



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**(75) Inventors: **Yoshiharu Mizui**, Ibaraki-Ken (JP);
Naoko Hata, Ibaraki-ken (JP);
Masao Iwata, Ibaraki-Ken (JP);
Koji Sagane, Ibaraki-Ken (JP); **Mai**
Uesugi, Ibaraki-Ken (JP); **Tadashi**
Kadowaki, Ibaraki-Ken (JP); **Taku**
Yoshida, Ibaraki-Ken (JP)

Correspondence Address:

FISH & RICHARDSON P.C.**P.O. BOX 1022****MINNEAPOLIS, MN 55440-1022 (US)**(73) Assignee: **Eisai R&D Management Co.,
Ltd.**, Tokyo-To (JP)(21) Appl. No.: **12/529,959**(22) PCT Filed: **Mar. 5, 2008**(86) PCT No.: **PCT/JP2008/053977**

§ 371 (c)(1),

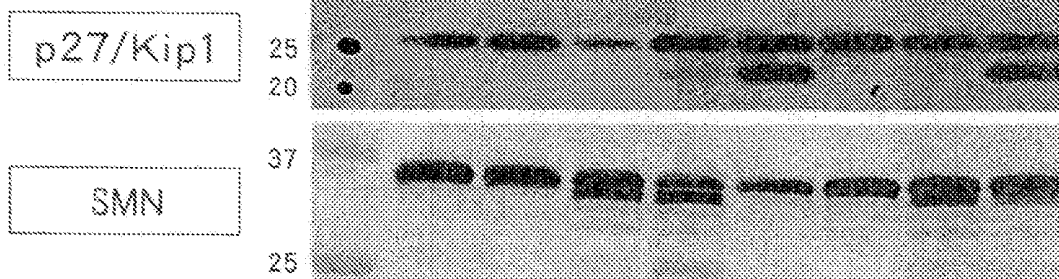
(2), (4) Date: **Sep. 4, 2009****Related U.S. Application Data**(60) Provisional application No. 60/904,774, filed on Mar.
5, 2007, provisional application No. 60/960,403, filed
on Sep. 28, 2007.**Publication Classification**(51) **Int. Cl.****C12Q 1/68** (2006.01)**C07H 21/04** (2006.01)**G01N 33/53** (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.

PLADIENOLIDE B

E7107

NONE 1 10 25 100 1 10 100 (nM)



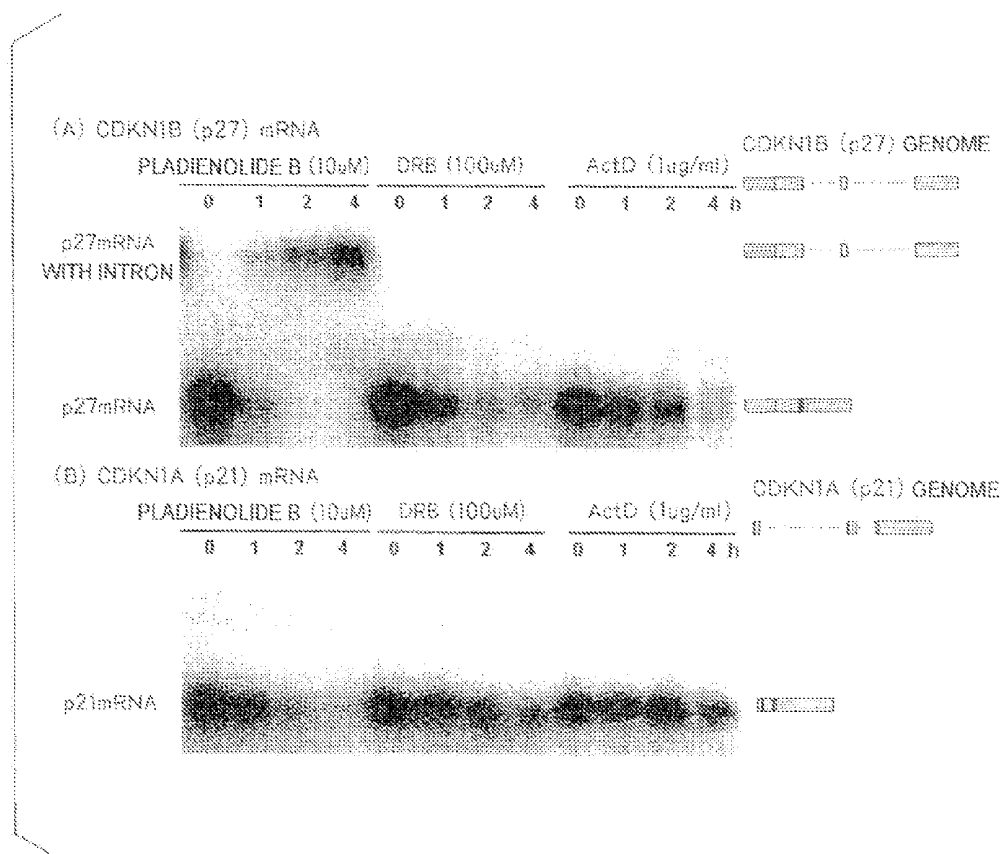


FIG. 1

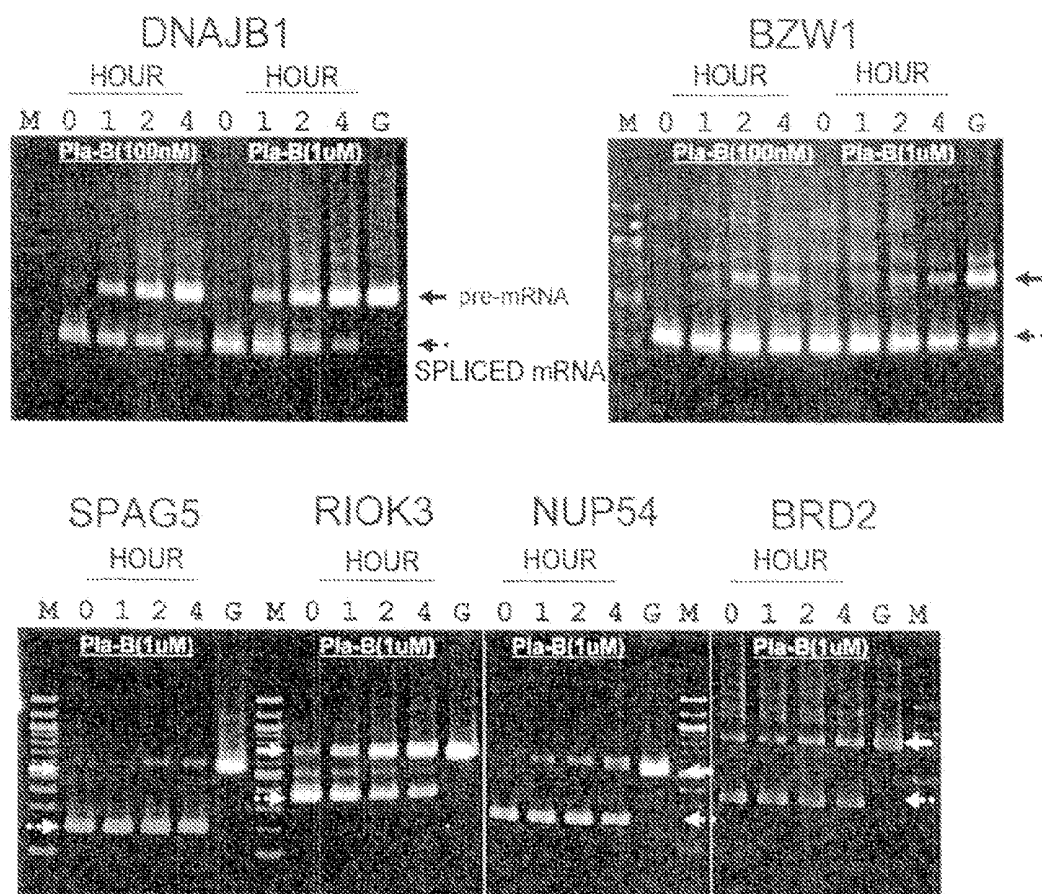
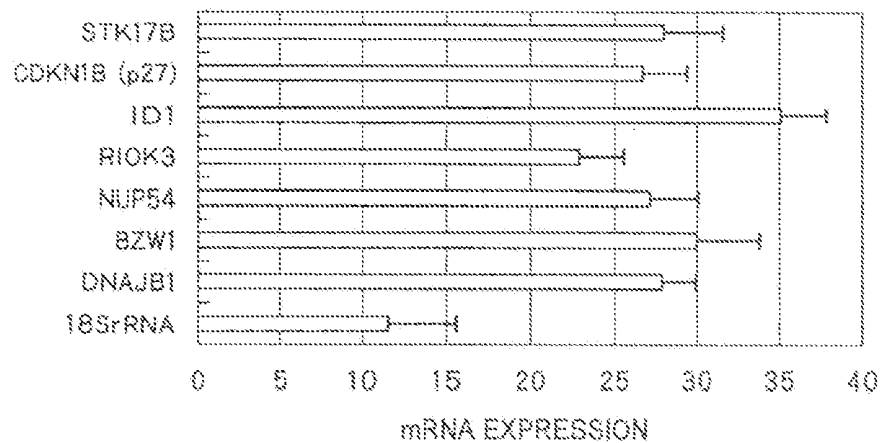


FIG. 2

(A)



(B)

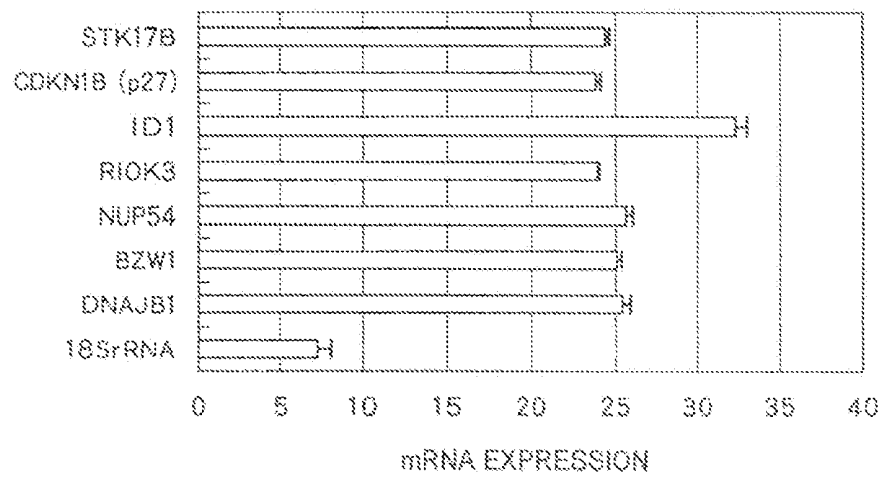


FIG. 3

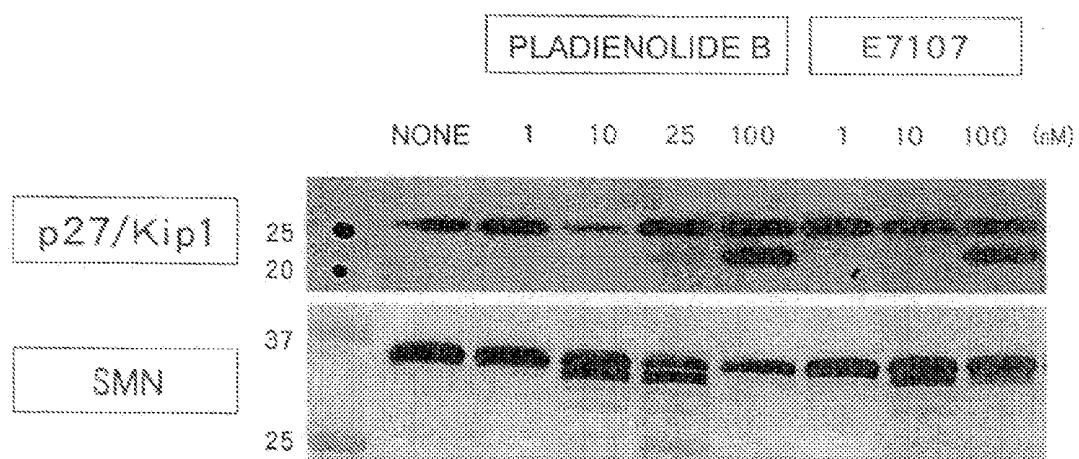


FIG. 4

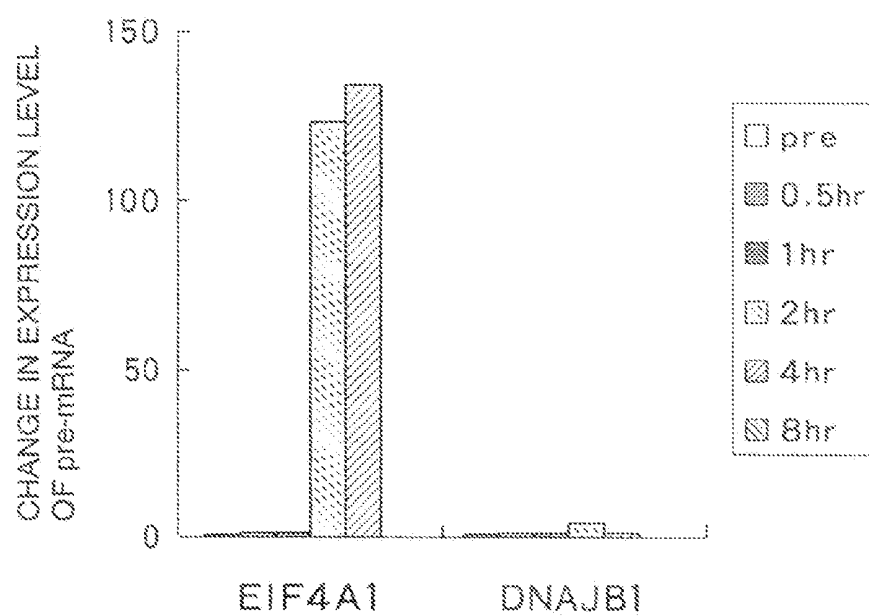


FIG. 5

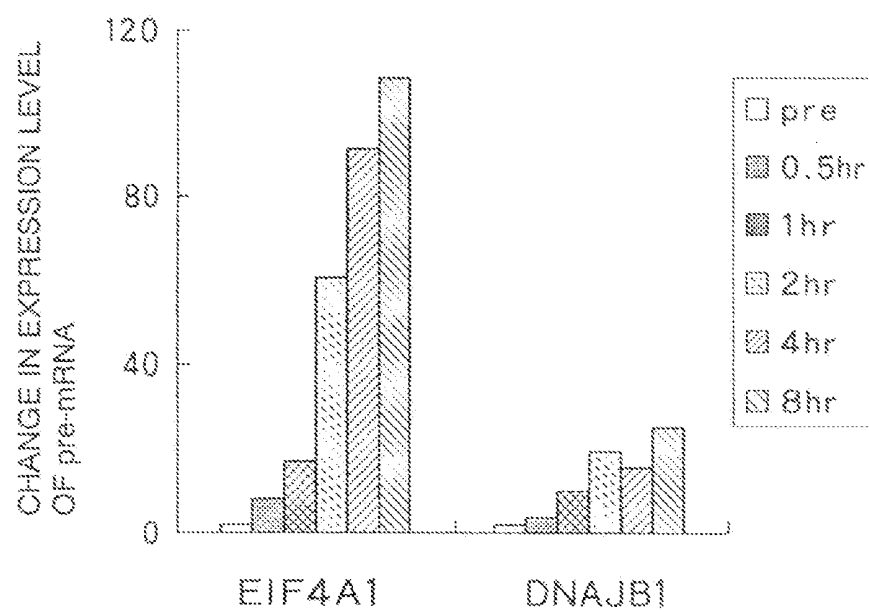


FIG. 6

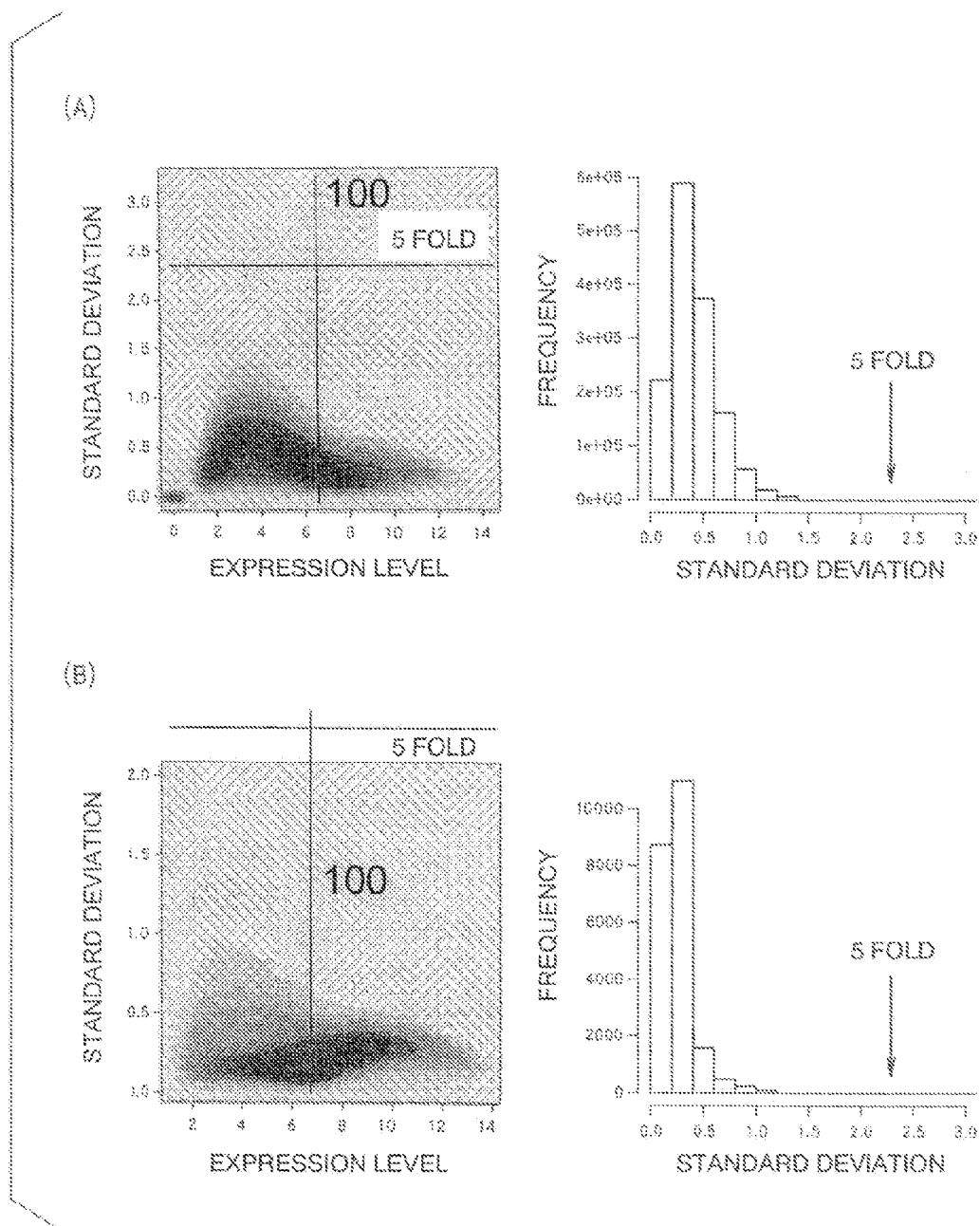


FIG. 7

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).

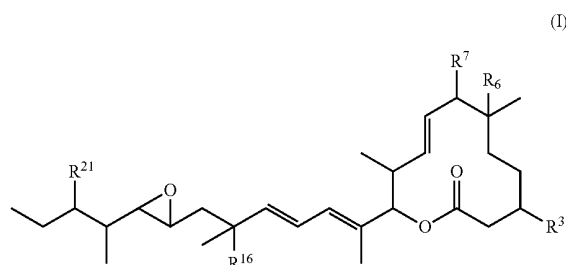
SUMMARY OF THE INVENTION

[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:



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] 1) 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 C₂₋₂₂ alkoxy group,

[0044] e) an optionally substituted C₆₋₁₄ aryloxy group,

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

[0046] g) an optionally substituted C₇₋₂₂ 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 C₁₋₂₂ alkyl group,

[0049] b) an optionally substituted unsaturated C₂₋₂₂ alkyl group,

[0050] c) an optionally substituted C₆₋₁₄ aryl group,

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

[0052] e) an optionally substituted C₇₋₂₂ 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 R³, R⁶, R⁷ and R²¹ are all hydroxyl groups, and a compound in which R³, R⁶ and R²¹ are all hydroxyl groups and R⁷ is an acetoxy group are excluded,

[0054] R¹⁵ 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-epoxytriosa-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)carbonyloxy)-18,19-epoxytriosa-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)carbonyloxy)-18,19-epoxytriosa-8,12,14-trien-11-olide;

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

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

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

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

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

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

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

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

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

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

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

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

[0075] (8E,12E,14E)-7-((4-(2,2-Dimethylpropyl)homopiperazin-1-yl)carbonyloxy)-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytriosa-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)carbonyloxy)-18,19-epoxytriosa-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 administered. 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-butylnyl group, 2-butylnyl group, 3-butylnyl group, 1-ethynyl-2-propynyl group, 2-methyl-3-butylnyl group, 1-pentylnyl 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-butylnyl group, 2-butylnyl group, 3-butylnyl 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, indolizynyl group, purinyl group, indazolyl group, quinolyl group, isoquinolyl group, quinolizynyl 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 pyrazolopyrimidinyl group; sulfur-containing aromatic heterocyclic groups such as thienyl group and benzothieryl 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, isoxazolyl group, benzoxazolyl group, oxadiazolyl group, pyrazolooxazolyl group, imidazothiazolyl group, thienofuranyl group, furopyrryl 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, azetidynyl group,

pyrrolidinyl group, pyrrolyl group, piperidinyl group, piperazinyl group, homopiperidinyl group, homopiperazinyl group, imidazolyl group, pyrazolidyl group, imidazolidyl group, morpholyl group, thiomorpholyl group, imidazoliny group, oxazoliny 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 “C₇₋₂₂ aralkyl group” used in the specification of the present application means a group corresponding to the above-defined “C₁₋₂₂ alkyl group” of which substitutable moiety is replaced by the above-defined “C₆₋₁₄ 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 “C₁₋₂₂ 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 “C₃₋₁₄ 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 “C₄₋₉ cycloalkyl alkyl group” used in the specification of the present application means a group corresponding to the above-defined “C₁₋₂₂ alkyl group” of which substitutable moiety is replaced by the above-defined “C₃₋₁₄ 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 “C₁₋₂₂ alkoxy group” used in the specification of the present application means a group corresponding to the above-defined “C₁₋₂₂ 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-dimethylpropyloxy 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-dimethylbutoxy group, 1,3-dimethylbutoxy group, 2-ethylbutoxy group, 2-methylpentyloxy 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 C₂₋₂₂ alkoxy group” used in the specification of the present application means a group corresponding to the above-defined “unsaturated C₂₋₂₂ 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-pentyloxy group, 1-hexenyloxy group, 1,3-hexadienyloxy group, 1,5-hexadienyloxy group, propargyloxy group and 2-butyloxy group; and preferred examples include allyloxy group, propargyloxy group and 2-butyloxy group.

[0102] The “C₆₋₁₄ aryloxy group” used in the specification of the present application means a group corresponding to the above-defined “C₆₋₁₄ 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, indacenenyloxy 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 “C₇₋₂₂ aralkyloxy group” used in the specification of the present application means a group corresponding to the above-defined “C₇₋₂₂ 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 pyridylmethyloxy 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, quinolizinyloxy group, phthalazyloxy group, naphthyridinyloxy group, quinoxalyloxy group, quinazolinolyloxy group, cinnolinyloxy group, pteridinyloxy group, imidazotriazinyloxy group, pyrazinopyridazinyloxy group, acridinyloxy group, phenanthridinyloxy group, carbazolyloxy group, carbazolinolyloxy group, perimidinyloxy group, phenanthrolinyloxy group, phenazinyloxy group, imidazopyridinyloxy group, imidazopyrimidinyloxy group, pyrazolopyridinyloxy group, pyrazolopyrimidinyloxy group, thienyloxy group, ben-

zothienyloxy group, furyloxy group, pyraniloxy group, cyclopentapyraniloxy 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 pyrazolyloxy 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 acetoxyl group, propionyloxy group and acryloxy group; and preferred examples include acetoxyl group and propionyloxy group.

[0111] The “ C_{2-22} alkoxy carbonyl 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} alkoxy carbonyl 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 vinylloxycarbonyl group, allyloxycarbonyl group, 1-propenyloxycarbonyl group, isopropenyloxycarbonyl group, propargyloxycarbonyl group and 2-butyntyloxycarbonyl 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) an 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, iso-propenyl group, ethynyl group, 1-propynyl group, 2-propynyl group, 1-butylnyl group, 2-butylnyl group and 3-butylnyl 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, imidazolyl group, oxazolyl 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-butyloxy group and 2-butyloxy group),

(18) a C_{6-14} aryloxy group (for example, phenoxy 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, acetoxyl 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, vinyloxy carbonyl group, allyloxy carbonyl group, 1-propenyloxy carbonyl group, 2-propenyloxy carbonyl group, isopropenyloxy carbonyl group, propargyloxy carbonyl group and 2-butyloxy carbonyl 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 above-mentioned (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 expedient 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, hydroiodic 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 2nd 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 2nd 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 lymph 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 adminis-

trated 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 μ M of pladienolide B, 100 μ M of DRB, or 1 μ g/mL of Actinomycin D for 0, 1, 2, and 4 hours. Subsequently, total RNA was obtained using RNeasy mini kit (Qiagen) and absorbance at 260 nm was measured to quantify an amount of RNA. Each total RNA sample (10 μ g) 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.

Primers for CDKN1B

P27-1F:

5'-ATGTCAAACGTGCGAGTGCTAAC-3' (SEQ ID NO: 1)

P27-2:

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

Primers for CDKN1A

P21-1F:

5'-GCCATGTCTAGAACCGGCTGGGGAT-3' (SEQ ID NO: 3)

P21-2:

5'-TTAGGGCTTCCTCTTGAGAAGAT-3' (SEQ ID NO: 4)

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 $\times$ SSC and 0.05% SDS, followed by a buffer containing 0.1 $\times$ 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. 1A 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 μ M 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, 10 μ M of pladienolide B and without the treatment, using μ MACS 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 μ g 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 μ M 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 μ M of pladienolide B and without the treatment was obtained using Big-Dye 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' - GAACCAAAATCACTTTCCCAAGGAAGGAG-3'

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

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

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

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

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

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

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

Total RNA was collected from HeLa cells treated with 100 nM or 1 μ M 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-epoxytriosa-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-epoxytriosa-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-epoxytriosa-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 μ g 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 deter-

mine 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

Gene Name	Gene Symbol	Accession	Synonym	Human Exon 1.0 ST					Fold Change
				Array	Chromosome	Strand	Start	Stop	
sprouty-related, EVH1 domain containing 2 WD repeat domain 73 muscleblind-like 2 (<i>Drosophila</i>)	SPRED2	NM_181784	FLJ12897 // FLJ131917 // MGC163164 // Sprad-2	2556752	chr2	-	65391279	65513247	31.56
	WDR73	NM_032856	FLJ14888 // HSPC264	3636956	chr15	-	82987018	82998719	30.61
	MBNL2	NM_144778 // NM_207304	DKFZp781H1296 // MBLL // MBLL39 // MGC120625 // MGC120626 //	3497586	chr13	+	96672563	96844371	28.86
	BXDC2	NM_018321	MGC120628 // PRO2032						
brix domain containing 2 development and differentiation enhancing factor 2	DDEF2	NM_003887	BRX // FLJ11100 AMAP2 // FLJ42910 // KIAA0400 // PAG3 // PAP // Pap-alpha // SHAG1	2806231 2468811	chr5 chr2	+	34951248 9264345	34962845 9463243	25.94 22.92
	ITGB1	NM_002211 // NM_033667 // NM_033668 //	CD29 // FNRR // GPIIA // MDF2 // MSK12 // VLAB	3284186	chr10	-	33211051	33321367	21.48
	EIF2C2	NM_012154	AGO2 // MGC3183 // Q10	3156193	chr8	-	141599440	141726037	21.33
	C10orf18	XM_374765	DKFZp781E1986 //	3233322	chr10	+	5766851	5846629	19.86
KIAA0174 discoilin, CUB and LCCL domain containing 2 ubiquitin protein ligase E3A (human papilloma virus E8- associated protein, Angelman syndrome) isopentenyl-diphosphate delta isomerase 1 chromosome 6 open reading frame 166 pumilio homolog 2 (<i>Drosophila</i>)	KIAA0174	NM_014761	FLJ20360 // BA318E3.2	3667766	chr16	+	70481983	70522196	19.65
	DCBLD2	NM_080927	MGC117220	2686023	chr3	-	99997526	100124598	19.52
	UBE3A	NM_000462 // NM_130838 // NM_130839	ANCR // AS // E8-AP // EPV66AP // FLJ26981 // HPV8A	3614087	chr15	-	23006655	23355108	19.35
	ID11	NM_004508	IPP1 // IPP11	3273601	chr10	-	1075869	1092634	19.25
suppressor of var1, 3-like 1 (<i>S. cerevisiae</i>) forkhead box K2 WW domain containing adaptor with coiled-coil	C6orf166	NM_018064	FLJ10342 // dJ486L4.2	2963784	chr6	-	88441297	88476721	19.23
	PUM2	NM_015317	FLJ36528 // KIAA0235 // MGC138251 // MGC136253 // PUMH2 // PUM12	2542816	chr2	-	20291440	20450197	19.01
	SUPV3L1	NM_003171	SUV3	3250204	chr10	+	70609946	70638996	18.81
	FOXK2	NM_004514	ILF // ILF-1 // ILF1	3738969	chr17	+	78070883	78195807	18.79
LTV1 homolog (<i>S. cerevisiae</i>) CDC20 cell division cycle 20 homolog (<i>S. cerevisiae</i>) TAR DNA binding protein fetal Alzheimer antigen villin 2 (ezrin)	WAC	NM_016628 // NM_100264 // NM_100486	BM-016 // MGC10753 // PRO1741 // Wwp4 // bA48B24 // bA48B24.1 C6orf93 // FLJ14909 //	3240340	chr10	+	28828043	29005095	18.53
	LTV1	NM_032860	dJ468K18.4	2929036	chr6	+	144194149	144227146	18.37
	CDC20	NM_001255	CDC20A // MGC102824 //	2333136	chr1	+	43597180	43601431	18.22
	TARDBP	NM_007375	bA276H19.3 // p55CDC						
BPTF	BPTF	NM_004459 // NM_182641	TDP-43	2370048	chr1	+	10995025	11013170	18.13
	VIL2	NM_003379	FAC1 // FAIZ // NURF301 CVIL // CVL //	3732448 2981912	chr17 chr6	+	63252111 159106770	63410954 159160432	17.61 17.50

TABLE 1-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon 1.0 ST					Fold Change
				Array	Chromosome	Strand	Start	Stop	
sorting nexin 19	SNX19	NM_014758	DKFZp762H157 //						
			FLJ26216 // MGC1584						
Cdk5 and Abl enzyme substrate 1	CABLES1	NM_138375	CHET8 // DKFZp667I205	3398482	chr11	-	130250320	130291615	17.12
			// KIAA0254						
SMAD specific E3 ubiquitin protein ligase 2	SMURF2	NM_022739	FLJ35924 // HsT2563	3781531	chr18	+	18940699	19101596	16.94
soluble carrier family 2 (facilitated glucose transporter), member 1	SLC2A1	NM_006516	DKFZp686F0270 //	3766980	chr17	-	59968891	60088896	16.60
			MGC138150						
v-raf-1 murine leukemia viral oncogene homolog 1	RAF1	NM_022490	GLUT // GLUT1 //	2409104	chr1	-	43124794	43338329	16.44
			MGC141895 // MGC141896						
chromosome 16 open reading frame 80	C16orf80	NM_013242	CRAF // Raf-1 // c-Raf	2663244	chr3	-	12600117	12680654	16.41
eukaryotic translation initiation factor 4A, isoform 1	EIF4A1	NM_001416	EVORF // GIL3	3693511	chr16	-	56683698	56739201	16.25
testis derived transcript (3 LIM domains)	TES	NM_015641 // NM_152829	DDX2A // EIF-4A // EIF4A	3708826	chr17	+	7416768	7423040	16.15
ring finger protein 40	RNF40	NM_014771	DKFZp586B2022 //	3020192	chr7	+	115637811	115743800	15.95
			MGC1146 // TESS //						
squamous cell carcinoma antigen recognised by T cells 3	SART3	NM_014706	TESS-2 // TESTIN	3856555	chr16	+	30681120	30695182	15.84
			BRE1B // DKFZp686K191						
heat shock 105 kDa/110 kDa protein 1	HSPH1	NM_006644	// KIAA0661 // MGC13051	3470253	chr12	-	107440140	107479296	15.13
			// RBP95 // STARING						
kelch-like 18 (<i>Drosophila</i>) myosin 1E	KLHL18	NM_025010	KIAA00156 // MGC138188	3508330	chr13	-	30558258	30651695	15.12
			// RP11-13G14 // TIP110						
LIM domain 7	LMO7	NM_005358	// p110(nrb)						
			DKFZp686M05240 //						
ring finger and SPRY domain containing 1	RSPRY1	NM_133368	HSP105 // HSP105A //	2621275	chr3	+	47298888	47367590	15.00
			HSP105B // KIAA0201 //	3626828	chr15	-	57215720	57452363	14.49
centromere protein L	CENPL	NM_033319	NY-CO-25	3494137	chr13	+	75092571	75586974	14.34
			FLJ13703 // KIAA0795	3662612	chr16	+	55777703	55831882	14.32
Smey homolog, X-linked (mouse)	JARID1C	NM_004187	HumeM-1C // MGC104638	3145020	chr8	-	95569109	95634851	14.19
			// MYO1C						
guanine nucleotide binding protein-like 3 (nucleolar)	GNL3	NM_014366 // NM_206825	FBX20 // FBXO20 //						
			KIAA0858 // LOMP						
protein-like 3 (nucleolar)	GNL3	NM_014366 // NM_206825	KIAA1972						
protein-like 3 (nucleolar)	GNL3	NM_014366 // NM_206825	DKFZp434I116 //						
			DKFZp781B2117 //						
protein-like 3 (nucleolar)	GNL3	NM_014366 // NM_206825	MGC136493 // MGC141940						
			// MSTP054						
protein-like 3 (nucleolar)	GNL3	NM_014366 // NM_206825	C1orf155 // CENP-L //	2444451	chr1	-	172035313	172104622	14.13
			FLJ31044 // RP3-383J4.1						
protein-like 3 (nucleolar)	GNL3	NM_014366 // NM_206825	// d383J4.3						
			DXS1272E // MRXJ //						
protein-like 3 (nucleolar)	GNL3	NM_014366 // NM_206825	MRXSJ // SMCX //	4009062	chrX	-	53159032	53271329	14.09
			C77032 // E2IG3 //						
protein-like 3 (nucleolar)	GNL3	NM_014366 // NM_206825	MGC800 // NS	2624074	chr3	+	52694976	52705212	14.08

TABLE 1-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon 1.0 ST					Fold Change
				Array	Chromosome	Strand	Start	Stop	
RIO kinase 3 (yeast) interleukin enhancer binding factor 2, 45 kDa	RIOK3 ILF2	NM_003831 // NM_145906 NM_004515	DKFZp79L1370 // SUDD MGC8391 // NE45 // PRO3063	3781654 2436132	chr18 chr1	+	19161035 151900372	19320545 151910103	13.67 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 GP110 // MGC29536 // Rpn13	3194635	chr9	+	138810077	138855460	13.66
adhesion regulating molecule 1	ADRM1	NM_007002	216L13.9 // bA216L13.7	3892607	chr20	+	60305485	60317305	13.51
keratin 18	KRT18	NM_000224	CSA // GRP75 // HSPA9B	3415576	chr12	+	51596769	51632949	13.41
heat shock 70 kDa protein 9B (mortalin-2)	HSPA9	NM_004134	// 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 (<i>Drosophila</i>)	SMAD3	NM_005902	DKFZp586N0721 // DKFZp686I10186 // 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 // ST3GAL1A.1 // ST3O	3154398	chr8	-	134535811	134653449	12.77
WD repeat domain 74 cyclin D1	WDR74 CCND1	NM_018093 NM_053058	FLJ10439 // FLJ21730 BCL1 // D115287E // PRAD1 // U21B31	3376235 3338192	chr11 chr11	- +	62358627 69161881	62365857 69178408	12.70 12.66
nucleoporin like 1	NUPL1	NM_014089 // NM_001008564 //	KIAA0410 // PRO2463	3482219	chr13	+	24773258	24822202	12.63
WDR45-like ubiquitin specific peptidase 47	WDR45L USP47	NM_01008565 NM_019613 NM_017944	WIPI-3 // WIPI3 DKFZp686C13257 // FLJ20727 // TRFP	3775157 3320604	chr17 chr11	- +	78185748 11819556	78199803 11937446	12.59 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 // SAM2	2491615	chr2	+	85597809	85625908	12.29

TABLE 1-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon 1.0 ST					Human Genome hg18		
				Array	Chromosome	Strand	Start	Stop	Fold Change		
WEE1 homolog (<i>S. pombe</i>)	WEE1	NM_003390	DKFZp686I18166 // FLJ16446 // WEE1hu	3319937	chr11	+	9550916	9579143	12.26		
GTP binding protein 4	GTPBP4	NM_012341	CREFG // 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	ATP1B1	NM_001677 // NM_001001787	ATP1B // MGC1798	2366422	chr1	+	167342204	167368946	12.11		
ADP-ribosylation factor interacting protein 2 (arlapin 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 // Hsp1 // 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 // FIG21 // 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 // YTS21 // YTS21-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-epoxytricoso-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 μ l 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-epoxytricoso-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/ μ l 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 Biosys-

tems) 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 rRNA 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-epoxytricoso-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'-GGCCTGATGGGTCTTATCATATGG-3'
Antisense:	5'-TTAGATGGAAGCTGGCTCAAGAG-3'
BZW1:	(SEQ ID NO: 20)
Sense:	5'-GAACTTTGCCTCATTCTTTTGCA-3'
Antisense:	5'-CTGAGCTCCAGTCTCTGTATTTCTG-3'
NUP54:	(SEQ ID NO: 22)
Sense:	5'-CAAGGTAACCACTTCTAAGACCATAATTC-3'
Antisense:	5'-CCTGCTGAAGATTACATAACTTTTGT-3'
RIOK3:	(SEQ ID NO: 24)
Sense:	5'-TCAATGGAGATAGCAAAGGTATTATAACC-3'
Antisense:	5'-AGATTACTTAGGAGCACATTATGAGTGT-3'
CDKN1B (p27):	(SEQ ID NO: 26)
Sense:	5'-ATGTTTATCAACGGTCCGGCT-3'
Antisense:	5'-CATCCCCAGTGGCTTTTAAGG-3'
STK17B:	(SEQ ID NO: 28)
Sense:	5'-TGCGCGGAGACAGCATAG-3'
Antisense:	5'-TGGGTTCAAAATGCCAGGT-3'
ADRM1:	(SEQ ID NO: 30)
Sense:	5'-GGCCCTTCAGAAATGCTTGTC-3'
Antisense:	5'-CCCATTACACAATTATGTGCTTAG-3'

-continued		-continued	
EIF4A1:	(SEQ ID NO: 32)	Antisense:	5'-CCTTCTCAGCCACCATGGAA-3' (SEQ ID NO: 41)
Sense:	5'-CAGATCATCTAGAAGCAGCTGGTT-3'	KLHL18:	(SEQ ID NO: 42)
	(SEQ ID NO: 33)	Sense:	5'-CCAGGTTTCCCTGCAGTT-3'
Antisense:	5'-ACAGAATCTGGTGCCTACTAACAAA-3'		(SEQ ID NO: 43)
FOXK2:	(SEQ ID NO: 34)	Antisense:	5'-CCCCCTGACTTAGTCCTCGTT-3'
Sense:	5'-GAGCAGAAGGAAGCGTGGTT-3'	VIL2:	(SEQ ID NO: 44)
	(SEQ ID NO: 35)	Sense:	5'-CCCCTGCCTTGATCTAGTTGAT-3'
Antisense:	5'-GACACATGAATTTCCACACAGTAAA-3'		(SEQ ID NO: 45)
GNB2L1:	(SEQ ID NO: 36)	Antisense:	5'-GTCAAGCAATCTATGGCTACCA-3'
Sense:	5'-ACGTAATGACATTTGGTCTGAGTAACT-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.	
Antisense:	5'-AAATGCTGCTAAACATCCTGGAA-3' (SEQ ID NO: 37)		

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 (<i>Drosophila</i>)	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

-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'-ACCTTCTTCTCACAAGACTTTTAAGC-3'

[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/ μ L and cDNA was synthesized by using High Capacity cDNA Reverse Transcription Kits (Applied Biosystems). A probe corresponding respectively to DNAB1, 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. 3A (Tempus Blood RNA Tube) and FIG. 3B (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 serve 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-epoxytriosa-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-epoxytriosa-8,12,14-trien-11-olide was examined by using cancer cells (HaLa). As a result, insertion of an 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 cm²), 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 μ m filter to remove insoluble matters and then combined with an equal

amount of 2 $\times$ 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 μ L 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-epoxytriosa-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-epoxytriosa-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 mm³, the mice were administered (8E,12E,14E)-7-((4-cycloheptylpiperazin-1-yl)carbonyl)oxy-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytriosa-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-epoxytricos-8,12,14-trien-11-olide, two mice per each time point were put down by euthanasia with CO₂. 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-epoxytricos-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'-GGCTGGCTTAGAGGCTTCACT-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-epoxytricos-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'-TTAGATGGAGCTGGCTCAAGAG-3' (SEQ ID NO: 51)

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

Antisense:
5'-CTGAGCTCCAGTCTCTTGATTCTG-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-epoxytricos-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

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Array	Human Genome hg18			
					Transcript Cluster ID	Chromosome	Strand	Fold Change
TSR1, 20S rRNA accumulation, translocase of inner mitochondrial membrane 23 homolog (yeast)	TSR1	NM_018128	FLJ10534 //	3740998	chr17	-	2172438	2187551
	TMM23	XM_001133798 //	MGC22767 //	3289031	chr10	-	51180787	51293382
pellino homolog 1 (<i>Drosophila</i>)	PELI1	NM_020651	PRO1197 // TIM23 //					
			TMM23B	2556302	chr2	-	64173290	64225291
chromosome 15 open reading frame 42	C15orf42	NM_152259	MGC50990	3607698	chr15	+	87857353	87975281
			FLJ41618 //					
RNA binding motif protein 26	RBM26	NM_022118	MGC45866	3519119	chr13	-	78783968	78878613
			C13orf10 //					
integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	ITGB1	NM_002211 //	FLJ20957 //					
			MGC133295 //					
ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)	ARFGEF1	NM_133376	MGC133296 //					
			PRO1777 // RP11- 255E21.1 // SE70-2	3284188	chr10	-	33211051	33321367
clathrin interactor 1	CLINT1	NM_014666	CD29 // FNRF2 //					
			GPIIA // MDF2 //					
CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase like 2	CTDSP2	NM_016396	MSK12 // VLAB					
			ARFGEEP1 // BIG1 //	3139035	chr8	-	68250009	68418446
WD repeat domain 73	WDRC73	NM_032856	D730028O18Rik //					
			DKEZP434L057 //					
zinc finger protein 317 // zinc finger protein 658	ZNF317 //	NM_020933 //	P200	2883609	chr5	-	157145339	157284818
	ZNF658	XM_001125688 //	CLINT // ENTH //					
integrin, alpha 6	ITGA6	NM_000210 //	EPN4 // EPNR //					
			EPSNR // KIAA0171	3591909	chr15	+	42506834	42607712
ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) muscleblind-like 2 (<i>Drosophila</i>)	UBE3A	NM_001079818	FLJ10523 //					
			HSPC058 //	3581386	chr14	-	104546975	104585458
			HSPC129	3636956	chr15	-	82987018	82998719
			FLJ20764 // HEPP //					
			MGC19517	3819880	chr19	+	9112073	9135082
			FLJ14888 //					
			HSPC264					
			KIAA1588 //					
			DKEZP572C163 //					
			FLJ32813 //					
			MGC35232	2515627	chr2	+	173000563	173079416
			CD49f // ITGA6B //					
			VLA-6	3614087	chr15	-	23006655	23355108
			ANCR // AS // E6- AP // EPVE6AP //					
			FLJ26981 // HPV E6A	3497586	chr13	+	96672563	96844371
			DKEZP781H1296 //					
			MBLL // MBLL39 //					
			MGC120625 //					

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	Stop
chromosome 6 open reading frame 166	C6orf166	NM_018064	MGC120626 // MGC120628 // PRO2032					
homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	HERPUD1	NM_001010989 // NM_001010990 // NM_014685	FLJ10342 // dI486L4.2		chr6	-	88441297	88476721
RAP1 interacting factor homolog (yeast)	RIF1	NM_018151	HERP // KIAA0025 // Mif1 // SUP		chr16	+	55523269	55552122
development and differentiation enhancing factor 2	DDEF2	NM_003887	DKFZ781N1478 // FLJ12870		chr2	+	151974674	152072768
cell division cycle 20 homolog (<i>S. cerevisiae</i>)	CDC20	NM_001255	AMAP2 // FLJ42910 // KIAA0400 // PAG3 // PAP // Pap-alpha // SHAG1		chr2	+	9264345	9463243
BMI1 polycomb ring finger oncogene	BMI1	NM_005180	CDC20A // MGC102824 // bA276H19.3 // p55CDC		chr1	+	43597180	43601431
golgi-specific brefeldin A resistance factor 1	GBF1	NM_004193	MGC12685 // PCGF4 // RNF51		chr10	+	22650103	22660820
strawberry notch homolog 1 (<i>Drosophila</i>)	SENO1	NM_018183	FLJ21263 // FLJ21500 // KIAA0248 // MGC134877 // MGC134878		chr10	+	103993260	104132642
protein phosphatase 4, regulatory subunit 2	PPP4R2	NM_174907	FLJ10701 // FLJ10833 // FLJ16176 // MOP3 // Sio		chr12	-	122342423	122435284
brix domain containing 2	BXDC2	NM_018321	MGC131930		chr3	+	73019849	73201035
far upstream element (FUSE) binding protein 1	FUBP1	NM_003902	BRX // FLJ11100		chr5	+	34951248	34962845
RAE1 RNA export 1 homolog (<i>S. pombe</i>)	RAE1	NM_001015885 // NM_003610	FBP // FUBP		chr1	-	78182330	78217881
CCHC-type zinc finger, nucleic acid binding protein	CNBP	NM_003418	FLJ30608 // MGC117333 // MGC126076 // MGC126077 // MIG14 // MRNP41 // Mmrp41 // dI481F12.3 // dI800J21.1		chr20	+	55359493	55386992
acyl-CoA synthetase long-chain family member 3	ACSL3	NM_004457 // NM_203372	CNBP1 // DM2 // PROMM // RNF163 // ZCCHC22 // ZNF9		chr3	-	130369369	130385467
			ACCS // EACL3 // PRO2194		chr2	+	223433916	223539136

