTA		
399668	MGC39606	NM_203306	CAGCGTGAAGGGCCTGAACAA	CAGGTCCTGAATGAAGCTGTA		
399671	MGC48595	NM_203309	CACTATGTTTATAAAGAGAAA	CTGCTTGGATATGAAACATAA		
399706	RP11-529L18.1	XM_378200	AAGAGCTTCGTGTTAGAGAAA	AAGACAAATGAGACAGAGCTA		
399708	LOC399708	XM_378203	CAGGGTATCAAGAGTCAGTAA	AAGGATAGAATTATCCATCTA		
399715	LOC399715	XM_374766	ACCCAATAGCATAAGTATTAA	CAGCCTCAGTACTGTAAGAAA		
399763	LOC399763	XM_374803	CGGTATATAAATAGAATTAAA	CAGGTGTTTCTGAAAGATTAA		
399833	FLJ44653	NM_001001678	AACCCTAAGCCTAAACCTTAA	ACCCTTAACCATAACCCTTAA		
399851	LOC399851	NM_207427	TGGCTTGAACCCAGAGGTGAA	CAGAGTCACACTGGATTTACA		
399919	LOC399919	XM_378299	CTCGCTCAGGTGAGCATTCAA	TAGAGAGGTAATTAAGTTAAA		
399921	LOC399921	XM_374904	CCCATCCAGGAAGGTTATATA	CAGGGTCAAAGTTCTGAGCAT		
399937	LOC399937	XM_374917	AAGAGACAGAATGACAAGATA	CTGAAGCAAATGTACCATAAA	CAGCAACTCAATGAAAGCCAA	CAGAGTGTGAGTGATACTTTA
399940	LOC399940	XM_374920	AAGAGACAGAATGACAAGATA	CTGAAGCAAATGTACCATAAA	CCGGCCCTGTTTCTACCTCAA	CAGCAACTCAATGAAAGCCAA
399961	LOC399961	XM_378317	CTGAGAAATGAAAGTGTGAAA	ATGGTGCTTCCTATAATCCAA		
400047	LOC400047	XM_378363	TTGGACTTGACCCTACTGTAA	AAGGAGTCTTCAGGAATCAAA		
400083	FLJ43808	NM_207438	TACATTTAATATCCCAATTAA	AAGGATGAAATTTGACGAATA		
400099	LOC400099	XM_378399	AAGGTCTGACAGAAACTTTAA	CAGGTTCATGTCCCAATGAAA		
400156	LOC400156	XM_375035	CAAGCTGTATGTGAAGCTACA	AAGGACAACGCCATTAAGAAA		
400201	LOC400201	XM_378449	ATGGAGCTATGAAATGGCAAA	AAGGATATTACCAACAATGGA		
400224	LOC400224	XM_375090	AGGGTGGGTGATGACCTTCTA	AAGAGCTTTGAAACCAATAAA		
400238	LOC400238	XM_378473	CAGGTCAACTGTGGAATTTGA	CACCATTTAGAGGACAATGAA		
400263	LOC400263	XM_378491	AAGAGCCATCATGGTGATCAA	ACGGAGCAACGTCCAGTTTAA		
400353	LOC400353	XM_375183	CAGGCATAACTGAAGGTGAAA	CAGGCAGGAGAATCACCTAAA		
400400	LOC400400	XM_378529	CAGGGTCTCACCTTACAGCAA	CACATCTAGCATGGCATATAA		
400446	LOC400446	XM_496093	AAGGCTTTCTTAGGTGTGAAA	CTGGTTAAGTTGTGTACTAAA		
400475	LOC400475	XM_378553	TTGCAGAGTCTCAATACCCAA	TAGCTATAAATTATCATATAT		
400481	LOC400481	XM_375284	CAGCAGCAACAACAACAACTA	CCCGACCTACCTCCTGTTCAA	AGGCACCTTTCTAGAGATTAA	CAGGGTGAAGAGAATCTTCTA
400496	LOC400496	XM_378562	ACCAATTTAGGTGTAATTTAA	AACGCTTTGCTTTATCATTAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
400523	LOC400523	XM_378582	AACGCAGGATATTGCATCATA	CTCGTGGGTCTTCATACCTAA		
400552	LOC400552	XM_378623	CCAGAGTGTATTGCTTATAAA	ACCGTGTTTGGCAGACATTAA		
400569	MGC88387	NM_001001683	CGCGCTCTGGAAGACATTGAA	CAGAGTGATAATGGCTACCTA		
400586	LOC400586	XM_375424	CCCGCAGAATGGAGGAGATAA	CTGGAGAAACATCATCCTTAT		
400591	FLJ44815	NM_207454	CAGGATTTCATATATAGCAAA	CAGGAGAATGTCAGCAGTGAA		
400619	LOC400619	XM_378703	CTGGAGTAACTATTCCACTAA	CTGAGTCTTCTCTTTCTTCAA		
400623	LOC400623	XM_378708	CTGCGACATTTAGTCCTTTAA	ACCAGTGTGTTTGAGCATTAA		
400624	FLJ45079	NM_001001685	CAGGGTCTGAACTAAGAGCAA	CTGGGTCTGCGTGAAGATAAA		
400642	LOC400642	XM_378735	CACATCTTCCATATACTTTAA	CCAGAGTTTCTTATCAAGTAA		
400651	LOC400651	XM_378747	CAGGCTGAATTTGACGTTAAT	AAGGACATACATGCAAATGAA		
400658	FLJ44313	NM_207460	TCCGCGAGTCCTCAAATGTAA	CAGGGCATTGTCTGTCTACAA		
400664	LOC400664	XM_375549	CTGGTGATTTCCAGTAGGTGA	CGCCCACTAATTCTACATTAT		
400668	PRSSL1	NM_214710	CACACCCATTCCACATGCAAA	CGCCCTGATGCTGCCCGTGAA		
400673	VMAC	XM_375560	TTCGAAAGTGCTGCAGTTATA	CTGTCTGTGCTCAAGAATAAA		
400679	FLJ46230	NM_207463	CCCGGAAGGAAAGGAAAGGAA	CTGGACTTTGGTCAAGTACTA		
400681	LOC400681	XM_375589	GACCCTATATTTGGAATTTAA	TAGATTAAATTGGCTAATTAA		
400684	LOC400684	XM_378793	CCACTGTTTATTTCAGCATAA	CACGAAATCCTCCCATCTCAA		
400685	LOC400685	XM_378795	TAGAGTAATACTGGCCTTATA	CTGCTTGTGGTGGAAACATAA		
400709	SIGLECP16	XM_375634	CTCCGTGTGGCCTCCCTGGAA	AAGGGCAGCATTGGGCATGGA		
400721	LOC400721	XM_375664	CACACTGGTCACACCACCTTA	GTGGGAAATCATTTAGTTCAA		
400729	LOC400729	XM_378824	CGGCTCCTGTCTGACCAGGAA	ATGATGTACTAGATCCCTTAA		
400764	LOC400764	XM_378880	CAGGGAGCAGAAGACATTAAT	AAGGGCTATGAAGAAACATAT		
400790	LOC400790	XM_375814	CAGGAGCTCCTGCTACATAAA	AAGGAACATATTTCCACATAA		
400800	LOC400800	XM_378925	AAGGTACAAATTACAGATATA	AAGGAAATGATTTAACTTCAA		
400842	LOC400842	XM_375914	CCCATGAAGAATGAAGCACAA	CCGAGCGATCGCAGAGACCTA	TTCATACAGAATGGCACTAAA	CTGGGATTATTGATTACAACA
400846	LOC400846	XM_378981	CACGTACTTTCTGAATCTAAA	CACAAAGATGTGAGCAATAAA		
400850	FLJ44790	NM_001001691	CCCGGCGTTCCTGGAAGCCAA	CCCGCAGCAAGTTAAATCTAA		
400865	LOC400865	XM_379006	AAGGCAAACCATAGCCATTAA	AAGAATTTGCATCATAATTAA		
400876	LOC400876	XM_379023	CAGCTCGGACAGCATCCATAA	CTGTCTGAAATTGAATGTTTA		
400888	LOC400888	XM_375955	CAGGCATCACCTTGCCTGGAA	CCGGTGATTGATGATACTACA		
400890	LOC400890	XM_379036	AACCAGAATAATCAGCCCTAA	ACGCAGAGATGCACACATTAA		
400916	C22orf16	NM_213720	CCCAGATAGCTGGGATTGGAA	CACAGATAACCCAAGACACAA		
400921	LOC400921	XM_376001	CTGGCTGACGTGCTCCATCCA	CATTGTGGACTTGGACATTTA	CTGACACTAAGCTCGGCTTCA	GCCCTCTACTCAGCATGGATA
400931	FLJ27365	NM_207477	CTGGGTAAGTCTAGCCCAGAA	CAGGTGATGCCTGAAGCTCAA		
400932	FLJ46257	NM_001001693	ATGCATTCGTTTATCAATCAA	CCGGGAAGTGTTCACAAATAT		
