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Staudt et al.

(54) **METHODS FOR IDENTIFYING, DIAGNOSING, AND PREDICTING SURVIVAL OF LYMPHOMAS**

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(52) **U.S. Cl.** **506/9**

(57) **ABSTRACT**

The present invention discloses methods for identifying, diagnosing, and predicting survival in a lymphoma or lymphoproliferative disorder on the basis of gene expression patterns. The invention discloses a novel microarray, the Lymph Dx microarray, for obtaining gene expression data from a lymphoma sample. The invention also discloses a variety of methods for utilizing lymphoma gene expression data to determine the identity of a particular lymphoma and to predict survival in a subject diagnosed with a particular lymphoma. This information is useful in developing the appropriate therapeutic approach for use with a particular subject.

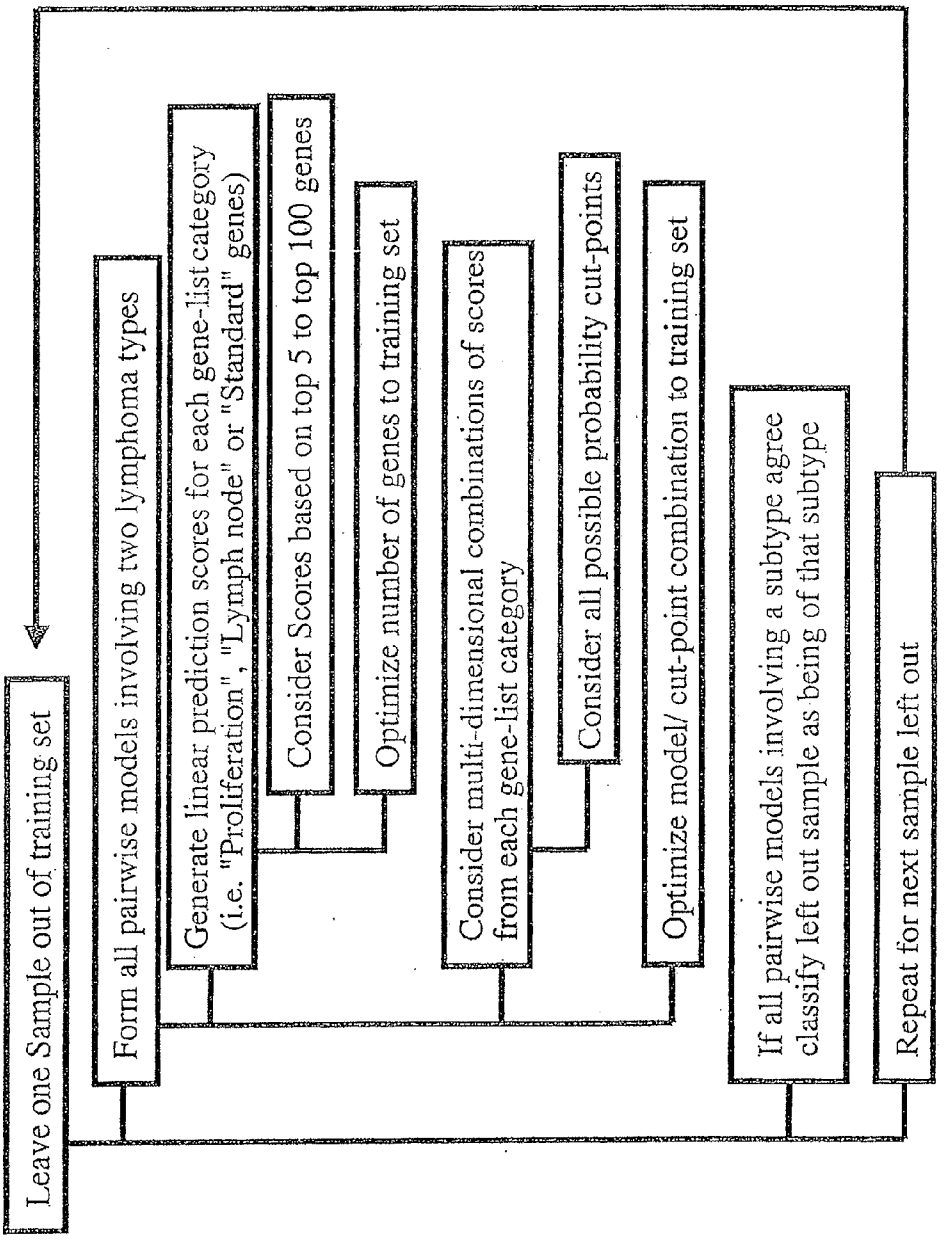

Leave one Sample out of training set
Form all pairwise models involving two lymphoma types
Generate linear prediction scores for each gene-list category (i.e. "Proliferation", "Lymph node" or "Standard" genes)
Consider Scores based on top 5 to top 100 genes
Optimize number of genes to training set
Consider multi-dimensional combinations of scores from each gene-list category
Consider all possible probability cut-points
Optimize model/ cut-point combination to training set
If all pairwise models involving a subtype agree classify left out sample as being of that subtype
Repeat for next sample left out

Figure 1

Figure 2

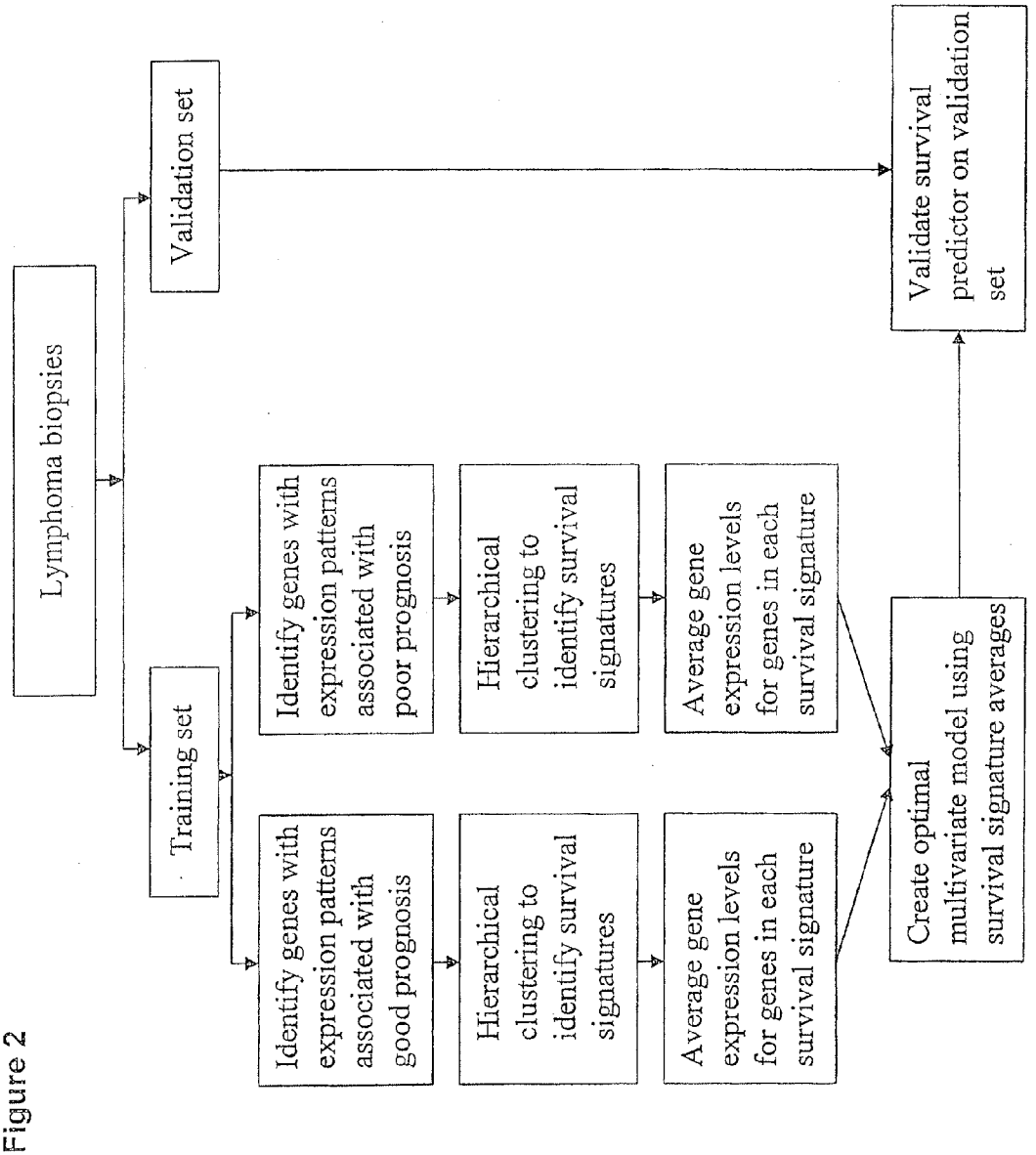

Lymphoma biopsies
Training set
Validation set
Identify genes with expression patterns associated with good prognosis
Hierarchical clustering to identify survival signatures
Average gene expression levels for genes in each survival signature
Identify genes with expression patterns associated with poor prognosis
Hierarchical clustering to identify survival signatures
Average gene expression levels for genes in each survival signature
Create optimal multivariate model using survival signature averages
Validate survival predictor on validation set

Figure 3

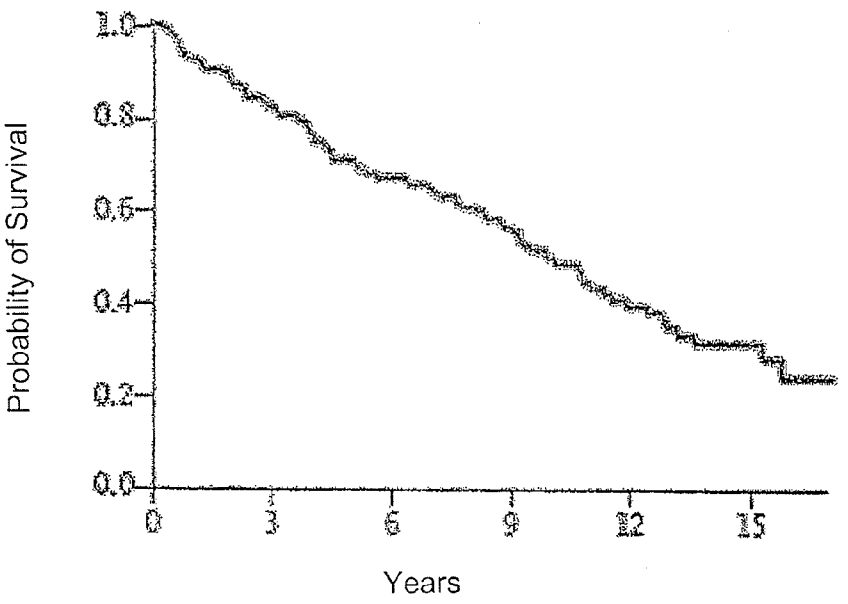


Figure 4

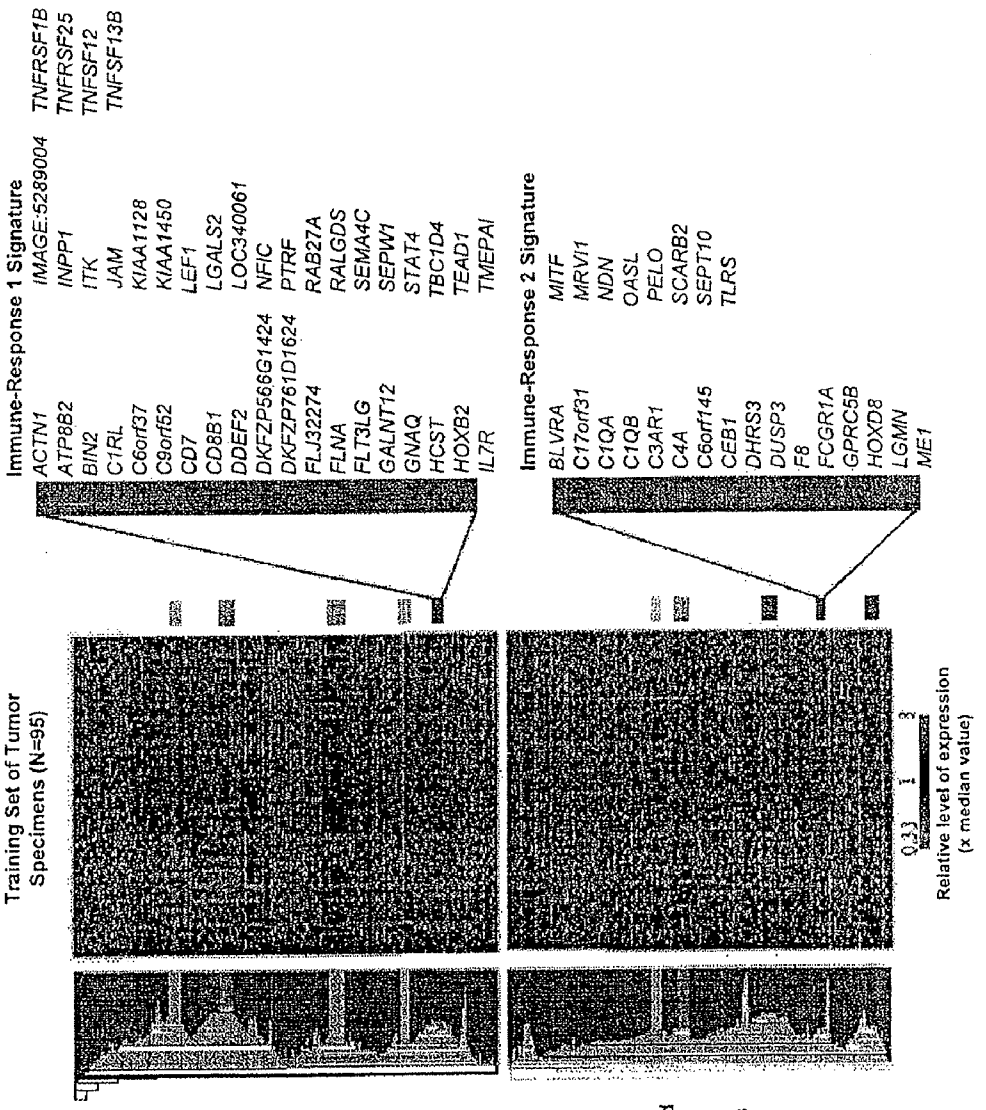

Immune-Response 1 Signature
ACTN1
ATP8B2
BIN2
C1RL
C6orf37
C9orf52
CD7
CD8B1
DDEF2
DKFZP566G1424
DKFZP761D1624
FLJ32274
FLNA
FLT3LG
GALNT12
GNAQ
HCST
HOXB2
IL7R
IMAGE:5289004
INPP1
ITK
JAM
KIAA1128
KIAA1450
LEF1
LGALS2
LOC340061
NFIC
PTRF
RAB27A
RALGDS
SEMA4C
SEPW1
STAT4
TBC1D4
TEAD1
TMEPAI
TNFRSF1B
TNFRSF25
TNFSF12
TNFSF13B
Immune-Response 2 Signature
BLVRA
C17orf31
C1QA
C1QB
C3AR1
C4A
C6orf145
CEB1
DHRS3
DUSP3
F8
FCGR1A
GPRC5B
HOXD8
LGMN
ME1
Training Set of Tumor Specimens (N=95)
Genes Associated with Favorable Prognosis
Genes Associated with Poor Prognosis
0.33
1
3
Relative level of expression (x median value)

Figure 5

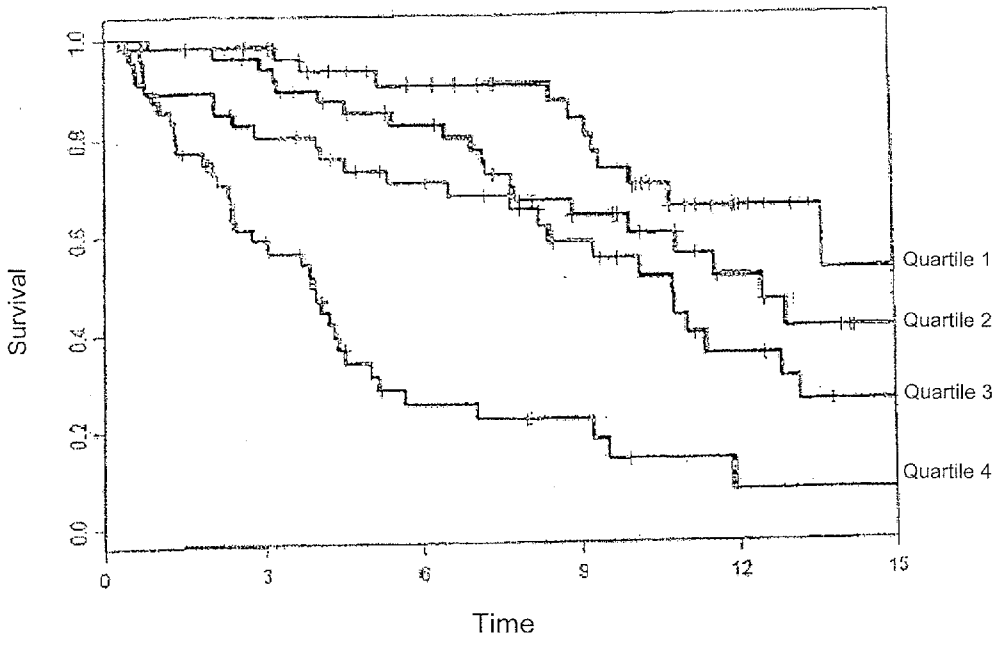
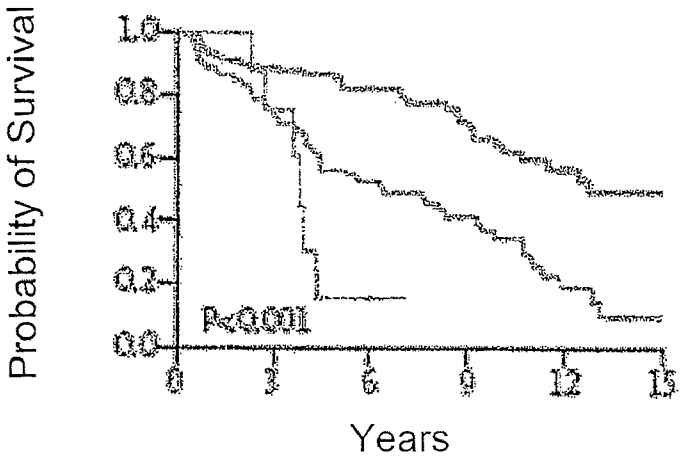
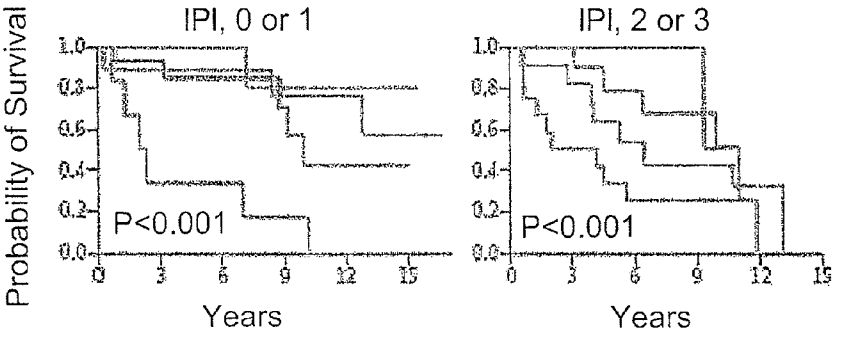

Survival
0.0
0.2
0.4
0.6
0.8
1.0
0
3
6
9
12
15
Time
Quartile 1
Quartile 2
Quartile 3
Quartile 4

Figure 6



No. at Risk						
---IPI, 0 or 1	91	75	55	38	19	8
---IPI, 2 or 3	64	48	31	18	5	1
---IPI, 4 or 5	9	6	1	0	0	0

Figure 7



No. at Risk												
---SPS quartile 1	15	9	13	5	3	1	3	3	3	2	0	0
---SPS quartile 2	8	5	7	3	2	1	10	10	7	4	0	0
---SPS quartile 3	9	8	8	6	4	2	11	9	5	4	2	0
---SPS quartile 4	6	2	2	1	0	0	12	6	3	2	0	0

Figure 8

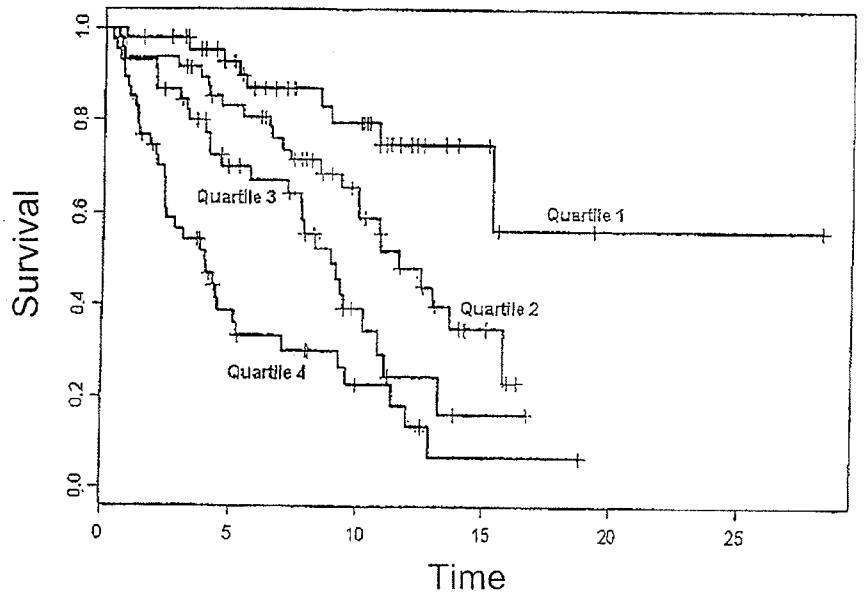

Survival
1.0
0.8
0.6
0.4
0.2
0.0
Quartile 3
Quartile 1
Quartile 2
Quartile 4
0
5
10
15
20
25
Time

Figure 9

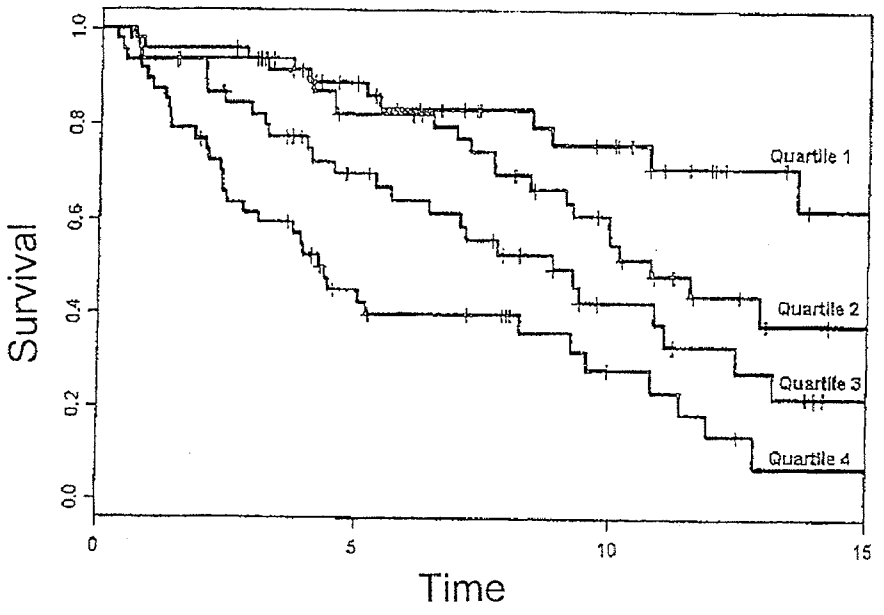

Survival
1.0
0.8
0.6
0.4
0.2
0.0
0
5
10
15
Time
Quartile 1
Quartile 2
Quartile 3
Quartile 4

Figure 10

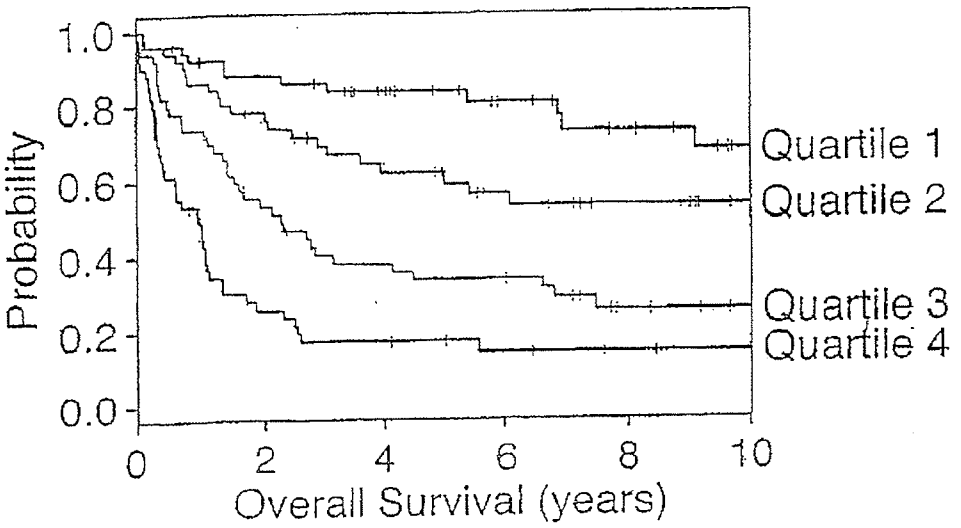

1.0
0.8
0.6
0.4
0.2
0.0
Probability
0
2
4
6
8
10
Overall Survival (years)
Quartile 1
Quartile 2
Quartile 3
Quartile 4

Figure 11

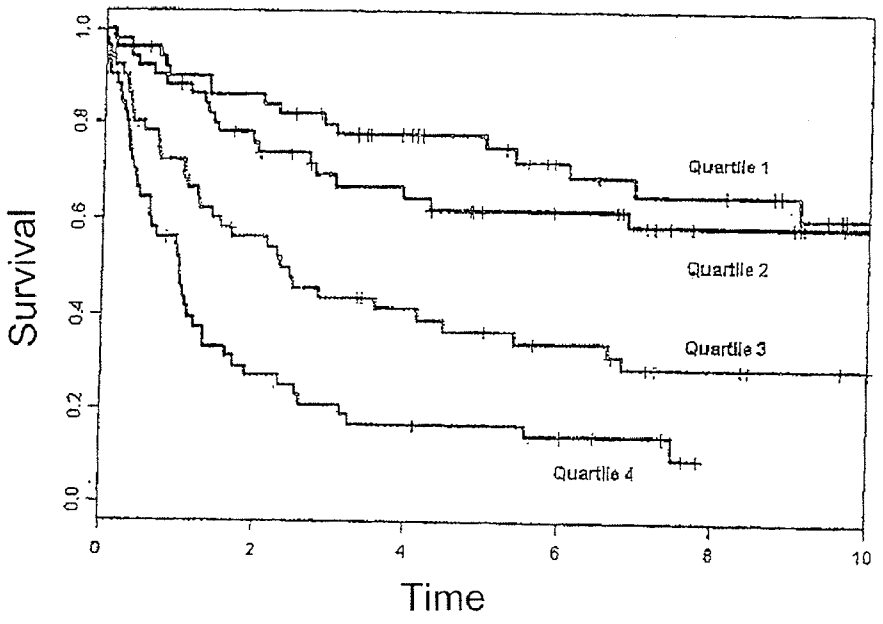

Survival
1.0
0.8
0.6
0.4
0.2
0.0
0
2
4
6
8
10
Time
Quartile 1
Quartile 2
Quartile 3
Quartile 4

Figure 12

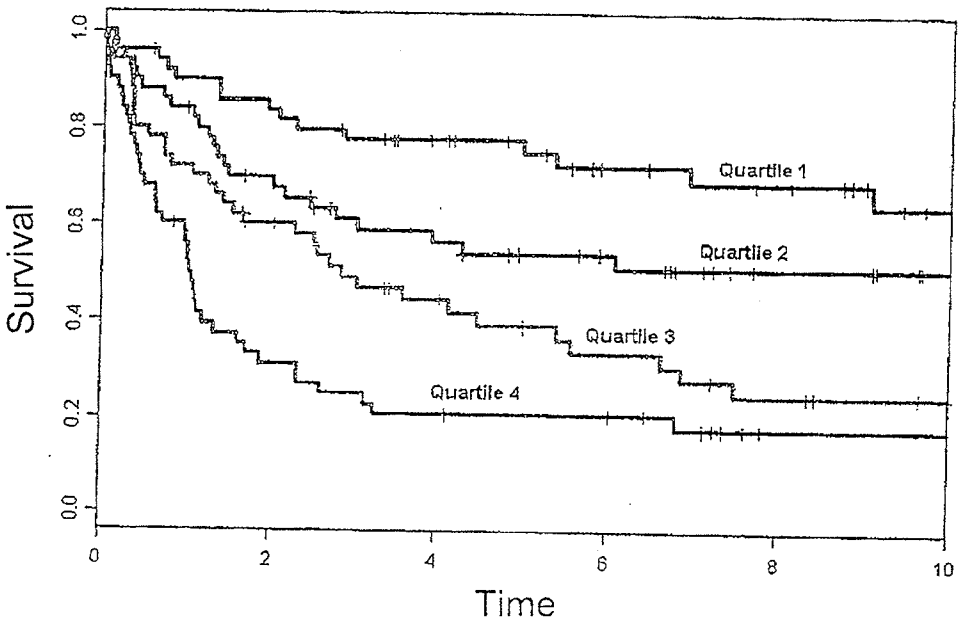

Survival
1.0
0.8
0.6
0.4
0.2
0.0
0
2
4
6
8
10
Time
Quartile 1
Quartile 2
Quartile 3
Quartile 4

Figure 13

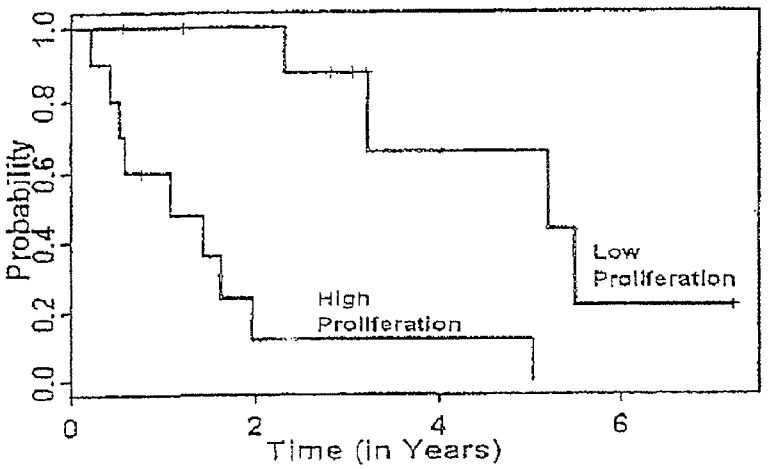

Probability
0.0
0.2
0.4
0.6
0.8
1.0
0
2
4
6
Time (in Years)
Low
Proliferation
High
Proliferation

Figure 14

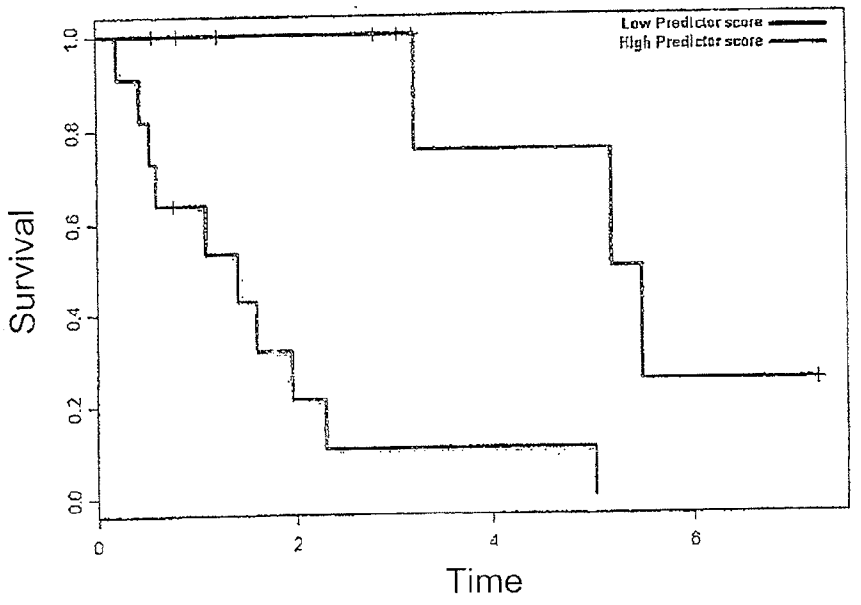

Low Predictor score
High Predictor score
Survival
0.0
0.2
0.4
0.6
0.8
1.0
0
2
4
6
Time

Figure 15

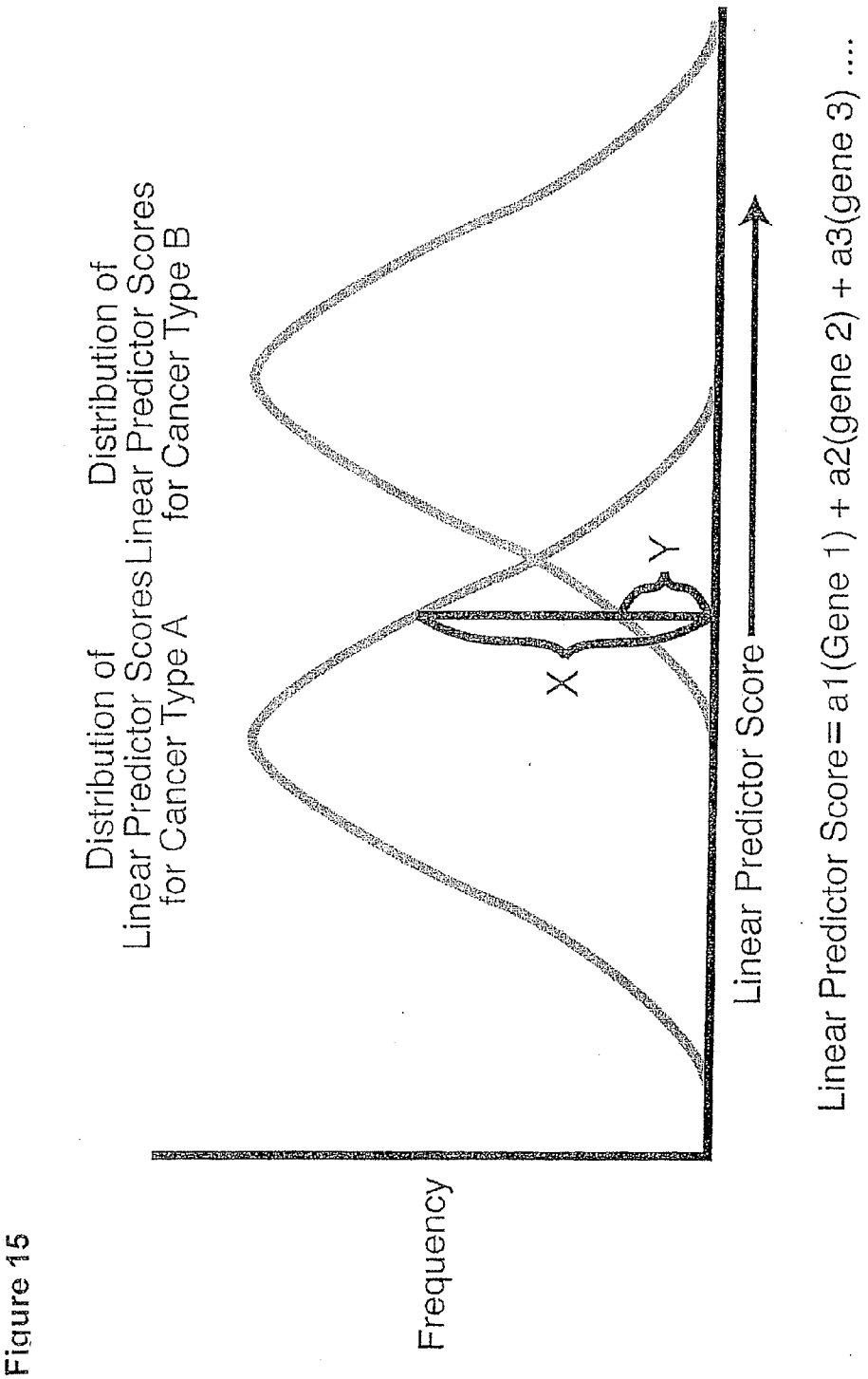

Distribution of Linear Predictor Scores for Cancer Type A
Distribution of Linear Predictor Scores for Cancer Type B
X
Y
Frequency
Linear Predictor Score
Linear Predictor Score = a1(Gene 1) + a2(gene 2) + a3(gene 3) ....
Bayes' Rule: Probability that cancer is Type A = X / (X + Y)

Figure 16

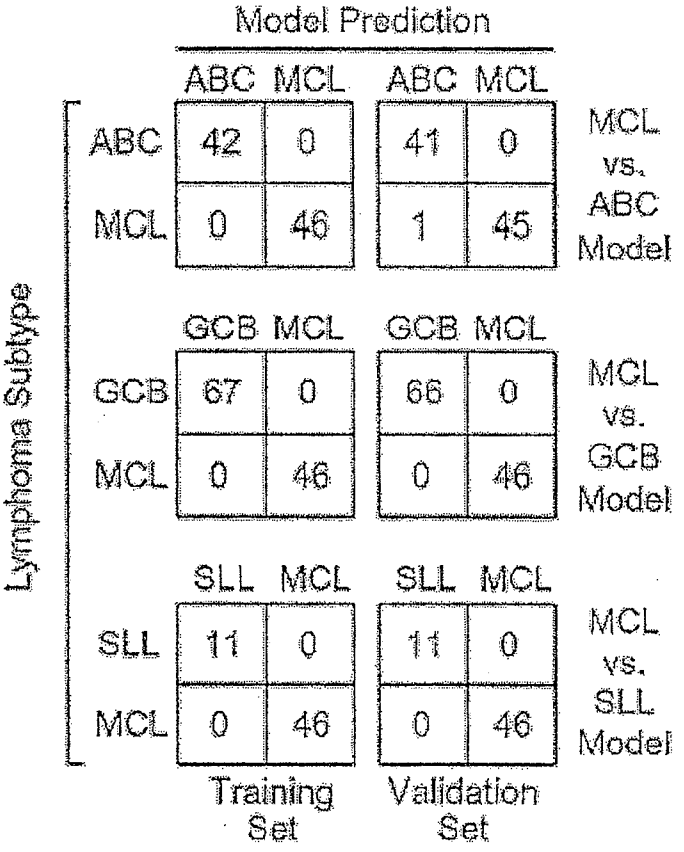

Model Prediction
Lymphoma Subtype
ABC MCL ABC MCL
ABC 42 0 41 0
MCL 0 46 1 45
MCL vs. ABC Model
GCB MCL GCB MCL
GCB 67 0 66 0
MCL 0 46 0 46
MCL vs. GCB Model
SLL MCL SLL MCL
SLL 11 0 11 0
MCL 0 46 0 46
MCL vs. SLL Model
Training Set
Validation Set

Figure 17

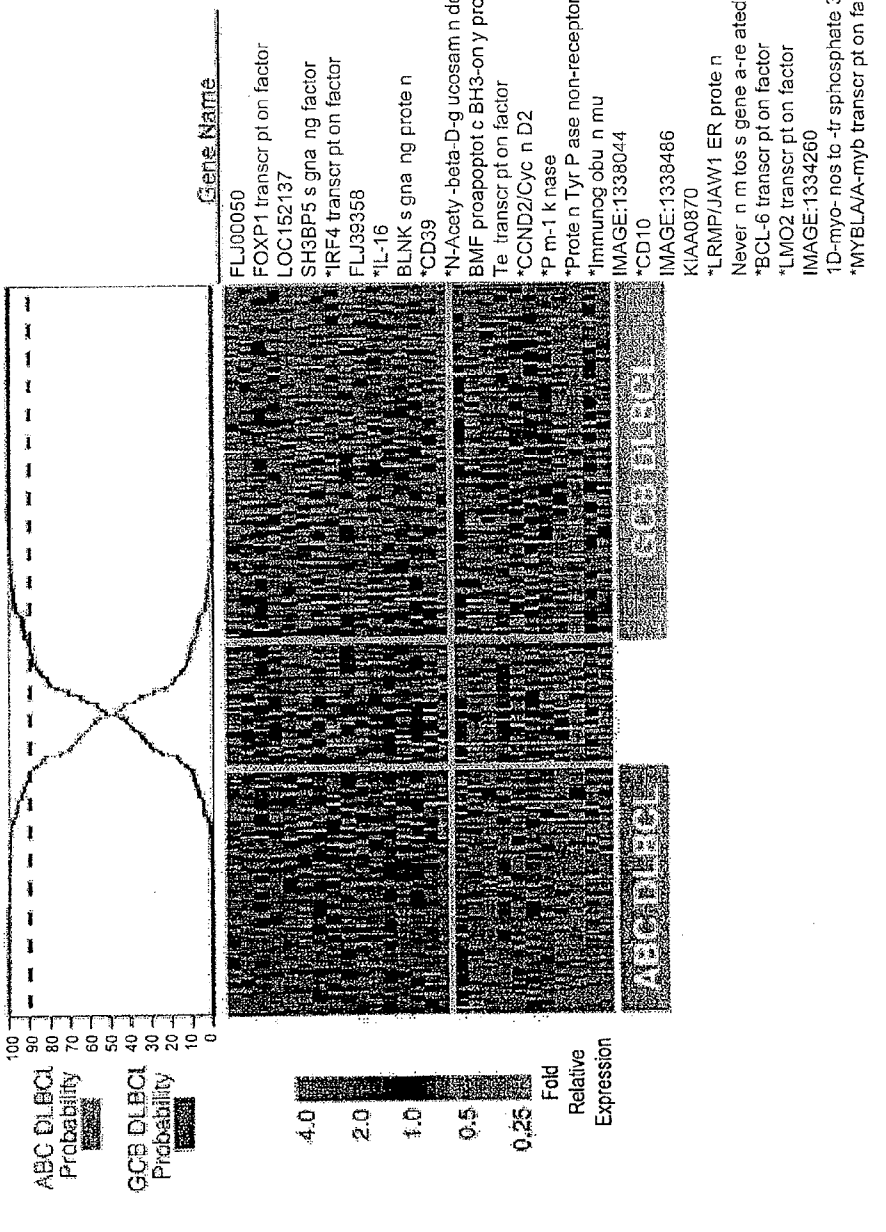

Gene Name
FLJ00050
FOXP1 transcription factor
LOC152137
SH3BP5 signaling factor
*IRF4 transcription factor
FLJ39358
*IL-16
BLNK signaling protein
*CD39
*N-Acetyl-beta-D-glucosaminide
BMF proapoptotic BH3-only protein
Testis transcription factor
*CCND2/Cyclin D2
*P1-1 kinase
*Protein Tyrosine phosphatase non-receptor type 1
*Immunoglobulin mu
IMAGE:1338044
*CD10
IMAGE:1338486
KIAA0870
*LRMP/JAW1 ER protein
Neuronatin gene arrested kinase
*BCL-6 transcription factor
*LMO2 transcription factor
IMAGE:1334260
1D-myo-inositol-trisphosphate 3-kinase
*MYBLA/A-myb transcription factor
ABC DLBCL
GCB DLBCL
ABC DLBCL Probability
GCB DLBCL Probability
100
90
80
70
60
50
40
30
20
10
0
4.0
2.0
1.0
0.5
0.25
Fold Relative Expression

Figure 18

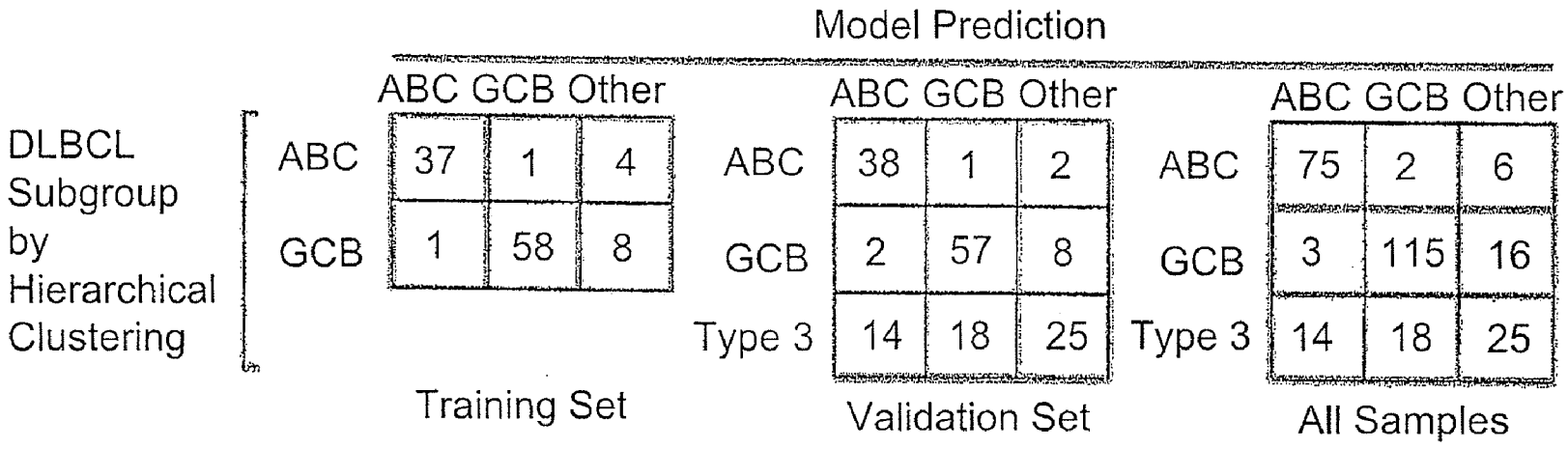

Model Prediction
DLBCL Subgroup by Hierarchical Clustering
ABC GCB Other
ABC 37 1 4
GCB 1 58 8
Training Set
ABC GCB Other
ABC 38 1 2
GCB 2 57 8
Type 3 14 18 25
Validation Set
ABC GCB Other
ABC 75 2 6
GCB 3 115 16
Type 3 14 18 25
All Samples

Figure 19

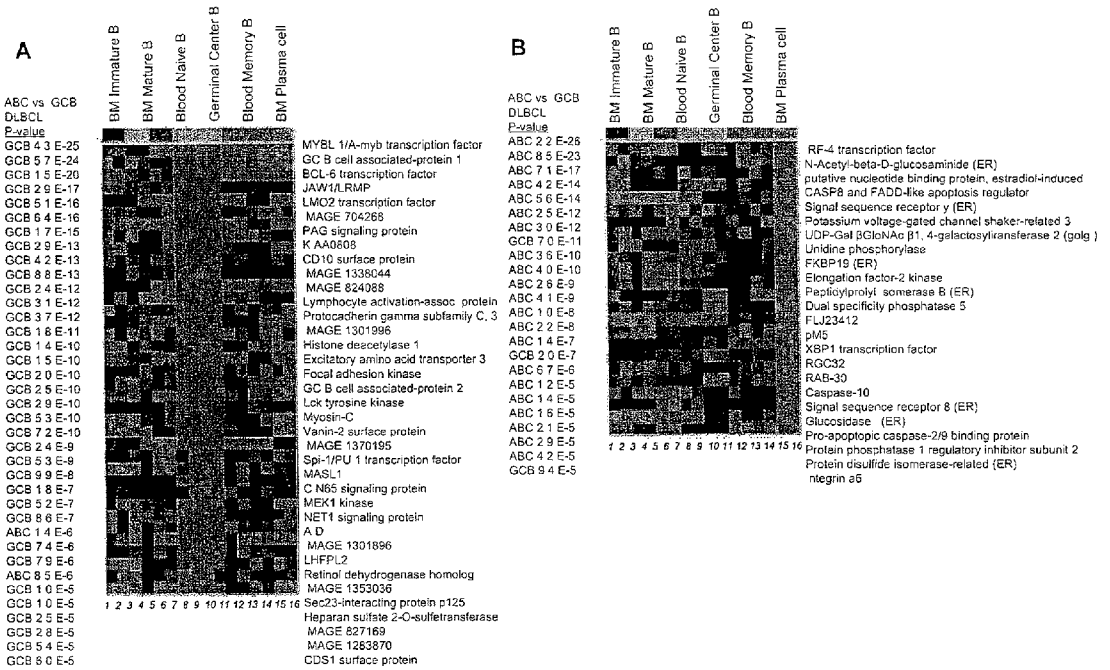
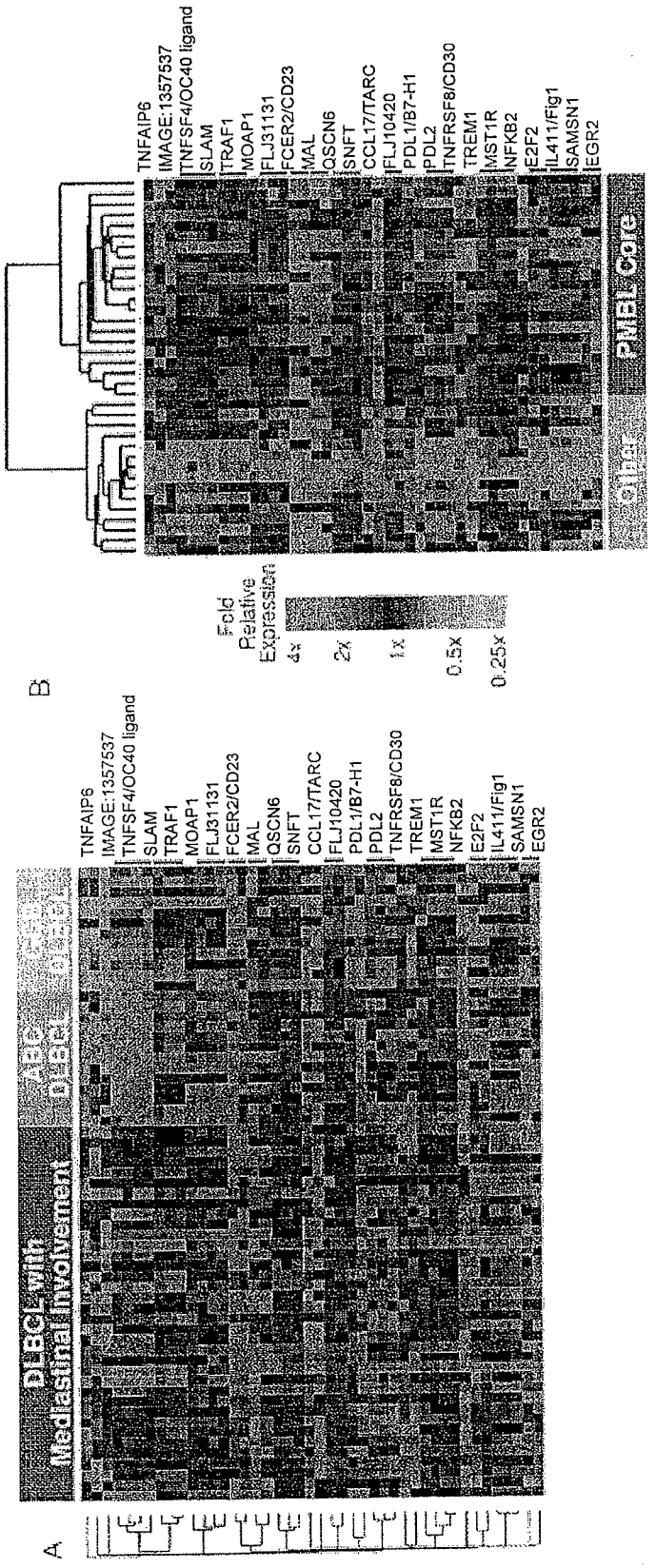

