US 20100021918A1

(19) **United States**

(12) **Patent Application Publication**

Mizui et al.

(10) **Pub. No.: US 2010/0021918 A1**

(43) **Pub. Date: Jan. 28, 2010**

(54) METHOD FOR ASSAYING ACTION OF ANTITUMOR AGENT USING SPLICING DEFECTS AS INDEX

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(21) Appl. No.: **12/529,959**

(22) PCT Filed: **Mar. 5, 2008**

(86) PCT No.: **PCT/JP2008/053977**

§ 371 (c)(1),
(2), (4) Date: **Sep. 4, 2009**

Related U.S. Application Data

(60) Provisional application No. 60/904,774, filed on Mar. 5, 2007, provisional application No. 60/960,403, filed on Sep. 28, 2007.

Publication Classification

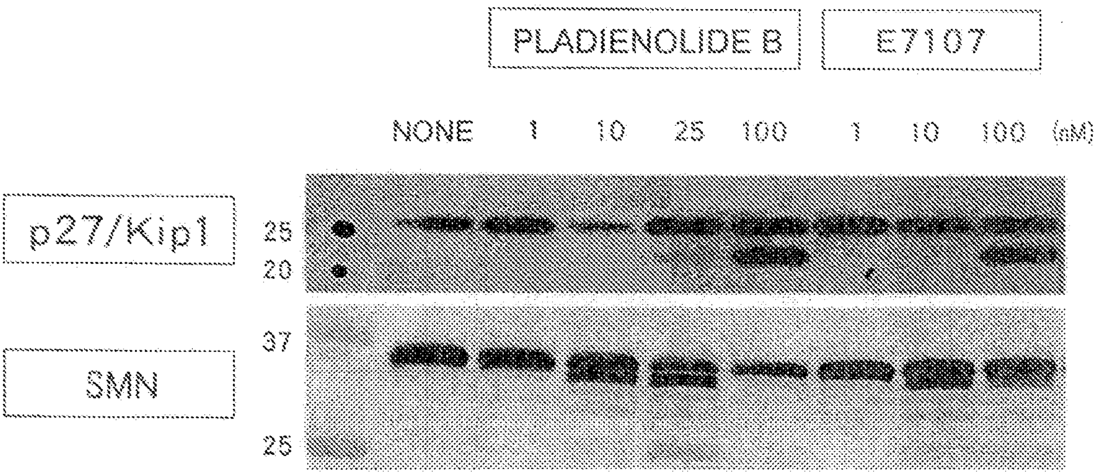
(51) **Int. Cl.**

C12Q 1/68	(2006.01)
C07H 21/04	(2006.01)
G01N 33/53	(2006.01)
C07K 16/00	(2006.01)

(52) **U.S. Cl.** **435/6**; 536/24.31; 435/7.1; 530/387.1

(57) ABSTRACT

An object of the present invention is to provide a method, a probe, a primer, an antibody, a reagent, and a kit for assaying an action of a pladienolide derivative to a living subject. According to the present invention, there is provided a method for assaying an action of the pladienolide derivative using splicing defect as an index.



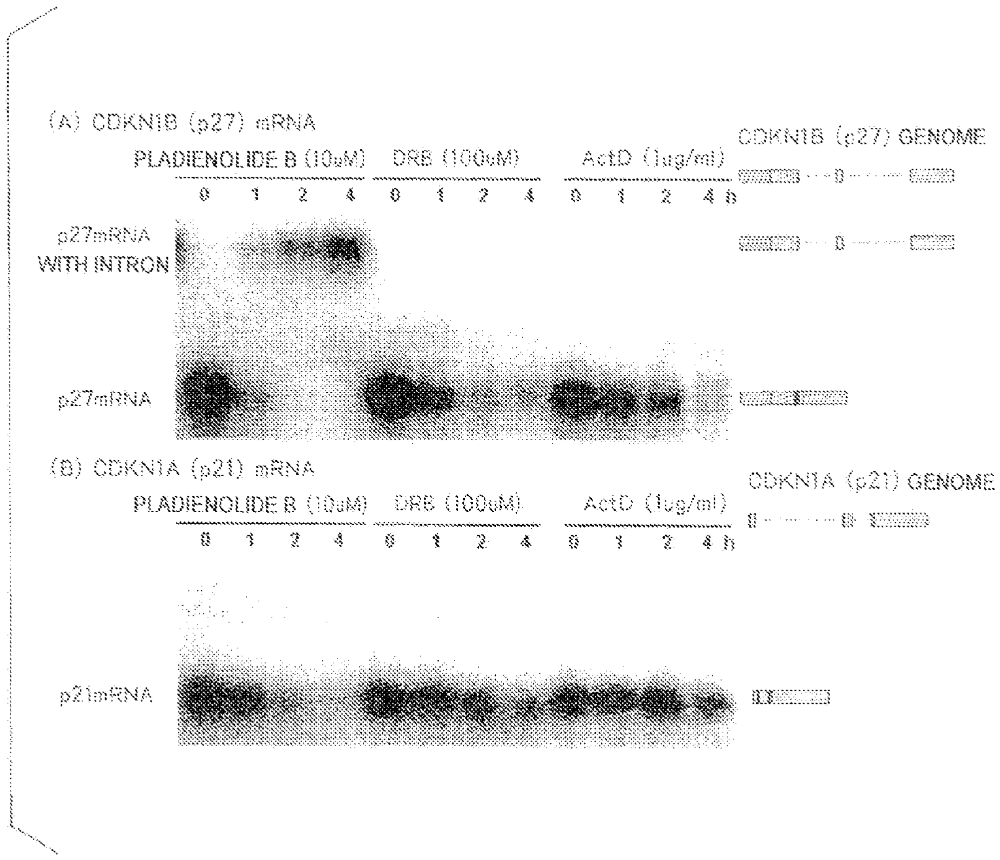

(A) CDKN1B (p27) mRNA
PLADIENOLIDE B (10uM)
DRB (100uM)
ActD (1ug/ml)
0 1 2 4
0 1 2 4
0 1 2 4 h
CDKN1B (p27) GENOME
p27mRNA WITH INTRON
p27mRNA
(B) CDKN1A (p21) mRNA
PLADIENOLIDE B (10uM)
DRB (100uM)
ActD (1ug/ml)
0 1 2 4
0 1 2 4
0 1 2 4 h
CDKN1A (p21) GENOME
p21mRNA

FIG. 1

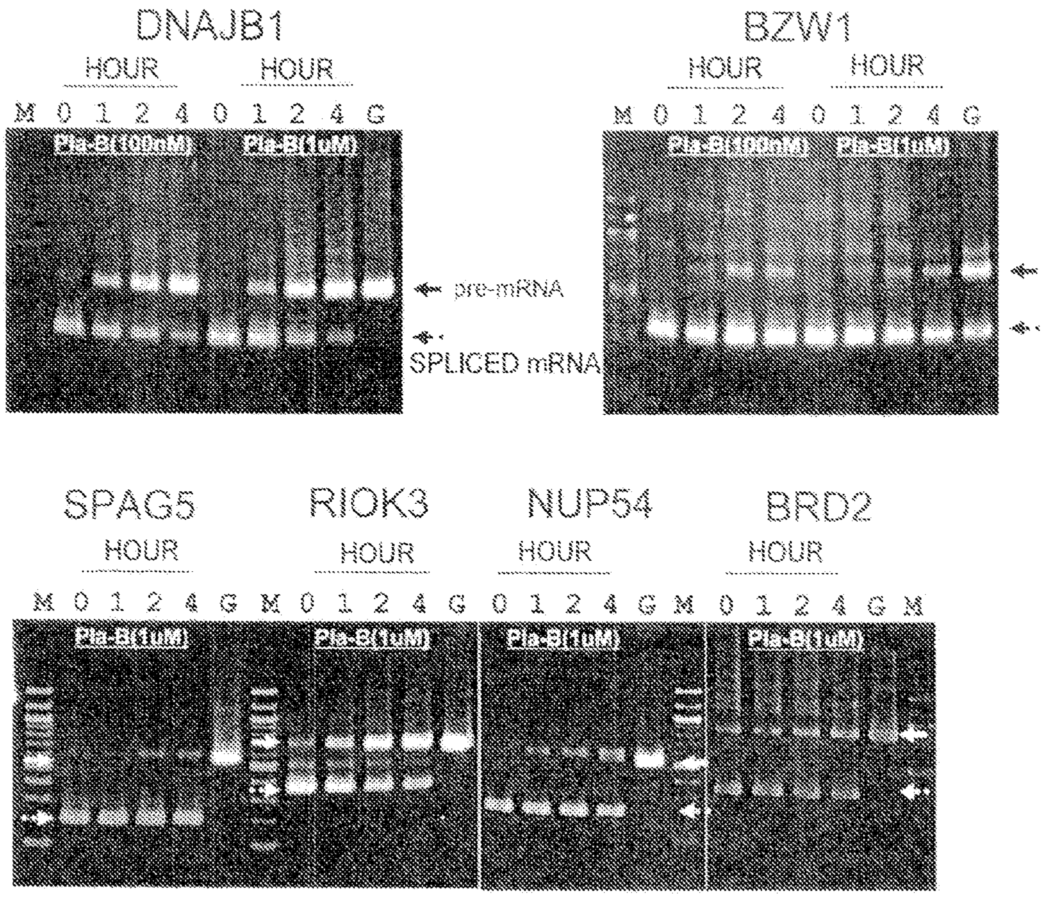

DNAJB1
HOUR
HOUR
M 0 1 2 4 0 1 2 4 G
Pla-B(100nM)
Pla-B(1uM)
pre-mRNA
SPLICED mRNA
BZW1
HOUR
HOUR
M 0 1 2 4 0 1 2 4 G
Pla-B(100nM)
Pla-B(1uM)
SPAG5
HOUR
M 0 1 2 4 G
Pla-B(1uM)
RIOK3
HOUR
M 0 1 2 4 G
Pla-B(1uM)
NUP54
HOUR
0 1 2 4 G M
Pla-B(1uM)
BRD2
HOUR
0 1 2 4 G M
Pla-B(1uM)

FIG. 2

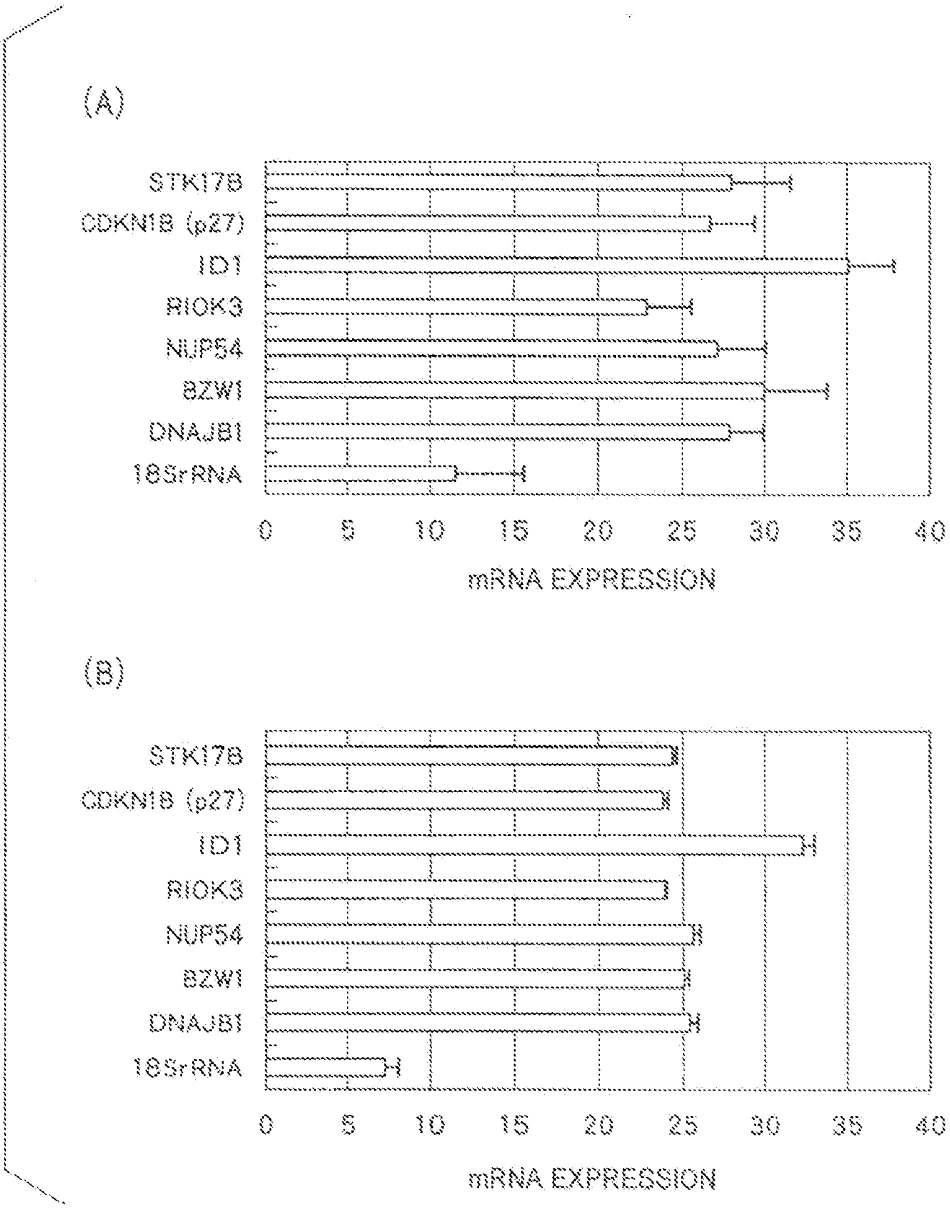

(A)
STK17B
CDKN1B (p27)
ID1
RIOK3
NUP54
BZW1
DNAJB1
18SrRNA
0
5
10
15
20
25
30
35
40
mRNA EXPRESSION
(B)
STK17B
CDKN1B (p27)
ID1
RIOK3
NUP54
BZW1
DNAJB1
18SrRNA
0
5
10
15
20
25
30
35
40
mRNA EXPRESSION

FIG. 3

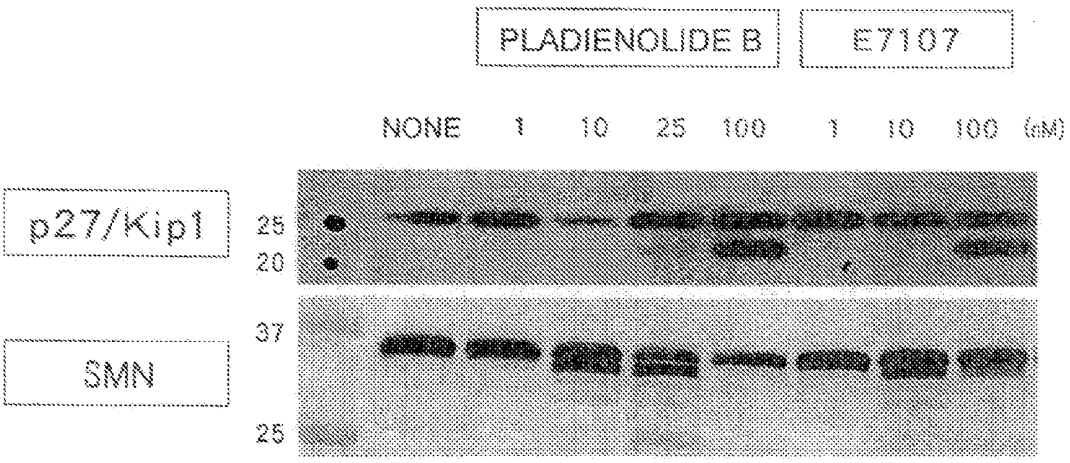

PLADIENOLIDE B
E7107
NONE
1
10
25
100
1
10
100
(nM)
p27/Kip1
25
20
SMN
37
25

FIG. 4

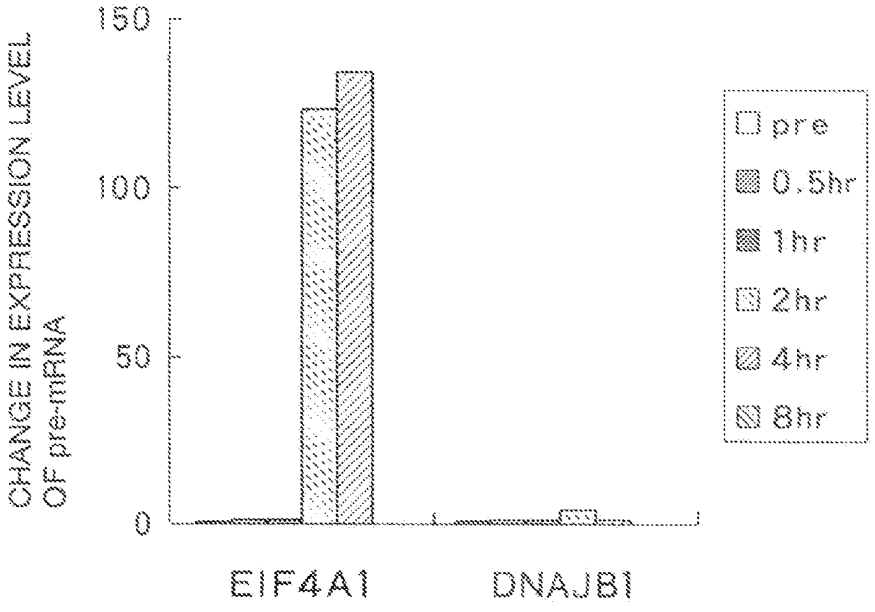

CHANGE IN EXPRESSION LEVEL OF pre-mRNA
150
100
50
0
EIF4A1
DNAJB1
pre
0.5hr
1hr
2hr
4hr
8hr

FIG. 5

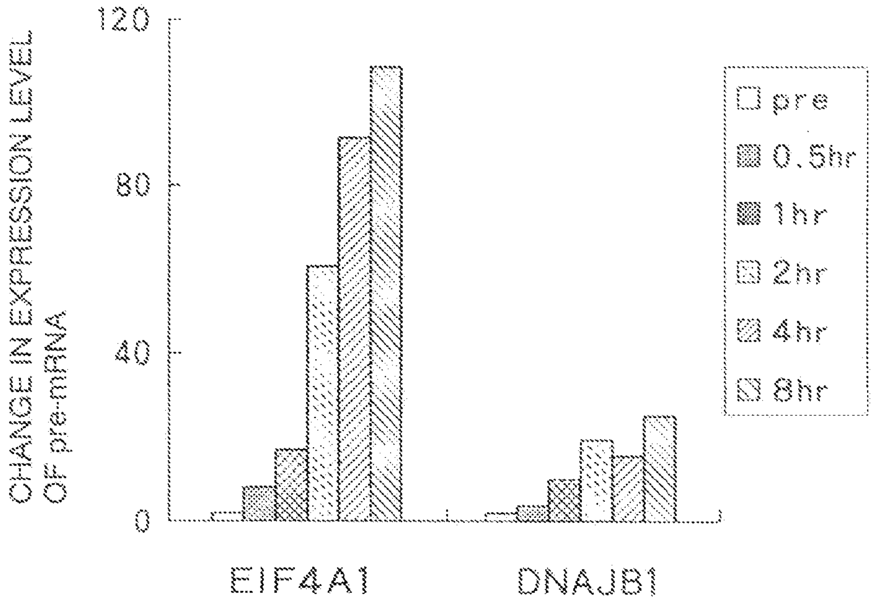
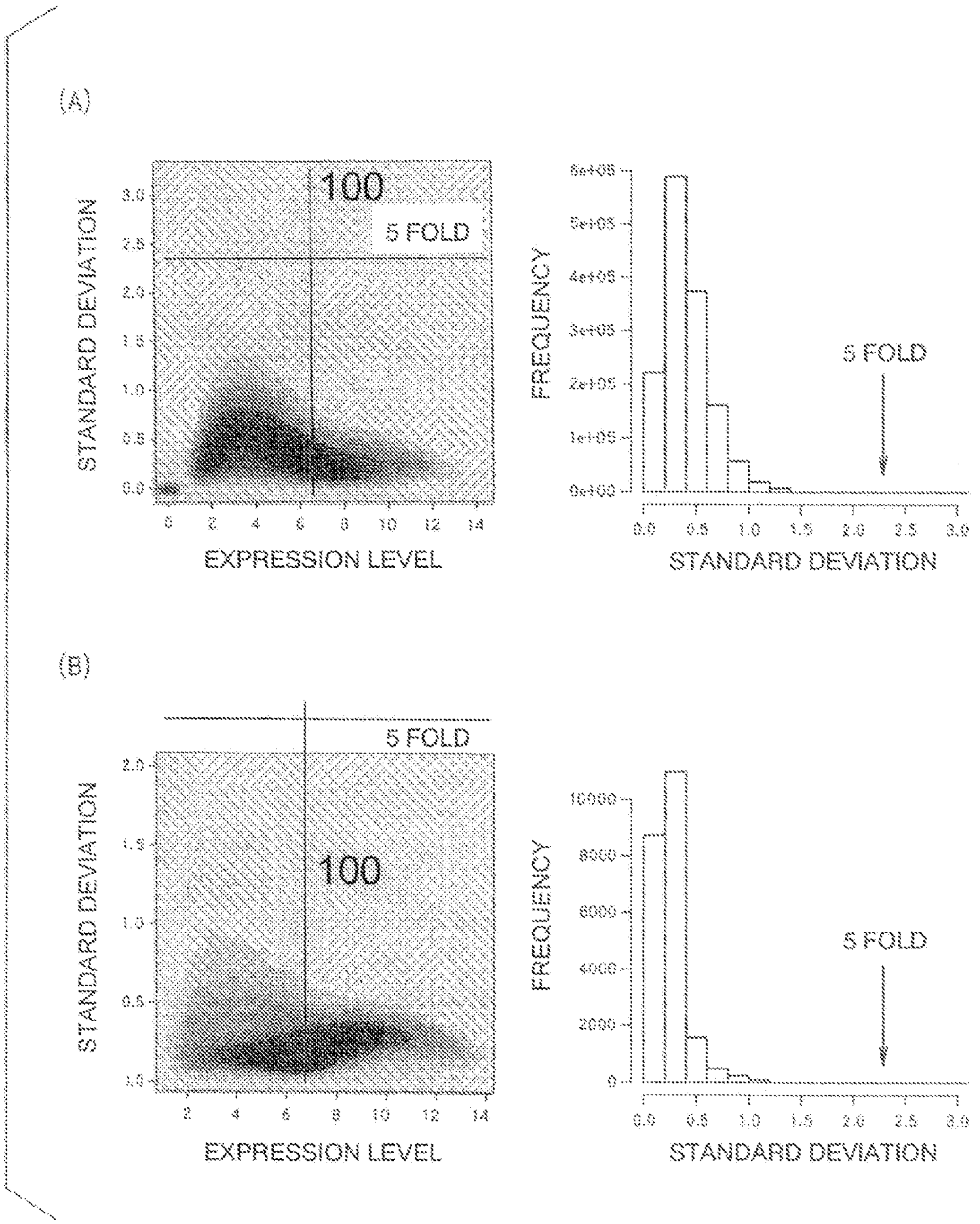

CHANGE IN EXPRESSION LEVEL OF pre-mRNA
120
80
40
0
EIF4A1
DNAJB1
pre
0.5hr
1hr
2hr
4hr
8hr

FIG. 6


(A)
100
5 FOLD
STANDARD DEVIATION
3.0
2.5
2.0
1.5
1.0
0.5
0.0
0
2
4
6
8
10
12
14
EXPRESSION LEVEL
FREQUENCY
6e+05
5e+05
4e+05
3e+05
2e+05
1e+05
0e+00
5 FOLD
0.0
0.5
1.0
1.5
2.0
2.5
3.0
STANDARD DEVIATION
(B)
5 FOLD
100
STANDARD DEVIATION
2.0
1.5
1.0
0.5
0.0
2
4
6
8
10
12
14
EXPRESSION LEVEL
FREQUENCY
10000
8000
6000
4000
2000
0
5 FOLD
0.0
0.5
1.0
1.5
2.0
2.5
3.0
STANDARD DEVIATION

F I G . 7

METHOD FOR ASSAYING ACTION OF ANTITUMOR AGENT USING SPLICING DEFECTS AS INDEX

BACKGROUND OF THE INVENTION

[0001] 1. Field of the Invention

[0002] The present invention relates to a method for assaying an action of an antitumor agent using splicing defect as an index, more particularly, a method for assaying an action of an antitumor agent using an increase in the expression level of pre-mRNA or abnormal protein as an index.

[0003] 2. Background Art

[0004] Pladienolide derivatives are derivatives of natural pladienolide. Since pladienolide exhibits an excellent antitumor activity (Mizui et al., 2004, *J. Antibiotics* 577:188-196), search for a compound with higher antitumor activities has been performed to find the pladienolide derivatives (WO2002/060890 and WO2003/099813).

SUMMARY OF THE INVENTION

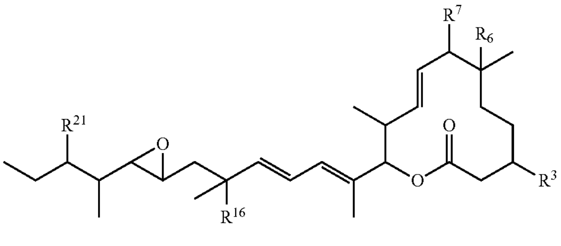
[0005] The present inventors have found that pre-mRNA of a certain group of genes and abnormal proteins increase when a pladienolide derivative is contacted with a sample obtained from living cells including cancerous cells, and peripheral blood (PBMC) and whole blood (PBC) of a subject. Without wishing to be bound by any theory, administration of the pladienolide derivative may cause an introduction of a mutation in pre-mRNA of a certain group of genes thereby inducing splicing defect. The present invention was made based on such findings.

[0006] It is an object of the present invention to provide a method, a probe, a primer, an antibody, a reagent and a kit for assaying an action of the pladienolide derivative on a living subject.

[0007] According to the present invention, there are provided inventions (1) to (19) as follows.

(1) A method for assaying an action of a compound represented by formula (I), a pharmaceutically acceptable salt thereof, or a solvate of them to a mammal, which comprises detecting splicing defect caused by the compound represented by formula (I), the pharmaceutically acceptable salt thereof, or the solvate of them:

(I)



wherein R^3, R^6, R^7 and R^{21}, the same or different, each represents

1) a hydroxyl group or an oxo group formed together with the carbon atom to which it is bound, provided that R^6 is limited to a hydroxyl group,

2) an optionally substituted C_{1-22} alkoxy group,

3) an optionally substituted unsaturated C_{2-22} alkoxy group,

4) an optionally substituted C_{7-22} aralkyloxy group,

5) an optionally substituted 5- to 14-membered heteroaralkyloxy group,

6) RCO—O— wherein R represents

[0008] a) a hydrogen atom,

[0009] b) an optionally substituted C_{1-22} alkyl group,

[0010] c) an optionally substituted unsaturated C_{2-22} alkyl group,

[0011] d) an optionally substituted C_{6-14} aryl group,

[0012] e) an optionally substituted 5- to 14-membered heteroaryl group,

[0013] f) an optionally substituted C_{7-22} aralkyl group,

[0014] g) an optionally substituted 5- to 14-membered heteroaralkyl group,

[0015] h) an optionally substituted C_{1-22} alkoxy group,

[0016] i) an optionally substituted unsaturated C_{2-22} alkoxy group,

[0017] j) an optionally substituted C_{6-14} aryloxy group or

[0018] k) an optionally substituted 5- to 14-membered heteroaryloxy group,

7) $R^{S1}R^{S2}R^{S3}SiO$— wherein R^{S1}, R^{S2}, and R^{S3}, the same or different, each represents

[0019] a) a C_{1-6} alkyl group or

[0020] b) a C_{6-14} aryl group,

8) a halogen atom,

9) $R^{N1}R^{N2}N—R^{M}$— wherein R^{M} represents

[0021] a) a single bond,

[0022] b) —CO—O—,

[0023] c) —SO_2—O—,

[0024] d) —CS—O— or

[0025] e) —CO—NR^{N3}— wherein R^{N3} represents a hydrogen atom or an optionally substituted C_{1-6} alkyl group, provided that each of the leftmost bond in b) to e) is bound to the nitrogen atom; and R^{N1} and R^{N2}, the same or different from each other and each represents

[0026] a) a hydrogen atom,

[0027] b) an optionally substituted C_{1-22} alkyl group,

[0028] c) an optionally substituted unsaturated C_{2-22} alkyl group,

[0029] d) an optionally substituted aliphatic C_{2-22} acyl group,

[0030] e) an optionally substituted aromatic C_{7-15} acyl group,

[0031] f) an optionally substituted C_{6-14} aryl group,

[0032] g) an optionally substituted 5- to 14-membered heteroaryl group,

[0033] h) an optionally substituted C_{7-22} aralkyl group,

[0034] i) an optionally substituted C_{1-22} alkylsulfonyl group,

[0035] j) an optionally substituted C_{6-14} arylsulfonyl group,

[0036] k) an optionally substituted 3- to 14-membered non-aromatic heterocyclic group formed by R^{N1} and R^{N2} together with the nitrogen atom to which R^{N1} and R^{N2} are bound, and the non-aromatic heterocyclic group optionally has substituent(s),

[0037] l) an optionally substituted 5- to 14-membered heteroaralkyl group,

[0038] m) an optionally substituted C_{3-14} cycloalkyl group or

[0039] n) an optionally substituted 3- to 14-membered non-aromatic heterocyclic group,

10) $R^{N4}SO_2$— wherein R^{N4} represents

[0040] a) an optionally substituted C_{1-22} alkyl group,

[0041] b) an optionally substituted C_{6-14} aryl group,

[0042] c) an optionally substituted C_{1-22} alkoxy group,

[0043] d) an optionally substituted unsaturated C_{2-22} alkoxy group,

[0044] e) an optionally substituted C_{6-14} aryloxy group,

[0045] f) an optionally substituted 5- to 14-membered heteroaryloxy group,

[0046] g) an optionally substituted C_{7-22} aralkyloxy group or

[0047] h) an optionally substituted 5- to 14-membered heteroaralkyloxy group,

11) $(R^{N5}O)_2PO$—O— wherein R^{N5} represents

[0048] a) an optionally substituted C_{1-22} alkyl group,

[0049] b) an optionally substituted unsaturated C_{2-22} alkyl group,

[0050] c) an optionally substituted C_{6-14} aryl group,

[0051] d) an optionally substituted 5- to 14-membered heteroaryl group,

[0052] e) an optionally substituted C_{7-22} aralkyl group or

[0053] f) an optionally substituted 5- to 14-membered heteroaralkyl group,

12) $(R^{N1}R^{N2}N)_2PO$—O— wherein R^{N1} and R^{N2} have the same meanings as defined above or

13) $(R^{N1}R^{N2}N)(R^{N5}O)PO$—O— wherein R^{N1}, R^{N2} and R^{N5} have the same meanings as defined above, provided that a compound in which R^3, R^6, R^7 and R^{21} are all hydroxyl groups, and a compound in which R^3, R^6 and R^{21} are all hydroxyl groups and R^7 is an acetoxy group are excluded,

[0054] R^{15} represents a hydrogen atom or hydroxyl group.

(2) The method according to (1), wherein the compound represented by formula (I) is selected from the group consisting of:

[0055] (8E,12E,14E)-7-(N-(2-(N',N'-Dimethylamino)ethyl)-N-methylcarbamoyloxy)-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide;

[0056] (8E,12E,14E)-3,6,16,21-Tetrahydroxy-6,10,12,16,20-pentamethyl-7-((4-methylhomopiperazin-1-yl)carbonyl)oxy-18,19-epoxytricosa-8,12,14-trien-11-olide;

[0057] (8E,12E,14E)-3,6,16,21-Tetrahydroxy-6,10,12,16,20-pentamethyl-7-((4-methylpiperazin-1-yl)carbonyl)oxy-18,19-epoxytricosa-8,12,14-trien-11-olide;

[0058] (8E,12E,14E)-7-((4-Butylpiperazin-1-yl)carbonyl)oxy-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide;

[0059] (8E,12E,14E)-7-((4-Ethylpiperazin-1-yl)carbonyl)oxy-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide;

[0060] (8E,12E,14E)-3,6,16,21-Tetrahydroxy-6,10,12,16,20-pentamethyl-7-((4-propylpiperazin-1-yl)carbonyl)oxy-18,19-epoxytricosa-8,12,14-trien-11-olide;

[0061] (8E,12E,14E)-7-((4-Cyclohexylpiperazin-1-yl)carbonyl)oxy-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide;

[0062] (8E,12E,14E)-7-((4-(Cyclopropylmethyl)piperazin-1-yl)carbonyl)oxy-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide;

[0063] (8E,12E,14E)-3,6,16,21-Tetrahydroxy-6,10,12,16,20-pentamethyl-7-((4-propylhomopiperazin-1-yl)carbonyl)oxy-18,19-epoxytricosa-8,12,14-trien-11-olide;

[0064] (8E,12E,14E)-7-((4-(Cyclopropylmethyl)homopiperazin-1-yl)carbonyl)oxy-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide;

[0065] (8E,12E,14E)-7-((4-Cyclopentylpiperazin-1-yl)carbonyl)oxy-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide;

[0066] (8E,12E,14E)-3,6,16,21-Tetrahydroxy-7-((4-isopropylpiperazin-1-yl)carbonyl)oxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide;

[0067] (8E,12E,14E)-7-((4-Cycloheptylpiperazin-1-yl)carbonyl)oxy-3,6,16,21-Tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide;

[0068] (8E,12E,14E)-7-(N-(2-(N',N'-Diethylamino)ethyl)-N-methylcarbamoyloxy)-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide;

[0069] (8E,12E,14E)-3,6,16,21-Tetrahydroxy-7-((4-isobutylhomopiperazin-1-yl)carbonyl)oxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide;

[0070] (8E,12E,14E)-7-((4-Ethylhomopiperazin-1-yl)carbonyl)oxy-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide;

[0071] (8E,12E,14E)-7-((4-Butylhomopiperazin-1-yl)carbonyl)oxy-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide;

[0072] (8E,12E,14E)-3,16,21-Trihydroxy-6-methoxy-6,10,12,16,20-pentamethyl-7-((4-methylpiperazin-1-yl)carbonyl)oxy-18,19-epoxytricosa-8,12,14-trien-11-olide;

[0073] (8E,12E,14E)-3,16,21-Trihydroxy-6-methoxy-6,10,12,16,20-pentamethyl-7-((4-(piperidin-1-yl)piperidin-1-yl)carbonyl)oxy-18,19-epoxytricosa-8,12,14-trien-11-olide;

[0074] (8E,12E,14E)-3,6,7,21-Tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide;

[0075] (8E,12E,14E)-7-((4-(2,2-Dimethylpropyl)homopiperazin-1-yl)carbonyl)oxy-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide; and

[0076] (8E,12E,14E)-3,6,16-Trihydroxy-21-methoxy-6,10,12,16,20-pentamethyl-7-((4-methylpiperazin-1-yl)carbonyl)oxy-18,19-epoxytricosa-8,12,14-trien-11-olide.

(3) The method according to (1), wherein the detection of splicing defect comprises the steps of:

[0077] (a) measuring the expression level of pre-mRNA before and after administration of the compound represented by formula (I), the pharmaceutically acceptable salt thereof, or the solvate of them to a mammal;

[0078] (b) comparing, based on the expression level measured in (a), the expression level of pre-mRNA before and after administration of the compound represented by formula (I), the pharmaceutically acceptable salt thereof, or the solvate of them, to determine that the compound represented by formula (I), the pharmaceutically acceptable salt thereof, or the solvate of them exerts an action to the mammal when the expression level of pre-mRNA after the administration increases.

(4) The method according to (3), wherein the pre-mRNA of which expression level is measured is pre-mRNA of at least one gene selected from the genes listed in Table 1, Table 2, Table 3, Table 4, and Table 5, or a homologous gene thereof.

(5) The method according to (4), wherein the gene(s) are selected from DNAJB1, BZW1, NUP54, RIOK3, CDKN1B, STK17B, EIF4A1, and ID1.

(6) The method according to (3), wherein in step (a), the expression level of pre-mRNA in samples obtained from a subject before and after administration of the compound rep-

resented by formula (I), the pharmaceutically acceptable salt thereof, or the solvate of them, is measured.

(7) The method according to (6), wherein the samples obtained from the subject are selected from hemocytes in peripheral blood, plasma, and serum.

(8) A probe or primer for assaying an action of a compound represented by formula (I), a pharmaceutically acceptable salt thereof, or a solvate of them to a mammal, which consists of a polynucleotide capable of hybridizing with a polynucleotide consisting of a nucleotide sequence of at least one gene selected from the genes listed in Table 1, Table 2, Table 3, Table 4, and Table 5, or a homologous gene thereof, or a complementary sequence thereof.

(9) The probe or primer according to (8), which is capable of detecting a genomic intron region or a part thereof in a gene listed in Table 1, Table 2, Table 3, Table 4 and Table 5, or which is capable of detecting a polynucleotide lacking a part of a genomic exon region in a gene listed in Table 1, Table 2, Table 3, Table 4 and Table 5.

(10) A reagent or kit for assaying an action of a compound represented by formula (I), a pharmaceutically acceptable salt thereof, or a solvate of them to a mammal, which comprises the probe or the primer according to (8).

(11) The method according to (1), wherein the detection of splicing defect comprises the steps of:

[0079] (f) measuring the expression level of an abnormal protein before and after administration of the compound represented by formula (I), the pharmaceutically acceptable salt thereof, or the solvate of them to a mammal;

[0080] (g) comparing, based on the expression level measured in (f), the expression level of the abnormal protein before and after administration of the compound represented by formula (I), the pharmaceutically acceptable salt thereof or the solvate of them, to determine that the compound represented by formula (I), the pharmaceutically acceptable salt thereof, or the solvate of them exerts an action to the mammal when the expression level of the abnormal protein after administration increases.

(12) The method according to (11), wherein the abnormal protein of which expression level is measured is a protein consisting of amino acids encoded by a polynucleotide of at least one gene selected from the genes listed in Table 1 and Table 3, or a homologous gene thereof where splicing defect has been caused in the polynucleotide, or a protein consisting of amino acids encoded by a polynucleotide of at least one gene selected from the genes listed in Table 2, Table 4 and Table 5 or a homologous gene thereof where splicing defect has been caused in the polynucleotide.

(13) The method according to (11), wherein the abnormal protein of which expression level is measured is a protein consisting of amino acids encoded by a polynucleotide of at least one gene selected from DNAJB1, BZW1, NUP54, RIOK3, CDKN1B, STK17B, EIF4A1 and ID1 where splicing defect has been caused in the polynucleotide.

(14) The method according to (11), wherein in step (f), the expression level of the abnormal protein in the samples obtained from a subject before and after administration of the compound represented by formula (I) or the pharmaceutically acceptable salt thereof or the solvate of them, is measured.

(15) The method according to (14), wherein the samples obtained from the subject are selected from hemocytes in peripheral blood, plasma, and serum.

(16) An antibody against an abnormal protein consisting of amino acids encoded by a polynucleotide of at least one gene selected from the genes listed in Table 1, Table 2, Table 3, Table 4 and Table 5 where splicing defect has been caused in the polynucleotide, or a fragment thereof.

(17) A reagent or kit for assaying an action of a compound represented by formula (I), a pharmaceutically acceptable salt thereof, or a solvate of them to a mammal, comprising the antibody or the fragment thereof according to (16).

(18) Use of a probe or primer consisting of a polynucleotide capable of hybridizing with a polynucleotide consisting of a nucleotide sequence of at least one gene selected from the genes listed in Table 1, Table 2, Table 3, Table 4, and Table 5, and homologous genes thereof, or complementary sequences thereof, for assaying an action of a compound represented by formula (I), a pharmaceutically acceptable salt thereof, or a solvate of them to a mammal.

(19) Use of an antibody against a protein consisting of amino acids encoded by a polynucleotide of at least one gene selected from the genes listed in Table 1, Table 2, Table 3, Table 4 and Table 5, or a fragment of the antibody, for assaying an action of a compound represented by formula (I), a pharmaceutically acceptable salt thereof, or a solvate of them to a mammal.

[0081] According to the present invention, an action of the compound represented by formula (I) to a living body can be confirmed using splicing defect in a cancerous or normal tissue of a cancer patient or normal tissue of a healthy individual, more specifically, the expression level of pre-mRNA or an abnormal protein as an index. For instance, when splicing defect is found in the cancerous or normal tissue of the cancer patient, more specifically, the expression level of pre-mRNA or the abnormal protein increases, it can be determined that the compound represented by formula (I) exerts the action in the body and that thus administration of the drug is no longer required or less amount of the drug should be administrated. Further, when splicing defect is not found in the cancerous or normal tissue of the cancer patient, more specifically, the expression level of pre-mRNA or the abnormal protein exhibits the same amount as before the administration, it can be determined that the compound represented by formula (I) does not exert the action and further administration of the drug is required. Hence, according to the invention, by monitoring periodically the expression of pre-mRNA or the abnormal protein, the antitumor agent can be administered more effectively to the patient and a minimally required amount of the drug can be administered to the patient. In particular, since the action of the compound represented by formula (I) can be judged by monitoring the expression level of pre-mRNA or the abnormal protein in samples obtained from normal tissue such as blood of the patient, it is an advantage that the action of the compound represented by formula (I) to the living body can be readily and reliably assessed.

BRIEF DESCRIPTION OF THE DRAWINGS

[0082] FIG. **1** shows accumulation of pre-mRNA of CDKN1B (p27) and CDKN1A (p21) in HeLa cells.

[0083] FIG. **2** shows accumulation of pre-mRNA of DNAJB1, BZW1, SPAG5, RIOK3, NUP54, and BRD2 in HeLa cells.

[0084] FIG. **3** shows the expression of mRNA in whole blood (PBC) samples obtained from human peripheral blood. A: Results of samples obtained with the Tempus Blood RNA Tube. B: Results of samples obtained with the PAXgene Blood RNA Tube.

[0085] FIG. **4** shows expression of a protein translated from the pre-mRNA.

[0086] FIG. **5** shows results measured expression of precursor genes (DNAJB1 and EIF4A1) in blood of nude mice to which human colon cancer cells were subcutaneously transplanted and the pladienolide derivative was administered.

[0087] FIG. **6** shows results measured expression of precursor genes (DNAJB1 and EIF4A1) in the tumor of nude mice to which human colon cancer cells were subcutaneously transplanted and the pladienolide derivative was administered.

[0088] FIG. **7** shows a scatter diagram of the expression level of probe sets and genes of control cells, and standard deviation thereof. "A" represents the expression level and standard deviation of exons. "B" represents the expression level and standard deviation of genes.

DETAILED DESCRIPTION OF THE INVENTION

[0089] All technical terms, scientific terms and terminologies used in the present specification have the same meanings as those that are generally understood by those ordinary skilled in the art in the technical fields to which the present invention belongs, and are used merely for the purpose of explaining a specific embodiment but are not intended to make limitation. The present invention can be carried out in various embodiments as long as not departing from the spirit thereof. All the prior art documents, published publications, patent publications and other patent documents cited in the present specification are incorporated into the present specification as references, and can be used for carrying out the present invention.

[0090] The "halogen atom" used in the specification of the present application means a fluorine atom, a chlorine atom, a bromine atom and an iodine atom. Among them, for example, a fluorine atom, a chlorine atom or a bromine atom is preferred, of which a fluorine atom or a chlorine atom is preferred.

[0091] The "C_{1-22} alkyl group" used in the specification of the present application indicates a linear or branched alkyl group having 1 to 22 carbon atoms, such as methyl group, ethyl group, n-propyl group, iso-propyl group, n-butyl group, iso-butyl group, sec-butyl group, tert-butyl group, n-pentyl group, 1,1-dimethylpropyl group, 1,2-dimethylpropyl group, 2,2-dimethylpropyl group, 1-ethylpropyl group, n-hexyl group, 1-ethyl-2-methylpropyl group, 1,1,2-trimethylpropyl group, 1-propylpropyl group, 1-methylbutyl group, 2-methylbutyl group, 1,1-dimethylbutyl group, 1,2-dimethylbutyl group, 2,2-dimethylbutyl group, 1,3-dimethylbutyl group, 2,3-dimethylbutyl group, 2-ethylbutyl group, 2-methylpentyl group, 3-methylpentyl group, n-heptyl group, n-octyl group, n-nonyl group or n-decyl group; preferably a linear or branched alkyl group having 1 to 6 carbon atoms, such as methyl group, ethyl group, n-propyl group, iso-propyl group, n-butyl group, iso-butyl group, sec-butyl group, tert-butyl group or n-pentyl group; and more preferably, for example, methyl group, ethyl group, propyl group, iso-propyl group, n-butyl group, iso-butyl group or tert-butyl group.

[0092] The "unsaturated C_{2-22} alkyl group" used in the specification of the present application indicates a linear or branched alkenyl group having 2 to 22 carbon atoms or a linear or branched alkynyl group having 2 to 22 carbon atoms, such as vinyl group, allyl group, 1-propenyl group, isopropenyl group, 2-methyl-1-propenyl group, 2-methyl-2-propenyl group, 1-butenyl group, 2-butenyl group, 3-butenyl group, 1-pentenyl group, 1-hexenyl group, 1,3-hexadienyl group, 1,5-hexadienyl group, ethynyl group, 1-propynyl group, 2-propynyl group, 1-butynyl group, 2-butynyl group, 3-butynyl group, 1-ethynyl-2-propynyl group, 2-methyl-3-butynyl group, 1-pentynyl group, 1-hexynyl group, 1,3-hexanediynyl group or 1,5-hexanediynyl group. It preferably indicates a linear or branched alkenyl group having 2 to 10 carbon atoms or a linear or branched alkynyl group having 2 to 10 carbon atoms, such as vinyl group, allyl group, 1-propenyl group, 2-propenyl group, isopropenyl group, 3-methyl-2-butenyl group, 3,7-dimethyl-2,6-octadienyl group, ethynyl group, 1-propynyl group, 2-propynyl group, 1-butynyl group, 2-butynyl group, 3-butynyl group or 3-methyl-1-propynyl group.

[0093] The "C_{6-14} aryl group" used in the specification of the present application means an aromatic cyclic hydrocarbon group having 6 to 14 carbon atoms, and a monocyclic group and condensed rings such as a bicyclic group and a tricyclic group are included. Examples thereof include phenyl group, indenyl group, 1-naphthyl group, 2-naphthyl group, azulenyl group, heptalenyl group, indacenyl group, acenaphthyl group, fluorenyl group, phenalenyl group, phenanthrenyl group and anthracenyl group; and preferred examples include phenyl group, 1-naphthyl group and 2-naphthyl group.

[0094] The "5- to 14-membered heteroaryl group" used in the specification of the present application means a monocyclic, bicyclic or tricyclic 5- to 14-membered aromatic heterocyclic group which contains one or more of hetero atoms selected from the group consisting of nitrogen atom, sulfur atom and oxygen atom. Preferred examples thereof include nitrogen-containing aromatic heterocyclic groups such as pyrrolyl group, pyridyl group, pyridazinyl group, pyrimidinyl group, pyrazinyl group, triazolyl group, tetrazolyl group, benzotriazolyl group, pyrazolyl group, imidazolyl group, benzimidazolyl group, indolyl group, isoindolyl group, indolizinyl group, purinyl group, indazolyl group, quinolyl group, isoquinolyl group, quinolizinyl group, phthalazinyl group, naphthyridinyl group, quinoxalinyl group, quinazolinyl group, cinnolinyl group, pteridinyl group, imidazotriazinyl group, pyrazinopyridazinyl group, acridinyl group, phenanthridinyl group, carbazolyl group, carbazolinyl group, perimidinyl group, phenanthrolinyl group, phenazinyl group, imidazopyridinyl group, imidazopyrimidinyl group, pyrazolopyridinyl group and pyrazolopyridinyl group; sulfur-containing aromatic heterocyclic groups such as thienyl group and benzothienyl group; and oxygen-containing aromatic heterocyclic groups such as furyl group, pyranyl group, cyclopentapyranyl group, benzofuryl group and isobenzofuryl group; aromatic heterocyclic groups containing two or more different hetero atoms, such as thiazolyl group, isothiazolyl group, benzothiazolyl group, benzthiadiazolyl group, phenothiazinyl group, isoxazolyl group, furazanyl group, phenoxazinyl group, oxazolyl group, isoxazoyl group, benzoxazolyl group, oxadiazolyl group, pyrazolooxazolyl group, imidazothiazolyl group, thienofuranyl group, furopyrrolyl group and pyridoxazinyl group; and preferred examples include thienyl group, furyl group, pyridyl group, pyridazyl group, pyrimidyl group and pyrazyl group.

[0095] The "3- to 14-membered non-aromatic heterocyclic group" used in the specification of the present application indicates a monocyclic, bicyclic or tricyclic 3- to 14-membered non-aromatic heterocyclic group which may contain one or more hetero atoms selected from the group consisting of nitrogen atom, sulfur atom and oxygen atom. Preferred examples thereof include aziridinyl group, azetidinyl group, pyrrolidinyl group, pyrrolyl group, piperidinyl group, piperazinyl group, homopiperidinyl group, homopiperazinyl group, imidazolyl group, pyrazolidyl group, imidazolidyl group, morpholyl group, thiomorpholyl group, imidazolinyl group, oxazolinyl group, 2,5-diazabicyclo[2.2.1]heptyl group, 2,5-diazabicyclo[2.2.2]octyl group, 3,8-diazabicyclo [3.2.1]octyl group, 1,4-diazabicyclo[4.3.0]nonyl group, quinuclidyl group, tetrahydrofuran-yl group and tetrahydrothiophen-yl group. The non-aromatic heterocyclic groups also include groups derived from pyridone ring, and non-aromatic fused rings (e.g., a group derived from, for example, phthalimide ring or succinimide ring).

[0096] The "C_{7-22} aralkyl group" used in the specification of the present application means a group corresponding to the above-defined "C_{1-22} alkyl group" of which substitutable moiety is replaced by the above-defined "C_{6-14} aryl group". Specific examples thereof include benzyl group, phenethyl group, 3-phenylpropyl group, 4-phenylbutyl group, 1-naphthylmethyl group and 2-naphthylmethyl group; and preferred examples include aralkyl groups having 7 to 10 carbon atoms such as benzyl group and phenethyl group.

[0097] The "5- to 14-membered heteroaralkyl group" used in the specification of the present application means a group corresponding to the above-defined "C_{1-22} alkyl group" of which substitutable moiety is replaced by the above-defined "5- to 14-membered heteroaryl group". Specific examples thereof include thienylmethyl group, furylmethyl group, pyridylmethyl group, pyridazylmethyl group, pyrimidylmethyl group and pyrazylmethyl group; and preferred examples include thienylmethyl group, furylmethyl group and pyridylmethyl group.

[0098] The "C_{3-14} cycloalkyl group" used in the specification of the present application indicates a cycloalkyl group having 3 to 14 carbon atoms, and suitable examples thereof include cyclopropyl group, cyclobutyl group, cyclopentyl group, cyclohexyl group, cycloheptyl group and cyclooctyl group; and preferred examples include cyclopentyl group, cyclohexyl group, cycloheptyl group and cyclooctyl group.

[0099] The "C_{4-9} cycloalkyl alkyl group" used in the specification of the present application means a group corresponding to the above-defined "C_{1-22} alkyl group" of which substitutable moiety is replaced by the above-defined "C_{3-14} cycloalkyl group". Specific examples thereof include cyclopropylmethyl group, cyclobutylmethyl group, cyclopentylmethyl group, cyclohexylmethyl group, cycloheptylmethyl group and cyclooctylmethyl group; and preferred example include cyclopropylmethyl group, cyclobutylmethyl group and cyclopentylmethyl group.

[0100] The "C_{1-22} alkoxy group" used in the specification of the present application means a group corresponding to the above-defined "C_{1-22} alkyl group" to which end an oxygen atom is bonded. Suitable examples thereof include methoxy group, ethoxy group, n-propoxy group, iso-propoxy group, n-butoxy group, iso-butoxy group, sec-butoxy group, tert-butoxy group, n-pentyloxy group, iso-pentyloxy group, sec-pentyloxy group, n-hexoxy group, iso-hexoxy group, 1,1-dimethylpropyloxy group, 1,2-dimethylpropyloxy group, 2,2-dimethylpropoxy group, 1-methyl-2-ethylpropoxy group, 1-ethyl-2-methylpropoxy group, 1,1,2-trimethylpropoxy group, 1,2,2-trimethylpropoxy group, 1,1-dimethylbutoxy group, 1,2-dimethylbutoxy group, 2,2-dimethylbutoxy group, 2,3-dimethylbutyloxy group, 1,3-dimethylbutoxy group, 2-ethylbutoxy group, 2-methylpentoxy group, 3-methylpentyloxy group and hexyloxy group; and preferred examples include methoxy group, ethoxy group, n-propoxy group, iso-propoxy group, iso-butoxy group and 2,2-dimethylpropyloxy group.

[0101] The "unsaturated C_{2-22} alkoxy group" used in the specification of the present application means a group corresponding to the above-defined "unsaturated C_{2-22} alkyl group" to which end an oxygen atom is bonded. Suitable examples thereof include vinyloxy group, allyloxy group, 1-propenyloxy group, 2-propenyloxy group, isopropenyloxy group, 2-methyl-1-propenyloxy group, 2-methyl-2-propenyloxy group, 1-butenyloxy group, 2-butenyloxy group, 3-butenyloxy group, 1-pentenyloxy group, 1-hexenyloxy group, 1,3-hexadienyloxy group, 1,5-hexadienyloxy group, propargyloxy group and 2-butynyloxy group; and preferred examples include allyloxy group, propargyloxy group and 2-butynyloxy group.

[0102] The "C_{6-14} aryloxy group" used in the specification of the present application means a group corresponding to the above-defined "C_{6-14} aryl group" to which end an oxygen atom is bonded. Specific examples thereof include phenyloxy group, indenyloxy group, 1-naphthyloxy group, 2-naphthyloxy group, azulenyloxy group, heptalenyloxy group, indacenyloxy group, acenaphthyloxy group, fluorenyloxy group, phenalenyloxy group, phenanthrenyloxy group and anthracenyloxy group; and preferred examples include phenyloxy group, 1-naphthyloxy group and 2-naphthyloxy group.

[0103] The "C_{7-22} aralkyloxy group" used in the specification of the present application means a group corresponding to the above-defined "C_{7-22} aralkyl group" to which end an oxygen atom is bonded. Specific examples thereof include benzyloxy group, phenethyloxy group, 3-phenylpropyloxy group, 4-phenylbutyloxy group, 1-naphthylmethyloxy group and 2-naphthylmethyloxy group; and preferred examples include benzyloxy group.

[0104] The "5- to 14-membered heteroaralkyloxy group" used in the specification of the present application means a group corresponding to the above-defined "5- to 14-membered heteroaralkyl group" to which end an oxygen atom is bonded. Specific examples thereof include thienylmethyloxy group, furylmethyloxy group, pyridylmethyloxy group, pyridazylmethyloxy group, pyrimidylmethyloxy group and pyrazylmethyloxy group; and preferred examples include thienylmethyloxy group, furylmethyloxy group and pyridinylmethyloxy group.

[0105] The "5- to 14-membered heteroaryloxy group" used in the specification of the present application means a group corresponding to the above-defined "5- to 14-membered heteroaryl group" to which end an oxygen atom is bonded. Specific examples thereof include pyrrolyloxy group, pyridyloxy group, pyridazinyloxy group, pyrimidinyloxy group, pyrazinyloxy group, triazolyloxy group, tetrazolyloxy group, benzotriazolyloxy group, pyrazolyloxy group, imidazolyloxy group, benzimidazolyloxy group, indolyloxy group, isoindolyloxy group, indolizinyloxy group, purinyloxy group, indazolyloxy group, quinolyloxy group, isoquinolyloxy group, quinolizyloxy group, phthalazyloxy group, naphthyridinyloxy group, quinoxalyloxy group, quinazolinyloxy group, cinnolinyloxy group, pteridinyloxy group, imidazotriazinyloxy group, pyrazinopyridazinyloxy group, acridinyloxy group, phenanthridinyloxy group, carbazolyloxy group, carbazolinyloxy group, perimidinyloxy group, phenanthrolinyloxy group, phenazinyloxy group, imidazopyridinyloxy group, imidazopyrimidinyloxy group, pyrazolopyridinyloxy group, pyrazolopyridinyloxy group, thienyloxy group, benzothienyloxy group, furyloxy group, pyranyloxy group, cyclopentapyranyloxy group, benzofuryloxy group, isobenzofuryloxy group, thiazolyloxy group, isothiazolyloxy group, benzothiazolyloxy group, benzothiadiazolyloxy group, phenothiazinyloxy group, isoxazoyloxy group, furazanyloxy group, phenoxazinyloxy group, oxazolyloxy group, isoxazolyloxy group, benzoxazolyloxy group, oxadiazolyloxy group, pyrazolooxazolyloxy group, imidazothiazolyloxy group, thienofuranyloxy group, furopyrrolyloxy group and pyridoxazinyloxy group; and preferred examples include thienyloxy group, pyridyloxy group, pyrimidyloxy group and pyrazyloxy group.

[0106] The "aliphatic C_{2-22} acyl group" used in the specification of the present application means a group corresponding to the above-defined "C_{1-22} alkyl group" or "unsaturated C_{2-22} alkyl group" to which end a carbonyl group is bonded. Examples thereof include acetyl group, propionyl group, butyryl group, iso-butyryl group, valeryl group, iso-valeryl group, pivaloyl group, caproyl group, decanoyl group, lauroyl group, myristoyl group, palmitoyl group, stearoyl group, arachidoyl group, acryloyl group, propiol group, crotonyl group, iso-crotonyl group, olenoyl group and linolenoyl group; and preferred examples include aliphatic acyl groups having 2 to 6 carbon atoms, such as acetyl group, propionyl group, butyryl group, iso-butyryl group and acryloyl group.

[0107] The "aromatic C_{7-15} acyl group" used in the specification of the present application means a group corresponding to the above-defined "C_{6-14} aryl group" or "5- to 14-membered heteroaryl group" to which end a carbonyl group is bonded. Examples thereof include benzoyl group, 1-naphthoyl group, 2-naphthoyl group, picolinoyl group, nicotinoyl group, isonicotinoyl group, furoyl group and thiophenecarbonyl group; and preferred examples include benzoyl group, picolinoyl group, nicotinoyl group and isonicotinoyl group.

[0108] The "C_{1-22} alkylsulfonyl group" used in the specification of the present application means a group corresponding to the above-defined "C_{1-22} alkyl group" to which a sulfonyl group is bound. Specific examples thereof include methylsulfonyl group, ethylsulfonyl group, n-propylsulfonyl group and iso-propylsulfonyl group; and preferred examples include methylsulfonyl group.

[0109] The "C_{6-14} arylsulfonyl group" used in the specification of the present application means a group corresponding to the above-defined "C_{6-14} aryl group" to which a sulfonyl group is bound. Specific examples thereof include benzenesulfonyl group, 1-naphthalenesulfonyl group and 2-naphthalenesulfonyl group; and preferred examples include benzenesulfonyl group.

[0110] The "aliphatic C_{2-22} acyloxy group" used in the specification of the present application means a group corresponding to the above-defined "aliphatic C_{2-22} acyl group" to which end an oxygen atom is bonded. Specific examples thereof include acetoxy group, propionyloxy group and acryloxy group; and preferred examples include acetoxy group and propionyloxy group.

[0111] The "C_{2-22} alkoxycarbonyl group" used in the specification of the present application means a group corresponding to the above-defined "C_{1-22} alkoxy group" to which end a carbonyl group is bonded. Examples thereof include methoxycarbonyl group, ethoxycarbonyl group, n-propoxycarbonyl group, iso-propoxycarbonyl group, n-butoxycarbonyl group, iso-butoxycarbonyl group, sec-butoxycarbonyl group and tert-butoxycarbonyl group; and preferred examples include ethoxycarbonyl group, iso-propoxycarbonyl group and tert-butoxycarbonyl group.

[0112] The "unsaturated C_{3-22} alkoxycarbonyl group" used in the specification of the present application means a group corresponding to the above-defined "unsaturated C_{2-22} alkoxy group" to which end a carbonyl group is bonded. Examples thereof include vinyloxycarbonyl group, allyloxycarbonyl group, 1-propenyloxycarbonyl group, isopropenyloxycarbonyl group, propargyloxycarbonyl group and 2-butynyloxycarbonyl group; and preferred examples include allyloxycarbonyl group.

[0113] The "C_{1-22} alkylthio group" used in the specification of the present application means a group corresponding to the above-defined "C_{1-22} alkyl group" to which end a sulfur atom is bonded. Examples thereof include methylthio group, ethylthio group, n-propylthio group and iso-propylthio group; and preferred examples include methylthio group or ethylthio group.

[0114] The "C_{1-22} alkylsulfinyl group" used in the specification of the present application means a group corresponding to the above-defined "C_{1-22} alkyl group" to which end a sulfinyl group is bonded. Examples thereof include methylsulfinyl group, ethylsulfinyl group, n-propylsulfinyl group and iso-propylsulfinyl group; and preferred examples include methanesulfinyl group or ethanesulfinyl group.

[0115] The "C_{1-22} alkylsulfonyloxy group" used in the specification of the present application means a group corresponding to the above-defined "C_{1-22} alkylsulfonyl group" to which end an oxygen atom is bonded. Examples thereof include methylsulfonyloxy group, ethylsulfonyloxy group, n-propylsulfonyloxy group and iso-propylsulfonyloxy group; and preferred examples include methylsulfonyloxy group.

[0116] The substituent of the phrase "an optionally substituted" used in the specification of the present application may be one or more groups selected from:

(1) a halogen atom,

(2) a hydroxyl group,

(3) a thiol group,

(4) a nitro group,

(5) a nitroso group,

(6) a cyano group,

(7) a carboxyl group,

(8) a hydroxysulfonyl group,

(9) a amino group,

(10) a C_{1-22} alkyl group (for example, methyl group, ethyl group, n-propyl group, iso-propyl group, n-butyl group, iso-butyl group, sec-butyl group and tert-butyl group),

(11) an unsaturated C_{2-22} alkyl group (for example, vinyl group, allyl group, 1-propenyl group, 2-propenyl group, isopropenyl group, ethynyl group, 1-propynyl group, 2-propynyl group, 1-butynyl group, 2-butynyl group and 3-butynyl group),

(12) a C_{6-14} aryl group (for example, phenyl group, 1-naphthyl group and 2-naphthyl group),

(13) a 5- to 14-membered heteroaryl group (for example, thienyl group, furyl group, pyridyl group, pyridazyl group, pyrimidyl group and pyrazyl group),

(14) a 3- to 14-membered non-aromatic heterocyclic group (for example, aziridinyl group, azetidyl group, pyrrolidinyl group, pyrrolyl group, piperidinyl group, piperazinyl group, homopiperidinyl group, homopiperazinyl group, imidazolyl group, pyrazolidyl group, imidazolidyl group, morpholyl

group, thiomorpholyl group, imidazolinyl group, oxazolinyl group and quinuclidyl group),

(15) a C_{3-14} cycloalkyl group (for example, cyclopropyl group, cyclobutyl group, cyclopentyl group, cyclohexyl group, cycloheptyl group and cyclooctyl group),

(16) a C_{1-22} alkoxy group (for example, methoxy group, ethoxy group, n-propoxy group, iso-propoxy group, sec-propoxy group, n-butoxy group, iso-butoxy group and tert-butoxy group),

(17) an unsaturated C_{2-22} alkoxy group (for example, vinyloxy group, allyloxy group, 1-propenyloxy group, 2-propenyloxy group, isopropenyloxy group, ethynyloxy group, 1-propynyloxy group, 2-propynyloxy group, 1-butynyloxy group and 2-butynyloxy group),

(18) a C_{6-14} aryloxy group (for example, phenyloxy group, 1-naphthyloxy group and 2-naphthyloxy group),

(19) a C_{7-22} aralkyloxy group (for example, benzyloxy group, phenethyloxy group, 3-phenylpropyloxy group, 4-phenylbutyloxy group, 1-naphthylmethyloxy group and 2-naphthylmethyloxy group),

(20) a 5- to 14-membered heteroaralkyloxy group (for example, thienylmethyloxy group, furylmethyloxy group, pyridylmethyloxy group, pyridazylmethyloxy group, pyrimidylmethyloxy group and pyrazylmethyloxy group),

(21) a 5- to 14-membered heteroaryloxy group (for example, thienyloxy group, furyloxy group, pyridyloxy group, pyridazyloxy group, pyrimidyloxy group and pyrazyloxy group),

(22) an aliphatic C_{2-22} acyl group (for example, acetyl group, propionyl group, butyryl group, iso-butyryl group, valeryl group, iso-valeryl group, pivalyl group, caproyl group, decanoyl group, lauroyl group, myristoyl group, palmitoyl group, stearoyl group, arachidoyl group, acryl group, propiol group, crotonyl group, iso-crotonyl group, olenoyl group and linolenoyl group),

(23) an aromatic C_{7-15} acyl group (for example, benzoyl group, 1-naphthoyl group and 2-naphthoyl group),

(24) an aliphatic C_{2-22} acyloxy group (for example, acetoxy group, propionyloxy group and acryloxy group),

(25) a C_{2-22} alkoxycarbonyl group (for example, methoxycarbonyl group, ethoxycarbonyl group, n-propoxycarbonyl group, iso-propoxycarbonyl group, n-butoxycarbonyl group, iso-butoxycarbonyl group, sec-butoxycarbonyl group and tert-butoxycarbonyl group),

(26) an unsaturated C_{3-22} alkoxycarbonyl group (for example, vinyloxycarbonyl group, allyloxycarbonyl group, 1-propenyloxycarbonyl group, 2-propenyloxycarbonyl group, isopropenyloxycarbonyl group, propargyloxycarbonyl group and 2-butynyloxycarbonyl group),

(27) a C_{1-22} alkylthio group (for example, methylthio group, ethylthio group, n-propylthio group and iso-propylthio group),

(28) a C_{1-22} alkylsulfinyl group (for example, methylsulfinyl group, ethylsulfinyl group, n-propylsulfinyl group and iso-propylsulfinyl group),

(29) a C_{1-22} alkylsulfonyl group (for example, methylsulfonyl group, ethylsulfonyl group, n-propanesulfonyl group and iso-propanesulfonyl group),

(30) a C_{6-14} arylsulfonyl group (for example, benzenesulfonyl group, 1-naphthalenesulfonyl group and 2-naphthalenesulfonyl group),

(31) a C_{1-22} alkylsulfonyloxy group (for example, methylsulfonyloxy group, ethylsulfonyloxy group, n-propylsulfonyloxy group and iso-propanesulfonyloxy group),

(32) carbamoyl group, and

(33) formyl group.

Among them, a preferred example is an amino group, a C_{1-22} alkyl group, an unsaturated C_{2-22} alkyl group, a C_{6-14} aryl group, a 5- to 14-membered heteroaryl group, a 3- to 14-membered non-aromatic heterocyclic group and a C_{3-14} cycloalkyl group, and a more preferred example is an amino group, a C_{1-22} alkyl group, a 3- to 14-membered nonaromatic heterocyclic group and a C_{3-14} cycloalkyl group. The abovementioned (9) amino group and (31) carbamoyl group as the substituent in "an optionally substituted" may each be further substituted with one or two of a C_{1-22} alkyl group, an unsaturated C_{2-22} alkyl group or a C_{6-14} aryl group.

[0117] In the present specification, the chemical formula of the compound according to the present invention is illustrated as a planimetric chemical formula for convenience but the compound can include certain isomers drawn from the chemical formula. The present invention can include all isomers and mixtures of the isomers such as a geometric isomer which is generated from the configuration of the compound, an optical isomer based on an asymmetric carbon, a rotamer, a stereoisomer and a tautomer. The present invention is not limited to the expediential description of the chemical formula, and can include either of isomers or a mixture thereof. Accordingly, when the compound according to the present invention has an asymmetric carbon in the molecule, and its optically active substance and racemate exist, any one is included. Further, when polymorphic crystals exist, the crystal form according to the present invention is not specifically limited to one form, and any one of the crystal forms may be single or a mixture of the crystal forms.

[0118] The "pharmaceutically acceptable salt" used in the present invention is not particularly restricted as long as it can form a salt with the compound represented by formula (I), and is pharmaceutically acceptable. Preferred examples thereof include halide hydroacid salt such as hydrochloric acid salt, hydrobromic acid salt, hydrolodic acid salt; inorganic acid salt such as sulphic acid salt, nitric acid salt, perchloric acid salt, phosphoric acid salt, carbonic acid salt, bicarbonic acid salt; organic carboxylic acid salt such as acetic acid salt, trifluoroacetic acid salt, maleic acid salt, tartaric acid salt, fumaric acid salt, citric acid salt; organic sulfonic acid salt such as methanesulfonic acid salt, trifluoro methanesulfonic acid salt, ethanesulfonic acid salt, benzenesulfonic acid salt, toluenesulfonic acid salt, camphorsulfonic acid salt; amino acid salt such as aspartic acid salt, glutamic acid salt; quaternary amine salt; alkaline metal salt such as sodium salt, potassium salt; and alkaline earth metal salt such as magnesium salt, calcium salt.

[0119] The "solvate" used in the present invention is not particularly restricted as long as it can form a solvate with the compound represented by formula (I) or the salt thereof, and is pharmaceutically acceptable. Preferred examples include hydrate, alcoholate such as ethanolate, and etherate.

[0120] The present invention also includes a metabolite generated by degradation of the compound represented by formula (I) within a living body, as well as a prodrug of the compound represented by formula (I) and the salt thereof. The "prodrug" used herein means an inert substance to which "an active moiety of a drug" (meaning "drug" corresponding to a prodrug) has been chemically modified, for the purpose of improvement of bioavailability and reduction of a side effect. After absorbed, it is metabolized into the active moiety in vivo and exerts an action. Accordingly, the term "prodrug" refers to any compound having a lower intrinsic activity than the corresponding "drug", which is, once administrated to a biological system, converted into the "drug" substance via a spontaneous chemical reaction, enzyme catalyzed reaction or metabolic reaction. Examples of such prodrugs include various prodrugs, for example, compounds produced by acylation, alkylation, phosphorylation, boration, carbonation, esterification, amidation, or urethanation of a functional group such as an amino, hydroxyl, or carboxyl group in the compound represented by formula (I). However, it should be noted that the exemplified prodrugs are not comprehensive but are merely typical, and other conventional various prodrugs can be prepared by a conventional method by a person having ordinary skill in the art from the compound represented by formula (I).

[0121] When the compound represented by formula (I) is administrated to a mammal in the method according to the present invention, the compound represented by formula (I) may be formulated by known methods. Conventional carriers are used for formulation, and the pharmaceutical products are prepared by conventional methods. Namely, when a solid formulation for oral use is prepared, a filler is added to the main drug, and if necessary, a binder, a disintegrant, a lubricant, a colorant, a flavoring agent and the like are added thereto, and then tablets, coated tablets, granules, powders, capsules and the like are prepared by conventional methods. It is needless to say that sugar coating, gelatin coating or suitable coating may be conducted on the tablet and granule, if necessary. When the compounds are formulated as an injection, a pH regulator, a buffer, a stabilizer, a solubilizer and the like are added to the main drug, if necessary, to prepare an subcutaneous, intramuscular, intra-articular or intravenous injection according to conventional procedures. When the compound represented by formula (I) is administered as a therapeutic or preventive agent for various diseases, it may be orally administered as tablets, powders, granules, capsules, syrups and the like, and may be parenterally administered as a spray, a suppository, an injection, a topical preparation or an infusion. Although the dose remarkably varies according to the severity of symptom, age, the kind of disease etc., approximately 1 mg to 100 mg per day for an adult is administered in general at one time or several times per day.

[0122] When the expression level of pre-mRNA of the genes listed in Table 1, Table 2, Table 3, Table 4, and Table 5 or homologous genes thereof, preferably the genes listed in Table 1 and Table 2 or homologous genes thereof as well as an abnormal protein generated by splicing defect of the gene is monitored in the method according to the present invention, the expression level may be preferably monitored before administration of the compound represented by formula (I), followed by another monitoring at 3, 6, 8, 24, or 48 hours after the administration. In a preferred embodiment, follow-up monitoring of the expression level is carried out at the earliest three hours after the administration of the compound represented by formula (I).

[0123] Upon implementing the method according to the present invention the splicing defect can be detected using an increase in the expression level of pre-mRNA or the abnormal protein caused by the splicing defect as an index.

[0124] According to a first aspect of the invention, a method for assaying the action of the compound represented by formula (I), using the increase in the expression level of pre-mRNA as an index (invention (3)) is provided.