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Array				Fold Change
				Transcript Cluster ID	Chromosome	Strand	Start	Stop
peptidase (mitochondrial processing) alpha	PMPCA	NM_015160	Alpha-MPP // INPPE // KIAA0123 // MGC104197	3194338	chr9	+	138424942	138438030
CGI-09 protein	CGI-09	NM_015939	MGC5029	3896524	chr20	-	5865881	5879370
baculoviral IAP repeat-containing 6 (apollon)	BIRC6	NM_016252	APOLLON // BRUCE // FLJ13726 // FLJ13786 //	2476219	chr2	+	32435095	32697447
BCI2/adenovirus E1B 19 kDa interacting protein 2	BNIP2	NM_004330	KIAA1289 BNIP-2 // NIP2	3627076	chr15	-	57742025	57768916
DEAD (Asp-Glu-Ala-Asp) box polypeptide 23	DDX23	NM_004818	MGC8416 // PRPF28 // U5-100K // ptp28	3453319	chr12	-	47509816	47532322
DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	DDX17	NM_006386 // NM_030881	DKEP761H2016 // P72 // RH70	3960629	chr22	-	37202800	37232288
SAPS domain family, member 3	SAPS3	NM_018312	C11orf23 // DKEP781E17107 // DKEP781E2374 // DKEP781O2362 //	3337618	chr11	+	67984785	68173381
PAK1 interacting protein 1 // chromosome 20 open reading frame 7	PAK1IP1 // C20orf7	NM_017906 // NM_001039375 // NM_024120	FLJ11058 // FLJ43065 // MGC125711 // MGC125712 // PP6R3 // SAP190 // SAPL // SAPL _a FLJ20624 // MAK11 // PIP1 // RP11- bA421M1.5 // WDR84 // bA421M1.5 // hPIP1 // FLJ22324 // MGC90272 // bA526K24.2 // dJ842G6.1 FLJ21897 // FLJ31917 // MGC163164 //	2894663	chr6	+	10799016	10817955
sprouty-related, EVH1 domain containing 2	SPRED2	NM_181784	dJ842G6.1 FLJ21897 // FLJ31917 // MGC163164 //	2556752	chr2	-	65391279	65513247
kelch-like 18 (<i>Drosophila</i>)	KLHL18	NM_025010	Spred-2 FLJ13703 // KIAA0795	2621275	chr3	+	47298888	47367590
suppressor of var1, 3-like 1 (<i>S. cerevisiae</i>) KIAA0174	SUPV3L1 KIAA0174	NM_003171 NM_014761	SUV3 MGC117220	3250204	chr10	+	70609946	70638996
flap structure-specific endonuclease 1	FEN1	NM_004111	FEN-1 // MF1 // RAD2	3667766 3333226	chr16 chr11	+	70481983 61312929	70522196 61350560
atrophin 1	ATN1	NM_001007026 // NM_001940	B37 // D12S755E // DRPLA // NOD	3403045	chr12	+	6903897	6921744
poliovirus receptor	PVR	NM_006505	CD155 // HVED // NECL5 // Necl-5 // PVS // TAGE4	3835645	chr19	+	49839030	49860075

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	Stop
KIAA0317	KIAA0317	NM_001039479	—	3572041	chr14	-	74189599	74249655
DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked brix domain containing 1	DDX3X	XM_001129278 //	DBX // DDX14 //	3974838	chrX	+	41055591	41108668
	BXDC1	NM_001356	DDX3 // HLP2	2921374	chr6	+	111409800	111408743
		NM_032194	FLJ21087 // RPF2 //					
			bA397G5.4					
actinin, alpha 1	ACTN1	NM_001102	FLJ40884	3569814	chr14	-	68409817	68515815
Rho guanine nucleotide exchange factor (GEF) 12	ARHGEF12	NM_015313	DKFZp698O2372 //	3352503	chr11	+	119711882	119896306
			KIAA0382 // LARG //					
			PRO2792					
KIAA0859	KIAA0859	NM_001007239 //	5630401D24Rik //	2367287	chr1	+	170017287	170053841
		NM_014955 //	CGI-01 // FLJ10310					
		NM_015935						
THO complex 5	THOC5	NM_001002877 //	C22orf19 // Fmip //	3956854	chr22	-	28224935	28280423
		NM_001002878 //	PK1.3					
		NM_001002879 //						
		NM_003678						
polo-like kinase 2 (<i>Drosophila</i>)	PLK2	NM_006622	SNK	2858023	chr5	-	57785572	57792624
forkhead box K2	FOXK2	XM_001134363 //	ILF // ILF-1 // ILF1	3738969	chr17	+	78070883	78195807
		XM_001134364 //						
		NM_004514						
calcium binding protein 39	CAB39	NM_016289	CGI-66 // FLJ22682	2531522	chr2	+	231285781	231394027
			// MO25					
ubiquitin specific peptidase 38	USP38	NM_032557	FLJ35970 //	2745499	chr4	+	144325529	144364549
			HP43.8KD //					
			KIAA1891					
SMAD specific E3 ubiquitin protein ligase 2	SMURF2	NM_022739	DKFZp686F0270 //	3766960	chr17	-	59968891	60088896
			MGC138150					
RIO kinase 3 (yeast)	RIOK3	NM_003831 //	DKFZp779L1370 //	3781654	chr18	+	19161035	19320545
		NM_145906	SUDD					
protein phosphatase 1, catalytic subunit, gamma isoform	PPP1CC	NM_002710	PPP1G	3471374	chr12	-	109642007	109665131
erbb2 interacting protein // caspase 6, apoptosis-related cysteine peptidase	ERBB2IP //	NM_001006600 //	ERBIN // LAP2 //	2812435	chr5	+	65258079	65451372
	CASP6	NM_018695 //	MCH2					
		NM_001226 //						
		NM_032992						
MK167 (FHA domain) interacting nucleolar phosphoprotein	MKI67IP	NM_032390	NIFK // Nopp34	2573786	chr2	-	122132489	122231052
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, Ctr9, Paf1/RNA polymerase II complex component, homolog (<i>S. cerevisiae</i>)	YWHAB	NM_003404 //	GW128 // HSI //	3886639	chr20	+	42927275	42970748
		NM_139323	KCIP-1					
methylinomethyl-2-thiouridylylate methyltransferase	CTR9 //	NM_014633 //	KIAA0155 // SH2BP1	3320301	chr11	+	10684027	10774985
	TRMU	NM_018006	// TSBP // p150 //					
			p150TSP //					
			MGC99627 // MTO2					
			// MTU1 // TRMT //					
			TRMT1 // TRNT1					

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	
karyopherin (importin) beta 1	KPNB1	NM_002265	IMB1 // IPOB // Impnb // MGC2155 // MGC2156 //	3724782	chr17	+	43082272	43117868
A kinase (PRKA) anchor protein 13	AKAP13	NM_006738 // NM_007200 // NM_144767	MGC2157 // NTF97 AKAP-Lbc // BRX // FLJ11952 // FLJ43341 // HA-3 // Hf31 // LBC //	3606304	chr15	+	83681343	84102785
nucleolar protein 9	NOL9	NM_024654	PROTO-LB // PROTO-LBC // c-lbc FLJ23323 // MGC131821 //	2394784	chr1	-	6504004	6537329
ADP-ribosylation factor-like 6 interacting protein 2	ARL6IP2	NM_022374	MGC138483 ARL3IP2 // ATL2 // FLJ23293 // atlastin2	2548776	chr2	-	38374621	38516141
pumilio homolog 2 (<i>Drosophila</i>)	PUM2	NM_015317	FLJ36528 // KIAA0235 // MGC138251 //	2542816	chr2	-	20291440	20450197
calmodulin 2 (phosphorylase kinase, delta)	CALM2	NM_001743	MGC138253 // PUMH2 // PUML2 CAMIL // PHKD //	2551924	chr2	-	47232159	47286178
nucleolar protein family A, member 1 (H/ACA small nucleolar RNPs)	NOLA1	NM_018983 // NM_032993	PHKD2 GARI	2739242	chr4	+	110956115	110965340
chromosome 6 open reading frame 94 // LTV1 homolog (<i>S. cerevisiae</i>)	C6orf94 // LTV1	XM_928657 // XM_941265 // NM_032860	dJ468K18.5 // C6orf93 // FLJ14909 // dJ468K18.4	2929036	chr6	+	144194149	144227146
PPAR binding protein	PPARBP	NM_004774	CRSP1 // CRSP200 // DRIP205 //	3755714	chr17	-	34801544	34861069
3-hydroxy-3-methylglutaryl-Coenzyme A reductase	HMGCR	NM_000859	DRIP230 // MED1 // MGC71488 // PBP // PPARGBP // RB18A // TRAP220 // TRIP2	2815965	chr5	+	74668800	74700136
15 kDa selenoprotein	15-Sep	NM_004261 // NM_203341	—	2421271	chr1	-	87100720	87153273
phosphatidylinositol binding clathrin assembly protein	PICALM	NM_001008660 // NM_007166	CALM // CLTH // LAP	3385175	chr11	-	85345353	85458481
proteasome (prosome, macropain) 26S subunit, non-ATPase, 3	PSMD3	NM_002809	P58 // RPN3 // S3	3720636	chr17	+	35390438	35407732
COP9 constitutive photomorphogenic homolog subunit 2 (<i>Arabidopsis</i>)	COPS2	NM_004236	ALIEN // CSN2 // SGN2 // TRIP15	3623424	chr15	-	47203877	47235198
B-cell CLL/lymphoma 10	BCL10	NM_003921	CARMEN // CIPER // CLAP // c-E10 // mE10	2420808	chr1	-	85504067	85516171

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18				Fold Change
					Chromosome	Strand	Start	Stop	
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 (<i>S. pombe</i>)	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 SIII // TCEB3A	3326252	chr11	+	34083688	34125769	12.51
transcription elongation factor B (SIII), polypeptide 3 (110 kDa, elongin microtubule-associated protein, RP/EB family, member 1	TCEB3	NM_003198	EB1 // MGC117374 // MGC129946	2325251	chr1	+	23942459	23961135	12.38
Cdk5 and Abl enzyme substrate 1	CABLES1	NM_138375	FLJ35924 // H8T2563	3882069	chr20	+	30871304	30901864	12.37
ubiquitin specific peptidase 47	USP47	NM_017944	DKFZp686C13257 // FLJ20727 // TRFP	3781531 3320604	chr18 chr11	+	18940699 11819556	19101596 11937446	12.37 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_182917 // NM_001017926 // NM_007222	FLJ14825 // MGC9784 //—	3151473	chr8	-	124291083	124356860	12.17
chromosome 10 open reading frame 18	C10orf18	XM_374765 // XM_937970	DKFZp781E1986 // FLJ20360 // bA318F3.2	3233322	chr10	+	5766851	5846629	12.16
guanine nucleotide binding protein- like 2 (nuclear)	GNL2	NM_013285	FLJ40906 // HUMAUAANTIG // NGP1 // Ngp-1 // d423B22.6	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 (<i>Drosophila</i>) // 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	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	Stop
Rho GTPase activating protein 11A	ARHGAP11A	NM_014783 // NM_199357	GAP (1-12) // KIAA0013 //	3587457	chr15	+	30693622	30719422
high-mobility group nucleosome binding domain 1	HMGN1	NM_004965	MGC70740 // FLJ27265 // HMG14 // MGC104230 //	3932270	chr21	-	39636124	39643423
mortality factor 4 / mortality factor 4 like 1	MORF4 // MORF4L1	NM_006792 // NM_006791 // NM_206839	MGC117425 // CSR // CSRB // SEN // SEN1 // Eaf3 // FWP006 // HsT17725 // MGC10631 // MORFRG15 // MRG15 // S863-6	3603532	chr15	+	76889894	76979806
cytotoxic and regulatory T cell molecule	KIAA0690 // CRTAM	NM_019604	—	3302240	chr10	-	99098933	99175486
TERF1 (TRF1)-interacting nuclear factor 2	TINF2	NM_012461	TIN2	3558012	chr14	-	23776465	23781950
DCN1, defective in cullin neddylation	DCUN1D5	NM_032299	FLJ32431 //	3388914	chr11	-	102342328	102485844
1, domain containing 5 (<i>S. cerevisiae</i>) isopenicillin-diphosphate delta isomerase 1	ID11	NM_004508	MGC2714 // IPP1 // IPP11	3273601	chr10	-	1075869	1092634
exosome component 9	EXOSC9	NM_001034194 // NM_005033	PM/ScL-75 // RRP45 // PMSC11 // RRP45 // Rrp45p // p5 // p6	2741768	chr4	+	122941935	122957724
diablo homolog (<i>Drosophila</i>)	DIABLO	NM_019887 // NM_138929 // NM_138930	DIABLO-S // FLJ10537 // FLJ25049 // SMAC // SMAC3	3475511	chr12	-	121257461	121277963
eukaryotic translation elongation factor 2	EEF2	NM_001961	EEF-2 // EEF2	3846538	chr19	-	3926677	3936451
calcium activated nucleotidase 1	CANT1	NM_138793	SCAN-1 // SHAPY	3772775	chr17	-	74499403	74517744
moesin	MSN	NM_002444	—	3979659	chrX	+	64804248	64878488
aquarius homolog (mouse)	AQR	NM_014691	KIAA0560	3617757	chr15	-	32935042	33160557
EPH receptor A2	EPHA2	NM_004431	ECK	2397948	chr1	-	16323428	16355151
ATPase, Na ⁺ /K ⁺ transporting, beta 1	ATP1B1	NM_001001787 // NM_001677	ATP1B // MGC1798	2366422	chr1	+	167342204	167368946
polypeptide ring finger protein 40	RNF40	NM_014771	BRE1B // DKE/Zp686K191 // KIAA0661 //	3656555	chr16	+	30681120	30695182
KIAA0406	KIAA0406	NM_014657	MGC13051 // RBP95	3905073	chr20	-	36044840	36095268
TIMP metalloproteinase inhibitor 1	TIMP1	NM_003254	// STARING	3976341	chrX	+	47326654	47332978
			CLG // EPA // EPO // FLJ90373 // HCI // TIMP					

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	Stop
DCP1 decapping enzyme homolog A (<i>S. cerevisiae</i>)	DCP1A	NM_018403	HS275986 // Nbl00360 // SMAD4IP1 // SMIF BIP // FLJ29106 // GRP78 // MIF2	2676726	chr3	-	53296412	53356692
heat shock 70 kDa protein 5 (glucose-regulated protein, 78 kDa) chromosome 4 open reading frame 23	HSPA5	NM_005347	FLJ12891 // FLJ35725	3225398	chr9	-	127036953	127064590
RAB5A, member RAS oncogene importin 7	C4orf23	NM_152544	RAB5	2717757	chr4	+	8474582	8545892
	RAB5A	NM_004162	FLJ14581 // MGC138673 // RANBP7	2613386	chr3	+	19963571	20002852
	IPO7	NM_006391	CAIN // CAIN // CAN // D9S46E // MGC104525 // N214	3319840	chr11	+	9362702	9426296
nucleoporin 214 kDa	NUP214	NM_005085	PRPF8 // PRPF8 // PRP8 // PRPC8 // RP13	3191900	chr9	+	132990780	133102339
PRP8 pre-mRNA processing factor 8 homolog (<i>S. cerevisiae</i>)	PRPF8	NM_006445	KYK18 // K18	3740479	chr17	-	1500681	1534906
Snf2-related CBP activator protein keratin 18	SRCAP	NM_006662	ACDCR2 // FLJ121432 // MGC4640 // PAQR2	3656418	chr16	+	30616551	30663998
	KRT18	NM_000224 // NM_199187	SRP20	3415576	chr12	+	51596769	51632949
adiponectin receptor 2	ADIPOR2	NM_024551	CCNB	3400625	chr12	+	1670418	1768071
splicing factor, arginine/serine-rich 3 cyclin B1	SFRS3	NM_003017	FLJ23713 // FLJ33918 // Mf-GrpE#2	2905118	chr6	+	36669658	36741293
GrpE-like 2, mitochondrial (<i>E. coli</i>)	CCNB1	NM_031966	YAP // YAP2 // YAP65	2813414	chr5	+	68498462	68509822
	GRPEL2	NM_152407	NRF3	2835006	chr5	+	148705190	148714338
Yes-associated protein 1, 65 kDa	YAP1	NM_006106	KIAA0410 // PRO2463	3346453	chr11	+	101486379	101609466
nuclear factor (erythroid-derived 2)- like 3	NFE2L3	NM_004289	FBP // RAB-14	2993590	chr7	+	26158385	26194013
nucleoporin like 1	NUPL1	NM_001008564 // NM_001008565	CS-1 // CS1 // DKFZp31301039 // DKFZp779G0129 // FLJ45996 // KIAA1927 // KRAP // SPAG13	3482219	chr13	+	24773258	24822202
RAB14, member RAS oncogene sperm specific antigen 2	RAB14	NM_016322	HSP40	3223872	chr9	-	122980236	123025093
	SSFA2	NM_006751	BCL1 // D11S287E // PRAD1 // U21B31	2518428	chr2	+	182464815	182516732
DnaJ (Hsp40) homolog, subfamily B, member 1	DNAJB1	NM_006145		3852783	chr19	-	14485622	14501114
cyclin D1	CCND1	NM_053056		3338192	chr11	+	69161881	69178408

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	
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 //	3258168	chr10	+	94292951	94405130 10.90
diclkopf homolog 1 (<i>Xenopus laevis</i>)	DKK1	NM_012242	KNSL1 // TRIP5	3247172	chr10	+	53744067	53807545 10.89
polo-like kinase 4 (<i>Drosophila</i>)	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	RSRY1	NM_133368	KIAA1972	3662612	chr16	+	55777703	55831882 10.87
leucine rich repeat containing 59	LRRCS9	NM_018509	FLJ21675 //	3762355	chr17	-	45813504	45836593 10.85
exosome component 2	EXOSC2	NM_014285	RRP4 // Rrp4p //	3191695	chr9	+	132559000	132572797 10.83
polo-like kinase 1 (<i>Drosophila</i>)	PLK1	NM_005030	hRrp4p // p7	3653072	chr16	+	23597664	23609180 10.82
chromosome 20 open reading frame 24	C20orf24	NM_018840 // NM_199483	PLK // STPK13	3883971	chr20	+	34667571	34674368 10.81
KIAA1984 // chromosome 9 open reading frame 86	KIAA1984 // C9orf86	NM_001039374 // NM_024718	PNAS-11 // RIP5	3194635	chr9	+	138810077	138855460 10.81
molecular protein 1, 120 kDa	NOL1	NM_001033714 // NM_006170	MGC15438 // PARF // RP11-216L13.7 // RP11-216L13.9 // bA216L13.7 // FLJ10101 // FLJ13045 // Parf // bA216L13.9 // pp8875	3442024	chr12	-	6536290	6547817 10.79
			MGC117384 // MGC149287 // MGC149288 // NOP120 // NSUN1 // p120	2688882	chr3	-	113926517	114253449 10.73
			DKFZP434F2021					
			DOT1 // KIAA1814	3816264	chr19	+	2114945	2183576 10.70
			HSOA11916	3743501	chr17	-	7087644	7096514 10.70
chromosome 3 open reading frame 17	C3orf17	NM_001025072 // NM_001025073 // NM_015412 NM_032482	CRAF // Raf-1 // c-Raf //	2663244	chr3	-	12600117	12680654 10.61
			DKFZp686I2148 // MAP2A // MAP2B // MAP2C					
			DOT1-like, histone H3 methyltransferase (<i>S. cerevisiae</i>)					
			dullard homolog (<i>Xenopus laevis</i>)					
			v-raf-1 murine leukemia viral oncogene homolog 1 // microtubule-associated protein 2					
solite 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

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	
protein 1		NM_002931	// HKE4 // KE4 // RING5 // ZIP7 //					
testis derived transcript (3 LIM domains)	TES	NM_015641 // NM_152829	RNF1 DKFZP586B2022 // MGC1146 // TESS // TES-2 // TESTIN	3020192	chr7	+	115637811	10.53
chromosome 12 open reading frame 11	C12orf11	NM_018164	FLJ10630 // FLJ10637	3448428	chr12	-	26949277	10.50
golgi associated PDZ and coiled-coil motif containing // v-ros UR2	GOPC //	NM_001017408 //	CAL // FIG //	2971378	chr6	-	117988142	10.49
sarcoma virus oncogene homolog 1 (avian)	ROS1	NM_020399 // NM_002944	GOPC1 // PIST // d94G16.2 // MCF3 // ROS					
protein regulator of cytokinesis 1 // interferon-related developmental regulator 1	PRC1 // IFRD1	NM_003981 // NM_199413 // NM_199414 // NM_001007245 //	ASE1 // MGC1671 // MGC3669 // PC4 // TIS7	3639031	chr15	-	89310285	10.49
RNA methyltransferase like 1	RNMTL1	NM_001550						
forkhead box O1A (thabdomyosarcoma)	FOXO1A	NM_018146 NM_002015	FLJ10581 // HC90 FKH1 // FKHR //	3705539 3510858	chr17 chr13	+	632263 40027817	10.45 10.41
mitochondrial ribosomal protein S7	MRPS7	NM_015971	FOXO1 MRP-S // MRP-S7 // RP-S7 // RPM87	3734760	chr17	+	70769374	10.41
suppressor of Ty 6 homolog (<i>S. cerevisiae</i>)	SUPT6H	NM_003170	KIAA0162 // MGC87943 // SPT6 // SPT6H // emb-5	3715703	chr17	+	24013260	10.38
splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)	SFRS1	NM_001078166 // NM_006924	ASF // MGC5228 // SF2 // SF2p33 //	3764103	chr17	-	53421412	10.37
heterogeneous nuclear ribonucleoprotein M	HNRPM	NM_005968 // NM_031203	SRp30a DKFZp547H118 // HNRNPM //	3819543	chr19	+	8415651	10.37
neuroepithelial cell transforming gene 1	NET1	NM_001047160 // NM_003863	HNRNPM4 // HNRPM4 // HTGR1 ARHGEF8 // NET1A	3233182	chr10	+	5444535	10.35
ribonucleotide reductase M2 polypeptide	RRM2	NM_001034	R2 // RRM2M	2469252	chr2	+	10179982	10.35
chromosome 16 open reading frame 80	C16orf80	NM_013242	EVORF // GTL3	3693511	chr16	-	56683698	10.32
exosome component 4	EXOSC4	NM_019037	FLJ20591 // RRP41 // RRP41A // Rrp41p // SKI6 // Sk6p //	3120008	chr8	+	145205527	10.30
UTP6, small subunit (SSU) processome component, homolog (yeast)	UTP6	NM_018428	hRrp41p // p12A C17orf40 // HCA66	3752437	chr17	-	27211153	10.30
polymerase (RNA) I polypeptide C, 30 kDa	POLR1C	NM_004875 // NM_203290	RPA39 // RPA40 // RPA5 // RPAC1	2908052	chr6	+	43592769	10.29

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Human Genome hg18			Fold Change
						Strand	Start	Stop	
centromere protein L	CENPL	NM_033319	C1orf155 // CENP-L // FLJ1044 // RP3- 38334.1 // d38334.3	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	ABCF3	NM_018358	EST201864 //	2655511	chr3	+	185386580	185395316	10.26
(GCN20), member 3			FLJ11198						
telomeric repeat binding factor 2,	TERF2IP	NM_018975	DRIP5 // RAP1	3669092	chr16	+	74238853	74353272	10.25
interacting protein									
ADP-ribosylation factor interacting	ARFIP2 //	NM_012402 //	POR1 // GST //	3360941	chr11	-	6453496	6459171	10.24
protein 2 (arlapin 2) // solute	SLCO6A1	NM_173488	MGC26949 //						
carrier organic anion transporter			OATP6A1 // OATPY						
family, member 6A1									
RNA binding motif protein 25	RBM25	NM_021239	MGC105088 // MGC117168 //	3543411	chr14	+	72594776	72658577	10.23
			RNPC7 // SL64						
zinc finger protein 410	ZNF410	NM_021188	APA-1 // APA1	3543884	chr14	+	73423093	73468718	10.23
3-hydroxy-3-methylglutaryl-	HMGS1	NM_002130	HMGS //	2855501	chr5	-	43324231	43349337	10.19
Coenzyme A synthase 1 (soluble)			MGC90332						
transcription elongation regulator 1	TCERG1	NM_001040006 //	CA150 //	2834093	chr5	+	145754916	145871713	10.18
		NM_006706	MGC133200 //						
WD repeat domain 74	WDR74	XM_001125771 //	FLJ10439 //	3376235	chr11	-	62356627	62365857	10.13
		NM_018093	FLJ21730						
sperm associated antigen 5	SPAG5	NM_006461	DEEPST // MAP126 // hMAP126	3750785	chr17	-	23928719	23950424	10.12
G protein-coupled receptor 126	GPR126	NM_001032394 //	DREG // PSI1P2 //	2928461	chr6	+	142622079	142853981	10.05
		NM_001032395 //	VIGR						
		NM_020455 //							
		NM_198569							
Dna-like protein // guanine	bA16L21.2.1	NM_001015882 //	—	3184940	chr9	+	113412172	113474576	10.05
nucleotide binding protein (G	// GNG10	NM_001017998							
protein), gamma 10									
general transcription factor IIIC,	GTF3C4	NM_012204	FLJ21002 // MGC138450 // TFIIH90 // TFIIIC90 //	3192525	chr9	+	134535243	134581784	10.00
polypeptide 4, 90 kDa			TFIIICdelta //						
			TFIIIC2-90						
eukaryotic translation initiation factor 5	EIF5	NM_001969 //	EIF-5A	3553607	chr14	+	102743652	102881108	10.00
		NM_183004							
programmed cell death 7	PDCD7	NM_005707	ES18 // HES18 //	3629475	chr15	-	63196772	63213308	9.97
			MGC22015						
dual specificity phosphatase 14	DUSP14	NM_007026	MKP-L // MKP6	3719515	chr17	+	32922795	32947707	9.97
RAD18 homolog (<i>S. cerevisiae</i>)	RAD18	NM_020165	RNF73	2662020	chr3	-	8792108	8980146	9.94
myeloid cell leukemia sequence 1	MCL1	NM_021960 //	EAT // MCL1L //	2434438	chr1	-	148799312	148818878	9.93
(BCL2-related)		NM_182763	MCL1S //						
oxysterol binding protein-like 2	OSBP1.2	NM_014835 //	MGC104264 //	3892565	chr20	+	60245389	60304834	9.91
		NM_144498	FLJ20223 // KIAA0772 //						

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Array				Fold Change
				Transcript Cluster ID	Chromosome	Strand	Start Stop	
inhibitor of DNA binding 2B, dominant negative helix-loop-helix protein // inhibitor of DNA binding 2, dominant negative helix-loop-helix protein cytoskeleton associated protein 5	ID2B // ID2	NM_001039082 // NM_002166	MGC4307 // MGC8342 // ORP-2 // ORP2 —// GIG8 // ID2A // ID2H // MGC26389	2468622	chr2	+	8513132 8750492	9.91
	CKAP5	NM_001008938 // NM_014756	FLJ35359 // KIAA0097 // TOG // TOGP // ch-TOG	3371719	chr11	-	46721250 46824660	9.90
	TMSB10	NM_021103	MIG12	2491271	chr2	+	84959319 84988131	9.85
	DDX27	NM_017895	DKFZp667N057 // FLJ12917 // FLJ20596 // FLJ22238 // HSPC259 // MGC1018 // MGC163147 //	3888217	chr20	+	47237780 47294013	9.83
thymosin, beta 10			PP3241 // RHLP // TDP-43					
DEAD (Asp-Glu-Ala-Asp) box polypeptide 27			DLDBP // E3BP // OPDX // PDX1 // proX // FLJ12099 // FLJ33785 // JNK3 // JNK3A // MGC50974 // PRKM10 // p493F12 //	2320048 3326540	chr1 chr11	+	10995025 11013170 34870003 34998695	9.82 9.81
TAR DNA binding protein pyruvate dehydrogenase complex, component X // mitogen-activated protein kinase 10	TARDBP PDHX // MAPK10	NM_007375 NM_003477 // NM_002753 // NM_138980 // NM_138981 // NM_138982	DUS3 // FLJ13896 POM100 // PSF	3847420 2406064	chr9 chr1	-	5735867 5759311 35351696 35506894	9.80 9.80
dihydrouridine synthase 3-like (<i>S. cerevisiae</i>) splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	DUS3L SFPQ	NM_020175 NM_005066	MGC102700 // VPS15 // p150 SCR3	2695200 3417583	chr3 chr12	-	131801268 132026111 55202025 55277435	9.79 9.78
phosphoinositide-3-kinase, regulatory subunit 4, p150 RNA binding motif, single stranded interacting protein 2 eukaryotic translation initiation factor 2C, 2	PIK3R4 RBMS2 EIF2C2	NM_014602 NM_002898 NM_012154	AGO2 // MGC3183 // Q10 FLJ1633 // MGC111393	3156193 3333358	chr8 chr11	-	141599440 141726037 61648046 61677757	9.74 9.73
inner centromere protein antigens 135/155 kDa cofilin 1 (non-muscle) heat shock 105 kDa/110 kDa protein 1	INCENP CFL1 HSPH1	NM_001040694 // NM_020238 NM_005507 NM_006644	CFL DKFZp686M05240 // HSP105 // HSP105A // HSP105B // KIAA0201 // NY-CO- 25	3377886 3508330	chr11 chr13	-	65347069 65386796 30558258 30651692	9.72 9.68
nuclear import 7 homolog (<i>S. cerevisiae</i>)	NIP7	NM_016101	CGI-37 // FLJ10296 // HSPC031 // KD93	3666686	chr16	+	67930869 67935044	9.64

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	Stop
epiregulin mannosidase, alpha, class 1A, member 2 // urothelial cancer tumor necrosis factor receptor superfamily, member 1A	EREG	NM_001432	ER	2731513	chr4	+	75440309	75473341
	MAN1A2	NM_006699	MAN1B	2353881	chr1	+	117689854	117931990
	UCA1							
	TNFRSF1A	NM_001065	CD120a // FPF // MGC19588 // TBP1 // TNF-R // TNF-R-1 // TNF-R55 // // TNF-R55 // TNFR1 // TNFR1 // TNFR55 // TNFR60 // p55 // p55-R // BM-001 // PRO1073 // ania-6a	3441849	chr12	-	6308185	6321522
cyclin L1	CCNL1	NM_020307	DKEZp547K0918 // LARK // MGC75138 // RBM4A // ZCHC21 // ZCRB3A DKEZp434H116 // DKEZp781B2117 // MGC138493 // MGC141940 // MSTP054	2702307	chr3	-	158305077	158361233
RNA binding motif protein 4	RBM4	NM_002896		3336422	chr11	+	66161951	66190547
KIAA1429	KIAA1429	NM_015496 // NM_183009		3145020	chr8	-	95569109	95634851
nucleoporin 153 kDa zinc finger protein 91 homolog (mouse) // ciliary neurotrophic factor	NUP153 ZFP91	NM_005124 NM_053023	HNUPI53 // N153 FKSG11 // PZF // ZNF757 // HCN1F	2943808 3331730	chr6 chr11	- +	17723255 58101868	17855638 58149782
tetraspanin 5	TSPAN5	NM_000614 NM_005723	NET-4 // TM4SF9 // TSPAN-5	2778856	chr4	-	99589201	99798839
resistance to inhibitors of cholinesterase 8 homolog A (<i>C. elegans</i>)	RIC8A	NM_021932	MGC104517 // MGC131931 // MGC148073 // MGC148074 // RIC8 // synembryn	3315512	chr11	+	197139	206202
splicing factor 3b, subunit 1, 155 kDa	SF3B1	NM_001005526 // NM_012433	PRP10 // PRPF10 // SAP155 // SF3b155	2593670	chr2	-	197962756	198039327
DEAD (Asp-Glu-Ala-Asp) box polypeptide 47 // apolipoprotein L domain containing 1	DDX47 APOLD1	NM_016355 // NM_201224 // NM_030817	DKEZp5640176 // E4-DBP // FLJ30012 // HQ0256 // MSTP162 // DKEZp434F0318 // CTEN // FLJ14950 // PP14434	3405531	chr12	+	12856462	12874176
tensin 4	TNS4	NM_032865		3756262	chr17	-	35881491	35911365
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
v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	YES1	NM_005433	HsT441 // P61-YES // Yes // c-yes	3795942	chr18	-	711592	803236

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	
nuclear factor (erythroid-derived 2)-like 2 // hypothetical protein	NFE2L2 //	NM_006164 //	NRF2 // —	2588827	chr2	-	177794809	177837753
DKFZp451M2119	DKFZp451M2119	NM_182585						
eukaryotic translation initiation factor 4A, isoform 1 //	EIF4A1 //	NM_001416 //	DDX2A // EIF-4A //	3708826	chr17	+	7416768	7423040
SUMO1/sentrin/SMT3 specific peptidase 3	SENP3	NM_015670	EIF4A //					
			DKFZp586K0919 //					
			DKFZp762A152 //					
			SMT3IP1 // SSP3					
nucleolar protein 11	NOL11	NM_015462	DKFZp586L0724	3732373	chr17	+	63144526	63205942
adenylate kinase 2	AK2	NM_001625 //	ADK2	2405364	chr1	-	33245959	33275155
		NM_013411						
splicing factor, arginine/serine-rich 5	SFRS5	NM_001039465 //	HRS // SRP40	3542207	chr14	+	69263363	69308465
		NM_006925	—// FLJ23757	2560254	chr2	-	74607294	74610455
ancient ubiquitous protein 1 //	AUP1 //	NM_014423						
DEAQ box polypeptide 1 (RNA-dependent ATPase)	DQX1	NM_181575 //						
AF4/FMR2 family, member 4	AF4	NM_014423	AFSQ31 // MCEF //	2875555	chr5	-	132238768	132327205
			MGC75036					
guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	GNB2L1	NM_006098	Gnb2-rs1 // H12.3 //	2891052	chr5	-	180596592	180612024
			HLC-7 // PIG21 //					
			RACK1					
survival motor neuron domain containing 1	SMNDC1	NM_005871	SMNR // SPF30	3306516	chr10	-	112042540	112106248
BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)	BUB1	NM_004336	BUB1A // BUB1L //	2570616	chr2	-	111088456	111174950
SET domain containing 5	SETD5	XM_926615 //	hBUB1					
		XM_931376 //	DKFZp686I18276 //	2609608	chr3	+	9414309	9495916
		XM_931417 //	FLJ10707 //					
		XM_931444 //	KIAA1757					
		XM_931447 //						
		XM_931455 //						
		XM_931478 //						
		XM_939712 //						
		XM_944260 //						
		XM_944276 //						
		XM_944280 //						
		XM_944295 //						
		XM_944298 //						
		XM_944303 //						
heat shock protein 90 kDa beta (Grp94), member 1 // thymine-DNA glycosylase // heat shock protein 90 kDa beta (Grp94), member 2 (pseudogene)	HSP90B1 //	NM_001080517	ECGP // GP96 //	3429312	chr12	+	102848291	102871551
	TDG //	NM_003299 //	GRP94 // TRA1 //					
	HSP90B2P	NM_003211 //	// GRP94P1 //					
			GRP94b // HSP //					
			HSPCP2 // HsGrp94b					
			// TRAP1 // TRAP1					

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Array				Fold Change
				Transcript Cluster ID	Chromosome	Strand	Start	Stop
actin, gamma 1	ACTG1	NM_001614	ACT // ACTG // DFNA20 // DFNA26	3773932	chr17	-	77091456	77105797
dual specificity phosphatase 6	DUSP6	NM_001946 // NM_022652	MKP3 // PYST1	3464860	chr12	-	88223376	88273467
LATS, large tumor suppressor, homolog 2 (<i>Drosophila</i>)	LATS2	NM_014572	FLJ13161 // KPM	3504526	chr13	-	20445178	20533718
SERPINE1 mRNA binding protein 1	SERBP1	NM_001018067 // NM_001018068 // NM_001018069 // NM_015640	CGI-55 // CHD3IP // DKFZp564M2423 // FLJ90489 // HABP4L // PAIRBP1 // PAIRBP1	2417174	chr1	-	67646101	67669020
DnaJ (Hsp40) homolog, subfamily A, member 3	DNAJA3	NM_005147	FLJ45758 // TID1 // hTid-1	3646164	chr16	+	4415465	4446773
nuclear cap binding protein subunit 2, 20 kDa	NCBP2	NM_007362	CBC2 // CBP20 // NIP1 // PIG55	2713074	chr3	-	198146677	198154763
TRK-fused gene	TFG	NM_001007565 // NM_006070	FLJ36137 // TFG // TRKT3	2633773	chr3	+	101910681	101950800
LIM domain 7	LMO7	NM_005358	FBX20 // FBXO20 // KIAA0858 // LOMP	3494137	chr13	+	75092571	75566974
KIAA0090	KIAA0090	NM_015047	RPI-43E13.1	2399620	chr1	-	19413665	19450633
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 // FLJ3706 // SR278	3556888	chr14	-	22439714	22458231
suppressor of Ty 7 (<i>S. cerevisiae</i>)- like	SUPT7L	NM_014860	ART1 // KIAA0764 // MGC90306 // SP T7L // STAF65 // STAF65(gamma)	2546008	chr2	-	27718957	27740160
transforming, acidic coiled-coil containing protein 3	TACC3	NM_006342	ERIC1 // MGC117382 // MGC133242	2714955	chr4	+	1692616	1716693
signal transducing adaptor molecule (SH3 domain and ITAM motif) 1	STAM	NM_003473	DKFZp686D2352 // STAM1	3237088	chr10	+	17726140	17798809
neurotensin receptor 1 (high affinity)	NTSR1	NM_002531	NTR	3892873	chr20	+	60810575	60864568
sorting nexin associated golgi protein 1	SNAG1	NM_052870	MGC150827 // MGC150829 // SH3PX2 // SH3PX2	2809628	chr5	+	53849348	53878172
DEAD (Asp-Glu-Ala-Asp) box polypeptide 42	DDX42	NM_007372 // NM_203499	FLJ43179 // RHELP // RNAHP //	3730899	chr17	+	59204975	59250510
adhesion regulating molecule 1	ADRM1	NM_007002 // NM_175573	GP110 // MGC29536 // Rpn13	3892607	chr20	+	60305485	60317305
dykeratosis congenita 1, dyskerin	DKC1	NM_001363	DKC // NAP57 // NOLA4 // XAP101 // dyskerin	3996667	chrX	+	153644243	153659150
GNAS complex locus	GNAS	NM_000516 // NM_001077488 //	AHO // C20orf45 // GNAS1 // GPSA //	3891163	chr20	+	56848165	56919604

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Array				Fold Change
				Transcript Cluster ID	Chromosome	Strand	Start	Stop
protein inhibitor of activated STAT, 1	PIAS1	NM_001077489 //	GSA // GSP //	3599280	chr15	+	65898917	66277975
		NM_001077490 //	MGC33735 // PHP1A					
		NM_016592 //	// PHP1B // POH //					
WD repeat domain 36	WDR36	NM_080425 //	dJ309F20.1.1 //	2823820	chr5	+	110455769	110517812
		NM_080426 //	dJ806M20.3.3					
		NR_003259						
tripartite motif-containing 44	TRIM44	NM_017583	DDXBP1 // GIBP //	3326842	chr11	+	35600246	35826001
		NM_004749 //	GU/RH-II //					
		NM_030900 //	MGC141878 //					
transforming growth factor beta regulator 4	TBRG4	NM_199122	MGC141879 // ZMIZ3	3049025	chr7	-	45103738	45128368
		NM_014366 //	DKEZp6861650 //					
		NM_206826 //	GLCIG // TA-WDRP					
guanine nucleotide binding protein- like 3 (nucleolar)	GNL3	NM_01077440 //	// TAWDRP //	2624074	chr3	+	52694976	52705212
		NM_014739	DIPB // HSA249128					
		NM_030937 //	// MC7 // MGC3490					
BCL2-associated transcription factor 1	BCLAF1	NM_017900	CPR2 // FASTKD4 //	2975680	chr6	-	136619703	136652847
		NM_001077441 //	KIAA0948					
		NM_01039577 //	C77032 // E2IG3 //					
cyclin L2 // aurora kinase A interacting protein 1	CCNL2 // AURKAIP1	NM_030937 //	MGC800 // NS	4041923	chr11_random	+	359569	372958
		NM_017900	BTF // KIAA0164 //					
		NM_01039577 //	bK211L9.1					
cirrhosis, autosomal recessive 1A (cfrin)	CIRH1A	NM_032830	ANIA-6B //	3666566	chr16	+	67722728	67761072
		NM_005902	DKEZp761A1210 //					
		NM_017900	DKEZp762O195 //					
SMAD family member 3	SMAD3	NM_005902	HCLA-ISO // HLA- ISO // PCEE //	3598959	chr15	+	65145043	65296818
		NM_005902	SBI38 // AIP //					
		NM_005902	AKIP // FLJ20608					
proteasome (prosome, macropain) subunit, beta type, 7	PSMB7	NM_002799	CIRHIN // FLJ14728	3225003	chr9	-	126155580	126223284
		NM_002799	// KIAA1988 // NAIC					
		NM_002799	// TEX292					
cyclin L2 // aurora kinase A interacting protein 1	CCNL2 // AURKAIP1	NM_030937 //	DKEZp68610186 //	2391532	chr1	-	1314609	1324575
		NM_017900	HSPC193 //					
		NM_017900	HsT17436 // J15-2					
cyclin L2 // aurora kinase A interacting protein 1	CCNL2 // AURKAIP1	NM_030937 //	// MADH3 //	2391532	chr1	-	1314609	1324575
		NM_017900	MGC60396 // Snad 3					
		NM_017900	Z					
cyclin L2 // aurora kinase A interacting protein 1	CCNL2 // AURKAIP1	NM_030937 //	ANIA-6B //	2391532	chr1	-	1314609	1324575
		NM_017900	DKEZp761A1210 //					
		NM_017900	DKEZp762O195 //					
cyclin L2 // aurora kinase A interacting protein 1	CCNL2 // AURKAIP1	NM_030937 //	HCLA-ISO // HLA- ISO // PCEE //	2391532	chr1	-	1314609	1324575
		NM_017900						
		NM_017900						

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	
mediator of RNA polymerase II transcription, subunit 28 homolog (<i>S. cerevisiae</i>)	MED28	NM_025205	SB138 // AIP // AKIP // FLJ20608 150003D12Rik // DKFZP434N185 // EGI // ngagin	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 (Mow34 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	KIAA0144 // NICE-4	2360083	chr1	+	152459139	152510701 8.91
solute carrier family 20 (phosphate transporter), member 1	SLC20A1	NM_005415	DKFZp686D2397 // FLJ41426 // GLVR1 // Givr-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	DKFZp86L2022 // HCNBP // HTRG // HTRP // BSE3 // 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 // RNASEL1 // RNS4H	2746024	chr4	+	146238626	146270126 8.86
BTAF1 RNA polymerase II, B-TFIIID transcription factor-associated, 170 kDa (Mot1 homolog, <i>S. cerevisiae</i>)	BTAF1	NM_003972	KIAA0940 // MGC138406 // MOT1 // TAF10 // TAF1170 // TAF172 // TAF1170	3257938	chr10	+	93673509	93821994 8.84
synaptaxin 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 // 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

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Human Genome hg18			Fold Change
						Strand	Start	Stop	
upstream binding protein 1 (LBP-1a)	UBP1	NM_014517	DKF/p686L1745 // LBP-1B // LBP-1a // LBP1A // LBP1B CAGH1 // CAGH1A // CIZ // ERDA2 // NMP4 // NP // TNRC1	2668351	chr3	-	33404835	33456874	8.80
zinc finger protein 384	ZNF384	NM_001039916 // NM_001039917 // NM_001039918 // NM_001039919 // NM_001039920 // NM_133476		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	PSITP5BP1	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 // SPEG2	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 // DKF/p686B1823 // ERBA-BETA // ERBA2 // GRTH // MGC126109 // MGC126110 // NR1A2 // THR1 // THR1 // THR2	2555490	chr2	-	61558490	61619343	8.71
D4, zinc and double PHD fingers family 2	DPE2	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 family with sequence similarity 83, member D	BHLHB3	NM_030762	DEC2 // SHARP-1 // SHARP1	3448088	chr12	-	26141435	26179615	8.69
thioredoxin domain containing 14 // catenin (cadherin-associated protein), delta 1	FAM83D	NM_030919	C20orf129 // FLJ38341 // d1616B8.3	3884892	chr20	+	36988369	37015223	8.69
	TXNDC14 // CTNND1	NM_015959 // XM_001126721 // XM_001126756 // XM_001126767	CGI-31 // DKF/p781O2021 // MGC111151 // CAS // TMX2 // CAS	3331487	chr11	+	57235839	57391291	8.68

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	Stop
thymopoietin	TMPO	XM_001126781 //	CTNND // KIAA0384	3427767	chr12	+	97395927	97502543
		XM_001126793 //	// P120CAS //					
		XM_001126823 //	P120CTN // p120					
		NM_001331						
junonji, AT rich interactive domain 1A	JARID1A	NM_001032283 //	CMD1T // LAP2 //	3439603	chr12	-	269504	368944
		NM_003276	MGC61508 //					
		NM_001042603 //	PRO0868 // TP					
		NM_005056	RBBP2 // RBP2					
sorting nexin 19	SNX19	NM_014758	CHET8 //	3398482	chr11	-	130250320	130291615
			DKFZp667L205 //					
			KIAA0254					
		NM_024295	DER-1 // DER1 //					
Der1-like domain family, member 1	DERL1		FLJ13784 //	3151401	chr8	-	124094605	124123781
			FLJ42092 //					
			MGC3067 //					
		NM_001037283 //	EIF3-ETA // EIF3-					
eukaryotic translation initiation factor 3, subunit 9 eta, 116 kDa	EIF3S9	NM_003751	P110 // EIF3-P116 //	2987441	chr7	+	2315929	2386896
			MGC104664 //					
			MGC131875 // PRT1					
			// eIF3b					
WDR45-like conserved helix-loop-helix ubiquitous kinase	WDR45L CHUK	NM_019613	WPL-3 // WIP3	3775157	chr17	-	78165748	78199803
		NM_001278	IKBKA // IKK-alpha					
			// IKK1 // IKKA //					
			NFKBKA // TCF16					
WD repeat domain 77 // oviductal glycoprotein 1, 120 kDa (mucin 9, oviductin)	WDR77 // OVGP1	NM_024102 //	HKMT1069 // MEP50	2427930	chr1	-	111782351	111793512
		NM_002557	// MGC2722 //					
			Nblal0071 // RP11-					
			552M11.3 // CHIT5 //					
Paf1, RNA polymerase II associated factor, homolog (<i>S. cerevisiae</i>) kinesin family member 23	PAF1	NM_019088	EGP // MUC9 //	3861978	chr19	-	44568113	44592162
			F23149_1 //					
			FLJ11123 // PD2					
		NM_004856 //	CHO1 // KNSL5 //					
BMS1-like, ribosome assembly protein (yeast) // tetrairicopeptide repeat domain 7B	BMS1L // TTC7B	NM_138555	MKLP-1 // MKLP1	3243708	chr10	+	42597978	42682443
		NM_014753 //	KIAA0187 // TTC7L1					
		NM_001010854	// c14_5685					
ubiquitin specific peptidase 9, X-linked // ubiquitin specific peptidase 9, Y-linked (far facets-like, squamous cell carcinoma antigen recognized by T cells 3)	INSIG2 USP9X // USP9Y	NM_016133	MGC26273	2502424	chr2	+	118558758	118593436
		NM_001039590 //	DFFRX // EAF //					
		NM_001039591 //	AZF // AZFA //					
		NM_004654	DFFRY // SP3					
SART3	SART3	NM_014706	KIAA0156 //	3470253	chr12	-	107440140	107479296
			MGC138188 // RP11-13G14 // TIP110 //					
			p110(mnb)					