A
BM Immature B
BM Mature B
Blood Naive B
Germinal Center B
Blood Memory B
BM Plasma cell
ABC vs GCB DLBCL
P-value
GCB 4 3 E-25
GCB 5 7 E-24
GCB 1 5 E-20
GCB 2 9 E-17
GCB 5 1 E-16
GCB 6 4 E-16
GCB 1 7 E-15
GCB 2 9 E-13
GCB 4 2 E-13
GCB 8 8 E-13
GCB 2 4 E-12
GCB 3 1 E-12
GCB 3 7 E-12
GCB 1 8 E-11
GCB 1 4 E-10
GCB 1 5 E-10
GCB 2 0 E-10
GCB 2 5 E-10
GCB 2 9 E-10
GCB 5 3 E-10
GCB 7 2 E-10
GCB 2 4 E-9
GCB 5 3 E-9
GCB 9 9 E-8
GCB 1 8 E-7
GCB 5 2 E-7
GCB 8 6 E-7
ABC 1 4 E-6
GCB 7 4 E-6
GCB 7 9 E-6
ABC 8 5 E-6
GCB 1 0 E-5
GCB 1 0 E-5
GCB 2 5 E-5
GCB 2 8 E-5
GCB 5 4 E-5
GCB 8 0 E-5
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16
MYBL 1/A-myb transcription factor
GC B cell associated-protein 1
BCL-6 transcription factor
JAW1/LRMP
LMO2 transcription factor
MAGE 704268
PAG signaling protein
K AA0808
CD10 surface protein
MAGE 1338044
MAGE 824088
Lymphocyte activation-assoc protein
Protocadherin gamma subfamily C, 3
MAGE 1301996
Histone deacetylase 1
Excitatory amino acid transporter 3
Focal adhesion kinase
GC B cell associated-protein 2
Lck tyrosine kinase
Myosin-C
Vanin-2 surface protein
MAGE 1370195
Spi-1/PU 1 transcription factor
MASL1
C N65 signaling protein
MEK1 kinase
NET1 signaling protein
A D
MAGE 1301896
LHFPL2
Retinol dehydrogenase homolog
MAGE 1353036
Sec23-interacting protein p125
Heparan sulfate 2-O-sulfetransferase
MAGE 827169
MAGE 1283870
CDS1 surface protein
B
BM Immature B
BM Mature B
Blood Naive B
Germinal Center B
Blood Memory B
BM Plasma cell
ABC vs GCB DLBCL
P-value
ABC 2 2 E-26
ABC 8 5 E-23
ABC 7 1 E-17
ABC 4 2 E-14
ABC 5 6 E-14
ABC 2 5 E-12
ABC 3 0 E-12
GCB 7 0 E-11
ABC 3 6 E-10
ABC 4 0 E-10
ABC 2 6 E-9
ABC 4 1 E-9
ABC 1 0 E-8
ABC 2 2 E-8
ABC 1 4 E-7
GCB 2 0 E-7
ABC 6 7 E-6
ABC 1 2 E-5
ABC 1 4 E-5
ABC 1 6 E-5
ABC 2 1 E-5
ABC 2 9 E-5
ABC 4 2 E-5
GCB 9 4 E-5
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16
RF-4 transcription factor
N-Acetyl-beta-D-glucosaminide (ER)
putative nucleotide binding protein, estradiol-induced
CASP8 and FADD-like apoptosis regulator
Signal sequence receptor γ (ER)
Potassium voltage-gated channel shaker-related 3
UDP-Gal βGlcNAc β1, 4-galactosyltransferase 2 (golg)
Uridine phosphorylase
FKBP19 (ER)
Elongation factor-2 kinase
Peptidylprolyl isomerase B (ER)
Dual specificity phosphatase 5
FLJ23412
pM5
XBP1 transcription factor
RGC32
RAB-30
Caspase-10
Signal sequence receptor δ (ER)
Glucosidase (ER)
Pro-apoptopic caspase-2/9 binding protein
Protein phosphatase 1 regulatory inhibitor subunit 2
Protein disulfide isomerase-related (ER)
ntegrin a6

Figure 20


A
DLBCL with Mediastinal Involvement
TNFAIP6
IMAGE:1357537
TNFSF4/OC40 ligand
SLAM
TRAF1
MOAP1
FLJ31131
FCER2/CD23
MAL
QSCN6
SNFT
CCL17/TARC
FLJ10420
PDL1/B7-H1
PDL2
TNFRSF8/CD30
TREM1
MST1R
NFKB2
E2F2
IL411/Fig1
SAMSN1
EGR2
B
Fold Relative Expression
4x
2x
1x
0.5x
0.25x
PMBL Core

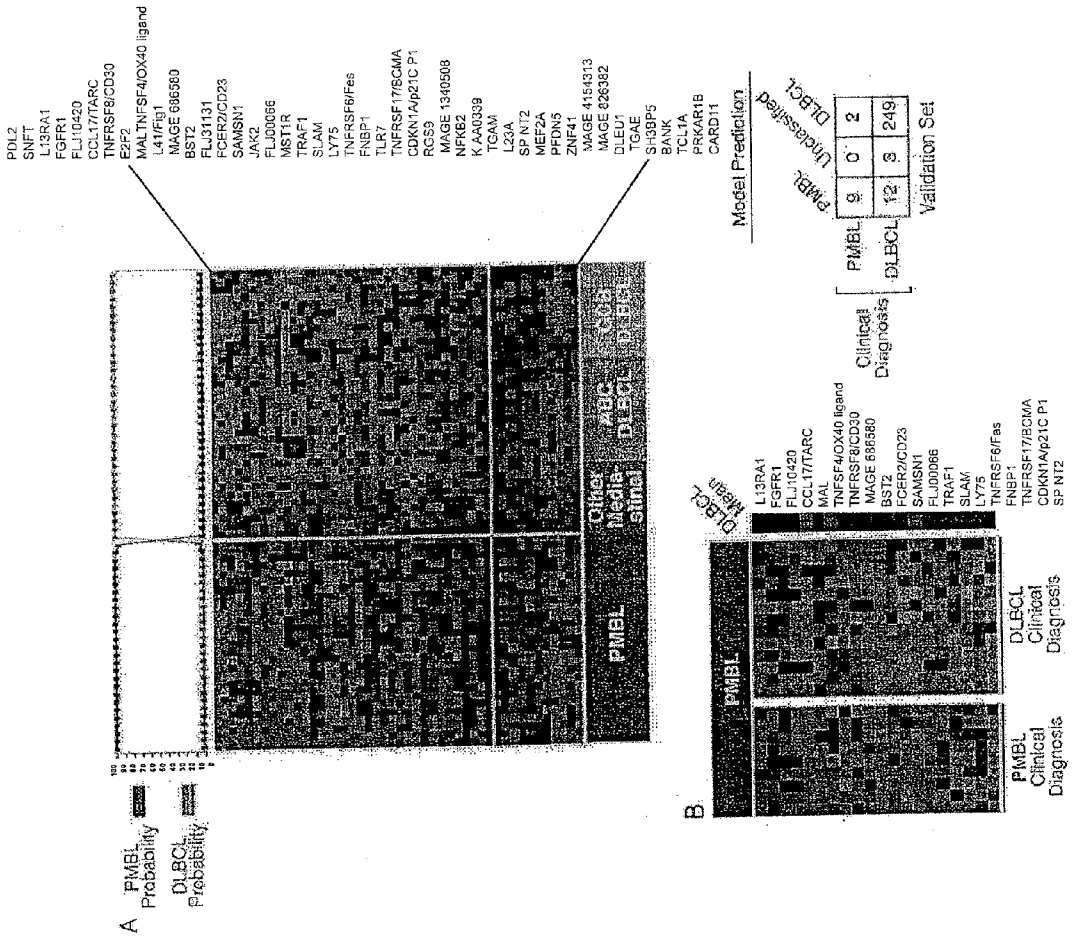
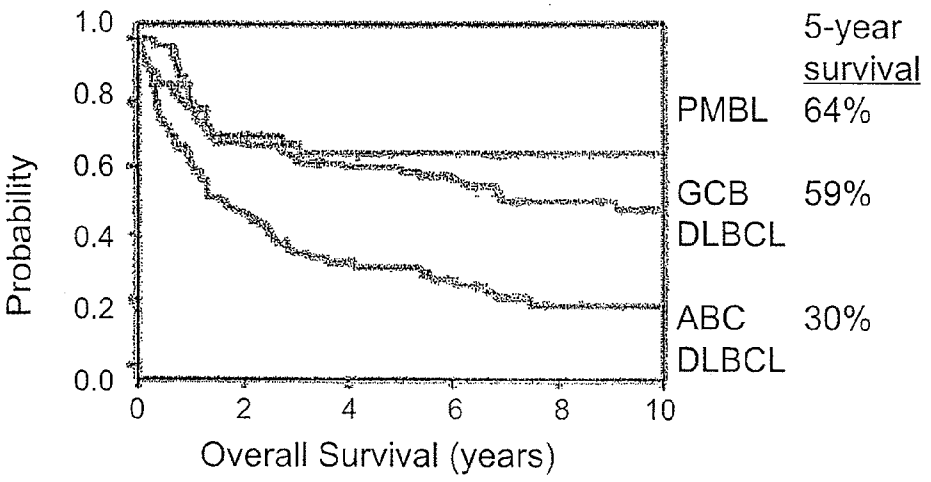

A
PMBL Probability
DLBCL Probability
PDL2
SNFT
IL13RA1
FGFR1
FLJ10420
CCL17/TARC
TNFRSF8/CD30
E2F2
MALTNFSF4/OX40 ligand
IL41/Fig1
MAGE 686580
BST2
FLJ31131
FCER2/CD23
SAMSN1
JAK2
FLJ00066
MST1R
TRAF1
SLAM
LY75
TNFRSF6/Fas
FNBP1
TLR7
TNFRSF17/BCMA
CDKN1A/p21C P1
RGS9
MAGE 1340508
NFKB2
KIAA0339
TGAM
L23A
SP N12
MEF2A
PPDN5
ZNF41
MAGE 4154313
MAGE 626382
DLEU1
TGAE
SH3BP5
BANK
TCL1A
PRKAR1B
CARD11
PMBL
Other
Media-stinal
ABC DLBCL
GCB DLBCL
PMBL Clinical Diagnosis
DLBCL Clinical Diagnosis
B
PMBL
DLBCL Mean
L13RA1
FGFR1
FLJ10420
CCL17/TARC
MAL
TNFSF4/OX40 ligand
TNFRSF8/CD30
MAGE 686580
BST2
FCER2/CD23
SAMSN1
FLJ00066
TRAF1
SLAM
LY75
TNFRSF6/Fas
FNBP1
TNFRSF17/BCMA
CDKN1A/p21C P1
SP N12
PMBL Clinical Diagnosis
DLBCL Clinical Diagnosis
Model Prediction
PMBL
Unassigned
DLBCL
PMBL 9 0 2
DLBCL 12 3 249
Validation Set

Figure 21

Figure 22


1.0
0.8
0.6
0.4
0.2
0.0
Probability
0
2
4
6
8
10
Overall Survival (years)
5-year survival
PMBL 64%
GCB DLBCL 59%
ABC DLBCL 30%

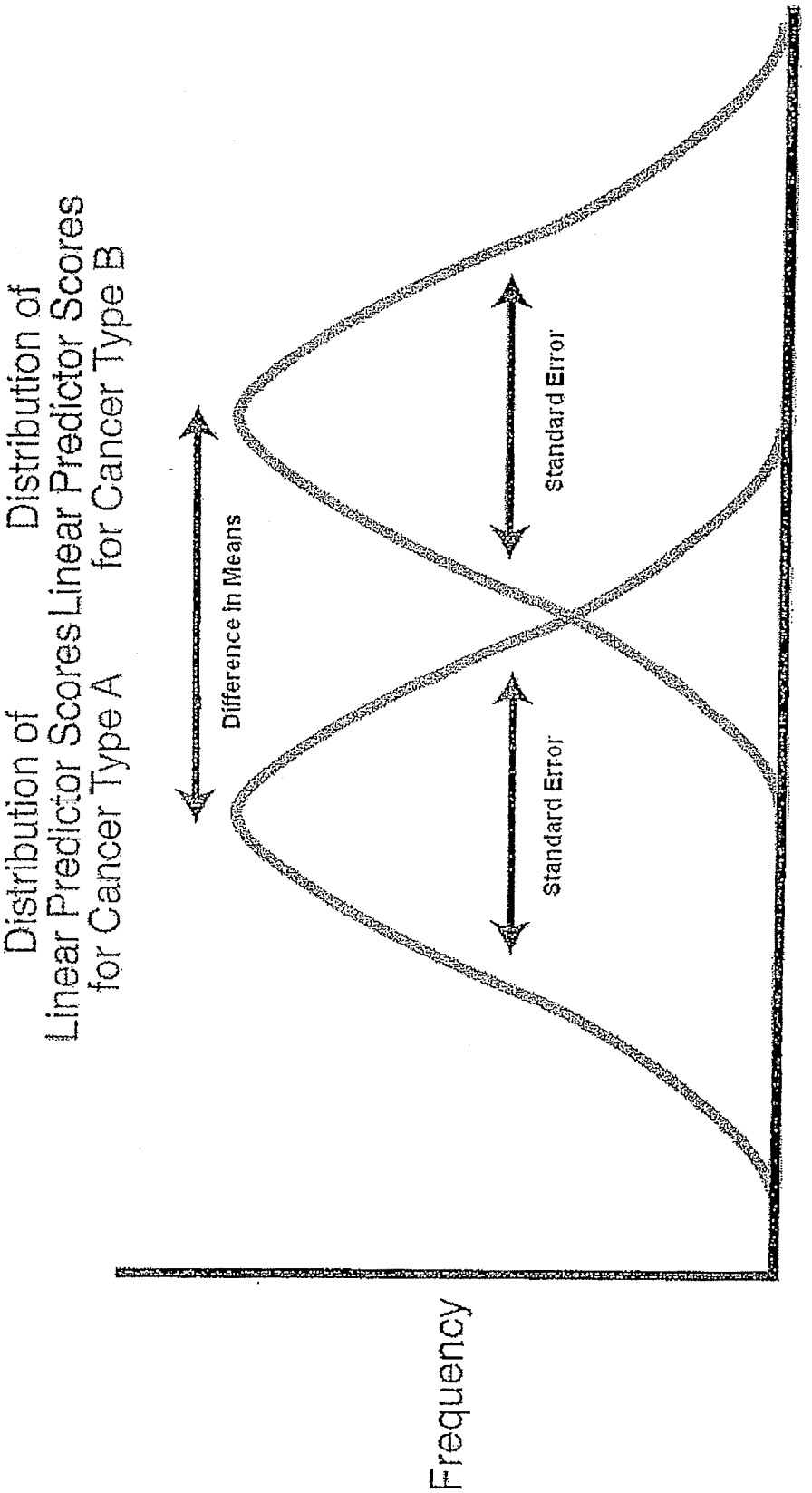

Distribution of Linear Predictor Scores for Cancer Type A
Distribution of Linear Predictor Scores for Cancer Type B
Difference in Means
Standard Error
Standard Error
Frequency

Figure 23

Figure 24

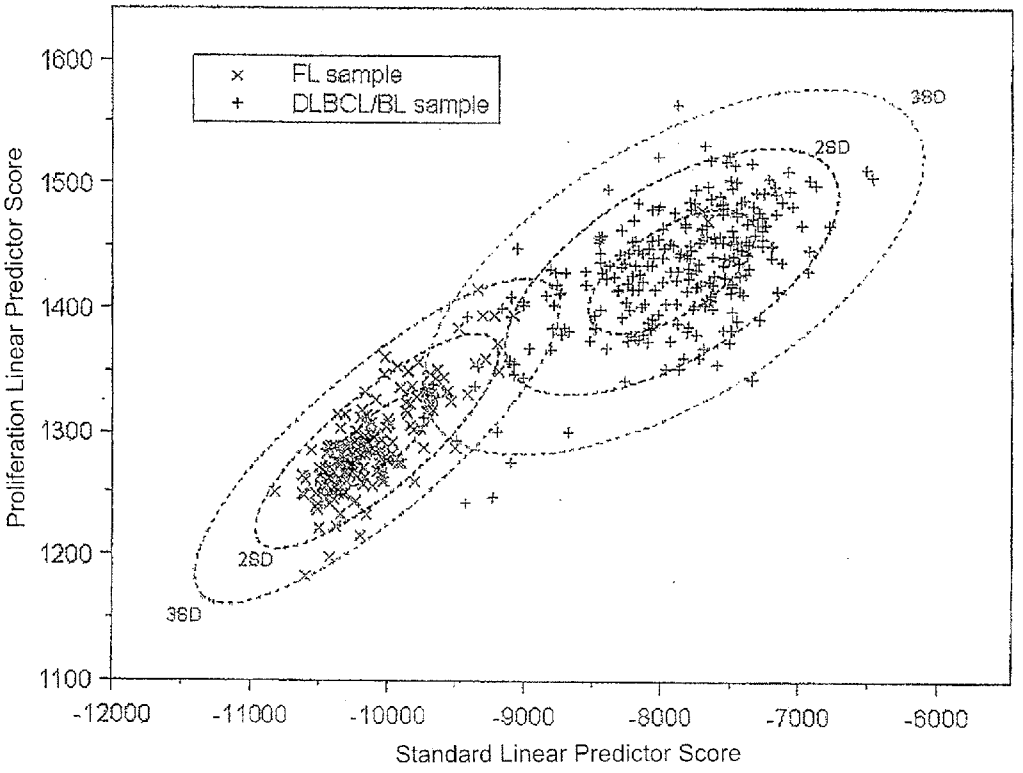
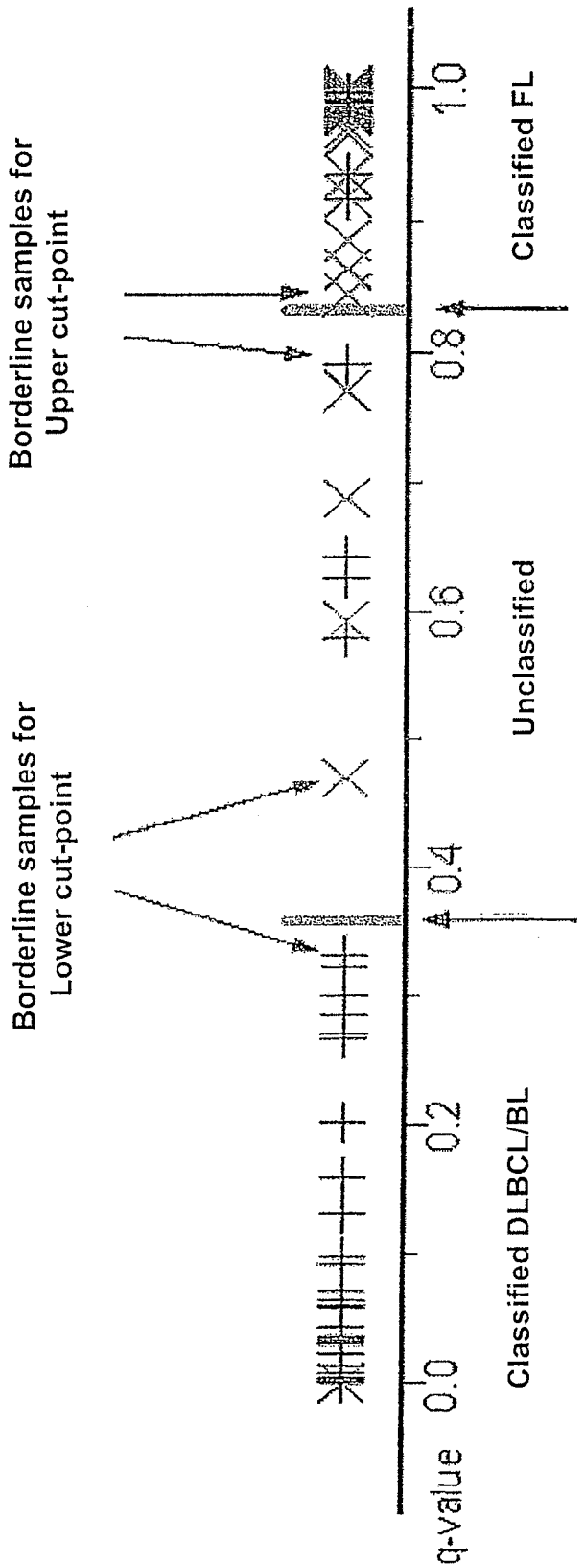
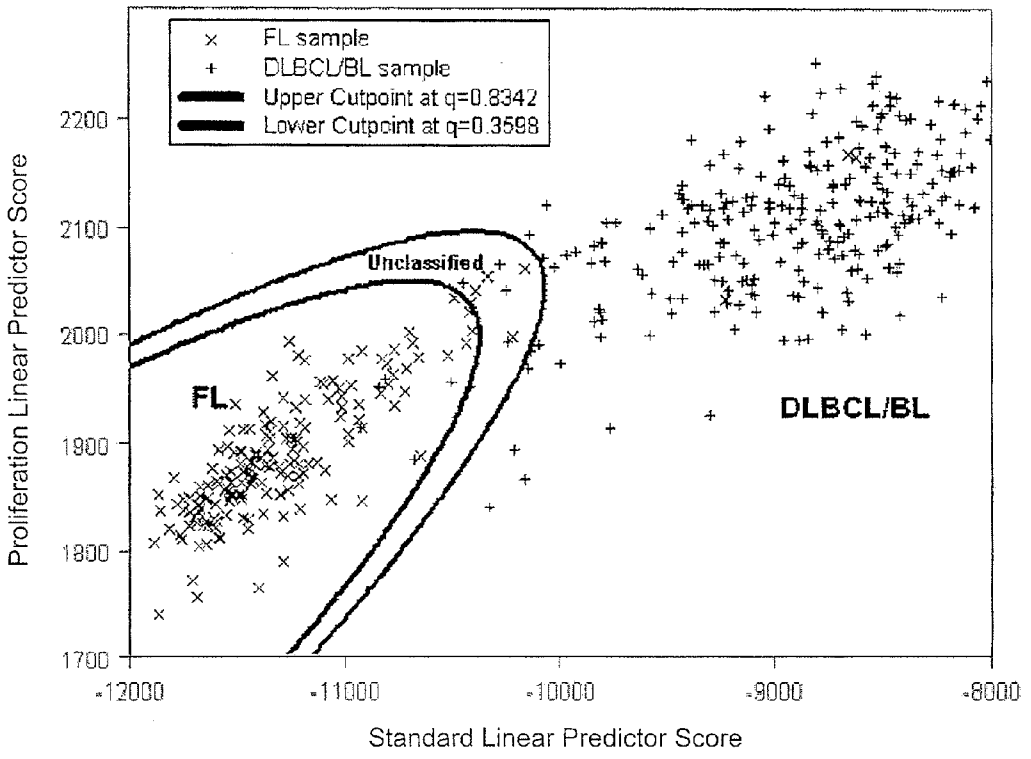

FL sample
DLBCL/BL sample
3SD
2SD
2SD
3SD
Proliferation Linear Predictor Score
1600
1500
1400
1300
1200
1100
-12000
-11000
-10000
-9000
-8000
-7000
-6000
Standard Linear Predictor Score

Figure 25



$$\text{Error score} = 4*(\text{Error Rate}) + \text{Unclassified Rate}$$

Figure 26


FL sample
DLBCL/BL sample
Upper Cutpoint at q=0.8342
Lower Cutpoint at q=0.3598
Unclassified
FL
DLBCL/BL
Proliferation Linear Predictor Score
2200
2100
2000
1900
1800
1700
-12000
-11000
-10000
-9000
-8000
Standard Linear Predictor Score

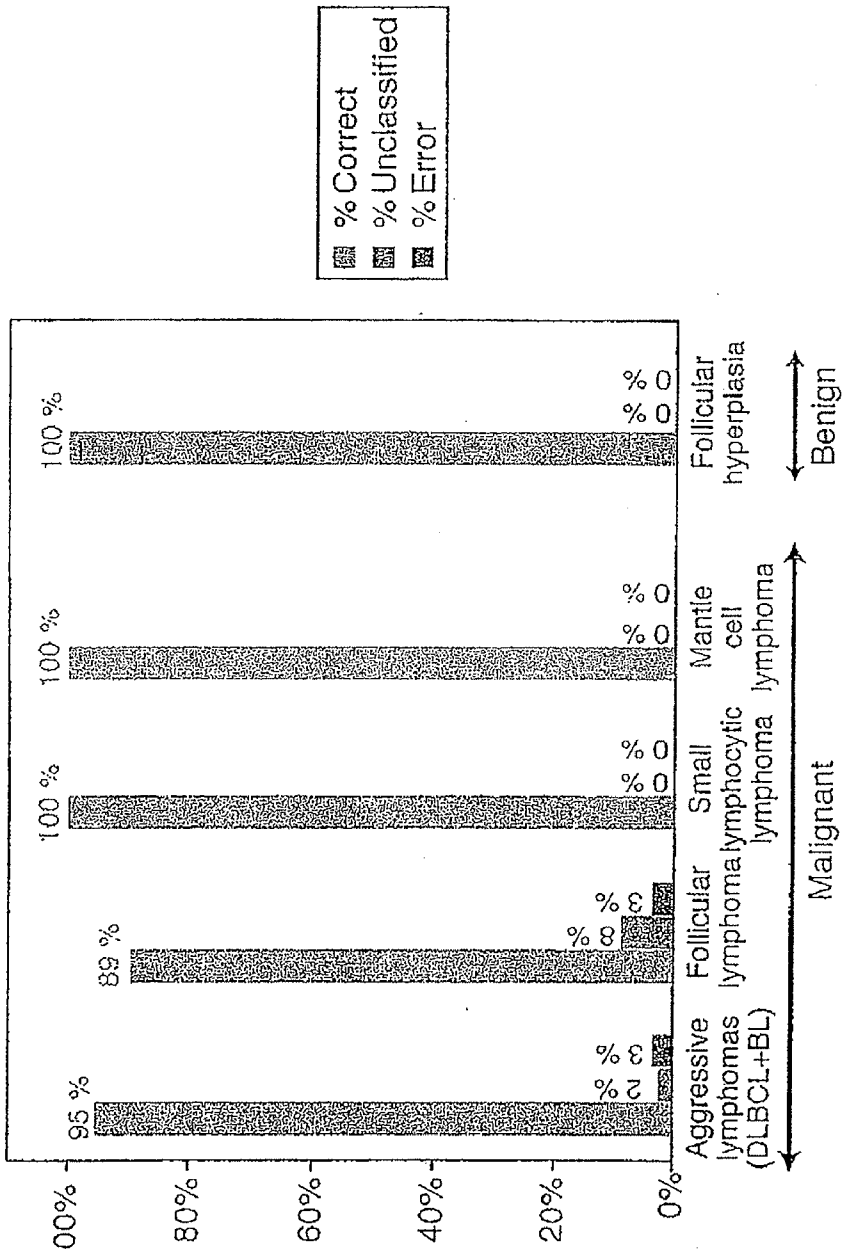

% Correct
% Unclassified
% Error
100%
80%
60%
40%
20%
0%
95 %
89 %
100 %
100 %
100 %
Aggressive lymphomas (DLBCL+BL)
Follicular lymphoma
Small lymphocytic lymphoma
Mantle cell lymphoma
Follicular hyperplasia
Malignant
Benign

Figure 27

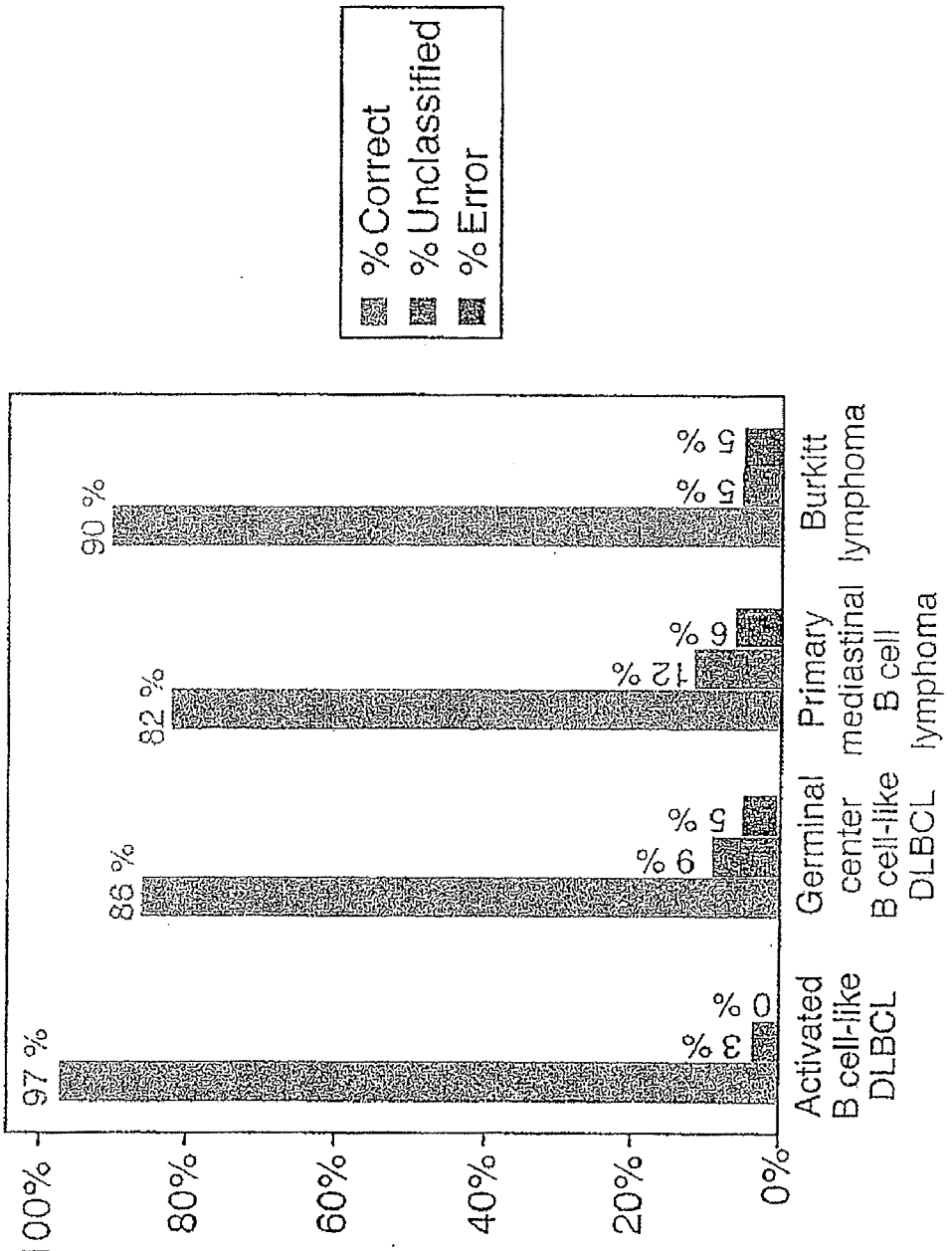

% Correct
% Unclassified
% Error
100%
80%
60%
40%
20%
0%
97 %
3 %
0 %
86 %
9 %
5 %
82 %
12 %
6 %
90 %
5 %
5 %
Activated B cell-like DLBCL
Germinal center B cell-like DLBCL
Primary mediastinal B cell lymphoma
Burkitt lymphoma

Figure 28

METHODS FOR IDENTIFYING, DIAGNOSING, AND PREDICTING SURVIVAL OF LYMPHOMAS

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This patent application is a continuation-in-part of copending U.S. patent application Ser. No. 12/592,778, filed Dec. 2, 2009, which is a divisional of U.S. patent application Ser. No. 10/934,930, filed Sep. 3, 2004, issued as U.S. Pat. No. 7,711,492, which claims the benefit of U.S. Provisional Patent Application No. 60/500,377, filed Sep. 3, 2003, which are incorporated by reference in their entirety herein.

REFERENCE TO TABLES AND COMPUTER PROGRAM LISTING APPENDIX PREVIOUSLY SUBMITTED ON COMPACT DISC

[0002] Tables 2-1723 and 1725-2358 are contained on 21 CD-ROMs submitted with U.S. patent application Ser. No. 10/934,930, now issued as U.S. Pat. No. 7,711,492, and U.S. patent application Ser. No. 12/592,778, filed Dec. 2, 2009. These CD-ROMs are numbered 1-21 of 22. The name, size, and date of creation for each file is presented in the file entitled "Tableofcontents.txt," located on CD number 21 of 22. The name of each file incorporates the number of the corresponding table. Any reference to a table or file should be considered an incorporation by reference of the contents of the table and/or file at that particular place in the specification.

[0003] A computer program listing appendix is contained on one CD-ROM numbered 22 of 22 submitted with U.S. patent application Ser. No. 10/934,930, now issued U.S. as U.S. Pat. No. 7,711,492, and U.S. patent application Ser. No. 12/592,778, filed Dec. 2, 2009. The computer program listing appendix contains files related to the implementation of an algorithm for determining lymphoma type. The name, size, and date of creation for each file in the computer program listing appendix is presented in the file entitled "Table_of_contents.txt," located on CD-ROM 22. Any reference to a file contained in the computer program listing appendix should be considered an incorporation by reference of the contents of that file at that particular place in the specification.

BACKGROUND OF INVENTION

[0004] A variety of systems for identifying and classifying lymphomas have been proposed over the last 20 years. In the 1980's, the Working Formulation was introduced as a method of classifying lymphomas based on morphological and clinical characteristics. In the 1990's, the Revised European-American Lymphoma (REAL) system was introduced in an attempt to take into account immunophenotypic and genetic characteristics in classifying lymphomas (Harris 1994). The most recent standard, set forth by the World Health Organization (WHO), attempts to build on these previous systems (Jaffe 2001). The WHO classification of lymphomas is based on several factors, including tumor morphology, immunophenotype, recurrent genetic abnormalities, and clinical features. Table 1, below, contains a list of the B and T cell neoplasms that have been recognized by the WHO classification. Each malignancy is listed according to its WHO classification nomenclature, followed by a WHO classification number.

TABLE 1

Category	Name	WHO ID #
	B-cell neoplasms	
Precursor B-cell neoplasms	Precursor B-cell lymphoblastic leukemia	9835/3
	Precursor B-cell lymphoblastic lymphoma	9728/3
Mature B-cell neoplasms	Chronic lymphocytic leukemia	9823/3
	Small lymphocytic lymphoma	9670/3
	B-cell prolymphocytic leukemia	9833/3
	Lymphoplasmacytic lymphoma	9671/3
	Splenic marginal zone lymphoma	9689/3
	Hairy cell leukemia	9940/3
	Plasma cell myeloma	9732/3
	Solitary plasmacytoma of bone	9731/3
	Extraosseous plasmacytoma	9734/3
	Extranodal marginal zone B-cell lymphoma of mucosa-associated lymphoid tissue (MALT lymphoma)	9699/3
	Nodal marginal zone B-cell lymphoma	9699/3
	Follicular lymphoma (Grade 1, 2, 3a, 3b)	9690/3
	Mantle cell lymphoma	9673/3
	Diffuse large B-cell lymphoma	9680/3
	Mediastinal (thymic) large B-cell lymphoma	9679/3
	Intravascular large B-cell lymphoma	9680/3
	Primary effusion lymphoma	9678/3
	Burkitt lymphoma	9687/3
	Burkitt leukemia	9826/3
B-cell proliferations of uncertain malignant potential	Lymphomatoid granulomatosis	9766/1
	Post-transplant lymphoproliferative disorder, polymorphic	9970/1
	T-cell and NK-cell neoplasms	
Precursor T-cell and NK-cell neoplasms	Precursor T lymphoblastic leukemia	9837/3
	Precursor T lymphoblastic lymphoma	9729/3
	Elastic NK-cell lymphoma	9727/3
Mature T-cell and NK-cell neoplasms	T-cell prolymphocytic leukemia	9834/3
	T-cell large granular lymphocytic leukemia	9831/3
	Aggressive NK-cell leukemia	9948/3
	Adult T-cell leukemia/lymphoma	9827/3
	Extranodal NK-/T-cell lymphoma, nasal type	9719/3
	Enteropathy-type T-cell lymphoma	9717/3
	Hepatosplenic T-cell lymphoma	9716/3
	Subcutaneous panniculitis-like T-cell lymphoma	9708/3
	Mycosis fungoides	9700/3
	Sezary syndrome (9701/3)	9701/3
	Primary cutaneous anaplastic large cell lymphoma (C-ALCL)	9718/3
	Peripheral T-cell lymphoma, unspecified	9702/3
	Angioimmunoblastic T-cell lymphoma	9705/3
	Anaplastic large cell lymphoma	9714/3
T-cell proliferation of uncertain malignant potential	Lymphomatoid papulosis	9718/3

TABLE 1-continued

Category	Name	WHO ID #
Hodgkin lymphoma	Nodular lymphocyte predominant Hodgkin lymphoma	9659/3
	Classical Hodgkin lymphoma	9650/3
	Classical Hodgkin lymphoma, nodular sclerosis	9663/3
	Classical Hodgkin lymphoma, lymphocyte-rich	9651/3
	Classical Hodgkin lymphoma, mixed cellularity	9652/3
	Classical Hodgkin lymphoma, lymphocyte depleted	9653/3

Other diagnoses that have not been given WHO diagnostic numbers include HIV-associated lymphoma, germinal center B cell-like subtype of diffuse large B cell lymphoma, activated B cell-like subtype of diffuse large B-cell lymphoma, follicular hyperplasia (non-malignant), and infectious mononucleosis (non-malignant).

[0005] Although the WHO classification has proven useful in patient management and treatment, patients assigned to the same WHO diagnostic category often have noticeably different clinical outcomes. In many cases, these different outcomes appear to be due to molecular differences between tumors that cannot be readily observed by analyzing tumor morphology. More precise methods are needed for identifying and classifying lymphomas based on their molecular characteristics.

SUMMARY OF THE INVENTION

[0006] Accurate identification of lymphoma type or subtype in a subject suffering from a lymphoproliferative disorder is important for developing an appropriate therapeutic strategy. Previous attempts have been made to identify lymphomas using gene expression data obtained using a microarray. However, there is a need in the art for more accurate and predictive methods of analyzing this gene expression data. In addition, there is a need for more specific and efficient methods of obtaining gene expression data.

[0007] The present invention discloses a novel microarray for obtaining gene expression data to be used in identifying lymphoma types and predicting survival in a subject. The present invention further discloses a variety of methods for analyzing gene expression data obtained from a lymphoma sample, and specific algorithms for predicting survival and clinical outcome in a subject suffering from a lymphoma.

[0008] One embodiment of the present invention provides a composition comprising the set of probes listed in Table 2, which is set forth below and contained in the file entitled "Tableb.-0002_LymphDx_Probe_List.txt." Preferably, this composition comprises a microarray.

[0009] In another embodiment, the present invention provides a method of generating a survival predictor for a particular lymphoma type. In this method, one or more biopsy samples that have been diagnosed as belonging to a particular lymphoma type are obtained. Gene expression data is obtained for these samples, and genes with expression patterns associated with longer or shorter survival are identified. Hierarchical clustering is performed to group these genes into gene expression signatures, and the expression of all genes within each signature are averaged to obtain a gene expression signature value for each signature. These gene expression signature values are then used to generate a multivariate survival predictor.

[0010] In another embodiment, the present invention provides a method for predicting survival in a follicular lymphoma (FL) subject. In this method, a biopsy sample is obtained from the subject and gene expression data is obtained from the biopsy sample. The expression level of those genes belonging to an immune response-1 or immune response-2 gene expression signature are averaged to generate gene expression signature values for each signature. A survival predictor score is then calculated using an equation: [2.71*(immune response-2 gene expression signature value)]−[2.36*(immune response-1 gene expression signature value)]. A higher survival predictor score is associated with a less favorable outcome. In one embodiment, the gene expression data used in this method is obtained using a microarray.

[0011] In another embodiment, the present invention provides another method for predicting survival in a follicular lymphoma (FL) subject. In this method, a biopsy sample is obtained from the subject and gene expression data is obtained from the biopsy sample. The expression level of those genes belonging to a B cell differentiation, T-cell, or macrophage gene expression signature are averaged to generate gene expression signature values for each signature. A survival predictor score is then calculated using an equation: [2.053*(macrophage gene expression signature value)]−[2.344*(T-cell gene expression signature value)]−[0.729*(B-cell gene expression signature value)]. A higher survival predictor score is associated with a less favorable outcome. In one embodiment, the gene expression data used in this method is obtained using a microarray.

[0012] In another embodiment, the present invention provides yet another method for predicting survival in a follicular lymphoma (FL) subject. In this method, a biopsy sample is obtained from the subject and gene expression data is obtained from the biopsy sample. The expression level of those genes belonging to a macrophage, T-cell, or B-cell differentiation gene expression signature are averaged to generate gene expression signature values for each signature. A survival predictor score is then calculated using an equation: [1.51*(macrophage gene expression signature value)]−[2.11*(T-cell gene expression signature value)]−[0.505*(B-cell differentiation gene expression signature value)]. A higher survival predictor score is associated with a less favorable outcome. In one embodiment, the gene expression data used in this method is obtained using a microarray.

[0013] In another embodiment, the present invention provides a method for predicting survival in a diffuse large B cell lymphoma (DLBCL) subject. In this method, a biopsy sample is obtained from the subject and gene expression data is obtained from the biopsy sample. The expression level of those genes belonging to an ABC DLBCL high, lymph node, or MHC class II gene expression signature are averaged to generate gene expression signature values for each signature. A survival predictor score is then calculated using an equation: [0.586*(ABC DLBCL high gene expression signature value)]−[0.468*(lymph node gene expression signature value)]−[0.336*(MHC class II gene expression signature value)]. A higher survival predictor score is associated with a less favorable outcome. In one embodiment, the gene expression data used in this method is obtained using a microarray.

[0014] In another embodiment, the present invention provides another method for predicting survival in a diffuse large B cell lymphoma (DLBCL) subject. In this method, a biopsy sample is obtained from the subject and gene expression data is obtained from the biopsy sample. The expression level of those genes belonging to a lymph node, germinal B cell, proliferation, or MHC class II gene expression signature are averaged to generate gene expression signature values for each signature. A survival predictor score is then calculated using an equation: [−0.4337*(lymph node gene expression signature)]+[0.09*(proliferation gene expression signature)]−[0.4144*(germinal center B-cell gene expression signature)]−[0.2006*(MHC class II gene expression signature)]. A higher survival predictor score is associated with a less favorable outcome. In one embodiment, the gene expression data used in this method is obtained using a microarray.

[0015] In another embodiment, the present invention provides yet another method for predicting survival in a diffuse large B cell lymphoma (DLBCL) subject. In this method, a biopsy sample is obtained from the subject and gene expression data is obtained from the biopsy sample. The expression level of those genes belonging to a lymph node, germinal B cell, or MHC class II gene expression signature are averaged to generate gene expression signature values for each signature. A survival predictor score is then calculated using an equation: [−0.32*(lymph node gene expression signature)]−[0.176*(germinal B cell gene expression signature)]−[0.206*(MHC class II gene expression signature)]. A higher survival predictor score is associated with a less favorable outcome. In one embodiment, the gene expression data used in this method is obtained using a microarray. In another embodiment, the gene expression data is obtained using RT-PCR.

[0016] In another embodiment, the present invention provides a method for predicting survival in a mantle cell lymphoma (MCL) subject. In this method, a biopsy sample is obtained from the subject and gene expression data is obtained from the biopsy sample. The expression level of those genes belonging to a proliferation gene expression signature are averaged to generate a gene expression signature value. A survival predictor score is then calculated using an equation: [1.66*(proliferation gene expression signature value)]. A higher survival predictor score is associated with a less favorable outcome. In one embodiment, the gene expression data used in this method is obtained using a microarray.

[0017] In another embodiment, the present invention provides a method for determining the probability that a sample X belongs to a first lymphoma type or a second lymphoma type. In this method, a set of genes is identified that is differentially expressed between the two lymphoma types in question, and a set of scale factors representing the difference in expression between the lymphoma types for each of these genes are calculated. A series of linear predictor scores are generated for samples belonging to either of the two lymphoma types based on expression of these genes. Gene expression data is then obtained for sample X, and a linear predictor score is calculated for this sample. The probability that sample X belongs to the first lymphoma type is calculated using an equation that incorporates the linear predictor score of sample X and the mean and variance of the linear predictor scores for the known samples of either lymphoma type.

[0018] In another embodiment, the present invention provides a method for determining the lymphoma type of a sample X In this method, a set of genes is identified that is differentially expressed between a first lymphoma type and a second lymphoma type, and a set of scale factors representing the difference in expression of each of these genes between the two lymphoma types are calculated. A series of linear predictor scores are generated for samples belonging to either of the two lymphoma types based on expression of these genes. Gene expression data is then obtained for sample X, and a linear predictor score is calculated for this sample. The probability that sample X belongs to the first lymphoma type is calculated using an equation that incorporates the linear predictor score of sample X and the mean and variance of the linear predictor scores for the known samples of either lymphoma type. This entire process is then repeated with various lymphoma types being substituted for the first lymphoma type, the second lymphoma type, or both.

[0019] In another embodiment, the present invention provides another method for determining the lymphoma type of a sample X. In this method, a series of lymphoma type pairs are created, with each pair consisting of a first lymphoma type and a second lymphoma type. For each type pair, gene expression data is obtained for a set of genes, and a series of scale factors representing the difference in expression of each of these genes between the two lymphoma types are calculated. A subset of z genes with the largest scale factors are identified, and a series of linear predictor scores are generated for samples belonging to either of the two lymphoma types. Linear predictor scores are calculated for anywhere from 1 to z of these genes. The number of genes from 1 to z that results in the largest difference in linear predictor scores between the two lymphoma types is selected, and gene expression data for these genes is obtained for sample X. A linear predictor score is generated for sample X, and the probability that the sample belongs to the first lymphoma type is calculated using an equation that incorporates the linear predictor score for sample X and the mean and variance of the linear predictor scores for the known samples of either lymphoma type.

[0020] In another embodiment, the present invention provides another method for determining the lymphoma type of a sample X. In this method, a series of lymphoma type pairs are created, with each pair consisting of a first lymphoma type and a second lymphoma type. For each type pair, gene expression data is obtained for a set of genes, and a series of scale factors representing the difference in expression of each of these genes between the two lymphoma types are calculated. The set of genes is divided into gene-list categories indicating correlation with a gene expression signature. Within each gene-list category, a subset of z genes with the largest scale factors are identified, and a series of linear predictor scores are generated for samples belonging to either of the two lymphoma types. Linear predictor scores are calculated for anywhere from 1 to z of these genes. The number of genes from 1 to z that results in the largest difference in linear predictor scores between the two lymphoma types is selected, and gene expression data for these genes is obtained for sample X. A linear predictor score is generated for sample X, and the probability q that the sample belongs to the first lymphoma type is calculated using an equation that incorporates the linear predictor score for sample X and the mean and variance of the linear predictor scores for the known samples of either lymphoma type. A high probability q indicates that sample X belongs to the first lymphoma type, a low probability q indicates that sample X belongs to the second lymphoma type, and a middle probability q indicates that sample X belongs to neither lymphoma type. The cut-off point between high, middle, and low probability values is determined by

ranking samples of known lymphoma type according to their probability values, then analyzing every possible cut-off point between adjacent samples using the equation: 3.99*[(% of first lymphoma type misidentified as second lymphoma type)+(% of second lymphoma type misidentified as a first lymphoma type)]+[(% of first lymphoma type identified as belonging to neither lymphoma type)+(% of second lymphoma type identified as belonging to neither lymphoma type)]. The final cut-off points are those that minimize the value of this equation.

BRIEF DESCRIPTION OF THE DRAWINGS

[0021] FIG. **1**: Method for identifying lymphoma type. Flow chart depicts a general method for identifying lymphoma type using gene expression data.

[0022] FIG. **2**: Survival signature analysis. Flow chart depicts method for developing a lymphoma survival predictor based on gene expression patterns.

[0023] FIG. **3**: FL survival data. Survival data for 191 subjects diagnosed with FL. Median age at diagnosis was 51 years (ranging from 23 to 81 years), and the subjects had a median follow-up of 6.6 years (8.1 years for survivors, with a range of <1 to 28.2 years).

[0024] FIG. **4**: Hierarchical clustering of survival associated genes in FL samples. Each column represents a single FL sample, while each row represents a single gene. Relative gene expression is depicted according to the scale at the bottom of the figure. The dendrogram to the left indicates the degree to which the expression pattern of each gene is correlated with that of the other genes. The colored bars indicate sets of coordinately regulated genes defined as gene expression signatures. Genes comprising the immune response-1 and immune response-2 gene expression signature are listed on the right.

[0025] FIG. **5**: Kaplan-Meier plot of survival in FL samples based on survival predictor scores. 191 FL samples were divided into quartiles based on their survival predictor scores. The survival predictor scores were calculated by: [(2.71*immune response-2 gene expression signature value)]−[(2.36× immune response-1 gene expression signature value)].

[0026] FIG. **6**: Kaplan-Meier plot of survival in FL samples based on IPI score. 96 FL samples were divided into three groups based on their IPI scores.

[0027] FIG. **7**: Kaplan-Meier plot of survival in FL samples with low or high risk IPI scores based on survival predictor scores. 96 FL samples with low risk (left panel) or intermediate risk (right panel) IPI scores were divided into quartiles based on their survival predictor scores. The survival predictor scores were calculated by: [(2.71*immune response-2 gene expression signature value)]−[(2.36 x immune response-1 gene expression signature value)].

[0028] FIG. **8**: Kaplan-Meier plot of survival in FL samples based on survival predictor scores. 191 FL samples were divided into quartiles based on their survival predictor scores. The survival predictor scores were calculated by: [2.053*(macrophage gene expression signature value)]−[2.344*(T-cell gene expression signature value)]−[0.729*(B-cell differentiation gene expression signature value)].

[0029] FIG. **9**: Kaplan-Meier plot of survival in FL samples based on survival predictor scores. 191 FL samples were divided into quartiles based on their survival predictor scores. The survival predictor scores were calculated by: [1.51*(macrophage gene expression signature value)]−[2.11*(T-cell gene expression signature value)]−[0.505*(B-cell differentiation gene expression signature value)].

[0030] FIG. **10**: Kaplan-Meier plot of survival in DLBCL samples based on survival predictor scores. 231 DLBCL samples were divided into quartiles based on their survival predictor scores. The survival predictor scores were calculated by: [0.586*(ABC DLBCL high gene expression signature value)]−[0.468*(lymph node gene expression signature value)]−[(0.336*MHC Class II gene expression signature value)].

[0031] FIG. **11**: Kaplan-Meier plot of survival in DLBCL samples based on survival predictor scores. 200 DLBCL samples were divided into quartiles based on their survival predictor scores. The survival predictor scores were calculated by: [−0.4337*(lymph node gene expression signature value)]+[0.09*(proliferation gene expression signature value)]−[0.4144*(germinal center B-cell gene expression signature value)]−[0.2006*(MHC class II gene expression signature value)].

[0032] FIG. **12**: Kaplan-Meier plot of survival in DLBCL samples based on survival predictor scores. 200 DLBCL samples were divided into quartiles based on their survival predictor scores. The survival predictor scores were calculated by: [−0.32*(lymph node gene expression signature value)]−[0.176*(germinal center B-cell gene expression signature value)]−[0.206*(MHC class II gene expression signature value)].

[0033] FIG. **13**: Kaplan-Meier plot of survival in MCL samples based on survival predictor scores. 21 MCL samples were divided into two equivalent groups based on their survival predictor scores. The survival predictor scores were calculated by: 1.66*(proliferation gene expression signature value).

[0034] FIG. **14**: Kaplan-Meier plot of survival in MCL samples based on survival predictor scores. 21 MCL samples were divided into two equivalent groups based on their survival predictor scores. The survival predictor scores were calculated by: 1.66*(proliferation gene expression signature value).

[0035] FIG. **15**: Predicting lymphoma type using Bayesian analysis. Bayes' rule can be used to determine the probability that an unknown sample belongs to a first lymphoma type rather than a second lymphoma type. A linear predictor score is generated for the sample, and the probability that the sample belongs to the first lymphoma type is determined based on the distribution of linear predictor scores within the first and second lymphoma type.

[0036] FIG. **16**: Performance of MCL predictor model. Results of the gene-expression based predictor model for MCL are shown for three models (MCL vs. ABC, MCL vs. GCB, MCL vs. SLL). Performance is shown for both the training set and the validation set.