400934	FLJ44385	NM_207478	AAGAAGGAAACTGGACACATA	CAGGACAATTATTAAGTTCCA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
400937	LOC400937	XM_379068	CAGGATCTACGTTATAATTAT	CACAATTATGAAATAATGTAA		
400944	LOC400944	XM_379077	CACCAACTCCTTGTATTGCAA	CTGGGATGGAATCCTAATGAA		
400945	LOC400945	XM_379078	CAGGTTTATAATATGCATTCA	CAGCAATTTAATAATAATGCA		
400964	LOC400964	XM_379106	CTGGGATTACACAGTCGGTAA	CAGGTTAATGGAAATAATTAA		
400997	FLJ44006	NM_001001696	ATGGAGATATACAATTGTTAA	AAGGTCTTAATGAGAATGAAA		
401025	LOC401025	XM_379149	CCCATCCTGAGTGACTACTAA	CCAGCATGTCTTTCCACTATA		
401034	LOC401034	XM_376179	CCACCGGAGACTCAAGATGAA	CACACTCACAGTTACCAGCTA		
401037	LOC401037	XM_379161	CCAGTGCAGCTAGAAATGTAA	TCCCTCAGAATTTACATCTAA		
401050	LOC401050	XM_379173	TTAGATAATAATGGAACTGAA	CCCAGTTTAGTTTATATATAA		
401054	LOC401054	XM_376207	TTGGCTGGACACAATCCTGAA	CAGGTTGACCTTGGTGAACTA		
401056	LOC401056	XM_379180	TAGGACTCTGGAGAAGATCAA	TGGAAGCTCTTTGGAAACCAA		
401058	LOC401058	XM_379182	AAGAATACATAAGAAGTCAAA	TACAATATATTCTTAATTTGA		
401059	LOC401059	XM_379184	TACATTCTGAGTTGAAGGAAA	TCCAAGTATGATTGGAAATTA	TAGATATTTATTATCCAGGTA	ACGAAATTCATTGGCAGATTA
401078	LOC401078	XM_379200	CTGCGTGGTGGCAGTTGTTGA	CGGGTTTGTAGTTACCTATAA		
401081	LOC401081	XM_379206	AAGCAGGTATTTGTATTAGAA	CTGATAGAAGAAGACATTAAA		
401087	LOC401087	XM_376267	AACAAGTACGAATTTGCCAAA	CTCCTTGTGTTTCATTGGCTA	ACGAATTTGCCAAATGGACAA	ACGGTCTATGGTGGCACAAGA
401089	LOC401089	XM_376269	CACGTTCCAGATACACTTTAA	TTGGATTTCTATCACCATAAA		
401097	LOC401097	XM_376281	CGCCAACTGCCTCAGACCTTA	GCGGGCTGCCTCTGACATTTA		
401101	LOC401101	XM_379234	AACGATCTGCGATGAAGATAA	CAGCTGTGACTTGATAAACAA		
401103	LOC401103	XM_379235	CAGGACCTCTGAATCCTATAA	ATGTAGTAATATACTCAATAA		
401114	FLJ35816	NM_207489	CTGACTTTACTCTGAGATCAA	AAAGGTAATGACCAAGATAAA		
401123	FLJ45721	NM_207490	TAGGAAGTAATTACTAATAAT	AACCATGTAGCTCATAAGTAA		
401149	LOC401149	XM_379273	CCGGGACAACAGGCTCTCCAA	CTGGCTGTAGATCCCAATGAA		
401165	LOC401165	XM_379299	TAGGGTTAATGCTACATGGAA	AAGGCAAATTCTATCTTCAAA		
401172	FLJ33360	NM_001001702	CAGGCTTTGCTTCTCTCCCAA	AGGAACCTTACTGATAATTTA		
401176	LOC401176	XM_379318	AACCAAGAGTTATAAACTATA	AACGTAAATATTATTACGTTA		
401180	LOC401180	XM_379325	CACGTCCTCCTTACTCCCGAA	CAGAAACTAAACCGACACCAA		
401206	LOC401206	XM_376420	AACCAGCTGTACATTTGGAAA	GACGAGAAGAAGGACGCTGGA		
401207	LOC401207	XM_376423	AAGGGAGAGACAGACAATAAA	AAGATACAACTTAACTTTAAA		
401210	LOC401210	XM_379359	CCGGTCCACTGTGGAAGGCAA	CAGCCAGAATCTCGCATGTAA		
401215	LOC401215	XM_379368	AAGCTCAGGCTGTGAAATTAA	AACGATAATTTGTGAAAGTAA		
401217	FLJ40453	NM_001007542	AAGAGATTGCTTTGTCCTGAA	CACGATGTCTATTAAACAGAT		
401220	LOC401220	XM_379378	AAGAAATTAGGTGAAGAATTA	AACAATCACTATAGTAAGATA		
401224	AACSL	XM_376454	CTGGTTGACCTTGCAAATTGA	AAGCAGATGCTTGTAAGCTAA		
401236	LOC401236	XM_376469	ATCAATCTATATTATCTTAAA	AAGGTTAGTTGAGTAAATTAA		
401254	LOC401254	XM_379406	CCAAATGGGACTGAACTTTAA	CAGGAGAACCATCACAAGCTA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
401262	CRIP3	NM_206922	ATGCCTGAAGTATGGCATGTA	AAGTGATGTCATTAAGCAGAA		
401278	FLJ44955	NM_207500	CCCATTTCATCTAGAAAGTAA	TAGAGGTTTGTTAATCTAATA		
401281	FLJ27255	NM_207501	CAGCTAGGTAAGATCATGTAA	GACCATGATACTAACAATAAA		
401308	LOC401308	XM_376576	TGCCCAGTTTGAAGAATTGAA	ATCCTCTATTGTTCTGACAAA		
401328	LOC401328	XM_379485	AACGTTTAACACAGACATTAA	AACCTAATAGTCTTAGCCAAA		
401400	LOC401400	XM_379518	CTGGAATTCTACAGCCATGAT	CTGCTGGGAGAAAGAATGGAA		
401431	LOC401431	NM_001008745	ATGACTTTGATTTCTGCATAA	CAGGGAATTATTCACATGGCA		
401470	LOC401470	XM_376787	AAGGGCAAGGCCATTAAGAAA	CCGCCACCACGCGCAGCCTAT		
401472	FLJ45248	NM_207505	AGGGTATTTCCTAGCAAGAAA	TAGGAAGAATTTCCTGACAAA		
401476	LOC401476	XM_379603	AAGCAATTTGCTCAAGATAAT	ACCCATCAAGAGATTAAGTAA		
401477	LOC401477	XM_379605	CAGGATGCTGTCACAATTACA	TCAGGAGTAATTGTTAACTAA		
401480	LOC401480	XM_379608	CAGCTTTGAGGTCCTAGGAAA	CAGAGTTTCCTTCCCAGCTAA		
401495	LOC401495	XM_379625	TACCAGGAAACTTGAGACCAA	CACACCCTTACCAGACTTCAA		
401497	LOC401497	XM_376822	CACAACAACAGTATAACATAA	TTCAATAAAGTTATCAATAAA		
401499	LOC401499	XM_379628	AACGGGAAAGCTCTTGGAACA	TTGAGCCAGTTTACAAAGAAA		
401508	FLJ45202	NM_207507	CTCAAAGGCTGTCCACAAGAA	AACCCTGTCTGTCTCTACTAA		
401537	LOC401537	XM_376888	CCAGATGAAACAGTACATCTA	CACCTACATCACAAATCTGAA	CACGGAGGCATCTTATGTTAA	CAGACTGGTTTGAAGGAAGAA
401539	LOC401539	XM_379648	AAGACGTAATAGAGATTTCAA	CTCGTAGTCAGTGACAAGTAA		
401550	C9orf148	XM_379667	AAGAAGAATCCTAACCTCAAA	AAGGGTCGTGGTGAGAATCAA		
401584	LOC401584	XM_376986	ACCAAGTACTCCAGATTAATA	CAGCTTGAACTGTTGCCTTAA		
401607	LOC401607	XM_379717	ATTGATCAGCCAGCAGTCAAA	CACTCGCCAATTAGAGATTGA		
401679	LOC401679	XM_377185	CTGCAAGGCGTGCCACCTGAA	CCGGTGCTCCTGCCTTGTGAA		
401704	LOC401704	XM_377231	CTACTGGATGATGACAATGAA	AAGCAGTAGATATGAATAATA		
401713	LOC401713	XM_377259	TGCCAATATGGTCAACAGGAA	TCACAAGACCTTCAATTTAAA		
401855	LOC401855	XM_497509	CTGGCCTACAAGAACACATAA	AAAGTGGGTCACCAAATGCTA	CCAGGCCGCTTTGGAAGCGAA	CCCTCGAGAGTTGGAAGTCAA