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18				Fold Change
					Chromosome	Strand	Start	Stop	
LIM domain only 4	LMO4	NM_006769	—	2345286	chr1	+	8745833	8758817	8.56
peptidylprolyl isomerase G (cyclophilin G)	PP1G	NM_004792	CARS-Cyp // CYP // MGC133241 //	2514441	chr2	+	170149096	170206156	8.55
guanine nucleotide binding protein (G protein), α polypeptide	GNAQ	NM_002072	G-ALPHA-q // GAQ	3210808	chr9	-	79475043	79836455	8.53
TSC22 domain family, member 1	TSC22D1	NM_006022 // NM_183422	DKFZp686019206 // MGC17597 // RP11-269C23.2 // TGFBI4 // TSC22	3512294	chr13	-	43905532	44202063	8.53
serine/arginine repetitive matrix 2	SRRM2	NM_016333	300-KD // DKFZp686015166 // FLJ21926 // FLJ22250 // KIAA0324 // MGC40295 // SRL300 // SRm300	3645253	chr16	+	2742650	2761908	8.52
methionine adenosyltransferase II, alpha	MAT2A	NM_005911	MAT2A // MATII // SAMS2	2491615	chr2	+	85597809	85625908	8.51
ubiquitin 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 (<i>E. coli</i>)	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	CXorf59	NM_207318	CD107a // LAMPA // LGP120	3985866	chrX	+	103297819	103323642	8.45
lysosomal-associated membrane protein 1	LAMP1	NM_005561	—	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 (<i>S. pombe</i>)	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	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	Stop
Rho GTPase activating protein 29	ARHGAP29	NM_004815	MGC126055 // SCA17 // THID PARG1 // RP11- 255E17.1	2423829	chr1	-	94409906	94549874
PRP4 pre-mRNA processing factor 4 homolog (yeast)	PRPF4	NM_004697	HPRP4 // HPRP4P // PRP4 // Prp4p	3185558	chr9	+	115077230	115095267
myosin phosphatase-Rho interacting protein	M-RIP // C17orf84	NM_0165134 // NM_201274	KIAA0864 // RHOIP3 // p116Rip	3712363	chr17	+	16886542	17062286
E2F transcription factor 4, p107/p130-binding glutamine-rich 1	E2F4	NM_001950	E2F-4	3665288	chr16	+	65783266	65790299
annexin A1	QRICH1	NM_017730 // NM_198880	FLJ20259 // MGC131838	2673902	chr3	-	49042148	49106498
serine/threonine kinase 4	ANXA1 STK4	NM_000700 NM_006282	ANX1 // LPC1 DKFZp686A2068 // KRS2 // MST1 //	3174816 3886704	chr9 chr20	+	74914324 43028534	74983394 43142041
chromosome X open reading frame 15	CXorf15	NM_018360	YSK3 FIAT // FLJ11209 // LSR5 // MGC126621 // MGC126625	3970166	chrX	+	16714433	16772561
transportin 2 (importin 3, karyopherin beta 2b)	TNPO2	NM_013433	FLJ12155 // IPO3 // KPNB2B // TRN2	3851651	chr19	-	12670912	12695776
pleckstrin homology-like domain, family B, member 1	PHLDB1	NM_015157	DKFZp686H039 // DKFZp686O24210 // FLJ00141 // FLJ90266 //	3351564	chr11	+	117982385	118033939
tumor necrosis factor receptor superfamily, member 12A	TNFRSF12A	NM_016639	KIAA0638 // LL5A // MGC111531 CD266 // FN14 //	3645555	chr16	+	3010334	3012380
SLC7A5 pseudogene	LAT1-3TM // IMAA	NR_002593 // NR_002594	TWEAKR DC49 // MLAS // hLAT1-3TM // MAAA	3684100	chr16	-	21320984	22449842
CD3e molecule, epsilon associated protein	CD3EAP	NM_012099	ASE-1 // CAST // MGC118851 // PAF49	3836243	chr19	+	50597660	50605831
kinesin family member 2C	KIF2C	NM_006845	KNSL6 // MCAK	2334098	chr1	+	44978097	45005994
CD55 molecule, decay accelerating factor for complement (Cromer blood group)	CD55	NM_000574	CR // DAF // TC	2377229	chr1	+	205561488	205607671
aldolase A, fructose-bisphosphate	ALDOA	NM_000034 // NM_184041 //	ALDA // MGC10942 // MGC17716 //	3655920	chr16	+	29968869	29991009
denticless homolog (<i>Drosophila</i>)	DTL	NM_184043 NM_016448	MGC17767 CDT2 // DCAF2 // L2DTL // RAMP	2378937	chr1	+	210275565	210399046
adhesion molecule with Ig-like domain 2	AMIGO2	NM_181847	ALI1 // DEGA	3452478	chr12	-	45726359	45874177
ST3 beta-galactoside alpha-2,3- sialyltransferase 1	ST3GAL1	NM_003033 // NM_173344	Gal-NAC6S // MGC9183 // SIAT4A // SIATFL //	3154398	chr8	-	134535811	134653449

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start Stop	
tripartite motif-containing 8 fibroblast growth factor (acidic) intracellular binding protein PAP associated domain containing 1 // collagen, type XI, alpha 1	TRIM8	NM_030912	ST3GalA // ST3GalA.1 // GERP // RNF27	3261820	chr10	+	104384137 104419190	8.29
	FIBP	NM_004214 // NM_198897	FGFIBP // FIBP-1	3377964	chr11	-	65407787 65412586	8.29
	PAPD1 // COL11A1	NM_018109 // NM_001854 // NM_080629 // NM_080630	FLJ10486 // RP11- 305E6.3 // mtPAP // COL1A1 // COL16 // STL2	3283378	chr10	-	30511316 30764402	8.26
	EXOSC10	NM_001001998 // NM_002685	PM-Scl // PM/Scl- 100 // PMSCL // PMSCL2 // RRP6 // Rpp6 // p2 // p3 // p4	2396480	chr1	-	11049173 11082811	8.26
	BCL9L	NM_182557	BC19-2 // DLNB11	3393993	chr11	-	118272076 118304947	8.23
1-acylglycerol-3-phosphate O- acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon) chaperonin containing TCP1, subunit 6A (zeta 1)	AGPAT5	NM_018361	1-AGPAT5 // LPAAT-e // LPAAT- epsilon	3083936	chr8	+	6553307 6633056	8.22
	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
	JARID1B	NM_006618	FLJ10538 // FLJ12459 // FLJ12491 // FLJ16281 // FLJ23670 // PLU-1 // PUT1 // RBBP2H1A	2451309	chr1	-	200963111 201048571	8.22
	SLC25A37	XM_001128238 // XM_001128248 // XM_001128255 // XM_001128269 // NM_016612	HT015 // MFRN // MSC // MSCP // PRO1278 // PRO1584 // PRO2217	3090006	chr8	+	23439117 23485313	8.21
	NUP50	NM_007172 // NM_153645	MGC39961 // NPAP60 // NPAP60L	3948461	chr22	+	43938390 43960160	8.21
mediator of RNA polymerase II transcription, subunit 8 homolog (<i>S. cerevisiae</i>)	MED8	NM_001001651 // NM_001001653 // NM_001001654 // NM_052877 // NM_201542	ARC32 // MGC17544 // MGC19641	2409344	chr1	-	43622176 43628144	8.20
	EIF4A2	NM_001967	BM-010 // DDX2B // EIF4A // EIF4F	2656738	chr3	+	187961636 187990742	8.20
	EIF4A2	NM_001967						

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Chromosome	Human Genome hg18			Fold Change
						Strand	Start	Stop	
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 // FLJ10290 // ZC3H16	3623683	chr15	-	48356681	48434794	8.18
RNA binding motif protein 22 meningioma expressed antigen 5 (hyaluronidase)	RBM22 MGEA5	NM_018047 NM_012215	FLJ11229 // FLJ23355 // KIAA0679 // MEA5 // NCOAT	2881521 3304012	chr5 chr10	-	150050460 103534201	150060885 103568420	8.16 8.15
low density lipoprotein receptor (familial hypercholesterolemia)	LDLR	NM_000527	FLJ10564 // EHB3 // PRPF17	3821015	chr19	+	11061114	11115050	8.15
cell division cycle 40 homolog (<i>S. cerevisiae</i>)	CDC40	NM_015891	HSPC185	2921086	chr6	+	110606544	110682171	8.13
hypothetical protein HSPC111 solute carrier family 2 (facilitated glucose transporter), member 1	HSPC111 SLC2A1	NM_016391 NM_006516	GLUT1 // GLUT1 // MGC141895 // MGC141896	2888284 2409104	chr5 chr1	-	175743557 43124794	175749348 43338329	8.13 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 (<i>Drosophila</i>)	ARIH1	NM_005744	ARI // HARI // HHARI // UBCH7BP	3600744	chr15	+	70553731	70666726	8.09
RNA binding motif protein, X-linked 2 family with sequence similarity 29, member A	RBMX2 FAM29A	NM_016024 NM_017645	CGI-79 MGC102696 // MGC138798 // MGC138799 // RP11-296P7.3	3990795 3200611	chrX chr9	+	129356824 19042752	129381607 19093153	8.09 8.09
NGFL-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 methyltransferase like 2B // methyltransferase like 2A	ZCCHC8 METTL2B // METTL2A	NM_017612 NM_018396 // NM_001005372 // NM_181725	DKFZp434E2220 FLJ11350 // FLJ12760 // METL // METTL2 // METTL2A // PSENIP1	3475679 3730211	chr12 chr17	-	121522105 57854988	121551469 57881176	8.07 8.06

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	Stop
fibrosin 1 splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot homolog, <i>Drosophila</i>)	FBS1	NM_022452	FBS // FLJ11618	365362	chr16	+	30577810	30590035
	SFRS8	NM_004592	SWAP	3438417	chr12	+	130761587	130852472
CCR4-NOT transcription complex, subunit 7	CNOT7	NM_013354 //	CAFI // hCAF-1	3125775	chr8	-	17128912	17148758
	BTBD7	NM_054026	DKEZp68N0544 //	3577277	chr14	-	92773656	92966460
chromosome 17 open reading frame 79	C17orf79	NM_018167	FUP1 // MGC48310	3752424	chr17	-	27203014	27210424
	TCF12	NM_003205 //	HSA272196 // TTP1	3595096	chr15	+	54963208	55402126
ATP binding domain 1 family, member B PRP3 pre-mRNA processing factor 3 homolog (<i>S. cerevisiae</i>) // KIAA0460	ATPBD1B	NM_0207037 //	HEB // HTE4 //					
	PRPF3 //	NM_207036 //	HsT17266					
G1 to S phase transition 1	GSPT1	NM_002094	FLJ10349	2402838	chr1	-	27073870	27089311
	ZNF408	NM_024741	HPRP3 // HPRP3P //	2358171	chr1	+	148560583	148592321
zinc finger protein 408 chromosome 20 open reading frame 4	C20orf4	NM_015511	PRP3 // Prp3p //					
			RP18 // FLJ32145 //					
DnaJ (Hsp40) homolog, subfamily A, member 2	DNAJ2	NM_003880	HSPC099	3680610	chr16	-	11865619	11917408
			551G9.2 // ETE3A //					
splicing factor, arginine/serine-rich 10 (transformer 2 homolog, <i>Drosophila</i>)	SFRS10	NM_004593	GST1 // eRF3a					
			FLJ12827	3329461	chr11	+	46678944	46684037
trinucleotide repeat containing 6A	TNRC6A	NM_014494	CGI-23 //	3883787	chr20	+	34287657	34322234
			DKEZp564N1363 //					
testis expressed sequence 10	TEX10	NM_017746	bA234K24.2	3690084	chr16	-	45546783	45565155
			CPR3 // DIA2 //					
nucleoporin 107 kDa hypoxia-inducible factor 1, alpha subunit inhibitor	NUP107	NM_020401	DNAJ // DNJ3 //	2709062	chr3	-	187048509	187160523
	HIF1AN	NM_017902	HIRP4 // PRO3015					
			// RDJ2					
			DKEZp686F18120 //					
			Htra2-beta //					
			SFRS10 // TRA2-					
			BETA // TRA2B					
			CAGH26 //					
			DKEZp666E117 //					
			FLJ22043 // GW1 //					
			GW182 // KIAA1460					
			// MGC75384 //					
			TNRC6					
			FLJ20287 //					
			bA208F1.2					
			NUP84					
			DKEZp762F1811 //					
			FIH1 // FLJ20615 //					
			FLJ22027					

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Array				Fold Change
				Transcript Cluster ID	Chromosome	Strand	Start Stop	
myosin IE	MYOIE	NM_004998	HuncM-IC // MGC104638 //	3626826	chr15	-	57215720 57452363	7.97
v-ref murine sarcoma 3611 viral oncogene homolog	ARAF	NM_001654	MYOIC A-RAF // ARAF1 //	3976299	chrX	+	47300826 47316249	7.96
nucleolar protein family 6 (RNA- associated)	NOL6	NM_130793 // NM_022917 // NM_139235	PKS2 // RAE1 FLJ21959 // MGC14896 // MGC14921 // MGC20838 // NRAP // UTP22 //	3203582	chr9	-	33442676 33464087	7.96
chromosome 21 open reading frame 66	C21orf66	NM_145328 // NM_013329 // NM_016631 // NM_058191	bA311H10.1 BM4020 // FLJ90561 // GCFC	3929395	chr21	-	33028084 33066030	7.96
casein kinase 1, alpha 1	CSNK1A1	NM_001025105 // NM_001892 NM_018410	CK1 // HLCDCGP1 // PRO2975 hFLEG1	2880932	chr5	-	148800168 148922811	7.96
hypothetical protein DKFZp762E1312	DKFZp762E1312	NM_018410	ANT-1 // C20orf14	2604254	chr2	-	234406876 234427931	7.95
PRP6 pre-mRNA processing factor 6 homolog (<i>S. cerevisiae</i>)	PRPF6	NM_012469	// TOM // U5-102K // hPp6	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 (<i>S. pombe</i>)	CDC25B	NM_004358 // NM_021872 // NM_021873 NM_020831	—	3874438	chr20	+	3715655 3734756	7.93
megakaryoblastic leukemia (translocation) 1	MKL1	NM_003286	BSAC // MAL // MRITF-A	3961496	chr22	-	39136248 39362660	7.93
topoisomerase (DNA) I	TOP1	NM_016628 //	TOPI	3885464	chr20	+	39090891 39186535	7.93
WW domain containing adapter with coiled-coil	WAC	NM_100264 // NM_100486	BM-016 // MGC10753 // PRO1741 // Wwp4 //	3240340	chr10	+	28828043 29005095	7.92
ubiquitin specific peptidase 36	USP36	NM_025090	bA48B24 //	3772581	chr17	-	74295075 74348574	7.92
t-complex 1	TCP1	NM_001008897 // NM_030752	DUB1 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

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	
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 (<i>S. cerevisiae</i>)	PRPF40A	XM_371575 // XM_938514	FBP-11 // FBP11 // FLAF1 // FLJ20585 // FBP3 // HIP10 // HYPA // NY-REN-6 CASP8P1 // DEDD1 // DEFT // FLDED1 // KE05	2581548	chr2	-	153212414	153283546 7.89
death effector domain containing	DEDD	NM_001039711 // NM_001039712 // NM_032998	—	2440625	chr1	-	159357395	159569167 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	D6881E // DDX39B // UAP56 // ATP6G // ATP6G2 // NG38 // VMA10	2949038	chr6	-	31605990	31625606 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 (<i>S. cerevisiae</i>)	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 B-cell CLL/lymphoma 7B	YTHDF1 BCL7B	NM_017798 NM_001707 // NM_138707	C20orf21 // —	3913712 3056108	chr20 chr7	-	61297230 72588624	61330873 7.83 72610244 7.82
HIR histone cell cycle regulation defective homolog A (<i>S. cerevisiae</i>)	HIRA	NM_003325	DGCR1 // TUP1 // TUPLE1	3952637	chr22	-	17696576	17799452 7.82
Josephin domain containing 3 // small nucleolar RNA, H/ACA box 25 // small nucleolar RNA, H/ACA box 32 // small nucleolar RNA, H/ACA GTP binding protein 4	JOSD3 // SNORA25 // SNORA32 // SNORA18 GTPBP4	NM_024116 // NR_003028 // NR003032 // NR_002959 NM_012341	MGC5306 // ACA25 // ACA32 // ACA18	3386814	chr11	-	93102831	93114308 7.81
eukaryotic translation elongation factor 1 beta 2	EEF1B2	NM_001037663 // NM_001959 // NM_021121	CRFG // FLJ10686 // FLJ10690 // // FLJ39774 // NGB EEF1B // EEF1B1 // EF1B	3231774	chr10	+	942450	1055862 7.79
SMAD family member 5	SMAD5	NM_001001419 // NM_001001420 //	DKFZp781C1895 // DKFZp781O1323 //	2524577 2830010	chr2 chr5	+	206732303 135464462	206735884 7.78 135552314 7.77

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Array				Fold Change
				Transcript Cluster ID	Chromosome	Strand	Start	Stop
epidermal growth factor receptor (erythroblastic leukemia viral (v-erb- b) oncogene homolog, avian)	EGFR	NM_005903	Dwfc // JV5-1 //					
		NM_005228 //	MADH5					
		NM_201282 //	ERBB // ERBB1 //	3002640	chr7	+	55054070	55291773
mitogen-activated protein kinase kinase kinase 11	MAP3K11	NM_201283 //	mENA					
		NM_201284						
		NM_002419	MGC17114 // MLK-3 // MLK3 // PTK1 //	3377752	chr11	-	65121806	65139693
apoptosis inhibitor 5	API5	NM_006595	SPRK					
		NM_017812	AAC-11 // AAC11 //	3327906	chr11	+	43290109	43322649
		NM_017812	API5L1	3073597	chr7	-	132062426	132500566
coiled-coil-helix-coiled-coil-helix domain containing 3	CHCHD3	NM_015527	FLJ20420					
		NM_015527	DKEZP434P1750 //	3687715	chr16	-	30275789	30289100
		NM_015934	FP2461					
nucleolar protein NOP5/NOP58 ribosomal protein S6 kinase, 70 kDa, polypeptide 1	NOP5/NOP58 RPS6KB1	NM_003161	HSPC120	2523144	chr2	+	20281346	202926967
			PS6K // S6K // S6K1 // STK14A //	3729294	chr17	+	55325239	55429105
			p70(S6K)-alpha //					
GDP dissociation inhibitor 1	GDI1	NM_001493	p70-S6K // p70-alpha FLJ41411 // GDIL //	3996404	chrX	+	153318480	153324978
			MRX41 // MRX48 //					
			OPHN2 // RABGD1A // RABGD1A // XAP-					
PHD finger protein 12	PHF12	NM_001033561 //	KIAA1523 //	3751184	chr17	-	24256404	24302905
		NM_020889	MGC131914 // PF1					
		NM_024700	FLJ12553 // RP3- 423B22.3 //	2407163	chr1	-	37774050	37792490
stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein)	STP1	NM_006819	d423B22.2					
		NM_001007226 //	HOP // HIF-SSP-	3334224	chr11	+	63709341	63728586
		NM_001007227 //	3521 // P60 // STIL					
speckle-type POZ protein	SPOP	NM_001007228 //	TEF2	3761905	chr17	-	45031245	45110541
		NM_001007229 //						
		NM_001007230 //						
eukaryotic translation elongation factor 1 alpha 1	EEF1A1	NM_003563	CCS-3 // CCS3 //					
		NM_001402	EEF-1 // EEF1A //	2960903	chr6	-	74281167	74335800
			EF-1a // EEF1A //					
			FLJ25721 // GRAF- 1EF // HNGC: 16303 // LENG7 //					
			MGC102687 //					
			MGC131894 //					
			MGC16224 // PTL1 //					
			eEF1A-1					

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Exon ST 1.0 Array					Fold Change
					Chromosome	Strand	Start	Stop		
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	
	DDX18 // WNT8B	NM_006773 // NM_003393	FLJ33908 // Mrfb // —	2502300	chr2	+	118243834	118323562	7.70	
	ATAD2	NM_014109	DKFZp667N1320 // MGC131938 // MGC142216 // MGC29843 // MGC3254 // DKFZP564D0478 // MGC111002 // RP11-4K3_A.4	3151534	chr8	-	124393174	124477871	7.69	
chromosome 1 open reading frame 160	C1orf160	NM_032125	MGC3254 // DKFZP564D0478 // MGC111002 // RP11-4K3_A.4	2326954	chr1	+	27521221	27535639	7.69	
RNA binding motif protein 5	RBM5	NM_005778	FLJ39876 // G15 // H37 // LUCA15 // RBM5	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 interleukin enhancer binding factor 3, 90 kDa	IRS2 ILF3	NM_003749 NM_004516 // NM_012218 // NM_153464	DRBF // DRBP76 // MNP4 // MPHOSPH4 // MPP4 // NF-AT-90 // NF90 // NFAR	3525234 3820663	chr13 chr19	- +	109196024 10625547	109238228 10664074	7.68 7.68	
	UBE2J1	NM_016021	NEAR-1 // TCP80 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 (<i>S. cerevisiae</i>) // 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

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	
transcription factor 2			RP5-976013.1 // dJ976013.2					
general transcription factor IIIC, polypeptide 2, beta 110 kDa	GTF3C2	NM_001035521 //	KIAA0011 // TFIIC-BETA // TFIIC110	2545681	chr2	-	27402231	27433372 7.63
general transcription factor IIH, polypeptide 1, 62 kDa	GTF2H1	NM_001521 NM_005316	BTf2 // TFIH	3322717	chr11	+	18300412	18345156 7.62
mitochondrial ribosomal protein L17	MRPL17	NM_022061	MRP-L26 // RPL17L // RPM126	3361116	chr11	-	6657673	6690484 7.62
Yip1 domain family, member 3 // chromosome 6 open reading frame 154	YIPF3 // C6orf154	NM_015388 // NM_001012974	C6orf109 // DKEZF566C243 // 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	AAAG1 // DAP5 // FLJ41344 // NAT1 // p97	3362719	chr11	-	10487574	10788746 7.60
MYST histone acetyltransferase 2 SIN3A homolog A, transcription regulator (yeast)	MYST2 SIN3A	NM_007067 NM_015477	HBO1 // HBOA DKEZF434K2235 // FLJ90319 //	3725779 3633403	chr17 chr15	+	45196447 73448786	45261455 73535167 7.60
centaurin, delta 1	CENTD1	NM_015230 // NM_139182	KIAA0700 ARAP2 // FLJ13675 // FLJ44916 //	2765590	chr4	-	35626248	35922356 7.60
KIT ligand	KITLG	NM_000899 // NM_003994	KIAA0580 // PARX DKEZF686F2250 // KL-1 // Kitl // MGF // SCF // SF	3464747	chr12	-	87349442	87498371 7.58
F-box and leucine-rich repeat protein 11	FBXL11	NM_012308	CXXC8 // DKEZF434M1735 // FBL11 // FBL7 // FLJ00115 // FLJ46431 // JHDM1A // KIAA1004 // LILNA	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)gen // p27BBP	3903836	chr20	-	33276003	33336225 7.55
chromosome 10 open reading frame 119	C10orf119	NM_024834	FLJ15081 // FLJ36756	3309755	chr10	-	121568302	121642742 7.55

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	
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 //	HSP90AA1	NM_001017963 //	FLJ31884 // HSP86	3580179	chr14	-	101616842	101676327 7.53
heat shock protein 90 kDa alpha (cytosolic), class A member 2 //	HSP90AA2	NM_005348 //	// HSP90A //					
heat shock protein 90 kDa alpha (cytosolic), class A member 2 //	HSP90AA2	NM_001040141 //	HSP90N // HSPC1 //					
heat shock protein 90 kDa alpha (cytosolic), class A member 6 (pseudogene)	HSP90AA6P		HSPCA // HSPCAL1 // HSPCAL4 //					
			HSPN // Hsp89 //					
			Hsp90 // LAP2 //					
			HSP90ALPHA //					
			HSPCAL3 //					
peroxisomal biogenesis factor 5	PEX5	NM_000319	PTSIR // PXR1	3403299	chr12	+	7232607	7262437 7.53
chromosome 4 open reading frame 30	C4orf30	NM_017741	FLJ20280 //	2762468	chr4	-	17404173	17421482 7.53
			MGC126765 //					
			MGC126767					
transmembrane protein 2	TMEM2	NM_013390	—	3209384	chr9	-	73452177	73573229 7.52
forkhead box M1	FOXM1	NM_021953 //	FKHL16 // FOXM1B	3440598	chr12	-	2836207	2856564 7.52
		NM_202002 //	// HFH-11 // HFH11					
		NM_202003	// HNF-3 // INS-1					
			// MPHOSPH2 //					
			MPP-2 // MPP2 //					
			PIG29 // TRIDENT					
			DKEZp434E0211 //					
			FLJ21430 //					
			FLJ23239 //					
			KIAA1646 // LK4 //					
			MGC131878 //					
			dA59H18.2 //					
			dA59H18.3 // ICERK					
small nuclear ribonucleoprotein 70 kDa polypeptide (RNP antigen)	SNRP70	NM_001009820 //	RNPUIZ // RPU1 //	3838185	chr19	+	54280358	54304714 7.52
		NM_003089	U170K // ULAP //					
			U1RNP					
anthrax toxin receptor 2	ANTXR2	NM_058172	CMG-2 // CMG2 //	2774971	chr4	-	80762874	81219758 7.51
			FLJ31074 // ISH //					
			JHF // MGC111533					
			// MGC45856					
			MGC3832 // MGC691					
			// OAZ1 // OAZIN //					
			ODOIL					
			FLJ11773					
antizyme inhibitor 1	AZIN1	NM_015878 //	CRSP77 // DRIP80	3147591	chr8	-	103907725	103953967 7.51
		NM_148174	// FLJ10812 //					
			MED17 // TRAP80					
			DBC-1 // DBC1					
chromosome 12 open reading frame 44	C12orf44	NM_021934	—	3415273	chr12	+	50749317	50757534 7.51
cofactor required for Sp1 transcriptional activation, subunit 6, 77 kDa	CRSP6	NM_004268	—	3344897	chr11	+	93157019	93186225 7.49
KIAA1967	KIAA1967	NM_021174 //	—	3089597	chr8	+	22518038	22534618 7.49
		NM_199205	—					

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	Stop
serologically defined colon cancer antigen 3 // small nuclear RNA activating complex, polypeptide 4, 190 kDa	SDCCAG3	NM_001039707 //	NY-CO-3 //	3229943	chr9	-	138416210	138425418
	// SNAPC4	NM_001039708 //	FLJ13451 //					
		NM_006643 //	PTFalpha //					
		NM_003086	SNAP190					
potassium channel tetramerisation domain containing 10	KCTD10	NM_031954	FLJ41739 //	3470793	chr12	-	108370845	108399528
			MSTP028 // UIRO61					
			BL3 // C1-13KD-B //					
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13 kDa	NDUFA5	NM_005000	DKEZp78IK1356 //	3070658	chr7	-	122968075	122985216
			FLJ12147 // NUFM					
			// UQOR13					
			AEN // FLJ12484 //					
interferon stimulated exonuclease gene 20 kDa-like 1	ISG20L1	NM_022767	FLJ12562 // pp12744	3607232	chr15	+	86948254	86976501
paxillin	PXN	NM_002859	FLJ16691	3474372	chr12	-	119132644	119187926
synaptotagmin binding, cytoplasmic RNA interacting protein	SYNCRIP	NM_006372	GRY-RBP //	2963407	chr6	-	86374062	86410282
			HNRPO1 // NSAP1					
			// RP1-3J17.2 //					
			dJ3117.2 // pp68					
proteasome (prosome, macropain)	PSMD6	NM_014814	KIAA0107 // S10 //	2679864	chr3	-	63971281	63984700
26S subunit, non-ATPase, 6			SGA-113M // p44S10					
chromosome 7 open reading frame	C7orf50	NM_138446	—	2992863	chr7	+	23305462	23317894
heterogeneous nuclear ribonucleoprotein K	HNRPK	NM_002140 //	CSBP // FLJ41122	3212294	chr9	-	85772377	85785355
		NM_031262 //	// HNRNPK // TUNP					
		NM_031263						
		NM_001005335 //	FLJ35509 //	3861617	chr19	-	44018883	44034809
heterogeneous nuclear ribonucleoprotein L	HNRPL	NM_001533	P/OKcl.14 // hnRNP-L					
SEC14-like 1 (<i>S. cerevisiae</i>)	SEC14L1	NM_001039573 //	DKEZp686C06176 //	3735752	chr17	+	72596335	72767744
		NM_003003	PRELID4A // SEC14L					
hippocampus abundant transcript-like 1	HIATL1	NM_001130181 //	FLJ14753 //	3180263	chr9	+	96176674	96325754
eukaryotic translation initiation factor 5A	EIF5A	NM_032558	MGC117350					
		NM_001970	EIF-5A // EIF5A1 //	3708422	chr17	+	7151037	7156478
			MGC104255 //					
			MGC99547 // uORF					
			// uORF A					
			CLCP1 // ESDN					
discoidin, CUB and LCCL domain containing 2	DCBLD2	NM_080927		2686023	chr3	-	99997526	100124598
voltage-dependent anion channel 2 polycarbonyl group ring finger 3	VDAC2	NM_003375	FLJ23841	3252577	chr10	+	76639941	76661389
	PCGF3	NM_006315	DKEZp686D20235 //	2714230	chr4	+	689573	754428
			DONG1 // FLJ36550					
			// FLJ43813 //					
			MGC129615 //					
			MGC40413 // RNF3					
			// RNF3A					
			—					
NADH dehydrogenase (ubiquinone) Fe—S protein 3, 30 kDa (NADH-coenzyme Q reductase)	NDUFS3	NM_004551		3329904	chr11	+	47557156	47562663

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	
signal recognition particle 68 kDa thioredoxin reductase 1	SRP68 TXNRD1	NM_014230	—	3771297	chr17	-	71546467	7.41
		NM_003330 //	GRM-12 // MGC9145	3429460	chr12	+	103130628	7.39
		NM_182729 //	// TR // TR1 //					
		NM_182742 //	TRXR1 // TXNR					
PDZ domain containing 8	PDZD8	NM_182743						
		NM_173791	FLJ25412 //	3308619	chr10	-	119029422	7.39
			FLJ34427 // PDZK8					
IKAROS family zinc finger 5 (Pegasus)	IKZF5	NM_022466	// bA129M16.2					
			DKFZp781B0249 //	3310757	chr10	-	124740316	7.38
			FLJ22973 //					
TPX2, microtubule-associated, homolog (<i>Xenopus laevis</i>)	TPX2	NM_012112	PEGASUS //	3881443	chr20	+	29774755	7.37
			C20orf1 // C20orf2					
			// DIL-2 // DIL2 //					
RNA binding motif protein 39	RBM39		FLS353 //					
			GD: C20orf1 //					
			HCA519 // HCTP4 //	3904226	chr20	-	33754569	7.35
ubiquitin specific peptidase 53 vesicle-associated membrane protein 3 (cellubrevin)	USP53 VAMP3	NM_184237 //	CAPER //					
		NM_184241 //	CAPERalpha // CC1.3					
		NM_184244 //	// DKFZp781C0423					
DEAH (Asp-Glu-Ala-His) box polypeptide 36 fibronectin type III domain containing 3B	DHX36 FNDC3B	NM_004902 //	// FLJ44170 //					
		NM_184234	HCC1 // RNPC2	2741236	chr4	+	120353195	7.35
		NM_019050	DKFZp781E1417	2318637	chr1	+	7753916	7.35
E74-like factor 1 (ets domain transcription factor) keratin 19	ELF1 KRT19	NM_004781	CEB	2701595	chr3	-	155475346	7.33
		NM_020865	DDX36 // KIAA1488	2652410	chr3	+	173240112	7.33
		NM_022763	// MLEL1					
Integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor) ribosomal protein L30 IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast) origin recognition complex, subunit 2-like (yeast) Kruppel-like factor 10	ITGA2 RPL30 IMP4 ORC2L // MGC39518 KLF10		DKFZp686D14170 //					
			DKFZp762K137 //					
			EAD104 // FLJ23399					
tight junction protein 1 (zona occludens 1)	TJP1		// MGC10002 //					
			PRO4979 //					
			YVTM2421	3511031	chr13	-	40394613	7.32
Integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor) ribosomal protein L30 IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast) origin recognition complex, subunit 2-like (yeast) Kruppel-like factor 10	ITGA2 RPL30 IMP4 ORC2L // MGC39518 KLF10	NM_172373	—					
		NM_002276	CK19 // K19 // K1CS	3757108	chr17	-	36933431	7.32
		NM_002203	// MGC15366					
tight junction protein 1 (zona occludens 1)	TJP1	NM_000989	BR // CD49B // GPIa	2809245	chr5	+	52320949	7.31
		NM_033416	// VLA-2 // VLA2					
			—	3145953	chr8	-	99123079	7.31
tight junction protein 1 (zona occludens 1)	TJP1		BXDC4 // MGC19606	2505501	chr2	+	130816288	7.31
			—					
			ORC2	2594569	chr2	-	201482783	7.31
tight junction protein 1 (zona occludens 1)	TJP1	NM_001032282 //	EGRA // TIEG //					
		NM_005655	TIEG1	3147508	chr8	-	103682306	7.30
		NM_003257 //	DKFZp686M05161 //					
tight junction protein 1 (zona occludens 1)	TJP1	NM_175610	MGC133289 // ZO-1	3615579	chr15	-	27703228	7.30

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	
tRNA 5-methylaminomethyl-2-thiouridylate methyltransferase	TRMU	NM_018006	MGC9627 // MITO2 // 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	DKEZp781F2016 // DKEZp781L0254 // 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 //	3671873	chr16	+	83291080	83371023 7.27
A kinase (PRKA) anchor protein (gravin) 12	AKAP12	NM_005100 // NM_144497	MGC2621 // UBPO AKAP250 // DKEZp686M0430 // DKEZp686O0331	2931569	chr6	+	151602720	151721361 7.27
ornithine decarboxylase 1 matrin 3	ODC1 MATR3	NM_002539 NM_018834 // NM_199189	— DKEZp686K0542 // DKEZp686K23100 // KIAA0723 //	2540157 2831124	chr2 chr5	- +	10485474 138505686	10606340 138695245 7.27 7.26
chromosome 5 open reading frame 22	C5orf22	NM_018356	MGC9105 DKEZp667N066 // FLJ11193 // FLJ23805 //	2805176	chr5	+	31568161	31590902 7.26
nuclear mitotic apparatus protein 1 macrophage erythroblast attacher	NUMA1 MAEA	NM_006185 NM_001017405 // NM_005882	MGC33010 NUMA EMP // HLC-10 //	3380901 2714672	chr11 chr4	- +	71389909 1273702	71469367 1323891 7.25 7.25
nucleolar protein 8	NOL8	NM_017948	PIG5 C9orf34 // DKEZp686P12242 // FLJ20736 // Nop132 // bA62C3.3 //	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	bA62C3.4 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 // GPI7 // FLJ39925 // LAS21 // MGC131903 // PRO4405 //	2714025	chr4	+	483010	523985 7.22
SON DNA binding protein	SON	NM_032195 // NM_138927	RLGS1930 BASS1 // C21orf50 // DBP-5 // FLJ21099 // FLJ33914 //	3918696	chr21	+	33836804	33872881 7.20

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	Stop
kelch-like ECH-associated protein 1 // ADAM metalloproteinase with thrombospondin type 1 motif, 6	KEAP1 // ADAMTS6	NM_012289 // NM_203500 // NM_197941	KIAA1019 // NREBP					
			// SON3					
			INH2 // KIAA0132 //					
			KLHL19 //					
			MGC10630 //					
bromodomain containing 2	BRD2	NM_005104	MGC1114 //					
			MGC20887 //					
			MGC4407 //					
			MGC9454 // ADAM-					
			D6S113E //					
squalene epoxidase lamin B receptor	SOLE LBR	NM_003129 NM_002296 // NM_194442 NM_005243 // NM_013986	DKFZp686N0336 //					
			FLJ31942 // FSRG1					
			// KIAA9001 // NAT					
			// RING3 // RNF3					
			—					
Ewing sarcoma breakpoint region 1	EWSR1	NM_005243 // NM_013986	DHCR14B // LMN2R					
			// MGC9041 // PHA					
			EWS					
			MGC13170					
			—					
chromosome 19 open reading frame 48	C19orf48	NM_199249 // NM_199250	FCHL // FCHL1 //					
			HYPLIP1 // MLTF //					
			MLTF1 // UEF //					
			FLJ00267 //					
			FLJ44128 // RP11-					
WD repeat domain 46	WDR46	NM_005452	544M22.6					
			BING4 // C6orf11 //					
			FP221					
			TOP2 // TP2A					
			ATP5K // MGC12532					
topoisomerase (DNA) II alpha 170 kDa ATP synthase, H+ transporting, mitochondrial F0 complex, subunit E splicing factor 3b, subunit 2, 145 kDa	TOP2A ATP5I SF3B2	NM_001067 NM_007100 NM_006842	SAP145 // SF3B145					
			// SF3b1 // SF3b150					
			DKFZp686M13204 //					
			d677H15.2 // p54					
			MP100 // PSA					
splicing factor, arginine/serine-rich 11	SFRS11	NM_004768	—					
			—					
			—					
			—					
			—					
aminopeptidase puromycin sensitive	NPEPPS	XM_001128588 // NM_006310	—					
			—					
			—					
			—					
			—					
influenza virus NS1A binding protein	IVNS1ABP	NM_006469 // NM_016389	DKFZp686K06216 //					
			FLARA3 // FLJ10069					
			// FLJ10411 //					
			FLJ10962 //					
			FLJ35593 //					
			FLJ36593 //					
			HSPC068 //					
			KIAA0850 // ND1 //					
			NS-1 // NS1-BP //					
			—					

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	
Smg-7 homolog, nonsense mediated mRNA decay factor (<i>C. elegans</i>)	SMG7	NM_014837 // NM_173156 // NM_201568 // NM_201569 // NM_014877	C1orf16 // EST1C // FLJ23717 // KIAA0250 // SGA56M // SMG-7	2371255	chr1	+	181708036	7.09
helicase with zinc finger	HELZ		DRHC // HUMOREF5 // KIAA0054 // MGC163454	3768015	chr17	-	62485987	7.08
cytochrome P450, family 1, subfamily B, polypeptide 1	CYP1B1	NM_000104	CYP1B // GLC3A	2548699	chr2	-	38138730	7.08
sprouty homolog 2 (<i>Drosophila</i>)	SPRY2	NM_005842	MGC23039 //	3519309	chr13	-	79683810	7.07
golgi phosphoprotein 4	GOLPH4	NM_014498	GIMPC // GPP130 //	2704567	chr3	-	169208832	7.07
Rab geranyltransferase, beta subunit // mutS homolog 4 (<i>E. coli</i>)	RABGGTB	NM_004582 //	P138	2342624	chr1	+	76024474	7.07
angiotensin like 2	MSH4	NM_002440	GGTB //					
MAK10 homolog, amino-acid N-acetyltransferase subunit, (<i>S. cerevisiae</i>)	AMOTL2	NM_016201	LCCP	2696309	chr3	-	135527277	7.06
	MAK10	NM_024635	FLJ21613 //	3177563	chr9	+	87733620	7.06
			FLJ22643 //					
			bA379P1.1					
NOL1/NOP2/Sun domain family, member 2	NSUN2	NM_017755	FLJ20303 // SAK1 //	2847292	chr5	-	6510634	7.06
leptin receptor overlapping transcript-like 1	LEPROTL1	NM_015344	TRM4	3092276	chr8	+	30059542	7.06
geminin, DNA replication inhibitor	GMNN	NM_015895	HSPC112 // Vps55	2898597	chr6	+	24857262	7.06
FAT tumor suppressor homolog 1 (<i>Drosophila</i>)	FAT	NM_005245	// my047	2797393	chr4	-	187745970	7.05
forkhead box J3	FOXJ3	NM_014947	Gem // RP3-					
nucleoporin 54 kDa	NUP54	NM_017426	CDHF7 // FAT1 //	2408855	chr1	-	42414807	7.05
kinesin family member 5B	KIF5B	NM_004521	ME5 // hFat1	2773997	chr4	-	77254731	7.04
			—	3283991	chr10	-	32337798	7.04
interferon gamma receptor 1	IFNGR1	NM_000416	KINH // KNS // KNS1					
mortality factor-4 like 2	MORF4L2	NM_012286	// UKHC	2976113	chr6	-	137560317	7.04
mastermind-like 1 (<i>Drosophila</i>)	MAML1	XM_001126853 //	CD119 // FLJ45734					
zinc finger and BTB domain containing 11	ZBTB11	NM_014415	// IFNGR	4016572	chrX	-	102817114	7.03
mitochondrial ribosomal protein S2	MRPS2	NM_016034	KIAA0026 // MORFL2	2844410	chr5	+	179092457	7.03
adaptor-related protein complex 2, alpha 2 subunit	AP2A2	NM_012305	// MRGX	2686727	chr3	-	102780272	7.02
serine arginine-rich pre-mRNA splicing factor SR-A1	SR-A1	NM_021228	KIAA0200 // Mam-1					
NMDA receptor regulated 1	NARG1	NM_057175	// Mam1	3193900	chr9	+	137531661	7.02
triple functional domain (PTPRF interacting)	TRIO	NM_007118	FLJ3426 //	3316447	chr11	+	912387	7.01
			MGC13303 // ZNF-U69274	3838757	chr19	+	54837204	7.01
			CGI-91 // MRP-S2	2744597	chr4	+	140442091	7.00
			ADTAP // CLAPA2	2802398	chr5	+	14196590	7.00
			// HIP9 // HYPJ					
			SRA1					
			Gal19 // NATH //					
			TBDN100					
			tgat					

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18				Fold Change
					Chromosome	Strand	Start	Stop	
myotubularin related protein 12 cyclin G associated kinase	MTMR12	NM_001040446	3-PAP // PIP3AP	2852274	chr5	-	32262872	32248897	7.00
	GAK	XM_001127411 //	FLJ40395 //	2756673	chr4	-	833110	916149	7.00
GRB2-associated binding protein 1	GAB1	NM_005255	MGC99654	2745547	chr4	+	144476834	144615158	7.00
		NM_002039 //	—						
senataxin	SETX	NM_207123	ALS4 // AOA2 //	3228007	chr9	-	134126584	134220359	7.00
		NM_015046	DKFZp781B151 //						
chromosome 12 open reading frame 41	C12orf41	NM_017822	FLJ12840 //						
			FLJ43459 //						
WNK lysine deficient protein kinase 1	WNK1	NM_018979	KIAA0625 // SCAR1	3453177	chr12	-	47333281	47362268	7.00
			// bA479K20.2						
myotubularin related protein 1 met proto-oncogene (hepatocyte growth factor receptor)	MTMR1	NM_003828	FLJ20436	3400034	chr12	+	278104	891189	6.98
	MET	NM_000245	KDP // KIAA0344 //						
ADP-ribosylation factor 4	ARF4	XM_001132763 //	PHA2C // PRKWNK1	3994846	chrX	+	149612503	149684226	6.97
			—	3020343	chr7	+	116099694	116230307	6.97
four and a half LIM domains 2	FHL2	NM_001660	HGFR // RCCP2	2678090	chr3	-	57532172	57558635	6.96
			—						
polypyrimidine tract binding protein 1	PTBP1	NM_001450 //	AAG11 // DRAL //	2568687	chr2	-	105335877	105501005	6.96
		NM_201555 //	SLM3						
glutamate-rich WD repeat containing 1	GRWD1	NM_031485	HNRNP1 // HNRP1 //	3815165	chr19	+	747768	763505	6.96
			MGC10830 //						
signal sequence receptor, alpha (translocon-associated protein alpha)	SSR1	NM_003144	GRWD // KIAA1942	3837796	chr19	+	53640874	53652090	6.95
			// RRB1 // WDR28						
GC-rich promoter binding protein 1- like 1	GPBP1L1	NM_021639	DKFZp78IN23103 //	2940551	chr6	-	7213542	7258526	6.94
			TRAPA						
chromosome 20 open reading frame 72	C20orf72	NM_052865	RP11-767N6.1 //	2410330	chr1	-	45865575	45926352	6.94
			SPI92						
ELAV (embryonic lethal, abnormal vision, <i>Drosophila</i>)-like 1 (Hu antigen R) // translocase of inner mitochondrial membrane 44 homolog (yeast)	ELAVL1 //	NM_001419 //	FLJ14597 //	3878220	chr20	+	17896912	17919759	6.94
	TIMM44	NM_006351	bA504H3.4						
heat shock protein 90 kDa alpha (cytosolic), class B member 1	HSP90AB1	NM_007355	ELAV1 // HUR //	3848689	chr19	-	7929463	7999655	6.93
			Hua // MeG //						
			DKFZp686H05241 //						
			TIM44						
			D6S182 // FLJ26984	2908474	chr6	+	44319983	44330383	6.93
			// HSP90-BETA //						
			HSP90B // HSPC2 //						
			HSPCB						

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	
TSC22 domain family, member 2	TSC22D2	NM_014779	KIAA0669 // TILZ4a // TILZ4b // TILZ4c	2647647	chr3	+	151385441	151660841
Pentatricopeptide repeat domain 3 // kinesin family member 5A	PTCD3 // KIF5A	NM_017952 // NM_004984	DKFZp666K071 // FLJ20758 // D12S1889 // MYO50	2491935	chr2	+	86186849	86222791
kelch-like 20 (<i>Drosophila</i>)	KLHL20	NM_014458	// NKHC // SPG10 KHLHX // KLEIP // KLHLX // RP3-383J4.3	2367793	chr1	+	171950703	172028914
sorting nexin 5	SNX5	NM_014426 // NM_152227	FLJ10931	3899346	chr20	-	17855335	17897603
KIAA0179	KIAA0179	NM_015056	—	3923218	chr21	+	43903644	43940364
protease, serine, 23	PRSS23	NM_007173	MGC5107 // SIG13 // SPUVE // ZSIG13	3343452	chr11	+	86189210	86341580
transmembrane, prostate androgen induced RNA	TMEPAI	NM_020182 // NM_199169 // NM_199170 // NM_199171	PMEPA1 // STAG1	3911217	chr20	-	55656877	55781123
zinc finger protein 330	ZNF330	NM_014487	HSA6591 // NOA36	2745220	chr4	+	142336669	142381405
chromodomain helicase DNA binding protein 2	CHD2	NM_001042572 // NM_001271	DKFZp781D1727	3609138	chr15	+	91227096	91387351
development and differentiation enhancing factor 1	DDEF1	NM_018482	AMAP1 // ASAP1 // KIAA1249 // PAG2 // PAP // ZG14P	3153428	chr8	-	131133540	131525100
mitogen-activated protein kinase kinase kinase 14	MAP3K14	NM_003954	FTDCR1B // HS // HSNIK // NIK	3759704	chr17	-	40696283	40750550
zinc finger protein 289, ID1 regulated	ZNF289	NM_032389	FLJ14576 // FLJ26000 // IRZ // Nbla10535 // Zfp289	3371928	chr11	-	47142451	47155114
heterogeneous nuclear ribonucleoprotein R	HNRPR	NM_005826	FLJ25714 // HNRNP // hnRNP-R	2401275	chr1	-	23486545	23543926
coiled-coil domain containing 47	CCDC47	NM_020198	GK001 // MSTP041	3766334	chr17	-	59176353	59204726
CUG triplet repeat, RNA binding protein 1	CUGBP1	NM_001025596 // NM_006560 // NM_198700	BRUNOL2 // CUG-BP // CUGBP // NAB50 // hNab50	3372253	chr11	-	47444068	47543613
cancer susceptibility candidate 3	CASC3	NM_007359	BTZ // MLN51	3720739	chr17	+	35518075	35586901
SUMO1/sentrim/SMIT3 specific peptidase 3	SEN3	NM_015670	DKFZp386K0919 // DKFZp762A152 // SMT3P1 // SSP3	3708798	chr17	+	7405827	7416006
MAX dimerization protein 1	MXD1	NM_002357	MAD // MAD1 // MGC104659	2487549	chr2	+	69995330	70023575
protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha isoform	PPP2R2A	NM_002717	B55A // FLJ26613 // MGC52248 // PR52A // PR55A	3090922	chr8	+	26156860	26286261
fusion (involved in t(12; 16) in malignant liposarcoma)	FUS	NM_001010850 // NM_004960	MGC52248 // PR52A // PR55A CHOP // FUS-CHOP // FUS1 // TLS // TLS/CHOP	3656904	chr16	+	31093395	31111003

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	
programmed cell death 6 // aryl-hydrocarbon receptor repressor	PDCD6 // AHR	NM_013232 //	ALG-2 //	2798586	chr5	+	324634	491368
		NM_020731	MGC111017 //					
			MGC119050 //					
nucleolar protein 5A (56 kDa with KKE/D repeat)	NOL5A	NM_006392	MGC9123 // PEF1B					
			// AHH // AHR //					
			NOP56	3873874	chr20	+	2580791	2587030
WAS protein family, member 2	WASF2	NM_006990	SCAR2 // WAVE2 //	2403111	chr1	-	27603331	27689256
			dJ393P12.2					
			DKE/ZP434F195 //	3229529	chr9	-	137840157	137938826
calmodulin regulated spectrin-associated protein 1	CAMSAP1	NM_015447	FLJ1228 //					
			MGC163452 //					
			PRO2405 //					
chromosome 18 open reading frame 25	C18orf25	NM_001008239 //	bA100C15.1	3787031	chr18	+	42008011	42123527
		NM_145055	ARKL1 // MGC12909					
			// MGC87799					
cullin 3	CUL3	NM_003590	—	2601544	chr2	-	225025520	225158348
			MSAP // c86fus	3164914	chr9	+	21792645	22022975
			FLJ90470	2686371	chr3	-	101565001	101614635
methylthioadenosine phosphorylase translocase of outer mitochondrial membrane 70 homolog A (<i>S. cerevisiae</i>)	TOMM70A	NM_014820	FLJ14494	3396883	chr11	-	125577202	125586743
RNA pseudouridylate synthase domain containing 4	RPUSD4	NM_032795	FLJ33903	3589141	chr15	+	36331548	36468943
sprouty-related, EVH1 domain containing 1	SPRED1	NM_152594	PAST4	3620276	chr15	-	39977674	40052063
			MGC75406 // p55	3768103	chr17	-	62764497	62804392
EH-domain containing 4	EHD4	NM_139265						
proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	PSMD12	XM_001134070 //						
		XM_001134072 //						
		XM_001134073 //						
nucleoporin 160 kDa	NUP160	NM_002816	MGC150678 //	3371986	chr11	-	47169280	47858048
		NM_015231	MGC150679					
EPS8-like 1	EPS8L1	NM_017729 //	DRC3 // EPS8R1 //	3841949	chr19	+	60273799	60291530
		NM_133180 //	FLJ20258 //					
		NM_139204	MGC23164 //					
chromatin modifying protein 4B	CHMP4B	NM_176812	MGC4642 // PP10566	3882681	chr20	+	31862780	31905829
			C20orf178 //					
			CHMP4A // SNF7-2					
thioredoxin interacting protein	TXNIP		// Shax1 //					
		NM_006472	EST01027 //	2356115	chr1	+	144149846	144164251
			HHCFA78 // THIF //					
eukaryotic translation initiation factor 1A, X-linked // eukaryotic translation initiation factor 1A	EIF1AX // EIF1AP1	XM_001134077 //	VDUP1	4002148	chrX	-	20052567	20069880
		NM_001412 //	EIF1A // EIF4C //					
			eIF-1A // eIF-4C //					