[0037] FIG. **17**: Gene expression-based identification of DLBCL. Expression levels for 27 genes in a subgroup predictor are shown for 274 DLBCL samples. Expression levels are depicted according to the scale shown at the left. The 14 genes used to predict the DLBCL subgroups in the Affymetrix data set are indicated with asterisks. The probabilities that the DLBCL samples belong to the ABC or GCB subtypes are graphed at the top, and the DLBCL cases are arranged accordingly. Cases belonging to either ABC or GCB with 90% or greater probability are indicated.

[0038] FIG. **18**: Performance of DLBCL subtype predictor model. Assignments of DLBCL samples to the ABC or GCB

subtypes based on hierarchical clustering vs. the predictor model disclosed herein are compared within the training, validation, and total set of samples.

[0039] FIG. **19**: Relationship of gene expression in normal B cell subpopulations to DLBCL subtypes. Relative gene expression in the indicated purified B cell populations is depicted according to the scale in FIG. **17**. The P value of the difference in expression of these genes between the GCB and ABC DLBCL subtypes is shown, and the subtype with the higher expression is indicated. A. DLBCL subtype distinction genes that are more highly expressed in germinal center B cells than at other B cell differentiation stages. B. DLBCL subtype distinction genes that are more highly expressed in plasma cells than at other B cell differentiation stages.

[0040] FIG. **20**: Identification of a PMBL gene expression signature. A. Hierarchical clustering identified a set of 23 PMBL signature genes that were more highly expressed in most lymphomas with a clinical diagnosis of PMBL than in lymphomas assigned to the GCB or ABC subtypes. Each row presents gene expression measurements from a single Lymphochip microarray feature representing the genes indicated. Each column represents a single lymphoma biopsy sample. Relative gene expression is depicted according to the scale shown. B. Hierarchical clustering of the lymphoma biopsy samples based on expression of the PMBL signature genes identified in (A). A "core" cluster of lymphoma cases was identified that highly expressed the PMBL signature genes.

[0041] FIG. **21**: Development of a gene expression-based molecular diagnosis of PMBL. A. A PMBL predictor was created based on expression of the 46 genes shown. Relative gene expression for each lymphoma biopsy sample is presented according to the color scale shown in FIG. **20**. The probability that each sample is PMBL or DLBCL based on gene expression is shown at the top. B. The PMBL predictor was used to classify 274 lymphoma samples as PMBL or DLBCL. Prediction results are summarized on the right, and the relative gene expression for each case that was classified by the predictor as PMBL is shown on the left. Average expression of each gene in samples classified as DLBCL is also shown. The 20 genes listed are those represented on the Lymphochip that were more highly expressed in PMBL than in DLBCL. Not shown are eight genes from the PMBL predictor that were more highly expressed in DLBCL than in PMBL.

[0042] FIG. **22**: Clinical characteristics of PMBL patients. Kaplan-Meier plot of overall survival in PMBL, GCB, and ABC patients after chemotherapy.

[0043] FIG. **23**: Optimization of gene number in lymphoma predictor. The optimal number of genes for inclusion in the lymphoma type predictor model is that number which generates a maximum t-statistic when comparing the LPS of two samples from different lymphoma types.

[0044] FIG. **24**: LPS distribution among FL and DLBCL/BL samples. Standard and proliferation LPSs for FL (x) and DLBCL/BL (+) samples. Dotted lines indicate standard deviations from the fitted multivariate normal distributions.

[0045] FIG. **25**: Determination of cut-off points for lymphoma classification. The cut-off points between samples classified as DLBCL/BL, FL, or unclassified were optimized to minimize the number of samples classified as the wrong lymphoma type. The optimal lower cut-off point was at q=0.49, while the optimal upper cut-off point was at q=0.84.

[0046] FIG. **26**: Division of LPSs among FL and DLBCL/FL samples. Illustration of how the cut-off points described in FIG. **25** divided the space between the LPSs of FL (x) and DLBCL/BL (+) samples.

[0047] FIG. **27**: Lymphoma classification results. Results of lymphoma classification based on gene expression. 100% of SLL, MCL, and FH samples were classified correctly, and only 3% of DLBCL/BL and FL samples were classified incorrectly.

[0048] FIG. **28**: DLBCL subtype classification based on gene expression. None of the ABC samples were classified as the wrong subtype, while only one of the BL samples was classified incorrectly. Of the GCB and PMBL samples, only 5% and 6%, respectively, were classified incorrectly.

DETAILED DESCRIPTION

[0049] The following description is merely intended to illustrate various embodiments of the invention. As such, the specific modifications discussed are not to be construed as limitations on the scope of the invention. It will be apparent to one skilled in the art that various equivalents, changes, and modifications may be made without departing from the scope of the invention, and it is understood that such embodiments are to be included herein.

[0050] Gene expression profiling of a cancer cell or biopsy reflects the molecular phenotype of a cancer at the time of diagnosis. As a consequence, the detailed picture provided by the genomic expression pattern provides the basis for a new systematic classification of cancers and more accurate predictors of survival and response to treatment. The present invention discloses methods for identifying, diagnosing, and/or classifying a lymphoma, lymphoid malignancy, or lymphoproliferative disorder based on its gene expression patterns. The present invention also discloses methods for predicting survival in a subject diagnosed with a particular lymphoma type or subtype using gene expression data. The information obtained using these methods will be useful in evaluating the optimal therapeutic approach to be employed with regards to a particular subject.

[0051] The term "lymphoproliferative disorder" as used herein refers to any tumor of lymphocytes, and may refer to both malignant and benign tumors. The terms "lymphoma" and "lymphoid malignancy" as used herein refer specifically to malignant tumors derived from lymphocytes and lymphoblasts. Examples of lymphomas include, but are not limited to, follicular lymphoma (FL), Burkitt lymphoma (BL), mantle cell lymphoma (MCL), follicular hyperplasia (FH), small cell lymphocytic lymphoma (SLL), mucosa-associated lymphoid tissue lymphoma (MALT), splenic lymphoma, multiple myeloma, lymphoplasmacytic lymphoma, post-transplant lymphoproliferative disorder (PTLD), lymphoblastic lymphoma, nodal marginal zone lymphoma (NMZ), germinal center B cell-like diffuse large B cell lymphoma (GCB), activated B cell-like diffuse large B cell lymphoma (ABC) and primary mediastinal B cell lymphoma (PMBL).

[0052] The phrase "lymphoma type" (or simply "type") as used herein refers to a diagnostic classification of a lymphoma. The phrase may refer to a broad lymphoma class (e.g., DLBCL, FL, MCL, etc.) or to a subtype or subgroup falling within a broad lymphoma class (e.g., GCB DLBCL, ABC DLBCL).

[0053] The phrase "gene expression data" as used herein refers to information regarding the relative or absolute level of expression of a gene or set of genes in a cell or group of

cells. The level of expression of a gene may be determined based on the level of RNA, such as mRNA, encoded by the gene. Alternatively, the level of expression may be determined based on the level of a polypeptide or fragment thereof encoded by the gene. "Gene expression data" may be acquired for an individual cell, or for a group of cells such as a tumor or biopsy sample.

[0054] The term "microarray," "array," or "chip" refers to a plurality of nucleic acid probes coupled to the surface of a substrate in different known locations. The substrate is preferably solid. Microarrays have been generally described in the art in, for example, U.S. Pat. Nos. 5,143,854 (Pirrung), 5,424,186 (Fodor), 5,445,934 (Fodor), 5,677,195 (Winkler), 5,744,305 (Fodor), 5,800,992 (Fodor), 6,040,193 (Winkler), and Fodor et al. 1991. Light-directed, spatially addressable parallel chemical synthesis. Science, 251:767-777. Each of these references is incorporated by reference herein in their entirety.

[0055] The term "gene expression signature" or "signature" as used herein refers to a group of coordinately expressed genes. The genes making up this signature may be expressed in a specific cell lineage, stage of differentiation, or during a particular biological response. The genes can reflect biological aspects of the tumors in which they are expressed, such as the cell of origin of the cancer, the nature of the non-malignant cells in the biopsy, and the oncogenic mechanisms responsible for the cancer (Shaffer 2001). Examples of gene expression signatures include lymph node (Shaffer 2001), proliferation (Rosenwald 2002), MHC class II, ABC DLBCL high, B-cell differentiation, T-cell, macrophage, immune response-1, immune response-2, and germinal center B cell.

[0056] The phrase "survival predictor score" as used herein refers to a score generated by a multivariate model used to predict survival based on gene expression. A subject with a higher survival predictor score is predicted to have poorer survival than a subject with a lower survival predictor score.

[0057] The term "survival" as used herein may refer to the probability or likelihood of a subject surviving for a particular period of time. Alternatively, it may refer to the likely term of survival for a subject, such as expected mean or median survival time for a subject with a particular gene expression pattern.

[0058] The phrase "linear predictor score" or "LPS" as used herein refers to a score that denotes the probability that a sample belongs to a particular lymphoma type. An LPS may be calculated using an equation such as:

$$LPS(S) = \sum_{j \in G} t_j S_j,$$

where S_j is the expression of gene j from gene set G in a sample S, and t_j is a scale factor representing the difference in expression of gene j between a first lymphoma type and a second lymphoma type. Alternatively, a linear predictor score may be generated by other methods including but not limited to linear discriminant analysis (Dudoit 2002), support vector machines (Furey 2000), or shrunken centroids (Tibshirani 2002)

[0059] The phrase "scale factor" as used herein refers to a factor that defines the relative difference in expression of a particular gene between two samples. An example of a scale factor is a t-score generated by a Student's t-test.

[0060] The phrase "lymphoma subject," wherein "lymphoma" is a specific lymphoma type (e.g., "follicular lymphoma subject"), may refer to a subject that has been diagnosed with a particular lymphoma by any method known in the art or discussed herein. This phrase may also refer to a subject with a known or suspected predisposition or risk of developing a particular lymphoma type.

[0061] The pattern of expression of a particular gene is closely connected to the biological role and effect of its gene product. For this reason, the systematic study of variations in gene expression provides an alternative approach for linking specific genes with specific diseases and for recognizing heritable gene variations that are important for immune function. For example, allelic differences in the regulatory region of a gene may influence the expression levels of that gene. An appreciation for such quantitative traits in the immune system may help elucidate the genetics of autoimmune diseases and lymphoproliferative disorders.

[0062] Genes that encode components of the same multisubunit protein complex are often coordinately regulated. Coordinate regulation is also observed among genes whose products function in a common differentiation program or in the same physiological response pathway. Recent application of gene expression profiling to the immune system has shown that lymphocyte differentiation and activation are accompanied by parallel changes in expression among hundreds of genes. Gene expression databases may be used to interpret the pathological changes in gene expression that accompany autoimmunity, immune deficiencies, cancers of immune cells and of normal immune responses.

[0063] Scanning and interpreting large bodies of relative gene expression data is a formidable task. This task is greatly facilitated by algorithms designed to organize the data in a way that highlights systematic features, and by visualization tools that represent the differential expression of each gene as varying intensities and hues of color (Eisen 1998). The development of microarrays, which are capable of generating massive amounts of expression data in a single experiment, has greatly increased the need for faster and more efficient methods of analyzing large-scale expression data sets. In order to effectively utilize microarray gene expression data for the identification and diagnosis of lymphoma and for the prediction of survival in lymphoma patients, new algorithms must be developed to identify important information and convert it to a more manageable format. In addition, the microarrays used to generate this data should be streamlined to incorporate probe sets that are useful for diagnosis and survival prediction. Disclosed herein are various methods and compositions that address both of these issues.

[0064] Mathematical analysis of gene expression data is a rapidly evolving science based on a rich mathematics of pattern recognition developed in other contexts (Kohonen 1997). Mathematical analysis of gene expression generally has three goals. First, it may be used to identify groups of genes that are coordinately regulated within a biological system. Second, it may be used to recognize and interpret similarities between biological samples on the basis of similarities in gene expression patterns. Third, it may be used to recognize and identify those features of a gene expression pattern that are related to distinct biological processes or phenotypes.

[0065] Mathematical analysis of gene expression data often begins by establishing the expression pattern for each gene on

an array across n experimental samples. The expression pattern of each gene can be represented by a point in n-dimensional space, with each coordinate specified by an expression measurement in one of the n samples (Eisen 1998). A clustering algorithm that uses distance metrics can then be applied to locate clusters of genes in this n-dimensional space. These clusters indicate genes with similar patterns of variation in expression over a series of experiments. Clustering methods that have been applied to microarray data in the past include hierarchical clustering (Eisen 1998), self-organizing maps (SOMs) (Tamayo 1999), k-means (Tavazoie 1999), and deterministic annealing (Alon 1999). A variety of different algorithms, each emphasizing distinct orderly features of the data, may be required to glean the maximal biological insight from a set of samples (Alizadeh 1998). One such algorithm, hierarchical clustering, begins by determining the gene expression correlation coefficients for each pair of the n genes studied. Genes with similar gene expression correlation coefficients are grouped next to one another in a hierarchical fashion. Generally, genes with similar expression patterns under a particular set of conditions encode protein products that play related roles in the physiological adaptation to those conditions. Novel genes of unknown function that are clustered with a large group of functionally related genes are likely to participate in the same biological process. Likewise, the other clustering methods mentioned herein may also group genes together that encode proteins with related biological function.

[0066] Gene expression maps may be constructed by organizing gene expression data from multiple samples using any of the various clustering algorithms outlined herein. The ordered tables of data may then be displayed graphically in a way that allows researchers and clinicians to assimilate both the choreography of gene expression on a broad scale and the fine distinctions in expression of individual genes.

[0067] In such a gene expression map, genes that are clustered together reflect a particular biological function, and are termed gene expression signatures (Shaffer 2001). One general type of gene expression signature includes genes that are characteristically expressed in a particular cell type or at a particular stage of cellular differentiation or activation. Another general type of gene expression signature includes genes that are regulated in their expression by a particular biological process such as proliferation, or by the activity of a particular transcription factor or signaling pathway.

[0068] The pattern of gene expression in a biological sample provides a distinctive and accessible molecular picture of its functional state and identity (DeRisi 1997; Cho 1998; Chu 1998; Holstege 1998; Spellman 1998). Each cell transduces variations in its environment, internal state, and developmental state into readily measured and recognizable variations in its gene expression patterns. Two different samples that have related gene expression patterns are therefore likely to be biologically and functionally similar to one another. Some biological processes are reflected by the expression of genes in a specific gene expression signature, as described above. The expression of a specific gene expression signature in a sample can provide important biological insights into its cellular composition and the function of various intracellular pathways within those cells.

[0069] The present invention discloses a variety of gene expression signatures related to the clinical outcome of lymphoma patients. While several of these signatures share a name with a previously disclosed signature, each of the gene expression signatures disclosed herein comprises a novel combination of genes. For example, the lymph node signature disclosed herein includes genes encoding extracellular matrix components and genes that are characteristically expressed in macrophage, NK, and T cells (e.g., α-Actinin, collagen type III α 1, connective tissue growth factor, fibronectin, KIAA0233, urokinase plasminogen activator). The proliferation signature includes genes that are characteristically expressed by cells that are rapidly multiplying or proliferating (e.g., c-myc, E21G3, NPM3, BMP6). The MHC class II signature includes genes that interact with lymphocytes in order to allow the recognition of foreign antigens (e.g., HLA-DPα, HLA-DQα, HLA-DRα, HLA-DRβ). The immune response-1 signature includes genes encoding T cell markers (e.g., CD7, CD8B1, ITK, LEF1, STAT4), as well as genes that are highly expressed in macrophages (e.g., ACTN1, TNFSF13B). The immune response-2 signature includes genes known to be preferentially expressed in macrophages and/or dendritic cells (e.g., TLR5, FCGR1A, SEPT10, LGMN, C3AR1). The germinal center B cell signature includes genes known to be overexpressed at this stage of B cell differentiation (e.g., MME, MEF2C, BCL6, LMO2, PRSPAP2, MBD4, EBF, MYBL1).

[0070] Databases of gene expression signatures have proven quite useful in elucidating the complex gene expression patterns of various cancers. For example, expression of genes from the germinal center B-cell signature in a lymphoma biopsy suggests that the lymphoma is derived from this stage of B cell differentiation. In the same lymphoma biopsy, the expression of genes from the T cell signature can be used to estimate the degree of infiltration of the tumor by host T cells, while the expression of genes from the proliferation signature can be used to quantitate the tumor cell proliferation rate. In this manner, gene expression signatures provide an "executive summary" of the biological properties of a tumor specimen. Gene expression signatures can also be helpful in interpreting the results of a supervised analysis of gene expression data. Supervised analysis generates a long list of genes with expression patterns that are correlated with survival. Gene expression signatures can be useful in assigning these "predictive" genes to functional categories. In building a multivariate model of survival based on gene expression data, this functional categorization helps to limit the inclusion of multiple genes in the model that measure the same aspect of tumor biology.

[0071] Gene expression profiles can be used to create multivariate models for predicting survival. The methods for creating these models are called "supervised" because they use clinical data to guide the selection of genes to be used in the prognostic classification. For example, a supervised method might identify genes with expression patterns that correlate with the length of overall survival following chemotherapy. The general method used to create a multivariate model for predicting survival may utilize the following steps:

[0072] 1. Identify genes with expression patterns that are univariately associated with a particular clinical outcome using a Cox proportional hazards model. Generally, a univariate p-value of <0.01 is considered the cut-off for significance. These genes are termed "predictor" genes.

[0073] 2. Within a set of predictor genes, identify gene expression signatures.

[0074] 3. For each gene expression signature that is significantly associated with survival, average the expres-

sion of the component genes within this signature to generate a gene expression signature value.

[0075] 4. Build a multivariate Cox model of clinical outcome using the gene expression signature values.

[0076] 5. If possible, include additional genes in the model that do not belong to a gene expression signature but which add to the statistical power of the model.

This approach has been utilized in the present invention to create novel survival prediction models for FL, DLBCL, and MCL. Each of these models generates a survival predictor score, with a higher score being associated with worse clinical outcome. Each of these models may be used separately to predict survival. Alternatively, these models may be used in conjunction with one or more other models, disclosed herein or in other references, to predict survival.

[0077] A first FL survival predictor was generated using gene expression data obtained using Affymetrix U133A and U133B microarrays. This predictor incorporated immune response-1 and immune response-2 gene expression signatures. Fitting the Cox proportional hazards model to the gene expression signature values obtained from these signatures resulted in the following model:

> Survival predictor score=[(2.71*immune response-2 gene expression signature value)]−[(2.36×immune response-1 gene expression signature value)].

[0078] A second FL survival predictor was generated using gene expression data obtained using Affymetrix U133A and U133B microarrays. This predictor incorporated macrophage, T-cell, and B-cell differentiation gene expression signatures. Fitting the Cox proportional hazards model to the gene expression signature values obtained from these signatures resulted in the following model:

> Survival predictor score=[2.053*(macrophage gene expression signature value)]−[2.344*(*T*-cell gene expression signature value)]−[0.729*(*B*-cell differentiation gene expression signature value)].

[0079] A third FL survival predictor was generated using gene expression data obtained using the Lymph Dx microarray. This predictor incorporated macrophage, T-cell, and B-cell differentiation gene expression signatures. Fitting the Cox proportional hazards model to the gene expression signature values obtained from these signatures resulted in the following model:

> Survival predictor score=[1.51*(macrophage gene expression signature value)]−[2.11*(*T*-cell gene expression signature value)]−[0.505*(*B*-cell differentiation gene expression signature value)].

[0080] A first DLBCL survival predictor was generated using gene expression data obtained using Affymetrix U133A and U133B microarrays. This predictor incorporated ABC DLBCL high, lymph node, and MHC class II gene expression signatures. Fitting the Cox proportional hazards model to the gene expression signature values obtained from these signatures resulted in the following model:

> Survival predictor score=[0.586*(ABC DLBCL high gene expression signature value)]−[0.468*(lymph node gene expression signature value)]−0.336*(MHC class II gene expression signature value)].

[0081] A second DLBCL survival predictor was generated using gene expression data obtained using the Lymph Dx microarray. This predictor incorporated lymph node, proliferation, germinal center B-cell, and MHC class II gene expression signatures. Fitting the Cox proportional hazards model to the gene expression signature values obtained from these signatures resulted in the following model:

> Survival predictor score=[−0.4337*(lymph node gene expression signature value)]+[0.09*(proliferation gene expression signature value)]−[0.4144*(germinal center *B*-cell gene expression signature value)]−[0.2006*(MHC class II gene expression signature value)].

[0082] A third DLBCL survival predictor was generated using gene expression data obtained using the Lymph Dx microarray. This predictor incorporated lymph node, germinal center B cell, and MHC class II gene expression signatures. Fitting the Cox proportional hazards model to the gene expression signature values obtained from these signatures resulted in the following model:

> Survival predictor score=[−0.32*(lymph node gene expression signature value)]−[0.176*(germinal center *B*-cell gene expression signature value)]−[0.206*(MHC class II gene expression signature value)].

[0083] An MCL survival predictor was generated using gene expression data obtained using Affymetrix U133A, Affymetrix U133B, and Lymph Dx microarrays. This predictor incorporated a proliferation gene expression signature. Fitting the Cox proportional hazards model to the gene expression signature values obtained from these signatures resulted in the following model:

> Survival predictor score=[1.66*(proliferation gene expression signature value)].

[0084] Gene expression data can also be used to diagnose and identify lymphoma types. In an embodiment of the present invention, a statistical method based on Bayesian analysis was developed to classify lymphoma specimens according to their gene expression profiles. This method does not merely assign a tumor to a particular lymphoma type, but also determines the probability that the tumor belongs to that lymphoma type. Many different methods have been formulated to predict cancer subgroups (Golub 1999; Ramaswamy 2001; Dudoit 2002; Radmacher 2002). These methods assign tumors to one of two subgroups based on expression of a set of differentially expressed genes. However, they do not provide a probability of membership in a subgroup. By contrast, the method disclosed herein used Bayes' rule to estimate this probability, thus allowing one to vary the probability cut-off for assignment of a tumor to a particular subgroup. In tumor types in which unknown additional subgroups may exist, the present method allows samples that do not meet the gene expression criteria of known subgroups to fall into an unclassified group with intermediate probability. A cancer subgroup predictor of the type described herein may be used clinically to provide quantitative diagnostic information for an individual cancer patient. This information can in turn be used to provide a predictor of treatment outcome for a particular cancer patient.

[0085] For any two lymphoma types A and B, there is a set of genes with significantly higher expression in type A than type B, and a set of genes with significantly lower expression in type A than in type B. By observing the expression of these genes in an unknown sample, it is possible to determine to which of the two types the sample belongs. Evaluating the likelihood that a particular sample belongs to one or the other lymphoma type by Bayesian analysis may be done using the following steps:

[0086] 1. Identify those genes that are most differentially expressed between the two lymphoma types. This can be

done by selecting those genes with the largest t-statistic between the two lymphoma types. The genes in this step may be subdivided into gene expression signatures in certain cases, with genes from each signature analyzed separately.

[0087] 2. Create a series of linear predictor score (LPS) for samples belonging to either lymphoma type.

[0088] 3. Evaluate the LPS for each sample in a training set, and estimate the distribution of these scores within each lymphoma type according to a normal distribution.

[0089] 4. Use Bayes' rule to evaluate the probability that each subsequent sample belongs to one or the other lymphoma type.

If only two types of lymphoma are being distinguished, then a single probability score is sufficient to discriminate between the two types. However, if more than two lymphoma types are being distinguished, multiple scores will be needed to highlight specific differences between the types.

[0090] A novel microarray termed the Lymph Dx microarray is disclosed herein for the identification and diagnosis of various lymphoma types. The Lymph Dx microarray contains cDNA probes corresponding to approximately 2,653 genes, fewer than the number seen on microarrays that have been used previously for lymphoma diagnosis. The reduced number of probes on the Lymph Dx microarray is the result of eliminating genes that are less useful for the identification of lymphoma types and predicting clinical outcome. This reduction allows for simplified analysis of gene expression data. The genes represented on the Lymph Dx microarray can be divided into four broad categories: 1,101 lymphoma predictor genes identified previously using the Affymetrix U133 microarray, 171 outcome predictor genes, 167 new genes not found on the Affymetrix U133 microarray, and 1,121 named genes. A list of the probe sets on the Lymph Dx microarray is presented in Table 2, contained in the file "Table_0002_LymphDx_Probe_List.txt."

[0091] Gene expression data obtained using the Lymph Dx microarray may be used to identify and classify lymphomas using Bayesian analysis using a strategy similar to that set forth above. In certain embodiments, this strategy may include additional steps designed to optimize the number of genes used and the cut-off points between lymphoma types. A general overview of such a method is presented in FIG. **1**. In one example of the method, each gene represented on the Lymph Dx microarray was placed into one of three gene-list categories based on its correlation with the lymph node or proliferation gene expression signatures: lymph node, proliferation, or standard. These signatures were identified by clustering of the DLBCL cases using hierarchical clustering and centroid-correlation of 0.35. Standard genes were those with expression patterns that did not correlate highly with expression of the lymph node or proliferation signatures. Lymph Dx gene expression data was first used to identify samples as FL, MCL, SLL, FH, or DLBCL/BL, then to identify DLBCL/BL samples as ABC, GCB, PMBL, or BL. For each stage, a series of pair-wise models was created, with each model containing a different pair of lymphoma types (e.g., FL vs. MCL, SLL vs. FH, etc.). For each pair, the difference in expression of each gene on the microarray was measured, and a t-statistic was generated representing this difference. Genes from each gene-list category were ordered based on their t-statistic, and those with the largest t-statistics were used to generate a series of LPSs for samples belonging to either lymphoma type. The number of genes used to generate the LPSs was optimized by repeating the calculation using between five and 100 genes from each gene-list category. The number of genes from each category used in the final LPS calculation was that which gave rise to the largest difference in LPS between the two lymphoma types. Once the number of genes in each gene-list category was optimized, four different LPSs were calculated for each sample. The first included genes from the standard gene-list category only, the second included genes from the proliferation and standard gene-list categories, the third included genes from the lymph node and standard gene-list categories, and the fourth included genes from all three categories. The probability q that a sample X belongs to the first lymphoma type of a pair-wise model can then be calculated using an equation:

$$q = \frac{\phi(LPS(X);\hat{\mu}_1,\hat{\sigma}_1)}{\phi(LPS(X);\hat{\mu}_1,\hat{\sigma}_1)+\phi(LPS(X);\hat{\mu}_2,\hat{\sigma}_2)}$$

LPS(X) is the LPS for sample X, $\phi(x;\mu,\sigma)$ is the normal density function with mean μ and standard deviation σ, and $\hat{\mu}_1$ and $\hat{\sigma}_1$ are the mean and variance of the LPSs for samples belonging to the first lymphoma type, and, $\hat{\mu}_2$ and $\hat{\sigma}_2$ are the mean and variance of the LPSs for samples belonging to the second lymphoma type. Samples with high q values were classified as the first lymphoma type, samples with low q values were classified as the second lymphoma type, and samples with middle range q values were deemed unclassified. To determine the proper cut-off point between high, low, and middle q values, every possible cut-off point between adjacent samples was analyzed by an equation:

> 3.99*[(% of type 1 misidentified as type 2)+(% of type 2 misidentified as type 1)]+[(% of type 1 unclassified)+(% of type 2 misidentified)].

This equation was used to favor the assignment of a sample to an "unclassified" category rather than to an incorrect lymphoma type. The final cut-off points were those which minimized this equation. The coefficient of 3.99 was chosen arbitrarily to allow an additional classification error only if the adjustment resulted in four or more unclassified samples becoming correctly classified. The coefficient can be varied to achieve a different set of trade-offs between the number of unclassified and misidentified samples.

[0092] To ensure that the accuracy of the model was not a result of overfitting, each model was validated by leave-one-out cross-validation. This entailed removing each sample of known lymphoma type from the data one at a time, and then determining whether the model could predict the missing sample. This process confirmed the accuracy of the prediction method.

[0093] The classification of a lymphoproliferative disorder in accordance with embodiments of the present invention may be used in combination with any other effective classification feature or set of features. For example, a disorder may be classified by a method of the present invention in conjunction with WHO suggested guidelines, morphological properties, histochemical properties, chromosomal structure, genetic mutation, cellular proliferation rates, immunoreactivity, clinical presentation, and/or response to chemical, biological, or other agents. Embodiments of the present invention may be used in lieu of or in conjunction with other

methods for lymphoma diagnosis, such as immunohistochemistry, flow cytometry, FISH for translocations, or viral diagnostics.

[0094] Accurate determination of lymphoma type in a subject allows for better selection and application of therapeutic methods. Knowledge about the exact lymphoma affecting a subject allows a clinician to select therapies or treatments that are most appropriate and useful for that subject, while avoiding therapies that are nonproductive or even counterproductive. For example, CNS prophylaxis may be useful for treating BL but not DLBCL, CHOP treatment may be useful for treating DLBCL but not blastic MCL (Fisher 1993; Khouri 1998), and subjects with follicular lymphoma frequently receive treatment while subjects with follicular hyperplasia do not. In each of these situations, the lymphoma types or subtypes in question can be difficult to distinguish using prior art diagnostic methods. The diagnostic and identification methods of the present invention allow for more precise delineation between these lymphomas, which simplifies the decision of whether to pursue a particular therapeutic option. Likewise, the survival prediction methods disclosed in the present invention also allow for better selection of therapeutic options. A subject with a very low survival predictor score (i.e., very good prognosis) may not receive treatment, but may instead be subjected to periodic check-ups and diligent observation. As survival predictor scores increase (i.e., prognosis gets worse), subjects may receive more intensive treatments. Those subjects with the highest survival predictor scores (i.e., very poor prognosis) may receive experimental treatments or treatments with novel agents. Accurate survival prediction using the methods disclosed herein provides an improved tool for selecting treatment options and for predicting the likely clinical outcome of those options.

[0095] Any effective method of quantifying the expression of at least one gene, gene set, or group of gene sets may be used to acquire gene expression data for use in embodiments of the present invention. For example, gene expression data may be measured or estimated using one or more microarrays. The microarrays may be of any effective type, including but not limited to nucleic acid based or antibody based. Gene expression may also be measured by a variety of other techniques, including but not limited to PCR, quantitative RT-PCR, real-time PCR, RNA amplification, in situ hybridization, immunohistochemistry, immunocytochemistry, FACS, serial analysis of gene expression (SAGE) (Velculescu 1995), Northern blot hybridization, or western blot hybridization.

[0096] Nucleic acid microarrays generally comprise nucleic acid probes derived from individual genes and placed in an ordered array on a support. This support may be, for example, a glass slide, a nylon membrane, or a silicon wafer. Gene expression patterns in a sample are obtained by hybridizing the microarray with the gene expression product from the sample. This gene expression product may be, for example, total cellular mRNA, rRNA, or cDNA obtained by reverse transcription of total cellular mRNA. The gene expression product from a sample is labeled with a radioactive, fluorescent, or other label to allow for detection. Following hybridization, the microarray is washed, and hybridization of gene expression product to each nucleic acid probe on the microarray is detected and quantified using a detection device such as a phosphorimager or scanning confocal microscope.

[0097] There are two broad classes of microarrays: cDNA and oligonucleotide arrays. cDNA arrays consist of hundreds or thousands of cDNA probes immobilized on a solid support. These cDNA probes are usually 100 nucleotides or greater in size. There are two commonly used designs for cDNA arrays. The first is the nitrocellulose filter array, which is generally prepared by robotic spotting of purified DNA fragments or lysates of bacteria containing cDNA clones onto a nitrocellulose filter (Southern 1992; Southern 1994; Gress 1996; Pietu 1996). The other commonly used cDNA arrays is fabricated by robotic spotting of PCR fragments from cDNA clones onto glass microscope slides (Schena 1995; DeRisi 1996; Schena 1996; Shalon 1996; DeRisi 1997; Heller 1997; Lashkari 1997). These cDNA microarrays are simultaneously hybridized with two fluorescent cDNA probes, each labeled with a different fluorescent dye (typically Cy3 or Cy5). In this format, the relative mRNA expression in two samples is directly compared for each gene on the microarray. Oligonucleotide arrays differ from cDNA arrays in that the probes are 20- to 25-mer oligonucleotides. Oligonucleotide arrays are generally produced by in situ oligonucleotide synthesis in conjunction with photolithographic masking techniques (Pease 1994; Lipshutz 1995; Chee 1996; Lockhart 1996; Wodicka 1997). The solid support for oligonucleotide arrays is typically a glass or silicon surface.

[0098] Methods and techniques applicable to array synthesis and use have been described in, for example, U.S. Pat. Nos. 5,143,854 (Pirrung), 5,242,974 (Holmes), 5,252,743 (Barrett), 5,324,633 (Fodor), 5,384,261 (Winkler), 5,424,186 (Fodor), 5,445,934 (Fodor), 5,451,683 (Barrett), 5,482,867 (Barrett), 5,491,074 (Aldwin), 5,527,681 (Holmes), 5,550,215 (Holmes), 5,571,639 (Hubbell), 5,578,832 (Trulson), 5,593,839 (Hubbell), 5,599,695 (Pease), 5,624,711 (Sundberg), 5,631,734 (Stern), 5,795,716 (Chee), 5,831,070 (Pease), 5,837,832 (Chee), 5,856,101 (Hubbell), 5,858,659 (Sapolsky), 5,936,324 (Montagu), 5,968,740 (Fodor), 5,974,164 (Chee), 5,981,185 (Matson), 5,981,956 (Stern), 6,025,601 (Trulson), 6,033,860 (Lockhart), 6,040,193 (Winkler), 6,090,555 (Fiekowsky), and 6,410,229 (Lockhart), and U.S. Patent Application Publication No. 20030104411 (Fodor). Each of the above patents and applications is incorporated by reference herein in its entirety.

[0099] Microarrays may generally be produced using a variety of techniques, such as mechanical or light directed synthesis methods that incorporate a combination of photolithographic methods and solid phase synthesis methods. Techniques for the synthesis of microarrays using mechanical synthesis methods are described in, for example, U.S. Pat. Nos. 5,384,261 (Winkler) and 6,040,193 (Winkler). Although a planar array surface is preferred, the microarray may be fabricated on a surface of virtually any shape, or even on a multiplicity of surfaces. Microarrays may be nucleic acids on beads, gels, polymeric surfaces, fibers such as fiber optics, glass or any other appropriate substrate. See, for example, U.S. Pat. Nos. 5,708,153 (Dower); 5,770,358 (Dower); 5,789,162 (Dower); 5,800,992 (Fodor); and 6,040,193 (Winkler), each of which is incorporated by reference herein in its entirety.

[0100] Microarrays may be packaged in such a manner as to allow for diagnostic use, or they can be an all-inclusive device. See, for example, U.S. Pat. Nos. 5,856,174 (Lipshutz) and 5,922,591 (Anderson), both of which are incorporated by reference herein in their entirety.

[0101] Microarrays directed to a variety of purposes are commercially available from Affymetrix (Affymetrix, Santa Clara, Calif.). For instance, these microarrays may be used for

genotyping and gene expression monitoring for a variety of eukaryotic and prokaryotic species.

[0102] The following examples are provided to better illustrate the claimed invention and are not to be interpreted as limiting the scope of the invention. To the extent that specific materials are mentioned, it is merely for purposes of illustration and is not intended to limit the invention. One skilled in the art may develop equivalent means or reactants without the exercise of inventive capacity and without departing from the scope of the invention. It will be understood that many variations can be made in the procedures herein described while still remaining within the bounds of the present invention. It is the intention of the inventors that such variations are included within the scope of the invention.

EXAMPLES

Example 1

Collection and Analysis of Gene Expression Data Using Affymetrix U133A and U133B Microarrays

[0103] 568 cell samples representing various forms of human lymphoid malignancies were obtained by biopsy using known methods described in the literature. The samples were reviewed by a panel of hematopathologists and classified into the following lymphoma types based on current diagnostic criteria:

[0104] 231 diffuse large B cell lymphomas (DLBCL)

[0105] 191 follicular lymphomas (FL)

[0106] 26 Burkitt lymphomas (BL)

[0107] 21 mantle cell lymphoma (MCL)

[0108] 18 follicular hyperplasias (FH)

[0109] 17 small cell lymphocytic lymphomas (SLL)

[0110] 16 mucosa-associated lymphoid tissue lymphomas (MALT)

[0111] 13 splenic lymphomas (Splenic)

[0112] 10 cyclin-D1 negative lymphomas with MCL morphology (CD1negMCL)

[0113] 9 multiple myeloma (Mult_Myeloma)

[0114] 6 lymphoplasmacytic lymphomas (LPC)

[0115] 4 post-transplant lymphoproliferative disorders (PTLD)

[0116] 3 lymphoblastic lymphomas (Lymbl)

[0117] 3 nodal marginal zone lymphomas (NMZ)

The 231 DLBCL samples were subdivided into the following lymphoma types based on gene expression (see below):

[0118] 88 germinal center B cell-like (GCB)

[0119] 78 activated B cell-like (ABC)

[0120] 33 primary mediastinal B cell lymphoma (PMBL)

[0121] 32 samples for which the subtype could not be determined (UC_DLBCL)

The 16 MALT samples were subdivided into the following four group based on tumor origin:

[0122] 9 from the gastric region (MALT_gastric)

[0123] 1 from the salivary gland (MALT_salivary)

[0124] 1 from the lung (MALT_lung)

[0125] 1 from the tonsil (MALT_tonsil)

[0126] 4 of unknown origin (MALT_unk)

[0127] Each of the 568 cell samples was given a unique sample ID number consisting of the lymphoma type followed by a unique numerical identifier. For example, "ABC_304" refers to an ABC DLBCL sample numbered 304. Cells were purified and RNA was isolated from the purified cells according to known methods described in the literature.

[0128] Aliquots of RNA from each sample were applied to Affymetrix U133A and Affymetrix U133B microarrays according to standard Affymetrix protocol. The U133A and U133B microarrays are divided into probe sets, with each probe set consisting of up to 69 oligonucleotide probes 25 nucleotides in length. Each probe set represents a distinct human gene. Information pertaining to these microarrays is available at the Affymetrix company web site. Each microarray was scanned using an Affymetrix scanner, which records signal intensity for every probe on the microarray. This information can be transformed into summary signal values for each probe set using a number of different algorithms, including MAS 5.0, D-chip (Li 2001), or Bioconductor's RMA algorithms (Irizarry 2003). The images produced by the scanner were evaluated by Affymetrix MAS 5.0 software and stored as tables in .txt format. Since each sample was scanned on both microarrays, there are two .txt files for each sample. Each .txt file was given a unique name consisting of the table number, sample ID number (discussed above), and a letter denoting the microarray used. For example, Table_0588_ABC_304A.txt is the .txt file for Table 588, which contains data for sample ID number ABC_304 from the U133A array. The data for each sample tested is contained in Tables 3-1138.

[0129] The signal value for each probe on the U133A and U133B microarrays was normalized to a target value of 500, and the base-2 log of the normalized values was used for the following analyses. Log-signal values for each probe set are presented in Tables 1139-1706, contained in files with the title format "Table_No._NAME_log_signal.txt," where NAME refers to the sample ID number (e.g., ABC_304). The first column provides the UNIQID for the probe set, while the second column provides the log-signal value.

[0130] Log-signal files were statistically analyzed using S+ software and the S+ subtype predictor script contained in the file entitled "Subtype_Predictor.txt," located in the computer program listing appendix contained on CD number 22 of 22. Although the log-signal values were analyzed using S+ software and the above algorithm, any effective software/algorithm combination may be used. Tables 1707-1721 provide descriptive statistical characteristics for each of the lymphoma types tested except for CD1 negMCL, non-gastric MALT, and UC_DLBCL. Table 1722 provides statistical characteristics for all MALT samples combined, while Table 1723 does likewise for all DLBCL samples.

[0131] The files containing Tables 1707-1723 have the title format "Table_No._TYPE_Stats.txt," where TYPE refers to the lymphoma type. Each row of these tables represents a particular probe set. The first column of each table provides the UNIQID for the probe set, while the second column provides the average log-signal for the probe set over all samples of a particular lymphoma type. The third column provides the log-fold change in expression of the probe set between the lymphoma type in question and a second lymphoma type. For example, if logfold.ABC.vs.GCB is −0.21 for gene X, expression of gene X in the ABC samples is, on average, 0.86 (i.e., $2^{-0.21}$) times greater than expression of gene X in the GCB samples. The fourth column provides a two-sided P-value derived from a t-test of the log signals of the two lymphoma types compared in column three. If, for example, P.value.ABC.vs.GCB was 0.00001 for gene X, this would indicate that the observed difference in expression of gene X between ABC and GCB would only occur approximately one time in 100,000 if there was no actual difference in gene X expression between the two lymphoma types. The

remainder of the columns can be read as pairs that repeat the pattern of columns three and four, presenting the log-fold change and P-value of the difference in expression of the probe set for the lymphoma type in question versus all other lymphoma types being tested. Tables 1710, 1715, and 1723 (corresponding to FL, MCL, and DLBCL, respectively) contain two additional columns entitled "TYPE_Cox_coefficient" and "TYPE_Cox_P_value." The content of these columns is discussed in the following examples.

Example 2

Collection of Gene Expression Data Using the Novel Lymph Dx Microarray

[0132] The novel Lymph Dx microarray contains cDNA probes corresponding to approximately 2,734 genes. 174 of these are "housekeeping" genes present for quality control, since they represent genes that are most variably expressed across all lymphoma samples. Other genes represented on the microarray were selected for their utility in identifying particular lymphoma samples and predicting survival in those samples. The genes represented on the Lymph Dx microarray can be divided into four broad categories: 1,101 lymphoma predictor genes identified previously using the Affymetrix U133 microarray, 171 outcome predictor genes identified using the Affymetrix 0133 microarray, 167 genes not found on the Affymetrix U133 microarray but represented on the Lymphochip microarray (Alizadeh 1999), and 1,121 named genes. The types of genes making up each of these broad categories are summarized in Table 1724, below, while the specific genes represented on the Lymph Dx microarray are listed in Table 2 and contained in the file "Table_0002_Lymph Dx_Probe_List.txt."

TABLE 2

UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1119003	200004_at	183684	EIF4G2
1119007	200009_at	56845	GDI2
1119015	200024_at	378103	RPS5
1130426	200039_s_at	432607	PSMB2
1130429	200048_s_at	6396	JTB
1130430	200052_s_at	75117	ILF2
1130433	200058_s_at	246112	U5-200KD
1130446	200076_s_at	369785	MGC2749
1130447	200077_s_at	446427	OAZ1
1119039	200084_at	447513	SMAP
1130465	200098_s_at	7101	ANAPC5
1130468	200594_x_at	166463	HNRPU
1130472	200599_s_at	192374	TRA1
1119046	200606_at	349499	DSP
1130482	200616_s_at	181418	KIAA0152
1130483	200622_x_at	334330	CALM3
1119056	200633_at	356190	UBB
1119061	200644_at	75061	MLP
1130501	200650_s_at	2795	LDHA
1119068	200660_at	417004	S100A11
1119070	200663_at	445570	CD63
1130509	200665_s_at	111779	SPARC
1119071	200667_at	411826	UBE2D3
1119072	200670_at	437638	XBP1
1119074	200675_at	54457	CD81
1130518	200679_x_at	434102	HMGB1
1119076	200681_at	268849	GLO1
1130527	200692_s_at	184233	HSPA9B
1130533	200706_s_at	76507	LITAF
1119090	200709_at	374638	FKBP1A
1130588	200775_s_at	307544	HNRPK
1130603	200797_s_at	86386	MCL1
1119111	200804_at	35052	TEGT
1130618	200822_x_at	83848	GRCC9
1130622	200829_x_at	97128	ZNF207
1130624	200832_s_at	119597	SCD
1130629	200839_s_at	135226	CTSB
1130631	200842_s_at	171292	EPRS
1130645	200860_s_at	279949	KIAA1007
1130653	200875_s_at	376064	NOL5A
1119139	200880_at	388392	DNAJA1
1130658	200886_s_at	447492	PGAM1
1130668	200897_s_at	194431	KIAA0992
1130674	200905_x_at	381008	HLA-E
1130676	200907_s_at	194431	KIAA0992
1130680	200912_s_at	511904	EIF4A2
1130687	200924_s_at	79748	SLC3A2
1119155	200934_at	110713	DEK
1130704	200951_s_at	376071	CCND2
1130707	200956_s_at	79162	SSRP1
1130712	200965_s_at	442540	ABLIM1

TABLE 2-continued

UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1119171	200974_at	208641	ACTA2
1119173	200978_at	75375	MDH1
1119183	200997_at	211203	RBM4
1130732	201002_s_at	381025	UBE2V1
1119186	201005_at	387579	CD9
1130735	201009_s_at	179526	TXNIP
1130744	201027_s_at	158688	EIF5B
1130746	201029_s_at	283477	CD99
1130747	201030_x_at	234489	LDHB
1119202	201042_at	512708	TGM2
1130755	201043_s_at	356089	ANP32A
1119209	201063_at	167791	RCN1
1130771	201068_s_at	61153	PSMC2
1119212	201069_at	367877	MMP2
1130799	201114_x_at	233952	PSMA7
1130812	201131_s_at	194657	CDH1
1119237	201141_at	389964	GPNMB
1130820	201144_s_at	151777	EIF2S1
1119239	201145_at	199625	HAX1
1130835	201163_s_at	435795	IGFBP7
1130839	201167_x_at	159161	ARHGDIA
1119243	201171_at	440165	ATP6V0E
1119245	201178_at	5912	FBXO7
1130852	201184_s_at	74441	CHD4
1130855	201189_s_at	77515	ITPR3
1119251	201194_at	433941	SEPW1
1119258	201209_at	88556	HDAC1
1119260	201212_at	18069	LGMN
1119263	201216_at	511762	C12orf8
1130871	201222_s_at	159087	RAD23B
1130879	201231_s_at	433455	ENO1
1119268	201234_at	6196	ILK
1130882	201236_s_at	75462	BTG2
1130888	201244_s_at	257266	RAF1
1130898	201260_s_at	80919	SYPL
1130900	201262_s_at	821	BGN
1130906	201277_s_at	81361	HNRPAB
1130910	201284_s_at	221589	APEH
1130911	201287_s_at	82109	SDC1
1119294	201292_at	156346	TOP2A
1130914	201294_s_at	315379	WSB1
1130922	201305_x_at	459987	ANP32B
1130923	201306_s_at	459987	ANP32B
1130926	201310_s_at	508741	C5orf13
1119300	201314_at	155206	STK25
1130936	201331_s_at	437475	STAT6
1130942	201338_x_at	445977	GTF3A
1119311	201341_at	104925	ENC1
1119317	201349_at	396783	SLC9A3R1
1119325	201365_at	74563	OAZ2
1119334	201389_at	149609	ITGA5
1130972	201393_s_at	76473	IGF2R
1130977	201401_s_at	83636	ADRBK1
1119350	201425_at	331141	ALDH2
1130994	201431_s_at	150358	DPYSL3
1119361	201448_at	391858	TIA1
1119365	201460_at	75074	MAPKAPK2
1131012	201464_x_at	78465	JUN
1119369	201473_at	25292	JUNB
1131019	201474_s_at	265829	ITGA3
1119375	201489_at	381072	PPIF
1131038	201502_s_at	81328	NFKBIA
1119383	201508_at	1516	IGFBP4
1119390	201518_at	77254	CBX1
1119400	201536_at	181046	DUSP3
1119401	201540_at	421383	FHL1
1131068	201564_s_at	118400	FSCN1
1131069	201565_s_at	180919	ID2
1131074	201572_x_at	76894	DCTD
1119417	201579_at	166994	FAT
1131081	201586_s_at	180610	SFPQ
1131082	201587_s_at	182018	IRAK1
1119424	201599_at	75485	OAT

TABLE 2-continued

UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1131107	201628_s_at	432330	RRAGA
1131110	201631_s_at	76095	IER3
1119438	201641_at	118110	BST2
1131119	201647_s_at	349656	SCARB2
1119443	201648_at	436004	JAK1
1119445	201650_at	309517	KRT19
1119448	201656_at	212296	ITGA6
1131140	201684_s_at	194035	C14orf92
1131149	201694_s_at	326035	EGR1
1131150	201695_s_at	75514	NP
1119460	201696_at	76122	SFRS4
1119462	201700_at	83173	CCND3
1119466	201710_at	179718	MYBL2
1119467	201714_at	21635	TUBG1
1119475	201739_at	296323	SGK
1119477	201743_at	163867	CD14
1131181	201744_s_at	406475	LUM
1119479	201746_at	408312	TP53
1119488	201761_at	154672	MTHFD2
1131197	201778_s_at	269902	KIAA0494
1119503	201803_at	149353	POLR2B
1131218	201809_s_at	76753	ENG
1131219	201810_s_at	109150	SH3BP5
1119510	201820_at	433845	KRT5
1119515	201833_at	3352	HDAC2
1119516	201834_at	6061	PRKAB1
1119519	201849_at	79428	BNIP3
1131246	201853_s_at	153752	CDC25B
1131260	201872_s_at	12013	ABCE1
1131263	201877_s_at	249955	PPP2R5C
1119533	201886_at	283976	WDR23
1131268	201888_s_at	285115	IL13RA1
1119537	201895_at	446641	TIMP1
1131274	201897_s_at	374378	CKS1B
1119541	201910_at	207428	FARP1
1119546	201921_at	433898	GNG10
1131290	201925_s_at	408864	DAF
1119557	201939_at	398157	PLK2
1119559	201941_at	5057	CPD
1119561	201945_at	59242	FURIN
1119564	201952_at	10247	ALCAM
1119565	201953_at	135471	CIB1
1119566	201954_at	433506	ARPC1B
1119568	201957_at	269777	PPP1R12B
1131321	201983_s_at	77432	EGFR
1131325	201990_s_at	13313	CREBL2
1119582	201998_at	2554	SIAT1
1131336	202010_s_at	405945	ZNF410
1131340	202018_s_at	437457	LTF
1131342	202020_s_at	13351	LANCL1
1131379	202075_s_at	439312	PLTP
1119611	202076_at	289107	BIRC2
1131395	202102_s_at	278675	BRD4
1131401	202119_s_at	14158	CPNE3
1131405	202123_s_at	446504	ABL1
1131407	202125_s_at	154248	ALS2CR3
1119633	202126_at	198891	PRPF4B
1119636	202130_at	209061	RIOK3
1131411	202135_s_at	2477	ACTR1B
1119639	202136_at	145894	BS69
1131414	202140_s_at	511790	CLK3
1119647	202161_at	2499	PRKCL1
1119652	202175_at	458374	CHPF
1119655	202178_at	407181	
1131450	202200_s_at	369358	SRPK1
1119667	202206_at	111554	ARL7
1119680	202237_at	364345	NNMT
1119683	202241_at	444947	C8FW
1119684	202242_at	439586	TM4SF2
1131473	202243_s_at	89545	PSMB4
1131474	202246_s_at	95577	CDK4
1119694	202265_at	380403	COMMD3
1119699	202273_at	307783	PDGFRB