401876	LOC401876	XM_497534	CATGGTATCAAGGGAAATATA	CCCACTTGAATTGCTCAACAA		
401891	LOC401891	XM_377488	CTGCTCGTAATGGATCAACAA	CAGATTTAACTGCAATAGATA		
401895	LOC401895	XM_377500	AACAGACCTTCCGCAACTTCA	CAGCAAGACGGCAGAGGTACA		
401896	LOC401896	XM_377511	ACCAAGTTCAATGCTGATGAA	ACGCTCGGAAGGGTTGACATT		
401921	LOC401921	XM_497630	CAGGTCTTCGGTGGCAAGAAA	CCCGGTCACTACACTATGAAA		
401943	LOC401943	XM_497659	TGGGAGGACGAGAAGAGCCAA	AAGCCCTTGGAGAATGAACTA		
401945	LOC401945	XM_377579	ACCGGATATGCAGCTCTGAAA	CCGGAGAAATCTGCAGGTAAA		
401980	LOC401980	XM_497729	CTGAGTGACGTTAATCACTCA	CGGGAAGCTGCTGGTGATCAA		
402011	LOC402011	XM_497758	CACAATATTGGTGGTATCAAT	TACCATCAACTTGTCCAACTA		
402036	LOC402036	XM_377696	CACGGTGCTCTGGACCGTCTT	CCTCATCAACATTGACTTTCA	CTGGAGAATGACAGCCACACA	CACGGAGGTGAGAGAGAGCAA
402037	LOC402037	XM_497793	CTGGGCCTGCCTGGACCATAA	AAGGATGAGAGGGAAGCAGAA	CAGACGCTGAGGATTCTTGTA	CCCGAAAGATGTGGGCATTAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
402055	LOC402055	XM_377713	CCAGGATTGAAGGAAGGGAAA	CAGGAGTTTGCTAGTGGGACA		
402057	LOC402057	XM_377716	AAGAAGCTCCGCAACAAGATA	CACGCATCTGATGAAATGGAT		
402072	LOC402072	XM_377741	CTGGTACTTCTTATGACACTA	AACATGGTCTATAATGTGTAA		
402094	LOC402094	XM_377755	CCGGGCATCTGCATTCCGGAA	CAGAAGGAAGAGAAAGTGCTA		
402095	LOC402095	XM_377756	TGCCATGGAAATGGTCCAATA	CAGGTTTAACCACCAGTTTAA		
402112	LOC402112	XM_496610	CTGTCTCAGGAGATTCTCAAA	CACCCAAGAGATTATCCTGAA		
402146	LOC402146	XM_497943	AAGCCTGAGCCCATGGAGAAA	ACGGTTATGTATGTAGCAAGA		
402184	LOC402184	XM_497977	GACAAGAAACTAGAGCAATAA	CCAGCATGTGGAATTCTTGAA		
402196	LOC402196	XM_497991	CTCCTTGTGGCCCACAGCCCA	AAGCCATTCCTCATGCCAGAA		
402199	LOC402199	XM_377875	CCGCTGCAGCCCAAGCATTTA	CTGCAGAAGAATCATGTTCTA		
402200	LOC402200	XM_377877	TGCCATGGCTGGAATAGCCAA	CCGCTGCAGCCCAAGCATTTA		
402253	LOC402253	XM_377935	TCGCCTCAGATCTGACCAGAA	TCAGAGTGTTTCAAATGTGTA		
402330	LOC402330	XM_378015	GAACTACGATAAGTTCTCATA	GAGAACTACGATAAGTTCTCA		
402353	LOC402353	XM_378043	ACGGGACGGCTGCCCAATGAA	CGCGGATAATCGAGACTGCAA		
402367	LOC402367	XM_378064	CAGGCACATGCTCCTGCTTCA	CCCAAGCATTCCCGACAGGAA		
402388	LOC402388	XM_378103	CAGATGTGCATTGGAGACTCT	GACGTGGGCATTGGAGACTGA		
402397	LOC402397	XM_497102	TCTGGAAGTATGTATCTACCA	CAGGATTTGATGGTGCTAGTA		
402485	LOC402485	XM_380104	CTCATTGACAAGATTAACATA	AACGTTTAACACAGACATTAA		
402504	LOC402504	XM_380107	CAGAGCTGGATCTACCATGAA	AAAGATGACTGAAGAATGGCA		
402522	LOC402522	XM_379849	CGCCGAGGATTTCAGAAGATA	CAGGAGGGTTGGACACGGCAA		
402523	LOC402523	XM_380114	AAGGGCATACATGGTAATTAT	AACGTGCTAAGTATCAGTAAA		
402532	LOC402532	XM_380117	CGGAGAAAGACTGGTCTTGAA	CAGACTTGGTGTTATGGTAAA		
402563	LOC402563	XM_380128	GCCGGGAGGTTGAGTAGAGAA	CAGAAGGAGTGGAGACATTGA		
402604	LOC402604	XM_379939	CAGGAATTCCTTATGTGTGAA	ACGGTACTGAACAGACAATTA	ACCAATGTTTACAAATATGTA	CACCATGAAATATGTCTTCTA
402634	LOC402634	XM_379987	CAGAAGGTGGAGAGGTCATCA	CCGGCGATGCTGCGTTGCCAA		
402641	LOC402641	XM_379995	AAGACATGAGGGAATCATTAA	ACAGCTGGATATAAACCTGAA	CAGAAGAAGTCTTGTCATCAA	TTCCAGGTTATTGATAAGAAA
402669	LOC402669	XM_380011	AGGCACCACTCTGAAGACAAA	CAGGTGGTGTCTATGATGCAA		
402716	LOC402716	XM_380072	AACACTGGTTATGGGAACAAA	CAGGGTTTGGAGAACATTCAA		
403282	OR6C65	NM_001005518	CCCGTGATTATGGGCCTCCAA	CTCCTACACACTCATCCTTAA		
404033	FLJ34077	XM_495846	AAGGGAAACAAGAGCATAAAT	CAGCCTGATGATGCAGTAGAA		
404550	MGC17624	NM_206967	CCCAGATGATGGAGAAATCGA	CCGCAGTGAGCCCACCAAGAA		
404552	SCGB1D4	NM_206998	AAGAAACGACTCTCATTGAAA	CTCCAAGTTGCCAAACTTAAT		
404785	POTE14	NM_001005356	CAGAAGCAACTTTCTGAAGAA	CAGGAAGAAATTGTCATGCTA		
407835	LOC407835	NR_002144	CAGGGAGATCAGCATCTGCAT	CAGCCCGTGGTCGACAGGGAA	CTGCTGGACTATATTGTGAAA	TTCCAGGAGTTTGTCAATAAA
408263	MGC27121	NM_001001343	AAACAAGATAATATTAAATAA	CAGCCTTATATTACTCCATAA		
414153	SNRPEL1	XM_034623	AACCTCATCTTCAGATACTTA	TTGCAAGTGTGCTCTTTGTGA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
414918	MGC33692	NM_001001794	CCGCGACAAGGCGCTGCTCAA	CACCATTGTCTCAGCAGTAAA		
415116	PIM3	NM_001001852	CACCGCGACATTAAGGACGAA	GAGCGTTTAATTTATTCAGTA	CTGTCAGAAGATGAACATGTA	ATGAACATGTATAGTGGCTAA
439919	LOC439919	XM_498448	TGGGTATTAATTCTCACTGTA	CTGTATAAGTGAAGACATTAA		
439928	LOC439928	XM_498427	AACCAGCAGAACAAATACAAA	TTCTTACTTTGATGGGAACAA		
439952	LOC439952	XM_495799	ATGCTGAAACATCGAAGTCCA	CCGAGAAATCAACGACCTATA		
439957	LOC439957	XM_495805	TACCCTTACCATCAATGCCAA	CCGGGAGACAGCCAGACTCAA		
439959	LOC439959	XM_495806	CACCAAGACTATCAATTTGAT	AGGGAAATTCATCTATTTATA	AAGATGCAGGATCATGGCCAA	TAGGTATTCAATAGCATTAGA
439982	LOC439982	XM_495828	CAGAATCAGATGTTCCAGCTT	ACGGGCTTATTGAGACCCTCA		
439985	LOC439985	XM_495832	AAAGCGATACATTGTCTATTA	AAAGATAAGAAGAAGAAGTAA		
439994	LOC439994	XM_498491	CAATGTCTTTCTTGTATTAAA	TACAGATAGGATTACACTAAA		
440000	LOC440000	XM_498494	CCGGCTGCTCGTCACCGCGAA	GACAATTTACTTGACTGGAAA		
440004	LOC440004	XM_498497	ATGGTATTTCTGGTTATTAAA	CCGGAGTGGTTCTGACTTTAA		
440021	KRTAP5-2	NM_001004325	CTCTCATGTCTGTAAATCAAA	AATGAATTTCCTTGCAATAAA		