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Array				Fold Change
				Transcript Cluster ID	Chromosome	Strand	Start	Stop
mitochondrial ribosomal protein S30	MRPS30	NM_016640	DKFZp566B2024 //	28086122	chr5	+	44844784	45054668
			MRP-S30 // PAP //					
Rho GTPase activating protein 21	ARHGAP21	NM_020824	PDCE9	3281621	chr10	-	24912552	25052583
			ARHGAP10 //					
regulator of G-protein signalling 3	RGS3	NM_017790 //	DKFZp761L0424 //	3185643	chr9	+	115246842	115399812
			FLJ33323					
NFKB inhibitor interacting Ras-like 2	NKIRAS2	NM_001001349 //	C2PA // FLJ20370 //	3721579	chr17	+	37422156	37431177
			FLJ31516 //					
polypyrimidine tract binding protein 2	PTBP2	NM_021190	FLJ90496 // PDZ-	2348060	chr1	+	96959805	97144643
			RGS3 // RGP3					
splicing factor 1	SF1	NM_004630 //	DKFZp434N1526 //	3377044	chr11	-	64287827	64302817
			KBRAS2 //					
Nipped-B homolog (<i>Drosophila</i>) //	NRBP1	NM_013384 //	MG74742 //	2806799	chr5	+	36894163	37115932
			FLJ34897 // MIBP //					
ring finger and WD repeat domain 3	RFXD3	NM_018124	PTB // PTBLP //	3699044	chr16	-	73212799	73258283
			brPTB // nPTB //					
BCL2-associated athanogene	BAG1	NM_004323	nPTB5 // nPTB6 //	3203482	chr9	-	33237838	33255392
			nPTB7 // nPTB8 //					
chromosome 6 open reading frame	C6orf111 //	NM_032870 //	D11S636 // ZFM1 //	2966253	chr6	-	99952648	99980235
			ZNF162					
111 // ubiquitin specific peptidase	USP45	XM_371838 //	CDLS //	3699044	chr16	-	73212799	73258283
			DKFZp434L1319 //					
45		NM_013392	FLJ11203 //	3203482	chr9	-	33237838	33255392
			FLJ12597 //					
		XM_931094 //	FLJ13354 //	2966253	chr6	-	99952648	99980235
			FLJ13648 //					
		XM_931115 //	FLJ44854 // IDN3 //	3699044	chr16	-	73212799	73258283
			IDN3-B // BCON3 //					
		XM_931124 //	FLJ27109 //	3203482	chr9	-	33237838	33255392
			FLJ35541 // MADM					
		XM_939661 //	// MUDPNP // NRBP	2966253	chr6	-	99952648	99980235
			FLJ14752 //					
		XM_944255 //	FLJ14853 //	3699044	chr16	-	73212799	73258283
			FLJ14992 //					
		XM_944271 //	FLJ90147 //	3203482	chr9	-	33237838	33255392
			HSPC306 //					
		XM_944273 //	MGC104269 // RP11-	2966253	chr6	-	99952648	99980235
			9819.2 // SRP 130 //					
		NM_001080481	bA9819.2 //	3699044	chr16	-	73212799	73258283
			MGC14793					

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	Stop
dynactin 5 (p25) integrator complex subunit 10	DCTN5	NM_032486	MGC3248 // p25	3653042	chr16	+	23560236	23588668
	INTS10	NM_018142	C8orf35 // FLI10569 // INT10	3088405	chr8	+	19666766	19753848
arrestin domain containing 3 CD59 molecule, complement regulatory protein	ARRDC3	NM_020801	KIAA1376 // TLIMP	2866704	chr5	-	90700311	90782084
	CD59	NM_000611 // NM_203329 // NM_203330 // NM_203331	16.3A5 // E116 // E130 // EL32 // G344 // MGC2354 // MIC11 // MIN1 // MIN2 // MIN3 // MSK21 // PROTECTIN // p18- TWA1	3368707	chr11	-	33676397	33714806
opioid growth factor receptor chromosome 20 open reading frame 11	OGFR	NM_007346	—	3892941	chr20	+	60906461	60915796
	C20orf11	NM_017896	—	3893072	chr20	+	61039681	61050570
ERBB receptor feedback inhibitor 1	ERRF1	NM_018948	GENE-33 // MIG-6 // MIG6 // RALT	2395177	chr1	-	7987071	8194824
DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	DDX5	NM_004396	DKEZp68601190 // G17P1 // HLR1 // HUMP68 // p68 99D8.1 // CCT-beta // CCTB //	3766893	chr17	-	59924843	59935796
chaperonin containing TCP1, subunit 2 (beta)	CCT2	NM_006431	MGC142074 // MGC142076 // PRO1633 // TCP-1- beta	3421630	chr12	+	68265508	68281612
TROVE domain family, member 2	TROVE2	NM_001042369 // NM_001042370 // NM_004600	SSA2	2372924	chr1	+	191281274	191327514
casein kinase 1, delta	CSNK1D	XM_001132734 // NM_001893 // NM_139062	HCKID	3774823	chr17	-	77789955	77824878
nucleoside phosphorylase	NP	NM_000270	MGC117396 // MGC125915 // MGC125916 // PNP // PRO1837 // PUNP	3527514	chr14	+	20007398	20015985
ubiquitin C	UBC	XM_001132949 // NM_021009	HMG20	3476741	chr12	-	123962213	123965631
general transcription factor IIF, polypeptide 2, 30 kDa	GTF2F2	NM_004128	BTF4 // RAP30 // TF2F2 // TFHIF	3488094	chr13	+	44592617	44756234
RAS p21 protein activator (GTPase activating protein) 1	RASA1	NM_002890 // NM_022650	CM-AVM // CMAYM // DKEZp434N071 // GAP // PKWS // RASA // RASGAP // p120GAP	2819044	chr5	+	86599391	86724647
chromosome 8 open reading frame activator of basal transcription 1	C8orf53 ABT1	NM_032334 NM_013375	MGC14595 hABT1	3112543 2899519	chr8 chr6	+	117847923 26661709	117930859 26708945

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	
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	DKEZp762L1710 // KIAA1381 // LDLB	3733938	chr17	+	68695573	68739952 6.58
adaptor-related protein complex 1, gamma 1 subunit	APIG1	NM_001030007 // NM_001128	ADTG // CLAPG1 // MGC18255	3697799	chr16	-	70320417	70400594 6.57
UTP15, U3 small nucleolar ribonucleoprotein, homolog (<i>S. cerevisiae</i>)	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 // RH-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	FLJ16157	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	DKEZp761C169 // 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	DKEZp686F19123 // HSD25 // TLAP // TRAPB	2437871	chr1	-	154245480	154257371 6.52
RAS and EF-hand domain containing cold shock domain protein A	RASEF CSDA	NM_152573 NM_003651	FLJ1614 // RAB45 CSDA1 // DBPA // ZONAB	3211938 3444252	chr9 chr12	- -	84772206 10742960	84937805 10775038 6.52 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	CTAK1 // KP78 // PAR1A	3374698	chr1	-	59098455	59140193 6.51
MAP/microtubule affinity-regulating kinase 3	MARK3	NM_002376		3553690	chr14	+	102921419	103370656 6.50

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Array			Fold Change
				Transcript Cluster ID	Chromosome	Strand	
oxidation resistance 1	OXR1	NM_181354	FLJ10125 //	3110999	chr8	+	107834092
			FLJ38829 //				
			FLJ41673 //				
			FLJ42450 //				
ATG16 autophagy related 16-like 1 (<i>S. cerevisiae</i>)	ATG16L1	NM_198890 //	FLJ45656 //	2532793	chr2	+	233869050
			Nb1a00307				
			APG16L // ATG16L				
			// FLJ00045 //				
ankyrin repeat domain 17	ANKRD17	NM_032217 //	FLJ10035 //	2773023	chr4	-	74343428
			FLJ10828 //				
			FLJ22677 // WDR30				
			FLJ22206 // GTAR				
small nuclear ribonucleoprotein polypeptide B ^a protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	SNRBP2	NM_003092 //	// KIAA0697 // NY- BR-16	3877776	chr20	+	16645421
			MGC24807 //				
			MGC45309				
			CAR // CNC //				
chromosome 20 open reading frame 20 ADP-ribosylation-like factor 6 interacting protein 4	C20orf20	NM_018270	CNC1 //	3732885	chr17	+	64059052
			NM_212471 //				
			NM_212472				
			DKFZp779L0468 //				
pre-mRNA cleavage factor 1, 59 kDa subunit RNA binding motif protein 17 actin binding LIM protein family, member 3 asparagine synthetase domain containing 1	ARL6IP4	NM_001002251 //	MGC17251 // PKR1	3892918	chr20	+	60903524
			Eaf7 // FLJ10914 //				
			MRG15BP // MRGBP				
			MGC814 // SR-25 //				
poly(A) polymerase alpha transmembrane protein 87A KIAA0907 DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 protein tyrosine phosphatase, non- receptor type 1 insulin-like growth factor 2 mRNA binding protein 2 zinc finger protein 592	FLJ12529	NM_024811	SRp25	3375340	chr11	-	60954030
			FLJ39024 //				
			MGC9315				
			MGC14439 // SPF45				
poly(A) polymerase alpha transmembrane protein 87A KIAA0907 DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 protein tyrosine phosphatase, non- receptor type 1 insulin-like growth factor 2 mRNA binding protein 2 zinc finger protein 592	RBM17	NM_032905	HMFN1661	3233547	chr10	+	6225410
			ABLM3				
			ASNSD1				
			FLJ20752 //				
poly(A) polymerase alpha transmembrane protein 87A KIAA0907 DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 protein tyrosine phosphatase, non- receptor type 1 insulin-like growth factor 2 mRNA binding protein 2 zinc finger protein 592	PAPOLA	NM_032632	NBLA00058 //	2519860	chr2	+	190244286
			NS3TP1				
			MGC5378 // PAP				
			DKFZP564G2022				
poly(A) polymerase alpha transmembrane protein 87A KIAA0907 DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 protein tyrosine phosphatase, non- receptor type 1 insulin-like growth factor 2 mRNA binding protein 2 zinc finger protein 592	TMEM87A	NM_015497	RP11-336K24.1	3550392	chr14	+	96038038
			DDX10				
			PTPN1				
			IMP-2 // IMP2 //				
poly(A) polymerase alpha transmembrane protein 87A KIAA0907 DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 protein tyrosine phosphatase, non- receptor type 1 insulin-like growth factor 2 mRNA binding protein 2 zinc finger protein 592	IGF2BP2	NM_001007225 //	VICKZ2 // p62	3620515	chr15	-	40289650
			KIAA0211 //				
			MGC138437 //				
			MGC138439				

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	
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	2934801	chr6	+	161332723	161458399 6.42
ubiquitin specific peptidase 15	USP15	NM_006313	// MTK1 // PRO0412 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 (<i>S. cerevisiae</i>)	ATG3	NM_022488	APG3 // APG3L // DKFZp564M1178 // FLJ22125 //	2688759	chr3	-	113726408	113769332 6.39
PTPRF interacting protein, binding protein 1 (liprin beta 1)	PTPRF	NM_003622 // NM_177444	MGC15201 // PC3-96	3409211	chr12	+	27567649	27739981 6.39
flotillin 1	FLOT1	NM_005803	L2 // hSGT2 // hSGT2p	2948587	chr6	-	30796156	30818490 6.38
isolectin/4RNA 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 // FCGR3	3395416	chr11	-	122429309	122438895 6.33

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Array				Fold Change
				Transcript Cluster ID	Chromosome	Strand	Start	Stop
cullin-associated and neddylation-dissociated 1	CAND1	NM_018448	DKFZp343M1414 // FLJ10114 // FLJ10929 // FLJ38691 // FLJ90441 // KIAA0829 // TIP120 // TIP120A BKLDHD4 // FLJ10450 // HSPC252 IPOA3 // MGC12217 // MGC26703 // QIP1 // SRP3 FLJ14827	3420713	chr12	+	65946048	65994719
kelch repeat and BTB (POZ) domain containing 4 karyopherin alpha 4 (importin alpha 3)	KBTD4 KPNA4	NM_016506 // NM_018095 NM_002268		3372337 2703217	chr11 chr3	- -	47550326 161663997	47557362 161766070
chromosome 12 open reading frame 52 aurora kinase A // serine/threonine kinase 6 pseudogene	C12orf52 AURKA // STK6P	NM_032848 NM_003600 // NM_198433 // NM_198434 // NM_198435 // NM_198436 // NM_198437 // NR_001587 NM_004094	AIK // ARK1 // AURA // AURORA2 // BTAK // MGC34538 // STK15 // STK6 // STK7 // —	3432641 3910785	chr12 chr20	+	112107758 54377855	112114543 54402553
eukaryotic translation initiation factor 2, subunit 1 alpha, 35 kDa	EIF2S1		EIF-2 // EIF-2A // EIF-2alpha // EIF2 // EIF2A	3541137	chr14	+	66896518	66922983
ubiquitin specific peptidase 7 (herpes virus-associated) SH3 domain containing ring finger 2	USP7 SH3RF2	NM_003470 NM_152550	HAUSP // TEF1 FLJ23654 // MGC149788 // MGC149789 // MGC90410 // PBG-D // PBGD // UPS	3679564 2833924	chr16 chr5	- +	8893458 145296335	8964832 145441529
hydroxymethylbilane synthase	HMBS	NM_000190 // NM_001024382 NM_001968	MGC11573 DKFZP434E098 // FLJ23364 // KIAA1172 // SRA4	3351841	chr11	+	118460803	118470689
eukaryotic translation initiation factor 4E	EIF4E		CBP // EIF4E1 // EIF4EL1 // EIF4F // MGC11573	2778980	chr4	-	99888790	100070801
splicing factor, arginine/serine-rich 15	SFRS15	NM_020706	DKFZP434E098 // FLJ23364 // KIAA1172 // SRA4	3928866	chr21	-	31965222	32077764
gem (nuclear organelle) associated protein 5 TNF receptor-associated factor 6	GEMIN5 TRAF6	NM_015465 NM_004620 // NM_145803 NM_000268 // NM_016418 // NM_181825 // NM_181828 // NM_181829 //	DKFZP586M1824 // MGC142174 MGC: 3310 // RNF85	2882897 3369890	chr5 chr11	- -	154247066 36465173	154309713 36488940
neurofibromin 2 (bilateral acoustic neuroma)	NF2		ACN // BDNF // Merlin // SCH	3942062	chr22	+	28329446	28424577

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Array				Fold Change
				Transcript Cluster ID	Chromosome	Strand	Start	Stop
structural maintenance of chromosomes 3	SMC3	NM_181830 //	BAM // BMH //	3263790	chr10	+	112317039	112365483
		NM_181831 //	CSFG6 // HCAP //					
		NM_181832 //	SMC3L1					
		NM_181833	KIAA1010 // TUBA	3303165	chr10	-	101624846	101759656
dynamitin binding protein	DNMBP	NM_015221	CST6 // EPM1 //	3934245	chr21	-	44016298	44020687
cystatin B (stefin B)	CSTB	NM_000100	PME // STFB					
mucin 20, cell surface associated	MUC20	NM_152673	FLJ14408 //	2659039	chr3	+	196867150	196953662
			KIAA1359					
tuberous sclerosis 1	TSC1	NM_000368 //	KIAA0243 // LAM //	3228373	chr9	-	134756560	134809831
abl interactor 2	ABI2	NM_001008567	MGC86987 // TSC					
		NM_001126750 //	ABI-2 // ABI2B //	2523689	chr2	+	203901161	204005128
		NM_005759	AIP-1 // AbiBP3 //					
			SSH3BP2 // argBPIA // argBP1B					
golgi reassembly stacking protein 2, 55 kDa // dehydrogenase/reductase (SDR family) member 9	GORASP2 // DHRS9	NM_015530 //	DKFZP434D156 //	2515050	chr2	+	171457150	171551619
		NM_005771 //	FLJ13139 // GOLPH6					
		NM_199204	// GRASP55 // GRS2					
			// p59 // 3alpha-HSD // RDH15 // RDHL // RETSDR8					
ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	ATP2A2	NM_001681 //	ATP2B // DAR // DD	3431483	chr12	+	109203332	109352495
		NM_170665	// MGC45367 //					
hypothetical protein HSPC148 EH-domain containing 1	HSPC148 EHD1	NM_016403	SERCA2					
		NM_006795	FLJ42622 //	3387171	chr11	-	94322815	94346692
			FLJ44618 // H-PAST // HPAST1 // PAST // PAST1	3377226	chr11	-	64376790	64404202
X-box binding protein 1 enhancer of zeste homolog 2 (<i>Drosophila</i>) SEC24 related gene family, member B (<i>S. cerevisiae</i>)	XBP1 EZH2 SEC24B	NM_001079539 //	TREB5 // XBP2	3956589	chr22	-	27520140	27526564
		NM_005080						
		NM_004456 //	ENX-1 // EZH1 //	3078348	chr7	-	148135436	148212647
		NM_152998	MGC9169					
RAB, member RAS oncogene family- like 5	RABL5	NM_001130118 //	MGC48822 // SEC24	2739079	chr4	+	110510304	110681811
		NM_006323						
RCD1 required for cell differentiation 1 homolog (<i>S. pombe</i>) // phospholipase C, delta 4	RQCD1 // PLCD4	NM_022777	DKFZp761N0823 //	3064638	chr7	-	100742601	100751793
			FLJ13225 //					
			FLJ14117					
		NM_005444 //	CNOT9 // RCD1 //	2527856	chr2	+	219141552	219170027
		NM_032726	RCD1+ // MGC12837					

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Array				Fold Change
				Transcript Cluster ID	Chromosome	Strand	Start	Stop
poly(IG) binding protein 2	PCBP2	NM_005016 // NM_031989	HNRP2 // MGC110998 // hnRNP-E2	3416036	chr12	+	52132173	52161417
solute carrier family 30 (zinc transporter), member 9	SLC30A9	NM_006345	C4orf1 // GAC63 // HUEL // ZNT9	2725381	chr4	+	41684531	41812215
zinc finger protein 192	ZNF192	NM_006298	LD5-1 // ZKSCAN8	2900299	chr6	+	28217285	28232872
jumonji domain containing 2A	JMJD2A	NM_014663	JHDM3A // JMJD2 // KIAA0677	2333429	chr1	+	43888407	43943994
HtrA serine peptidase 2	HTRA2	NM_013247 // NM_145074	OMI // PARK13 // PRSS25	2489411	chr2	+	74609783	74614240
epidermal growth factor receptor pathway substrate 8	EP8	NM_004447	—	3445908	chr12	-	15664367	15833589
glutamine and serine rich 1	QSER1	NM_024774 // NM_001076786	FLJ21924	3325768	chr11	+	32871321	32971438
phosphomannomutase 2	PMM2	NM_000303	CDG1 // CDG1a // CDGS	3647504	chr16	+	8798971	8850664
DEAH (Asp-Glu-Ala-His) box polypeptide 15	DHX15	NM_001358	DBP1 // DDX15 // HRH2 // PRP43 // PRPF43 // PRP43p	2763805	chr4	-	24128159	24250940
transforming growth factor, beta receptor II (70/80 kDa)	TGFBR2	NM_001024847 // NM_003242	AAAT3 // FAA3 // HNPC6 // MFS2 // RIIC // TAAAD2 // TGFBR-2 // TGFbeta-RII	2615360	chr3	+	30492214	30710745
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
HLA-B associated transcript 4	BAT4	NM_033177	ANKRD59 // D6S54E // G5 // GPANK1 // GPATCH10	2949210	chr6	-	31736995	31742029
COX4 neighbor	COX4NB	NM_006067	C16orf4 // NOC4	3703164	chr16	-	84362936	84391266
RNA binding motif protein 7	RBM7	NM_016090	FLJ11153	3349918	chr11	+	113776539	113790335
suppressor of Ty 4 homolog 1 (<i>S. cerevisiae</i>)	SUPT4H1	NM_003168	SPT4H // SUPT4H	3764384	chr17	-	53777538	53784705
PRP4 pre-mRNA processing factor 4 homolog B (yeast)	PRPF4B	NM_003913	KIAA0536 // PR4H // PRP4 // PRP4H // PRP4K // dJ1013A10.1	2892738	chr6	+	3966500	4010215
phosphoglycerate kinase 1	PGK1	NM_000291	MGC117307 // MGC142128 // MGC8947 // MIG10 // PGKA	3982462	chrX	+	77207320	77269191

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	
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 // NM_052932	ABC29 // ABCC // DKFZp686N04233 // DKFZp781G125 // GS-X // MRP // MRP1	3649890	chr16	+	15950935	6.18
transmembrane protein 123	TMEM123	NM_052932	KCT3 // PORIMIN // PORMIN	3388631	chr11	-	101772285	6.18
SEH1-like (<i>S. cerevisiae</i>)	SEH1L	NM_001013437 // NM_031216	SEC13L // SEH1A // SEHUB // Sehl	3779756	chr18	+	12886655	6.17
ferritin, heavy polypeptide-like 7 //	FTHL7 //	NR_002202 //	—// FTH // FTHL6	3375648	chr11	-	61488337	6.16
ferritin, heavy polypeptide 1 //	FTH1 //	NM_002032 //	// MGC104426 //					
ferritin, heavy polypeptide-like 3 //	FTHL3 //	NR_002201 //	PIG15 // PLIF //					
ferritin, heavy polypeptide	FTHP1 //	NR_002205 //	FTHL5					
pseudogene 1 // ferritin, heavy	FTHL12 //	NR_002204 //						
polypeptide-like 12 // ferritin, heavy	FTHL11 //	NR_002203						
polypeptide-like 11 // ferritin, heavy	FTHL8							
DNA polymerase-transactivated protein 6	DNATP6	NM_015535	DKFZp564A2416	2522094	chr2	+	200879035	6.15
serologically defined colon cancer antigen 10	SDCCAG10	NM_003869	NY-CO-10	2812120	chr5	+	64100099	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	6.15
tetratricopeptide repeat domain 17	TTC17	NM_018259	DKFZp686D20222 // FLJ10890 // FLJ13099 // FLJ23673	3327948	chr11	+	43337004	6.13
polymerase (RNA) III (DNA directed) polypeptide E (80 KD)	POLR3E	NM_018119	RPC5 // SIN	3652489	chr16	+	22216140	6.13
bromodomain containing 1	BRD1	NM_014577	BRL // BRPF1 // BRPF2	3965314	chr22	-	48552694	6.12
SET translocation (myeloid leukemia-associated)	SET	NM_003011	DKFZp686F0325	3190659	chr9	+	130485775	6.12
glutamate-cysteine ligase, catalytic subunit	GCLC	NM_001498	2PP2A // I2PP2A // IGAAD // PHAPII // TAF-IBETA	2957700	chr6	-	53438876	6.12
SCY1-like 2 (<i>S. cerevisiae</i>)	SCYL2	NM_017988	GCS // GLCL // GLCLC	3428131	chr12	+	99185070	6.12
ribosomal protein L8	RPL8	NM_000973 // NM_033301	CVAK104 // FLJ10074 //	3159040	chr8	-	145985994	6.11
protein tyrosine phosphatase type IVA, member 1	PTP4A1	NM_003463	—	2911903	chr6	+	64289625	6.10
			DKFZp779M0721 // HH72 // PRL-1 // PRL1 // PTP(CAAX1) // PTPCAAX1					

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Array				Fold Change
				Transcript Cluster ID	Chromosome	Strand	Start	Stop
Rac GTPase activating protein 1	RACGAP1	NM_013277	H3CYK-4 // ID-GAP // MgcRacGAP	3454223	chr12	-	48657002	48705537
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
translocation protein 1	TL0C1	NM_003262	Drp1 // FLJ32803 // HTP1 // SEC62	2651782	chr3	+	171166446	171194653
muscleblind-like (<i>Drosophila</i>)	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
chromosome X open reading frame 40A // chromosome X open reading frame 40B	CXorf40A // CXorf40B	NM_178124 // NM_001013845	CXorf40 // EOLA1 // —	3994451	chrX	+	148413672	148439412
ubiquitin B // chromosome 17 open reading frame 45	UBB // C17orf45	NM_018955 // NM_152350	FLJ25987 // MGC8385 // FLJ25777 // MGC40157	3712041	chr17	+	16223047	16228977
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
smu-1 suppressor of nec-8 and unc-52 homolog (<i>C. elegans</i>)	SMU1	NM_018225	BWD // FLJ10805 // FLJ11970 // MGC117363 // RP11-54K16.3 // SMU-1	3203382	chr9	-	33031772	33072208
annexin A2	ANXA2	NM_001002857 // NM_001002858 // NM_004039	ANX2 // ANX2L4 // CALIH // LIP2 // LPC2 // LPC2D // P36 // PAP-IV	3627248	chr15	-	58247806	58482354
COP9 constitutive photomorphogenic homolog subunit 7B (<i>Arabidopsis</i>)	COPS7B	NM_022730	FLJ12612 // MGC111077	2532064	chr2	+	232354256	232382342
chromosome 1 open reading frame 174	C1orf174	NM_207356	RP13-531C17.2	2393816	chr1	-	3791939	3812760
v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	ETS2	NM_005239	—	3921068	chr21	+	39059147	39118744
actinin, alpha 4	ACTN4	NM_004924	DKFZp686K23158 // FSGS1	3832643	chr19	+	43830130	43913003
protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	PPP2CA	NM_002715	PP2Ac // PP2CA // RP-C	2876046	chr5	-	133557588	133589841
glycogen synthase kinase 3 beta	GSK3B	NM_002093	—	2691014	chr3	-	121018519	121297142
hypothetical protein FLJ14154	FLJ14154	NM_024845	—	3645901	chr16	+	3433714	3476953

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	
poliovirus receptor-related 2 (herpesvirus entry mediator B) DnaJ homolog subfamily A member 5	PVRL2	NM_001042724 // NM_002856	CD112 // HVEB // PRR2 // PVRR2	3835814	chr19	+	50041409	50084314
	DNAJ5	NM_001012339 // NM_194283	—	2806256	chr5	+	34965441	34994822
	ZRANB2	NM_005455 // NM_203350	DKEZp686J1831 // DKEZp686N09117 // FLJ41119 // ZIS // ZIS1 // ZIS2 //	2418000	chr1	-	71292434	71355820
								6.03
GDP dissociation inhibitor 2	GDI2	NM_001494	ZNF265 FLJ16452 // FLJ37352 //	3275132	chr10	-	5844502	5924081
								6.03
transmembrane protein 138 CDC28 protein kinase regulatory subunit 2 ADAM metalloproteinase domain 10	TMEM138	NM_016464	RABGDIB	3332886	chr11	+	60885939	60900898
	CKS2	NM_001827	HSPC196 CKSHS2	3178583	chr9	+	91050736	91121542
	ADAM10	NM_001110	CD156c // HsT18717 // MADM // kuz	3626555	chr15	-	56651514	56829469
								6.00
telomeric repeat binding factor 2 elongation factor, RNA polymerase II, proteasome maturation protein	TERF2	NM_005652	TRBF2 // TRF2	3696571	chr16	-	67946973	68001605
	ELL2	NM_012081	—	2867873	chr5	-	95246561	95237333
	POMP	NM_015932	C13orf12 // HSPC014 // PNAS-110 //	3483348	chr13	+	28125188	28151050
								5.99
mitochondrial ribosomal protein L16 glucosaminyl (N-acetyl) transferase 3, mucin type KIAA0409 tannase 1 binding protein 1, 182 kDa	MRPL16	NM_017840	UMP1 FLJ20484 // L16mt // PNAS-111	3374856	chr11	-	59330154	59334921
	GCNT3	NM_004751	C24Gnt // C2GntF- M // C2Gnt2 //	3596147	chr15	+	57628756	57719710
	KIAA0409	NM_015324	RRP8	3360982	chr11	-	6492639	6582206
	TNKS1BP1	NM_033396	FLJ45975 // KIAA1741 // TAB182	3373675	chr11	-	56823694	56848992
polymerase (RNA) I polypeptide E, 53 kDa	POLR1E	NMP_022490	FLJ13390 // PAF53 // PRAF1 // RP11- 405L183	3168938	chr9	+	37475945	37500379
								5.97
E3 ubiquitin protein ligase, HECT domain containing, 1	EDD1	NM_015902	DD5 // EDD // FLJ11310 // HYD //	3147321	chr8	-	103333634	103493671
								5.97
G protein-coupled receptor, family C, group 5, member A fragile X mental retardation 1 thyroid hormone receptor associated protein 2	GPRC5A	NM_003979	MGC57263 GPCR5A // RA13 //	3405587	chr12	+	12929011	12986488
	FMR1	NM_002024	RAIG1 FMRP // FRAXA //	3994100	chrX	+	146801098	146840329
	THRAP2	NM_015335	MGC87458 DKEZp781D0112 //	3473083	chr12	-	114868953	115419724
			FLJ21627 // KIAA1025 // MED13L // PROSIT240 // TRAP240L					5.96

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	Stop
epithelial membrane protein 1	EMP1	NM_001423	CL-20 // EMP-1 // TMP	3405748	chr12	+	13230082	13264499
SUMO1/sentrin specific peptidase 5	SENPS	NM_152699	FLJ42398 // MGC27076	2659631	chr3	+	198079101	198143960
FUS interacting protein (serine/arginine-rich) 1	FUSIP1	NM_006625 // NM_054016	FUSIP2 // NSSR // SFRS13 // SRP38 // SRP40 // TASR // TASR1 // TASR2	4045780	chr1_random	-	1493804	1514582
UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast)	UTP14A	NM_006649	KIAA0266 // NY-CO-16 // SDCCAG16 // dJ537K23.3	3990566	chrX	+	128832975	128912087
cell division cycle associated 3	CDCA3	NM_031299	GRCC8 // MGC2577 // TOME-1	3442322	chr12	-	6824231	6831482
zinc finger, AN1-type domain 3	ZFAND3	NM_021943	FLJ13222 // TEX27	2905664	chr6	+	37895285	38231400
glucocorticoid receptor DNA binding factor 1	GRLF1	NM_004491	GRF-1 // KIAA1722 // MGC10745 // P190-A // P190A // p190RhoGAP	3837001	chr19	+	52113779	52200169
GPI-anchored membrane protein 1	GPIAP1	NM_005898 // NM_203364	GPP137 // MI151 // p137GPI	3326183	chr11	+	34009711	34081946
AT hook containing transcription factor 1	AHCTF1	XM_001126456 // NM_015446	DKFZp434N093 // ELYS // MST108 // MSTP108 // TMSB62	2465324	chr1	-	245069027	245162066
aurora kinase B	AURKB	NM_004217	AIK2 // AIM-1 // AIM1 // ARK2 // AurB // IPL1 // STK12 // STK5	3744263	chr17	-	8034636	8054649
ariadne homolog 2 (<i>Drosophila</i>)	ARIH2	NM_006321	ARI2 // FLJ10938 // FLJ3921 // TRIAD1	2621827	chr3	+	48930742	48997971
chromosome 11 open reading frame 68	C11orf68	NM_031450	Bles03 // P5326	3378007	chr1	-	65440893	65443107
nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	NFKBIA	NM_020529	IKBA // MAD-3 // NFKBI	3561039	chr14	-	34940473	34944214
caveolin binding protein	CACYBP	NM_001007214 // NM_014412	GIG5 // MGC87971 // PNAS-107 // RPI-102G20.6 // SI00A6BP // SIP	2368198	chr1	+	173235214	173247469
zinc finger protein 593	ZNF593	NM_015871	ZT86	2326311	chr1	+	26368813	26371688
proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	PSMD2	NM_002808	MGC14274 // P97 // S2 // TRAP2	2655650	chr3	+	185499199	185509504
YY1 transcription factor	YY1	NM_003403	DELTA // NF-E1 // UCRBP // YIN-YANG-1	3551677	chr14	+	99750383	99818868
Smith-Magenis syndrome chromosome region, candidate 7-like	SMCR7L	NM_019008	FLJ20232 // HSU79252 // dJ1104E15.3	3945877	chr22	+	38226061	38244079

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	
CDC-like kinase 1	CLK1	NM_001024646 // NM_004071	CLK // CLK/STY // STY	2594497	chr2	-	201425997	201437659
phosphatidylinositol transfer protein, beta	PTPNB	NM_012399	PT-TP-beta //	3956290	chr22	-	26577440	26645487
A kinase (PRKA) anchor protein 8- like	AKAP8L	NM_014371	PtdInsTP // VIB1B DKEZp434L0650 // HAP95 // NAKAP //	3853345	chr19	-	15351869	15390819
chromosome 17 open reading frame 70	C17orf70	NM_025161	NAKAP95 FLJ212175 //	3773980	chr17	-	77117366	77130137
ring finger protein 34	RNF34	NM_025126 // NM_194271	FLJ21786 // RFI // RIF // RIFF	3434823	chr12	+	120322070	120352805
solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	SLC7A6	NM_001076785 // NM_003983	DKEZp686K15246 // KIAA0245 // LAT-2 // LAT3 // y+LAT-2	3666146	chr16	+	66855932	66893223
solute carrier family 39 (zinc transporter), member 14	SLC39A14	NM_015359	KIAA0062 // LZT-Hs4 // ZIP14 // cig19	3089360	chr8	+	22280765	22347587
PI-3-kinase-related kinase SMG-1	SMG1	NM_015092	61E3.4 // ATX // KIAA0421 // LIP	3683050	chr16	-	18719381	18845318
zinc finger protein 259	ZNF259	NM_003904	MGC110983 // ZPR1	3392871	chr11	-	116153652	116163944
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11, 17.3 kDa	NDUFB11	NM_019056	ESSS // FLJ20494 // MGC111182 //	4007009	chrX	-	46886563	46902114
heterogeneous nuclear ribonucleoprotein L1 (scaffold attachment factor A)	HNRPU	NM_004501 // NM_031844	NP17.3 // Np15 // HNRNPU // SAF-A // U2L1	2464499	chr1	-	243078713	243094975
BCL2-like 1	BCL2L1	NM_001191 // NM_138578	BCL-XL/S // BCL2L // BCLX // Bel-X // DKEZp781P2092 //	3902489	chr20	-	29715925	29775453
stem-loop (histone) binding protein retinitis pigmentosa 2 (X-linked recessive)	SLBP RP2	NM_006527 NM_006915	bel-xL // bel-xS HBP	2757319 3975869	chr4 chrX	- +	1664276 46381319	1684080 46637601
cullin 4A	CUL4A	NM_001008895 // NM_003589	KIAA0215 // TBCCD2	3502497	chr13	+	112905835	112967356
tripartite motif-containing 28	TRIM28	NM_005762	—	3844238	chr19	+	63740597	63753931
DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	DDX39	NM_005804	FLJ29029 // KAP1 // RNF96 // TIF1B // TIF1B	3852691	chr19	-	14380562	14404078
lectin, galactoside-binding, soluble, 8 (galectin 8)	LGALS8	NM_006499 // NM_201543 // NM_201544 // NM_201545	BAT1 // BAT1L // DDXL // MGC18203 // MGC8417 // URH49	2386867	chr1	+	234717161	234782890
ankyrin repeat domain 10	ANKRD10	NM_017664	Gal-8 // PCTA-1 // PCTA1 // Po66-CBP	3525679	chr13	-	110322146	110365417

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	
zinc finger and BTB domain containing 9 // synaptic Ras GTPase activating protein 1 homolog (rat)	ZBTB9 // SYNGAP1	NM_152735 //	MG23166 //	2903703	chr6	+	33494813	33533290
		NM_006772	DKFZp761G1421 // KIAA1938 // RASA1 // RASA5 // FLJ20533					
transmembrane protein 70	TMEM70	NM_001040613 //		3103494	chr8	+	75046321	75057572
afipilin	AFTPH	NM_017866	FLJ20080 //	2485433	chr2	+	64604969	64714437
		NM_001002243 //	FLJ23793 //					
		NM_017657 //	MG233965 //					
		NM_203437	Nblat0388					
polymerase (RNA) 1 polypeptide A, 194 kDa	POLR1A	NM_015425	DKFZP586M0122 //	2562605	chr2	-	86103197	86186509
			FLJ21915 //					
			MG287965 // RPA1 // RPO1-4					
general transcription factor IIIC, polypeptide 5, 63 kDa	GTF3C5	NM_012087	FLJ20857 // TFIIIC63 // TFIIICepsilon // TfrilC2-63	3192653	chr9	+	134895917	134923708
tumor necrosis factor receptor superfamily, member 21	TNFRSF21	NM_014452	BM-018 // DR6 //	2956052	chr6	-	47307230	47385639
sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B	SEMA4B	NM_020210 //	MG231965	3607927	chr15	+	88529156	88573879
		NM_198925	KIAA1745 // MG231831 // SEMAC // SemC					
mitochondrial ribosomal protein S11	MRPS11	NM_022839 //	FLJ22512 //	3607183	chr15	+	86811688	86822612
		NM_176805	FLJ23406 // HCC-2					
nuclear factor of activated T-cells 5, tonicity-responsive	NEAT5	NM_006599 //	KIAA0827 // NF-AT5 // NFATL1 // NFATZ // OREBP // TONEBP	3666779	chr16	+	68156498	68296054
		NM_138713 //						
		NM_138714 //						
		NM_173214 //						
		NM_173215						
nuclear receptor subfamily 2, group F, member 2	NR2F2	NM_021005	ARP1 // COUP-TFII // COUP-TFB // MG2117452 //	3610110	chr15	+	94448164	94683620
			SVP40 // TFCOUP2					
SH3 domain containing ring finger 1	SH3RF1	NM_020870	FLJ21602 //	2793137	chr4	-	170220651	170428725
			KIAA1494 // POSH // RNF142 //					
splicing factor 3b, subunit 3, 130 kDa	SF3B3	NM_012426	KIAA0017 // RSE1 // SAP130 // SF3b130 // STAF130	3667281	chr16	+	69115212	69169072
PTC7 protein phosphatase homolog (<i>S. cerevisiae</i>)	PPTC7	NM_139283	DKFZp686M07120 //	3471300	chr12	-	109455446	109514152
			MG2133072 // TA-PP2C					
homeodomain interacting protein kinase 1	HIPK1	NM_152696 //	KIAA0630 //	2352758	chr1	+	114273467	114322014
		NM_181358 //	MG26642 //					
		NM_198268 //	MG233446 //					

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	
nuclear receptor binding protein 1	NRBP1	NM_198269	MG33548 // Myak // Nbk2	2474527	chr2	+	27504171	27518620
		NM_013392	BCON3 // FLU27109 // FLJ35541 // MADM // MUDPNP // NRBP					
cleavage stimulation factor, 3' pre-RNA, subunit 1, 50 kDa	CSTF1	NM_001033521 // NM_001033522 // NM_001324 NM_005746 // —	Cstf-50 // CstfP50	3890154	chr20	+	54393411	54413257
pre-B-cell colony enhancing factor 1 // pre-B cell enhancing factor 1 pseudogene	PBEF1 // RP11- 92J19.4	NM_001324 NM_005746 // —	1110035014Rik // DKFZP666B131 // MGC117256 // NAMPT // PBEF // LOC646309 C17orf35 // PM1 // PMI	3066818	chr7	-	105625846	105713266
transmembrane protein 11	TMEM11	NM_003876	LOC646309	3749767	chr17	-	21041205	21058509
transmembrane protein 115	TMEM115	NM_007024	PMI	2675304	chr3	-	50367198	50372046
catenin (cadherin-associated protein), alpha-like 1	CTNNA1	NM_003798	CLLP // alpha-CATU	3219621	chr9	-	110744011	110815625
clathrin, heavy chain (Hc)	CLTC	NM_004859	CHC17 // CLH-17 // CLTC12 // Hc //	3729172	chr17	+	55052021	55127299
cyclin H	CCNH	NM_001239	KIAA0034	2865860	chr5	-	86707385	86782317
SECIS binding protein 2	SECISBP2	NM_024077	CAK // p34 // p37 DKFZp686C09169 // SBP2	3178611	chr9	+	91122988	91146214
WD repeat domain 26	WDR26	NM_025160	FLJ21016 // MIP2	2458082	chr1	-	222639474	222691338
stomatin (EPB72)-like 2 // Fanconianemia, complementation group G	STOML2 // FANCG	NM_013442 // NM_004629	HSPC108 // SLP-2 // FAG // XRCC9	3204534	chr9	-	35089540	35093157
nucleolar and coiled-body phosphoprotein 1	NOLC1	NM_004741	KIAA0035 // NOPP130 // NOPP140 //	3261492	chr10	+	103901962	103913597
ADP-ribosylhydrolase like 2	ADPRHL2	NM_017825	NS5ATP13 // P130	2330253	chr1	+	36327093	36332113
chromosome 1 open reading frame 164	C1orf164	NM_018150	ARH3 // FLJ20446 // dJ665N4.2 FLJ10597	2333907	chr1	+	44643293	44889968
platelet-activating factor acetylhydrolase, isoform Ib, beta subunit 30 kDa	PAFAH1B2	NM_002572	—	3350749	chr11	+	116520229	116552810
DPH2 homolog (<i>S. cerevisiae</i>) // 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 // HAIPL // VMA16	2333635	chr1	+	44208244	44211909
chromosome 4 open reading frame 14	C4orf14	NM_032313	MGC33232 // hAINOS1 //	2770427	chr4	-	57496489	57539746

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	
ST3 beta-galactoside alpha-2,3-sialyltransferase 4	ST3GAL4	NM_006278	CGS23 // FLJ11867 // NANT3 // SAT3 // SIAT4 // SIAT4C // ST3Gal IV // ST3GalIV // STZ	3355145	chr11	+	125730175	126063667
myeloid differentiation primary response gene (88)	MYD88	NM_002468	—	2617563	chr3	+	38155029	38159513
interferon-related developmental regulator 2	IFRD2	NM_006764	FLJ40446 // IFNRP // SKMe1.5 // SMI5	2675088	chr3	-	50300134	50305282
TNF receptor-associated factor 4	TRAF4	NM_145751 // NM_004295	CART1 // MLN62 // RNF83	3715839	chr17	+	24095168	24102103
Kruppel-like factor 5 (intestinal)	KLF5	NM_001730	BTEB2 // CKLF // IKLF	3493543	chr13	+	72527115	72549671
melanophilin	MLPH	NM_001042467 // NM_024101	MGC2771 // MGC59733 // SLAC2-A	2534252	chr2	+	238025804	238135783
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'-3' exoribonuclease 2	XRN2	NM_012255	—	3879467	chr20	+	21219705	21322172
large subunit GTPase 1 homolog (<i>S. cerevisiae</i>)	LSG1	NM_018385	FLJ11301	2711818	chr3	-	195842815	195874226
ubiquitin protein ligase E3C	UBE3C	NM_014671	KIAA0010 // KIAA10	3033924	chr7	+	156624381	156754823
Rho GTPase-activating protein	RICS	NM_014715	GC-GAP // GRIT // KIAA0712 // MGC1892 // p200RhoGAP // p250GAP	3397877	chr11	-	128343040	128567297
v-rat murine sarcoma viral oncogene homolog B1	BRAF	NM_004333	B-raf1 // BRAF1 // MGC126806 // MGC138284 // 2H9	3076340	chr7	-	139994192	140274640
heterogeneous nuclear ribonucleoprotein H3 (2H9)	HNRPH3	NM_012207 // NM_021644	CML66 // FLJ14991	3249738	chr10	+	69760947	69772949
NudC domain containing 1	NUDCD1	NM_032869	—	3148796	chr8	-	110322324	110415934
GATA binding protein 6	GATA6	NM_005257	—	3781245	chr18	-	18003412	18060817
preimplantation protein 3 // heat shock 10 kDa protein 1 (chaperonin 10)	PREH3 // HSPE1	NM_015387 // NM_199482 // NM_002157	2C4D // CGF-95 // MGC12264 // MOB1 // MOB3 // CPN10 // GROES // HSP10 MGC13251	2521500	chr2	+	198088565	198125849
chromosome 14 open reading frame 151	C14orf151	NM_032714	—	3554282	chr14	+	104227008	104244902
ADAM metalloproteinase domain 9	ADAM9	NM_001005845 // NM_003816	KIAA0021 // MCMP // MDC9 // Mltng	3095002	chr8	+	38973642	39082294
target of EGFR1, member 1 (nuclear)	TOE1	NM_025077	FLJ13949	2334319	chr1	+	45577929	45582381
acidic (leucine-rich) nuclear phosphoprotein 32 family, member B	ANP32B	NM_006401	APRIL // PHAP12 // SSP29	3181417	chr9	+	99784907	99823167

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	
cleavage and polyadenylation specific factor 4, 30 kDa IK cytokine, down-regulator of HLA II phosphoribosyl pyrophosphate amidotransferase proteasome (prosome, macropain) 26S subunit, ATPase, 2 N-acetyltransferase 5	CPSF4	NM_001081559 // NM_006693 NM_006083	CPSF30 // NAR // NEB1 OSA2 // IK protein // MGC59741 // RED ATASE // GPAT	3014764	chr7	+	98874515	98905314
	IK			2831932	chr5	+	140006890	140022229
	PPAT	NM_002703		2770242	chr4	-	56954288	57029053
	PSMC2	NM_002803	MGC3004 // MSS1 // Nblal.0058 // S7	3017206	chr7	+	102771969	102797076
	NAT5	NM_016100 // NM_181527 //	NAT3 // dJ1002M8.1	3878934	chr20	+	19935711	19962808
USP6 N-terminal like	USP6NL	NM_181528 XM_374768 // XM_927409 // XM_938665 // XM_943800 // NM_001080491 NM_006331	KIAA0019 // RNTRE // TRE2NL	3277468	chr10	-	11523200	11725919
EMG1 nucleolar protein homolog (<i>S. cerevisiae</i>) glutaminase	EMG1 GLS	NM_014905	C2F // Grec2f // NEP1 DKFZp686015119 // FLJ10358 // GLS1 //	3403140 2520291	chr12 chr2	+	6949871 191453802	6966191 191538513
pleiomorphic adenoma gene-like 2 TM2 domain containing 3	PLAGL2 TM2D3	NM_002657 NM_025141 // NM_078474	KIAA0838 FLJ23283 BLP2	3902682 3642358	chr20 chr15	- -	30243975 99977972	30259284 100010609
SEC24 related gene family, member C (<i>S. cerevisiae</i>) ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	SEC24C UBE2D3	NM_004922 // NM_198597 NM_003340 // NM_181886 // NM_181887 // NM_181888 // NM_181889 // NM_181890 // NM_181891 // NM_181892 // NM_181893	KIAA0079 E217/KCB3 // MGC43926 // MGC5416 // UBC4/5 // UBCH5C	3251848 2779992	chr10 chr4	+	75174138	75210008
Rho guanine nucleotide exchange factor (GEF) 7	ARHGEF7	NM_003899 // NM_145735	BETA-PIX // COOL1 // DKFZp761K1021 // KIAA0142 // KIAA0142 // Nblal0314 // P50 // P50BP // P85 // P85COOL1 // P85SPR // PAK3 // HRCA1 // MGC31961 // RCA1 // TRC8	3501661	chr13	+	110565635	110756075
ring-finger protein 139	RNF139	NM_007218		3114618	chr8	+	1255556189	125570389