TABLE 2-continued

UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1119706	202281_at	153227	GAK
1119708	202283_at	173594	SERPINF1
1131490	202284_s_at	370771	CDKN1A
1119709	202288_at	338207	FRAP1
1131497	202295_s_at	114931	CTSH
1131503	202303_x_at	135705	SMARCA5
1131507	202311_s_at	172928	COL1A1
1119725	202329_at	77793	CSK
1119729	202338_at	164457	TK1
1131531	202350_s_at	153647	MATN2
1119734	202351_at	436873	ITGAV
1131541	202369_s_at	310230	TRAM2
1119752	202391_at	511745	BASP1
1131561	202403_s_at	232115	COL1A2
1119765	202421_at	81234	IGSF3
1119766	202423_at	93231	MYST3
1131578	202431_s_at	202453	MYC
1131584	202439_s_at	303154	IDS
1131592	202450_s_at	83942	CTSK
1131594	202454_s_at	306251	ERBB3
1119775	202455_at	9028	HDAC5
1119780	202472_at	75694	MPI
1119782	202478_at	155418	TRB2
1131614	202483_s_at	24763	RANBP1
1119799	202518_at	408219	BCL7B
1119802	202522_at	7370	PITPNB
1131636	202524_s_at	436193	SPOCK2
1131637	202527_s_at	75862	MADH4
1119807	202530_at	79107	MAPK14
1119808	202531_at	80645	IRF1
1131640	202534_x_at	83765	DHFR
1131645	202542_s_at	105656	SCYE1
1119813	202545_at	155342	PRKCD
1131654	202555_s_at	386078	MYLK
1119817	202561_at	409194	TNKS
1131663	202568_s_at	437625	MARK3
1119820	202573_at	181390	CSNK1G2
1119826	202589_at	87491	TYMS
1131687	202606_s_at	369280	TLK1
1119838	202615_at	469951	GNAQ
1119841	202625_at	80887	LYN
1119846	202634_at	351475	POLR2K
1131705	202638_s_at	386467	ICAM1
1131710	202644_s_at	211600	TNFAIP3
1119860	202670_at	132311	MAP2K1
1131733	202686_s_at	83341	AXL
1119868	202688_at	387871	TNFSF10
1131737	202693_s_at	9075	STK17A
1119872	202696_at	95220	OSR1
1119873	202697_at	446393	CPSF5
1119876	202703_at	14611	DUSP11
1119878	202705_at	194698	CCNB2
1119880	202709_at	442844	FMOD
1119884	202716_at	418004	PTPN1
1131752	202724_s_at	170133	FOXO1A
1131753	202727_s_at	180866	IFNGR1
1131755	202729_s_at	241257	LTBP1
1119889	202731_at	257697	PDCD4
1131757	202736_s_at	76719	LSM4
1119894	202740_at	334707	ACY1
1119895	202741_at	156324	PRKACB
1119903	202753_at	350939	p44S10
1131767	202758_s_at	296776	RFXANK
1119906	202762_at	58617	ROCK2
1119907	202763_at	141125	CASP3
1131778	202779_s_at	396393	UBE2S
1119916	202780_at	177584	OXCT
1119919	202786_at	199263	STK39
1119920	202788_at	234521	MAPKAPK3
1119924	202794_at	32309	INPP1
1119928	202799_at	317335	CLPP
1131786	202803_s_at	375957	ITGB2
1119936	202811_at	407994	STAMBP

TABLE 2-continued

UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1119939	202820_at	170087	AHR
1119946	202834_at	19383	AGT
1119950	202840_at	402752	TAF15
1131806	202842_s_at	6790	DNAJB9
1131808	202845_s_at	75447	RALBP1
1131813	202853_s_at	285346	RYK
1131815	202856_s_at	386678	SLC16A3
1131816	202859_x_at	624	IL8
1131827	202880_s_at	1050	PSCD1
1131835	202888_s_at	1239	ANPEP
1119972	202894_at	437008	EPHB4
1131839	202899_s_at	405144	SFRS3
1131845	202906_s_at	25812	NBS1
1131847	202910_s_at	3107	CD97
1119979	202911_at	445052	MSH6
1119983	202920_at	409783	ANK2
1131854	202923_s_at	414985	GCLC
1131861	202933_s_at	194148	YES1
1131863	202936_s_at	2316	SOX9
1131868	202947_s_at	81994	GYPC
1119995	202948_at	82112	IL1R1
1119997	202951_at	367811	STK38
1131870	202952_s_at	8850	ADAM12
1119998	202953_at	8986	C1QB
1131875	202965_s_at	169172	CAPN6
1120008	202969_at	173135	DYRK2
1120011	202983_at	3068	SMARCA3
1120016	202991_at	77628	STARD3
1120023	203005_at	1116	LTBR
1120024	203006_at	408063	INPP5A
1120026	203010_at	437058	STAT5A
1131916	203035_s_at	435761	PIAS3
1131918	203037_s_at	77694	MTSS1
1120038	203044_at	110488	CHSY1
1120044	203053_at	22960	BCAS2
1131925	203054_s_at	250894	TCTA
1120053	203073_at	82399	COG2
1120055	203075_at	110741	MADH2
1120059	203083_at	458354	THBS2
1131940	203085_s_at	1103	TGFB1
1120063	203090_at	118684	SDF2
1120069	203104_at	174142	CSF1R
1120072	203110_at	405474	PTK2B
1131955	203112_s_at	21771	WHSC2
1120079	203126_at	5753	IMPA2
1131964	203130_s_at	6641	KIF5C
1120081	203131_at	74615	PDGFRA
1120082	203132_at	408528	RB1
1120088	203138_at	13340	HAT1
1120089	203139_at	244318	DAPK1
1120090	203140_at	155024	BCL6
1131972	203154_s_at	20447	PAK4
1131975	203160_s_at	24439	RNF8
1120108	203175_at	75082	ARHG
1120120	203196_at	307915	ABCC4
1120121	203198_at	150423	CDK9
1131998	203210_s_at	443227	RFC5
1120127	203213_at	334562	CDC2
1132004	203217_s_at	415117	SIAT9
1120128	203218_at	348446	MAPK9
1120129	203221_at	406491	TLE1
1132011	203229_s_at	73986	CLK2
1132013	203232_s_at	434961	SCA1
1120134	203233_at	75545	IL4R
1132016	203238_s_at	8546	NOTCH3
1120137	203240_at	111732	FCGBP
1132022	203247_s_at	173911	ZNF24
1120145	203256_at	191842	CDH3
1132031	203266_s_at	134106	MAP2K4
1132034	203271_s_at	410455	UNC119
1132035	203272_s_at	8186	TUSC2
1120152	203275_at	83795	IRF2
1120153	203276_at	89497	LMNB1

TABLE 2-continued

UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1120160	203288_at	436976	KIAA0355
1120163	203302_at	709	DCK
1132058	203313_s_at	161999	TGIF
1120191	203373_at	405946	SOCS2
1120194	203379_at	149957	RPS6KA1
1120196	203386_at	173802	TBC1D4
1132104	203387_s_at	173802	TBC1D4
1120205	203405_at	5198	DSCR2
1120214	203416_at	443057	CD53
1120216	203418_at	85137	CCNA2
1132122	203434_s_at	307734	MME
1132132	203454_s_at	279910	ATOX1
1120254	203485_at	99947	RTN1
1120261	203499_at	171596	EPHA2
1120266	203507_at	246381	CD68
1120267	203508_at	256278	TNFRSF1B
1120269	203510_at	419124	MET
1120272	203514_at	29282	MAP3K3
1120274	203517_at	31584	MTX2
1132159	203521_s_at	147868	ZNF318
1120278	203528_at	511748	SEMA4D
1120288	203547_at	17483	CD4
1120289	203552_at	246970	MAP4K5
1132178	203554_x_at	350966	PTTG1
1120299	203574_at	79334	NFIL3
1120300	203575_at	82201	CSNK2A2
1132196	203591_s_at	381027	CSF3R
1120316	203611_at	63335	TERF2
1120317	203612_at	106880	BYSL
1120324	203627_at	239176	IGF1R
1132220	203632_s_at	448805	GPRC5B
1132223	203638_s_at	404081	FGFR2
1132230	203649_s_at	76422	PLA2G2A
1120335	203652_at	432787	MAP3K11
1132236	203661_s_at	374849	TMOD1
1120350	203679_at	446686	IL1RL1LG
1120353	203685_at	79241	BCL2
1120355	203687_at	80420	CX3CL1
1120356	203688_at	458291	PKD2
1120359	203697_at	128453	FRZB
1132256	203702_s_at	169910	KIAA0173
1132260	203706_s_at	173859	FZD7
1120361	203708_at	188	PDE4B
1120362	203709_at	196177	PHKG2
1120366	203717_at	44926	DPP4
1120370	203723_at	78877	ITPKB
1120373	203728_at	93213	BAK1
1120378	203738_at	151046	FLJ11193
1120385	203755_at	36708	BUB1B
1120387	203758_at	75262	CTSO
1120389	203761_at	75367	SLA
1132288	203767_s_at	79876	STS
1132292	203771_s_at	435726	BLVRA
1132294	203777_s_at	32156	RPS6KB2
1120400	203787_at	152207	SSBP2
1120402	203794_at	18586	CDC42BPA
1132306	203795_s_at	371758	BCL7A
1120417	203827_at	9398	FLJ10055
1120419	203830_at	9800	NJMU-R1
1120422	203835_at	151641	GARP
1120423	203837_at	151988	MAP3K5
1132329	203839_s_at	528296	ACK1
1120425	203843_at	188361	RPS6KA3
1132336	203853_s_at	30687	GAB2
1120433	203856_at	422662	VRK1
1132345	203868_s_at	109225	VCAM1
1120438	203870_at	109268	USP46
1132349	203881_s_at	169470	DMD
1132353	203887_s_at	2030	THBD
1132354	203890_s_at	153908	DAPK3
1120465	203915_at	77367	CXCL9
1120477	203934_at	12337	KDR
1120478	203935_at	150402	ACVR1

TABLE 2-continued

UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1132375	203942_s_at	157199	MARK2
1132376	203944_x_at	169963	BTN2A1
1120483	203947_at	180034	CSTF3
1120484	203949_at	458272	MPO
1120494	203967_at	405958	CDC6
1120500	203979_at	82568	CYP27A1
1132396	203988_s_at	118722	FUT8
1120509	204000_at	155090	GNB5
1132407	204005_s_at	406074	PAWR
1120520	204023_at	35120	RFC4
1120524	204033_at	436187	TRIP13
1120529	204039_at	76171	CEBPA
1132426	204049_s_at	102471	C6orf56
1132428	204051_s_at	105700	SFRP4
1120538	204057_at	14453	ICSBP1
1132433	204059_s_at	14732	ME1
1132434	204060_s_at	147996	PRKX
1132435	204062_s_at	168762	ULK2
1120544	204068_at	166684	STK3
1120553	204086_at	30743	PRAME
1120555	204090_at	444	STK19
1132449	204092_s_at	250822	STK6
1120562	204103_at	75703	CCL4
1120564	204106_at	79358	TESK1
1120572	204116_at	84	IL2RG
1120574	204118_at	901	CD48
1132460	204126_s_at	114311	CDC45L
1120580	204127_at	115474	RFC3
1120581	204129_at	415209	BCL9
1132462	204131_s_at	14845	FOXO3A
1120583	204133_at	153768	RNU3IP2
1120588	204140_at	421194	TPST1
1132468	204147_s_at	79353	TFDP1
1120593	204150_at	301989	STAB1
1120594	204154_at	442378	CDO1
1120595	204156_at	444909	KIAA0999
1120596	204159_at	4854	CDKN2C
1120601	204166_at	441129	KIAA0963
1132479	204170_s_at	83758	CKS2
1120605	204171_at	86858	RPS6KB1
1132485	204183_s_at	445563	ADRBK2
1120615	204191_at	181315	IFNAR1
1120616	204192_at	166556	CD37
1120617	204193_at	439777	CPT1B
1120625	204208_at	27345	RNGTT
1132498	204211_x_at	439523	PRKR
1120630	204218_at	38044	DKFZP564M082
1132504	204222_s_at	511765	GLIPR1
1120633	204225_at	222874	HDAC4
1120637	204232_at	433300	FCER1G
1132519	204247_s_at	166071	CDK5
1132520	204249_s_at	283063	LMO2
1120643	204252_at	19192	CDK2
1132525	204255_s_at	2062	VDR
1120645	204257_at	21765	FADS3
1132529	204265_s_at	288316	GPSM3
1132531	204267_x_at	77783	PKMYT1
1120651	204269_at	80205	PIM2
1132536	204285_s_at	96	PMAIP1
1120673	204301_at	5333	KIAA0711
1132545	204306_s_at	512857	CD151
1132547	204310_s_at	78518	NPR2
1120695	204352_at	385685	TRAF5
1120697	204355_at	323462	DHX30
1132572	204357_s_at	36566	LIMK1
1120700	204362_at	410745	SCAP2
1120703	204368_at	83974	SLCO2A1
1132584	204379_s_at	1420	FGFR3
1120716	204392_at	512804	CAMK1
1120717	204394_at	444159	SLC43A1
1132592	204396_s_at	211569	GRK5
1120720	204401_at	10082	KCNN4
1120730	204415_at	287721	G1P3

TABLE 2-continued

UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1120743	204440_at	79197	CD83
1132614	204446_s_at	89499	ALOX5
1120750	204454_at	45231	LDOC1
1132628	204468_s_at	78824	TIE
1120755	204470_at	789	CXCL1
1120765	204484_at	343329	PIK3C2B
1132636	204490_s_at	306278	CD44
1120770	204493_at	300825	BID
1120779	204510_at	28853	CDC7
1120780	204511_at	301283	FARP2
1120785	204517_at	110364	PPIC
1120789	204524_at	154729	PDPK1
1132651	204529_s_at	439767	TOX
1120792	204533_at	413924	CXCL10
1120803	204549_at	321045	IKBKE
1120808	204562_at	127686	IRF4
1120809	204563_at	82848	SELL
1120813	204568_at	414809	KIAA0831
1120814	204569_at	417022	ICK
1120818	204579_at	165950	FGFR4
1120824	204589_at	200598	ARK5
1120825	204591_at	388344	CRL1
1120828	204600_at	2913	EPHB3
1120832	204604_at	57856	PFTK1
1120834	204606_at	57907	CCL21
1120838	204612_at	433700	PKIA
1120839	204613_at	512298	PLCG2
1120846	204632_at	105584	RPS6KA4
1132700	204633_s_at	109058	RPS6KA5
1120847	204634_at	433008	NEK4
1120853	204641_at	153704	NEK2
1120854	204642_at	154210	EDG1
1120858	204647_at	410683	HOMER3
1120863	204655_at	489044	CCL5
1120875	204674_at	124922	LRMP
1120880	204682_at	105689	LTBP2
1120881	204683_at	433303	ICAM2
1132726	204707_s_at	433728	MAPK4
1120900	204718_at	380089	EPHB6
1132734	204724_s_at	126248	COL9A3
1120918	204754_at	250692	HLF
1120923	204765_at	334	ARHGEF5
1120925	204773_at	204891	IL11RA
1132762	204777_s_at	80395	MAL
1132766	204781_s_at	82359	TNFRSF6
1132768	204785_x_at	512211	IFNAR2
1132775	204803_s_at	1027	RRAD
1132780	204811_s_at	389415	CACNA2D2
1120946	204813_at	25209	MAPK10
1120952	204822_at	169840	TTK
1120955	204825_at	184339	MELK
1120958	204831_at	397734	CDK8
1132787	204832_s_at	2534	BMPR1A
1132799	204859_s_at	373575	APAF1
1120976	204867_at	245644	GCHFR
1120980	204872_at	494269	TLE4
1132809	204878_s_at	291623	PSK
1120986	204886_at	172052	PLK4
1132818	204891_s_at	1765	LCK
1132825	204900_x_at	512813	SAP30
1132830	204908_s_at	31210	BCL3
1120993	204912_at	327	IL10RA
1132834	204914_s_at	432638	SOX11
1121000	204924_at	519033	TLR2
1121005	204932_at	81791	TNFRSF11B
1121007	204936_at	440835	SF1
1121012	204947_at	96055	E2F1
1121013	204949_at	353214	ICAM3
1132850	204954_s_at	130988	DYRK1B
1121021	204958_at	153640	PLK3
1132851	204961_s_at	1583	
1132852	204962_s_at	1594	CENPA
1121028	204968_at	247323	APOM

TABLE 2-continued

UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1121029	204971_at	412999	CSTA
1121033	204975_at	356835	EMP2
1132860	204986_s_at	291623	PSK
1132862	204990_s_at	85266	ITGB4
1132866	204998_s_at	9754	ATF5
1132874	205013_s_at	197029	ADORA2A
1121054	205016_at	170009	TGFA
1121057	205026_at	434992	STAT5B
1132883	205027_s_at	432453	MAP3K8
1121061	205032_at	387725	ITGA2
1121062	205034_at	408658	CCNE2
1132890	205049_s_at	79630	CD79A
1132892	205051_s_at	81665	KIT
1121073	205052_at	81886	AUH
1121076	205055_at	389133	ITGAE
1121082	205067_at	126256	IL1B
1121100	205098_at	301921	CCR1
1121102	205101_at	126714	MHC2TA
1132918	205114_s_at	73817	CCL3
1132920	205119_s_at	753	FPR1
1121115	205124_at	78881	MEF2B
1121117	205126_at	82771	VRK2
1121120	205130_at	104119	RAGE
1121129	205159_at	285401	CSF2RB
1121136	205168_at	440905	DDR2
1132953	205180_s_at	86947	ADAM8
1121143	205184_at	447973	GNG4
1121149	205192_at	440315	MAP3K14
1132959	205198_s_at	606	ATP7A
1121159	205205_at	307905	RELB
1121161	205207_at	512234	IL6
1132961	205212_s_at	337242	CENTB1
1121166	205214_at	88297	STK17B
1121170	205220_at	458425	HM74
1121186	205242_at	100431	CXCL13
1121190	205247_at	436100	NOTCH4
1121195	205253_at	408222	PBX1
1132973	205255_x_at	169294	TCF7
1121201	205263_at	193516	BCL10
1121203	205266_at	2250	LIF
1121205	205269_at	2488	LCP2
1132979	205271_s_at	26322	CCRK
1121217	205291_at	75596	IL2RB
1121220	205296_at	87	RBL1
1132990	205297_s_at	89575	CD79B
1132994	205301_s_at	380271	OGG1
1132996	205306_x_at	409081	KMO
1121228	205312_at	157441	SPI1
1133004	205327_s_at	389846	ACVR2
1121248	205345_at	54089	BARD1
1133011	205347_s_at	56145	TMSNB
1121265	205372_at	14968	PLAG1
1133021	205377_s_at	154495	ACHE
1133024	205383_s_at	436987	ZNF288
1133030	205392_s_at	272493	CCL15
1121276	205394_at	24529	CHEK1
1121278	205399_at	21355	DCAMKL1
1121281	205403_at	25333	IL1R2
1121287	205411_at	35140	STK4
1121290	205418_at	7636	FES
1121291	205419_at	784	EBI2
1133042	205422_s_at	311054	ITGBL1
1133047	205434_s_at	528338	AAK1
1133049	205436_s_at	147097	H2AFX
1121301	205437_at	449971	ZNF134
1121306	205443_at	179312	SNAPC1
1121309	205449_at	23642	HSU79266
1121315	205455_at	2942	MST1R
1121316	205456_at	3003	CD3E
1121322	205467_at	5353	CASP10
1121326	205476_at	75498	CCL20
1133065	205479_s_at	77274	PLAU
1133068	205483_s_at	458485	G1P2

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UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1121329	205484_at	88012	SIT
1121331	205486_at	8980	TESK2
1121343	205504_at	159494	BTK
1133076	205512_s_at	18720	PDCD8
1133080	205526_s_at	440341	KATNA1
1133091	205544_s_at	73792	CR2
1133093	205546_s_at	75516	TYK2
1121368	205551_at	8071	SV2B
1133099	205554_s_at	88646	DNASE1L3
1121371	205558_at	444172	TRAF6
1133102	205565_s_at	360041	FRDA
1121380	205569_at	10887	LAMP3
1121383	205572_at	115181	ANGPT2
1121387	205578_at	208080	ROR2
1133111	205593_s_at	389777	PDE9A
1121400	205599_at	223474	TRAF1
1133117	205607_s_at	435560	PACE-1
1121404	205609_at	2463	ANGPT1
1121406	205611_at		TNFSF12
1121408	205613_at	258326	LOC51760
1133119	205614_x_at	512587	MST1
1121414	205621_at	94542	ALKBH
1121436	205659_at	487662	HDAC9
1121444	205668_at	153563	LY75
1133138	205671_s_at	1802	HLA-DOB
1133141	205677_s_at	344524	DLEU1
1121452	205681_at	227817	BCL2A1
1133148	205692_s_at	174944	CD38
1133150	205698_s_at	256924	MAP2K6
1121468	205707_at	129751	IL17R
1133156	205713_s_at	1584	COMP
1121473	205718_at	1741	ITGB7
1121482	205729_at	238648	OSMR
1121497	205758_at	85258	CD8A
1121511	205780_at	155419	BIK
1133184	205786_s_at	172631	ITGAM
1121516	205789_at	1799	CD1D
1121518	205792_at	194679	WISP2
1133192	205801_s_at	24024	RASGRP3
1133195	205805_s_at	274243	ROR1
1121533	205821_at	387787	KLRK1
1121542	205831_at	89476	CD2
1133210	205842_s_at	434374	JAK2
1121546	205844_at	12114	VNN1
1121554	205854_at	437046	TULP3
1121558	205858_at	415768	NGFR
1121559	205859_at	184018	LY86
1121560	205861_at	437905	SPIB
1121564	205865_at	437783	ARID3A
1133216	205872_x_at	502577	PDE4DIP
1121572	205876_at	446501	LIFR
1121573	205878_at	2815	POU6F1
1133219	205879_x_at	350321	RET
1121574	205880_at	2891	PRKCM
1133227	205895_s_at	75337	NOLC1
1121584	205898_at	78913	CX3CR1
1121585	205899_at	417050	CCNA1
1121587	205901_at	371809	PNOC
1121589	205904_at	90598	MICA
1133232	205910_s_at	406160	CEL
1121629	205965_at	41691	BATF
1133252	205977_s_at	89839	EPHA1
1121643	205986_at	514575	AATK
1121645	205988_at	398093	CD84
1133260	205992_s_at	528402	IL15
1121650	206002_at	421137	GPR64
1121655	206009_at	222	ITGA9
1133272	206028_s_at	306178	MERTK
1133275	206036_s_at	44313	REL
1121680	206049_at	73800	SELP
1133296	206070_s_at	123642	EPHA3
1133299	206075_s_at	446484	CSNK2A1
1121689	206076_at	155586	B7

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UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1121693	206080_at	170156	KIAA0450
1121695	206082_at	511759	HCP5
1133300	206085_s_at	19904	CTH
1121711	206106_at	432642	MAPK12
1121717	206114_at	73964	EPHA4
1121720	206118_at	80642	STAT4
1121722	206120_at	83731	CD33
1121726	206126_at	113916	BLR1
1121739	206142_at	85863	ZNF135
1121743	206148_at	460433	IL3RA
1121745	206150_at	355307	TNFRSF7
1121757	206170_at	2551	ADRB2
1121759	206172_at	336046	IL13RA2
1121760	206176_at	285671	BMP6
1121762	206181_at	32970	SLAMF1
1121767	206187_at	458324	PTGIR
1121780	206206_at	87205	LY64
1121783	206211_at	89546	SELE
1121788	206216_at	104865	STK23
1121792	206222_at	119684	TNFRSF10C
1121793	206223_at	122708	LMTK2
1121809	206247_at	211580	MICB
1121814	206255_at	389900	BLK
1133355	206267_s_at	437808	MATK
1121828	206271_at	29499	TLR3
1121834	206279_at	183165	PRKY
1133358	206283_s_at	73828	TAL1
1121841	206291_at	80962	NTS
1121844	206295_at	83077	IL18
1121848	206301_at	278005	TEC
1121853	206310_at	98243	SPINK2
1121854	206312_at	171470	GUCY2C
1121857	206315_at	114948	CRLF1
1133376	206324_s_at	129208	DAPK2
1121869	206336_at	164021	CXCL6
1121870	206337_at	1652	CCR7
1121874	206341_at	130058	IL2RA
1133388	206362_x_at	435014	MAP3K10
1121887	206363_at	134859	MAF
1133389	206366_x_at	174228	XCL1
1133392	206380_s_at	53155	PFC
1133397	206390_x_at	81564	PF4
1133400	206398_s_at	96023	CD19
1133405	206407_s_at	414629	CCL13
1133406	206411_s_at	159472	ABL2
1121918	206412_at	121558	FER
1133407	206413_s_at	144519	TCL6
1133408	206414_s_at	12802	DDEF2
1121947	206464_at	27372	BMX
1133430	206467_x_at	348183	TNFRSF6B
1121953	206478_at	38365	KIAA0125
1121956	206482_at	51133	PTK6
1121959	206486_at	409523	LAG3
1121963	206493_at	411312	ITGA2B
1121966	206498_at	82027	OCA2
1133445	206499_s_at	196769	CHC1
1121970	206508_at	99899	TNFSF7
1133453	206518_s_at	117149	RGS9
1121996	206545_at	1987	CD28
1122007	206569_at	411311	IL24
1133476	206571_s_at	3628	MAP4K4
1122009	206575_at	50905	CDKL5
1122021	206591_at	73958	RAG1
1122036	206618_at	159301	IL18R1
1122051	206637_at	2465	GPR105
1122053	206641_at	2556	TNFRSF17
1122065	206660_at	348935	IGLL1
1122075	206674_at	385	FLT3
1133515	206687_s_at	63489	PTPN6
1122087	206693_at	72927	IL7
1122091	206702_at	89640	TEK
1122104	206718_at	1149	LMO1
1122112	206729_at	1314	TNFRSF8

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UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1122131	206756_at	138155	CHST7
1133538	206760_s_at	1416	FCER2
1122139	206766_at	158237	ITGA10
1122156	206794_at	1939	ERBB4
1122165	206804_at	2259	CD3G
1122181	206828_at	29877	TXK
1133565	206846_s_at	6764	HDAC6
1133568	206854_s_at	290346	MAP3K7
1133569	206855_s_at	76873	HYAL2
1133576	206864_s_at	87247	HRK
1133577	206874_s_at	105751	SLK
1133580	206881_s_at	113277	LILRA3
1122215	206887_at	528317	CCBP2
1122217	206890_at	223894	IL12RB1
1122219	206892_at	437877	AMHR2
1122230	206907_at	1524	TNFSF9
1122241	206923_at	349611	PRKCA
1133595	206926_s_at	1721	IL11
1122253	206943_at	28005	TGFBR1
1122274	206974_at	34526	CXCR6
1122275	206975_at	36	LTA
1122277	206978_at	511794	CCR2
1122281	206983_at	46468	CCR6
1122284	206988_at	310511	CCL25
1133618	206991_s_at	511796	CCR5
1122288	206999_at	413608	IL12RB2
1122292	207008_at	846	IL8RB
1133629	207011_s_at	90572	PTK7
1122304	207029_at	1048	KITLG
1122327	207061_at	137575	ERN1
1122335	207073_at	143241	CDKL2
1133652	207076_s_at	160786	ASS
1122344	207094_at	194778	IL8RA
1122353	207111_at	2375	EMR1
1133672	207113_s_at	241570	TNF
1133676	207121_s_at	271980	MAPK6
1122380	207160_at	673	IL12A
1133694	207163_s_at	368861	AKT1
1122382	207165_at	72550	HMMR
1133700	207173_x_at	443435	CDH11
1133701	207176_s_at	838	CD80
1133702	207178_s_at	89426	FRK
1122388	207179_at	89583	TLX1
1133704	207181_s_at	9216	CASP7
1122394	207188_at	100009	CDK3
1133708	207194_s_at	512159	ICAM4
1122400	207199_at	439911	TERT
1122412	207216_at	177136	TNFSF8
1122420	207228_at	158029	PRKACG
1133724	207239_s_at	171834	PCTK1
1122428	207245_at	183596	UGT2B17
1133731	207253_s_at	21479	UBN1
1122449	207277_at	278694	CD209
1122471	207312_at	512612	PHKG1
1133753	207314_x_at	380156	KIR3DL1
1133755	207318_s_at	404501	CDC2L5
1133757	207320_x_at	6113	STAU
1133766	207339_s_at	376208	LTB
1122491	207354_at	10458	CCL16
1133778	207375_s_at	12503	IL15RA
1133786	207396_s_at	153591	ALG3
1133801	207426_s_at	181097	TNFSF4
1133802	207428_x_at	454861	CDC2L2
1122537	207433_at	193717	IL10
1122541	207442_at	2233	CSF3
1133810	207445_s_at	225946	CCR9
1122544	207446_at	366986	TLR6
1133829	207497_s_at	386748	MS4A2
1122581	207505_at	41749	PRKG2
1133834	207509_s_at	43803	LAIR2
1122596	207533_at	72918	CCL1
1133846	207536_s_at	528403	TNFRSF9
1122599	207538_at	73917	IL4

TABLE 2-continued

UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1133848	207540_s_at	192182	SYK
1122602	207550_at	82906	CDC20
1122609	207568_at	103128	CHRNA6
1122610	207569_at	1041	ROS1
1133867	207571_x_at	10649	C1orf38
1133869	207574_s_at	110571	GADD45B
1133901	207633_s_at	156465	MUSK
1122640	207634_at	158297	PDCD1
1122645	207641_at	158341	TNFRSF13B
1133904	207643_s_at	159	TNFRSF1A
1133910	207655_s_at	167746	BLNK
1122664	207681_at	198252	CXCR3
1133931	207697_x_at	306230	LILRB2
1122680	207709_at	256067	PRKAA2
1122710	207766_at	380788	CDKL1
1133998	207826_s_at	76884	ID3
1122738	207840_at	81743	CD160
1122740	207844_at	845	IL13
1122743	207849_at	89679	IL2
1122744	207850_at	89690	CXCL3
1122749	207861_at	80420	CX3CL1
1122763	207884_at	309958	GUCY2D
1122767	207892_at	652	TNFSF5
1122772	207900_at	66742	CCL17
1122773	207901_at	674	IL12B
1122774	207902_at	68876	IL5RA
1122775	207906_at	694	IL3
1122776	207907_at	129708	TNFSF14
1122796	207952_at	2247	IL5
1134069	207979_s_at	405667	CD8B1
1134076	207988_s_at	83583	ARPC2
1134083	207996_s_at	285091	C18orf1
1134095	208018_s_at	89555	HCK
1134109	208037_s_at	102598	MADCAM1
1122824	208038_at	416814	IL1RL2
1122834	208059_at	113222	CCR8
1134133	208075_s_at	251526	CCL7
1134145	208091_s_at	4750	DKFZP564K0822
1134200	208161_s_at	90786	ABCC3
1134212	208178_x_at	367689	TRIO
1134220	208189_s_at	370421	MYO7A
1122863	208193_at	960	IL9
1122864	208195_at	434384	TTN
1122865	208200_at	1722	IL1A
1134230	208206_s_at	99491	RASGRP2
1134233	208212_s_at	410680	ALK
1134270	208284_x_at	352119	GGT1
1134271	208286_x_at	249184	POU5F1
1134280	208303_s_at	287729	CRLF2
1122914	208304_at	506190	CCR3
1134296	208335_s_at	183	FY
1134316	208365_s_at	32959	GRK4
1122939	208376_at	184926	CCR4
1134361	208426_x_at	515605	KIR2DL4
1134370	208438_s_at	1422	FGR
1122956	208450_at	113987	LGALS2
1134379	208451_s_at	150833	C4A
1122983	208495_at	249125	TLX3
1122994	208524_at	159900	GPR15
1134422	208536_s_at	84063	BCL2L11
1134424	208540_x_at		S100A14
1123026	208578_at	250443	SCN10A
1134457	208605_s_at	406293	NTRK1
1134480	208634_s_at	372463	MACF1
1123038	208636_at	119000	ACTN1
1123039	208638_at	212102	P5
1134494	208657_s_at	288094	MSF
1123052	208680_at	180909	PRDX1
1123053	208683_at	350899	CAPN2
1134517	208690_s_at	75807	PDLIM1
1123055	208691_at	185726	TFRC
1134523	208700_s_at	89643	TKT
1134532	208711_s_at	371468	CCND1

TABLE 2-continued

UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1134533	208716_s_at	93832	LOC54499
1134542	208729_x_at	77961	HLA-B
1123086	208774_at	378918	CSNK1D
1134582	208794_s_at	78202	SMARCA4
1134593	208812_x_at	274485	HLA-C
1123105	208820_at	434281	PTK2
1123108	208828_at	108112	POLE3
1134615	208851_s_at	134643	THY1
1134618	208854_s_at	168913	STK24
1134647	208892_s_at	298654	DUSP6
1123127	208894_at	409805	HLA-DRA
1134653	208901_s_at	253536	TOP1
1134665	208921_s_at	422340	SRI
1134674	208937_s_at	410900	ID1
1134676	208942_s_at	158193	TLOC1
1123148	208944_at	82028	TGFBR2
1134679	208946_s_at	12272	BECN1
1134682	208949_s_at	411701	LGALS3
1134687	208959_s_at	154023	TXNDC4
1134699	208974_x_at	439683	KPNB1
1123160	208982_at	78146	PECAM1
1134706	208987_s_at	219614	FBXL11
1123163	208991_at	421342	STAT3
1134710	208993_s_at	77965	PPIG
1134727	209018_s_at	439600	PINK1
1134738	209033_s_at	75842	DYRK1A
1134753	209053_s_at	110457	WHSC1
1134778	209085_x_at	166563	RFC1
1123188	209089_at	73957	RAB5A
1123192	209100_at	315177	IFRD2
1123193	209101_at	410037	CTGF
1123198	209112_at	238990	CDKN1B
1134797	209118_s_at	433394	TUBA3
1123213	209154_at	12956	TIP-1
1123223	209173_at	226391	AGR2
1134837	209185_s_at	143648	IRS2
1123231	209189_at	25647	FOS
1123233	209193_at	81170	PIM1
1123235	209196_at	436930	C6orf11
1134843	209199_s_at	368950	MEF2C
1134850	209210_s_at	270411	PLEKHC1
1134852	209214_s_at	374477	EWSR1
1134858	209226_s_at	405954	TNPO1
1123250	209233_at	135643	C2F
1123255	209239_at	160557	NFKB1
1134865	209241_x_at	112028	MINK
1134880	209265_s_at	168799	METTL3
1134888	209278_s_at	438231	TFPI2
1123278	209295_at	51233	TNFRSF10B
1134903	209306_s_at	153026	SWAP70
1123286	209311_at	410026	BCL2L2
1123289	209317_at	5409	POLR1C
1123293	209333_at	47061	ULK1
1123298	209339_at	20191	SIAH2
1134921	209341_s_at	413513	IKBKB
1134928	209352_s_at	13999	SIN3B
1123304	209354_at	279899	TNFRSF14
1134933	209360_s_at	410774	RUNX1
1123308	209364_at	76366	BAD
1123310	209368_at	212088	EPHX2
1134945	209379_s_at	81897	KIAA1128
1123317	209386_at	351316	TM4SF1
1123321	209392_at	23719	ENPP2
1123331	209409_at	512118	GRB10
1134961	209417_s_at	50842	IFI35
1123346	209443_at	76353	SERPINA3
1123358	209464_at	442658	AURKB
1134988	209467_s_at	79516	MKNK1
1134991	209474_s_at	444105	ENTPD1
1123369	209481_at	79025	SNRK
1123372	209487_at	195825	RBPMS
1123376	209496_at	37682	RARRES2
1135002	209500_x_at	54673	TNFSF13

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UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1123399	209541_at	308053	IGF1
1135023	209543_s_at	374990	CD34
1135024	209545_s_at	103755	RIPK2
1123401	209550_at	50130	NDN
1135028	209555_s_at	443120	CD36
1123413	209575_at	418291	IL10RB
1135042	209582_s_at	79015	MOX2
1135047	209589_s_at	125124	EPHB2
1123419	209590_at	170195	BMP7
1135056	209604_s_at	169946	GATA3
1123429	209619_at	446471	CD74
1135068	209621_s_at	71719	PDLIM3
1123430	209622_at	153003	STK16
1123437	209636_at	73090	NFKB2
1123439	209642_at	287472	BUB1
1135080	209644_x_at	421349	CDKN2A
1135085	209650_s_at	505862	C22orf4
1135088	209656_s_at	8769	TM4SF10
1135093	209666_s_at	198998	CHUK
1135101	209680_s_at	20830	KIFC1
1123455	209682_at	436986	CBLB
1123457	209684_at	446304	RIN2
1135102	209685_s_at	349845	PRKCB1
1123459	209687_at	436042	CXCL12
1123470	209704_at	31016	M96
1123476	209711_at	82635	SLC35D1
1123479	209716_at	173894	CSF1
1123490	209732_at	85201	CLECSF2
1123497	209747_at	2025	TGFB3
1135130	209757_s_at	25960	MYCN
1171502	209760_at	511944	KIAA0922
1123507	209770_at	284283	BTN3A1
1135138	209771_x_at	375108	CD24
1135141	209774_x_at	75765	CXCL2
1135151	209790_s_at	3280	CASP6
1123529	209815_at	159526	PTCH
1135164	209825_s_at	458360	UMPK
1135165	209827_s_at	170359	IL16
1123535	209829_at	389488	C6orf32
1135168	209831_x_at	118243	DNASE2
1135173	209841_s_at	3781	LRRN3
1135186	209860_s_at	386741	ANXA7
1135189	209863_s_at	137569	TP73L
1123552	209879_at	423077	SELPLG
1135209	209899_s_at	74562	SIAHBP1
1123566	209906_at	155935	C3AR1
1135214	209908_s_at	169300	TGFB2
1123573	209924_at	16530	CCL18
1135226	209929_s_at	43505	IKBKG
1135227	209930_s_at	75643	NFE2
1135229	209932_s_at	367676	DUT
1123581	209941_at	390758	RIPK1
1135234	209945_s_at	282359	GSK3B
1123584	209946_at	79141	VEGFC
1123586	209948_at	93841	KCNMB1
1123587	209949_at	949	NCF2
1135240	209955_s_at	436852	FAP
1135251	209969_s_at	21486	STAT1
1135253	209971_x_at	301613	JTV1
1135267	209995_s_at	2484	TCL1A
1135270	209999_x_at	50640	SOCS1
1123608	210017_at	180566	MALT1
1135285	210024_s_at	449501	UBE2E3
1123611	210029_at	840	INDO
1123613	210031_at	97087	CD3Z
1123614	210038_at	408049	PRKCQ
1135299	210044_s_at	46446	LYL1
1123622	210051_at	8578	EPAC
1123628	210058_at	178695	MAPK13
1123634	210072_at	50002	CCL19
1123635	210073_at	408614	SIAT8A
1123643	210092_at	421576	MAGOH
1135322	210095_s_at	450230	IGFBP3

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UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1135328	210105_s_at	390567	FYN
1123663	210133_at	54460	CCL11
1123671	210148_at	30148	HIPK3
1135350	210151_s_at	164267	DYRK3
1123672	210152_at	67846	LILRB4
1123679	210163_at	103982	CXCL11
1123680	210164_at	1051	GZMB
1123682	210166_at	114408	TLR5
1123690	210176_at	111805	TLR1
1123694	210184_at	385521	ITGAX
1135374	210214_s_at	53250	BMPR2
1135379	210225_x_at	511766	LILRB3
1135380	210229_s_at	1349	CSF2
1135383	210240_s_at	435051	CDKN2D
1123731	210258_at	17165	RGS13
1135395	210260_s_at	17839	TNFAIP8
1135399	210275_s_at	406096	ZNF216
1123744	210279_at	88269	GPR18
1123760	210313_at	406708	ILT7
1123762	210316_at	415048	FLT4
1123778	210349_at	440638	CAMK4
1123780	210354_at	856	IFNG
1135467	210404_x_at	321572	CAMK2B
1135475	210416_s_at	146329	CHEK2
1135487	210432_s_at	300717	SCN3A
1135489	210438_x_at	288178	SSA2
1123814	210439_at	56247	ICOS
1123816	210442_at	66	IL1RL1
1135492	210448_s_at	408615	P2RX5
1135513	210481_s_at	421437	CD209L
1123833	210487_at	397294	DNTT
1123842	210506_at	457	FUT7
1135526	210512_s_at	73793	VEGF
1135529	210517_s_at	197081	AKAP12
1123847	210523_at	87223	BMPR1B
1135541	210538_s_at	127799	BIRC3
1135549	210549_s_at	169191	CCL23
1135550	210550_s_at	221811	RASGRF1
1135571	210582_s_at	278027	LIMK2
1135583	210606_x_at	41682	KLRD1
1123875	210607_at	428	FLT3LG
1135592	210621_s_at	758	RASA1
1135593	210622_x_at	77313	CDK10
1123889	210643_at	333791	TNFSF11
1135606	210644_s_at	407964	LAIR1
1123890	210654_at	129844	TNFRSF10D
1123892	210659_at	159553	CMKLR1
1135622	210671_x_at	445864	MAPK8
1135645	210715_s_at	31439	SPINT2
1135665	210749_x_at	423573	DDR1
1135673	210759_s_at	82159	PSMA1
1123938	210772_at	99855	FPRL1
1135684	210775_x_at	329502	CASP9
1135685	210776_x_at	371282	TCF3
1135735	210838_s_at	410104	ACVRL1
1135743	210847_x_at	299558	TNFRSF25
1123954	210865_at	2007	TNFSF6
1135755	210869_s_at	511397	MCAM
1135773	210889_s_at	126384	FCGR2B
1135778	210895_s_at	27954	CD86
1135795	210933_s_at	55923	Lin10
1135801	210943_s_at	130188	CHS1
1135802	210944_s_at	439343	CAPN3
1135826	210976_s_at	75160	PFKM
1135830	210981_s_at	235116	GRK6
1135835	210986_s_at	133892	TPM1
1123988	211005_at	498997	LAT
1135852	211008_s_at	302903	UBE2I
1135858	211015_s_at	90093	HSPA4
1135866	211026_s_at	409826	MGLL
1135871	211031_s_at	104717	CYLN2
1135899	211070_x_at	78888	DBI
1135925	211100_x_at	149924	LILRB1

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UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1135929	211105_s_at	96149	NFATC1
1135930	211107_s_at	98338	AURKC
1135966	211155_s_at	1166	THPO
1135968	211160_x_at	119000	ACTN1
1135974	211168_s_at	388125	RENT1
1135982	211178_s_at	129758	PSTPIP1
1135994	211197_s_at	14155	ICOSL
1136002	211208_s_at	288196	CASK
1124049	211276_at	401835	my048
1136048	211282_x_at	299558	TNFRSF25
1136051	211286_x_at	520937	CSF2RA
1136055	211296_x_at	183704	UBC
1136056	211297_s_at	184298	CDK7
1136087	211339_s_at	211576	ITK
1136109	211370_s_at	436145	MAP2K5
1136150	211432_s_at	381282	TYRO3
1136152	211434_s_at	458436	CCRL2
1136162	211453_s_at	326445	AKT2
1136172	211470_s_at	38084	SULT1C1
1136185	211488_s_at	355722	ITGB8
1136193	211499_s_at	57732	MAPK11
1136216	211528_x_at	512152	HLA-G
1136269	211593_s_at	101474	MAST2
1136273	211597_s_at	13775	HOP
1136285	211615_s_at	182490	LRPPRC
1124132	211658_at	432121	PRDX2
1136329	211675_s_at	132739	HIC
1136337	211685_s_at	90063	NCALD
1136343	211692_s_at	87246	BBC3
1124137	211693_at	366	MGC27165
1136357	211709_s_at	512680	SCGF
1136362	211714_x_at	356729	OK/SW-cl.56
1136369	211724_x_at	387140	FLJ20323
1136371	211726_s_at	361155	FMO2
1136379	211734_s_at	897	FCER1A
1136391	211748_x_at	446429	PTGDS
1136393	211750_x_at	406578	TUBA6
1136401	211761_s_at	27258	SIP
1136408	211771_s_at	1101	POU2F2
1136427	211795_s_at	276506	FYB
1136430	211798_x_at	102950	IGLJ3
1136459	211828_s_at	252550	KIAA0551
1136464	211833_s_at	159428	BAX
1136540	211924_s_at	179657	PLAUR
1124176	211966_at	407912	COL4A2
1124177	211967_at	172089	PORIMIN
1124178	211969_at	446579	HSPCA
1124187	211986_at	378738	MGC5395
1124188	211987_at	282346	TOP2B
1136573	211991_s_at	914	HLA-DPA1
1124192	211992_at	275999	PRKWNK1
1124195	211998_at	180877	H3F3B
1136585	212022_s_at	80976	MKI67
1124215	212037_at	409965	PNN
1136595	212038_s_at	404814	VDAC1
1136599	212046_x_at	861	MAPK3
1136601	212048_s_at	322735	YARS
1136605	212064_x_at	448398	MAZ
1124237	212080_at	258855	MLL
1136620	212091_s_at	415997	COL6A1
1124254	212110_at	301743	SLC39A14
1124266	212123_at	438991	DKFZP564D116
1124283	212144_at	406612	UNC84B
1124296	212158_at	1501	SDC2
1124304	212168_at	166887	CPNE1
1124316	212186_at	449863	ACACA
1124318	212190_at	21858	SERPINE2
1124321	212196_at	529772	
1136655	212218_s_at	388387	FBXO9
1124342	212230_at	432840	PPAP2B
1136662	212240_s_at	6241	PIK3R1
1124357	212247_at	413636	NUP205
1124362	212252_at	297343	CAMKK2

TABLE 2-continued

UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1124365	212261_at	334871	TNRC15
1124377	212282_at	199695	MAC30
1124381	212288_at	440808	FNBP1
1124384	212291_at	12259	HIPK1
1124391	212299_at	7200	NEK9
1136681	212303_x_at	91142	KHSRP
1124400	212312_at	305890	BCL2L1
1124411	212326_at	194737	VPS13D
1124416	212331_at	283604	RBL2
1124429	212344_at	409602	SULF1
1136687	212345_s_at	59943	CREB3L2
1124438	212358_at	7357	CLIPR-59
1136692	212359_s_at	65135	KIAA0913
1124456	212382_at	359289	TCF4
1136702	212399_s_at	155584	KIAA0121
1136710	212429_s_at	75782	GTF3C2
1136712	212442_s_at	503941	LOC253782
1136718	212459_x_at	446476	SUCLG2
1136722	212481_s_at	250641	TPM4
1136724	212491_s_at	433540	DNAJC8
1124539	212494_at	6147	TENC1
1124543	212500_at	99821	C10orf22
1124549	212508_at	24719	MOAP1
1124561	212530_at	24119	NEK7
1124563	212533_at	249441	WEE1
1124577	212552_at	3618	HPCAL1
1124583	212558_at	20977	GDAP1L1
1124594	212572_at	184523	STK38L
1124606	212588_at	444324	PTPRC
1124610	212592_at	381568	IGJ
1124613	212599_at	296720	AUTS2
1124616	212603_at	154655	MRPS31
1136759	212605_s_at	188882	
1124620	212610_at	83572	PTPN11
1136762	212624_s_at	380138	CHN1
1136765	212629_s_at	69171	PRKCL2
1124646	212646_at	436432	RAFTLIN
1136774	212657_s_at	81134	IL1RN
1124655	212658_at	79299	LHFPL2
1124658	212663_at	522351	KIAA0674
1136777	212671_s_at	387679	HLA-DQA1
1124666	212672_at	526394	ATM
1136781	212680_x_at	120197	PPP1R14B
1136784	212689_s_at	321707	JMJD1
1136786	212694_s_at	63788	PCCB
1136788	212698_s_at	355455	9/10/2004
1124692	212713_at	296049	MFAP4
1124705	212730_at	381347	DMN
1124712	212738_at	80305	ARHGAP19
1124713	212740_at	306747	PIK3R4
1124723	212753_at	435065	RNF3
1124733	212771_at	66762	LOC221061
1124734	212774_at	446677	ZNF238
1124745	212789_at	438550	KIAA0056
1136819	212798_s_at	112605	DKFZP564O043
1124753	212801_at	528307	CIT
1124755	212805_at	23311	KIAA0367
1124760	212813_at	419149	JAM3
1124768	212824_at	98751	FUBP3
1124770	212827_at	153261	IGHM
1136831	212841_s_at	12953	PPFIBP2
1136832	212842_x_at	434959	RANBP2L1
1124782	212843_at	78792	NCAM1
1124786	212847_at	22370	NEXN
1124798	212867_at	446678	NCOA2
1124800	212871_at	413901	MAPKAPK5
1136844	212875_s_at	16007	C21orf25
1124806	212881_at	105779	PIASY
1124820	212899_at	129836	CDK11
1124830	212911_at	9059	KIAA0962
1124831	212912_at	301664	RPS6KA2
1124833	212914_at	356416	CBX7
1136853	212922_s_at	66170	SMYD2

TABLE 2-continued

UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1136859	212942_s_at	212584	KIAA1199
1124862	212954_at	439530	DYRK4
1136865	212959_s_at	412128	MGC4170
1124864	212960_at	411317	KIAA0882
1124875	212975_at	18166	KIAA0870
1124889	212993_at	244847	BTBD14A
1136876	212997_s_at	445078	TLK2
1136877	212998_x_at	409934	HLA-DQB1
1124893	213002_at	318603	MARCKS
1124913	213027_at	288178	SSA2
1124920	213039_at	6150	ARHGEF18
1124921	213044_at	306307	ROCK1
1124922	213045_at	173864	MAST3
1124941	213068_at	80552	DPT
1124942	213069_at	433452	HEG
1124948	213075_at	357004	LOC169611
1124953	213083_at	386278	SLC35D2
1136902	213086_s_at	442592	
1136903	213087_s_at	334798	EEF1D
1124967	213108_at	143535	CAMK2A
1136913	213113_s_at	99962	SLC43A3
1124972	213116_at	2236	NEK3
1136925	213154_s_at	436939	BICD2
1125001	213158_at	16193	
1125009	213169_at	27621	
1125010	213170_at	43728	GPX7
1125013	213174_at	79170	TTC9
1136938	213188_s_at	23294	MINA53
1136939	213193_x_at	419777	
1125025	213196_at	301094	
1125027	213198_at	371974	ACVR1B
1125058	213238_at	437241	ATP10D
1125079	213264_at	211601	MAP3K12
1125122	213324_at	436015	SRC
1125124	213326_at	20021	VAMP1
1136971	213330_s_at	257827	STIP1
1136972	213331_s_at	414410	NEK1
1125130	213338_at	35861	RIS1
1125132	213341_at	47367	FEM1C
1125136	213348_at	106070	CDKN1C
1136983	213360_s_at	450237	LOC340318
1136984	213364_s_at	498154	SNX1
1136987	213370_s_at	21695	SFMBT1
1136988	213373_s_at	243491	CASP8
1136996	213397_x_at	283749	RNASE4
1125181	213418_at	3268	HSPA6
1125195	213438_at	7309	
1137022	213475_s_at	174103	ITGAL
1125231	213489_at	446375	MAPRE2
1137026	213490_s_at	366546	MAP2K2
1125245	213517_at	132977	PCBP2
1125246	213518_at	496511	PRKCI
1125249	213523_at	244723	CCNE1
1137042	213524_s_at	432132	G0S2
1125279	213575_at	445652	TRA2A
1125305	213627_at	376719	MAGED2
1137097	213656_s_at	20107	KNS2
1137109	213689_x_at	469653	RPL5
1137112	213693_s_at	89603	MUC1
1137137	213746_s_at	195464	FLNA
1125377	213748_at	196966	KIAA0298
1125397	213784_at	415172	RABL4
1137158	213794_s_at	9043	C14orf120
1137201	213877_x_at	433343	SRRM2
1137202	213881_x_at	380973	SMT3H2
1125456	213906_at	300592	MYBL1
1125459	213909_at	288467	LRRC15
1125462	213915_at	10306	NKG7
1125485	213958_at	436949	CD6
1137247	213975_s_at	234734	LYZ
1137273	214020_x_at	149846	ITGB5
1125516	214032_at	234569	ZAP70
1125520	214038_at	271387	CCL8