[0125] In step (a), cancer tissue or normal tissue such as hemocytes in peripheral blood, platelets, and serum can be taken from the mammal subjected to the assay and pre-mRNA samples can be prepared from the obtained samples to quantify the expression level of pre-mRNA. Preparation of pre-mRNA is well known (for example, "Molecular Cloning, A Laboratory Manual 3^{d} ed." (Cold Spring Harbor Press (2001)), and required devices, instruments, and reagents therefor are commercially available. Hence those skilled in the art may prepare pre-mRNA with no difficulties using the devices, apparatuses, and reagents as needed.

[0126] Measurement of the expression level of pre-mRNA in step (a) can be performed with any method selected from a Northern blot method, a dot blot method, an RT-PCR method, and a microarray (preferably, Human Exon 1.0 ST Array). The principles of these methods and how to carry out these methods are well-known, and the required devices and apparatuses therefor are commercially available. Moreover, in Examples below, an example in which the expression level of pre-mRNA is measured with these methods will be described. Those skilled in the art can measure the expression level of pre-mRNA with no difficulties using the Northern blot method, the dot blot method, the RT-PCR method, and the microarray. In the measurement of the expression level of pre-mRNA in step (a), preferably, the microarray can be used.

[0127] For the measurement of the expression level of pre-mRNA in step (a), a probe and a primer which consist of a polynucleotide capable of hybridizing with nucleotide sequences of genes listed in Table 1, Table 2, Table 3, Table 4, and Table 5 and homologous genes thereof, preferably genes listed in Table 1 and Table 2 or homologous genes thereof, or their complementary sequences can be employed as a detection marker.

[0128] Any probe and primer according to the present invention may be employed as long as it can detect the expression of pre-mRNA (including a part thereof) of the genes listed in Table 1, Table 2, Table 3, Table 4, and Table 5 and homologous genes thereof, preferably the genes listed in Table 1 and Table 2 or homologous genes thereof. The probe and the primer according to the present invention refers to a polymer consisting of bases or base pairs such as deoxyribonucleic acid (DNA) or ribonucleic acid (RNA). It has been known that double stranded cDNA can be used in tissue in situ hybridization, and the probe and the primer according to the present invention include such double stranded cDNA. Particularly preferred RNA probe and primer for detecting RNA in tissue include RNA probes (riboprobe).

[0129] The probe and the primer according to the present invention includes a probe or a primer which consists of a polynucleotide comprising a nucleotide sequence of at least 10, preferably at least 15, more preferably at least 20, further preferably at least 25 continuous nucleotides of the genes listed in Table 1, Table 2, Table 3, Table 4 and Table 5, and homologous genes thereof, preferably genes listed in Table 1 and Table 2 or homologous genes thereof, or complementary sequences thereof as well as all mutated polynucleotide sequences thereof. The probe and the primer according to the present invention include a probe or a primer which consists of a polynucleotide comprising a nucleotide sequence of 10 to 50 or 10 to 30 continuous nucleotides, 15 to 50 or 15 to 30 continuous nucleotides, 20 to 50 or 20 to 30 continuous nucleotides, 25 to 50 or 25 to 30 continuous nucleotides, of the genes listed in Table 1, Table 2, Table 3, Table 4 and Table 5, and homologous genes thereof, preferably the genes listed in Table 1 and Table 2 or homologous genes thereof or mutated polynucleotide sequences thereof.

[0130] The probe and the primer according to the present invention may be at least 10 bases in length, preferably at least 15 bases in length, more preferably at least 20 bases in length, further preferably at least 25 bases in length. The probe and the primer according to the present invention may also be 10 to 50 bases or 10 to 30 bases in length, 15 to 50 bases or 15 to 30 bases in length, 20 to 50 bases or 20 to 30 bases in length, 25 to 50 bases or 25 to 30 bases in length.

[0131] According to the preferred embodiment of the probe and the primer according to the present invention, there are provided the probe and the primer having 15 to 30 bases in length for assaying the action of the compound represented by formula (I) to the mammals, which consist of a polynucleotide comprising at least 10, preferably at least 15, more preferably at least 20, further preferably at least 25 continuous nucleotides of a polynucleotide sequence of the genes listed in Table 1, Table 2, Table 3, Table 4, and Table 5 or homologous genes thereof, preferably the genes listed in Table 1 and Table 2 or homologous genes thereof, as well as all mutated sequences thereof, and which are capable of hybridizing with a polynucleotide sequence of the genes listed in Table 1, Table 2, Table 3, Table 4, and Table 5 or homologous genes thereof, preferably the genes listed in Table 1 and Table 2 or homologous genes thereof.

[0132] According to a preferred aspect of the probe and the primer according to the present invention, there are provided a probe and a primer which are capable of hybridizing with a more distinct region within a nucleotide sequence of the genes listed in Table 1, Table 2, Table 3, Table 4, and Table 5 or homologous genes thereof, preferably the genes listed in Table 1 and Table 2 or homologous genes thereof. The above probe and primer allow more precise detection of the action of the compound represented by formula (I) to the mammal.

[0133] The probe according to the present invention can be chemically synthesized based on the nucleotide sequence of the gene subjected to be detected. Preparation of the probes is well known and can be carried out in accordance with, for example, "Molecular Cloning, A Laboratory Manual 2^{nd} ed." (Cold Spring Harbor Press (1989)), "Current Protocols in Molecular Biology" (John Wiley & Sons (1987-1997)).

[0134] The primers according to the present invention can be used as a primer set comprising of two or more types of the primers.

[0135] The primer and the primer set according to the present invention can be used as a primer and a primer set in accordance with a conventional method in a known method for detecting the target gene using a nucleic acid amplification method such as a PCR method, a RT-PCR method, a real-time PCR method, and an in situ PCR method.

[0136] The primer set according to the present invention can be selected such that the nucleotide sequence of the target gene can be amplified with the nucleic acid amplification method such as the PCR method. The nucleic acid amplification method is well known and selection of the primer pair therein is obvious for those skilled in the art. For example, in the PCR method, the primers can be selected such that one of two primers (a primer pair) undergoes base pairing with the plus strand of the double stranded DNA of the gene subjected to be detected whereas the other of the primers undergoes base pairing with the minus strand of the double stranded DNA, as well as an extending strand extended with one primer can be paired with the other primer. In a LAMP method (WO00/28082), three regions from the 3' terminus termed F3c, F2c and F1c, and three regions from the 5' terminus termed B1, B2 and B3 are respectively defined for the gene subjected to be detected. Four types of primers can be designed using these six regions.

[0137] The primer according to the present invention may be chemically synthesized based on the nucleotide sequence of the gene subjected to be detected. Preparation of the primer is well known and can be carried out in accordance with, for example, "Molecular Cloning, A Laboratory Manual 2^{nd} ed." (Cold Spring Harbor Press (1989)), "Current Protocols in Molecular Biology" (John Wiley & Sons (1987-1997)).

[0138] Table 1, Table 2, Table 3, Table 4, and Table 5 describe information specifying the genes and homologous genes thereof listed in these tables. Accordingly those skilled in the art can obtain information on the nucleotide sequence of the subject gene to be detected based on the information described in Table 1, Table 2, Table 3, Table 4, and Table 5 to design the probe and primer based thereon.

[0139] In addition, the genes listed in Table 1, Table 2, Table 3, Table 4, and Table 5 are known genes and probes and primers for detecting them are commercially available individually or as a detection kit or detection array.

[0140] The term "to hybridize" used in the specification of the present application means to hybridize with a target polynucleotide under stringent conditions. A specific example of the polynucleotide which hybridizes under stringent conditions includes a polynucleotide having at least 70% or more, preferably 80% or more, more preferably 85% or more, further preferably 90% or more, further more preferably 95% or more, particularly preferably 98% or more, and most preferably 99% or more homology to the target polynucleotide when the homology is calculated by a homology search software, such as FASTA, BLAST, Smith-Waterman (*Meth. Enzym.*, 164, 765, (1988)), using default parameters. Further, hybridization "under stringent conditions" can be performed, for example, by a method of carrying out the reaction at a temperature of 40° C. to 70° C., preferably at a temperature of 60° C. to 65° C., in a hybridization buffer solution generally used by those skilled in the art, and carrying out washing in a washing solution at a salt concentration of 15 to 300 mmol/L, preferably at 15 to 60 mmol/L. The temperature and salt concentration can be appropriately adjusted depending on the length of the probe to be used. Further the hybridized product can be washed under conditions in 0.2× or 2×SSC and 0.1% SDS at a temperature of 20° C. to 68° C. Whether stringent (high stringency) or mild (low stringency) conditions is used depends on a difference in salt concentrations and temperatures while the washing process. In cases where the difference in hybridizing depends on the salt concentration, the washing process can be carried out in 0.2×SSC and 0.1% SDS as a stringent washing buffer (high stringency wash buffer) and 2×SSC and 0.1% SDS as a mild washing buffer (low stringency wash buffer). Also, in cases where the difference in hybridizing depends on the temperature, the washing process may be carried out at 68° C. for stringent conditions, at 42° C. for medium (moderate stringency) conditions, or at room temperature (20-25° C.) for mild conditions, but 0.2×SSC and 0.1% SDS are used in all the cases.

[0141] When pre-hybridization is carried out, it is carried out under the same condition as in hybridization, but pre (preliminary)-washing is not necessarily carried out under the same condition as in hybridization.

[0142] The "homologous gene" used in the specification of the present application means a gene encoding a protein functionally equivalent to a protein encoded by a certain gene. Whether it is "functionally equivalent" or not can be determined by evaluating if the protein has functions equivalent to biological phenomena or functions related to the expression of the gene. Such a gene encoding the functionally equivalent protein includes not only the so-called homologous gene but also a gene with polymorphism and a gene having a mutation without affecting the function.

[0143] Examples of the homologous gene include genes which have a nucleotide sequence of a certain gene wherein one or more (preferably one to several, or 1, 2, 3 or 4) nucleotides are inserted, substituted or deleted, or added to one or both termini, and which encode the functionally equivalent protein.

[0144] Examples of the homologous gene also include genes which encode an amino acid sequence encoded by a certain gene wherein one or more amino acids are inserted, substituted, or deleted, or added to one or both termini (modified amino acid sequence), and which encode the functionally equivalent protein.

[0145] "One or more amino acids are inserted, substituted, or deleted, or added to one or both termini" used in the specification of the present application means that a modification is made by a known technical method such as a site specific mutagenesis method or by substitution of several amino acids as in naturally occurring mutation.

[0146] The "modified amino acid sequence" used in the specification of the present application can be an amino acid sequence wherein, for example, 1 to 30 amino acids, preferably 1 to 20 amino acids, more preferably 1 to 9 amino acids, further preferably 1 to 5 amino acids, particularly preferably 1 to 2 amino acids have been inserted, substituted, or deleted, or added to one or both termini. Preferably, the modified amino acid sequence may be an amino acid sequence having one or more (preferably one or several or 1, 2, 3, or 4) conservative substitutions.

[0147] The term "conservative substitution" is used herein to mean that one or more amino acid residues are substituted with other chemically similar amino acid residues, so as not to substantially modify the functions of a protein. Examples of such conservative substitution include a case where a certain hydrophobic residue is substituted with another hydrophobic residue and a case where a certain polar residue is substituted with another polar residue having the same electric charge. Such functionally similar amino acids that can be used in such substitution are known as every amino acid types in the present technical field. Specific examples of a nonpolar (hydrophobic) amino acid include alanine, valine, isoleucine, leucine, proline, tryptophan, phenylalanine, and methionine. Examples of a polar (neutral) amino acid include glycine, serine, threonine, tyrosine, glutamine, asparagine, and cysteine. Examples of a (basic) amino acid having a positive charge include arginine, histidine, and lysine. Examples of an (acidic) amino acid having a negative charge include aspartic acid and glutamic acid.

[0148] In cases where the first aspect of the present invention is carried out using a cancer tissue and its surrounding tissue as assay samples, the action of the compound represented by formula (I) can be assayed preferably by using the expression level of pre-mRNA of the genes listed in Table 1 and Table 3 or homologous genes thereof as an index. Measurement of the expression level of the pre-mRNA in cases where the cancer tissue and the surrounding tissue are used as the samples, the microarray can be preferably used.

[0149] In cases where the first aspect of the present invention is carried out using a normal tissue, in particular peripheral blood and whole blood as the assay samples, the action of the compound represented by formula (I) can be assayed preferably by using the expression level of pre-mRNA of the genes listed in Table 2, Table 4, and Table 5, or homologous genes thereof as an index. Measurement of the expression level of the pre-mRNA in cases where the peripheral blood and whole blood are used as the samples, the microarray can be preferably used.

[0150] According to a second aspect of the present invention, a method for assaying the action of the compound represented by formula (I), using an increase in the expression level of an abnormal protein expressed resulting from splicing defect of pre mRNA (invention (11)) is provided.

[0151] The abnormal protein measured in step (f) is an abnormal protein resulting from splicing defect of the genes listed Table 1, Table 2, Table 3, Table 4, and Table 5, or homologous genes thereof. Table 1, Table 2, Table 3, Table 4, and Table 5 describe information specifying the genes listed in these tables and homologous genes thereof.

[0152] In step (f), samples are taken from a cancer tissue or normal tissue such as hemocytes in peripheral blood, plasma, and serum from a mammal subjected to the assay. Measurement of the expression level of the abnormal protein may be carried out with the collected samples as they are or a protein extracted therefrom. Extraction of the protein is well known (for example, Campa, M. J. et al. *Cancer Res.* 63, 1652-1656, 2003), and devices, instruments, and reagents necessary for carrying out the extraction are commercially available. Hence those skilled in the art may extract the protein with no difficulties using such the commercially available devices, apparatuses, and reagents as needed.

[0153] The measurement of the expression level of the abnormal protein in step (f) can be carried out with a method selected from a fluorescent antibody method, an enzyme immunoassay (ELISA) method, a radioimmunoassay (RIA) method, a Western blot method and an immunostaining (immunohistochemistry) method. The principle and implementation procedures of these methods are well known and devices and instruments necessary for carrying out the methods are commercially available. Furthermore, in Examples below, an example in which the expression level of pre-mRNA is measured with those methods will be described. Those skilled in the art may measure the expression level of pre-mRNA with no difficulties using the fluorescent antibody method, the enzyme immunoassay (ELISA) method, the radioimmunoassay (RIA) method, the Western blot method and the immunostaining (immunohistochemistry) method. In the measurement of the expression level of the abnormal protein in step (f), the enzyme immunoassay (ELISA) method, the Western blot method, the immunostaining (immunohistochemistry) method and a mass spectrometry method can be used.

[0154] In the measurement of the abnormal protein in step (f), an antibody against the abnormal protein generated from the splicing defect of the genes listed Table 1, Table 2, Table 3, Table 4, and Table 5 and a fragment thereof can be used as a detection marker.

[0155] Any abnormal protein may be employed for obtaining the antibody according to the present invention as long as it has antigenicity. A protein having an amino acid sequence of the abnormal protein wherein one or more amino acids are deleted, inserted, substituted or added can be used as the antigen for the abnormal protein. It is known that such a protein maintains the same biological activity as the original protein (Mark et al. (1984) *Proc. Natl. Acad. Sci. USA* 81:5662-6; Zoller and Smith (1982) *Nucleic Acids Res.* 10:6487-500; Wang et al. (1984) *Science* 224:1431-3; Dalbadie-McFarland et al. (1982) *Proc. Natl. Acad. Sci. USA* 79:6409-13). A technique to delete, insert, substitute or add one or more amino acids while maintaining the antigenicity of the original protein is known. For example, such a protein may be obtained by preparing and properly expressing a polynucleotide encoding an abnormal protein by site directed mutagenesis technique (*Molecular Cloning, A Laboratory Manual* 2nd ed., Cold Spring Harbor Press (1989); *Current Protocols in Molecular Biology*, John Wiley & Sons, (1987-1997), Section 8.1-8.5; Hashimoto-Goto et al. (1995) *Gene* 152:271-5; Kinkel (1985) *Proc. Natl. Acad. Sci. USA* 82:488-92; Kramer and Fritz (1987) *Method. Enzymol.* 154:350-67; Kunkel (1988) *Method. Enzymol.* 85:2763-6).

[0156] The antibody according to the present invention includes an antibody having specificity against a part of the abnormal protein. That is, the abnormal protein for obtaining the antibody according to the present invention includes a polypeptide having the full length amino acid sequence of the abnormal protein as well as a fragment thereof having at least six amino acid residues (for example, not less than 6, 8, 10, 12 or 15 amino acid residues). A preferred fragment is a polypeptide fragment such as an amino terminus and a carboxyl terminus of the abnormal protein. An antigen determination site of the polypeptide can be predicted by a method analyzing the hydrophobicity/hydrophilicity of the amino acid sequence of the protein (Kyte-Doolittle (1982) *J. Mol. Biol.* 157:105-22), and a method analyzing a secondary structure (Chou-Fasman (1978) *Ann. Rev. Biochem.* 47:251-76) and further confirmed by a computer program (*Anal. Biochem.* 151:540-6 (1985)) or a technique such as PEPSCAN analysis (patent application publication JP60500684T) involving the synthesis of a short peptide to confirm the antigenicity.

[0157] Table 1, Table 2, Table 3, Table 4 and Table 5 describe information specifying the genes listed in these Tables and homologous genes thereof. Accordingly, those skilled in the art can obtain information on an amino acid encoded by the subject gene to be detected based on the information described in Table 1, Table 2, Table 3, Table 4 and Table 5, and can design and obtain an antibody based thereon.

[0158] In addition, the genes listed in Table 1, Table 2, Table 3, Table 4 and Table 5 are known genes and an antibody for detecting a protein encoded thereby is commercially available individually or as a detection kit or detection array.

[0159] The antibody according to the present invention may be obtained with a method known those skilled in the art (for example, "Current Protocols in Molecular Biology" (John Wiley & Sons (1987), *Antibodies: A Laboratory Manual*, Ed. Harlow and David Lane, Cold Spring Harbor Laboratory (1988)).

[0160] The antibody according to the present invention includes a polyclonal antibody, a monoclonal antibody, a chimeric antibody, a single chain antibody (scFv), a humanized antibody and a multispecific antibody. Also, the fragment of the antibody according to the present invention includes an antibody fragment such as Fab, Fab', F(ab')$_2$, Fc, and Fv.

[0161] For a polyclonal antibody, blood can be taken from a mammal sensitized with an antigen and blood serum can be isolated with known procedures from the blood to yield blood serum containing the polyclonal antibody. As needed, a fraction containing the polyclonal antibody can further be isolated from this blood serum.

[0162] For a monoclonal antibody, antibody-producing cells are taken from spleen or lympho node of a mammal sensitized with the above-mentioned antigen, and then undergo cell fusion with myeloma cell. The resultant hybridoma is subjected to cloning and the antibody was recovered from the culture thereof to yield the monoclonal antibody.

[0163] A fragment of the abnormal protein can be used as an immunogen. Alternatively, the synthesized one based on the amino acid sequence of the abnormal protein can be used. The antigen can be used as a complex with a carrier protein. A variety of condensing agents can be used for preparation of the complex between the antigen and the carrier protein, which condensing agents include glutaraldehyde, carbodiimide, and maleimide active ester. The carrier protein may be a usually used one such as bovine serum albumin, thyroglobulin, and hemocyanin. A procedure for coupling at a rate (volume) of 1 time to 5 times is usually employed.

[0164] Examples of the animal immunized include mice, rats, rabbits, guinea pigs, hamsters. An example of a method of inoculation is subcutaneous, intramuscular or intraperitoneal administration. The administration may be done in combination with Freund's complete adjuvant and Freund's incomplete adjuvant, and usually once every two to five weeks.

[0165] The antibody-producing cells obtained from the spleen or lymph node of the animal immunized undergo cell fusion with myeloma cells, and is isolated as hybridoma. As the myeloma cells, cells derived from mouse, rat, *Homo sapiens* and etc. are used. It is preferred that antibody-producing cell be derived from the same species. Yet there are cases where the cell fusion can be carried out between different species.

[0166] Procedures for the cell fusion may be carried out with a known method, in accordance with, for example, *Nature,* 256, 495, 1975. Examples of fusion accelerator include polyethylene glycols and Sendai virus. The cell fusion can be usually carried out by using about 20 to 50% of concentration of polyethylene glycols (average molecular weight 1000 to 4000); at a temperature of 20 to 40° C., preferably 30 to 37° C.; at a ratio in number of cells between antibody production cells and myeloma of usually about 1:1 to 10:1, and for about 1 to 10 minutes.

[0167] Various immunochemical methods can be employed for screening the antibody-producing hybridoma. Examples thereof include ELISA method using a microtiter plate coated with the abnormal protein, EIA method using a microtiter plate coated with an anti-immunoglobulin antibody, immune blot method using a nitrocellulose blotting membrane after electrophoresis of samples containing the abnormal protein.

[0168] Using such wells, cloning by, for example, a limiting dilution method can be further carried out to obtain a clone. Selection and breeding of the hybridoma is usually carried out culture medium for mammalian cells (such as RPMI1640) containing 10~20% bovine fetus serum and supplemented with HAT (hypoxanthine, aminopterin, and thymidine). The clone obtained in such a way is intraperitoneally transplanted into a SCID mouse previously administrated with pristine. Ten to fourteen days later, ascites containing the monoclonal antibody at a high concentration is obtained, which ascites can be used as a raw material for antibody purification. Also the clone may be cultured and the obtained culture may be used as a raw material for antibody purification

[0169] Any purification method may be used for purifying the monoclonal antibody as long as it is a known method for purifying an immunoglobulin. The purification can be readily accomplished by, for example, an ammonium sulfate fractionation method, a PEG fractionation method, an ethanol fractionation method, and use of an anion exchanger, as well as means such as affinity chromatography using the abnormal protein.

[0170] Purification of the polyclonal antibody from serum can be carried out in the same manner.

[0171] In cases where the procedure in the second aspect according to the present invention is carried out by using the cancer tissue and its surrounding tissue as assay samples, the action of the compound represented by formula (I) can preferably be assayed by using the expression level of the abnormal protein(s) expressed resulting from splicing defect of the genes listed in Table 1 and Table 3 or homologous genes thereof as an index. In cases where the cancer tissue and the surrounding tissue are used as the samples, the measurement of the expression level of the abnormal proteins can preferably be employed with the enzyme immunoassay (ELISA) method, the Western blot technique, the immunostaining (immunohistochemistry) method and the mass spectrometry method.

[0172] In cases where the procedure in the second aspect of the present invention using peripheral blood or whole blood as assay samples, the action of the compound represented by formula (I) can preferably be assayed by using the expression level of the abnormal protein(s) expressed resulting from splicing defect of the genes listed in Table 2, Table 4, and Table 5 or homologous genes thereof as an index. In cases where peripheral blood or whole blood are used as the samples, the measurement of the expression level of the abnormal proteins can preferably be employed with the enzyme immunoassay (ELISA) method, the Western blot method, the immunostaining (immunohistochemistry) method and the mass spectrometry method.

[0173] The samples obtained from a subject refer to tissues, cells, body fluids, and the like which are obtained from the subject. Specific examples include biopsy, blood (including hemocytes, plasma, and serum), urine, tissue samples such as curettage tissue (buccal scrapes) of oral cavity, and tumor cells (cells from tumors of breast, lung, stomach, head and neck, colorectum, kidney, pancreas, uterus, liver, urinary bladder, endometrium, and prostate, as well as hemocytes of leukemia patients or of lymphocytes).

EXAMPLES

[0174] The present invention is described in more detail by the examples below. The followings are illustrative of the invention and by no means intended to limit the invention to the embodiments described herein.

Example 1

Analysis with Northern Blotting

[0175] Gene expression that affects the cell cycle was examined by Northern blotting analysis using RNA from HeLa cells treated with pladienolide B. As a result, it was discovered that CDKN1B (p27) gene caused pre-mRNA accumulation.

[0176] HeLa cells (5×10^5 cells/mL) were first seeded in a six-well plate and cultured overnight in RPMI1640 medium (containing 10% FCS, penicillin, and streptomycin). The cells were then treated with 10 μM of pladienolide B, 100 μM of DRB, or 1 μg/mL of Actinomycin D for 0, 1, 2, and 4 hours. Subsequently, total RNA was obtained using RNeay mini kit (Qiagen) and absorbance at 260 nm was measured to quantify an amount of RNA. Each total RNA sample (10 μg) was, after combined with RNA SAMPLE LOADING BUFFER (SIGMA), subjected to electrophoresis in 1% denatured agarose gel containing formaldehyde, followed by blotting to nylon membrane and cross-linking with UV to make a Northern membrane.

[0177] In order to make a probe for CDKN1B(p27) and CDKN1A(p21), the entire length of gene was amplified by PCR with the following primers using cDNA reverse-transcribed from total RNA prepared from U251 cells as a template.

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Primers for CDKN1B
P27-1F:
5'-ATGTCAAACGTGCGAGTGTCTAAC-3'     (SEQ ID NO: 1)

P27-2:
5'-TTACGTTTGACGTGTTGTGAGGCC-3'     (SEQ ID NO: 2)

Primers for CDKN1A
P21-1F:
5'-GCCATGTCAGAACCGGCTGGGGAT-3'     (SEQ ID NO: 3)

P21-2:
5'-TTAGGGCTTCCTCTTGGAGAAGAT-3'     (SEQ ID NO: 4)
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The obtained fragment was separated by electrophoresis in agarose gel and purified. The fragment was labeled using Megaprime DNA labeling kit (Amersham) and Redivue ^{32}P (Amersham) and purified with ProbeQuant G-50 Micro Columns (Amersham). Using PerfectHyb hybridization solution (TOYOBO), the labeled probe was hybridized onto the blotting membrane. The membrane was washed with a buffer containing 2×SSC and 0.05% SDS, followed by a buffer containing 0.1×SSC and 0.1% SDS. The membrane was exposed to Imaging Plate (FUJIFILM) to determine intensity of photosensitivity with BAS2000 (FUJIFILM). Accumulation of CDKN1B pre-mRNA was observed only when the cells were treated with pladienolide (FIGS. **1**A and B).

Example 2

Analysis with cDNA Library

[0178] In order to check if any other gene accumulated its pre-mRNA, a cDNA library was constructed from HeLa cells treated with pladienolide and by randomly sequencing 42 clones, genes containing an intron were screened. Primers were designed within the introns surrounding an exon of those genes. RT-PCR was performed for the total RNA of HeLa cells treated with pladienolide. DNAJB1, BZW1, SPAG5, RIOK3, NUP54, and BRD2 were identified as pre-mRNA-accumulating genes.

[0179] Semi-confluent HeLa cells cultured in a 10 cm dish in DMEM high glucose medium (containing 10% FCS, penicillin, and streptomycin) were treated with 10 nM, 100 nM, and 10 μM of pladienolide B for 4 hours and 6 mL of TRIzol

(Invitrogen) was added thereto so that the cells were dissolved. Total RNA was obtained in accordance with the protocol of TRIzol and absorbance at 260 nm was measured to quantify an amount of RNA.

[0180] Subsequently, mRNA was purified from total RNA collected from HeLa cells treated with 10 nM, 100 nM, 10μ of pladienolide B and without the treatment, using μMACS mRNA Isolation Kit (Miltenyi Biotec). mRNA was concentrated by ethanol precipitation and absorbance at 260 nm was measured to quantify an amount of RNA. For 1 μg of mRNA, single stranded cDNA synthesis, double stranded cDNA synthesis, adaptor ligation in order was carried out using SuperScript Plasmid System for cDNA Synthesis and Cloning (Invitrogen), and the resultant DNA fragment was ligated to pCLex, which is a retrovirus vector. The resultant vector construct was then transformed into XL10-Gold ultracompetent cells (STRATAGENE). The transformed cells were seeded on LB plates containing ampicillin and cultured overnight. From each plate of the sample treated with 10 nM, 100 nM, and 10 μM of pladienolide B and without the treatment, 42 clones were separately picked up. A total of 42 clones was individually cultured and the plasmid was purified.

[0181] A nucleotide sequence of the genes inserted in the plasmid of the 42 clones extracted from the cDNA library of the sample treated with 10 nM, 100 nM, and 10 μM of pladienolide B and without the treatment was obtained using BigDye Terminator (Applied Biosystems) and senseXIY primer (sequence: CCTCGATCCTCCCTTTATCCAGCCCTCACT) (SEQ ID NO: 5) with ABI PRISM3130 (Applied Biosystems). The obtained sequence was then compared with genome information with UCSC/BLAT to collect genes containing a sequence of an intron region. For the genes containing the sequence of the intron region, the following primers were designed within both-sided exon regions surrounding the intron region.

DNAJB1-FW:
(SEQ ID NO: 6)
5'-GAACCAAAATCACTTTCCCCAAGGAAGGAG-3'

DNAJB1-RV:
(SEQ ID NO: 7)
5'-AATGAGGTCCCCACGTTTCTCGGGTGT-3'

BZW1-FW:
(SEQ ID NO: 8)
5'-GCCAATAAGCAAAGTGTTGAACACTTCAC-3'

BZW1-RV:
(SEQ ID NO: 9)
5'-AAGTGCTTGATGGCTTGCTCTGCTAC-3'

SPAG5-FW:
(SEQ ID NO: 10)
5'-ACATGGACAGCTTTGCTGAGTCGGTCC-3'

SPAG5-RV:
(SEQ ID NO: 11)
5'-TTGCTAGACGACTGTTTTCCAACTCCAG-3'

RIOK3-FW:
(SEQ ID NO: 12)
5'-GCTGAAGGACCATTTATTACTGGAG-3'

RIOK3-RV:
(SEQ ID NO: 13)
5'-TTCTTGCTGTGTTCTTTCTCCCACA-3'

-continued

NUP54-FW:
(SEQ ID NO: 14)
5'-CTAATCAAACAGGAAATTCAAAGGAAGAG-3'

NUP54-RV:
(SEQ ID NO: 15)
5'-CTTGATTTCTCGTAACAGATCTGCATC-3'

BRD2-FW:
(SEQ ID NO: 16)
5'-ACTCTCAGCAACAACACCAGAGCTCTA-3'

BRD2-RV:
(SEQ ID NO: 17)
5'-TAGCTTTCGTGCCATTGCCACAACATC-3'

Total RNA was collected from HeLa cells treated with 100 nM or 1 μM of Pladienolide B for 1, 2, or 4 hours or untreated. The total RNA was treated with DNase, and then subjected to reverse transcription reaction to yield cDNA. The obtained cDNA was then subjected to PCR using FastStart HiFi Polymerase (Roche Diagnostics) with the designed primers. Based on an electrophoresis pattern in agarose gel, a decrease in the expression of mature RNA and an increase in the expression of premature mRNA upon the Pladienolide B treatment was confirmed in DNAJB1, BZW1, SPAG5, RIOK3, NUP54, and BRD2 (FIG. **2**).

Example 3

Analysis with Microarray

[0182] Using RNA purified from human colon carcinoma cell strain WiDr treated with 14 nM of (8E,12E,14E)-7-((4-cycloheptylpiperazin-1-yl)carbonyl)oxy-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide (also referred to as "E7101") for six hours, microarray analysis (Human Exon 1.0 ST Array: Affymetrix) was carried out. Not only does this array comprehensively cover the exons for all genes, but it is also designed to have probes for regions estimated as potential exons by a computer prediction program, which enables detection of the expression of the exons and introns of all genes in theory. As a result, genes of which mature mRNA was sufficiently expressed when untreated and of which intron exhibited not less than ten times increase upon the treatment with (8E,12E,14E)-7-((4-cycloheptylpiperazin-1-yl)carbonyl)oxy-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide in at least two probe sets were identified.

[0183] WiDr cells were first suspended in RPMI1640 medium (containing 10% FBS, penicillin, and streptomycin) and seeded in a 10 cm dish (2×10^6 cells/dish). After an overnight culture in an incubator with 5% carbon dioxide gas at 37° C., the medium was changed with medium containing 14 nM of (8E,12E,14E)-7-((4-cycloheptylpiperazin-1-yl)carbonyl)oxy-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide or containing vehicle alone. After cultured for additional six hours, TRI reagent (SIGMA) were added to the cells and the cells were harvested. RNA was purified in accordance with the protocol of TRI reagent, followed by further purification with RNeasy (QIAGEN). Absorbance at 260 nm was measured to quantify an amount of RNA. This experiment was repeated three times and RNA samples (n=3) were prepared.

[0184] Ribosomal RNA was removed from 1 μg of each total RNA of control cells (n=3) and cells with the treatment (n=3) by using RiboMinus Human/Mouse Transcriptome

Isolation Kit (Invitrogen). Single stranded cDNA synthesis, double stranded cDNA synthesis, cRNA synthesis, second single stranded cDNA synthesis, cDNA fragmentation, and cDNA labeling in order were carried out for the total RNA from which ribosomal RNA was removed, by using GeneChip Whole Transcript Sense Target Labeling and Control Reagents (Affymetrix) to make a cDNA probe. The cDNA probe was used for hybridization with Human Exon 1.0 ST Array (Affymetrix). The array was washed and stained, and luminescence intensity was measured by a scanner.

[0185] The expression level of the probe set and the gene was quantified by using Expression Console Ver. 1.0 (Affymetrix) with Summarization Method and Normalization Method being set to "Median polish as used in RMA" and "None", respectively. The expression level of the probe was normalized with that of the gene. Welch's t-test was conducted for the treated group and the control group to determine a p value, which was converted into a q value by controlling False Discovery Ratio to pick out a significant probe set.

[0186] Probe sets showing that the q value was less than 1%; the normalized change in the level expression of the probe set in the group with the treatment was more than 10 times; the expression level of the probe set and the gene in the group with the treatment was more than 100; and probe set annotation was "extended, full, free", were picked out and further arranged by gene. A gene was, when more than one probe sets therefor were found, determined as a candidate gene with increased expression level of the intron regions (Table 1). In Table 1, for the gene evaluated, gene name (Gene Name), abbreviated name (Gene Symbol), accession number (Accession), alias name (Synonym), transcription number in Human Exon 1.0 ST Array (Human Exon 1.0 ST Array), chromosome number (Chromosome), type of strand (Strand), start region (Start), stop region (Stop), and change in expression level (Fold Change) were respectively shown.

TABLE 1

				Human Exon 1.0 ST	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Array	Chromosome	Strand	Start	Stop	Fold Change
sprouty-related, EVH1 domain containing 2	SPRED2	NM_181784	FLJ21897 // FLJ31917 // MGC163164 // Spred-2	2556752	chr2	–	65391279	65513247	31.56
WD repeat domain 73	WDR73	NM_032856	FLJ14888 // HSPC264	3636956	chr15	–	82987018	82998719	30.61
muscleblind-like 2 (*Drosophila*)	MBNL2	NM_144778 // NM_207304	DKFZp781H1296 // MBLL // MBLL39 // MGC120625 // MGC120626 // MGC120628 // PRO2032	3497586	chr13	+	96672563	96844371	28.86
brix domain containing 2	BXDC2	NM_018321	BRIX // FLJ11100	2806231	chr5	+	34951248	34962845	25.94
development and differentiation enhancing factor 2	DDEF2	NM_003887	AMAP2 // FLJ42910 // KIAA0400 // PAG3 // PAP // Pap-alpha // SHAG1	2468811	chr2	+	9264345	9463243	22.92
integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	ITGB1	NM_002211 // NM_033667 // NM_033668 // NM_033669	CD29 // FNRB // GPIIA // MDF2 // MSK12 // VLAB	3284186	chr10	–	33211051	33321367	21.48
eukaryotic translation initiation factor 2C, 2	EIF2C2	NM_012154	AGO2 // MGC3183 // Q10	3156193	chr8	–	141599440	141726037	21.33
chromosome 10 open reading frame 18	C10orf18	XM_374765	DKFZp781E1986 // FLJ20360 // bA318E3.2	3233322	chr10	+	5766851	5846629	19.86
KIAA0174	KIAA0174	NM_014761	MGC117220	3667766	chr16	+	70481983	70522196	19.65
discoidin, CUB and LCCL domain containing 2	DCBLD2	NM_080927	CLCP1 // ESDN	2686023	chr3	–	99997526	100124598	19.52
ubiquitin protein ligase E3A (human papilloma virus E8-associated protein, Angelman syndrome)	UBE3A	NM_000462 // NM_130838 // NM_130839	ANCR // AS // E8-AP // EPVE6AP // FLJ26981 // HPVE8A	3614087	chr15	–	23006655	23355108	19.35
isopentenyl-diphosphate delta isomerase 1	IDI1	NM_004508	IPP1 // IPPI1	3273601	chr10	–	1075869	1092634	19.25
chromosome 6 open reading frame 166	C6orf166	NM_018064	FLJ10342 // dJ486L4.2	2963784	chr6	–	88441297	88476721	19.23
pumilio homolog 2 (*Drosophila*)	PUM2	NM_015317	FLJ36528 // KIAA0235 // MGC138251 // MGC136253 // PUMH2 // PUML2	2542816	chr2	–	20291440	20450197	19.01
suppressor of var1, 3-like 1 (*S. cerevisiae*)	SUPV3L1	NM_003171	SUV3	3250204	chr10	+	70609946	70638996	18.81
forkhead box K2	FOXK2	NM_004514	ILF // ILF-1 // ILF1	3738969	chr17	+	78070883	78195807	18.79
WW domain containing adaptor with coiled-coil	WAC	NM_016628 // NM_100264 // NM_100486	BM-016 // MGC10753 // PRO1741 // Wwp4 // bA48B24 // bA48B24.1	3240340	chr10	+	28828043	29005095	18.53
LTV1 homolog (*S. cerevisiae*)	LTV1	NM_032860	C6orf93 // FLJ14909 // dJ468K18.4	2929036	chr6	+	144194149	144227146	18.37
CDC20 cell division cycle 20 homolog (*S. cerevisiae*)	CDC20	NM_001255	CDC20A // MGC102824 // bA276H19.3 // p55CDC	2333136	chr1	+	43597180	43601431	18.22
TAR DNA binding protein	TARDBP	NM_007375	TDP-43	2320048	chr1	+	10995025	11013170	18.13
fetal Alzheimer antigen	BPTF	NM_004459 // NM_182641	FAC1 // FALZ // NURF301	3732448	chr17	+	63252111	63410954	17.61
villin 2 (ezrin)	VIL2	NM_003379	CVIL // CVL //	2981912	chr6	–	159106770	159160432	17.50

TABLE 1-continued

				Human Exon 1.0 ST	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Array	Chromosome	Strand	Start	Stop	Fold Change
sorting nexin 19	SNX19	NM_014758	DKFZp762H157 // FLJ26216 // MGC1584 CHET8 // DKFZp667I205 // KIAA0254	3398482	chr11	–	130250320	130291615	17.12
Cdk5 and Abl enzyme substrate 1	CABLES1	NM_138375	FLJ35924 // HsT2563	3781531	chr18	+	18940699	19101596	16.94
SMAD specific E3 ubiquitin protein ligase 2	SMURF2	NM_022739	DKFZp686F0270 // MGC138150	3766980	chr17	–	59968891	60088896	16.60
solute carrier family 2 (facilitated glucose transporter), member 1	SLC2A1	NM_006516	GLUT // GLUT1 // MGC141895 // MGC141896	2409104	chr1	–	43124794	43338329	16.44
v-raf-1 murine leukemia viral oncogene homolog 1	RAF1	NM_022490	CRAF // Raf-1 // c-Raf	2663244	chr3	–	12600117	12680654	16.41
chromosome 16 open reading frame 80	C16orf80	NM_013242	EVORF // GTL3	3693511	chr16	–	56683698	56739201	16.25
eukaryotic translation initiation factor 4A, isoform 1	EIF4A1	NM_001416	DDX2A // EIF-4A // EIF4A	3708826	chr17	+	7416768	7423040	16.15
testis derived transcript (3 LIM domains)	TES	NM_015641 // NM_152829	DKFZP586B2022 // MGC1146 // TESS // TESS-2 // TESTIN	3020192	chr7	+	115637811	115743800	15.95
ring finger protein 40	RNF40	NM_014771	BRE1B // DKFZp686K191 // KIAA0661 // MGC13051 // RBP95 // STARING	3856555	chr16	+	30681120	30695182	15.84
squamous cell carcinoma antigen recognised by T cells 3	SART3	NM_014706	KIAA0156 // MGC138188 // RP11-13G14 // TIP110 // p110(nrb)	3470253	chr12	–	107440140	107479296	15.13
heat shock 105 kDa/110 kDa protein 1	HSPH1	NM_006644	DKFZp686M05240 // HSP105 // HSP105A // HSP105B // KIAA0201 // NY-CO-25	3508330	chr13	–	30558258	30651695	15.12
kelch-like 18 (*Drosophila*)	KLHL18	NM_025010	FLJ13703 // KIAA0795	2621275	chr3	+	47298888	47367590	15.00
myosin 1E	MYO1E	NM_004998	HuncM-1C // MGC104638 // MYO1C	3626828	chr15	–	57215720	57452363	14.49
LIM domain 7	LMO7	NM_005358	FBX20 // FBXO20 // KIAA0858 // LOMP	3494137	chr13	+	75092571	75586974	14.34
ring finger and SPRY domain containing 1	RSPRY1	NM_133368	KIAA1972	3662612	chr16	+	55777703	55831882	14.32
KIAA1429	KIAA1429	NM_015496 // NM_183009	DKFZP434I116 // DKFZp781B2117 // MGC136493 // MGC141940 // MSTP054	3145020	chr8	–	95569109	95634851	14.19
centromere protein L	CENPL	NM_033319	C1orf155 // CENP-L // FLJ31044 // RP3-383J4.1 // dJ383J4.3	2444451	chr1	–	172035313	172104622	14.13
Smcy homolog, X-linked (mouse)	JARID1C	NM_004187	DXS1272E // MRXJ // MRXSJ // SMCX // XE169	4009062	chrX	–	53159032	53271329	14.09
guanine nucleotide binding protein-like 3 (nucleolar)	GNL3	NM_014366 // NM_206825	C77032 // E2IG3 // MGC800 // NS	2624074	chr3	+	52694976	52705212	14.08

TABLE 1-continued

				Human Exon 1.0 ST	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Array	Chromosome	Strand	Start	Stop	Fold Change
RIO kinase 3 (yeast)	RIOK3	NM_003831 // NM_145906	DKFZp779L1370 // SUDD	3781654	chr18	+	19161035	19320545	13.67
interleukin enhancer binding factor 2, 45 kDa	ILF2	NM_004515	MGC8391 // NF45 // PRO3063	2436132	chr1	–	151900372	151910103	13.79
chromosome 9 open reading frame 86 // KIAA1984	C9orf86 // KIAA1984	NM_024718 // NM_001039374	FLJ10101 // FLJ13045 // Parf // RP11-216L13.9 // bA216L13.9 // pp8875 // MGC15438 // PARF // RP11-216L13.7 // RP11-216L13.9 // bA216L13.7	3194635	chr9	+	138810077	138855460	13.66
adhesion regulating molecule 1	ADRM1	NM_007002	GP110 // MGC29536 // Rpn13	3892607	chr20	+	60305485	60317305	13.51
keratin 18	KRT18	NM_000224	CYK18 // K18	3415576	chr12	+	51596769	51632949	13.41
heat shock 70 kDa protein 9B (mortalin-2)	HSPA9	NM_004134	CSA // GRP75 // HSPA9B // MGC4500 // MOT // MOT2 // MTHSP75 // PBP74 // mot-2	2877508	chr5	–	137917364	137939144	13.33
3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	HMGCS1	NM_002130	HMGCS // MGC90332	2855501	chr5	–	43324231	43349337	13.21
neuroepithelial cell transforming gene 1	NET1	NM_005863	ARHGEF8 // NET1A	3233182	chr10	+	5444535	5491001	13.02
SMAD, mothers against DPP homolog 3 (*Drosophila*)	SMAD3	NM_005902	DKFZP586N0721 // DKFZp686J10186 // HSPC193 // HsT17436 // JV15-2 // MADH3 // MGC60396 // Smad 3	3598959	chr15	+	65145043	65296818	12.88
cyclin L2	CCNL2	NM_030937	ANIA-6B // DKFZp761A1210 // DKFZp762O195 // HCLA-ISO // HLA-ISO // PCEE // SB138	4041923	chr1_random	+	359569	372958	12.84
ST3 beta-galactoside alpha-2,3-sialyltransferase 1	ST3GAL1	NM_003033	Gal-NAc6S // MGC9183 // SIAT4A // SIATFL // ST3GalA // ST3GalA.1 // ST3GalIA.1 // ST3O	3154398	chr8	–	134535811	134653449	12.77
WD repeat domain 74	WDR74	NM_018093	FLJ10439 // FLJ21730	3376235	chr11	–	62358627	62365857	12.70
cyclin D1	CCND1	NM_053058	BCL1 // D11S287E // PRAD1 // U21B31	3338192	chr11	+	69161881	69178408	12.66
nucleoporin like 1	NUPL1	NM_014089 // NM_001008564 // NM_001008565	KIAA0410 // PRO2463	3482219	chr13	+	24773258	24822202	12.63
WDR45-like	WDR45L	NM_019613	WIPI-3 // WIPI3	3775157	chr17	–	78185748	78199803	12.59
ubiquitin specific peptidase 47	USP47	NM_017944	DKFZp686C13257 // FLJ20727 // TRFP	3320604	chr11	+	11819556	11937446	12.32
eukaryotic translation initiation factor 5	EIF5	NM_001969	EIF-5A	3553607	chr14	+	102743652	102881108	12.30
methionine adenosyltransferase II, alpha	MAT2A	NM_005911	MATA2 // MATII // SAMS2	2491615	chr2	+	85597809	85625908	12.29

TABLE 1-continued

				Human Exon 1.0 ST	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Array	Chromosome	Strand	Start	Stop	Fold Change
WEE1 homolog (*S. pombe*)	WEE1	NM_003390	DKFZp686I18166 // FLJ16446 // WEE1hu	3319937	chr11	+	9550916	9579143	12.26
GTP binding protein 4	GTPBP4	NM_012341	CRFG // FLJ10686 // FLJ10690 // FLJ39774 // NGB	3231774	chr10	+	942450	1055862	12.24
zinc finger protein 384	ZNF384	NM_133476	CAGH1 // CAGH1A // CIZ // ERDA2 // NMP4 // NP // TNRC1	3442205	chr12	−	6645924	6668961	12.13
ATPase, Na+/K+ transporting, beta 1 polypeptide	ATP1B1	NM_001677 // NM_001001787	ATP1B // MGC1798	2366422	chr1	+	167342204	167368946	12.11
ADP-ribosylation factor interacting protein 2 (arfaptin 2)	ARFIP2	NM_012402	POR1	3360941	chr11	−	6453496	6459171	12.04
zinc finger protein 410	ZNF410	NM_021188	APA-1 // APA1	3543884	chr14	+	73423093	73468718	12.01
DnaJ (Hsp40) homolog, subfamily B, member 1	DNAJB1	NM_006145	HSPF1 // Hdj1 // Hsp40	3852783	chr19	−	14485622	14501114	11.95
guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	GNB2L1	NM_006098	Gnb2-rs1 // H12.3 // HLC-7 // PIG21 // RACK1	2891052	chr5	−	180596592	180612024	11.87
Rho GTPase activating protein 12	ARHGAP12	NM_018287	DKFZp779N2050 // FLJ10971 // FLJ20737 // FLJ21785 // FLJ45709	3283920	chr10	−	32134245	32261226	11.60
tight junction protein 1 (zona occludens 1)	TJP1	NM_003257 // NM_175610	DKFZp686M05161 // MGC133289 // ZO-1	3615579	chr15	−	27703228	28048334	11.55
dyskeratosis congenita 1, dyskerin	DKC1	NM_001363	DKC // NAP57 // NOLA4 // XAP101 // dyskerin	3996667	chrX	+	153644243	153659150	11.53
BAT2 domain containing 1	BAT2D1	NM_015172	BAT2-iso // XTP2	2367154	chr1	+	169716078	169829282	11.26
TERF1 (TRF1)-interacting nuclear factor 2	TINF2	NM_012461	TIN2	3558012	chr14	−	23776465	23781950	11.05
YTH domain containing 1	YTHDC1	NM_001031732	KIAA1966 // YT521 // YT521-B	2772017	chr4	−	68858700	68934802	10.66
adenylate kinase 2	AK2	NM_001625 // NM_013411	ADK2	2405364	chr1	−	33245959	33275155	10.05

Example 4

Analysis in PBMC

[0187] Since it is not easy to obtain a cancer tissue clinically, the measurement of the marker in hemocytes readily obtainable in peripheral blood would be more useful. It was then examined whether the marker gene obtained in cancer cells could change in peripheral blood mononuclear cells in a similar manner as observed in the cancer cells. Specifically peripheral blood was taken from three normal individuals (volunteers) and peripheral blood mononuclear cells were purified and treated with (8E,12E,14E)-7-((4-cycloheptylpiperazin-1-yl)carbonyl)oxy-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide for three hours, followed by measurement of change in expression of the precursor gene (pre-mRNA) by qPCR. In cases where an increase in the expression of pre-mRNA is used as a marker, the genes in Table 2 below, as a representative example, were found to be usable.

(1) Isolation of Peripheral Blood Mononuclear Cells (PBMC)

[0188] Ficoll-Paque PLUS solution (Amersham, 17-1440-02) was slowly added to the blood taken (with heparin added) from healthy individuals to form a layer underneath the blood (15 mL of Ficoll-Paque PLUS solution was added to 25 mL of blood). After the mixture was centrifuged at 1500 rpm for 30 min, the upper part containing platelets was removed and then a layer containing mononuclear cells was transferred to another tube. The cells were suspended in PBS and centrifuged at 1500 rpm for 5 min, followed by removal of the supernatant. After these steps were repeated twice, the PBMC was suspended in RPMI1640 (containing 10% FBS, penicillin, and streptomycin) and the number of the cells was then counted.

(2) Preparation of Total RNA

[0189] PBMC was suspended in RPMI1640 medium (containing 10% FBS, penicillin, and streptomycin) to 5×10^6 cells/ml and 1 ml of the suspension was plated per well of a 24-well plate. Immediately, 111 μl of 10 times-concentrated (8E,12E,14E)-7-((4-cycloheptylpiperazin-1-yl)carbonyl)oxy-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide was added to the well (six wells per each concentration tested). The cells were then cultured in an incubator with 5% carbon dioxide gas at 37° C. Three hours later, the supernatant was collected and centrifuged at 1500 rpm for five minutes. TRI reagent (SIGMA) (1 ml) was added to each well of the plate from which the supernatant was removed to harvest the cells, which was added to the centrifuged pellet to dissolve. RNA was purified in accordance with the protocol of TRI reagent. RNA was further purified using RNeasy (QIAGEN) and, in accordance with the protocol, DNaseI was added to the samples during the procedure. Absorbance at 260 nm was measured to quantify an amount of RNA.

(3) Measurement of the Expression Level of a Precursor Gene (pre-mRNA)

[0190] RNA was prepared to 30 ng/μl and cDNA was synthesized using TaqMan Reverse Transcription Reagents (Applied Biosystems). For the expression level of pre-mRNA of ID1, amplification was carried out by using TaqMan Universal PCR Master Mix (Applied Biosystems) with TaqMan Gene Expression Assays (Hs00704053_s1, Applied Biosystems) as a probe. For the expression level of pre-mRNA of DNAJB1, BZW1, NUP54, RIOK3, CDKN1B, STK17B, ADRM1, EIF4A1, FOXK2, GNB2L1, HSPA9B, HSPH1, KLHL18 and VIL2, reagents were prepared in accordance with each protocol by using POWER SYBR GREEN PCR MASTER MIX (Applied Biosystems) and primers with the sequence below (Invitrogen), and the expression level was measured with ABI7900 (Applied Biosystems). 18S rRNA was measured by both the TaqMan and SYBR methods. The expression level of 18S r RNA was measured with Hs99999901_s1 (Applied Biosystems) as primers for TaqMan and with 18S primers included in TaqMan Ribosomal RNA control reagents (4308329: Applied Biosystems) as primers for SYBR. Measured values were corrected using the expression level of 18S rRNA as an internal control. The expression level of each gene was calculated with the expression level in the cells treated without (8E,12E,14E)-7-((4-cycloheptylpiperazin-1-yl)carbonyl)oxy-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide as 1. Genes of which expression level in PBMC reached about 250% or more were shown in Table 2.

DNAJB1:

(SEQ ID NO: 18)
Sense: 5'-GGCCTGATGGGTCTTATCTATGG-3'

(SEQ ID NO: 19)
Antisense: 5'-TTAGATGGAAGCTGGCTCAAGAG-3'

BZW1:

(SEQ ID NO: 20)
Sense: 5'-GAACTTTGCCTCATTCTTTTGCA-3'

(SEQ ID NO: 21)
Antisense: 5'-CTGAGCTCCAGTCTCTTGTATTTCTG-3'

NUP54:

(SEQ ID NO: 22)
Sense: 5'-CAAGGTAACCACTTCTAAGACCATAATTC-3'

(SEQ ID NO: 23)
Antisense: 5'-CCTGCTTGAAGATTACATAACTTTTTGT-3'

RIOK3:

(SEQ ID NO: 24)
Sense: 5'-TCAATGGAGATAGCAAAGGTATTATAACC-3'

(SEQ ID NO: 25)
Antisense: 5'-AGATTTACTTAGGAGCACATTATGAGTGTT-3'

CDKN1B (p27):

(SEQ ID NO: 26)
Sense: 5'-ATGTTTATCAACGGTCCGGCT-3'

(SEQ ID NO: 27)
Antisense: 5'-CATCCCCAGTGGCTTTTAAGG-3'

STK17B:

(SEQ ID NO: 28)
Sense: 5'-TGCGCGGAGACAGCATAG-3'

(SEQ ID NO: 29)
Antisense: 5'-TGGGTTCAAAATGCCAGGTT-3'

ADRM1:

(SEQ ID NO: 30)
Sense: 5'-GGCCCTTCAGAAATGCTTGTC-3'

(SEQ ID NO: 31)
Antisense: 5'-CCCATTACACAATTCATGTGCTTAG-3'

-continued

EIF4A1:

(SEQ ID NO: 32)
Sense: 5'-CAGATCATCTAGAAGCAGCTGGTTT-3'

(SEQ ID NO: 33)
Antisense: 5'-ACAGAATCTGGTGCCTACTAACAAAA-3'

FOXK2:

(SEQ ID NO: 34)
Sense: 5'-GAGCAGAAGGAAGCGTGGTT-3'

(SEQ ID NO: 35)
Antisense: 5'-GACACATGAATTTCCACAACAGTAAA-3'

GNB2L1:

(SEQ ID NO: 36)
Sense: 5'-ACGTAATGACATTTTGGTCTGAGTAACT-3'

(SEQ ID NO: 37)
Antisense: 5'-AAATGCTGCTAAACATCCTGGAA-3'

-continued

HSPA9B:

(SEQ ID NO: 38)
Sense: 5'-TGAATCCTGAATACTATGCCTCCTT-3'

(SEQ ID NO: 39)
Antisense: 5'-TCCCTTCTTCTCAAGACTACTCAGTATG-3'

HSPH1:

(SEQ ID NO: 40)
Sense: 5'-ACCTTCTTCTCACAAGACTTTTTAAGC-3'

-continued

(SEQ ID NO: 41)
Antisense: 5'-CCTTCTCAGCCACCATGGAA-3'

KLHL18:

(SEQ ID NO: 42)
Sense: 5'-CCAGGTTTCCCCTGCAGTT-3'

(SEQ ID NO: 43)
Antisense: 5'-CCCCCTGACTTAGTCCTCGTT-3'

VIL2:

(SEQ ID NO: 44)
Sense: 5'-CCCACTGCCTTGATCTAGTTGAT-3'

(SEQ ID NO: 45)
Antisense: 5'-GTCAAGCAATCTATGGCCTACCA-3'

In Table 2, for the gene evaluated, abbreviated name (Gene Symbol), accession number (Accession), alias name (Synonym), gene name (Gene Name), chromosome number (Chromosome), type of strand (Strand), start region (Start), stop region (Stop), and the expression level at 0 hours, three hours, 10 hours and 30 hours after the E7107 treatment were respectively shown.

TABLE 2

Gene				E7107 (nM)			
Symbol	Accession	Synonym	Gene Name	0	3	10	30
DNAJB1	NM_006145	HSPF1 // Hdj1 // Hsp40	DnaJ (Hsp40) homolog, subfamily B, member 1	1	2.25	4.46	7.42
BZW1	XM_001126385 // NM_014670	BZAP45 // KIAA0005 // Nbla10236	basic leucine zipper and W2 domains 1	1	1.72	2.34	3.26
NUP54	NM_017426	MGC13407	nucleoporin 54 kDa	1	2.31	2.46	1.93
RIOK3	NM_003831 // NM_145906	DKFZp779L1370 // SUDD	RIO kinase 3 (yeast)	1	2.59	3.57	2.89
CDKN1B	NM_004064	CDKN4 // KIP1 // P27KIP1	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	1	1.27	2.35	4.9
STK17B	NM_004226	DRAK2	serine/threonine kinase 17b	1	1.94	3.44	3.99
ID1	NM_002165 // NM_181353	ID	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	1	3.31	6	10.57
ADRM1	NM_007002 // NM_175573	GP110 // MGC29536 // Rpn13	adhesion regulating molecule 1	1	1.8	2.68	2.59
EIF4A1	NM_001418	DDX2A // EIF-4A // EIF4A	eukaryotic translation initiation factor 4A, isoform 1	1	2.17	3.64	4.36
FOXK2	XM_001134363 // XM_001134364 // NM_004514	ILF // ILF-1 // ILF1	forkhead box K2	1	2.1	2.68	2.31
GNB2L1	NM_006098	Gnb2-rs1 // H12.3 // HLC-7 // PIG21 // RACK1	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	1	2.47	2.74	2.23
HSPA9	NM_004134	CSA // GRP75 // HSPA9B // MGC4500 // MOT // MOT2 // MTHSP75 // PBP74 // mot-2	heat shock 70 kDa protein 9 (mortalin)	1	1.87	3.45	2.33
HSPH1	NM_006644	DKFZp686M05240 // HSP105 // HSP105A // HSP105B // KIAA0201 // NY-CO-25	heat shock 105 kDa/110 kDa protein 1	1	1.26	1.88	2.68
KLHL18	NM_025010	FLJ13703 // KIAA0795	kelch-like 18 (*Drosophila*)	1	2.36	2.97	2.6
VIL2	NM_003379	CVIL // CVL // DKFZp762NH157 // FLJ26216 // MGC1584	villin 2 (ezrin)	1	1.27	2.87	4.89

Example 5

Analysis in PBC

[0191] Since fractionation of hemocytes is required for employing PBMC, use of PBMC in a clinical test is complicated. If change of pre-mRNA can be confirmed in whole blood (PBC), such a test would be clinically more useful. However, since it is difficult to culture PBC, it is not easy to monitor the change of pre-mRNA in vitro. If expression of mRNA in PBC, like in PBMC, is confirmed, the change of pre-mRNA can be monitored. Accordingly, in regard to the genes of Table 2 confirmed for PBMC (DNAJB1, BZW1, NUP54, RIOK3, CDKN1B, STK17B, and ID1), it is examined whether mRNA can be detected for RNA obtained from PBC by the same RNA purification method as in the clinical setting (Tempus PAX gene).

[0192] (1) Preparation of RNA with Tempus Blood RNA Tube (Applied Biosystems)

[0193] Human peripheral blood was collected in the tube (3 ml/tube) and combined with Stabilizing Reagent. In accordance with the protocol of the Tube, RNA was purified by the RNA Blood-DNA Method in ABI 6100 PrepStation (Applied Biosystems). Absorbance at 260 nm was measured to quantify an amount of RNA.

[0194] (2) Preparation of RNA with PAXgene Blood RNA Tube (QIAGEN)

[0195] Human peripheral blood was collected in the tube (2.5 ml/tube), combined with Stabilizing Reagent, and left to stand overnight at room temperature. In accordance with the protocol of the Tube, RNA was purified with PAXgene Blood RNA Kit (QIAGEN). Absorbance at 260 nm was measured to quantify an amount of RNA.

[0196] (3) Quantification of the Expression Level of mRNA

[0197] RNA was prepared to 30 ng/μL and cDNA was synthesized by using High Capacity cDNA Reverse Transcription Kits (Applied Biosystems). A probe corresponding respectively to DNAJB1, BZW1, NUP54, RIOK3, CDKN1B, STK17B, ID1 and 18S rRNA was purchased from TaqMan Gene Expression Assays (Applied Biosystems). Reagents were prepared in accordance with the protocol of TaqMan Universal PCR Master Mix (Applied Biosystems) and the expression level of mRNA was measured with ABI7900 (Applied Biosystems). As shown in FIG. **3**A (Tempus Blood RNA Tube) and FIG. **3**B (PAXgene Blood RNA Tube), it was demonstrated that gene expression could sufficiently be confirmed in RNA obtained by both methods.

Example 6

Analysis by Western Blotting

[0198] Since pre-mRNA contains a part of the introns, a protein translated from such pre-mRNA is one which does not normally exist. Consequently the protein may serves as a protein marker to monitor the action of (8E,12E,14E)-7-((4-cycloheptylpiperazin-1-yl)carbonyl)oxy-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide. Whether the pre-mRNA-dependent abnormal protein practically emerged upon the treatment of (8E,12E,14E)-7-((4-cycloheptylpiperazin-1-yl)carbonyl)oxy-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide was examined by using cancer cells (HaLa). As a result, insertion of a intron sequence was found to introduce a termination codon, which led to generation of small-molecule p27 and SMN different from normal CDKN1B (p27) (FIG. **4**). Based on these findings, the protein generated from pre-mRNA can serve as the marker as well.

[0199] About 3×10^5 cells of HeLa cells were first seeded in a 24-well culture plate (bottom area: 2 cm^2), and 18 hours later, the compound was added thereto at the indicated concentration, followed by additional 24-hour culturing. The cells were washed once with PBS(−), and then were lysed by treating with 0.2 ml of M-PER reagent (PIERCE) for 30 minutes. The collected lysate was filtered with a 0.45 μm filter to remove insoluble matters and then combined with an equal amount of 2×SDS-PAGE sample solution. The mixture was heated to be denatured at 95° C. for five minutes to yield a sample to be analyzed.

[0200] The analysis sample (15 μl each) was separated with 5-20% SDS-PAGE and transferred onto a PVDF membrane (Hybond-P: GE-Amersham). The membrane was treated to be blocked with Blockace (Dainippon Pharma Co., Ltd.) by one-hour incubation. The membrane was then incubated with a primary antibody for two hours, washed three times for 10 minutes each, incubated with a secondary antibody for one hour, washed (10 minutes each) three times followed by signal detection.

[0201] Detection of p27/Kip1 was carried out as follows. Specifically, a mouse anti-p27/Kip1 monoclonal antibody (BD Bioscience, #610242) was used as the primary antibody at a 1:1000 dilution rate. An HRP-labeled mouse anti-IgG antibody (GE-Amersham) was used as the secondary antibody at a 1:2500 dilution rate. An ECL-Plus reagent (GE-Amersham) was used for the signal detection.

[0202] Detection of SMN was carried out as follows. Specifically, a mouse anti-SMN monoclonal antibody (BD Bioscience, #610646) was used as the primary antibody at a 1:1000 dilution rate. An AP-labeled mouse anti-IgG antibody (CHEMICON) was used as the secondary antibody at a 1:2500 dilution rate. NBT/BCIP reagent (PIERCE) was used for signal detection.

[0203] As shown in FIG. **4**, only a 27 kDa band was detected for p27/Kip1 when the cells were treated without the compounds. On the other hand, appearance of a band with about 22 kDa was confirmed in the cells treated with about 100 nM of Pladienolide B or (8E,12E,14E)-7-((4-cycloheptylpiperazin-1-yl)carbonyl)oxy-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide for 24 hours. In addition, only a 35 kDa band was detected for SMN in the cells treated without the compounds. When the cells were treated with 10 nM and 25 nM of Pladienolide B or 10 nM and 100 nM of (8E,12E,14E)-7-((4-cycloheptylpiperazin-1-yl)carbonyl)oxy-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide for 24 hours, multiple bands with a molecular weight of less than 35 kDa were confirmed.

Example 7

Analysis in a Nude Mouse

[0204] (1) Administration of the Pladienolide Derivative to Nude Mice Subcutaneously Transplanted with WiDr Human Colon Carcinoma Cells.

[0205] Nude mice (BALB/cAJcl-nu/nu, 6 weeks old, female) were purchased from CLEA Japan, Inc. After an acclimated period of a week, the mice were subcutaneously transplanted WiDr cells suspended in Hanks' Balanced Salt Solution (GIBCO) (5×10^6 cells per a mouse). Two weeks after the transplantation, when tumor volume was confirmed to grow to more than 200 mm^3, the mice were administrated (8E,12E,14E)-7-((4-cycloheptylpiperazin-1-yl)carbonyl)oxy-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide (30 mg/kg) in a single dose via tail vein injection.

[0206] (2) Blood Collection and Isolation of the Tumor

[0207] At the time point of 30 minutes, 1 hour, 2 hours, 4 hours, and 8 hours, after the administration of (8E,12E,14E)-7-((4-cycloheptylpiperazin-1-yl)carbonyl)oxy-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide, two mice per each time point were put down by euthanasia with CO_2. Whole blood (with heparin added) was taken from abdominal aorta of each mouse, TRIzol LS Reagent (Invitrogen) was added thereto, and the mixture was stored at −20° C. The tumor was removed, cut in shape of a about 0.5 cm×0.5 cm square, and stored −20° C. in RNAlater (Ambion).

[0208] (3) Preparation of RNA

[0209] RNA preparation from blood was carried out in accordance with the protocol of TRIzol LS Reagent (Invitrogen). The obtained RNA was further purified with RNeasy (QIAGEN). During the process, a treatment with DNase I was performed in accordance with the protocol. The tumor treated with RNA later (Ambion) was placed in TRI reagent (SIGMA) and grinded by a homogenizer, followed by the operations following the protocol of TRI reagent. The obtained RNA was then purified using RNeasy (QIAGEN). During the process, a treatment with DNase I was performed in accordance with the protocol. Absorbance at 260 nm was measured to quantify an amount of each RNA.

[0210] (4) Measurement of the Expression Level of the Precursor Gene (pre-mRNA) in Blood

[0211] RNA was prepared to 100 ng/μl and cDNA was synthesized by using TaqMan Reverse Transcription Reagents (Applied Biosystems). For the expression level of pre-mRNA of mouse DNAJB1 and mouse EIF4A, reagents were prepared in accordance with each protocol by using POWER SYBR GREEN PCR MASTER MIX (Applied Biosystems) and primers with the sequence below (Invitrogen), and the expression level was measured with ABI7900 (Applied Biosystems). The expression level of 18S rRNA was measured by using 18S primers included in TaqMan Ribosomal RNA control reagents (4308329: Applied Biosystems). Measured values were corrected using the expression level of 18S rRNA as an internal control. The expression level of each gene was calculated with the expression level in the group of mice treated without (8E,12E,14E)-7-((4-cycloheptylpiperazin-1-yl)carbonyl)oxy-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide as 1. Results were shown in FIG. **5**.

```
[mouse DNAJB1]
Sense:
5'-TGCTGTGAGAATAATGGGTTGTG-3'      (SEQ ID NO: 46)

Antisense:
5'-GGCTGGCTTAGGAGCTTCACT-3'        (SEQ ID NO: 47)

[mouse EIF4A1]
Sense:
5'-ACCTGCGGTTCCCACTTTATT-3'        (SEQ ID NO: 48)

Antisense:
5'-ACCACTCCAAATGTCTAAGGTCACT-3'    (SEQ ID NO: 49)
```

[0212] (5) Measurement of the expression level of the precursor gene (pre-mRNA) in tumor

[0213] RNA was prepared to 100 ng/μl and cDNA was synthesized by using TaqMan Reverse Transcription Reagents (Applied Biosystems). For the expression level of pre-mRNA of human DNAJB1 and human EIF4A, reagents were prepared in accordance with each protocol by using POWER SYBR GREEN PCR MASTER MIX (Applied Biosystems) and primers with the sequence below (Invitrogen), and the expression level was measured with ABI7900 (Applied Biosystems). The expression level of 18S rRNA was measured by using 18S primers included in TaqMan Ribosomal RNA control reagents (4308329: Applied Biosystems). Measured values were corrected using the expression level of 18S rRNA as an internal control. The expression level of each gene was calculated with the expression level in the group of mice treated without (8E,12E,14E)-7-((4-cycloheptylpiperazin-1-yl)carbonyl)oxy-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide as 1. Results were shown in FIG. **6**.

```
[Human DNAJB1]
Sense:
5'-GGCCTGATGGGTCTTATCTATGG-3'      (SEQ ID NO: 50)

Antisense:
5'-TTAGATGGAAGCTGGCTCAAGAG-3'      (SEQ ID NO: 51)

[Human EIF4A1]
Sense:
5'-GAACTTTGCCTCATTCTTTTGCA-3'      (SEQ ID NO: 52)

Antisense:
5'-CTGAGCTCCAGTCTCTTGTATTTCTG-3'   (SEQ ID NO: 53)
```

Example 8

Analysis with Microarray (2)

[0214] Analysis conditions were reviewed in the data used in Example 3. Genes containing increased introns upon treatment with (8E,12E,14E)-7-((4-cycloheptylpiperazin-1-yl)carbonyl)oxy-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide were identified.

[0215] In order to consider the analysis conditions, variations in the data from the samples with identical conditions were studied. FIG. **7** shows a scatter diagram of the expression level of probe sets and genes of the control cells, and standard deviation thereof. It turned out that, by analyzing under conditions where the expression level was more than 100 and change in the expression level was more than five times, a probe set with increased expression can be extracted.

[0216] Probe sets showing that the normalized change in the level expression of the probe set in the group with the treatment was more than 5 times; the expression level of the probe set and the gene in the group with the treatment were more than 100; and probe set annotation was "extended, full, free", were picked out. Welch's t-test was conducted with the probe sets extracted for the treated group and the control group to determine a p and q value. A gene containing the probe sets with the q value of less than 5% was determined as a candidate gene with increased expression level of the intron regions (Table 3).

[0217] In Table 3, for each gene evaluated, gene name (Gene Name), abbreviated name (Gene Symbol), accession number (Accession), alias name (Synonym), transcription cluster number in Human Exon 1.0 ST Array (Human Exon 1.0 ST Array Transcript Cluster ID), chromosome number (Chromosome), type of strand (Strand), start region (Start), stop region (Stop), and change in expression level (Fold Change) were respectively shown.