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	
valosin-containing protein // Fanconi anemia, complementation group G	VCF //	NM_007126	IBMPFD //	3204404	chr9	-	35026106	5.58
	FANCG	NM_004629	MGC131997 //					
			MGC148092 //					
ADP-ribosylation factor 1	ARF1	NM_001024226 //	MGC8560 // TERA //					
		NM_001024227 //	p97 // FAG //	2383726	chr1	+	226313262	5.58
		NM_001024228 //	—					
bladder cancer associated protein heterogeneous nuclear ribonucleoprotein H1 (H)	BLCAP	NM_001658	BC10	3904928	chr20	-	35554050	5.57
	HNRPH1	NM_006698	DKEZp686A15170 //	2890148	chr5	-	178970155	5.57
		NM_005520	HNRPH // hmRNP					
programmed cell death 2-like TNF receptor-associated factor 2	PDCD2L	NM_032346	MGC13096	3829751	chr19	+	39587143	5.57
	TRAF2	NM_021138	MGC: 45012 // TRAP	3194896	chr9	+	138896205	5.56
			// TRAP3					
ring finger protein 43	RNF43	NM_017763	DKEZp781H02126 //	3764399	chr17	-	53785272	5.56
			DKEZp781H0392 //					
			FLJ20315 //					
tousled-like kinase 1	TLK1	NM_012290	MGC125630 //					
			RNF124 // URCC	2586603	chr2	-	171538552	5.55
			KIAA0137 // PKU-					
suppressor of zeste 12 homolog (<i>Drosophila</i>)	SUZ12	NM_015355	BETA	3717395	chr17	+	27258855	5.55
			CHET9 // JIAZ1 //					
			KIAA0160					
dynactin 4 (p62)	DCTN4	NM_016221	—	2881554	chr5	-	150065753	5.54
	LRR1 //	NM_018214 //	FLJ10775 //	2910680	chr6	+	53695560	5.54
	leucine rich repeat containing 1 // chromosome 20 open reading frame 44	NM_018244 //	FLJ11834 // LANO					
GTPase activating protein (SH3 domain) binding protein 2 // NMDA receptor regulated 2 // RAR-related orphan receptor A	G3BP2 //	NM_012297 //	// d523E19.1 //					
	NARG2 //	NM_203504 //	BFZB // CBP3 //					
	RORA	NM_203505 //	MGC104353 //					
ubiquitin specific peptidase 3		NM_001018089 //	MGC141902	2773756	chr4	-	76786807	5.54
		NM_024611 //	— // MGC119326 //					
		NM_002943 //	MGC119329 //					
peptidylprolyl isomerase (cyclophilin)-like 4 // solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 24	PP1L4 //	NM_139126 //	NR1F1 // ROR1 //	3597603	chr15	+	61554385	5.54
	SLC25A24	NM_013386 //	ROR2 // ROR3 //	2978876	chr6	-	149811664	5.54
		NM_213651	RZRA					

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	
structural maintenance of chromosomes 1A	SMC1A	NM_006306	DKEZp686L19178 //	4009238	chrX	-	53417797	53466400
			DXS423E //					
NM23-LV // non-metastatic cells 1, protein (NM23A) expressed in	NME1-NME2 // NME1	NM_001018136 //	KIAA0178 //	3726934	chr17	+	46564693	46594905
			MGC138332 // SB1.8 // SMC1 // SMC1L1 // SMC1alpha //					
taxilin alpha // doublecortin domain containing 2B	TXLNA // DCDC2B	NM_198175 NM_175852 // XM_926306 // XM_940631	NME2 // AWD //	2328713	chr1	+	32417884	32436467
			GAAD // NDPKA // NM23 // NM23-H1 DKEZp451J0118 // IL14 // MGC118870 // MGC118871 // RP4-62L5.4 // TXLN // —					
cysteine-rich, angiogenic inducer, 61	CYR61	NM_001554	CCN1 // GIG1 // IGFBP10	2344888	chr1	+	85816676	85867516
prothymosin, alpha (gene sequence 28) // family with sequence similarity 22, member G	PTMA // FAM22G	NM_002823 // XM_001127718 //	MGC104802 // TMSA // —	2532021	chr2	+	232280604	232286493
casein kinase 1, epsilon // KIAA1660 protein	CSNK1E // KIAA1660	NM_001045477 NM_001894 // NM_152221 // XM_929784 // XM_940170 NM_002388	HCKIE // MGC10398 // —	3960478	chr22	-	37010115	37150916
MCM3 minichromosome maintenance deficient 3 (<i>S. cerevisiae</i>)	MCM3	NM_001554	HCC5 // MGC1157 // P1-MCM3 // P1.h //	2957126	chr6	-	52236739	52356643
solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3	SLC25A3	NM_213612 // NM_002635 // NM_005888 // NM_213611 NM_018992	RLFB OK/SW-cl.48 // PHC	3427820	chr12	+	97511471	97519906
potassium channel tetramerisation domain containing 5	KCTD5	NM_014720	FLJ20040	3645204	chr16	+	2640820	2700477
STE20-like kinase (yeast)	SLK	NM_014720	KIAA0204 // MGC133067 // STK2 // bA16H23.1 // se20-9	3262433	chr10	+	105716666	105778975
glutathione reductase par-3 partitioning defective 3 homolog (<i>C. elegans</i>)	GSR PARD3	NM_000637 NM_019619	MGC78522 ASIP // Baz // Bazooka // FLJ21015 // PAR3 // PAR3alpha // PARD3A // SE2-5L16 // SE2-5LT1 // SE2- CGI-48 // WDR50	3130161 3284596	chr8 chr10	- -	30655000 34413632	30705038 35144249
UTP18, small subunit (SSU) processome component, homolog (yeast)	UTP18	NM_016001		3726992	chr17	+	46692081	46730289

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Array				Fold Change
				Transcript Cluster ID	Chromosome	Strand	Start Stop	
serine/arginine repetitive matrix 1 // chromosome 1 open reading frame 130 conserved nuclear protein NHN1	SRRM1 //	NM_005839 //	160-KD // MGC39488	2325526	chr1	+	24830814 24929968	5.49
	C1orf130	NM_001010980	// POP101					
	NHN1	NM_144604	SRM160 // FLJ42528 FLJ22664 // FLJ34530 // FLJ36075	3673515	chr16	+	87152329 87225870	5.49
UBX domain containing 8 elongation protein 4 homolog (<i>S. cerevisiae</i>)	UBXD8	NM_014613	ETE A // KIAA0887	2842570	chr5	+	175807217 175870117	5.48
	ELP4	NM_019040	C11orf19 //	3325307	chr11	+	31487883 31764940	5.48
			FLJ20498 // PAX6NEB // PAXNEB // d68P15A.1					
hypothetical protein FLJ20366 SYF2 homolog, RNA splicing factor (<i>S. cerevisiae</i>) // MAX interactor 1 // chromosome 1 open reading frame 63	FLJ20366	NM_017786	GOLSYN	3148871	chr8	-	110655383 110964912	5.48
	SYF2 //	NM_015484 //	CBPIN //	2402068	chr1	-	25324131 25431599	5.47
	MXI1 //	NM_207170 //	DKFZp564O2082 //					
exosomes (multiple) 1 polymerase (RNA) II (DNA directed) polypeptide D // WD repeat domain 33	C1orf63	NM_001008541 //	NTC31 // P29 //					
		NM_005962 //	MAD2 // MGC43220					
		NM_130439 //	// MXD2 // MXI //					
ankyrin repeat domain 13 family, member D serum amyloid A-like 1 C1q domain containing 1	EXT1	NM_000127	NPDP014 // RP3- 465N24.4	3150060	chr8	-	118880792 119193382	5.46
	POLR2D //	NM_004805 //	EXT // HV	2575134	chr2	-	128317597 128334003	5.45
	WDR33	NM_001006622 //	HSRBP4 // HSRBP4 // RBP4 // FLJ11294 // WDC146					
chromosome 11 open reading frame 30 ubiquitin 1 // death inducer- obliterator 1	ANKRD13D	NM_018383	MGC50828	3336857	chr11	+	66812660 66826524	5.45
	SAAL1	NM_138421	FLJ141463	3365249	chr11	-	18048076 18084203	5.45
	C1QDC1	NM_001002259 //	BEG-1 // BEG1 //	3449368	chr12	-	30753755 30799712	5.44
chromosome 11 open reading frame 30 ubiquitin 1 // death inducer- obliterator 1		NM_023925 //	FLJ11391 //					
		NM_032156	FLJ22569 //					
			MGC102894 //					
chromosome 11 open reading frame 30 ubiquitin 1 // death inducer- obliterator 1			MGC134847 //					
			MGC134848	3340913	chr11	+	75803897 75941697	5.44
			EMSY // FLJ90741					
chromosome 11 open reading frame 30 ubiquitin 1 // death inducer- obliterator 1	C11orf50	NM_020193	// GL002	3212143	chr9	-	85464717 85512928	5.44
	UBQLN1 //	NM_013438 //	DA41 // DSK2 //					
	DIDO1	NM_053067 //	FLJ90054 // PLIC-1					
chromosome 11 open reading frame 30 ubiquitin 1 // death inducer- obliterator 1		NM_022105 //	// XDRP1 // BYE1					
		NM_033081 //	// C20orf158 //					
		NM_080796 //	DATE1 // DIO2 //					
chromosome 11 open reading frame 30 ubiquitin 1 // death inducer- obliterator 1		NM_080797	DIDO3 // DIO-1 //					
			DIO1 //					
			DKFZp434P1115 //					
chromosome 11 open reading frame 30 ubiquitin 1 // death inducer- obliterator 1			FLJ11265 //					
			KIAA0333 //					
			MGC16140 //					

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Array				Fold Change
				Transcript Cluster ID	Chromosome	Strand	Start	Stop
similar to ribosomal protein P0 // ribosomal protein, large, P0	RPLP0-like // RPLP0	XR_015741 //	BLOCK 23 // L10E //	3474344	chr12	-	119118908	119123401
		XR_017813 //	MGC111226 //					
		NM_001002 //	MGC88175 // P0 //					
zinc finger, NFX1-type containing 1 // gasdermin-like	ZNF51 // GSDML	NM_053275	PRLP0 // RPP0	3908831	chr20	-	47233911	47420063
		NM_021035 //	FLJ39275 //					
		NM_00104247 //	MGC131926 //					
exportin 4	XPO4	NM_018530	PP4052 // PRO2521	3504434	chr13	-	20251014	20375187
		NM_022459	FLJ13046 //					
			KIAA1721					
centrosomal protein 72 kDa	CEP72	NM_018140	FLJ10565 //	2798777	chr5	+	608522	720187
			KIAA1519 //					
			MGC5307					
basic transcription factor 3	BTF3	NM_001037637 //	BETA-NAC // BTF3a	2815331	chr5	+	72704665	72850839
		NM_001207	// BTF3b // NACB					
		NM_030629 //	KIAA1694	3670772	chr16	+	80030441	80323852
c-Maf-inducing protein	CMIP	NM_198390						
cerebellar degeneration-related protein 2, 62 kDa	CDR2	NM_001802	CDR62 // Yo	3684782	chr16	-	22264766	22356527
ubiquitin-like 3	UBL3	NM_007106	DKFZP434K151 //	3507798	chr13	-	29200782	29371040
			FLJ32018 // HCG-1					
			// PNSC1					
ATP-binding cassette, sub-family F (GCN20), member 1	ABCF1	NM_001025091 //	ABC27 // ABC50	2901687	chr6	+	30647103	30667268
		NM_001090						
		NM_020673	MGC16770	3890870	chr20	+	56318177	56375962
RAB22A, member RAS oncogene family	RAB22A							
axin 1	AXIN1	NM_003502 //	AXIN // MGC52315	3675047	chr16	-	277442	351633
		NM_181050						
mitochondrial ribosomal protein L44	MRPL44	NM_022915	FLJ12701 //	2529782	chr2	+	224530378	224540666
			FLJ13990					
			MGC125660 //					
zinc finger protein 146 // zinc finger protein 268	ZNF146 // ZNF268	NM_007145 //	MGC125661 // OZF	3831260	chr19	+	41397873	41421503
		NM_152943 //	// HZF3 //					
		NM_003415	MGC126498					
golgi SNAP receptor complex member 1	GOSR1	NM_001007024 //	GOS28 //	3716481	chr17	+	25828452	25893594
		NM_001007025 //	GOS28P28 // GS28					
		NM_004871	// P28					
zinc finger protein 512	ZNF512	NM_032434	KIAA1805 //	2474651	chr2	+	27659393	27699586
			MGC111046					
			DKFZp779L1064 //	3372459	chr11	-	47694235	47745657
formin binding protein 4	FNBP4	NM_015308	FBP30 // FLJ41904					
			KIAA1014					
zinc finger protein 707 FERM domain containing 5	ZNF707 FRMD5	NM_173831	FLJ41022 //	3119765	chr8	+	144771273	144849532
		NM_032892	MGC14161	3621728	chr15	-	41950261	42274751
serum/glucocorticoid regulated hypoxia-inducible factor 1, alpha	SGK HIF1A	NM_005627	SGK1	2975014	chr6	-	134532088	134680889
		NM_001530 //	HIF-1 alpha // HIF-1-	3539070	chr14	+	61225495	61285222

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Array				Fold Change
				Transcript Cluster ID	Chromosome	Strand	Start	Stop
subunit (basic helix-loop-helix transcription factor) deoxyhypusine synthase	DHPS	NM_181054	ALPHA // MOP1 //					
		NM_001930 //	PASD8	3851603	chr19	-	12647534	12653680
		NM_013406 //	MIG13					5.37
thioredoxin-like 1	TXNL1	NM_013407	TRP32 // TXL-1 //	3809324	chr18	-	52334063	52469773
		NM_004786	TXNL // TxI	3438027	chr12	+	129922411	129928164
		NM_006325	ARA24 // Gsp1 //					5.36
RAN, member RAS oncogene family	RAN		TC4					
		NM_006141	DNCL12 // LIC2	3695199	chr16	-	65312304	65343212
								5.36
dynein, cytoplasmic 1, light intermediate chain 2	ERH	XM_001130537 //	DROER // FLJ27340	3570049	chr14	-	68916605	68935306
		NM_004450	// TAAL6	2700365	chr3	-	150567718	150578270
		NM_014220	H-16 // L6 // M3S1					5.34
transmembrane 4 L six family member 1	TM4SF1		EDL // EL //	3787855	chr18	+	45341077	45481323
		NM_006033	EXP6 // FLJ22519 //	3686339	chr16	-	28016804	28130734
		NM_015171	KIAA0370 //					5.34
lipase, endothelial exportin 6	LIPG		RANBP20					
		NM_018348	—	3697563	chr16	-	69872813	69881003
		NM_002911	FLJ43809 //	3825383	chr19	+	18803757	18840030
hypothetical protein FLJ11171 UPF1 regulator of nonsense transcripts homolog (yeast)	UPF1		FLJ46894 // HUPF1					
			// KIAA0221 //					
			NORF1 // RENT1 //					
surfeit 6 neural precursor cell expressed, developmentally down-regulated 4-like // sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4G tetraspatin 14	SURF6	NM_006753	pNORF1	3228621	chr9	-	135186667	135193036
		NM_015277 //	FLJ33870 //	3789947	chr18	+	53862627	54232131
		NM_017893	KIAA0439 // RSP5 //					5.30
core-binding factor, beta subunit	CBFB		hNedd4-2 //					
		NM_030927	FLJ20590 //	3254521	chr10	+	82203922	82272901
			KIAA1619 //					5.30
baculoviral IAP repeat-containing 5 (survivin)	BIRC5		MGC102867					
		NM_001755 //	DC-TM4F2 //	3665116	chr16	+	65620522	65692457
		NM_022845	MGC11352 //					5.29
grainyhead-like 2 (<i>Drosophila</i>)	GRHL2	NM_001012270 //	TM4SF14	3736290	chr17	+	73721882	73733311
		NM_001168	PEBP2B					
		NM_024915	API4 // EPR-1	3109687	chr8	+	102573566	102751110
			BOM // DFNA28 //					5.29
			FLJ11172 //					
			FLJ13782 //					
			MGC149294 //					
			MGC149295 //					
			TFCP2L3					

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18				Fold Change
					Chromosome	Strand	Start	Stop	
acydsonless homolog (<i>Drosophila</i>) RBM13 CDCA2	ECD	NM_007265	GCR2 // HSGT1	3294242	chr10	-	74559939	74598411	5.29
	RBM13	NM_032509	MAK16 // MAK16L	3093259	chr8	+	33462192	33478316	528
	CDCA2	NM_152562	FLJ25804 //	3090697	chr8	+	25362573	25431420	5.28
			MGC129906 // MGCI29906 // Repoman						
myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, <i>Drosophila</i>); translocated to, 4 nuclear receptor subfamily 1, group H, member 2	MLLT4	NM_001040000 //	AF-6 // AF6 //	2936857	chr6	+	167970473	168115537	5.28
		NM_001040001 //	AFADIN // FLJ34371						
		NM_005936	// RP3-431P23.3						
	NR1H2	NM_007121	LXR-b // LXRb // NER // NER-1 // RIP15 // UNR	3839276	chr19	+	55524771	55578457	5.28
TIP2 occludens 2) neutarkyotic translation initiation factor 2A, 65 kDa	TIP2	NM_004817 //	MGC26306 // X104	3173880	chr9	+	70925894	71059931	5.27
		NM_201629	// ZO-2 // ZO2						
	EIF2A	NM_032025	CDA02 // EIF-2A // MST089 // MSTP004	2647742	chr3	+	151747168	151788822	5.27
			// MSTP089						
histone acetyltransferase 1 ring finger protein 138	HAT1	NM_001033085 //	—	2515369	chr2	+	172487173	172556842	5.26
		NM_003642							
	RNF138	NM_016271 //	HSD-4 // MGC8758	3783749	chr18	+	27925835	28030948	5.26
		NM_198128	// NARE // STRIN						
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
	RANGAP1	NM_002883	Fug1 // KIAA1835 //	3961842	chr22	-	39969442	40028027	5.24
			MGC20266 // SD						
zinc finger and BTB domain containing 7A	ZBTB7A	NM_015898	DKFZp47O146 // FBI-1 // FBI1 // LRF // MGC99631 // ZBTB7 // pokemon	3846594	chr19	-	3990713	4033507	5.24
	METAP2 //	NM_006838 //	MNPEP // p67 //	3426917	chr12	+	94391437	94696442	5.23
	FLJ11292	NM_018382	p67aF2 // —						
small nuclear ribonucleoprotein polypeptides B and B1	SNRPB	NM_003091 //	COD // SNRPB1 // Smb/Smb' //	3894995	chr20	-	2369715	2399499	5.23
		NM_198216	snRNP-B						
	CD151 //	NM_001039490 //	GP27 // MER2 //	3316344	chr11	+	822755	828824	5.23
CDI51 molecule (Raph blood group) // FK506 binding protein 9-like	FKBP9L	NM_004357 //	PETA-3 // RAPH //						
		NM_139029 //	SEAI // TSPAN24 //						
		NM_139030 //	FKBP9 // MGC20531						
		NM_182827							
wolf-Hirschhorn syndrome candidate 1	WHSC1	NM_001042424 //	FLJ23286 //	2715076	chr4	+	1842909	1953717	5.23
		NM_007331 //	KIAA1090 // MMSET						
		NM_133330 //	// NSD2 // REHBP						
		NM_133331 //	// TRX5 // WHS						
		NM_133334 //							
		NM_133335 //							
		NM_133336							

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	
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 // d4447E3.2 // CDKN1A // MRX30 // MRX47 // OPHN3 // PAK3beta // bPaK // hPAK3	3887049	chr20	+	43874662	43878994 5.22
ribosomal L1 domain containing 1	RSL1D1	NM_002578 NM_015659	CSIG // DKFZP564M182 // L12 // MGC138433 // MGC142259 // N14 // NA-14 // NA14	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-Mmr	NM_003885	KIAA0597 // MARCH-VI	2801608	chr5	+	10406824	10490959 5.20
Sp3 transcription factor // Sp3 transcription factor pseudogene	SP3 // RP11-114G1.1	NM_001017371 // NM_003111 // —	DKFZp68601631 // 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

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	
chromosome 1 open reading frame 77	C1orf77	NM_015607	DKEZP547E1010 // MGC131924 // MGC86949 // RP1-178F15.2 // pp7704	2359736	chr1	+	151872948	151885444 5.18
zinc finger protein 787	ZNF787	NM_001002836	—	3871730	chr19	-	61361349	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_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) transmembrane protein 170	MPHOSPH10	NM_005791	MPP10 // MPP10P	2488078	chr2	+	71210952	71237711 5.16
YTH domain family, member 2	YTHDF2	NM_145254	FLJ37611	3699581	chr16	-	74034456	74107659 5.15
breast cancer anti-estrogen resistance 3	BCAR3	NM_016258	HGRG8 // NY-REN-2	2327630	chr1	+	28935740	28968859 5.15
KH domain containing, RNA binding, signal transduction associated 1	KHDRBS1	NM_003567	KIAA0554 // NSP2 // SH2D3B	2423422	chr1	-	93790445	94085633 5.15
reticulon 4	RTN4	NM_006559	FLJ34027 // Sam68 // p62	2328465	chr1	+	32212249	32299034 5.15
		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	GRIP-RCP // CRCP // MGC111194 // RCP	3005332	chr7	+	65131004	65262097 5.15

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	Stop
solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	SLC3A2	NM_001012661 //	4F2 // 4F2HC //	3333711	chr11	+	62380117	62412872
		NM_001012662 //	4T2HC // CD98 //					
		NM_001012663 //	CD98HC // MIDU1 //					
		NM_001012664 //	NACAE					
		NM_001013251 //						
zinc finger, DHHC-type containing 5	ZDHHC5	NM_002394	DKEZP586K0524 //	3331433	chr11	+	57192053	57225319
		NM_015457	KIAA1748 // ZNF375					
Smg-5 homolog, nonsense mediated mRNA decay factor (<i>C. elegans</i>)	SMG5	NM_015327	EST1B // FLJ34864	2438042	chr1	-	154485643	154519254
			// KIAA1089 //					
alkB, alkylation repair homolog 2 (<i>E. coli</i>)	ALKBH2	NM_001001655	LPTS-RP1 //	3470689	chr12	-	108010254	108015656
			54H19 // SMG-5					
			ABH2 // MGC90512					
BUD31 homolog (<i>S. cerevisiae</i>)	BUD31	NM_003910	// hABH2	3014742	chr7	+	98844221	98855171
			EDG-2 // EDG2 //					
MIS12, MIND kinetochore complex component, homolog (yeast)	MIS12	NM_024039	G10 // MGC111202	3707759	chr17	+	5330450	5334853
			// YCR063W					
			2510025F08Rik //					
tripartite motif-containing 26	TRIM26	NM_003449	KNTC2AP //	2948259	chr6	-	30260217	30290029
			MGC2488 // MTW1					
			// hMis12					
similar to FRG1 protein (FSHD region gene 1 protein) // FSHD region gene 1 ATPase family, AAA domain containing 1	MGC72104 // FRG1 ATAD1	NM_207350 // NM_004477 NM_032810	AFP // RNF95 //	2756029	chr4	+	191051868	191138306
			ZNF173					
			—// FSG1					
BTB (POZ) domain containing 3	BTBD3	NM_014962 // NM_181443	AFDC1 // FLJ14600	3299255	chr10	-	89500784	89591413
			// FNP001					
			KIAA0952 //					
sterol regulatory element binding transcription factor 2	SREBF2	NM_004599	MGC130038 //	3947123	chr22	+	40559049	40633247
			MGC130039 //					
			dJ742124.1					
splicing factor 3a, subunit 3, 60 kDa	SF3A3	NM_006802	SREBP2	2407439	chr1	-	38195241	38229180
			PRP9 // PRPF9 //					
ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide	ATP5B	NM_001686	SAF61 // SF3a60	3458033	chr12	-	55318243	55326110
			ATPMB // ATPSB //					
mitochondrial ribosomal protein L55	MRPL55	NM_181441 // NM_181454 // NM_181455 // NM_181456 //	MGC5231	2459438	chr1	-	226360734	226367172
			AAVG5835 //					
			DKEZp686D1387 //					
			MGC61802 //					
			PRO19675					

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18		
					Chromosome	Strand	Fold Change
SMAD specific E3 ubiquitin protein ligase 1 myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, <i>Drosophila</i>)	SMURF1	NM_181462 //	KIAA1625	3063083	chr7	-	98449133
		NM_181463 //					98579664
		NM_181464 //					
	MLL	NM_181465	ALL-1 // CXXC7 //				5.11
		NM_020429 //	HRX // HTRX1 //	3351385	chr1	+	117811029
		NM_181349	MLL/GAS7 // MLL1A // TRX1				5.10
family with sequence similarity 89, member B alkB, alkylation repair homolog 3 (<i>E. coli</i>)	FAM89B	NM_152832	MIVR1	3335338	chr1	+	65096490
	ALKBH3	NM_139178	ABH3 // DEPC-1 //			+	43858633
			DEPC1 //	3328214	chr1	+	43898486
	SETD2	NM_014159	MGC118790 // MGC118792 // FLJ16420 // FLJ22472 // FLJ23184 // FLJ45883 // HIF-1 // HSPC069 // HYPB // KIAA1732	2672532	chr3	-	47032936
p53 and DNA damage regulated 1 ubiquitin carboxyl-terminal esterase L3 (ubiquitin thioesterase) hepatocyte growth factor-regulated tyrosine kinase substrate proteasome (prosome, macropain) 26S subunit, ATPase, 4	PDRG1	NM_030815	C20orf126 // PDRG	3902609	chr20	-	29995826
	UCHL3	NM_006002	—	3494102	chr3	+	75021620
	HGS	NM_004712	HRS // ZFYVE8	3738138	chr17	+	77260785
	PSMC4	NM_006503 // NM_153001	MGC13687 // MGC23214 // MGC8570 // MIP224 // S6 // TBP7	3833291	chr19	+	45168772
tubulin, beta	TUBB	NM_178014	M40 // MGC117247 // MGC16435 //	2901913	chr6	+	30795977
	KIF20A	NM_005733	OK/SW-cl.56 // TUBB1 // TUBB5				30801165
			FLJ21151 // MKLP2	2830638	chr5	+	137542289
	RARS	NM_002887	// RAB6KIFL ArgRS // DALRD1 //	2839671	chr5	+	137542289
calpain 2, (mII) large subunit	CAPN2	NM_001748	MGC8641	2382117	chr1	+	167845940
			CANPL2 // CANPnl // FLJ39928 // mCANP	2382117	chr1	+	221955990
							222031806
							5.08

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start Stop	
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 // DKEZp686P18118 // ELP120 // FLJ10942 // FLJ32318 // ROP120	2478748	chr2	+	42250017 42418636	5.06
splicing factor 3b, subunit 4, 49 kDa	SF3B4	NM_003850	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 //	3315952	chr11	+	550321 554016	5.05
Wilms tumor 1 associated protein // acetyl-Coenzyme A	WTAP // ACAT2	NM_004906 // NM_152857 // NM_152858 // NM_005891	DKEZp686P20131 // KIAA0105 // MGC3925 // —	2934089	chr6	+	160066607 160097332	5.04
Coenzyme A thiolase	ORC5L	NM_002553 // NM_181747	ORC5 // ORC5P // ORC5T	3065963	chr7	-	103553146 103719295	5.04
origin recognition complex, subunit 5-like (yeast)	CDYL	NM_004824 // NM_170751 // NM_170752	CDYL1 // DKEZP586C1622 // MGC131936	2892979	chr6	+	4651344 4900768	5.03
chromodomain protein, Y-like	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
apataxin	PIK4CB // RFX5	NM_002651 // NM_000449 // NM_001025603	PI4K-BETA // PI4KIIbeta // PI4Kbeta // —	2434925	chr1	-	149530589 149567792	5.03
phosphatidylinositol 4-kinase, catalytic, beta polypeptide // regulatory factor X, 5 (influences HLA class II expression)								

TABLE 3-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	Stop
serine palmitoyltransferase, long chain base subunit 2	SPTLC2	NM_004863	KIAA0526 // LCB2 // SPT2	3573152	chr14	-	77042100	77202740
cell division cycle associated 5	CDC45	NM_080668	MGC16386	3377423	chr11	-	64592075	64608249
myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, <i>Drosophila</i>)	MLL5	NM_018682 // NM_182931	FLJ10078 // FLJ14026 // HDCMC04P // MGC70452	3017547	chr7	+	104436029	104542698
F-box protein 28	FBXO28	NM_015176	FLJ10766 // Fbx28 // KIAA0483	2382336	chr1	+	222368455	222416368
eukaryotic translation initiation factor 3, subunit, 1 alpha, 35 kDa	EIF3S1	NM_003758	EIF3-alpha // EIF3-p35 // EIF3j	3591963	chr15	+	42616580	42644124
polymerase (RNA) III (DNA directed) polypeptide C (62 kD)	POLR3O	NM_006468	RPC3 // RPC62	2432647	chr1	-	144297192	144333220
bromodomain adjacent to zinc finger domain, 1B	BAZ1B	NM_023005 // NM_032408	WBSCR10 // WBSCR9 // WSTF	3056044	chr7	-	72492710	72574552
isocitrate dehydrogenase 3 (NAD+) beta	IDH3B	NM_006899 // NM_174855 // NM_174856	FLJ11043 // H-IDHB // MGC903	3895075	chr20	-	2586736	2592862
basic transcription factor 3-like 4	BTFL4	NM_152265	MGC23908 // MGC88389 // RP4-800M22.5	2336271	chr1	+	52293292	52339895
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

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

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0	Human Genome hg18			
					Transcript Cluster ID	Chromosome	Strand	Start Stop Fold Change
TIMP metalloproteinase inhibitor 1	TIMP1	NM_003254	CLGI // EPA // EPO // FLJ90373 // HCL // TIMP FKSG34 // MADDAM //		3976341	chrX	+	47326654 47332978 14.98
ADAM metalloproteinase domain 19 (meltrin beta)	ADAM19	NM_023038 //	FLJ90373 // HCL // TIMP FKSG34 // MADDAM //		2883440	chr5	-	156755122 156935351 9.71
phosphodiesterase 4A, cAMP-specific (phosphodiesterase E2 duncce homolog. Rap guanine nucleotide exchange factor (GEF) 1	PDE4A	NM_033274 NM_006202	MLTNB DPDE2 // PDE4		3820501	chr19	+	10388560 10451531 9.64
	RAPGEF1	NM_005312 //	C3G // DKFZp781P1719 // GRF2		3227696	chr9	-	133441988 133605262 9.27
myosin, heavy chain 9, non-muscle	MYH9	NM_198679 NM_002473	DEFNA17 // FTNS EPSTS // FTNS // MGC104539 // MHA //		3959451	chr22	-	35007278 35113982 7.90
serpin peptidase inhibitor, clade B (ovalbumin), member 9 // serpin peptidase inhibitor, clade B (ovalbumin), member 6	SERPINF9 // SERPINB6	NM_004155 // NM_004568	NMHC-II-A // NMHC CAP-3 // CAP3 // P19 // CAP // DKFZp686I04222 //		2939034	chr6	-	2832402 2858242 7.75
RNA binding motif protein 23	RBM23	NM_001077351 // NM_001077352 //	MGC111370 // MSTP057 // CAPERbeta // FLJ10482 // MGC4458 // PP239 //		3556888	chr14	-	22439714 22458231 7.63
polyhomeotic homolog 3 (<i>Drosophila</i>)	PHC3	NM_018107 NM_024947	RNPC4 DKFZp313K1221 // EDR3 // FLJ12729 // FLJ12967 // HPH3 //		2704894	chr3	-	171287994 171381537 7.30
splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated) BTB (POZ) domain containing 11	SFPQ BTBD11	NM_005066 NM_001017523 //	MGC88144 POMP100 // PSF FLJ33957 // FLJ42845		2406064 3430462	chr1 chr12	- +	35351696 35506894 7.08 106237825 106577543 7.07

TABLE 4-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Exon ST 1.0				Fold Change
					Chromosome	Strand	Start	Stop	
v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	SRC	NM_001018072 // NM_152322 NM_005417 //	ASV // SRC1 // c-SRC //	3884191	chr20	+	35406502	35467847	6.98
		NM_198291 NM_015556	p60-Src DKFZp686G1344 // E6TP1 //	3542847	chr14	+	70857592	71468470	6.93
signal-induced proliferation-associated 1 like 1	SIPA1L1	NM_007067 NM_005898 //	KIAA0440 HBO1 // HBOA GPIP137 //	3725779 3326183	chr17 chr11	+	45196447 34009711	45261455 34081946	6.84 6.78
		NM_203364 XM_001127869 //	M11S1 // p137GPI CD11C	3657041	chr16	+	31274012	31301819	6.76
integrin, alpha X (complement component 3 receptor 4 subunit)	ITGAX	NM_000887 NM_012325	EB1 // MGC117374 //	3882069	chr20	+	30871304	30901864	6.65
microtubule-associated protein, RP/EB family, member 1	MAPRE1	NM_015213	MGC129946 FLJ22354 // FLJ33829 //	3362263	chr11	-	9116953	9243468	6.61
RAB6 interacting protein 1	RAB6IP1	NM_015213	FLJ43455 // KIAA1091 DKFZP586B2022 // MGC1146	3020192	chr7	+	115637811	115743800	6.22
testis derived transcript (3 LIM domains)	TES	NM_015641 // NM_152829	TESS-2 // CCT1-alpha //	2982381	chr6	-	160119521	160130731	6.19
t-complex 1	TCP1	NM_001008897 // NM_030752	CCT1 // CCTa // D6S230E //	3089853 3186966	chr8 chr9	+	23157105 119506334	23176288 119670150	6.08 6.00
CHMP family, member 7 toll-like receptor 4	CHMP7 TLR4	NM_152272 NM_138554	TCP-1-alpha MGC29816 CD284 // TOLL // hToll	2652410	chr3	+	173240112	173601176	5.97
fibronectin type III domain containing 3B	FNDC3B	NM_022763	DKFZp686D14170 // DKFZp762K137 // FAD104 // FLJ33399 // MGC10002 //						

TABLE 4-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18			Fold Change
					Chromosome	Strand	Start	
serine/threonine kinase 38 like	STK38L	NM_015000	PRO4979 //	3409081	chr12	+	27288343	27370157
			YV7M2421					
eukaryotic translation initiation factor 4 gamma, 2	EIF4G2	NM_001042559	KIAA0965 //	3362719	chr11	-	10487574	10788746
			NDR2					
aminopeptidase puromycin sensitive	NPEPPS	NM_001418	AAG1 // DAP5	3724698	chr17	+	42955347	43057168
			// FLJ41344 //					
membrane protein, palmitoylated 1, 55 kDa	MPP1	NM_006310	NAT1 // p97	4027585	chrX	-	153658739	154075618
			XM_001128588					
eukaryotic translation initiation factor 4 gamma, 1	EIF4G1	NM_004953	MP100 // PSA	2655688	chr3	+	185514970	185535829
			//					
leucine rich repeat containing 8 family, member C	LRRC8C	NM_032270	AAG12 //	2345929	chr1	+	89871229	90008050
			NM_002436					
EH-domain containing 1	EHD1	NM_006795	DXS552E //	3377226	chr11	-	64376790	64404202
			EMP5 //					
3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	HMGCS1	NM_002130	MRG1 // PEMP	2855501	chr5	-	43324231	43349337
			DKFZp686A1451					
insulin induced gene 1	INSIG1	NM_005542	// EIF4F //	3033209	chr7	+	154649208	154732868
			EIF4G // p220					
chromodomain helicase DNA binding protein 2	CHD2	NM_198337	AD158 //	3609138	chr15	+	91227096	91387351
			DKFZp586J1119					

TABLE 4-continued

Gene Name	Gene Symbol	Accession	Synonym	Transcript Cluster ID	Human Genome hg18				Fold Change
					Chromosome	Strand	Start	Stop	
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 //	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	MGC26147 LYT-10 // LYT10	3261643	chr10	+	104144262	104152716	5.61
ubiquitin-activating enzyme E1-like 2	UBE1L2	NM_002502 NM_018227	FLJ10808 // FLJ23367	2771718	chr4	-	68130308	68249472	5.57
ras homolog gene family, member A	RHOA	NM_001664	ARH12 // ARHA //	2674242	chr3	-	49371587	49424514	5.54
HECT, UBA and WWE domain containing 1	HUWE1	NM_031407	RHO12 // ARE-BP1 // HECTH9 // HSPC272 // lb772 // KIAA0312 // LASU1 //	4009315	chrX	-	53575796	53740871	5.54
cyclin-dependent kinase 8	CDK8	NM_001260	MULE // K35 // MGC126074 //	3482498	chr13	+	25701360	25877335	5.53
E3 ubiquitin protein ligase, HECT domain containing, 1	EDD1	NM_015902	MGC126075 DDS // EDD // FLJ11310 // HYD //	3147321	chr8	-	103333634	103493671	5.49
dedicator of cytokinesis 4	DOCK4	NM_014705	KIAA0896 // MGC57263 FLJ34238 //	3068097	chr7	-	111152902	111633744	5.42
sterol regulatory element binding transcription factor 2	SREBF2	NM_004599	MGC134911 // MGC134912 SREBF2	3947123	chr22	+	40559049	40633247	5.40
heterogeneous nuclear ribonucleoprotein M	HNRFM	NM_005968 // NM_031203	DKFZp547H118 // HNRNPM // HNRNPM4 // HNRPM4 //	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	HTGR1 // NAGR1 SH3BP-1 // TIP-B1 // DKFZP434L0117 //	2326448	chr1	+	26478669	26480591	5.34

TABLE 4-continued

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

Gene Name	Gene Symbol	Accession	Synonym	Cluster ID	Chromosome	Human Genome hg18			Fold Change/
						Strand	Start	Stop	
epiregulin	EREG	NM_001432	ER	2731513	chr4	+	75440309	75473341	1.08
pellino homolog 1 (<i>Drosophila</i>)	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 // beta4Gal-T5 // gt-beta4Gal-T5 // CYTOHESIN-1 // DI7S811E // FLJ34050 // FLJ41900 // SEC7	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 // DI7S811E // FLJ34050 // FLJ41900 // SEC7	3772525	chr17	-	74181731	74289973	1.08
EH-domain containing 4	EHD4	NM_139265	PAST4	3620276	chr15	-	39977674	40052063	1.08
TIMP metalloproteinase inhibitor 1	TIMP1	NM_003254	CLGI // EPA // EPO // FLJ90373 // HCL // 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 (<i>S. cerevisiae</i>)	PRPF40A	NM_371575 // XM_938514	FBP-11 // FBP11 // FLAF1 // FLJ20585 // FNBP3 // HIP10 // HYPA // NY-REN-ABC-1 // ABC1 // CERP // FLJ14958 // HDLDT1 // TGD	2581548	chr2	-	153212414	153283546	1.08
ATP-binding cassette, sub-family A (ABC1), member 1	ABCA1	NM_005502	FNBP3 // HIP10 // HYPA // NY-REN-ABC-1 // ABC1 // CERP // FLJ14958 // HDLDT1 // TGD	3218528	chr9	-	106583121	106748222	1.08
RAB5A, member RAS oncogene family protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	RAB5A PPP2CA	NM_004162 NM_002715	RAB5 PP2Ac // PP2CA // RP-C	2613386 2876046	chr3 chr5	+	19963571 133557588	20002852 133589841	1.07 1.07
membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	MPP7	NM_173496	FLJ32798	3282601	chr10	-	28377816	28631969	1.07

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
RAB6 interacting protein 1	RAB6IP1	NM_015213	FLJ2354 // FLJ3829 // FLJ4345 // KIAA1091 KIAA0571	3362263	chr11	-	9116953	9243468
GRB2-associated binding protein 2	GAB2	NM_012296 // NM_080491	CLIC4L //	3383227	chr11	-	77603886	77989843
chloride intracellular channel 4 // adducin 3 (gamma)	CLIC4 // ADD3	NM_013943 // NM_001121 // NM_016824 // NM_019903	DKFZP566G223 // FLJ38640 // H1 // huH1 // p64H1 //	2325593	chr1	+	24943202	25071376
TBC1 domain family, member 23	TBC1D23	NM_018309	ADDL DKFZp667G062 // FLJ11046 //	2633587	chr3	+	101462368	101526762
solute carrier family 16, member 3 (monocarboxylic acid transporter 4)	SLC16A3	NM_001042422 // NM_001042423 // NM_004207	NS4ATP1 MCT3 // MCT4 // MGC138472 //	3738629	chr17	+	77775274	77812305
sestrin 3	SESN3	NM_144665	MGC29667 //	3387259	chr11	-	94545767	94605309
nuclear RNA export factor 1	NXF1	NM_001081491 // NM_006362	SEST3 DKFZp667O0311 //	3376155	chr11	-	62316178	62329529
myristoylated alanine-rich protein kinase C substrate	MARCKS	NM_002356	MEX67 // TAP 80K-L // FLJ14368 // FLJ90045 // MACS // MRACKS // PKCSL //	2922215	chr6	+	114284762	114292853
retinitis pigmentosa 2 (X-linked recessive)	RP2	NM_006915	PRKCSL KIAA0215 //	3975869	chrX	+	46581319	46637601
DnaJ (Hsp40) homolog, subfamily C, member 3	DNAJC3	NM_006260	TBCD2 HP58 // P58 //	3497270	chr13	+	95125276	95245596
interleukin 1, alpha	IL1A	NM_000575	P58PK // PRKRI IL-1A // IL1 //	2571483	chr2	-	113247977	113259446
TANK-binding kinase 1	TBK1	NM_013254	IL1-ALPHA // FLJ11330 // NAK // T2K	3419849	chr12	+	63132014	63202097
adaptor-related protein complex 3, beta 1 subunit	AP3B1	NM_003664	ADTB3 // ADTB3A // HPS // HPS2 //	2863730	chr5	-	77318390	77671471
ATPase type 13A3	ATP13A3	XM_931948 // XM_942079	PE AFURS1 // DKFZp686K16189 // FLJ90613	2711644	chr3	-	195604703	195757213
coiled-coil domain containing 131	CCDC131	NM_144982	DKFZp686A0722 // KIAA0546 // MGC23401 // MGC90200 // PSCR2	3462094	chr12	-	70269806	70344289

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
calmodulin 2 (phosphorylase kinase, delta)	CALM2	NM_001743	CAMII // PHKD // PHKD2	2551924	chr2	-	47232159	47286178
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
brain abundant, membrane attached signal protein 1	BASP1	NM_006317	CAP-23 // CAP23 // MGC8555 // NAP-22 // NAP22	2803329	chr5	+	17118727	17381190
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
proteasome (prosome, macropain) 26S subunit, non-ATPase, 3	PSMD3	NM_002809	P58 // RPN3 // S3	3720636	chr17	+	35390438	35407732
acyl-CoA synthetase long-chain family member 1	ACSL1	NM_001995	ACSL1 // FAEL1 // FAEL2 // LACS // LACS1 // LACS2	2796553	chr4	-	185913758	186002178
numb homolog (<i>Drosophila</i>)	NUMB	NM_001005743 // NM_001005744 // NM_001005745 // NM_003744	S171	3571347	chr14	-	72811631	73000081
protein kinase C, epsilon	PRKCE	NM_005400	MGC125656 // MGC125657 // PKCE // nPKC-epsilon	2480168	chr2	+	45731934	46343070
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
eukaryotic translation initiation factor 2C, 2	EIF2C2	NM_012154	AGO2 // MGC3183 // Q10	3156193	chr8	-	141599440	141726037
CD2 molecule	CD2	NM_001767	SRBC // TI1	2353669	chr1	+	117098550	117149098
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
transcription elongation factor B (SIII), polypeptide 3 (110 kDa, elongin A)	TCEB3	NM_003198	SIII // TCEB3A	2325251	chr1	+	23942459	23961135
COP9 constitutive photomorphogenic homolog subunit 2 (<i>Arabidopsis</i>)	COPS2	NM_004236	ALIEN // CSN2 // SGN2 // TRIP15	3623424	chr15	-	47203877	47235198

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	
pyridoxal (pyridoxine, vitamin B6) kinase // chromosome 21 open reading frame 124	PDXK //	NM_003681 //	C21orf97 // PKH //	3923257	chr21	+	43963416	44006601	1.07
	C21orf124	NM_032920	PNK // FLJ31940 // MGC15873 //						
nucleoporin 98 kDa	NUP98	NM_005387 //	PRED79	3359910	chr11	-	3652836	3775353	1.07
		NM_016320 //	ADIR2 // NUP196						
		NM_139131 //							
		NM_139132							
muskelin 1, intracellular mediator containing kelch motifs	MKLN1	NM_013255	FLJ11162	3024275	chr7	+	130445315	130837940	1.07
	CERK	NM_022766 //	DKFZp434E0211 //	3964154	chr22	-	45454343	45537349	1.07
ceramide kinase		NM_182661	FLJ21430 //						
			FLJ23239 //						
non-POU domain containing, octamer-binding neuroepithelial cell transforming gene 1	NONO	NM_007363	KIAA1646 // LK4 // MGC131878 //	3980887	chrX	+	70420006	70437726	1.07
	NET1	NM_001047160 //	da59H18.2 //	3233182	chr10	+	5444535	5491001	1.07
mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A // hypothetical protein MGC52110	MGAT4A //	NM_005863	ICERK	2566414	chr2	-	98600132	98714000	1.07
	MGC52110	NM_012214 //	NMT55 // NRB54 // P54 // P54NRB	2948425	chr6	-	30676177	30694348	1.07
protein phosphatase 1, regulatory (inhibitor) subunit 10	PPP1R10	NM_002714	NET1A	3272205	chr10	+	134201308	134446967	1.07
	INPP5A	NM_001133189 //	GNT-IV // GNT-IVA //						
inositol polyphosphate-5-phosphatase, 40 kDa		NM_005539	6330578E17Rik						
			CAT53 // FB19 //						
plasminogen activator, urokinase receptor	PLAUR	NM_001005376 //	PNUTS	3864551	chr19	-	48841865	48866539	1.06
		NM_001005377 //	SPTASE //						
PHD finger protein 12	PHF12	NM_002659	DKFZp434A1721 //	3751184	chr17	-	24256404	24302905	1.06
	SYAP1	NM_032796	MGC116947 //	3970130	chrX	+	16639861	16690708	1.06
synapse associated protein 1, SAP47 homolog (<i>Drosophila</i>)			MGCI16949						
			CD87 // UPAR //						
chromosome 1 open reading frame 152 // phosphodiesterase 4D interacting protein (myomegalin)	C1orf152 //	NR_003242 //	URKR	2431886	chr1	-	142444924	143804054	1.06
	PDE4DIP	NM_001002810 //	KIAA1523 //						
		NM_001002811 //	MGC131914 // PF1						
		NM_001002812 //	DKFZp686K221 //						
			FLJ14495 //						
			FLJ44185 //						
			PRO3113						
			COAS3 // CMYA2						
			// DKFZp781J054						
			// MGC75440 //						
			MMGL						

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	
homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	HERPUD1	NM_014644 //							
		NM_022359							
		NM_001010989 //	HERP // KIAA0025	3662387	chr16	+	55523269	55552122	1.06
		NM_001010990 //	// Mif1 // SUP						
TNF receptor-associated factor 1 pimilio homolog 2 (<i>Drosophila</i>)	TRAF1 PUM2	NM_014685							
		NM_005658	EBI6 // MGC: 10353	3223738	chr9	-	122699696	122731521	1.06
			FLJ36528 //	2542816	chr2	-	20291440	20450197	1.06
		NM_015317	KIAA0235 //						
Dmx-like 2	DMXL2		MGC138251 //						
			MGC138253 //						
			PUMH2 // PUMIL2						
		NM_015263	FLJ26672 //	3624145	chr15	-	49527223	49702258	1.06
RAB8B, member RAS oncogene family tight junction protein 2 (zona occludens 2)	RAB8B TJP2		KIAA0856 // RC3						
		NM_016530	FLJ38125	3597476	chr15	+	61268620	61347018	1.06
		NM_004817 //	MGC26306 // X104	3173880	chr9	+	70925894	71059931	1.06
		NM_201629	// ZO-2 // ZO2						
BCL2/adenovirus E1B 19 kDa interacting protein 2 sorting nexin 9 // synaptojanin 2	BNIP2 SNX9 // SYNJ2	NM_004330	BNIP-2 // NIP2	3627076	chr15	-	57742025	57768916	1.06
		NM_016224 //	MST155 //						
		NM_003898	MSTP155 // SDP1	2933331	chr6	+	158164282	158286097	1.06
programmed cell death 4 (neoplastic transformation inhibitor) leupaxin solite carrier family 7 (cationic amino acid transporter, y+ system), member 5 // SLC7A5 pseudogene	PDCD4 LPXN SLC7A5 // LAT1-3TM		// SH3PX1 //						
			SH3PXD3A // WISP						
			// INP5H //						
			KIAA0348 //						
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		MGC44422						
		NM_014456 //	H731 // MGC33046	3263944	chr10	+	112621575	112649753	1.06
		NM_145341	// MGC33047						
		NM_004811	LDPL	3374402	chr11	-	58050925	58102459	1.06
TNFAIP3 interacting protein 1 NECAP endocytosis associated 2	TNIP1 NECAP2		4F2LC // CD98 //	3703885	chr16	-	86421130	86460615	1.06
			D16S469E // E16						
			// LAT1 // MPE16						
			// hLAT1 // DC49						
TNFAIP3 interacting protein 1 NECAP endocytosis associated 2	TNIP1 NECAP2		// MLAS //						
			hLAT1-3TM						
		NM_003299 //	ECGP // GP96 //	3429312	chr12	+	102848291	102871551	1.06
		NM_003211 //	GRP94 // TRAI //						
TNFAIP3 interacting protein 1 NECAP endocytosis associated 2	TNIP1 NECAP2		// GRP94P1 //						
			GRP94b // HSP //						
			HSPCP2 //						
			HsGrp94b //						
TNFAIP3 interacting protein 1 NECAP endocytosis associated 2	TNIP1 NECAP2		TRAIP1 // TRAP1						
			ABIN-1 //						
		NM_006058	KIAA0113 // NAF1	2881672	chr5	-	150389707	150446947	1.06
			// VAN						
TNFAIP3 interacting protein 1 NECAP endocytosis associated 2	TNIP1 NECAP2		FLJ10420 // RP4-798A10.1	2322389	chr1	+	16639774	16659570	1.06
		NM_018090							