TABLE 2-continued

UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1137289	214049_x_at	36972	CD7
1125527	214051_at	422848	MGC39900
1137291	214055_x_at	446197	XTP2
1125532	214058_at	437922	MYCL1
1125546	214081_at	125036	PLXDC1
1137308	214093_s_at	118962	FUBP1
1137328	214130_s_at	502577	PDE4DIP
1137332	214146_s_at	2164	PPBP
1137343	214170_x_at	391168	FH
1125593	214180_at	8910	MAN1C1
1137360	214196_s_at	429658	CLN2
1137378	214228_x_at	129780	TNFRSF4
1125634	214265_at	171025	ITGA8
1125658	214322_at	12436	CAMK2G
1137439	214339_s_at	95424	MAP4K1
1137447	214359_s_at	74335	HSPCB
1137449	214363_s_at	223745	MATR3
1125685	214371_at	103978	STK22B
1137481	214428_x_at	150833	C4A
1137486	214442_s_at	441069	MIZ1
1137488	214448_x_at	9731	NFKBIB
1137492	214459_x_at	274485	HLA-C
1125742	214470_at	169824	KLRB1
1137506	214501_s_at	75258	H2AFY
1137512	214512_s_at	229641	PC4
1137534	214551_s_at	36972	CD7
1125789	214560_at	511953	FPRL2
1137539	214567_s_at	458346	XCL2
1125818	214607_at	152663	PAK3
1125826	214617_at	2200	PRF1
1137561	214639_s_at	67397	HOXA1
1125852	214660_at	439320	ITGA1
1125854	214663_at	6874	DustyPK
1137582	214683_s_at	433732	CLK1
1137583	214687_x_at	273415	ALDOA
1125872	214696_at	417157	MGC14376
1137594	214710_s_at	23960	CCNB1
1137597	214721_x_at	3903	CDC42EP4
1137601	214730_s_at	78979	GLG1
1125901	214745_at	193143	KIAA1069
1125916	214764_at	497770	
1125917	214769_at	417091	CLCN4
1125919	214772_at	432369	G2
1125921	214777_at	512003	
1125927	214787_at	511742	IRLB
1125928	214790_at	435628	SUSP1
1137626	214797_s_at	445402	PCTK3
1137643	214864_s_at	155742	GRHPR
1137663	214909_s_at	247362	DDAH2
1126047	214969_at	437214	MAP3K9
1137687	214974_x_at	89714	CXCL5
1137698	215001_s_at	442669	GLUL
1126081	215030_at	309763	GRSF1
1137742	215111_s_at	114360	TSC22
1126131	215117_at	159376	RAG2
1137751	215127_s_at	241567	RBMS1
1126148	215143_at	408264	FLJ36166
1137760	215158_s_at	169681	DEDD
1137771	215193_x_at	308026	HLA-DRB3
1137782	215223_s_at	384944	SOD2
1137806	215313_x_at	181244	HLA-A
1137809	215332_s_at	405667	CD8B1
1126293	215346_at	504816	TNFRSF5
1137838	215411_s_at	437508	C6orf4
1137868	215493_x_at	169963	BTN2A1
1126387	215499_at	180533	MAP2K3
1126408	215528_at	22689	
1137908	215603_x_at	454906	
1137955	215722_s_at	434901	SNRPA1
1126540	215750_at	474916	KIAA1659
1126554	215767_at	159528	LOC91752
1126559	215776_at	248138	INSRR
1138030	215925_s_at	116481	CD72

TABLE 2-continued

UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1138048	215967_s_at	403857	LY9
1138120	216178_x_at	287797	ITGB1
1138128	216199_s_at	390428	MAP3K4
1138132	216207_x_at	390427	IGKV1D-13
1138136	216215_s_at	433574	RBM9
1138147	216234_s_at	194350	PRKACA
1138150	216237_s_at	77171	MCM5
1138157	216251_s_at	82563	KIAA0153
1126858	216261_at	87149	ITGB3
1138192	216321_s_at	126608	NR3C1
1126892	216331_at	74369	ITGA7
1138244	216442_x_at	418138	FN1
1138259	216484_x_at	89525	HDGF
1138279	216520_s_at	374596	TPT1
1138312	216598_s_at	303649	CCL2
1138331	216640_s_at	212102	P5
1138355	216705_s_at	407135	ADA
1138379	216836_s_at	446352	ERBB2
1127214	216837_at	201920	EPHA5
1138392	216862_s_at	3548	MTCP1
1138400	216876_s_at	41724	IL17
1138417	216905_s_at	56937	ST14
1138421	216913_s_at	434251	KIAA0690
1138441	216945_x_at	397891	PASK
1138443	216950_s_at	77424	FCGR1A
1127290	217019_at	447032	
1127294	217028_at	421986	CXCR4
1138507	217066_s_at	898	DMPK
1138515	217080_s_at	93564	HOMER2
1138532	217128_s_at	199068	CAMK1G
1138537	217140_s_at		
1138538	217143_s_at	2014	TRD@
1138541	217149_x_at	203420	TNK1
1127371	217164_at	391858	TIA1
1138555	217184_s_at	434481	LTK
1138567	217200_x_at	355264	CYB561
1138645	217373_x_at	212217	MDM2
1138647	217377_x_at	171262	ETV6
1138652	217388_s_at	444471	KYNU
1138670	217422_s_at	262150	CD22
1138671	217427_s_at	415735	HIRA
1138677	217436_x_at	390440	
1127567	217529_at	440667	FLJ20013
1127576	217544_at	529751	
1138721	217552_x_at	334019	CR1
1138759	217707_x_at	396404	SMARCA2
1138765	217716_s_at	306079	SEC61A1
1138778	217736_s_at	434986	HRI
1138780	217739_s_at	293464	PBEF1
1138783	217742_s_at	370152	WAC
1138789	217750_s_at	369120	FLJ13855
1127720	217765_at	272736	NRBP
1138801	217774_s_at	333579	HSPC152
1127742	217814_at	8207	GK001
1127744	217817_at	323342	ARPC4
1138832	217829_s_at	12820	USP39
1138845	217849_s_at	436985	CDC42BPB
1127756	217850_at	313544	NS
1127761	217863_at	75251	PIAS1
1138858	217871_s_at	407995	MIF
1127775	217886_at	79095	EPS15
1138867	217892_s_at	10706	EPLIN
1138874	217910_x_at	383019	TCFL4
1138878	217917_s_at	100002	DNCL2A
1138887	217937_s_at	200063	HDAC7A
1127805	217947_at	380627	CKLFSF6
1127807	217950_at	7236	NOSIP
1127813	217962_at	14317	NOLA3
1138905	217970_s_at	437844	KIAA1194
1127822	217977_at	279623	SEPX1
1138910	217982_s_at	374503	MORF4L1
1127833	218001_at	382044	MRPS2
1138920	218002_s_at	24395	CXCL14

TABLE 2-continued

UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1127838	218012_at	136164	SE20-4
1127849	218032_at	76691	SNN
1138944	218051_s_at	84753	FLJ12442
1127864	218066_at	172613	SLC12A7
1138959	218076_s_at	203605	RICH1
1127873	218089_at	11314	C20orf4
1138973	218097_s_at	11270	C10orf66
1127885	218113_at	160417	TMEM2
1138994	218143_s_at	238030	SCAMP2
1138995	218144_s_at	24956	FLJ22056
1127901	218145_at	344378	C20orf97
1139005	218168_s_at	273186	CABC1
1139017	218189_s_at	274424	NANS
1139026	218205_s_at	512094	MKNK2
1127931	218208_at	288284	PQLC1
1139037	218223_s_at	173380	CKIP-1
1127940	218227_at	256549	NUBP2
1139039	218228_s_at	280776	TNKS2
1127943	218232_at	9641	C1QA
1139048	218250_s_at	170553	CNOT7
1139054	218263_s_at	25726	LOC58486
1139076	218306_s_at	133411	HERC1
1139100	218350_s_at	234896	GMNN
1139105	218367_x_at	8015	USP21
1139106	218368_s_at	355899	TNFRSF12A
1139127	218409_s_at	13015	DNAJC1
1128042	218436_at	297875	SIL1
1128066	218475_at	63609	HTF9C
1128070	218481_at	283741	RRP46
1128079	218499_at	23643	MST4
1128095	218520_at	432466	TBK1
1128099	218529_at	333427	8D6A
1128100	218530_at	95231	FHOD1
1139185	218535_s_at	27021	RIOK2
1128106	218542_at	14559	C10orf3
1128111	218552_at	170915	FLJ10948
1139196	218559_s_at	169487	MAFB
1139202	218569_s_at	440695	KBTBD4
1128125	218581_at	445665	ABHD4
1139215	218597_s_at	43549	C10orf70
1128144	218613_at	236438	DKFZp761K1423
1128151	218625_at	103291	NRN1
1128157	218631_at	23918	VIP32
1139226	218633_x_at	266514	FLJ11342
1139230	218640_s_at	29724	PLEKHF2
1128164	218646_at	44344	FLJ20534
1139235	218651_s_at	416755	FLJ11196
1128167	218653_at	78457	SLC25A15
1128174	218665_at	19545	FZD4
1128192	218696_at	102506	EIF2AK3
1128195	218699_at	115325	RAB7L1
1139265	218722_s_at	187657	FLJ12436
1139266	218723_s_at	76640	RGC32
1128214	218734_at	408443	FLJ13848
1139274	218740_s_at	20157	CDK5RAP3
1139277	218747_s_at	267993	TAPBP-R
1139280	218751_s_at	312503	FBXW7
1128223	218753_at	55024	FLJ10307
1128231	218764_at	315366	PRKCH
1139301	218792_s_at	108502	BSPRY
1139303	218794_s_at	134406	FLJ20511
1128248	218802_at	234149	FLJ20647
1139314	218831_s_at	111903	FCGRT
1128283	218856_at	159651	TNFRSF21
1128287	218862_at	300063	ASB13
1128298	218887_at	55041	MRPL2
1128311	218909_at	30352	RPS6KC1
1128321	218921_at	433036	SIGIRR
1139360	218947_s_at	173946	FLJ10486
1128341	218955_at	274136	BRF2
1128356	218983_at	415792	C1RL
1128360	218988_at	445043	SLC35E3
1128377	219014_at	371003	PLAC8

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UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1128386	219025_at	195727	CD164L1
1128387	219028_at	397465	HIPK2
1139393	219032_x_at	170129	OPN3
1128395	219039_at	7188	SEMA4C
1128401	219049_at	341073	ChGn
1139411	219073_s_at	368238	OSBPL10
1128418	219082_at	433499	CGI-14
1128435	219109_at	6783	PF20
1128439	219118_at	438695	FKBP11
1128447	219130_at	40337	FLJ10287
1128457	219148_at	104741	TOPK
1139444	219151_s_at	355874	RABL2B
1128469	219173_at	390817	FLJ22686
1128471	219176_at	3592	FLJ22555
1139461	219191_s_at	14770	BIN2
1128494	219209_at	389539	MDA5
1139466	219210_s_at	365655	RAB8B
1128506	219226_at	416108	CRK7
1139483	219249_s_at	3849	FKBP10
1128535	219278_at	194694	MAP3K6
1128536	219279_at	21126	DOCK10
1139526	219356_s_at	415534	C9orf83
1139528	219360_s_at	31608	TRPM4
1139531	219365_s_at	145156	MGC8407
1128585	219366_at	63168	AVEN
1139542	219396_s_at	512732	NEIL1
1128615	219410_at	104800	FLJ10134
1128626	219424_at	501452	EBI3
1139552	219441_s_at	413386	LRRK1
1128648	219452_at	499331	DPEP2
1139556	219457_s_at	413374	RIN3
1128653	219461_at	21420	PAK6
1128655	219463_at	22920	C20orf103
1128660	219471_at	413071	C13orf18
1128681	219500_at	191548	CLC
1128688	219509_at	238756	MYOZ1
1139572	219511_s_at	24948	SNCAIP
1128694	219517_at	171466	ELL3
1139575	219519_s_at	31869	SN
1139579	219528_s_at	57987	BCL11B
1128705	219535_at	109437	HUNK
1128710	219542_at	159146	NEK11
1128713	219545_at	17296	KCTD14
1128733	219572_at	489847	CADPS2
1128738	219581_at	335550	MGC2776
1139603	219603_s_at	145956	ZNF226
1128757	219618_at	142295	IRAK4
1128781	219648_at	79741	FLJ10116
1128786	219654_at	114062	PTPLA
1128787	219655_at	114611	C7orf10
1139623	219667_s_at	193736	BANK1
1128801	219676_at	288539	ZNF435
1128807	219686_at	58241	HSA250839
1128845	219734_at	272416	FLJ20174
1128860	219753_at	323634	STAG3
1139645	219757_s_at	134051	C14orf101
1139654	219787_s_at	293257	ECT2
1139661	219806_s_at	416456	FN5
1128900	219812_at	323634	STAG3
1128901	219813_at	487239	LATS1
1139663	219816_s_at	4997	RNPC4
1128915	219831_at	105818	CDKL3
1139669	219837_s_at	13872	C17
1128965	219901_at	170623	FGD6
1128969	219906_at	446590	FLJ10213
1129024	220005_at	13040	GPR86
1129026	220007_at	135146	FLJ13984
1129043	220028_at	23994	ACVR2B
1129049	220034_at	268552	IRAK3
1129059	220054_at	98309	IL23A
1129061	220056_at	110915	IL22RA1
1129064	220059_at	121128	BRDG1
1129071	220068_at	136713	VPREB3

TABLE 2-continued

UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1129085	220088_at	2161	C5R1
1129103	220118_at	99430	TZFP
1139767	220127_s_at	12439	FBXL12
1139774	220140_s_at	15827	SNX11
1129120	220146_at	179152	TLR7
1129151	220196_at	432676	MUC16
1139805	220230_s_at	414362	CYB5R2
1129203	220273_at	110040	IL17B
1129223	220296_at	13785	GALNT10
1129228	220302_at	148496	MAK
1129232	220307_at	157872	CD244
1129245	220322_at	211238	IL1F9
1139830	220330_s_at	221851	SAMSN1
1139831	220335_x_at	268700	FLJ21736
1129265	220351_at	310512	CCRL1
1139839	220357_s_at	62863	SGK2
1129269	220358_at	62919	SNFT
1139842	220367_s_at	133523	SAP130
1129281	220377_at	395486	C14orf110
1129310	220415_at	414091	TNNI3K
1129336	220448_at	252617	KCNK12
1129419	220565_at	278446	GPR2
1139925	220643_s_at	173438	FAIM
1129495	220684_at	272409	TBX21
1129517	220712_at		
1139949	220725_x_at	528684	FLJ23558
1139950	220731_s_at	437385	FLJ10420
1129535	220737_at	368153	RPS6KA6
1139955	220740_s_at	4876	SLC12A6
1139957	220742_s_at	63657	NGLY1
1129537	220745_at	71979	IL19
1139962	220751_s_at	10235	C5orf4
1139969	220761_s_at	12040	JIK
1139971	220765_s_at	127273	LIMS2
1140007	220865_s_at	279865	TPRT
1140018	220917_s_at	438482	PWDMP
1140027	220933_s_at	12742	ZCCHC6
1140031	220937_s_at	3972	SIAT7D
1129661	220971_at	302036	IL17E
1140072	220984_s_at	199750	SLCO5A1
1140075	220987_s_at	172012	SNARK
1140088	221002_s_at	509050	DC-TM4F2
1140127	221044_s_at	125300	TRIM34
1140151	221080_s_at	236449	FAM31C
1129681	221085_at	241382	TNFSF15
1129694	221111_at	272350	IL26
1129743	221191_at	429531	DKFZP434A0131
1140214	221215_s_at	55565	ANKRD3
1140236	221239_s_at	194976	SPAP1
1140238	221241_s_at	11962	BCL2L14
1129754	221271_at	302014	IL21
1129760	221287_at	404277	RNASEL
1129812	221355_at	248101	CHRNG
1129821	221367_at	248146	MOS
1129825	221371_at	248197	TNFSF18
1129874	221463_at	247838	CCL24
1129879	221468_at	248116	XCR1
1140344	221479_s_at	132955	BNIP3L
1129887	221485_at	107526	B4GALT5
1140370	221520_s_at	48855	CDCA8
1140378	221530_s_at	437282	BHLHB3
1129907	221539_at	406408	EIF4EBP1
1129911	221549_at	400625	GRWD1
1140391	221558_s_at	44865	LEF1
1129917	221560_at	118843	MARK4
1129923	221571_at	297660	TRAF3
1140399	221577_x_at	296638	GDF15
1140404	221584_s_at	354740	KCNMA1
1140416	221601_s_at	58831	TOSO
1129943	221626_at	512828	ZNF506
1140457	221658_s_at	210546	IL21R
1140464	221667_s_at	111676	HSPB8
1140473	221676_s_at	17377	CORO1C

TABLE 2-continued

UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1140491	221696_s_at	24979	DKFZp761P1010
1140497	221704_s_at	77870	FLJ12750
1129967	221739_at	10927	C19orf10
1140520	221741_s_at	11747	C20orf21
1129978	221753_at	60377	SSH1
1140524	221766_s_at	10784	C6orf37
1129993	221777_at	412981	FLJ14827
1140534	221790_s_at	184482	ARH
1130007	221796_at	439109	NTRK2
1130030	221834_at	301872	LONP
1130040	221855_at	356460	
1130054	221872_at	82547	RARRES1
1140565	221875_x_at	411958	HLA-F
1140567	221881_s_at	25035	CLIC4
1140570	221891_x_at	180414	HSPA8
1140571	221893_s_at	210397	ADCK2
1130072	221898_at	468675	T1A-2
1130078	221905_at	386952	CYLD
1140574	221912_s_at	17987	MGC1203
1130088	221918_at	258536	PCTK2
1130090	221922_at	278338	GPSM2
1140584	221932_s_at	294083	C14orf87
1140589	221942_s_at	433488	GUCY1A3
1130114	221965_at	445084	MPHOSPH9
1130117	221969_at	22030	PAX5
1130121	221978_at	411958	HLA-F
1140613	221998_s_at	443330	VRK3
1140630	222033_s_at	347713	FLT1
1140632	222036_s_at	460184	MCM4
1130155	222043_at	436657	CLU
1130168	222061_at	75626	CD58
1130169	222062_at	132781	IL27RA
1130201	222126_at	278502	HRBL
1140729	222223_s_at	207224	IL1F5
1140745	222245_s_at	72222	FER1L4
1130293	222315_at	292853	
1130337	222368_at	491069	
1095985	222450_at	83883	TMEPAI
1095996	222482_at	288801	SSBP3
1114679	222503_s_at	16470	FLJ10904
1096028	222557_at	285753	STMN3
1114715	222565_s_at	434387	PRKCN
1096035	222569_at	105794	UGCGL1
1096038	222572_at	22265	PPM2C
1114726	222590_s_at	3532	NLK
1096054	222606_at	21331	FLJ10036
1096070	222640_at	241565	DNMT3A
1096077	222659_at	441043	IPO11
1096078	222661_at	284216	HSU84971
1114766	222666_s_at	113052	RCL1
1096085	222674_at	224137	HSPC109
1096108	222731_at	292871	ZDHHC2
1114824	222762_x_at	193370	LIMD1
1114853	222812_s_at	512618	ARHF
1096149	222824_at	410205	NUDT5
1096152	222828_at	288240	IL20RA
1096158	222838_at	132906	SLAMF7
1096163	222848_at	164018	FKSG14
1114877	222862_s_at	18268	AK5
1096172	222880_at	300642	AKT3
1096180	222890_at	11614	HSPC065
1114893	222891_s_at	314623	BCL11A
1096182	222899_at	256297	ITGA11
1114913	222920_s_at	33187	KIAA0748
1096220	222974_at	287369	IL22
1114967	223028_s_at	7905	SNX9
1114970	223032_x_at	279529	PX19
1096248	223040_at	109253	NAT5
1096251	223044_at	409875	SLC40A1
1114977	223052_x_at	30026	HSPC182
1114981	223057_s_at	203206	XPO5
1114988	223075_s_at	4944	C9orf58
1115008	223117_s_at	441028	USP47

TABLE 2-continued

UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1115012	223122_s_at	31386	SFRP2
1096297	223141_at	9597	UCK1
1096300	223151_at	74284	MGC2714
1115034	223158_s_at	387222	NEK6
1115052	223190_s_at	380021	MLL5
1115071	223218_s_at	390476	MAIL
1115073	223220_s_at	131315	BAL
1096341	223241_at	12169	SNX8
1096356	223266_at	259230	ALS2CR2
1096357	223267_at	57898	FLJ20432
1096362	223274_at	512706	TCF19
1096364	223276_at	29444	NID67
1096369	223286_at	417029	DERP6
1096378	223303_at	180535	URP2
1096379	223304_at	439590	SLC37A3
1115128	223349_s_at	293753	BOK
1096406	223361_at	238205	C6orf115
1096429	223405_at	64896	NPL
1115160	223413_s_at	425427	LYAR
1096440	223423_at	231320	GPR160
1096442	223430_at	306864	SIK2
1096446	223434_at	92287	GBP3
1115176	223451_s_at	15159	CKLF
1096456	223454_at	82407	CXCL16
1096460	223460_at	8417	CAMKK1
1096466	223467_at	25829	RASD1
1096469	223471_at	103267	RAB3IP
1115186	223480_s_at	283734	MRPL47
1115194	223502_s_at	270737	TNFSF13B
1096499	223514_at	293867	CARD11
1096503	223522_at	21379	C9orf45
1115203	223534_s_at	414481	RPS6KL1
1096530	223565_at	409563	PACAP
1115226	223600_s_at	279718	KIAA1683
1096570	223624_at	409813	ANUBL1
1096579	223640_at	117339	HCST
1115253	223664_x_at	310922	BCL2L13
1096609	223696_at	528631	ARSD
1115271	223705_s_at	71252	DKFZp761C169
1096615	223707_at	356342	RPL27A
1096616	223708_at	119302	C1QTNF4
1096617	223710_at	131342	CCL26
1096621	223715_at	170819	STK29
1115286	223750_s_at	120551	TLR10
1115290	223759_s_at	193666	GSG2
1115303	223787_s_at	236257	LOC51244
1115309	223804_s_at	443081	DKFZP434F091
1096690	223827_at	334174	TNFRSF19
1096693	223834_at	443271	PDCD1LG1
1115329	223852_s_at	439658	MGC4796
1096719	223874_at	250153	ARP3BETA
1115338	223883_s_at	224355	STK31
1096738	223903_at	87968	TLR9
1115347	223909_s_at	112272	HDAC8
1096742	223910_at	114905	ERN2
1115360	223940_x_at	187199	PRO1073
1096805	224027_at	334633	CCL28
1096829	224071_at	272373	IL20
1096834	224079_at	278911	IL17C
1096877	224132_at	326732	MGC13008
1115441	224156_x_at	5470	IL17RB
1096903	224185_at	437460	FLJ10385
1096936	224262_at	306974	IL1F10
1115519	224302_s_at	408914	MRPS36
1096965	224346_at	433466	PRO1853
1115566	224369_s_at	163825	SP329
1096981	224399_at	61929	PDCD1LG2
1115587	224402_s_at	120260	IRTA1
1115589	224406_s_at	415950	IRTA2
1115591	224409_s_at	367871	SSTK
1115607	224428_s_at	435733	CDCA7
1115621	224450_s_at	437474	RIOK1
1115646	224481_s_at	210850	HECTD1

TABLE 2-continued

UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1115668	224509_s_at	155839	RTN4IP1
1115673	224514_x_at	129959	IL17RC
1115679	224523_s_at	8345	MGC4308
1115695	224553_s_at	212680	TNFRSF18
1115696	224555_x_at	166371	IL1F7
1115704	224569_s_at	350268	IRF2BP2
1097030	224574_at	511801	
1097065	224621_at	324473	MAPK1
1097096	224659_at	8518	SEPN1
1097107	224673_at	502378	LENG8
1097109	224675_at	78871	MESDC2
1097126	224694_at	274520	ANTXR1
1097143	224716_at	74335	HSPCB
1097156	224733_at	298198	CKLFSF3
1097161	224740_at	5064	
1097172	224753_at	434886	CDCA5
1097177	224761_at	9691	GNA13
1097195	224785_at	149931	MGC29814
1097202	224796_at	386779	DDEF1
1097229	224830_at	446393	CPSF5
1097236	224837_at	235860	FOXP1
1115763	224839_s_at	355862	GPT2
1097247	224851_at	388761	CDK6
1097253	224859_at	77873	B7H3
1097255	224861_at	380144	
1097271	224880_at	6906	RALA
1097280	224891_at	423523	
1097281	224892_at	7037	PLDN
1097282	224893_at	356719	LOC283241
1097290	224903_at	151001	CIRH1A
1097297	224917_at	166254	VMP1
1097307	224929_at	379754	LOC340061
1097310	224934_at	5672	SMAP-5
1097325	224951_at	458450	LASS5
1097329	224955_at	528675	TEAD1
1097334	224960_at	71573	FLJ10074
1097359	224990_at	518723	
1097365	224998_at	325825	CKLFSF4
1097371	225005_at	7299	PHF13
1097383	225019_at	111460	CAMK2D
1097388	225024_at	278839	C20orf77
1097395	225032_at	299883	FAD104
1115800	225040_s_at	282260	RPE
1097424	225067_at	7978	DKFZP434C131
1097441	225086_at	6799	FLJ38426
1097448	225093_at	250607	UTRN
1115812	225164_s_at	412102	EIF2AK4
1115813	225175_s_at	105509	CTL2
1097540	225195_at	388087	
1097553	225214_at	197071	PSMB7
1097561	225224_at	19221	DKFZP566G1424
1097563	225226_at	169577	FLJ14743
1097564	225227_at	272108	SKIL
1115829	225253_s_at	433213	METTL2
1097600	225272_at	10846	SAT2
1097609	225283_at	6093	ARRDC4
1097610	225284_at	6019	DNAJC3
1097611	225285_at	438993	BCAT1
1097614	225289_at	410491	MGC16063
1115840	225308_s_at	437362	KIAA1728
1097637	225317_at	63220	ACBD6
1097665	225351_at	434241	HT011
1097676	225366_at	23363	PGM2
1097683	225373_at	132569	PP2135
1097684	225374_at	368878	MGC45714
1097704	225399_at	440663	C1orf19
1097707	225402_at	440263	C20orf64
1097717	225412_at	23317	FLJ14681
1097735	225436_at	26765	LOC58489
1097804	225519_at	446590	FLJ10213
1097814	225529_at	21446	CENTB5
1115876	225535_s_at	11866	TIMM23
1097824	225540_at	167	MAP2

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UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1115877	225552_x_at	76239	MGC3047
1097887	225611_at	212787	KIAA0303
1097897	225622_at	266175	PAG
1097899	225624_at	145047	LOC92017
1097901	225626_at	266175	PAG
1115888	225629_s_at	35096	ZBTB4
1097902	225630_at	412318	KIAA1706
1115892	225649_s_at	100057	STK35
1097918	225650_at	140309	LOC90378
1097928	225660_at	443012	SEMA6A
1097930	225662_at	115175	ZAK
1097940	225673_at	380906	MYADM
1115895	225682_s_at	202505	RPC8
1097948	225684_at	69476	LOC348235
1097961	225699_at	25892	
1097966	225704_at	127270	KIAA1545
1097976	225715_at	218017	raptor
1098012	225756_at	355669	CSNK1E
1115905	225757_s_at	301478	CLMN
1098023	225773_at	181161	KIAA1972
1098065	225817_at	10119	FLJ14957
1098069	225823_at	356626	
1115916	225836_s_at	157148	MGC13204
1115917	225849_s_at	284265	C6orf83
1098095	225852_at	131059	ANKRD17
1098103	225864_at	124951	NSE2
1098145	225913_at	9587	KIAA2002
1098152	225922_at	377588	KIAA1450
1098156	225927_at	170610	MAP3K1
1098168	225943_at	22151	NLN
1098174	225949_at	274401	LOC340371
1098179	225956_at	163725	LOC153222
1098186	225964_at	288697	MGC11349
1098195	225974_at	88594	DKFZp762C1112
1098204	225984_at	43322	PRKAA1
1098220	226002_at	80720	GAB1
1098234	226016_at	446414	CD47
1098235	226017_at	440494	CKLFSF7
1098242	226025_at	273104	KIAA0379
1098252	226035_at	16953	USP31
1098256	226041_at	431871	SVH
1098258	226043_at	239370	GPSM1
1098268	226053_at	110299	MAP2K7
1098271	226056_at	300670	CDGAP
1098277	226065_at	6786	PRICKLE1
1098278	226066_at	166017	MITF
1098303	226096_at	15463	FNDC5
1115953	226111_s_at	278422	ZNF385
1115955	226132_s_at	7988	FLJ31434
1098338	226136_at	269857	HRB2
1115960	226145_s_at	15420	FRAS1
1115965	226166_x_at	26996	STK36
1098405	226218_at	362807	IL7R
1098412	226225_at	409515	MCC
1098415	226230_at	130900	KIAA1387
1098433	226250_at	202577	
1098447	226267_at	154095	JDP2
1098459	226279_at	25338	SPUVE
1098461	226281_at	234074	DNER
1098476	226299_at	300485	pknbeta
1098495	226318_at	443668	TBRG1
1098506	226333_at	193400	IL6R
1098521	226350_at	170129	OPN3
1098548	226377_at	436639	NFIC
1098550	226381_at	355655	
1098553	226384_at	437179	HTPAP
1098574	226410_at	79077	KIAA0233
1098592	226431_at	283707	ALS2CR13
1098604	226444_at	32793	SLC39A10
1098607	226448_at	38516	MGC15887
1098611	226452_at	433611	PDK1
1098613	226454_at	388125	RENT1
1098618	226459_at	374836	PIK3AP1

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UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1116001	226465_s_at	430541	SON
1098629	226473_at	103305	
1116006	226491_x_at	172550	PTBP1
1098658	226507_at	64056	PAK1
1098668	226517_at	438993	BCAT1
1098669	226518_at	302746	KCTD10
1098678	226530_at	386140	BMF
1098683	226535_at	57664	ITGB6
1098694	226548_at	97837	
1098718	226574_at	16364	PSPC1
1116022	226611_s_at	433422	p30
1098771	226638_at	374446	KIAA1501
1098784	226653_at	12808	MARK1
1098809	226682_at	359394	
1098821	226694_at	42322	PALM2
1098822	226695_at	443452	PRRX1
1098832	226705_at	748	FGFR1
1098840	226713_at	55098	C3orf6
1098862	226737_at	303669	MGC26694
1098865	226741_at	250905	LOC51234
1098883	226760_at	412014	MBTPS2
1098893	226771_at	43577	ATP8B2
1098898	226777_at	8850	ADAM12
1098909	226789_at	446408	
1098918	226799_at	170623	FGD6
1098927	226811_at	356216	FLJ20202
1116045	226828_s_at	23823	HEYL
1098946	226834_at	135121	ASAM
1098951	226840_at	75258	H2AFY
1098952	226841_at	62264	KIAA0937
1098954	226844_at	128905	MOBKL2B
1098962	226853_at	20137	BMP2K
1098978	226869_at	124863	
1098987	226879_at	412559	FLJ21127
1098991	226884_at	126085	LRRN1
1116056	226913_s_at	243678	SOX8
1099028	226930_at	334838	FNDC1
1099032	226936_at	35962	
1099040	226944_at	390421	HTRA3
1116063	226957_x_at	75447	RALBP1
1099053	226959_at	376041	
1099058	226964_at	425116	
1099072	226979_at	28827	MAP3K2
1099088	226996_at	14355	
1099105	227013_at	78960	LATS2
1099112	227020_at	368672	
1099120	227030_at	371680	
1099124	227034_at	355455	9/10/2004
1099128	227039_at	350631	AKAP13
1099135	227046_at	3402	SLC39A11
1099140	227052_at	500350	
1099148	227060_at	434975	TNFRSF19L
1099150	227062_at	240443	
1099152	227064_at	351247	MGC15396
1099154	227066_at	97927	MOBKL2C
1116071	227067_x_at	502564	FLJ20719
1099167	227080_at	381105	MGC45731
1116073	227103_s_at	146161	MGC2408
1099204	227121_at	193784	
1116085	227173_s_at	88414	BACH2
1099265	227193_at	375762	
1099291	227222_at	130774	FBXO10
1099292	227223_at	282901	RNPC2
1099299	227232_at	241471	EVL
1099318	227255_at	29911	LOC149420
1099328	227267_at	432726	FLJ35779
1099332	227272_at	32433	
1099358	227300_at	93135	
1116103	227308_x_at	289019	LTBP3
1099377	227324_at	130712	ADCK4
1099388	227336_at	124024	DTX1
1099396	227346_at	435949	ZNFN1A1
1099403	227354_at	266175	PAG

TABLE 2-continued

UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1099418	227370_at	172792	KIAA1946
1099444	227407_at	434489	FLJ90013
1116122	227408_s_at	42768	DKFZp761O0113
1116126	227432_s_at	438669	INSR
1099510	227482_at	15251	ADCK1
1099526	227502_at	521240	LCHN
1099539	227520_at	201624	CXorf15
1099549	227533_at	446665	
1099563	227550_at	388347	
1099598	227590_at	511859	
1116150	227606_s_at	16229	AMSH-LP
1099631	227624_at	367639	FLJ20032
1099633	227627_at	380877	SGKL
1099651	227646_at	120785	EBF
1099669	227666_at	45057	MGC45428
1099680	227677_at	210387	JAK3
1099686	227684_at	117721	
1099699	227697_at	436943	SOCS3
1099711	227713_at	243596	
1099734	227740_at	127310	KIS
1099743	227750_at	162189	TRAD
1099748	227755_at	356481	
1099760	227767_at	129206	CSNK1G3
1099798	227811_at	411081	FGD3
1099826	227842_at	445862	RAB30
1099830	227847_at	28020	EPM2AIP1
1099847	227867_at	36723	LOC129293
1099857	227877_at	119768	
1116181	227891_s_at	402752	TAF15
1099886	227917_at	511708	
1099900	227934_at	444508	
1099939	227983_at	488173	MGC7036
1099951	227999_at	157728	LOC170394
1099953	228001_at	433668	C21orf4
1099960	228008_at	144583	
1099965	228014_at	71962	LOC138428
1099978	228035_at	148135	STK33
1116219	228056_s_at	322854	NAP1L
1099995	228057_at	107515	DDIT4L
1100005	228069_at	121536	DUFD1
1100027	228094_at	16291	AMICA
1100040	228109_at	410953	RASGRF2
1100042	228113_at	351413	RAB37
1116233	228128_x_at	440769	PAPPA
1100054	228130_at	125353	
1100060	228139_at	268551	RIPK3
1100071	228153_at	432653	IBRDC2
1100130	228224_at	76494	PRELP
1100136	228231_at	413078	NUDT1
1100138	228234_at	278391	TIRP
1100144	228240_at	436379	
1100150	228248_at	9343	MGC39830
1100159	228258_at	32156	RPS6KB2
1100161	228261_at	135805	LOC142678
1100171	228273_at	528654	FLJ11029
1100183	228286_at	180582	FLJ40869
1100249	228367_at	388674	HAK
1100258	228377_at	88442	KIAA1384
1100263	228382_at	406335	LOC90268
1116277	228384_s_at	118210	C10orf33
1100288	228411_at	26981	ALS2CR19
1100290	228414_at	4241	
1100301	228426_at	356250	LLT1
1100311	228437_at	445890	HSPC163
1100335	228464_at	268474	
1100339	228468_at	276905	MASTL
1100384	228524_at	283374	ADCK5
1100405	228549_at	119387	KIAA0792
1100420	228565_at	50883	KIAA1804
1100423	228568_at	50841	FLJ30973
1100433	228580_at	390421	HTRA3
1100443	228592_at	438040	MS4A1
1100496	228654_at	111496	LOC139886

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UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1116317	228661_s_at	526415	
1100538	228709_at	432458	PRG4
1100561	228736_at	194109	HEL308
1100562	228737_at	26608	C20orf100
1100581	228758_at	155024	BCL6
1100585	228762_at	159142	LFNG
1100591	228769_at	388162	HKR2
1100598	228776_at	531058	
1100609	228788_at	447045	PPIL2
1100625	228806_at	232803	
1100721	228918_at	18713	
1100750	228955_at	280387	
1100753	228958_at	512717	ZNF19
1100770	228976_at	65578	
1100847	229070_at	97411	C6orf105
1100849	229072_at	184430	
1100851	229074_at	55058	EHD4
1100871	229101_at	48353	
1100873	229103_at	445884	
1100879	229111_at	119983	MASP2
1100904	229145_at	426296	LOC119504
1100911	229152_at	320147	C4orf7
1100916	229158_at	105448	PRKWNK4
1100977	229233_at	444783	NRG3
1100995	229256_at	26612	PGM2L1
1101004	229265_at	2969	SKI
1101023	229288_at	73962	EPHA7
1101054	229322_at	173328	PPP2R5E
1116432	229356_x_at	409362	KIAA1259
1101096	229373_at	527236	
1101119	229401_at	390823	IL17RE
1101128	229411_at	436667	MGC45419
1116445	229436_x_at	301927	C6.1A
1101149	229437_at	517226	BIC
1101211	229513_at	287659	STRBP
1101272	229584_at	179089	DKFZp434H2111
1101276	229588_at	1098	ERdj5
1101291	229606_at	272458	PPP3CA
1101295	229610_at	99807	FLJ40629
1101305	229623_at	112742	
1101322	229645_at	227699	
1101354	229686_at	111377	P2RY8
1101416	229764_at	338851	FLJ41238
1101430	229779_at	418040	
1101439	229790_at	63335	TERF2
1101477	229838_at	423095	NUCB2
1101478	229839_at	146246	MGC45780
1101514	229886_at	88801	FLJ32363
1101566	229947_at	98558	
1101582	229967_at	195685	CKLFSF2
1101586	229971_at	187884	GPR114
1101628	230021_at	441708	MGC45866
1101634	230028_at	510588	
1101687	230086_at	440808	FNBP1
1101708	230110_at	459526	MCOLN2
1101758	230170_at	248156	OSM
1101775	230191_at	343820	TTBK1
1101777	230193_at	359981	MGC33630
1101829	230252_at	155538	GPR92
1101892	230327_at	225948	
1116593	230329_s_at	422889	NUDT6
1101905	230345_at	170843	
1101944	230391_at	439064	
1101948	230395_at	14411	
1101974	230425_at	272311	EPHB1
1102027	230489_at	58685	CD5
1102030	230494_at	110855	SLC20A1
1102081	230551_at	506977	
1102165	230650_at	152460	
1102193	230680_at	22668	
1102282	230788_at	934	GCNT2
1116666	230803_s_at	442801	DKFZP564B1162
1102350	230864_at	25845	MGC42105

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UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1116676	230894_s_at	185084	MSI2
1102408	230934_at	306327	RAB3GAP
1102415	230942_at	99272	CKLFSF5
1102437	230966_at	437023	IL4I1
1102470	231007_at	292915	
1102471	231008_at	158357	UNC5CL
1102479	231017_at	301772	STK11
1102537	231087_at	202151	
1102540	231093_at	434881	FCRH3
1116715	231149_s_at	123427	FLJ20574
1102633	231198_at	511124	
1102652	231219_at	343717	CKLFSF1
1102654	231221_at	380599	KIAA0350
1102725	231303_at	234016	C21orf42
1102744	231324_at	198671	
1102821	231412_at	202024	
1102859	231455_at	446195	
1102885	231481_at	130310	CCNB3
1102898	231496_at	145519	FKSG87
1102912	231514_at	194610	MGC15882
1103054	231690_at	341531	
1103107	231759_at	247978	TAL2
1103111	231763_at	436896	RPC155
1103120	231775_at	401745	TNFRSF10A
1103124	231779_at	424542	IRAK2
1103134	231792_at	86092	MYLK2
1103137	231796_at	283613	EPHA8
1103139	231798_at	248201	NOG
1116826	231823_s_at	26204	KIAA1295
1116829	231840_x_at	115467	LOC90624
1103224	231906_at	301963	HOXD8
1116844	231920_s_at	405789	CSNK1G1
1103264	231954_at	142307	DKFZP434I0714
1103272	231964_at	137206	
1103284	231978_at	186655	TPCN2
1116854	231992_x_at	438623	
1103303	232000_at	49605	C9orf52
1103304	232001_at	46919	
1116863	232068_s_at	174312	TLR4
1103390	232103_at	271752	BPNT1
1103398	232112_at	220745	FLJ10244
1103420	232138_at	372571	MBNL2
1116879	232160_s_at	325630	TNIP2
1103475	232204_at	120785	EBF
1103497	232231_at	50115	
1103504	232239_at	142517	
1103540	232282_at	92423	PRKWNK3
1103639	232399_at	388304	KIAA1765
1103711	232478_at	288718	
1103766	232546_at	192132	TP73
1103855	232645_at	259625	LOC153684
1103858	232648_at	246240	PSMA3
1116958	232693_s_at	27410	PBF
1103921	232724_at	371612	MS4A6A
1103932	232741_at	31330	
1116966	232744_x_at	301124	
1103982	232798_at	142926	MGC26226
1104072	232906_at	287429	
1104175	233029_at	287383	KIAA1639
1104195	233052_at	172101	DNAH8
1117023	233110_s_at	289052	BCL2L12
1104254	233121_at	492700	
1104373	233271_at		
1104545	233476_at	254477	
1104552	233483_at	193857	LOC96597
1104840	233867_at	482250	
1104870	233916_at	210958	KIAA1486
1117211	233955_x_at	356509	HSPC195
1104905	233964_at	13453	FLJ14753
1104910	233969_at	458262	IGL@
1105001	234088_at	527386	
1117245	234107_s_at	527974	HARS2
1105178	234284_at	283961	GNG8

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UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1117278	234312_s_at	14779	ACAS2
1117298	234366_x_at	449586	
1105248	234403_at		
1117343	234643_x_at	306812	BUCS1
1117350	234672_s_at	435982	FLJ10407
1117373	234725_s_at	416077	SEMA4B
1117394	234792_x_at		
1117403	234863_x_at	272027	FBXO5
1105668	234954_at		
1105684	234973_at	195155	SLC38A5
1105728	235022_at	13034	MGC24180
1105732	235026_at	396626	FLJ32549
1105751	235046_at	176376	
1105759	235056_at	171262	ETV6
1105798	235099_at	154986	CKLFSF8
1105814	235117_at	105223	
1105832	235136_at	306777	GSDML
1105838	235142_at	129837	ZBTB8
1105842	235146_at	173392	KIAA1145
1105854	235158_at	267245	FLJ14803
1105866	235170_at	9521	ZNF92
1105900	235211_at	525015	
1105915	235229_at	332649	
1105935	235251_at	444290	
1105936	235252_at	276238	KSR
1105959	235278_at	399982	
1105986	235310_at	49614	GCET2
1106013	235341_at	6019	DNAJC3
1106015	235343_at	96885	FLJ12505
1106025	235353_at	49500	KIAA0746
1106030	235359_at	162185	UNQ3030
1106043	235372_at	266331	FREB
1106053	235383_at	154578	MYO7B
1106088	235421_at	499235	
1106110	235444_at	235860	FOXP1
1106124	235458_at	155111	HAVCR2
1106126	235460_at	434937	PPIB
1106159	235496_at	208081	
1106196	235536_at	142074	
1106204	235545_at	445098	SDP35
1106230	235572_at	381225	Spc24
1106279	235626_at	130065	CAMK1D
1106306	235657_at	14204	
1106317	235668_at	381140	PRDM1
1106323	235674_at	442690	
1106394	235750_at	126932	
1106401	235758_at	11849	MGC15827
1106415	235774_at	169071	
1117517	235816_s_at	148656	Rgr
1106478	235843_at	119898	
1106522	235890_at	31903	
1106589	235965_at	22627	MIST1
1106722	236109_at	150458	FLJ14494
1106781	236172_at	445013	LTB4R
1106855	236255_at	455101	KIAA1909
1117555	236295_s_at	128357	NOD3
1106908	236313_at	72901	CDKN2B
1106935	236341_at	247824	CTLA4
1106990	236401_at	369561	
1107044	236458_at	163426	
1107076	236491_at	283672	BCL2L10
1107124	236543_at	130203	
1107190	236614_at	50601	MGC10986
1107197	236621_at	40838	
1107329	236761_at	439124	LHFPL3
1107348	236782_at	440508	SAMD3
1107369	236805_at	512466	
1107457	236901_at	120330	ADAMTS2
1117599	236918_s_at	120277	MGC27085
1107527	236981_at	14706	
1107575	237033_at	424589	MGC52498
1107637	237104_at		

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UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1107762	237244_at	58597	
1107838	237322_at	355618	
1117644	237451_x_at	34174	
1107997	237493_at	126891	IL22RA2
1108088	237591_at	441601	
1108200	237710_at	156135	
1108237	237753_at	126232	
1108323	237849_at	526982	
1108347	237880_at	121476	
1108467	238018_at	346333	LOC285016
1108473	238025_at	119878	FLJ34389
1108515	238071_at	98132	LCN6
1108745	238323_at	528776	TEAD2
1117747	238365_s_at	158272	
1108776	238376_at	513346	
1108910	238536_at	351848	
1108925	238552_at	136102	KIAA0853
1108961	238593_at	292088	FLJ22531
1108970	238604_at	140489	
1108988	238624_at	3532	NLK
1117800	238701_x_at	125166	
1109058	238706_at	220277	FLJ38499
1109107	238759_at	292925	KIAA1212
1109188	238846_at	204044	TNFRSF11A
1109195	238853_at	416155	
1109210	238870_at	117010	KCNK9
1109220	238880_at	445977	GTF3A
1109505	239186_at	8162	MGC39372
1109519	239201_at	348711	ALS2CR7
1117835	239205_s_at	89688	CR1L
1109530	239214_at	123244	
1109545	239231_at	63187	
1109557	239243_at	444548	NP220
1109560	239246_at	207428	FARP1
1109603	239292_at		
1109732	239427_at	374124	
1109756	239453_at	530304	
1117853	239479_x_at	268724	
1109827	239533_at	127196	GPR155
1109913	239629_at	355724	CFLAR
1110019	239744_at		
1110070	239803_at		
1110099	239835_at	116665	TA-KRP
1110198	239946_at	189046	
1110214	239964_at	144519	TCL6
1110223	239973_at	212709	
1110284	240038_at	192221	ELL2
1110309	240066_at	105623	
1110313	240070_at	421750	FLJ39873
1110486	240260_at	445054	
1110608	240392_at	306227	CARD14
1110610	240394_at	436906	
1110740	240538_at	416810	
1110852	240661_at	196026	
1110871	240681_at	431753	
1117977	240854_x_at		
1111070	240899_at	202201	
1111478	241357_at	133017	ERK8
1111486	241365_at	33024	
1111494	241373_at	75432	IMPDH2
1111503	241383_at	502910	KBRAS2
1111694	241592_at	157302	
1111807	241751_at	6483	OFD1
1111946	241928_at	280881	
1112019	242013_at	196484	
1118148	242020_s_at	302123	ZBP1
1112052	242052_at	525361	
1112061	242064_at	43410	
1112256	242293_at	143198	ING3
1112344	242406_at	163242	
1118228	242520_s_at	173679	
1112510	242595_at	314432	C14orf20
1112521	242611_at	244818	

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UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1112552	242650_at	89029	
1112674	242794_at	310320	MAML3
1112689	242814_at	104879	SERPINB9
1118286	242866_x_at	147381	
1112762	242901_at	208179	
1112764	242903_at	180866	IFNGR1
1112837	242994_at	4099	NRD1
1112849	243006_at	208965	
1112871	243030_at	269493	
1112935	243099_at	436677	NFAM1
1112981	243154_at	86650	
1113020	243198_at	373484	LOC161577
1118347	243366_s_at	528404	ITGA4
1113263	243467_at	435736	
1113435	243659_at	100636	
1113488	243717_at	129435	
1113500	243729_at	165900	
1113545	243780_at	435736	
1113555	243791_at	291993	
1113589	243829_at	162967	BRAF
1118414	243968_x_at	415473	FCRH1
1113730	243993_at	293771	
1113769	244035_at	46996	
1113783	244052_at	71616	FLJ14431
1113930	244214_at	24725	MGC35521
1113972	244261_at	386334	IL28RA
1113993	244286_at	131811	
1114017	244313_at	133255	
1114064	244364_at	148228	MYO3A
1114109	244413_at	203041	DCAL1
1114162	244467_at	526942	
1114351	244677_at	445534	PER1
1114503	244845_at	170577	
1114543	244887_at	156189	
1118612	32625_at		
1118621	33307_at		
1130354	33323_r_at	184510	SFN
1118659	35617_at		
1118681	36711_at		
1118684	36830_at		
1118708	37408_at		
1118736	38340_at		
1118772	40420_at		
1130378	44783_s_at	234434	HEY1
1118835	47069_at		
1118861	49878_at		
1130387	50314_i_at	274422	C20orf27
1130393	58780_s_at	22451	FLJ10357
1118939	60528_at		
1118573	632_at		
1118949	64064_at		
1118963	65472_at		
1130400	74694_s_at	170253	FRA
1140788	AFFX-DapX-3_at		
1140834	AFFX-HSAC07/X00351_3_at	426930	ACTB
1140835	AFFX-HSAC07/X00351_5_at	426930	ACTB
1140836	AFFX-HSAC07/X00351_M_at	426930	ACTB
1140842	AFFX-HUMGAPDH/M33197_3_at	169476	GAPD
1140843	AFFX-HUMGAPDH/M33197_5_at	169476	GAPD
1140844	AFFX-HUMGAPDH/M33197_M_at	169476	GAPD
1140845	AFFX-HUMISGF3A/M97935_3_at	21486	STAT1
1140846	AFFX-HUMISGF3A/M97935_5_at	21486	STAT1
1140847	AFFX-HUMISGF3A/M97935_MA_at	21486	STAT1
1140848	AFFX-HUMISGF3A/M97935_MB_at	21486	STAT1
1140837	AFFX-HUMRGE/M10098_3_at		
1140838	AFFX-HUMRGE/M10098_5_at		
1140839	AFFX-HUMRGE/M10098_M_at		
1140791	AFFX-LysX-3_at		
1140792	AFFX-LysX-5_at		
1140793	AFFX-LysX-M_at		
1140806	AFFX-M27830_3_at		
1140807	AFFX-M27830_5_at		
1140808	AFFX-M27830_M_at		

TABLE 2-continued

UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1140794	AFFX-PheX-3_at		
1140795	AFFX-PheX-5_at		
1140796	AFFX-PheX-M_at		
1140797	AFFX-ThrX-3_at		
1140798	AFFX-ThrX-5_at		
1140799	AFFX-ThrX-M_at		
1140802	AFFX-TrpnX-3_at		
1140803	AFFX-TrpnX-5_at		
1140804	AFFX-TrpnX-M_at		
1140805	AFFX-hum_alu_at		
1140809	AFFX-r2-Bs-dap-3_at		
1140810	AFFX-r2-Bs-dap-5_at		
1140811	AFFX-r2-Bs-dap-M_at		
1140812	AFFX-r2-Bs-lys-3_at		
1140813	AFFX-r2-Bs-lys-5_at		
1140814	AFFX-r2-Bs-lys-M_at		
1140815	AFFX-r2-Bs-phe-3_at		
1140816	AFFX-r2-Bs-phe-5_at		
1140817	AFFX-r2-Bs-phe-M_at		
1140827	AFFX-r2-Bs-thr-3_s_at		
1140828	AFFX-r2-Bs-thr-5_s_at		
1140829	AFFX-r2-Bs-thr-M_s_at		
1140820	AFFX-r2-Ec-bioB-3_at		
1140821	AFFX-r2-Ec-bioB-5_at		
1140822	AFFX-r2-Ec-bioB-M_at		
1140823	AFFX-r2-Ec-bioC-3_at		
1140824	AFFX-r2-Ec-bioC-5_at		
1140825	AFFX-r2-Ec-bioD-3_at		
1140826	AFFX-r2-Ec-bioD-5_at		
1140818	AFFX-r2-P1-cre-3_at		
1140819	AFFX-r2-P1-cre-5_at		
1529284	Lymph_Dx_001_at	409515	MCC
1529285	Lymph_Dx_002_at	348929	KIAA1219
1529286	Lymph_Dx_003_at	167700	MADH5
1529287	Lymph_Dx_004_s_at	212787	KIAA0303
1529288	Lymph_Dx_005_at	13291	CCNG2
1529443	Lymph_Dx_006_at	88886	
1529289	Lymph_Dx_007_at	96557	
1529290	Lymph_Dx_008_at	101761	N4BP3
1529291	Lymph_Dx_009_at	104450	
1529292	Lymph_Dx_010_at		
1529293	Lymph_Dx_011_at	113117	
1529294	Lymph_Dx_011_s_at	113117	
1529295	Lymph_Dx_012_at	116441	
1529296	Lymph_Dx_013_at	122428	
1529444	Lymph_Dx_014_at	126905	
1529297	Lymph_Dx_015_at	132335	
1529298	Lymph_Dx_016_at	136707	
1529299	Lymph_Dx_017_at	444290	
1529300	Lymph_Dx_018_at	449608	
1529301	Lymph_Dx_019_at		
1529445	Lymph_Dx_020_at		
1529302	Lymph_Dx_021_at	67928	ELF3
1529303	Lymph_Dx_022_at		
1529304	Lymph_Dx_022_s_at		
1529305	Lymph_Dx_023_at	173957	
1529306	Lymph_Dx_024_at	190043	MGC26706
1529446	Lymph_Dx_025_at	190626	
1529307	Lymph_Dx_026_at	435736	
1529308	Lymph_Dx_027_x_at	193014	
1529309	Lymph_Dx_028_at	512797	HSH2
1529310	Lymph_Dx_029_x_at	3136	PRKAG1
1529311	Lymph_Dx_030_at	251214	
1529312	Lymph_Dx_031_s_at	255809	
1529313	Lymph_Dx_032_at	271998	
1529314	Lymph_Dx_033_at		
1529315	Lymph_Dx_034_at	530912	
1529316	Lymph_Dx_035_at	315241	ZNF198
1529447	Lymph_Dx_036_at	291886	
1529317	Lymph_Dx_037_at		
1529318	Lymph_Dx_038_at	291954	
1529319	Lymph_Dx_039_at	103329	KIAA0970
1529320	Lymph_Dx_040_at	309149	