TABLE 3

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
TSR1, 20S rRNA accumulation,	TSR1	NM_018128	FLJ10534 //	3740998	chr17	−	2172438	2187551	44.77
translocase of inner mitochondrial membrane 23 homolog (yeast)	TIMM23	XM_001133798 // NM_006327	MGC22767 // PRO1197 // TIM23 // TIMM23B	3289031	chr10	−	51180787	51293382	28.32
pellino homolog 1 (*Drosophila*)	PELI1	NM_020651	DKFZp686C18116 // MGC50990	2556302	chr2	−	64173290	64225291	27.36
chromosome 15 open reading frame 42	C15orf42	NM_152259	FLJ41618 // MGC45866	3607698	chr15	+	87857353	87975281	26.27
RNA binding motif protein 26	RBM26	NM_022118	C13orf10 // FLJ20957 // MGC133295 // MGC133296 // PRO1777 // RP11-255E21.1 // SE70-2	3519119	chr13	−	78783968	78878613	21.52
integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	ITGB1	NM_002211 // NM_033666 // NM_033667 // NM_033668 // NM_033669 // NM_133376	CD29 // FNRB // GPIIA // MDF2 // MSK12 // VLAB	3284188	chr10	−	33211051	33321367	21.20
ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)	ARFGEF1	NM_006421	ARFGEEP1 // BIG1 // D730028O18Rik // DKFZP434L057 // P200	3139035	chr8	−	68250009	68418446	21.19
clathrin interactor 1	CLINT1	NM_014666	CLINT // ENTH // EPN4 // EPNR // EPSINR // KIAA0171	2883609	chr5	−	157145339	157284818	20.51
CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase like 2	CTDSPL2	NM_016396	FLJ10523 // HSPC058 // HSPC129	3591909	chr15	+	42506834	42607712	20.40
cell division cycle associated 4	CDCA4	NM_017955 // NM_145701	FLJ20764 // HEPP // MGC19517	3581386	chr14	−	104546975	104585458	20.39
WD repeat domain 73	WDR73	NM_032856	FLJ14888 // HSPC264	3636956	chr15	−	82987018	82998719	20.03
zinc finger protien 317 // zinc finger protein 658	ZNF317 // ZNF658	NM_020933 // XM_001125688 // NM_033160	KIAA1588 // DKFZp572C163 // FLJ32813 // MGC35232	3819880	chr19	+	9112073	9135082	19.64
integrin, alpha 6	ITGA6	NM_000210 // NM_001079818	CD49f // ITGA6B // VLA-6	2515627	chr2	+	173000563	173079416	19.59
ubiquitin protein ligase E3A (human papilioma virus E6-associated protein, Angelman syndrome)	UBE3A	NM_000462 // NM_130838 // NM_130839	ANCR // AS // E6-AP // EPVE6AP // FLJ26981 // HPVE6A	3614087	chr15	−	23006655	23355108	19.35
muscleblind-like 2 (*Drosophila*)	MBNL2	NM_144778 // NM_207304	DKFZp781H1296 // MBLL // MBLL39 // MGC120625 //	3497586	chr13	+	96672563	96844371	19.31

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Array Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change
			MGC120626 // MGC120628 // PRO2032						
chromosome 6 open reading frame 166	C6orf166	NM_018064	FLJ10342 // dJ486L4.2	2963784	chr6	−	88441297	88476721	19.23
homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	HERPUD1	NM_001010989 // NM_001010990 // NM_014685	HERP // KIAA0025 // Mif1 // SUP	3662387	chr16	+	55523269	55552122	19.03
RAP1 interacting factor homolog (yeast)	RIF1	NM_018151	DKFZp781N1478 // FLJ12870	2510485	chr2	+	151974674	152072768	18.85
development and differentiation enhancing factor 2	DDEF2	NM_003887	AMAP2 // FLJ42910 // KIAA0400 // PAG3 // PAP // Pap-alpha // SHAG1	2468811	chr2	+	9264345	9463243	18.43
cell division cycle 20 homolog (*S. cerevisiae*)	CDC20	NM_001255	CDC20A // MGC102824 // bA276H19.3 // p55CDC	2333136	chr1	+	43597180	43601431	18.22
BMI1 polycomb ring finger oncogene	BMI1	NM_005180	MGC12685 // PCGF4 // RNF51	3238491	chr10	+	22650103	22660820	18.11
golgi-specific brefeldin A resistance factor 1	GBF1	NM_004193	FLJ21263 // FLJ21500 // KIAA0248 // MGC134877 // MGC134878	3261544	chr10	+	103993260	104132642	17.47
strawberry notch homolog 1 (*Drosophila*)	SBNO1	NM_018183	FLJ10701 // FLJ10833 // FLJ16176 // MOP3 // Sno	3476130	chr12	−	122342423	122435284	17.44
protein phosphatase 4, regulatory subunit 2	PPP4R2	NM_174907	MGC131930	2629693	chr3	+	73019849	73201035	17.19
brix domain containing 2	BXDC2	NM_018321	BRIX // FLJ11100	2806231	chr5	+	34951248	34962845	17.08
far upstream element (FUSE) binding protein 1	FUBP1	NM_003902	FBP // FUBP	2419235	chr1	−	78182330	78217881	16.59
RAE1 RNA export 1 homolog (*S. pombe*)	RAE1	NM_001015885 // NM_003610	FLJ30608 // MGC117333 // MGC126076 // MGC126077 // MIG14 // MRNP41 // Mnrp41 // dJ481F12.3 // dJ800J21.1	3890555	chr20	+	55359493	55386992	16.46
CCHC-type zinc finger, nucleic acid binding protein	CNBP	NM_003418	CNBP1 // DM2 // PROMM // RNF163 // ZCCHC22 // ZNF9	2694644	chr3	−	130369369	130385467	16.43
acyl-CoA synthetase long-chain family member 3	ACSL3	NM_004457 // NM_203372	ACS3 // FACL3 // PRO2194	2529546	chr2	+	223433916	223539136	16.27

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
peptidase (mitochondrial processing) alpha	PMPCA	NM_015160	Alpha-MPP // INPP5E // KIAA0123 // MGC104197	3194338	chr9	+	138424942	138438030	16.01
CGI-09 protein	CGI-09	NM_015939	MGC5029	3896524	chr20	−	5865881	5879370	16.01
baculoviral IAP repeat-containing 6 (apollon)	BIRC6	NM_016252	APOLLON // BRUCE // FLJ13726 // FLJ13786 // KIAA1289	2476219	chr2	+	32435095	32697447	15.96
BCL2/adenovirus E1B 19 kDa interacting protein 2	BNIP2	NM_004330	BNIP-2 // NIP2	3627076	chr15	−	57742025	57768916	15.96
DEAD (Asp-Glu-Ala-Asp) box polypeptide 23	DDX23	NM_004818	MGC8416 // PRPF28 // U5-100K // prp28	3453319	chr12	−	47509816	47532322	15.78
DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	DDX17	NM_006386 // NM_030881	DKFZp761H2016 // P72 // RH70	3960629	chr22	−	37202800	37232288	15.42
SAPS domain family, member 3	SAPS3	NM_018312	C11orf23 // DKFZp781E17107 // DKFZp781E2374 // DKFZp781O2362 // FLJ11058 // FLJ43065 // MGC125711 // MGC125712 // PP6R3 // SAP190 // SAPL // SAPLa	3337618	chr11	+	67984785	68173381	15.25
PAK1 interacting protein 1 // chromosome 20 open reading frame 7	PAK1IP1 // C20orf7	NM_017906 // NM_001039375 // NM_024120	FLJ20624 // MAK11 // PIP1 // RP11-421M1.5 // WDR84 // bA421M1.5 // hPIP1 // FLJ22324 // MGC90272 // bA526K24.2 // dJ842G6.1	2894663	chr6	+	10799016	10817955	15.04
sprouty-related, EVH1 domain containing 2	SPRED2	NM_181784	FLJ21897 // FLJ31917 // MGC163164 // Spred-2	2556752	chr2	−	65391279	65513247	15.03
kelch-like 18 (*Drosophila*)	KLHL18	NM_025010	FLJ13703 // KIAA0795	2621275	chr3	+	47298888	47367590	15.00
suppressor of var1, 3-like 1 (*S. cerevisiae*)	SUPV3L1	NM_003171	SUV3	3250204	chr10	+	70609946	70638996	14.99
KIAA0174	KIAA0174	NM_014761	MGC117220	3667766	chr16	+	70481983	70522196	14.78
flap structure-specific endonuclease 1	FEN1	NM_004111	FEN-1 // MF1 // RAD2	3333226	chr11	+	61312929	61350560	14.75
atrophin 1	ATN1	NM_001007026 // NM_001940	B37 //D12S755E // DRPLA // NOD	3403045	chr12	+	6903897	6921744	14.70
poliovirus receptor	PVR	NM_006505	CD155 // HVED // NECL5 // Necl-5 // PVS // TAGE4	3835645	chr19	+	49839030	49860075	14.67

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Array Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change
KIAA0317	KIAA0317	NM_001039479	—	3572041	chr14	–	74189599	74249655	14.49
DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	DDX3X	XM_001129278 // NM_001356	DBX // DDX14 // DDX3 // HLP2	3974838	chrX	+	41055591	41108668	14.39
brix domain containing 1	BXDC1	NM_032194	FLJ21087 // RPF2 // bA397G5.4	2921374	chr6	+	111409800	111408743	14.38
actinin, alpha 1	ACTN1	NM_001102	FLJ40884	3569814	chr14	–	68409817	68515815	14.26
Rho guanine nucleotide exchange factor (GEF) 12	ARHGEF12	NM_015313	DKFZp698O2372 // KIAA0382 // LARG // PRO2792	3352503	chr11	+	119711882	119896306	14.21
KIAA0859	KIAA0859	NM_001007239 // NM_014955 // NM_015935	5630401D24Rik // CGI-01 // FLJ10310	2367287	chr1	+	170017287	170053841	14.17
THO complex 5	THOC5	NM_001002877 // NM_001002878 // NM_001002879 // NM_003678	C22orf19 // Fmip // PK1.3	3956854	chr22	–	28224935	28280423	14.15
polo-like kinase 2 (*Drosophila*)	PLK2	NM_006622	SNK	2858023	chr5	–	57785572	57792624	14.01
forkhead box K2	FOXK2	XM_001134363 // XM_001134364 // NM_004514	ILF // ILF-1 // ILF1	3738969	chr17	+	78070883	78195807	14.01
calcium binding protein 39	CAB39	NM_016289	CGI-66 // FLJ22682 // MO25	2531522	chr2	+	231285781	231394027	13.97
ubiquitin specific peptidase 38	USP38	NM_032557	FLJ35970 // HP43.8KD // KIAA1891	2745499	chr4	+	144325529	144364549	13.94
SMAD specific E3 ubiquitin protein ligase 2	SMURF2	NM_022739	DKFZp686F0270 // MGC138150	3766960	chr17	–	59968891	60088896	13.92
RIO kinase 3 (yeast)	RIOK3	NM_003831 // NM_145906	DKFZp779L1370 // SUDD	3781654	chr18	+	19161035	19320545	13.87
protein phosphatase 1, catalytic subunit, gamma isoform	PPP1CC	NM_002710	PPP1G	3471374	chr12	–	109642007	109665131	13.87
erbb2 interacting protein // caspase 6, apoptosis-related cysteine peptidase	ERBB2IP // CASP6	NM_001006600 // NM_018695 // NM_001226 // NM_032992	ERBIN // LAP2 // MCH2	2812435	chr5	+	65258079	65451372	13.87
MKI67 (FHA domain) interacting nucleolar phosphoprotein	MKI67IP	NM_032390	NIFK // Nopp34	2573786	chr2	–	122132489	122231052	13.76
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein,	YWHAB	NM_003404 // NM_139323	GW128 // HS1 // KCIP-1	3886639	chr20	+	42927275	42970748	13.72
Ctr9, Paf1/RNA polymerase II complex component, homolog (*S. cerevisiae*) // tRNA 5-methylaminomethyl-2-thiouridylate methyltransferase	CTR9 // TRMU	NM_014633 // NM_018006	KIAA0155 // SH2BP1 // TSBP // p150 // p150TSP // MGC99627 // MTO2 // MTU1 // TRMT // TRMT1 // TRNT1	3320301	chr11	+	10684027	10774985	13.68

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
karyopherin (importin) beta 1	KPNB1	NM_002265	IMB1 // IPOB // Impnb // MGC2155 // MGC2156 // MGC2157 // NTF97	3724782	chr17	+	43082272	43117868	13.68
A kinase (PRKA) anchor protein 13	AKAP13	NM_006738 // NM_007200 // NM_144767	AKAP-Lbc // BRX // FLJ11952 // FLJ43341 // HA-3 // Ht31 // LBC // PROTO-LB // PROTO-LBC // c-lbc	3606304	chr15	+	83681343	84102785	13.65
nucleolar protein 9	NOL9	NM_024654	FLJ23323 // MGC131821 // MGC138483	2394784	chr1	–	6504004	6537329	13.58
ADP-ribosylation factor-like 6 interacting protein 2	ARL6IP2	NM_022374	ARL3IP2 // ATL2 // FLJ23293 // atlastin2	2548776	chr2	–	38374621	38516141	13.57
pumilio homolog 2 (*Drosophila*)	PUM2	NM_015317	FLJ36528 // KIAA0235 // MGC138251 // MGC138253 // PUMH2 // PUML2	2542816	chr2	–	20291440	20450197	13.55
calmodulin 2 (phosphorylase kinase, delta)	CALM2	NM_001743	CAMII // PHKD // PHKD2	2551924	chr2	–	47232159	47286178	13.54
nucleolar protein family A, member 1 (H/ACA small nucleolar RNPs)	NOLA1	NM_018983 // NM_032993	GAR1	2739242	chr4	+	110956115	110965340	13.42
chromosome 6 open reading frame 94 // LTV1 homolog (*S. cerevisiae*)	C6orf94 // LTV1	XM_928657 // XM_941265 // NM_032860	dJ468K18.5 // C6orf93 // FLJ14909 // dJ468K18.4	2929036	chr6	+	144194149	144227146	13.35
PPAR binding protein	PPARBP	NM_004774	CRSP1 // CRSP200 // DRIP205 // DRIP230 // MED1 // MGC71488 // PBP // PPARGBP // RB18A // TRAP220 // TRIP2	3755714	chr17	–	34801544	34861069	13.29
3-hydroxy-3-methylglutaryl-Coenzyme A reductase	HMGCR	NM_000859	—	2815965	chr5	+	74668800	74700136	13.12
15 kDa selenoprotein	15-Sep	NM_004261 // NM_203341	—	2421271	chr1	–	87100720	87153273	13.02
phosphatidylinosital binding clathrin assembly protein	PICALM	NM_001008660 // NM_007166	CALM // CLTH // LAP	3385175	chr11	–	85345353	85458481	13.00
proteasome (prosome, macropain) 26S subunit, non-ATPase, 3	PSMD3	NM_002809	P58 // RPN3 // S3	3720636	chr17	+	35390438	35407732	12.85
COP9 constitutive photomorphogenic homolog subunit 2 (*Arabidopsis*)	COPS2	NM_004236	ALIEN // CSN2 // SGN2 // TRIP15	3623424	chr15	–	47203877	47235198	12.73
B-cell CLL/lymphoma 10	BCL10	NM_003921	CARMEN // CIPER // CLAP // c-E10 // mE10	2420808	chr1	–	85504067	85516171	12.67

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
villin 2 (ezrin)	VIL2	NM_003379	CVIL // CVL // DKFZp762H157 // FLJ26216 // MGC1584	2981912	chr6	–	159106770	159160432	12.62
solute carrier family 25, member 32	SLC25A32	NM_030780	FLJ23872 // MFTC	3147726	chr8	–	104247068	104496640	12.60
DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	DDX21	NM_004728	DKFZp686F21172 // GUA // GURDB // RH-II/GU // RH-II/GuA	3250055	chr10	+	70380584	70414821	12.56
WEE1 homolog (*S. pombe*)	WEE1	NM_003390	DKFZp686I18166 // FLJ16446 // WEE1hu	3319937	chr11	+	9550916	9579143	12.54
N-acetyltransferase 10	NAT10	NM_024662	ALP // DKFZp434C116 // FLJ10774 // FLJ12179 // FLJ23850 // KIAA1709 // hALP	3326252	chr11	+	34083688	34125769	12.51
transcription elongation factor B (SIII), polypeptide 3 (110 kDa, elongin	TCEB3	NM_003198	SIII // TCEB3A	2325251	chr1	+	23942459	23961135	12.38
microtubule-associated protein, RP/EB family, member 1	MAPRE1	NM_012325	EB1 // MGC117374 // MGC129946	3882069	chr20	+	30871304	30901864	12.37
Cdk5 and Abl enzyme substrate 1	CABLES1	NM_138375	FLJ35924 // HsT2563	3781531	chr18	+	18940699	19101596	12.37
ubiquitin specific peptidase 47	USP47	NM_017944	DKFZp686C13257// FLJ20727 // TRFP	3320604	chr11	+	11819556	11937446	12.32
DEAD (Asp-Glu-Ala-Asp) box polypeptide 31	DDX31	NM_022779 // NM_138620	FLJ13633 // FLJ14578 // FLJ23349 // helicain A // helicain B // helicain C	3228191	chr9	–	134456969	134535609	12.21
chromosome 8 open reading frame 76 // zinc fingers and homeoboxes 1	C8orf76 // ZHX1	NM_032847 // NM_001017926 // NM_007222	FLJ14825 // MGC9784 //—	3151473	chr8	–	124291083	124356860	12.17
chromoseme 10 open reading frame 18	C10orf18	XM_374765 // XM_937970	DKFZp781E1986 // FLJ20360 // bA318E3.2	3233322	chr10	+	5766851	5846629	12.16
guanine nucleotide binding protein-like 2 (nucleolar)	GNL2	NM_013285	FLJ40906 // HUMAUANTIG // NGP1 // Ngp-1 // dJ423B22.6	2407191	chr1	–	37805043	37834120	12.14
eukaryotic translation initiation factor 4 gamma, 1	EIF4G1	NM_004953 // NM_182917 // NM_198241 // NM_198242 // NM_198244	DKFZp686A1451 // EIF4F // EIF4G // p220	2655688	chr3	+	185514970	185535829	12.13
peter pan homolog (*Drosophila*) // PPAN-P2RY11	PPAN // PPAN-P2RY11	NM_020230 // NM_001040664	BXDC3 // MGC14226 // MGC45852 // SSF // SSF1 // SSF2 //	3820342	chr19	+	10077989	10082841	12.07

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Array	Human Genome hg18				
				Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
Rho GTPase activating protein 11A	ARHGAP11A	NM_014783 // NM_199357	GAP (1-12) // KIAA0013 // MGC70740	3587457	chr15	+	30693622	30719422	12.06
high-mobility group nucleosome binding domain 1	HMGN1	NM_004965	FLJ27265 // FLJ31471 // HMG14 // MGC104230 // MGC117425	3932270	chr21	–	39636124	39643423	11.92
mortality factor 4 // mortality factor 4 like 1	MORF4 // MORF4L1	NM_006792 // NM_006791 // NM_206839	CSR // CSRB // SEN // SEN1 // Eaf3 // FWP006 // HsT17725 // MGC10631 // MORFRG15 // MRG15 // S863-6	3603532	chr15	+	76889894	76979806	11.90
cytotoxic and regulatory T cell molecule	KIAA0690 // CRTAM	NM_019604	—	3302240	chr10	–	99098933	99175486	11.86
TERF1 (TRF1)-interacting nuclear factor 2	TINF2	NM_012461	TIN2	3558012	chr14	–	23776465	23781950	11.82
DCN1, defective in cullin neddylation 1, domain containing 5 (*S. cerevisiae*)	DCUN1D5	NM_032299	FLJ32431 // MGC2714	3388914	chr11	–	102342328	102485844	11.81
isopentenyl-diphosphate delta isomerase 1	IDI1	NM_004508	IPP1 // IPPI1	3273601	chr10	–	1075869	1092634	11.81
exosome component 9	EXOSC9	NM_001034194 // NM_005033	PM/Scl-75 // PMSCL1 // RRP45 // Rrp45p // p5 // p6	2741768	chr4	+	122941935	122957724	11.79
diablo homolog (*Drosophila*)	DIABLO	NM_019887 // NM_138929 // NM_138930	DIABLO-S // FLJ10537 // FLJ25049 // SMAC // SMAC3	3475511	chr12	–	121257461	121277963	11.73
eukaryotic translation elongation factor 2	EEF2	NM_001961	EEF-2 // EF2	3846538	chr19	–	3926677	3936451	11.73
calcium activated nucleotidase 1	CANT1	NM_138793	SCAN-1 // SHAPY	3772775	chr17	–	74499403	74517744	11.68
moesin	MSN	NM_002444	—	3979659	chrX	+	64804248	64878488	11.57
aquarius homolog (mouse)	AQR	NM_014691	KIAA0560	3617757	chr15	–	32935042	33160557	11.56
EPH receptor A2	EPHA2	NM_004431	ECK	2397948	chr1	–	16323428	16355151	11.54
ATPase, Na+/K+ transporting, beta 1 polypeptide	ATP1B1	NM_001001787 // NM_001677	ATP1B // MGC1798	2366422	chr1	+	167342204	167368946	11.44
ring finger protein 40	RNF40	NM_014771	BRE1B // DKFZp686K191 // KIAA0661 // MGC13051 // RBP95 // STARING	3656555	chr16	+	30681120	30695182	11.42
KIAA0406	KIAA0406	NM_014657	—	3905073	chr20	–	36044840	36095268	11.38
TIMP metallopeptidase inhibitor 1	TIMP1	NM_003254	CLGI // EPA // EPO // FLJ90373 // HCI // TIMP	3976341	chrX	+	47326654	47332978	11.27

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
DCP1 decapping enzyme homolog A (*S. cerevisiae*)	DCP1A	NM_018403	HSA275986 // Nbla00360 // SMAD4IP1 // SMIF	2676726	chr3	–	53296412	53356692	11.27
heat shock 70 kDa protein 5 (glucose-regulated protein, 78 kDa)	HSPA5	NM_005347	BIP // FLJ29106 // GRP78 // MIF2	3225398	chr9	–	127036953	127064590	11.27
chromosome 4 open reading frame 23	C4orf23	NM_152544	FLJ12891 // FLJ35725	2717757	chr4	+	8474582	8545892	11.25
RAB5A, member RAS oncogene	RAB5A	NM_004162	RAB5	2613386	chr3	+	19963571	20002852	11.19
importin 7	IPO7	NM_006391	FLJ14581 // MGC138673 // RANBP7	3319840	chr11	+	9362702	9426296	11.19
nucleoporin 214 kDa	NUP214	NM_005085	CAIN // CAN // D9S46E // MGC104525 // N214	3191900	chr9	+	132990780	133102339	11.18
PRP8 pre-mRNA processing factor 8 homolog (*S. cerevisiae*)	PRPF8	NM_006445	HPRP8 // PRP8 // PRPC8 // RP13	3740479	chr17	–	1500681	1534906	11.12
Snf2-related CBP activator protein	SRCAP	NM_006662	KIAA0309	3656418	chr16	+	30616551	30663998	11.09
keratin 18	KRT18	NM_000224 // NM_199187	CYK18 // K18	3415576	chr12	+	51596769	51632949	11.07
adiponectin receptor 2	ADIPOR2	NM_024551	ACDCR2 // FLJ21432 // MGC4640 // PAQR2	3400625	chr12	+	1670418	1768071	11.05
splicing factor, arginine/serine-rich 3	SFRS3	NM_003017	SRp20	2905118	chr6	+	36669658	36741293	11.05
cyclin B1	CCNB1	NM_031966	CCNB	2813414	chr5	+	68498462	68509822	11.03
GrpE-like 2, mitochondrial (*E. coli*)	GRPEL2	NM_152407	DKFZp451C205 // FLJ23713 // FLJ33918 // Mt-GrpE#2	2835006	chr5	+	148705190	148714338	11.03
Yes-associated protein 1, 65 kDa	YAP1	NM_006106	YAP // YAP2 // YAP65	3346453	chr11	+	101486379	101609466	11.01
nuclear factor (erythroid-derived 2)-like 3	NFE2L3	NM_004289	NRF3	2993590	chr7	+	26158385	26194013	11.01
nucleoporin like 1	NUPL1	NM_001008564 // NM_001008565 NM_014089	KIAA0410 // PRO2463	3482219	chr13	+	24773258	24822202	10.97
RAB14, member RAS oncogene	RAB14	NM_016322	FBP // RAB-14	3223872	chr9	–	122980236	123025093	10.96
sperm specific antigen 2	SSFA2	NM_006751	CS-1 // CS1 // DKFZp313O1039 // DKFZp779G0129 // FLJ45996 // KIAA1927 // KRAP // SPAG13	2518428	chr2	+	182464815	182516732	10.95
DnaJ (Hsp40) homolog, subfamily B, member 1	DNAJB1	NM_006145	HSPF1 // Hdj1 // Hsp40	3852783	chr19	–	14485622	14501114	10.94
cyclin D1	CCND1	NM_053056	BCL1 // D11S287E // PRAD1 // U21B31	3338192	chr11	+	69161881	69178408	10.91

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
chromosome 20 open reading frame 77	C20orf77	NM_021215	CREPT // DKFZp434P0735 // FLJ44520 // dJ1057B20.2	3884450	chr20	+	36095232	36189576	10.91
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 1	SMARCD1	NM_003076 // NM_139071	BAF60A // CRACD1 // Rsc6p	3414390	chr12	+	48765279	48780742	10.90
kinesin family member 11	KIF11	NM_004523	EG5 // HKSP // KNSL1 // TRIP5	3258168	chr10	+	94292951	94405130	10.90
dickkopf homolog 1 (*Xenopus laevis*)	DKK1	NM_012242	DKK-1 // SK	3247172	chr10	+	53744067	53807545	10.89
polo-like kinase 4 (*Drosophila*)	PLK4	NM_014264	SAK // STK18	2742985	chr4	+	129021450	129039809	10.88
OTU domain containing 4	OTUD4	NM_017493 // NM_199324	DKFZp434I0721 // HIN1 // HSHIN1 // KIAA1046	2788195	chr4	–	146274170	146471942	10.88
ring finger and SPRY domain containing 1	RSPRY1	NM_133368	KIAA1972	3662612	chr16	+	55777703	55831882	10.87
leucine rich repeat containing 59	LRRC59	NM_018509	FLJ21675 //	3762355	chr17	–	45813504	45836593	10.85
exosome component 2	EXOSC2	NM_014285	RRP4 // Rrp4p // hRrp4p // p7	3191695	chr9	+	132559000	132572797	10.83
polo-like kinase 1 (*Drosophila*)	PLK1	NM_005030	PLK // STPK13	3653072	chr16	+	23597664	23609180	10.82
chromosome 20 open reading frame 24	C20orf24	NM_018840 // NM_199483	PNAS-11 // RIP5	3883971	chr20	+	34667571	34674368	10.81
KIAA1984 // chromosome 9 open reading frame 86	KIAA1984 // C9orf86	NM_001039374 // NM_024718	MGC15438 // PARF // RP11-216L13.7 // RP11-216L13.9 // bA216L13.7 // FLJ10101 // FLJ13045 // Parf // bA216L13.9 // pp8875	3194635	chr9	+	138810077	138855460	10.81
nucleolar protein 1, 120 kDa	NOL1	NM_001033714 // NM_006170	MGC117384 // MGC149287 // MGC149288 // NOP120 // NSUN1 // p120	3442024	chr12	–	6536290	6547817	10.79
chromosome 3 open reading frame 17	C3orf17	NM_001025072 // NM_001025073 // NM_015412	DKFZP434F2021	2688882	chr3	–	113926517	114253449	10.73
DOT1-like, histone H3 methyltransferase (*S. cerevisiae*)	DOT1L	NM_032482	DOT1 // KIAA1814	3816264	chr19	+	2114945	2183576	10.70
dullard homolog (*Xenopus laevis*)	DULLARD	NM_015343	HSA011916	3743501	chr17	–	7087644	7096514	10.70
v-raf-1 murine leukemia viral oncogene homolog 1 // microtubule-associated protein 2	RAF1 // MAP2	NM_002880 // NM_001039538 // NM_002374 // NM_031845 // NM_031847	CRAF // Raf-1 // c-Raf // DKFZp686I2148 // MAP2A // MAP2B // MAP2C	2663244	chr3	–	12600117	12680654	10.61
solute carrier family 39 (zinc transporter), member 7 // ring finger	SLC39A7 // RING1	NM_001077516 // NM_006979 //	D6S115E // D6S2244E // H2-KE4	2903470	chr6	+	33276220	33280187	10.55

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
protein 1		NM_002931	// HKE4 // KE4 // RING5 // ZIP7 // RNF1						
testis derived transcript (3 LIM domains)	TES	NM_015641 // NM_152829	DKFZP586B2022 // MGC1146 // TESS // TESS-2 // TESTIN	3020192	chr7	+	115637811	115743800	10.53
chromosome 12 open reading frame 11	C12orf11	NM_018164	FLJ10630 // FLJ10637	3448428	chr12	−	26949277	26982501	10.50
golgi associated PDZ and coiled-coil motif containing // v-ros UR2 sarcoma virus oncogene homolog 1 (avian)	GOPC // ROS1	NM_001017408 // NM_020399 // NM_002944	CAL // FIG // GOPC1 // PIST // dJ94G16.2 // MCF3 // ROS	2971378	chr6	−	117988142	118030384	10.49
protein regulator of cytokinesis 1 // interferon-related developmental regulator 1	PRC1 // IFRD1	NM_003981 // NM_199413 // NM_199414 // NM_001007245 // NM_001550	ASE1 // MGC1671 // MGC3669 // PC4 // TIS7	3639031	chr15	−	89310285	89338950	10.49
RNA methyltransferase like 1	RNMTL1	NM_018146	FLJ10581 // HC90	3705539	chr17	+	632263	642481	10.45
forkhead box O1A (rhabdomyosarcoma)	FOXO1A	NM_002015	FKH1 // FKHR // FOXO1	3510858	chr13	−	40027817	40162098	10.41
mitochondrial ribosomal protein S7	MRPS7	NM_015971	MRP-S // MRP-S7 // RP-S7 // RPMS7	3734760	chr17	+	70769374	70774626	10.41
suppressor of Ty 6 homolog (*S. cerevisiae*)	SUPT6H	NM_003170	KIAA0162 // MGC87943 // SPT6 // SPT6H // emb-5	3715703	chr17	+	24013260	24053809	10.38
splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)	SFRS1	NM_001078166 // NM_006924	ASF // MGC5228 // SF2 // SF2p33 // SRp30a	3764103	chr17	−	53421412	53439635	10.37
heterogeneous nuclear ribonucleoprotein M	HNRPM	NM_005968 // NM_031203	DKFZp547H118 // HNRNPM // HNRNPM4 // HNRPM4 // HTGR1	3819543	chr19	+	8415651	8459993	10.37
neuroepithelial cell transforming gene 1	NET1	NM_001047160 // NM_005863	ARHGEF8 // NET1A	3233182	chr10	+	5444535	5491001	10.35
ribonucleotide reductase M2 polypeptide	RRM2	NM_001034	R2 // RR2M	2469252	chr2	+	10179982	10279478	10.35
chromosome 16 open reading frame 80	C16orf80	NM_013242	EVORF // GTL3	3693511	chr16	−	56683698	56739201	10.32
exosome component 4	EXOSC4	NM_019037	FLJ20591 // RRP41 // RRP41A // Rrp41p // SKI6 // Ski6p // hRrp41p // p12A	3120008	chr8	+	145205527	145207529	10.30
UTP6, small subunit (SSU) processome component, homolog (yeast)	UTP6	NM_018428	C17orf40 // HCA66	3752437	chr17	−	27211153	27252839	10.30
polymerase (RNA) I polypeptide C, 30 kDa	POLR1C	NM_004875 // NM_203290	RPA39 // RPA40 // RPA5 // RPAC1	2908052	chr6	+	43592769	43605071	10.29

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Array Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change
centromere protein L	CENPL	NM_033319	C1orf155 // CENP-L // FLJ31044 // RP3-383J4.1 // dJ383J4.3	2444451	chr1	−	172035313	172104622	10.28
coronin, actin binding protein, 1C	CORO1C	NM_014325	HCRNN4 // coronin-3	3470549	chr12	−	107563018	107697353	10.27
ATP-binding cassette, sub-family F (GCN20), member 3	ABCF3	NM_018358	EST201864 // FLJ11198	2655511	chr3	+	185386580	185395316	10.26
telomeric repeat binding factor 2, interacting protein	TERF2IP	NM_018975	DRIP5 // RAP1	3669092	chr16	+	74238853	74353272	10.25
ADP-ribosylation factor interacting protein 2 (arfaptin 2) // solute carrier organic anion transporter family, member 6A1	ARFIP2 // SLCO6A1	NM_012402 // NM_173488	POR1 // GST // MGC26949 // OATP6A1 // OATPY	3360941	chr11	−	6453496	6459171	10.24
RNA binding motif protein 25	RBM25	NM_021239	MGC105088 // MGC117168 // RNPC7 // S164	3543411	chr14	+	72594776	72658577	10.23
zinc finger protein 410	ZNF410	NM_021188	APA-1 // APA1	3543884	chr14	+	73423093	73468718	10.23
3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	HMGCS1	NM_002130	HMGCS // MGC90332	2855501	chr5	−	43324231	43349337	10.19
transcription elongation regulator 1	TCERG1	NM_001040006 // NM_006706	CA150 // MGC133200 //	2834093	chr5	+	145754916	145871713	10.18
WD repeat domain 74	WDR74	XM_001125771 // NM_018093	FLJ10439 // FLJ21730	3376235	chr11	−	62356627	62365857	10.13
sperm associated antigen 5	SPAG5	NM_006461	DEEPEST // MAP126 // hMAP126	3750785	chr17	−	23928719	23950424	10.12
G protein-coupled receptor 126	GPR126	NM_001032394 // NM_001032395 // NM_020455 // NM_198569	DREG // PS1TP2 // VIGR	2928461	chr6	+	142622079	142853981	10.05
DnaJ-like protein // guanine nucleotide binding protein (G protein), gamma 10	bA16L21.2.1 // GNG10	NM_001015882 // NM_001017998	—	3184940	chr9	+	113412172	113474576	10.05
general transcription factor IIIC, polypeptide 4, 90 kDa	GTF3C4	NM_012204	FLJ21002 // MGC138450 // TFIII90 // TFIIIC90 // TFIIICdelta // TFiiiC2-90	3192525	chr9	+	134535243	134581784	10.00
eukaryotic translation initiation factor 5	EIF5	NM_001969 // NM_183004	EIF-5A	3553607	chr14	+	102743652	102881108	10.00
programmed cell death 7	PDCD7	NM_005707	ES18 // HES18 // MGC22015	3629475	chr15	−	63196772	63213308	9.97
dual specificity phosphatase 14	DUSP14	NM_007026	MKP-L // MKP6	3719515	chr17	+	32922795	32947707	9.97
RAD18 homolog (*S. cerevisiae*)	RAD18	NM_020165	RNF73	2662020	chr3	−	8792108	8980146	9.94
myeloid cell leukemia sequence 1 (BCL2-related)	MCL1	NM_021960 // NM_182763	EAT // MCL1L // MCL1S // MGC104264 //	2434438	chr1	−	148799312	148818878	9.93
oxysterol binding protein-like 2	OSBPL2	NM_014835 // NM_144498	FLJ20223 // KIAA0772 //	3892565	chr20	+	60245389	60304834	9.91

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
			MGC4307 // MGC8342 // ORP-2 // ORP2						
inhibitor of DNA binding 2B, dominant negative helix-loop-helix protein // inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	ID2B //ID2	NM_001039082 // NM_002166	—// GIG8 // ID2A // ID2H // MGC26389	2468622	chr2	+	8513132	8750492	9.91
cytoskeleton associated protein 5	CKAP5	NM_001008938 // NM_014756	FLJ35359 // KIAA0097 // TOG // TOGp // ch-TOG	3371719	chr11	–	46721250	46824660	9.90
thymosin, beta 10	TMSB10	NM_021103	MIG12	2491271	chr2	+	84959319	84988131	9.85
DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	DDX27	NM_017895	DKFZp667N057 // FLJ12917 // FLJ20596 // FLJ22238 // HSPC259 // MGC1018 // MGC163147 // PP3241 // RHLP //	3888217	chr20	+	47237780	47294013	9.83
TAR DNA binding protein	TARDBP	NM_007375	TDP-43	2320048	chr1	+	10995025	11013170	9.82
pyruvate dehydrogenase complex, component X // mitogen-activated protein kinase 10	PDHX // MAPK10	NM_003477 // NM_002753 // NM_138980 // NM_138981 // NM_138982	DLDBP // E3BP // OPDX // PDX1 // proX // FLJ12099 // FLJ33785 // JNK3 // JNK3A // MGC50974 // PRKM10 // p493F12 //	3326540	chr11	+	34870003	34998695	9.81
dihydrouridine synthase 3-like (*S. cerevisiae*)	DUS3L	NM_020175	DUS3 // FLJ13896	3847420	chr19	–	5735867	5759311	9.80
splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	SFPQ	NM_005066	POMP100 // PSF	2406064	chr1	–	35351696	35506894	9.80
phosphoinositide-3-kinase, regulatory subunit 4, p150	PIK3R4	NM_014602	MGC102700 // VPS15 // p150	2695200	chr3	–	131801268	132026111	9.79
RNA binding motif, single stranded interacting protein 2	RBMS2	NM_002898	SCR3	3417583	chr12	+	55202025	55277435	9.78
eukaryotic translation initiation factor 2C, 2	EIF2C2	NM_012154	AGO2 // MGC3183 // Q10	3156193	chr8	–	141599440	141726037	9.74
inner centromere protein antigens 135/155 kDa	INCENP	NM_001040694 // NM_020238	FLJ31633 // MGC111393	3333358	chr11	+	61648046	61677757	9.73
cofilin 1 (non-muscle)	CFL1	NM_005507	CFL	3377886	chr11	–	65347069	65386796	9.72
heat shock 105 kDa/110 kDa protein 1	HSPH1	NM_006644	DKFZp686M05240 // HSP105 // HSP105A // HSP105B // KIAA0201 // NY-CO-25	3508330	chr13	–	30558258	30651692	9.68
nuclear import 7 homolog (*S. cerevisiae*)	NIP7	NM_016101	CGI-37 // FLJ10296 // HSPC031 // KD93	3666686	chr16	+	67930869	67935044	9.64

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
epiregulin	EREG	NM_001432	ER	2731513	chr4	+	75440309	75473341	9.62
mannosidase, alpha, class 1A, member 2 // urothelial cancer	MAN1A2 // UCA1	NM_006699 // —	MAN1B // —	2353881	chr1	+	117689854	117931990	9.61
tumor necrosis factor receptor superfamily, member 1A	TNFRSF1A	NM_001065	CD120a // FPF // MGC19588 // TBP1 // TNF-R // TNF-R-I // TNF-R55 // TNFAR // TNFR1 // TNFR55 // TNFR60 // p55 // p55-R //	3441849	chr12	–	6308185	6321522	9.60
cyclin L1	CCNL1	NM_020307	BM-001 // PRO1073 // ania-6a	2702307	chr3	–	158305077	158361233	9.60
RNA binding motif protein 4	RBM4	NM_002896	DKFZp547K0918 // LARK // MGC75138 // RBM4A // ZCCHC21 // ZCRB3A	3336422	chr11	+	66161951	66190547	9.60
KIAA1429	KIAA1429	NM_015496 // NM_183009	DKFZP434I116 // DKFZp781B2117 // MGC138493 // MGC141940 // MSTP054	3145020	chr8	–	95569109	95634851	9.57
nucleoporin 153 kDa	NUP153	NM_005124	HNUP153 // N153	2943808	chr6	–	17723255	17855638	9.56
zinc finger protein 91 homolog (mouse) // ciliary neurotrophic factor	ZFP91 // CNTF	NM_053023 // NM_170768 // NM_000614	FKSG11 // PZF // ZNF757 // HCNTF	3331730	chr11	+	58101868	58149782	9.54
tetraspanin 5	TSPAN5	NM_005723	NET-4 // TM4SF9 // TSPAN-5	2778856	chr4	–	99589201	99798839	9.53
resistance to inhibitors of cholinesterase 8 homolog A (*C. elegans*)	RIC8A	NM_021932	MGC104517 // MGC131931 // MGC148073 // MGC148074 // RIC8 // synembryn	3315512	chr11	+	197139	206202	9.52
splicing factor 3b, subunit 1, 155 kDa	SF3B1	NM_001005526 // NM_012433	PRP10 // PRPF10 // SAP155 // SF3b155	2593670	chr2	–	197962756	198039327	9.52
DEAD (Asp-Glu-Ala-Asp) box polypeptide 47 // apolipoprotein L domain containing 1	DDX47 // APOLD1	NM_016355 // NM_201224 // NM_030817	DKFZp564O176 // E4-DBP // FLJ30012 // HQ0256 // MSTP162 // DKFZP434F0318 //	3405531	chr12	+	12856462	12874176	9.51
tensin 4	TNS4	NM_032865	CTEN // FLJ14950 // PP14434	3756262	chr17	–	35881491	35911365	9.51
heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37 kDa)	HNRPD	NM_001003810 // NM_002138 // NM_031369 // NM_031370	AUF1 // AUF1A // P37 // hnRNPD0	2775463	chr4	–	83492676	83515077	9.50
v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	YES1	NM_005433	HsT441 // P61-YES // Yes // c-yes	3795942	chr18	–	711592	803236	9.48

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Array	Human Genome hg18				
				Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
nuclear factor (erythroid-derived 2)-like 2 // hypothetical protein DKFZp451M2119	NFE2L2 // DKFZp451M2119	NM_006164 // NM_182585	NRF2 // —	2588827	chr2	−	177794809	177837753	9.48
eukaryotic translation initiation factor 4A, isoform 1 // SUMO1/sentrin/SMT3 specific peptidase 3	EIF4A1 // SENP3	NM_001416 // NM_015670	DDX2A // EIF-4A // EIF4A // DKFZP586K0919 // DKFZp762A152 // SMT3IP1 // SSP3	3708826	chr17	+	7416768	7423040	9.46
nucleolar protein 11	NOL11	NM_015462	DKFZP586L0724	3732373	chr17	+	63144526	63205942	9.45
adenylate kinase 2	AK2	NM_001625 // NM_013411	ADK2	2405364	chr1	−	33245959	33275155	9.45
splicing factor, arginine/serine-rich 5	SFRS5	NM_001039465 // NM_006925	HRS // SRP40	3542207	chr14	+	69263363	69308465	9.42
ancient ubiquitous protein 1 // DEAQ box polypeptide 1 (RNA-dependent ATPase)	AUP1 // DQX1	NM_181575 // NM_133637	—// FLJ23757	2560254	chr2	−	74607294	74610455	9.38
AF4/FMR2 family, member 4	AFF4	NM_014423	AF5Q31 // MCEF // MGC75036	2875555	chr5	−	132238768	132327205	9.38
guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	GNB2L1	NM_006098	Gnb2-rs1 // H12.3 // HLC-7 // PIG21 // RACK1	2891052	chr5	−	180596592	180612024	9.38
survival motor neuron domain containing 1	SMNDC1	NM_005871	SMNR // SPF30	3306516	chr10	−	112042540	112106248	9.38
BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)	BUB1	NM_004336	BUB1A // BUB1L // hBUB1	2570616	chr2	−	111088456	111174950	9.36
SET domain containing 5	SETD5	XM_926615 // XM_931376 // XM_931417 // XM_931444 // XM_931447 // XM_931455 // XM_931478 // XM_939712 // XM_944260 // XM_944276 // XM_944280 // XM_944295 // XM_944298 // XM_944303 // NM_001080517	DKFZp686J18276 // FLJ10707 // KIAA1757	2609608	chr3	+	9414309	9495916	9.36
heat shock protein 90 kDa beta (Grp94), member 1 // thymine-DNA glycosylase // heat shock protein 90 kDa beta (Grp94), member 2 (pseudogene)	HSP90B1 // TDG // HSP90B2P	NM_003299 // NM_003211 // —	ECGP // GP96 // GRP94 // TRA1 // — // GRP94P1 // GRP94b // HSP // HSPCP2 // HsGrp94b // TRA1P1 // TRAP1	3429312	chr12	+	102848291	102871551	9.34

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
actin, gamma 1	ACTG1	NM_001614	ACT // ACTG // DFNA20 // DFNA26	3773932	chr17	−	77091456	77105797	9.32
dual specificity phosphatase 6	DUSP6	NM_001946 // NM_022652	MKP3 // PYST1	3464860	chr12	−	88223376	88273467	9.31
LATS, large tumor suppressor, homolog 2 (*Drosophila*)	LATS2	NM_014572	FLJ13161 // KPM	3504526	chr13	−	20445178	20533718	9.28
SERPINE1 mRNA binding protein 1	SERBP1	NM_001018067 // NM_001018068 // NM_001018069 // NM_015640	CGI-55 // CHD3IP // DKFZp564M2423 // FLJ90489 // HABP4L // PAI-RBP1 // PAIRBP1	2417174	chr1	−	67646101	67669020	9.26
DnaJ (Hsp40) homolog, subfamily A, member 3	DNAJA3	NM_005147	FLJ45758 // TID1 // hTid-1	3646164	chr16	+	4415465	4446773	9.23
nuclear cap binding protein subunit 2, 20 kDa	NCBP2	NM_001042540 // NM_007362	CBC2 // CBP20 // NIP1 // PIG55	2713074	chr3	−	198146677	198154763	9.23
TRK-fused gene	TFG	NM_001007565 // NM_006070	FLJ36137 // TF6 // TRKT3	2633773	chr3	+	101910681	101950800	9.22
LIM domain 7	LMO7	NM_005358	FBX20 // FBXO20 // KIAA0858 // LOMP	3494137	chr13	+	75092571	75566974	9.22
KIAA0090	KIAA0090	NM_015047	RP1-43E13.1	2399620	chr1	−	19413665	19450633	9.22
RNA binding motif protein 23 // chromosome 9 open reading frame 102	RBM23 // C9orf102	NM_001077351 // NM_001077352 // NM_018107 // NM_001034155 // NM_020207	CAPERbeta // FLJ10482 // MGC4458 // PP239 // RNPC4 // FLJ37706 // SR278	3556888	chr14	−	22439714	22458231	9.18
suppressor of Ty 7 (*S. cerevisiae*)-like	SUPT7L	NM_014860	ART1 // KIAA0764 // MGC90306 // SPT7L // STAF65 // STAF65(gamma)	2546008	chr2	−	27718957	27740160	9.15
transforming, acidic coiled-coil containing protein 3	TACC3	NM_006342	ERIC1 // MGC117382 // MGC133242	2714955	chr4	+	1692616	1716693	9.12
signal transducing adaptor molecule (SH3 domain and ITAM motif) 1	STAM	NM_003473	DKFZp686J2352 // STAM1	3237088	chr10	+	17726140	17798809	9.11
neurotensin receptor 1 (high affinity)	NTSR1	NM_002531	NTR	3892873	chr20	+	60810575	60864568	9.10
sorting nexin associated golgi protein 1	SNAG1	NM_052870	MGC150827 // MGC150829 // SH3PX2 // SH3PXD3B // SNX18	2809628	chr5	+	53849348	53878172	9.07
DEAD (Asp-Glu-Ala-Asp) box polypeptide 42	DDX42	NM_007372 // NM_203499	FLJ43179 // RHELP // RNAHP //	3730899	chr17	+	59204975	59250510	9.05
adhesion regulating molecule 1	ADRM1	NM_007002 // NM_175573	GP110 // MGC29536 // Rpn13	3892607	chr20	+	60305485	60317305	9.05
dyskeratosis congenita 1, dyskerin	DKC1	NM_001363	DKC // NAP57 // NOLA4 // XAP101 // dyskerin	3996667	chrX	+	153644243	153659150	9.04
GNAS complex locus	GNAS	NM_000516 // NM_001077488 //	AHO // C20orf45 // GNAS1 // GPSA //	3891163	chr20	+	56848165	56919604	9.04

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Array Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change
		NM_001077489 // NM_001077490 // NM_016592 // NM_080425 // NM_080426 // NR_003259	GSA // GSP // MGC33735 // PHP1A // PHP1B // POH // dJ309F20.1.1 // dJ806M20.3.3						
protein inhibitor of activated STAT, 1	PIAS1	NM_016166	DDXBP1 // GBP // GU/RH-II // MGC141878 // MGC141879 // ZMIZ3	3599280	chr15	+	65898917	66277975	9.03
WD repeat domain 36	WDR36	NM_139281	DKFZp686I1650 // GLC1G // TA-WDRP // TAWDRP //	2823820	chr5	+	110455769	110517812	9.03
tripartite motif-containing 44	TRIM44	NM_017583	DIPB // HSA249128 // MC7 // MGC3490	3326842	chr11	+	35600246	35826001	9.03
transforming growth factor beta regulator 4	TBRG4	NM_004749 // NM_030900 // NM_199122	CPR2 // FASTKD4 // KIAA0948	3049025	chr7	−	45103738	45128368	9.01
guanine nucleotide binding protein-like 3 (nucleolar)	GNL3	NM_014366 // NM_206825 // NM_206826	C77032 // E2IG3 // MGC800 // NS	2624074	chr3	+	52694976	52705212	9.00
BCL2-associated transcription factor 1	BCLAF1	NM_001077440 // NM_001077441 // NM_014739	BTF // KIAA0164 // bK211L9.1	2975680	chr6	−	136619703	136652847	8.99
cyclin L2 // aurora kinase A interacting protein 1	CCNL2 // AURKAIP1	NM_001039577 // NM_030937 // NM_017900	ANIA-6B // DKFZp761A1210 // DKFZp762O195 // HCLA-ISO // HLA- ISO // PCEE // SB138 // AIP // AKIP // FLJ20608	4041923	chr1_random	+	359569	372958	8.99

cirrhosis, autosomal recessive 1A (cirhin)	CIRH1A	NM_032830	CIRHIN // FLJ14728
			// KIAA1988 // NAIC
			// TEX292
				3666566	chr16	+	67722728	67761072	8.98

SMAD family member 3	SMAD3	NM_005902	DKFZP586N0721 // DKFZp686J10186 // HSPC193 // HsT17436 // JV15-2 // MADH3 // MGC60396 // Smad 3	3598959	chr15	+	65145043	65296818	8.97
proteasome (prosome, macropain) subunit, beta type, 7	PSMB7	NM_002799	Z	3225003	chr9	−	126155580	126223284	8.97
cyclin L2 // aurora kinase A interacting protein 1	CCNL2 // AURKAIP1	NM_001039577 // NM_030937 // NM_017900	ANIA-6B // DKFZp761A1210 // DKFZp762O195 // HCLA-ISO // HLA- ISO // PCEE //	2391532	chr1	−	1314609	1324575	8.96

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
mediator of RNA polymerase II transcription, subunit 28 homolog (*S. cerevisiae*)	MED28	NM_025205	SB138 // AIP // AKIP // FLJ20608 1500003D12Rik // DKFZP434N185 // EG1 // magicin	2720181	chr4	+	17225344	17244808	8.95
Rho GTPase activating protein 12	ARHGAP12	NM_018287	DKFZp779N2050 // FLJ10971 // FLJ20737 // FLJ21785 // FLJ45709	3283920	chr10	–	32134245	32261226	8.93
proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog)	PSMD7	NM_002811	MOV34 // P40 // S12	3668617	chr16	+	72888182	72901528	8.92
hypothetical protein MGC10433	MGC10433	NM_024321	—	3830612	chr19	+	40811767	40820425	8.91
ubiquitin associated protein 2-like	UBAP2L	NM_014847	FLJ42300 // KIAA0144 // NICE-4	2360083	chr1	+	152459139	152510701	8.91
solute carrier family 20 (phosphate transporter), member 1	SLC20A1	NM_005415	DKFZp686J2397 // FLJ41426 // GLVR1 // Glvr-1 // PIT1 // PiT-1	2500919	chr2	+	113117773	113137861	8.90
protein phosphatase 1, regulatory (inhibitor) subunit 10	PPP1R10	NM_002714	CAT53 // FB19 // PNUTS	2948425	chr6	–	30676177	30694348	8.87
SAP30 binding protein // cardiotrophin-like cytokine factor 1	SAP30BP // CLCF1	NM_013260 // NM_013246	DKFZp586L2022 // HCNGP // HTRG // HTRP // BSF3 // CISS2 // CLC // NNT1 // NR6	3735107	chr17	+	71174801	71215729	8.86
ATP-binding cassette, sub-family E (OABP), member 1	ABCE1	NM_001040876 // NM_002940	ABC38 // OABP // RLI // RNASEL1 // RNASELI // RNS4I	2746024	chr4	+	146238626	146270126	8.86
BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, 170 kDa (Mot1 homolog, *S. cerevisiae*)	BTAF1	NM_003972	KIAA0940 // MGC138406 // MOT1 // TAF(II)170 // TAF172 // TAFII170	3257938	chr10	+	93673509	93821994	8.84
syntaxin 5	STX5	XM_001128716 // NM_003164	SED5 // STX5A	3376193	chr11	–	62330946	62356126	8.84
cyclin A2	CCNA2	NM_001237	CCN1 // CCNA	2784113	chr4	–	122956335	122964516	8.81
integrator complex subunit 7	INTS7	NM_015434	C1orf73 // DKFZP434B168 // INT7	2454532	chr1	–	210180312	210275613	8.81
regulator of chromosome condensation 1 // small nucleolar RNA host gene (non-protein coding) 3	RCC1 // SNHG3	NM_001048194 // NM_001048195 // NM_001269 // NR_002909	CHC1 // RCC1-1 // RNU17C // RNU17D // U17HG // U17HG-A	2327482	chr1	+	28705062	28802493	8.81
LEM domain containing 3	LEMD3	NM_014319	MAN1	3420079	chr12	+	63806051	63928317	8.80

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
upstream binding protein 1 (LBP-1a)	UBP1	NM_014517	DKFZp686L1745 // LBP-1B // LBP-1a // LBP1A // LBP1B	2668351	chr3	–	33404835	33456874	8.80
zinc finger protein 384	ZNF384	NM_001039916 // NM_001039917 // NM_001039918 // NM_001039919 // NM_001039920 // NM_133476	CAGH1 // CAGH1A // CIZ // ERDA2 // NMP4 // NP // TNRC1	3442205	chr12	–	6645924	6668961	8.79
caveolin 2	CAV2	NM_001233 // NM_198212	CAV // MGC12294	3020273	chr7	+	115926553	115935830	8.78
actin, beta	ACTB	NM_001101	PS1TP5BP1	3036924	chr7	–	5533433	5537011	8.77
acyl-Coenzyme A binding domain containing 3	ACBD3	NM_022735	GCP60 // GOCAP1 // GOLPH1 // PAP7	2458701	chr1	–	224398953	224463924	8.76
eukaryotic translation initiation factor 3, subunit 10 theta, 150/170 kDa	EIF3S10	NM_003750	EIF3 // EIF3A // KIAA0139 // P167 // eIF3-p170 // eIF3-theta // p180 // p185	3309215	chr10	–	120621551	120830522	8.75
CDC42 small effector 2	CDC42SE2	NM_001038702 // NM_020240	FLJ21967 // SPEC2	2828146	chr5	+	130616639	130781182	8.75
zinc finger, AN1-type domain 2B	ZFAND2B	NM_138802	—	2528308	chr2	+	219779769	219782603	8.72
ribosomal protein S20	RPS20	NM_001023	FLJ27451 // MGC102930	3136129	chr8	–	57139946	57185891	8.72
exportin 1 (CRM1 homolog, yeast) // thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian)	XPO1 // THRB	NM_003400 // NM_000461	CRM1 // DKFZp686B1823 // ERBA-BETA // ERBA2 // GRTH // MGC126109 // MGC126110 // NR1A2 // THR1 // THRB1 // THRB2	2555490	chr2	–	61558490	61619343	8.71
D4, zinc and double PHD fingers family 2	DPF2	NM_006268	MGC10180 // REQ // UBID4 // ubi-d4	3335089	chr11	+	64857703	64877276	8.71
basic leucine zipper and W2 domains 1	BZW1	XM_001126385 // NM_014670	BZAP45 // KIAA0005 // Nbla10236	2522439	chr2	+	201384456	201418386	8.71
pogo transposable element with ZNF domain	POGZ	NM_015100 // NM_145796 // NM_207171	KIAA0461 // MGC71543 // SUHW5 // ZNF635	2435044	chr1	–	149641830	149753035	8.70
basic helix-loop-helix domain containing, class B, 3	BHLHB3	NM_030762	DEC2 // SHARP-1 // SHARP1	3448088	chr12	–	26141435	26179615	8.69
family with sequence similarity 83, member D	FAM83D	NM_030919	C20orf129 // FLJ38341 // dJ616B8.3	3884892	chr20	+	36988369	37015223	8.69
thioredoxin domain containing 14 // catenin (cadherin-associated protein), delta 1	TXNDC14 // CTNND1	NM_015959 // XM_001126721 // XM_001126756 // XM_001126767 //	CGI-31 // DKFZp781O2021 // MGC111151 // PIG26 // TMX2 // CAS //	3331487	chr11	+	57235839	57391291	8.68

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Array Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change
		XM_001126781 // XM_001126793 // XM_001126823 // NM_001331	CTNND // KIAA0384 // P120CAS // P120CTN // p120						
thymopoietin	TMPO	NM_001032283 // NM_001032284 // NM_003276	CMD1T // LAP2 // MGC61508 // PRO0868 // TP	3427767	chr12	+	97395927	97502543	8.68
jumonji, AT rich interactive domain 1A	JARID1A	NM_001042603 // NM_005056	RBBP2 // RBP2	3439603	chr12	–	269504	368944	8.67
sorting nexin 19	SNX19	NM_014758	CHET8 // DKFZp667I205 // KIAA0254	3398482	chr11	–	130250320	130291615	8.67
Der1-like domain family, member 1	DERL1	NM_024295	DER-1 // DER1 // FLJ13784 // FLJ42092 // MGC3067 //	3151401	chr8	–	124094605	124123781	8.67
eukaryotic translation initiation factor 3, subunit 9 eta, 116 kDa	EIF3S9	NM_001037283 // NM_003751	EIF3-ETA // EIF3-P110 // EIF3-P116 // MGC104664 // MGC131875 // PRT1 // eIF3b	2987441	chr7	+	2315929	2386896	8.66
WDR45-like	WDR45L	NM_019613	WIPI-3 // WIPI3	3775157	chr17	–	78165748	78199803	8.65
conserved helix-loop-helix ubiquitous kinase	CHUK	NM_001278	IKBKA // IKK-alpha // IKK1 // IKKA // NFKBIKA // TCF16	3303300	chr10	–	101938115	101979345	8.62
WD repeat domain 77 // oviductal glycoprotein 1, 120 kDa (mucin 9, oviductin)	WDR77 // OVGP1	NM_024102 // NM_002557	HKMT1069 // MEP50 // MGC2722 // Nbla10071 // RP11-552M11.3 // CHIT5 // EGP // MUC9 //	2427930	chr1	–	111782351	111793512	8.60
Paf1, RNA polymerase II associated factor, homolog (*S. cerevisiae*)	PAF1	NM_019088	F23149_1 // FLJ11123 // PD2	3861978	chr19	–	44568113	44592162	8.60
kinesin family member 23	KIF23	NM_004856 // NM_138555	CHO1 // KNSL5 // MKLP-1 // MKLP1	3599811	chr15	+	67493677	67527808	8.60
BMS1-like, ribosome assembly protein (yeast) // tetratricopeptide repeat domain 7B	BMS1L // TTC7B	NM_014753 // NM_001010854	KIAA0187 // TTC7L1 // c14_5685	3243708	chr10	+	42597978	42682443	8.58
insulin induced gene 2	INSIG2	NM_016133	MGC26273	2502424	chr2	+	118558758	118593436	8.57
ubiquitin specific peptidase 9, X-linked // ubiquitin specific peptidase 9, Y-linked (fat facets-like,	USP9X // USP9Y	NM_001039590 // NM_001039591 // NM_004654	DFFRX // FAF // AZF // AZFA // DFFRY // SP3	3974708	chrX	+	40829542	40980776	8.57
squamous cell carcinoma antigen recognized by T cells 3	SART3	NM_014706	KIAA0156 // MGC138188 // RP11-13G14 // TIP110 // p110(nrb)	3470253	chr12	–	107440140	107479296	8.57

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
LIM domain only 4	LMO4	NM_006769	—	2345286	chr1	+	87458333	87588817	8.56
peptidylprolyl isomerase G (cyclophilin G)	PPIG	NM_004792	CARS-Cyp // CYP // MGC133241 //	2514441	chr2	+	170149096	170206156	8.55
guanine nucleotide binding protein (G protein), q polypeptide	GNAQ	NM_002072	G-ALPHA-q // GAQ	3210808	chr9	–	79475043	79836455	8.53
TSC22 domain family, member 1	TSC22D1	NM_006022 // NM_183422	DKFZp686O19206 // MGC17597 // RP11-269C23.2 // TGFB1I4 // TSC22	3512294	chr13	–	43905532	44202063	8.53
serine/arginine repetitive matrix 2	SRRM2	NM_016333	300-KD // DKFZp686O15166 // FLJ21926 // FLJ22250 // KIAA0324 // MGC40295 // SRL300 // SRm300	3645253	chr16	+	2742650	2761908	8.52
methionine adenosyltransferase II, alpha	MAT2A	NM_005911	MATA2 // MATII // SAMS2	2491615	chr2	+	85597809	85625908	8.51
ubinuclein 1	UBN1	NM_001079514 // NM_016936	VT // VT4	3646434	chr16	+	4836677	4872358	8.51
solute carrier family 38, member 2	SLC38A2	NM_018976	ATA2 // KIAA1382 // PRO1068 // SAT2 // SNAT2	3452323	chr12	–	45038242	45132603	8.50
GrpE-like 1, mitochondrial (*E. coli*)	GRPEL1	NM_025196	FLJ25609 // HMGE	2759404	chr4	–	7107908	7187815	8.48
BAT2 domain containing 1	BAT2D1	NM_015172	BAT2-iso // XTP2	2367154	chr1	+	169716078	169829262	8.48
eukaryotic translation initiation factor 3, subunit 7 zeta, 66/67 kDa	EIF3S7	NM_003753	MGC126526 // MGC17258 // eIF3-p66 // eIF3-zeta // eIF3d	3959631	chr22	–	35236857	35255429	8.48
polymerase (DNA directed) sigma	POLS	NM_006999	LAK-1 // POLK // TRF4 // TRF4-1	2800503	chr5	+	6736994	6893446	8.47
interleukin enhancer binding factor 2, 45 kDa	ILF2	NM_004515	MGC8391 // NF45 // PRO3063	2436132	chr1	–	151900372	151910103	8.46
chromosome X open reading frame	CXorf39	NM_207318	—	3985866	chrX	+	103297819	103323642	8.45
lysosomal-associated membrane protein 1	LAMP1	NM_005561	CD107a // LAMPA // LGP120	3502570	chr13	+	112999460	113025981	8.45
YTH domain containing 1	YTHDC1	NM_001031732 // NM_133370	KIAA1966 // YT521 // YT521-B	2772017	chr4	–	68858700	68934802	8.45
RAD21 homolog (*S. pombe*)	RAD21	NM_006265	FLJ25655 // FLJ40596 // HR21 // HRAD21 // KIAA0078 // MCD1 // NXP1 // SCC1 // hHR21	3149843	chr8	–	117909861	117956284	8.45
TATA box binding protein	TBP	NM_003194	GTF2D // GTF2D1 // MGC117320 // MGC126054 //	2937984	chr6	+	170705200	170723945	8.44

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Array Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change
			MGC126055 // SCA17 // TFIID						
Rho GTPase activating protein 29	ARHGAP29	NM_004815	PARG1 // RP11-255E17.1	2423829	chr1	–	94409906	94549874	8.43
PRP4 pre-mRNA processing factor 4 homolog (yeast)	PRPF4	NM_004697	HPRP4 // HPRP4P // PRP4 // Prp4p	3185558	chr9	+	115077230	115095267	8.42
myosin phosphatase-Rho interacting protein	M-RIP // C17orf84	NM_0165134 // NM_201274	KIAA0864 // RHOIP3 // p116Rip	3712363	chr17	+	16886542	17062286	8.42
E2F transcription factor 4, p107/p130-binding	E2F4	NM_001950	E2F-4	3665288	chr16	+	65783266	65790299	8.42
glutamine-rich 1	QRICH1	NM_017730 // NM_198880	FLJ20259 // MGC131838	2673902	chr3	–	49042148	49106498	8.42
annexin A1	ANXA1	NM_000700	ANX1 // LPC1	3174816	chr9	+	74914324	74983394	8.41
serine/threonine kinase 4	STK4	NM_006282	DKFZp686A2068 // KRS2 // MST1 // YSK3	3886704	chr20	+	43028534	43142041	8.38
chromosome X open reading frame 15	CXorf15	NM_018360	FIAT // FLJ11209 // LSR5 // MGC126621 // MGC126625	3970166	chrX	+	16714433	16772561	8.36
transportin 2 (importin 3, karyopherin beta 2b)	TNPO2	NM_013433	FLJ12155 // IPO3 // KPNB2B // TRN2	3851651	chr19	–	12670912	12695776	8.35
pleckstrin homology-like domain, family B, member 1	PHLDB1	NM_015157	DKFZp686H039 // DKFZp686O24210 // FLJ00141 // FLJ90266 // KIAA0638 // LL5A // MGC111531	3351564	chr11	+	117982385	118033939	8.34
tumor necrosis factor receptor superfamily, member 12A	TNFRSF12A	NM_016639	CD266 // FN14 // TWEAKR	3645555	chr16	+	3010334	3012380	8.34
SLC7A5 pseudogene	LAT1-3TM // IMAA	NR_002593 // NR_002594	DC49 // MLAS // hLAT1-3TM // MMAA	3684100	chr16	–	21320984	22449842	8.33
CD3e molecule, epsilon associated protein	CD3EAP	NM_012099	ASE-1 // CAST // MGC118851 // PAF49	3836243	chr19	+	50597660	50605831	8.33
kinesin family member 2C	KIF2C	NM_006845	KNSL6 // MCAK	2334098	chr1	+	44978097	45005994	8.33
CD55 molecule, decay accelerating factor for complement (Cromer blood group)	CD55	NM_000574	CR // DAF // TC	2377229	chr1	+	205561488	205607671	8.32
aldolase A, fructose-bisphosphate	ALDOA	NM_000034 // NM_184041 // NM_184043	ALDA // MGC10942 // MGC17716 // MGC17767	3655920	chr16	+	29968869	29991009	8.31
denticleless homolog (*Drosophila*)	DTL	NM_016448	CDT2 // DCAF2 // L2DTL // RAMP	2378937	chr1	+	210275565	210399046	8.30
adhesion molecule with Ig-like domain 2	AMIGO2	NM_181847	ALI1 // DEGA	3452478	chr12	–	45726359	45874177	8.30
ST3 beta-galactoside alpha-2,3-sialyltransferase 1	ST3GAL1	NM_003033 // NM_173344	Gal-NAc6S // MGC9183 // SIAT4A // SIATFL //	3154398	chr8	–	134535811	134653449	8.29

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Array Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change
			ST3GalA // ST3GalA.1 //						
tripartite motif-containing 8	TRIM8	NM_030912	GERP // RNF27	3261820	chr10	+	104384137	104419190	8.29
fibroblast growth factor (acidic) intracellular binding protein	FIBP	NM_004214 // NM_198897	FGFIBP // FIBP-1	3377964	chr11	−	65407787	65412586	8.29
PAP associated domain containing 1 // collagen, type XI, alpha 1	PAPD1 // COL11A1	NM$_{13}$ 018109 // NM_001854 // NM_080629 // NM_080630	FLJ10486 // RP11-305E6.3 // mtPAP // CO11A1 // COLL6 // STL2	3283378	chr10	−	30511316	30764402	8.26
exosome component 10	EXOSC10	NM_001001998 // NM_002685	PM-Scl // PM/Scl-100 // PMSCL // PMSCL2 // RRP6 // Rrp6p // p2 // p3 // p4	2396480	chr1	−	11049173	11082811	8.26
B-cell CLL/lymphoma 9-like	BCL9L	NM_182557	BCL9-2 // DLNB11	3393993	chr11	−	118272076	118304947	8.23
1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon)	AGPAT5	NM_018361	1-AGPAT5 // LPAAT-e // LPAAT-epsilon	3083936	chr8	+	6553307	6633056	8.22
chaperonin containing TCP1, subunit 6A (zeta 1)	CCT6A	NM_001009186 // NM_001762	CCT-zeta // CCT-zeta-1 // CCT6 // Cctz // HTR3 // MGC126214 // MGC126215 // MoDP-2 // TCP-1-zeta // TCP20 // TCPZ // TTCP20	3003193	chr7	+	56086894	56099148	8.22
jumonji, AT rich interactive domain 1B	JARID1B	NM_006618	FLJ10538 // FLJ12459 // FLJ12491 // FLJ16281 // FLJ23670 // PLU-1 // PUT1 // RBBP2H1A	2451309	chr1	−	200963111	201048571	8.22
solute carrier family 25, member 37	SLC25A37	XM_001128238 // XM_001128248 // XM_001128255 // XM_001128269 // NM_016612	HT015 // MFRN // MSC // MSCP // PRO1278 // PRO1584 // PRO2217	3090006	chr8	+	23439117	23485313	8.21
nucleoporin 50 kDa	NUP50	NM_007172 // NM_153645	MGC39961 // NPAP60 // NPAP60L	3948461	chr22	+	43938390	43960160	8.21
mediator of RNA polymerase II transcription, subunit 8 homolog (*S. cerevisiae*)	MED8	NM_001001651 // NM_001001653 // NM_001001654 // NM_052877 // NM_201542	ARC32 // MGC17544 // MGC19641	2409344	chr1	−	43622176	43628144	8.20
eukaryotic translation initiation factor 4A, isofom 2	EIF4A2	NM_001967	BM-010 // DDX2B // EIF4A // EIF4F	2656738	chr3	+	187961636	187990742	8.20

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Array Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change
GA binding protein transcription factor, beta subunit 2	GABPB2	NM_002041 // NM_005254 // NM_016654 // NM_016655 // NM_181427	BABPB2 // E4TF1 // E4TF1-47 // E4TF1-53 // E4TF1B // GABPB // GABPB1 // NRF2B1 //	3623683	chr15	–	48356681	48434794	8.18
RNA binding motif protein 22	RBM22	NM_018047	FLJ10290 // ZC3H16	2881521	chr5	–	150050460	150060885	8.16
meningioma expressed antigen 5 (hyaluronidase)	MGEA5	NM_012215	FLJ11229 // FLJ23355 // KIAA0679 // MEA5 // NCOAT	3304012	chr10	–	103534201	103568420	8.15
low density lipoprotein receptor (familial hypercholesterolemia)	LDLR	NM_000527	FH // FHC	3821015	chr19	+	11061114	11115050	8.15
cell division cycle 40 homolog (*S. cerevisiae*)	CDC40	NM_015891	EHB3 // FLJ10564 // MGC102802 // PRP17 // PRPF17	2921086	chr6	+	110606544	110682171	8.13
hypothetical protein HSPC111	HSPC111	NM_016391	HSPC185	2888284	chr5	–	175743557	175749348	8.13
solute carrier family 2 (facilitated glucose transporter), member 1	SLC2A1	NM_006516	GLUT // GLUT1 // MGC141895 // MGC141896	2409104	chr1	–	43124794	43338329	8.12
caspase 2, apoptosis-related cysteine peptidase (neural precursor cell expressed, developmentally down-regulated 2)	CASP2	NM_032982 // NM_032983	CASP-2 // ICH-1L // ICH-1L/1S // ICH1 // NEDD2	3029030	chr7	+	142695524	142714904	8.11
HECT domain containing 1	HECTD1	NM_015382	FLJ38315 // KIAA1131	3559570	chr14	–	30629936	31002364	8.10
ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (*Drosophila*)	ARIH1	NM_005744	ARI // HARI // HHARI // UBCH7BP	3600744	chr15	+	70553731	70666726	8.09
RNA binding motif protein, X-linked 2	RBMX2	NM_016024	CGI-79	3990795	chrX	+	129356824	129381607	8.09
family with sequence similarity 29, member A	FAM29A	NM_017645	MGC102696 // MGC138798 // MGC138799 // RP11-296P7.3	3200611	chr9	–	19042752	19093153	8.09
NGFI-A binding protein 1 (EGR1 binding protein 1)	NAB1	NM_005966	—	2520225	chr2	+	191205069	191437200	8.08
zinc finger protein 706	ZNF706	NM_001042510 // NM_001042511 // NM_016096	HSPC038 // PNAS-106 // PNAS-113	3147020	chr8	–	102226101	102376609	8.08
chaperonin containing TCP1, subunit 4 (delta)	CCT4	NM_006430	Cctd // MGC126164 // MGC126165 // SRB	2555630	chr2	–	61939693	61970469	8.07
zinc finger, CCHC domain containing	ZCCHC8	NM_017612	DKFZp434E2220	3475679	chr12	–	121522105	121551469	8.07
methyltransferase like 2B // methyltransferase like 2A	METTL2B // METTL2A	NM 018396 // NM_001005372 // NM_181725	FLJ11350 // FLJ12760 // METL // METTL2 // METTL2A // PSENIP1	3730211	chr17	+	57854988	57881176	8.06