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	
proteasome (prosome, macropain) subunit, alpha type, 5	PSMA5	NM_002790	MGC117302 //	2427074	chr1	-	109742573	109770611	1.06
			MGC125802 //						
			MGC125803 //						
			MGC125804 //						
guanine nucleotide binding protein-like 2 (nucleolar)	GNL2	NM_013285	PSC5 // ZETA	2407191	chr1	-	37805043	37834120	1.06
			FLJ40906 //						
			HUMAUANTIG //						
			NGP1 // Ngp-1 //						
GRIP and coiled-coil domain containing 2	GCC2	NM_014635 //	dJ423B22.6	2498977	chr2	+	108431315	108492470	1.06
			GCC185 //						
			KIAA0336						
			RAD50-2 //						
RAD50 homolog (<i>S. cerevisiae</i>)	RAD50	NM_005732 //	hRad50	2828564	chr5	+	131774479	132009928	1.06
			NM_133482						
			NM_022763						
			DKFZp686D14170						
fibronectin type III domain containing 3B	FNDC3B	NM_022763	// DKFZp762K137	2652410	chr3	+	173240112	173601176	1.06
			// FAD104 //						
			FLJ23399 //						
			MGC10002 //						
son of sevenless homolog 2 (<i>Drosophila</i>) 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)	SOS2	NM_006939	PRO4979 //	3563734	chr14	-	49654812	49768331	1.06
			YVTM2421						
			FLJ1884 // HSP86						
			// HSP90A //						
phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 duncce homolog, <i>Drosophila</i>)	PDE4B	NM_001037340 //	HSP90N // HSPC1	3580179	chr14	-	101616842	101676327	1.06
			// HSPCA //						
			HSPCAL1 //						
			HSPCAL4 // HSPN						
interleukin-1 receptor-associated kinase 2	IRAK2	NM_001570	// Hsp89 // Hsp90	2340529	chr1	+	66030487	66612844	1.06
			// LAP2 //						
			HSP90ALPHA //						
			HSPCAL3 //						
chromosome 14 open reading frame 32	C14orf32	NM_144578	HSP90AF	2610359	chr3	+	10181579	10260427	1.06
			DKFZp686F2182 //						
			DPDE4 //						
			MGC126529 //						
nucleoside phosphorylase	NP	NM_000270	PDEIVB	3536663	chr14	+	54588114	54606655	1.06
			IRAK-2 //						
			MGC150550						
			MGC23138 // MISS						
nucleoside phosphorylase	NP	NM_000270	// c14_5346	3527514	chr14	+	20007398	20015985	1.06
			MGC117396 //						
			MGC125915 //						
			MGC125916 // PNP						
nucleoside phosphorylase	NP	NM_000270	// PRO1837 //	3527514	chr14	+	20007398	20015985	1.06
			PUNP						

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	
proline-serine-threonine phosphatase interacting protein 2 growth factor receptor-bound protein 2	PSTPIP2	NM_024430	MAYP // MGC34175	3806211	chr18	-	41817502	41906221	1.06
	GRB2	NM_002086 // NM_203506	ASH // EGRBP- GRB2 // Grb3-3 // MST084 //	3770743	chr17	-	70805871	70913384	1.06
			MSTP084						
signal-induced proliferation-associated 1 like 1	SIPA1L1	NM_015556	DKFZp686G1344 // EGTP1 // 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 // MGC136110 //	2555490	chr2	-	61558490	61619343	1.06
centromere protein C 1	CENPC1	NM_001812	NR1A2 // THR1 // THRB1 // THRB2 CENP-C // CENPC // MIF2 // hcp-4 ABLL // ARG	2771654	chr4	-	68020183	68093837	1.06
v-abl Abelson murine leukemia viral oncogene homolog 2 (arg, Abelson-related gene) rine finger protein 10	ABL2 RNF10	NM_005158 // NM_007314 NM_014868	KIAA0262 // MGC126758 // MGC126764 //	2446047 3434413	chr1 chr12	- +	177335093 119456489	177528267 119500226	1.06 1.06
Notch homolog 2 (<i>Drosophila</i>) // neuroblastoma breakpoint family, member 14	NOTCH2 // NBPF14	XM_001133349 // NM_024408 // NM_015383	AGS2 // hN2 // DI328E19/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 //	2400518	chr1	-	21394307	21544720	1.06
phosphoinositide-3-kinase adaptor protein 1	PIK3AP1	NM_152309	MGC35575 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 AT-hook transcription factor	TNIK AKNA	NM_015028 NM_030767	AD 2 KIAA1968 // RP11- 8211.4	2705266 3221916	chr3 chr9	- -	172258898 116138238	172660964 116200584	1.06 1.06
Fas (TNF receptor superfamily, member 6)	FAS	NM_000043 // NM_152871 // NM_152872 // NM_152873 // NM_152874 // NM_152875 //	ALPSIA // APO-1 // APT1 // CD95 // FAS1 // FASTM // TNFRSF6	3257098	chr10	+	90721519	90765521	1.06

Gene Name	Gene Symbol	Accession	Synonym	Cluster ID	Human Genome hg18			Fold Change/			
					Chromosome	Strand	Start		Stop	mM	
ankyrin repeat domain 17	ANKRD17	NM_152876 //	FLJ2206 // GTAR // KIAA0697 // NY-BR-16	2773023	chr4	-	74158547	74343428	1.06		
elafalin interactor 1	CLINT1	NM_014666	CLINT // ENTH // EPN4 // EPNR // EPSNR //	2883609	chr5	-	157145339	157284818	1.06		
PRP8 pre-mRNA processing factor 8 homolog (<i>S. cerevisiae</i>)	PRPF8	NM_006445	HRP8 // PRP8 // PRPC8 // RP13	3740479	chr17	-	1500681	1534906	1.06		
AT4/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 //	UV20	3865378	chr19	-	50602433	50673926	1.06		
		NM_202001									
ubiquitously transcribed tetratricopeptide repeat, X chromosome // ubiquitously transcribed tetratricopeptide repeat gene, Y- linked	UTX // UTY	NM_021140 //	DKFZp686A03225	3975467	chrX	+	44590716	44896185	1.06		
		NM_007125 //	// MGC141941 //								
		NM_182659 //	BA386N14.2 //								
ATPase, Ca++ transporting, plasma membrane 1	ATP2B1	NM_182660	DKFZp686L12190 // UTY1	3464983	chr12	-	88505965	88620030	1.06		
v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	ETS2	NM_001682	PMCA1	3921068	chr21	+	39059147	39118744	1.06		
zinc finger protein 91 homolog (mouse) // ciliary neurotrophic factor	ZFP91 // CNTF	NM_053023 //	FKSG11 // PZF //	3331730	chr11	+	58101868	58149782	1.06		
		NM_170768 //	ZNF757 // HCN1F								
		NM_000614									
integrin, alpha 5 (fibronectin receptor, alpha polypeptide)	ITGA5	NM_002205	CD49e // FNRA //	3456732	chr12	-	53075332	53099491	1.06		
			VLA5A								
IBR domain containing 3 cofactor required for Sp1 transcriptional activation, subunit 2, 150 kDa	IBRDC3 CRSP2	NM_153341	FLJ90005	2405312	chr1	-	33172120	33203343	1.06		
		XM_001126052 //	CRSP150 // CSRP	4005644	chrX	-	40392502	40480045	1.06		
		NM_004229	// CXorf4 // DRP150 // EXLM1 // MED14 //								
aryl hydrocarbon receptor solute carrier family 43, member 2	AHR SLC43A2	NM_001621	MGCI04513 //	2991233	chr7	+	17304771	17363729	1.06		
		NM_152346	RGR1 // TRAP170	3740367	chr17	-	1423948	1478920	1.06		
			FLJ23848 // LAT4 // MGC34680								
chemokine (C-C motif) ligand 20	CCL20	NM_004591	CKb4 // LARC // MIP-3a // MIP3A // SCYA20 //	2530713	chr2	+	228386802	228427090	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
serpin peptidase inhibitor, clade B (ovalbumin), member 8	SERPINF8	NM_001031848 // NM_002640 // NM_198833	CAP2 // P18	3791996	chr18	+	59787618	59823238
chaperonin containing TCP1, subunit 4 (delta)	CCT4	NM_006430	Cctd // MGC126164 // MGC126165 // SRB	2555630	chr2	-	61939693	61970469
AP2 associated kinase 1	AAK1	NM_014911	KIAA1048 // MGC138170	2558150	chr2	-	69538639	69783824
musculin (activated B-cell factor-1)	MSC	NM_005098	ABF-1 // ABF1 // MYOR	3140213	chr8	-	72843959	73059105
Yip1 domain family, member 5	YIPF5	NM_001024947 // NM_030799	DKFZp313L2216 // FinGERS // SB140 // SMAP-5 // SMAP5 // YIP1A	2879509	chr5	-	143463451	143565514
START domain containing 7	STARD7	NM_020151 // NM_139267	GTT1	2565143	chr2	-	96214334	96238296
ADP-ribosylation factor guanine nucleotide-exchange factor 1 (brefeldin A-inhibited)	ARFGEF1	NM_006421	ARFGEF1 // BIG1 // D730028O18Rik // DKFZP434L057 // P200	3139035	chr8	-	68250009	68418446
myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, <i>Drosophila</i>)	MLL5	NM_018682 // NM_182931	FLJ10078 // FLJ14026 // HDCMC04P // MGC70452	3017547	chr7	+	104436029	104542698
DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	DDX3X	XM_001129278 // NM_001356	DBX // DDX14 // DDX3 // HLP2	3974838	chrX	+	41055591	41108668
nibrin	NBN	NM_001024688 // NM_002485	AT-V1 // AT-V2 // ATV // FLJ10155 // MGC87362 // NBS	3143970	chr8	-	91014745	91066433
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
ankyrin repeat domain 44	ANKRD44	NM_153697	MGC21968 // MGC70444	2593464	chr2	-	197512324	197901798
RB1-inducible coiled-coil 1	RB1CC1	NM_014781	CC1 // DRAGOU14 // FIP200	3135184	chr8	-	53641628	93789545
ubiquitin specific peptidase 12	USP12	NM_182488	USP12L1	3506738	chr13	-	26518485	26644264
apoptosis inhibitor 5	API5	NM_006595	AAC-11 // AAC11 // API5L1	3327906	chr11	+	43290109	43322649
HIR histone cell cycle regulation defective homolog A (<i>S. cerevisiae</i>)	HIRA	NM_003325	DGCR1 // TUP1 // TUPLE1	3952637	chr22	-	17696576	17799452

Gene Name	Gene Symbol	Accession	Synonym	Chromosome	Human Genome hg18			Fold Change/
					Strand	Start	Stop	
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	chr1	-	89343675	89496682	1.06
	CFLAR	NM_003879	CASH // CASP8A1 // CLARP // Casper // FLAME // FLAME-1 // FLIP // L-FLICE // MRIT // USURPIN // c-FLIP // c-FLIPL // HIV-EP2 // MBP-2 // MIBP1	chr2	+	201689135	201744701	1.06
	HIVEP2	NM_006734	FLIP // c-FLIPL // HIV-EP2 // MBP-2 // MIBP1	chr6	-	143065515	143308841	1.06
	SERPINB9 // SERPINB6	NM_004155 // NM_004568	CAP-3 // CAP3 // P19 // CAP // DKFZp686l04222 // MGC111370 // MSTP057 // P16 // PTI	chr6	-	2832402	2858242	1.06
human immunodeficiency virus type 1 enhancer binding protein 2								
serpin peptidase inhibitor, clade B (ovalbumin), member 9 // serpin peptidase inhibitor, clade B (ovalbumin), member 6								
myxovirus (influenza virus) resistance 2 (mouse) soluble carrier family 25, member 37	MX2 SLC25A37	NM_002463 XM_00128238 // XM_00128248 // XM_00128255 // XM_00128269 // NM_016612 NM_016312	MXB HT015 // MFRN // MSC // MSCP // PRO1278 // PRO1584 // PRO2217 DKFZp779M1063 // NPWB // SIPP1	chr21	+	41655820	41703177	1.06
WW domain binding protein 11	WBP11	NM_016312	ACF1 // NPWB // SIPP1	chr12	-	14829481	14848171	1.06
bromodomain adjacent to zinc finger domain, 1A	BAZ1A	NM_013448 // NM_182648	ACF1 // DKFZP586E0518 // FLJ14383 // WALp1 // WCRF180 // hACF1	chr14	-	34291692	34414604	1.06
aquaporin 9	AQP9	NM_020980	Hs6					
solute carrier family 39 (zinc transporter), member 8	SLC39A8	NM_022154	BIGM103 // LZT-1	chr15	+	56217766	56280468	1.06
FYFN oncogene related to SRC, FGR, YES	FYN	NM_002037 // NM_153047 // NM_153048	MGC45350 // SLK // SYN	chr4	-	103393022	103486067	1.06
elongation factor, RNA polymerase II, 2	ELL2	NM_012081	IAK1A // IAK1B	chr6	-	112088237	112301348	1.06
Janus kinase 1 (a protein tyrosine kinase)	IAK1	NM_002227	I-REL	chr5	-	95246561	95323733	1.06
v-r1 reticuloendotheliosis viral oncogene homolog B, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (avian)	RELB	NM_006509		chr1	-	65071504	65278035	1.06
chemokine (C-C motif) ligand 2	CCL2	NM_002982	GDCF-2 // GDCF-2 HC11 // HC11 // HSMCR30 // MCAF	chr19	+	50196537	50233287	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
hexokinase 2	HK2	NM_000189	// MCP-1 // MCP1 // MGC9434 // SCYA2 // SMC-CF DKFZp686M1669 // HKII // HXK2 ERP // NET // SAP2 MSK // SIK CMT1C // FLJ38636 // MGC116698 // MGC116700 // MGC116701 // MGC125274 // MGC125275 // MGC125276 // PIG7 // SIMPLE // TP53I7	2489545	chr2	+	74913290	74974310
ELK3, ETS-domain protein (SRF accessory protein 2)	ELK3	NM_005230		3427098	chr12	+	95112269	95187725
SNF1-like kinase	SNF1LK	NM_173354		3934111	chr21	-	43637578	43705100
lipopolysaccharide-induced TNF factor	LITAF	NM_004862		3680434	chr16	-	11549088	11599620
tRNA splicing endonuclease 54 homolog (<i>S. cerevisiae</i>)	TSEN54	NM_207346	// NAP-3 // FYVE-DSP1 // KIAA0371 // ZFYVE10 ADTB1 // AP105A // BAM22 // CLAPB2 FLJ40884 FLH21957 // FLJ10410 // FLJ20373 // FLJ90111 // HGK // KIAA0687 // NIK CD166 // FLJ38514 // MEMD // MGC71733 IBMPHD // MGC131997 // MGC148092 // MGC8560 // TERA	3734865	chr17	+	71022989	71032409
chromodomain helicase DNA binding protein 6	CHD6	NM_032221		3906160	chr20	-	39464169	39680547
chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)	CXCL1	NM_001511		2731381	chr4	+	74953973	74983954
myotubularin related protein 3	MTMR3	NM_021090 // NM_153050 // NM_153051 NM_001127 // NM_145730	// NAP-3 // FYVE-DSP1 // KIAA0371 // ZFYVE10 ADTB1 // AP105A // BAM22 // CLAPB2 FLJ40884 FLH21957 // FLJ10410 // FLJ20373 // FLJ90111 // HGK // KIAA0687 // NIK CD166 // FLJ38514 // MEMD // MGC71733 IBMPHD // MGC131997 // MGC148092 // MGC8560 // TERA	3942179	chr22	+	28609182	28762301
adaptor-related protein complex 1, beta 1 subunit	AP1B1	NM_001127 // NM_145730		3956781	chr22	-	28053592	28206955
actinin, alpha 1	ACTN1	NM_001102		3569814	chr14	-	68409817	68515815
mitogen-activated protein kinase kinase kinase 4	MAP4K4	NM_004834 // NM_145686 // NM_145687		2496727	chr2	+	101600496	101877880
activated leukocyte cell adhesion molecule	ALCAM	NM_001627	// KIAA0687 // NIK CD166 // FLJ38514 // MEMD // MGC71733 IBMPHD // MGC131997 // MGC148092 // MGC8560 // TERA	2634494	chr3	+	106304077	106816151
valosin-containing protein // Fanconi anemia, complementation group G	VCP // FANCG	NM_007126 // NM_004629		3204404	chr9	-	35026106	35062648

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
heat shock 105 kDa/110 kDa protein 1	HSPH1	NM_006644	// p97 // FAG //					
			XRCC9					
			DKFZp686M05240		3508330	chr13	-	30651692
			// HSP105 //				30558258	1.06
WAS protein family, member 2	WASF2	NM_006990	HSP105A //					
			HSP105B //					
			KIAA0201 // NY-					
			CO-25					
RAP1 interacting factor homolog (yeast)	RIF1	NM_018151	SCAR2 // WAVE2		2403111	chr1	-	27689256
			// dJ393P12.2					
			DKFZp781N1478 //		2510485	chr2	+	152072768
			FLJ12870				151974674	1.06
chromosome 20 open reading frame 77	C20orf77	NM_021215	CREPT //		3884450	chr20	+	36189576
			DKFZp434P0735 //				36095232	1.06
			FLJ44520 //					
			dJ1057B20.2					
Wilms tumor 1 associated protein // acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thiolase)	WTAP // ACAT2	NM_004906 // NM_152857 // NM_152858 // NM_005891 // NM_006813	DKFZp686F20131		2934089	chr6	+	160097332
			// KIAA0105 //				160066607	1.06
			MGC3925 // —					
			B4-2 // PNAS-145					
proline-rich nuclear receptor coactivator 1	PNRC1	NM_006813	// PRO12 // PRR2		2916716	chr6	+	89852045
			// RP11-63L7.5				89847048	1.06
			DKFZp761F0118 //					
			FLJ14374 //		3291682	chr10	-	64951821
jumonji domain containing 1C	JMJD1C	NM_004241 // NM_032776	KIAA1380 // RP11-10C13.2 // TRIP8					
			—					
			—					
			—					
ELL associated factor 1, mitogen-activated protein kinase-activated importin 7	EAF1 MAPKAPK2 IPO7	NM_033083 NM_004759 // NM_032960 NM_006391	FLJ14581 //		2612371	chr3	+	15466824
			MGC138673 //		2376922	chr1	+	204974249
			RANBP7				9362702	1.06
			EIF-2 // EIF-2A //		3541137	chr14	+	66922983
eukaryotic translation initiation factor 2, subunit 1 alpha, 35 kDa	EIF2S1	NM_004094	EIF-2alpha // EIF2					
			// EIF2A					
			4F9 // C33 //		3328520	chr1	+	44543723
			GR15 // IA4 //					
CD82 molecule	CD82	NM_001024844 // NM_002231	KAI1 // R2 //					
			SAR2 // ST6 //					
			DKFZp667H044 //		3131916	chr8	-	38359646
			FLJ20353 //					
Wolf-Hirschhorn syndrome candidate 1-like 1	WHSC1L1	NM_017778 // NM_023034	MGC126766 //					
			MGC142029 //					
			NSD3 // pp14328					
			—					

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
ADP-ribosylation factor-like 8B	ARL8B	NM_018184	ARL10C // FLJ10702 // Giel	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-GEF // Rap-GEF	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 polypeptide 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-1 // Pgp1 // FLJ12099 // FLJ33785 // INK3 // INK3A // MGC50974 //	3326635	chr11	+	35117003	35210509	1.06

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript	Human Genome hg18			Fold Change/ nM
					Cluster ID	Chromosome	Strand	
mitogen-activated protein kinase kinase 1	MAP2K1	NM_002755	PRKM10 //					
			p493F12 //					
chromosome 16 open reading frame 72	C16orf72	NM_014117	MAPPK1 // MEK1		3598662	chr15	+	64466253
			// MKK1 //					64571690
tumor necrosis factor receptor superfamily, member 1B	TNFRSF1B	NM_001066	PRKMK1		3647632	chr16	+	9092682
			FLJ41272 //					9121055
protein phosphatase 2, regulatory subunit B', gamma isoform	PPP2R5C	NM_002719 //	PRO0149		2320727	chr1	+	12149647
			CD120b // TBP1 //					12192323
TSPY-like 2 // paraoxonase 3	TSPYL2 // PON3	NM_001128695 //	TNF-R-II // TNF-R75 // TNFR //					
			TNFR2 // TNFR80					
serine/threonine kinase 17a	STK17A	NM_004760	// p75 // p75TNFR		3552729	chr14	+	101296771
			B56G // MGC23064					101464066
ELAV (embryonic lethal, abnormal vision, <i>Drosophila</i>)-like 1 (Hu antigen R) // translocase of inner mitochondrial membrane 44 homolog (yeast)	ELAVL1 // TIMM44	NM_006351	// PR61G					
			CDA1 // CINAP //					
basic leucine zipper and W2 domains 1	BZW1	NM_001126385 //	CTCL // DENT1 //		3978169	chrX	+	53124038
			HRHFB2216 //					53134445
fibronectin type III domain containing 3A // cancer/testis antigen CT45-3	FNDC3A // RP13-36C9.3	NM_014923 //	SE20-4 // —					
			DRAK1		2999485	chr7	+	43573961
MAX dimerization protein 1	MXD1	NM_002357	ELAV1 // HUR //		3848689	chr19	-	7929463
			Hua // MeIG //					7999655
TLA1 cytotoxic granule-associated RNA binding protein-like 1	TLA1	NM_001033925 //	DKFZp686H05241					
			// TIM44					
nuclear receptor subfamily 4, group A, member 3	NR4A3	NM_001017435	BZAP45 //		2522439	chr2	+	201384456
			KIAA0005 //					201418386
SAM domain, SH3 domain and nuclear localization signals 1	SAMS1	NM_022136	Nbia10236		3489212	chr13	+	48428770
			FLJ1509 //					48681909
sperm specific antigen 2	SSFA2	NM_006751	FNDC3 //					
			RP13-36C9.3					
TIA1 cytotoxic granule-associated RNA binding protein-like 1	TIA1	NM_001033925 //	KIAA0970 //					
			bA203116.1 //					
nuclear receptor subfamily 4, group A, member 3	NR4A3	NM_001017435	bA203116.5 //					
			CT45-3 // RP13-					
SAM domain, SH3 domain and nuclear localization signals 1	SAMS1	NM_022136	MAD // MAD1 //		2487549	chr2	+	69995330
			MGC104659					70023575
sperm specific antigen 2	SSFA2	NM_006751	MGC33401 //		3309629	chr10	-	121291481
			TCBP // TIA1					121346521
MAX dimerization protein 1	MXD1	NM_002357	CHN // CSMF //		3181976	chr9	+	101623410
			MINOR // NOR1 //					101669157
TIA1 cytotoxic granule-associated RNA binding protein-like 1	TIA1	NM_001033925 //	TEC					
			HACS1 // NASH1		3925473	chr21	-	14779427
nuclear receptor subfamily 4, group A, member 3	NR4A3	NM_001017435	CS-1 // CSI //		2518428	chr2	+	182464815
			DKFZp313O1039 //					182516732

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
zinc finger protein 317 // zinc finger protein 658	ZNF317 // ZNF658	NM_020933 // XM_001125688 // NM_033160	DKFZp779G0129 //					
			FLJ45996 //					
			KIAA1927 // KRAP					
			// SPAG13					
vactolar protein sorting 35 homolog (<i>S. cerevisiae</i>)	VPS35	NM_018206	KIAA1588 //				9112073	9135082
			DKFZp572C163 //					
			FLJ32813 //					
			MGC35232					
CD8a molecule	CD8A	NM_001768 // NM_171827 // NM_001514	DKFZp434E1211 //				45220566	45280598
			DKFZp434P1672 //					
			FLJ10752 //					
			FLJ13588 //					
general transcription factor IIB	GTF2B // RP11-82K18.3	NM_001768 // NM_171827 // NM_001514	FLJ20388 // MEM3				86857923	86889020
			CD8 // Leu2 //					
			MAL // p32					
			TF2B // TFHIB				89090909	89130195
ring finger and WD repeat domain 2	RFWD2	NM_001001740 // NM_022457 // NM_015033	COP1 // FLJ10416				174150358	174443232
			// RNF200					
			FBP17 // KIAA0554				131689314	131845274
			// MGC126804					
transmembrane protein 23	TMEM23	NM_147156	MGC17342 // MOB				51706090	52054733
			// MOB1 // SMS1					
			HIF-1alpha //				612225495	61285222
			HIF1-ALPHA //					
hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	HIF1A	NM_001530 // NM_181054	MOP1 // PASD8					
			ANX5 // ENX2 //				122695163	122838353
			PP4					
			FKSG15 //				159375488	159517834
annexin A5	ANXA5	NM_001154	FLJ32631 //					
			NM_13810 //					
			NM_152133					
			FLJ39711 //					
T-cell activation GTPase activating protein	TAGAP	NM_003859	MGC133247 //					
			MGC27381 //					
			TAGAP1					
			CDGIE // MPDS				48984632	49008494
dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit	TIA1	NM_022037 // NM_022173	—					
							70290081	70329315
			BL11 // HB15				14118209	14485106
CD83 molecule	CD83	NM_004233	300-KD //				2742650	2761908
			DKFZp686O15166					
			// FLJ21926 //					
			FLJ22250 //					
serine/arginine repetitive matrix 2	SRRM2	NM_016333	KIAA0324 //					

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
mitogen-activated protein kinase kinase 3	MAP2K3	XM_001130488 //	MGC40295 //					
		NM_145110 //	SRL300 // SRM300					
		NM_002756 //	MAPKK3 // MEK3		3714729	chr17	+	21128581
		NM_145109	// MKK3 //					21159113
mitogen-activated protein kinase kinase 1	MAP2K1IP1	NM_021970	PRKMK3					
interacting protein 1	FLJ131951	NM_144726	MP1		2779408	chr4	-	101018538
								101034726
capping protein (actin filament) muscle Z-line, alpha 1	CAPZA1	NM_006135	DKFZp686M11215		2884216	chr5	-	158516997
			CAPPA1 // CAPZ		2352228	chr1	+	112945824
			// CAZ1					113015736
chemokine (C-X-C motif) ligand 10	CXCL10	NM_001565	C7 // IFI10 //		2773958	chr4	-	77151393
			INP10 // IP-10 //					77163693
			SCYB10 // crg-2					
			// gIP-10 // mob-1					
v-rat murine sarcoma 3611 viral oncogene homolog	ARAF	NM_001654	A-RAF // ARAF1		3976299	chrX	+	47300826
			// PKS2 // RAFA1					47316249
ADAM metalloproteinase domain 17 (tumor necrosis factor, alpha, converting enzyme)	ADAM17	NM_003183	CD156b //		2539821	chr2	-	9546070
			MGC71942 //					9630637
			TACE // gSVP					
protein tyrosine phosphatase type IVA, member 1	PTP4A1	NM_003463	DKFZp779M0721 //		2911903	chr6	+	64289625
			HH72 // PRL-1 //					64351448
			PRL1 //					
			PTP(CAAX1) //					
poly (ADP-ribose) polymerase family, member 9	PARP9	NM_031458	PTPCAAX1		2692060	chr3	-	123729469
			BAL // BAL1 //					123766193
			DKFZp666B0810 //					
			DKFZp686M15238					
WD repeat domain 74	WDR74	XM_001125771 //	// FLJ26637 //					
		NM_018093	FLJ41418 //					
		NM_014701 //	MGC: 7868		3376235	chr11	-	62356627
		NM_001042461 //	FLJ10439 //					62365857
KIAA0256 gene product // trafficking protein particle complex 5	TRAPPC5	NM_001042462 //	FLJ21730		3623320	chr15	-	47055671
		NM_174894	—// MGC52424					47126043
CD47 molecule	CD47	NM_001025079 //	IAP // MER6 //		2687739	chr3	-	109143203
		NM_001777 //	OAS3					109306052
		NM_198793						
inositol polyphosphate-5-phosphatase, 145 kDa	INPP5D	XM_929960 //	MGC104855 //		2532699	chr2	+	233632835
		NM_001017915 //	MGC142140 //					233823600
		NM_005541	MGC142142 //					
			SHIP // SHIP1 //					
			SIP-145 // hp51CN					

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript	Human Genome hg18			Fold Change/
					Cluster ID	Chromosome	Strand	
					Cluster ID	Chromosome	Strand	Start
								Stop
								nM
slingshot homolog 2 (<i>Drosophila</i>)	SSH2	NM_033389	KIAA1725 // MGC78588 // SSH-2	3751625	chr17	-	-	24977091
oxysterol binding protein-like 8	OSBP18	NM_001003712 // NM_020841	DKFZp686A11164 // MGC126578 // MGC133203	3462949	chr12	-	-	75269250
RAS p21 protein activator 3	RASA3	NM_007368	ORP8 // OSBP10 GAP1IP4BP // GAPIII // MGC46517	3526831	chr13	-	-	113765177
stromal antigen 2	STAG2	NM_001042749 // NM_001042750 // NM_001042751 // NM_006603	DKFZp686P168 // DKFZp781H1753 // FLJ25871 // SA-2 // SA2 // ba51701.1	3989721	chrX	+	+	122922013
NIMA (never in mitosis gene a)-related kinase 7 protein tyrosine phosphatase, receptor type, E	NEK7 PTPRE	NM_133494 NM_006504 // NM_130435	DKFZp313F1310 // HPTPE // PTP // R-PTP-EPSILON	2373736 3270270	chr1 chr10	+	+	196225008 129595315
solite carrier organic anion transporter family, member 4A1	SLCO4A1	NM_016354	OATP-E // OATP1 // OATP4A1 // OATPRP1 // POAT // SLC21A12	3892812	chr20	+	+	60744242
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
phosphoinositide-3-kinase, regulatory subunit 5, p101	PIK3R5	NM_014308	F730038U.SRik // FOAP-2 // P101-PBK	3744680	chr17	-	-	8718740
HECT, UBA and WWE domain containing 1 // paraoxonase 1 // paraoxonase 3	HUWE1 // PON1 // PON3	NM_031407 // NM_000446 // NM_000940	ARE-BP1 // HECTH9 // HSPC272 // lb772 // KIAA0312 // LASU1 // MULE // UREB1 // ESA // PON // —	4009315	chrX	-	-	53575796
antizyme inhibitor 1	AZIN1	NM_015878 // NM_148174 //	MGC3832 // MGC691 // OAZI // OAZIN //	3147591	chr8	-	-	103907725
A kinase (PRKA) anchor protein 13	AKAP13	NM_006738 // NM_007200 // NM_144767	AKAP-Lbc // BRX // FLJ11952 // FLJ43341 // HA-3 // H31 // LBC // PROTO-LB // PROTO-LBC // c-lbc	3606304	chr15	+	+	83681343

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript	Human Genome hg18			Fold Change/
					Cluster ID	Chromosome	Strand	
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 (<i>S. cerevisiae</i>)	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 (<i>S. cerevisiae</i>)	DOT1L	NM_032482	DOT1 // KIAA1814	3816264	chr19	+	2114945	2183576 1.06
epithelial stromal interaction 1 (breast) //	EPSTI1	NM_001002264 //	BRIS11 //	3511698	chr13	-	42309603	42464520 1.06
junctionophilin 3	JPH3	NM_033255 // NM_020655	MGC29634 // CAGL237 // FLJ44707 // HDL2 // JP-3 // JP3 //					
promyelocytic leukemia	PML	XM_001132060 // NM_002675 // NM_033238 // NM_033239 // NM_033240 // NM_033244 // NM_033246 // NM_033247 // NM_033249 // NM_033250 NM_001539	TNRC22 MYL // PP8675 // RNF71 // TRIM19	3601387	chr15	+	72073603	72126162 1.06
DnaJ (Hsp40) homolog, subfamily A, member 1	DNAJA1	NM_001539	DI-2 // Dja1 // HD12 // 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 // DSIP1 // GILZ // TSC-22R // hDIP	4017381	chrX	-	106803586	106916423 1.06
RNA binding motif protein 4	RBM4	NM_002896	DKFZp547K0918 // LARK // MGC75138 // RBM4A // ZCCHC21 //	3336422	chr11	+	66161951	66190547 1.06
Smg-7 homolog, nonsense mediated mRNA decay factor (<i>C. elegans</i>)	SMG7	NM_014837 // NM_173156 // NM_201568 // NM_201569 NM_001166	ZCRB3A C1orf16 // EST1C // FLJ23717 // KIAA0250 // SGA56M // SMG-7 API1 // H1AP2 // H1ap-2 // M1HB // RNF48 // cIAP1	2371255	chr1	+	181708036	181834004 1.06
baculoviral IAP repeat-containing 2	BIRC2			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	
DEAH (Asp-Glu-Ala-His) box polypeptide 15	DHX15	NM_001358	DBP1 // DDX15 //	2763805	chr4	-	24128159	24250940
			HRH2 // PRP43 //					
echinoderm microtubule associated protein like 4	EML4	NM_019063	PRPF43 // PrPp43p	2478748	chr2	+	42250017	42418636
			C2orf2 //					
protein phosphatase 6, catalytic subunit bromodomain and WD repeat domain containing 1	PPP6C BRWD1	NM_002721 NM_001007246 //	DKFZp686P18118	3225348 3932148	chr9 chr21	-	126948675 39479279	12691992 39615332
			// ELP120 //					
any/old beta (A4) precursor-like protein 2	APLP2	NM_033656 NM_001642	FLJ10942 //	3356115	chr11	+	129444931	129519895
			FLJ32318 //					
sperm associated antigen 9	SPAG9	NM_003971 // NM_172345	ROPP120	3762519	chr17	-	46394554	46553215
			—					
Rap guanine nucleotide exchange factor (GEF) 6 // folliculin interacting protein 1	RAPGEF6 // FNIP1	NM_016340 // NM_001008738 // NM_133372	C21orf107 //	2874794	chr5	-	130760272	131160628
			FLJ43918 // N143					
ATPase, Na ⁺ /K ⁺ transporting, beta 3 polypeptide	ATP1B3	XM_001133533 // XM_001133534 //	// WDR9	2645764	chr3	+	143077611	143128338
			APPH // APPL2 //					
leukocyte-associated immunoglobulin-like receptor 1	LAIR1	NM_002287 // NM_021706	CDEBP	3870824	chr19	-	59557066	59578582
			FLJ14006 //					
interleukin enhancer binding factor 2, 45 kDa	ILF2	NM_004515	FLJ34602 // HLC4	2436132	chr1	-	151900372	151910103
			// HSS // JLP //					
solute carrier family 38, member 1	SLC38A1	NM_001077484 // NM_030674	KIAA0516 //	3452231	chr12	-	44863120	44952390
			MGC117291 //					
tumor domain containing 7	TDRD7	NM_014290	MGC14967 //	3181193	chr9	+	99202471	99298225
			MGC74461 // PHET					
			// PIG6					
			DKFZp667N084 //					
			DKFZp686I5116 //					
			KIA0011B // PDZ-					
			GEF2 // PDZGEF2					
			// RA-GEF-2 //					
			DKFZp686E18167					
			// DKFZp781P0215					
			// KIAA1961 //					
			MGC667					
			ATPB-3 // CD298					
			// FLJ29027					
			CD305 // LAIR-1					
			MGC8391 // NF45					
			// PRO3063					
			ATA1 // NAT2 //					
			SAT1 // SNAT1					
			KIAA1529 //					
			PCTAIRE2BP //					
			RP11-508D10.1 //					
			TRAP					

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	
thioredoxin domain containing 14 // catenin (cadherin-associated protein), delta 1	TXNDC14 // CTNND1	NM_015959 //	CGI-31 //	3331487	chr11	+	57235839	57391291	1.06	
		XM_001126721 //	DKFZp781O2021 //							
		XM_001126756 //	MGC111151 //							
		XM_001126767 //	PIG26 // TMX2 //							
		XM_001126781 //	CAS // CTNND //							
zinc finger protein 207	ZNF207	XM_001126793 //	KIAA0384 //							
		XM_001126823 //	PI20CAS //							
		NM_001331	PI20CTN // p120	3717635	chr17	+	27701159	27759429	1.06	
		NM_001032293 //	DKFZp761N202							
		NM_003457								
zinc finger, AN1-type domain 3 catenin (cadherin-associated protein), beta 1, 88 kDa	ZFAND3 CTNNB1	NM_021943	FLJ13222 // TEX27	2905664	chr6	+	37895285	38231400	1.06	
		XM_001133660 //	CTNNB //	2618940	chr3	+	41211356	41256934	1.06	
		XM_001133664 //	FLJ25606							
		XM_001133673 //								
		XM_001133675 //								
NCK-associated protein 1-like upstream binding protein 1 (LBP-1a)	NCKAP1L UBP1	NM_001904	HEM1	3416577	chr12	+	53177769	53224156	1.06	
		NM_005337	DKFZp686L1745 //	2668351	chr3	-	33404835	33456874	1.06	
		NM_014517	LBP-1B // LBP-1a // LBP1A //							
			CLIMP-63 //	3469687	chr12	-	105155796	105222139	1.06	
		NM_006825	ERGIC-63 //							
cytoskeleton-associated protein 4	CKAP4		MGC99554 // p63							
		NM_018955 //	FLJ25987 //	3712041	chr17	+	16223047	16228977	1.06	
		NM_152350	MGC8385 //							
			FLJ25777 //							
			MGC40157							
ATPase, Class V, type 10D cytoplasmic polyadenylation element binding protein 4	ATP10D CPEB4	NM_020453	ATPVD //	2726072	chr4	+	47179942	47290260	1.06	
		NM_030627	KIAA1673	2841699	chr5	+	173177911	173320580	1.06	
			COASTER //							
		NM_001031623 //	FLJ90693 //	2911303	chr6	+	57062631	57143064	1.06	
		NM_015555	KIAA0576 //							
superoxide dismutase 2, mitochondrial	SOD2 // MGC5618		MGC26701 //							
			dJ417L1.1							
		NM_000636 //	IPO-B // MNSOD	2982319	chr6	-	160020086	160103541	1.06	
		NM_001024465 //	// Mn-SOD							
		NM_001024466								
optic atrophy 1 (autosomal dominant)	OPA1	NM_015560 //	FLJ12460 //							
		NM_130831 //	KIAA0567 // NPG	2658346	chr3	+	194793673	194902403	1.06	
		NM_130832 //	// NTG // largeG							
		NM_130833 //								
		NM_130834 //								

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	
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	FLJ22835 // IFI41	3922100	chr21	+	41714183	41752955	1.06	
SP110 nuclear body protein	SP110	NM_004509 // NM_004510 // NM_080424	MX // MxA // IFI75 // VOD1	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	MAT2 // MATIII // SAMB2	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 (<i>S. cerevisiae</i>)	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 (HITF4, helix-loop-helix transcription factors 4)	TCF12	NM_003205 // NM_207036 // NM_207037 // NM_207038 // NM_207040	HEB // HITF4 // HsT17266	3595096	chr15	+	54963208	55402126	1.06	
ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	ATP2A2	NM_001681 // NM_170665	ATP2B // DAR // DD // MGC45367	3431483	chr12	+	109203332	109352495	1.06	
ubiquitin associated protein 1	UBAP1	NM_016525	SERCA2 // MGC119669 // MGC8710 // NAG20 // UAP	3167325	chr9	+	34168995	34243205	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	
heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1 arrestin domain containing 2	HS3ST3B1 ARRDC2	NM_006041 NM_001025604 // NM_015683	3OST3B1 // 3OST3B1 CLONE24945 // PP2703	3711262 3824713	chr17 chr19	+	14145125 17972961	14193444 17985905	1.06 1.06
casein kinase 1, alpha 1	CSNK1A1	NM_001025105 // NM_001892	CK1 // HLCDDGP1 // PRO2975	2880932 3421897	chr5 chr12	-	148800168 68901823	148922811 69035035	1.06 1.06
CCR4-NOT transcription complex, subunit 2	CNOT2	NM_014515	CDC36 //	3240987	chr10	+	30762872	30791283	1.06
mitogen-activated protein kinase kinase 8	MAP3K8	NM_005204	HSPC131 // NOT2 COT // EST // ESTF // FLJ10486 // TPL2 // Tpl-2 // e-COT	2574798	chr2	-	127772731	127863022	1.06
mitogen-activated protein kinase kinase 2	MAP3K2	XM_001128799 // NM_006609	MEKK2 // MEKK2B	2629693	chr3	+	73019946	73201035	1.06
protein phosphatase 4, regulatory subunit 2	PPP4R2	NM_174907	MGC131930	3885464	chr20	+	39090891	39186535	1.06
topoisomerase (DNA) 1	TOP1	NM_003286	TOP1	3679564	chr16	-	8893458	8964832	1.06
ubiquitin specific peptidase 7 (herpes virus-associated)	USP7	NM_003470	HAUSP // TEF1	3422269	chr12	+	70434927	70470787	1.06
RAB21, member RAS oncogene family	RAB21	NM_014999	KIAA0118	3263624	chr10	+	111944059	112037108	1.06
MAX interactor 1	MXI1	NM_001008541 // NM_005962 // NM_130439	MAD2 // MGC43220 // MXD2 // MXI	2520225 2548699	chr2 chr2	+	191205069 38138730	191437200 38196009	1.06 1.06
NGF1-A binding protein 1 (EGR1 binding protein cytochrome P450, family 1, subfamily B, polypeptide 1 chromosome 1 open reading frame 63	NAB1 CYP1B1 C1orf63	NM_005966 NM_000104 NM_020317	CP1B // GLC3A	2402111	chr1	-	25440667	25538017	1.06
nucleoporin 153 kDa protein phosphatase 1K (PP2C domain containing)	NUP153 PPM1K	NM_005124 NM_152542	DJ465N24.2.1 // NPD014 // RP3- 465N24.4 HNUP153 // N153 DKFZp667B084 // DKFZp761G058 // PTMP // UG0882E07	2943808 2777333	chr6 chr4	-	17723255 89401891	17855638 89424935	1.06 1.06
phosphoinositide-3-kinase, class 3 CCHC-type zinc finger, nucleic acid binding protein	PIK3C3 CNBP	NM_002647 NM_003418	MGC61518 // CNBP1 // DM2 // PROMM // RNF163 // ZCCHC22 //	3786039 2694644	chr18 chr3	+	37534028 130369369	37985705 130385467	1.05 1.05
ubiquitin specific peptidase 9, X-linked // ubiquitin specific peptidase 9, Y-linked (fat facets-like, <i>Drosophila</i>) baculoviral IAP repeat-containing 6 (apollon)	USP9X // USP9Y BIRC6	NM_001039590 // NM_001039591 // NM_004654 NM_016252	ZNF9 DFFRX // FAF // AZF // AZFA // DFFRY // SP3 APOLLON // BRUCE // FLJ13726 // FLJ13786 //	3974708 2476219	chrX chr2	+	40829542 32435095	40980776 32697447	1.05 1.05

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Cluster ID	Chromosome	Human Genome hg18		Fold Change/		
						Strand	Start		Stop	nM
chromosome 11 open reading frame 30 pleckstrin homology domain containing, family M (with RUN domain) member 1 autism susceptibility candidate 2 YME1-like 1 (<i>S. cerevisiae</i>) toll-like receptor 4 splicing factor 3b, subunit 1, 155 kDa E3 ubiquitin protein ligase, HECT domain containing, 1 ATP-binding cassette, sub-family C (CFTR/MRP), member 1	C11orf30	NM_020193	EMSY // FLJ90741 // GL002	3340913	chr11	+	75803897	75941697	1.05	
	PLEKHM1	XM_001128220 // NM_014798	AP162 // B2 // KIAA0356	3759849	chr17	-	40869050	40923923	1.05	
	AUTS2	NM_015570	KIAA0442 // MGC13140	3006572	chr7	+	68695979	69896399	1.05	
	YME1L1	NM_014263 // NM_139312 // NM_139313	FTSH // MEG4 // PAMP // YME1L	3282213	chr10	-	27439066	27484191	1.05	
	TLR4	NM_138554	CD284 // TOLL // hToll	3186966	chr9	+	119506334	119670150	1.05	
	SF3B1	NM_001005526 // NM_012433	PRP10 // PRPF10 // SAP155 // SF3b155	2593670	chr2	-	197962756	198039327	1.05	
	EDD1	NM_015902	DD5 // EDD // FLJ11310 // HYD // KIAA0896 // MGC57263	3147321	chr8	-	103333634	103493671	1.05	
	ABCC1	NM_004996 // NM_019862 // NM_019898 // NM_019899 // NM_019900 // NM_019901 // NM_019902	ABC29 // ABCC // DKFZp68N04233 // DKFZp781G125 // GS-X // MRP // MRP1	3649890	chr16	+	15950935	16144419	1.05	
	PLEK	NM_002664	FLJ27168 // P47	2486811	chr2	+	68415853	68526386	1.05	
	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 pleckstrin farnesyltransferase, CAAX box, alpha centrosomal protein 170 kDa // centrosomal protein 170 kDa-like forkhead box K2 B-cell CLL/lymphoma 9-like cell division cycle 2-like 5 (cholinesterase-related cell division controller) proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	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	
	FOXK2	XM_001134363 // XM_001134364 // NM_004514	ILF // ILF-1 // ILF1	3738969	chr17	+	78070883	78195807	1.05	
	BCL9L	NM_182557	BCL9-2 // DLNB11	3393993	chr11	-	118272076	118304947	1.05	
	CDC2L5	NM_003718 // NM_031267	CDC2L // CHED // FLJ35215 // KIAA1791	2998536	chr7	+	39897668	40103253	1.05	
	PSMD11	NM_002815	MGC3844 // S9 // p44.5	3717737	chr17	+	27795087	27834449	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	
calreticulin	CALR	NM_004343	FLJ26680 // RO // SSA // cC1qR	3822049	chr19	+	12910423	12916480 1.05
schlafen family member 11	SLEF11	NM_152270	FLJ34922 // SLEF8/9	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 // GIR // 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	SRP20	2905118	chr6	+	36669658	36741293 1.05
guanine nucleotide binding protein (G protein) alpha 12	GNA12	NM_007353	MGC104623 // MGC99644 // NNX3	3035892	chr7	-	2724003	2910140 1.05
chromosome 13 open reading frame 18	C13orf18	NM_025113	// RNP // gep	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	FLJ43762	3261643	chr10	+	104144262	104152716 1.05
chromosome 22 open reading frame 28	C22orf28	NM_014306	DI149A16.6 // HSPC117 // RP1-149A16.6	3958253	chr22	-	31113563	31138223 1.05
ubiquitin specific peptidase 4 (proto-oncogene)	USP4	NM_003363 // NM_199443	MGC149848 // MGC149849 // UNP	2674179	chr3	-	49290730	49353046 1.05
F-box protein 11	FBXO11	NM_012167 // NM_018693 // NM_025133	// Unph	2552153	chr2	-	47869608	47988296 1.05
PRP4 pre-mRNA processing factor 4 homolog B (yeast)	PRPF4B	NM_003913	FBX11 // FLJ12673 // MGC44383 // PRMT9 // UG063H01 // VIT1	2892738	chr6	+	39665500	4010215 1.05
ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 // protocadherin LKC	ATP8A1 // PCLKC	NM_006095 // NM_017675	KIAA0536 // PR4H // PRP4 // PRP4K // dJ1013A10.1	2767378	chr4	-	42105160	42353857 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
zinc finger protein 267 BAT2 domain containing 1 DEAD (Asp-Glu-Ala-Asp) box polypeptide 18 // wingless-type MMTV integration site family, member 8B Ran GTPase activating protein 1 protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	ZNF267	NM_003414	FLJ20124 // FLJ20383 // MGC163154	3657367	chr16	+	31730255	31836159	1.05
	BAT2D1	NM_015172	HZF2	2367164	chr1	+	169716078	169829262	1.05
	DDX18 //	NM_006773 //	BAT2-iso // XTP2	2502300	chr2	+	118243834	118323562	1.05
	WNT8B	NM_003393	FLJ33908 // MHDb // —						
	RANGAP1	NM_002883	Fug1 // KIAA1835 // MGC20266 //	3961842	chr22	-	39969442	40028027	1.05
	PRKAR1A	NM_002734 // NM_212471 // NM_212472	CAR // CNC // CNC1 // DKFZp779L0468 // MGC17251 // PKR1 // PRKAR1 // FLJ35970 // HP43.8KD //	3732885	chr17	+	64019700	64059052	1.05
	USP38	NM_032557	FLJ35970 // HP43.8KD // KIAA1891	2745499	chr4	+	144325529	144364549	1.05
	DRAM	NM_018370	FLJ11259	3428783	chr12	+	100795270	100930011	1.05
	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
	MYD88	NM_002468	—	2617563	chr3	+	38155029	38159513	1.05
TMEM1	NM_00107723 // 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 //	NM_001077351 // NM_001077352 // NM_018107 // NM_001034155 // NM_020207	CAPERbeta // FLJ10482 // MGC4458 // PP239 // RNPC4 // FLJ37706 // SR278	3556888	chr14	-	22439714	22458231	1.05
	C9orf102	NM_004529	AF9 // FLJ2035 // YEATS3						
myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, <i>Drosophila</i>); translocated to,	MLLT3	NM_004529	FLJ37706 // SR278	3200982	chr9	-	20334968	20612522	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
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
chromosome 3 open reading frame 63	C3orf63	NM_015224	DKFZp686C2456 // KIAA1105 // RAP140 // se89-1	2677653	chr3	-	56629203	56692517
adenosine monophosphate deaminase (isoform E) // peroxisome proliferator-activated receptor alpha // RNA 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	MGC2452 // NRIC1 // PPAR // hPPAR // MGC99627 // MTO2 // MTU1 // TRMT // TRMT1 // TRNT1 // B99	3320169	chr11	+	10428461	10485703
retinoic acid receptor, alpha	RARA	NM_001033603 // NM_000964 // NM_001024809	NR1B1 // RAR	3720921	chr17	+	35718982	35767411
p21 (CDKN1A)-activated kinase 2	PAK2	NM_001126110 // NM_002577	PAK65 // PAKgamma	2659577	chr3	+	197951145	198043895
splicing factor 3b, subunit 2, 145 kDa	SF3B2	NM_006842	SAP145 // SF3B145 // SF3b1 // SF3b1S0	3335907	chr11	+	65573499	65593343
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
syntaxin 6	STX6	NM_005819	—	2446567	chr1	-	179095658	179258656
carbohydrate (chondroitin 4) sulfotransferase 11	CHST11	NM_018413	C4ST // C4ST-1 // C4ST1 // HSA269537	3429566	chr12	+	103374529	103679918
protein phosphatase 1, catalytic subunit, beta isoform	PPP1CB	NM_206877 // NM_002709 // NM_206876	MGC3672 // PP-1B // PPP1CD	2475209	chr2	+	28828128	28879300
mitogen-activated protein kinase 6	MAPK6	NM_002748	DKFZp686F03189 // ERK3 // HsT17250 // PRKM6 // CRFG // FLJ10686 // FLJ10690 // FLJ39774 // NGB	3694129	chr15	+	50098740	50146174
GTP binding protein 4	GTPBP4	NM_012341	—	3231774	chr10	+	942450	1055862