TABLE 2-continued

UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1529321	Lymph_Dx_041_s_at	411311	IL24
1529322	Lymph_Dx_042_x_at	514291	
1529323	Lymph_Dx_043_at		
1529324	Lymph_Dx_044_at	348264	GZMH
1529325	Lymph_Dx_045_at		
1529326	Lymph_Dx_046_s_at	200063	HDAC7A
1529327	Lymph_Dx_047_s_at	288986	SMN2
1529328	Lymph_Dx_048_s_at	369056	
1529448	Lymph_Dx_049_at	369101	
1529329	Lymph_Dx_049_s_at	369101	
1529330	Lymph_Dx_050_at	259625	LOC153684
1529331	Lymph_Dx_051_s_at	374126	
1529332	Lymph_Dx_052_at	140443	LOC134492
1529333	Lymph_Dx_053_at	378849	
1529334	Lymph_Dx_054_at	529494	
1529335	Lymph_Dx_055_s_at	400872	
1529336	Lymph_Dx_056_at	405474	PTK2B
1529337	Lymph_Dx_057_at	201864	C6orf166
1529338	Lymph_Dx_058_s_at	284275	PAK2
1529339	Lymph_Dx_059_s_at		
1529449	Lymph_Dx_060_s_at		
1529340	Lymph_Dx_061_at		
1529341	Lymph_Dx_062_at	153563	LY75
1529342	Lymph_Dx_063_at		
1529343	Lymph_Dx_064_at	521948	
1529344	Lymph_Dx_065_at	317970	SERPINA11
1529450	Lymph_Dx_066_at		
1529345	Lymph_Dx_067_s_at	443475	
1529346	Lymph_Dx_068_at	443935	
1529347	Lymph_Dx_069_at	444019	
1529348	Lymph_Dx_070_s_at	326392	SOS1
1529349	Lymph_Dx_071_at	445500	
1529451	Lymph_Dx_072_at	396853	JMY
1529350	Lymph_Dx_073_at	445884	
1529351	Lymph_Dx_074_s_at	445898	
1529352	Lymph_Dx_075_at	446195	
1529353	Lymph_Dx_076_at	446198	
1529354	Lymph_Dx_077_at	314623	BCL11A
1529452	Lymph_Dx_078_at	422550	AIM1
1529355	Lymph_Dx_079_at	370675	
1529356	Lymph_Dx_080_at	303775	C14orf170
1529357	Lymph_Dx_081_at	444651	
1529358	Lymph_Dx_082_at	127178	
1529359	Lymph_Dx_083_at		
1529360	Lymph_Dx_084_at	443036	
1529453	Lymph_Dx_085_at	372679	FCGR3A
1529361	Lymph_Dx_086_s_at	388681	HDAC3
1529362	Lymph_Dx_087_at	329989	PLK1
1529363	Lymph_Dx_088_at	311559	NOTCH1
1529364	Lymph_Dx_089_at	526394	ATM
1529365	Lymph_Dx_090_at	344088	TNFRSF13C
1529366	Lymph_Dx_091_at		
1529367	Lymph_Dx_092_at		
1529368	Lymph_Dx_093_at		
1529369	Lymph_Dx_095_at		
1529370	Lymph_Dx_096_at		
1529371	Lymph_Dx_097_at		
1529372	Lymph_Dx_098_at		
1529373	Lymph_Dx_099_at		
1529374	Lymph_Dx_100_at		
1529454	Lymph_Dx_101_at		
1529375	Lymph_Dx_102_at		
1529376	Lymph_Dx_103_at		
1529377	Lymph_Dx_104_at		
1529378	Lymph_Dx_105_at		
1529455	Lymph_Dx_107_at		
1529379	Lymph_Dx_108_at		
1529380	Lymph_Dx_109_at		
1529381	Lymph_Dx_110_at		
1529382	Lymph_Dx_111_at	371468	CCND1
1529383	Lymph_Dx_112_at	371468	CCND1
1529456	Lymph_Dx_113_at	371468	CCND1
1529384	Lymph_Dx_114_at	371468	CCND1

TABLE 2-continued

UNIQID	Probe Set	Unigene ID Build 167	Unigene Symbol
1529385	Lymph_Dx_115_at	371468	CCND1
1529386	Lymph_Dx_116_at	371468	CCND1
1529387	Lymph_Dx_117_at	79241	BCL2
1529388	Lymph_Dx_118_at	79241	BCL2
1529389	Lymph_Dx_119_at	79241	BCL2
1529390	Lymph_Dx_120_at	79241	BCL2
1529391	Lymph_Dx_121_at	79241	BCL2
1529392	Lymph_Dx_122_at	352338	ACVR1C
1529393	Lymph_Dx_123_s_at	182081	KIAA1811
1529394	Lymph_Dx_124_s_at	339846	LOC91807
1529395	Lymph_Dx_125_at	403201	
1529396	Lymph_Dx_126_at	512897	MGC33182
1529397	Lymph_Dx_127_s_at	406557	CLK4
1529398	Lymph_Dx_128_at	293590	HSMDPKIN
1529399	Lymph_Dx_129_at	256916	LOC203806
1529457	Lymph_Dx_130_at	351818	GRK7
1529400	Lymph_Dx_131_s_at	210697	HIPK4
1529401	Lymph_Dx_132_at	399752	MAP4K3
1529402	Lymph_Dx_133_at	375836	KSR2
1529403	Lymph_Dx_134_s_at	511780	LMTK3
1529404	Lymph_Dx_135_at	170610	MAP3K1
1529405	Lymph_Dx_136_s_at	227489	SAST
1529406	Lymph_Dx_137_s_at	409066	MYO3B
1529458	Lymph_Dx_138_at	448468	NEK8
1529407	Lymph_Dx_139_s_at	284275	PAK2
1529408	Lymph_Dx_141_at	336929	PSKH2
1529409	Lymph_Dx_142_s_at	351173	FLJ25006
1529410	Lymph_Dx_143_s_at	380991	SNF1LK
1529411	Lymph_Dx_144_at	80181	APEG1
1529459	Lymph_Dx_145_at	411061	SRMS
1529412	Lymph_Dx_146_at	512763	STK22C
1529413	Lymph_Dx_147_at	232116	PRKWNK2
1529414	Lymph_Dx_148_s_at	352370	MGC22688
1529415	Lymph_Dx_149_at	369523	DKFZp686A17109
1529416	Lymph_Dx_150_s_at	421349	CDKN2A
1529417	Lymph_Dx_151_at	421349	CDKN2A
1529418	Lymph_Dx_152_at	421349	CDKN2A
1529419	Lymph_Dx_153_s_at	104182	
1529420	Lymph_Dx_154_at	272295	IL17F
1529421	Lymph_Dx_156_at	375043	IL27
1529422	Lymph_Dx_157_s_at	375184	IL23R
1529423	Lymph_Dx_158_at	381264	ITGAD
1529424	Lymph_Dx_159_s_at	512683	CCL3L1
1529425	Lymph_Dx_160_at	406228	IL9R
1529426	Lymph_Dx_162_at	406744	IL28B
1529427	Lymph_Dx_163_at	406745	IL29
1529428	Lymph_Dx_164_at	415768	NGFR
1529429	Lymph_Dx_165_at	434103	IL17D
1529430	Lymph_Dx_166_at	444484	SPHK2
1529431	Lymph_Dx_167_at		
1529432	Lymph_Dx_168_at		
1529433	Lymph_Dx_168_x_at		
1529434	Lymph_Dx_171_at	103995	FLJ27099
1529435	Lymph_Dx_172_s_at		
1529436	Lymph_Dx_174_at		
1529437	Lymph_Dx_175_at	445162	BTLA

TABLE 1724

Gene type	Number of genes
Lymphoma predictor genes	1101
Subtype specific	763
Lymph node signature	178
Proliferation signature	160
Outcome predictor genes	171
DLBCL	79
FL	81

TABLE 1724-continued

Gene type	Number of genes
MCL	11
New genes not on U133	167
Lymphochip lymphoma predictor genes	84
EBV and HHV8 viral genes	18
BCL-2/cyclin D1/INK4a specialty probes	14
Named genes missing from U133	51
Named genes	1121

TABLE 1724-continued

Gene type	Number of genes
Protein kinase	440
Interleukin	35
Interleukin receptor	29
Chemokine	51
Chemokine receptor	29
TNF family	26
TNF receptor family	51
Adhesion	45
Surface marker	264
Oncogene/tumor suppressor	49
Apoptosis	46
Drug target	10
Regulatory	46

[0133] Cell samples representing various forms of human lymphoid malignancy were obtained by biopsy using known methods described in the literature. These 634 biopsy samples were reviewed by a panel of hematopathologists and classified into the following lymphoma types based on current diagnostic criteria:

[0134] 201 diffuse large B-cell lymphomas (DLBCL)

[0135] 191 follicular lymphomas (FL)

[0136] 60 Burkitt lymphomas (BL)

[0137] 21 mantle cell lymphomas (MCL)

[0138] 30 primary mediastinal B cell lymphoma (PMBL)

[0139] 18 follicular hyperplasias (FH)

[0140] 18 small cell lymphocytic lymphomas (SLL)

[0141] 17 mucosa-associated lymphoid tissue lymphomas (MALT), including 9 gastric MALTs (GMALT)

[0142] 16 chronic lymphocytic leukemias (CLL)

[0143] 13 splenic lymphomas (SPL)

[0144] 11 lymphoplasmacytic lymphomas (LPC)

[0145] 11 transformed DLBCL (trDLBCL) (DLBCL that arose from an antecedent FL)

[0146] 10 cyclin D1 negative lymphomas with MCL morphology (CD1N)

[0147] 6 peripheral T-cell lymphoma (PTCL)

[0148] 4 post-transplant lymphoproliferative disorders (PTLD)

[0149] 4 nodal marginal zone lymphomas (NMZ)

[0150] 3 lymphoblastic lymphomas (LBL)

[0151] Each of the 634 samples was given a unique sample ID number consisting of the lymphoma type followed by a unique numerical identifier. For example, "BL_2032_52748" refers to a Burkitt lymphoma sample with the numerical identifier 2032_52748. Cells were purified and RNA was isolated from the purified cells according to known methods described in the literature.

[0152] Aliquots of purified RNA from each sample were applied to the Lymph Dx microarrays according to standard Affymetrix microarray protocol. Each microarray was scanned on an Affymetrix scanner. This scanner produced an image of the microarray, which was then evaluated by Affymetrix MAS 5.0 software. This information was stored in tables in .txt format. Each of these .txt files was given a unique name consisting of the table number, the sample ID number (discussed above), and the UNIQID for identifying the array data in the National Cancer Institute Database. For example, Table_1725_BL_2032_52748.txt is the .txt file for Table 1725, which contains data for sample ID number BL_2032. The data for each sample analyzed is contained in Tables 1725-2358. The signal intensity for each probe on the microarray can be transformed into summary signal values for each probe set through a number of different algorithms, including but not limited to MAS 5.0, D-chip (Li 2001), or Bioconductor's RMA algorithms (Irizarry 2003).

Example 3

Development of a First FL Survival Predictor Using Gene Expression Data from Affymetrix U133A and U133B Microarrays

[0153] An analytical method entitled Survival Signature Analysis was developed to create survival prediction models for lymphoma. This method is summarized in FIG. **2**. The key feature of this method is the identification of gene expression signatures. Survival Signature Analysis begins by identifying genes whose expression patterns are statistically associated with survival. A hierarchical clustering algorithm is then used to identify subsets of these genes with correlated expression patterns across the lymphoma samples. These subsets are operationally defined as "survival-associated signatures." Evaluating a limited number of survival-associated signatures mitigates the multiple comparison problems that are inherent in the use of large-scale gene expression data sets to create statistical models of survival (Ransohoff 2004).

[0154] FL samples were divided into two equivalent groups: a training set (95 samples) for developing the survival prediction model, and a validation set (96 samples) for evaluating the reproducibility of the model. The overall survival of this cohort is depicted in FIG. **3**. The median age at diagnosis was 51 years (ranging from 23 to 81 years), and the patients had a median follow-up of 6.6 years (8.1 years for survivors, with a range of <1 to 28.2 years). Gene expression data from Affymetrix U133A and U133B microarrays was obtained for each sample. Within the training set, a Cox proportional hazards model was used to identify "survival predictor" genes, which were genes whose expression levels were associated with long survival (good prognosis genes) or short survival (poor prognosis genes). A hierarchical clustering algorithm (Eisen 1998) was used to identify gene expression signatures within the good and poor prognosis genes according to their expression pattern across all samples. Ten gene expression signatures were observed within either the good prognosis or poor prognosis gene sets (FIG. **4**). The expression level of every component gene in each of these ten gene expression signatures was averaged to create a gene expression signature value.

[0155] To create a multivariate model of survival, different combinations of the ten gene expression signature values were generated and evaluated for their ability to predict survival within the training set. Among models consisting of two signatures, an exceptionally strong statistical synergy was observed between one signature from the good prognosis group and one signature from the poor prognosis group. These signatures were deemed "immune response-1" and "immune response-2," respectively, based on the biological function of certain genes within each signature. The immune response-1 gene expression signature included genes encoding T cell markers (e.g., CD7, CD8B1, ITK, LEF1, STAT4) and genes that are highly expressed in macrophages (e.g., ACTN1, TNFSF13B). The immune response-1 signature is not merely a surrogate for the number of T cells in the FL biopsy sample because many other standard T cell genes (e.g.,

CD2, CD4, LAT, TRIM, SH2D1A) were not associated with survival. The immune response-2 gene expression signature included genes known to be preferentially expressed in macrophages and/or dendritic cells (e.g., TLR5, FCGR1A, SEPT10, LGMN, C3AR1). Table 2359 lists the genes that were used to generate the gene expression signature values for the immune response-1 and immune response-2 signatures. The Unigene ID Build database referenced in the following tables is hosted by the hosted by the National Center for Biotechnology Information (NCBI) web site

TABLE 2359

Signature	UNIQID	Unigene ID Build 167	Gene symbol
Immune response-1	1095985	83883	TMEPAI
Immune response-1	1096579	117339	HCST
Immune response-1	1097255	380144	
Immune response-1	1097307	379754	LOC340061
Immune response-1	1097329	528675	TEAD1
Immune response-1	1097561	19221	C20orf112
Immune response-1	1098152	377588	KIAA1450
Immune response-1	1098405	362807	IL7R
Immune response-1	1098548	436639	NFIC
Immune response-1	1098893	43577	ATP8B2
Immune response-1	1099053	376041	
Immune response-1	1100871	48353	
Immune response-1	1101004	2969	SKI
Immune response-1	1103303	49605	C9orf52
Immune response-1	1107713	171806	
Immune response-1	1115194	270737	TNFSF13B
Immune response-1	1119251	433941	SEPW1
Immune response-1	1119838	469951	GNAQ
Immune response-1	1119924	32309	INPP1
Immune response-1	1120196	173802	TBC1D4
Immune response-1	1120267	256278	TNFRSF1B
Immune response-1	1121313	290432	HOXB2
Immune response-1	1121406	NA	TNFSF12
Immune response-1	1121720	80642	STAT4
Immune response-1	1122956	113987	LGALS2
Immune response-1	1123038	119000	ACTN1
Immune response-1	1123092	437191	PTRF
Immune response-1	1123875	428	FLT3LG
Immune response-1	1124760	419149	JAM3
Immune response-1	1128356	415792	C1RL
Immune response-1	1128395	7188	SEMA4C
Immune response-1	1132104	173802	TBC1D4
Immune response-1	1133408	12802	DDEF2
Immune response-1	1134069	405667	CD8B1
Immune response-1	1134751	106185	RALGDS
Immune response-1	1134945	81897	KIAA1128
Immune response-1	1135743	299558	TNFRSF25
Immune response-1	1135968	119000	ACTN1
Immune response-1	1136048	299558	TNFRSF25
Immune response-1	1136087	211576	ITK
Immune response-1	1137137	195464	FLNA
Immune response-1	1137289	36972	CD7
Immune response-1	1137534	36972	CD7
Immune response-1	1139339	47099	GALNT12
Immune response-1	1139461	14770	BIN2
Immune response-1	1140391	44865	LEF1
Immune response-1	1140524	10784	C6orf37
Immune response-1	1140759	298530	RAB27A
Immune response-2	1118755	127826	EPOR
Immune response-2	1118966	19196	LOC51619
Immune response-2	1121053	1690	FGFBP1
Immune response-2	1121267	334629	SLN
Immune response-2	1121331	8980	TESK2
Immune response-2	1121766	396566	MPP3
Immune response-2	1121852	421391	LECT1
Immune response-2	1122624	126378	ABCG4
Immune response-2	1122679	232770	ALOXE3
Immune response-2	1122770	66578	CRHR2
Immune response-2	1123767	1309	CD1A

TABLE 2359-continued

Signature	UNIQID	Unigene ID Build 167	Gene symbol
Immune response-2	1123841	389	ADH7
Immune response-2	1126097	498015	
Immune response-2	1126380	159408	
Immune response-2	1126628	254321	CTNNA1
Immune response-2	1126836	414410	NEK1
Immune response-2	1127277	121494	SPAM1
Immune response-2	1127519	NA	
Immune response-2	1127648	285050	
Immune response-2	1128483	444359	SEMA4G
Immune response-2	1128818	115830	HS3ST2
Immune response-2	1129012	95497	SLC2A9
Immune response-2	1129582	272236	C21orf77
Immune response-2	1129658	58356	PGLYRP4
Immune response-2	1129705	289368	ADAM19
Immune response-2	1129867	283963	G6PC2
Immune response-2	1130003	432799	
Immune response-2	1130388	19196	LOC51619
Immune response-2	1131837	156114	PTPNS1
Immune response-2	1133843	6682	SLC7A11
Immune response-2	1133949	502092	PSG9
Immune response-2	1134447	417628	CRHR1
Immune response-2	1135117	512646	PSG6
Immune response-2	1136017	1645	CYP4A11
Immune response-2	1137478	315235	ALDOB
Immune response-2	1137745	26776	NTRK3
Immune response-2	1137768	479985	
Immune response-2	1138476	351874	HLA-DOA
Immune response-2	1138529	407604	CRSP2
Immune response-2	1138601	149473	PRSS7
Immune response-2	1139862	251383	CHST4
Immune response-2	1140189	287369	IL22
Immune response-2	1140389	22116	CDC14B

[0156] Although the immune response-1 and immune response-2 gene expression signatures taken individually were not ideal predictors of survival, the binary model formed by combining the two was more predictive of survival in the training set than any other binary model ($p<0.001$). Using this binary model as an anchor, other signatures were added to the model using a step up procedure (Drapner 1966). Of the remaining eight signatures, only one signature contributed significantly to the model in the training set ($p<0.01$), resulting in a three-variable model for survival. This model was associated with survival in a highly statistically significant fashion in both the training ($p<0.001$) and validation sets ($p=0.003$). However, only the immune response-1 and immune response-2 gene expression signatures contributed to the predictive power of the model in both the training set and the validation set. The predictive power of each of these signatures is summarized in Table 2360.

TABLE 2360

Gene expression signature	Contribution of signature to model in validation set (p-value)	Relative risk of death among patients in validation set (95% C.I.)	Effect of increased expression on survival
Immune response-1	<0.001	0.15 (0.05-0.46)	Favorable
Immune response-2	<0.001	9.35 (3.02-28.9)	Poor

[0157] Based on this information, the third signature was removed from the model and the two-signature model was used to generate a survival predictor score using the following equation:

> Survival predictor score=[(2.71*immune response-2 gene expression signature value)]−[(2.36×immune response-1 gene expression signature value)].

A higher survival predictor score was associated with worse outcome. The two-signature model was associated with survival in a statistically significant fashion in both the training set ($p<0.001$) and the validation set ($p<0.001$), which demonstrated that the model was reproducible. For the 187 FL samples with available clinical data, the survival predictor score had a mean of 1.6 and a standard deviation of 0.894, with each unit increase in the predictor score corresponding to a 2.5 fold increase in the relative risk of death. Data for all 191 samples is shown in Table 2361.

TABLE 2361

Sample ID #	Set	Length of follow-up (years)	Status at follow-up	Immune response-1 signature value	Immune response-2 signature value	Survival predictor score
FL_1073	Training	7.68	Dead	9.20	8.67	1.77
FL_1074	Training	4.52	Dead	9.10	8.57	1.74
FL_1075	Validation	4.52	Dead	8.97	8.69	2.38
FL_1076	Training	3.22	Dead	9.20	8.55	1.44
FL_1077	Training	7.06	Alive	9.80	8.46	−0.20
FL_1078	Training	4.95	Alive	9.32	8.23	0.30
FL_1080	Training	6.05	Alive	9.45	8.94	1.93
FL_1081	Validation	6.61	Alive	9.00	8.22	1.05
FL_1083	Training	10.01	Alive	9.82	8.72	0.47
FL_1085	Validation	8.84	Alive	9.31	8.58	1.29
FL_1086	Validation	1.98	Dead	9.49	9.09	2.22
FL_1087	Training	8.19	Alive	9.98	9.27	1.57
FL_1088	Validation	5.30	Alive	9.22	8.47	1.20
FL_1089	Training	10.72	Alive	9.42	8.35	0.40
FL_1090	Validation	10.20	Alive	9.27	8.37	0.82
FL_1097	Validation	8.79	Dead	9.87	8.92	0.87
FL_1098	Validation	5.34	Dead	9.33	8.81	1.87
FL_1099	Training	7.65	Alive	9.73	9.04	1.54
FL_1102	Validation	13.20	Dead	9.45	8.89	1.79
FL_1104	Training	8.42	Dead	9.30	8.27	0.48
FL_1106	Validation	7.94	Alive	9.13	9.19	3.36
FL_1107	Training	5.01	Dead	9.41	9.32	3.07
FL_1183	Training	11.56	Dead	9.31	8.53	1.16
FL_1184	Training	6.93	Dead	9.66	8.83	1.13
FL_1185	Validation	7.02	Dead	9.23	9.09	2.86
FL_1186	Training	1.34	Dead	9.01	8.84	2.68
FL_1416	Validation	6.21	Alive	9.50	8.67	1.08
FL_1417	Training	2.40	Dead	8.47	8.39	2.73
FL_1418	Validation	3.59	Alive	8.94	8.42	1.72
FL_1419	Training	3.85	Alive	9.82	8.56	0.03
FL_1422	Training	5.72	Alive	9.46	8.49	0.68
FL_1425	Validation	4.26	Alive	8.93	8.50	1.98
FL_1426	Training	7.32	Alive	9.08	8.26	0.97
FL_1427	Training	5.22	Alive	8.57	8.28	2.22
FL_1428	Validation	5.41	Dead	9.22	8.44	1.10
FL_1432	Training	3.66	Alive	9.22	8.95	2.51
FL_1436	Training	9.08	Dead	9.48	8.63	1.02
FL_1440	Training	7.85	Alive	9.07	8.35	1.22
FL_1445	Training	9.24	Dead	8.67	8.66	3.01
FL_1450	Validation	0.65	Dead	9.83	9.99	3.86
FL_1472	Validation	16.72	Alive	8.85	8.49	2.10
FL_1473	Training	15.07	Alive	9.75	8.50	0.02
FL_1474	Validation	2.75	Dead	9.34	9.10	2.62
FL_1476	Validation	4.08	Dead	9.51	8.87	1.60
FL_1477	Training	0.59	Dead	9.64	9.06	1.83

TABLE 2361-continued

Sample ID #	Set	Length of follow-up (years)	Status at follow-up	Immune response-1 signature value	Immune response-2 signature value	Survival predictor score
FL_1478	Training	12.47	Dead	9.60	8.87	1.39
FL_1479	Training	2.29	Dead	8.71	9.07	4.01
FL_1480	Training	16.29	Alive	9.40	8.67	1.30
FL_1579	Training	8.22	Dead	8.81	8.44	2.10
FL_1580	Training	19.30	Alive	9.58	8.52	0.49
FL_1581	Training	9.52	Dead	9.08	9.02	3.00
FL_1582	Validation	1.30	Dead	8.40	8.18	2.36
FL_1583	Training	15.26	Dead	9.47	8.79	1.48
FL_1584	Training	15.73	Dead	9.44	8.55	0.89
FL_1585	Validation	0.01	Alive	8.96	8.53	1.96
FL_1586	Validation	3.11	Alive	9.38	8.55	1.03
FL_1588	Training	0.49	Dead	9.52	9.06	2.08
FL_1589	Training	3.15	Alive	9.72	8.74	0.72
FL_1591	Training	11.22	Alive	9.49	8.62	0.97
FL_1594	Validation	11.19	Alive	9.25	8.59	1.47
FL_1595	Training	8.03	Alive	9.75	9.60	3.01
FL_1598	Validation	2.80	Dead	8.81	8.33	1.79
FL_1599	Validation	6.17	Alive	9.48	8.65	1.06
FL_1603	Training	5.17	Dead	9.66	9.75	3.63
FL_1604	Training	3.98	Dead	9.24	8.86	2.20
FL_1606	Validation	4.22	Dead	9.45	9.18	2.57
FL_1607	Validation	8.12	Alive	9.40	8.60	1.13
FL_1608	Validation	9.70	Alive	8.92	8.41	1.72
FL_1610	Validation	2.05	Dead	9.33	9.35	3.32
FL_1611	Validation	10.15	Alive	9.42	8.69	1.31
FL_1616	Training	2.36	Dead	9.38	8.82	1.78
FL_1617	Validation	7.85	Alive	8.96	8.49	1.87
FL_1619	Validation	9.24	Dead	9.43	8.56	0.94
FL_1620	Validation	9.36	Dead	9.14	8.35	1.04
FL_1622	Training	14.01	Alive	9.23	8.53	1.33
FL_1623	Training	9.72	Alive	9.67	8.93	1.38
FL_1624	Validation	3.98	Dead	9.05	8.50	1.70
FL_1625	Validation	11.16	Alive	8.98	8.47	1.75
FL_1626	Validation	6.47	Dead	8.59	8.14	1.76
FL_1628	Validation	0.82	Dead	9.80	8.72	0.51
FL_1637	Validation	18.81	Alive	9.95	9.58	2.48
FL_1638	Validation	4.06	Alive	9.13	8.88	2.51
FL_1639	Training	4.75	Alive	9.53	8.89	1.62
FL_1643	Training	0.77	Dead	9.73	9.06	1.58
FL_1644	Validation	3.84	Alive	9.55	8.68	0.98
FL_1645	Training	3.56	Alive	9.49	8.70	1.18
FL_1646	Training	1.97	Dead	9.25	8.61	1.50
FL_1647	Training	1.22	Dead	9.12	8.89	2.55
FL_1648	Training	11.01	Alive	9.13	8.12	0.46
FL_1652	Training	3.72	Dead	9.50	9.14	2.35
FL_1654	Validation	0.30	Dead	8.74	8.28	1.82
FL_1655	Training	8.45	Alive	9.51	8.85	1.53
FL_1656	Validation	9.36	Alive	9.06	8.58	1.87
FL_1657	Training	10.09	Alive	9.53	8.46	0.44
FL_1660	Training	2.32	Alive	8.81	8.38	1.91
FL_1661	Validation	1.48	Alive	9.86	8.90	0.85
FL_1662	Validation	0.74	Dead	9.57	9.15	2.21
FL_1664	Validation	4.53	Dead	9.34	8.62	1.31
FL_1669	Training	4.40	Dead	8.87	8.58	2.30
FL_1670	Training	1.88	Alive	9.64	9.45	2.86
FL_1675	Training	4.57	Alive	9.36	8.46	0.84
FL_1681	Validation	4.23	Alive	9.52	8.63	0.91
FL_1683	Validation	4.03	Dead	9.95	9.10	1.19
FL_1684	Training	2.88	Dead	9.53	8.73	1.18
FL_1716	Validation	9.69	Alive	8.95	8.35	1.50
FL_1717	Validation	2.01	Dead	9.35	8.88	1.98
FL_1718	Training	10.35	Alive	9.23	8.13	0.26
FL_1719	Validation	7.70	Dead	9.13	8.50	1.49
FL_1720	Training	3.91	Dead	8.78	8.88	3.33
FL_1729	Training	8.06	Alive	9.35	8.65	1.39
FL_1732	Validation	0.71	Dead	7.81	8.59	4.86
FL_1761	Validation	10.83	Alive	9.31	8.55	1.22
FL_1764	Training	0.42	Dead	9.25	8.87	2.21
FL_1768	Training	13.04	Alive	9.42	8.47	0.72
FL_1771	Training	9.26	Dead	9.09	8.67	2.06
FL_1772	Validation	13.64	Dead	9.49	8.49	0.61

TABLE 2361-continued

Sample ID #	Set	Length of follow-up (years)	Status at follow-up	Immune response-1 signature value	Immune response-2 signature value	Survival predictor score
FL__1788	Training	1.00	Dead	9.09	9.13	3.29
FL__1790	Training	1.42	Alive	9.85	9.40	2.22
FL__1792	Validation	2.01	Dead	9.33	8.72	1.61
FL__1795	Training	0.71	Dead	10.19	9.27	1.08
FL__1797	Validation	7.17	Alive	9.34	8.92	2.14
FL__1799	Training	14.18	Alive	9.32	8.63	1.38
FL__1810	Validation	9.91	Alive	8.66	8.41	2.35
FL__1811	Validation	3.04	Alive	9.38	8.27	0.29
FL__1825	Training	2.98	Alive	9.46	9.07	2.25
FL__1827	Training	3.66	Alive	9.80	8.84	0.83
FL__1828	Validation	11.51	Alive	8.99	8.09	0.72
FL__1829	Validation	4.11	Alive	9.57	8.73	1.08
FL__1830	Validation	5.65	Dead	9.01	8.68	2.25
FL__1833	Training	11.95	Alive	9.74	8.67	0.51
FL__1834	Validation	15.92	Alive	9.22	8.72	1.88
FL__1835	Validation	12.49	Alive	9.26	8.83	2.10
FL__1836	Validation	12.24	Alive	9.55	8.64	0.85
FL__1837	Validation	0.55	Dead	9.47	8.84	1.62
FL__1838	Validation	2.54	Alive	9.90	9.12	1.34
FL__1839	Training	4.48	Alive	8.56	8.32	2.34
FL__1841	Training	0.88	Dead	9.32	9.10	2.66
FL__1842	Validation	4.56	Alive	9.73	8.87	1.07
FL__1844	Validation	13.39	Alive	9.41	8.55	0.98
FL__1845	Training	12.92	Dead	9.89	9.04	1.16
FL__1846	Validation	1.80	Dead	9.79	9.61	2.93
FL__1848	Training	12.52	Alive	9.76	8.81	0.82
FL__1851	Training	4.08	Dead	9.43	9.01	2.18
FL__1853	Validation	12.50	Alive	9.28	8.54	1.25
FL__1854	Validation	13.81	Alive	9.32	8.84	1.98
FL__1855	Validation	9.96	Dead	9.31	8.39	0.75
FL__1857	Validation	8.39	Dead	9.80	9.14	1.65
FL__1861	Validation	3.19	Dead	9.47	8.57	0.88
FL__1862	Validation	7.22	Dead	8.96	8.33	1.44
FL__1863	Validation	10.77	Dead	9.31	8.85	2.00
FL__1864	Training	14.25	Alive	9.98	9.12	1.17
FL__1866	Training	10.72	Dead	9.93	8.94	0.79
FL__1870	Validation	6.41	Dead	10.01	9.22	1.36
FL__1873	Training	7.78	Dead	9.39	8.66	1.30
FL__1874	Validation	3.15	Dead	9.38	8.74	1.53
FL__1876	Validation	15.07	Alive	9.59	8.72	0.98
FL__1879	Training	7.13	Dead	9.25	8.62	1.53
FL__1880	Validation	12.84	Dead	8.82	8.35	1.82
FL__1882	Training	8.84	Dead	9.43	8.76	1.49
FL__1884	Validation	11.92	Dead	9.48	9.14	2.41
FL__1885	Validation	15.49	Alive	9.70	8.85	1.11
FL__1887	Training	5.14	Dead	9.47	8.57	0.87
FL__1888	Training	15.08	Alive	9.83	8.97	1.11
FL__1890	Training	3.03	Dead	9.29	9.05	2.60
FL__1894	Training	11.37	Dead	9.01	8.64	2.13
FL__1896	Training	12.03	Alive	9.80	8.56	0.08
FL__1897	Training	9.63	Alive	9.02	8.33	1.29
FL__1898	Training	5.20	Alive	8.82	8.25	1.54
FL__1900	Validation	7.38	Alive	9.13	8.26	0.85
FL__1903	Validation	28.25	Alive	9.07	8.46	1.54
FL__1904	Validation	7.36	Alive	9.16	8.53	1.50
FL__1905	Validation	3.68	Dead	9.25	8.38	0.87
FL__1906	Training	2.35	Dead	8.04	8.69	4.56
FL__1907	Validation	2.35	Dead	8.11	8.21	3.11
FL__1910	Training	13.84	Alive	9.36	8.72	1.56
FL__1912	Validation	0.73	Dead	9.30	9.21	3.02
FL__1913	Training	2.57	Alive	9.77	8.51	0.01
FL__1916	Validation	11.61	Alive	9.22	8.49	1.24
FL__1918	Validation	9.95	Dead	9.54	8.77	1.26
FL__1919	Training	10.84	Dead	9.51	8.81	1.44
FL__735	Validation	11.05	Dead	8.81	8.23	1.53
FL__738	Validation	10.15	Dead	9.19	8.79	2.13
FL__739	Training	10.80	Dead	9.29	8.77	1.85
FL__878	Validation	3.87	Dead	8.85	8.54	2.26
FL__879	Training	4.34	Dead	8.95	8.74	2.56
FL__886	Validation	3.29	Alive	9.43	8.72	1.40
FL__888	Validation	1.32	Dead	8.76	8.49	2.34

TABLE 2361-continued

Sample ID #	Set	Length of follow-up (years)	Status at follow-up	Immune response-1 signature value	Immune response-2 signature value	Survival predictor score
FL_1627	Training	NA	NA	9.60	8.51	0.40
FL_1429	Training	NA	NA	8.69	8.28	1.93
FL_1850	Validation	NA	NA	9.75	8.83	0.92
FL_1735	Validation	NA	NA	7.32	8.30	5.24

[0158] In order to visualize the predictive power of the model, the FL samples were ranked according to their survival predictor scores and divided into four quartiles. Kaplan-Meier plots of overall survival showed clear differences in survival rate in the validation set (FIG. **5**). The median survival for each of the four quartiles is set forth in Table 2362.

TABLE 2362

Quartile	Median survival (years)
1	13.6
2	11.1
3	10.8
4	3.9

[0159] Various clinical variables were found to be significantly associated with survival, including the IPI and some of its components and the presence of B-symptoms. The gene expression-based model was independent of each of these variables at predicting survival. These clinical variables and the relative risk of death associated with each are summarized in Table 2363.

TABLE 2363

		% of patients[1]	% of patients[1]	Univariate (clinical variable only) relative risk of death among patients in validation set		Multivariate (clinical variable + survival predictor score) relative risk of death among patients in validation set	
Clinical variable	Criteria	Training set	Validation set	RR[2] (95% C.I.)	p-value	RR[2] (95% C.I.)	p-value
Age	60	64.5	70.2	1.90	0.044	2.21	<0.001
	>60	35.5	29.8	(1.02-3.56)		(1.48-3.29)	
Stage	I-II	33.3	25	1.31	0.447	2.31	<0.001
	III-IV	66.7	75	(0.65-2.64)		(1.51-3.52)	
Extranodal sites (#)	2	5.4	20.2	1.58	0.163	2.21	<0.001
	<2	94.6	79.8	(0.83-2.99)		(1.48-3.30)	
LDH	Normal	77.1	66.2	1.77	0.065	2.40	<0.001
	Greater than normal	22.9	33.8	(0.97-3.24)		(1.57-3.67)	
ECOG performance status	2	9.4	12.5	2.05	0.090	2.17	<0.001
	<2	90.6	87.5	(0.89-4.71)		(1.40-3.35)	
Gender	Male	42	65	1.62	0.105	2.17	<0.001
	Female	58	35	(0.90-2.90)		(1.45-3.25)	
B-symptoms	Present	17.2	21.3	2.05	0.029	2.10	<0.001
	Absent	82.8	78.7	(1.08-3.89)		(1.37-3.23)	
Grade[3]	1	45	43.4	N/A	0.118	2.55	<0.001
	2	34.8	33.3	2.03 (1.04-3.96)		(1.63-3.99)	
	3	20.2	23.3	1.39 (0.65-2.98)			
Int'l. Prognostic Index[4]	Scores 0-1	63.1	47.5	N/A	0.029	2.28 (1.46-3.57)	<0.001
	Scores 2-3	33.3	45	2.07 (1.07-4.00)			
	Scores 4-5	3.6	7.5	3.73 (1.18-11.18)			

[1]Due to rounding, percentages may not total 100

[2]Relative risk of death (RR) based on 2-fold increase in expression

[3]RR for grades 2 and 3 calculated with respect to risk of death for grade 1. The p-value is calculated for all grades.

[4]RR for scores 2-3 and 4-5 calculated with respect to risk of death for scores 0-1. The p-value is calculated for all grades.

[0160] The samples in the validation set were divided into three groups based on their IPI score, and the relationship between survival and IPI score was visualized by Kaplan-Meier plot (FIG. **6**). Among validation set samples from the low-risk (IPI 0-1) and intermediate risk (IPI 2-3) IPI groups, the gene-expression-based survival predictor could stratify patients into groups differing by more than 5 years with regards to median survival (FIG. **7**). The high-risk IPI group (IPI 4-5) comprised less than 5% of the samples, and was omitted from this analysis. These results demonstrate that the gene expression-based model is not merely acting as a surrogate for clinical variables that are known to predict survival in FL, but rather it identifies distinct biological attributes of the tumors that are associated with survival.

Example 4

Development of a Second FL Survival Predictor Using Gene Expression Data from Affymetrix U133A and U133B Microarrays

[0161] 191 FL were divided into two equivalent groups: a training set (95 samples) for developing the survival prediction model, and a validation set (96 samples) for evaluating the reproducibility of the model. Gene expression data from Affymetrix U133A and U133B microarrays was obtained for each of the samples. A Cox proportional hazards model was used to identify survival predictor genes whose expression levels were associated with long survival (good prognosis genes) or short survival (poor prognosis genes) in the training set. The correlation between expression and survival for each gene on the microarrays is provided in the final two columns of Table 1710. The first of these two columns ("FL_Cox_coefficient") provides a Cox coefficient indicating the extent to which a 2-fold increase in expression of a particular gene affects mortality. A positive Cox coefficient indicates increasing mortality with increasing expression of the gene, while a negative Cox coefficient indicates decreasing mortality with increasing expression of the gene. The second of these two columns provides a Cox p-value indicating the estimated probability that the increase or decrease in survival associated with the gene would occur by chance if there was no connection between the expression of the gene and survival.

[0162] A hierarchical clustering algorithm (Eisen 1998) was used to identify gene expression signatures within the good and poor prognosis genes according to their expression pattern across all samples. Eight clusters of coordinately regulated genes were observed within the good prognosis gene set and six clusters were observed in the poor prognosis gene sets. The expression level of every component gene in each of these gene expression signatures was averaged to create a gene expression signature value. After averaging, only ten of the gene expression signatures were found to be significantly associated with survival in the training set ($p<0.01$). To create a multivariate model of survival, different combinations of these ten gene expression signature averages were generated and evaluated for their ability to predict survival within the training set. Among models consisting of two signatures, an exceptionally strong statistical synergy was noted between one signature from the good prognosis group and one from the poor prognosis group. These gene expression signatures were termed "T-cell" and "macrophage" based on the biological function of certain genes within each signature. The T-cell gene expression signature included genes that were typically expressed in T-cells, while the macrophage gene expression signature included a number of genes typically expressed in macrophages. Although these two signatures taken individually were not the best predictors of survival, the binary model formed by combining the two was more predictive than any combination of three signatures that did not contain these two signatures. Using these two signatures as an anchor, other signatures were added to the model using a step up procedure (Drapner 1966). Only one of the remaining eight signatures, termed the B-cell differentiation signature, contributed significantly to the model in the training set ($p=0.054$). The B-cell differentiation signature included a number of genes that appear to be involved in B-cell signal transduction. Table 2364 lists the genes that were used to generate the gene expression signature values for the T-cell, macrophage, and B-cell differentiation gene expression signatures.

TABLE 2364

Signature	UNIQID	Unigene ID Build 167	Gene symbol
B-cell differentiation	1119350	331141	ALDH2
B-cell differentiation	1130922	459987	ANP32B
B-cell differentiation	1130923	459987	ANP32B
B-cell differentiation	1099291	130774	C9orf105
B-cell differentiation	1102859	446195	FLJ42418
B-cell differentiation	1120976	245644	GCHFR
B-cell differentiation	1098862	303669	MGC26694
B-cell differentiation	1111070	202201	
B-cell differentiation	1105935		
B-cell differentiation	1139017	274424	NANS
B-cell differentiation	1108988	3532	NLK
B-cell differentiation	1114726	3532	NLK
B-cell differentiation	1097897	266175	PAG
B-cell differentiation	1097901	266175	PAG
B-cell differentiation	1119813	155342	PRKCD
B-cell differentiation	1123298	20191	SIAH2
B-cell differentiation	1101439	63335	TERF2
B-cell differentiation	1120316	63335	TERF2
B-cell differentiation	1096035	105794	UGCGL1
T-cell	1134945	81897	KIAA1128
T-cell	1134069	405667	CD8B1
T-cell	1137809	405667	CD8B1
T-cell	1119251	433941	SEPW1
T-cell	1096579	117339	HCST
T-cell	1101004	2969	SKI
T-cell	1137137	195464	FLNA
T-cell	1100871	48353	
T-cell	1139461	14770	BIN2
T-cell	1128395	7188	SEMA4C
T-cell	1119880	442844	FMOD
T-cell	1130676	194431	KIAA0992
T-cell	1130668	194431	KIAA0992
T-cell	1135968	119000	ACTN1
T-cell	1097329	528675	TEAD1
T-cell	1098548	436639	NFIC
T-cell	1123038	119000	ACTN1
T-cell	1128356	415792	C1RL
T-cell	1133408	12802	DDEF2
T-cell	1140524	10784	C6orf37
T-cell	1119838	469951	GNAQ
T-cell	1097255	380144	
T-cell	1098152	377588	KIAA1450
T-cell	1115194	270737	TNFSF13B
T-cell	1124760	419149	JAM3
T-cell	1120267	256278	TNFRSF1B
T-cell	1137289	36972	CD7
T-cell	1137534	36972	CD7
T-cell	1097307	379754	LOC340061
T-cell	1123613	97087	CD3Z
T-cell	1121720	80642	STAT4
T-cell	1120196	173802	TBC1D4
T-cell	1136087	211576	ITK
T-cell	1132104	173802	TBC1D4

TABLE 2364-continued

Signature	UNIQID	Unigene ID Build 167	Gene symbol
T-cell	1140391	44865	LEF1
T-cell	1098405	362807	IL7R
T-cell	1135743	299558	TNFRSF25
T-cell	1136048	299558	TNFRSF25
T-cell	1123875	428	FLT3LG
T-cell	1098893	43577	ATP8B2
T-cell	1097561	19221	C20orf112
T-cell	1122956	113987	LGALS2
T-cell	1121406		TNFSF12
T-cell	1125532		
T-cell	1138538	2014	TRD
T-cell	1103303	49605	C9orf52
T-cell	1119924	32309	INPP1
Macrophage	1123682	114408	TLR5
Macrophage	1099124	355455	SEPT10
Macrophage	1123401	50130	NDN
Macrophage	1134379	150833	C4A
Macrophage	1137481	150833	C4A
Macrophage	1132220	448805	GPRC5B
Macrophage	1119400	181046	DUSP3
Macrophage	1131119	349656	SCARB2
Macrophage	1123566	155935	C3AR1
Macrophage	1138443	77424	FCGR1A
Macrophage	1127943	9641	C1QA
Macrophage	1119998	8986	C1QB
Macrophage	1132433	14732	ME1
Macrophage	1119260	18069	LGMN
Macrophage	1098278	166017	MITF

The three signatures were used to generate a survival predictor score using the following equation:

> Survival predictor score=[2.053*(macrophage gene expression signature value)]−[2.344*(*T*-cell gene expression signature value)]−[0.729*(*B*-cell differentiation gene expression signature value)].

A higher survival predictor score was associated with worse outcome. According to a likelihood ratio test adjusted for the number of variables included, this model was significant in predicting survival in both the training set ($p=1.8\times10^{-8}$) and the validation set ($p=2.0\times10^{-5}$). For the 187 FL samples with available clinical data, the survival predictor score had a mean of −11.9 and a standard deviation of 0.9418, with each unit increase in the predictor score corresponding to a 2.5 fold increase in the relative risk of death. Data for all 191 samples is shown in Table 2365.

TABLE 2365

Sample ID #	Set	B cell differentiation signature value	T-cell signature value	Macrophage signature value	Survival predictor score
FL_1073	Training	9.70	9.14	8.58	−10.89
FL_1074	Training	11.11	9.06	8.52	−11.84
FL_1075	Validation	11.23	8.92	8.75	−11.15
FL_1076	Training	10.02	9.21	8.59	−11.25
FL_1077	Training	9.94	9.77	8.44	−12.82
FL_1078	Training	10.67	9.32	8.21	−12.76
FL_1080	Training	10.62	9.44	8.88	−11.64
FL_1081	Validation	10.38	9.00	8.09	−12.04
FL_1083	Training	10.29	9.77	8.74	−12.47
FL_1085	Validation	9.87	9.24	8.43	−11.55
FL_1086	Validation	10.03	9.50	9.02	−11.06
FL_1087	Training	9.83	9.98	9.37	−11.31
FL_1088	Validation	10.57	9.21	8.29	−12.27
FL_1089	Training	10.30	9.38	8.27	−12.53

TABLE 2365-continued

Sample ID #	Set	B cell differentiation signature value	T-cell signature value	Macrophage signature value	Survival predictor score
FL_1090	Validation	9.74	9.24	8.20	−11.93
FL_1097	Validation	9.57	9.82	8.80	−11.93
FL_1098	Validation	11.08	9.40	8.97	−11.69
FL_1099	Training	10.23	9.70	9.12	−11.46
FL_1102	Validation	9.66	9.46	8.90	−10.93
FL_1104	Training	10.72	9.19	8.20	−12.53
FL_1106	Validation	11.11	9.17	9.57	−9.96
FL_1107	Training	9.70	9.42	9.55	−9.54
FL_1183	Training	9.85	9.25	8.44	−11.54
FL_1184	Training	10.12	9.57	8.86	−11.63
FL_1185	Validation	10.75	9.21	9.13	−10.68
FL_1186	Training	9.76	8.88	8.83	−9.80
FL_1416	Validation	9.94	9.45	8.59	−11.77
FL_1417	Training	10.12	8.53	8.43	−10.08
FL_1418	Validation	9.35	8.86	8.27	−10.59
FL_1419	Training	10.20	9.76	8.53	−12.81
FL_1422	Training	10.22	9.48	8.40	−12.43
FL_1425	Validation	9.61	8.89	8.58	−10.23
FL_1426	Training	10.80	9.06	8.13	−12.41
FL_1427	Training	10.27	8.56	8.13	−10.87
FL_1428	Validation	10.76	9.25	8.38	−12.32
FL_1432	Training	10.51	9.17	9.04	−10.59
FL_1436	Training	9.69	9.40	8.61	−11.42
FL_1440	Training	9.82	9.04	8.21	−11.50
FL_1445	Training	9.24	8.69	8.62	−9.41
FL_1450	Validation	9.70	9.88	10.37	−8.93
FL_1472	Validation	10.78	8.96	8.51	−11.40
FL_1473	Training	9.99	9.70	8.41	−12.75
FL_1474	Validation	10.21	9.27	9.05	−10.59
FL_1476	Validation	9.82	9.44	8.78	−11.27
FL_1477	Training	9.32	9.61	9.03	−10.78
FL_1478	Training	10.19	9.60	8.81	−11.83
FL_1479	Training	10.69	8.78	9.09	−9.71
FL_1480	Training	10.10	9.42	8.70	−11.57
FL_1579	Training	10.15	8.82	8.24	−11.15
FL_1580	Training	10.31	9.59	8.50	−12.54
FL_1581	Training	9.91	8.96	9.05	−9.66
FL_1582	Validation	9.73	8.31	8.06	−10.03
FL_1583	Training	10.95	9.45	8.86	−11.95
FL_1584	Training	9.98	9.38	8.46	−11.89
FL_1585	Validation	10.53	8.88	8.46	−11.11
FL_1586	Validation	10.00	9.30	8.42	−11.81
FL_1588	Training	9.59	9.41	8.94	−10.68
FL_1589	Training	10.29	9.68	8.73	−12.27
FL_1591	Training	10.44	9.45	8.56	−12.18
FL_1594	Validation	10.01	9.25	8.56	−11.41
FL_1595	Training	9.61	9.75	9.65	−10.07
FL_1598	Validation	11.18	8.80	8.31	−11.71
FL_1599	Validation	10.55	9.48	8.60	−12.24
FL_1603	Training	9.40	9.60	9.77	−9.31
FL_1604	Training	9.92	9.21	8.90	−10.54
FL_1606	Validation	9.87	9.45	9.17	−10.52
FL_1607	Validation	9.76	9.37	8.50	−11.63
FL_1608	Validation	9.92	8.90	8.39	−10.85
FL_1610	Validation	10.02	9.38	9.74	−9.30
FL_1611	Validation	10.18	9.41	8.69	−11.64
FL_1616	Training	9.62	9.33	8.85	−10.71
FL_1617	Validation	9.90	8.95	8.39	−10.98
FL_1619	Validation	9.98	9.37	8.47	−11.85
FL_1620	Validation	9.43	8.95	8.12	−11.19
FL_1622	Training	9.84	9.15	8.31	−11.56
FL_1623	Training	9.95	9.61	8.97	−11.37
FL_1624	Validation	10.55	9.06	8.43	−11.61
FL_1625	Validation	10.00	8.89	8.23	−11.22
FL_1626	Validation	11.05	8.62	8.10	−11.62
FL_1628	Validation	10.08	9.81	8.66	−12.57
FL_1637	Validation	9.77	9.95	9.59	−10.76
FL_1638	Validation	10.25	9.20	9.07	−10.41
FL_1639	Training	10.29	9.52	8.99	−11.35
FL_1643	Training	9.80	9.72	9.00	−11.46
FL_1644	Validation	9.51	9.46	8.61	−11.43

TABLE 2365-continued

Sample ID #	Set	B cell differentiation signature value	T-cell signature value	Macrophage signature value	Survival predictor score
FL_1645	Training	9.39	9.46	8.70	−11.15
FL_1646	Training	9.90	9.25	8.52	−11.42
FL_1647	Training	9.51	9.12	8.95	−9.92
FL_1648	Training	10.02	9.18	7.86	−12.67
FL_1652	Training	9.62	9.39	9.19	−10.16
FL_1654	Validation	10.32	8.59	8.10	−11.02
FL_1655	Training	10.12	9.53	8.75	−11.74
FL_1656	Validation	10.54	9.08	8.55	−11.42
FL_1657	Training	10.53	9.53	8.55	−12.46
FL_1660	Training	10.24	8.75	8.27	−10.99
FL_1661	Validation	10.08	9.85	9.00	−11.97
FL_1662	Validation	9.85	9.56	9.49	−10.11
FL_1664	Validation	10.16	9.35	8.48	−11.92
FL_1669	Training	9.48	8.76	8.28	−10.45
FL_1670	Training	9.76	9.66	9.66	−9.92
FL_1675	Training	10.57	9.28	8.41	−12.18
FL_1681	Validation	10.48	9.52	8.66	−12.19
FL_1683	Validation	9.88	9.92	9.07	−11.83
FL_1684	Training	9.64	9.53	8.85	−11.20
FL_1716	Validation	9.90	8.91	8.22	−11.23
FL_1717	Validation	9.87	9.34	8.95	−10.71
FL_1718	Training	10.00	9.21	7.98	−12.49
FL_1719	Validation	9.87	9.06	8.42	−11.14
FL_1720	Training	10.70	8.77	8.92	−10.05
FL_1729	Training	10.50	9.23	8.65	−11.53
FL_1732	Validation	9.91	7.68	8.54	−7.69
FL_1761	Validation	9.81	9.22	8.39	−11.54
FL_1764	Training	9.81	9.24	8.77	−10.80
FL_1768	Training	10.12	9.36	8.50	−11.86
FL_1771	Training	9.92	9.12	8.68	−10.79
FL_1772	Validation	9.72	9.42	8.43	−11.87
FL_1788	Training	9.65	9.05	9.12	−9.51
FL_1790	Training	9.58	9.83	9.48	−10.56
FL_1792	Validation	9.79	9.29	8.67	−11.11
FL_1795	Training	9.58	10.18	9.33	−11.69
FL_1797	Validation	9.93	9.26	8.79	−10.90
FL_1799	Training	10.49	9.28	8.64	−11.65
FL_1810	Validation	10.06	8.55	8.21	−10.52
FL_1811	Validation	9.84	9.37	8.08	−12.56
FL_1825	Training	10.49	9.44	9.03	−11.24
FL_1827	Training	10.06	9.76	8.84	−12.08
FL_1828	Validation	10.55	8.93	7.67	−12.87
FL_1829	Validation	9.85	9.58	8.65	−11.87
FL_1830	Validation	10.80	8.99	8.67	−11.15
FL_1833	Training	10.41	9.83	8.82	−12.52
FL_1834	Validation	10.81	9.25	8.63	−11.85
FL_1835	Validation	9.36	9.25	8.91	−10.21
FL_1836	Validation	10.58	9.58	8.61	−12.50
FL_1837	Validation	10.22	9.47	8.76	−11.68
FL_1838	Validation	10.51	9.89	9.19	−11.98
FL_1839	Training	10.79	8.54	8.19	−11.09
FL_1841	Training	10.32	9.31	9.18	−10.48
FL_1842	Validation	10.36	9.69	8.92	−11.95
FL_1844	Validation	10.92	9.43	8.49	−12.65
FL_1845	Training	9.87	9.87	9.06	−11.73
FL_1846	Validation	9.66	9.81	9.93	−9.63
FL_1848	Training	9.82	9.74	8.70	−12.14
FL_1851	Training	9.89	9.47	9.03	−10.87
FL_1853	Validation	9.96	9.28	8.54	−11.49
FL_1854	Validation	9.97	9.29	8.73	−11.12
FL_1855	Validation	9.95	9.33	8.42	−11.85
FL_1857	Validation	10.35	9.81	9.28	−11.50
FL_1861	Validation	9.73	9.46	8.43	−11.96
FL_1862	Validation	10.42	8.94	8.22	−11.69
FL_1863	Validation	10.79	9.29	8.82	−11.54
FL_1864	Training	9.67	9.97	9.07	−11.80
FL_1866	Training	10.19	9.88	8.89	−12.33
FL_1870	Validation	9.78	10.07	9.30	−11.63
FL_1873	Training	10.09	9.41	8.77	−11.40
FL_1874	Validation	10.05	9.33	8.69	−11.37
FL_1876	Validation	10.15	9.59	8.67	−12.08

TABLE 2365-continued

Sample ID #	Set	B cell differentiation signature value	T-cell signature value	Macrophage signature value	Survival predictor score
FL_1879	Training	9.73	9.21	8.58	−11.06
FL_1880	Validation	10.02	8.79	8.35	−10.77
FL_1882	Training	9.59	9.44	8.80	−11.05
FL_1884	Validation	9.76	9.51	9.26	−10.38
FL_1885	Validation	10.48	9.66	8.75	−12.32
FL_1887	Training	9.98	9.42	8.47	−11.96
FL_1888	Training	9.73	9.83	8.99	−11.67
FL_1890	Training	10.06	9.33	8.98	−10.76
FL_1894	Training	9.85	8.99	8.75	−10.29
FL_1896	Training	10.21	9.80	8.51	−12.94
FL_1897	Training	10.67	8.99	8.26	−11.90
FL_1898	Training	9.59	8.77	8.21	−10.68
FL_1900	Validation	10.12	9.10	8.10	−12.08
FL_1903	Validation	11.08	8.99	8.39	−11.93
FL_1904	Validation	10.20	9.16	8.30	−11.87
FL_1905	Validation	9.73	9.21	8.22	−11.80
FL_1906	Training	9.95	8.15	8.44	−9.01
FL_1907	Validation	10.12	7.95	7.99	−9.62
FL_1910	Training	11.03	9.38	8.74	−12.10
FL_1912	Validation	9.83	9.38	9.36	−9.95
FL_1913	Training	9.81	9.75	8.43	−12.69
FL_1916	Validation	9.83	9.18	8.40	−11.43
FL_1918	Validation	9.86	9.52	8.79	−11.45
FL_1919	Training	9.87	9.53	8.79	−11.48
FL_735	Validation	10.48	8.73	8.23	−11.20
FL_738	Validation	11.05	9.10	8.75	−11.43
FL_739	Training	9.66	9.25	8.74	−10.78
FL_878	Validation	10.61	8.92	8.65	−10.89
FL_879	Training	9.92	8.94	8.78	−10.14
FL_886	Validation	10.16	9.41	8.63	−11.73
FL_888	Validation	9.35	8.76	8.38	−10.15
FL_1627	Training	9.82	9.48	8.49	−11.94
FL_1429	Training	10.06	8.70	8.14	−11.01
FL_1850	Validation	9.58	9.73	8.70	−11.93
FL_1735	Validation	9.60	7.46	8.42	−7.19

[0163] In order to visualize the predictive power of the model, the FL samples were ranked according to their survival predictor scores and divided into four quartiles. Kaplan-Meier plots of overall survival showed clear differences in survival rate in the validation set (FIG. **8**). The median survival for each of the four quartiles is set forth in Table 2366.