440042	LOC440042	XM_498516	ATAGTAGATTCTATCAATCAA	CAGGTGAACAGAAGTTCTCAA		
440050	LOC440050	XM_498520	AGGGTCCATTCCTCACTATAA	AGGAGAGTCCACCCTAATTAA		
440055	LOC440055	XM_495885	CAAGATTCAGGTTCACCCGTA	CAGGTTCACCCGTAACCCACT		
440058	LOC440058	XM_498524	TTGGAAGAATTGTGTTATATA	AAGGGTAGACTGAGTCTTGAA		
440066	LOC440066	XM_495897	TAGGGTCAAATCAGTCACTCA	CACCTGCATTGTGCAAGGAAA		
440071	LOC440071	XM_498531	CCGGAGAGGCCGAGTGATCTA	CACAATTCTCTCTCTCCTTAA		
440077	FLJ16353	NM_001004328	CAGCACATAGTTAGTGCTCCA	TTGACAAATCAATATATTAAA		
440079	LOC440079	XM_498535	TGCAAGGTACTTGACACGCAA	AAGAGAGAATAGATAACTTCA		
440083	LOC440083	XM_498536	AAGAAGATGAGAGTGATTCAA	AAGGAGACAACAAGTCCCGAA		
440093	LOC440093	XM_495919	ATGCATGTTTCTGTATGTTAA	ACCAAGCAGACTGCTCGTAAA		
440098	LOC440098	XM_498543	ATCGGGTAAAGGAGTCGATAA	CTGGAGACAAGTGGACCCTAA		
440101	LOC440101	XM_498545	CAGAAGTTTATTTCTCACTTA	CACATAGATTACACTAAATAA		
440102	LOC440102	XM_498546	GAGAATGTTGCTGCCACTCAA	AAAGAAAGGAATATCATTATA		
440106	LOC440106	XM_495929	AAGAGGGTCCATCGCCATCAT	AGGGCTGGAAGTAGGCCTGAA		
440112	LOC440112	XM_498548	AAGATGTTGTTTCAACCTGTA	AAGCTTTAAGTTGCAAATGAA		
440134	LOC440134	XM_498562	CCACTCCATAGTGAATGGTTA	TTGATTGTCTTTCATCGGAAA		
440138	LOC440138	NM_001004127	AACGGTCAACAGATACTAGAA	CTCATTGTATGTGGAACTTTA		
440142	LOC440142	XM_495960	ATCCAGTTCATCTCACTTCAA	AAGCCTTTGAGAAGCATGAAA		
440151	LOC440151	XM_498568	CACCAGCATTCCAGAGTCCAA	CTGGAAATAAATAATTCATAA		
440153	LOC440153	XM_495967	CAACATATGCACTGACTATAA	CTCACTCTTTACTACAACATA	CAGCAACTTCACAACCCAGTA	CAGGCCTCAGATAGACGCCAA
440155	LOC440155	XM_498569	TACAAATGGAGACACAGGAAA	CCGGCTGCTGCTTACACCTTT		
440157	LOC440157	XM_495969	AAGGGAAGCCAGGCTGAGATA	CAGAGTCTGCCTCCATGAGAA		
440186	LOC440186	XM_498579	AGCCTCGGAAATTTCCTTTAA	CCCGGAAAGCAGGGCATTCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
440190	LOC440190	XM_498580	AAGGAACTTTGGGAAGATGAT	CCGGGCCTCCTTGAAGGTTGA		
440191	LOC440191	XM_498582	TAGCATAAGATGCTTCCTTAA	TACTTAATAAATAAACATTTA		
440228	LOC440228	XM_496031	CTCCTGGGTAGATGCATATAA	CAGCCCAAGGACAGCCAATTA		
440232	LOC440232	XM_496036	CTGTGCCTGGCCTGTATTGTA	AAGCAGGTGGATGCAAATGAA		
440233	LOC440233	XM_496037	CAAGAAGGCAAAGACAATAAA	CACCTGGAAGCTGCCATCTAA		
440242	LOC440242	XM_496040	TGCAGAGATCCAGGATACAAA	ATACAACAGCTTCTTAGGTAA		
440243	LOC440243	XM_496041	CACCTGGAAGCTGCCATCTAA	GTGCATCCTCACGTAAGTGCA		
440245	LOC440245	XM_496042	CCCAAACGAGGTGATCGACTT	CTCCTTTCGGTGCATGAACAA		
440252	LOC440252	XM_496049	AACAAGAAACAGAAAGCCAAA	AGAGATGAGTATTCTGAACAT		
440254	LOC440254	XM_498602	CAGCTGCTGCGGCGCCATGAT	TTGCAAATAATGAGAAGCCGA		
440266	LOC440266	XM_496062	CTGCAGCAAAGCACATACAGA	GATGAGTGTGCTGAACATATA		
440274	LOC440274	XM_498608	CTTGAGAATTATGTAGAATAA	CAGAGGTCATCTTTAAGTAAA		
440277	LOC440277	XM_498610	AACATTGGCCAGGGAAGTTAA	CAGGATGGTGACTTGTCTTTA		
440284	LOC440284	XM_498614	ACGGAAAGCCTTTATAATGTA	CAGAATGTTATTAATCTTTAA		
440298	LOC440298	XM_496086	CCGGGACCCTGCAGAAATGAA	ACCCGGGATCCTCAAATAGAA		
440301	LOC440301	XM_498620	ATAAATTCTCACACACACATA	CTGCCCTGTTCTATAGCTATA		
440303	DNM1DN11-13	XM_498621	TTGACCGTTGCTGAAACTTGT	CTGAGCATTCATCTGAACTAT		
440307	LOC440307	XM_496092	ACGCAGATCACTGGCCATCAA	ATCGAGGACATCATCATCAAA		
440317	LOC440317	XM_496097	AACCCTAGTGTTGGTACAGCA	CAGAGCGTTTCAGGCAATGAA		
440329	LOC440329	XM_498628	TCCCAAGTCAAAGACACTCCA	CGGCTTGAAGGAACAGGGCTA		
440334	LOC440334	XM_498631	TTGTAACTACTTGAAGTTAAA	ACGGTCTTTCTTTGCCAACTA		
440344	LOC440344	XM_496123	CACGGGAGGTGACATGAGCAA	GAAGGAGAAATTCCAAAGAAA	CAAAGAAATGTAGTTTATTTA	CTGGCTGTGAAGGACCCTTTA
440361	LOC440361	XM_496145	AGGGAGCAGTGAGGACACCAA	CACAACGATGTGCTTAGTAAA		
440370	LOC440370	XM_496158	CTCCTTGTATCTTCAAATGAA	ATGGTATACTTTATTAAGAAA		
440372	LOC440372	XM_496161	GCCGATGGAGATGCCTATGAA	CACGGAGAATGACCAGCTCAA	ATGGACAAGAAGAAAGAGTAA	CGCGGGCGTCTAGGCAAGAAA
440374	LOC440374	XM_370980	ACCTATTTATGAATATACAAA	AAACCATTAAACAGATTTCTA		
440380	LOC440380	XM_498645	AACCCAAGAGAAAGTCAGAAA	ATGGAGGAATGAGGAGTTCAA		
440387	LOC440387	XM_496169	TACCACCACGCCCGCTGTGTA	CTGCCTTAAGATTTCCCATTA		
440391	LOC440391	XM_498650	ATGGTATTGGTGTAACATGTA	AAGGATCGCATGGCAGAACTA		
440414	LOC440414	XM_496194	CGCGGATAGTGTGCAGGCATA	CCTGGTGTTGTCAATCATGAA		
440426	LOC440426	XM_498662	TCCCAAGTGGCTAAGACTTAA	CAGGATTAGCTTGTGGTTTAT		
440432	LOC440432	XM_498666	CCGGGCATACTTAGTATCTTT	CTGGTTGGTAAAGAACATTAA		
440434	LOC440434	XM_496214	GCCGCAGGCGTTATTCCTAAA	CAGCCGAAAGAGCAACTCATA		
440435	GPR158L1	NM_001004334	AACCAAGGAAATGGCCGCAAA	CAGGTGTGTATAAATCTGACA	ACAGAAGAATTCACTACTGAA	CACCATCATACTCAAGCTTTA
440447	LOC440447	XM_496231	TCCCAGGGTCTCTACAGATTT	AAGGAGTTGCAGGAAGCATTT		
440449	LOC440449	XM_498675	CTAGATGAAGAGTTATCTTAA	CTGGAGTTCCTTGACTAGGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
440455	LOC440455	XM_498678	CCCGAGGCTCCACGTACTCAA	CGCGCTTGTCAGGGAACAGAA		
440461	LOC440461	XM_498680	CTTGTGATGTGTGGAGATCAA	CTCCCTGGTTATACTGTTATA		
440462	LOC440462	XM_498681	CCGGGCCTTGTGAACCTGCAA	CACCCTGGTCTTCTCCTGTAA		