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
forkhead box O3A	FOXO3A	NM_001455 // NM_201559	AF6q21 // DKFZp781A0677 // FKHL1 // FKHL1P2 // MGC12739 // MGC31925	2920475	chr6	+	108987684	109112650
transmembrane protein 2	TMEM2	NM_013390	—	3209384	chr9	-	73452177	73573229
cyclin G associated kinase	GAK	XM_001127411 // NM_005255	FLJ40395 // MGC99654	2756673	chr4	-	833110	916149
tumor necrosis factor (ligand) superfamily, member 8	TNFSF8	NM_001244	CD153 // CD30L // CD30LG // MGC138144	3222144	chr9	-	116695445	116732620
presenilin 1 (Alzheimer disease 3)	PSEN1	NM_000021	AD3 // EAD // PS1 // S182	3543481	chr14	+	72672571	72760151
D4, zinc and double PHD fingers family 2	DPF2	NM_006268	MGC10180 // REQ // UBID4 // ubi-d4	3335089	chr11	+	64857703	64877276
splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated) development and differentiation enhancing factor 1	SFPQ	NM_005066	POMP100 // PSF	2406064	chr1	-	35351696	35506894
DDEF1	DDEF1	NM_018482	AMAP1 // ASAP1 // KIAA1249 //	3153428	chr8	-	131133540	131525100
TNF receptor-associated factor 3	TRAF3	NM_003300 // NM_145725 // NM_145726	PAG2 // PAP // CAP-1 // CD40bp // CRAF1 // LAP1	3553337	chr14	+	102313566	102447585
thyroid hormone receptor associated protein 1	THRAP1	NM_005121	ARC250 // DRIP250 // HSPC221 // KIAA0593 //	3765689	chr17	-	57374750	57498031
general transcription factor IIIC, polypeptide 4, 90 kDa	GTF3C4	NM_012204	FLJ21002 // MGC138450 // TFII90 // TFIIIC90 // TFIIICdelta // TFIIIC2-90	3192525	chr9	+	134535243	134581784
praja 2, RING-H2 motif containing	PJA2	NM_014819	KIAA0438 // Neurodapl // RNF131	2870397	chr5	-	108614328	108773545
suppressor of var1, 3-like 1 (<i>S. cerevisiae</i>) ADP-ribosylation factor 1	SUPV3L1 ARF1	NM_003171 NM_001024226 // NM_001024227 // NM_001024228 // NM_001658	SUV3	3250204	chr10	+	70609946	70638996
cullin-associated and neddylation-dissociated 1	CAND1	NM_018448	DKFZp434M1414 // FLJ10114 // FLJ10929 // FLJ38691 // FLJ90441 //	2383726	chr1	+	226313262	226353506
				3420713	chr12	+	65946048	65994719

TABLE 5-continued

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

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript	Human Genome hg18			Fold Change/		
					Cluster ID	Chromosome	Strand	Start	Stop	mM
cyclin D2	CCND2	NM_001759	// PCNP // PCPNI // hPCPNI // FLJ23119 // FLJ27465 // KIAA1790 // RPK6 // Rocol // —	3401704	chr12	+		4232432	4284764	1.05
isopentenyl-diphosphate delta isomerase 1 ST8 alpha-N-acetyl-neuraminide alpha-2,8- sialyltransferase 4	ID1L ST8SLA4	NM_004508 NM_005668 // NM_175052	MGC102758 IPPI // IPP1I MGC34450 // MGC61459 // PST // PST1 // SLA18D // ST8SLA-IV	3273601 2868904	chr10 chr5	- -		1075869 100116166	1092634 100293602	1.05 1.05
Kruppel-like factor 9 splicing factor, arginine/serine-rich 2, interacting protein ubiquitin specific peptidase 47	KLF9 SFRS2IP USP47	NM_001206 NM_004719 NM_017944	BTEB // BTEB1 CASP11 // SIP1 // SRRP129 DKFZp686C13257 // FLJ20727 // FH // FHC	3208995 3452145 3320604	chr9 chr12 chr11	- - +		72189344 44599187 11819556	72219360 44672160 11937446	1.05 1.05 1.05
low density lipoprotein receptor (familial hypercholesterolemia) Rho GDP dissociation inhibitor (GDI) beta	LDLR ARHGDIIB	NM_000527 NM_001175	D4 // GDIA2 // GDID4 // LYGDI // Ly-GDI // RPC5 // SIN	3821015 3445786	chr19 chr12	+ -		11061114 14986174	11115050 15005951	1.05 1.05
polymerase (RNA) III (DNA directed) polypeptide E (80 kD) DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y- linked adenosine deaminase, RNA-specific	POLR3E DDX3Y ADAR	NM_018119 NM_004660 NM_001025107 // NM_001111 // NM_015840 // NM_015841	DBY ADAR1 // DRADA // DSH // DSRAD // G1P1 // IFL4 // IFI4 // K88dsRBP // p136	3652489 4030162 2436754	chr19 chrY chr1	+ + -		22216140 13525423 152821187	22253905 13555808 152867095	1.05 1.05 1.05
actin binding LIM protein 1	ABLIM1	NM_001003407 // NM_001003408 // NM_002313 // NM_006720	ABLM // DKFZp781D01							

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
RAD21 homolog (<i>S. pombe</i>)	RAD21	NM_006265	FLJ25655 // ELJ40596 // HR21 // HRAD21 // KIAA0078 // MCD1 // NXP1 // SCC1 // hHR21	3149843	chr8	-	117909861	117956284
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
lactate dehydrogenase A	LDHA	NM_005566	LDH-M // LDH1 // PG19	3322775	chr11	+	18372531	18386528
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 // HPV E6A	3614087	chr15	-	23006655	23355108
nuclear receptor subfamily 4, group A, member 1	NR4A1	NM_002135 // NM_173157 // NM_173158	GPR1 // HMR // MGC9485 // N10 // NAK-1 // NGFIB // NP10 // NUR77 // TR3	3415229	chr12	+	50717248	50739539
diaphanous homolog 1 (<i>Drosophila</i>)	DIAPH1	NM_001079812 // NM_005219	DFNA1 // DRF1 // FLJ25265 // LFHL1 // HDIA1	2878662	chr5	-	140874773	140978866
zinc finger CCCH-type, antiviral 1	ZC3HAV1	NM_020119 // NM_024625	DKFZp686E2052 // DKFZp686H1869 // DKFZp686O19171 // FLB6421 // FLJ13288 // MGC48898 // ZAP // ZC3H2 // ZC3HDC2	3075566	chr7	-	138378808	138445046
SEC24 related gene family, member C (<i>S. cerevisiae</i>)	SEC24C	NM_004922	KIAA0079	3251848	chr10	+	75174138	75210008
calpain 2, (m/l) large subunit	CAPN2	NM_198597	CANPL2 // CANPml // FLJ39928 // DKFZp4340721 // HIN1 // HSHIN1 // KIAA1046	2382117	chr1	+	221955990	222031806
OTU domain containing 4	OTUD4	NM_017493 // NM_199324	FLJ31821 // KIAA0615	2788195	chr4	-	146274170	146471942
Nedd4 binding protein 1	N4BP1	NM_153029	IPFK2 // PFK2	3690597	chr16	-	47130140	47324384
6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3	PFKFB3	NM_004566		3233605	chr10	+	6226893	6336597

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	
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	DDXB1 // 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 // IF160 // 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 EH-domain containing 1	SH2D2A EHD1	NM_003975 NM_006795	F2771 // TSAad FL42622 // FL44618 // H-PAST // HPAST1 // PAST // PAST1	2438575 3377226	chr11 chr11	- -	155038957 64376790	15503637 64404202	1.05 1.05	
SH2B adaptor protein 3 tropomodulin 3 (ubiquitous) SMAD family member 3	SH2B3 TMOD3 SMAD3	NM_005475 NM_014547 NM_005902	LNK UTMOD DKFZF586N0721 // DKFZF686I10186 // HSPC193 // HsT17436 // IV15-2 // MADH3 // MGC60396 // Smad 3	3431892 3594066 3598959	chr12 chr15 chr15	+	110328135 49909087 65145043	110373802 50026784 65296818	1.05 1.05 1.05	
vacuolar protein sorting 53 homolog (<i>S. cerevisiae</i>)	VP53	NM_018289	FLJ10979 // MGC39512 // IVps53L // AD022 // EAP2 // MGC111021 // MGC9099 // d30M3.3	3739679	chr17	-	375959	564837	1.05	
TRAF and TNF receptor associated protein	TTRAP	NM_016614	EMK1 // MGC99619 // PAR-1	2945645	chr6	-	24758144	24775240	1.05	
MAP/microtubule affinity-regulating kinase 2	MARK2	NM_001039468 // NM_001039469 // NM_004954 // NM_017490	—	3334025	chr11	+	63362634	63435067	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
helicase with zinc finger	HELZ	NM_014877	DRHC // HUMORE5 // KIAA0054 // MGC163454	3768015	chr17	-	62485987	62672547
golgi-specific brefeldin A resistance factor 1	GBF1	NM_004193	FLJ21263 // FLJ21500 // KIAA0248 // MGC134877 // MGC134878	3261544	chr10	+	103993260	104132642
serine/threonine kinase 38 like BCL2-related protein A1	STK38L BCL2A1	NM_015000 NM_004049	KIAA0965 // NDR2 ACC-1 // ACC-2 // BCL2L5 // BFL1	3409081 3635198	chr12 chr15	+	27288343 78040295	27370157 78138851
membrane-associated ring finger (C3HC4) 7	MARCH7	NM_022826	// GRS // HBPA1 AXO // AXOT // DKFZP586F1122 // MARCH-VII // RNF177	2512330	chr2	+	160277236	160333585
periplin 1	PPHLN1	NM_016488 // NM_201438 // NM_201439 // NM_201440 // NM_201515 NM_025235	HSPC206 // HSPC232 // MGC48786	3412008	chr12	+	40917957	41128677
tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	TNKS2	NM_025235	PARP-5b // PARP-5c // PARP5B // PARP5C // TANK2 // TNKL	3257850	chr10	+	93548049	93633726
kelch-like 6 (<i>Drosophila</i>) Kruppel-like factor 10	KLHL6 KLF10	NM_130446 NM_001032282 // NM_005655	FLJ00029 EGRA // TIEG // TIEG1	2708066 3147508	chr3 chr8	-	184688052 103682306	184789879 103767558
neugrin, neurite outgrowth associated	NGRN	NM_001033088 // NM_016645 NM_004396	DSC92 // NEUGRIN	3607998	chr15	+	88586640	88670084
DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	DDX5	NM_004396	DKFZp686j01190 // G17P1 // HLR1	3766893	chr17	-	59924843	59935796
SMEK homolog 2, suppressor of mek1 (<i>Dictyostelium</i>)	SMEK2	NM_020463	// HUMBP68 // p68 FLEL2 // FLJ31474 // KIAA1387 // PSY2 // smk1	2553911	chr2	-	55627936	55699519
thioredoxin reductase 1	TXNRD1	NM_003330 // NM_182729 // NM_182742 // NM_182743 NM_024832	GRIM-12 // TR // MGC9145 // TRX1 // TRXR1 // TXNR	3429460	chr12	+	103130628	103354079
Ras and Rab interactor 3	RIN3	NM_024832	DKFZp762H1613 // FLJ11700 // FLJ22439	3548929	chr14	+	92049804	92225160
itohy homolog E3 ubiquitin protein ligase (mouse)	ITCH	NM_031483	AIFA // AIP4 // NAPP1 // dJ468O1.1	3882854	chr20	+	32414702	32562859

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
KIAA0174	KIAA0174	NM_014761	MGC117220	3667766	chr16	+	70481983	70522196
formin-like 3	FMNL3	NM_175736 // NM_198900	DKFZp62B245 // FHOD3 // FL45265 //	3454006	chr12	-	48316548	48387433
ARP3 actin-related protein 3 homolog (yeast) cyclin T2 // aminocarboxymuconate semialdehyde decarboxylase	ACTR3 CCNT2 // ACMSD	NM_005721 NM_001241 // NM_058241 //	MGC45819 // ARP3 FLJ90560 // MGC134840 //	2501697 2507209	chr2 chr2	+	114360575 135392283	114502125 135432746
topoisomerase (DNA) II beta 180 kDa RNA binding motif protein 16 // T-cell lymphoma invasion and metastasis 2	TOP2B RBM16 // TIAM2	NM_001068 NM_014892 // NM_001010927 //	TOP1IB // top2beta KIAA1116 // FLJ41865 // STEF	2566478 2932360	chr3 chr6	- +	25614141 155029299	25681392 155324283
solite carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	SLC3A2	NM_012454 NM_001012661 // NM_001012662 // NM_001012663 // NM_001012664 // NM_001013251 //	4F2 // 4F2HC // 4T2HC // CD98 // CD98HC // MDU1 // NACAE	3333711	chr11	+	62380117	62412872
Der1-like domain family, member 1	DERL1	NM_002394 NM_024295	DER-1 // DER1 // FLJ13784 // FLJ42092 // MGC3067 //	3151401	chr8	-	124094605	124123781
phosphodiesterase 7A	PDE7A	NM_002603 // NM_002604	PRO2577 HCP1 // PDE7	3138464	chr8	-	66789124	67101393
formin-like 1	FMNL1	NM_005892	C17orf1 // C17orf1B // FHOD4 // FMNL // KW-13 // MGC133052 // MGC1894 //	3723378	chr17	+	40654831	40680464
Rap guanine nucleotide exchange factor (GEF) 1	RAPGEF1	NM_005312 // NM_198679	DKFZp781P1719 // GRF2	3227696	chr9	-	133441988	133605262
transmembrane BAX inhibitor motif containing 4	TMBIM4	NM_016056	CGI-119 // SIR // ZPRO	3460593	chr12	-	64816984	64850064
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

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Cluster ID	Chromosome	Human Genome hg18		Fold Change/	
						Strand	Start		Stop
MYST histone acetyltransferase 2 KIAA0247 ubiquitin specific peptidase 36 protein kinase, AMP-activated, gamma 2 non-catalytic subunit	MYST2	NM_007067	HBO1 // HBOA	3725779	chr17	+	45196447	45261455	1.05
	KIAA0247	NM_014734	—	3542145	chr14	+	69145907	69256533	1.05
	USP36	NM_025090	DUB1	3772581	chr17	—	74295075	74348574	1.05
	PRKAG2	NM_001040633 //	AAKG // AAKG2 //	3079803	chr7	—	150865031	151205160	1.05
		NM_016203 //	CMH6 // H91620p						
		NM_024429	// WPWS						
	RAB18	NM_021252	RAB18L1	3240095	chr10	+	27791811	27930577	1.05
	WAC	NM_016628 //	BM-016 //	3240340	chr10	+	28828043	29005095	1.05
		NM_100264 //	MGC10753 //						
		NM_100486	PRO1741 //Wwp4						
stromal interaction molecule 2 actin, gamma 1 ash1 (absent, small, or homeotic)-like (<i>Drosophila</i>)	STIM2	NM_020860	FLJ39527 // KIAA1482	2722377	chr4	+	26415653	26636427	1.05
	ACTG1	NM_001614	ACT // ACTG // DFNA20 // DFNA26	3773932	chr17	—	77091456	77105797	1.05
	ASH1L	NM_018489	ASH1 // ASH1L1 // FLJ10504 //	2437417	chr1	—	153571685	153798937	1.05
			KIAA1420						
	FLJ36874	NM_152716	MGC125671 //	3374746	chr11	—	59160770	59193099	1.05
	THRAP2	NM_015335	MGC125672 DKFZp781D0112 // FLJ1627 //	3473083	chr12	—	114868953	115419724	1.05
			KIAA1025 // MED13L // PROSIT240 //						
			TRAP240L						
			CARMEN // CIPER // CLAP // c-E10 // mE10	2420808	chr1	—	85504067	85516171	1.05
			CERT // CERTL // FLJ20597 // GPBP // STARD11	2862950	chr5	—	74700067	74843717	1.05
collagen, type IV, alpha 3 (Goodpasture antigen) binding protein wings apart-like homolog (<i>Drosophila</i>) SFRS protein kinase 2 RNA binding motif protein 22 chromodomain helicase DNA binding protein 1 G1 to S phase transition 1 ubiquitin 1 // death inducer-obliteror 1	COL4A3BP	NM_005731 // NM_031361	FOE // KIAA0261 // WAPL	3298738	chr10	—	88184999	88286267	1.05
	WAPAL	NM_015045	FLJ36101 //	3066267	chr7	—	104537547	104842466	1.05
	SRPK2	NM_182691 // NM_182692	SFRSK2	2881521	chr5	—	150050460	150060885	1.05
	RBM22	NM_018047	FLJ10290 // ZC3H16	2868523	chr5	—	98218502	98293051	1.05
	CHD1	NM_001270	DKFZp686E2337	3680610	chr16	—	11865619	11917408	1.05
	GSPT1	NM_002094	551G9.2 // EIF3A // GST1 // eRF3a	3212143	chr9	—	85464717	85512928	1.05
	UBQLN1 //	NM_013438 //	DA41 // DSK2 //						
	DIDO1	NM_053067 // NM_022105 // NM_033081 //	FLJ90054 // PLIC-1 // XDRP1 // BYE1 // C20orf158						

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Cluster ID	Chromosome	Human Genome hg18			Fold Change/ nM
						Strand	Start	Stop	
		NM_080796 // NM_080797	// D1AF1 // D1DO2 // D1DO3 // D1O-1 // D1O1 // DKFZp434P1115 // FLJ11265 // K1AA0333 // MGC16140 // d1885L7.8						
		NM_015044	FLJ20966 //	3685183	chr16	-	23381059	23429320	1.05
	golgi associated, gamma adaptin ear containing, ARF binding protein 2		K1AA1080 // VEAR						
	solute carrier family 2 (facilitated glucose transporter), member 3	NM_006931	FLJ09380 // GLUT3	3442854	chr12	-	7917549	7980138	1.05
	protein tyrosine phosphatase, non-receptor type 1	NM_002827	PTPIB	3888721	chr20	+	48560298	48634700	1.05
	hematopoietic progenitor cell leukemia (translocation) 1								
	sequestosome 1	NM_020831	MKL1	3961496	chr22	-	39136248	39362660	1.05
		NM_003900	SQSTM1 // OSIL	2844479	chr5	+	179166014	179198853	1.05
		NM_033387	FAM78A	3227574	chr9	-	133123292	133147120	1.05
	family with sequence similarity 78, member A								
		NM_015697 NM_003092 // NM_198220 NM_013449	FLJ00024 CL640 // FLJ26072 MGC24807 // MGC45309 DKFZp781B109 // FLJ13768 // FLJ13780 // FLJ45876 // K1AA0314 // TIP5 // WALp3	2775965 3877776 3457947	chr4 chr20 chr12	- + -	84404005 16645421 55275319	84424988 16670916 55316417	1.05 1.05 1.05
	coenzyme Q2 homolog, prenyltransferase small nuclear ribonucleoprotein polypeptide B"								
	bromodomain adjacent to zinc finger domain, 2A								
		NM_021239	RBM25	3543411	chr14	+	72594776	72658577	1.05
	RNA binding motif protein 25								
		NM_001039937 // NM_002392 // NM_012141	INTS6	3514488	chr13	-	50826009	50927014	1.05
	integrator complex subunit 6								
		XN_001127059 // NM_017623 // NM_199078 NM_002392 // NM_006878 // NM_006879 // NM_006881 // NM_006882	CNNM3	2494749	chr2	+	96843277	96864841	1.05
	eycelein M3								
MDm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse)	MDM2		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
colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog thioresoxin-like 1	CSF1R	NM_005211	C-FMS // CD115 CSFR // FIM2 // FMS	2881187	chr5	-	149412410	149473128
	TXNL1	NM_004786	TRP32 // TXL-1 // TXNL // Txl	3809324	chr18	-	52334063	52469773
ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)	ELOVL5	NM_021814	HELO1 // RP3-483K16.1 // d483K16.1	2957596	chr6	-	53179349	53321902
PFTAIRE protein kinase 1	PFTK1	NM_012395	d483K16.1 KIAA0834 // PFTAIRE1	3012064	chr7	+	90002707	90677837
nuclear mitotic apparatus protein 1	NUMA1	NM_006185	NUMA	3380901	chr11	-	71389909	71469367
sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2	SPOCK2	NM_014767	testican-2	3293840	chr10	-	73457514	73518527
clathrin, heavy chain (Hc)	CLTC	NM_004859	CHC17 // CLH-17 // CLTCL2 // Hc	3729172	chr17	+	55052021	55127299
F-box and leucine-rich repeat protein 11	FBXL11	NM_012308	// KIAA0034 CXXC8 // DKFZP434M1735 // FBL11 // FBL7 // FLJ00115 // FLJ46431 // JHDM1A // KAA1004 // LILNA	3336696	chr11	+	66643299	66782124
signal-induced proliferation-associated gene 1	SIPA1	NM_006747 // NM_153253	MGC102688 // MGC17037 // SPA1	3335465	chr11	+	65162171	65174965
kelch-like 24 (<i>Drosophila</i>) // YEATS domain containing 2	KLHL24 // YEATS2	NM_017644 // NM_018023	DRE1 // FLJ25796 // FLJ10201 // FLJ12841 // FLJ13308 // KIAA1197	2655113	chr3	+	184836105	184882100
thymopoietin	TMPO	NM_001032283 // NM_001032284 // NM_003276	CMD1T // LAP2 // MGC61508 // PRO0866 // TP	3427767	chr12	+	97395927	97502543
STT3, subunit of the oligosaccharyltransferase complex, homolog B (<i>S. cerevisiae</i>)	STT3B	NM_178862	FLJ90106 // SIMP // STT3-B	2615600	chr3	+	31544326	31662283
ATP-binding cassette, sub-family F (GCM20), member 1	ABCF1	NM_001025091 // NM_001090	ABC27 // ABC50	2901687	chr6	+	30647103	30667268
CUG triplet repeat, RNA binding protein 2	CUGBP2	NM_001025076 // NM_001025077 // NM_006561	BRUNOL3 // ETR-3 // NAPOR	3234760	chr10	+	10544225	11418680
major histocompatibility complex, class II, DR	HLA-DRA	NM_019111	HLA-DRA1	2903189	chr6	+	32496972	32520923
RAN binding protein 2	RANBP2 // RRPD4	NM_006267	NUP358 // TRP1 // TRP2	2499158	chr2	+	108702376	108768725

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript	Human Genome hg18			Fold Change/	
					Cluster ID	Chromosome	Strand		
G protein-coupled receptor Kinase 5 FRY-like	GRK5	NM_005308	GPRK5	3267036	chr10	+	120957193	121256088	1.05
	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	NEATC2	NM_012340 // NM_173091	KIAA0611 // NEAT1 // NEATP	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	FYTID1	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	DKFZP434I16 // 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

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript	Human Genome hg18			Fold Change/
					Cluster ID	Chromosome	Strand	
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, (<i>S. cerevisiae</i>)	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	CHR28YT // 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 // 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

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript	Human Genome hg18			Fold Change/
					Chromosome	Strand	Start	Stop
quiescin Q6	QSCN6 // FLJ23867	NM_001004128 // NM_002826	Q6 // QSOX1	2369950	chr1	+	178353067	178436483
splicing factor, arginine/serine-rich 6	SFRS6	NM_006275	B52 // MGC5045 // SRP55	3886050	chr20	+	41519932	41526301
mosesin	MSN	NM_002444	KIAA1256 //	3979659	chrX	+	64804248	64878488
intersectin 2	ITSN2	NM_006277 // NM_019595 // NM_147152	SH3D1B // SH3P18 // SWA // SWAP	2544238	chr2	-	24279241	24436906
SAFB-like, transcription modulator	SLTM	NM_001013843 // NM_017968 // NM_024755	DKFZp762G052 // FLJ10005 // FLJ13213 // Met	3626704	chr15	-	56949072	57013564
transcription factor 4	TCF4	NM_003199	E2-2 // ITF2 // MGC149724 // MGC149724 // SEF2 // SEF2-1 // SEF2-1A // SEF2-1B	3808854	chr18	-	51010981	51506795
DEAH (Asp-Glu-Ala-His) box polypeptide 9	DHX9	NM_001357	DDX9 // LKP // NDH II // NDHIII // RHA	2370991	chr1	+	181075106	181123738
chromosome 10 open reading frame 119	C10orf119	NM_024834	FLJ13081 // FLJ36756	3309755	chr10	-	121568302	121642742
SET domain containing 2	SETD2	NM_014159	FLJ16420 // FLJ22472 // FLJ23184 // FLJ45883 // HIF-1 // HSPC069 //	2672532	chr3	-	47032936	47180418
golgi reassembly stacking protein 2, 55 kDa // dehydrogenase/reductase (SDR family) member 9	GORASP2 // DHRS9	NM_015530 // NM_005771 // NM_199204	HYPB // KIAA1732	2515050	chr2	+	171457150	171551619
target of myb1 (chicken) ATPase, H+ transporting, lysosomal 42 kDa, V1 subunit C1	TOM1 ATP6V1C1	NM_005488	FLJ33404	3944084	chr22	+	34025845	34073962
potassium channel tetramerisation domain containing 20	KCTD20	NM_002040 // NM_001695	ATP6C // ATP6D // FLJ20057 // VATIC // Yma5	3110171	chr8	+	104102441	104171800
serine/threonine kinase 10	STK10	NM_173562	Coor69 // MGC14254 // dJ108K11.3	2905069	chr6	+	36518349	36566874
GA binding protein transcription factor, alpha subunit 60 kDa // GA binding protein transcription factor, alpha subunit pseudogene	GABPA // GABPA	NM_005990	LOK // PRO2729	2887048	chr5	-	171401689	171547855
		NM_002040 // NR_002723	E4TF1-60 // E4TF1A // NFT2 // NRF2 // NRF2A //	3916576	chr21	+	26028762	260666641

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Cluster ID	Chromosome	Strand	Human Genome hg18		Fold Change/
							Start	Stop	
centaurin, beta 2	CENTB2	NM_012287	E4TF1 // E4TF1B // GABPB1 ACAP2 // CNT-B2 // KIAA0041	2712040	chr3	-	196476779	196645492	1.05
fibronin 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 // KPMB2 // MIP // MIP1 //	2815043	chr5	+	72148176	72245960	1.05
heterogeneous nuclear ribonucleoprotein U-like 1	HNRPUL1	NM_144733 // NM_144734 // NM_007040 // NM_144732	EIB-AP5 // EIBAP5 // FLJ12944	3834089	chr19	+	46460006	46505508	1.05
CD300c molecule // fibrillin 2 (congenital contractural arachnoidactyly)	CD300E // FBN2	NM_181449 // NM_001999	CD300LE // CLM2 // REM2 // 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 //	3422326	chr12	+	70519754	70604360	1.05
v-raf murine sarcoma viral oncogene homolog 1	BRAF	NM_004333	FLJ12085 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	Human Genome hg18			Fold Change/			
					Cluster ID	Chromosome	Strand		Start	Stop	nM
splicing factor, arginine/serine-rich 5 GRAM domain containing 1A	SFRS5	NM_001039465 //	MGC138284 //								
		NM_006925	RAFBI		3542207	chr14	+	69263363	69308465	1.05	
	GRAMD1A	NM_020895	HRS // SRP40		3830002	chr19	+	40161899	40210121	1.05	
			FLJ22411 //	FLJ90346 //							
	MED28	NM_025205	KIAA1533		2720181	chr4	+	17225344	17244808	1.05	
			1500003D12Rik //	DKFZP434N185 //							
	JARID1A	NM_001042603 //	EG1 // magidin		3439603	chr12	-	259504	368944	1.05	
		NM_005056	RBP2 // RBP2								
	ATF6	NM_007348	-		2363919	chr1	+	160002678	160208836	1.05	
		MATR3	NM_018834 //	DKFZp686K0542 //	2831124	chr5	+	138505686	138695245	1.05	
granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	GZMB	NM_199189	DKFZp686K23100								
			// KIAA0723 //								
			MGC9105								
		NM_004131	CCPI // CGL-1 //		3558375	chr14	-	24169951	24173308	1.05	
			CGL1 // CSP-B //								
			CSPB // CTLA1 //								
			CTSG1 // HLP //								
			SECT								
	CCNL1	NM_020307	BM-001 //		2702307	chr3	-	158305077	158361233	1.05	
	neighbor of BRCA1 gene 1	NBR1	XM_001124650 //	PRO1073 // amia-							
XM_001124827 //			1A1-3B //		3722417	chr17	+	38563761	38719231	1.05	
		XM_001127781 //	KIAA0049 // M17S2								
		NM_005899 //	// MIG19								
		NM_031858 //									
		NM_031862									
		NM_003680									
YARS			CMTDIC // TYRBS		2405192	chr1	-	33012453	33056331	1.05	
SLC25A3			// YRS // YTS								
		NM_213612 //	OK/SW-cl.48 //		3427820	chr12	+	97511471	97519906	1.05	
CCR4-NOT transcription complex, subunit 1	CNOT1	NM_002635 //	PHC								
		NM_005888 //									
		NM_213611									
		NM_016284 //									
		NM_206999	AD-005 // CDC39		3693673	chr16	-	57111094	57236550	1.05	
			// DKFZp686E0722								
			// FLJ90644 //								
			KIAA1007 // NOT1								
			// NOT1H								
			MGC50828								
ankyrin repeat domain 13 family, member D	ANKRD13D	XM_001129739 //		3336857	chr11	+	66812660	66826524	1.05		
		NM_207354									
	PHF10	NM_018288 //	FLJ10975 //		2986084	chr6	-	169845929	169866056	1.05	
		NM_133325	MGC111009 //								
			XAP135								

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
hypothetical protein KIAA1434	RP5-1022P6.2	NM_019593	FLJ1085 // KIAA1434 // MGC26147	3896370	chr20	-	5473033	5546357
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
UPF2 regulator of nonsense transcripts homolog (Yeast)	UPF2	NM_015542 // NM_080599	HUPF2 // KIAA1408 // MGC138834 // MGC138835 // EST01027 // HHCPA78 // THIF // VDUP1	3277662	chr10	-	11984615	12125155
thioredoxin interacting protein	TXNIP	NM_006472	ANKRD4 // KIAA0823 // TIMAP	2356115	chr1	+	144149846	144164251
protein phosphatase 1, regulatory (inhibitor) subunit 16B	PPP1R16B	NM_015568	CYP3 // Cyp-D // FLJ90798 // MGC117207	3884830	chr20	+	36866338	36985066
peptidylprolyl isomerase F (cyclophilin F)	PPIF	NM_005729	—	3253880	chr10	+	80777230	80785093
3-hydroxy-3-methylglutaryl-Coenzyme A reductase	HMGCR	NM_000859	—	2815965	chr5	+	74668800	74700136
chloride intracellular channel 1	CLIC1	NM_001288	G6 // NCC27	2949330	chr6	-	31806365	31815144
HBS1-like (<i>S. cerevisiae</i>) // aldehyde dehydrogenase 8 family, member A1	HBS1L // ALDH8A1	NM_006620 // NM_022568 // NM_170771	DKFZp686L13262 // EF-1a // ERFS // HBS1 // HSPC276 // ALDH12	2975287	chr6	-	135314409	135417715
vav 3 oncogene	VAV3	NM_001079874 // NM_006113	DKFZp779D2315 // FL40431	2426385	chr1	-	107914594	108309371
Rho guanine nucleotide exchange factor (GEF) 7	ARHGEF7	NM_003899 // NM_145735	BETA-PIX // COOL1 // DKFZp761K1021 // KIAA0142 // KIAA0412 // Nblat10314 // P50 // P50BP // P85 // P85COOL1 // P85SPR // PAK3 // PIXB	3501661	chr13	+	110565635	110756075

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	
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily 4, member 5	SMARCA5	NM_003601	ISWI // SNF2H // WCRF135 // hISWI	2745646	chr4	+	144616165	144697227	1.05
proteasome maturation protein	POMP	NM_015932	C13orf12 // hSNF2H	3483348	chr13	+	28125188	28151050	1.05
DnaJ (Hsp40) homolog, subfamily B, member 6	DNAJB6	NM_005494 // NM_058246	HSPC014 // PNAS-110 // UMP1 DKFZp566D0824 // FLJ42837 // HHDI1 // HSF-2 // HSF2 // MGC1152 // MGC117297 // FLJ41312	3034027	chr7	+	156799667	156902887	1.05
zinc finger RNA binding protein	ZFR	NM_016107	DC-TM4E2 // MGC11352 // TM4SF14	2852333	chr5	-	32390101	32537319	1.05
tetraspavin 14	TSPAN14	NM_030927	MGC99675	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		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/IBLC3	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	API1 // Alix // DRP4 // 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	NR1H1	3452818	chr12	-	46521596	46606823	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
diablo homolog (<i>Drosophila</i>)	DIABLO	NM_019887 // NM_138929 // NM_138930	DIABLO-S // FLJ10537 // FLJ25049 // SMAC // SMAC3	3475511	chr12	-	121257461	121277963
B-cell translocation gene 1, anti-proliferative CD53 molecule	BTG1 CD53	NM_001731 NM_000560 // NM_001040033	MOX44 // TSPAN25	3465409 2351572	chr12 chr1	- +	90902887 111215352	91063960 111296983
damage-specific DNA binding protein 1, 127 kDa	DDB1	NM_001128974 // NM_00128983 // NM_001923 NM_006321	DDBA // UV-DDB1 // XAP1 // XPCE // XPE // XPE-BF AR2 // FLJ10938	3375245	chr11	-	60823513	60857553
ariadne homolog 2 (<i>Drosophila</i>)	ARIH2	NM_006321	ARI2 // FLJ10938	2621827	chr3	+	48930742	48997971
protein tyrosine phosphatase, non-receptor type 12	PTPN12	NM_002835	PTP-PEST // TRIAD1	3009959	chr7	+	77004361	77123074
metetrin, glial cell differentiation regulator-like // mediator of RNA polymerase II transcription, subunit 25 homolog (<i>S. cerevisiae</i>)	METRNL // MED25	NM_00104431 // NM_030973	PTPG1 ACID1 // ARC92 // DKFZp434K0512 // MGC70671 // P78 // TCBAP0758	3739431	chr17	+	78630769	78653225
trinucleotide repeat containing 6A	TNRC6A	NM_020847 // NM_014494	CAGH26 // DKFZp666E117 // FLJ22043 // GW1 // GW182 // KIAA1460 // MGC75384 // TNRC6	3653398	chr16	+	24583665	24748478
ubiquitin specific peptidase 10	USP10	NM_005153	KIAA0190 // MGC2621 // UBPO	3671873	chr16	+	83291080	83371023
DnaJ (Hsp40) homolog, subfamily A, member 2	DNAJA2	NM_005880	CPR3 // DIA2 // DNAJ // DNJ3 // HIRP4 // PRO3015 // RDJ2	3690084	chr16	-	45546783	45565155
MYC binding protein 2	MYCBP2	NM_015057	DKFZp686M08244 // FLJ10106 // FLJ13826 // FLJ21597 // FLJ21646	3518496	chr13	-	76500672	76799212
SEC24 related gene family, member B (<i>S. cerevisiae</i>)	SEC24B	NM_001130118 // NM_001042734 // NM_006323 NM_005534	KIAA0916 // PAM MGC48822 // SEC24	2739079	chr4	+	110510304	110681811
interferon gamma receptor 2 (interferon gamma transducer 1)	IFNGR2	NM_005534	AF-1 // IFGR2 // IFNGT1	3918635	chr21	+	33696906	33774607

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
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
SP100 nuclear antigen	SP100	NM_001080391 // NM_003113	DKFZp686E07254 // FLJ00340 // FLJ34579	2531377	chr2	+	230985008	231142598
transforming growth factor beta regulator 1	TBRG1	NM_032811	FLJ14621 // FLJ25020 // FLJ90113 // MGC129890 // NIAM // TB-5	3354174	chr11	+	123997906	124011654
growth arrest and DNA-damage-inducible, beta	GADD45B	NM_015675	DKFZP566B133 // GADD45BETA // MYD118	3816509	chr19	+	2425718	2469133
alanyl (membrane) aminopeptidase (aminopeptidase N, aminopeptidase M, microsomal aminopeptidase, CD13, pI 50)	ANPEP	NM_001150	APN // CD13 // LAP1 // PEPN // gpl50	3638607	chr15	-	88129142	88159617
proteasome (prosome, macropain) activator subunit 4	PSME4	NM_014614	FLJ21864 // KIAA0077 // MGC138374 // MGC142228 // PA200	2553282	chr2	-	53944710	54160919
microtubule-associated protein, RP/EB family, member 1	MAPRE1	NM_012325	EB1 // MGC117374 // MGC129946	3882069	chr20	+	30871304	30901864
BM11 polycarb ring finger oncogene	BM11	NM_005180	MGC12685 // PCGF4 // RNF51	3238491	chr10	+	22650103	22660820
CUG triplet repeat, RNA binding protein 1	CUGBP1	NM_001025596 // NM_006560 // NM_198700	BRUNOL2 // CUG-BP // CUGBP // NAB50 // hNab50	3372253	chr11	-	47444068	47543613
transforming, acidic coiled-coil containing protein 3	TACC3	NM_006342	ERIC1 // MGC117382 // MGC133242	2714955	chr4	+	1692616	1716693
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
C-type lectin domain family 4, member E	CLEC4E	NM_014358	CLEC4SF9 // MINCLE	3443183	chr12	-	8577026	8584811
interferon, gamma-inducible protein 18	IFI16	NM_005531	IFNGIP1 // MGC9466 // PYHIN2	2362394	chr1	+	157215279	157291561

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
LMBR1 domain containing 1	LMBRD1	NM_018368	C6orf209 // FLJ11240 // RP11-810122.1 // bA81022.1	2960010	chr6	-	70361077	70634121
protein kinase D3	PRKD3	NM_005813	EPK2 // PKC-NU // PKD3 // PRKCN // nPKC-NU	2548500	chr2	-	37331165	37405413
CCR4-NOT transcription complex, subunit 7	CNOT7	NM_013354 // NM_054026	CAF1 // hCAF-1	3125775	chr8	-	17128912	17148758
heterogeneous nuclear ribonucleoprotein M	HNRPM	NM_005968 // NM_031203	DKFZp547H118 // HNRNPM // HNRNPM4 // HNRPM4 // HTGR1 // NAGR1	3819543	chr19	+	8415651	8459993
heterogeneous nuclear ribonucleoprotein H1 (H)	HNRPH1	NM_005520	DKFZp686A15170 // HNRPH	2890148	chr5	-	178970155	178993890
adenosine A2a receptor	ADORA2A	NM_000675	ADORA2 // RDC8 // hA2aR	3940099	chr22	+	23143709	23200243
PPAR binding protein	PPARB	NM_004774	CRSP1 // CRSP200 // DRIP205 // DRIP230 // MED1 // MGC71488 // PBP // PPARGBP // RB18A	3755714	chr17	-	34801544	34861069
serine/threonine kinase 17b	STK17B	NM_004226	DRAK2	2593159	chr2	-	196706552	196744596
adhesion regulating molecule 1	ADRM1	NM_007002	GP110	3892607	chr20	+	60305485	60317305
splicing factor, arginine/serine-rich 9	SFRS9	NM_175573	MGC29536	3474502	chr12	-	119372834	119407274
E2F transcription factor 4, p107/p130-binding	E2F4	NM_003769	SRP30c	3665288	chr16	+	65783266	65790299
chromodomain helicase DNA binding protein 2	CHD2	NM_001950	E2F-4	3609138	chr15	+	91227096	91387351
serpin peptidase inhibitor, clade B (ovalbumin), member 2	SERPINF2	NM_001042572 // NM_001271	DKFZp781D1727	3791935	chr18	+	59704265	59722138
phosphatidylinositol 3,4,5-trisphosphate-dependent RAC exchanger 1	PREX1	NM_020820	HsT1201 // PAI // PAI-2 // PAI2 // PLANH2	3908631	chr20	-	46674205	46938090
pre-B-cell colony enhancing factor 1 // pre-B cell enhancing factor 1 pseudogene	PBEF1 // RP11-92119.4	NM_005746	KIAA1415	3066818	chr7	-	105625846	105713266
interferon regulatory factor 1	IRF1	NM_002198	1110035014Rik // DKFZp666B131 // MGC117256	2875348	chr5	-	131846280	131893043
nuclear receptor coactivator 4	NCOA4	NM_005437	NAMPT // PBEF // LOC646309	3246372	chr10	+	51202191	51260947
			IRF-1 // MAR					
			ARA70 // DKFZp762E1112					

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
adrenergic, beta, receptor kinase 1	ADRBK1	NM_001619	ELE1 // PTC3 // RFG	3336801	chr11	+	66790523	66810933
BTAF1 RNA polymerase II, B-TFIIID transcription factor-associated, 170 kDa (Mot1 homolog, <i>S. cerevisiae</i>)	BTAF1	NM_003972	ARK1 // GRK2 KIAA0940 // MGC138406 // MOT1 // TAF(II)170 //TAF172 // TAFII170	3257938	chr10	+	93673509	93821994
golgi autoantigen, golgin subfamily a, 4	GOLGA4	NM_002078	GCP2 // GOLG // MU-RMS-40.18 // p230	2617041	chr3	+	37259518	37452233
ras homolog gene family, member A	RHOA	NM_001664	ARH12 // ARHA // RHO12 // RHOH12	2674242	chr3	-	49371587	49424514
regulatory factor X, 5 (influences HLA class II expression)	RFX5	NM_000449 //	—	2434971	chr1	-	149578882	149586373
protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha isoform	PPP2R2A	NM_001025603 NM_002717	B55A // FLJ26613 // MGC52248 // PR52A // PR55A	3090922	chr8	+	26156860	26286261
chromosome 20 open reading frame 11	C20orf11	NM_017896	TWA1	3893072	chr20	+	61039681	61050570
PCI domain containing 2	PCID2	NM_018386	F10 // FLJ11305 // MGC16774	3526378	chr13	-	112877970	112912799
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
arrestin domain containing 3	ARRDC3	NM_020801	KIAA1376 // TLIMP	2866704	chr5	-	90700311	90782084
chromosome 14 open reading frame 103	C14orf103	NM_018036	FLJ10242	3578278	chr14	-	95817349	95900740
myosin IXB	MYO9B	NM_004145	CELIAC4 // MYR5	3823982	chr19	+	17047591	17185088
t-complex 1	TCP1	NM_001008897 // NM_030752	CCT1 // CCTa // CCT1 // CCTb // D6S230E // TCP-1-alpha	2982381	chr6	-	160119521	160130731
translocation protein 1	TLOC1	NM_003262	Drp1 // FLJ32803 // HTP1 // SEC62	2651782	chr3	+	171166446	171194653
far upstream element (FUSE) binding protein 1	FUBP1	NM_003902	FBP // FUBP	2419235	chr1	-	78182330	78217881
mannosidase, alpha, class 1A, member 2 // urothelial cancer associated 1	MAN1A2 // UCA1	NM_006699 // —	MAN1B // —	2353881	chr1	+	117689854	117931990
engulfment and cell motility 2	ELMO2	NM_133171 // NM_182764	CED-12 // CED12 // ELMO-2 // FLJ1656 // KIAA1834	3907830	chr20	-	44426906	44495031
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

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
heterogeneous nuclear ribonucleoprotein R	HNRPR	NM_005826	FLJ25714 // HNRNPR // HNRNP-R	2401275	chr1	-	23486545	23543926
membrane-bound transcription factor peptidase, site 1	MBTPS1	NM_003791 // NM_201268	KIAA0091 // MGC138711 // MGC138712 // PCSK8 // SIP // SKI-1	3702293	chr16	-	82644885	82708018
RAB35, member RAS oncogene family	RAB35	NM_006861	H-ray // RAB1C // RAY	3474228	chr12	-	119017289	119039689
farnesyl-diphosphate farnesyltransferase 1	FDF1	NM_004462	DGPT // ERG9 // SQS // SS	3086206	chr8	+	11690497	11740987
SATB homeobox 1	SATB1	NM_002971	—	2665199	chr3	-	18364435	18462086
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
interferon-related developmental regulator 1	IFRD1	NM_001007245 // NM_001590	PC4 // TIS7	3019519	chr7	+	111835465	111903788
coatamer protein complex, subunit alpha // peroxisomal biogenesis factor 19	COPA // PEX19	NM_004371 // NM_002857	FLJ26320 // HEP-COP // DIS2223E // HK33 // PMP1 // PMP1 // PFX // PXMP1	2440143	chr1	-	158525015	158580073
SCY1-like 2 (<i>S. cerevisiae</i>)	SCYL2	NM_017988	CVAK104 // FLJ10074 // KIAA1360	3428131	chr12	+	99185070	99260564
Clr9, Paf1/RNA polymerase II complex component, homolog (<i>S. cerevisiae</i>) // tRNA 5-methylaminomethyl-2-thiouridylate methyltransferase	CTR9 // TRMU	NM_014633 // NM_018006	KIAA0155 // SH2BP1 // TSBP // p150 // p150TSP // MGC99627 // MTO2 // MTU1 // TRMT // TRMT1 // MGC4796 // RP11-26815.4 // SHIK // Sgk495 // 4.1 R // EL1 // HE	3320301	chr11	+	10684027	10774985
serine/threonine kinase 40 // erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked)	STK40 // EPB41	NM_032017 // NM_004437 // NM_203342 // NM_203343	TRMT // TRMT1 // MGC4796 // RP11-26815.4 // SHIK // Sgk495 // 4.1 R // EL1 // HE	2406677	chr1	-	36577822	36626062
heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	HNRPU	NM_004501 // NM_031844 // NM_015156	HNRNPU // SAF-A U21.1	2464499	chr1	-	243078713	243094575
REST corepressor 1	RCOR1	NM_001079846 // NM_004380	COREST // KIAA0071 // RCOR	3553228	chr14	+	102053947	102266629
CREB binding protein (Rubinstein-Taybi syndrome)	CREBP	NM_001079846 // NM_004380	CBP // RSTS // RTS	3677795	chr16	-	3715075	3870713