TABLE 2366

Quartile	Median survival (yrs.)	5-year survival	10-year survival
1	NR	94%	79%
2	11.6	82%	62%
3	8.8	69%	39%
4	3.9	38%	22%

Example 5

Development of a Third FL Survival Predictor Using Gene Expression Data from the Lymph Dx Microarray

[0164] 191 FL samples were divided into two equivalent groups: a training set for developing the survival prediction model, and a validation set for evaluating the reproducibility of the model. Gene expression data from the Lymph Dx microarray was obtained for those genes listed in Table 2364, above. This gene expression data was used to calculate gene

expression signature values for the macrophage, T-cell, and B-cell differentiation gene expression signatures, and these signature values were used to generate a survival predictor score using the following equation:

> Survival predictor score=[1.51*(macrophage gene expression signature value)]−[2.11*(*T*-cell gene expression signature value)]−[0.505*(*B*-cell differentiation gene expression signature value)].

A higher survival predictor score was associated with worse outcome. For the 187 FL samples with available clinical data, the survival predictor score had a mean of −10.1 and a standard deviation of 0.69, with each unit increase in the predictor score corresponding to a 2.7 fold increase in the relative risk of death. Data for all 191 samples is shown in Table 2367.

TABLE 2367

Sample ID #	Set	B cell differentiation signature value	T-cell signature value	Macrophage signature value	Survival predictor score
FL_1073	Training	8.26	8.17	7.36	−10.30
FL_1074	Training	9.53	8.12	7.56	−10.53
FL_1075	Validation	9.81	8.00	7.99	−9.77
FL_1076	Training	8.46	8.10	7.62	−9.86
FL_1077	Training	8.45	8.66	7.32	−11.49
FL_1078	Training	9.23	8.32	7.32	−11.18
FL_1080	Training	9.18	8.37	7.86	−10.42
FL_1081	Validation	8.96	8.01	6.94	−10.96
FL_1083	Training	8.72	8.65	7.89	−10.75
FL_1085	Validation	8.34	8.17	7.54	−10.07
FL_1086	Validation	8.50	8.35	7.94	−9.94
FL_1087	Training	8.02	8.88	8.48	−10.00
FL_1088	Validation	9.10	8.15	7.38	−10.65
FL_1089	Training	8.76	8.31	7.35	−10.86
FL_1090	Validation	8.18	8.23	7.43	−10.28
FL_1097	Validation	8.07	8.81	7.90	−10.73
FL_1098	Validation	9.53	8.30	8.09	−10.11
FL_1099	Training	8.44	8.56	8.26	−9.86
FL_1102	Validation	7.92	8.43	7.94	−9.80
FL_1104	Training	9.17	8.07	7.21	−10.78
FL_1106	Validation	9.71	8.15	8.77	−8.85
FL_1107	Training	8.16	8.44	8.60	−8.95
FL_1183	Training	8.49	8.15	7.23	−10.56
FL_1184	Training	8.81	8.49	7.91	−10.43
FL_1185	Validation	9.31	8.19	8.06	−9.80
FL_1186	Training	8.43	7.87	7.83	−9.04
FL_1416	Validation	8.42	8.34	7.63	−10.34
FL_1417	Training	8.65	7.51	7.05	−9.58
FL_1418	Validation	7.96	7.82	7.22	−9.62
FL_1419	Training	8.80	8.71	7.55	−11.43
FL_1422	Training	8.63	8.35	7.39	−10.83
FL_1425	Validation	8.21	7.92	7.62	−9.36
FL_1426	Training	9.39	8.09	7.15	−11.01
FL_1427	Training	8.66	7.51	7.00	−9.65
FL_1428	Validation	9.33	8.18	7.39	−10.81
FL_1432	Training	8.98	8.17	7.93	−9.81
FL_1436	Training	8.04	8.17	7.35	−10.20
FL_1440	Training	8.29	7.82	7.15	−9.89
FL_1445	Training	8.04	7.78	7.63	−8.94
FL_1450	Validation	8.25	8.81	9.52	−8.39
FL_1472	Validation	9.29	7.88	7.33	−10.26
FL_1473	Training	8.49	8.57	7.52	−11.03
FL_1474	Validation	8.59	8.09	8.53	−8.54
FL_1476	Validation	8.25	8.39	7.71	−10.23
FL_1477	Training	7.94	8.57	7.88	−10.21
FL_1478	Training	8.57	8.40	7.88	−10.16
FL_1479	Training	9.15	7.83	7.87	−9.27
FL_1480	Training	8.25	8.38	7.44	−10.63
FL_1579	Training	8.70	7.73	7.43	−9.48
FL_1580	Training	8.86	8.46	7.64	−10.79
FL_1581	Training	8.41	7.89	8.08	−8.69
FL_1582	Validation	8.20	7.42	6.99	−9.24
FL_1583	Training	9.34	8.34	7.94	−10.32
FL_1584	Training	8.50	8.33	7.75	−10.17
FL_1585	Validation	9.08	7.96	7.72	−9.72
FL_1586	Validation	8.52	8.25	7.36	−10.61
FL_1588	Training	7.97	8.35	7.73	−9.98
FL_1589	Training	8.85	8.48	7.76	−10.66
FL_1591	Training	8.92	8.36	7.77	−10.42
FL_1594	Validation	8.54	8.22	7.74	−9.96
FL_1595	Training	8.05	8.82	8.68	−9.57
FL_1598	Validation	9.74	7.81	6.97	−10.88
FL_1599	Validation	9.13	8.42	7.69	−10.77
FL_1603	Training	7.97	8.66	8.90	−8.86
FL_1604	Training	8.47	8.14	7.75	−9.75
FL_1606	Validation	8.34	8.32	8.11	−9.51
FL_1607	Validation	8.33	8.30	7.39	−10.57
FL_1608	Validation	8.35	7.88	6.98	−10.31
FL_1610	Validation	8.48	8.35	8.86	−8.52
FL_1611	Validation	8.54	8.33	7.64	−10.37
FL_1616	Training	8.03	8.39	7.67	−10.18
FL_1617	Validation	8.30	7.85	7.52	−9.40
FL_1619	Validation	8.53	8.31	7.64	−10.32
FL_1620	Validation	8.09	7.99	7.17	−10.11
FL_1622	Training	8.14	8.10	7.36	−10.09
FL_1623	Training	8.45	8.52	8.15	−9.93
FL_1624	Validation	9.13	8.12	7.46	−10.49
FL_1625	Validation	8.53	7.94	7.17	−10.23
FL_1626	Validation	9.63	7.67	7.17	−10.22
FL_1628	Validation	8.63	8.76	7.95	−10.86
FL_1637	Validation	8.07	8.81	8.79	−9.38
FL_1638	Validation	8.52	8.18	8.19	−9.18
FL_1639	Training	8.70	8.33	7.89	−10.06
FL_1643	Training	8.26	8.62	8.01	−10.26
FL_1644	Validation	8.28	8.33	7.77	−10.02
FL_1645	Training	7.84	8.32	7.68	−9.91
FL_1646	Training	8.40	8.26	7.71	−10.01
FL_1647	Training	8.10	8.04	7.92	−9.10
FL_1648	Training	8.33	8.08	6.87	−10.90
FL_1652	Training	8.15	8.33	8.37	−9.07
FL_1654	Validation	8.67	7.62	7.03	−9.85
FL_1655	Training	8.53	8.41	7.75	−10.36
FL_1656	Validation	9.09	8.09	7.62	−10.16
FL_1657	Training	8.95	8.44	7.58	−10.89
FL_1660	Training	8.82	7.79	7.26	−9.93
FL_1661	Validation	8.56	8.79	8.17	−10.53
FL_1662	Validation	8.30	8.47	8.69	−8.93
FL_1664	Validation	8.62	8.23	7.56	−10.31
FL_1669	Training	7.89	7.67	7.39	−9.02
FL_1670	Training	8.01	8.54	8.64	−9.03
FL_1675	Training	9.00	8.21	7.36	−10.76
FL_1681	Validation	8.83	8.39	7.59	−10.72
FL_1683	Validation	8.14	8.85	7.97	−10.74
FL_1684	Training	7.99	8.42	7.84	−9.97
FL_1716	Validation	8.28	7.90	7.26	−9.88
FL_1717	Validation	8.27	8.21	7.89	−9.60
FL_1718	Training	8.50	8.17	7.15	−10.75
FL_1719	Validation	8.35	8.02	7.21	−10.26
FL_1720	Training	9.03	7.65	8.01	−8.61
FL_1729	Training	8.97	8.27	7.69	−10.37
FL_1732	Validation	8.49	6.82	7.71	−7.02
FL_1761	Validation	8.36	8.19	7.29	−10.49
FL_1764	Training	8.52	8.24	7.94	−9.69
FL_1768	Training	8.70	8.25	7.63	−10.28
FL_1771	Training	8.55	8.19	7.65	−10.04
FL_1772	Validation	8.30	8.38	7.41	−10.71
FL_1788	Training	8.14	8.06	8.11	−8.87
FL_1790	Training	7.95	8.69	8.36	−9.74
FL_1792	Validation	8.16	8.20	7.64	−9.88
FL_1795	Training	7.94	9.08	8.37	−10.54
FL_1797	Validation	8.17	8.21	7.87	−9.57
FL_1799	Training	9.02	8.21	7.77	−10.14
FL_1810	Validation	8.43	7.52	7.06	−9.47
FL_1811	Validation	8.33	8.24	7.07	−10.93

TABLE 2367-continued

Sample ID #	Set	B cell differentiation signature value	T-cell signature value	Macrophage signature value	Survival predictor score
FL_1825	Training	8.90	8.39	7.97	−10.18
FL_1827	Training	8.47	8.77	7.96	−10.76
FL_1828	Validation	9.13	7.87	6.76	−11.01
FL_1829	Validation	8.34	8.51	7.59	−10.71
FL_1830	Validation	9.26	8.04	7.62	−10.13
FL_1833	Training	8.82	8.86	7.88	−11.26
FL_1834	Validation	9.25	8.17	7.62	−10.39
FL_1835	Validation	7.71	8.16	8.01	−9.02
FL_1836	Validation	9.06	8.52	7.59	−11.09
FL_1837	Validation	8.57	8.33	7.37	−10.79
FL_1838	Validation	8.78	8.72	8.04	−10.69
FL_1839	Training	9.27	7.36	7.37	−9.08
FL_1841	Training	8.66	8.35	8.17	−9.64
FL_1842	Validation	8.62	8.50	8.02	−10.19
FL_1844	Validation	9.37	8.40	7.47	−11.18
FL_1845	Training	8.33	8.84	8.30	−10.32
FL_1846	Validation	8.11	8.75	9.06	−8.89
FL_1848	Training	8.19	8.60	7.91	−10.33
FL_1851	Training	8.37	8.50	8.15	−9.84
FL_1853	Validation	8.37	8.14	7.43	−10.19
FL_1854	Validation	8.50	8.29	7.96	−9.78
FL_1855	Validation	8.63	8.34	7.54	−10.58
FL_1857	Validation	8.73	8.82	8.45	−10.26
FL_1861	Validation	8.21	8.50	7.50	−10.77
FL_1862	Validation	8.98	7.96	7.31	−10.28
FL_1863	Validation	9.30	8.22	7.86	−10.18
FL_1864	Training	8.13	8.93	8.27	−10.46
FL_1866	Training	8.62	8.78	7.91	−10.93
FL_1870	Validation	8.16	8.97	8.52	−10.18
FL_1873	Training	8.55	8.30	8.00	−9.74
FL_1874	Validation	8.43	8.20	7.59	−10.10
FL_1876	Validation	8.48	8.52	7.70	−10.64
FL_1879	Training	8.29	8.21	7.66	−9.94
FL_1880	Validation	8.56	7.76	7.34	−9.61
FL_1882	Training	8.02	8.40	7.71	−10.14
FL_1884	Validation	8.14	8.46	8.42	−9.24
FL_1885	Validation	8.88	8.57	7.78	−10.81
FL_1887	Training	8.38	8.39	7.38	−10.78
FL_1888	Training	8.14	8.74	8.07	−10.37
FL_1890	Training	8.45	8.24	8.11	−9.41
FL_1894	Training	8.38	7.97	7.82	−9.25
FL_1896	Training	8.63	8.71	7.52	−11.37
FL_1897	Training	9.01	7.91	6.93	−10.78
FL_1898	Training	8.08	7.75	7.09	−9.74
FL_1900	Validation	8.61	7.94	6.84	−10.77
FL_1903	Validation	9.63	7.96	7.30	−10.64
FL_1904	Validation	8.79	8.14	7.15	−10.82
FL_1905	Validation	8.22	8.24	7.36	−10.43
FL_1906	Training	8.40	7.40	7.24	−8.93
FL_1907	Validation	8.61	7.11	6.59	−9.40
FL_1910	Training	9.47	8.28	7.63	−10.73
FL_1912	Validation	8.32	8.45	8.52	−9.18
FL_1913	Training	8.24	8.60	7.23	−11.41
FL_1916	Validation	8.31	8.04	7.27	−10.19
FL_1918	Validation	8.30	8.49	7.78	−10.37
FL_1919	Training	8.05	8.42	8.00	−9.75
FL_735	Validation	9.03	7.83	7.41	−9.88
FL_738	Validation	9.54	8.07	7.65	−10.30
FL_739	Training	8.14	8.09	7.69	−9.57
FL_878	Validation	9.17	7.91	7.70	−9.69
FL_879	Training	8.37	7.96	7.67	−9.45
FL_886	Validation	8.59	8.38	7.67	−10.44
FL_888	Validation	7.85	7.71	7.07	−9.56
FL_1627	Training	8.26	8.17	7.36	−10.30
FL_1429	Training	9.53	8.12	7.56	−10.53
FL_1850	Validation	9.81	8.00	7.99	−9.77
FL_1735	Validation	8.46	8.10	7.62	−9.86

[0165] In order to visualize the predictive power of the model, the FL samples were ranked according to their survival predictor scores and divided into four quartiles. Kaplan-Meier plots of overall survival showed clear differences in survival rate in the validation set (FIG. **9**).

Example 6

Development of a First DLBCL Survival Predictor Using Gene Expression Data from Affymetrix U133A and U133B Microarrays

[0166] Gene expression data from Affymetrix U133A and U133B microarrays was obtained for 231 DLBCL samples. The follow-up time and status at follow-up for each of the subjects from whom these samples were acquired is listed in Table 2368. Table 2368 also indicates which samples were used in creating the survival predictor.

TABLE 2368

Sample ID #	Length of follow-up (years)	Status at follow-up	Used in creating survival predictor?
ABC_1000	0.69	Dead	Yes
ABC_1002	0.28	Dead	Yes
ABC_1023	5.57	Dead	Yes
ABC_1027	0.25	Dead	Yes
ABC_1031	6.64	Dead	Yes
ABC_1034	2.31	Dead	Yes
ABC_1038	0.71	Dead	Yes
ABC_1043	2.31	Dead	Yes
ABC_1045	2.26	Dead	Yes
ABC_1055	7.81	Alive	Yes
ABC_1057	2.13	Dead	Yes
ABC_1059	2.00	Dead	Yes
ABC_1061	1.04	Dead	Yes
ABC_1946	0.68	Dead	No
ABC_1994	1.21	Dead	No
ABC_2001	1.32	Dead	No
ABC_304	1.31	Dead	Yes
ABC_305	0.82	Alive	Yes
ABC_309	2.80	Alive	Yes
ABC_413	0.60	Dead	Yes
ABC_428	11.38	Alive	Yes
ABC_432	0.38	Dead	Yes
ABC_446	2.82	Dead	Yes
ABC_462	7.49	Dead	Yes
ABC_477	1.70	Dead	Yes
ABC_481	10.75	Alive	Yes
ABC_482	7.72	Alive	Yes
ABC_538	0.34	Dead	Yes
ABC_541	4.11	Alive	Yes
ABC_544	1.31	Dead	Yes
ABC_547	0.05	Dead	Yes
ABC_577	1.65	Alive	Yes
ABC_616	0.99	Dead	Yes
ABC_626	2.49	Dead	Yes
ABC_633	2.02	Alive	Yes
ABC_642	0.34	Dead	Yes
ABC_644	0.31	Dead	Yes
ABC_645	6.08	Dead	Yes
ABC_646	2.59	Dead	Yes
ABC_651	2.34	Alive	Yes
ABC_652	0.01	Dead	Yes
ABC_660	0.20	Dead	Yes
ABC_663	0.62	Dead	Yes
ABC_668	6.44	Alive	Yes
ABC_676	1.00	Dead	Yes
ABC_678	0.06	Dead	Yes
ABC_687	0.94	Dead	Yes
ABC_689	2.54	Dead	Yes
ABC_692	10.53	Alive	Yes
ABC_694	4.83	Alive	Yes
ABC_700	5.40	Dead	Yes
ABC_702	4.13	Dead	Yes
ABC_704	9.67	Alive	Yes
ABC_709	0.47	Dead	Yes

TABLE 2368-continued

Sample ID #	Length of follow-up (years)	Status at follow-up	Used in creating survival predictor?
ABC_712	3.26	Dead	Yes
ABC_714	2.45	Dead	Yes
ABC_717	0.42	Dead	Yes
ABC_725	0.96	Dead	Yes
ABC_726	7.62	Alive	Yes
ABC_730	1.03	Dead	Yes
ABC_753	0.04	Dead	Yes
ABC_756	7.21	Alive	Yes
ABC_771	6.80	Dead	Yes
ABC_779	0.35	Dead	Yes
ABC_800	0.33	Dead	Yes
ABC_807	0.31	Dead	Yes
ABC_809	0.51	Dead	Yes
ABC_816	1.86	Dead	Yes
ABC_820	1.59	Dead	Yes
ABC_823	0.16	Dead	Yes
ABC_835	1.22	Dead	Yes
ABC_839	0.29	Dead	Yes
ABC_841	10.14	Alive	Yes
ABC_858	3.58	Dead	Yes
ABC_872	5.00	Alive	Yes
ABC_875	8.45	Alive	Yes
ABC_912	16.79	Alive	Yes
ABC_996	0.21	Dead	Yes
GCB_1005	5.77	Alive	Yes
GCB_1008	6.46	Alive	Yes
GCB_1009	9.68	Alive	Yes
GCB_1021	14.59	Alive	Yes
GCB_1025	2.86	Dead	Yes
GCB_1026	6.94	Dead	Yes
GCB_1037	0.23	Dead	Yes
GCB_1039	2.05	Dead	Yes
GCB_1049	1.33	Dead	Yes
GCB_1051	0.12	Dead	Yes
GCB_1058	0.42	Dead	Yes
GCB_1060	6.45	Alive	Yes
GCB_1990	0.06	Dead	No
GCB_1991	1.01	Dead	No
GCB_2017	0.08	Dead	No
GCB_2018	0.17	Dead	No
GCB_2095	0.97	Alive	No
GCB_412	12.12	Alive	Yes
GCB_415	5.38	Dead	Yes
GCB_421	1.24	Dead	Yes
GCB_424	10.62	Dead	Yes
GCB_433	0.76	Dead	Yes
GCB_434	10.53	Alive	Yes
GCB_438	8.15	Alive	Yes
GCB_459	9.65	Alive	Yes
GCB_470	11.17	Alive	Yes
GCB_479	7.24	Alive	Yes
GCB_492	11.29	Alive	Yes
GCB_517	3.03	Dead	Yes
GCB_523	8.36	Alive	Yes
GCB_524	5.88	Alive	Yes
GCB_529	1.06	Dead	Yes
GCB_533	0.71	Dead	Yes
GCB_537	4.99	Dead	Yes
GCB_543	3.47	Alive	Yes
GCB_545	1.10	Dead	Yes
GCB_549	2.68	Dead	Yes
GCB_550	21.78	Alive	Yes
GCB_553	0.82	Dead	Yes
GCB_565	9.11	Dead	Yes
GCB_572	14.24	Alive	Yes
GCB_617	5.88	Alive	Yes
GCB_618	5.65	Alive	Yes
GCB_619	8.76	Alive	Yes
GCB_623	2.43	Alive	Yes
GCB_627	1.27	Dead	Yes
GCB_654	7.37	Alive	Yes
GCB_661	0.56	Alive	Yes

TABLE 2368-continued

Sample ID #	Length of follow-up (years)	Status at follow-up	Used in creating survival predictor?
GCB_669	7.11	Alive	Yes
GCB_672	6.78	Alive	Yes
GCB_674	7.22	Alive	Yes
GCB_675	6.02	Alive	Yes
GCB_681	9.70	Alive	Yes
GCB_688	0.33	Dead	Yes
GCB_695	0.15	Dead	Yes
GCB_698	3.88	Alive	Yes
GCB_701	3.90	Alive	Yes
GCB_710	1.08	Dead	Yes
GCB_711	3.93	Dead	Yes
GCB_722	3.32	Alive	Yes
GCB_724	1.40	Dead	Yes
GCB_731	10.18	Alive	Yes
GCB_742	4.09	Alive	Yes
GCB_744	8.86	Alive	Yes
GCB_745	1.33	Dead	Yes
GCB_747	15.41	Alive	Yes
GCB_749	10.40	Alive	Yes
GCB_758	1.10	Dead	Yes
GCB_772	2.48	Alive	Yes
GCB_777	4.27	Dead	Yes
GCB_792	5.53	Alive	Yes
GCB_795	3.43	Alive	Yes
GCB_797	6.87	Dead	Yes
GCB_803	1.45	Dead	Yes
GCB_810	11.72	Alive	Yes
GCB_817	2.76	Dead	Yes
GCB_818	0.10	Dead	Yes
GCB_819	0.72	Dead	Yes
GCB_821	9.47	Alive	Yes
GCB_832	4.01	Alive	Yes
GCB_836	4.29	Alive	Yes
GCB_840	3.40	Alive	Yes
GCB_847	4.16	Alive	Yes
GCB_860	3.03	Dead	Yes
GCB_871	0.41	Dead	Yes
GCB_874	0.12	Dead	Yes
GCB_995	6.65	Alive	Yes
PMBL_1006	7.12	Alive	Yes
PMBL_1024	19.83	Alive	Yes
PMBL_1048	7.70	Alive	Yes
PMBL_1053	1.04	Dead	Yes
PMBL_1920	1.97	Alive	No
PMBL_1921	4.16	Alive	No
PMBL_1923	1.60	Alive	No
PMBL_1924	6.11	Alive	No
PMBL_1935	12.42	Alive	No
PMBL_1941	0.71	Alive	No
PMBL_1942	0.88	Alive	No
PMBL_1943	8.96	Alive	No
PMBL_1945	0.84	Dead	No
PMBL_1948	7.96	Alive	No
PMBL_1949	4.28	Alive	No
PMBL_1989	1.33	Dead	No
PMBL_1992	1.00	Dead	No
PMBL_1993	1.33	Dead	No
PMBL_2002	6.62	Alive	No
PMBL_2019	0.99	Dead	No
PMBL_2020	2.08	Alive	No
PMBL_2092	1.27	Alive	No
PMBL_484	1.40	Dead	Yes
PMBL_546	0.78	Dead	Yes
PMBL_570	14.40	Alive	Yes
PMBL_621	8.14	Alive	Yes
PMBL_638	0.70	Dead	Yes
PMBL_691	0.32	Dead	Yes
PMBL_791	1.33	Dead	Yes
PMBL_824	12.24	Alive	Yes
PMBL_906	16.80	Alive	Yes
PMBL_994	4.79	Alive	Yes
PMBL_998	9.11	Alive	Yes

TABLE 2368-continued

Sample ID #	Length of follow-up (years)	Status at follow-up	Used in creating survival predictor?
UC_DLBCL_1001	0.33	Dead	Yes
UC_DLBCL_1004	6.72	Alive	Yes
UC_DLBCL_1007	2.26	Dead	Yes
UC_DLBCL_1018	0.03	Dead	Yes
UC_DLBCL_1041	3.13	Dead	Yes
UC_DLBCL_1054	12.34	Alive	Yes
UC_DLBCL_306	2.69	Alive	Yes
UC_DLBCL_310	0.97	Alive	Yes
UC_DLBCL_449	9.16	Alive	Yes
UC_DLBCL_452	9.17	Alive	Yes
UC_DLBCL_458	1.18	Dead	Yes
UC_DLBCL_460	9.02	Alive	Yes
UC_DLBCL_491	4.47	Dead	Yes
UC_DLBCL_528	1.64	Alive	Yes
UC_DLBCL_615	4.94	Alive	Yes
UC_DLBCL_625	5.24	Alive	Yes
UC_DLBCL_664	0.62	Dead	Yes
UC_DLBCL_671	3.35	Alive	Yes
UC_DLBCL_682	0.11	Dead	Yes
UC_DLBCL_683	7.42	Alive	Yes
UC_DLBCL_684	1.92	Dead	Yes
UC_DLBCL_748	1.01	Dead	Yes
UC_DLBCL_751	9.99	Alive	Yes
UC_DLBCL_808	0.37	Dead	Yes
UC_DLBCL_831	11.02	Dead	Yes
UC_DLBCL_834	1.64	Dead	Yes
UC_DLBCL_838	0.00	Dead	Yes
UC_DLBCL_851	0.05	Dead	Yes
UC_DLBCL_854	1.51	Dead	Yes
UC_DLBCL_855	1.67	Alive	Yes
UC_DLBCL_856	0.60	Dead	Yes

[0167] The correlation between expression of each gene represented on the microarrays and survival was estimated using a Cox proportional hazards model. The results of this survival analysis are provided in the final two columns of Table 1723. The first of these two columns ("DLBCL_Cox_coefficient") provides a Cox coefficient indicating the extent to which a 2-fold increase in expression of a particular gene affects mortality. A positive Cox coefficient indicates increasing mortality with increasing expression of the gene, while a negative Cox coefficient indicates decreasing mortality with increasing expression of the gene. The second of these two columns ("DLBCL_Cox_P_value") provides a Cox p-value indicating the estimated probability that the increase or decrease in survival associated with the gene would occur by chance if there was no connection between the expression of the gene and survival.

[0168] Genes that were significantly correlated with survival ($p<0.001$) were grouped into gene expression signatures using a hierarchical clustering algorithm. The expression level of every component gene in each of these gene expression signatures was averaged for each sample to create a gene expression signature value. A step-up procedure (Drapner 1966) was applied to determine the optimal number of gene signatures to use in the survival predictor model. First, the gene expression signature that was most significantly associated with survival was included in the model. Next, the gene expression signature with the second highest association with survival was added to the model to form a two-component model. This procedure was repeated until there was no gene expression signature to add to the model with a p-value of <0.05.

[0169] The final prediction model incorporated gene expression signature values from three gene expression signatures. The first gene expression signature added to the model was termed "ABC DLBCL high," because it included genes that were more highly expressed in ABC than in GCB (Rosenwald 2002). The second gene expression signature added to the model was termed "lymph node," because it reflected the response of non-tumor cells in the lymph node to the malignant lymphoma cells. The final gene expression signature added to the model was termed "MHC class II," because it included all of the genes encoding the MHC class II alpha and beta chains. Table 2369 shows the genes that were averaged to form each of these signatures.

TABLE 2369

Signature	UNIQID	Gene symbol	Survival p-value
ABC DLBCL high	1134271	POU5F1	3.09E-05
ABC DLBCL high	1121564	DRIL1	4.06E-05
ABC DLBCL high	1119889	PDCD4	7.28E-05
ABC DLBCL high	1133300	CTH	1.23E-04
ABC DLBCL high	1106030	MGC: 50789	1.70E-04
ABC DLBCL high	1139301	FLJ20150	4.49E-04
ABC DLBCL high	1122131	CHST7	5.18E-04
ABC DLBCL high	1114824	LIMD1	5.20E-04
ABC DLBCL high	1100161	LOC142678	6.24E-04
ABC DLBCL high	1120129	TLE1	6.95E-04
Lymph node	1097126	TEM8	5.14E-09
Lymph node	1120880	LTBP2	9.80E-07
Lymph node	1098898	FLJ31066	1.09E-06
Lymph node	1123376	RARRES2	1.68E-06
Lymph node	1128945	SLC12A8	2.90E-06
Lymph node	1130994	DPYSL3	3.37E-06
Lymph node	1124429	SULF1	3.53E-06
Lymph node	1099358	FLJ39971	4.09E-06
Lymph node	1130509	SPARC	6.23E-06
Lymph node	1095985	TMEPAI	7.07E-06
Lymph node	1123038	ACTN1	7.90E-06
Lymph node	1133700	CDH11	8.20E-06
Lymph node	1122101	TFEC	9.66E-06
Lymph node	1124296	SDC2	9.99E-06
MHC Class II	1123127	HLA-DRA	1.21E-06
MHC Class II	1136777	HLA-DQA1	3.45E-06
MHC Class II	1137771	HLA-DRB1	3.95E-06
MHC Class II	1134281	HLA-DRB4	2.70E-05
MHC Class II	1136573	HLA-DPA1	2.92E-05
MHC Class II	1132710	HLA-DRB3	7.09E-05

[0170] Fitting the Cox proportional hazards model to the three gene expression signature values resulted in the following model:

> Survival predictor score=[0.586*(ABC DLBCL high gene expression signature value)]−[0.468*(lymph node gene expression signature value)]−[0.336*(MHC Class II gene expression signature value)].

A higher survival predictor score was associated with worse outcome. According to a likelihood ratio test adjusted for the number of variables included, this model was significant in predicting survival at $p=2.13\times10^{-13}$. In order to visualize the predictive power of the model, the 205 samples used to create the model were ranked according to their survival predictor scores and divided into four quartiles. Kaplan-Meier plots of overall survival probability show clear differences in survival rate between these four quartiles (FIG. **10**). The five-year survival probabilities for each quartile are set forth in Table 2370.

TABLE 2370

Quartile	5-year survival
1	83%
2	59%
3	33%
4	17%

Example 7

Development of a Second DLBCL Survival Predictor Using Gene Expression Data from the Lymph Dx Microarray

[0171] A DLBCL survival model based on gene expression had been developed previously using proliferation, germinal center B-cell, lymph node, and MHC class II gene expression signatures and the expression of the single gene BMP-6 (Rosenwald 2002). BMP-6 expression was poorly measured on the Lymph Dx microarray, but genes associated with each of these four gene expression signatures exhibited associations with survival similar to those observed using Lymphochip microarrays. DLBCL samples were divided into two groups: a training set (100 samples) for developing the survival prediction model, and a validation set (100 samples) for evaluating the reproducibility of the model. Gene expressed in the training set samples were clustered, and lymph node, germinal center B-cell, MHC class II, and proliferation gene expression signatures were identified. Within each signature, expression of genes that were associated with survival ($p<0.01$) was averaged to generate a gene expression signature value for each signature. Table 2371 lists the genes that were used to generate the gene expression signature value for each signature.

TABLE 2371

Signature	UNIQID	Unigene ID Build 167	Gene symbol
Germinal center B-cell	1099686	117721	
Germinal center B-cell	1099711	243596	
Germinal center B-cell	1103390	271752	BPNT1
Germinal center B-cell	1106025	49500	KIAA0746
Germinal center B-cell	1128287	300063	ASB13
Germinal center B-cell	1132520	283063	LMO2
Germinal center B-cell	1138192	126608	NR3C1
Germinal center B-cell	1529318	291954	
Germinal center B-cell	1529344	317970	SERPINA11
Germinal center B-cell	1529352	446195	
Germinal center B-cell	1096570	409813	ANUBL1
Germinal center B-cell	1097897	266175	PAG
Germinal center B-cell	1097901	266175	PAG
Germinal center B-cell	1098611	433611	PDK1
Germinal center B-cell	1100581	155024	BCL6
Germinal center B-cell	1115034	387222	NEK6
Germinal center B-cell	1120090	155024	BCL6
Germinal center B-cell	1120946	25209	MAPK10
Germinal center B-cell	1121248	54089	BARD1
Germinal center B-cell	1123105	434281	PTK2
Germinal center B-cell	1125456	300592	MYBL1
Germinal center B-cell	1128694	171466	ELL3
Germinal center B-cell	1128787	114611	C7orf10
Germinal center B-cell	1132122	307734	MME
Germinal center B-cell	1136269	101474	MAST2
Germinal center B-cell	1136702	155584	KIAA0121
Germinal center B-cell	1139230	29724	PLEKHF2
Germinal center B-cell	1529292	NA	
Germinal center B-cell	1529295	116441	
Lymph node	1097126	274520	ANTXR1
Lymph node	1099028	334838	FNDC1
Lymph node	1099358	93135	
Lymph node	1101478	146246	MGC45780
Lymph node	1103497	50115	
Lymph node	1121029	412999	CSTA
Lymph node	1124429	409602	SULF1
Lymph node	1135068	71719	PDLIM3
Lymph node	1136051	520937	CSF2RA
Lymph node	1136172	38084	SULT1C1
MHC class II	1136777	387679	HLA-DQA1
MHC class II	1136877	409934	HLA-DQB1
Proliferation	1096903	437460	FLJ10385
Proliferation	1120583	153768	RNU3IP2
Proliferation	1123289	5409	POLR1C
Proliferation	1131808	75447	RALBP1
Proliferation	1133102	360041	FRDA
Proliferation	1136595	404814	VDAC1

[0172] Table 2372 lists p-values for the association of each signature with survival in the training set, the validation set, and overall.

TABLE 2372

Signature	Training set	Validation set	Overall
Lymph node	4.0×10^{-5}	2.3×10^{-6}	6.8×10^{-10}
Proliferation	8.1×10^{-5}	3.4×10^{-3}	2.1×10^{-6}
Germinal center B-cell	6.2×10^{-6}	2.1×10^{-3}	5.0×10^{-8}
MHC class II	2.4×10^{-2}	2.7×10^{-3}	3.1×10^{-4}

[0173] The four gene expression signatures were used to generate a survival predictor score using the following equation:

> Survival predictor score=[−0.4337*(lymph node gene expression signature value)]+[0.09*(proliferation gene expression signature value)]−[0.4144*(germinal center *B*-cell gene expression signature value)]−[0.2006*(MHC class II gene expression signature value)].

A higher survival predictor score was associated with worse outcome. For the 200 DLBCL samples used to generate the model, the survival predictor score had a mean of 5.7 and a standard deviation of 0.78, with each unit increase in the predictor score corresponding to an approximately 2.7 fold increase in the relative risk of death. Data for all 200 samples is presented in Table 2373.

TABLE 2373

Sample ID #	Set	Lymph node signature value	Proliferation signature value	Germinal center B-cell signature value	MHC class II signature value	Survival predictor score
ABC_1000	Validation	6.50	8.92	7.60	11.50	−5.08
ABC_1002	Validation	7.00	8.58	7.27	12.54	−5.50
ABC_1023	Validation	7.43	8.99	6.80	11.42	−5.05
ABC_1027	Training	5.68	9.00	6.87	12.31	−4.70
ABC_1031	Validation	8.02	9.00	7.17	11.68	−5.53
ABC_1034	Validation	6.06	9.61	6.72	11.83	−4.58
ABC_1038	Training	6.83	8.97	7.17	12.30	−5.23
ABC_1043	Training	6.96	9.01	6.77	12.29	−5.11
ABC_1045	Validation	8.18	8.21	6.77	12.07	−5.66
ABC_1055	Validation	5.58	9.16	7.30	13.05	−4.76
ABC_1057	Training	7.33	8.94	7.74	12.05	−5.53
ABC_1059	Validation	9.02	8.46	7.15	11.35	−6.08
ABC_1061	Training	7.13	9.18	7.09	12.28	−5.21
ABC_304	Validation	5.92	8.80	6.76	12.76	−4.84
ABC_305	Training	5.92	8.74	7.50	11.89	−4.91
ABC_309	Validation	8.86	8.39	7.62	12.53	−6.46
ABC_413	Validation	6.45	9.32	6.55	9.04	−4.16
ABC_428	Training	7.52	9.19	7.98	10.25	−5.51
ABC_432	Validation	6.48	9.33	7.45	9.56	−4.56
ABC_446	Training	7.91	9.42	7.41	10.55	−5.46
ABC_462	Validation	6.41	8.85	6.67	13.36	−5.03
ABC_477	Validation	6.26	9.02	6.69	12.45	−4.89
ABC_481	Training	8.18	8.30	7.35	11.98	−5.91
ABC_482	Training	8.59	9.01	7.66	12.35	−6.16
ABC_538	Validation	8.06	8.84	7.17	11.83	−5.69
ABC_541	Training	6.14	8.52	7.42	10.59	−4.71
ABC_544	Training	6.91	9.03	6.82	11.87	−4.89
ABC_547	Validation	5.80	8.96	7.14	11.38	−4.60
ABC_577	Validation	7.84	8.65	8.16	11.95	−5.94
ABC_616	Validation	6.03	9.05	7.36	12.64	−4.84
ABC_626	Validation	7.48	9.22	7.25	11.11	−5.27
ABC_633	Training	7.74	8.35	7.39	12.45	−5.80
ABC_642	Training	5.71	8.82	6.41	13.80	−4.62
ABC_644	Validation	6.64	9.15	7.05	13.28	−5.20
ABC_645	Training	8.44	8.81	7.93	13.39	−6.43
ABC_646	Validation	5.94	9.11	6.71	11.60	−4.63
ABC_652	Validation	5.87	8.85	6.88	12.73	−4.77
ABC_660	Training	5.19	9.34	6.64	10.17	−3.86
ABC_663	Training	5.69	9.02	7.33	12.82	−4.91
ABC_668	Validation	7.12	9.28	7.03	10.57	−4.91
ABC_676	Training	4.95	8.90	7.09	13.32	−4.61
ABC_678	Training	5.84	9.11	7.34	11.26	−4.41
ABC_687	Validation	5.15	9.89	6.56	10.46	−3.76
ABC_689	Training	6.49	8.86	7.10	12.56	−4.88
ABC_692	Validation	7.32	8.96	7.25	11.57	−5.32
ABC_694	Validation	8.28	9.21	8.01	12.41	−6.23
ABC_700	Training	7.29	8.97	7.55	12.10	−5.48
ABC_702	Validation	7.60	8.66	6.86	12.55	−5.45
ABC_704	Training	7.07	8.92	7.03	12.83	−5.35
ABC_709	Validation	5.92	8.58	6.37	13.40	−4.66
ABC_712	Validation	5.79	9.12	6.34	12.02	−4.23
ABC_714	Training	7.49	8.88	7.49	11.97	−5.54
ABC_717	Training	7.17	9.45	7.01	11.34	−5.05
ABC_725	Training	6.71	9.01	6.52	12.76	−4.86
ABC_726	Validation	6.91	8.72	6.71	11.91	−4.90
ABC_730	Validation	6.28	9.22	7.28	12.14	−4.88
ABC_753	Training	6.84	9.64	7.05	13.00	−5.22
ABC_756	Training	7.67	8.45	7.59	12.48	−5.85
ABC_771	Training	6.98	8.76	6.91	12.20	−5.18
ABC_779	Training	6.73	9.32	6.78	9.82	−4.44
ABC_800	Validation	8.75	8.31	7.45	11.91	−6.04
ABC_807	Training	5.50	9.53	6.92	7.56	−3.79
ABC_809	Training	7.40	8.70	7.68	10.83	−5.50
ABC_816	Training	5.20	9.91	7.65	10.64	−4.14
ABC_820	Training	6.71	8.94	6.55	11.98	−4.85
ABC_823	Validation	5.58	9.26	6.44	10.09	−3.97
ABC_835	Validation	6.95	8.68	8.04	12.31	−5.59
ABC_839	Training	6.63	9.17	7.23	11.89	−5.04
ABC_841	Validation	6.35	9.51	7.52	13.19	−5.28
ABC_858	Training	7.63	8.51	7.12	11.74	−5.42

TABLE 2373-continued

Sample ID #	Set	Lymph node signature value	Proliferation signature value	Germinal center B-cell signature value	MHC class II signature value	Survival predictor score
ABC_872	Training	6.78	8.73	7.41	12.47	−5.44
ABC_875	Training	7.59	8.81	7.20	11.26	−5.25
ABC_912	Validation	7.01	8.55	7.45	12.79	−5.64
ABC_996	Validation	5.00	9.53	6.70	10.02	−3.94
GCB_1005	Validation	8.28	8.67	9.11	13.27	−6.98
GCB_1008	Training	8.17	8.59	9.83	12.83	−7.06
GCB_1009	Training	6.63	9.02	10.07	12.28	−6.19
GCB_1021	Validation	6.44	8.83	9.34	13.20	−6.15
GCB_1025	Validation	7.87	8.48	9.27	12.37	−6.57
GCB_1026	Training	7.71	8.30	9.81	13.52	−6.85
GCB_1037	Training	4.95	8.83	9.35	12.57	−5.22
GCB_1039	Training	7.63	8.65	9.01	13.28	−6.47
GCB_1049	Validation	8.54	8.61	8.12	12.60	−6.41
GCB_1051	Validation	6.26	9.09	9.48	12.76	−5.97
GCB_1058	Validation	7.12	8.89	8.34	12.80	−5.85
GCB_1060	Validation	8.27	8.84	8.94	12.96	−6.75
GCB_412	Training	7.22	8.33	8.50	13.09	−6.09
GCB_415	Training	9.01	8.62	8.38	11.99	−6.47
GCB_421	Training	7.59	7.89	7.49	12.20	−5.80
GCB_424	Training	9.29	8.42	8.51	12.44	−6.79
GCB_433	Training	8.45	8.34	8.02	12.64	−6.54
GCB_434	Training	8.46	8.55	9.17	12.54	−6.98
GCB_438	Validation	8.14	8.71	9.13	12.51	−6.67
GCB_459	Validation	8.98	8.39	8.42	11.37	−6.49
GCB_470	Validation	7.72	8.57	8.67	12.23	−6.12
GCB_479	Validation	6.86	8.25	7.13	13.07	−5.35
GCB_492	Training	8.01	8.61	9.51	12.34	−6.63
GCB_517	Validation	8.57	8.73	7.99	12.76	−6.48
GCB_523	Training	5.96	8.56	8.74	12.77	−5.72
GCB_524	Training	8.51	8.09	8.76	12.51	−6.57
GCB_529	Training	5.12	9.17	8.88	10.77	−4.86
GCB_533	Training	8.88	8.81	8.36	12.44	−6.60
GCB_537	Validation	7.42	8.19	9.73	13.29	−6.68
GCB_543	Validation	8.49	8.02	8.66	12.06	−6.45
GCB_545	Training	8.65	8.28	6.90	12.90	−6.13
GCB_549	Validation	6.87	8.24	8.65	12.15	−6.00
GCB_550	Validation	8.98	8.29	8.76	12.24	−6.94
GCB_553	Validation	8.51	8.64	8.62	12.63	−6.69
GCB_565	Validation	7.97	8.79	9.79	13.42	−6.98
GCB_572	Training	7.61	8.60	9.39	12.58	−6.42
GCB_617	Validation	8.31	7.89	7.54	13.17	−6.12
GCB_618	Training	5.66	8.97	9.20	13.32	−5.54
GCB_619	Validation	7.83	8.65	9.34	12.12	−6.36
GCB_623	Training	7.16	8.88	9.26	12.35	−6.21
GCB_627	Validation	8.13	8.83	8.62	11.85	−6.31
GCB_654	Training	6.30	9.60	8.45	10.00	−4.88
GCB_661	Validation	8.46	8.51	8.18	12.66	−6.33
GCB_669	Training	7.88	8.65	8.59	12.32	−6.19
GCB_672	Training	8.29	8.61	8.14	12.41	−6.21
GCB_674	Validation	8.36	8.62	7.76	12.33	−6.14
GCB_675	Validation	6.01	9.52	8.90	10.12	−5.09
GCB_681	Training	9.25	8.72	8.72	12.59	−6.89
GCB_688	Validation	6.97	9.01	9.90	9.94	−5.99
GCB_695	Validation	8.80	8.73	9.23	12.45	−6.84
GCB_698	Validation	9.27	8.35	8.85	11.99	−6.96
GCB_701	Training	7.77	7.93	8.68	13.10	−6.33
GCB_710	Validation	6.12	8.78	7.65	13.19	−5.24
GCB_711	Training	7.57	8.80	8.43	11.44	−5.84
GCB_722	Training	7.78	8.31	8.93	12.61	−6.51
GCB_724	Training	7.88	9.08	8.74	11.53	−6.21
GCB_731	Validation	7.72	8.92	9.08	12.20	−6.46
GCB_742	Validation	8.33	8.55	8.58	12.95	−6.70
GCB_744	Training	8.02	8.64	9.36	11.85	−6.52
GCB_745	Training	8.47	8.34	8.93	11.95	−6.67
GCB_747	Validation	7.64	8.48	8.32	13.06	−6.27
GCB_749	Training	7.57	8.61	9.40	12.55	−6.56
GCB_758	Validation	5.66	8.77	7.89	12.51	−4.63
GCB_772	Validation	8.52	7.81	7.95	12.25	−6.34
GCB_777	Validation	7.52	8.65	8.57	11.69	−6.10
GCB_792	Training	8.14	8.64	9.21	12.08	−6.65

TABLE 2373-continued

Sample ID #	Set	Lymph node signature value	Proliferation signature value	Germinal center B-cell signature value	MHC class II signature value	Survival predictor score
GCB_795	Validation	9.19	8.17	8.81	11.60	−6.92
GCB_797	Validation	7.50	8.62	8.08	12.84	−6.09
GCB_803	Validation	6.19	8.65	9.49	13.18	−6.11
GCB_810	Training	8.46	8.32	8.10	13.13	−6.50
GCB_817	Training	6.93	8.51	9.49	11.09	−6.04
GCB_818	Training	7.18	8.96	8.08	12.23	−5.76
GCB_819	Validation	7.16	8.97	8.06	13.22	−5.79
GCB_821	Validation	8.13	8.59	8.90	12.41	−6.61
GCB_832	Training	7.83	8.35	8.71	12.47	−6.37
GCB_836	Validation	7.84	8.99	8.50	11.46	−5.85
GCB_840	Training	8.24	7.75	7.40	11.74	−5.77
GCB_847	Training	7.82	8.17	8.97	12.55	−6.51
GCB_860	Training	7.12	8.39	9.34	11.54	−6.10
GCB_871	Training	5.59	9.60	7.28	11.16	−4.23
GCB_874	Training	8.53	9.14	8.95	11.65	−6.47
GCB_995	Validation	6.98	8.68	8.54	12.22	−5.76
PMBL_1006	Validation	7.34	8.51	7.66	10.94	−5.33
PMBL_1024	Validation	7.62	8.48	8.56	10.89	−5.96
PMBL_1048	Validation	8.68	8.16	7.23	12.18	−6.08
PMBL_1053	Training	7.02	8.28	8.24	11.12	−5.31
PMBL_484	Training	7.15	8.45	7.01	13.62	−5.41
PMBL_546	Validation	8.19	7.88	7.66	11.73	−6.06
PMBL_570	Training	9.34	8.21	8.48	12.70	−6.86
PMBL_621	Training	8.08	8.60	9.14	12.96	−6.72
PMBL_638	Training	7.56	8.26	8.00	11.37	−5.75
PMBL_691	Validation	6.48	8.92	8.40	10.17	−5.04
PMBL_791	Validation	7.72	8.65	8.94	11.56	−6.16
PMBL_824	Validation	8.06	8.01	7.76	13.28	−6.11
PMBL_994	Training	9.15	8.36	7.46	12.43	−6.29
PMBL_998	Training	6.70	8.35	9.24	13.19	−6.20
UC_DLBCL_1001	Validation	6.74	8.43	7.10	12.76	−5.31
UC_DLBCL_1004	Validation	7.54	8.75	8.01	13.09	−6.10
UC_DLBCL_1007	Training	9.97	8.44	7.64	12.97	−6.85
UC_DLBCL_1018	Training	6.42	8.38	6.97	12.71	−5.03
UC_DLBCL_1041	Validation	5.76	8.69	6.78	13.38	−4.71
UC_DLBCL_1054	Training	8.92	8.65	8.51	11.48	−6.59
UC_DLBCL_306	Validation	7.85	8.90	8.31	12.36	−6.23
UC_DLBCL_310	Training	8.14	8.80	7.63	12.27	−6.03
UC_DLBCL_449	Validation	9.03	8.48	7.07	12.17	−6.01
UC_DLBCL_458	Training	5.92	8.53	8.28	9.60	−4.96
UC_DLBCL_460	Validation	7.92	9.08	8.30	12.29	−6.13
UC_DLBCL_491	Training	7.65	8.33	7.35	12.39	−5.53
UC_DLBCL_528	Validation	6.99	8.56	7.36	11.63	−5.35
UC_DLBCL_615	Validation	7.11	8.32	8.77	12.80	−6.10
UC_DLBCL_625	Training	8.93	7.78	7.85	12.62	−6.46
UC_DLBCL_664	Training	7.62	8.15	8.17	12.72	−6.04
UC_DLBCL_671	Training	8.09	8.48	7.61	11.53	−5.78
UC_DLBCL_682	Training	7.38	8.35	7.14	12.33	−5.43
UC_DLBCL_683	Training	7.91	8.36	7.78	12.57	−6.02
UC_DLBCL_684	Validation	8.06	8.63	8.29	12.76	−6.29
UC_DLBCL_748	Validation	5.38	8.57	7.45	9.55	−4.23
UC_DLBCL_751	Training	6.33	8.65	8.88	13.14	−5.74
UC_DLBCL_808	Training	7.42	9.01	7.44	13.09	−5.63
UC_DLBCL_831	Validation	8.33	8.30	7.46	11.58	−5.84
UC_DLBCL_834	Training	6.98	9.09	8.61	11.77	−5.66
UC_DLBCL_838	Validation	7.25	8.40	7.23	12.56	−5.36
UC_DLBCL_851	Validation	6.28	9.05	6.78	8.19	−4.10
UC_DLBCL_854	Validation	7.36	8.50	7.39	12.59	−5.53
UC_DLBCL_855	Training	8.31	7.94	7.49	12.08	−6.07
UC_DLBCL_856	Validation	5.65	9.01	8.52	9.32	−4.68

[0174] In order to visualize the predictive power of the model, the 200 samples were ranked according to their survival predictor scores and divided into four quartiles. Kaplan-Meier plots of overall survival probability show clear differences in survival rate between these four quartiles (FIG. **11**).