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
fibrosin 1	FBS1	NM_022452	FBS // FLJ11618	3656362	chr16	+	30577810	30590035	8.06
splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot homolog, *Drosophila*)	SFRS8	NM_004592	SWAP	3438417	chr12	+	130761587	130852472	8.05
CCR4-NOT transcription complex, subunit 7	CNOT7	NM_013354 // NM_054026	CAF1 // hCAF-1	3125775	chr8	–	17128912	17148758	8.05
BTB (POZ) domain containing 7	BTBD7	NM_001002860 // NM_018167	DKFZp686N0544 // FUP1 // MGC48310	3577277	chr14	–	92773656	92966460	8.05
chromosome 17 open reading frame 79	C17orf79	NM_018405	FLJ21119 // HSA272196 // TTP1	3752424	chr17	–	27203014	27210424	8.04
transcription factor 12 (HTF4, helix-loop-helix transcription factors 4)	TCF12	NM_003205 // NM_207036 // NM_207037 // NM_207038 // NM_207040	HEB // HTF4 // HsT17266	3595096	chr15	+	54963208	55402126	8.03
ATP binding domain 1 famliy, member B	ATPBD1B	NM_018066	FLJ10349	2402838	chr1	–	27073870	27089311	8.03
PRP3 pre-mRNA processing facter 3 homolog (*S. cerevisiae*) // KIAA0460	PRPF3 // KIAA0460	NM_004698 // NM_015203	HPRP3 // HPRP3P // PRP3 // Prp3p // RP18 // FLJ32145 // HSPC099	2358171	chr1	+	148560583	148592321	8.03
G1 to S phase transition 1	GSPT1	NM_002094	551G9.2 // ETF3A // GST1 // eRF3a	3680610	chr16	–	11865619	11917408	8.00
zinc finger protein 408	ZNF408	NM_024741	FLJ12827	3329461	chr11	+	46678944	46684037	7.99
chromosome 20 open reading frame 4	C20orf4	NM_015511	CGI-23 // DKFZp564N1363 // bA234K24.2	3883787	chr20	+	34287657	34322234	7.99
DnaJ (Hsp40) homolog, subfamily A, member 2	DNAJA2	NM_005880	CPR3 // DJA2 // DNAJ // DNJ3 // HIRIP4 // PRO3015 // RDJ2	3690084	chr16	–	45546783	45565155	7.98
splicing factor, arginine/serine-rich 10 (transformer 2 homolog, *Drosophila*)	SFRS10	NM_004593	DKFZp686F18120 // Htra2-beta // SRFS10 // TRA2-BETA // TRA2B	2709062	chr3	–	187048509	187160523	7.98
trinucleotide repeat containing 6A	TNRC6A	NM_020847 // NM_014494	CAGH26 // DKFZp666E117 // FLJ22043 // GW1 // GW182 // KIAA1460 // MGC75384 // TNRC6	3653398	chr16	+	24583665	24748478	7.98
testis expressed sequence 10	TEX10	NM_017746	FLJ20287 // bA208F1.2	3217807	chr9	–	102104197	102155471	7.98
nucleoporin 107 kDa	NUP107	NM_020401	NUP84	3421177	chr12	+	67366998	67423025	7.97
hypoxia-inducible factor 1, alpha subunit inhibitor	HIF1AN	NM_017902	DKFZp762F1811 // FIH1 // FLJ20615 // FLJ22027	3260666	chr10	+	102279093	102303662	7.97

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
myosin IE	MYO1E	NM_004998	HuncM-IC // MGC104638 // MYO1C	3626826	chr15	−	57215720	57452363	7.97
v-ref murine sarcoma 3611 viral oncogene homolog	ARAF	NM_001654	A-RAF // ARAF1 // PKS2 // RAFA1	3976299	chrX	+	47300826	47316249	7.96
nucleolar protein family 6 (RNA-associated)	NOL6	NM_130793 // NM_022917 // NM_139235	FLJ21959 // MGC14896 // MGC14921 // MGC20838 // NRAP // UTP22 // bA311H10.1	3203582	chr9	−	33442676	33464087	7.96
chromosome 21 open reading frame 66	C21orf66	NM_145328 // NM_013329 // NM_016631 // NM_058191	BM-020 // FLJ90561 // GCFC	3929395	chr21	−	33028084	33066030	7.96
casein kinase 1, alpha 1	CSNK1A1	NM_001025105 // NM_001892	CK1 // HLCDGP1 // PRO2975	2880932	chr5	−	148800168	148922811	7.96
hypothetical protein DKFZp762E1312	DKFZp762E1312	NM_018410	hFLEG1	2604254	chr2	−	234406876	234427931	7.95
PRP6 pre-mRNA processing factor 6 homolog (*S. cerevisiae*)	PRPF6	NM_012469	ANT-1 // C20orf14 // TOM // U5-102K // hPrp6	3893849	chr20	+	62082901	62134891	7.95
tumor suppressing subtransferable candidate 4	TSSC4	NM_005706	—	3317338	chr11	+	2378304	2381662	7.93
cell division cycle 25 homolog B (*S. pombe*)	CDC25B	NM_004358 // NM_021872 // NM_021873	—	3874438	chr20	+	3715655	3734756	7.93
megakaryobiastic leukemia (translocation) 1	MKL1	NM_020831	BSAC // MAL // MRTF-A	3961496	chr22	−	39136248	39362660	7.93
topoisomerase (DNA) I	TOP1	NM_003286	TOPI	3885464	chr20	+	39090891	39186535	7.93
WW domain containing adapter with coiled-coil	WAC	NM_016628 // NM_100264 // NM_100486	BM-016 // MGC10753 // PRO1741 // Wwp4 // bA48B24 //	3240340	chr10	+	28828043	29005095	7.92
ubiquitin specific peptidase 36	USP36	NM_025090	DUB1	3772581	chr17	−	74295075	74348574	7.92
t-complex 1	TCP1	NM_001008897 // NM_030752	CCT-alpha // CCT1 // CCTa // D6S230E // TCP-1-alpha	2982381	chr6	−	160119521	160130731	7.92
protein phosphatase 6, catalytic subunit	PPP6C	NM_002721	—	3225348	chr9	−	126948675	126991992	7.91
CDC-like kinase 3	CLK3	NM_001292 // NM_003992	FLJ22858	3601741	chr15	+	72677906	72719105	7.91
anillin, actin binding protein	ANLN	NM_018685	ANILLIN // DKFZp779A055 // Scraps // scra	2997376	chr7	+	36395957	36462017	7.90
adenosylmethionine decarboxylase 1	AMD1	NM_001033059 // NM_001634	ADOMETDC // AMD // DKFZp313L1234 // FLJ26964	2921296	chr6	+	111287588	111324441	7.90

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
farnesyl-diphosphate farnesyltransferase 1	FDFT1	NM_004462	DGPT // ERG9 // SQS // SS	3086206	chr8	+	11690497	11740987	7.90
PRP40 pre-mRNA processing factor 40 homolog A (*S. cerevisiae*)	PRPF40A	XM_371575 // XM_938514	FBP-11 // FBP11 // FLAF1 // FLJ20585 // FNBP3 // HIP10 // HYPA // NY-REN-6	2581548	chr2	−	153212414	153283546	7.89
death effector domain containing	DEDD	NM_001039711 // NM_001039712 // NM_032998	CASP8IP1 // DEDD1 //DEFT // FLDED1 // KE05	2440625	chr1	−	159357395	159369167	7.89
integrin, beta 6	ITGB6	NM_000888	—	2583465	chr2	−	160664438	160818586	7.88
zinc finger protein 473	ZNF473	NM_001006656 // NM_015428	HZFP100 // ZN473	3839142	chr19	+	55220811	55248476	7.87
HLA-B associated transcript 1 // ATPase, H+ transporting, lysosomal 13 kDa, V1 subunit G2	BAT1 // ATP6V1G2	NM_004640 // NM_080598 // NM_130463 // NM_138282	D6S81E // DDX39B // UAP56 // ATP6G // ATP6G2 // NG38 // VMA10	2949038	chr6	−	31605990	31622606	7.87
casein kinase 2, alpha 1 polypeptide // casein kinase 2, alpha 1 polypeptide pseudogene	CSNK2A1 // CSNK2A1P	NM_001895 // NM_177559 // NM_177560 // NR_002207	CK2A1 // CKII // CKII alpha // —	3894228	chr20	−	402069	472534	7.87
peroxisome proliferator-activated receptor gamma, coactivator-related 1	PPRC1	NM_015062	KIAA0595 // MGC74642 // PRC // RP11-302K17.6	3261447	chr10	+	103882745	103900072	7.86
YME1-like 1 (*S. cerevisiae*)	YME1L1	NM_014263 // NM_139312 // NM_139313	FTSH // MEG4 // PAMP // YME1L	3282213	chr10	−	27439066	27484191	7.84
thyroid hormone receptor associated protein 1	THRAP1	NM_005121	ARC250 // DRIP250 // HSPC221 // KIAA0593 // MED13 // TRAP240	3765689	chr17	−	57374750	57498031	7.84
YTH domain family, member 1	YTHDF1	NM_017798	C20orf21 //	3913712	chr20	−	61297230	61330873	7.83
B-cell CLL/lymphoma 7B	BCL7B	NM_001707 // NM_138707	—	3056108	chr7	−	72588624	72610244	7.82
HIR histone cell cycle regulation defective homolog A (*S. cerevisiae*)	HIRA	NM_003325	DGCR1 // TUP1 // TUPLE1	3952637	chr22	−	17696576	17799452	7.82
Josephin domain containing 3 // small nucleolar RNA, H/ACA box 25 // small nucleoler RNA, H/ACA box 32 // small nucleolar RNA, H/ACA	JOSD3 // SNORA25 // SNORA32 // SNORA18	NM_024116 // NR_003028 // NR003032 // NR_002959	MGC5306 // ACA25 // ACA32 // ACA18	3386814	chr11	−	93102831	93114308	7.81
GTP binding protein 4	GTPBP4	NM_012341	CRFG // FLJ10686 // FLJ10690 // // FLJ39774 // NGB	3231774	chr10	+	942450	1055862	7.79
eukaryotic translation elongation factor 1 beta 2	EEF1B2	NM_001037663 // NM_001959 // NM_021121	EEF1B // EEF1B1 // EF1B	2524577	chr2	+	206732303	206735884	7.78
SMAD family member 5	SMAD5	NM_001001419 // NM_001001420 //	DKFZp781C1895 // DKFZp781O1323 //	2830010	chr5	+	135464462	135552314	7.77

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
		NM_005903	Dwfc // JV5-1 // MADH5						
epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	EGFR	NM_005228 // NM_201282 // NM_201283 // NM_201284	ERBB // ERBB1 // mENA	3002640	chr7	+	55054070	55291773	7.77
mitogen-activated protein kinase kinase kinase 11	MAP3K11	NM_002419	MGC17114 // MLK-3 // MLK3 // PTK1 // SPRK	3377752	chr11	–	65121806	65139693	7.77
apoptosis inhibitor 5	API5	NM_006595	AAC-11 // AAC11 // API5L1	3327906	chr11	+	43290109	43322649	7.77
coiled-coil-helix-coiled-coil-helix domain containing 3	CHCHD3	NM_017812	FLJ20420	3073597	chr7	–	132062426	132500566	7.75
TBC1 domain family, member 10B	TBC1D10B	NM_015527	DKFZP434P1750 // FP2461	3687715	chr16	–	30275789	30289100	7.74
nucleolar protein NOP5/NOP58	NOP5/NOP58	NM_015934	HSPC120	2523144	chr2	+	202811346	202926967	7.73
ribosomal protein S6 kinase, 70 kDa, polypeptide 1	RPS6KB1	NM_003161	PS6K // S6K // S6K1 // STK14A // p70(S6K)-alpha // p70-S6K // p70-alpha	3729294	chr17	+	55325239	55429105	7.73
GDP dissociation inhibitor 1	GDI1	NM_001493	FLJ41411 // GDIL // MRX41 // MRX48 // OPHN2 // RABGD1A // RABGDIA // XAP-	3996404	chrX	+	153318480	153324978	7.73
PHD finger protein 12	PHF12	NM_001033561 // NM_020889	KIAA1523 // MGC131914 // PF1	3751184	chr17	–	24256404	24302905	7.73
Smad nuclear interacting protein 1	SNIP1	NM_024700	FLJ12553 // RP3-423B22.3 // dJ423B22.2	2407163	chr1	–	37774050	37792490	7.72
stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein)	STIP1	NM_006819	HOP // IEF-SSP-3521 // P60 // STI1L	3334224	chr11	+	63709341	63728586	7.71
speckle-type POZ protein	SPOP	NM_001007226 // NM_001007227 // NM_001007228 // NM_001007229 // NM_001007230 // NM_003563	TEF2	3761905	chr17	–	45031245	45110541	7.71
eukaryotic translation elongation factor 1 alpha 1	EEF1A1	NM_001402	CCS-3 // CCS3 // EEF-1 // EEF1A // EF-Tu // EF1A // FLJ25721 // GRAF-1EF // HNGC: 16303 // LENG7 // MGC102687 // MGC131894 // MGC16224 // PTI1 // eEF1A-1	2960903	chr6	–	74281167	74335800	7.70

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
mitogen-activated protein kinase kinase 3	MAP2K3	XM_001130488 // NM_145110 // NM_002756 // NM_145109	MAPKK3 // MEK3 // MKK3 // PRKMK3	3714729	chr17	+	21128581	21159113	7.70
DEAD (Asp-Glu-Ala-Asp) box polypeptide 18 // wingless-type MMTV integration site family.	DDX18 // WNT8B	NM_006773 // NM_003393	FLJ33908 // MrDb // —	2502300	chr2	+	118243834	118323562	7.70
ATPase family, AAA domain containing 2	ATAD2	NM_014109	DKFZp667N1320 // MGC131938 // MGC142216 // MGC29843 // MGC5254 //	3151534	chr8	−	124393174	124477871	7.69
chromosome 1 open reading frame 160	C1orf160	NM_032125	DKFZP564D0478 // MGC111002 // RP11-4K3_A.4	2326954	chr1	+	27521221	27535639	7.69
RNA binding motif protein 5	RBM5	NM_005778	FLJ39876 // G15 // H37 // LUCA15 // RMB5	2622469	chr3	+	50101372	50134000	7.69
thioredoxin domain containing 9 // lysozyme-like	TXNDC9 // LYG2	NM_005783 // NM_175735	APACD // LYGH // MGC119046 // MGC119047 // MGC119049	2566740	chr2	−	99301923	99319337	7.69
zinc finger protein 148	ZNF148	NM_021964	BERF-1 // BFCOL1 // HT-BETA // ZBP-89 // ZFP148 // pHZ-52	2693081	chr3	−	126427204	126577074	7.69
insulin receptor substrate 2	IRS2	NM_003749	—	3525234	chr13	−	109196024	109238228	7.68
interleukin enhancer binding factor 3, 90 kDa	ILF3	NM_004516 // NM_012218 // NM_153464	DRBF // DRBP76 // MMP4 // MPHOSPH4 // MPP4 // NF-AT-90 // NF90 // NFAR // NFAR-1 // TCP80	3820663	chr19	+	10625547	10664074	7.68
ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)	UBE2J1	NM_016021	CGI-76 // HSPC153 // HSPC205 // HSU93243 // MGC12555 // NCUBE1 // Ubc6p	2964200	chr6	−	90093065	90119338	7.66
START domain containing 7	STARD7	NM_020151 // NM_139267	GTT1	2565143	chr2	−	96214334	96238296	7.65
DPH1 homolog (*S. cerevisiae*) // candidate tumor suppressor in ovarian cancer 2	DPH1 // OVCA2	NM_001383 // NM_080822	DPH2L // DPH2L1 // FLJ33211 // OVCA1 // —	3706071	chr17	+	1874907	1895099	7.64
non-POU domain containing, octamer-binding	NONO	NM_007363	NMT55 // NRB54 // P54 // P54NRB	3980887	chrX	+	70420006	70437726	7.64
scaffold attachment factor B2	SAFB2	NM_014649	KIAA0138	3847252	chr19	−	5533105	5575015	7.64
WD repeat domain 3	WDR3	NM_006784	FLJ12796	2354082	chr1	+	118273827	118304572	7.63
metal response element binding	MTF2	NM_007358	M96 // PCL2 //	2346934	chr1	+	93147511	93377202	7.63

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
transcription factor 2			RP5-976O13.1 // dJ976O13.2						
general transcription factor IIIC, polypeptide 2, beta 110 kDa	GTF3C2	NM_001035521 // NM_001521	KIAA0011 // TFIIIC-BETA // TFIIIC110	2545681	chr2	–	27402231	27433372	7.63
general transcription factor IIH, polypeptide 1, 62 kDa	GTF2H1	NM_005316	BTF2 // TFIIH	3322717	chr11	+	18300412	18345156	7.62
mitochondrial ribosomal protein L17	MRPL17	NM_022061	MRP-L26 // RPL17L // RPML26	3361116	chr11	–	6657673	6690484	7.62
Yip1 domain family, member 3 // chromosome 6 open reading frame 154	YIPF3 // C6orf154	NM_015388 // NM_001012974	C6orf109 // DKFZP566C243 // FinGER3 // KLIP1 // dJ337H4.3 // FLJ44836 // MGC131686 // dJ337H4.2	2954646	chr6	–	43587500	43592701	7.61
eukaryotic translation initiation factor 4 gamma, 2	EIF4G2	NM_001042559 // NM_001418	AAG1 // DAP5 // FLJ41344 // NAT1 // p97	3362719	chr11	–	10487574	10788746	7.60
MYST histone acetyltransferase 2	MYST2	NM_007067	HBO1 // HBOA	3725779	chr17	+	45196447	45261455	7.60
SIN3 homolog A, transcription regulator (yeast)	SIN3A	NM_015477	DKFZP434K2235 // FLJ90319 // KIAA0700	3633403	chr15	–	73448786	73535167	7.60
centaurin, delta 1	CENTD1	NM_015230 // NM_139182	ARAP2 // FLJ13675 // FLJ44916 // KIAA0580 // PARX	2765590	chr4	–	35626248	35922356	7.60
KIT ligand	KITLG	NM_000899 // NM_003994	DKFZp686F2250 // KL-1 // Kitl // MGF // SCF // SF	3464747	chr12	–	87349442	87498371	7.58
F-box and leucine-rich repeat protein 11	FBXL11	NM_012308	CXXC8 // DKFZP434M1735 // FBL11 // FBL7 // FLJ00115 // FLJ46431 // JHDM1A // KIAA1004 // LILINA	3336696	chr11	+	66643299	66782124	7.57
POM (POM121 homolog, rat) and ZP3 fusion	POMZP3	NM_012230 // NM_152992	MGC8359 // POM-ZP3 // POM121	3057755	chr7	–	76037679	76196100	7.56
VAMP (vesicle-associated membrane protein)-associated protein A, 33 kDa	VAPA	NM_003574 // NM_194434	MGC3745 // VAP-33 // VAP-A // VAP33 // hVAP-33	3778601	chr18	+	9903984	9950012	7.56
integrin beta 4 binding protein	ITGB4BP	NM_002212 // NM_181466 // NM_181467 // NM_181468 // NM_181469	CAB // EIF3A // EIF6 // b(2)gcn // p27BBP	3903836	chr20	–	33276003	33336225	7.55
chromosome 10 open reading frame 119	C10orf119	NM_024834	FLJ13081 // FLJ36756	3309755	chr10	–	121568302	121642742	7.55

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
chromosome 11 open reading frame 57	C11orf57	NM_018195	FLJ10726	3348891	chr11	+	111450087	111461067	7.54
heat shock protein 90 kDa alpha (cytosolic), class A member 1 // heat shock protein 90 kDa alpha (cytosolic), class A member 2 // heat shock protein 90 kDa alpha (cytosolic), class A member 6 (pseudogene)	HSP90AA1 // HSP90AA2 // HSP90AA6P	NM_001017963 // NM_005348 // NM_001040141 // —	FLJ31884 // HSP86 // HSP90A // HSP90N // HSPC1 // HSPCA // HSPCAL1 // HSPCAL4 // HSPN // Hsp89 // Hsp90 // LAP2 // HSP90ALPHA // HSPCAL3 //	3580179	chr14	–	101616842	101676327	7.53
peroxisomal biogenesis factor 5	PEX5	NM_000319	PTS1R // PXR1	3403299	chr12	+	7232607	7262437	7.53
chromosome 4 open reading frame 30	C4orf30	NM_017741	FLJ20280 // MGC126765 // MGC126767	2762468	chr4	–	17404173	17421482	7.53
transmembrane protein 2	TMEM2	NM_013390	—	3209384	chr9	–	73452177	73573229	7.52
forkhead box M1	FOXM1	NM_021953 // NM_202002 // NM_202003	FKHL16 // FOXM1B // HFH-11 // HFH11 // HNF-3 // INS-1 // MPHOSPH2 // MPP-2 // MPP2 // PIG29 // TRIDENT	3440598	chr12	–	2836207	2856564	7.52
ceramide kinase	CERK	NM_022766 // NM_182661	DKFZp434E0211 // FLJ21430 // FLJ23239 // KIAA1646 // LK4 // MGC131878 // dA59H18.2 // dA59H18.3 // hCERK	3964154	chr22	–	45454343	45537349	7.52
small nuclear ribonucleoprotein 70 kDa polypeptide (RNP antigen)	SNRP70	NM_001009820 // NM_003089	RNPU1Z // RPU1 // U170K // U1AP // U1RNP	3838185	chr19	+	54280358	54304714	7.52
anthrax toxin receptor 2	ANTXR2	NM_058172	CMG-2 // CMG2 // FLJ31074 // ISH // JHF // MGC111533 // MGC45856	2774971	chr4	–	80762874	81219758	7.51
antizyme inhibitor 1	AZIN1	NM_015878 // NM_148174	MGC3832 // MGC691 // OAZI // OAZIN // ODO1L	3147591	chr8	–	103907725	103953967	7.51
chromosome 12 open reading frame 44	C12orf44	NM_021934	FLJ11773	3415273	chr12	+	50749317	50757534	7.51
cofactor required for Sp1 transcriptional activation, subunit 6, 77 kDa	CRSP6	NM_004268	CRSP77 // DRIP80 // FLJ10812 // MED17 // TRAP80	3344897	chr11	+	93157019	93186225	7.49
KIAA1967	KIAA1967	NM_021174 // NM_199205	DBC-1 // DBC1	3089597	chr8	+	22518038	22534618	7.49

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
serologically defined colon cancer antigen 3 // small nuclear RNA activating complex, polypeptide 4, 190 kDa	SDCCAG3 // SNAPC4	NM_001039707 // NM_001039708 // NM_006643 // NM_003086	NY-CO-3 // FLJ13451 // PTFalpha // SNAP190	3229943	chr9	–	138416210	138425418	7.49
potassium channel tetramerisation domain containing 10	KCTD10	NM_031954	FLJ41739 // MSTP028 // ULRO61	3470793	chr12	–	108370845	108399528	7.48
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13 kDa	NDUFA5	NM_005000	B13 // CI-13KD-B // DKFZp781K1356 // FLJ12147 // NUFM // UQOR13	3070658	chr7	–	122968075	122985216	7.48
interferon stimulated exonuclease gene 20 kDa-like 1	ISG20L1	NM_022767	AEN // FLJ12484 // FLJ12562 // pp12744	3607232	chr15	+	86948254	86976501	7.47
paxillin	PXN	NM_002859	FLJ16691	3474372	chr12	–	119132644	119187926	7.47
synaptotagmin binding, cytoplasmic RNA interacting protein	SYNCRIP	NM_006372	GRY-RBP // HNRPQ1 // NSAP1 // RP1-3J17.2 // dJ3J17.2 // pp68	2963407	chr6	–	86374062	86410282	7.47
proteasome (prosome, macropain) 26S subunit, non-ATPase, 6	PSMD6	NM_014814	KIAA0107 // S10 // SGA-113M // p44S10	2679864	chr3	–	63971281	63984700	7.47
chromosome 7 open reading frame	C7orf30	NM_138446	—	2992863	chr7	+	23305462	23317894	7.46
heterogeneous nuclear ribonucleoprotein K	HNRPK	NM_002140 // NM_031262 // NM_031263	CSBP // FLJ41122 // HNRNPK // TUNP	3212294	chr9	–	85772377	85785355	7.45
heterogeneous nuclear ribonucleoprotein L	HNRPL	NM_001005335 // NM_001533	FLJ35509 // P/OKcl.14 // hnRNP-L	3861617	chr19	–	44018883	44034809	7.45
SEC14-like 1 (*S. cerevisiae*)	SEC14L1	NM_001039573 // NM_003003	DKFZp686C06176 // PRELID4A // SEC14L	3735752	chr17	+	72596335	72767744	7.45
hippocampus abundant transcript-like 1	HIATL1	XM_001130181 // NM_032558	FLJ14753 // MGC117350	3180263	chr9	+	96176674	96325754	7.43
eukaryotic translation initiation factor 5A	EIF5A	NM_001970	EIF-5A // EIF5A1 // MGC104255 // MGC99547 // uORF // uORF A	3708422	chr17	+	7151037	7156478	7.42
discoidin, CUB and LCCL domain containing 2	DCBLD2	NM_080927	CLCP1 // ESDN	2686023	chr3	–	99997526	100124598	7.42
voltage-dependent anion channel 2	VDAC2	NM_003375	FLJ23841	3252577	chr10	+	76639941	76661389	7.41
polycomb group ring finger 3	PCGF3	NM_006315	DKFZp686D20235 // DONG1 // FLJ36550 // FLJ43813 // MGC129615 // MGC40413 // RNF3 // RNF3A	2714230	chr4	+	689573	754428	7.41
NADH dehydrogenase (ubiquinone) Fe—S protein 3, 30 kDa (NADH-coenzyme Q reductase)	NDUFS3	NM_004551	—	3329904	chr11	+	47557156	47562663	7.41

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
signal recognition particle 68 kDa	SRP68	NM_014230	—	3771297	chr17	–	71546467	71580323	7.41
thioredoxin reductase 1	TXNRD1	NM_003330 // NM_182729 // NM_182742 // NM_182743	GRIM-12 // MGC9145 // TR // TR1 // TRXR1 // TXNR	3429460	chr12	+	103130628	103354079	7.39
PDZ domain containing 8	PDZD8	NM_173791	FLJ25412 // FLJ34427 // PDZK8 // bA129M16.2	3308619	chr10	–	119029422	119124958	7.39
IKAROS family zinc finger 5 (Pegasus)	IKZF5	NM_022466	DKFZp781B0249 // FLJ22973 // PEGASUS //	3310757	chr10	–	124740316	124774190	7.38
TPX2, microtubule-associated, homolog (*Xenopus laevis*)	TPX2	NM_012112	C20orf1 // C20orf2 // DIL-2 // DIL2 // FLS353 // GD: C20orf1 // HCA519 // HCTP4 //	3881443	chr20	+	29774755	29853260	7.37
RNA binding motif protein 39	RBM39	NM_184237 // NM_184241 // NM_184244 // NM_004902 // NM_184234	CAPER // CAPERalpha // CC1.3 // DKFZp781C0423 // FLJ44170 // HCC1 // RNPC2	3904226	chr20	–	33754569	33793768	7.35
ubiquitin specific peptidase 53	USP53	NM_019050	DKFZp781E1417	2741236	chr4	+	120353195	120436746	7.35
vesicle-associated membrane protein 3 (cellubrevin)	VAMP3	NM_004781	CEB	2318637	chr1	+	7753916	7764072	7.35
DEAH (Asp-Glu-Ala-His) box polypeptide 36	DHX36	NM_020865	DDX36 // KIAA1488 // MLEL1	2701595	chr3	–	155475346	155524965	7.33
fibronectin type III domain containing 3B	FNDC3B	NM_022763	DKFZp686D14170 // DKFZp762K137 // FAD104 // FLJ23399 // MGC10002 // PRO4979 // YVTM2421	2652410	chr3	+	173240112	173601176	7.33
E74-like factor 1 (ets domain transcription factor)	ELF1	NM_172373	—	3511031	chr13	–	40394613	40533811	7.32
keratin 19	KRT19	NM_002276	CK19 // K19 // K1CS // MGC15366	3757108	chr17	–	36933431	36938160	7.32
Integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	ITGA2	NM_002203	BR // CD49B // GPIa // VLA-2 // VLAA2	2809245	chr5	+	52320949	52432778	7.31
ribosomal protein L30	RPL30	NM_000989	—	3145953	chr8	–	99123079	99127371	7.31
IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)	IMP4	NM_033416	BXDC4 // MGC19606	2505501	chr2	+	130816288	130828310	7.31
origin recognition complex, subunit 2-like (yeast)	ORC2L // MGC39518	NM_006190	ORC2	2594569	chr2	–	201482783	201536750	7.31
Kruppel-like factor 10	KLF10	NM_001032282 // NM_005655	EGRA // TIEG // TIEG1	3147508	chr8	–	103682306	103767558	7.30
tight junction protein 1 (zona occludens 1)	TJP1	NM_003257 // NM_175610	DKFZp686M05161 // MGC133289 // ZO-1	3615579	chr15	–	27703228	28048334	7.30

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Array	Human Genome hg18				Fold Change
				Transcript Cluster ID	Chromosome	Strand	Start	Stop	
tRNA 5-methylaminomethyl-2-thiouridylate methyltransferase	TRMU	NM_018006	MGC99627 // MTO2 // MTU1 // TRMT // TRMT1 // TRNT1	3949097	chr22	+	45109982	45131896	7.29
ribosomal protein L18	RPL18	NM_000979	—	3867223	chr19	–	53810441	53814585	7.29
Nance-Horan syndrome (congenital cataracts and dental anomalies)	NHS	XM_001134060 // NM_198270	DKFZp781F2016 // DKFZp781L0254 // SCML1	3970338	chrX	+	17303441	17664033	7.29
chromosome 16 open reading frame 72	C16orf72	NM_014117	FLJ41272 // PRO0149	3647632	chr16	+	9092682	9121055	7.28
ubiquitin specific peptidase 10	USP10	NM_005153	KIAA0190 // MGC2621 // UBPO	3671873	chr16	+	83291080	83371023	7.27
A kinase (PRKA) anchor protein (gravin) 12	AKAP12	NM_005100 // NM_144497	AKAP250 // DKFZp686M0430 // DKFZp686O0331	2931569	chr6	+	151602720	151721361	7.27
ornithine decarboxylase 1	ODC1	NM_002539	—	2540157	chr2	–	10485474	10606340	7.27
matrin 3	MATR3	NM_018834 // NM_199189	DKFZp686K0542 // DKFZp686K23100 // KIAA0723 // MGC9105	2831124	chr5	+	138505686	138695245	7.26
chromosome 5 open reading frame 22	C5orf22	NM_018356	DKFZp667N066 // FLJ11193 // FLJ23805 // MGC33010	2805176	chr5	+	31568161	31590902	7.26
nuclear mitotic apparatus protein 1	NUMA1	NM_006185	NUMA	3380901	chr11	–	71389909	71469367	7.25
macrophage erythroblast attacher	MAEA	NM_001017405 // NM_005882	EMP // HLC-10 // PIG5	2714672	chr4	+	1273702	1323891	7.25
nucleolar protein 8	NOL8	NM_017948	C9orf34 // DKFZp686P12242 // FLJ20736 // Nop132 // bA62C3.3 // bA62C3.4	3214749	chr9	–	94099471	94127688	7.25
proliferation-associated 2G4, 38 kDa // dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	PA2G4 // DLST	NM_006191 // NM_001933	EBP1 // HG4-1 // p38-2G4 // DLTS	3417309	chr12	+	54784566	54793956	7.23
mitochondrial ribosomal protein L46	MRPL46	NM_022163	C15orf4 // LIECG2 // MGC22762 //	3638048	chr15	–	86795015	86811600	7.23
phosphatidylinositol glycan anchor biosynthesis, class G	PIGG	NM_017733	FLJ20265 // FLJ39925 // GP17 // LAS21 // MGC131903 // PRO4405 // RLGS1930	2714025	chr4	+	483010	523985	7.22
SON DNA binding protein	SON	NM_032195 // NM_138927	BASS1 // C21orf50 // DBP-5 // FLJ21099 // FLJ33914 //	3918696	chr21	+	33836804	33872881	7.20

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
			KIAA1019 // NREBP // SON3						
kelch-like ECH-associated protein 1 // ADAM metallopeptidase with thrombospondin type 1 motif, 6	KEAP1 // ADAMTS6	NM_012289 // NM_203500 // NM_197941	INrf2 // KIAA0132 // KLHL19 // MGC10630 // MGC1114 // MGC20887 // MGC4407 // MGC9454 // ADAM-	3850363	chr19	−	10457571	10475233	7.20
bromodomain containing 2	BRD2	NM_005104	D6S113E // DKFZp686N0336 // FLJ31942 // FSRG1 // KIAA9001 // NAT // RING3 // RNF3	2903343	chr6	+	33044392	33057253	7.20
squalene epoxidase	SQLE	NM_003129	—	3114832	chr8	+	126063738	126105522	7.20
lamin B receptor	LBR	NM_002296 // NM_194442	DHCR14B // LMN2R // MGC9041 // PHA	2458289	chr1	−	223655840	223683230	7.19
Ewing sarcoma breakpoint region 1	EWSR1	NM_005243 // NM_013986	EWS	3941907	chr22	+	27994201	28026501	7.19
chromosome 19 open reading frame 48	C19orf48	NM_199249 // NM_199250	MGC13170	3868659	chr19	−	55992774	56012596	7.17
upstream transcription factor 1 // Rho GTPase activating protein 30	USF1 // ARHGAP30	NM_007122 // NM_207005 // NM_001025598 // NM_181720	FCHL // FCHL1 // HYPLIP1 // MLTF // MLTF1 // UEF // FLJ00267 // FLJ44128 // RP11-544M22.6	2440523	chr1	−	159275665	159282355	7.17
WD repeat domain 46	WDR46	NM_005452	BING4 // C6orf11 // FP221	2950561	chr6	−	33354871	33365259	7.16
topoisomerase (DNA) II alpha 170 kDa	TOP2A	NM_001067	TOP2 // TP2A	3756193	chr17	−	35717597	35847034	7.15
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit E	ATP5I	NM_007100	ATP5K // MGC12532	2756497	chr4	−	654679	658269	7.14
splicing factor 3b, subunit 2, 145 kDa	SF3B2	NM_006842	SAP145 // SF3B145 // SF3b1 // SF3b150	3335907	chr11	+	65573499	65593343	7.14
splicing factor, arginine/serine-rich 11	SFRS11	NM_004768	DKFZp686M13204 // dJ677H15.2 // p54	2341565	chr1	+	70443686	70492014	7.12
aminopeptidase puromycin sensitive	NPEPPS	XM_001128588 // NM_006310	MP100 // PSA	3724698	chr17	+	42955347	43057168	7.11
influenza virus NS1A binding protein	IVNS1ABP	NM_006469 // NM_016389	DKFZp686K06216 // FLARA3 // FLJ10069 // FLJ10411 // FLJ10962 // FLJ35593 // FLJ36593 // HSPC068 // KIAA0850 // ND1 // NS-1 // NS1-BP //	2448073	chr1	−	183532162	183553081	7.10

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
Smg-7 homolog, nonsense mediated mRNA decay factor (*C. elegans*)	SMG7	NM_014837 // NM_173156 // NM_201568 // NM_201569	C1orf16 // EST1C // FLJ23717 // KIAA0250 // SGA56M // SMG-7	2371255	chr1	+	181708036	181834004	7.09
helicase with zinc finger	HELZ	NM_014877	DRHC // HUMORF5 // KIAA0054 // MGC163454	3768015	chr17	−	62485987	62672547	7.08
cytochrome P450, family 1, subfamily B. polypeptide 1	CYP1B1	NM_000104	CP1B // GLC3A	2548699	chr2	−	38138730	38196009	7.08
sprouty homolog 2 (*Drosophila*)	SPRY2	NM_005842	MGC23039 //	3519309	chr13	−	79683810	79813918	7.07
golgi phosphoprotein 4	GOLPH4	NM_014498	GIMPC // GPP130 // P138	2704267	chr3	−	169208832	169296426	7.07
Rab geranylgeranyltransferase, beta subunit // mutS homolog 4 (*E. coli*)	RABGGTB // MSH4	NM_004582 // NM_002440	GGTB // —	2342624	chr1	+	76024474	76033333	7.07
angiomotin like 2	AMOTL2	NM_016201	LCCP	2696309	chr3	−	135527277	135576097	7.06
MAK10 homolog, amino-acid N-acetyltransferase subunit, (*S. cerevisiae*)	MAK10	NM_024635	FLJ21613 // FLJ22643 // bA379P1.1	3177563	chr9	+	87733620	87828205	7.06
NOL1/NOP2/Sun domain family, member 2	NSUN2	NM_017755	FLJ20303 // SAKI // TRM4	2847292	chr5	−	6510634	6686394	7.06
leptin receptor overlapping transcript-like 1	LEPROTL1	NM_015344	HSPC112 // Vps55 // my047	3092276	chr8	+	30059542	30115386	7.06
geminin, DNA replication inhibitor	GMNN	NM_015895	Gem // RP3-	2898597	chr6	+	24857262	24894306	7.06
FAT tumor suppressor homolog 1 (*Drosophila*)	FAT	NM_005245	CDHF7 // FAT1 // ME5 // hFat1	2797393	chr4	−	187745970	187885048	7.05
forkhead box J3	FOXJ3	NM_014947	—	2408855	chr1	−	42414807	42574125	7.05
nucleoporin 54 kDa	NUP54	NM_017426	MGC13407	2773997	chr4	−	77254731	77288679	7.04
kinesin family member 5B	KIF5B	NM_004521	KINH // KNS // KNS1 // UKHC	3283991	chr10	−	32337798	32385342	7.04
interferon gamma receptor 1	IFNGR1	NM_000416	CD119 // FLJ45734 // IFNGR	2976113	chr6	−	137560317	137582279	7.04
mortality factor 4 like 2	MORF4L2	NM_012286	KIAA0026 // MORFL2 // MRGX	4016572	chrX	−	102817114	102844278	7.03
mastermind-like 1 (*Drosophila*)	MAML1	XM_001126853 // NM_014757	KIAA0200 // Mam-1 // Mam1	2844410	chr5	+	179092457	179151795	7.03
zinc finger and BTB domain containing 11	ZBTB11	NM_014415	FLJ13426 // MGC133303 // ZNF-U69274	2686727	chr3	−	102780272	102878819	7.02
mitochondrial ribosomal protein S2	MRPS2	NM_016034	CGI-91 // MRP-S2	3193900	chr9	+	137531661	137536331	7.02
adaptor-related protein complex 2, alpha 2 subunit	AP2A2	NM_012305	ADTAB // CLAPA2 // HIP9 // HYPJ	3316447	chr11	+	912387	1002226	7.01
serine arginine-rich pre-mRNA splicing factor SR-A1	SR-A1	NM_021228	SRA1	3838757	chr19	+	54837204	54853671	7.01
NMDA receptor regulated 1	NARG1	NM_057175	Ga19 // NATH // TBDN100	2744597	chr4	+	140442091	140560627	7.00
triple functional domain (PTPRF interacting)	TRIO	NM_007118	tgat	2802398	chr5	+	14196590	14585215	7.00

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
myotubularin related protein 12	MTMR12	NM_001040446	3-PAP // PIP3AP	2852274	chr5	–	32262872	32348897	7.00
cyclin G associated kinase	GAK	XM_001127411 // NM_005255	FLJ40395 // MGC99654	2756673	chr4	–	833110	916149	7.00
GRB2-associated binding protein 1	GAB1	NM_002039 // NM_207123	—	2745547	chr4	+	144476834	144615158	7.00
senataxin	SETX	NM_015046	ALS4 // AOA2 // DKFZp781B151 // FLJ12840 // FLJ43459 // KIAA0625 // SCAR1 // bA479K20.2	3228007	chr9	–	134126584	134220359	7.00
chromosome 12 open reading frame 41	C12orf41	NM_017822	FLJ12670 // FLJ20436	3453177	chr12	–	47333281	47362268	7.00
WNK lysine deficient protein kinase 1	WNK1	NM_018979	KDP // KIAA0344 // PHA2C // PRKWNK1	3400034	chr12	+	278104	891189	6.98
myotubularin related protein 1	MTMR1	NM_003828	—	3994846	chrX	+	149612503	149684226	6.97
met proto-oncogene (hepatocyte growth factor receptor)	MET	NM_000245	HGFR // RCCP2	3020343	chr7	+	116099694	116230307	6.97
ADP-ribosylation factor 4	ARF4	XM_001132763 // NM_001660	—	2678090	chr3	–	57532172	57558635	6.96
four and a half LIM domains 2	FHL2	NM_001039492 // NM_001450 // NM_201555 // NM_201557	AAG11 // DRAL // SLIM3	2568687	chr2	–	105335877	105501005	6.96
polypyrimidine tract binding protein 1	PTBP1	NM_002819 // NM_031990 // NM_031991 // NM_175847	HNRNPI // HNRPI // MGC10830 // MGC8461 // PTB // PTB-1 // PTB-T // PTB2 // PTB3 // PTB4 // pPTB	3815165	chr19	+	747768	763505	6.96
glutamate-rich WD repeat containing 1	GRWD1	NM_031485	GRWD // KIAA1942 // RRB1 // WDR28	3837796	chr19	+	53640874	53652090	6.95
signal sequence receptor, alpha (translocon-associated protein alpha)	SSR1	NM_003144	DKFZp781N23103 // TRAPA	2940551	chr6	–	7213542	7258526	6.94
GC-rich promoter binding protein 1-like 1	GPBP1L1	NM_021639	RP11-767N6.1 // SP192	2410330	chr1	–	45865575	45926352	6.94
chromosome 20 open reading frame 72	C20orf72	NM_052865	FLJ14597 // bA504H3.4	3878220	chr20	+	17896912	17919759	6.94
ELAV (embryonic lethal, abnormal vision, *Drosophila*)-like 1 (Hu antigen R) // translocase of inner mitochondrial membrane 44 homolog (yeast)	ELAVL1 // TIMM44	NM_001419 // NM_006351	ELAV1 // HUR // Hua // MelG // DKFZp686H05241 // TIM44	3848689	chr19	–	7929463	7999655	6.93
heat shock protein 90 kDa alpha (cytosolic), class B member 1	HSP90AB1	NM_007355	D6S182 // FLJ26984 // HSP90-BETA // HSP90B // HSPC2 // HSPCB	2908474	chr6	+	44319983	44330383	6.93

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Array Transcript Cluster ID	Human Genome hg18 Chromosome	Human Genome hg18 Strand	Human Genome hg18 Start	Human Genome hg18 Stop	Fold Change
TSC22 domain family, member 2	TSC22D2	NM_014779	KIAA0669 // TILZ4a // TILZ4b // TILZ4c	2647647	chr3	+	151585441	151660841	6.91
Pentatricopeptide repeat domain 3 // kinesin family member 5A	PTCD3 // KIF5A	NM_017952 // NM_004984	DKFZp666K071 // FLJ20758 // D12S1889 // MY050 // NKHC // SPG10	2491935	chr2	+	86186849	86222791	6.91
kelch-like 20 (*Drosophila*)	KLHL20	NM_014458	KHLHX // KLEIP // KLHLX // RP3-383J4.3	2367793	chr1	+	171950703	172028914	6.90
sorting nexin 5	SNX5	NM_014426 // NM_152227	FLJ10931	3899346	chr20	−	17855335	17897603	6.89
KIAA0179	KIAA0179	NM_015056	—	3923218	chr21	+	43903644	43940364	6.87
protease, serine, 23	PRSS23	NM_007173	MGC5107 // SIG13 // SPUVE // ZSIG13	3343452	chr11	+	86189210	86341580	6.87
transmembrane, prostate androgen induced RNA	TMEPAI	NM_020182 // NM_199169 // NM_199170 // NM_199171	PMEPA1 // STAG1	3911217	chr20	−	55656877	55781123	6.87
zinc finger protein 330	ZNF330	NM_014487	HSA6591 // NOA36	2745220	chr4	+	142336669	142381405	6.87
chromodomain helicase DNA binding protein 2	CHD2	NM_001042572 // NM_001271	DKFZp781D1727	3609138	chr15	+	91227096	91387351	6.86
development and differentiation enhancing factor 1	DDEF1	NM_018482	AMAP1 // ASAP1 // KIAA1249 // PAG2 // PAP // ZG14P	3153428	chr8	−	131133540	131525100	6.85
mitogen-activated protein kinase kinase kinase 14	MAP3K14	NM_003954	FTDCR1B // HS // HSNIK // NIK	3759704	chr17	−	40696283	40750550	6.85
zinc finger protein 289, ID1 regulated	ZNF289	NM_032389	FLJ14576 // FLJ26000 // IRZ // Nbla10535 // Zfp289	3371928	chr11	−	47142451	47155114	6.84
heterogeneous nuclear ribonucleoprotein R	HNRPR	NM_005826	FLJ25714 // HNRNPR // hnRNP-R	2401275	chr1	−	23486545	23543926	6.84
coiled-coil domain containing 47	CCDC47	NM_020198	GK001 // MSTP041	3766334	chr17	−	59176353	59204726	6.84
CUG triplet repeat, RNA binding protein 1	CUGBP1	NM_001025596 // NM_006560 // NM_198700	BRUNOL2 // CUG-BP // CUGBP // NAB50 // hNab50	3372253	chr11	−	47444068	47543613	6.83
cancer susceptibility candidate 3	CASC3	NM_007359	BTZ // MLN51	3720739	chr17	+	35518075	35586901	6.82
SUMO1/sentrin/SMT3 specific peptidase 3	SENP3	NM_015670	DKFZP586K0919 // DKFZp762A152 // SMT3IP1 // SSP3	3708798	chr17	+	7405827	7416006	6.82
MAX dimerization protein 1	MXD1	NM_002357	MAD // MAD1 // MGC104659	2487549	chr2	+	69995330	70023575	6.82
protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha isoform	PPP2R2A	NM_002717	B55A // FLJ26613 // MGC52248 // PR52A // PR55A	3090922	chr8	+	26156860	26286261	6.82
fusion (involved in t(12; 16) in malignant liposarcoma)	FUS	NM_001010850 // NM_004960	CHOP // FUS-CHOP // FUS1 // TLS // TLS/CHOP	3656904	chr16	+	31093395	31111003	6.82

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
programmed cell death 6 // aryl-hydrocarbon receptor repressor	PDCD6 // AHRR	NM_013232 // NM_020731	ALG-2 // MGC111017 // MGC119050 // MGC9123 // PEF1B // AHH // AHHR //	2798586	chr5	+	324634	491368	6.81
nucleolar protein 5A (56 kDa with KKE/D repeat)	NOL5A	NM_006392	NOP56	3873874	chr20	+	2580791	2587030	6.81
WAS protein family, member 2	WASF2	NM_006990	SCAR2 // WAVE2 // dJ393P12.2	2403111	chr1	−	27603331	27689256	6.81
calmodulin regulated spectrin-associated protein 1	CAMSAP1	NM_015447	DKFZP434F195 // DKFZp434G2311 // FLJ31228 // MGC163452 // PRO2405 // bA100C15.1	3229529	chr9	−	137840157	137938826	6.81
chromosome 18 open reading frame 25	C18orf25	NM_001008239 // NM_145055	ARKL1 // MGC12909 // MGC87799	3787031	chr18	+	42008011	42123527	6.78
cullin 3	CUL3	NM_003590	—	2601544	chr2	−	225025520	225158348	6.78
methylthioadenosine phosphorylase	MTAP	NM_002451	MSAP // c86fus	3164914	chr9	+	21792645	22022975	6.77
translocase of outer mitochondrial membrane 70 homolog A (*S. cerevisiae*)	TOMM70A	NM_014820	FLJ90470	2686371	chr3	−	101565001	101614635	6.76
RNA pseudouridylate synthase domain containing 4	RPUSD4	NM_032795	FLJ14494	3396883	chr11	−	125577202	125586743	6.76
sprouty-related, EVH1 domain containing 1	SPRED1	NM_152594	FLJ33903	3589141	chr15	+	36331548	36468943	6.76
EH-domain containing 4	EHD4	NM_139265	PAST4	3620276	chr15	−	39977674	40052063	6.75
proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	PSMD12	XM_001134070 // XM_001134072 // XM_001134073 // NM_002816	MGC75406 // p55	3768103	chr17	−	62764497	62804392	6.75
nucleoporin 160 kDa	NUP160	NM_015231	MGC150678 // MGC150679	3371986	chr11	−	47169280	47858048	6.74
EPS8-like 1	EPS8L1	NM_017729 // NM_133180 // NM_139204	DRC3 // EPS8R1 // FLJ20258 // MGC23164 // MGC4642 // PP10566	3841949	chr19	+	60273799	60291530	6.74
chromatin modifying protein 4B	CHMP4B	NM_176812	C20orf178 // CHMP4A // SNF7-2 // Shax1 //	3882681	chr20	+	31862780	31905829	6.74
thioredoxin interacting protein	TXNIP	NM_006472	EST01027 // HHCPA78 // THIF // VDUP1	2356115	chr1	+	144149846	144164251	6.72
eukaryotic translation initiation factor 1A, X-linked // eukaryotic translation initiation factor 1A	EIF1AX // EIF1AP1	XM_001134077 // NM_001412 // —	EIF1A // EIF4C // eIF-1A // eIF-4C // —	4002148	chrX	−	20052567	20069880	6.71

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
mitochondrial ribosomal protein S30	MRPS30	NM_016640	DKFZp566B2024 // MRP-S30 // PAP // PDCD9	28086122	chr5	+	44844784	45054668	6.71
Rho GTPase activating protein 21	ARHGAP21	NM_020824	ARHGAP10 // DKFZp761L0424 // FLJ33323	3281621	chr10	–	24912552	25052583	6.71
regulator of G-protein signalling 3	RGS3	NM_017790 // NM_021106 // NM_130795 // NM_134427 // NM_144488 // NM_144489	C2PA // FLJ20370 // FLJ31516 // FLJ90496 // PDZ-RGS3 // RGP3	3185643	chr9	+	115246842	115399812	6.71
NFKB inhibitor interacting Ras-like 2	NKIRAS2	NM_001001349 // NM_017595	DKFZP434N1526 // KBRAS2 // MGC74742 //	3721579	chr17	+	37422156	37431177	6.70
polypyrimidine tract binding protein 2	PTBP2	NM_021190	FLJ34897 // MIBP // PTB // PTBLP // brPTB // nPTB // nPTB5 // nPTB6 // nPTB7 // nPTB8	2348060	chr1	+	96959805	97144643	6.70
splicing factor 1	SF1	NM_004630 // NM_201995 // NM_201997 // NM_201998	D11S636 // ZFM1 // ZNF162	3377044	chr11	–	64287827	64302817	6.69
Nipped-B homolog (*Drosophila*) // nuclear receptor binding protein 1	NIPBL // NRBP1	NM_015384 // NM_133433 // NM_013392	CDLS // DKFZp434L1319 // FLJ11203 // FLJ12597 // FLJ13354 // FLJ13648 // FLJ44854 // IDN3 // IDN3-B // BCON3 // FLJ27109 // FLJ35541 // MADM // MUDPNP // NRBP	2806799	chr5	+	36894163	37115932	6.68
ring finger and WD repeat domain 3	RFWD3	NM_018124	FLJ10520 // RNF201	3699044	chr16	–	73212799	73258283	6.68
BCL2-associated athanogene	BAG1	NM_004323	—	3203482	chr9	–	33237838	33255392	6.68
chromosome 6 open reading frame 111 // ubiquitin specific peptidase 45	C6orf111 // USP45	NM_032870 // XM_371838 // XM_931094 // XM_931115 // XM_931124 // XM_939661 // XM_944255 // XM_944271 // XM_944273 // NM_001080481	DKFZp564B0769 // FLJ14752 // FLJ14853 // FLJ14992 // FLJ90147 // HSPC306 // MGC104269 // RP11-98I9.2 // SRrp 130 // bA98I9.2 // MGC14793	2966253	chr6	–	99952648	99980235	6.68

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
dynactin 5 (p25)	DCTN5	NM_032486	MGC3248 // p25	3653042	chr16	+	23560236	23588668	6.67
integrator complex subunit 10	INTS10	NM_018142	C8orf35 // FLJ10569 // INT10	3088405	chr8	+	19666766	19753848	6.67
arrestin domain containing 3	ARRDC3	NM_020801	KIAA1376 // TLIMP	2866704	chr5	–	90700311	90782084	6.67
CD59 molecule, complement regulatory protein	CD59	NM_000611 // NM_203329 // NM_203330 // NM_203331	16.3A5 // EJ16 // EJ30 // EL32 // G344 // MGC2354 // MIC11 // MIN1 // MIN2 // MIN3 // MSK21 // PROTECTIN // p18-	3368707	chr11	–	33676397	33714806	6.65
opioid growth factor receptor	OGFR	NM_007346	—	3892941	chr20	+	60906461	60915796	6.65
chromosome 20 open reading frame 11	C20orf11	NM_017896	TWA1	3893072	chr20	+	61039681	61050570	6.63
ERBB receptor feedback inhibitor 1	ERRFI1	NM_018948	GENE-33 // MIG-6 // MIG6 // RALT	2395177	chr1	–	7987071	8194824	6.62
DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	DDX5	NM_004396	DKFZp686J01190 // G17P1 // HLR1 // HUMP68 // p68	3766893	chr17	–	59924843	59935796	6.62
chaperonin containing TCP1, subunit 2 (beta)	CCT2	NM_006431	99D8.1 // CCT-beta // CCTB // MGC142074 // MGC142076 // PRO1633 // TCP-1-beta	3421630	chr12	+	68265508	68281612	6.62
TROVE domain family, member 2	TROVE2	NM_001042369 // NM_001042370 // NM_004600	SSA2	2372924	chr1	+	191281274	191327514	6.62
casein kinase 1, delta	CSNK1D	XM_001132734 // NM_001893 // NM_139062	HCKID	3774823	chr17	–	77789955	77824878	6.62
nucleoside phosphorylase	NP	NM_000270	MGC117396 // MGC125915 // MGC125916 // PNP // PRO1837 // PUNP	3527514	chr14	+	20007398	20015985	6.61
ubiquitin C	UBC	XM_001132949 // NM_021009	HMG20	3476741	chr12	–	123962213	123965631	6.61
general transcription factor IIF, polypeptide 2, 30 kDa	GTF2F2	NM_004128	BTF4 // RAP30 // TF2F2 // TFIIF	3488094	chr13	+	44592617	44756234	6.60
RAS p21 protein activator (GTPase activating protein) 1	RASA1	NM_002890 // NM_022650	CM-AVM // CMAVM // DKFZp434N071 // GAP // PKWS // RASA // RASGAP // p120GAP	2819044	chr5	+	86599391	86724647	6.60
chromosome 8 open reading frame	C8orf53	NM_032334	MGC14595	3112543	chr8	+	117847923	117930859	6.60
activator of basal transcription 1	ABT1	NM_013375	hABT1	2899519	chr6	+	26661709	26708945	6.59

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Array	Human Genome hg18				
				Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
DEAD (Asp-Glu-Ala-Asp) box polypeptide 50	DDX50	NM_024045	GU2 // GUB // MGC3199 // RH-II/GuB	3250019	chr10	+	70330615	70377158	6.58
component of oligomeric golgi complex 1	COG1	NM_018714	DKFZp762L1710 // KIAA1381 // LDLB	3733938	chr17	+	68695573	68739952	6.58
adaptor-related protein complex 1, gamma 1 subunit	AP1G1	NM_001030007 // NM_001128	ADTG // CLAPG1 // MGC18255	3697799	chr16	–	70320417	70400594	6.57
UTP15, U3 small nucleolar ribonucleoprotein, homolog (*S. cerevisiae*)	UTP15	NM_032175	FLJ12787	2815455	chr5	+	72897308	72915109	6.57
PR domain containing 4 // protein kinase, cAMP-dependent, regulatory, type II, beta	PRDM4 // PRKAR2B	NM_012406 // NM_002736	MGC45046 // PFM1 // PRKAR2 // RII-BETA	3470037	chr12	–	106650784	106679235	6.56
nuclear transcription factor, X-box binding-like 1	NFXL1	NM_152995	FLJ16294 // HOZFP	2768273	chr4	–	47543715	47612453	6.55
YTH domain family, member 3	YTHDF3	NM_152758	FLJ31657	3100909	chr8	+	64213088	64392289	6.55
MAP/microtubule affinity-regulating kinase 2	MARK2	NM_001039468 // NM_001039469 // NM_004954 // NM_017490	EMK1 // MGC99619 // PAR-1	3334025	chr11	+	63362634	63435067	6.55
GC-rich promoter binding protein 1	GPBP1	NM_022913	DKFZp761C169 // GPBP // MGC126339	2810458	chr5	+	56504841	56597388	6.55
CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1	CTDP1	NM_004715 // NM_048368	CCFDN // FCP1	3795312	chr18	+	75540799	75617601	6.54
protein tyrosine phosphatase, non-receptor type 12	PTPN12	NM_002835	PTP-PEST // PTPG1	3009959	chr7	+	77004361	77123074	6.54
ubiquitin-conjugating enzyme E2M (UBC12 homolog, yeast) // ubiquitin-conjugating enzyme E2M pseudogene 1	UBE2M // UBE2MP1	NM_003969 // NR_002837	UBC-RS2 // UBC12 // hUbc12 // —	3872999	chr19	–	63758732	63762147	6.54
wingless-type MMTV integration site family, member 11	WNT11	NM_004626	HWNT11 // MGC141946 // MGC141948	3382523	chr11	–	75542387	75599441	6.53
chromosome 14 open reading frame 32	C14orf32	NM_144578	MGC23138 // MISS // c14_5346	3536663	chr14	+	54588114	54606655	6.53
signal sequence receptor, beta (translocon-associated protein beta)	SSR2	XM_001128341 // NM_003145	DKFZp686F19123 // HSD25 // TLAP // TRAPB	2437871	chr1	–	154245480	154257371	6.52
RAS and EF-hand domain containing	RASEF	NM_152573	FLJ31614 // RAB45	3211938	chr9	–	84772206	84937805	6.52
cold shock domain protein A	CSDA	NM_003651	CSDA1 // DBPA // ZONAB	3444252	chr12	–	10742960	10775038	6.51
leucine-rich PPR-motif containing	LRPPRC	NM_133259	CLONE-23970 // GP130 // LRP130 // LSFC	2550790	chr2	–	43961504	44085128	6.51
oxysterol binding protein	OSBP	NM_002556	OSBP1	3374698	chr11	–	59098455	59140193	6.51
MAP/microtubule affinity-regulating kinase 3	MARK3	NM_002376	CTAK1 // KP78 // PAR1A	3553690	chr14	+	102921419	103370656	6.50

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
oxidation resistance 1	OXR1	NM_181354	FLJ10125 // FLJ38829 // FLJ41673 // FLJ42450 // FLJ45656 // Nbla00307	3110999	chr8	+	107351659	107834092	6.50
ATG16 autophagy related 16-like 1 (*S. cerevisiae*)	ATG16L1	NM_198890 // NM_017974 // NM_030803	APG16L // ATG16L // FLJ00045 // FLJ10035 // FLJ10828 // FLJ22677 // WDR30	2532793	chr2	+	233825030	233869050	6.50
ankyrin repeat domain 17	ANKRD17	NM_032217 // NM_198889	FLJ22206 // GTAR // KIAA0697 // NY-BR-16	2773023	chr4	−	74158547	74343428	6.50
small nuclear ribonucleoprotein polypeptide B"	SNRPB2	NM_003092 // NM_198220	MGC24807 // MGC45309	3877776	chr20	+	16645421	16670916	6.49
protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	PRKAR1A	NM_002734 // NM_212471 // NM_212472	CAR // CNC // CNC1 // DKFZp779L0468 // MGC17251 // PKR1	3732885	chr17	+	64019700	64059052	6.49
chromosome 20 open reading frame 20	C20orf20	NM_018270	Eaf7 // FLJ10914 // MRG15BP // MRGBP	3892918	chr20	+	60898107	60903524	6.49
ADP-ribosylation-like factor 6 interacting protein 4	ARL6IP4	NM_001002251 // NM_001002252 // NM_016638 // NM_018694	MGC814 // SR-25 // SRp25	3435681	chr12	+	122030886	122033406	6.48
pre-mRNA cleavage factor 1, 59 kDa subunit	FLJ12529	NM_024811	FLJ39024 // MGC9315	3375340	chr11	−	60926704	60954030	6.48
RNA binding motif protein 17	RBM17	NM_032905	MGC14439 // SPF45	3233547	chr10	+	6170982	6225410	6.47
actin binding LIM protein family, member 3	ABLIM3	NM_014945	HMFN1661	2834863	chr5	+	148497619	148620192	6.47
asparagine synthetase domain containing 1	ASNSD1	NM_019048	FLJ20752 // NBLA00058 // NS3TP1	2519860	chr2	+	190198920	190244286	6.46
poly(A) polymerase alpha	PAPOLA	NM_032632	MGC5378 // PAP	3550392	chr14	+	96038038	96104627	6.46
transmembrane protein 87A	TMEM87A	NM_015497	DKFZP564G2022	3620515	chr15	−	40289650	40353024	6.46
KIAA0907	KIAA0907	NM_014949	RP11-336K24.1	2437753	chr1	−	154149414	154174836	6.45
DEAD (Asp-Glu-Ala-Asp) box polypeptide 10	DDX10	NM_004398	HRH-J8	3347831	chr11	+	108041010	108316858	6.45
protein tyrosine phosphatase, non-receptor type 1	PTPN1	NM_002827	PTP1B	3888721	chr20	+	48560298	48634700	6.45
insulin-like growth factor 2 mRNA binding protein 2	IGF2BP2	NM_001007225 // NM_006548	IMP-2 // IMP2 // VICKZ2 // p62	2708922	chr3	−	186844235	187025506	6.45
zinc finger protein 592	ZNF592	NM_014630	KIAA0211 // MGC138437 // MGC138439	3605832	chr15	+	83092594	83150653	6.44

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Array	Human Genome hg18				
				Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
HIV-1 Rev binding protein	HRB	XM_941338 // NM_004504	MGC116938 // MGC116940 // RAB // RIP	2530599	chr2	+	228045122	228134167	6.43
mitogen-activated protein kinase kinase kinase 4	MAP3K4	NM_005922 // NM_006724	FLJ42439 // KIAA0213 // MAPKKK4 // MEKK4 // MTK1 // PRO0412	2934801	chr6	+	161332723	161458399	6.42
ubiquitin specific peptidase 15	USP15	NM_006313	KIAA0529 // MGC131982 // MGC149838 // MGC74854 // UNPH4	3419147	chr12	+	60940328	61086166	6.41
cullin 1	CUL1	NM_003592	MGC149834 // MGC149835	3030285	chr7	+	148026213	148129128	6.41
family with sequence similarity 104, member A	FAM104A	NM_032837	FLJ14775	3769969	chr17	−	68715100	68740203	6.41
nucleoporin 88 kDa	NUP88	NM_002532	MGC8530	3742652	chr17	−	5204992	5264204	6.41
kinesin family member 22	KIF22	NM_007317	KID // KNSL4 // OBP // OBP-1 //	3655628	chr16	+	29708911	29724778	6.40
zinc finger protein 313	ZNF313	NM_018683	RNF114	3888474	chr20	+	47986321	48003818	6.39
ATG3 autophagy related 3 homolog (*S. cerevisiae*)	ATG3	NM_022488	APG3 // APG3L // DKFZp564M1178 // FLJ22125 // MGC15201 // PC3-96	2688759	chr3	−	113726408	113769332	6.39
PTPRF interacting protein, binding protein 1 (liprin beta 1)	PPFIBP1	NM_003622 // NM_177444	L2 // hSGT2 // hSgt2p	3409211	chr12	+	27567649	27739981	6.39
flotillin 1	FLOT1	NM_005803	—	2948587	chr6	−	30796156	30818490	6.38
isoleucyl-tRNA synthetase	IARS	NM_002161 // NM_013417	FLJ20736 // IARS1 // ILRS // PRO0785	3214668	chr9	−	94012330	94096287	6.38
TM2 domain containing 2	TM2D2	NM_001024380 // NM_001024381 // NM_031940 // NM_078473	BLP1 // MGC125813 // MGC125814	3132333	chr8	−	38965485	38973467	6.38
hypothetical protein MGC22014	MGC22014	XM_371501 // XM_942026	KIAA0401	2489071	chr2	+	74066761	74188804	6.37
THO complex 1	THOC1	NM_005131	HPR1 // P84 // P84N5	3795680	chr18	−	201783	258461	6.36
chromosome 14 open reading frame 129	C14orf129	NM_016472	HSPC210 // MGC4945	3550328	chr14	+	95899075	95923378	6.35
vascular endothelial zinc finger 1	VEZF1	NM_007146	DB1 // ZNF161	3764066	chr17	−	53359568	53420600	6.34
heat shock 70 kDa protein 8 // Fc fragment of IgG, low affinity IIIb, receptor (CD16b)	HSPA8 // FCGR3B	NM_006597 // NM_153201 // NM_000570	HSC54 // HSC70 // HSC71 // HSP71 // HSP73 // HSPA10 // LAP1 // MGC131511 // MGC29929 // NIP71 // CD16 // CD16b // FCG3 // FCGR3	3395416	chr11	−	122429309	122438895	6.33

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
cullin-associated and neddylation-dissociated 1	CAND1	NM_018448	DKFZp434M1414 // FLJ10114 // FLJ10929 // FLJ38691 // FLJ90441 // KIAA0829 // TIP120 // TIP120A	3420713	chr12	+	65946048	65994719	6.32
kelch repeat and BTB (POZ) domain containing 4	KBTBD4	NM_016506 // NM_018095	BKLHD4 // FLJ10450 // HSPC252	3372337	chr11	−	47550326	47557362	6.32
karyopherin alpha 4 (importin alpha 3)	KPNA4	NM_002268	IPOA3 // MGC12217 // MGC26703 // QIP1 // SRP3	2703217	chr3	−	161663997	161766070	6.31
chromosome 12 open reading frame 52	C12orf52	NM_032848	FLJ14827	3432641	chr12	+	112107758	112114543	6.31
aurora kinase A // serine/threonine kinase 6 pseudogene	AURKA // STK6P	NM_003600 // NM_198433 // NM_198434 // NM_198435 // NM_198436 // NM_198437 // NR_001587	AIK // ARK1 // AURA // AURORA2 // BTAK // MGC34538 // STK15 // STK6 // STK7 // —	3910785	chr20	−	54377855	54402553	6.30
eukaryotic translation initiation factor 2, subunit 1 alpha, 35 kDa	EIF2S1	NM_004094	EIF-2 // EIF-2A // EIF-2alpha // EIF2 // EIF2A	3541137	chr14	+	66896518	66922983	6.30
ubiquitin specific peptidase 7 (herpes virus-associated)	USP7	NM_003470	HAUSP // TEF1	3679564	chr16	−	8893458	8964832	6.30
SH3 domain containing ring finger 2	SH3RF2	NM_152550	FLJ23654 // MGC149788 // MGC149789 // MGC90410 //	2833924	chr5	+	145296335	145441529	6.30
hydroxymethylbilane synthase	HMBS	NM_000190 // NM_001024382	PBG-D // PBGD // UPS	3351841	chr11	+	118460803	118470689	6.30
eukaryotic translation initiation factor 4E	EIF4E	NM_001968	CBP // EIF4E1 // EIF4EL1 // EIF4F // MGC111573	2778980	chr4	−	99888790	100070801	6.30
splicing factor, arginine/serine-rich 15	SFRS15	NM_020706	DKFZP434E098 // FLJ23364 // KIAA1172 // SRA4	3928866	chr21	−	31965222	32077764	6.30
gem (nuclear organelle) associated protein 5	GEMIN5	NM_015465	DKFZP586M1824 // MGC142174	2882897	chr5	−	154247066	154309713	6.30
TNF receptor-associated factor 6	TRAF6	NM_004620 // NM_145803	MGC: 3310 // RNF85	3369890	chr11	−	36465173	36488940	6.29
neurofibromin 2 (bilateral acoustic neuroma)	NF2	NM_000268 // NM_016418 // NM_181825 // NM_181828 // NM_181829 //	ACN // BANF // Merlin // SCH	3942062	chr22	+	28329446	28424577	6.29

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
		NM_181830 // NM_181831 // NM_181832 // NM_181833							
structural maintenance of chromosomes 3	SMC3	NM_005445	BAM // BMH // CSPG6 // HCAP // SMC3L1	3263790	chr10	+	112317039	112365483	6.28
dynamin binding protein	DNMBP	NM_015221	KIAA1010 // TUBA	3303165	chr10	–	101624846	101759656	6.28
cystatin B (stefin B)	CSTB	NM_000100	CST6 // EPM1 // PME // STFB	3934245	chr21	–	44016298	44020687	6.28
mucin 20, cell surface associated	MUC20	NM_152673	FLJ14408 // KIAA1359	2659039	chr3	+	196867150	196953662	6.27
tuberous sclerosis 1	TSC1	NM_000368 // NM_001008567	KIAA0243 // LAM // MGC86987 // TSC	3228373	chr9	–	134756560	134809831	6.27
abl interactor 2	ABI2	XM_001126750 // NM_005759	ABI-2 // ABI2B // AIP-1 // AblBP3 // SSH3BP2 // argBPIA // argBPIB	2523689	chr2	+	203901161	204005128	6.27
golgi reassembly stacking protein 2, 55 kDa // dehydrogenase/reductase (SDR family) member 9	GORASP2 // DHRS9	NM_015530 // NM_005771 // NM_199204	DKFZP434D156 // FLJ13139 // GOLPH6 // GRASP55 // GRS2 // p59 // 3alpha-HSD // RDH15 // RDHL // RETSDR8	2515050	chr2	+	171457150	171551619	6.27
ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	ATP2A2	NM_001681 // NM_170665	ATP2B // DAR // DD // MGC45367 // SERCA2	3431483	chr12	+	109203332	109352495	6.26
hypothetical protein HSPC148	HSPC148	NM_016403	—	3387171	chr11	–	94322815	94346692	6.26
EH-domain containing 1	EHD1	NM_006795	FLJ42622 // FLJ44618 // H-PAST // HPAST1 // PAST // PAST1	3377226	chr11	–	64376790	64404202	6.26
X-box binding protein 1	XBP1	NM_001079539 // NM_005080	TREB5 // XBP2	3956589	chr22	–	27520140	27526564	6.25
enhancer of zeste homolog 2 (*Drosophila*)	EZH2	NM_004456 // NM_152998	ENX-1 // EZH1 // MGC9169	3078348	chr7	–	148135436	148212647	6.25
SEC24 related gene family, member B (*S. cerevisiae*)	SEC24B	XM_001130118 // NM_001042734 // NM_006323	MGC48822 // SEC24	2739079	chr4	+	110510304	110681811	6.24
RAB, member RAS oncogene family-like 5	RABL5	NM_022777	DKFZp761N0823 // FLJ13225 // FLJ14117	3064638	chr7	–	100742601	100751793	6.24
RCD1 required for cell differentiation 1 homolog (*S. pombe*) // phospholipase C, delta 4	RQCD1 // PLCD4	NM_005444 // NM_032726	CNOT9 // RCD1 // RCD1+ // MGC12837	2527856	chr2	+	219141552	219170027	6.24

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
poly(rC) binding protein 2	PCBP2	NM_005016 // NM_031989	HNRPE2 // MGC110998 // hnRNP-E2	3416036	chr12	+	52132173	52161417	6.23
solute carrier family 30 (zinc transporter), member 9	SLC30A9	NM_006345	C4orf1 // GAC63 // HUEL // ZNT9	2725381	chr4	+	41684531	41812215	6.23
zinc finger protein 192	ZNF192	NM_006298	LD5-1 // ZKSCAN8	2900299	chr6	+	28217285	28232872	6.23
jumonji domain containing 2A	JMJD2A	NM_014663	JHDM3A // JMJD2 // KIAA0677	2333429	chr1	+	43888407	43943994	6.23
HtrA serine peptidase 2	HTRA2	NM_013247 // NM_145074	OMI // PARK13 // PRSS25	2489411	chr2	+	74609783	74614240	6.23
epidermal growth factor receptor pathway substrate 8	EPS8	NM_004447	—	3445908	chr12	–	15664367	15833589	6.23
glutamine and serine rich 1	QSER1	NM_024774 // NM_001076786	FLJ21924	3325768	chr11	+	32871321	32971438	6.22
phosphomannomutase 2	PMM2	NM_000303	CDG1 // CDG1a // CDGS	3647504	chr16	+	8798971	8850664	6.22
DEAH (Asp-Glu-Ala-His) box polypeptide 15	DHX15	NM_001358	DBP1 // DDX15 // HRH2 // PRP43 // PRPF43 // PrPp43p	2763805	chr4	–	24128159	24250940	6.22
transforming growth factor, beta receptor II (70/80 kDa)	TGFBR2	NM_001024847 // NM_003242	AAT3 // FAA3 // HNPCC6 // MFS2 // RIIC // TAAD2 // TGFR-2 // TGFbeta-RII	2615360	chr3	+	30492214	30710745	6.21
tropomyosin 1 (alpha)	TPM1	NM_000366 // NM_001018004 // NM_001018005 // NM_001018006 // NM_001018007 // NM_001018008 // NM_001018020	HTM-alpha // TMSA // TPM1-alpha // TPM1-kappa	3597338	chr15	+	61105711	61151151	6.21
HLA-B associated transcript 4	BAT4	NM_033177	ANKRD59 // D6S54E // G5 // GPANK1 // GPATCH10	2949210	chr6	–	31736995	31742029	6.21
COX4 neighbor	COX4NB	NM_006067	C16orf4 // NOC4	3703164	chr16	–	84362936	84391266	6.21
RNA binding motif protein 7	RBM7	NM_016090	FLJ11153	3349918	chr11	+	113776539	113790335	6.20
suppressor of Ty 4 homolog 1 (*S. cerevisiae*)	SUPT4H1	NM_003168	SPT4H // SUPT4H	3764384	chr17	–	53777538	53784705	6.19
PRP4 pre-mRNA processing factor 4 homolog B (yeast)	PRPF4B	NM_003913	KIAA0536 // PR4H // PRP4 // PRP4H // PRP4K // dJ1013A10.1	2892738	chr6	+	3966500	4010215	6.19
phosphoglycerate kinase 1	PGK1	NM_000291	MGC117307 // MGC142128 // MGC8947 // MIG10 // PGKA	3982462	chrX	+	77207320	77269191	6.19