440472	LOC440472	XM_496255	ATGGCTATAACAACAAACTAA	CAGACTCTTCTTAGAAGTCTA		
440484	LOC440484	XM_496268	CAGGATCATCCATACCCTAAA	CACTGTAACATAATCCATTAA		
440493	LOC440493	XM_498698	GCGGCTCAGTTTCACTAACAA	CCCGACTTTCCGTGCAATAAA		
440495	LOC440495	XM_498700	GGCGACATATACTAACAACAA	CTGGTGTTACATTATCAACAT		
440498	LOC440498	XM_498704	ATGGTGCAAGCTGGCATTGAA	CTGGTAGATTATCATGGAGTA		
440501	LOC440501	XM_498706	CGGAGCAGAGTTCTCCTCAGA	CAGATTTCAGTGGTACTGCGA		
440508	LOC440508	XM_496285	CAGGGCTACTCCCACTGGTTA	CTCCATAAGCCTCAGAATGAA		
440526	LOC440526	XM_498718	CAGCAACCACGCCACCATGAA	CTGAACAGGGTTCTAACCAAA		
440536	LOC440536	XM_498721	CAGGCATCACATCCAGACTCA	AGCCTTTGTAGGAACGAGAAA		
440546	LOC440546	XM_496328	AAGCAGAGAAATGCAAACTAA	TTGCTTCAAATAGGGCCAGTA		
440551	LOC440551	XM_496331	GAGGGAGATGCGCTCCCTGGA	CCCGCCTCTCGTGGTGCTCTA		
440552	LOC440552	XM_496332	CTCCAAATATCTCATCAACAA	AACCAACACACTAACCATATA		
440554	LOC440554	XM_498731	AAGCACAGTTTCCTATGACAA	CACGTCACTCAGAAAGTTGAA		
440563	LOC440563	XM_496344	TCGAAACACCAGCGCATATCA	ACCAGCTTCATTTGATCAAGA		
440567	LOC440567	XM_496348	GAGCTCTATGATGAGCATGTA	CTGCTCGTGTTAAATCTAGAA		
440568	LOC440568	XM_496349	AAGGTCTTAAGTGCAGCAGGA	AAGCTCTTTGTTGGAGAAGGA		
440572	LOC440572	XM_498736	CCGTTTAATATCAGAGAGAAA	AACCATATTTATGAAAGTAAA		
440583	LOC440583	XM_498743	CCGGGATGACCTAAGGAACAA	CAGAGAGTGATGACTGCTTAA		
440586	LOC440586	XM_496361	TCAGGTTATGTTGGAGCTAAA	AAGCGAATTTATGATCTGAAA		
440587	LOC440587	XM_496362	CAGGCAGTCATGTGGCCCGAA	CCCAAACATCTTATTGATACT		
440596	LOC440596	XM_498746	TTGGGTTTCCTTCAGTCTCAA	GTGGGTGAAGTGGAAGAACAA		
440606	LOC440606	XM_496385	CTGGAACATGTAGGCCTTGTA	TAGCTACAGCATATTATTTAA		
440607	LOC440607	NM_001004340	ACTGTGAAAGGCCTCCAGTTA	CAGCAGGAATATCACAATACA		
440609	LOC440609	XM_498754	AAGCCTTGTTAACTTGCTGAA	CACATCGTGTTTGGGATCAAA		
440665	LOC440665	XM_498809	CACCAAGAAGTTTCTGACAAT	GAGAATGTTCCTCTTCAGTAA		
440667	LOC440667	XM_498810	CAGCAGCTGTTGCCAAATGAA	CACGCGGGTTCTGCCCTCAAA		
440678	LOC440678	XM_496401	AAGGATGTCATCAAAGTAGTT	TAGGAGATCTTTCACTTGTAA		
440683	LOC440683	XM_496404	GAACATAAGTTTCTATTTCAA	CAGAGGCGCTTCAGGAAGCAA	AGGAATGAACATAAGTTTCTA	GTGCAATTCGTCAGAACTTAA
440684	LOC440684	XM_496405	CTCCTTGTCAGGAGCACCTAA	AGGGATTATTACTCACTGCAA	CTGCAACTTAGCCTAGCATTA	TAGCATTAAGTTGCTTGACTA
440692	LOC440692	XM_498820	AAGCAGATCAGTGCTCAAGTA	TAGGAGTTGTAGAGCAGAGAA		
440696	LOC440696	XM_496420	AAGCCAATTGATGACATATAT	AAGCGTAAAGCTTGAAATATA		
440705	LOC440705	XM_496427	CACCTTCATGCTCAGCATTCA	TCCGAATTTCTTGATCAAGAA		
440707	LOC440707	XM_498827	CCGAGACTCAGACTTACCCAA	CTGCATCTTCTCATCCCATAT		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
440722	LOC440722	XM_498831	AGGCATCACGTCCACATGCAA	CAGTGTGGCATGGGCATGTAA		
440724	LOC440724	XM_498833	AAGGGAAAGGGTGACCACATA	CACTGTGAAGAATATATTAAA		
440725	LOC440725	XM_498834	TTGCATCAAATGGGACCTTAA	ACGAGACTTACAAATAATAAA		
440730	TRIM67	NM_001004342	CTGGCTTTAATAGTGATTCAT	TACCTAAGTTCTGGTATCTAA	CCGGGAAGTGTACGTCGGTAA	CACAACTATCTCAGGCCTTAA
440747	LOC440747	XM_380170	ATCCAATTCTCTACACCATAA	ATGCAGAATCAACAACAACAA		
440752	LOC440752	XM_498844	CTGCTTGAAGCTGGCATTTGA	ATGGCTGGTTACTGTGCTAAA		
440757	MGC44328	NM_001004344	ACAAGTGTTAATCCCAATAAA	CAGGGAAGACACAGTCACTAA		
440764	LOC440764	XM_496476	CACGGTGCTCCTGGAGGCCTA	CACGCTCACGGTCAAGTATGA		
440765	LOC440765	XM_498851	CAGCAGTAACTTATTAAATCT	CACAGCCGAGTTGCTAGCTAA		
440766	LOC440766	XM_498852	ACCCATGAACATGTACAATTA	ATGGCTAATAATCACATGATA		
440771	LOC440771	XM_498856	CCGGTAGCCAGTCAGAATTTA	CACGGTCAAGACGGAAGCAAA		
440772	LOC440772	XM_498857	AAGCAAATGGCTCATTTCCAA	AACCTCTAAGATTTGAATGAA		
440773	LOC440773	XM_496481	CAGGTAGATGATAAGGAGATT	AAAGAAGAATCTGAAGTGAAA		
440786	LOC440786	XM_496488	CTGGCGTTAAAGAGGTCCATA	TAGAATATGGAGGCCCTGAAA		
440787	LOC440787	XM_496489	TAGACTCAGAGAGATGGCAAA	CAGAACAAACATAGTACGGCA		
440788	LOC440788	XM_496490	ACGGAGCATTACATTCCCAGA	CCCGGAATCAATGGGAATGAA		
440790	LOC440790	XM_498869	AACATTCTTCATTATGCATAA	CAGCAGGTGTTGCTTAGTGAA		
440793	LOC440793	XM_496494	AAGGTCTTCTCAAATATTGTA	CTGCAGCGGAGCCATGGCCCA		
440804	LOC440804	XM_036936	AACAGAGATCCTGGATACCAA	CTGGAGGAAGACAGCTTATTA		
440815	LOC440815	XM_498875	GCAGATGGCGAGCATGGCAAA	AAGGGAGACCAAAGTTGGAAA		
440824	LOC440824	XM_496523	CAGATCCATGCTGATCCCGCA	CAGGGCGCTGAGTACCATGTA		
440839	LOC440839	XM_496539	TTGAGGGATTTCAGACTTCAA	AAGTCTTATTTAAGAAATATA		
440843	LOC440843	XM_498885	TTGAATTTGTGTTCAAAGTAA	CTGGGAAGAAAGCAACACAAA		
440854	CAPN14	XM_496548	CTGGAGTGACAGTTCAAGTAA	CAGGATGAATTCTTCACCAAA		
440855	LOC440855	XM_498894	CTGGACATATTTCTTCTGGAA	CCGGAACAGAGATTTACTCAA		
440856	LOC440856	XM_498895	ACGAACGTAATTTGTTTCTGA	AAGGGAGAGAAGAGAGTTGAA		
440857	LOC440857	XM_498896	TCCAGTCTGTTTACTATACAT	GGGACTCAAAGTATTAGCTAA		
440859	LOC440859	XM_498898	CCGGGAAGCCTGGCTCCGAAA	CACATTACAGTTAATCTGTAA		
440866	LOC440866	XM_496551	CAGAAAGTTTGTGAAGATCTT	ATGGTCTGACTTTCACAGAAA	CCGGTTCATCTAATACAGACA	CAGATTTGTCAAGGTTTGAAA
440867	FLJ16124	NM_001004345	AAGGAAGGAATTTATCTACCA	CACGAGAAATATTACGTTGTA		