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	
golgi apparatus protein 1 // CDC42 small affector 1 // sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6C	GLG1 //	NM_012201 //	CFR-1 // ESL-1 //	3698919	chr16	-	73015604	73209803	1.05
	CDC42SE1 //	NM_001038707 //	FLJ23319 //						
	SEMA6C	NM_020239 //	FLJ23967 // MG-160 // MGI60 //						
		NM_030913	SCIP1 // SPEC1 // SEMAY // m-SemaY // m-Sema Y2						
PHD finger protein 3	PHF3	NM_015153	KIAA0244 // MGC142210 //	2911944	chr6	+	64403666	64547188	1.05
WDR45-like HMG-box transcription factor 1 chromosome 2 open reading frame 25 heat shock 70 kDa protein 8 // Fc fragment of IgG, low affinity IIb, receptor (CD166)	WDR45L	NM_019613	MGC142212	3775157	chr17	-	78165748	78199803	1.05
	HBP1	NM_012257	WIP1-3 // WIP3	3018420	chr7	+	106596679	106630194	1.05
	C2orf25	NM_015702	FLJ16340	2580635	chr2	-	150101637	150152607	1.05
	HSPA8 //	NM_006597 //	CL25022	3395416	chr11	-	122429305	122438895	1.05
	FCGR3B	NM_153201 //	HSC54 // HSC70						
		NM_000570	// HSC71 // HSP71 // HSP73 // HSPA10 //						
chromosome 6 open reading frame 62			LAP1 //						
			MGC131511 //						
			MGC29929 //						
	C6orf62	NM_030939	NIP71 // CD16 // DKFZP564G182 //	2945677	chr6	-	24798431	24851423	1.05
leptin receptor overlapping transcript-like 1			FLJ12619 //						
			Nhlal00237 //						
	LEPROTL1	NM_015344	XTP12 // dJ30M3.2	3092276	chr8	+	30059542	30115386	1.05
			HSPC112 // Vps55 // my047						
ubiquitin-conjugating enzyme E21 (UBC9 homolog, yeast)	UBE2I	NM_003345 //	C358B7.1 // P18 //	3643703	chr16	+	1289451	1317016	1.05
		NM_194259 //	UBC9						
		NM_194260 //							
		NM_194261							
nucleoporin 155 kDa	NUP155	NM_004298 //	KIAA0791 // N155	2853768	chr5	-	37325714	37407016	1.05
lysosomal trafficking regulator	LYST	NM_153485	CHS // CHS1	2461999	chr1	-	233878999	234113611	1.05
mitogen-activated protein kinase 14		NM_001005736	CSBP1 // CSBP2	2904877	chr6	+	36103487	36186989	1.05
		NM_001315 //	// CSBP1 // EXIP						
		NM_139012 //	// Mxi2 // PRKM14						
		NM_139013 //	// PRKM15 // RK						
nuclear factor (erythroid-derived 2)-like 2 // hypothetical protein DKFZp451M2119		NM_139014	// SAPK2A // p38						
			// p38ALPHA						
	NFE2L2 //	NM_006164 //	NRF2 //	2588827	chr2	-	177794809	177837753	1.05
	DKFZp451M2119	NM_182585							

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript	Human Genome hg18			Fold Change/
					Cluster ID	Chromosome	Strand	
WD repeat domain 26 heterogeneous nuclear ribonucleoprotein K	WDR26 HNRPK	NM_025160	FLJ21016 // MIP2	2458082	chr1	-	222639474	222691338
		NM_002140 //	CSBP // FLJ41122	3212294	chr9	-	85772377	85785355
		NM_031262 //	// HNRNPK //					
transducin-like enhancer of split 4 (E(sp1) homolog, <i>Drosophila</i>)	TLE4	NM_031263	TUNP	3176209	chr9	+	81269283	81552230
		NM_007005	BCE-1 // E(sp1) //					
			ESG // ESG4 //					
bromodomain containing 2	BRD2		GRG4	2903343	chr6	+	33044392	33057253
		NM_005104	DGS113E //					
			DKFZp686N0336 //					
signal transducer and activator of transcription 3 (acute-phase response factor)	STAT3		FLJ31942 //					
			FSRG1 //					
			KIAA9001 // NAT	3757840	chr17	-	37718873	37794201
ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (<i>Drosophila</i>)	ARIH1	NM_003150 //	APRF // FLJ20882					
		NM_139276 //	// RING3 // RNF3					
		NM_213662	// MGC16063					
zinc finger, NFX1-type containing 1 // gasdermin-like	ZNF1 // GSDML	NM_005744	ARI // HARI //	3600744	chr15	+	70553731	70666726
		NM_021035 //	HHARI //					
		NM_001042471 //	FLJ39275 //	3908831	chr20	-	47233911	47420063
SUMO1/sentrin specific peptidase 6	SENP6	NM_018530	MGC131936 //					
		NM_015571	PP4052 //					
			FLJ11355 //	2913983	chr6	+	76367955	76484717
DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	DDX17		FLJ11887 //					
			KIAA0389 //					
			KIAA0797 // SSP1					
ubiquitin specific peptidase 15	USP15	NM_006386 //	// SUSP1	3960629	chr22	-	37202800	37232288
		NM_030881	DKFZp761H2016 //					
		NM_006313	P72 // RH70	3419147	chr12	+	60940328	61086166
Ras association (RalGDS/AF-6) domain family 2	RASSF2		KIAA0529 //					
			MGC131982 //					
			MGC149838 //					
dual specificity phosphatase 6	DUSP6		MGC74854 //					
			UNPH4	3896034	chr20	-	4655529	4752291
			DKFZp781O1747 //					
E1A binding protein p300 solite carrier family 7 (cationic amino acid transporter, y+ system), member 6	EP300 SLC7A6	NM_170774	KIAA0168	3464860	chr12	-	88223376	88273467
		NM_022652	MKP3 // PYST1					
		NM_001429	p300	3946615	chr22	+	39817736	39906025
RNA binding motif protein 5	RBM5	NM_001076785 //	DKFZp686K15246	3666146	chr16	+	66855932	66893223
		NM_003983	// KIAA0245 //					
			LAT-2 // LAT3 //					
			y+LAT2	2622469	chr3	+	50101372	50134000
			FLJ39876 // G15					
			// H37 // LUCA15					
			// RMB5					

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	
nuclear protein localization 4 homolog (<i>S. cerevisiae</i>)	NPLOC4	NM_017921	FLJ20657 // FLJ23742 //	3774029	chr17	-	77134363	77214526	1.05	
			KIAA1499 // NPL4							
cyclin L2 // aurora kinase A interacting protein 1	CCNL2 // AURKAIP1	NM_001039577 //	ANIA-6B //	4041923	chr1_random	+	359569	372958	1.05	
		NM_030937 //	DKFZp761A1210 //							
		NM_017900	DKFZp762O195 //							
			HCLA-ISO // HLA-ISO // PCEE // SB138 // AIP //							
poly(cG) binding protein 2	PCBP2	NM_005016 //	AKIP // FLJ20608	3416036	chr12	+	52132173	52161417	1.05	
		NM_031989	HNRPE2 //							
afipilin	AFTPH	NM_001002243 //	MGC110998 //	2485433	chr2	+	64604969	64714437	1.05	
		NM_017657 //	FLJ20080 //							
		NM_203437	FLJ23793 //							
			MGC33965 //							
GTP binding protein 1	GTPBP1	NM_004286	Nblal0388	3945396	chr22	+	37431694	37459514	1.05	
			GP-1 // GP1 //							
protein kinase C, eta	PRKCH	NM_006255	HSPC018 //	3538893	chr14	+	60816958	61087440	1.05	
			MGC20069							
glutaminase	GLS	NM_014905	MGC26269 // PKC-L // PKCL //	2520291	chr2	+	191453802	191538513	1.05	
			PRKCL // nPKC-// FLJ10358 //							
tubulin, beta	TUBB	NM_178014	DKFZp686O15119	2901913	chr6	+	30795977	30801165	1.05	
			GLS1 // KIAA0838							
neurogulin, EIF4E binding protein	NGDN	XM_033371 //	M40 // MGC117247	3529156	chr14	+	23008821	23048896	1.05	
		XM_932898 //	// MGC16435 //							
zinc finger, RAN-binding domain containing 2	ZRANB2	XM_932900 //	OK/SW-el.56 //							
		XM_932903 //	TUBB1 // TUBB5							
		XM_932906 //	C14orf120 //							
		XM_941350 //	DKFZp564O092 //							
		XM_945161 //	LCP5 // NGD //							
		XM_945163 //	Ipd-2							
		XM_945166 //								
		XM_945170 //								
		NM_001042635 //								
		NM_015514								
		NM_005455 //	DKFZp686J1831 //	2418000	chr1	-	71292434	71355820	1.05	
		NM_203350	DKFZp686N09117							
			// FLJ41119 // ZIS							

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Cluster ID	Chromosome	Human Genome hg18			Fold Change/
						Strand	Start	Stop	
DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	DDX21	NM_004728	// ZIS1 // ZIS2 // ZNF265 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
	SMG1	NM_015092	61E3.4 // ATX // KIAA0421 // LIP	3683050	chr16	-	18719381	18845318	1.05
MON2 homolog (<i>S. cerevisiae</i>)	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	DGS182 // 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	PNPLA10P // PNPLA8	XM_927062 // XM_938392 // NM_015723	—// IPLA2(GAMMA) // IPLA2-2 // IPLA2G	3067592	chr7	-	107880325	107956012	1.05
	OAS3	NM_006187	MGC133260 // MP100 // PSA	3432467	chr12	+	111860550	111895663	1.05
2'-5'-oligoadenylate synthetase 3, 100 kDa 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	Human Genome hg18			Fold Change/
					Cluster ID	Chromosome	Strand	
							Start	Stop
								nM
stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein)	STP1	NM_006819	// SNF2L2 // SNF2LA // SWI2 // Sh1p // hBRM // hSNF2a HOP // IEF-SSP-3521 // P60 // STIL 9G8 // AAG3 // HSSG1 // RBM37 // ZCCHC20 // ZCRB2	chr11	+	63709341	63728586	1.05
splicing factor, arginine/serine-rich 7, 35 kDa	SFRS7	NM_001031684	9G8 // AAG3 // HSSG1 // RBM37 // ZCCHC20 // ZCRB2	chr2	-	38824253	38832154	1.05
ribosomal protein L14 // ribosomal protein L14-like	RPL14 // RPL14L	NM_001034996 // NM_003973 // XR_017789 // XR_017790	CAG-LSL-7 // CTG-B33 // L14 // MGC88594 // RL14 // hRL14 // bemb298	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 // IIPP2A // LANP // MAPM // MGC119787 // MGC150373 // PHAP1 // PHAPI // PP32	chr15	-	66857944	66900452	1.05
endoglin (Osler-Rendu-Weber syndrome 1)	ENG	NM_000118	CD105 // END // FLJ41744 // HHT1 // ORW // ORW1	chr9	-	129615329	129660473	1.05
lysosomal associated multispanning membrane protein 5 family with sequence similarity 108, member A2 // family with sequence similarity 108, member A1	LAPTM5 FAM108A2 // FAM108A1	NM_006762 XM_039721 // XM_933830 // NM_001080422 // NM_031213 NM_004513 // NM_172217	MGC125860 // MGC125861 C1orf47 // C19orf27 // MGC5244	chr1	-	30977913	31095913	1.05
interleukin 16 (lymphocyte chemoattractant factor)	IL16	NM_031213 NM_004513 // NM_172217	FLJ16806 // FLJ42735 // FLJ4234 // HsT19289 // IL-16 // LCF // prIL-16 DKEFp434O0515 // SOLO beta-COP	chr15	+	79262148	79392377	1.05
SEC14 and spectrin domains 1	SESTD1	NM_178123	FLJ16806 // FLJ42735 // FLJ4234 // HsT19289 // IL-16 // LCF // prIL-16 DKEFp434O0515 // SOLO	chr2	-	179644888	180002479	1.05
coatamer protein complex, subunit beta 2 (beta prime)	COPB2	NM_004766	beta-COP	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	chr11	-	64644697	64646234	1.05
AHA1, activator of heat shock 90 kDa protein ATPase homolog 1 (yeast)	AHA1	NM_012111	AHA1 // C14orf3 // p38	chr14	+	76993989	77005560	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	
SLU7 splicing factor homolog (<i>S. cerevisiae</i>)	SLU7	NM_006425	9G8 // MGC9280 // hslu7	2884658	chr5	-	159761226	15978959	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	MGC40489	XR_016048	FLJ30780	3767053	chr17	-	60176255	60263758	1.05	
ATG9 autophagy related 9 homolog A (<i>S. cerevisiae</i>)	ATG9A //	NM_001077198 //	APG9L1 //	2599955	chr2	-	219781799	219802587	1.05	
// ATP-binding cassette, sub-family B (MDR/TAP), member 6	ABCB6	NM_024085 // NM_005689	MGD3208 // ABC // ABC14 //							
			EST45597 // FLJ22414 //							
			MTABC3 // PRP // unat							
isoleucyl-tRNA synthetase	IARS	NM_002161 // NM_013417	FLJ20736 // IARS1 // ILRS //	3214668	Chr9	-	94012330	94096287	1.05	
			PRO0785							
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 //	Aig21 // CGI-50 // DKFZP434J154 // DKFZp686P02188 // FLJ12979 //	2988536	chr7	+	5196360	5239975	1.05	
		NM_016003	FLJ14217 //							
			FLJ42984 // WIPI-2							
BCL2-associated transcription factor 1	BCLAF1	NM_001077440 // NM_001077441 // NM_014739	BTF // KIAA0164 // BK211L9.1	2975680	chr6	-	136619703	136652847	1.05	
ADAM metalloproteinase domain 19 (meltrin beta)	ADAM19	NM_023038 //	FKSG34 //	2883440	chr5	-	156755122	156935351	1.05	
RAE1 RNA export 1 homolog (<i>S. pombe</i>)	RAE1	NM_001015885 // NM_003610	MADDAM // FLJ30608 // MGC117333 //	3890555	chr20	+	55359493	55386992	1.05	
			MGC126076 // MGC126077 //							
			MIG14 // MRNP41 // Mmrp41 //							
			dJ481F12.3 // dJ800J21.1							
cyclin L2 // aurora kinase A interacting protein 1	CCNL2 // AURKAIP1	NM_001039577 // NM_030937 // NM_017900	ANLA-6B // DKFZp761A1210 // DKFZp762O195 // HCLA-ISO // HLA-ISO // PCEE //	2391532	chr1	-	1314609	1324575	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
nucleolar and colled-body phosphoprotein 1	NOLC1	NM_004741	SB138 // AIP // AKIP // FLJ20608 KIAA0035 // NOPP130 // NOPP140 // NS5AIP13 // P130 CTIP-2 // CTIP2 // RIT1 // hRIT1-MOV34 // P40 // S12	3261492	chr10	+	103901962	103913597
B-cell CLL/lymphoma 11B (zinc finger protein)	BCL11B	NM_022898 // NM_138576	NS5AIP13 // P130 CTIP-2 // CTIP2	3579114	chr14	-	98705377	98931503
proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog)	PSMD7	NM_002811	// RIT1 // hRIT1-MOV34 // P40 // S12	3668617	chr16	+	72888182	72901528
chromosome 14 open reading frame 118	C14orf118	NM_017926 // NM_017972	FLJ10033 // FLJ20689 // MGC61896	3544905	chr14	+	75688015	75800924
translocase of inner mitochondrial membrane 23 homolog (yeast)	TIMM23	XM_001133798 // NM_006327	MGC22767 // PRO1197 // TIM23 // TIMM23B	3289031	chr10	-	51180787	51293392
proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	PSMD2	NM_002808	MGC14274 // P97	2655650	chr3	+	185499199	185509504
LSM14A, SOD6 homolog A (<i>S. cerevisiae</i>)	LSM14A	NM_015578	// S2 // TRAP2 C19orf13 // DKFZP434D1335 // FAM61A // RAP55	3829575	chr19	+	39355192	39416345
phosphatidylinositol transfer protein, alpha // myosin IC	PTPN // MYO1C	NM_006224 // NM_001080779 // NM_001080950 // NM_033375	PTPN // VTB1A // FLJ23603 // MMI-beta // MM1b // NMI // myr2	3740304	chr17	-	1367883	1412932
centaurin, delta 1	CENTD1	NM_015230 // NM_139182	ARAP2 // FLJ13675 // FLJ4916 // DKFZp686L19178	2765590	chr4	-	35626248	35922356
structural maintenance of chromosomes 1A	SMC1A	NM_006306	// DXS423E // KIAA0178 // MGC138332 // SB1.8 // SMC1 // SMC1L1 // SMC1alpha // DKFZp762A227 // BEG1 // FOAP-13 // PRO1659 // SEEG-1	4009238	chrX	-	53417797	53466400
solute carrier family 43, member 3	SLC43A3	NM_014096 // NM_017611 // NM_199329	DKFZp762A227 // BEG1 // FOAP-13 // PRO1659 // SEEG-1	3373845	chr11	-	56931008	56951629
ninjurin 1	NINJ1	NM_004148	NIN1 // NINJURIN	3215146	chr9	-	94923613	94939639
CDC-like kinase 3	CLK3	NM_001292 // NM_003992	FLJ22858	3601741	chr15	+	72677906	72719105
sortilin-related receptor, I (DLR class) A	SORL1 // C11orf52	NM_003105	LR11 // LRP9 // SORLA // SorLA-1 // gp250	3352948	chr11	+	120828130	121077997
repeats-containing				3352948	chr11	+	120828130	121077997

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	
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 1, 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 (<i>S. cerevisiae</i>)	CDC40	NM_015891	EBH3 // 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 fusion (involved in t(12; 16) in malignant liposarcoma)	GTPBP2 FUS	NM_019096 NM_001010850 // NM_004960	MGC74725 CHOP // FUS-CHOP // FUS1 // TLS // TLS/CHOP	29544771	chr6	-	43681031	43704877	1.04	
KIAA0430 lymphocyte cytosolic protein 1 (L-plastin)	KIAA0430 LCP1	NM_014647 NM_002298	A-362G6.1 // LKAP CP64 // DKFZp781A23186 // FLJ25423 // FLJ26114 // FLJ39956 // L-PLASTIN // LC64P // PLS2	3681956	chr16	-	15595757	15654441	1.04	
DENN/MADD domain containing 3	DENN3	NM_014957	—	3512874	chr13	-	45595067	45684007	1.04	
KIAA0317	KIAA0317	NM_001039479	KIAA0870	3118651	chr8	+	142207943	142289494	1.04	
ninein (GSK3B interacting protein)	NIN	NM_016350 // NM_020921 // NM_182944 // NM_182945 // NM_182946	KIAA1565	3572041	chr14	-	74189599	74249655	1.04	
				3564071	chr14	-	50256234	50403020	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
transmembrane protein 161B // integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41)	TMEM161B // ITGA2B	NM_153354 //	FLB3342 //	2866045	chr5	-	87526693	87600565	1.04
		NM_000419	MGC33214 //						
		PRO1313 // CD41							
Ewing sarcoma breakpoint region 1	EWSR1	NM_005243 //	HPA3	3941907	chr22	+	27994201	28026501	1.04
		NM_013986	EWS						
		NM_001031732 //	KIAA1966 // YTS21						
YTH domain containing 1	YTHDC1	NM_133370	// YTS21-B	2772017	chr4	-	68858700	68934802	1.04
squamous cell carcinoma antigen recognized by T cells 3	SART3	NM_014706	KIAA0156 //	3470253	chr12	-	107440140	107479296	1.04
		MGC138188 //	RP11-13G14 //						
		RP110 // p110(unb)	TIP110 // p110(unb)						
cytoplasmic linker associated protein 1	CLASP1	NM_015282	DKFZp686D1968 //	2573641	chr2	-	121811825	122169321	1.04
		DKFZp686H2039 //	FLJ33821 //						
		FLJ41222 //	FLJ41222 //						
nuclear receptor interacting protein 1 protein phosphatase 1, regulatory (inhibitor) subunit 12A	NRIP1 PPP1R12A	NM_003489	MAST1 //	3925639	chr21	-	15255125	15359182	1.04
		NM_002480	RIP140						
		MBS //	MBS //						
STE20-like kinase (yeast)	SLK	NM_014720	MGC133042 //	3463571	chr12	-	78690959	78853356	1.04
		KIAA0204 //	KIAA0204 //						
		MGC133067 //	MGC133067 //						
polymerase (RNA) II (DNA directed) polypeptide B, 140 kDa	POLR2B	NM_000938	STK2 // bA16H23.1	2728448	chr4	+	57539163	57592513	1.04
		// se20-9	POL2RB // RPB2						
		// hRPB140 //	// hRPB140 //						
HIV-1 Rev binding protein	HRB	XM_941338 //	hSRPB2	2530599	chr2	+	228045122	228134167	1.04
		NM_004504	MGC116938 //						
		MGC116940 //	MGC116940 // RAB						
zinc finger CCCH-type containing 12A	ZC3H12A	NM_025079	// RIP	2330687	chr1	+	37712740	37722550	1.04
		FLJ23231 //	FLJ23231 //						
		MCPBP // RP3-	MCPBP // RP3-						
transforming growth factor, beta 1	TGFB1	NM_000660	423B22.1 //	3863021	chr19	-	46499343	46551636	1.04
		CED // DPD1 //	CED // DPD1 //						
		TGFB	TGFB						
ADP-ribosylation factor 4	ARF4	XM_001132763 //	—	2678090	chr3	-	57532172	57558635	1.04
		NM_001660	—						
		NM_002657	—						
pleiotropic adenoma gene-like 2 jumonji domain containing 2C	PLAGL2 JMD2C	NM_015061	FLJ23283	3902682	chr20	-	30243975	30259284	1.04
		FLJ25949 //	FLJ25949 //						
		GASCI // JHDM3C	GASCI // JHDM3C						
			// KIAA0780 //						
			bA146B14.1						

TABLE 5-continued

Gene Name	Gene Symbol	Accession	Synonym	Human Exon ST 1.0 Transcript	Human Genome hg18			Fold Change/
					Cluster ID	Chromosome	Strand	
transmembrane BAX inhibitor motif containing 1 GPI-anchored membrane protein 1	TMBIM1	NM_022152	PP1201 // RECS1	2599371	chr2	-	218847185	218865515
	GPIAP1	NM_005898 // NM_203364	GP1P137 // M11S1 // p137GPI	3326183	chr11	+	34009711	34081946
	DDX47 // APOLD1	NM_016355 // NM_201224 // NM_030817	DKFZp564O176 // E4-DBP // FLJ30012 // HQ0256 // MSTP162 // DKFZP434F0318 // FLJ25138	3405531	chr12	+	12856462	12874176
SERPINE1 mRNA binding protein 1	SERP1	NM_001018067 // NM_001018068 // NM_001018069 // NM_015640	CGI-55 // CHD3IP // DKFZp564M2423 // FLJ90489 // HAPB4L // PAI-1	2417174	chr1	-	67646101	67669020
	CCDC47	NM_020198	RBP1 // PAIRBP1	3766334	chr17	-	59176353	59204726
	LBR	NM_002296 // NM_194442	GK001 // MSTP041 // DHOR14B // LMN2R // MGC9041 // PHA	2458289	chr1	-	223655840	223683230
caspase 3, apoptosis-related cysteine peptidase Burkitt lymphoma receptor 1, GTP binding protein (chemokine (C-X-C motif) receptor 5)	CASP3	NM_004346 // NM_032991	CPP32 // CPP32B // SCA-1	2796484	chr4	-	185782536	185807608
	BLR1	NM_001716 // NM_032966	CD185 // CXCR5 // MDR15 // MGC117347	3351675	chr11	+	118259777	118272180
	HLA-E	NM_005516	DKFZp686P19218 // EA1.2 // EA2.1 // HLA-6.2 // MHC	2901620	chr6	+	30565243	30620086
v-yes-1 Yamaguchi sarcoma viral related oncogene homolog MYC-associated zinc finger protein (purine-binding transcription factor) // kinesin family member 22	LYN	NM_002350	FLJ26625 // JTK8	3098977	chr8	+	56954505	57087291
	MAZ // KIF22	NM_001042539 // NM_002383 // NM_007317	PUR1 // Pur-1 // SAF-1 // SAF-2 // ZF87 // ZNF801 // ZNF87 // KID // KNSL4 // OBP // OBP-1 // OBP-2	3655665	chr16	+	29724956	29729977
	C3orf58	NM_173552	MGC33365	2646327	chr3	+	145173603	145669744
chromosome 3 open reading frame 58 hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1 KIAA0652 PX domain containing serine/threonine kinase jumonji, AT rich interactive domain 2	HERC1	NM_003922	p532 // p619	3628650	chr15	-	61687879	61913158
	KIAA0652	NM_014741	FLJ20698	3329404	chr11	+	46595671	46652934
	PXK	NM_017771	FLJ20335 // MONAKA	2626167	chr3	+	58293657	58386884
JARID2 // C20orf120	JARID2 // C20orf120	NM_004973	JMJ	2896177	chr6	+	15261674	15630231

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	
GGI-09 protein syndecan binding protein (syntenin)	GGI-09	NM_015939	MGC5029	3896524	chr20	-	5865881	5879370	1.04
	SDCBP	NM_001007067 //	MDA-9 // ST1 //	3099750	chr8	+	59605208	59658960	1.04
		NM_001007068 //	SYCL // TACIP18						
		NM_001007069 //							
		NM_001007070 //							
2, 3'-cyclic nucleotide 3' phosphodiesterase family with sequence similarity 48, member A // family with sequence similarity 48, member B2	CNP	NM_005625	CNP1	3721548	chr17	+	37372285	37383765	1.04
		NM_033133	CL3 // C13orf19 //	3509910	chr13	-	36480880	3656254	1.04
	FAM48A //	NM_001014286 //	FP757 // P38IP //						
	FAM48B2	NM_017569 //	bA421P11.4 //						
	UBE1L2	XM_293352	ELJ10808 //	2771718	chr4	-	68130308	68249472	1.04
ubiquitin-activating enzyme E1-like 2		NM_018227	FLJ23367						
			UGTREL1	3761959	chr17	-	45133304	45141355	1.04
		NM_005827	KIAA0461 //	2435044	chr1	-	149641830	149753035	1.04
	SLC35B1	NM_015100 //	MGC71543 //						
	POGZ	NM_145796 //	SUHW5 // ZNF635						
pogo transposable element with ZNF domain		NM_207171	FKH1 // FKHR //	3510858	chr13	-	40027817	40162098	1.04
	FOXO1A	NM_002015	FOXO1						
			FBP // RAB-14	3223872	chr9	-	122980236	123025093	1.04
	RAB14, member RAS oncogene family	NM_016322	RNF114	3888474	chr20	+	47986321	48003818	1.04
	zinc finger protein 313	NM_018683	DNAI1 // ERdj1	3280902	chr10	-	22078144	22332877	1.04
DnaI (Hsp40) homolog, subfamily C, member 1	DNAJC1	NM_022365	// HTJ1 //						
			MGC131954						
	ITGB1	NM_002211 //	CD29 // ENRB //	3284188	chr10	-	33211051	33321367	1.04
		NM_033666 //	GPIIA // MDF2 //						
		NM_033667 //	MSK12 // VLAB						
MMDA receptor regulated 2		NM_033668 //							
		NM_033669 //							
		NM_133376							
	NARG2	NM_001018089 //	—	3627363	chr15	-	58500956	58558626	1.04
		NM_024611							
mitochondrial ribosomal protein S7	MRPS7	NM_015971	MRP-S // MRP-S7	3734760	chr17	+	70769374	70774626	1.04
			// RP-S7 //						
	TBP	NM_003194	GTF2D // GTF2D1	2937984	chr6	+	170705200	170723945	1.04
			// MGC117320 //						
			MGC126054 //						
polymerase (RNA) I polypeptide C, 30 kDa			MGC126055 //						
			SCA7 // TFID						
	POIR1C	NM_004875 //	RPA39 // RPA40	2908052	chr6	+	43592769	43605071	1.04
		NM_203290	// RPA5 // RPAC1						
	SPTAN1	NM_003127	(ALPHA)II-	3190558	chr9	+	130354704	130435758	1.04
spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)			SPECTRIN //						
			FLJ44613						
			PPP1G						
	PPP1CC	NM_002710		3471374	chr12	-	109642007	109665131	1.04
	protein phosphatase 1, catalytic subunit, gamma isoform								

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	
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 // TRPC4AP //	3903708	chr20	33053899	33144297	1.04
actin, beta	ACTB	NM_001101	PS1TPSBP1	3036924	chr7	5533433	5537011	1.04
polypyrimidine tract binding protein 1	PTBP1	NM_002819 // NM_031990 // NM_031991 // NM_175847	HNRNP1 // HNRP1 // MGC10830 // MGC8461 // PTB // PTB-1 // PTB-2 // PTB3 // PTB4 // pPTB	3815165	chr19	747768	763505	1.04
chromosome 6 open reading frame 166	C6orf166	NM_018064	FLJ10342 // dJ4861.4.2	2963784	chr6	88441297	88476721	1.04
ring finger protein 40	RNF40	NM_014771	BRE1B // DKFZp686K191 // KIAA0661 // MGC13051 //	3656555	chr16	30681120	30695182	1.04
coiled-coil domain containing 100	CCDC100	NM_133223	RBP95 // STARING DKFZp686106246 // FLJ36090 //	2873168	chr5	122642038	122832582	1.04
ubiquitin specific peptidase B	USP8	NM_005154	FLJ38327 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 reticuloendotheliosis 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	Human Genome hg18			Fold Change/
					Cluster ID	Chromosome	Strand	
chromodomain helicase DNA binding protein 4	CHD4	NM_001273	DKFZp686E06161 // Mf-2b // Mf2-CD71 // TFR // TFR1 // TFR	3442054	chr12	-	6549521	6587067 1.04
transferrin receptor (p90, CD71)	TFR	NM_003234	—	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	RNP1U1Z // RPU1 // UI70K // UIAP // UIRNP	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 (<i>S. cerevisiae</i>)	VPS4B	NM_004869	MIG1 // SKD1 // VPS4-2	3811497	chr18	-	59207407	59240734 1.04
KIAA1128	KIAA1128	NM_018999	FLJ14262 // FLJ25809 // Geap14 // bA486022.1	3255402	chr10	+	86020629	86268247 1.04
c-src tyrosine kinase pleiotropic regulator 1 (PRL1 homolog, <i>Arabidopsis</i>)	CSK PLRG1	NM_004383 NM_002669	MGC117393 MGC110880 // PRL1	3601840 2790570	chr15 chr4	+	72841734 155675613	72882558 155691014 1.04
WD repeat domain 1	WDR1	NM_005112 // NM_017491	API1 // NORI-1	2760371	chr4	-	9685078	9772600 1.04
FB1 murine osteosarcoma viral oncogene homolog B	FOSB	NM_006732	DKFZp686C0818 // GOS3 // GOS3 // GOSB // KIAA1694	3836266	chr19	+	50624036	50671180 1.04
c-Maf-inducing protein	CMIP	NM_030629 // NM_198390	—	3670772	chr16	+	80030441	80323852 1.04
aldolase A, fructose-bisphosphate	ALDOA	NM_000034 // NM_184041 // NM_184043	ALDA // MGC10942 // MGC17716 // CGH-143 // MGC75015 // RP11-196G18.18	3655920	chr16	+	29968869	29991009 1.04
bolA homolog 1 (<i>E. coli</i>)	BOLA1	NM_016074	—	2357961	chr1	+	148126062	148138968 1.04
ring finger and SPRY domain containing 1 centaurin, delta 2	RSPRY1 CENTD2	NM_133368 NM_001040118 // NM_015242 // NM_139181	KIAA1972 ARAP1 KIAA0782	3662612 3381241	chr16 chr11	+	55777703 72073021	55831882 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	
brix domain containing 2 tumor necrosis factor receptor superfamily, member 25 // pleckstrin homology domain containing, family G (with RhoGef domain) member 5	BXDC2	NM_018321	BRIX // FLJ11100	2806231	chr5	+	34951248	34962845	1.04
	TNFRSF25 //	NM_001039664 //	ARO-3 // DDR3 //	2394699	chr1	-	6443807	6448816	1.04
	PLEKHG5	NM_003790 //	DR3 // LARD //						
		NM_148965 //	TNFRSF12 // TR3						
		NM_148966 //	// TRAMP // WSL-						
		NM_148967 //	1 // WSL-LR //						
		NM_148970 //	KIAA0720 // RP4-						
		NM_001042663 //	650H14.3						
		NM_001042664 //							
		NM_001042665 //							
nucleoporin like 1	NUPL1	NM_020631 //							
		NM_198681	KIAA0410 //	3482219	chr13	+	24773258	24822202	1.04
		NM_001008564 //	PRO2463						
		NM_001008565 //							
		NM_014089	IKBE	2955076	chr6	-	44333884	44341478	1.04
		NM_004556							
		NM_030912	GERP // RNF27	3261820	chr10	+	104384137	104419190	1.04
		NM_015626 //	SWIP1 // WSB-1	3715109	chr17	+	22644482	22684326	1.04
		NM_134265							
		NM_018312	C11orf23 //	3337618	chr11	+	67984785	68173381	1.04
hypothetical protein FLJ21438			DKFZp781E17107						
			// DKFZp781E2374						
			// DKFZp781O2362						
			// FLJ11058 //						
			FLJ43065 //						
			MGC125711 //						
			MGC125712 //						
			PP6R3 // SAP190						
			// SAPL // SAPLa						
			DKFZp667E013 //						
CD14 molecule	FLJ21438	XM_029084	FLJ00087	3853453	chr19	-	15423181	15436377	1.04
	CD14	NM_000591 //		2878437	chr5	-	139991507	139993422	1.04
		NM_001040021							
		NM_004698 //							
		NM_015203							
			PRP3 // HPRP3P	2358171	chr1	+	148560583	148592321	1.04
			// PRP3 // Prp3p						
			// RP18 //						
			FLJ32145 //						
			HSPC099						
PRP3 pre-mRNA processing factor 3 homolog (<i>S. cerevisiae</i>) // KIAA0460	PRPF3 //	NM_012448	STAT5	3757770	chr17	-	37604727	37682109	1.04
	KIAA0460	NM_018433	DKFZp686A24246	2492064	chr2	+	86509150	86574548	1.04
			//						
signal transducer and activator of transcription junonji domain containing 1A	STAT5B								
	JMJD1A								

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
IQ motif containing GTPase activating protein 1	IQGAP1	NM_003870	DKFZp686P07111 // JHMD2A //					
			JMJD1 //		3608113	chr15	+	88732454 88846463 1.04
ubiquitin-conjugating enzyme E2B (RAD6 homolog)	UBE2B	NM_003337	KIAA0051 // SAR1 // p195					
			E2-17 kDa // HHR6B // HHR6B // RAD6B // UBC2		2829275	chr5	+	133734769 133788148 1.04
splicing factor, arginine/serine-rich 10 (transformer 2 homolog, <i>Drosophila</i>)	SFRS10	NM_004593	DKFZp686F18120 // Htra2-beta //					
			SFRS10 // TRA2-BETA // TRA2B		2709062	chr3	-	187048509 187160523 1.04
poly(A) polymerase alpha kelch-like 18 (<i>Drosophila</i>)	PAPOLA KLHL18	NM_032632 NM_025010	MGC5378 // PAP FLJ13703 //					
			KIAA0795		3550392	chr14	+	96038038 96104627 1.04
G protein-coupled receptor 132	GPR132	NM_013345	MGC5378 // PAP		2621275	chr3	+	47298888 47367590 1.04
			FLJ13703 //					
phosphatidylinositol transfer protein, beta	PITPNB	NM_012399	KIAA0795					
			PE-TP-beta //		3581404	chr14	-	104586779 104622593 1.04
Snf2-related CBP activator protein engulfment and cell motility 1	SRCAP ELMO1	NM_006662 NM_001039459 // NM_014800 // NM_130442	PtdInsTP // VIB1B					
			KIAA0309		3956290	chr22	-	26577440 26645487 1.04
metal response element binding transcription factor 2	MTF2	NM_007358	CED-12 // CED12 // ELMO-1 //					
			KIAA0281 //		3656418	chr16	+	30616551 30663998 1.04
hemopoietic cell kinase SIN3 homolog A, transcription regulator (yeast)	HCK SIN3A	NM_002110 NM_015477	MGC126406					
			M96 // PCL2 //		3046197	chr7	-	36860492 37455389 1.04
eukaryotic translation initiation factor 3, subunit 9 eta, 116 kDa	EIF3S9	NM_001037283 // NM_003751	RP5-976O13.1 //					
			d976O13.2		2346934	chr1	+	93147511 93377202 1.04
transmembrane 9 superfamily member 3	TM9SF3	NM_020123	DKFZp434K2235 //					
			FLJ90319 //		3881651	chr20	+	30086433 30153306 1.04
chromosome 1 open reading frame 50	C1orf50	NM_024097	KIAA0700					
			EIF3-ETA // EIF3-P110 // EIF3-P116 // MGC104664 //		3633403	chr15	-	73448786 73535167 1.04
			MGC131875 //					
			PRT1 // eIF3b					
			EP70-P-iso //					
			RP11-34E5.1 //					
			SNBP					
			MGC955					
					2987441	chr7	+	2315929 2386896 1.04
					3301857	chr10	-	98267858 98337079 1.04
					2332767	chr1	+	43005527 43036633 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	
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 // 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 // Elk // OGDH	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	CLEC5F5 // 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 // DKFZp68B0877 // FLJ36517 // HLC-11 // NY-LU-12 // gl6	2622359	chr3	+	49942372	50089683 1.04
nucleotide binding protein 1 (MinD homolog, <i>E. coli</i>)	NUBP1	NM_002484	MGC117406 // MGC130052 // MGC130053 // NBP	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 // FL44836 // MGC131686 // dJ337H4.2	2954646	chr6	-	43587500	43592701 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
chromosome 6 open reading frame 94 // LTV1 homolog (<i>S. cerevisiae</i>)	C6orf94 // LTV1	XM_928657 //	dJ468K18.5 //	2929036	chr6	+	144194149	144227146	1.04
		XM_941265 //	C6orf93 //						
		NM_032860	FLJ14909 //						
intercellular adhesion molecule 1 (CD54), human rhinovirus receptor	ICAM1	NM_000201	BB2 // CD54 //	3820443	chr19	+	10242765	10258289	1.04
		P3.58	dJ468K18.4						
		ECM29 //	3220513						
KIAA0368	KIAA0368	XM_001129450 //	ECM29 //	3220513	chr9	-	113131941	113286475	1.04
		XM_001131778 //	FLJ22036 //						
		NM_001080398	KIAA1962 // RP11-						
CD3d molecule, delta (CD3-TCR complex)	CD3D	NM_000732 //	CD3-DELTA //	3393744	chr11	-	117698596	117718659	1.04
		NM_001040651	T3D						
		NM_014820	FLJ90470						
translocase of outer mitochondrial membrane 70 homolog A (<i>S. cerevisiae</i>)	TOMM70A	NM_001012651 //	DKFZp686F1754 //	2686371	chr3	-	101565001	101614635	1.04
		NM_005385	DKFZp686G0426 //						
			DKFZp686J06106 //						
molecular protein 9	NOL9	NM_024654	DKFZp686N24126	2394784	chr1	-	6504004	6537329	1.04
			FLJ23323 //						
			MGC131821 //						
proteasome (prosome, macropain) 26S subunit, ATPase, 4	PSMC4	NM_006503 //	MGC138483	3833291	chr19	+	45168772	45179181	1.04
		NM_153001	MGC13687 //						
			MGC23214 //						
			MGC8570 //						
			MIP224 // S6 //						

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 53

<210> SEQ ID NO 1

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: primer

<400> SEQUENCE: 1

atgtcaaacg tgcgagtgtc taac 24

<210> SEQ ID NO 2

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: primer

<400> SEQUENCE: 2

ttacggttga cgtgttgtga ggcc 24

<210> SEQ ID NO 3

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: primer

<400> SEQUENCE: 3

gccatgtcag aaccggctgg ggat 24

<210> SEQ ID NO 4

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: primer

<400> SEQUENCE: 4

ttagggcttc ctcttgaga agat 24

<210> SEQ ID NO 5

<211> LENGTH: 30

<212> TYPE: DNA

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: primer

<400> SEQUENCE: 5

cctcgatcct ccctttatcc agccctcact 30

<210> SEQ ID NO 6

<211> LENGTH: 30

<212> TYPE: DNA

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: primer

<400> SEQUENCE: 6

gaacccaaat cactttcccc aaggaaggag 30

-continued

<210> SEQ ID NO 7
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 7

aatgaggtcc ccacgtttct cgggtgt

27

<210> SEQ ID NO 8
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 8

gccaataagc aaagtgttga acacttcac

29

<210> SEQ ID NO 9
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 9

aagtgttga tggcttgctc tgctac

26

<210> SEQ ID NO 10
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 10

acatggacag ctttgctgag tcggtcc

27

<210> SEQ ID NO 11
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 11

ttgctagacg actgttttcc aactccag

28

<210> SEQ ID NO 12
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 12

gctgaaggac catttattac tggag

25

<210> SEQ ID NO 13
<211> LENGTH: 25
<212> TYPE: DNA

-continued

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

<400> SEQUENCE: 13

ttcttgetgt gttctttctc ccaca 25

<210> SEQ ID NO 14
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 14

ctaatcaaac aggaaattca aaggaagag 29

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

<400> SEQUENCE: 15

cttgatttct cgtaacagat ctgcatc 27

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

<400> SEQUENCE: 16

actctcagca acaacaccag agctcta 27

<210> SEQ ID NO 17
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 17

tagctttcgt gccattgcca caacatc 27

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

<400> SEQUENCE: 18

ggcctgatgg gtcttatcta tgg 23

<210> SEQ ID NO 19
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

-continued

<400> SEQUENCE: 19

ttagatggaa gctggctcaa gag 23

<210> SEQ ID NO 20

<211> LENGTH: 23

<212> TYPE: DNA

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: primer

<400> SEQUENCE: 20

gaactttgcc tcattctttt gca 23

<210> SEQ ID NO 21

<211> LENGTH: 26

<212> TYPE: DNA

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: primer

<400> SEQUENCE: 21

ctgagctcca gtctcttgta tttctg 26

<210> SEQ ID NO 22

<211> LENGTH: 29

<212> TYPE: DNA

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: primer

<400> SEQUENCE: 22

caaggtaacc acttctaaga ccataattc 29

<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

tcaatggaga tagcaaaggt attataacc 29

<210> SEQ ID NO 25

<211> LENGTH: 30

<212> TYPE: DNA

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: primer

<400> SEQUENCE: 25

agatttactt aggagcacat tatgagtgtt 30

-continued

<210> SEQ ID NO 26
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 26

atgtttatca acggtccgcc t 21

<210> SEQ ID NO 27
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 27

catccccagt ggcttttaag g 21

<210> SEQ ID NO 28
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 28

tgcgcggaga cagcatag 18

<210> SEQ ID NO 29
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 29

tgggttcaaa atgccaggtt 20

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

<400> SEQUENCE: 30

ggcccttcag aaatgcttgt c 21

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

<400> SEQUENCE: 31

cccattacac aattcatgtg cttag 25

<210> SEQ ID NO 32
<211> LENGTH: 25
<212> TYPE: DNA

-continued

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

<400> SEQUENCE: 32

cagatcatct agaagcagct ggttt 25

<210> SEQ ID NO 33
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 33

acagaatctg gtcctacta acaaaa 26

<210> SEQ ID NO 34
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial
<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

-continued

<400> SEQUENCE: 38
tgaatcctga atactatgcc tcctt 25

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

<400> SEQUENCE: 39
tccctttcttc 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
ccagggttcc 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
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 44
cccactgcct tgatctagtt gat 23

-continued

<210> SEQ ID NO 45
<211> LENGTH: 23
<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
<213> ORGANISM: Artificial
<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 tcaact 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

-continued

<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

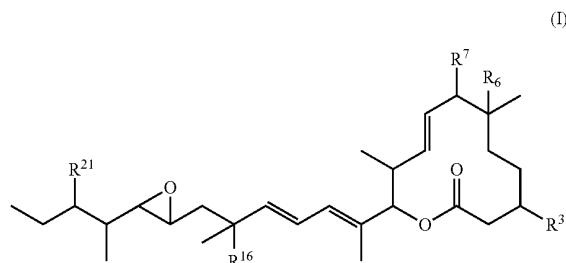
<210> SEQ ID NO 53
 <211> LENGTH: 26
 <212> TYPE: DNA
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: primer

<400> SEQUENCE: 53

ctgagctcca gtctcttgta tttctg

26

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:



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-epoxytriosa-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)carbonyloxy)-18,19-epoxytriosa-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)carbonyloxy)-18,19-epoxytriosa-8,12,14-trien-11-olide;
- (8E,12E,14E)-7-((4-Butylpiperazin-1-yl)carbonyloxy)-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytriosa-8,12,14-trien-11-olide;
- (8E,12E,14E)-7-((4-Ethylpiperazin-1-yl)carbonyloxy)-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytriosa-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)carbonyloxy)-18,19-epoxytriosa-8,12,14-trien-11-olide;
- (8E,12E,14E)-7-((4-Cyclohexylpiperazin-1-yl)carbonyloxy)-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytriosa-8,12,14-trien-11-olide;
- (8E,12E,14E)-7-((4-(Cyclopropylmethyl)piperazin-1-yl)carbonyloxy)-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytriosa-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)carbonyloxy)-18,19-epoxytriosa-8,12,14-trien-11-olide;
- (8E,12E,14E)-7-((4-(Cyclopropylmethyl)homopiperazin-1-yl)carbonyloxy)-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytriosa-8,12,14-trien-11-olide;
- (8E,12E,14E)-7-((4-Cyclopentylpiperazin-1-yl)carbonyloxy)-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytriosa-8,12,14-trien-11-olide;
- (8E,12E,14E)-3,6,16,21-Tetrahydroxy-7-((4-isopropylpiperazin-1-yl)carbonyloxy)-6,10,12,16,20-pentamethyl-18,19-epoxytriosa-8,12,14-trien-11-olide;
- (8E,12E,14E)-7-((4-Cycloheptylpiperazin-1-yl)carbonyloxy)-3,6,16,21-Tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytriosa-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-epoxytriosa-8,12,14-trien-11-olide;
- (8E,12E,14E)-3,6,16,21-Tetrahydroxy-7-((4-isobutylhomopiperazin-1-yl)carbonyloxy)-6,10,12,16,20-pentamethyl-18,19-epoxytriosa-8,12,14-trien-11-olide;
- (8E,12E,14E)-7-((4-Ethylhomopiperazin-1-yl)carbonyloxy)-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytriosa-8,12,14-trien-11-olide;
- (8E,12E,14E)-7-((4-Butylhomopiperazin-1-yl)carbonyloxy)-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytriosa-8,12,14-trien-11-olide;
- (8E,12E,14E)-3,6,16,21-Trihydroxy-6-methoxy-6,10,12,16,20-pentamethyl-7-((4-methylpiperazin-1-yl)carbonyloxy)-18,19-epoxytriosa-8,12,14-trien-11-olide;
- (8E,12E,14E)-3,6,16,21-Trihydroxy-6-methoxy-6,10,12,16,20-pentamethyl-7-((4-(piperidin-1-yl)piperidin-1-yl)carbonyloxy)-18,19-epoxytriosa-8,12,14-trien-11-olide;
- (8E,12E,14E)-3,6,7,21-Tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytriosa-8,12,14-trien-11-olide;
- (8E,12E,14E)-7-((4-(2,2-Dimethylpropyl)homopiperazin-1-yl)carbonyloxy)-3,6,16,21-tetrahydroxy-6,10,12,16,20-pentamethyl-18,19-epoxytriosa-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)carbonyloxy)-18,19-epoxytriosa-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.

* * * * *

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
[标]申请(专利权)人(译)	卫材株式会社		
申请(专利权)人(译)	EISAI研发MANAGEMENT CO. , LTD.		
当前申请(专利权)人(译)	EISAI研发MANAGEMENT CO. , LTD.		
[标]发明人	MIZUI YOSHIHARU HATA NAOKO IWATA MASAO SAGANE KOJI UESUGI MAI KADOWAKI TADASHI YOSHIDA TAKU		
发明人	MIZUI, YOSHIHARU HATA, NAOKO IWATA, MASAO SAGANE, KOJI UESUGI, MAI KADOWAKI, TADASHI YOSHIDA, TAKU		
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。