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
ATP-binding cassette, sub-family C (CFTR/MRP), member 1	ABCC1	NM_004996 // NM_019862 // NM_019898 // NM_019899 // NM_019900 // NM_019901 // NM_019902	ABC29 // ABCC // DKFZp686N04233 // DKFZp781G125 // GS-X // MRP // MRP1	3649890	chr16	+	15950935	16144419	6.18
transmembrane protein 123	TMEM123	NM_052932	KCT3 // PORIMIN // PORMIN	3388631	chr11	−	101772285	101828945	6.18
SEH1-like (*S. cerevisiae*)	SEH1L	NM_001013437 // NM_031216	SEC13L // SEH1A // SEH1B // Seh1	3779756	chr18	+	12886655	12981306	6.17
ferritin, heavy polypeptide-like 7 // ferritin, heavy polypeptide 1 // ferritin, heavy polypeptide-like 3 // ferritin, heavy polypeptide pseudogene 1 // ferritin, heavy polypeptide-like 12 // ferritin, heavy polypeptide-like 11 // ferritin, heavy	FTHL7 // FTH1 // FTHL3 // FTHP1 // FTHL12 // FTHL11 // FTHL8	NR_002202 // NM_002032 // NR_002201 // —// NR_002205 // NR_002204 // NR_002203	—// FTH // FTHL6 // MGC104426 // PIG15 // PLIF // FTHL5	3375648	chr11	−	61488337	61492603	6.16
DNA polymerase-transactivated protein 6	DNAPTP6	NM_015535	DKFZp564A2416	2522094	chr2	+	200879035	201053805	6.15
serologically defined colon cancer antigen 10	SDCCAG10	NM_005869	NY-CO-10	2812120	chr5	+	64100099	64417210	6.15
SHC (Src homology 2 domain containing) transforming protein 1	SHC1	NM_003029 // NM_183001	FLJ26504 // SHC // SHCA // p52SHC // p66 // p66SHC	2436985	chr1	−	153201334	153213510	6.15
tetratricopeptide repeat domain 17	TTC17	NM_018259	DKFZp686D20222 // FLJ10890 // FLJ13099 // FLJ23673	3327948	chr11	+	43337004	43473027	6.13
polymerase (RNA) III (DNA directed) polypeptide E (80 KD)	POLR3E	NM_018119	RPC5 // SIN	3652489	chr16	+	22216140	22253905	6.13
bromodomain containing 1	BRD1	NM_014577	BRL // BRPF1 // BRPF2 // DKFZp686F0325	3965314	chr22	−	48552694	48636916	6.12
SET translocation (myeloid leukemia-associated)	SET	NM_003011	2PP2A // I2PP2A // IGAAD // PHAPII // TAF-IBETA	3190659	chr9	+	130485775	130498483	6.12
glutamate-cysteine ligase, catalytic subunit	GCLC	NM_001498	GCS // GLCL // GLCLC	2957700	chr6	−	53438876	53589510	6.12
SCY1-like 2 (*S. cerevisiae*)	SCYL2	NM_017988	CVAK104 // FLJ10074 //	3428131	chr12	+	99185070	99260564	6.12
ribosomal protein L8	RPL8	NM_000973 // NM_033301	—	3159040	chr8	−	145985994	145988615	6.11
protein tyrosine phosphatase type IVA, member 1	PTP4A1	NM_003463	DKFZp779M0721 // HH72 // PRL-1 // PRL1 // PTP(CAAX1) // PTPCAAX1	2911903	chr6	+	64289625	64351448	6.10

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
Rac GTPase activating protein 1	RACGAP1	NM_013277	H3CYK-4 // ID-GAP // MgcRacGAP	3454223	chr12	–	48657002	48705537	6.09
cold shock domain containing E1, RNA-binding // neuroblastoma RAS viral (v-ras) oncogene homolog	CSDE1 // NRAS	NM_001007553 // NM_007158 // NM_002524	D1S155E // DKFZp779B0247 // DKFZp779J1455 // FLJ26882 // RP5-1000E10.3 // UNR // N-ras // NRAS1	2429277	chr1	–	115061068	115102225	6.09
translocation protein 1	TLOC1	NM_003262	Dtrp1 // FLJ32803 // HTP1 // SEC62	2651782	chr3	+	171166446	171194653	6.09
muscleblind-like (*Drosophila*)	MBNL1	NM_021038 // NM_207292 // NM_207293 // NM_207294 // NM_207295 // NM_207296 // NM_207297	DKFZp686P06174 // EXP // EXP35 // EXP40 // EXP42 // KIAA0428 // MBNL	2648141	chr3	+	153444327	153670549	6.08
chromosome X open reading frame 40A // chromosome X open reading frame 40B	CXorf40A // CXorf40B	NM_178124 // NM_001013845	CXorf40 // EOLA1 // —	3994451	chrX	+	148413672	148439412	6.08
ubiquitin B // chromosome 17 open reading frame 45	UBB // C17orf45	NM_018955 // NM_152350	FLJ25987 // MGC8385 // FLJ25777 // MGC40157	3712041	chr17	+	16223047	16228977	6.08
solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	SLC7A1	NM_003045	ATRC1 // CAT-1 // ERR // HCAT1 // REC1L	3507710	chr13	–	28981563	29067721	6.07
smu-1 suppressor of mec-8 and unc-52 homolog (*C. elegans*)	SMU1	NM_018225	BWD // FLJ10805 // FLJ11970 // MGC117363 // RP11-54K16.3 // SMU-1	3203382	chr9	–	33031772	33072208	6.06
annexin A2	ANXA2	NM_001002857 // NM_001002858 // NM_004039	ANX2 // ANX2L4 // CAL1H // LIP2 // LPC2 // LPC2D // P36 // PAP-IV	3627248	chr15	–	58247806	58482354	6.06
COP9 constitutive photomorphogenic homolog subunit 7B (*Arabidopsis*)	COPS7B	NM_022730	FLJ12612 // MGC111077	2532064	chr2	+	232354256	232382342	6.06
chromosome 1 open reading frame 174	C1orf174	NM_207356	RP13-531C17.2	2393816	chr1	–	3791939	3812760	6.06
v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	ETS2	NM_005239	—	3921068	chr21	+	39059147	39118744	6.06
actinin, alpha 4	ACTN4	NM_004924	DKFZp686K23158 // FSGS // FSGS1	3832643	chr19	+	43830130	43913003	6.06
protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	PPP2CA	NM_002715	PP2Ac // PP2CA // RP-C	2876046	chr5	–	133557588	133589841	6.05
glycogen synthase kinase 3 beta	GSK3B	NM_002093	—	2691014	chr3	–	121018519	121297142	6.05
hypothetical protein FLJ14154	FLJ14154	NM_024845	—	3645901	chr16	+	3433714	3476953	6.04

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Array	Human Genome hg18				
				Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
poliovirus receptor-related 2 (herpesvirus entry mediator B)	PVRL2	NM_001042724 // NM_002856	CD112 // HVEB // PRR2 // PVRR2	3835814	chr19	+	50041409	50084314	6.04
DnaJ homolog subfamily A member 5	DNAJA5	NM_001012339 // NM_194283	—	2806256	chr5	+	34965441	34994822	6.03
zinc finger, RAN-binding domain containing 2	ZRANB2	NM_005455 // NM_203350	DKFZp686J1831 // DKFZp686N09117 // FLJ41119 // ZIS // ZIS1 // ZIS2 // ZNF265	2418000	chr1	–	71292434	71355820	6.03
GDP dissociation inhibitor 2	GDI2	NM_001494	FLJ16452 // FLJ37352 // RABGDIB	3275132	chr10	–	5844502	5924081	6.03
transmembrane protein 138	TMEM138	NM_016464	HSPC196	3332886	chr11	+	60885939	60900898	6.02
CDC28 protein kinase regulatory subunit 2	CKS2	NM_001827	CKSHS2	3178583	chr9	+	91050736	91121542	6.01
ADAM metallopeptidase domain 10	ADAM10	NM_001110	CD156c // HsT18717 // MADM // kuz	3626555	chr15	–	56651514	56829469	6.00
telomeric repeat binding factor 2	TERF2	NM_005652	TRBF2 // TRF2	3696571	chr16	–	67946973	68001605	6.00
elongation factor, RNA polymerase II,	ELL2	NM_012081	—	2867873	chr5	–	95246561	95323733	5.99
proteasome maturation protein	POMP	NM_015932	C13orf12 // HSPC014 // PNAS-110 // UMP1	3483348	chr13	+	28125188	28151050	5.99
mitochondrial ribosomal protein L16	MRPL16	NM_017840	FLJ20484 // L16mt // PNAS-111	3374856	chr11	–	59330154	59334921	5.99
glucosaminyl (N-acetyl) transferase 3, mucin type	GCNT3	NM_004751	C2/4GnT // C2GnT-M // C2GnT2 //	3596147	chr15	+	57628756	57719710	5.98
KIAA0409	KIAA0409	NM_015324	RRP8	3360982	chr11	–	6492639	6582206	5.98
tankyrase 1 binding protein 1, 182 kDa	TNKS1BP1	NM_033396	FLJ45975 // KIAA1741 // TAB182	3373675	chr11	–	56823694	56848992	5.98
polymerase (RNA) I polypeptide E, 53 kDa	POLR1E	NMP_022490	FLJ13390 // FLJ13970 // PAF53 // PRAF1 // RP11-405L18.3	3168938	chr9	+	37475945	37500379	5.97
E3 ubiquitin protein ligase, HECT domain containing, 1	EDD1	NM_015902	DD5 // EDD // FLJ11310 // HYD // KIAA0896 // MGC57263	3147321	chr8	–	103333634	103493671	5.97
G protein-coupled receptor, family C, group 5, member A	GPRC5A	NM_003979	GPCR5A // RAI3 // RAIG1	3405587	chr12	+	12929011	12986488	5.96
fragile X mental retardation 1	FMR1	NM_002024	FMRP // FRAXA // MGC87458	3994100	chrX	+	146801098	146840329	5.96
thyroid hormone receptor associated protein 2	THRAP2	NM_015335	DKFZp781D0112 // FLJ21627 // KIAA1025 // MED13L // PROSIT240 // TRAP240L	3473083	chr12	–	114868953	115419724	5.96

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
epithelial membrane protein 1	EMP1	NM_001423	CL-20 // EMP-1 // TMP	3405748	chr12	+	13230082	13264499	5.95
SUMO1/sentrin specific peptidase 5	SENP5	NM_152699	FLJ42398 // MGC27076	2659631	chr3	+	198079101	198143960	5.94
FUS interacting protein (serine/arginine-rich) 1	FUSIP1	NM_006625 // NM_054016	FUSIP2 // NSSR // SFRS13 // SRp38 // SRrp40 // TASR // TASR1 // TASR2	4045780	chr1_random	–	1493804	1514582	5.93
UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast)	UTP14A	NM_006649	KIAA0266 // NY-CO-16 // SDCCAG16 // dJ537K23.3	3990566	chrX	+	128832975	128912087	5.93
cell division cycle associated 3	CDCA3	NM_031299	GRCC8 // MGC2577 // TOME-1	3442322	chr12	–	6824231	6831482	5.93
zinc finger, AN1-type domain 3	ZFAND3	NM_021943	FLJ13222 // TEX27	2905664	chr6	+	37895285	38231400	5.93
glucocorticoid receptor DNA binding factor 1	GRLF1	NM_004491	GRF-1 // KIAA1722 // MGC10745 // P190-A // P190A // p190RhoGAP	3837001	chr19	+	52113779	52200169	5.92
GPI-anchored membrane protein 1	GPIAP1	NM_005898 // NM_203364	GPIP137 // M11S1 // p137GPI	3326183	chr11	+	34009711	34081946	5.92
AT hook containing transcription factor 1	AHCTF1	XM_001126456 // NM_015446	DKFZp434N093 // ELYS // MST108 // MSTP108 // TMBS62	2465324	chr1	–	245069027	245162066	5.92
aurora kinase B	AURKB	NM_004217	AIK2 // AIM-1 // AIM1 // ARK2 // AurB // IPL1 // STK12 // STK5	3744263	chr17	–	8034636	8054649	5.92
ariadne homolog 2 (*Drosophila*)	ARIH2	NM_006321	ARI2 // FLJ10938 // FLJ33921 // TRIAD1	2621827	chr3	+	48930742	48997971	5.91
chromosome 11 open reading frame 68	C11orf68	NM_031450	Bles03 // P5326	3378007	chr11	–	65440893	65443107	5.91
nuclear factor of kappa light polypeptide gene enhancer in B-cells ihibitor, alpha	NFKBIA	NM_020529	IKBA // MAD-3 // NFKBI	3561039	chr14	–	34940473	34944214	5.90
calcyclin binding protein	CACYBP	NM_001007214 // NM_014412	GIG5 // MGC87971 // PNAS-107 // RP1-102G20.6 // S100A6BP // SIP	2368198	chr1	+	173235214	173247469	5.90
zinc finger protein 593	ZNF593	NM_015871	ZT86	2326311	chr1	+	26368813	26371688	5.90
proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	PSMD2	NM_002808	MGC14274 // P97 // S2 // TRAP2	2655650	chr3	+	185499199	185509504	5.89
YY1 transcription factor	YY1	NM_003403	DELTA // NF-E1 // UCRBP // YIN-YANG-1	3551677	chr14	+	99750383	99818868	5.89
Smith-Magenis syndrome chromosome region, candidate 7-like	SMCR7L	NM_019008	FLJ20232 // HSU79252 // dJ1104E15.3	3945877	chr22	+	38226061	38244079	5.88

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
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CDC-like kinase 1	CLK1	NM_001024646 // NM_004071	CLK // CLK/STY // STY	2594497	chr2	–	201425997	201437659	5.88
phosphatidylinositol transfer protein, beta	PITPNB	NM_012399	PI-TP-beta // PtdInsTP // VIB1B	3956290	chr22	–	26577440	26645487	5.87
A kinase (PRKA) anchor protein 8-like	AKAP8L	NM_014371	DKFZp434L0650 // HAP95 // NAKAP // NAKAP95	3853345	chr19	–	15351869	15390819	5.87
chromosome 17 open reading frame 70	C17orf70	NM_025161	FLJ22175 // FLJ30151	3773980	chr17	–	77117366	77130137	5.87
ring finger protein 34	RNF34	NM_025126 // NM_194271	FLJ21786 // RFI // RIF // RIFF	3434823	chr12	+	120322070	120352805	5.87
solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	SLC7A6	NM_001076785 // NM_003983	DKFZp686K15246 // KIAA0245 // LAT-2 // LAT3 // y+LAT-2	3666146	chr16	+	66855932	66893223	5.86
solute carrier family 39 (zinc transporter), member 14	SLC39A14	NM_015359	KIAA0062 // LZT-Hs4 // ZIP14 // cig19	3089360	chr8	+	22280765	22347587	5.86
PI-3-kinase-related kinase SMG-1	SMG1	NM_015092	61E3.4 // ATX // KIAA0421 // LIP	3683050	chr16	–	18719381	18845318	5.86
zinc finger protein 259	ZNF259	NM_003904	MGC110983 // ZPR1	3392871	chr11	–	116153652	116163944	5.86
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11, 17.3 kDa	NDUFB11	NM_019056	ESSS // FLJ20494 // MGC111182 // NP17.3 // Np15 //	4007009	chrX	–	46886563	46902114	5.86
heterogeneous nuclear ribonucleoprotein LI (scaffold attachment factor A)	HNRPU	NM_004501 // NM_031844	HNRNPU // SAF-A // U21.1	2464499	chr1	–	243078713	243094975	5.85
BCL2-like 1	BCL2L1	NM_001191 // NM_138578	BCL-XL/S // BCL2L // BCLX // Bcl-X // DKFZp781P2092 // bcl-xL // bcl-xS	3902489	chr20	–	29715925	29775453	5.85
stem-loop (histone) binding protein	SLBP	NM_006527	HBP	2757319	chr4	–	1664276	1684080	5.85
retinitis pigmentosa 2 (X-linked recessive)	RP2	NM_006915	KIAA0215 // TBCCD2	3975869	chrX	+	46581319	46637601	5.85
cullin 4A	CUL4A	NM_001008895 // NM_003589	—	3502497	chr13	+	112905835	112967356	5.85
tripartite motif-containing 28	TRIM28	NM_005762	FLJ29029 // KAP1 // RNF96 // TF1B // TIF1B	3844238	chr19	+	63740597	63753931	5.84
DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	DDX39	NM_005804	BAT1 // BAT1L // DDXL // MGC18203 // MGC8417 // URH49	3852691	chr19	–	14380562	14404078	5.84
lectin, galactoside-binding, soluble, 8 (galectin 8)	LGALS8	NM_006499 // NM_201543 // NM_201544 // NM_201545	Gal-8 // PCTA-1 // PCTA1 // Po66-CBP	2386867	chr1	+	234717161	234782890	5.84
ankyrin repeat domain 10	ANKRD10	NM_017664	DKFZp686B07190 // FLJ20093	3525679	chr13	–	110322146	110365417	5.83

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
zinc finger and BTB domain containing 9 // synaptic Ras GTPase activating protein 1 homolog (rat)	ZBTB9 // SYNGAP1	NM_152735 // NM_006772	MGC23166 // DKFZp761G1421 // KIAA1938 // RASA1 // RASA5 //	2903703	chr6	+	33494813	33533290	5.82
transmembrane protein 70	TMEM70	NM_001040613 // NM_017866	FLJ20533	3103494	chr8	+	75046321	75057572	5.82
aftiphilin	AFTPH	NM_001002243 // NM_017657 // NM_203437	FLJ20080 // FLJ23793 // MGC33965 // Nbla10388	2485433	chr2	+	64604969	64714437	5.82
polymerase (RNA) 1 polypeptide A, 194 kDa	POLR1A	NM_015425	DKFZP586M0122 // FLJ21915 // MGC87965 // RPA1 // RPO1-4	2562605	chr2	−	86103197	86186509	5.81
general transcription factor IIIC, polypeptide 5, 63 kDa	GTF3C5	NM_012087	FLJ20857 // TFIIIC63 // TFIIICepsilon // TFiiiC2-63	3192653	chr9	+	134895917	134923708	5.81
tumor necrosis factor receptor superfamily, member 21	TNFRSF21	NM_014452	BM-018 // DR6 // MGC31965	2956052	chr6	−	47307230	47385639	5.80
sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B	SEMA4B	NM_020210 // NM_198925	KIAA1745 // MGC131831 // SEMAC // SemC	3607927	chr15	+	88529156	88573879	5.80
mitochondrial ribosomal protein S11	MRPS11	NM_022839 // NM_176805	FLJ22512 // FLJ23406 // HCC-2	3607183	chr15	+	86811688	86822612	5.80
nuclear factor of activated T-cells 5, tonicity-responsive	NFAT5	NM_006599 // NM_138713 // NM_138714 // NM_173214 // NM_173215	KIAA0827 // NF-AT5 // NFATL1 // NFATZ // OREBP // TONEBP	3666779	chr16	+	68156498	68296054	5.80
nuclear receptor subfamily 2, group F, member 2	NR2F2	NM_021005	ARP1 // COUP-TFII // COUPTFB // MGC117452 // SVP40 // TFCOUP2	3610110	chr15	+	94448164	94683620	5.79
SH3 domain containing ring finger 1	SH3RF1	NM_020870	FLJ21602 // KIAA1494 // POSH // RNF142 //	2793137	chr4	−	170220651	170428725	5.78
splicing factor 3b, subunit 3, 130 kDa	SF3B3	NM_012426	KIAA0017 // RSE1 // SAP130 // SF3b130 // STAF130	3667281	chr16	+	69115212	69169072	5.78
PTC7 protein phosphatase homolog (*S. cerevisiae*)	PPTC7	NM_139283	DKFZp686M07120 // MGC133072 // TA-PP2C	3471300	chr12	−	109455446	109514152	5.77
homeodomain interacting protein kinase 1	HIPK1	NM_152696 // NM_181358 // NM_198268 //	KIAA0630 // MGC26642 // MGC33446 //	2352758	chr1	+	114273467	114322014	5.77

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Array Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change
		NM_198269	MGC33548 // Myak // Nbak2						
nuclear receptor binding protein 1	NRBP1	NM_013392	BCON3 // FLU27109 // FLJ35541 // MADM // MUDPNP // NRBP	2474527	chr2	+	27504171	27518620	5.77
cleavage stimulation factor, 3' pre-RNA, subunit 1, 50 kDa	CSTF1	NM_001033521 // NM_001033522 // NM_001324	CstF-50 // CstFp50	3890154	chr20	+	54393411	54413257	5.77
pre-B-cell colony enhancing factor 1 // pre-B cell enhancing factor 1 pseudogene	PBEF1 // RP11-92J19.4	NM_005746 // —	1110035O14Rik // DKFZP666B131 // MGC117256 // NAMPT // PBEF // LOC646309	3066818	chr7	−	105625846	105713266	5.77
transmembrane protein 11	TMEM11	NM_003876	C17orf35 // PM1 // PMI	3749767	chr17	−	21041205	21058509	5.77
transmembrane protein 115	TMEM115	NM_007024	PL6	2675304	chr3	−	50367198	50372046	5.76
catenin (cadherin-associated protein), alpha-like 1	CTNNAL1	NM_003798	CLLP // alpha-CATU	3219621	chr9	−	110744011	110815625	5.76
clathrin, heavy chain (Hc)	CLTC	NM_004859	CHC17 // CLH-17 // CLTCL2 // Hc // KIAA0034	3729172	chr17	+	55052021	55127299	5.76
cyclin H	CCNH	NM_001239	CAK // p34 // p37	2865860	chr5	−	86707385	86782317	5.74
SECIS binding protein 2	SECISBP2	NM_024077	DKFZp686C09169 // SBP2	3178611	chr9	+	91122988	91146214	5.74
WD repeat domain 26	WDR26	NM_025160	FLJ21016 // MIP2	2458082	chr1	−	222639474	222691338	5.74
stomatin (EPB72)-like 2 // Fanconianemia, complementation group G	STOML2 // FANCG	NM_013442 // NM_004629	HSPC108 // SLP-2 // FAG // XRCC9	3204534	chr9	−	35089540	35093157	5.74
nucleolar and coiled-body phosphoprotein 1	NOLC1	NM_004741	KIAA0035 // NOPP130 // NOPP140 // NS5ATP13 // P130	3261492	chr10	+	103901962	103913597	5.73
ADP-ribosylhydrolase like 2	ADPRHL2	NM_017825	ARH3 // FLJ20446 // dJ665N4.2	2330253	chr1	+	36327093	36332113	5.73
chromosome 1 open reading frame 164	C1orf164	NM_018150	FLJ10597	2333907	chr1	+	44643293	44889968	5.72
platelet-activating factor acetylhydrolase, isoform Ib, beta subunit 30 kDa	PAFAH1B2	NM_002572	—	3350749	chr11	+	116520229	116552810	5.72
DPH2 homolog (*S. cerevisiae*) // UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 2 // ATPase, H+ transporting, lysosomal 21 kDa, V0 subunit b	DPH2 // B4GALT2 // ATP6V0B	NM_001039589 // NM_001384 // NM_001005417 // NM_003780 // NM_001039457 // NM_004047	DPH2L2 // B4Gal-T2 // B4Gal-T3 // beta4Gal-T2 // ATP6F // HATPL // VMA16	2333635	chr1	+	44208244	44211909	5.72
chromosome 4 open reading frame 14	C4orf14	NM_032313	MGC3232 // hAtNOS1 //	2770427	chr4	−	57496489	57539746	5.72

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Array Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change
ST3 beta-galactoside alpha-2,3-sialyltransferase 4	ST3GAL4	NM_006278	CGS23 // FLJ11867 // NANTA3 // SAT3 // SIAT4 // SIAT4C // ST3Gal IV // ST3GalIV // STZ	3355145	chr11	+	125730175	126063667	5.71
myeloid differentiation primary response gene (88)	MYD88	NM_002468	—	2617563	chr3	+	38155029	38159513	5.71
interferon-related developmental regulator 2	IFRD2	NM_006764	FLJ40446 // IFNRP // SKMc15 // SM15	2675088	chr3	–	50300134	50305282	5.71
TNF receptor-associated factor 4	TRAF4	NM_145751 // NM_004295	CART1 // MLN62 // RNF83	3715839	chr17	+	24095168	24102103	5.71
Kruppel-like factor 5 (intestinal)	KLF5	NM_001730	BTEB2 // CKLF // IKLF	3493543	chr13	+	72527115	72549671	5.70
melanophilin	MLPH	NM_001042467 // NM_024101	MGC2771 // MGC59733 // SLAC2-A	2534252	chr2	+	238025804	238135783	5.70
pleckstrin homology, Sec7 and coiled-coil domains 2 (cytohesin-2)	PSCD2	NM_004228 // NM_017457	ARNO // CTS18 // CTS18.1 // PSCD2L // SEC7L // Sec7p-L // Sec7p-like	3837836	chr19	+	53664134	53690474	5.69
5'-3' exoribonuclease 2	XRN2	NM_012255	—	3879467	chr20	+	21219705	21322172	5.69
large subunit GTPase 1 homolog (*S. cerevisiae*)	LSG1	NM_018385	FLJ11301	2711818	chr3	–	195842815	195874226	5.69
ubiquitin protein ligase E3C	UBE3C	NM_014671	KIAA0010 // KIAA10	3033924	chr7	+	156624381	156754823	5.68
Rho GTPase-activating protein	RICS	NM_014715	GC-GAP // GRIT // KIAA0712 // MGC1892 // p200RhoGAP // p250GAP	3397877	chr11	–	128343040	128567297	5.68
v-raf murine sarcoma viral oncogene homolog B1	BRAF	NM_004333	B-raf I // BRAF1 // MGC126806 // MGC138284 //	3076340	chr7	–	139994192	140274640	5.68
heterogeneous nuclear ribonucleoprotein H3 (2H9)	HNRPH3	NM_012207 // NM_021644	2H9	3249738	chr10	+	69760947	69772949	5.68
NudC domain containing 1	NUDCD1	NM_032869	CML66 // FLJ14991	3148796	chr8	–	110322324	110415934	5.68
GATA binding protein 6	GATA6	NM_005257	—	3781245	chr18	+	18003412	18060817	5.67
preimplantation protein 3 // heat shock 10 kDa protein 1 (chaperonin 10)	PREI3 // HSPE1	NM_015387 // NM_199482 // NM_002157	2C4D // CGI-95 // MGC12264 // MOB1 // MOB3 // CPN10 // GROES // HSP10	2521500	chr2	+	198088565	198125849	5.67
chromosome 14 open reading frame 151	C14orf151	NM_032714	MGC13251	3554282	chr14	+	104227008	104244902	5.67
ADAM metallopeptidase domain 9 meltrin gamma)	ADAM9	NM_001005845 // NM_003816	KIAA0021 // MCMP // MDC9 // Mltng	3095002	chr8	+	38973642	39082294	5.67
target of EGR1, member 1 (nuclear)	TOE1	NM_025077	FLJ13949	2334319	chr1	+	45577929	45582381	5.67
acidic (leucine-rich) nuclear phosphoprotein 32 family, member B	ANP32B	NM_006401	APRIL // PHAPI2 // SSP29	3181417	chr9	+	99784907	99823167	5.66

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
cleavage and polyadenylation specific factor 4, 30 kDa	CPSF4	NM_001081559 // NM_006693	CPSF30 // NAR // NEB1	3014764	chr7	+	98874515	98905314	5.66
IK cytokine, down-regulator of HLA II	IK	NM_006083	OSA2 // IK protein // MGC59741 // RED	2831932	chr5	+	140006890	140022229	5.66
phosphoribosyl pyrophosphate amidotransferase	PPAT	NM_002703	ATASE // GPAT	2770242	chr4	−	56954288	57029053	5.65
proteasome (prosome, macropain) 26S subunit, ATPase, 2	PSMC2	NM_002803	MGC3004 // MSS1 // Nbla10058 // S7	3017206	chr7	+	102771969	102797076	5.65
N-acetyltransferase 5	NAT5	NM_016100 // NM_181527 // NM_181528	NAT3 // dJ1002M8.1	3878934	chr20	+	19935711	19962808	5.65
USP6 N-terminal like	USP6NL	XM_374768 // XM_927409 // XM_938665 // XM_943800 // NM_001080491	KIAA0019 // RNTRE // TRE2NL	3277468	chr10	−	11523200	11725919	5.65
EMG1 nucleolar protein hemolog (*S. cerevisiae*)	EMG1	NM_006331	C2F // Grcc2f // NEP1	3403140	chr12	+	6949871	6966191	5.65
glutaminase	GLS	NM_014905	DKFZp686O15119 // FLJ10358 // GLS1 // KIAA0838	2520291	chr2	+	191453802	191538513	5.65
pleiomorphic adenoma gene-like 2	PLAGL2	NM_002657	FLJ23283	3902682	chr20	−	30243975	30259284	5.63
TM2 domain containing 3	TM2D3	NM_025141 // NM_078474	BLP2	3642358	chr15	−	99977972	100010609	5.62
SEC24 related gene family, member C (*S. cerevisiae*)	SEC24C	NM_004922 // NM_198597	KIAA0079	3251848	chr10	+	75174138	75210008	5.62
ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	UBE2D3	NM_003340 // NM_181886 // NM_181887 // NM_181888 // NM_181889 // NM_181890 // NM_181891 // NM_181892 // NM_181893	E2(17)KB3 // MGC43926 // MGC5416 // UBC4/5 // UBCH5C	2779992	chr4	−	103934623	104009473	5.61
Rho guanine nucleotide exchange factor (GEF) 7	ARHGEF7	NM_003899 // NM_145735	BETA-PIX // COOL1 // DKFZp761K1021 // KIAA0142 // KIAA0142 // Nbla10314 // P50 // P50BP // P85 // P85COOL1 // P85SPR // PAK3 //	3501661	chr13	+	110565635	110756075	5.61
ring-finger protein 139	RNF139	NM_007218	HRCA1 // MGC31961 // RCA1 // TRC8	3114618	chr8	+	125556189	125570389	5.59

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
valosin-containing protein // Fanconi anemia, complementation group G	VCP // FANCG	NM_007126 NM_004629	IBMPFD // MGC131997 // MGC148092 // MGC8560 // TERA // p97 // FAG //	3204404	chr9	–	35026106	35062648	5.58
ADP-ribosylation factor 1	ARF1	NM_001024226 // NM_001024227 // NM_001024228 // NM_001658	—	2383726	chr1	+	226313262	226353506	5.58
bladder cancer associated protein	BLCAP	NM_006698	BC10	3904928	chr20	–	35554050	35589711	5.57
heterogeneous nuclear ribonucleoprotein H1 (H)	HNRPH1	NM_005520	DKFZp686A15170 // HNRPH // hnRNPH	2890148	chr5	–	178970155	178993890	5.57
programmed cell death 2-like	PDCD2L	NM_032346	MGC13096	3829751	chr19	+	39587143	39608910	5.57
TNF receptor-associated factor 2	TRAF2	NM_021138	MGC: 45012 // TRAP // TRAP3	3194896	chr9	+	138896205	138943484	5.56
ring finger protein 43	RNF43	NM_017763	DKFZp781H02126 // DKFZp781H0392 // FLJ20315 // MGC125630 // RNF124 // URCC	3764399	chr17	–	53785272	53849935	5.56
tousled-like kinase 1	TLK1	NM_012290	KIAA0137 // PKU-BETA	2586603	chr2	–	171538552	171796060	5.55
suppressor of zeste 12 homolog (*Drosophila*)	SUZ12	NM_015355	CHET9 // JJAZ1 // KIAA0160	3717395	chr17	+	27258855	27352177	5.55
dynactin 4 (p62)	DCTN4	NM_016221	—	2881554	chr5	–	150065753	150135890	5.54
leucine rich repeat containing 1 // chromosome 20 open reading frame 44	LRRC1 // C20orf44	NM_018214 // NM_018244 // NM_199487 // NM_199513	FLJ10775 // FLJ11834 // LANO // dJ523E19.1 // BFZB // CBP3 // MGC104353 // MGC141902	2910680	chr6	+	53695560	53897416	5.54
GTPase activating protein (SH3 domain) binding protein 2 // NMDA receptor regulated 2 // RAR-related orphan receptor A	G3BP2 // NARG2 // RORA	NM_012297 // NM_203504 // NM_203505 // NM_001018089 // NM_024611 // NM_002943 // NM_134260 // NM_134261 // NM_134262	—// MGC119326 // MGC119329 // NR1F1 // ROR1 // ROR2 // ROR3 // RZRA	2773756	chr4	–	76786807	76869171	5.54
ubiquitin specific peptidase 3	USP3	NM_006537	MGC129878 // MGC129879 // SIH003 // UBP	3597603	chr15	+	61554385	61673885	5.54
peptidylprolyl isomerase (cyclophilin)-like 4 // solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 24	PPIL4 // SLC25A24	NM_139126 // NM_013386 // NM_213651	HDCME13P // APC1 // DKFZp586G0123 // SCAMC-1	2978876	chr6	–	149811664	149908884	5.54

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Array Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change
structural maintenance of chromosomes 1A	SMC1A	NM_006306	DKFZp686L19178 // DXS423E // KIAA0178 // MGC138332 // SB1.8 // SMC1 // SMC1L1 // SMC1alpha //	4009238	chrX	–	53417797	53466400	5.53
NM23-LV // non-metastatic cells 1, protein (NM23A) expressed in	NME1-NME2 // NME1	NM_001018136 // NM_000269 // NM_198175	NME2 // AWD // GAAD // NDPKA // NM23 // NM23-H1	3726934	chr17	+	46564693	46594905	5.52
taxilin alpha // doublecortin domain containing 2B	TXLNA // DCDC2B	NM_175852 // XM_926306 // XM_940631	DKFZp451J0118 // IL14 // MGC118870 // MGC118871 // RP4-622L5.4 // TXLN // —	2328713	chr1	+	32417884	32436467	5.52
cysteine-rich, angiogenic inducer, 61	CYR61	NM_001554	CCN1 // GIG1 // IGFBP10	2344888	chr1	+	85816676	85867516	5.52
prothymosin, alpha (gene sequence 28) // family with sequence similarity 22, member G	PTMA // FAM22G	NM_002823 // XM_001127718 // NM_001045477	MGC104802 // TMSA // —	2532021	chr2	+	232280604	232286493	5.52
casein kinase 1, epsilon // KIAA1660 protein	CSNK1E // KIAA1660	NM_001894 // NM_152221 // XM_929784 // XM_940170	HCKIE // MGC10398 // —	3960478	chr22	–	37010115	37150916	5.51
MCM3 minichromosome maintenance deficient 3 (*S. cerevisiae*)	MCM3	NM_002388	HCC5 // MGC1157 // P1-MCM3 // P1.h // RLFB	2957126	chr6	–	52236739	52356643	5.50
solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3	SLC25A3	NM_213612 // NM_002635 // NM_005888 // NM_213611	OK/SW-cl.48 // PHC	3427820	chr12	+	97511471	97519906	5.50
potassium channel tetramerisation domain containing 5	KCTD5	NM_018992	FLJ20040	3645204	chr16	+	2640820	2700477	5.50
STE20-like kinase (yeast)	SLK	NM_014720	KIAA0204 // MGC133067 // STK2 // bA16H23.1 // se20-9	3262433	chr10	+	105716666	105778975	5.49
glutathione reductase	GSR	NM_000637	MGC78522	3130161	chr8	–	30655000	30705038	5.49
par-3 partitioning defective 3 homolog (*C. elegans*)	PARD3	NM_019619	ASIP // Baz // Bazooka // FLJ21015 // PAR3 // PAR3alpha // PARD3A // SE2-5L16 // SE2-5LT1 // SE2-	3284596	chr10	–	34413632	35144249	5.49
UTP18, small subunit (SSU) processome component, homolog (yeast)	UTP18	NM_016001	CGI-48 // WDR50	3726992	chr17	+	46692081	46730289	5.49

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
serine/arginine repetitive matrix 1 // chromosome 1 open reading frame 130	SRRM1 // C1orf130	NM_005839 // NM_001010980	160-KD // MGC39488 // POP101 // SRM160 // FLJ42528	2325526	chr1	+	24830814	24929968	5.49
conserved nuclear protein NHN1	NHN1	NM_144604	FLJ22664 // FLJ34530 // FLJ36075	3673515	chr16	+	87152329	87225870	5.49
UBX domain containing 8	UBXD8	NM_014613	ETEA // KIAA0887	2842570	chr5	+	175807217	175870117	5.48
elongation protein 4 homolog (*S. cerevisiae*)	ELP4	NM_019040	C11orf19 // FLJ20498 // PAX6NEB // PAXNEB // dJ68P15A.1	3325307	chr11	+	31487883	31764940	5.48
hypothetical protein FLJ20366	FLJ20366	NM_017786	GOLSYN	3148871	chr8	−	110655383	110964912	5.48
SYF2 homolog, RNA splicing factor (*S. cerevisiae*) // MAX interactor 1 // chromosome 1 open reading frame 63	SYF2 // MXI1 // C1orf63	NM_015484 // NM_207170 // NM_001008541 // NM_005962 // NM_130439 // NM_020317	CBPIN // DKFZp564O2082 // NTC31 // P29 // MAD2 // MGC43220 // MXD2 // MXI // DJ465N24.2.1 // NPD014 // RP3-465N24.4	2402068	chr1	−	25324131	25431599	5.47
exostoses (multiple) 1	EXT1	NM_000127	EXT // ttv	3150060	chr8	−	118880792	119193382	5.46
polymerase (RNA) II (DNA directed) polypeptide D // WD repeat domain 33	POLR2D // WDR33	NM_004805 // NM_001006622 // NM_001006623 // NM_018383	HSRBP4 // HSRPB4 // RBP4 // FLJ11294 // WDC146	2575134	chr2	−	128317597	128334003	5.45
ankyrin repeat domain 13 family, member D	ANKRD13D	XM_001129739 // NM_207354	MGC50828	3336857	chr11	+	66812660	66826524	5.45
serum amyloid A-like 1	SAAL1	NM_138421	FLJ41463	3365249	chr11	−	18048076	18084203	5.45
C1q domain containing 1	C1QDC1	NM_001002259 // NM_023925 // NM_032156	EEG-1 // EEG1 // FLJ11391 // FLJ22569 // MGC102894 // MGC134847 // MGC134848	3449368	chr12	−	30753755	30799712	5.44
chromosome 11 open reading frame 30	C11orf30	NM_020193	EMSY // FLJ90741 // GL002	3340913	chr11	+	75803897	75941697	5.44
ubiquilin 1 // death inducer-obliterator 1	UBQLN1 // DIDO1	NM_013438 // NM_053067 // NM_022105 // NM_033081 // NM_080796 // NM_080797	DA41 // DSK2 // FLJ90054 // PLIC-1 // XDRP1 // BYE1 // C20orf158 // DATF1 // DIDO2 // DIDO3// DIO-1 // DIO1 // DKFZp434P1115 // FLJ11265 // KIAA0333 // MGC16140 //	3212143	chr9	−	85464717	85512928	5.44

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
similar to ribosomal protein P0 // ribosomal protein, large, P0	RPLP0-like // RPLP0	XR_015741 // XR_017813 // NM_001002 // NM_053275	BLOCK 23 // LI0E // MGC111226 // MGC88175 // P0 // PRLP0 // RPP0	3474344	chr12	–	119118908	119123401	5.44
zinc finger, NFX1-type containing 1 // gasdermin-like	ZNFX1 // GSDML	NM_021035 // NM_00104247 // NM_018530	FLJ39275 // MGC131926 // PP4052 // PRO2521	3908831	chr20	–	47233911	47420063	5.44
exportin 4	XPO4	NM_022459	FLJ13046 // KIAA1721	3504434	chr13	–	20251014	20375187	5.43
centrosomal protein 72 kDa	CEP72	NM_018140	FLJ10565 // KIAA1519 // MGC5307	2798777	chr5	+	608522	720187	5.43
basic transcription factor 3	BTF3	NM_001037637 // NM_001207	BETA-NAC // BTF3a // BTF3b // NACB	2815331	chr5	+	72704665	72850839	5.43
c-Maf-inducing protein	CMIP	NM_030629 // NM_198390	KIAA1694	3670772	chr16	+	80030441	80323852	5.42
cerebellar degeneration-related protein 2, 62 kDa	CDR2	NM_001802	CDR62 // Yo	3684782	chr16	–	22264766	22356527	5.42
ubiquitin-like 3	UBL3	NM_007106	DKFZP434K151 // FLJ32018 // HCG-1 // PNSC1	3507798	chr13	–	29200782	29371040	5.42
ATP-binding cassette, sub-family F (GCN20), member 1	ABCF1	NM_001025091 // NM_001090	ABC27 // ABC50	2901687	chr6	+	30647103	30667268	5.42
RAB22A, member RAS oncogene family	RAB22A	NM_020673	MGC16770	3890870	chr20	+	56318177	56375962	5.42
axin 1	AXIN1	NM_003502 // NM_181050	AXIN // MGC52315	3675047	chr16	–	277442	351633	5.41
mitochondrial ribosomal protein L44	MRPL44	NM_022915	FLJ12701 // FLJ13990	2529782	chr2	+	224530378	224540666	5.41
zinc finger protein 146 // zinc finger protein 268	ZNF146 // ZNF268	NM_007145 // NM_152943 // NM_003415	MGC125660 // MGC125661 // OZF // HZF3 // MGC126498	3831260	chr19	+	41397873	41421503	5.40
golgi SNAP receptor complex member 1	GOSR1	NM_001007024 // NM_001007025 // NM_004871	GOS28 // GOS28/P28 // GS28 // P28	3716481	chr17	+	25828452	25893594	5.40
zinc finger protein 512	ZNF512	NM_032434	KIAA1805 // MGC111046	2474651	chr2	+	27659393	27699586	5.40
formin binding protein 4	FNBP4	NM_015308	DKFZp779I1064 // FBP30 // FLJ41904 KIAA1014	3372459	chr11	–	47694235	47745657	5.39
zinc finger protein 707	ZNF707	NM_173831	—	3119765	chr8	+	144771273	144849532	5.39
FERM domain containing 5	FRMD5	NM_032892	FLJ41022 // MGC14161	3621728	chr15	–	41950261	42274751	5.39
serum/glucocorticoid regulated	SGK	NM_005627	SGK1	2975014	chr6	–	134532088	134680889	5.38
hypoxia-inducible factor 1, alpha	HIF1A	NM_001530 //	HIF-1 alpha // HIF1-	3539070	chr14	+	61225495	61285222	5.38

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
subunit (basic helix-loop-helix transcription factor)		NM_181054	ALPHA // MOP1 // PASD8						
deoxyhypusine synthase	DHPS	NM_001930 // NM_013406 // NM_013407	MIG13	3851603	chr19	−	12647534	12653680	5.37
thioredoxin-like 1	TXNL1	NM_004786	TRP32 // TXL-1 // TXNL // Txl	3809324	chr18	−	52334063	52469773	5.37
RAN, member RAS oncogene family	RAN	NM_006325	ARA24 // Gsp1 // TC4	3438027	chr12	+	129922411	129928164	5.36
dynein, cytoplasmic 1, light intermediate chain 2	DYNC1LI2	NM_006141	DNCLI2 // LIC2	3695199	chr16	−	65312304	65343212	5.36
enchancer of rudimentary homolog (*Drosophila*)	ERH	XM_001130537 // NM_004450	DROER // FLJ27340	3570049	chr14	−	68916605	68935306	5.35
transmembrane 4 L six family member 1	TM4SF1	NM_014220	H-L6 // L6 // M3S1 // TAAL6	2700365	chr3	−	150567718	150578270	5.34
lipase, endothelial	LIPG	NM_006033	EDL // EL //	3787855	chr18	+	45341077	45481323	5.34
exportin 6	XPO6	NM_015171	EXP6 // FLJ22519 // KIAA0370 // RANBP20	3686339	chr16	−	28016804	28130734	5.34
hypothetical protein FLJ11171	FLJ11171	NM_018348	—	3697563	chr16	−	69872813	69881003	5.34
UPF1 regulator of nonsense transcripts homolog (yeast)	UPF1	NM_002911	FLJ43809 // FLJ46894 // HUPF1 // KIAA0221 // NORF1 // RENT1 // pNORF1	3825383	chr19	+	18803757	18840030	5.34
surfeit 6	SURF6	NM_006753	FLJ30322	3228621	chr9	−	135186667	135193036	5.32
neural precursor cell expressed, developmentally down-regulated 4-like // sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4G	NEDD4L // SEMA4G	NM_015277 // NM_017893	FLJ33870 // KIAA0439 // RSP5 // hNedd4-2 // FLJ20590 // KIAA1619 // MGC102867	3789947	chr18	+	53862627	54232131	5.30
tetraspanin 14	TSPAN14	NM_030927	DC-TM4F2 // MGC11352 // TM4SF14	3254521	chr10	+	82203922	82272901	5.30
core-binding factor, beta subunit	CBFB	NM_001755 // NM_022845	PEBP2B	3665116	chr16	+	65620522	65692457	5.30
baculoviral IAP repeat-containing 5 (survivin)	BIRC5	NM_001012270 // NM_001012271 // NM_001168	API4 // EPR-1	3736290	chr17	+	73721882	73733311	5.29
grainyhead-like 2 (*Drosophila*)	GRHL2	NM_024915	BOM // DFNA28 // FLJ11172 // FLJ13782 // MGC149294 // MGC149295 // TFCP2L3	3109687	chr8	+	102573566	102751110	5.29

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Array	Human Genome hg18				
				Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
acdysoneless homolog (*Drosophila*)	ECD	NM_007265	GCR2 // HSGT1	3294242	chr10	–	74559939	74598411	5.29
RNA binding motif protein 13	RBM13	NM_032509	MAK16 // MAK16L	3093259	chr8	+	33462192	33478316	528
cell division cycle associated 2	CDCA2	NM_152562	FLJ25804 // MGC129906 // MGC129907 // Repo-Man	3090697	chr8	+	25362573	25431420	5.28
myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, *Drosophila*); translocated to, 4	MLLT4	NM_001040000 // NM_001040001 // NM_005936	AF-6 // AF6 // AFADIN // FLJ34371 // RP3-431P23.3	2936857	chr6	+	167970473	168115537	5.28
nuclear receptor subfamily 1, group H, member 2	NR1H2	NM_007121	LXR-b // LXRB // NER // NER-1 // RIP15 // UNR	3839276	chr19	+	55524771	55578457	5.28
tight junction protein 2 (zona occludens 2)	TJP2	NM_004817 // NM_201629	MGC26306 // X104 // ZO-2 // ZO2	3173880	chr9	+	70925894	71059931	5.27
eukaryotic translation initiation factor 2A, 65 kDa	EIF2A	NM_032025	CDA02 // EIF-2A // MST089 // MSTP004 // MSTP089	2647742	chr3	+	151747168	151788822	5.27
histone acetyltransferase 1	HAT1	NM_001033085 // NM_003642	—	2515369	chr2	+	172487173	172556842	5.26
ring finger protein 138	RNF138	NM_016271 // NM_198128	HSD-4 // MGC8758 // NARF // STRIN	3783749	chr18	+	27925835	28030948	5.26
phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	PTEN	NM_000314	BZS // MGC11227 // MHAM // MMAC1 // PTEN1 // TEP1	3256689	chr10	+	89598814	89722145	5.25
Ran GTPase activating protein 1	RANGAP1	NM_002883	Fug1 // KIAA1835 // MGC20266 // SD	3961842	chr22	–	39969442	40028027	5.24
zinc finger and BTB domain containing 7A	ZBTB7A	NM_015898	DKFZp547O146 // FBI-1 // FBI1 // LRF // MGC99631 // ZBTB7 // pokemon	3846594	chr19	–	3990713	4033507	5.24
methionyl aminopeptidase 2 // hypothetical protein FLJ11292	METAP2 // FLJ11292	NM_006838 // NM_018382	MNPEP // p67 // p67eIF2 // —	3426917	chr12	+	94391437	94696442	5.23
small nuclear ribonucleoprotein polypeptides B and B1	SNRPB	NM_003091 // NM_198216	COD // SNRPB1 // SmB/SmB' // snRNP-B	3894995	chr20	–	2369715	2399499	5.23
CD151 molecule (Raph blood group) // FK506 binding protein 9-like	CD151 // FKBP9L	NM_001039490 // NM_004357 // NM_139029 // NM_139030 // NM_182827	GP27 // MER2 // PETA-3 // RAPH // SFA1 // TSPAN24 // FKBP9 // MGC20531	3316344	chr11	+	822755	828824	5.23
wolf-Hirschhorn syndrome candidate 1	WHSC1	NM_001042424 // NM_007331 // NM_133330 // NM_133331 // NM_133334 // NM_133335 // NM_133336	FLJ23286 // KIAA1090 // MMSET // NSD2 // REIIBP // TRX5 // WHS	2715076	chr4	+	1842909	1953717	5.23

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
heterogeneous nuclear ribonucleoprotein U-like 1	HNRPUL1	NM_144733 // NM_144734 // NM_007040 // NM_144732	E1B-AP5 // E1BAP5 // FLJ12944	3834089	chr19	+	46460006	46505508	5.22
ubiquitin-conjugating enzyme E2C // p21 (CDKN1A)-activated kinase 3	UBE2C // PAK3	NM_007019 // NM_181799 // NM_181800 // NM_181801 // NM_181802 // NM_181803 // NM_002578	UBCH10 // dJ447F3.2 // CDKN1A // MRX30 // MRX47 // OPHN3 // PAK3beta // bPaK // hPAK3	3887049	chr20	+	43874662	43878994	5.22
ribosomal L1 domain containing 1	RSL1D1	NM_015659	CSIG // DKFZP564M182 // L12 // MGC138433 // MGC142259 //	3680583	chr16	–	11835208	11852988	5.22
Sjogren's syndrome nuclear autoantigen 1	SSNA1	NM_003731	N14 // NA-14 // NA14	3195296	chr9	+	139202850	139204636	5.22
zinc finger protein 227 // zinc finger protein 155	ZNF227 // ZNF155	NM_182490 // NM_003445 // NM_198089	—// MGC161655 // pHZ-96	3835544	chr19	+	49408524	49433254	5.21
splicing factor, arginine/serine-rich 6	SFRS6	NM_006275	B52 // MGC5045 // SRP55	3886050	chr20	+	41519932	41526301	5.21
transmembrane protein 5	TMEM5	NM_014254	HP10481	3419585	chr12	+	62440396	62489599	5.20
peptide deformylase (mitochondrial) // component of oligomeric golgi complex 8	PDF // COG8	NM_0022341 // NM_032382	—// DOR1 // FLJ22315	3696524	chr16	–	67914755	67931014	5.20
membrane-associated ring finger (C3HC4) 6	6-Mar	NM_005885	KIAA0597 // MARCH-VI //	2801608	chr5	+	10406824	10490959	5.20
Sp3 transcription factor // Sp3 transcription factor pseudogene	SP3 // RP11-114G1.1	NM_001017371 // NM_003111 // —	DKFZp686O1631 // SPR-2 // LOC160824	2587520	chr2	–	174445149	174610682	5.20
ubiquitin specific peptidase like 1	USPL1	NM_005800	C13orf22 // D13S106E // DKFZp781K2286 // FLJ32952 // RP11-121O19.1 // bA121O19.1	3484005	chr13	+	30028543	30132897	5.20
nucleolin	NCL	NM_005381	C23 // FLJ45706	2603460	chr2	–	232027713	232080578	5.19
myotubularin related protein 3	MTMR3	NM_021090 // NM_153050 // NM_153051	FYVE-DSP1 // KIAA0371 // ZFYVE10	3942179	chr22	+	28609182	28762301	5.19
Sec61 gamma subunit	SEC61G	NM_001012456 // NM_014302	SSS1	3051395	chr7	–	54753676	54847174	5.19
signal recognition particle 72 kDa	SRP72	NM_006947	—	2728224	chr4	+	57028214	57064696	5.19

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
chromosome 1 open reading frame 77	C1orf77	NM_015607	DKFZP547E1010 // MGC131924 // MGC86949 // RP1-178F15.2 // pp7704	2359736	chr1	+	151872948	151885444	5.18
zinc finger protein 787	ZNF787	NM_001002836	—	3871730	chr19	−	61261349	61355028	5.18
TAF5-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65 kDa // mucin 4, cell surface associated	TAF5L // MUC4	NM_001025247 // NM_014409 // XM_001125749 // NM_004532 // NM_018406 // NM_138297	PAF65B // HSA276359	2459971	chr1	−	227795491	227828457	5.18
cyclin T1	CCNT1	NM_001240	CCNT // CYCT1	3453218	chr12	−	47372840	47397048	5.18
A kinase (PRKA) anchor protein 1	AKAP1	NM_003488	AKAP // AKAP121 // AKAP149 // AKAP84 // D-AKAP1 // MGC1807 // PRKA1 // SAKAP84	3728097	chr17	+	52517583	52667254	5.18
proteasome (prosome, macropain) 26S subunit, ATPase, 5	PSMC5	NM_002805	S8 // SUG1 // TBP10 // TRIP1 // p45 // p45/SUG	3730941	chr17	+	59258523	59263555	5.18
protein phosphatase 1, regulatory (inhibitor) subunit 15B // phosphoinositide-3-kinase, class 2, beta polypeptide	PPP1R15B // PIK3C2B	NM_032833 // NM_002646	FLJ14744 // C2-PI3K // DKFZp686G16234	2452049	chr1	−	202639152	202647598	5.17
myristoylated alanine-rich protein kinase C substrate	MARCKS	NM_002356	80K-L // FLJ14368 // FLJ90045 // MACS // MRACKS // PKCSL // PRKCSL	2922215	chr6	+	114284762	114292853	5.17
M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)	MPHOSPH10	NM_005791	MPP10 // MPP10P	2488078	chr2	+	71210952	71237711	5.16
transmembrane protein 170	TMEM170	NM_145254	FLJ37611	3699581	chr16	−	74034456	74107659	5.15
YTH domain family, member 2	YTHDF2	NM_016258	HGRG8 // NY-REN-2	2327630	chr1	+	28935740	28968859	5.15
breast cancer anti-estrogen resistance 3	BCAR3	NM_003567	KIAA0554 // NSP2 // SH2D3B	2423422	chr1	−	93790445	94085633	5.15
KH domain containing, RNA binding, signal transduction associated 1	KHDRBS1	NM_006559	FLJ34027 // Sam68 // p62	2328465	chr1	+	32212249	32299034	5.15
reticulon 4	RTN4	NM_007008 // NM_020532 // NM_153828 // NM_207520 // NM_207521	ASY // NI220/250 // NOGO // NOGO-A // NSP // NSP-CL // Nbla00271 // Nbla10545 // RTN-X // RTN4-A // RTN4-B1 // RTN4-B2 // RTN4-C	2553576	chr2	−	55051075	55161279	5.15
calcitonin gene-related peptide-receptor component protein	RCP9	NM_001040647 // NM_001040648 // NM_014478	CGRP-RCP // CRCP // MGC111194 // RCP	3005332	chr7	+	65131004	65262097	5.15

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Array Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change
solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	SLC3A2	NM_001012661 // NM_001012662 // NM_001012663 // NM_001012664 // NM_001013251 // NM_002394	4F2 // 4F2HC // 4T2HC // CD98 // CD98HC // MDU1 // NACAE	3333711	chr11	+	62380117	62412872	5.15
zinc finger, DHHC-type containing 5	ZDHHC5	NM_015457	DKFZP586K0524 // KIAA1748 // ZNF375	3331433	chr11	+	57192053	57225319	5.14
Smg-5 homolog, nonsense mediated mRNA decay factor (*C. elegans*)	SMG5	NM_015327	EST1B // FLJ34864 // KIAA1089 // LPTS-RP1 // LPTSRP1 // RP11-54H19.7 // SMG-5	2438042	chr1	−	154485643	154519254	5.14
alkB, alkylation repair homolog 2 (*E. coli*)	ALKBH2	NM_001001655	ABH2 // MGC90512 // hABH2	3470689	chr12	−	108010254	108015656	5.13
BUD31 homolog (*S. cerevisiae*)	BUD31	NM_003910	EDG-2 // EDG2 // G10 // MGC111202 // YCR063W	3014742	chr7	+	98844221	98855171	5.13
MIS12, MIND kinetochore complex component, homolog (yeast)	MIS12	NM_024039	2510025F08Rik // KNTC2AP // MGC2488 // MTW1 // hMis12	3707759	chr17	+	5330450	5334853	5.13
tripartite motif-containing 26	TRIM26	NM_003449	AFP // RNF95 // ZNF173	2948259	chr6	−	30260217	30290029	5.13
similar to FRG1 protein (FSHD region gene 1 protein) // FSHD region gene 1	MGC72104 // FRG1	NM_207350 // NM_004477	—// FSG1	2756029	chr4	+	191051868	191138306	5.13
ATPase family, AAA domain containing 1	ATAD1	NM_032810	AFDC1 // FLJ14600 // FNP001	3299255	chr10	−	89500784	89591413	5.12
BTB (POZ) domain containing 3	BTBD3	NM_014962 // NM_181443	KIAA0952 // MGC130038 // MGC130039 // dJ742J24.1	3876645	chr20	+	11722386	11855239	5.12
sterol regulatory element binding transcription factor 2	SREBF2	NM_004599	SREBP2	3947123	chr22	+	40559049	40633247	5.12
splicing factor 3a, subunit 3, 60 kDa	SF3A3	NM_006802	PRP9 // PRPF9 // SAP61 // SF3a60	2407439	chr1	−	38195241	38229180	5.11
ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide	ATP5B	NM_001686	ATPMB // ATPSB // MGC5231	3458033	chr12	−	55318243	55326110	5.11
mitochondrial ribosomal protein L55	MRPL55	NM_181441 // NM_181454 // NM_181455 // NM_181456 //	AAVG5835 // DKFZp686D1387 // MGC61802 // PRO19675	2459438	chr1	−	226360734	226367172	5.11

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
		NM_181462 // NM_181463 // NM_181464 // NM_181465							
SMAD specific E3 ubiquitin protein ligase 1	SMURF1	NM_020429 // NM_181349	KIAA1625	3063083	chr7	−	98449133	98579664	5.11
myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, *Drosophila*)	MLL	NM_005933	ALL-1 // CXXC7 // HRX // HTRX1 // MLL/GAS7 // MLL1A // TRX1	3351385	chr11	+	117811029	117902749	5.10
family with sequence similarity 89, member B	FAM89B	NM_152832	MTVR1	3335338	chr11	+	65096490	65098230	5.10
alkB, alkylation repair homolog 3 (*E. coli*)	ALKBH3	NM_139178	ABH3 // DEPC-1 // DEPC1 // MGC118790 // MGC118792 //	3328214	chr11	+	43858633	43898486	5.10
SET domain containing 2	SETD2	NM_014159	FLJ16420 // FLJ22472 // FLJ23184 // FLJ45883 // HIF-1 // HSPC069 // HYPB // KIAA1732	2672532	chr3	−	47032936	47180418	5.09
p53 and DNA damage regulated 1	PDRG1	NM_030815	C20orf126 // PDRG	3902609	chr20	−	29995826	30005314	5.09
ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)	UCHL3	NM_006002	—	3494102	chr13	+	75021620	75078250	5.08
hepatocyte growth factor-regulated tyrosine kinase substrate	HGS	NM_004712	HRS // ZFYVE8	3738138	chr17	+	77260785	77279549	5.08
proteasome (prosome, macropain) 26S subunit, ATPase, 4	PSMC4	NM_006503 // NM_153001	MGC13687 // MGC23214 // MGC8570 // MIP224 // S6 // TBP7	3833291	chr19	+	45168772	45179181	5.08
tubulin, beta	TUBB	NM_178014	M40 // MGC117247 // MGC16435 // OK/SW-cl.56 // TUBB1 // TUBB5	2901913	chr6	+	30795977	30801165	5.08
kinesin family member 20A	KIF20A	NM_005733	FLJ21151 // MKLP2 // RAB6KIFL	2830638	chr5	+	137542289	137552275	5.08
arginyl-tRNA synthetase	RARS	NM_002887	ArgRS // DALRD1 // MGC8641	2839671	chr5	+	167845940	167878885	5.08
calpain 2, (m/II) large subunit	CAPN2	NM_001748	CANPL2 // CANPml // FLJ39928 // mCANP	2382117	chr1	+	221955990	222031806	5.08

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
ribosomal protein S15a	RPS15A	NM_001019 // NM_001030009	FLJ27457 // MGC111208 // S15a	3683018	chr16	–	18700121	18709175	5.07
topoisomerase (DNA) II binding protein 1	TOPBP1	NM_007027	TOP2BP1	2695941	chr3	–	134799729	134863527	5.07
calcium homeostasis endoplasmic reticulum protein // cofactor required for Sp1 transcriptional activation, subunit 7, 70 kDa	CHERP // CRSP7	NM_006387 // NM_004831	DAN16 // SCAF6 // SRA1 // CRSP70 // MED26	3853942	chr19	–	16489710	16517113	5.06
echinoderm microtubule associated protein like 4	EML4	NM_019063	C2orf2 // DKFZp686P18118 // ELP120 // FLJ10942 // FLJ32318 // ROPP120	2478748	chr2	+	42250017	42418636	5.06
splicing factor 3b, subunit 4, 49 kDa	SF3B4	NM_005850	MGC10828 // SAP49 // SF3b49	2434159	chr1	–	148161628	148167125	5.05
rho/rac guanine nucleotide exchange factor (GEF) 18	ARHGEF18	NM_015318	KIAA0521 // MGC15913	3818732	chr19	+	7319892	7443363	5.05
pescadillo homolog 1, containing BRCT domain (zebrafish)	PES1	NM_014303	PES	3957445	chr22	–	29302623	29333107	5.05
Ras association (RalGDS/AF-6) domain family 7	RASSF7	NM_003475	C11orf13 // HRAS1 // HRC1 // MGC126069 // MGC126070	3315952	chr11	+	550321	554016	5.05
Wilms tumor 1 associated protein // acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thiolase)	WTAP // ACAT2	NM_004906 // NM_152857 // NM_152858 // NM_005891	DKFZp686F20131 // KIAA0105 // MGC3925 // —	2934089	chr6	+	160066607	160097332	5.04
origin recognition complex, subunit 5-like (yeast)	ORC5L	NM_002553 // NM_181747	ORC5 // ORC5P // ORC5T	3065963	chr7	–	103553146	103719295	5.04
chromodomain protein, Y-like	CDYL	NM_004824 // NM_170751 // NM_170752	CDYL1 // DKFZP586C1622 // MGC131936	2892979	chr6	+	4651344	4900768	5.03
aprataxin	APTX	NM_017692 // NM_175069 // NM_175071 // NM_175072 // NM_175073	AOA // AOA1 // AXA1 // EAOH // EOAHA // FHA-HIT // FLJ20157 // MGC1072	3203311	chr9	–	32962360	33015096	5.03
phosphatidylinositol 4-kinase, catalytic, beta polypeptide // regulatory factor X, 5 (influences HLA class II expression)	PIK4CB // RFX5	NM_002651 // NM_000449 // NM_001025603	PI4K-BETA // PI4KIIIbeta // PI4Kbeta // —	2434925	chr1	–	149530589	149567792	5.03

TABLE 3-continued

				Human Exon ST 1.0 Array	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
serine palmitoyltransferase, long chain base subunit 2	SPTLC2	NM_004863	KIAA0526 // LCB2 // SPT2	3573152	chr14	–	77042100	77202740	5.02
cell division cycle associated 5	CDCA5	NM_080668	MGC16386	3377423	chr11	–	64592075	64608249	5.02
myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, *Drosophila*)	MLL5	NM_018682 // NM_182931	FLJ10078 // FLJ14026 // HDCMC04P // MGC70452	3017547	chr7	+	104436029	104542698	5.02
F-box protein 28	FBXO28	NM_015176	FLJ10766 // Fbx28 // KIAA0483	2382336	chr1	+	222368455	222416368	5.02
eukaryotic translation initiation factor 3, subunit, 1 alpha, 35 kDa	EIF3S1	NM_003758	eIF3-alpha // eIF3-p35 // eIF3j	3591963	chr15	+	42616580	42644124	5.02
polymerase (RNA) III (DNA directed) polypeptide C (62 kD)	POLR3O	NM_006468	RPC3 // RPC62	2432647	chr1	–	144297192	144333220	5.01
bromodomain adjacent to zinc finger domain, 1B	BAZ1B	NM_023005 // NM_032408	WBSCR10 // WBSCR9 // WSTF	3056044	chr7	–	72492710	72574552	5.01
isocitrate dehydrogenase 3 (NAD+) beta	IDH3B	NM_006899 // NM_174855 // NM_174856	FLJ11043 // H-IDHB // MGC903	3895075	chr20	–	2586736	2592862	5.01
basic transcription factor 3-like 4	BTF3L4	NM_152265	MGC23908 // MGC88389 // RP4-800M22.5	2336271	chr1	+	52293292	52339895	5.01
Src homology 2 domain containing adaptor protein B // cytoskeleton associated protein 2 // mitochondrial carrier triple repeat 1	SHB // CKAP2 // MCART1	NM_003028 // NM_018204 // NM_033412	RP11-3J10.8 // bA3J10.2 // FLJ10749 // LB1 // CG7943 //	3205659	chr9	–	37901375	38059198	5.00

Example 9

Analysis with Microarray (3)

[0218] Using the PBMC samples in Example 4(2), genes of which introns exhibited increased expression were identified. Ribosomal RNA was removed from 1 μg of each total RNA of control cells (n=3) and cells with the treatment (n=3) using RiboMinus Human/Mouse Transcriptome Isolation Kit (Invitrogen). Single stranded cDNA synthesis, double stranded cDNA synthesis, cRNA synthesis, second single stranded cDNA synthesis, cDNA fragmentation, and cDNA labeling in order were carried out for total RNA from which ribosomal RNA was removed, using GeneChip Whole Transcript Sense Target Labeling and Control Reagents (Affymetrix) to make a cDNA probe. Subsequently, the cDNA probe was used for hybridization with Human Exon 1.0 ST Array (Affymetrix). The array was washed and stained, and luminescence intensity was measured by a scanner.

[0219] The expression level of the probe set and the gene was quantified by using Expression Console Ver. 1.0 (Affymetrix) with Summarization Method and Normalization Method being set to "Median polish as used in RMA" and "None", respectively. The expression level of the probe was normalized with that of the gene.

[0220] (1) Identification of a Gene of which Introns Exhibit Increased Expression in a Group with the Treatment at a Concentration of 3 nM

[0221] Probe sets showing that the normalized change in the level expression of the probe set in the group with the treatment at 3 nM was more than 5 times; the expression level of the probe set and the gene in the group with the treatment at 3 nM was more than 100; and probe set annotation was "extended, full, free", were picked out. Welch's t-test was conducted with the probe sets extracted for the group with the treatment at 3 nM and the control group to determine a p value and a q value. A gene containing the probe sets with the q value of less than 5% was determined as a candidate gene with increased expression level of the intron regions (Table 4).

[0222] In Table 4, for the gene evaluated, gene name (Gene Name), abbreviated name (Gene Symbol), accession number (Accession), alias name (Synonym), transcription cluster number in Human Exon 1.0 ST Array (Human Exon 1.0 ST Array Transcript Cluster ID), chromosome number (Chromosome), type of strand (Strand), start region (Start), stop region (Stop), and change in expression level (Fold Change) were respectively shown.