440872	LOC440872	XM_496559	AAAGAGATACGTATGTACTTA	CAGTGGCTGTGAAGAATATAA		
440900	LOC440900	XM_498909	ATCCGTCACACTAGATGCATA	CCGGAGCCGTTTACAGTTTGA		
440923	LOC440923	XM_498916	AACAGTGAATAAGCACCATAA	TAGGAGGAAGGCCACAACTAA		
440925	LOC440925	XM_496609	CAGAGGTTAGCCTAACTACAA	ATAGGTTTAAGAGTTAATATA		
440927	LOC440927	XM_496612	AAGATCAATGCCCTCATTAAA	AAGAAAGTGGAAGCAAAGAAA		
440930	LOC440930	XM_498918	CCGCTAGGTGTAGGACCGCTA	TTGGCAGAATACTCAGGTCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
440937	LOC440937	XM_498922	ACCTGAGAATTCAATGATGTA	CCCAACCTACAGGAAGCATAA		
440940	LOC440940	XM_498923	CAGGGCGACAGTGTAGGGCCA	AGCCTGCGTCTCAGCAGCAAA		
440954	LOC440954	XM_498932	CTCATTTACCTTCCACATAAA	AAGGAACAGATGTACAGTAAA		
440959	LOC440959	XM_498934	CTGCACCAATTCGCTCATTTA	CAGCCAGTTCATAGACACCAA		
440960	LOC440960	XM_498935	CGGGAGAATATGCAGCAATAA	CCGGCTCAGGTATTTATTGAA		
440965	LOC440965	XM_498938	CGGCAGACACACCACGTTCCA	TAGGTCTATCAGTGCTTTGGA		
440970	LOC440970	XM_496650	AAGGAAGAGAGTGATTATATA	CAACATCTTATTGCTATTTAA		
440971	LOC440971	XM_496651	ATGGAGTAAACTACAGCTTAA	TAGGATATATTTGTCCCTTAA		
440978	LOC440978	XM_496659	CAGGGTAATCACGGAATCCCA	AAGGGAGAGATTGGTGATGTA		
440990	LOC440990	XM_498952	GAGGATGTATGTGATGAGTAA	CTGCTGTAAACCAATGTTAAA		
440992	LOC440992	XM_496668	TTCGCTCTCGCCGCCGAGGAA	AAGGAGGAGTTCGAATGCCTT		
440995	LOC440995	XM_498955	CCAGAACTGGCAGCCCTTAAA	TAGCGTGCCGTGGCCATTGAA		
440997	LOC440997	XM_498957	AAGGTTCATAGTTGTGTTGTA	TAGGCTATTTCAAGAAATTAA		
440998	LOC440998	XM_498958	TGCAGAATTCATTATAATAAA	CAGGTGAGACTTCACCGTGAA		
441022	LOC441022	XM_496700	CACCCTATGGATGAACAGGAT	CACAAGCATCTGATGAAGCAA		
441023	LOC441023	XM_498970	TCCCTCCATCCTTGCCCTAAA	ACCATGAGTTGTCACATCTAA		
441027	LOC441027	XM_496707	CGGAATGACCTTACTTGGTAA	TACCATTAAATTCAGCTGAAA		
441030	LOC441030	XM_498973	AAGAATCTTTACAAAGCTGAA	AAGGATGAGAGTGGATGTCAA		
441035	LOC441035	XM_496713	CAACTTGGTAAGAACACATAA	GTGAGAAATAATACTCATAAA		
441042	LOC441042	XM_498981	AAGGTTTGCTCTAACCTAGAA	TAGCAGGAATTCTTATATCAA		
441050	LOC441050	XM_496721	CTGGAGTAAGAAATATTTCAT	CTGGCTTAGTATGGACTTCAA		
441053	LOC441053	XM_496723	ACCATTTGCAATGAAGAGGAA	AGGAAAGGAATTTGACATTAA		
441059	LOC441059	XM_498991	AACTCCCAATTTGGAAAGTAA	CTGCTAAAGAATAAATGTAAA		
441068	LOC441068	XM_496743	CTACAAGAAATCGAAGAGAAA	CACCAAGGAAATGAAAGTTCA		
441069	LOC441069	XM_498996	CGGGACCTGAACCGAGAGCAA	CAGGGTTCCATCAGGAAGGAA		
441071	LOC441071	XM_498997	CAGCTTGAACAACTCAGCTAA	CCCATGGATATTGAAAGGATA		
441073	LOC441073	XM_496746	AAGAGCTGAGACAGAAGTACA	AAACTGGACAAAGACTGTGAA		
441077	LOC441077	XM_496748	AGGGTTCAACCTCCAACCTTA	CCTGAGATCGATAAAGCTTAA		
441093	LOC441093	XM_499007	AAGATGGAGTTTGGAAGGATA	CTGGAAGATTCTGTTCATGTA		
441099	LOC441099	XM_496770	AAGCCTCAGAGTATTTCGAAA	AACATTTCACTTTACATCTAA		
441113	LOC441113	XM_496782	AACCACAGATCTCGTAGGAAA	CACGATGTATTTATTTGATTT		
441117	LOC441117	XM_496786	GTGGAAGAATTCATATATGAA	AAGGATCTTAGCTTTGAGAAA		
441118	LOC441118	XM_496787	CTGGAAGAGTAGAAACAGAGA	CAGGTGGTGTTTGGGTGCATA		
441128	LOC441128	XM_496793	AAGCCCAAATAGAGAACAGTA	AAGAGGCACCTAATTCCTTAA		
441129	LOC441129	XM_499026	CCCACTCACCGCACACCATCA	CAGGGCGCCTCTAGTCCCTCA		
441140	FLJ45422	NM_001004349	TTGGGAGGTGATGTCATATAA	CAGACGGTACATACACTCTAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
441141	LOC441141	XM_499031	CAGAATGACTACCCATGCAAA	AAGACAGGTACTGGAAGATAA		
441157	LOC441157	XM_499037	CCGGGATTCAGAATTGATCCA	CTGCACGTCACGGCTACTCAA		
441162	LOC441162	XM_499039	ATGGGACATGCATATAAACTA	TACCTAATACACTGCAATATA		
441165	LOC441165	XM_496820	CACCCTTAAACTACAAAGAGA	AAAGAAGACATCACCCTTAAA	CACCTGCTACTCAGAAAGCTA	TTGGAAGAGATTCTTATTAAA
441167	LOC441167	XM_499042	CAGGCAAGCTTTCAACTATAA	CTGAAGGTAATCAGAGATTAA		
441171	LOC441171	XM_499044	CCCAGAAACACTGTACTTTAT	ATGATGAATCACCAACACTAA		
441173	FLJ39824	XM_496827	CAGGACCATTTGACTATTTCA	TAAGTTATTTATACTCATTTA		
441189	LOC441189	XM_496843	CCGGGCCTCAGTTTCCCGGAA	CCCGGAGGAGATCGCGCGCAA		
441199	LOC441199	XM_496855	AAGGATACTTGTTAACCTTAA	TCCAGCTTTGTTGGTATTCAA		
441209	LOC441209	XM_496859	CTGGCTGTCAATTTATCAGTA	AGGAAGATTGTTGGTGATGAA		
441215	LOC441215	XM_496862	TTGCAAAGAGAAGAAGATCAA	CAGGGTGTATGAGGAGAGAAA		
441220	LOC441220	XM_496867	CAGCATGTCTTCAGCCAGGAA	CTGGTGGTTGTACTCAGATAA		
441221	LOC441221	XM_496868	CTGAGAAATGGAATAATCGTA	CAGGATGAACGGCGCCAGGTA		
441235	LOC441235	XM_496880	CAGGTCATATCCTGAGATCAA	CACTGTCCTGATTATAAATAA		
441243	LOC441243	XM_376622	AGGCCAAAGCTTTGTATTTCA	ACAGAGTGGTGTGGAGAATAA		
441268	LOC441268	XM_496908	TTGCTCCATACAGACCTCCCA	CTGCTGATTTCTTCACTTGCT		
441307	LOC441307	XM_499093	AAGGATGTTTGGAGGCTTCAA	CCGGCCTTCGTTTCCATTCAA		
441309	LOC441309	XM_496942	CTGAATGATATTTAAGCTGAA	GGCGACCTTGCTGCAGGACAA		
441313	LOC441313	XM_496945	GACGTTGTAGTTGGCGTGGTT	CTGGAATGCCTTTGTACATAT		
441328	LOC441328	XM_496957	ACCAAAGAGCGTGGAAGGAAA	TCCGGATCAGAAGGAGCAGGA		
441333	LOC441333	XM_496962	TAGGGAAGGGTGGTTCTGCAA	CACCTTGGATCTAGGAGACAA		