TABLE 4

				Human Exon ST 1.0	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
TIMP metallopeptidase inhibitor 1	TIMP1	NM_003254	CLGI // EPA // EPO // FLJ90373 // HCI // TIMP	3976341	chrX	+	47326654	47332978	14.98
ADAM metallopeptidase domain 19 (meltrin beta)	ADAM19	NM_023038 // NM_033274	FKSG34 // MADDAM // MLTNB	2883440	chr5	–	156755122	156935351	9.71
phosphodiesterase 4A, cAMP-specific (phosphodiesterase E2 dunce homolog.	PDE4A	NM_006202	DPDE2 // PDE4	3820501	chr19	+	10388560	10451531	9.64
Rap guanine nucleotide exchange factor (GEF) 1	RAPGEF1	NM_005312 // NM_198679	C3G // DKFZp781P1719 // GRF2	3227696	chr9	–	133441988	133605262	9.27
myosin, heavy chain 9, non-muscle	MYH9	NM_002473	DFNA17 // EPSTS // FTNS // MGC104539 // MHA // NMHC-II-A // NMMHCA	3959451	chr22	–	35007278	35113982	7.90
serpin peptidase inhibitor, clade B (ovalbumin), member 9 // serpin peptidase inhibitor, clade B (ovalbumin), member 6	SERPINB9 // SERPINB6	NM_004155 // NM_004568	CAP-3 // CAP3 // P19 // CAP // DKFZp686I04222 // MGC111370 // MSTP057 //	2939034	chr6	–	2832402	2858242	7.75
RNA binding motif protein 23	RBM23	NM_001077351 // NM_001077352 // NM_018107	CAPERbeta // FLJ10482 // MGC4458 // PP239 // RNPC4	3556888	chr14	–	22439714	22458231	7.63
polyhomeotic homolog 3 (*Drosophila*)	PHC3	NM_024947	DKFZp313K1221 // EDR3 // FLJ12729 // FLJ12967 // HPH3 // MGC88144	2704894	chr3	–	171287994	171381537	7.30
splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	SFPQ	NM_005066	POMP100 // PSF	2406064	chr1	–	35351696	35506894	7.08
BTB (POZ) domain containing 11	BTBD11	NM_001017523 //	FLJ33957 // FLJ42845	3430462	chr12	+	106237825	106577543	7.07

TABLE 4-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change
		NM_001018072 // NM_152322							
v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	SRC	NM_005417 // NM_198291	ASV // SRC1 // c-SRC // p60-Src	3884191	chr20	+	35406502	35467847	6.98
signal-induced proliferation-associated 1 like 1	SIPA1L1	NM_015556	DKFZp686G1344 // E6TP1 // KIAA0440	3542847	chr14	+	70857592	71468470	6.93
MYST histone acetyltransferase 2	MYST2	NM_007067	HBO1 // HBOA	3725779	chr17	+	45196447	45261455	6.84
GPI-anchored membrane protein 1	GPIAP1	NM_005898 // NM_203364	GPIP137 // M11S1 // p137GPI	3326183	chr11	+	34009711	34081946	6.78
integrin, alpha X (complement component 3 receptor 4 subunit)	ITGAX	XM_001127869 // NM_000887	CD11C	3657041	chr16	+	31274012	31301819	6.76
microtubule-associated protein, RP/EB family, member 1	MAPRE1	NM_012325	EB1 // MGC117374 // MGC129946	3882069	chr20	+	30871304	30901864	6.65
RAB6 interacting protein 1	RAB6IP1	NM_015213	FLJ22354 // FLJ33829 // FLJ43455 // KIAA1091	3362263	chr11	–	9116953	9243468	6.61
testis derived transcript (3 LIM domains)	TES	NM_015641 // NM_152829	DKFZP586B2022 // MGC1146 // TESS // TESS-2 //	3020192	chr7	+	115637811	115743800	6.22
t-complex 1	TCP1	NM_001008897 // NM_030752	CCT-alpha // CCT1 // CCTa // D6S230E // TCP-1-alpha	2982381	chr6	–	160119521	160130731	6.19
CHMP family, member 7	CHMP7	NM_152272	MGC29816	3089853	chr8	+	23157105	23176288	6.08
toll-like receptor 4	TLR4	NM_138554	CD284 // TOLL // hToll	3186966	chr9	+	119506334	119670150	6.00
fibronectin type III domain containing 3B	FNDC3B	NM_022763	DKFZp686D14170 // DKFZp762K137 // FAD104 // FLJ23399 // MGC10002 //	2652410	chr3	+	173240112	173601176	5.97

TABLE 4-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change
			PRO4979 // YVTM2421						
serine/threonine kinase 38 like	STK38L	NM_015000	KIAA0965 // NDR2	3409081	chr12	+	27288343	27370157	5.97
eukaryotic translation initiation factor 4 gamma, 2	EIF4G2	NM_001042559 // NM_001418	AAG1 // DAP5 // FLJ41344 // NAT1 // p97	3362719	chr11	−	10487574	10788746	5.97
aminopeptidase puromycin sensitive	NPEPPS	XM_001128588 // NM_006310	MP100 // PSA	3724698	chr17	+	42955347	43057168	5.96
membrane protein, palmitoylated 1, 55 kDa	MPP1	NM_002436	AAG12 // DXS552 // DXS552E // EMP55 // MRG1 // PEMP	4027585	chrX	−	153658739	154075618	5.94
eukaryotic translation initiation factor 4 gamma, 1	EIF4G1	NM_004953 // NM_182917 // NM_198241 // NM_198242 // NM_198244	DKFZp686A1451 // EIF4F // EIF4G // p220	2655688	chr3	+	185514970	185535829	5.83
leucine rich repeat containing 8 family, member C	LRRC8C	NM_032270	AD158 // DKFZp586J1119 // FAD158 // MGC138551	2345929	chr1	+	89871229	90008050	5.81
EH-domain containing 1	EHD1	NM_006795	FLJ42622 // FLJ44618 // H-PAST // HPAST1 // PAST // PAST1	3377226	chr11	−	64376790	64404202	5.78
3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	HMGCS1	NM_002130	HMGCS // MGC90332	2855501	chr5	−	43324231	43349337	5.74
insulin induced gene 1	INSIG1	NM_005542 // NM_198336 // NM_198337	CL-6 // MGC1405	3033209	chr7	+	154649208	154732868	5.72
chromodomain helicase DNA binding protein 2	CHD2	NM_001042572 // NM_001271	DKFZp781D1727	3609138	chr15	+	91227096	91387351	5.70

TABLE 4-continued

				Human Exon ST 1.0	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	DDX17	NM_006386 // NM_030881	DKFZp761H2016 // P72 // RH70	3960629	chr22	–	37202800	37232288	5.70
hypothetical protein KIAA1434	RP5-1022P6.2	NM_019593	FLJ11085 // KIAA1434 // MGC26147	3896370	chr20	–	5473033	5546357	5.68
nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	NFKB2	NM_001077493 // NM_001077494 // NM_002502	LYT-10 // LYT10	3261643	chr10	+	104144262	104152716	5.61
ubiquitin-activating enzyme E1-like 2	UBE1L2	NM_018227	FLJ10808 // FLJ23367	2771718	chr4	–	68130308	68249472	5.57
ras homolog gene family, member A	RHOA	NM_001664	ARH12 // ARHA // RHO12 //	2674242	chr3	–	49371587	49424514	5.54
HECT, UBA and WWE domain containing 1	HUWE1	NM_031407	ARF-BP1 // HECTH9 // HSPC272 // lb772 // KIAA0312 // LASU1 // MULE //	4009315	chrX	–	53575796	53740871	5.54
cyclin-dependent kinase 8	CDK8	NM_001260	K35 // MGC126074 // MGC126075	3482498	chr13	+	25701360	25877335	5.53
E3 ubiquitin protein ligase, HECT domain containing, 1	EDD1	NM_015902	DD5 // EDD // FLJ11310 // HYD // KIAA0896 // MGC57263	3147321	chr8	–	103333634	103493671	5.49
dedicator of cytokinesis 4	DOCK4	NM_014705	FLJ34238 // KIAA0716 // MGC134911 // MGC134912	3068097	chr7	–	111152902	111633744	5.42
sterol regulatory element binding transcription factor 2	SREBF2	NM_004599	SREBP2	3947123	chr22	+	40559049	40633247	5.40
heterogeneous nuclear ribonucleoprotein M	HNRPM	NM_005968 // NM_031203	DKFZp547H118 // HNRNPM // HNRNPM4 // HNRPM4 // HTGR1 // NAGR1	3819543	chr19	+	8415651	8459993	5.34
SH3 domain binding glutamic acid-rich protein like 3 // coiled-coil domain containing 21	SH3BGRL3 // CCDC21	NM_031286 // NM_022778	SH3BP-1 // TIP-B1 // DKFZP434L0117 //	2326448	chr1	+	26478669	26480591	5.34

TABLE 4-continued

				Human Exon ST 1.0	Human Genome hg18				
Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Strand	Start	Stop	Fold Change
exportin 4	XPO4	NM_022459	DKFZp434P232 // FLJ13976 // FLJ22000 FLJ13046 // KIAA1721	3504434	chr13	−	20251014	20375187	5.33
squalene epoxidase	SQLE	NM_003129	—	3114832	chr8	+	126063738	126105522	5.19
peptidylprolyl isomerase F (cyclophilin F)	PPIF	NM_005729	CYP3 // Cyp-D // FLJ90798 // MGC117207	3253880	chr10	+	80777230	80785093	5.19
serum response factor (c-fos serum response element-binding transcription factor)	SRF	NM_003131	MCM1	2907730	chr6	+	43246765	43257189	5.15
c-mer proto-oncogene tyrosine kinase	MERTK	NM_006343	MER // MGC133349 // c-mer	2500550	chr2	+	112372656	112513624	5.12
echinoderm microtubule associated protein like 4	EML4	NM_019063	C2orf2 // DKFZp686P18118 // ELP120 // FLJ10942 // FLJ32318 // ROPP120	2478748	chr2	+	42250017	42418636	5.02

[0223] (2) Identification of the Gene of which Introns Exhibit Increased Expression in a Dose-Dependent Fashion in Groups with the Treatment at a Concentration of 3 nM, 10 nM, and 30 nM.

[0224] Probe sets showing that the normalized change in the level expression of the probe set in the group with the treatment at 30 nM was more than 5 times; the expression level of the probe set and the gene in the group with the treatment at 30 nM was more than 100; and probe set annotation was "extended, full, free", were picked out. Regression analysis was performed with the probe sets extracted for the control group, the group with the treatment at 3 nM, the group with the treatment at 10 nM, and the group with the treatment at 30 nM to determine a p and q value for the slope of regression formula. A gene containing the probe sets with the q value of less than 5% was determined as a candidate gene with increased expression level of the intron regions (Table 5).

[0225] In Table 5, for the gene evaluated, gene name (Gene Name), abbreviated name (Gene Symbol), accession number (Accession), alias name (Synonym), transcription cluster number in Human Exon 1.0 ST Array (Human Exon 1.0 ST Array Transcription Cluster ID), chromosome number (Chromosome), type of strand (Strand), start region (Start), stop region (Stop), and change in expression level per 1 nM (Fold Change/nM) were respectively shown.

TABLE 5

				Human Exon ST 1.0 Transcript	Human Genome hg18				Fold Change/
Gene Name	Gene Symbol	Accession	Synonym	Cluster ID	Chromosome	Strand	Start	Stop	nM
epiregulin	EREG	NM_001432	ER	2731513	chr4	+	75440309	75473341	1.08
pellino homolog 1 (*Drosophila*)	PELI1	NM_020651	DKFZp686C18116 // MGC50990	2556302	chr2	−	64173290	64225291	1.08
integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)	ITGAV	NM_002210	CD51 // MSK8 // VNRA	2519229	chr2	+	187163045	187253869	1.08
heat shock 70 kDa protein 5 (glucose-regulated protein, 78 kDa)	HSPA5	NM_005347	BIP // FLJ26106 // GRP78 // MIF2	3225398	chr9	−	127036953	127064590	1.08
villin 2 (ezrin)	VIL2	NM_003379	CVIL // CVL // DKFZp762H157 // FLJ26216 // MGC1584	2981912	chr6	−	159106770	159160432	1.08
UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5	B4GALT5	NM_004776	B4Gal-T5 // BETA4-GALT-IV // MGC138470 // beta4Gal-T5 // beta4GalT-V // gt-	3908963	chr20	−	47682889	47809709	1.08
pleckstrin homology, Sec7 and coiled-coil domains 1(cytohesin 1)	PSCD1	NM_004762 // NM_017456	B2-1 // CYTOHESIN-1 // D17S811E // FLJ34050 // FLJ41900 // SEC7	3772525	chr17	−	74181731	74289973	1.08
EH-domain containing 4	EHD4	NM_139265	PAST4	3620276	chr15	−	39977674	40052063	1.08
TIMP metallopeptidase inhibitor 1	TIMP1	NM_003254	CLGI // EPA // EPO // FLJ90373 // HCI // TIMP	3976341	chrX	+	47326654	47332978	1.08
interleukin 1 receptor antagonist	IL1RN	NM_000577 // NM_173841 // NM_173842 // NM_173843	ICIL-1RA // IL-1ra3 // IL1F3 // IL1RA // IRAP // MGC10430	2501204	chr2	+	113573383	113608060	1.08
PRP40 pre-mRNA processing factor 40 homolog A (*S. cerevisiae*)	PRPF40A	XM_371575 // XM_938514	FBP-11 // FBP11 // FLAF1 // FLJ20585 // FNBP3 // HIP10 // HYPA // NY-REN-	2581548	chr2	−	153212414	153283546	1.08
ATP-binding cassette, sub-family A (ABC1), member 1	ABCA1	NM_005502	ABC-1 // ABC1 // CERP // FLJ14958 // HDLDT1 // TGD	3218528	chr9	−	106583121	106748222	1.08
RAB5A, member RAS oncogene family	RAB5A	NM_004162	RAB5	2613386	chr3	+	19963571	20002852	1.07
protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	PPP2CA	NM_002715	PP2Ac // PP2CA // RP-C	2876046	chr5	−	133557588	133589841	1.07
membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	MPP7	NM_173496	FLJ32798	3282601	chr10	−	28377816	28631969	1.07

TABLE 5-continued

				Human Exon ST 1.0 Transcript	Human Genome hg18				Fold Change/
Gene Name	Gene Symbol	Accession	Synonym	Cluster ID	Chromosome	Strand	Start	Stop	nM
RAB6 interacting protein 1	RAB6IP1	NM_015213	FLJ22354 // FLJ33829 // FLJ43455 // KIAA1091	3362263	chr11	–	9116953	9243468	1.07
GRB2-associated binding protein 2	GAB2	NM_012296 // NM_080491	KIAA0571	3383227	chr11	–	77603886	77989843	1.07
chloride intracellular channel 4 // adducin 3 (gamma)	CLIC4 // ADD3	NM_013943 // NM_001121 // NM_016824 // NM_019903	CLIC4L // DKFZP566G223 // FLJ38640 // H1 // huH1 // p64H1 // ADDL	2325593	chr1	+	24943202	25071376	1.07
TBC1 domain family, member 23	TBC1D23	NM_018309	DKFZp667G062 // FLJ11046 // NS4ATP1	2633587	chr3	+	101462368	101526762	1.07
solute carrier family 16, member 3 (monocarboxylic acid transporter 4)	SLC16A3	NM_001042422 // NM_001042423 // NM_004207	MCT3 // MCT4 // MGC138472 // MGC138474	3738629	chr17	+	77775274	77812305	1.07
sestrin 3	SESN3	NM_144665	MGC29667 // SEST3	3387259	chr11	–	94545767	94605309	1.07
nuclear RNA export factor 1	NXF1	NM_001081491 // NM_006362	DKFZp667O0311 // MEX67 // TAP	3376155	chr11	–	62316178	62329529	1.07
myristoylated alanine-rich protein kinase C substrate	MARCKS	NM_002356	80K-L // FLJ14368 // FLJ90045 // MACS // MRACKS // PKCSL // PRKCSL	2922215	chr6	+	114284762	114292853	1.07
retinitis pigmentosa 2 (X-linked recessive)	RP2	NM_006915	KIAA0215 // TBCCD2	3975869	chrX	+	46581319	46637601	1.07
DnaJ (Hsp40) homolog, subfamily C, member 3	DNAJC3	NM_006260	HP58 // P58 // P58IPK // PRKRI	3497270	chr13	+	95125276	95245596	1.07
interleukin 1, alpha	IL1A	NM_000575	IL-1A // IL1 // IL1-ALPHA //	2571483	chr2	–	113247977	113259446	1.07
TANK-binding kinase 1	TBK1	NM_013254	FLJ11330 // NAK // T2K	3419849	chr12	+	63132014	63202097	1.07
adaptor-related protein complex 3, beta 1 subunit	AP3B1	NM_003664	ADTB3 // ADTB3A // HPS // HPS2 // PE	2863730	chr5	–	77318390	77671471	1.07
ATPase type 13A3	ATP13A3	XM_931948 // XM_942079	AFURS1 // DKFZp686K16189 // FLJ90613	2711644	chr3	–	195604703	195757213	1.07
coiled-coil domain containing 131	CCDC131	NM_144982	DKFZp686A0722 // KIAA0546 // MGC23401 // MGC90200 // PSRC2	3462094	chr12	–	70269806	70344289	1.07

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change/ nM
calmodulin 2 (phosphorylase kinase, delta)	CALM2	NM_001743	CAMII // PHKD // PHKD2	2551924	chr2	–	47232159	47286178	1.07
ubiquitously transcribed tetratricopeptide repeat gene, Y-linked // ubiquitously transcribed tetratricopeptide repeat, X chromosome	UTY // UTX	NM_007125 // NM_182659 // NM_182660 // NM_021140	DKFZp686L12190 // UTY1 // DKFZp686A03225 // MGC141941 // bA386N14.2	4035017	chrY	–	13772846	14101944	1.07
brain abundant, membrane attached signal protein 1	BASP1	NM_006317	CAP-23 // CAP23 // MGC8555 // NAP-22 // NAP22	2803329	chr5	+	17118727	17381190	1.07
GTP cyclohydrolase 1 (dopa-responsive dystonia)	GCH1	NM_000161 // NM_001024024 // NM_001024070 // NM_001024071	DYT5 // GCH // GTP-CH-1 // GTPCH1	3565524	chr14	–	54375952	54439279	1.07
proteasome (prosome, macropain) 26S subunit, non-ATPase, 3	PSMD3	NM_002809	P58 // RPN3 // S3	3720636	chr17	+	35390438	35407732	1.07
acyl-CoA synthetase long-chain family member 1	ACSL1	NM_001995	ACS1 // FACL1 // FACL2 // LACS // LACS1 // LACS2	2796553	chr4	–	185913758	186002178	1.07
numb homolog (*Drosophila*)	NUMB	NM_001005743 // NM_001005744 // NM_001005745 // NM_003744	S171	3571347	chr14	–	72811631	73000081	1.07
protein kinase C, epsilon	PRKCE	NM_005400	MGC125656 // MGC125657 // PKCE // nPKC-epsilon	2480168	chr2	+	45731934	46343070	1.07
quaking homolog, KH domain RNA binding (mouse)	QKI	XM_945803 // NM_006775 // NM_206853 // NM_206854 // NM_206855	DKFZp586I0923 // Hqk // QK // QK3	2935475	chr6	+	163684268	163960462	1.07
eukaryotic translation initiation factor 2C, 2	EIF2C2	NM_012154	AGO2 // MGC3183 // Q10	3156193	chr8	–	141599440	141726037	1.07
CD2 molecule	CD2	NM_001767	SRBC // T11	2353669	chr1	+	117098550	117149098	1.07
nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	NFKB1	NM_003998	DKFZp686C01211 // EBP-1 // KBF1 // MGC54151 // NF-kappa-B // NFKB-p105 //	2737717	chr4	+	103568522	103757506	1.07
transcription elongation factor B (SIII), polypeptide 3 (110 kDa, elongin A)	TCEB3	NM_003198	SIII // TCEB3A	2325251	chr1	+	23942459	23961135	1.07
COP9 constitutive photomorphogenic homolog subunit 2 (*Arabidopsis*)	COPS2	NM_004236	ALIEN // CSN2 // SGN2 // TRIP15	3623424	chr15	–	47203877	47235198	1.07

TABLE 5-continued

				Human Exon ST 1.0 Transcript	Human Genome hg18				Fold Change/
Gene Name	Gene Symbol	Accession	Synonym	Cluster ID	Chromosome	Strand	Start	Stop	nM
pyridoxal (pyridoxine, vitamin B6) kinase // chromosome 21 open reading frame 124	PDXK // C21orf124	NM_003681 // NM_032920	C21orf97 // PKH // PNK // FLJ31940 // MGC15873 // PRED79	3923257	chr21	+	43963416	44006601	1.07
nucleoporin 98 kDa	NUP98	NM_005387 // NM_016320 // NM_139131 // NM_139132	ADIR2 // NUP196	3359910	chr11	–	3652836	3775353	1.07
muskelin 1, intracellular mediator containing kelch motifs	MKLN1	NM_013255	FLJ11162	3024275	chr7	+	130445315	130837940	1.07
ceramide kinase	CERK	NM_022766 // NM_182661	DKFZp434E0211 // FLJ21430 // FLJ23239 // KIAA1646 // LK4 // MGC131878 // dA59H18.2 // dA59H18.3 // hCERK	3964154	chr22	–	45454343	45537349	1.07
non-POU domain containing, octamer-binding	NONO	NM_007363	NMT55 // NRB54 // P54 // P54NRB	3980887	chrX	+	70420006	70437726	1.07
neuroepithelial cell transforming gene 1	NET1	NM_001047160 // NM_005863	ARHGEF8 // NET1A	3233182	chr10	+	5444535	5491001	1.07
mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A // hypothetical protein MGC52110	MGAT4A // MGC52110	NM_012214 // NM_001008215	GNT-IV // GNT-IVA // 6330578E17Rik	2566414	chr2	–	98600132	98714000	1.07
protein phosphatase 1, regulatory (inhibitor) subunit 10	PPP1R10	NM_002714	CAT53 // FB19 // PNUTS	2948425	chr6	–	30676177	30694348	1.07
inositol polyphosphate-5-phosphatase, 40 kDa	INPP5A	XM_001133189 // NM_005539	5PTASE // DKFZp434A1721 // MGC116947 // MGC116949	3272205	chr10	+	134201308	134446967	1.07
plasminogen activator, urokinase receptor	PLAUR	NM_001005376 // NM_001005377 // NM_002659	CD87 // UPAR // URKR	3864551	chr19	–	48841865	48866539	1.06
PHD finger protein 12	PHF12	NM_001033561 // NM_020889	KIAA1523 // MGC131914 // PF1	3751184	chr17	–	24256404	24302905	1.06
synapse associated protein 1, SAP47 homolog (*Drosophila*)	SYAP1	NM_032796	DKFZp686K221 // FLJ14495 // FLJ44185 // PRO3113	3970130	chrX	+	16639861	16690708	1.06
chromosome 1 open reading frame 152 // phosphodiesterase 4D interacting protein (myomegalin)	C1orf152 // PDE4DIP	NR_003242 // XM_943179 // NM_001002810 // NM_001002811 // NM_001002812 //	COAS3 // CMYA2 // DKFZp781J054 // MGC75440 // MMGL	2431886	chr1	–	142444924	143804054	1.06

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript	Human Genome hg18				Fold Change/
				Cluster ID	Chromosome	Strand	Start	Stop	nM
homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	HERPUD1	NM_014644 // NM_022359 // NM_001010989 // NM_001010990 // NM_014685	HERP // KIAA0025 // Mif1 // SUP	3662387	chr16	+	55523269	55552122	1.06
TNF receptor-associated factor 1	TRAF1	NM_005658	EBI6 // MGC: 10353	3223738	chr9	–	122699696	122731521	1.06
pumilio homolog 2 (*Drosophila*)	PUM2	NM_015317	FLJ36528 // KIAA0235 // MGC138251 // MGC138253 // PUMH2 // PUML2	2542816	chr2	–	20291440	20450197	1.06
Dmx-like 2	DMXL2	NM_015263	FLJ26672 // KIAA0856 // RC3	3624145	chr15	–	49527223	49702258	1.06
RAB8B, member RAS oncogene family	RAB8B	NM_016530	FLJ38125	3597476	chr15	+	61268620	61347018	1.06
tight junction protein 2 (zona occludens 2)	TJP2	NM_004817 // NM_201629	MGC26306 // X104 // ZO-2 // ZO2	3173880	chr9	+	70925894	71059931	1.06
BCL2/adenovirus E1B 19 kDa interacting protein 2	BNIP2	NM_004330	BNIP-2 // NIP2	3627076	chr15	–	57742025	57768916	1.06
sorting nexin 9 // synaptojanin 2	SNX9 // SYNJ2	NM_016224 // NM_003898	MST155 // MSTP155 // SDP1 // SH3PX1 // SH3PXD3A // WISP // INPP5H // KIAA0348 // MGC44422	2933331	chr6	+	158164282	158286097	1.06
programmed cell death 4 (neoplastic transformation inhibitor)	PDCD4	NM_014456 // NM_145341	H731 // MGC33046 // MGC33047	3263944	chr10	+	112621575	112649753	1.06
leupaxin	LPXN	NM_004811	LDPL	3374402	chr11	–	58050925	58102459	1.06
solute carrier family 7 (cationic amino acid transporter, y+ system), member 5 // SLC7A5 pseudogene	SLC7A5 // LAT1-3TM	NM_003486 // NR_002593	4F2LC // CD98 // D16S469E // E16 // LAT1 // MPE16 // hLAT1 // DC49 // MLAS // hLAT1-3TM	3703885	chr16	–	86421130	86460615	1.06
heat shock protein 90 kDa beta (Grp94), member 1 // thymine-DNA glycosylase // heat shock protein 90 kDa beta (Grp94), member 2 (pseudogene)	HSP90B1 // TDG // HSP90B2P	NM_003299 // NM_003211 // —	ECGP // GP96 // GRP94 // TRA1 // —// GRP94P1 // GRP94b // HSP // HSPCP2 // HsGrp94b // TRA1P1 // TRAP1	3429312	chr12	+	102848291	102871551	1.06
TNFAIP3 interacting protein 1	TNIP1	NM_006058	ABIN-1 // KIAA0113 // NAF1 // VAN	2881672	chr5	–	150389707	150446947	1.06
NECAP endocytosis associated 2	NECAP2	NM_018090	FLJ10420 // RP4-798A10.1	2322389	chr1	+	16639774	16659570	1.06

TABLE 5-continued

				Human Exon ST 1.0 Transcript	Human Genome hg18				Fold Change/
Gene Name	Gene Symbol	Accession	Synonym	Cluster ID	Chromosome	Strand	Start	Stop	nM
proteasome (prosome, macropain) subunit, alpha type, 5	PSMA5	NM_002790	MGC117302 // MGC125802 // MGC125803 // MGC125804 // PSC5 // ZETA	2427074	chr1	−	109742573	109770611	1.06
guanine nucleotide binding protein-like 2 (nucleolar)	GNL2	NM_013285	FLJ40906 // HUMAUANTIG // NGP1 // Ngp-1 // dJ423B22.6	2407191	chr1	−	37805043	37834120	1.06
GRIP and coiled-coil domain containing 2	GCC2	NM_014635 // NM_181453	GCC185 // KIAA0336	2498977	chr2	+	108431315	108492470	1.06
RAD50 homolog (*S. cerevisiae*)	RAD50	NM_005732 // NM_133482	RAD50-2 // hRad50	2828564	chr5	+	131774479	132009928	1.06
fibronectin type III domain containing 3B	FNDC3B	NM_022763	DKFZp686D14170 // DKFZp762K137 // FAD104 // FLJ23399 // MGC10002 // PRO4979 // YVTM2421	2652410	chr3	+	173240112	173601176	1.06
son of sevenless homolog 2 (*Drosophila*)	SOS2	NM_006939	—	3563734	chr14	−	49654812	49768331	1.06
heat shock protein 90 kDa alpha (cytosolic), class A member 1 // heat shock protein 90 kDa alpha (cytosolic), class A member 2 // heat shock protein 90 kDa alpha (cytosolic), class A member 6 (pseudogene)	HSP90AA1 // HSP90AA2 // HSP90AA6P	NM_001017963 // NM_005348 // NM_001040141 // —	FLJ31884 // HSP86 // HSP90A // HSP90N // HSPC1 // HSPCA // HSPCAL1 // HSPCAL4 // HSPN // Hsp89 // Hsp90 // LAP2 // HSP90ALPHA // HSPCAL3 // HSP90Af	3580179	chr14	−	101616842	101676327	1.06
phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce komolog, *Drosophila*)	PDE4B	NM_001037339 // NM_001037340 // NM_001037341 // NM_002600	DKFZp686F2182 // DPDE4 // MGC126529 // PDEIVB	2340529	chr1	+	66030487	66612844	1.06
interleukic-1 receptor-associated kinase 2	IRAK2	NM_001570	IRAK-2 // MGC150550	2610359	chr3	+	10181579	10260427	1.06
chromosome 14 open reading frame 32	C14orf32	NM_144578	MGC23138 // MISS // c14_5346	3536663	chr14	+	54588114	54606655	1.06
nucleoside phosphorylase	NP	NM_000270	MGC117396 // MGC125915 // MGC125916 // PNP // PRO1837 // PUNP	3527514	chr14	+	20007398	20015985	1.06

TABLE 5-continued

				Human Exon ST 1.0 Transcript	Human Genome hg18				Fold Change/
Gene Name	Gene Symbol	Accession	Synonym	Cluster ID	Chromosome	Strand	Start	Stop	nM
proline-serine-threonine phosphatase interacting protein 2	PSTPIP2	NM_024430	MAYP // MGC34175	3806211	chr18	−	41817502	41906221	1.06
growth factor receptor-bound protein 2	GRB2	NM_002086 // NM_203506	ASH // EGFRBP-GRB2 // Grb3-3 // MST084 // MSTP084	3770743	chr17	−	70805871	70913384	1.06
signal-induced proliferation-associated 1 like 1	SIPA1L1	NM_015556	DKFZp686G1344 // E6TP1 // KIAA0440	3542847	chr14	+	70857592	71468470	1.06
exportin 1 (CRM1 homolog, yeast) // thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian)	XPO1 // THRB	NM_003400 // NM_000461	CRM1 // DKFZp686B1823 // ERBA-BETA // ERBA2 // GRTH // MGC126109 // MGC126110 // NR1A2 // THR1 // THRB1 // THRB2	2555490	chr2	−	61558490	61619343	1.06
centromere protein C 1	CENPC1	NM_001812	CENP-C // CENPC // MIF2 // hcp-4	2771654	chr4	−	68020183	68093837	1.06
v-abl Abelson murine leukemia viral oncogene homolog 2 (arg, Abelson-related gene)	ABL2	NM_005158 // NM_007314	ABLL // ARG	2446047	chr1	−	177335093	177528267	1.06
rine finger protein 10	RNF10	NM_014868	KIAA0262 // MGC126758 // MGC126764 //	3434413	chr12	+	119456489	119500226	1.06
Notch homolog 2 (*Drosophila*) // neuroblastoma breakpoint family, member 14	NOTCH2 // NBPF14	XM_001133349 // NM_024408 // NM_015383	AGS2 // hN2 // DJ328E19.C1.1 // FLJ35032 // NBPF	2431112	chr1	−	120205744	120426930	1.06
endothelin converting enzyme 1 // amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like)	ECE1 // APBB2	NM_001397 // NM_173075	ECE // FE65L // FE65L1 // MGC35575	2400518	chr1	−	21394307	21544720	1.06
phosphoinositide-3-kinase adaptor protein 1	PIK3AP1	NM_152309	BCAP // RP11-34E5.3	3301914	chr10	−	98342808	98470259	1.06
BTB and CNC homology 1, basic leucine zipper transcription factor 2	BACH2	NM_021813	—	2964553	chr6	−	90692975	91063182	1.06
ATPase, H+ transporting, lysosomal 56/58 kDa, V1 subunit B2	ATP6V1B2	NM_001693	ATP6B1B2 // ATP6B2 // HO57 // VATB // VPP3 // Vma2	3088544	chr8	+	20098984	20143098	1.06
TRAF2 and NCK interacting kinase	TNIK	NM_015028	AD 2	2705266	chr3	−	172258898	172660964	1.06
AT-hook transcription factor	AKNA	NM_030767	KIAA1968 // RP11-82I1.4	3221916	chr9	−	116138238	116200584	1.06
Fas (TNF receptor superfamily, member 6)	FAS	NM_000043 // NM_152871 // NM_152872 // NM_152873 // NM_152874 // NM_152875 //	ALPS1A // APO-1 // APT1 // CD95 // FAS1 // FASTM // TNFRSF6	3257098	chr10	+	90721519	90765521	1.06

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change/ nM
ankyrin repeat domain 17	ANKRD17	NM_152876 // NM_152877 // NM_032217 // NM_198889	FLJ22206 // GTAR // KIAA0697 // NY-BR-16	2773023	chr4	−	74158547	74343428	1.06
clathrin interactor 1	CLINT1	NM_014666	CLINT // ENTH // EPN4 // EPNR // EPSINR // KIAA0171	2883609	chr5	−	157145339	157284818	1.06
PRP8 pre-mRNA processing factor 8 homolog (*S. cerevisiae*)	PRPF8	NM_006445	HPRP8 // PRP8 // PRPC8 // RP13	3740479	chr17	−	1500681	1534906	1.06
AF4/FMR2 family, member 4	AFF4	NM_014423	AF5Q31 // MCEF // MGC75036	2875555	chr5	−	132238768	132327205	1.06
v-rel reticuloendotheliosis viral oncogene homolog (avian)	REL	NM_002908	C-Rel	2484358	chr2	+	60962266	61004124	1.06
excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence)	ERCC1	NM_001983 // NM_202001	UV20	3865378	chr19	−	50602433	50673926	1.06
ubiquitously transcribed tetratricopeptide repeat, X chromosome // ubiquitously transcribed tetratricopeptide repeat gene, Y-linked	UTX // UTY	NM_021140 // NM_007125 // NM_182659 // NM_182660	DKFZp686A03225 // MGC141941 // bA386N14.2 // DKFZp686L12190 // UTY1	3975467	chrX	+	44590716	44896185	1.06
ATPase, Ca++ transporting, plasma membrane 1	ATP2B1	NM_001001323 // NM_001682	PMCA1	3464983	chr12	−	88505965	88620030	1.06
v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	ETS2	NM_005239	—	3921068	chr21	+	39059147	39118744	1.06
zinc finger protein 91 homolog (mouse) // ciliary neurotrophic factor	ZFP91 // CNTF	NM_053023 // NM_170768 // NM_000614	FKSG11 // PZF // ZNF757 // HCNTF	3331730	chr11	+	58101868	58149782	1.06
integrin, alpha 5 (fibronectin receptor, alpha polypeptide)	ITGA5	NM_002205	CD49e // FNRA // VLA5A	3456732	chr12	−	53075332	53099491	1.06
IBR domain containing 3	IBRDC3	NM_153341	FLJ90005	2405312	chr1	−	33172120	33203343	1.06
cofactor required for Sp1 transcriptional activation, subunit 2, 150 kDa	CRSP2	XM_001126052 // NM_004229	CRSP150 // CSRP // CXorf4 // DRIP150 // EXLM1 // MED14 // MGC104513 // RGR1 // TRAP170	4005644	chrX	−	40392502	40480045	1.06
aryl hydrocarbon receptor	AHR	NM_001621	—	2991233	chr7	+	17304771	17363729	1.06
solute carrier family 43, member 2	SLC43A2	NM_152346	FLJ23848 // LAT4 // MGC34680	3740367	chr17	−	1423948	1478920	1.06
chemokine (C-C motif) ligand 20	CCL20	NM_004591	CKb4 // LARC // MIP-3a // MIP3A // SCYA20 //	2530713	chr2	+	228386802	228427090	1.06

TABLE 5-continued

				Human Exon ST 1.0 Transcript	Human Genome hg18				Fold Change/
Gene Name	Gene Symbol	Accession	Synonym	Cluster ID	Chromosome	Strand	Start	Stop	nM
serpin peptidase inhibiter, clade B (ovalbumin), member 8	SERPINB8	NM_001031848 // NM_002640 // NM_198833	CAP2 // P18	3791996	chr18	+	59787618	59823238	1.06
chaperonin containing TCP1, subunit 4 (delta)	CCT4	NM_006430	Cctd // MGC126164 // MGC126165 // SRB	2555630	chr2	–	61939693	61970469	1.06
AP2 associated kinase 1	AAK1	NM_014911	KIAA1048 // MGC138170	2558150	chr2	–	69538639	69783824	1.06
musculin (activated B-cell factor-1)	MSC	NM_005098	ABF-1 // ABF1 // MYOR	3140213	chr8	–	72843959	73059105	1.06
Yip1 domain family, member 5	YIPF5	NM_001024947 // NM_030799	DKFZp313L2216 // FinGER5 // SB140 // SMAP-5 // SMAP5 // YIP1A	2879509	chr5	–	143463451	143565514	1.06
START domain containing 7	STARD7	NM_020151 // NM_139267	GTT1	2565143	chr2	–	96214334	96238296	1.06
ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)	ARFGEF1	NM_006421	ARFGEP1 // BIG1 // D730028O18Rik // DKFZP434L057 // P200	3139035	chr8	–	68250009	68418446	1.06
myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, *Drosophila*)	MLL5	NM_018682 // NM_182931	FLJ10078 // FLJ14026 // HDCMC04P // MGC70452	3017547	chr7	+	104436029	104542698	1.06
DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	DDX3X	XM_001129278 // NM_001356	DBX // DDX14 // DDX3 // HLP2	3974838	chrX	+	41055591	41108668	1.06
nibrin	NBN	NM_001024688 // NM_002485	AT-V1 // AT-V2 // ATV // FLJ10155 // MGC87362 // NBS	3143970	chr8	–	91014745	91066433	1.06
AT rich interactive domain 4B (RBP1-like) // RNA binding motif protein 34	ARID4B // RBM34	NM_016374 // NM_031371 // NM_015014	BCAA // BRCAA1 // DFZp313M2420 // MGC163290 // RBBP1L1 // RBP1L1 // SAP180 // KIAA0117	2461786	chr1	–	233396677	233558149	1.06
ankyrin repeat domain 44	ANKRD44	NM_153697	MGC21968 // MGC70444	2593464	chr2	–	197512324	197901798	1.06
RB1-inducible coiled-coil 1	RB1CC1	NM_014781	CC1 // DRAGOU14 // FIP200	3135184	chr8	–	53641628	93789545	1.06
ubiquitin specific peptidase 12	USP12	NM_182488	USP12L1	3506738	chr13	–	26518485	26644264	1.06
apoptosis inhibitor 5	API5	NM_006595	AAC-11 // AAC11 // API5L1	3327906	chr11	+	43290109	43322649	1.06
HIR histone cell cycle regulation defective homolog A (*S. cerevisiae*)	HIRA	NM_003325	DGCR1 // TUP1 // TUPLE1	3952637	chr22	–	17696576	17799452	1.06

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change/ nM
guanylate binding protein 7 // guanylate binding protein 2, interferon-inducible // guanylate binding protein 4	GBP7 // GBP2 // GBP4	NM_207398 // NM_004120 // NM_052941	FLJ38822 // GBP4L // —// Mpa2	2421925	chr1	–	89343675	89496682	1.06
CASP8 and FADD-like apoptosis regulator	CFLAR	NM_003879	CASH // CASP8AP1 // CLARP // Casper // FLAME // FLAME-1 // FLIP // I-FLICE // MRIT // USURPIN // c-FLIP // c-FLIPL //	2522616	chr2	+	201689135	201744701	1.06
human immunodeficiency virus type I enhancer binding protein 2	HIVEP2	NM_006734	HIV-EP2 // MBP-2 // MIBP1	2977265	chr6	–	143065515	143308841	1.06
serpin peptidase inhibitor, clade B (ovalbumin), member 9 // serpin peptidase inhibitor, clade B (ovalbumin), member 6	SERPINB9 // SERPINB6	NM_004155 // NM_004568	CAP-3 // CAP3 // PI9 // CAP // DKFZp686I04222 // MGC111370 // MSTP057 // PI6 // PTI	2939034	chr6	–	2832402	2858242	1.06
myxovirus (influenza virus) resistance 2 (mouse)	MX2	NM_002463	MXB	3922037	chr21	+	41655820	41703177	1.06
solute carrier family 25, member 37	SLC25A37	XM_001128238 // XM_001128248 // XM_001128255 // XM_001128269 // NM_016612	HT015 // MFRN // MSC // MSCP // PRO1278 // PRO1584 // PRO2217	3090006	chr8	+	23439117	23485313	1.06
WW domain binding protein 11	WBP11	NM_016312	DKFZp779M1063 // NPWBP // SIPP1	3445670	chr12	–	14829481	14848171	1.06
bromodomain adjacent to zinc finger domain, 1A	BAZ1A	NM_013448 // NM_182648	ACF1 // DKFZP586E0518 // FLJ14383 // WALp1 // WCRF180 // hACF1	3560711	chr14	–	34291692	34414604	1.06
aquaporin 9	AQP9	NM_020980	HsT17287 // SSC1	3595594	chr15	+	56217766	56280468	1.06
solute carrier family 39 (zinc transporter), member 8	SLC39A8	NM_022154	BIGM103 // LZT-Hs6	2779823	chr4	–	103393022	103486067	1.06
FYN oncogene related to SRC, FGR, YES	FYN	NM_002037 // NM_153047 // NM_153048	MGC45350 // SLK // SYN	2969886	chr6	–	112088237	112301348	1.06
elongation factor, RNA polymerase II, 2	ELL2	NM_012081	—	2867873	chr5	–	95246561	95323733	1.06
Janus kinase 1 (a protein tyrosine kinase)	JAK1	NM_002227	JAK1A // JAK1B	2416522	chr1	–	65071504	65278035	1.06
v-rel reticuloendotheliosis viral oncogene homolog B, nuclear factor of kappa light polypeptide gene enhancer is B-cells 3 (avian)	RELB	NM_006509	I-REL	3835966	chr19	+	50196537	50233287	1.06
chemokine (C-C motif) ligand 2	CCL2	NM_002982	GDCF-2 // GDCF-2 HC11 // HC11 // HSMCR30 // MCAF	7385547	chr17	+	29513430	29608325	1.06

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript	Human Genome hg18				Fold Change/
				Cluster ID	Chromosome	Strand	Start	Stop	nM
			// MCP-1 // MCP1 // MGC9434 // SCYA2 // SMC-CF						
hexokinase 2	HK2	NM_000189	DKFZp686M1669 // HKII // HXK2	2489545	chr2	+	74913290	74974310	1.06
ELK3, ETS-domain protein (SRF accessory protein 2)	ELK3	NM_005230	ERP // NET // SAP2	3427098	chr12	+	95112269	95187725	1.06
SNF1-like kinase	SNF1LK	NM_173354	MSK // SIK	3934111	chr21	−	43637578	43705100	1.06
lipopolysaccharide-induced TNF factor	LITAF	NM_004862	CMT1C // FLJ38636 // MGC116698 // MGC116700 // MGC116701 // MGC125274 // MGC125275 // MGC125276 // PIG7 // SIMPLE // TP53I7	3680434	chr16	−	11549088	11599620	1.06
tRNA splicing endonuclease 54 homolog (*S. cerevisiae*)	TSEN54	NM_207346	FLJ37147 // SEN54L // sen54	3734865	chr17	+	71022989	71032409	1.06
chromodomain helicase DNA binding protein 6	CHD6	NM_032221	CHD5 // KIAA1335 // RIGB	3906160	chr20	−	39464169	39680547	1.06
chemokine (C—X—C motif) ligand 1 (melanoma growth stimulating activity, alpha)	CXCL1	NM_001511	GRO1 // GROa // MGSA // MGSA alpha // MGSA-a // NAP-3 //	2731381	chr4	+	74953973	74983954	1.06
myotubularin related protein 3	MTMR3	NM_021090 // NM_153050 // NM_153051	FYVE-DSP1 // KIAA0371 // ZFYVE10	3942179	chr22	+	28609182	28762301	1.06
adaptor-related protein complex 1, beta 1 subunit	AP1B1	NM_001127 // NM_145730	ADTB1 // AP105A // BAM22 // CLAPB2	3956781	chr22	−	28053592	28206955	1.06
actinin, alpha 1	ACTN1	NM_001102	FLJ40884	3569814	chr14	−	68409817	68515815	1.06
mitogen-activated protein kinase kinase kinase kinase 4	MAP4K4	NM_004834 // NM_145686 // NM_145687	FLH21957 // FLJ10410 // FLJ20373 // FLJ90111 /// HGK // KIAA0687 // NIK	2496727	chr2	+	101600496	101877880	1.06
activated leukocyte cell adhesion molecule	ALCAM	NM_001627	CD166 // FLJ38514 // MEMD // MGC71733	2634494	chr3	+	106304077	106816151	1.06
valosin-containing protein // Fanconi anemia, complementation group G	VCP // FANCG	NM_007126 // NM_004629	IBMPFD // MGC131997 // MGC148092 // MGC8560 // TERA	3204404	chr9	−	35026106	35062648	1.06

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript	Human Genome hg18				Fold Change/
				Cluster ID	Chromosome	Strand	Start	Stop	nM
			// p97 // FAG // XRCC9						
heat shock 105 kDa/110 kDa protein 1	HSPH1	NM_006644	DKFZp686M05240 // HSP105 // HSP105A // HSP105B // KIAA0201 // NY-CO-25	3508330	chr13	−	30558258	30651692	1.06
WAS protein family, member 2	WASF2	NM_006990	SCAR2 // WAVE2 // dJ393P12.2	2403111	chr1	−	27603331	27689256	1.06
RAP1 interacting factor homolog (yeast)	RIF1	NM_018151	DKFZp781N1478 // FLJ12870	2510485	chr2	+	151974674	152072768	1.06
chromosome 20 open reading frame 77	C20orf77	NM_021215	CREPT // DKFZp434P0735 // FLJ44520 // dJ1057B20.2	3884450	chr20	+	36095232	36189576	1.06
Wilms tumor 1 associated protein // acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thiolase)	WTAP // ACAT2	NM_004906 // NM_152857 // NM_152858 // NM_005891	DKFZp686F20131 // KIAA0105 // MGC3925 // —	2934089	chr6	+	160066607	160097332	1.06
proline-rich nuclear receptor coactivator 1	PNRC1	NM_006813	B4-2 // PNAS-145 // PROL2 // PRR2 // RP11-63L7.5	2916716	chr6	+	89847048	89852045	1.06
jumonji domain containing 1C	JMJD1C	NM_004241 // NM_032776	DKFZp761F0118 // FLJ14374 // KIAA1380 // RP11-10C13.2 // TRIP8	3291682	chr10	−	64589487	64951821	1.06
ELL associated factor 1	EAF1	NM_033083	—	2612371	chr3	+	15443374	15466824	1.06
mitogen-activated protein kinase-activated protein kinase 2	MAPKAPK2	NM_004759 // NM_032960	—	2376922	chr1	+	204924896	204974249	1.06
importin 7	IPO7	NM_006391	FLJ14581 // MGC138673 // RANBP7	3319840	chr11	+	9362702	9426296	1.06
eukaryotic translation initiation factor 2, subunit 1 alpha, 35 kDa	EIF2S1	NM_004094	EIF-2 // EIF-2A // EIF-2alpha // EIF2 // EIF2A	3541137	chr14	+	66896518	66922983	1.06
CD82 molecule	CD82	NM_001024844 // NM_002231	4F9 // C33 // GR15 // IA4 // KAI1 // R2 // SAR2 // ST6 //	3328520	chr11	+	44543723	44598484	1.06
Wolf-Hirschhorn syndrome candidate 1-like 1	WHSC1L1	NM_017778 // NM_023034	DKFZp667H044 // FLJ20353 // MGC126766 // MGC142029 // NSD3 // pp14328	3131916	chr8	−	38251717	38359646	1.06

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change/ nM
ADP-ribosylation factor-like 8B	ARL8B	NM_018184	ARL10C // FLJ10702 // Gie1	2608765	chr3	+	5138874	5197592	1.06
Rap guanine nucleotide exchange factor (GEF) 2	RAPGEF2	XM_376350 // XM_934714 // XM_934717 // XM_934718 // XM_944403 // XM_944410 // XM_944412	CNrasGEF // PDZ-GEF1 // PDZGEF1 // RA-GEF // Rap GEP // Rap-GEP	2749699	chr4	+	160171745	160501468	1.06
guanine nucleotide binding protein (G protein), gamma 2	GNG2	NM_053064	—	3535628	chr14	+	51383702	51506715	1.06
influenza virus NS1A binding protein	IVNS1ABP	NM_006469 // NM_016389	DKFZp686K06216 // FLARA3 // FLJ10069 // FLJ10411 // FLJ10962 // FLJ35593 // FLJ36593 // HSPC068 // KIAA0850 // ND1 // NS-1 // NS1-BP // NS1BP	2448073	chr1	−	183532162	183553081	1.06
ancient ubiquitous protein 1 // DEAQ box polypetide 1 (RNA-dependent ATPase)	AUP1 // DQX1	NM_181575 // NM_133637	—// FLJ23757	2560254	chr2	−	74607294	74610455	1.06
TERF1 (TRF1)-interacting nuclear factor 2	TINF2	NM_012461	TIN2	3558012	chr14	−	23776465	23781950	1.06
N-myc downstream regulated gene 1	NDRG1	NM_006096	CAP43 // CMT4D // DRG1 // GC4 // HMSNL // NDR1 // NMSL // PROXY1 // RIT42 // RTP // TARG1 // TDD5	3154317	chr8	−	134318628	134379306	1.06
kinesin 2	KNS2	NM_005552 // NM_182923	KLC // KLC1 // KNS2A // MGC15245	3553872	chr14	+	103160147	103247456	1.06
CD44 molecule (Indian blood group) // mitogen-activated protein kinase 10	CD44 // MAPK10	NM_000610 // NM_001001389 // NM_001001390 // NM_001001391 // NM_001001392 // NM_002753 // NM_138980 // NM_138981 // NM_138982	CDW44 // CSPG8 // ECMR-III // HCELL // IN // LHR // MC56 // MDU2 // MDU3 // MGC10468 // MIC4 // MUTCH-I // Pgp1 // FLJ12099 // FLJ33785 // JNK3 // JNK3A // MGC50974 //	3326635	chr11	+	35117003	35210509	1.06

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change/ nM
			PRKM10 // p493F12 //						
mitogen-activated protein kinase kinase 1	MAP2K1	NM_002755	MAPKK1 // MEK1 // MKK1 // PRKMK1	3598662	chr15	+	64466253	64571690	1.06
chromosome 16 open reading frame 72	C16orf72	NM_014117	FLJ41272 // PRO0149	3647632	chr16	+	9092682	9121055	1.06
tumor necrosis factor receptor superfamily, member 1B	TNFRSF1B	NM_001066	CD120b // TBPII // TNF-R-II // TNF-R75 // TNFBR // TNFR2 // TNFR80 // p75 // p75TNFR	2320727	chr1	+	12149647	12192323	1.06
protein phosphatase 2, regulatory subunit B', gamma isoform	PPP2R5C	NM_002719 // NM_178586 // NM_178587 // NM_178588	B56G // MGC23064 // PR61G	3552729	chr14	+	101296771	101464066	1.06
TSPY-like 2 // paraoxonase 3	TSPYL2 // PON3	XM_001128695 // NM_022117 // NM_000940	CDA1 // CINAP // CTCL // DENTT // HRIHFB2216 // SE20-4 // —	3978169	chrX	+	53124038	53134445	1.06
serine/threonine kinase 17a	STK17A	NM_004760	DRAK1	2999485	chr7	+	43573961	43642649	1.06
ELAV (embryonic lethal, abnormal vision, *Drosophila*)-like 1 (Hu antigen R) // translocase of inner mitochondrial membrane 44 homolog (yeast)	ELAVL1 // TIMM44	NM_001419 // NM_006351	ELAV1 // HUR // Hua // MelG // DKFZp686H05241 // TIM44	3848689	chr19	−	7929463	7999655	1.06
basic leucine zipper and W2 domains 1	BZW1	XM_001126385 // NM_014670	BZAP45 // KIAA0005 // Nbia10236	2522439	chr2	+	201384456	201418386	1.06
fibronectin type III domain containing 3A // cancer/testis antigen CT45-3	FNDC3A // RP13-36C9.3	NM_001079673 // NM_014923 // NM_001017435	FLJ31509 // FNDC3 // KIAA0970 // bA203I16.1 // bA203I16.5 // CT45-3 // RP13-	3489212	chr13	+	48428770	48681909	1.06
MAX dimerization protein 1	MXD1	NM_002357	MAD // MAD1 // MGC104659	2487549	chr2	+	69995330	70023575	1.06
TIA1 cytotoxic granule-associated RNA binding protein-like 1	TIAL1	NM_001033925 // NM_003252	MGC33401 // TCBP // TIAR	3309629	chr10	−	121291481	121346521	1.06
nuclear receptor subfamily 4, group A, member 3	NR4A3	NM_006981 // NM_173198 // NM_173199 // NM_173200	CHN // CSMF // MINOR // NOR1 // TEC	3181976	chr9	+	101623410	101669157	1.06
SAM domain, SH3 domain and nuclear localization signals 1	SAMSN1	NM_022136	HACS1 // NASH1	3925473	chr21	−	14779427	14877594	1.06
sperm specific antigen 2	SSFA2	NM_006751	CS-1 // CS1 // DKFZp313O1039 //	2518428	chr2	+	182464815	182516732	1.06

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change/ nM
			DKFZp779G0129 // FLJ45996 // KIAA1927 // KRAP // SPAG13						
zinc finger protein 317 // zinc finger protein 658	ZNF317 // ZNF658	NM_020933 // XM_001125688 // NM_033160	KIAA1588 // DKFZp572C163 // FLJ32813 // MGC35232	3819880	chr19	+	9112073	9135082	1.06
vacuolar protein sorting 35 homolog (*S. cerevisiae*)	VPS35	NM_018206	DKFZp434E1211 // DKFZp434P1672 // FLJ10752 // FLJ13588 // FLJ20388 // MEM3	3689922	chr16	–	45220566	45280598	1.06
CD8a molecule	CD8A	NM_001768 // NM_171827	CD8 // Leu2 // MAL // p32	2562932	chr2	–	86857923	86889020	1.06
general transcription factor IIB	GTF2B // RP11-82K18.3	NM_001514	TF2B // TFIIB	2421753	chr1	–	89090909	89130195	1.06
ring finger and WD repeat domain 2	RFWD2	NM_001001740 // NM_022457	COP1 // FLJ10416 // RNF200	2445141	chr1	–	174150358	174443232	1.06
formin binding protein 1	FNBP1	NM_015033	FBP17 // KIAA0554 // MGC126804	3227159	chr9	–	131689314	131845274	1.06
transmembrane protein 23	TMEM23	NM_147156	MGC17342 // MOB // MOB1 // SMS1	3289235	chr10	–	51706090	52054733	1.06
hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	HIF1A	NM_001530 // NM_181054	HIF-1alpha // HIF1-ALPHA // MOP1 // PASD8	3539070	chr14	+	61225495	61285222	1.06
annexin A5	ANXA5	NM_001154	ANX5 // ENX2 // PP4	2784027	chr4	–	122695163	122838353	1.06
T-cell activation GTPase activating protein	TAGAP	NM_054114 // NM_138810 // NM_152133	FKSG15 // FLJ32631 // FLJ39771 // MGC133247 // MGC27381 // TAGAP1	2982076	chr6	–	159375488	159517834	1.06
dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit	DPM1	NM_003859	CDGIE // MPDS	3909395	chr20	–	48984632	49008494	1.06
TIA1 cytotoxic granule-associated RNA binding protein	TIA1	NM_022037 // NM_022173	—	2558511	chr2	–	70290081	70329315	1.06
CD83 molecule	CD83	NM_001040280 // NM_004233	BL11 // HB15	2895841	chr6	+	14118209	14485106	1.06
serine/arginine repetitive matrix 2	SRRM2	NM_016333	300-KD // DKFZp686O15166 // FLJ21926 // FLJ22250 // KIAA0324 //	3645253	chr16	+	2742650	2761908	1.06

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change/ nM
mitogen-activated protein kinase kinase 3	MAP2K3	XM_001130488 // NM_145110 // NM_002756 // NM_145109	MGC40295 // SRL300 // SRm300 MAPKK3 // MEK3 // MKK3 // PRKMK3	3714729	chr17	+	21128581	21159113	1.06
mitogen-activated protein kinase kinase 1 interacting protein 1	MAP2K1IP1	NM_021970	MP1	2779408	chr4	−	101018538	101034726	1.06
hypothetical protein FLJ31951	FLJ31951	NM_144726	DKFZp686M11215	2884216	chr5	−	158516997	158569129	1.06
capping protein (actin filament) muscle Z-line, alpha 1	CAPZA1	NM_006135	CAPPA1 // CAPZ // CAZ1	2352228	chr1	+	112945824	113015736	1.06
chemokine (C—X—C motif) ligand 10	CXCL10	NM_001565	C7 // IFI10 // INP10 // IP-10 // SCYB10 // crg-2 // gIP-10 // mob-1	2773958	chr4	−	77151393	77163693	1.06
v-raf murine sarcoma 3611 viral oncogene homolog	ARAF	NM_001654	A-RAF // ARAF1 // PKS2 // RAFA1	3976299	chrX	+	47300826	47316249	1.06
ADAM metallopeptidase domain 17 (tumor necrosis factor, alpha, converting enzyme)	ADAM17	NM_003183	CD156b // MGC71942 // TACE // cSVP	2539821	chr2	−	9546070	9630637	1.06
protein tyrosine phosphatase type IVA, member 1	PTP4A1	NM_003463	DKFZp779M0721 // HH72 // PRL-1 // PRL1 // PTP(CAAX1) // PTPCAAX1	2911903	chr6	+	64289625	64351448	1.06
poly (ADP-ribose) polymerase family, member 9	PARP9	NM_031458	BAL // BAL1 // DKFZp666B0810 // DKFZp686M15238 // FLJ26637 // FLJ41418 // MGC: 7868	2692060	chr3	−	123729469	123766193	1.06
WD repeat domain 74	WDR74	XM_001125771 // NM_018093	FLJ10439 // FLJ21730	3376235	chr11	−	62356627	62365857	1.06
KIAA0256 gene product // trafficking protein particle complex 5	KIAA0256 // TRAPPC5	NM_014701 // NM_001042461 // NM_001042462 // NM_174894	—// MGC52424	3623320	chr15	−	47055671	47126043	1.06
CD47 molecule	CD47	NM_001025079 // NM_001777 // NM_198793	IAP // MER6 // OA3	2687739	chr3	−	109143203	109306052	1.06
inositol polyphosphate-5-phosphatase, 145 kDa	INPP5D	XM_929960 // NM_001017915 // NM_005541	MGC104855 // MGC142140 // MGC142142 // SHIP // SHIP1 // SIP-145 // hp51CN	2532699	chr2	+	233632835	233823600	1.06

TABLE 5-continued

				Human Exon ST 1.0 Transcript	Human Genome hg18				Fold Change/
Gene Name	Gene Symbol	Accession	Synonym	Cluster ID	Chromosome	Strand	Start	Stop	nM
slingshot homolog 2 (*Drosophila*)	SSH2	NM_033389	KIAA1725 // MGC78588 // SSH-2	3751625	chr17	−	24977091	25281397	1.06
oxysterol binding protein-like 8	OSBPL8	NM_001003712 // NM_020841	DKFZp686A11164 // MGC126578 // MGC133203 // ORP8 // OSBP10	3462949	chr12	−	75269250	75477720	1.06
RAS p21 protein activator 3	RASA3	NM_007368	GAP1IP4BP // GAPIII // MGC46517 //	3526831	chr13	−	113765177	113916197	1.06
stromal antigen 2	STAG2	NM_001042749 // NM_001042750 // NM_001042751 // NM_006603	DKFZp686P168 // DKFZp781H1753 // FLJ25871 // SA-2 // SA2 // bA517O1.1	3989721	chrX	+	122922013	123384079	1.06
NIMA (never in mitosis gene a)-related kinase 7	NEK7	NM_133494	—	2373736	chr1	+	196225008	196558827	1.06
protein tyrosine phosphatase, receptor type, E	PTPRE	NM_006504 // NM_130435	DKFZp313F1310 // HPTPE // PTPE // R-PTP-EPSILON	3270270	chr10	+	129595315	129774152	1.06
solute carrier organic anion transporter family, member 4A1	SLCO4A1	NM_016354	OATP-E // OATP1 // OATP4A1 // OATPRP1 // POAT // SLC21A12	3892812	chr20	+	60744242	60787582	1.06
v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	SRC	NM_005417 // NM_198291	ASV // SRC1 // c-SRC // p60-Src	3884191	chr20	+	35406502	35467847	1.06
phosphoinositide-3-kinase, regulatory subunit 5, p101	PIK3R5	NM_014308	F730038I15Rik // FOAP-2 // P101-PI3K	3744680	chr17	−	8718740	8809747	1.06
HECT, UBA and WWE domain containing 1 // paraoxonase 1 // paraoxonase 3	HUWE1 // PON1 // PON3	NM_031407 // NM_000446 // NM_000940	ARF-BP1 // HECTH9 // HSPC272 // lb772 // KIAA0312 // LASU1 // MULE // UREB1 // ESA // PON // —	4009315	chrX	−	53575796	53740871	1.06
antizyme inhibitor 1	AZIN1	NM_015878 // NM_148174 //	MGC3832 // MGC691 // OAZI // OAZIN //	3147591	chr8	−	103907725	103953967	1.06
A kinase (PRKA) anchor protein 13	AKAP13	NM_006738 // NM_007200 // NM_144767	AKAP-Lbc // BRX // FLJ11952 // FLJ43341 // HA-3 // Ht31 // LBC // PROTO-LB // PROTO-LBC // c-lbc	3606304	chr15	+	83681343	84102785	1.06

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change/ nM
eukaryotic translation initiation factor 4 gamma, 2	EIF4G2	NM_001042559 // NM_001418	AAG1 // DAP5 // FLJ41344 // NAT1 // p97	3362719	chr11	−	10487574	10788746	1.06
suppressor of Ty 6 homolog (*S. cerevisiae*)	SUPT6H	NM_003170	KIAA0162 // MGC87943 // SPT6 // SPT6H // emb-5	3715703	chr17	+	24013260	24053809	1.06
solute carrier family 36 (proton/amino acid symporter), member 4	SLC36A4	NM_152313	FLJ38932 // PAT4	3386638	chr11	−	92485640	92570746	1.06
DOT1-like, histone H3 methyltransferase (*S. cerevisiae*)	DOT1L	NM_032482	DOT1 // KIAA1814	3816264	chr19	+	2114945	2183576	1.06
epithelial stromal interaction 1 (breast) // junctophilin 3	EPSTI1 // JPH3	NM_001002264 // NM_033255 // NM_020655	BRESI1 // MGC29634 // CAGL237 // FLJ44707 // HDL2 // JP-3 // JP3 // TNRC22	3511698	chr13	−	42309603	42464520	1.06
promyelocytic leukemia	PML	XM_001132060 // NM_002675 // NM_033238 // NM_033239 // NM_033240 // NM_033244 // NM_033246 // NM_033247 // NM_033249 // NM_033250	MYL // PP8675 // RNF71 // TRIM19	3601387	chr15	+	72073603	72126162	1.06
DnaJ (Hsp40) homolog, subfamily A, member 1	DNAJA1	NM_001539	DJ-2 // DjA1 // HDJ2 // HSDJ // HSJ2 // HSPF4 // hDJ-2	3166718	chr9	+	33015173	33029946	1.06
TSC22 domain family, member 3	TSC22D3	NM_001015881 // NM_004089 // NM_198057	DIP // DKFZp313A1123 // DSIPI // GILZ // TSC-22R // hDIP	4017381	chrX	−	106803586	106916423	1.06
RNA binding motif protein 4	RBM4	NM_002896	DKFZp547K0918 // LARK // MGC75138 // RBM4A // ZCCHC21 // ZCRB3A	3336422	chr11	+	66161951	66190547	1.06
Smg-7 homolog, nonsense mediated mRNA decay factor (*C. elegans*)	SMG7	NM_014837 // NM_173156 // NM_201568 // NM_201569	C1orf16 // EST1C // FLJ23717 // KIAA0250 // SGA56M // SMG-7	2371255	chr1	+	181708036	181834004	1.06
baculoviral IAP repeat-containing 2	BIRC2	NM_001166	API1 // HIAP2 // Hiap-2 // MIHB // RNF48 // cIAP1	3346584	chr11	+	101722704	101754720	1.06

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript	Human Genome hg18				Fold Change/
				Cluster ID	Chromosome	Strand	Start	Stop	nM
DEAH (Asp-Glu-Ala-His) box polypeptide 15	DHX15	NM_001358	DBP1 // DDX15 // HRH2 // PRP43 // PRPF43 // PrPp43p	2763805	chr4	−	24128159	24250940	1.06
echinoderm microtubule associated protein like 4	EML4	NM_019063	C2orf2 // DKFZp686P18118 // ELP120 // FLJ10942 // FLJ32318 // ROPP120	2478748	chr2	+	42250017	42418636	1.06
protein phosphatase 6, catalytic subunit	PPP6C	NM_002721	—	3225348	chr9	−	126948675	126991992	1.06
bromodomain and WD repeat domain containing 1	BRWD1	NM_001007246 // NM_018963 // NM_033656	C21orf107 // FLJ43918 // N143 // WDR9	3932148	chr21	−	39479279	39615332	1.06
amyloid beta (A4) precursor-like protein 2	APLP2	NM_001642	APPH // APPL2 // CDEBP	3356115	chr11	+	129444931	129519895	1.06
sperm associated antigen 9	SPAG9	NM_003971 // NM_172345	FLJ13450 // FLJ14006 // FLJ34602 // HLC4 // HSS // JLP // KIAA0516 // MGC117291 // MGC14967 // MGC74461 // PHET // PIG6	3762519	chr17	−	46394554	46553215	1.06
Rap guanine nucleotide exchange factor (GEF) 6 // folliculin interacting protein 1	RAPGEF6 // FNIP1	NM_016340 // NM_001008738 // NM_133372	DKFZp667N084 // DKFZp686I15116 // KIA001LB // PDZ-GEF2 // PDZGEF2 // RA-GEF-2 // DKFZp686E18167 // DKFZp781P0215 // KIAA1961 // MGC667	2874794	chr5	−	130760272	131160628	1.06
ATPase, Na+/K+ transporting, beta 3 polypeptide	ATP1B3	XM_001133533 // XM_001133534 // NM_001679	ATPB-3 // CD298 // FLJ29027	2645764	chr3	+	143077611	143128338	1.06
leukocyte-associated immunoglobulin-like receptor 1	LAIR1	NM_002287 // NM_021706	CD305 // LAIR-1	3870824	chr19	−	59557066	59578582	1.06
interleukin enhancer binding factor 2, 45 kDa	ILF2	NM_004515	MGC8391 // NF45 // PRO3063	2436132	chr1	−	151900372	151910103	1.06
solute carrier family 38, member 1	SLC38A1	NM_001077484 // NM_030674	ATA1 // NAT2 // SAT1 // SNAT1	3452231	chr12	−	44863120	44952390	1.06
tudor domain containing 7	TDRD7	NM_014290	KIAA1529 // PCTAIRE2BP // RP11-508D10.1 // TRAP	3181193	chr9	+	99202471	99298225	1.06

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change/ nM
thioredoxin domain containing 14 // catenin (cadherin-associated protein), delta 1	TXNDC14 // CTNND1	NM_015959 // XM_001126721 // XM_001126756 // XM_001126767 // XM_001126781 // XM_001126793 // XM_001126823 // NM_001331	CGI-31 // DKFZp781O2021 // MGC111151 // PIG26 // TMX2 // CAS // CTNND // KIAA0384 // P120CAS // P120CTN // p120	3331487	chr11	+	57235839	57391291	1.06
zinc finger protein 207	ZNF207	NM_001032293 // NM_003457	DKFZp761N202	3717635	chr17	+	27701159	27759429	1.06
zinc finger, AN1-type domain 3	ZFAND3	NM_021943	FLJ13222 // TEX27	2905664	chr6	+	37895285	38231400	1.06
catenin (cadherin-associated protein), beta 1, 88 kDa	CTNNB1	XM_001133660 // XM_001133664 // XM_001133673 // XM_001133675 // NM_001904	CTNNB // FLJ25606	2618940	chr3	+	41211356	41256934	1.06
NCK-associated protein 1-like	NCKAP1L	NM_005337	HEM1	3416577	chr12	+	53177769	53224156	1.06
upstream binding protein 1 (LBP-1a)	UBP1	NM_014517	DKFZp686L1745 // LBP-1B // LBP-1a // LBP1A //	2668351	chr3	−	33404835	33456874	1.06
cytoskeleton-associated protein 4	CKAP4	NM_006825	CLIMP-63 // ERGIC-63 // MGC99554 // p63	3469687	chr12	−	105155796	105222139	1.06
ubiquitin B // chromosome 17 open reading frame 45	UBB // C17orf45	NM_018955 // NM_152350	FLJ25987 // MGC8385 // FLJ25777 // MGC40157	3712041	chr17	+	16223047	16228977	1.06
ATPase, Class V, type 10D	ATP10D	NM_020453	ATPVD //	2726072	chr4	+	47179942	47290260	1.06
cytoplasmic polyadenylation element binding protein 4	CPEB4	NM_030627	KIAA1673	2841699	chr5	+	173177911	173320580	1.06
zinc finger protein 451	ZNF451 // KIAA1702	NM_001031623 // NM_015555	COASTER // FLJ90693 // KIAA0576 // MGC26701 // dJ417I1.1	2911303	chr6	+	57062631	57143064	1.06
superoxide dismutase 2, mitochondrial	SOD2 // MGC5618	NM_000636 // NM_001024465 // NM_001024466	IPO-B // MNSOD // Mn-SOD	2982319	chr6	−	160020086	160103541	1.06
optic atrophy 1 (autosomal dominant)	OPA1	NM_015560 // NM_130831 // NM_130832 // NM_130833 // NM_130834 // NM_130835 // NM_130836 // NM_130837	FLJ12460 // KIAA0567 // NPG // NTG // largeG	2658346	chr3	+	194793673	194902403	1.06

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change/ nM
Rho-associated, coiled-coil containing protein kinase 1	ROCK1	NM_005406	MGC131603 // MGC43611 // P160ROCK	3800619	chr18	−	16783710	17017478	1.06
GNAS complex locus	GNAS	NM_000516 // NM_001077488 // NM_001077489 // NM_001077490 // NM_016592 // NM_080425 // NM_080426 // NR_003259	AHO // C20orf45 // GNAS1 // GPSA // GSA // GSP // MGC33735 // PHP1A // PHP1B // POH // dJ309F20.1.1 // dJ806M20.3.3	3891163	chr20	+	56848165	56919604	1.06
myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	MX1	NM_002462	IFI-78K // IFI78 // MX // MxA	3922100	chr21	+	41714183	41752955	1.06
SP110 nuclear body protein	SP110	NM_004509 // NM_004510 // NM_080424	FLJ22835 // IFI41 // IFI75 // VODI	2603051	chr2	−	230740259	230797812	1.06
AP1 gamma subunit binding protein 1	AP1GBP1	NM_007247 // NM_080550	MGC104959 // SYNG	3754677	chr17	−	32949033	33043613	1.06
TAR DNA binding protein	TARDBP	NM_007375	TDP-43	2320048	chr1	+	10995025	11013170	1.06
methionine adenosyltransferase II, alpha	MAT2A	NM_005911	MATA2 // MATII // SAMS2	2491615	chr2	+	85597809	85625908	1.06
RNA binding motif protein 17	RBM17	NM_032905	MGC14439 // SPF45	3233547	chr10	+	6170982	6225410	1.06
asparaginyl-tRNA synthetase // sideroflexin 3	NARS // SFXN3	NM_004539 // NM_030971	ASNRS // BA108L7.2 // SFX3	3809671	chr18	−	53418770	53448841	1.06
PAN3 polyA specific ribonuclease subunit homolog (*S. cerevisiae*)	PAN3	NM_175854	—	3483159	chr13	+	27572646	27773671	1.06
SMAD specific E3 ubiquitin protein ligase 2	SMURF2	NM_022739	DKFZp686F0270 // MGC138150	3766960	chr17	−	59968891	60088896	1.06
ankyrin repeat domain 15	ANKRD15	NM_015158 // NM_153186	DKFZp451G231 // KANK // KIAA0172 // MGC43128	3159483	chr9	+	460301	746375	1.06
structural maintenance of chromosomes flexible hinge domain containing 1	SMCHD1	XM_113962 // XM_938891	DKFZp686O0631 // KIAA0650	3776193	chr18	+	2688138	2794997	1.06
transcription factor 12 (HTF4, helix-loop-helix transcription factors 4)	TCF12	NM_003205 // NM_207036 // NM_207037 // NM_207038 // NM_207040	HEB // HTF4 // HsT17266	3595096	chr15	+	54963208	55402126	1.06
ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	ATP2A2	NM_001681 // NM_170665	ATP2B // DAR // DD // MGC45367 // SERCA2	3431483	chr12	+	109203332	109352495	1.06
ubiquitin associated protein 1	UBAP1	NM_016525	MGC119669 // MGC8710 // NAG20 // UAP //	3167325	chr9	+	34168995	34243205	1.06

TABLE 5-continued

				Human Exon ST 1.0 Transcript	Human Genome hg18				Fold Change/
Gene Name	Gene Symbol	Accession	Synonym	Cluster ID	Chromosome	Strand	Start	Stop	nM
heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	HS3ST3B1	NM_006041	30ST3B1 // 3OST3B1	3711262	chr17	+	14145125	14193444	1.06
arrestin domain containing 2	ARRDC2	NM_001025604 // NM_015683	CLONE24945 // PP2703	3824713	chr19	+	17972961	17985905	1.06
casein kinase 1, alpha 1	CSNK1A1	NM_001025105 // NM_001892	CK1 // HLCDGP1 // PRO2975	2880932	chr5	−	148800168	148922811	1.06
CCR4-NOT transcription complex, subunit 2	CNOT2	NM_014515	CDC36 // HSPC131 // NOT2	3421897	chr12	+	68901823	69035035	1.06
mitogen-activated protein kinase kinase kinase 8	MAP3K8	NM_005204	COT // EST // ESTF // FLJ10486 // TPL2 // Tpl-2 // c-COT	3240987	chr10	+	30762872	30791283	1.06
mitogen-activated protein kinase kinase kinase 2	MAP3K2	XM_001128799 // NM_006609	MEKK2 // MEKK2B	2574798	chr2	−	127772731	127863022	1.06
protein phosphatase 4, regulatory subunit 2	PPP4R2	NM_174907	MGC131930	2629693	chr3	+	73019946	73201035	1.06
topoisomerase (DNA) 1	TOP1	NM_003286	TOP1	3885464	chr20	+	39090891	39186535	1.06
ubiquitin specific peptidase 7 (herpes virus-associated)	USP7	NM_003470	HAUSP // TEF1	3679564	chr16	−	8893458	8964832	1.06
RAB21, member RAS oncogene family	RAB21	NM_014999	KIAA0118	3422269	chr12	+	70434927	70470787	1.06
MAX interactor 1	MXI1	NM_001008541 // NM_005962 // NM_130439	MAD2 // MGC43220 // MXD2 // MXI	3263624	chr10	+	111944059	112037108	1.06
NGFI-A binding protein 1 (EGR1 binding protein	NAB1	NM_005966	—	2520225	chr2	+	191205069	191437200	1.06
cytochrome P450, family 1, subfamily B, polypeptide 1	CYP1B1	NM_000104	CP1B // GLC3A	2548699	chr2	−	38138730	38196009	1.06
chromosome 1 open reading frame 63	C1orf63	NM_020317	DJ465N24.2.1 // NPD014 // RP3-465N24.4	2402111	chr1	−	25440667	25538017	1.06
nucleoporin 153 kDa	NUP153	NM_005124	HNUP153 // N153	2943808	chr6	−	17723255	17855638	1.06
protein phosphatase 1K (PP2C domain containing)	PPM1K	NM_152542	DKFZp667B084 // DKFZp761G058 // PTMP // UG0882E07	2777333	chr4	−	89401891	89424935	1.06
phosphoinositide-3-kinase, class 3	PIK3C3	NM_002647	MGC61518 //	3786039	chr18	+	37534028	37985705	1.05
CCHC-type zinc finger, nucleic acid binding protein	CNBP	NM_003418	CNBP1 // DM2 // PROMM // RNF163 // ZCCHC22 // ZNF9	2694644	chr3	−	130369369	130385467	1.05
ubiquitin specific peptidase 9, X-linked // ubiquitin specific peptidase 9, Y-linked (fat facets-like, *Drosophila*)	USP9X // USP9Y	NM_001039590 // NM_001039591 // NM_004654	DFFRX // FAF // AZF // AZFA // DFFRY // SP3	3974708	chrX	+	40829542	40980776	1.05
baculoviral IAP repeat-containing 6 (apollon)	BIRC6	NM_016252	APOLLON // BRUCE // FLJ13726 // FLJ13786 //	2476219	chr2	+	32435095	32697447	1.05