441336	LOC441336	XM_499101	CACCAGGACCTGAAATGTTAT	CCAGCTGGATATCACGGGAAA		
441377	LOC441377	XM_496991	AAGGAACAACGGTCACACCAA	CCCACCTTGATTTAGACCTGT		
441386	GD:PTPRD	XM_497007	CCCAAGCTGTATGTGAAGCTA	AAGGACAAGGCCATTAAGAAA		
441395	LOC441395	XM_497014	ACAGATCCTGGTCAGAGTAAA	CAGGTGCTGGTTATGCTTTAT		
441401	LOC441401	XM_499136	CAGCCGGTCAAAGCAGCAGAA	ATGACAGATTATGAGAATGAA		
441421	LOC441421	XM_497042	AAGGCGTGCTGTCGCCTGCAA	AAGAGGTTTCTGGGTCATCTA		
441424	LOC441424	XM_497044	AACACCCATAAGAATTCCTAT	CAGAAGGAACAAGCACAATAT		
441432	LOC441432	XM_376852	CAGGAAATATGATGCGAGGAA	CAGGGTGTACCATGGCATGAA		
441447	LOC441447	XM_497061	AAGGAGGAATTTCAGGGTGAA	TAGCACGATTTCCTATGACCA		
441450	LOC441450	XM_499151	CTGGGTTCTGCTGACATGTGA	TAGGACGAATTTCTTGCTCCA		
441454	LOC441454	XM_499153	CAGCTCTGAAATCATTGCCAA	TTGGTTTATATGATCTAGTTA		
441455	LOC441455	XM_497068	AACTGCTGTGGAAACCAAGAA	GTGCCTCTCCATGGAGATTCA		
441458	LOC441458	XM_499155	CTAAGTGGAGTGGACCATAAA	ATGATAATAGCTTACCACAAA		
441460	LOC441460	XM_499156	TGGGAACAATAAAGCACTTCA	CTGCACCTATTGTCACAGCAA		
441464	LOC441464	XM_499160	CTGGGATTAAGACACAAACAA	CAGGGACAACTTGGATCTTCA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
441467	LOC441467	XM_499164	CTGCTTGGCGGTAGACCTTAA	CAGGATCCTAACGAAGACCAA		
441468	LOC441468	XM_499165	AAGCAAGGTCTCGCTGTGTTA	TAGGACTTTCTTTGCATTCAT		
441471	LOC441471	XM_351854	AAGCGTCTTCGTCTTGCTCAT	CTGCACCTCACTGGAGCGGAA		
441474	LOC441474	XM_499168	CGCCGCCTGCTTCACTTCTTA	CCCAGGAGATAGAACCTTCTA		
441483	LOC441483	XM_497093	GGCCCTGATAAGGCCACCCAA	CCACGCTGGGTTTAAGTGACA		
441490	LOC441490	XM_497100	ATGGAATCAGCGACCACACTA	TTTGACCATTGTTAACAATAA		
441491	LOC441491	XM_499175	CCCAGTGGAGCACGTCCTCAA	CTCCAGAAACATGAGCACAAA		
441494	LOC441494	XM_499177	CAGAGGCATGAAGCTAGAATA	CAGGTTCATCTCATTAGTGGA		
441515	LOC441515	XM_497146	CTCACTAAAGCTCTAGTGCAA	CAGCACATTCAGTTAATGTTA		
441525	SPANX-N4	NM_001009613	CTGGAGAATAACCAGCCTACA	CAGAGTTTGAAAGAGACAGAA		
441528	LOC441528	XM_497181	CTGGCCCAGCATTTAAACTTA	CTGAATATTGTGCGCATGAAA		
441529	LOC441529	XM_497182	CTGGAGGAATCACCCAGTGAA	CAGGCCACTCAGGATATCCAA		
441531	LOC441531	XM_497185	AAGCCATTCCTCATACCAATA	AAAGTATAGTATATATTAATA		
441540	LOC441540	XM_351948	CTGGCACCCTTCAGATCCTTT	CCTTACGGATTTCGCGGTTTA		
441542	LOC441542	XM_497201	CAGCATTCTGACGCTGAAGTA	CAGGACATATGAGACTTATTA		
441551	LOC441551	XM_497216	TCGACCAATTTGCCAACGTTA	CTGGGAATATGGCTCCTGAAA		
441560	LOC441560	XM_497230	GCGGATGAGCACCAACCCTGA	CAGACGGCTTGTATCTCGCAA		
441561	LOC441561	XM_497231	ATGGACCAAGTGGAAGGCAAA	CAAGAGATTATATGACATGAA		
441569	LOC441569	XM_499192	ATCAGAAGACATAGCCAGAAA	CTGCAAGAAAGGCCTCAACAA		
441599	LOC441599	XM_497281	ATGGGTGACTCTTAAAGGTTA	CTGAATCTAGAGCTCATTAAA		
441631	LOC441631	XM_497334	ATGGTCCATTATAAGACTGAA	CAGCATGATGCCATTGCTGAA		
441634	LOC441634	XM_497338	CTGGAGCTCACTCGCATTCAT	CGGGAGTTGAAGGACTTGGAA		
441636	LOC441636	XM_497341	CAGGAACAACTGAACCATCAA	ATCCATATTGATGACAATAAA		
441663	LOC441663	XM_497381	TAGCAACAAGATGAAGACCCA	TAGCCGCAAACTAGACCCAAA		
441665	LOC441665	XM_497385	CCGGGACCTGTGACCCACTCA	CACCTGAGACCTGTCCTGTGA		
441682	LOC441682	XM_497406	CACCATCCAAGGTATCGTGTA	CAGGCCTAGCATAGTCCTTTA		
441696	LOC441696	XM_499197	CTCAGACATGCCTCCGCGTAA	CACAAAGAGTTTGTTACTGTT		
441706	LOC441706	XM_497431	TGGGATGACAGATGCATTCAA	CCAGGATATCTAATTCGCTAA		
441709	LOC441709	XM_497434	TCTGGTATTTATTACTAGAAA	CACCCTAAGTCTGCACTTCAA		
441740	LOC441740	XM_497477	ACAGCTGTACATATTATACTA	CAGGAAACTGCCAGAAAGTAA		
441754	LOC441754	XM_497493	TTGGAACATCGGCAACACAAA	CAGGATGAAGCTCATGCCTCA		
441755	LOC441755	XM_497494	CAGGCAATGGAAGATGCATAT	TAGATGAAACTTACAATATAA		
441759	LOC441759	XM_497498	CTGGCCGAGTTGCACCCTTGA	ACGGACGATGGAGGTCTGTGA		
441790	LOC441790	XM_497536	TCCAAACAGATTCCTTGGGAA	CAGCTTGTGATTGAGGACCTA		
441798	LOC441798	XM_497553	TCCGCGGTCTTTACCCTGGAA	CAGGAGCATGCAGGCCTACAA		
441816	LOC441816	XM_497584	CAGCAGGTGTGGGAAATCCTA	ATGGACTTGGTCAACATCAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
441821	LOC441821	XM_497592	AAAGATTGCTCCAAAGATTAA	CAGCAATATCCCATCCACAAA		
441826	LOC441826	XM_499202	CTGGGAATTCTGGATGTTCCA	CTGGGTATTCTGGGCATTCCA		
441827	LOC441827	XM_499203	AAGCCTATCTAGATCTACTAA	CAGCCTATCTAGACCTACTAA		
441833	LOC441833	XM_497603	CTCTCGGACATTAGTCACCAA	TCCCGAGAATGTGACATCTAA		
441842	LOC441842	XM_497614	AAGCTTCTAACGGGTTCTCAA	CTGAATGTGAGATAATTTATA		
441847	LOC441847	XM_497623	ACCCACCTTGTTAGGCATAAA	TCCAACCTCATTAAATATAAA		
441848	LOC441848	XM_497624	CAGTTGAAGATCAATAAGAAA	ATGCATCGAGTTCACACTAAA		
441866	LOC441866	XM_497645	ACCCTGATTTGTCCTGATAAA	TCCTGATAAAGAGAAGGCATA		
441874	LOC441874	XM_497654	CACGTCAATTACCGCGAGGAA	CAGTTCTGTATCAGTCTTGAA		
441898	LOC441898	XM_497698	AAGCTCCTTCTCCTATTATTA	TAGGCAGAATCCCGTCAAGAA		
441915	LOC441915	XM_497724	CCAGTTACATCTGGTGATCAA	AACGCTTATGGTATGAAGAAA		
441916	LOC441916	XM_497726	ATCCAGAGTATGGAGAAGTAA	CAAATCCAATATATTAAGAAA		
441922	LOC441922	XM_497733	CAGGAGAGACAGGACCCATTA	CAGGAGAGACAGGACCTATTA		