TABLE 5-continued

				Human Exon ST 1.0 Transcript	Human Genome hg18				Fold Change/
Gene Name	Gene Symbol	Accession	Synonym	Cluster ID	Chromosome	Strand	Start	Stop	nM
chromosome 11 open reading frame 30	C11orf30	NM_020193	EMSY // FLJ90741 // GL002	3340913	chr11	+	75803897	75941697	1.05
pleckstrin homology domain containing, family M (with RUN domain) member 1	PLEKHM1	XM_001128220 // NM_014798	AP162 // B2 // KIAA0356	3759849	chr17	−	40869050	40923923	1.05
autism susceptibility candidate 2	AUTS2	NM_015570	KIAA0442 // MGC13140	3006572	chr7	+	68695979	69896399	1.05
YME1-like 1 (*S. cerevisiae*)	YME1L1	NM_014263 // NM_139312 // NM_139313	FTSH // MEG4 // PAMP // YME1L	3282213	chr10	−	27439066	27484191	1.05
toll-like receptor 4	TLR4	NM_138554	CD284 // TOLL // hToll	3186966	chr9	+	119506334	119670150	1.05
splicing factor 3b, subunit 1, 155 kDa	SF3B1	NM_001005526 // NM_012433	PRP10 // PRPF10 // SAP155 // SF3b155	2593670	chr2	−	197962756	198039327	1.05
E3 ubiquitin protein ligase, HECT domain containing, 1	EDD1	NM_015902	DD5 // EDD // FLJ11310 // HYD // KIAA0896 // MGC57263	3147321	chr8	−	103333634	103493671	1.05
ATP-binding cassette, sub-family C (CFTR/MRP), member 1	ABCC1	NM_004996 // NM_019862 // NM_019898 // NM_019899 // NM_019900 // NM_019901 // NM_019902	ABC29 // ABCC // DKFZp686N04233 // DKFZp781G125 // GS-X // MRP // MRP1	3649890	chr16	+	15950935	16144419	1.05
pleckstrin	PLEK	NM_002664	FLJ27168 // P47	2486811	chr2	+	68415853	68526386	1.05
farnesyltransferase, CAAX box, alpha	FNTA	NM_001018676 // NM_001018677 // NM_002027	FPTA // MGC99680 // PGGT1A	3096428	chr8	+	43030413	43060080	1.05
centrosomal protein 170 kDa // centrosomal protein 170 kDa-like	CEP170 // CEP170L	XM_001125768 // NM_001042404 // NM_001042405 // NM_014812 // XR_015931 // XR_017916 // NR_003135	FAM68A // KAB // KIAA0470 // FAM68B // KIAA0470L // MGC26143	2463864	chr1	−	241354364	241485236	1.05
forkhead box K2	FOXK2	XM_001134363 // XM_001134364 // NM_004514	ILF // ILF-1 // ILF1	3738969	chr17	+	78070883	78195807	1.05
B-cell CLL/lymphoma 9-like	BCL9L	NM_182557	BCL9-2 // DLNB11	3393993	chr11	−	118272076	118304947	1.05
cell division cycle 2-like 5 (cholinesterase-related cell division controller)	CDC2L5	NM_003718 // NM_031267	CDC2L // CHED // FLJ35215 // KIAA1791	2998536	chr7	+	39897668	40103253	1.05
proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	PSMD11	NM_002815	MGC3844 // S9 // p44.5	3717737	chr17	+	27795087	27834449	1.05

TABLE 5-continued

				Human Exon ST 1.0 Transcript	Human Genome hg18				Fold Change/
Gene Name	Gene Symbol	Accession	Synonym	Cluster ID	Chromosome	Strand	Start	Stop	nM
calreticulin	CALR	NM_004343	FLJ26680 // RO // SSA // cC1qR	3822049	chr19	+	12910423	12916480	1.05
schlafen family member 11	SLFN11	NM_152270	FLJ34922 // SLFN8/9	3753500	chr17	−	30696595	30724798	1.05
nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	NR3C1	NM_000176 // NM_001018074 // NM_001018075 // NM_001018076 // NM_001018077 // NM_101020825 // NM_001024094	GCCR // GCR // GR // GRL	2879312	chr5	−	142566614	142794517	1.05
dual specificity phosphatase 16	DUSP16	NM_030640	KIAA1700 // MGC129701 // MGC129702 // MKP-7 // MKP7	3444958	chr12	−	12510545	12606611	1.05
glycoprotein V (platelet) // zinc finger protein 394	GP5 // ZNF394	NM_004488 // NM_032164	CD42d // FLJ12298 // ZKSCAN14	3063337	chr7	−	98922007	98935856	1.05
nuclear protein, ataxia-telangiectasia locus	NPAT	NM_002519	E14	3390067	chr11	−	107533176	107599902	1.05
splicing factor, arginine/serine-rich 3	SFRS3	NM_003017	SRp2O	2905118	chr6	+	36669658	36741293	1.05
guanine nucleotide binding protein (G protein) alpha 12	GNA12	NM_007353	MGC104623 // MGC99644 // NNX3 // RMP // gep	3035892	chr7	−	2724003	2910140	1.05
chromosome 13 open reading frame 18	C13orf18	NM_025113	FLJ21562 // FLJ43762	3512948	chr13	−	45814156	45917111	1.05
nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	NFKB2	NM_001077493 // NM_001077494 // NM_002502	LYT-10 // LYT10	3261643	chr10	+	104144262	104152716	1.05
chromosome 22 open reading frame 28	C22orf28	NM_014306	DJ149A16.6 // HSPC117 // RP1-149A16.6	3958253	chr22	−	31113563	31138223	1.05
ubiquitin specific peptidase 4 (proto-oncogene)	USP4	NM_003363 // NM_199443	MGC149848 // MGC149849 // UNP // Unph	2674179	chr3	−	49290730	49353046	1.05
F-box protein 11	FBXO11	NM_012167 // NM_018693 // NM_025133	FBX11 // FLJ12673 // MGC44383 // PRMT9 // UG063H01 // VIT1	2552153	chr2	−	47869608	47988296	1.05
PRP4 pre-mRNA processing factor 4 homolog B (yeast)	PRPF4B	NM_003913	KIAA0536 // PR4H // PRP4 // PRP4H // PRP4K // dJ1013A10.1	2892738	chr6	+	3966500	4010215	1.05
ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 // protocadherin LKC	ATP8A1 // PCLKC	NM_006095 // NM_017675	ATPASEII // ATPIA // ATPP2 // MGC130042 // MGC130043 // MGC26327 //	2767378	chr4	−	42105160	42353857	1.05

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change/ nM
			FLJ20124 // FLJ20383 // MGC163154						
zinc finger protein 267	ZNF267	NM_003414	HZF2	3657367	chr16	+	31730255	31836159	1.05
BAT2 domain containing 1	BAT2D1	NM_015172	BAT2-iso // XTP2	2367164	chr1	+	169716078	169829262	1.05
DEAD (Asp-Glu-Ala-Asp) box polypeptide 18 // wingless-type MMTV integration site family, member 8B	DDX18 // WNT8B	NM_006773 // NM_003393	FLJ33908 // MrDb // —	2502300	chr2	+	118243834	118323562	1.05
Ran GTPase activating protein 1	RANGAP1	NM_002883	Fug1 // KIAA1835 // MGC20266 //	3961842	chr22	–	39969442	40028027	1.05
protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	PRKAR1A	NM_002734 // NM_212471 // NM_212472	CAR // CNC // CNC1 // DKFZp779L0468 // MGC17251 // PKR1 // PRKAR1 //	3732885	chr17	+	64019700	64059052	1.05
ubiquitin specific peptidase 38	USP38	NM_032557	FLJ35970 // HP43.8KD // KIAA1891	2745499	chr4	+	144325529	144364549	1.05
damage-regulated autophagy modulator	DRAM	NM_018370	FLJ11259	3428783	chr12	+	100795270	100930011	1.05
SET domain containing 5	SETD5	XM_926615 // XM_931376 // XM_931417 // XM_931444 // XM_931447 // XM_931455 // XM_931478 // XM_939712 // XM_944260 // XM_944276 // XM_944280 // XM_944295 // XM_944298 // XM_944303 // NM_001080517	DKFZp686J18276 // FLJ10707 // KIAA1757	2609608	chr3	+	9414309	9495916	1.05
myeloid differentiation primary response gene	MYD88	NM_002468	—	2617563	chr3	+	38155029	38159513	1.05
transmembrane protein 1	TMEM1	NM_001001723 // NM_003274	EHOC-1 // EHOC1 // GT334 // MGC126777	3923436	chr21	+	44256650	44350842	1.05
RNA binding motif protein 23 // chromosome 9 open reading frame 102	RBM23 // C9orf102	NM_001077351 // NM_001077352 // NM_018107 // NM_001034155 // NM_020207	CAPERbeta // FLJ10482 // MGC4458 // PP239 // RNPC4 // FLJ37706 // SR278	3556888	chr14	–	22439714	22458231	1.05
myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, *Drosophila*); translocated to,	MLLT3	NM_004529	AF9 // FLJ2035 // YEATS3	3200982	chr9	–	20334968	20612522	1.05

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change/ nM
eukaryotic translation initiation factor 3, subunit 10 theta, 150/170 kDa	EIF3S10	NM_003750	EIF3 // EIF3A // KIAA0139 // P167 // eIF3-p170 // eIF3-theta // p180 // p185	3309215	chr10	−	120621551	120830522	1.05
chromosome 3 open reading frame 63	C3orf63	NM_015224	DKFZp686C2456 // KIAA1105 // RAP140 // se89-1	2677653	chr3	−	56629203	56692517	1.05
adenosine monophosphate deaminase (isoform E) // peroxisome proliferator-activated receptor alpha // tRNA 5-methylaminomethyl-2-thiouridylate methyltransferase // G-2 and S-phase expressed 1	AMPD3 // PPARA // TRMU // GTSE1	NM_000480 // NM_001025389 // NM_001025390 // NM_001001929 // NM_001001930 // NM_032644 // NM_001001928 // NM_005036 // NM_018006 // NM_016426	—// MGC2237 // MGC2452 // NRIC1 // PPAR // hPPAR // MGC99627 // MTO2 // MTU1 // TRMT // TRMT1 // TRNT1 // B99	3320169	chr11	+	10428461	10485703	1.05
retinoic acid receptor, alpha	RARA	NM_001033603 // NM_000964 // NM_001024809	NR1B1 // RAR	3720921	chr17	+	35718982	35767411	1.05
p21 (CDKNIA)-activated kinase 2	PAK2	XM_001126110 // NM_002577	PAK65 // PAKgamma	2659577	chr3	+	197951145	198043895	1.05
splicing factor 3b, subunit 2, 145 kDa	SF3B2	NM_006842	SAP145 // SF3B145 // SF3b1 // SF3b150	3335907	chr11	+	65573499	65593343	1.05
eukaryotic translation initiation factor 4A, isoform 1 // SUMO1/sentrin/SMT3 specific peptidase 3	EIF4A1 // SENP3	NM_001416 // NM_015670	DDX2A // EIF-4A // EIF4A // DKFZP586K0919 // DKFZp762A152 // SMT3IP1 // SSP3	3708826	chr17	+	7416768	7423040	1.05
syntaxin 6	STX6	NM_005819	—	2446567	chr1	−	179095658	179258656	1.05
carbohydrate (chondroitin 4) sulfotransferase 11	CHST11	NM_018413	C4ST // C4ST-1 // C4ST1 // HSA269537	3429566	chr12	+	103374529	103679918	1.05
protein phosphatase 1, catalytic subunit, beta isoform	PPP1CB	NM_206877 // NM_002709 // NM_206876	MGC3672 // PP-1B // PPP1CD	2475209	chr2	+	28828128	28879300	1.05
mitogen-activated protein kinase 6	MAPK6	NM_002748	DKFZp686F03189 // ERK3 // HsT17250 // PRKM6 //	3694129	chr15	+	50098740	50146174	1.05
GTP binding protein 4	GTPBP4	NM_012341	CRFG // FLJ10686 // FLJ10690 // FLJ39774 // NGB	3231774	chr10	+	942450	1055862	1.05

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change/ nM
forkhead box O3A	FOXO3A	NM_001455 // NM_201559	AF6q21 // DKFZp781A0677 // FKHRL1 // FKHRL1P2 // MGC12739 // MGC31925	2920475	chr6	+	108987684	109112650	1.05
transmembrane protein 2	TMEM2	NM_013390	—	3209384	chr9	−	73452177	73573229	1.05
cyclin G associated kinase	GAK	XM_001127411 // NM_005255	FLJ40395 // MGC99654	2756673	chr4	−	833110	916149	1.05
tumor necrosis factor (ligand) superfamily, member 8	TNFSF8	NM_001244	CD153 // CD30L // CD30LG // MGC138144	3222144	chr9	−	116695445	116732620	1.05
presenilin 1 (Alzheimer disease 3)	PSEN1	NM_000021	AD3 // FAD // PS1 // S182	3543481	chr14	+	72672571	72760151	1.05
D4, zinc and double PHD fingers family 2	DPF2	NM_006268	MGC10180 // REQ // UBID4 // ubi-d4	3335089	chr11	+	64857703	64877276	1.05
splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	SFPQ	NM_005066	POMP100 // PSF	2406064	chr1	−	35351696	35506894	1.05
development and differentiation enhancing factor 1	DDEF1	NM_018482	AMAP1 // ASAP1 // KIAA1249 // PAG2 // PAP //	3153428	chr8	−	131133540	131525100	1.05
TNF receptor-associated factor 3	TRAF3	NM_003300 // NM_145725 // NM_145726	CAP-1 // CD40bp // CRAF1 // LAP1	3553337	chr14	+	102313566	102447585	1.05
thyroid hormone receptor associated protein 1	THRAP1	NM_005121	ARC250 // DRIP250 // HSPC221 // KIAA0593 //	3765689	chr17	−	57374750	57498031	1.05
general transcription factor IIIC, polypeptide 4, 90 kDa	GTF3C4	NM_012204	FLJ21002 // MGC138450 // TFIII90 // TFIIIC90 // TFIIICdelta // TFiiiC2-90	3192525	chr9	+	134535243	134581784	1.05
praja 2, RING-H2 motif containing	PJA2	NM_014819	KIAA0438 // Neurodap1 // RNF131	2870397	chr5	−	108614328	108773545	1.05
suppressor of var1, 3-like 1 (*S. cerevisiae*)	SUPV3L1	NM_003171	SUV3	3250204	chr10	+	70609946	70638996	1.05
ADP-ribosylation factor 1	ARF1	NM_001024226 // NM_001024227 // NM_001024228 // NM_001658	—	2383726	chr1	+	226313262	226353506	1.05
cullin-associated and neddylation-dissociated 1	CAND1	NM_018448	DKFZp434M1414 // FLJ10114 // FLJ10929 // FLJ38691 // FLJ90441 //	3420713	chr12	+	65946048	65994719	1.05

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript Cluster ID	Human Genome hg18 Chromosome	Human Genome hg18 Strand	Human Genome hg18 Start	Human Genome hg18 Stop	Fold Change/ nM
			KIAA0829 // TIP120 // TIP120A						
ankylosis, progressive homolog (mouse)	ANKH	XM_001132013 // NM_054027	ANK // CCAL2 // CMDJ // CPPDD // FLJ27166 // HANK // MANK	2849469	chr5	–	14757920	14924876	1.05
UBX domain containing 2	UBXD2	NM_014607	FLJ23318 // KIAA0242 // UBXDC1 // erasin	2507495	chr2	+	136215526	136259081	1.05
interferon gamma receptor 1	IFNGR1	NM_000416	CD119 // FLJ45734 // IFNGR	2976113	chr6	–	137560317	137582279	1.05
GDP dissociation inhibitor 1	GDI1	NM_001493	FLJ41411 // GDIL // MRX41 // MRX48 // OPHN2 // RABGD1A // RABGDIA // XAP-4	3996404	chrX	+	153318480	153324978	1.05
myotubularin related protein 6	MTMR6	NM_004685	—	3506153	chr13	–	24700317	24774271	1.05
KIAA0226	KIAA0226	XM_032901 // XM_936700	—	2713555	chr3	–	198863016	198960684	1.05
Nipped-B homolog (*Drosophila*) // nuclear receptor binding protein 1	NIPBL // NRBP1	NM_015384 // NM_133433 // NM_013392	CDLS // DKFZp434L1319 // FLJ11203 // FLJ12597 // FLJ13354 // FLJ13648 // FLJ44854 // IDN3 // IDN3-B // BCON3 // FLJ27109 // FLJ35541 // MADM // MUDPNP // NRBP	2806799	chr5	+	36894163	37115932	1.05
DENN/MADD domain containing 4A	DENND4A	NM_005848	FLJ33949 // IRLB // KIAA0476 // MYCPBP	3629811	chr15	–	63737458	63871676	1.05
MKI67 (FHA domain) interacting nucleolar phosphoprotein	MKI67IP	NM_032390	NIFK // Nopp34	2573786	chr2	–	122132489	122231052	1.05
myeloid/lymphoid or mixed-lineage leukemia 3 // ADAM metallopeptidase with thrombospondin type 1 motif, 2 // leucine-rich repeat kinase 1 // B melanoma antigen family, member 3	MLL3 // ADAMTS2 // LRRK1 // BAGE3	NM_021230 // NM_170606 // NM_014244 // NM_021599 // NM_024652 // NM_182481	DKFZp686C08112 // FLJ12625 // FLJ38309 // HALR // KIAA1506 // MGC119851 // MGC119852 // MGC119853 // ADAM-TS2 // ADAMTS-3 // NPI	3080033	chr7	–	151462947	151763974	1.05

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change/ nM
			// PCINP // PCPNI // hPCPNI // FLJ23119 // FLJ27465 // KIAA1790 // RIPK6 // Roco1 // —						
cyclin D2	CCND2	NM_001759	KIAK0002 // MGC102758	3401704	chr12	+	4232432	4284764	1.05
isopentenyl-diphosphate delta isomerase 1	IDI1	NM_004508	IPP1 // IPPI1	3273601	chr10	−	1075869	1092634	1.05
ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	ST8SIA4	NM_005668 // NM_175052	MGC34450 // MGC61459 // PST // PST1 // SIAT8D // ST8SIA-IV	2868904	chr5	−	100116166	100293602	1.05
Kruppel-like factor 9	KLF9	NM_001206	BTEB // BTEB1	3208995	chr9	−	72189344	72219360	1.05
splicing factor, arginine/serine-rich 2, interacting protein	SFRS2IP	NM_004719	CASP11 // SIP1 // SRRP129	3452145	chr12	−	44599187	44672160	1.05
ubiquitin specific peptidase 47	USP47	NM_017944	DKFZp686C13257 // FLJ20727 //	3320604	chr11	+	11819556	11937446	1.05
low density lipoprotein receptor (familial hypercholesterolemia)	LDLR	NM_000527	FH // FHC	3821015	chr19	+	11061114	11115050	1.05
Rho GDP dissociation inhibitor (GDI) beta	ARHGDIB	NM_001175	D4 // GDIA2 // GDID4 // LYGDI // Ly-GDI //	3445786	chr12	−	14986174	15005951	1.05
polymerase (RNA) III (DNA directed) polypeptide E (80 kD)	POLR3E	NM_018119	RPC5 // SIN	3652489	chr19	+	22216140	22253905	1.05
DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked	DDX3Y	NM_004660	DBY	4030162	chrY	+	13525423	13555808	1.05
adenosine deaminase, RNA-specific	ADAR	NM_001025107 // NM_001111 // NM_015840 // NM_015841	ADAR1 // DRADA // DSH // DSRAD // G1P1 // IFI-4 // IFI4 // K88dsRBP // p136	2436754	chr1	−	152821187	152867095	1.05
actin binding LIM protein 1	ABLIM1	NM_001003407 // NM_001003408 // NM_002313 // NM_006720	ABLIM // DKFZp781D0148 // FLJ14564 // KIAA0059 // LIMAB1 // LIMATIN // MGC1224	3307939	chr10	−	116180867	116571234	1.05
IBR domain containing 2	IBRDC2	NM_182757	KIAA0161 // MGC71786 // bA528A10.3 // p53RFP	2897172	chr6	+	18385558	18650038	1.05
IK cytokine, down-regulator of HLA II	IK	NM_006083	CSA2 // IK protein // MGC59741 // RED	2831932	chr5	+	140006890	140022229	1.05

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change/ nM
RAD21 homolog (*S. pombe*)	RAD21	NM_006265	FLJ25655 // FLJ40596 // HR21 // HRAD21 // KIAA0078 // MCD1 // NXP1 // SCC1 // hHR21	3149843	chr8	–	117909861	117956284	1.05
eukaryotic translation initiation factor 4 gamma, 1	EIF4G1	NM_004953 // NM_182917 // NM_198241 // NM_198242 // NM_198244	DKFZp686A1451 // EIF4F // EIF4G // p220	2655688	chr3	+	185514970	185535829	1.05
lactate dehydrogenase A	LDHA	NM_005566	LDH-M // LDH1 // PIG19	3322775	chr11	+	18372531	18386528	1.05
ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome)	UBE3A	NM_000462 // NM_130838 // NM_130839	ANCR // AS // E6-AP // EPVE6AP // FLJ26981 // HPVE6A	3614087	chr15	–	23006655	23355108	1.05
nuclear receptor subfamily 4, group A, member 1	NR4A1	NM_002135 // NM_173157 // NM_173158	GFRP1 // HMR // MGC9485 // N10 // NAK-1 // NGFIB // NP10 // NUR77 // TR3	3415229	chr12	+	50717248	50739539	1.05
diaphanous homolog 1 (*Drosophila*)	DIAPH1	NM_001079812 // NM_005219	DFNA1 // DRF1 // FLJ25265 // LFHL1 // hDIA1	2878662	chr5	–	140874773	140978866	1.05
zinc finger CCCH-type, antiviral 1	ZC3HAV1	NM_020119 // NM_024625	DKFZp686F2052 // DKFZp686H1869 // DKFZp686O19171 // FLB6421 // FLJ13288 // MGC48898 // ZAP // ZC3H2 // ZC3HDC2	3075566	chr7	–	138378808	138445046	1.05
SEC24 related gene family, member C (*S. cerevisiae*)	SEC24C	NM_004922 NM_198597	KIAA0079	3251848	chr10	+	75174138	75210008	1.05
calpain 2, (m/II) large subunit	CAPN2	NM_001748	CANPL2 // CANPml // FLJ39928 //	2382117	chr1	+	221955990	222031806	1.05
OTU domain containing 4	OTUD4	NM_017493 // NM_199324	DKFZp434I0721 // HIN1 // HSHIN1 // KIAA1046	2788195	chr4	–	146274170	146471942	1.05
Nedd4 binding protein 1	N4BP1	NM_153029	FLJ31821 // KIAA0615	3690597	chr16	–	47130140	47324384	1.05
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	PFKFB3	NM_004566	IPFK2 // PFK2	3233605	chr10	+	6226893	6336597	1.05

TABLE 5-continued

				Human Exon ST 1.0 Transcript	Human Genome hg18				Fold Change/
Gene Name	Gene Symbol	Accession	Synonym	Cluster ID	Chromosome	Strand	Start	Stop	nM
ATPase, H+ transporting, lysosomal 50/57 kDa, V1 subunit H	ATP6V1H	NM_015941 // NM_213619 // NM_213620	CGI-11 // MSTP042 // SFD // SFDalpha // SFDbeta // VMA13	3135452	chr8	−	54790669	54918651	1.05
ferritin, heavy polypeptide-like 7 // ferritin, heavy polypeptide 1 // ferritin, heavy polypeptide-like 3 // ferritin, heavy polypeptide pseudogene 1 // ferritin, heavy polypeptide-like 12 // ferritin, heavy polypeptide-like 11 // ferritin, heavy polypeptide-like 8	FTHL7 // FTH1 // FTHL3 // FTHP1 // FTHL12 // FTHL11 // FTHL8	NR_002202 // NM_002032 // NR_002201 // —// NR_002205 // NR_002204 // NR_002203	—// FTH // FTHL6 // MGC104426 // PIG15 // PLIF // FTHL5	3375648	chr11	−	61488337	61492603	1.05
protein inhibitor of activated STAT, 1	PIAS1	NM_016166	DDXBP1 // GBP // GU/RH-II // MGC141878 // MGC141879 // ZMIZ3	3599280	chr15	+	65898917	66277975	1.05
interferon-induced protein with tetratricopeptide repeats 3	IFIT3	NM_001031683 // NM_001549	CIG-49 // GARG-49 // IFI60 // IFIT4 // IRG2 // ISG60 // RIG-G	3257204	chr10	+	91059126	91090705	1.05
cullin 4A	CUL4A	NM_001008895 // NM_003589	—	3502497	chr13	+	112905835	112967356	1.05
SH2 domain protein 2A	SH2D2A	NM_003975	F2771 // TSAd	2438575	chr1	−	155038957	155053637	1.05
EH-domain containing 1	EHD1	NM_006795	FLJ42622 // FLJ44618 // H-PAST // HPAST1 // PAST // PAST1	3377226	chr11	−	64376790	64404202	1.05
SH2B adaptor protein 3	SH2B3	NM_005475	LNK	3431892	chr12	+	110328135	110373802	1.05
tropomodulin 3 (ubiquitous)	TMOD3	NM_014547	UTMOD	3594066	chr15	+	49909087	50026784	1.05
SMAD family member 3	SMAD3	NM_005902	DKFZP586N0721 // DKFZP686J10186 // HSPC193 // HsT17436 // JV15-2 // MADH3 // MGC60396 // Smad 3	3598959	chr15	+	65145043	65296818	1.05
vacuolar protein sorting 53 homolog (*S. cerevisiae*)	VPS53	NM_018289	FLJ10979 // MGC39512 // hVps53L //	3739679	chr17	−	375959	564837	1.05
TRAF and TNF receptor associated protein	TTRAP	NM_016614	AD022 // EAP2 // MGC111021 // MGC9099 // dJ30M3.3	2945645	chr6	−	24758144	24775240	1.05
MAP/microtubule affinity-regulating kinase 2	MARK2	NM_001039468 // NM_001039469 // NM_004954 // NM_017490	EMK1 // MGC99619 // PAR-1	3334025	chr11	+	63362634	63435067	1.05

TABLE 5-continued

				Human Exon ST 1.0 Transcript	Human Genome hg18				Fold Change/
Gene Name	Gene Symbol	Accession	Synonym	Cluster ID	Chromosome	Strand	Start	Stop	nM
helicase with zinc finger	HELZ	NM_014877	DRHC // HUMORF5 // KIAA0054 // MGC163454	3768015	chr17	−	62485987	62672547	1.05
golgi-specific brefeldin A resistance factor 1	GBF1	NM_004193	FLJ21263 // FLJ21500 // KIAA0248 // MGC134877 // MGC134878	3261544	chr10	+	103993260	104132642	1.05
serine/threonine kinase 38 like	STK38L	NM_015000	KIAA0965 // NDR2	3409081	chr12	+	27288343	27370157	1.05
BCL2-related protein A1	BCL2A1	NM_004049	ACC-1 // ACC-2 // BCL2L5 // BFL1 // GRS // HBPA1	3635198	chr15	−	78040295	78138851	1.05
membrane-associated ring finger (C3HC4) 7	MARCH7	NM_022826	AXO // AXOT // DKFZP586F1122 // MARCH-VII // RNF177	2512330	chr2	+	160277236	160333585	1.05
periphilin 1	PPHLN1	NM_016488 // NM_201438 // NM_201439 // NM_201440 // NM_201515	HSPC206 // HSPC232 // MGC48786	3412008	chr12	+	40917957	41128677	1.05
tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	TNKS2	NM_025235	PARP-5b // PARP-5c // PARP5B // PARP5C // TANK2 // TNKL	3257850	chr10	+	93548049	93633726	1.05
kelch-like 6 (*Drosophila*)	KLHL6	NM_130446	FLJ00029	2708066	chr3	−	184688052	184789879	1.05
Kruppel-like factor 10	KLF10	NM_001032282 // NM_005655	EGRA // TIEG // TIEG1	3147508	chr8	−	103682306	103767558	1.05
neugrin, neurite outgrowth associated	NGRN	NM_001033088 // NM_016645	DSC92 // NEUGRIN	3607998	chr15	+	88586640	88670084	1.05
DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	DDX5	NM_004396	DKFZp686J01190 // G17P1 // HLR1 // HUMP68 // p68	3766893	chr17	−	59924843	59935796	1.05
SMEK homolog 2, suppressor of mek1 (Dictyostelium)	SMEK2	NM_020463	FLFL2 // FLJ31474 // KIAA1387 // PSY2 // smk1	2553911	chr2	−	55627936	55699519	1.05
thioredoxin reductase 1	TXNRD1	NM_003330 // NM_182729 // NM_182742 // NM_182743	GRIM-12 // MGC9145 // TR // TR1 // TRXR1 // TXNR	3429460	chr12	+	103130628	103354079	1.05
Ras and Rab interactor 3	RIN3	NM_024832	DKFZp762H1613 // FLJ11700 // FLJ22439	3548929	chr14	+	92049804	92225160	1.05
itchy homolog E3 ubiquitin protein ligase (mouse)	ITCH	NM_031483	AIF4 // AIP4 // NAPP1 // dJ468O1.1	3882854	chr20	+	32414702	32562859	1.05

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change/ nM
KIAA0174	KIAA0174	NM_014761	MGC117220	3667766	chr16	+	70481983	70522196	1.05
formin-like 3	FMNL3	NM_175736 // NM_198900	DKFZp762B245 // FHOD3 // FLJ45265 // MGC45819 //	3454006	chr12	–	48316548	48387433	1.05
ARP3 actin-related protein 3 homolog (yeast)	ACTR3	NM_005721	ARP3	2501697	chr2	+	114360575	114502125	1.05
cyclin T2 // aminocarboxymuconate semialdehyde decarboxylase	CCNT2 // ACMSD	NM_001241 // NM_058241 // NM_138326	FLJ90560 // MGC134840 // —	2507209	chr2	+	135392283	135432746	1.05
topoisomerase (DNA) II beta 180 kDa	TOP2B	NM_001068	TOPIIB // top2beta	2566478	chr3	–	25614141	25681392	1.05
RNA binding motif protein 16 // T-cell lymphoma invasion and metastasis 2	RBM16 // TIAM2	NM_014892 // NM_001010927 // NM_012454	KIAA1116 // FLJ41865 // STEF	2932360	chr6	+	155029299	155324283	1.05
solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	SLC3A2	NM_001012661 // NM_001012662 // NM_001012663 // NM_001012664 // NM_001013251 // NM_002394	4F2 // 4F2HC // 4T2HC // CD98 // CD98HC // MDU1 // NACAE	3333711	chr11	+	62380117	62412872	1.05
Der1-like domain family, member 1	DERL1	NM_024295	DER-1 // DER1 // FLJ13784 // FL.J42092 // MGC3067 // PRO2577	3151401	chr8	–	124094605	124123781	1.05
phosphodiesterase 7A	PDE7A	NM_002603 // NM_002604	HCP1 // PDE7	3138464	chr8	–	66789124	67101393	1.05
formin-like 1	FMNL1	NM_005892	C17orf1 // C17orf1B // FHOD4 // FMNL // KW-13 // MGC133052 // MGC1894 //	3723378	chr17	+	40654831	40680464	1.05
Rap guanine nucleotide exchange factor (GEF) 1	RAPGEF1	NM_005312 // NM_198679	C3G // DKFZp781P1719 // GRF2	3227696	chr9	–	133441988	133605262	1.05
transmembrane BAX inhibitor motif containing 4	TMBIM4	NM_016056	CGI-119 // S1R // ZPRO	3460593	chr12	–	64816984	64850064	1.05

B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB	BDP1	NM_018429	DKFZp686C01233
			// DKFZp686KD831
			// HSA238520 //
			KIAA1241 //
			KIAA1689 //
			TAF3B1 // TFC5
			// TFIIIB" //
			TFIIIB150 //
			TFIIIB90 // TFNR
				2814527	chr5	+	70699177	70899402	1.05

TABLE 5-continued

				Human Exon ST 1.0 Transcript	Human Genome hg18				Fold Change/
Gene Name	Gene Symbol	Accession	Synonym	Cluster ID	Chromosome	Strand	Start	Stop	nM
MYST histone acetyltransferase 2	MYST2	NM_007067	HBO1 // HBOA	3725779	chr17	+	45196447	45261455	1.05
KIAA0247	KIAA0247	NM_014734	—	3542145	chr14	+	69145907	69256533	1.05
ubiquitin specific peptidase 36	USP36	NM_025090	DUB1	3772581	chr17	–	74295075	74348574	1.05
protein kinase, AMP-activated, gamma 2 non-catalytic subunit	PRKAG2	NM_001040633 // NM_016203 // NM_024429	AAKG // AAKG2 // CMH6 // H91620p // WPWS	3079803	chr7	–	150865031	151205160	1.05
RAB18, member RAS oncogene family	RAB18	NM_021252	RAB18LI1	3240095	chr10	+	27791811	27930577	1.05
WW domain containing adaptor with coiled-coil	WAC	NM_016628 // NM_100264 // NM_100486	BM-016 // MGC10753 // PRO1741 //Wwp4 // bA48B24 // bA48B24.1	3240340	chr10	+	28828043	29005095	1.05
stromal interaction molecule 2	STIM2	NM_020860	FLJ39527 // KIAA1482	2722377	chr4	+	26415653	26636427	1.05
actin, gamma 1	ACTG1	NM_001614	ACT // ACTG // DFNA20 // DFNA26	3773932	chr17	–	77091456	77105797	1.05
ash1 (absent, small, or homeotic)-like (*Drosophila*)	ASH1L	NM_018489	ASH1 // ASH1L1 // FLJ10504 // KIAA1420	2437417	chr1	–	153571685	153798937	1.05
FLJ36874 protein	FLJ36874	NM_152716	MGC125671 // MGC125672	3374746	chr11	–	59160770	59193099	1.05
thyroid hormone receptor associated protein 2	THRAP2	NM_015335	DKFZp781D0112 // FLJ21627 // KIAA1025 // MED13L // PROSIT240 // TRAP240L	3473083	chr12	–	114868953	115419724	1.05
B-cell CLL/lymphoma 10	BCL10	NM_003921	CARMEN // CIPER // CLAP // c-E10 // mE10	2420808	chr1	–	85504067	85516171	1.05
collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	COL4A3BP	NM_005731 // NM_031361	CERT // CERTL // FLJ20597 // GPBP // STARD11	2862950	chr5	–	74700067	74843717	1.05
wings apart-like homolog (*Drosophila*)	WAPAL	NM_015045	FOE // KIAA0261 // WAPL	3298738	chr10	–	88184999	88286267	1.05
SFRS protein kinase 2	SRPK2	NM_182691 // NM_182692	FLJ36101 // SFRSK2	3066267	chr7	–	104537547	104842466	1.05
RNA binding motif protein 22	RBM22	NM_018047	FLJ10290 // ZC3H16	2881521	chr5	–	150050460	150060885	1.05
chromodomain helicase DNA binding protein 1	CHD1	NM_001270	DKFZp686E2337	2868523	chr5	–	98218502	98293051	1.05
G1 to S phase transition 1	GSPT1	NM_002094	551G9.2 // ETF3A // GST1 // eRF3a	3680610	chr16	–	11865619	11917408	1.05
ubiquilin 1 // death inducer-obliterator 1	UBQLN1 // DIDO1	NM_013438 // NM_053067 // NM_022105 // NM_033081 //	DA41 // DSK2 // FLJ90054 // PLIC-1 // XDRP1 // BYE1 // C20orf158	3212143	chr9	–	85464717	85512928	1.05

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change/ nM
		NM_080796 // NM_080797	// DATF1 // DIDO2 // DIDO3 // DIO-1 // DIO1 // DKFZp434P1115 // FLJ11265 // KIAA0333 // MGC16140 // dJ885L7.8						
golgi associated, gamma adaptin ear containing, ARF binding protein 2	GGA2	NM_015044	FLJ20966 // KIAA1080 // VEAR	3685183	chr16	–	23381059	23429320	1.05
solute carrier family 2 (facilitated glucose transporter), member 3	SLC2A3	NM_006931	FLJ90380 // GLUT3	3442854	chr12	–	7917549	7980138	1.05
protein tyrosine phosphatase, non-receptor type 1	PTPN1	NM_002827	PTP1B	3888721	chr20	+	48560298	48634700	1.05
megakaryoblastic leukemia (translocation) 1	MKL1	NM_020831	BSAC // MAL // MRTF-A	3961496	chr22	–	39136248	39362660	1.05
sequestosome 1	SQSTM1 // OSIL	NM_003900	A170 // OSIL // PDB3 // ZIP3 // p60 // p62 // p62B	2844479	chr5	+	179166014	179198853	1.05
family with sequence similarity 78, member A	FAM78A	NM_033387	C9orf59 // FLJ00024	3227574	chr9	–	133123292	133147120	1.05
coenzyme Q2 homolog, prenyltransferase	COQ2	NM_015697	CL640 // FLJ26072	2775965	chr4	–	84404005	84424988	1.05
small nuclear ribonucleoprotein polypeptide B"	SNRPB2	NM_003092 // NM_198220	MGC24807 // MGC45309	3877776	chr20	+	16645421	16670916	1.05
bromodomain adjacent to zinc finger domain, 2A	BAZ2A	NM_013449	DKFZp781B109 // FLJ13768 // FLJ13780 // FLJ45876 // KIAA0314 // TIP5 // WALp3	3457947	chr12	–	55275319	55316417	1.05
RNA binding motif protein 25	RBM25	NM_021239	MGC105088 // MGC117168 // RNPC7 // S164	3543411	chr14	+	72594776	72658577	1.05
integrator complex subunit 6	INTS6	NM_001039937 // NM_001039938 // NM_012141	DBI-1 // DDX26 // DDX26A // DICE1 // DKFZP434B105 // HDB // INT6 // Notchl2	3514488	chr13	–	50826009	50927014	1.05
cyclin M3	CNNM3	XM_001127059 // NM_017623 // NM_199078	ACDP3 // DKFZp434I1016 // FLJ20018	2494749	chr2	+	96843277	96864841	1.05
Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse)	MDM2	NM_002392 // NM_006878 // NM_006879 // NM_006881 // NM_006882	HDMX // MGC71221 // hdm2	3421300	chr12	+	67488176	67525479	1.05

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript	Human Genome hg18				Fold Change/
				Cluster ID	Chromosome	Strand	Start	Stop	nM
colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog	CSF1R	NM_005211	C-FMS // CD115 CSFR // FIM2 // FMS	2881187	chr5	–	149412410	149473128	1.05
thioredoxin-like 1	TXNL1	NM_004786	TRP32 // TXL-1 // TXNL // Txl	3809324	chr18	–	52334063	52469773	1.05
ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)	ELOVL5	NM_021814	HELO1 // RP3-483K16.1 // dJ483K16.1	2957596	chr6	–	53179349	53321902	1.05
PFTAIRE protein kinase 1	PFTK1	NM_012395	KIAA0834 // PFTAIRE1	3012064	chr7	+	90002707	90677837	1.05
nuclear mitotic apparatus protein 1	NUMA1	NM_006185	NUMA	3380901	chr11	–	71389909	71469367	1.05
sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2	SPOCK2	NM_014767	testican-2	3293840	chr10	–	73457514	73518527	1.05
clathrin, heavy chain (Hc)	CLTC	NM_004859	CHC17 // CLH-17 // CLTCL2 // Hc // KIAA0034	3729172	chr17	+	55052021	55127299	1.05
F-box and leucine-rich repeat protein 11	FBXL11	NM_012308	CXXC8 // DKFZP434M1735 // FBL11 // FBL7 // FLJ00115 // FLJ46431 // JHDM1A // KAA1004 // LILINA	3336696	chr11	+	66643299	66782124	1.05
signal-induced proliferation-associated gene 1	SIPA1	NM_006747 // NM_153253	MGC102688 // MGC17037 // SPA1	3335465	chr11	+	65162171	65174965	1.05
kelch-like 24 (*Drosophila*) // YEATS domain containing 2	KLHL24 // YEATS2	NM_017644 // NM_018023	DRE1 // FLJ25796 // FLJ10201 // FLJ12841 // FLJ13308 // KIAA1197	2655113	chr3	+	184836105	184882100	1.05
thymopoietin	TMPO	NM_001032283 // NM_001032284 // NM_003276	CMD1T // LAP2 // MGC61508 // PRO0866 // TP	3427767	chr12	+	97395927	97502543	1.05
STT3, subunit of the oligosaccharyltransferase complex, homolog B (*S. cerevisiae*)	STT3B	NM_178862	FLJ90106 // SIMP // STT3-B	2615600	chr3	+	31544326	31662283	1.05
ATP-binding cassette, sub-family F (GCN20), member 1	ABCF1	NM_001025091 // NM_001090	ABC27 // ABC50	2901687	chr6	+	30647103	30667268	1.05
CUG triplet repeat, RNA binding protein 2	CUGBP2	NM_001025076 // NM_001025077 // NM_006561	BRUNOL3 // ETR-3 // NAPOR	3234760	chr10	+	10544225	11418680	1.05
major histocompatibility complex, class II, DR	HLA-DRA	NM_019111	HLA-DRA1	2903189	chr6	+	32496972	32520923	1.05
RAN binding protein 2	RANBP2 // RGPD4	NM_006267	NUP358 // TRP1 // TRP2	2499158	chr2	+	108702376	108768725	1.05

TABLE 5-continued

				Human Exon ST 1.0 Transcript	Human Genome hg18				Fold Change/
Gene Name	Gene Symbol	Accession	Synonym	Cluster ID	Chromosome	Strand	Start	Stop	nM
G protein-coupled receptor kinase 5	GRK5	NM_005308	GPRK5	3267036	chr10	+	120957193	121256088	1.05
FRY-like	FRYL	XM_001134434 // XM_001134456 // NM_015030	DKFZp686E205 // FLJ16177 // KIAA0826	2768468	chr4	–	48194140	48272015	1.05
bromodomain containing 1	BRD1	NM_014577	BRL // BRPF1 // BRPF2 // DKFZp686F0325	3965314	chr22	–	48552694	48636916	1.05
nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2	NFATC2	NM_012340 // NM_173091	KIAA0611 // NFAT1 // NFATP	3909553	chr20	–	49436909	49603743	1.05
TATA element modulatory factor 1	TMF1	NM_007114	ARA160	2681157	chr3	–	69151671	69184154	1.05
ral guanine nucleotide dissociation stimulator	RALGDS	NM_001042368 // NM_006266	FLJ20922 // RGF // RalGEF	3228463	chr9	–	134962931	135014381	1.05
GATA binding protein 2	GATA2	NM_032638	MGC2306 // NFE1B	2694314	chr3	–	129675850	129700720	1.05
forty-two-three domain containing 1	FYTTD1	NM_001011537 // NM_032288	DKFZp761B1514	2659887	chr3	+	198960821	198996244	1.05

splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)	SFRS1	NM_001078166 //
		NM_006924
			ASF // MGC5228
			// SF2 // SF2p33
			// SRp30a
				3764103	chr17	–	53421412	53439635	1.05

transcription elongation regulator 1	TCERG1	NM_001040006 // NM_006706	CA150 // MGC133200 // TAF2S	2834093	chr5	+	145754916	145871713	1.05
3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	HMGCS1	NM_002130	HMGCS // MGC90332	2855501	chr5	–	43324231	43349337	1.05
inositol 1,4,5-trisphosphate 3-kinase B	ITPKB	NM_002221	IP3K // IP3K-B // PIG37	2458921	chr1	–	224865889	225014518	1.05
insulin-like growth factor 1 receptor	IGF1R	NM_000875	CD221 // IGFIR // JTK13 // MGC142170 // MGC142172 // MGC18216	3610804	chr15	+	97010298	97320602	1.05
ribulose-5-phosphate-3-epimerase // chemokine binding protein 2	RPE // CCBP2	NM_006916 // NM_199229 // NM_001296	MGC2636 // RPE2- 1 // CCR10 // CCR9 // CMKBR9 // D6 // MGC126678 // MGC138250 // hD6	2525852	chr2	+	210575559	210637315	1.05
KIAA1429	KIAA1429	NM_015496 // NM_183009	DKFZP434I116 // DKFZp781B2117 // MGC138493 // MGC141940 // MSTP054	3145020	chr8	–	95569109	95634851	1.05
dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A	DYRK1A	NM_001396 // NM_101395 // NM_130436 // NM_130437 // NM_130438	DYRK // DYRK1 // HP86 // MNB // MNBH	3920566	chr21	+	37661116	37857051	1.05

TABLE 5-continued

				Human Exon ST 1.0 Transcript	Human Genome hg18				Fold Change/
Gene Name	Gene Symbol	Accession	Synonym	Cluster ID	Chromosome	Strand	Start	Stop	nM
coronin 7	CORO7	NM_024535	0610011B16Rik // CRN7 // FLJ22021 // FLJ44188	3678083	chr16	−	4343041	4406954	1.05
ribosomal protein S6 kinase, 70 kDa, polypeptide 1	RPS6KB1	NM_003161	PS6K // S6K // S6K1 // STK14A // p70(S6K)-alpha // p70-S6K // p70-alpha	3729294	chr17	+	55325239	55429105	1.05
MAK10 homolog, amino-acid N-acetyltransferase subunit, (*S. cerevisiae*)	MAK10	NM_024635	FLJ21613 // FLJ22643 // bA379P1.1	3177563	chr9	+	87733620	87828205	1.05
family with sequence similarity 62 (C2 domain containing) member B	FAM62B	NM_020728	CHR2SYT // ESYT2 // KIAA1228	3082248	chr7	−	158205107	158355198	1.05
guanylate binding protein 4 // guanylate binding protein 7	GBP4 // GBP7	NM_052941 // NM_207398	Mpa2 // FLJ38822 // GBP4L	2421995	chr1	−	89419435	89437211	1.05
5-methyltetrahydrofolate-homocysteine methyltransferase reductase	MTRR	NM_002454 // NM_024010	MGC129643 // MSR	2800906	chr5	+	7922217	7954221	1.05
tripeptidyl peptidase II	TPP2	NM_003291	FLJ40359	3499453	chr13	+	101981581	102131173	1.05
acyl-CoA synthetase short-chain family member 1	ACSS1	NM_032501	ACAS2L // AceCS2L // FLJ45659 // MGC33843	3901696	chr20	−	24934882	24987616	1.05
tousled-like kinase 1	TLK1	NM_012290	KIAA0137 // PKU-BETA	2586603	chr2	−	171538552	171796060	1.05
secretory carrier membrane protein 1	SCAMP1	NM_052822 // NM_004866	SCAMP // SCAMP37	2817053	chr5	+	77691978	77812317	1.05
tripartite motif-containing 28	TRIM28	NM_005762	FLJ29029 // KAP1 // RNF96 // TF1B // TIF1B	3844238	chr19	+	63740597	63753931	1.05
chromosome 11 open reading frame 58	C11orf58	NM_014267	IMAGE145052 // MGC117265 // SMAP	3322048	chr11	+	16716744	16734468	1.05
serine incorporator 1	SERINC1	NM_020755	KIAA1253 // TDE1L // TDE2 // TMS-2	2972310	chr6	−	122804811	122948968	1.05
karyopherin (importin) beta 1	KPNB1	NM_002265	IMB1 // IPOB // Impnb // MGC2155 // MGC2156 // MGC2157 // NTF97	3724782	chr17	+	43082272	43117868	1.05
hypothetical FLJ46363 // ataxin 2-like	FLJ46363 // ATXN2L	NM_207434 // XM_001127543 // NM_007245 // NM_017492 // NM_145714 // NM_148414 // NM_148415 // NM_148416	—// A2D // A2LG // A2LP // A2RP	3654859	chr16	+	28617718	28756043	1.05

TABLE 5-continued

				Human Exon ST 1.0 Transcript	Human Genome hg18				Fold Change/
Gene Name	Gene Symbol	Accession	Synonym	Cluster ID	Chromosome	Strand	Start	Stop	nM
quiescin Q6	QSCN6 // FLJ23867	NM_001004128 // NM_002826	Q6 // QSOX1	2369950	chr1	+	178353067	178436483	1.05
splicing factor, arginine/serine-rich 6	SFRS6	NM_006275	B52 // MGC5045 // SRP55	3886050	chr20	+	41519932	41526301	1.05
moesin	MSN	NM_002444	—	3979659	chrX	+	64804248	64878488	1.05
intersectin 2	ITSN2	NM_006277 // NM_019595 // NM_147152	KIAA1256 // SH3D1B // SH3P18 // SWA // SWAP	2544238	chr2	−	24279241	24436906	1.05
SAFB-like, transcription modulator	SLTM	NM_001013843 // NM_017968 // NM_024755	DKFZp762G052 // FLJ10005 // FLJ13213 // Met	3626704	chr15	−	56949072	57013564	1.05
transcription factor 4	TCF4	NM_003199	E2-2 // ITF2 // MGC149723 // MGC149724 // SEF2 // SEF2-1 // SEF2-1A // SEF2-1B	3808854	chr18	−	51010981	51506795	1.05
DEAH (Asp-Glu-Ala-His) box polypeptide 9	DHX9	NM_001357	DDX9 // LKP // NDH II // NDHII // RHA	2370991	chr1	+	181075106	181123738	1.05
chromosome 10 open reading frame 119	C10orf119	NM_024834	FLJ13081 // FLJ36756	3309755	chr10	−	121568302	121642742	1.05
SET domain containing 2	SETD2	NM_014159	FLJ16420 // FLJ22472 // FLJ23184 // FLJ45883 // HIF-1 // HSPC069 // HYPB // KIAA1732	2672532	chr3	−	47032936	47180418	1.05
golgi reassembly stacking protein 2, 55 kDa // dehydrogenase/reductase (SDR family) member 9	GORASP2 // DHRS9	NM_015530 // NM_005771 // NM_199204	DKFZP434D156 // FLJ13139 // GOLPH6 // GRASP55 // GRS2 // p59 // 3alpha-HSD // RDH15 // RDHL // RETSDR8	2515050	chr2	+	171457150	171551619	1.05
target of myb1 (chicken)	TOM1	NM_005488	FLJ33404	3944084	chr22	+	34025845	34073962	1.05
ATPase, H+ transporting, lysosomal 42 kDa, V1 subunit C1	ATP6V1C1	NM_001007254 // NM_001695	ATP6C // ATP6D // FLJ20057 // VATC // Vma5	3110171	chr8	+	104102441	104171800	1.05
potassium channel tetramerisation domain containing 20	KCTD20	NM_173562	C6orf69 // MGC14254 // dJ108K11.3	2905069	chr6	+	36518349	36566874	1.05
serine/threonine kinase 10	STK10	NM_005990	LOK // PRO2729	2887048	chr5	−	171401689	171547855	1.05
GA binding protein transcription factor, alpha subunit 60 kDa // GA binding protein transcription factor, alpha subunit pseudogene	GABPA // GABPAP	NM_002040 // —// NR_002723	E4TF1-60 // E4TF1A // NFT2 // NRF2 // NRF2A //	3916576	chr21	+	26028762	26066641	1.05

TABLE 5-continued

				Human Exon ST 1.0 Transcript	Human Genome hg18				Fold Change/
Gene Name	Gene Symbol	Accession	Synonym	Cluster ID	Chromosome	Strand	Start	Stop	nM
			E4TF1 // E4TF1B // GABPB1						
centaurin, beta 2	CENTB2	NM_012287	ACAP2 // CNT-B2 // KIAA0041	2712040	chr3	−	196476779	196645492	1.05
fibrosin 1	FBS1	NM_022452	FBS // FLJ11618	3656362	chr16	+	30577810	30590035	1.05
G protein-coupled receptor kinase interactor 2	GIT2	NM_014776 // NM_057169 // NM_057170 // NM_139201	CAT-2 // DKFZp686G01261 // KIAA0148 // MGC760	3471005	chr12	−	108852000	108918536	1.05
vimentin	VIM	NM_003380	FLJ36605	3236958	chr10	+	17296705	17357733	1.05
nuclear receptor coactivator 2	NCOA2	NM_006540	GRIP1 // MGC138808 // NCoA-2 // TIF2	3139722	chr8	−	71184397	71478626	1.05
thrombospondin 1	THBS1	NM_003246	THBS // TSP // TSP1	3589458	chr15	+	37614946	37678406	1.05
trinucleotide repeat containing 6B	TNRC6B	NM_001024843 // NM_015088	KIAA1093	3946192	chr22	+	38770332	39061757	1.05
GTPase activating protein (SH3 domain) binding protein 2 // NMDA receptor regulated 2 // RAR-related orphan receptor A	G3BP2 // NARG2 // RORA	NM_012297 // NM_203504 // NM_203505 // NM_001018089 // NM_024611 // NM_002943 // NM_134260 // NM_134261 // NM_134262	—// MGC119326 // MGC119329 // NR1F1 // ROR1 // ROR2 // ROR3 // RZRA	2773756	chr4	−	76786807	76869171	1.05
calcium/calmodulin-dependent protein kinase IV	CAMK4	NM_001744	CaMK-GR // MGC36771	2823880	chr5	+	110587242	110854177	1.05
oxidative-stress responsive 1	OXSR1	NM_005109	KIAA1101 // OSR1	2617579	chr3	+	38182030	38271979	1.05
ATPase, Na+/K+ transporting, alpha 1 polypeptide	ATP1A1	NM_000701 // NM_001001586	MGC3285 // MGC51750	2353477	chr1	+	116706775	116754386	1.05
transportin 1	TNPO1	NM_002270 // NM_153188	IPO2 // KPNB2 // MIP // MIP1 //	2815043	chr5	+	72148176	72245960	1.05
heterogeneous nuclear ribonucleoprotein U-like 1	HNRPUL1	NM_144733 // NM_144734 // NM_007040 // NM_144732	E1B-AP5 // E1BAP5 // FLJ12944	3834089	chr19	+	46460006	46505508	1.05
CD300e molecule // fibrillin 2 (congenital contractural arachnodactyly)	CD300E // FBN2	NM_181449 // NM_001999	CD300LE // CLM2 // IREM2 // CCA	3770345	chr17	−	70117621	70131474	1.05
CD55 molecule, decay accelerating factor for complement (Cromer blood group)	CD55	NM_000574	CR // DAF // TC	2377229	chr1	+	205561488	205607671	1.05
TBC1 domain family, member 15	TBC1D15	NM_022771	DKFZp686M1379 // DKFZp761D0223 // FLJ12085	3422326	chr12	+	70519754	70604360	1.05
v-raf murine sarcoma viral oncogene homolog B1	BRAF	NM_004333	B-raf1 // BRAF1 // MGC126806 //	3076340	chr7	−	139994192	140274640	1.05

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript Cluster ID	Human Genome hg18 Chromosome	Human Genome hg18 Strand	Human Genome hg18 Start	Human Genome hg18 Stop	Fold Change/ nM
			MGC138284 // RAFB1						
splicing factor, arginine/serine-rich 5	SFRS5	NM_001039465 // NM_006925	HRS // SRP40	3542207	chr14	+	69263363	69308465	1.05
GRAM domain containing 1A	GRAMD1A	NM_020895	FLJ22411 // FLJ90346 // KIAA1533	3830002	chr19	+	40161899	40210121	1.05
mediator of RNA polymerase II transcription, subunit 28 homolog (*S. cerevisiae*)	MED28	NM_025205	1500003D12Rik // DKFZP434N185 // EG1 // magicin	2720181	chr4	+	17225344	17244808	1.05
jumonji, AT rich interactive domain 1A	JARID1A	NM_001042603 // NM_005056	RBBP2 // RBP2	3439603	chr12	–	259504	368944	1.05
activating transcription factor 6	ATF6	NM_007348	–	2363919	chr1	+	160002678	160208836	1.05
matrin 3	MATR3	NM_018834 // NM_199189	DKFZp686K0542 // DKFZp686K23100 // KIAA0723 // MGC9105	2831124	chr5	+	138505686	138695245	1.05
granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	GZMB	NM_004131	CCPI // CGL-1 // CGL1 // CSP-B // CSPB // CTLA1 // CTSGL1 // HLP // SECT	3558375	chr14	–	24169951	24173308	1.05
cyclin L1	CCNL1	NM_020307	BM-001 // PRO1073 // ania-	2702307	chr3	–	158305077	158361233	1.05
neighbor of BRCA1 gene 1	NBR1	XM_001124650 // XM_001124827 // XM_001127781 // NM_005899 // NM_031858 // NM_031862	1A1-3B // KIAA0049 // M17S2 // MIG19	3722417	chr17	+	38563761	38719231	1.05
tyrosyl-tRNA synthetase	YARS	NM_003680	CMTDIC // TYRRS // YRS // YTS	2405192	chr1	–	33012453	33056331	1.05
solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3	SLC25A3	NM_213612 // NM_002635 // NM_005888 // NM_213611	OK/SW-cl.48 // PHC	3427820	chr12	+	97511471	97519906	1.05
CCR4-NOT transcription complex, subunit 1	CNOT1	NM_016284 // NM_206999	AD-005 // CDC39 // DKFZp686E0722 // FLJ90644 // KIAA1007 // NOT1 // NOT1H	3693673	chr16	–	57111094	57236550	1.05
ankyrin repeat domain 13 family, member D	ANKRD13D	XM_001129739 // NM_207354	MGC50828	3336857	chr11	+	66812660	66826524	1.05
PHD finger protein 10	PHF10	NM_018288 // NM_133325	FLJ10975 // MGC111009 // XAP135	2986084	chr6	–	169845929	169866056	1.05

TABLE 5-continued

				Human Exon ST 1.0 Transcript	Human Genome hg18				Fold Change/
Gene Name	Gene Symbol	Accession	Synonym	Cluster ID	Chromosome	Strand	Start	Stop	nM
hypothetical protein KIAA1434	RP5-1022P6.2	NM_019593	FLJ11085 // KIAA1434 // MGC26147	3896370	chr20	−	5473033	5546357	1.05
ribosomal protein S6 kinase, 90 kDa, polypeptide 3	RPS6KA3	NM_004586	CLS // HU-3 // ISPK-1 // MAPKAPK1B // MRX19 // RSK // RSK2 // S6K-alpha3 // p90-RSK2 // pp90RSK2	4002173	chrX	−	20077954	20254253	1.05
UPF2 regulator of nonsense transcripts homolog (yeast)	UPF2	NM_015542 // NM_080599	DKFZP434D222 // HUPF2 // KIAA1408 // MGC138834 // MGC138835 //	3277662	chr10	−	11984615	12125155	1.05
thioredoxin interacting protein	TXNIP	NM_006472	EST01027 // HHCPA78 // THIF // VDUP1	2356115	chr1	+	144149846	144164251	1.05
protein phosphatase 1, regulatory (inhibitor) subunit 16B	PPP1R16B	NM_015568	ANKRD4 // KIAA0823 // TIMAP	3884830	chr20	+	36866338	36985066	1.05
peptidylprolyl isomerase F (cyclophilin F)	PPIF	NM_005729	CYP3 // Cyp-D // FLJ90798 // MGC117207	3253880	chr10	+	80777230	80785093	1.05
3-hydroxy-3-methylglutaryl-Coenzyme A reductase	HMGCR	NM_000859	—	2815965	chr5	+	74668800	74700136	1.05
chloride intracellular channel 1	CLIC1	NM_001288	G6 // NCC27	2949330	chr6	−	31806365	31815144	1.05
HBS1-like (*S. cerevisiae*) // aldehyde dehydrogenase 8 family, member A1	HBS1L // ALDH8A1	NM_006620 // NM_022568 // NM_170771	DKFZp686L13262 // EF-1a // ERFS // HBS1 // HSPC276 // ALDH12 // DJ352A20.2 // DKFZp779D2315 //	2975287	chr6	−	135314409	135417715	1.05
vav 3 oncogene	VAV3	NM_001079874 // NM_006113	FLJ40431	2426385	chr1	−	107914594	108309371	1.05
Rho guanine nucleotide exchange factor (GEF) 7	ARHGEF7	NM_003899 // NM_145735	BETA-PIX // COOL1 // DKFZp761K1021 // KIAA0142 // KIAA0412 // Nbla10314 // P50 // P50BP// P85 // P85COOL1 // P85SPR // PAK3 // PIXB	3501661	chr13	+	110565635	110756075	1.05

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change/ nM
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	SMARCA5	NM_003601	ISWI // SNF2H // WCRF135 // hISWI // hSNF2H	2745646	chr4	+	144616165	144697227	1.05
proteasome maturation protein	POMP	NM_015932	C13orf12 // HSPC014 // PNAS-110 // UMP1	3483348	chr13	+	28125188	28151050	1.05
DnaJ (Hsp40) hamolog, subfamily B, member 6	DNAJB6	NM_005494 // NM_058246	DKFZp566D0824 // FLJ42837 // HHDJ1 // HSJ-2 // HSJ2 // MGC1152 // MGC117297 //	3034027	chr7	+	156799667	156902887	1.05
zinc finger RNA binding protein	ZFR	NM_016107	FLJ41312	2852333	chr5	–	32390101	32537319	1.05
tetraspanin 14	TSPAN14	NM_030927	DC-TM4F2 // MGC11352 // TM4SF14	3254521	chr10	+	82203922	82272901	1.05
myelin basic protein	MBP	NM_001025081 // NM_001025090 // NM_001025092 // NM_001025094 // NM_001025098 // NM_001025100 // NM_001025101 // NM_002385	MGC99675	3814063	chr18	–	72853742	73023063	1.05
testis derived transcript (3 LIM domains)	TES	NM_015641 // NM_152829	DKFZP586B2022 // MGC1146 // TESS // TESS-2 // TESTIN	3020192	chr7	+	115637811	115743800	1.05
microtubule-associated protein 1 light chain 3 beta	MAP1LC3B	NM_022818	MAP1A/1BLC3	3672830	chr16	+	85982917	85996864	1.05
transcription factor binding to IGHM enhancer 3	TFE3	NM_006521	RCCP2 // TFEA	4007734	chrX	–	48771186	48787973	1.05
CHMP family, member 7	CHMP7	NM_152272	MGC29816	3089853	chr8	+	23157105	23176288	1.05
potassium channel tetramerisation domain containing 10	KCTD10	NM_031954	FLJ41739 // MSTP028 // ULRO61	3470793	chr12	–	108370845	108399528	1.05
ets variant gene 6 (TEL oncogene)	ETV6	NM_001987	TEL // TEL/ABL	3405032	chr12	+	11645490	11939588	1.05
programmed cell death 6 interacting protein	PDCD6IP	NM_013374	AIP1 // Alix // DRIP4 // HP95 // MGC17003	2616317	chr3	+	33743952	33886195	1.05
ras homolog gene family, member F (in filopodia)	RHOF	NM_019034	ARHF // FLJ20247 // RIF	3475324	chr12	–	120698553	120716624	1.05
lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76 kDa)	LCP2	NM_005565	SLP-76 // SLP76	2886595	chr5	–	169607157	169657789	1.05
vitamin D (1,25-dihydroxyvitamin D3) receptor	VDR	NM_000376 // NM_001017535	NR1I1	3452818	chr12	–	46521596	46606823	1.05

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change/ nM

diablo homolog (*Drosophila*)	DIABLO	NM_019887 //
		NM_138929 //
		NM_138930
			DIABLO-S //
			FLJ10537 //
			// FLJ25049 // SMAC
			// SMAC3
				3475511	chr12	−	121257461	121277963	1.05

B-cell translocation gene 1, anti-proliferative	BTG1	NM_001731	—	3465409	chr12	−	90902887	91063960	1.05
CD53 molecule	CD53	NM_000560 // NM_001040033	MOX44 // TSPAN25	2351572	chr1	+	111215352	111296983	1.05

damage-specific DNA binding protein 1, 127 kDa	DDB1	XM_001128974 //
		XM_001128983 //
		NM_001923
			DDBA // UV-DDB1
			// XAP1 // XPCE
			// XPE // XPE-BF
				3375245	chr11	−	60823513	60857553	1.05

ariadne homolog 2 (*Drosophila*)	ARIH2	NM_006321	ARI2 // FLJ10938 // FLJ33921 // TRIAD1	2621827	chr3	+	48930742	48997971	1.05
protein tyrosine phosphatase, non-receptor type 12	PTPN12	NM_002835	PTP-PEST // PTPG1	3009959	chr7	+	77004361	77123074	1.05
meteorin, glial cell differentiation regulator-like // mediator of RNA polymerase II transcription, subunit 25 homolog (*S. cerevisiae*)	METRNL // MED25	XM_941466 // NM_001004431 // NM_030973	MGC99788 // ACID1 // ARC92 // DKFZp434K0512 // MGC70671 // P78 // TCBAP0758	3739431	chr17	+	78630769	78653225	1.05
trinucleotide repeat containing 6A	TNRC6A	NM_020847 // NM_014494	CAGH26 // DKFZp666E117 // FLJ22043 // GW1 // GW182 // KIAA1460 // MGC75384 // TNRC6	3653398	chr16	+	24583665	24748478	1.05
ubiquitin specific peptidase 10	USP10	NM_005153	KIAA0190 // MGC2621 // UBPO	3671873	chr16	+	83291080	83371023	1.05
DnaJ (Hsp40) homolog, subfamily A, member 2	DNAJA2	NM_005880	CPR3 // DJA2 // DNAJ // DNJ3 // HIRIP4 // PRO3015 // RDJ2	3690084	chr16	−	45546783	45565155	1.05
MYC binding protein 2	MYCBP2	NM_015057	DKFZp686M08244 // FLJ10106 // FLJ13826 // FLJ21597 // FLJ21646 // KIAA0916 // PAM	3518496	chr13	−	76500672	76799212	1.05
SEC24 related gene family, member B (*S. cerevisiae*)	SEC24B	XM_001130118 // NM_001042734 // NM_006323	MGC48822 // SEC24	2739079	chr4	+	110510304	110681811	1.05
interferon gamma receptor 2 (interferon gamma transducer 1)	IFNGR2	NM_005534	AF-1 // IFGR2 // IFNGT1	3918635	chr21	+	33696906	33774607	1.05

TABLE 5-continued

				Human Exon ST 1.0 Transcript	Human Genome hg18				Fold Change/
Gene Name	Gene Symbol	Accession	Synonym	Cluster ID	Chromosome	Strand	Start	Stop	nM
VAMP (vesicle-associeted membrane protein)-associated protein A, 33 kDa	VAPA	NM_003574 // NM_194434	MGC3745 // VAP-33 // VAP-A // VAP33 // hVAP-33	3778601	chr18	+	9903984	9950012	1.05
SP100 nuclear antigen	SP100	NM_001080391 // NM_003113	DKFZp686E07254 // FLJ00340 // FLJ34579	2531377	chr2	+	230985008	231142598	1.05
transforming growth factor beta regulator 1	TBRG1	NM_032811	FLJ14621 // FLJ25020 // FLJ90113 // MGC129890 // NIAM // TB-5	3354174	chr11	+	123997906	124011654	1.05
growth arrest and DNA-damage-inducible, beta	GADD45B	NM_015675	DKFZP566B133 // GADD45BETA // MYD118	3816509	chr19	+	2425718	2469133	1.05
alanyl (membrane) aminopeptidase (aminopeptidase N, aminopeptidase M, microsomal aminopeptidase, CD13, p150)	ANPEP	NM_001150	APN // CD13 // LAP1 // PEPN // gp150	3638607	chr15	–	88129142	88159617	1.05
proteasome (prosome, macropain) activator subunit 4	PSME4	NM_014614	FLJ21864 // KIAA0077 // MGC138374 // MGC142228 // PA200	2553282	chr2	–	53944710	54160919	1.05
microtubule-associated protein, RP/EB family, member 1	MAPRE1	NM_012325	EB1 // MGC117374 // MGC129946	3882069	chr20	+	30871304	30901864	1.05
BMI1 polycomb ring finger oncogene	BMI1	NM_005180	MGC12685 // PCGF4 // RNF51	3238491	chr10	+	22650103	22660820	1.05
CUG triplet repeat, RNA binding protein 1	CUGBP1	NM_001025596 // NM_006560 // NM_198700	BRUNOL2 // CUG-BP // CUGBP // NAB50 // hNab50	3372253	chr11	–	47444068	47543613	1.05
transforming, acidic coiled-coil containing protein 3	TACC3	NM_006342	ERIC1 // MGC117382 // MGC133242	2714955	chr4	+	1692616	1716693	1.05
zinc finger, CCHC domain containing 6 // hypothetical protein MGC13114	ZCCHC6 // MGC13114	NM_024617 // NM_001040160 // NM_001040161 // NM_001040162 // NM_001040163 // NM_001040164 // NM_001040165 // NM_001040166 // NM_032366	DKFZp666B142 // DKFZp686C11112 // DKFZp686F119 // DKFZp686I1269 // PAPD6 // JFP2	3212976	chr9	–	88092469	88159805	1.05
C-type lectin domain family 4, member E	CLEC4E	NM_014358	CLECSF9 // MINCLE	3443183	chr12	–	8577026	8584811	1.05
interferon, gamma-inducible protein 18	IFI16	NM_005531	IFNGIP1 // MGC9466 // PYHIN2	2362394	chr1	+	157215279	157291561	1.05

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change/ nM
LMBR1 domain containing 1	LMBRD1	NM_018368	C6orf209 // FLJ11240 // RP11-810I22.1 // bA810I22.1	2960010	chr6	−	70361077	70634121	1.05
protein kinase D3	PRKD3	NM_005813	EPK2 // PKC-NU // PKD3 // PRKCN // nPKC-NU	2548500	chr2	−	37331165	37405413	1.05
CCR4-NOT transcription complex, subunit 7	CNOT7	NM_013354 // NM_054026	CAF1 // hCAF-1	3125775	chr8	−	17128912	17148758	1.05
heterogeneous nuclear ribonucleoprotein M	HNRPM	NM_005968 // NM_031203	DKFZp547H118 // HNRNPM // HNRNPM4 // HNRPM4 // HTGR1 // NAGR1	3819543	chr19	+	8415651	8459993	1.05
heterogeneous nuclear ribonucleoprotein H1 (H)	HNRPH1	NM_005520	DKFZp686A15170 // HNRPH //	2890148	chr5	−	178970155	178993890	1.05
adenosine A2a receptor	ADORA2A	NM_000675	ADORA2 // RDC8 // hA2aR	3940099	chr22	+	23143709	23200243	1.05
PPAR binding protein	PPARBP	NM_004774	CRSP1 // CRSP200 // DRIP205 // DRIP230 // MED1 // MGC71488 // PBP // PPARGBP // RB18A //	3755714	chr17	−	34801544	34861069	1.05
serine/threonine kinase 17b	STK17B	NM_004226	DRAK2	2593159	chr2	−	196706552	196744596	1.05
adhesion regulating molecule 1	ADRM1	NM_007002 // NM_175573	GP110 // MGC29536 //	3892607	chr20	+	60305485	60317305	1.05
splicing factor, arginine/serine-rich 9	SFRS9	NM_003769	SRp30c	3474502	chr12	−	119372834	119407274	1.05
E2F transcription factor 4, p107/p130-binding	E2F4	NM_001950	E2F-4	3665288	chr16	+	65783266	65790299	1.05
chromodomain helicase DNA binding protein 2	CHD2	NM_001042572 // NM_001271	DKFZp781D1727	3609138	chr15	+	91227096	91387351	1.05
serpin peptidase inhibitor, clade B (ovalbumin), member 2	SERPINB2	NM_002575	HsT1201 // PAI // PAI-2 // PAI2 // PLANH2	3791935	chr18	+	59704265	59722138	1.05
phosphatidylinositol 3,4,5-trisphosphate-dependent RAC exchanger 1	PREX1	NM_020820	KIAA1415	3908631	chr20	−	46674205	46938090	1.05
pre-B-cell colony enhancing factor 1 // pre-B cell enhancing factor 1 pseudogene	PBEF1 // RP11-92J19.4	NM_005746 //	1110035O14Rik // DKFZP666B131 // MGC117256 // NAMPT // PBEF // LOC646309	3066818	chr7	−	105625846	105713266	1.05
interferon regulatory factor 1	IRF1	NM_002198	IRF-1 // MAR	2875348	chr5	−	131846280	131893043	1.05
nuclear receptor coactivator 4	NCOA4	NM_005437	ARA70 // DKFZp762E1112 //	3246372	chr10	+	51202191	51260947	1.05

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript Cluster ID	Human Genome hg18 Chromosome	Human Genome hg18 Strand	Human Genome hg18 Start	Human Genome hg18 Stop	Fold Change/ nM
			ELE1 // PTC3 // RFG						
adrenergic, beta, receptor kinase 1	ADRBK1	NM_001619	BARK1 // BETA-ARK1 // GRK2	3336801	chr11	+	66790523	66810933	1.05
BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, 170 kDa (Mot1 homolog, *S. cerevisiae*)	BTAF1	NM_003972	KIAA0940 // MGC138406 // MOT1 // TAF(II)170 // TAF172 // TAFII170	3257938	chr10	+	93673509	93821994	1.05
golgi autoantigen, golgin subfamily a, 4	GOLGA4	NM_002078	GCP2 // GOLG // MU-RMS-40.18 // p230	2617041	chr3	+	37259518	37452233	1.05
ras homolog gene family, member A	RHOA	NM_001664	ARH12 // ARHA // RHO12 // RHOH12	2674242	chr3	−	49371587	49424514	1.05
regulatory factor X, 5 (influences HLA class II expression)	RFX5	NM_000449 // NM_001025603	—	2434971	chr1	−	149578882	149586373	1.05
protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha isoform	PPP2R2A	NM_002717	B55A // FLJ26613 // MGC52248 // PR52A // PR55A	3090922	chr8	+	26156860	26286261	1.05
chromosome 20 open reading frame 11	C20orf11	NM_017896	TWA1	3893072	chr20	+	61039681	61050570	1.05
PCI domain containing 2	PCID2	NM_018386	F10 // FLJ11305 // MGC16774	3526378	chr13	−	112877970	112912799	1.05
lymphocyte antigen 9 // SLAM family member 7	LY9 // SLAMF7	NM_001033667 // NM_002348 // NM_021181	CD229 // SLAMF3 // hly9 // mLY9 // 19A // CD319 // CRACC // CS1	2363248	chr1	+	159032527	159064855	1.05
arrestin domain containing 3	ARRDC3	NM_020801	KIAA1376 // TLIMP	2866704	chr5	−	90700311	90782084	1.05
chromosome 14 open reading frame 103	C14orf103	NM_018036	FLJ10242	3578278	chr14	−	95817349	95900740	1.05
myosin IXB	MYO9B	NM_004145	CELIAC4 // MYR5	3823982	chr19	+	17047591	17185088	1.05
t-complex 1	TCP1	NM_001008897 // NM_030752	CCT-alpha // CCT1 // CCTa // D6S230E // TCP-1-alpha	2982381	chr6	−	160119521	160130731	1.05
translocation protein 1	TLOC1	NM_003262	Dtrp1 // FLJ32803 // HTP1 // SEC62	2651782	chr3	+	171166446	171194653	1.05
far upstream element (FUSE) binding protein 1	FUBP1	NM_003902	FBP // FUBP	2419235	chr1	−	78182330	78217881	1.05
mannosidase, alpha, class 1A, member 2 // urothelial cancer associated 1	MAN1A2 // UCA1	NM_006699 // —	MAN1B // —	2353881	chr1	+	117689854	117931990	1.05
engulfment and cell motility 2	ELMO2	NM_133171 // NM_182764	CED-12 // CED12 // ELMO-2 // FLJ11656 // KIAA1834	3907830	chr20	−	44426906	44495031	1.05
erbb2 interacting protein // caspase 6, apoptosis-related cysteine peptidase	ERBB2IP // CASP6	NM_001006600 // NM_018695 // NM_001226 NM_032992	ERBIN // LAP2 // MCH2	2812435	chr5	+	65258079	65451372	1.05

TABLE 5-continued

				Human Exon ST 1.0 Transcript	Human Genome hg18				Fold Change/
Gene Name	Gene Symbol	Accession	Synonym	Cluster ID	Chromosome	Strand	Start	Stop	nM
heterogeneous nuclear ribonucleoprotein R	HNRPR	NM_005826	FLJ25714 // HNRNPR // hnRNP-R	2401275	chr1	–	23486545	23543926	1.05
membrane-bound transcription factor peptidase, site 1	MBTPS1	NM_003791 // NM_201268	KIAA0091 // MGC138711 // MGC138712 // PCSK8 // S1P // SKI-1	3702293	chr16	–	82644885	82708018	1.05
RAB35, member RAS oncogene family	RAB35	NM_006861	H-ray // RAB1C // RAY	3474228	chr12	–	119017289	119039689	1.05
farnesyl-diphosphate farnesyltransferase 1	FDFT1	NM_004462	DGPT // ERG9 // SQS // SS	3086206	chr8	+	11690497	11740987	1.05
SATB homeobox 1	SATB1	NM_002971	—	2665199	chr3	–	18364435	18462086	1.05
RAS guanyl releasing protein 1 (calcium and DAG-regulated)	RASGRP1	NM_005739	CALDAG-GEFI // CALDAG-GEFII // MGC129998 // MGC129999 // RASGRP // V // hRasGRP1	3618736	chr15	–	36567598	36809973	1.05
interferon-related developmental regulator 1	IFRD1	NM_001007245 // NM_001590	PC4 // TIS7	3019519	chr7	+	111835465	111903788	1.05
coatomer protein complex, subunit alpha // peroxisomal biogenesis factor 19	COPA // PEX19	NM_004371 // NM_002857	FLJ26320 // HEP-COP // D1S2223E // HK33 // PMP1 // PMPI // PXF // PXMP1	2440143	chr1	–	158525015	158580073	1.05
SCY1-like 2 (*S. cerevisiae*)	SCYL2	NM_017988	CVAK104 // FLJ10074 // KIAA1360	3428131	chr12	+	99185070	99260564	1.05
Ctr9, Paf1/RNA polymerase II complex component, homolog (*S. cerevisiae*) // tRNA 5-methylaminomethyl-2-thiouridylate methyltransferase	CTR9 // TRMU	NM_014633 // NM_018006	KIAA0155 // SH2BP1 // TSBP // p150 // p150TSP // MGC99627 // MTO2 // MTU1 // TRMT // TRMT1 //	3320301	chr11	+	10684027	10774985	1.05
serine/threonine kinase 40 // erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked)	STK40 // EPB41	NM_032017 // NM_004437 // NM_203342 // NM_203343	MGC4796 // RP11-268J15.4 // SHIK // SgK495 // 4.1 R // EL1 // HE	2406677	chr1	–	36577822	36626062	1.05
heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	HNRPU	NM_004501 // NM_031844 //	HNRNPU // SAF-A U21.1	2464499	chr1	–	243078713	243094575	1.05
REST corepressor 1	RCOR1	NM_015156	COREST // KIAA0071 // RCOR	3553228	chr14	+	102053947	102266629	1.05
CREB binding protein (Rubinstein-Taybi syndrome)	CREBEP	NM_001079846 // NM_004380	CBP // RSTS // RTS	3677795	chr16	–	3715075	3870713	1.05

TABLE 5-continued

				Human Exon ST 1.0 Transcript	Human Genome hg18				Fold Change/
Gene Name	Gene Symbol	Accession	Synonym	Cluster ID	Chromosome	Strand	Start	Stop	nM
golgi apparatus protein 1 // CDC42 small affecter 1 // sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6C	GLG1 // CDC42SE1 // SEMA6C	NM_012201 // NM_001038707 // NM_020239 // NM_030913	CFR-1 // ESL-1 // FLJ23319 // FLJ23967 // MG-160 // MG160 // SCIP1 // SPEC1 // SEMAY // m-SemaY // m-Sema Y2	3698919	chr16	−	73015604	73209803	1.05
PHD finger protein 3	PHF3	NM_015153	KIAA0244 // MGC142210 // MGC142212	2911944	chr6	+	64403666	64547188	1.05
WDR45-like	WDR45L	NM_019613	WIPI-3 // WIPI3	3775157	chr17	−	78165748	78199803	1.05
HMG-box transcription factor 1	HBP1	NM_012257	FLJ16340	3018420	chr7	+	106596679	106630194	1.05
chromosome 2 open reading frame 25	C2orf25	NM_015702	CL25022	2580635	chr2	−	150101637	150152607	1.05
heat shock 70 kDa protein 8 // Fc fragment of IgG, low affinity IIIb, receptor (CD16b)	HSPA8 // FCGR3B	NM_006597 // NM_153201 // NM_000570	HSC54 // HSC70 // HSC71 // HSP71 // HSP73 // HSPA10 // LAP1 // MGC131511 // MGC29929 // NIP71 // CD16 //	3395416	chr11	−	122429305	122438895	1.05
chromosome 6 open reading frame 62	C6orf62	NM_030939	DKFZP564G182 // FLJ12619 // Nbla00237 // XTP12 // dJ30M3.2	2945677	chr6	−	24798431	24851423	1.05
leptin receptor overlapping transcript-like 1	LEPROTL1	NM_015344	HSPC112 // Vps55 // my047	3092276	chr8	+	30059542	30115386	1.05
ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast)	UBE2I	NM_003345 // NM_194259 // NM_194260 // NM_194261	C358B7.1 // P18 // UBC9	3643703	chr16	+	1289451	1317016	1.05
nucleoporin 155 kDa	NUP155	NM_004298 // NM_153485	KIAA0791 // N155	2853768	chr5	−	37325714	37407016	1.05
lysosomal trafficking regulator	LYST	NM_000081 // NM_001005736	CHS // CHS1	2461999	chr1	−	233878999	234113611	1.05
mitogen-activated protein kinase 14	MAPK14	NM_001315 // NM_139012 // NM_139013 // NM_139014	CSBP1 // CSBP2 // CSPB1 // EXIP // Mxi2 // PRKM14 // PRKM15 // RK // SAPK2A // p38 // p38ALPHA	2904877	chr6	+	36103487	36186989	1.05
nuclear factor (erythroid-derived 2)-like 2 // hypothetical protein DKFZp451M2119	NFE2L2 // DKFZp451M2119	NM_006164 // NM_182585	NRF2 // —	2588827	chr2	−	177794809	177837753	1.05

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript Cluster ID	Human Genome hg18 Chromosome	Human Genome hg18 Strand	Human Genome hg18 Start	Human Genome hg18 Stop	Fold Change/ nM
WD repeat domain 26	WDR26	NM_025160	FLJ21016 // MIP2	2458082	chr1	−	222639474	222691338	1.05
heterogeneous nuclear ribonucleoprotein K	HNRPK	NM_002140 // NM_031262 // NM_031263	CSBP // FLJ41122 // HNRNPK // TUNP	3212294	chr9	−	85772377	85785355	1.05
transducin-like enhancer of split 4 (E(sp1) homolog, *Drosophila*)	TLE4	NM_007005	BCE-1 // E(spI) // ESG // ESG4 // GRG4	3176209	chr9	+	81269283	81552230	1.05
bromodomain containing 2	BRD2	NM_005104	D6S113E // DKFZp686N0336 // FLJ31942 // FSRG1 // KIAA9001 // NAT // RING3 // RNF3	2903343	chr6	+	33044392	33057253	1.05
signal transducer and activator of transcription 3 (acute-phase response factor)	STAT3	NM_003150 // NM_139276 // NM_213662	APRF // FLJ20882 // MGC16063	3757840	chr17	−	37718873	37794201	1.05
ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (*Drosophila*)	ARIH1	NM_005744	ARI // HARI // HHARI //	3600744	chr15	+	70553731	70666726	1.05
zinc finger, NFX1-type containing 1 // gasdermin-like	ZNFX1 // GSDML	NM_021035 // NM_001042471 // NM_018530	FLJ39275 // MGC131926 // PP4052 //	3908831	chr20	−	47233911	47420063	1.05
SUMO1/sentrin specific peptidase 6	SENP6	NM_015571	FLJ11355 // FLJ11887 // KIAA0389 // KIAA0797 // SSP1 // SUSP1	2913983	chr6	+	76367955	76484717	1.05
DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	DDX17	NM_006386 // NM_030881	DKFZp761H2016 // P72 // RH70	3960629	chr22	−	37202800	37232288	1.05
ubiquitin specific peptidase 15	USP15	NM_006313	KIAA0529 // MGC131982 // MGC149838 // MGC74854 // UNPH4	3419147	chr12	+	60940328	61086166	1.05
Ras association (RalGDS/AF-6) domain family 2	RASSF2	NM_014737 // NM_170774	DKFZp781O1747 // KIAA0168	3896034	chr20	−	4655529	4752291	1.05
dual specificity phosphatase 6	DUSP6	NM_001946 // NM_022652	MKP3 // PYST1	3464860	chr12	−	88223376	88273467	1.05
E1A binding protein p300	EP300	NM_001429	p300	3946615	chr22	+	39817736	39906025	1.05
solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	SLC7A6	NM_001076785 // NM_003983	DKFZp686K15246 // KIAA0245 // LAT-2 // LAT3 // y+LAT-2	3666146	chr16	+	66855932	66893223	1.05
RNA binding motif protein 5	RBM5	NM_005778	FLJ39876 // G15 // H37 // LUCA15 // RMB5	2622469	chr3	+	50101372	50134000	1.05

TABLE 5-continued

				Human Exon ST 1.0 Transcript	Human Genome hg18				Fold Change/
Gene Name	Gene Symbol	Accession	Synonym	Cluster ID	Chromosome	Strand	Start	Stop	nM
nuclear protein localization 4 homolog (*S. cerevisiae*)	NPLOC4	NM_017921	FLJ20657 // FLJ23742 // KIAA1499 // NPL4	3774029	chr17	–	77134363	77214526	1.05
cyclin L2 // aurora kinase A interacting protein 1	CCNL2 // AURKAIP1	NM_001039577 // NM_030937 // NM_017900	ANIA-6B // DKFZp761A1210 // DKFZp762O195 // HCLA-ISO // HLA-ISO // PCEE // SB138 // AIP // AKIP // FLJ20608	4041923	chr1__random	+	359569	372958	1.05
poly(rC) binding protein 2	PCBP2	NM_005016 // NM_031989	HNRPE2 // MGC110998 // hnRNP-E2	3416036	chr12	+	52132173	52161417	1.05
aftiphilin	AFTPH	NM_001002243 // NM_017657 // NM_203437	FLJ20080 // FLJ23793 // MGC33965 // Nbla10388	2485433	chr2	+	64604969	64714437	1.05
GTP binding protein 1	GTPBP1	NM_004286	GP-1 // GP1 // HSPC018 // MGC20069	3945396	chr22	+	37431694	37459514	1.05
protein kinase C, eta	PRKCH	NM_006255	MGC26269 // MGC5363 // PKC-L // PKCL // PRKCL // nPKC-	3538893	chr14	+	60816958	61087440	1.05
glutaminase	GLS	NM_014905	DKFZp686O15119 // FLJ10358 // GLS1 // KIAA0838	2520291	chr2	+	191453802	191538513	1.05
tubulin, beta	TUBB	NM_178014	M40 // MGC117247 // MGC16435 // OK/SW-cl.56 // TUBB1 // TUBB5	2901913	chr6	+	30795977	30801165	1.05
neuroguidin, EIF4E binding protein	NGDN	XM_033371 // XM_932898 // XM_932900 // XM_932903 // XM_932906 // XM_941350 // XM_945161 // XM_945163 // XM_945166 // XM_945170 // NM_001042635 // NM_015514	C14orf120 // DKFZP564O092 // LCP5 // NGD // lpd-2	3529156	chr14	+	23008821	23048896	1.05
zinc finger, RAN-binding domain containing 2	ZRANB2	NM_005455 // NM_203350	DKFZp686J1831 // DKFZp686N09117 // FLJ41119 // ZIS	2418000	chr1	–	71292434	71355820	1.05

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change/ nM
			// ZIS1 // ZIS2 // ZNF265						
DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	DDX21	NM_004728	DKFZp686F21172 // GUA // GURDB // RH-II/GU // RH-II/GuA	3250055	chr10	+	70380584	70414821	1.05
sorting nexin 19	SNX19	NM_014758	CHET8 // DKFZp667I205 // KIAA0254	3398482	chr11	−	130250320	130291615	1.05
phosphatidylinositol binding clathrin assembly protein	PICALM	NM_001008660 // NM_007166	CALM // CLTH // LAP	3385175	chr11	−	85345353	85458481	1.05
PI-3-kinase-related kinase SMG-1	SMG1	NM_015092	61E3.4 // ATX // KIAA0421 // LIP	3683050	chr16	−	18719381	18845318	1.05
MON2 homolog (*S. cerevisiae*)	MON2	NM_015026	KIAA1040 // MGC35493	3419239	chr12	+	61146751	61280506	1.05
signal recognition particle receptor (‘docking protein’)	SRPR	NM_003139	DP // MGC17355 // MGC3650 // MGC9571 // SRP-alpha // Sralpha	3396916	chr11	−	125636504	125644013	1.05
heat shock protein 90 kDa alpha (cytosolic), class B member 1	HSP90AB1	NM_007355	D6S182 // FLJ26984 // HSP90-BETA // HSP90B // HSPC2 // HSPCB	2908474	chr6	+	44319983	44330383	1.05
eukaryotic translation initiation factor 5	EIF5	NM_001969 // NM_183004	EIF-5A	3553607	chr14	+	102743652	102881108	1.05
patatin-like phospholipase domain containing 10 pseudogene // patatin-like phospholipase domain containing 8	PNPLA10P // PNPLA8	XM_927062 // XM_938392 // NM_015723	—// IPLA2(GAMMA) // IPLA2-2 // IPLA2G	3067592	chr7	−	107880325	107956012	1.05
2'-5'-oligoadenylate synthetase 3, 100 KDa	OAS3	NM_006187	MGC133260 //	3432467	chr12	+	111860550	111895663	1.05
aminopeptidase puromycin sensitive	NPEPPS	XM_001128588 // NM_006310	MP100 // PSA	3724698	chr17	+	42955347	43057188	1.05
SAP30 binding protein // cardiotrophin-like cytokine factor 1	SAP30BP // CLCF1	NM_013260 // NM_013246	DKFZp586L2022 // HCNGP // HTRG // HTRP // BSF3 // CISS2 // CLC // NNT1 // NR6	3735107	chr17	+	71174801	71215729	1.05
bromodomain adjacent to zinc finger domain, 1B	BAZ1B	NM_023005 // NM_032408	WBSCR10 // WBSCR9 // WSTF	3056044	chr7	−	72492710	72574552	1.05
cullin 3	CUL3	NM_003590	—	2601544	chr2	−	225025520	225158348	1.05
DEAD (Asp-Glu-Ala-Asp) box polypeptide 42	DDX42	NM_007372 // NM_203499	FLJ43179 // RHELP // RNAHP // SF3b125	3730899	chr17	+	59204975	59250510	1.05
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SMARCA2	NM_003070 // NM_139045	BAF190 // BRM // FLJ36757 // MGC74511 // SNF2	3159946	chr9	+	1968220	2253060	1.05

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change/ nM
			// SNF2L2 // SNF2LA // SWI2 // Sth1p // hBRM // hSNF2a						
stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein)	STIP1	NM_006819	HOP // IEF-SSP-3521 // P60 // STI1L	3334224	chr11	+	63709341	63728586	1.05
splicing factor, arginine/serine-rich 7, 35 kDa	SFRS7	NM_001031684	9G8 // AAG3 // HSSG1 // RBM37 // ZCCHC20 // ZCRB2	2548970	chr2	–	38824253	38832154	1.05
ribosomal protein L14 // ribosomal protein L14-like	RPL14 // RPL14L	NM_001034996 // NM_003973 // XR_017789 // XR_017790	CAG-ISL-7 // CTG-B33 // L14 // MGC88594 // RL14 // hRL14 // bcm1298	2618640	chr3	+	40473807	40485068	1.05
acidic (leucine-rich) nuclear phosphoprotein 32 family, member C // acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	ANP32C // ANP32A	NM_012403 // NM_006305	PP32R1 // C15orf1 // I1PP2A // LANP // MAPM // MGC119787 // MGC150373 // PHAP1 // PHAPI // PP32	3630912	chr15	–	66857944	66900452	1.05
endoglin (Osler-Rendu-Weber syndrome 1)	ENG	NM_000118	CD105 // END // FLJ41744 // HHT1 // ORW // ORW1	3226097	chr9	–	129615329	129660473	1.05
lysosomal associated multispanning membrane protein 5	LAPTM5	NM_006762	MGC125860 // MGC125861	2404158	chr1	–	30977913	31095913	1.05
family with sequence similarity 108, member A2 // family with sequence similarity 108, member A1	FAM108A2 // FAM108A1	XM_039721 // XM_933830 // NM_001080422 // NM_031213	C1orf47 // C19orf27 // MGC5244	3845581	chr19	–	1827984	1836490	1.05
interleukin 16 (lymphocyte chemoattractant factor)	IL16	NM_004513 // NM_172217	FLJ16806 // FLJ42735 // FLJ44234 // HsT19289 // IL-16 // LCF // prIL-16	3604287	chr15	+	79262148	79392377	1.05
SEC14 and spectrin domains 1	SESTD1	NM_178123	DKFZp434O0515 // SOLO	2589929	chr2	–	179644888	180002479	1.05
coatomer protein complex, subunit beta 2 (beta prime)	COPB2	NM_004766	beta'-COP	2697792	chr3	–	140555482	140591192	1.05
Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived); ribosomal protein S30	FAU	NM_001997	FAU1 // RPS30	3377463	chr11	–	64644697	64646234	1.05
AHA1, activator of heat shock 90 kDa protein ATPase homolog 1 (yeast)	AHSA1	NM_012111	AHA1 // C14orf3 // p38	3545466	chr14	+	76993989	77005560	1.05

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change/ nM
SLU7 splicing factor homolog (*S. cerevisiae*)	SLU7	NM_006425	9G8 // MGC9280 // hSlu7	2884658	chr5	–	159761226	159778959	1.05
multiple C2 domains, transmembrane 1	MCTP1	NM_001002796 // NM_024717	FLJ22344	2867443	chr5	–	94066156	94646035	1.05
ubiquitin-conjugating enzyme E2Z (putative)	UBE2Z	NM_023079	FLJ13855 //	3725481	chr17	+	44340808	44361870	1.05
hypothetical protein MGC40489 XR_016048	MGC40489	XR_015622 //	FLJ30780	3767053	chr17	–	60176255	60263758	1.05
ATG9 autophagy related 9 homolog A (*S. cerevisiae*) // ATP-binding cassette, sub-family B (MDR/TAP), member 6	ATG9A // ABCB6	NM_001077198 // NM_024085 // NM_005689	APG9L1 // MGD3208 // ABC // ABC14 // EST45597 // FLJ22414 // MTABC3 // PRP // umat	2599955	chr2	–	219781799	219802587	1.05
isoleucyl-tRNA synthetase	IARS	NM_002161 // NM_013417	FLJ20736 // IARS1 // ILRS // PRO0785	3214668	Chr9	–	94012330	94096287	1.05
LIM domain binding 1	LDB1	NM_003893	CLIM2 // NLJ	3304215	chr10	–	103830793	103883389	1.05
YY1 transcription factor	YY1	NM_003403	DELTA // NF-E1 // UCRBP // YIN-YANG-1	3551677	chr14	+	99750383	99818868	1.05
WD repeat domain, phosphoinositide interacting	WIPI2	NM_001033518 // NM_001033519 // NM_001033520 // NM_015610 // NM_016003	Atg21 // CGI-50 // DKFZP434J154 // DKFZp686P02188 // FLJ12979 // FLJ14217 // FLJ42984 // WIPI-2	2988536	chr7	+	5196360	5239975	1.05
BCL2-associated transcription factor 1	BCLAF1	NM_001077440 // NM_001077441 // NM_014739	BTF // KIAA0164 // bK211L9.1	2975680	chr6	–	136619703	136652847	1.05
ADAM metallopeptidase domain 19 (meltrin beta)	ADAM19	NM_023038 // NM_033274	FKSG34 // MADDAM //	2883440	chr5	–	156755122	156935351	1.05
RAE1 RNA export 1 homolog (*S. pombe*)	RAE1	NM_001015885 // NM_)003610	FLJ30608 // MGC117333 // MGC126076 // MGC126077 // MIG14 // MRNP41 // Mnrp41 // dJ481F12.3 // dJ800J21.1	3890555	chr20	+	55359493	55386992	1.05
cyclin L2 // aurora kinase A interacting protein 1	CCNL2 // AURKAIP1	NM_001039577 // NM_030937 // NM_017900	ANIA-6B // DKFZp761A1210 // DKFZp762O195 // HCLA-ISO // HLA-ISO // PCEE //	2391532	chr1	–	1314609	1324575	1.05

TABLE 5-continued

				Human Exon ST 1.0 Transcript	Human Genome hg18				Fold Change/
Gene Name	Gene Symbol	Accession	Synonym	Cluster ID	Chromosome	Strand	Start	Stop	nM
nucleolar and coiled-body phosphoprotein 1	NOLC1	NM_004741	SB138 // AIP // AKIP // FLJ20608 KIAA0035 // NOPP130 // NOPP140 // NS5ATP13 // P130	3261492	chr10	+	103901962	103913597	1.05
B-cell CLL/lymphoma 11B (zinc finger protein)	BCL11B	NM_022898 // NM_138576	CTIP-2 // CTIP2 // RIT1 // hRIT1-	3579114	chr14	–	98705377	98931503	1.05
proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog)	PSMD7	NM_002811	MOV34 // P40 // S12	3668617	chr16	+	72888182	72901528	1.05
chromosome 14 open reading frame 118	C14orf118	NM_017926 // NM_017972	FLJ10033 // FLJ20689 // MGC61896	3544905	chr14	+	75688015	75800924	1.05
translocase of inner mitochondrial membrane 23 homoleg (yeast)	TIMM23	XM_001133798 // NM_006327	MGC22767 // PRO1197 // TIM23 // TIMM23B	3289031	chr10	–	51180787	51293392	1.05
proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	PSMD2	NM_002808	MGC14274 // P97 // S2 // TRAP2	2655650	chr3	+	185499199	185509504	1.05
LSM14A, SOD6 homolog A (*S. cerevislee*)	LSM14A	NM_015578	C19orf13 // DKFZP434D1335 // FAM61A // RAP55	3829575	chr19	+	39355192	39416345	1.05
phosphatidylinositol transfer protein, alpha // mysoin IC	PITPNA // MYO1C	NM_006224 // NM_001080779 // NM_001080950 // NM_033375	MGC99649 // PITPN // VIB1A // FLJ23603 // MMI-beta // MMIb // NMI // myr2	3740304	chr17	–	1367883	1412932	1.05
centaurin, delta 1	CENTD1	NM_015230 // NM_139182	ARAP2 // FLJ13675 // FLJ44916 //	2765590	chr4	–	35626248	35922356	1.05
structural maintenance of chromosomes 1A	SMC1A	NM_006306	DKFZp686L19178 // DXS423E // KIAA0178 // MGC138332 // SB1.8 // SMC1 // SMC1L1 // SMC1alpha //	4009238	chrX	–	53417797	53466400	1.05
solute carrier family 43, member 3	SLC43A3	NM_014096 // NM_017611 // NM_199329	DKFZp762A227 // EEG1 // FOAP-13 // PRO1659 // SEEEG-1	3373845	chr11	–	56931008	56951629	1.04
ninjurin 1	NINJ1	NM_004148	NIN1 // NINJURIN	3215146	chr9	–	94923613	94939639	1.04
CDC-like kinase 3	CLK3	NM_001292 // NM_003992	FLJ22858	3601741	chr15	+	72677906	72719105	1.04
sortilin-related receptor, L(DLR class) A	SORL1 //	NM_003105	LR11 // LRP9 //	3352948	chr11	+	120828130	121077997	1.04
repeats-containing	C11orf32		SORLA // SorLA-1 // gp250	3352948	chr11	+	120828130	121077997	1.04

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change/ nM
KIAA0831	KIAA0831	NM_014924	MGC126291 // MGC126292	3565739	chr14	–	54902008	54948457	1.04
CD6 molecule	CD6	NM_006725	TP120	3332663	chr11	+	60495619	60544422	1.04
pre-mRNA cleavage factor I, 59 kDa subunit	FLJ12529	NM_024811	FLJ39024 // MGC9315	3375340	chr11	–	60926704	60954030	1.04
SEC23 interacting protein	SEC23IP	NM_007190	MSTP053 // P125	3267455	chr10	+	121642213	121691984	1.04
cell division cycle 40 homolog (*S. cerevisiae*)	CDC40	NM_015891	EHB3 // FLJ10564 // MGC102802 // PRP17 // PRPF17	2921086	chr5	+	110606544	110682171	1.04
calnexin	CANX	NM_001024649 // NM_001746	CNX // FLJ26570 // IP90 // P90	2844203	chr5	+	179058077	179091243	1.04
chromosome 20 open reading frame 112	C20orf112	NM_080616	DKFZP566G1424 // dJ1184F4.2	3902764	chr20	–	30498759	30636537	1.04
splicing factor 3b, subunit 3, 130 kDa	SF3B3	NM_012426	KIAA0017 // RSE1 // SAP130 // SF3b130 // STAF130	3667281	chr16	+	69115212	69169072	1.04
family with sequence similarity 44, member A	FAM44A	NM_148894	FLJ33215 // KIAA1327	2761285	chr4	–	13179462	13207890	1.04
casein kinase 2, alpha 1 polypeptide // casein kinase 2, alpha 1 polypeptide pseudogene	CSNK2A1 // CSNK2A1P	NM_001895 // NM_177559 // NM_177560 // NR_002207	CK2A1 // CKII // CKII alpha // —	3894228	chr20	–	402069	472534	1.04
eukaryotic translation initiation factor 3, subunit 7 zeta, 66/67 kDa	EIF3S7	NM_003753	MGC126526 // MGC17258 // eIF3-p66 // eIF-zeta // eIF3d	3959631	chr22	–	35236857	35255429	1.04
GTP binding protein 2	GTPBP2	NM_019096	MGC74725	29544771	chr6	–	43681031	43704877	1.04
fusion (involved in t(12; 16) in malignant liposarcoma)	FUS	NM_001010850 // NM_004960	CHOP // FUS-CHOP // FUS1 // TLS // TLS/CHOP	3656904	chr16	+	31093395	31111003	1.04
KIAA0430	KIAA0430	NM_014647	A-362G6.1 // LKAP	3681956	chr16	–	15595757	15654441	1.04
lymphocyte cytosolic protein 1 (L-plastin)	LCP1	NM_002298	CP64 // DKFZp781A23186 // FLJ25423 // FLJ26114 // FLJ39956 // L-PLASTIN // LC64P // PLS2	3512874	chr13	–	45595067	45684007	1.04
DENN/MADD domain containing 3	DENND3	NM_014957	KIAA0870	3118651	chr8	+	142207943	142289494	1.04
KIAA0317	KIAA0317	NM_001039479	—	3572041	chr14	–	74189599	74249655	1.04
ninein (GSK3B interacting protein)	NIN	NM_016350 // NM_020921 // NM_182944 // NM_182945 // NM_182946	KIAA1565	3564071	chr14	–	50256234	50403020	1.04

TABLE 5-continued

				Human Exon ST 1.0 Transcript	Human Genome hg18				Fold Change/
Gene Name	Gene Symbol	Accession	Synonym	Cluster ID	Chromosome	Strand	Start	Stop	nM
transmembrane protein 161B // integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41)	TMEM161B // ITGA2B	NM_153354 // NM_000419	FLB3342 // MGC33214 // PRO1313 // CD41 // CD41B // GP2B // GPIIb // GTA // HPA3	2866045	chr5	−	87526693	87600565	1.04
Ewing sarcoma breakpoint region 1	EWSR1	NM_005243 // NM_013986	EWS	3941907	chr22	+	27994201	28026501	1.04
YTH domain containing 1	YTHDC1	NM_001031732 // NM_133370	KIAA1966 // YT521 // YT521-B	2772017	chr4	−	68858700	68934802	1.04
squamous cell carcinoma antigen recognized by T cells 3	SART3	NM_014706	KIAA0156 // MGC138188 // RP11-13G14 // TIP110 // p110(nrb)	3470253	chr12	−	107440140	107479296	1.04
cytoplasmic linker associated pretein 1	CLASP1	NM_015282	DKFZp686D1968 // DKFZp686H2039 // FLJ33821 // FLJ41222 // KIAA0622 // MAST1 //	2573641	chr2	−	121811825	122169321	1.04
nuclear receptor interacting protein 1	NRIP1	NM_003489	RIP140	3925639	chr21	−	15255125	15359182	1.04
protein phosphatase 1, regulatory (inhibitor) subunit 12A	PPP1R12A	NM_002480	MBS // MGC133042 //	3463571	chr12	−	78690959	78853356	1.04
STE20-like kinase (yeast)	SLK	NM_014720	KIAA0204 // MGC133067 // STK2 // bA16H23.1 // se20-9	3262433	chr10	+	105716666	105778975	1.04
polymerase (RNA) II (DNA directed) polypeptide B, 140 kDa	POLR2B	NM_000938	POL2RB // RPB2 // hRPB140 // hsRPB2	2728448	chr4	+	57539163	57592513	1.04
HIV-1 Rev binding protein	HRB	XM_941338 // NM_004504	MGC116938 // MGC116940 // RAB // RIP	2530599	chr2	+	228045122	228134167	1.04
zinc finger CCCH-type containing 12A	ZC3H12A	NM_025079	FLJ23231 // MCPIP // RP3-423B22.1 //	2330687	chr1	+	37712740	37722550	1.04
transforming growth factor, beta 1	TGFB1	NM_000660	CED // DPD1 // TGFB	3863021	chr19	−	46499343	46551636	1.04
ADP-ribosylation factor 4	ARF4	XM_001132763 // NM_001660	—	2678090	chr3	−	57532172	57558635	1.04
pleiomorphic adenoma gene-like 2	PLAGL2	NM_002657	FLJ23283	3902682	chr20	−	30243975	30259284	1.04
jumonji domain containing 2C	JMJD2C	NM_015061	FLJ25949 // GASC1 // JHDM3C // KIAA0780 // bA146B14.1	3161566	chr9	+	6747651	7165647	1.04

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change/ nM
transmembrane BAX inhibitor motif containing 1	TMBIM1	NM_022152	PP1201 // RECS1	2599371	chr2	−	218847185	218865515	1.04
GPI-anchored membrane protein 1	GPIAP1	NM_005898 // NM_203364	GPIP137 // M11S1 // p137GPI	3326183	chr11	+	34009711	34081946	1.04
DEAD (Asp-Glu-Ala-Asp) box polypeptide 47 // apolipoprotein L domain containing 1	DDX47 // APOLD1	NM_016355 // NM_201224 // NM_030817	DKFZp564O176 // E4-DBP // FLJ30012 // HQ0256 // MSTP162 // DKFZP434F0318 // FLJ25138	3405531	chr12	+	12856462	12874176	1.04
SERPINE1 mRNA binding protein 1	SERBP1	NM_001018067 // NM_001018068 // NM_001018069 // NM_015640	CGI-55 // CHD3IP // DKFZp564M2423 // FLJ90489 // HABP4L // PAI-RBP1 // PAIRBP1	2417174	chr1	−	67646101	67669020	1.04
coiled-coil domain containing 47	CCDC47	NM_020198	GK001 // MSTP041	3766334	chr17	−	59176353	59204726	1.04
lamin B receptor	LBR	NM_002296 // NM_194442	DHOR14B // LMN2R // MGC9041 // PHA	2458289	chr1	−	223655840	223683230	1.04
caspase 3, apoptosis-related cysteine peptidase	CASP3	NM_004346 // NM_032991	CPP32 // CPP32B // SCA-1	2796484	chr4	−	185782536	185807608	1.04
Burkitt lymphoma receptor 1, GTP binding protein (chemokine (C—X—C motif) receptor 5)	BLR1	NM_001716 // NM_032966	CD185 // CXCR5 // MDR15 // MGC117347	3351675	chr11	+	118259777	118272180	1.04
major histocompatibility complex, class I, E	HLA-E	NM_005516	DKFZp686P19218 // EA1.2 // EA2.1 // HLA-6.2 // MHC	2901620	chr6	+	30565243	30620086	1.04
v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	LYN	NM_002350	FLJ26625 // JTK8	3098977	chr8	+	56954505	57087291	1.04
MYC-associated zinc finger protein (purine-binding transcription factor) // kinesin family member 22	MAZ // KIF22	NM_001042539 // NM_002383 // NM_007317	PUR1 // Pur-1 // SAF-1 // SAF-2 // ZF87 // ZNF801 // Zif87 // KID // KNSL4 // OBP // OBP-1 // OBP-2	3655665	chr16	+	29724956	29729977	1.04
chromosome 3 open reading frame 58	C3orf58	NM_173552	MGC33365	2646327	chr3	+	145173603	145669744	1.04
hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1	HERC1	NM_003922	p532 // p619	3628650	chr15	−	61687879	61913158	1.04
KIAA0652	KIAA0652	NM_014741	FLJ20698	3329404	chr11	+	46595671	46652934	1.04
PX domain containing serine/threonine kinase	PXK	NM_017771	FLJ20335 // MONaKA	2626167	chr3	+	58293657	58386884	1.04
jumonji, AT rich interactive domain 2	JARID2 // C20orf120	NM_004973	JMJ	2896177	chr6	+	15261674	15630231	1.04

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change/ nM
GGI-09 protein	CGI-09	NM_015939	MGC5029	3896524	chr20	–	5865881	5879370	1.04
syndecan binding protein (syntenin)	SDCBP	NM_001007067 // NM_001007068 // NM_001007069 // NM_001007070 // NM_005625	MDA-9 // ST1 // SYCL // TACIP18	3099750	chr8	+	59605208	59658960	1.04
2',3'-cyclic nucleotide 3' phosphodiesterase	CNP	NM_033133	CNP1	3721548	chr17	+	37372285	37383765	1.04
family with sequence similarity 48, member A // family with sequence similarity 48, member B2	FAM48A // FAM48B2	NM_001014286 // NM_017569 // XM_293352	C13 // C13orf19 // FP757 // P38IP // bA421P11.4 // —	3509910	chr13	–	36480880	36556254	1.04
ubiquitin-activating enzyme E1-like 2	UBE1L2	NM_018227	FLJ10808 // FLJ23367	2771718	chr4	–	68130308	68249472	1.04
solute carrier family 35, member B1	SLC35B1	NM_005827	UGTREL1	3761959	chr17	–	45133304	45141355	1.04
pogo transposable element with ZNF domain	POGZ	NM_015100 // NM_145796 // NM_207171	KIAA0461 // MGC71543 // SUHW5 // ZNF635	2435044	chr1	–	149641830	149753035	1.04
forkhead box O1A (rhabdomyosarcoma)	FOXO1A	NM_002015	FKH1 // FKHR // FOXO1	3510858	chr13	–	40027817	40162098	1.04
RAB14, member RAS oncogene family	RAB14	NM_016322	FBP // RAB-14	3223872	chr9	–	122980236	123025093	1.04
zinc finger protein 313	ZNF313	NM_018683	RNF114	3888474	chr20	+	47986321	48003818	1.04
DnaJ (Hsp40) homolog, subfamily C, member 1	DNAJC1	NM_022365	DNAJL1 // ERdj1 // HTJ1 // MGC131954	3280902	chr10	–	22078144	22332877	1.04
integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	ITGB1	NM_002211 // NM_033666 // NM_033667 // NM_033668 // NM_033669 // NM_133376	CD29 // FNRB // GPIIA // MDF2 // MSK12 // VLAB	3284188	chr10	–	33211051	33321367	1.04
MMDA receptor regulated 2	NARG2	NM_001018089 // NM_024611	—	3627363	chr15	–	58500956	58558626	1.04
mitochondrial ribosomal protein S7	MRPS7	NM_015971	MRP-S // MRP-S7 // RP-S7 //	3734760	chr17	+	70769374	70774626	1.04
TATA box binding protein	TBP	NM_003194	GTF2D // GTF2D1 // MGC117320 // MGC126054 // MGC126055 // SCA17 // TFIID	2937984	chr6	+	170705200	170723945	1.04
polymerase (RNA) I polypeptide C, 30 kDa	POLR1C	NM_004875 // NM_203290	RPA39 // RPA40 // RPA5 // RPAC1	2908052	chr6	+	43592769	43605071	1.04
spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)	SPTAN1	NM_003127	(ALPHA)II-SPECTRIN // FLJ44613	3190558	chr9	+	130354704	130435758	1.04
protein phosphatase 1, catalytic subunit, gamma isoform	PPP1CC	NM_002710	PPP1G	3471374	chr12	–	109642007	109665131	1.04

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change/ nM
CDC-like kinase 1	CLK1	NM_001024646 // NM_004071	CLK // CLK/STY // STY	2594497	chr2	−	201425997	201437659	1.04
transient receptor potential cation channel, subfamily C, member 4 associated protein	TRPC4AP	NM_015638 // NM_199368	C20orf188 // TRRP4AP //	3903708	chr20	−	33053899	33144297	1.04
actin, beta	ACTB	NM_001101	PS1TP5BP1	3036924	chr7	−	5533433	5537011	1.04
polypyrimidine tract binding protein 1	PTBP1	NM_002819 // NM_031990 // NM_031991 // NM_175847	HNRNPI // HNRPI // MGC10830 // MGC8461 // PTB // PTB-1 // PTB-T // PTB2 // PTB3 // PTB4 // pPTB	3815165	chr19	+	747768	763505	1.04
chromosome 6 open reading frame 166	C6orf166	NM_018064	FLJ10342 // dJ486L4.2	2963784	chr6	−	88441297	88476721	1.04
ring finger protein 40	RNF40	NM_014771	BRE1B // DKFZp686K191 // KIAA0661 // MGC13051 // RBP95 // STARING	3656555	chr16	+	30681120	30695182	1.04
coiled-coil domain containing 100	CCDC100	NM_153223	DKFZp686106246 // FLJ36090 // FLJ38327	2873168	chr5	−	122642038	122832582	1.04
ubiquitin specific peptidase B	USP8	NM_005154	FLJ34456 // HumORF8 // KIAA0055 // MGC129718 // UBPY	3593652	chr15	+	48503634	48580565	1.04
splicing factor 1	SF1	NM_004630 // NM_201995 // NM_201997 // NM_201998	D11S636 // ZFM1 // ZNF162	3377044	chr11	−	64287827	64302817	1.04
family with sequence similarity 89, member B	FAM89B	NM_152832	MTVR1	3335338	chr11	+	65096490	65098230	1.04
eukaryotic translation initiation factor 4A, isoform 2	EIF4A2	NM_001967	BM-010 // DDX2B // EIF4A // EIF4F	2656738	chr3	+	187961636	187990742	1.04
leucine-rich PPR-motif containing	LRPPRC	NM_133259	CLONE-23970 // GP130 // LRP130 // LSFC	2550790	chr2	−	43961504	44085128	1.04
v-rel reticuloendothellosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian)	RELA	NM_021975	MGC131774 // NFKB3	3377789	chr11	−	65176856	65204491	1.04

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change/ nM
chromodomain helicase DNA binding protein 4	CHD4	NM_001273	DKFZp686E06161 // Mt-2b // Mi2-	3442054	chr12	–	6549521	6587067	1.04
transferrin receptor (p90, CD71)	TFRC	NM_003234	CD71 // TFR // TFR1 // TFRR	2712632	chr3	–	197238405	197334433	1.04
GRP1 (general receptor for phosphoinositides 1)-associated scaffold protein	GRASP	NM_181711	—	3415193	chr12	+	50686988	50695938	1.04
small nuclear ribonucleoprotein 70 kDa polypeptide (RNP antigen)	SNRP70	NM_001009820 // NM_003089	RNPU1Z // RPU1 // U170K // U1AP // U1RNP	3838185	chr19	+	54280358	54304714	1.04
1-acylglycerol-3-phosphate O-acyltransferase 3	AGPAT3	NM_001037553 // NM_020132	LPAAT-GAMMA1 // MGC4604	3923354	chr21	+	44105141	44245644	1.04
vacuolar protein sorting 4 homolog B (*S. cerevisiae*)	VPS4B	NM_004869	MIG1 // SKD1 // VPS4-2	3811497	chr18	–	59207407	59240734	1.04
KIAA1128	KIAA1128	NM_018999	FLJ14262 // FLJ25809 // Gcap14 // bA486O22.1	3255402	chr10	+	86020629	86268247	1.04
c-src tyrosine kinase	CSK	NM_004383	MGC117393	3601840	chr15	+	72841734	72882558	1.04
pleiotropic regulator 1 (PRL1 homolog, *Arabidopsis*)	PLRG1	NM_002669	MGC110880 // PRL1	2790570	chr4	–	155675613	155691014	1.04
WD repeat domain 1	WDR1	NM_005112 // NM_017491	AIP1 // NORI-1	2760371	chr4	–	9685078	9772600	1.04
FBJ murine osteosarcoma viral oncogene homolog B	FOSB	NM_006732	DKFZp686C0818 // G0S3 // GOS3 // GOSB //	3836266	chr19	+	50624036	50671180	1.04
c-Maf-inducing protein	CMIP	NM_030629 // NM_198390	KIAA1694	3670772	chr16	+	80030441	80323852	1.04
aldolase A, fructose-bisphosphate	ALDOA	NM_000034 // NM_184041 // NM_184043	ALDA // MGC10942 // MGC17716 //	3655920	chr16	+	29968869	29991009	1.04
bolA homolog 1 (*E. coli*)	BOLA1	NM_016074	CGI-143 // MGC75015 // RP11-196G18.18	2357961	chr1	+	148126062	148138968	1.04
ring finger and SPRY domain containing 1	RSPRY1	NM_133368	KIAA1972	3662612	chr16	+	55777703	55831882	1.04
centaurin, delta 2	CENTD2	NM_001040118 // NM_015242 // NM_139181	ARAP1 KIAA0782	3381241	chr11	–	72073021	72141062	1.04
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13 kDa	NDUFA5	NM_005000	B13 // CI-13KD-B // DKFZp781K1356 // FLJ12147 // NUFM //UQOR13	3070658	chr7	–	122968075	122985216	1.04

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript	Human Genome hg18				Fold Change/
				Cluster ID	Chromosome	Strand	Start	Stop	nM
brix domain containing 2	BXDC2	NM_018321	BRIX // FLJ11100	2806231	chr5	+	34951248	34962845	1.04
tumor necrosis factor receptor superfamily, member 25 // pleckstrin homology domain containing, family G (with RhoGef domain) member 5	TNFRSF25 // PLEKHG5	NM_001039664 // NM_003790 // NM_148965 // NM_148966 // NM_148967 // NM_148970 // NM_001042663 // NM_001042664 // NM_001042665 // NM_020631 // NM_198681	APO-3 // DDR3 // DR3 // LARD // TNFRSF12 // TR3 // TRAMP // WSL-1 // WSL-LR // KIAA0720 // RP4-650H14.3	2394699	chr1	−	6443807	6448816	1.04
nucleoporin like 1	NUPL1	NM_001008564 // NM_001008565 // NM_014089	KIAA0410 // PRO2463	3482219	chr13	+	24773258	24822202	1.04
nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon	NFKBIE	NM_004556	IKBE	2955076	chr6	−	44333884	44341478	1.04
tripartite motif-containing 8	TRIM8	NM_030912	GERP // RNF27	3261820	chr10	+	104384137	104419190	1.04
WD repeat and SOCS box-containing 1	WSB1	NM_015626 // NM_134265	SWIP1 // WSB-1	3715109	chr17	+	22644482	22684326	1.04
SAPS domain family, member 3	SAPS3	NM_018312	C11orf23 // DKFZp781E17107 // DKFZp781E2374 // DKFZp781O2362 // FLJ11058 // FLJ43065 // MGC125711 // MGC125712 // PP6R3 // SAP190 // SAPL // SAPLa	3337618	chr11	+	67984785	68173381	1.04
hypothetical protein FLJ21438	FLJ21438	XM_029084	DKFZp667E013 // FLJ00087	3853453	chr19	−	15423181	15436377	1.04
CD14 molecule	CD14	NM_000591 // NM_001040021	—	2878437	chr5	−	139991507	139993422	1.04
PRP3 pre-mRNA processing factor 3 homolog (*S. cerevisiae*) // KIAA0460	PRPF3 // KIAA0460	NM_004698 // NM_015203	HPRP3 // HPRP3P // PRP3 // Prp3p // RP18 // FLJ32145 // HSPC099	2358171	chr1	+	148560583	148592321	1.04
signal transducer and activator of transcription	STAT5B	NM_012448	STAT5	3757770	chr17	−	37604727	37682109	1.04
jumonji domain containing 1A	JMJD1A	NM_018433	DKFZp686A24246 //	2492064	chr2	+	86509150	86574548	1.04

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript Cluster ID	Human Genome hg18 Chromosome	Strand	Start	Stop	Fold Change/ nM
			DKFZp686P07111 // JHMD2A // JMJD1 //						
IQ motif containing GTPase activating protein 1	IQGAP1	NM_003870	HUMORFA01 // KIAA0051 // SAR1 // p195	3608113	chr15	+	88732454	88846463	1.04
ubiquitin-conjugating enzyme E2B (RAD6 homolog)	UBE2B	NM_003337	E2-17 kDa // HHR6B // HR6B // RAD6B // UBC2	2829275	chr5	+	133734769	133788148	1.04
splicing factor, arginine/serine-rich 10 (transformer 2 homolog, *Drosophila*)	SFRS10	NM_004593	DKFZp686F18120 // Htra2-beta // SRFS10 // TRA2-BETA // TRA2B	2709062	chr3	–	187048509	187160523	1.04
poly(A) polymerase alpha	PAPOLA	NM_032632	MGC5378 // PAP	3550392	chr14	+	96038038	96104627	1.04
kelch-like 18 (*Drosophila*)	KLHL18	NM_025010	FLJ13703 // KIAA0795	2621275	chr3	+	47298888	47367590	1.04
G protein-coupled receptor 132	GPR132	NM_013345	G2A // MGC99642	3581404	chr14	–	104586779	104622593	1.04
phosphatidylinositol transfer protein, beta	PITPNB	NM_012399	PI-TP-beta // PtdInsTP // VIB1B	3956290	chr22	–	26577440	26645487	1.04
Snf2-related CBP activator protein	SRCAP	NM_006662	KIAA0309	3656418	chr16	+	30616551	30663998	1.04
engulfment and cell motility 1	ELMO1	NM_001039459 // NM_014800 // NM_130442	CED-12 // CED12 // ELMO-1 // KIAA0281 // MGC126406	3046197	chr7	–	36860492	37455389	1.04
metal response element binding transcription factor 2	MTF2	NM_007358	M96 // PCL2 // RP5-976O13.1 // dJ976O13.2	2346934	chr1	+	93147511	93377202	1.04
hemopoietic cell kinase	HCK	NM_002110	JTK9	3881651	chr20	+	30086433	30153306	1.04
SIN3 homolog A, transcription regulator (yeast)	SIN3A	NM_015477	DKFZP434K2235 // FLJ90319 // KIAA0700	3633403	chr15	–	73448786	73535167	1.04
eukaryotic translation initiation factor 3, subunit 9 eta, 116 kDa	EIF3S9	NM_001037283 // NM_003751	EIF3-ETA // EIF3-P110 // EIF3-P116 // MGC104664 // MGC131875 // PRT1 // eIF3b	2987441	chr7	+	2315929	2386896	1.04
transmembrane 9 superfamily member 3	TM9SF3	NM_020123	EP70-P-iso // RP11-34E5.1 // SMBP	3301857	chr10	–	98267858	98337079	1.04
chromosome 1 open reading frame 50	C1orf50	NM_024097	MGC955	2332767	chr1	+	43005527	43036633	1.04

TABLE 5-continued

				Human Exon ST 1.0 Transcript	Human Genome hg18				Fold Change/
Gene Name	Gene Symbol	Accession	Synonym	Cluster ID	Chromosome	Strand	Start	Stop	nM
chaperonin containing TCP1, subunit 6A (zeta 1)	CCT6A	NM_001009186 // NM_001762	CCT-zeta // CCT-zeta-1 // CCT6 // Cctz // HTR3 // MGC126214 // MGC126215 // MoDP-2 // TCP-1-zeta // TCP20 // TCPZ // TTCP20	3003193	chr7	+	56086894	56099148	1.04
zinc finger protein 410	ZNF410	NM_021188	APA-1 // APA1	3543884	chr14	+	73423093	73468718	1.04
KIAA1468	KIAA1468	NM_020854	FLJ33841 // HsT3308 // HsT885	3791168	chr18	+	58005478	58125326	1.04
nucleolar protein NOP5/NOP58	NOP5/NOP58	NM_015934	HSPC120	2523144	chr2	+	202811346	202926967	1.04
guanylate binding protein 5	GBP5	NM_052942	GBP-5	2422035	chr1	–	89496930	89511122	1.04
5'-3' exoribonuclease 2	XRN2	NM_012255	—	3879467	chr20	+	21219705	21322172	1.04
fragile X mental retardation, autosomal homolog 1	FXR1	NM_001013438 // NM_001013439 // NM_005087	—	2654394	chr3	+	182113040	182179459	1.04
oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	OGDH	NM_001003941 // NM_002541	AKGDH // E1k // OGDC	2999948	chr7	+	44612716	44715181	1.04
KIAA1967	KIAA1967	NM_021174 // NM_199205	DBC-1 // DBC1	3089597	chr8	+	22518038	22534618	1.04
C-type lectin domain family 5, member A	CLEC5A	NM_013252	CLECSF5 // MDL-1 // MDL1 // MGC138304	3076868	chr7	–	141273626	141298905	1.04
exportin 4	XPO4	NM_022459	FLJ13046 // KIAA1721	3504434	chr13	–	20251014	20375187	1.04
RNA binding motif protein 6	RBM6	NM_005777	3G2 // DEF-3 // DEF3 // DKFZp686B0877 // FLJ36517 // HLC-11 // NY-LU-12 // g16	2622359	chr3	+	49942372	50089683	1.04
nucleotide binding protein 1 (MinD homolog, *E. coli*)	NUBP1	NM_002484	MGC117406 // MGC130052 // MGC130053 // NBP // NBP1	3647956	chr16	+	10729448	10771777	1.04
Yip1 domain family, member 3 // chromosome 6 open reading frame 154	YIPF3 // C6orf154	NM_015388 // NM_001012974	C6orf109 // DKFZP566C243 // FinGER3 // KLIP1 // dJ337H4.3 // FLJ44836 // MGC131686 // dJ337H4.2	2954646	chr6	–	43587500	43592701	1.04

TABLE 5-continued

				Human Exon ST 1.0 Transcript	Human Genome hg18				Fold Change/
Gene Name	Gene Symbol	Accession	Synonym	Cluster ID	Chromosome	Strand	Start	Stop	nM
chromosome 6 open reading frame 94 // LTV1 homolog (*S. cerevisiae*)	C6orf94 // LTV1	XM_928657 // XM_941265 // NM_032860	dJ468K18.5 // C6orf93 // FLJ14909 // dJ468K18.4	2929036	chr6	+	144194149	144227146	1.04
intercellular adhesion molecule 1 (CD54), human rhinovirus receptor	ICAM1	NM_000201	BB2 // CD54 // P3.58	3820443	chr19	+	10242765	10258289	1.04
KIAA0368	KIAA0368	XM_001129450 // XM_001131778 // NM_001080398	ECM29 // FLJ22036 // KIAA1962 // RP11-	3220513	chr9	−	113131941	113286475	1.04
CD3d molecule, delta (CD3-TCR complex)	CD3D	NM_000732 // NM_001040651	CD3-DELTA // T3D	3393744	chr11	−	117698596	117718659	1.04
translocase of outer mitochondrial membrane 70 homolog A (*S. cerevisiae*)	TOMM70A	NM_014820	FLJ90470	2686371	chr3	−	101565001	101614635	1.04
natural killer-tumor recognition sequence	NKTR	NM_001012651 // NM_005385	DKFZp686F1754 // DKFZp686G0426 // DKFZp686J06106 // DKFZp686N24126	2619344	chr3	+	42617105	42678166	1.04
nucleolar protein 9	NOL9	NM_024654	FLJ23323 // MGC131821 // MGC138483	2394784	chr1	−	6504004	6537329	1.04
proteasome (prosome, macropain) 26S subunit, ATPase, 4	PSMC4	NM_006503 // NM_153001	MGC13687 // MGC23214 // MGC8570 // MIP224 // S6 //	3833291	chr19	+	45168772	45179181	1.04

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<210> SEQ ID NO 11
<211> LENGTH: 28
<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 11

ttgctagacg actgttttcc aactccag                                         28


<210> SEQ ID NO 12
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<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

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<210> SEQ ID NO 13
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<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 13

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<210> SEQ ID NO 14
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<212> TYPE: DNA
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<220> FEATURE:
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<210> SEQ ID NO 15
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<212> TYPE: DNA
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<210> SEQ ID NO 16
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 16

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<210> SEQ ID NO 17
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<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 17

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<210> SEQ ID NO 18
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 18

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<210> SEQ ID NO 19
<211> LENGTH: 23
<212> TYPE: DNA
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<220> FEATURE:
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<210> SEQ ID NO 20
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<400> SEQUENCE: 20

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<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 21

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<210> SEQ ID NO 22
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<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 22

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<210> SEQ ID NO 23
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 23

cctgcttgaa gattacataa ctttttgt 28

<210> SEQ ID NO 24
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 24

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<210> SEQ ID NO 25
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<212> TYPE: DNA
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<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial
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<400> SEQUENCE: 26

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<210> SEQ ID NO 27
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<213> ORGANISM: Artificial
<220> FEATURE:
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<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 28

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<220> FEATURE:
<223> OTHER INFORMATION: primer

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<210> SEQ ID NO 30
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 30

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<210> SEQ ID NO 31
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 31

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<210> SEQ ID NO 32
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<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 32

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<210> SEQ ID NO 34
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 34

gagcagaagg aagcgtggtt                                                20


<210> SEQ ID NO 35
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 35

gacacatgaa tttccacaac agtaaa                                         26


<210> SEQ ID NO 36
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 36

acgtaatgac attttggtct gagtaact                                       28


<210> SEQ ID NO 37
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 37

aaatgctgct aaacatcctg gaa                                            23


<210> SEQ ID NO 38
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer
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<400> SEQUENCE: 38

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<210> SEQ ID NO 39
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 39

tcccttcttc tcaagactac tcagtatg                                     28


<210> SEQ ID NO 40
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 40

accttcttct cacaagactt tttaagc                                      27


<210> SEQ ID NO 41
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 41

ccttctcagc caccatggaa                                              20


<210> SEQ ID NO 42
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 42

ccaggtttcc cctgcagtt                                               19


<210> SEQ ID NO 43
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 43

ccccctgact tagtcctcgt t                                            21


<210> SEQ ID NO 44
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<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 44

cccactgcct tgatctagtt gat                                          23
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<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 45

gtcaagcaat ctatggccta cca                                              23


<210> SEQ ID NO 46
<211> LENGTH: 23
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 46

tgctgtgaga ataatgggtt gtg                                              23


<210> SEQ ID NO 47
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 47

ggctggctta ggagcttcac t                                                21


<210> SEQ ID NO 48
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 48

acctgcggtt cccactttat t                                                21


<210> SEQ ID NO 49
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 49

accactccaa atgtctaagg tcact                                            25


<210> SEQ ID NO 50
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 50

ggcctgatgg gtcttatcta tgg                                              23


<210> SEQ ID NO 51
<211> LENGTH: 23
<212> TYPE: DNA
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<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 51

ttagatggaa gctggctcaa gag                                               23


<210> SEQ ID NO 52
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 52

gaactttgcc tcattctttt gca                                               23


<210> SEQ ID NO 53
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 53

ctgagctcca gtctcttgta tttctg                                            26
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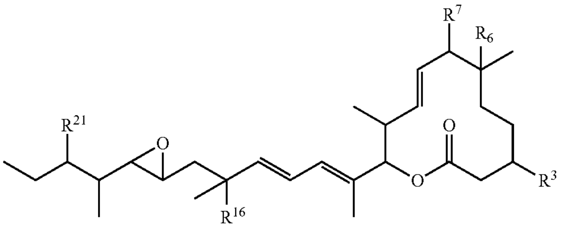
1. The method according to claim **18**, wherein the antitumor agent is a compound represented by formula (I), a pharmaceutically acceptable salt thereof, or a solvate of them:

(I)



wherein R^3, R^6, R^7 and R^{21}, the same or different, each represents

1) a hydroxyl group or an oxo group formed together with the carbon atom to which it is bound, provided that R^6 is limited to a hydroxyl group,
2) an optionally substituted C_{1-22} alkoxy group,
3) an optionally substituted unsaturated C_{2-22} alkoxy group,
4) an optionally substituted C_{7-22} aralkyloxy group,
5) an optionally substituted 5- to 14-membered heteroaralkyloxy group,
6) RCO—O— wherein R represents
    a) a hydrogen atom,
    b) an optionally substituted C_{1-22} alkyl group,
    c) an optionally substituted unsaturated C_{2-22} alkyl group,
    d) an optionally substituted C_{6-14} aryl group,
    e) an optionally substituted 5- to 14-membered heteroaryl group,
    f) an optionally substituted C_{7-22} aralkyl group,
    g) an optionally substituted 5- to 14-membered heteroaralkyl group,
    h) an optionally substituted C_{1-22} alkoxy group,
    i) an optionally substituted unsaturated C_{2-22} alkoxy group,
    j) an optionally substituted C_{6-14} aryloxy group or
    k) an optionally substituted 5- to 14-membered heteroaryloxy group,
7) $R^{S1}R^{S2}R^{S3}SiO$— wherein R^{S1}, R^{S2}, and R^{S3}, the same or different, each represents
    a) a C_{1-6} alkyl group or
    b) a C_{6-14} aryl group,
8) a halogen atom,
9) $R^{N1}R^{N2}N$—R^M— wherein R^M represents
    a) a single bond,
    b) —CO—O—,
    c) —SO_2—O—,
    d) —CS—O— or
    e) —CO—NR^{N3}— wherein R^{N3} represents a hydrogen atom or an optionally substituted C_{1-6} alkyl group, provided that each of the leftmost bond in b) to e) is bound to the nitrogen atom; and R^{N1} and R^{N2}, the same or different from each other and each represents
    a) a hydrogen atom,
    b) an optionally substituted C_{1-22} alkyl group,
    c) an optionally substituted unsaturated C_{2-22} alkyl group,
    d) an optionally substituted aliphatic C_{2-22} acyl group,
    e) an optionally substituted aromatic C_{7-15} acyl group,
    f) an optionally substituted C_{6-14} aryl group,

g) an optionally substituted 5- to 14-membered heteroaryl group,
h) an optionally substituted C_{7-22} aralkyl group,
i) an optionally substituted C_{1-22} alkylsulfonyl group,
j) an optionally substituted C_{6-14} arylsulfonyl group,
k) an optionally substituted 3- to 14-membered non-aromatic heterocyclic group formed by R^{N1} and R^{N2} together with the nitrogen atom to which R^{N1} and R^{N2} are bound, and the non-aromatic heterocyclic group optionally has substituent(s),
l) an optionally substituted 5- to 14-membered heteroaralkyl group,
m) an optionally substituted C_{3-14} cycloalkyl group or
n) an optionally substituted 3- to 14-membered non-aromatic heterocyclic group,

10) R^{N4} SO_2— wherein R^{N4} represents
a) an optionally substituted C_{1-22} alkyl group,
b) an optionally substituted C_{6-14} aryl group,
c) an optionally substituted C_{1-22} alkoxy group,
d) an optionally substituted unsaturated C_{2-22} alkoxy group,
e) an optionally substituted C_{6-14} aryloxy group,
f) an optionally substituted 5- to 14-membered heteroaryloxy group,
g) an optionally substituted C_{7-22} aralkyloxy group or
h) an optionally substituted 5- to 14-membered heteroaralkyloxy group,

11) $(R^{N5}O)_2PO$—O— wherein R^{N5} represents
a) an optionally substituted C_{1-22} alkyl group,
b) an optionally substituted unsaturated C_{2-22} alkyl group,
c) an optionally substituted C_{6-14} aryl group,
d) an optionally substituted 5- to 14-membered heteroaryl group,
e) an optionally substituted C_{7-22} aralkyl group or
f) an optionally substituted 5- to 14-membered heteroaralkyl group,

12) $(R^{N1}R^{N2}N)_2PO$—O— wherein R^{N1} and R^{N2} have the same meanings as defined above or

13) $(R^{N1}R^{N2}N)(R^{N5}O)PO$—O— wherein R^{N1}, R^{N2} and R^{N5} have the same meanings as defined above, provided that a compound in which R^3, R^6, R^7 and R^{21} are all hydroxyl groups, and a compound in which R^3, R^6 and R^{21} are all hydroxyl groups and R^7 is an acetoxy group are excluded,

R^{16} represents a hydrogen atom or hydroxyl group.

2. The method according to claim 1, wherein the antitumor agent is selected from the group consisting of:

(8E,12E,14E)-7-(N-(2-(N',N'-Dimethylamino)ethyl)-N-methylcarbamoyloxy)-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide;

(8E,12E,14E)-3,6,16,21-Tetrahydroxy-6,10,12,16,20-pentamethyl-7-((4-methylhomopiperazin-1-yl)carbonyl)oxy-18,19-epoxytricosa-8,12,14-trien-11-olide;

(8E,12E,14E)-3,6,16,21-Tetrahydroxy-6,10,12,16,20-pentamethyl-7-((4-methylpiperazin-1-yl)carbonyl)oxy-18,19-epoxytricosa-8,12,14-trien-11-olide;

(8E,12E,14E)-7-((4-Butylpiperazin-1-yl)carbonyl)oxy-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide;

(8E,12E,14E)-7-((4-Ethylpiperazin-1-yl)carbonyl)oxy-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide;

(8E,12E,14E)-3,6,16,21-Tetrahydroxy-6,10,12,16,20-pentamethyl-7-((4-propylpiperazin-1-yl)carbonyl)oxy-18,19-epoxytricosa-8,12,14-trien-11-olide;

(8E,12E,14E)-7-((4-Cyclohexylpiperazin-1-yl)carbonyl)oxy-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide;

(8E,12E,14E)-7-((4-(Cyclopropylmethyl)piperazin-1-yl)carbonyl)oxy-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide;

(8E,12E,14E)-3,6,16,21-Tetrahydroxy-6,10,12,16,20-pentamethyl-7-((4-propylhomopiperazin-1-yl)carbonyl)oxy-18,19-epoxytricosa-8,12,14-trien-11-olide;

(8E,12E,14E)-7-((4-(Cyclopropylmethyl)homopiperazin-1-yl)carbonyl)oxy-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide;

(8E,12E,14E)-7-((4-Cyclopentylpiperazin-1-yl)carbonyl)oxy-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide;

(8E,12E,14E)-3,6,16,21-Tetrahydroxy-7-((4-isopropylpiperazin-1-yl)carbonyl)oxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide;

(8E,12E,14E)-7-((4-Cycloheptylpiperazin-1-yl)carbonyl)oxy-3,6,16,21-Tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide;

(8E,12E,14E)-7-(N-(2-(N',N'-Diethylamino)ethyl)-N-methylcarbamoyloxy)-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide;

(8E,12E,14E)-3,6,16,21-Tetrahydroxy-7-((4-isobutylhomopiperazin-1-yl)carbonyl)oxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide;

(8E,12E,14E)-7-((4-Ethylhomopiperazin-1-yl)carbonyl)oxy-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide;

(8E,12E,14E)-7-((4-Butylhomopiperazin-1-yl)carbonyl)oxy-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide;

(8E,12E,14E)-3,16,21-Trihydroxy-6-methoxy-6,10,12,16,20-pentamethyl-7-((4-methylpiperazin-1-yl)carbonyl)oxy-18,19-epoxytricosa-8,12,14-trien-11-olide;

(8E,12E,14E)-3,16,21-Trihydroxy-6-methoxy-6,10,12,16,20-pentamethyl-7-((4-(piperidin-1-yl)piperidin-1-yl)carbonyl)oxy-18,19-epoxytricosa-8,12,14-trien-11-olide;

(8E,12E,14E)-3,6,7,21-Tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide;

(8E,12E,14E)-7-((4-(2,2-Dimethylpropyl)homopiperazin-1-yl)carbonyl)oxy-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytricosa-8,12,14-trien-11-olide; and

(8E,12E,14E)-3,6,16-Trihydroxy-21-methoxy-6,10,12,16,20-pentamethyl-7-((4-methylpiperazin-1-yl)carbonyl)oxy-18,19-epoxytricosa-8,12,14-trien-11-olide.

3. The method according to claim 1, wherein the detection of splicing defect comprises the steps of:

(a) measuring the expression level of pre-mRNA before and after administration of the antitumor agent to a mammal;

(b) comparing, based on the expression level measured in (a), the expression level of pre-mRNA before and after administration of the antitumor agent to determine that the antitumor agent exerts an action to the mammal when the expression level of pre-mRNA after the administration increases.

4. The method according to claim **3**, wherein the pre-mRNA of which expression level is measured is pre-mRNA of at least one gene selected from the genes listed in Table 1, Table 2, Table 3, Table 4, and Table 5, or a homologous gene thereof.

5. The method according to claim **4**, wherein the gene(s) are selected from DNAJB1, BZW1, NUP54, RIOK3, CDKN1B, STK17B, EIF4A1, and ID1.

6. The method according to claim **3**, wherein in step (a), the expression level of pre-mRNA in samples obtained from a subject before and after administration of the antitumor agent is measured.

7. The method according to claim **6**, wherein the samples obtained from the subject are selected from hemocytes in peripheral blood, plasma, and serum.

8. A probe or primer for assaying an action of a compound represented by formula (I), a pharmaceutically acceptable salt thereof, or a solvate of them to a mammal, which consists of a polynucleotide capable of hybridizing with a polynucleotide consisting of a nucleotide sequence of at least one gene selected from the genes listed in Table 1, Table 2, Table 3, Table 4, and Table 5, and a homologous gene thereof, or a complementary sequence thereof.

9. The probe or primer according to claim **8**, which is capable of detecting a genomic intron region or a part thereof in a gene listed in Table 1, Table 2, Table 3, Table 4 and Table 5, or which is capable of detecting a polynucleotide lacking a part of a genomic exon region in a gene listed in Table 1, Table 2, Table 3, Table 4 and Table 5.

10. A reagent or kit for assaying an action of a compound represented by formula (I), a pharmaceutically acceptable salt thereof, or a solvate of them to a mammal, which comprises the probe or the primer according to claim **8**.

11. The method according to claim **1**, wherein the detection of splicing defect comprises the steps of:

(f) measuring the expression level of an abnormal protein before and after administration of the antitumor agent to a mammal;

(g) comparing, based on the expression level measured in (f), the expression level of the abnormal protein before and after administration of the antitumor agent to determine that the antitumor agent exerts an action to the mammal when the expression level of the abnormal protein after the administration increases.

12. The method according to claim **11**, wherein the abnormal protein of which expression level is measured is a protein consisting of amino acids encoded by a polynucleotide of at least one gene selected from the genes listed in Table 1 and Table 3, or a homologous gene thereof where splicing defect has been caused in the polynucleotide, or a protein consisting of amino acids encoded by a polynucleotide of at least one gene selected from the genes listed in Table 2, Table 4 and Table 5 or a homologous gene thereof where splicing defect has been caused in the polynucleotide.

13. The method according to claim **11**, wherein the abnormal protein of which expression level is measured is a protein consisting of amino acids encoded by a polynucleotide of at least one gene selected from DNAJB1, BZW1, NUP54, RIOK3, CDKN1B, STK17B, EIF4A1 and ID1 where splicing defect has been caused in the polynucleotide.

14. The method according to claim **11**, wherein in step (f), the expression level of the abnormal protein in the samples obtained from a subject before and after administration of the antitumor agent is measured.

15. The method according to claim **14**, wherein the samples obtained from the subject are selected from hemocytes in peripheral blood, plasma, and serum.

16. An antibody against an abnormal protein consisting of amino acids encoded by a polynucleotide of at least one gene selected from the genes listed in Table 1, Table 2, Table 3, Table 4 and Table 5 where splicing defect has been caused in the polynucleotide, or a fragment thereof.

17. A reagent or kit for assaying an action of a compound represented by formula (I), a pharmaceutically acceptable salt thereof, or a solvate of them to a mammal, comprising the antibody or the fragment thereof according to claim **16**.

18. A method for assaying an action of an antitumor agent to a mammal, which comprises detecting splicing defect caused by the antitumor agent.

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专利名称(译)	以剪接缺陷为指标测定抗肿瘤剂作用的方法		
公开(公告)号	US20100021918A1	公开(公告)日	2010-01-28
申请号	US12/529959	申请日	2008-03-05
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IPC分类号	C12Q1/68 C07H21/04 G01N33/53 C07K16/00		
CPC分类号	C12Q1/6883 G01N33/68 G01N33/5011		
优先权	60/904774 2007-03-05 US 60/960403 2007-09-28 US		
外部链接	Espacenet USPTO		

摘要(译)

本发明的一个目的是提供用于测定pla二烯内酯衍生物对活体的作用的方法，探针，引物，抗体，试剂和试剂盒。根据本发明，提供了一种使用剪接缺陷作为指标来测定pladienolide衍生物的作用的方法。

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