441925	LOC441925	XM_497740	CAAGTTCATGCTTATAAATTT	CAGGGACTACAGTGCCTTGAA		
441928	LOC441928	XM_497743	TGGGAAATATGAGGTCATGAA	CTGGAGGTACCTGCAGCGGAA		
441955	LOC441955	XM_497773	AGGGATGAGGTAGCAGAGAAA	AAGGCTATGAGAATACACCAA		
441959	LOC441959	XM_497777	CAGACCATGACAACAACATCA	TGAGCAGATCGCGGAGATCAA		
441994	LOC441994	XM_497814	TCGACAGACCCTGGAGGTGTA	CAGCACCATATCCGACATCAT		
442008	LOC442008	XM_497828	GACGACAAGAACTTTAGCAAA	CAGAATCAAATGATCCTGCAA		
442011	LOC442011	XM_497831	AAGCTTATTGATGGCATTCAT	ACGGCTTCATTTAACAGTGAA		
442016	LOC442016	XM_497838	CAGATAGATCTGTTTCAAGAA	AAGGGAAATGCTTGATGGTTA		
442020	LOC442020	XM_497844	CAGCATCATGAGCCAGTTTCA	CAGGCTGACTCGGTACGCAAA		
442022	LOC442022	XM_497846	CGAGCAACTCTCTGGGAACTA	TGAGGTGGTGTCCTTCCGTAA		
442044	LOC442044	XM_497872	CCAGGTGTCAAGGACAGCAAA	CAGCTCCATTGTCTCCCATAA		
442081	LOC442081	XM_497923	CCGCCAGACATTCCAATTGGA	CACGGGCTACATGACCTGTGA		
442093	LOC442093	XM_497939	ATCGTCATTGTTAATGAGCTA	AAGGCTGATTACGAGAGCAAA		
442099	LOC442099	XM_497951	TCGGACAGACCTCCACTTCAA	AACCCTCAGCTTCCATTTAAA		
442108	LOC442108	XM_497964	AAGGGACATGTGGAAGTAATA	CAGATTAGTCAAGAAGATGAA		
442119	LOC442119	XM_497984	CAGGATTTGAAGGAAGCCACA	AACGACATCTTTGGCACCAAA		
442121	LOC442121	XM_497986	CAGAATAGCTTTGCACATACA	CAGCTGGACTTTAAGAATGTA		
442124	LOC442124	XM_497989	CCCGCCTTCGTTATCATTTGT	CACCTTCTACCTCTTATTCCA		
442140	LOC442140	XM_498021	CTCATGGCTCTTGGAAGGAAA	CACCCTGGAAGAAACCATCAA		
442141	LOC442141	XM_498022	CTCAAGGAGCCTCATATGGAA	CCGGAGCATGGCAGAACTCCA		
442145	LOC442145	XM_498027	CCGGGTCCTAAACTCTGGATA	TAGGCTCTGGGTATAAGCTTT		
442158	LOC442158	XM_498040	TGCCAGCAAAGTCCATGTAAA	AGGAACAATAATTGTGCCAAA		
442174	LOC442174	XM_498056	CTGGCTCTGTGAATTCGAATA	CTGGTGGGAGTGAGAATTGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
442208	LOC442208	XM_498091	GCGGATCAGGTTCAAAGTGAT	CAGGACCAACATCCTCTCCAT		
442209	LOC442209	XM_498092	AACAATAAAGGCGAGATGAAA	CAGATCAAGGGATCAAGGGAT		
442228	LOC442228	XM_498111	ACGGAAGTACTTGGCATATAA	CACCATGTAGTTGTAATTCAA		
442243	LOC442243	XM_498127	CTGACACCTCAGGGTCAGAAA	CAGAGGCACCTATACCACCAA		
442272	LOC442272	XM_498157	AAGCAGAAGGACACAGATGTA	CCGAACCAGATGAAACCCAAA		
442339	LOC442339	XM_498230	GTGACTTTGAAGATAGCTTCA	CCGGTGAGTGGCAAACAACGA		
442350	LOC442350	XM_498243	CAGAAACAGGGAAATCCTGAA	CGGAATGGAAATACTTTCTAA		
442375	LOC442375	XM_498266	ATGGCTTTGCAAAGGAGCCAA	TGGCATCATCTCAGGAAGAAA		
442397	LOC442397	XM_498297	CCCGTAACAGATTTCCATGAA	CAGGTAGTAGTGACACATATT		
442398	LOC442398	XM_499238	GTGCGAGATGAGAAATCTCAA	CCGGGACAACTGCACCAGTGA		
442400	LOC442400	XM_498299	AACGACAACATGAAGTTCGAA	CAGGGACGCTTTAGCACTCGA		
442401	LOC442401	XM_378044	CCGCCTCTTTGGGCACCTTAA	CAGCGAGATGACCAAGACGAA		
442410	LOC442410	XM_498312	CGGTGTGAGCATGGCAGAGAA	CAGGGCCATTTCCATTGTCAT		
442429	LOC442429	XM_498335	CTGGCCAAGAAGCCATTCACA	CAGAGCCTGCGCAGTGTGGTA		
442451	LOC442451	XM_498366	CATGATGAACACAGTGTGAAA	CAGCTGAAAGTCAGGATAGTA		
442454	LOC442454	XM_498369	TGCATTGGACCTGACCATGAA	TACCTTGAACTGTATGTGCAA		
442481	LOC442481	XM_498410	CAGGATGGAGGCTACGAAGGT	CCGACCCACAGGCTCCAGTAA		
442524	LOC442524	XM_499272	CAGACTTGAGGGCCCAGACAA	CTCGAAGATGCCAGTATTTCA		
442535	LOC442535	XM_499279	TACTATGACGTCTCCAACTCA	ACTGTTTGTCATAGTGCCGTA		
442562	LOC442562	XM_499306	CAGTCACAATGAGTAATTTAA	CCCGTCGAACACAGCCACCTA		
442573	LOC442573	XM_499315	ATCGGGTATTGAGTCCATGGA	AAGGGTGGAGCACAACGTCAA		
442578	LOC442578	XM_499318	TGGAATTGGCAGCGTGGCAAA	TCCACCTTACATGCAGTTGTA		
442606	LOC442606	XM_499352	GAACAACATCATGGAGTATTA	CCGTGCCTTCTTCCACTACAA		
442608	LOC442608	XM_499354	CTTCCACTTCCTGGCCAGGAA	TGCAGTCCAGGAGGATTTGAA		
442616	LOC442616	XM_499536	TTGGACATGCATATTCCCAAA	CCCGGCGGTTATTCCGTTTAA		
442622	LOC442622	XM_499365	CAAGGAGAAACTGGACTAATA	CTGGAGGGCCTTTGACTTCAA		
442625	LOC442625	XM_499368	AAGCAGGAGATTAGTAATGGA	AAGGAGAAATTGAGCGATGTA		
442696	LOC442696	XM_499441	CAGTTACATGTTCTCATTTCA	CTCAAGCGGTACTACACATAA		
442699	LOC442699	XM_499444	AAGCTCCACAATTGCCAGGAA	AGCTGTGACCTTAATAATTTA		
442708	LOC442708	XM_499454	AAGAATTTGACAAGAAGGATA	CTGCCTTGTCAAGGCCATTAA		
442709	LOC442709	XM_499455	ACAGATCACATTGCATGCAAA	TAGGAACAATGTGGCCTTCAA		
442711	LOC442711	XM_499457	CAGGAACATCAGCTTAACCAT	CTGGTGCATTTAGGCCACCTA		
442721	LOC442721	XM_499467	CACCACAGAAGTCAATTTGAA	AAAGTCAAATAGAGAACATAA		
445328	FLJ43692	NM_001003702	ATGTGTTTCATCAGCACTCAA	CTGGATGATTACTATCTCTTT		
445449	HBM	NM_001003938	TTGGTCTGTGCCTGTCAATAA	CAGGACGAGTTCACCGTGCAA		
474338	LOC474338	NR_002190	CAGAGAATTGCTGATAATCAT	CTCATTATTCATTATTGTTTA	AAGGAAGGTGAATATATTAAA	CAGGCTTGTGGTGATAAATAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
474343	SPIN-2	NM_001006681	CAGCAGGGAGGCGGAGGGCTA	CAAACTTGTGTGTACATGAAA		
474344	GIMAP6	NM_001007224	AGCGATCAATTTCCCATTGAA	CCCATTGAACTGAACATGCAA		
494143	LOC494143	NM_001008708	CAGAACCTCAATTGCATATAA	CTGGAAGACATTGCTGAACAA		
497049	FLJ25758	NM_001011541	CAGGCTGTTCCTAGTCATGGA	CACCCTCGAATTCTTCTTGAA		
503497	MS4A13	NM_001012417	CTGCAGTAACTCTAACAATAA	CTGGAATTATAAGTACTTTAA		