Example 8

Development of a Third DLBCL Survival Predictor Using Gene Expression Data from the Lymph Dx Microarray

[0175] The number of genes used to generate the DLBCL survival predictor in Example 7 was reduced in order to create a survival predictor compatible with RT-PCR. The list of genes from the lymph node and germinal center B-cell gene expression signatures was narrowed to those three genes from each signature that were most closely correlated with the lymph node and germinal center B-cell gene expression signature values, respectively. The genes from the proliferation gene expression signature did not add significantly to the reduced gene survival prediction model, so they were removed entirely. The expression of the genes within each signature was averaged on the $\log_2$ scale to generate a gene expression signature value for each signature. Table 2374 lists the genes that were used to generate these gene expression signature values.

TABLE 2374

Signature	UNIQID	Unigene ID Build 167	Gene symbol
Germinal center B-cell	1099686	117721	
Germinal center B-cell	1529318	291954	
Germinal center B-cell	1529344	317970	SERPINA11

TABLE 2374-continued

Signature	UNIQID	Unigene ID Build 167	Gene symbol
Lymph node	1097126	274520	ANTXR1
Lymph node	1099358	93135	
Lymph node	1121029	412999	CSTA
MHC class II	1136777	387679	HLA-DQA1
MHC class II	1136877	409934	HLA-DQB1

[0176] Table 2375 lists p-values for the association of each signature with survival in the training set, the validation set, and overall.

TABLE 2375

Signature	Training set	Validation set	Overall
Lymph node	6.1×10^{-6}	0.0021	2.1×10^{-17}
Germinal center B-cell	3.5×10^{-4}	0.0099	2.7×10^{-5}
MHC class II	0.024	0.0026	0.00031

[0177] The three gene expression signatures were used to generate a survival predictor score using the following equation:

> Survival predictor score=[−0.32*(lymph node gene expression signature value)]−[0.176*(germinal center *B*-cell gene expression signature value)]−[0.206*(MHC class II gene expression signature value)].

A higher survival predictor score was associated with worse outcome. For the 200 DLBCL samples used to generate the model, the survival predictor score had a mean of 6.54 and a standard deviation of 0.69, with each unit increase in the predictor score corresponding to an approximately 2.7 fold increase in the relative risk of death. Data for all 200 samples is presented in Table 2376.

TABLE 2376

Sample ID #	Set	Lymph node signature value	Germinal center B-cell signature value	MHC class II signature value	Survival predictor score
ABC_1000	Validation	8.08	5.68	11.50	−5.96
ABC_1002	Validation	8.32	6.06	12.54	−6.31
ABC_1023	Validation	9.36	4.74	11.42	−6.18
ABC_1027	Training	7.41	4.90	12.31	−5.77
ABC_1031	Validation	9.40	5.23	11.68	−6.33
ABC_1034	Validation	7.47	4.92	11.83	−5.69
ABC_1038	Training	7.89	5.84	12.30	−6.09
ABC_1043	Training	7.84	4.66	12.29	−5.86
ABC_1045	Validation	9.31	4.66	12.07	−6.29
ABC_1055	Validation	6.46	6.38	13.05	−5.88
ABC_1057	Training	9.13	7.93	12.05	−6.80
ABC_1059	Validation	10.93	4.82	11.35	−6.68
ABC_1061	Training	8.18	5.04	12.28	−6.04
ABC_304	Validation	7.31	6.47	12.76	−6.10
ABC_305	Training	7.02	6.60	11.89	−5.86
ABC_309	Validation	10.47	7.00	12.53	−7.16
ABC_413	Validation	7.99	4.80	9.04	−5.26
ABC_428	Training	9.43	7.59	10.25	−6.47
ABC_432	Validation	7.29	8.16	9.56	−5.74
ABC_446	Training	9.49	5.46	10.55	−6.17
ABC_462	Validation	7.72	4.97	13.36	−6.10
ABC_477	Validation	7.16	3.69	12.45	−5.51
ABC_481	Training	9.75	6.89	11.98	−6.80
ABC_482	Training	10.51	7.64	12.35	−7.25
ABC_538	Validation	8.79	5.00	11.83	−6.13
ABC_541	Training	7.70	5.80	10.59	−5.67
ABC_544	Training	8.90	3.98	11.87	−5.99

TABLE 2376-continued

Sample ID #	Set	Lymph node signature value	Germinal center B-cell signature value	MHC class II signature value	Survival predictor score
ABC_547	Validation	7.05	5.18	11.38	−5.51
ABC_577	Validation	9.93	8.05	11.95	−7.06
ABC_616	Validation	7.34	4.54	12.64	−5.75
ABC_626	Validation	8.78	6.77	11.11	−6.29
ABC_633	Training	9.63	5.02	12.45	−6.53
ABC_642	Training	7.31	4.95	13.80	−6.05
ABC_644	Validation	7.77	5.35	13.28	−6.15
ABC_645	Training	9.77	6.21	13.39	−6.98
ABC_646	Validation	7.39	3.75	11.60	−5.41
ABC_652	Validation	7.51	4.53	12.73	−5.82
ABC_660	Training	5.85	3.55	10.17	−4.59
ABC_663	Training	7.04	5.06	12.82	−5.78
ABC_668	Validation	8.00	5.65	10.57	−5.73
ABC_676	Training	6.53	4.29	13.32	−5.59
ABC_678	Training	6.87	7.48	11.26	−5.83
ABC_687	Validation	6.39	3.78	10.46	−4.87
ABC_689	Training	8.29	5.07	12.56	−6.13
ABC_692	Validation	8.10	5.26	11.57	−5.90
ABC_694	Validation	9.67	8.15	12.41	−7.09
ABC_700	Training	8.37	6.75	12.10	−6.36
ABC_702	Validation	8.44	4.59	12.55	−6.09
ABC_704	Training	8.51	4.34	12.83	−6.13
ABC_709	Validation	7.47	4.54	13.40	−5.95
ABC_712	Validation	7.12	3.99	12.02	−5.46
ABC_714	Training	9.57	7.03	11.97	−6.77
ABC_717	Training	8.33	5.54	11.34	−5.98
ABC_725	Training	8.04	4.40	12.76	−5.97
ABC_726	Validation	7.79	4.18	11.91	−5.68
ABC_730	Validation	8.13	7.36	12.14	−6.40
ABC_753	Training	9.24	6.60	13.00	−6.80
ABC_756	Training	9.51	5.21	12.48	−6.53
ABC_771	Training	8.08	4.74	12.20	−5.93
ABC_779	Training	8.11	4.09	9.82	−5.34
ABC_800	Validation	10.34	4.83	11.91	−6.61
ABC_807	Training	6.58	4.44	7.56	−4.44
ABC_809	Training	9.29	5.72	10.83	−6.21
ABC_816	Training	6.36	6.36	10.64	−5.35
ABC_820	Training	8.10	4.79	11.98	−5.90
ABC_823	Validation	6.63	4.85	10.09	−5.05
ABC_835	Validation	9.17	7.78	12.31	−6.84
ABC_839	Training	8.06	4.97	11.89	−5.90
ABC_841	Validation	8.05	6.24	13.19	−6.39
ABC_858	Training	9.02	4.86	11.74	−6.16
ABC_872	Training	8.67	5.85	12.47	−6.37
ABC_875	Training	9.60	5.59	11.26	−6.37
ABC_912	Validation	7.99	7.74	12.79	−6.56
ABC_996	Validation	6.89	6.23	10.02	−5.36
GCB_1005	Validation	9.02	9.56	13.27	−7.30
GCB_1008	Training	9.27	10.49	12.83	−7.46
GCB_1009	Training	7.80	10.09	12.28	−6.80
GCB_1021	Validation	8.73	9.20	13.20	−7.13
GCB_1025	Validation	9.94	9.97	12.37	−7.49
GCB_1026	Training	9.54	10.20	13.52	−7.63
GCB_1037	Training	6.34	8.79	12.57	−6.17
GCB_1039	Training	8.71	9.94	13.28	−7.27
GCB_1049	Validation	10.53	8.18	12.60	−7.41
GCB_1051	Validation	7.63	10.18	12.76	−6.86
GCB_1058	Validation	8.61	9.04	12.80	−6.98
GCB_1060	Validation	10.23	9.38	12.96	−7.59
GCB_412	Training	8.79	7.92	13.09	−6.90
GCB_415	Training	10.72	8.57	11.99	−7.41
GCB_421	Training	9.23	5.26	12.20	−6.39
GCB_424	Training	11.14	8.46	12.44	−7.62
GCB_433	Training	9.26	8.52	12.64	−7.07
GCB_434	Training	9.73	10.13	12.54	−7.48
GCB_438	Validation	9.60	9.99	12.51	−7.41
GCB_459	Validation	10.51	7.75	11.37	−7.07
GCB_470	Validation	9.56	6.63	12.23	−6.74
GCB_479	Validation	7.77	4.71	13.07	−6.01
GCB_492	Training	8.82	9.52	12.34	−7.04
GCB_517	Validation	9.92	6.96	12.76	−7.03

TABLE 2376-continued

Sample ID #	Set	Lymph node signature value	Germinal center B-cell signature value	MHC class II signature value	Survival predictor score
GCB_523	Training	6.59	9.17	12.77	−6.35
GCB_524	Training	10.00	7.83	12.51	−7.16
GCB_529	Training	5.61	7.93	10.77	−5.41
GCB_533	Training	9.55	5.54	12.44	−6.59
GCB_537	Validation	8.25	10.25	13.29	−7.18
GCB_543	Validation	9.92	8.85	12.06	−7.21
GCB_545	Training	9.69	4.91	12.90	−6.62
GCB_549	Validation	7.86	8.88	12.15	−6.58
GCB_550	Validation	10.64	9.53	12.24	−7.60
GCB_553	Validation	10.14	9.05	12.63	−7.44
GCB_565	Validation	9.08	10.80	13.42	−7.57
GCB_572	Training	8.93	10.03	12.58	−7.21
GCB_617	Validation	9.27	7.80	13.17	−7.05
GCB_618	Training	7.23	9.11	13.32	−6.66
GCB_619	Validation	9.63	9.63	12.12	−7.27
GCB_623	Training	8.94	9.07	12.35	−7.00
GCB_627	Validation	9.72	8.33	11.85	−7.02
GCB_654	Training	7.04	5.60	10.00	−5.30
GCB_661	Validation	10.27	7.92	12.66	−7.29
GCB_669	Training	9.15	9.29	12.32	−7.10
GCB_672	Training	9.69	7.36	12.41	−6.95
GCB_674	Validation	9.93	6.23	12.33	−6.81
GCB_675	Validation	7.48	8.46	10.12	−5.97
GCB_681	Training	10.77	9.52	12.59	−7.72
GCB_688	Validation	8.01	10.17	9.94	−6.40
GCB_695	Validation	10.58	9.38	12.45	−7.60
GCB_698	Validation	10.44	9.00	11.99	−7.39
GCB_701	Training	9.38	9.27	13.10	−7.33
GCB_710	Validation	6.96	5.59	13.19	−5.93
GCB_711	Training	9.28	8.49	11.44	−6.82
GCB_722	Training	8.93	9.51	12.61	−7.13
GCB_724	Training	9.51	8.39	11.53	−6.90
GCB_731	Validation	8.82	9.19	12.20	−6.95
GCB_742	Validation	9.95	9.37	12.95	−7.50
GCB_744	Training	10.23	10.11	11.85	−7.49
GCB_745	Training	10.29	9.71	11.95	−7.46
GCB_747	Validation	9.83	9.79	13.06	−7.56
GCB_749	Training	8.57	10.27	12.55	−7.14
GCB_758	Validation	6.88	5.69	12.51	−5.78
GCB_772	Validation	9.92	7.28	12.25	−6.98
GCB_777	Validation	9.03	9.63	11.69	−6.99
GCB_792	Training	9.49	9.06	12.08	−7.12
GCB_795	Validation	11.12	9.02	11.60	−7.54
GCB_797	Validation	8.42	5.90	12.84	−6.38
GCB_803	Validation	7.33	10.11	13.18	−6.84
GCB_810	Training	10.00	8.22	13.13	−7.35
GCB_817	Training	8.60	10.16	11.09	−6.82
GCB_818	Training	9.14	7.78	12.23	−6.81
GCB_819	Validation	9.08	8.63	13.22	−7.15
GCB_821	Validation	10.05	9.81	12.41	−7.50
GCB_832	Training	8.83	6.91	12.47	−6.61
GCB_836	Validation	9.49	7.86	11.46	−6.78
GCB_840	Training	9.45	5.02	11.74	−6.33
GCB_847	Training	9.41	8.77	12.55	−7.14
GCB_860	Training	9.02	6.66	11.54	−6.43
GCB_871	Training	6.60	4.46	11.16	−5.20
GCB_874	Training	10.39	9.13	11.65	−7.33
GCB_995	Validation	8.52	9.35	12.22	−6.89
PMBL_1006	Validation	8.72	4.67	10.94	−5.86
PMBL_1024	Validation	9.30	8.47	10.89	−6.71
PMBL_1048	Validation	10.30	4.98	12.18	−6.68
PMBL_1053	Training	8.75	9.78	11.12	−6.81
PMBL_484	Training	8.25	4.96	13.62	−6.32
PMBL_546	Validation	9.66	6.07	11.73	−6.57
PMBL_570	Training	10.58	8.54	12.70	−7.50
PMBL_621	Training	9.39	9.94	12.96	−7.43
PMBL_638	Training	9.81	8.35	11.37	−6.95
PMBL_691	Validation	8.37	7.51	10.17	−6.10
PMBL_791	Validation	9.29	8.65	11.56	−6.88
PMBL_824	Validation	9.87	7.19	13.28	−7.16
PMBL_994	Training	11.27	6.73	12.43	−7.35

TABLE 2376-continued

Sample ID #	Set	Lymph node signature value	Germinal center B-cell signature value	MHC class II signature value	Survival predictor score
PMBL_998	Training	7.92	8.34	13.19	−6.72
UC_DLBCL_1001	Validation	8.25	5.63	12.76	−6.26
UC_DLBCL_1004	Validation	9.01	7.01	13.09	−6.81
UC_DLBCL_1007	Training	11.42	6.73	12.97	−7.51
UC_DLBCL_1018	Training	7.77	4.58	12.71	−5.91
UC_DLBCL_1041	Validation	7.90	4.33	13.38	−6.05
UC_DLBCL_1054	Training	10.41	8.72	11.48	−7.23
UC_DLBCL_306	Validation	9.42	6.54	12.36	−6.71
UC_DLBCL_310	Training	9.97	5.50	12.27	−6.69
UC_DLBCL_449	Validation	10.01	5.37	12.17	−6.65
UC_DLBCL_458	Training	7.50	5.79	9.60	−5.40
UC_DLBCL_460	Validation	10.26	8.27	12.29	−7.27
UC_DLBCL_491	Training	9.43	4.73	12.39	−6.40
UC_DLBCL_528	Validation	8.42	6.19	11.63	−6.18
UC_DLBCL_615	Validation	8.44	9.01	12.80	−6.92
UC_DLBCL_625	Training	10.43	8.27	12.62	−7.39
UC_DLBCL_664	Training	9.80	8.74	12.72	−7.29
UC_DLBCL_671	Training	9.42	5.26	11.53	−6.32
UC_DLBCL_682	Training	9.01	4.73	12.33	−6.26
UC_DLBCL_683	Training	8.85	8.23	12.57	−6.87
UC_DLBCL_684	Validation	9.62	8.78	12.76	−7.25
UC_DLBCL_748	Validation	7.60	5.79	9.55	−5.42
UC_DLBCL_751	Training	6.40	9.91	13.14	−6.50
UC_DLBCL_808	Training	9.44	7.01	13.09	−6.95
UC_DLBCL_831	Validation	9.45	5.81	11.58	−6.43
UC_DLBCL_834	Training	8.52	7.66	11.77	−6.50
UC_DLBCL_838	Validation	8.49	4.60	12.56	−6.11
UC_DLBCL_851	Validation	7.50	4.82	8.19	−4.94
UC_DLBCL_854	Validation	8.35	5.82	12.59	−6.29
UC_DLBCL_855	Training	9.56	5.44	12.08	−6.51
UC_DLBCL_856	Validation	6.81	7.49	9.32	−5.42

[0178] In order to visualize the predictive power of the model, the 200 samples were ranked according to their survival predictor scores and divided into four quartiles. Kaplan-Meier plots of overall survival probability show clear differences in survival rate between these four quartiles (FIG. **12**).

Example 9

Development of an MCL Survival Predictor Using Gene Expression Data from Affymetrix U133A and U133B Microarrays

[0179] The connection between higher expression of proliferation genes and worse survival in MCL had previously been documented and validated (Rosenwald 2003a). A cluster of proliferation genes had been identified in the DLBCL samples used to create the DLBCL survival predictor described in Example 7. By averaging the expression of these genes, a proliferation gene expression signature value had been developed for the DLBCL samples. The correlation of this signature with each probe set on the U133A and U133B microarrays was determined, and the 22 genes for which the correlation was greater than 0.5 were labeled proliferation genes. The correlation between expression of these proliferation genes and survival in 21 MCL samples was estimated using the Cox proportional hazards model. Table 2377 lists these 21 MCL samples.

TABLE 2377

Sample ID #	Length of follow-up (years)	Status at follow-up	Used in creating survival predictor?
MCL_1012	3.19	Alive	Yes
MCL_1091	3.03	Alive	Yes
MCL_1114	0.59	Dead	Yes
MCL_1128	0.43	Dead	Yes
MCL_1150	3.21	Dead	Yes
MCL_1162	0.78	Alive	Yes
MCL_1166	0.53	Dead	Yes
MCL_1194	0.55	Alive	Yes
MCL_885	1.19	Alive	Yes
MCL_918	1.95	Dead	Yes
MCL_924	5.48	Dead	Yes
MCL_925	7.23	Alive	Yes
MCL_926	5.18	Dead	Yes
MCL_936	2.80	Alive	Yes
MCL_939	1.07	Dead	Yes
MCL_953	2.31	Dead	Yes
MCL_956	1.40	Dead	Yes
MCL_964	0.75	Alive	Yes
MCL_966	0.21	Dead	Yes
MCL_968	1.59	Dead	Yes
MCL_970	5.02	Dead	Yes

Out of the 22 proliferation genes, 11 were significant at a 0.001 level. The expression level of these 11 genes in each of the 21 MCL samples was averaged to generate a proliferation gene expression signature value. No other genes represented on the U133A or U133B microarrays correlated with MCL survival to an extent greater than would be expected by

chance, so the final model included only proliferation genes. The 11 genes used to generate the model are presented in Table 2378.

TABLE 2378

Signature	UNIQID	Gene Symbol
Proliferation	1097290	CIRH1A
Proliferation	1101295	FLJ40629
Proliferation	1119729	TK1
Proliferation	1120153	LMNB1
Proliferation	1120494	CDC6
Proliferation	1124745	KIAA0056
Proliferation	1126148	DKFZp586E1120
Proliferation	1130618	TPI1
Proliferation	1134753	WHSC1
Proliferation	1139654	ECT2
Proliferation	1140632	IMAGE: 52707

[0180] A survival predictor score for MCL was generated using the following equation:

Survival predictor score=1.66*(proliferation gene expression signature value).

This model was associated with survival in a statistically significant manner (p=0.00018). To illustrate the significance of the model in predicting survival, the 21 MCL samples were divided into two equivalent groups based on their survival predictor scores. Those samples with survival predictor scores above the median were placed in the high proliferation group, while those with survival predictor scores below the median were placed in the low proliferation group. FIG. **13** illustrates the Kaplan Meier survival estimates for these two groups. Median survival for the high proliferation group was 1.07 years, while median survival for the low proliferation group was 5.18 years.

Example 10

Development of an MCL Survival Predictor Using Gene Expression Data from the Lymph Dx Microarray

[0181] A set of 21 genes associated with proliferation and poor prognosis in MCL had been identified previously (Rosenwald 2003a). Of these 21 genes, only four were represented on the Lymph Dx microarray. In order to find a larger set of genes on the Lymph Dx microarray associated with survival in MCL, Lymphochip expression data (Rosenwald 2003a) was re-analyzed and another set of proliferation genes whose expression levels were correlated with poor survival in MCL were identified. Thirteen of these genes were represented on the Lymph Dx microarray (median expression >6 on $\log_2$ scale). These 13 genes are listed in Table 2379.

TABLE 2379

Signature	UNIQID	Unigene ID Build 167	Gene symbol
Proliferation	1119294	156346	TOP2A
Proliferation	1119729	164457	TK1
Proliferation	1120153	89497	LMNB1
Proliferation	1121276	24529	CHEK1
Proliferation	1123358	442658	AURKB
Proliferation	1124178	446579	HSPCA
Proliferation	1124563	249441	WEE1
Proliferation	1130799	233952	PSMA7
Proliferation	1131274	374378	CKS1B

TABLE 2379-continued

Signature	UNIQID	Unigene ID Build 167	Gene symbol
Proliferation	1131778	396393	UBE2S
Proliferation	1132449	250822	STK6
Proliferation	1135229	367676	DUT
Proliferation	1136585	80976	MKI67

[0182] The expression levels of the 13 genes listed in Table 2379 on the Lymph Dx microarray were transformed into the $\log_2$ scale and averaged to form a proliferation gene expression signature value. This was used to generate a survival predictor score using the following equation:

Survival predictor score=1.66*(proliferation gene expression signature value).

[0183] For the 21 MCL samples analyzed, the survival predictor score had a mean of 14.85 and a standard deviation of 1.13. Even in this limited sample set, the survival predictor score was significantly associated with prognosis (p=0.0049), with each unit increase in the score corresponding to a 2.7 fold increase in the relative risk of death. Data for all 21 samples is shown in Table 2380.

TABLE 2380

Sample ID #	Proliferation signature value	Survival predictor score
MCL_1012	8.83	14.658
MCL_1091	8.81	14.625
MCL_1114	10.39	17.247
MCL_1128	10.12	16.799
MCL_1150	8.33	13.828
MCL_1162	8.15	13.529
MCL_1166	9.40	15.604
MCL_1194	7.44	12.350
MCL_885	8.68	14.409
MCL_918	9.33	15.488
MCL_924	8.35	13.861
MCL_925	8.86	14.708
MCL_926	8.14	13.512
MCL_936	8.56	14.21
MCL_939	9.14	15.172
MCL_953	9.25	15.355
MCL_956	9.35	15.521
MCL_964	9.74	16.168
MCL_966	8.76	14.542
MCL_968	9.10	15.106
MCL_970	9.27	15.388

[0184] To illustrate the significance of the model in predicting survival, the 21 MCL samples were divided into two equivalent groups based on their survival predictor scores. Those samples with survival predictor scores above the median were placed in the high proliferation group, while those with survival predictor scores below the median were placed in the low proliferation group. FIG. **14** illustrates the Kaplan Meier survival estimates for these two groups.

Example 11

Identification of Lymphoma Samples as MCL Based on Bayesian Analysis of Gene Expression Data from Affymetrix U133A and U133B Microarrays

[0185] A statistical method based on Bayesian analysis was developed to distinguish MCL samples from samples belong-

ing to other lymphoma types based on gene expression profiling. This method was developed using the gene expression data obtained in Example 1 for the following lymphoma types: ABC, GCB, PMBL, BL, FH, FL, MALT, MCL, PTLD, SLL, and splenic marginal zone lymphoma (splenic). Tables 1707-1741 (discussed in Example 1) provide gene expression data for samples within each of these lymphoma types, including the expression level of each gene and the difference in expression of each gene between types. Tables 1710, 1715, and 1723 (corresponding to FL, MCL, and DLBCL, respectively) include the correlation between expression of each gene and survival.

[0186] To determine the lymphoma type of a sample, a series of predictor models are generated. Each predictor model calculates the probability that the sample belongs to a first lymphoma type rather than a second lymphoma type. A method was developed to determine whether a sample was MCL, or one of the following lymphoma types: ABC, BL, FH, FL, GCB, MALT, PMBL, PTLD, SLL, or splenic. This method required ten different predictor models, each designed to determine whether the sample belonged to MCL or one of the other ten lymphoma types (e.g., MCL vs. ABC, MCL vs. BL, etc.).

[0187] Several of the lymphoma samples analyzed displayed a tendency towards elevated or reduced expression of genes from the lymph node and proliferation gene expression signatures. These genes are likely to be highly differentially expressed between the lymphoma types, but they do not serve as good predictor genes because they are often variably expressed within a single lymphoma type. For this reason, any gene that displayed a correlation with the proliferation or lymph node signatures was eliminated from consideration.

[0188] For each lymphoma type pair (e.g., MCL vs. ABC, MCL vs. FL, etc.), 20 genes were identified that exhibited the greatest difference in expression between MCL and the second lymphoma type according to a Student's t-test. The choice to use 20 genes was arbitrary. For each sample X, the 20 genes were used to generate a linear predictor score (LPS) according to the following formula:

$$LPS(X) = \sum_{j=1}^{20} t_j X_j,$$

where X_j is the expression of gene j in sample X and t_j is the t-statistic for the difference in expression of gene j between a first lymphoma type and a second lymphoma type. This is merely one method for generating an LPS. Others methods include linear discriminant analysis (Dudoit 2002), support vector machines (Furey 2000), or shrunken centroids (Tibshirani 2002). In addition, there is no requirement that a t-statistic be used as the scaling factor.

[0189] After an LPS had been formulated for each lymphoma sample, the mean and standard deviation of these LPS's was calculated for each lymphoma type. For a new sample X, Bayes' rule can be used to estimate the probability that the sample belongs to a first lymphoma type rather than a second lymphoma type (FIG. **15**). In this example, Bayes' rule was used to calculate the probability q that sample X was MCL rather than a second lymphoma type using the following equation:

$$q(X \text{ is type } 1) = \frac{\phi(LPS(X); \hat{\mu}_1, \hat{\sigma}_1)}{\phi(LPS(X); \hat{\mu}_1, \hat{\sigma}_1) + \phi(LPS(X); \hat{\mu}_2, \hat{\sigma}_2)}$$

where type 1 is MCL, type 2 is one of the other nine lymphoma types, $\phi(x; \mu,\sigma)$ is the normal density function with mean μ and standard deviation σ, $\hat{\mu}_1$ and $\hat{\sigma}_1$ are the sample mean and variance of the LPS values for lymphoma type 1, and $\hat{\mu}_2$ and $\hat{\sigma}_2$ are the sample mean and variance of the LPS values for lymphoma type 2.

[0190] This method was used to develop ten predictor models, one for each pairing of MCL and a second lymphoma type. A sample was classified as MCL if each of the ten predictors generated at least a 90% probability that the sample was MCL. If any of the ten predictors indicated a probability of less than 90%, the sample was classified as non-MCL.

[0191] The 10 sets of 20 genes that were included in these models and the t-statistics for each gene are presented in Tables 2381-2490.

TABLE 2381

MCL vs. ABC predictor genes

UNIQID	Gene name	Scale Factor
1103711	*Homo sapiens* cDNA FLJ11833 fis, clone HEMBA1006579.	17.88496416
1133111	PDE9A—phosphodiesterase 9A	17.61579873
1137987	PLXNB1—plexin B1	17.47030156
1132835	SOX11—SRY (sex determining region Y)-box 11	16.89404131
1109505	*Homo sapiens*, Similar to LOC168058, clone MGC: 39372 IMAGE: 5089466, mRNA, complete cds	15.78111902
1139054	LOC58486—transposon-derived Buster1 transposase-like protein	15.77800815
1119361	TIA1—TIA1 cytotoxic granule-associated RNA binding protein	15.68070962
1115226	KIAA1683—KIAA1683 protein	15.67954057
1101211	*Homo sapiens* cDNA: FLJ21960 fis, clone HEP05517.	15.4183527
1118963	*Homo sapiens* cDNA FLJ35653 fis, clone SPLEN2013690.	15.36802586
1096503	GL012—hypothetical protein GL012	14.64776335
1127849	SNN—stannin	14.54859775
1099204	*Homo sapiens* mRNA; cDNA DKFZp586K1922 (from clone DKFZp586K1922)	14.32724822

TABLE 2381-continued

MCL vs. ABC predictor genes

UNIQID	Gene name	Scale Factor
1098840	C3orf6—chromosome 3 open reading frame 6	14.10346944
1139444	RABL2B—RAB, member of RAS oncogene family-like 2B	14.10016196
1106855	KIAA1909—KIAA1909 protein	13.9504946
1126695	KIAA0484—KIAA0484 protein	13.92285415
1120137	FCGBP—Fc fragment of IgG binding protein	13.86147896
1133011	TMSNB—thymosin, beta, identified in neuroblastoma cells	13.74377784
1133192	GRP3—guanine nucleotide exchange factor for Rap1	−17.09085725

TABLE 2382

MCL vs. BL predictor genes

UNIQID	Gene name	Scale Factor
1120900	EPHB6—EphB6	13.43582327
1112061	*Homo sapiens* cDNA FLJ90513 fis, clone NT2RP3004355.	12.73065392
1109505	*Homo sapiens*, Similar to LOC168058, clone MGC: 39372 IMAGE: 5089466, mRNA, complete cds	12.63674985
1133099	DNASE1L3—deoxyribonuclease I-like 3	12.43333984
1106855	KIAA1909—KIAA1909 protein	12.32623489
1110070	ESTs	12.05416064
1121739	ZNF135—zinc finger protein 135 (clone pHZ-17)	11.90460363
1098840	C3orf6—chromosome 3 open reading frame 6	11.90309143
1132833	SOX11—SRY (sex determining region Y)-box 11	11.60864812
1121693	KIAA0450—KIAA0450 gene product	11.33634052
1123760	ILT7—leukocyte immunoglobulin-like receptor, subfamily A (without TM domain), member 4	11.18744726
1125964	KIAA0792—KIAA0792 gene product	11.14762675
1112306	ESTs	11.02434114
1096070	DNMT3A—DNA (cytosine-5-)-methyltransferase 3 alpha	10.98991879
1129943	*Homo sapiens*, similar to Zinc finger protein 85 (Zinc finger protein HPF4) (HTF1), clone IMAGE: 3352451, mRNA	10.72494956
1118749	PRKWNK1—protein kinase, lysine deficient 1	10.64623382
1098954	FLJ13204—hypothetical protein FLJ13204	10.46164401
1134749	PRKCBP1—protein kinase C binding protein 1	10.40948157
1131860	BIN1—bridging integrator 1	10.31084561
1123148	TGFBR2—transforming growth factor, beta receptor II (70/80 kDa)	10.2956213

TABLE 2383

MCL vs. FH predictor genes

UNIQID	Gene name	Scale Factor
1132834	SOX11—SRY (sex determining region Y)-box 11	24.3531072
1100873	ESTs	16.83342764
1109603	ESTs	13.02401995
1139411	OSBPL10—oxysterol binding protein-like 10	12.54369577
1106855	KIAA1909—KIAA1909 protein	12.10316361
1125193	CNR1—cannabinoid receptor 1 (brain)	12.070579
1137450	ALOX5—arachidonate 5-lipoxygenase	11.74571823
1100258	KIAA1384—KIAA1384 protein	11.60998697
1133167	ZFD25—zinc finger protein (ZFD25)	11.52931491
1136831	PPFIBP2—PTPRF interacting protein, binding protein 2 (liprin beta 2)	11.50062692
1138222	NA	10.99674674
1099437	*Homo sapiens* mRNA; cDNA DKFZp667B1913 (from clone DKFZp667B1913)	10.90797288
1140236	SPAP1—SH2 domain containing phosphatase anchor protein 1	10.77082801
1114109	DCAL1—dendritic cell-associated lectin-1	10.65867119
1098277	PRICKLE1—prickle-like 1 (*Drosophila*)	10.55457068
1135138	CD24—CD24 antigen (small cell lung carcinoma cluster 4 antigen)	10.41999962
1103304	*Homo sapiens* clone CDABP0095 mRNA sequence	−10.46625233
1128460	RDGBB—retinal degeneration B beta	−10.91106245

TABLE 2383-continued

MCL vs. FH predictor genes

UNIQID	Gene name	Scale Factor
1121953	KIAA0125—KIAA0125 gene product	−11.22466255
1129281	C14orf110—chromosome 14 open reading frame 110	−15.54465448

TABLE 2384

MCL vs. FL predictor genes

UNIQID	Gene name	Scale Factor
1132835	SOX11—SRY (sex determining region Y)-box 11	22.14208817
1096070	DNMT3A—DNA (cytosine-5-)-methyltransferase 3 alpha	20.53740132
1103711	*Homo sapiens* cDNA FLJ11833 fis, clone HEMBA1006579.	20.49880004
1137987	PLXNB1—plexin B1	18.38081568
1109505	*Homo sapiens*, Similar to LOC168058, clone MGC: 39372 IMAGE: 5089466, mRNA, complete cds	17.17812448
1098840	C3orf6—chromosome 3 open reading frame 6	16.32703666
1130926	C5orf13—chromosome 5 open reading frame 13	15.34261878
1096396	SPG3A—spastic paraplegia 3A (autosomal dominant)	14.75437736
1132734	COL9A3—collagen, type IX, alpha 3	14.684583
1139393	OPN3—opsin 3 (encephalopsin, panopsin)	14.39118445
1115537	LOC84518—protein related with psoriasis	14.18446144
1102215	*Homo sapiens* cDNA FLJ11666 fis, clone HEMBA1004672.	14.16246426
1124585	*Homo sapiens* cDNA: FLJ21930 fis, clone HEP04301, highly similar to HSU90916 Human clone 23815 mRNA sequence.	−14.33315955
1137561	HOXA1—homeo box A1	−15.38404642
1100581	*Homo sapiens* mRNA; cDNA DKFZp667A1115 (from clone DKFZp667A1115)	−15.91666634
1124646	KIAA0084—KIAA0084 protein	−16.40577696
1114543	ESTs	−17.60167863
1120090	BCL6—B-cell CLL/lymphoma 6 (zinc finger protein 51)	−17.63091181
1123731	RGS13—regulator of G-protein signalling 13	−22.41602151
1133192	GRP3—guanine nucleotide exchange factor for Rap1	−27.28308723

TABLE 2385

MCL vs. GCB predictor genes

UNIQID	Gene name	Scale Factor
1098840	C3orf6—chromosome 3 open reading frame 6	22.26488562
1132835	SOX11—SRY (sex determining region Y)-box 11	17.76179754
1137987	PLXNB1—plexin B1	16.86845147
1098954	FLJ13204—hypothetical protein FLJ13204	16.65023669
1103711	*Homo sapiens* cDNA FLJ11833 fis, clone HEMBA1006579.	15.64719784
1096070	DNMT3A—DNA (cytosine-5-)-methyltransferase 3 alpha	15.22540494
1139393	OPN3—opsin 3 (encephalopsin, panopsin)	14.64030565
1127849	SNN—stannin	14.28242206
1098156	Human HeLa mRNA isolated as a false positive in a two-hybrid-screen.	14.00049272
1128845	FLJ20174—hypothetical protein FLJ20174	13.96064416
1129943	*Homo sapiens*, similar to Zinc finger protein 85 (Zinc finger protein HPF4) (HTF1), clone IMAGE: 352451, mRNA	13.85404507
1140116	DKFZP564B116—hypothetical protein DKFZp564B1162	13.81464172
1106855	KIAA1909—KIAA1909 protein	13.74521849
1120900	EPHB6—EphB6	13.46567004
1127371	*Homo sapiens* cDNA FLJ14046 fis, clone HEMBA1006461.	13.45735668
1119361	TIA1—TIA1 cytotoxic granule-associated RNA binding protein	13.37376559
1120854	EDG1—endothelial differentiation, sphingolipid G-protein-coupled receptor, 1	13.1047657
1098277	PRICKLE1—prickle-like 1 (*Drosophila*)	13.04993076
1140127	TRIM34—tripartite motif-containing 34	12.66260609
1100581	*Homo sapiens* mRNA; cDNA DKFZp667A1115 (from clone DKFZp667A1115)	−12.81251689

TABLE 2386

MCL vs. MALT predictor genes

UNIQID	Gene name	Scale Factor
1132834	SOX11—SRY (sex determining region Y)-box 11	20.7489202
1101987	KIAA1909—KIAA1909 protein	10.78991326
1100873	ESTs	10.11845036
1130764	HNRPA0—heterogeneous nuclear ribonucleoprotein A0	9.432459453
1102178	*Homo sapiens*, Similar to thymosin, beta, identified in neuroblastoma cells, clone MGC: 39900 IMAGE: 5247537, mRNA, complete cds	9.035605572
1098277	PRICKLE1—prickle-like 1 (*Drosophila*)	9.003360784
1130926	C5orf13—chromosome 5 open reading frame 13	8.712830747
1098694	LOC112868—hypothetical protein LOC112868	8.309789856
1103711	*Homo sapiens* cDNA FLJ11833 fis, clone HEMBA1006579.	8.248526605
1138099	NA	8.107440225
1120854	EDG1—endothelial differentiation, sphingolipid G-protein-coupled receptor, 1	8.045872672
1102215	*Homo sapiens* cDNA FLJ11666 fis, clone HEMBA1004672.	8.032351578
1121739	ZNF135—zinc finger protein 135 (clone pHZ-17)	8.020919565
1096070	DNMT3A—DNA (cytosine-5-)-methyltransferase 3 alpha	7.964477216
1101211	*Homo sapiens* cDNA: FLJ21960 fis, clone HEP05517.	7.738742472
1120825	CHL1—cell adhesion molecule with homology to L1CAM (close homolog of L1)	7.516130116
1099437	*Homo sapiens* mRNA; cDNA DKFZp667B1913 (from clone DKFZp667B1913)	7.209041652
1096503	GL012—hypothetical protein GL012	7.171540413
1135927	LILRA2—leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2	7.134470829
1120645	FADS3—fatty acid desaturase 3	7.039952979

TABLE 2387

MCL vs. PMBL predictor genes

UNIQID	Gene name	Scale Factor
1132834	SOX11—SRY (sex determining region Y)-box 11	28.17593839
1100873	ESTs	17.90004832
1096503	GL012—hypothetical protein GL012	17.43982729
1098840	C3orf6—chromosome 3 open reading frame 6	17.37421052
1124734	NA	16.73821457
1135102	PRKCB1—protein kinase C, beta 1	16.67436366
1103711	*Homo sapiens* cDNA FLJ11833 fis, clone HEMBA1006579.	16.57202026
1140416	TOSO—regulator of Fas-induced apoptosis	15.64802242
1121757	ADRB2—adrenergic, beta-2-, receptor, surface	15.57336633
1140236	SPAP1—SH2 domain containing phosphatase anchor protein 1	15.20264513
1099140	ESTs, Moderately similar to hypothetical protein FLJ20378 [*Homo sapiens*] [*H. sapiens*]	15.11929571
1099549	ESTs	14.92883027
1139054	LOC58486—transposon-derived Buster1 transposase-like protein	14.63422275
1138818	ILF3—interleukin enhancer binding factor 3, 90 kDa	14.50621028
1109444	ESTs, Highly similar to IL24_HUMAN Interleukin-24 precursor (Suppression of tumorigenicity 16 protein) (Melanoma differentiation associated protein 7) (MDA-7) [*H. sapiens*]	14.20430672
1124534	KIAA0553—KIAA0553 protein	14.18537487
1098277	PRICKLE1—prickle-like 1 (*Drosophila*)	13.98526258
1131687	TLK1—tousled-like kinase 1	13.97468703
1125112	PLCL2—phospholipase C-like 2	13.85714318
1125397	*Homo sapiens* cDNA FLJ33389 fis, clone BRACE2006871.	13.85049805

TABLE 2388

MCL vs. PTLD predictor genes

UNIQID	Gene name	Scale Factor
1109603	ESTs	19.95553782
1138222	NA	15.95397369
1135138	CD24—CD24 antigen (small cell lung carcinoma cluster 4 antigen)	15.89198725
1134230	RASGRP2—RAS guanyl releasing protein 2 (calcium and DAG-regulated)	15.80452978
1139411	OSBPL10—oxysterol binding protein-like 10	14.32818885
1140416	TOSO—regulator of Fas-induced apoptosis	13.89685188
1132834	SOX11—SRY (sex determining region Y)-box 11	13.78424818
1121739	ZNF135—zinc finger protein 135 (clone pHZ-17)	13.02195529
1098156	Human HeLa mRNA isolated as a false positive in a two-hybrid-screen.	12.95032505
1099270	*Homo sapiens* cDNA FLJ30555 fis, clone BRAWH2003818.	12.7877735
1139012	FLJ20373—hypothetical protein FLJ20373	12.70176225
1120854	EDG1—endothelial differentiation, sphingolipid G-protein-coupled receptor, 1	12.25264341
1120985	KIAA0053—KIAA0053 gene product	12.04626201
1115952	LOC146517—hypothetical protein LOC146517	11.96299478
1120825	CHL1—cell adhesion molecule with homology to L1CAM (close homolog of L1)	11.82402907
1131636	SPOCK2—sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2	11.80417657
1136706	MYT1—myelin transcription factor 1	11.74962191
1113560	*Homo sapiens*, clone IMAGE: 5725893, mRNA	11.72049882
1133851	P4HA1—procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I	−12.59876059
1137459	BCAT1—branched chain aminotransferase 1, cytosolic	−14.00465411

TABLE 2389

MCL vs. SLL predictor genes

UNIQID	Gene name	Scale Factor
1132834	SOX11—SRY (sex determining region Y)-box 11	23.59602107
1101987	KIAA1909—KIAA1909 protein	14.50254794
1103711	*Homo sapiens* cDNA FLJ11833 fis, clone HEMBA1006579.	13.31375894
1096070	DNMT3A—DNA (cytosine-5-)-methyltransferase 3 alpha	12.37453972
1130926	C5orf13—chromosome 5 open reading frame 13	11.27840239
1120645	FADS3—fatty acid desaturase 3	11.14057287
1138099	NA	10.92729287
1097887	KIAA0303—KIAA0303 protein	10.37913127
1099941	ESTs	10.33953409
1130373	KIAA0303—KIAA0303 protein	10.01524528
1110957	SYNE2—spectrin repeat containing, nuclear envelope 2	9.865436185
1130320	ESTs	9.807091644
1124373	LPIN1—lipin 1	9.024985551
1128813	KREMEN2—kringle containing transmembrane protein 2	8.903791941
1131130	MARCKS—myristoylated alanine-rich protein kinase C substrate	8.688979176
1120825	CHL1—cell adhesion molecule with homology to L1CAM (close homolog of L1)	8.685132271
1119752	BASP1—brain abundant, membrane attached signal protein 1	8.663402838
1131854	GCLC—glutamate-cysteine ligase, catalytic subunit	−8.761521136
1105801	*Homo sapiens* mRNA; cDNA DKFZp686H1529 (from clone DKFZp686H1529)	−8.828675125
1097824	MAP2—microtubule-associated protein 2	−9.345688564

TABLE 2390

MCL vs. splenic predictor genes

UNIQID	Gene name	Scale Factor
1106855	KIAA1909—KIAA1909 protein	14.48278638
1121739	ZNF135—zinc finger protein 135 (clone pHZ-17)	11.95918572
1111850	*Homo sapiens* cDNA FLJ36977 fis, clone BRACE2006344.	11.13464157
1098024	KIAA1972—KIAA1972 protein	10.10869886
1130764	HNRPA0—heterogeneous nuclear ribonucleoprotein A0	10.06898534
1135342	SHOX2—short stature homeobox 2	9.565884385
1097218	MGC45400—hypothetical protein MGC45400	9.187725705
1117193	RINZF—zinc finger protein RINZF	9.12522795
1139564	PSMD10—proteasome (prosome, macropain) 26S subunit, non-ATPase, 10	9.066714773
1132834	SOX11—SRY (sex determining region Y)-box 11	8.908574745
1131130	MARCKS—myristoylated alanine-rich protein kinase C substrate	8.732921026
1131756	PDCD4—programmed cell death 4 (neoplastic transformation inhibitor]	8.441424593
1102187	DKFZp586C102—hypothetical protein DKFZp586C1021	8.391861029
1098195	DKFZp762C111—hypothetical protein DKFZp762C1112	8.349839204
1101211	*Homo sapiens* cDNA: FLJ21960 fis, clone HEP05517.	8.337208237
1136673	GNAS—GNAS complex locus	8.254076655
1139116	USP16—ubiquitin specific protease 16	8.179384251
1098694	LOC112868—hypothetical protein LOC112868	7.935903681
1120519	WWP2—Nedd-4-like ubiquitin-protein ligase	−7.881202253
1114916	FLJ13993—hypothetical protein FLJ13993	−8.33683119

[0192] With so many candidate predictor genes being utilized, it is possible to generate a predictor model that accurately predicts every element of a training set but fails to perform on an independent sample. This occurs because the model incorporates and "learns" the individual characteristics of each sample in the training set. Leave-one-out cross-validation was used to verify that the prediction models generated above would work on independent samples that the models had not encountered previously. In this cross-validation method, a single sample is removed from the training set, and the predictor is developed again using the remaining data. The resulting model is then used to predict the sample that was removed. This method is repeated with each individual sample taken out. Since no sample is predicted from a model that includes that sample, this method provides an unbiased estimate of predictor accuracy.

[0193] When the predictors developed above were evaluated by leave-one-out cross-validation, all but one of the 21 MCL samples were correctly identified as MCL and none of the 489 non-MCL samples were mistakenly identified as MCL.

Example 12

Identification of Lymphoma Samples as MCL Based on Bayesian Analysis of Gene Expression Data from a Lymphochip Microarray

[0194] Lymphoma samples with morphology consistent with MCL were identified by pathological review. Since t(11; 14) translocation and cyclin D1 overexpression have been consistently associated with MCL, cyclin D1 mRNA levels were measured in each sample by quantitative RT-PCR. Of the 101 samples analyzed, 92 expressed cyclin D1 mRNA. These 92 samples, which were deemed the "core group" of MCLs, were divided into a training set and a validation set. Gene expression was measured in all 101 samples using a Lymphochip microarray (Alizadeh 1999). For comparison, gene expression was measured in 20 samples identified as SLL. In addition, MCL expression data was compared to expression data obtained previously for GCB (134 cases) and ABC (83 cases) (Rosenwald 2002). Several thousand genes were differentially expressed between cyclin D1-positive MCL and the other lymphoma types with high statistical significance ($p<0.001$). A complete listing of these genes is available at Rosenwald et al., *Cancer Cell,* 3: 185-197 (2003), which is referenced therein at page 194 and which is hosted by the Lymphoma/Leukemia Molecular Profiling Project Gateways at the National Institute of Health web site.

[0195] Three different binary predictor models were developed: MCL vs. SLL, MCL vs. GCB, and MCL vs. ABC. Each of these models was designed to calculate the probability that a sample was MCL rather than the other lymphoma type in the pair. For each pair, the genes that were most differentially expressed between MCL and the other lymphoma type in the pair were identified, and the difference in expression between the lymphoma types was quantified using a Student's t-test. An LPS was then calculated for each sample using the following formula:

$$LPS(X) = \sum_{j \in G} t_j X_j,$$

where X_j is the expression of gene j in sample X and t_j is the t-statistic for the difference in expression of gene j between the two lymphoma types in the pair. Cyclin D1 was excluded from the calculation of LPS so that the model could be used to identify potential MCL cases that were cyclin D1 negative.

[0196] After an LPS had been formulated for each lymphoma sample, the mean and standard deviation of these LPS's was calculated for each lymphoma type. For a new sample X, Bayes' rule can be used to estimate the probability

q that the sample belongs to MCL rather than the second lymphoma type in the pair using the following equation:

$$q(X \text{ is } MCL) = \frac{\phi(LPS(X); \hat{\mu}_{MCL}, \hat{\sigma}_{MCL})}{\phi(LPS(X); \hat{\mu}_{MCL}, \hat{\sigma}_{MCL}) + \phi(LPS(X); \hat{\mu}_2, \hat{\sigma}_2)}$$

where $\phi(x; \mu,\sigma)$ is the normal density function with mean μ and standard deviation σ, $\hat{\mu}_{MCL}$ and $\hat{\sigma}_{MCL}$ are the sample mean and variance of the LPS values for MCL, and $\hat{\mu}_2$ and σ_2 are the sample mean and variance of the LPS values for the second lymphoma type of the pair. A cut-off point of 90% was selected for assigning a sample to a particular lymphoma type. Every sample in the training set was classified correctly using this model (FIG. **16**). When applied to the validation set, the model correctly classified 98% of the cyclin D1-positive MCL cases as MCL (FIG. **16**).

[0197] This diagnostic test was applied to nine lymphoma cases that were morphologically consistent with MCL, but negative for cyclin D1 expression. Seven of these samples were classified as MCL, one was classified as GCB, and one was not assigned to any lymphoma type because none of the pairs generated a probability of 90% or greater.

Example 13

Classification of DLBCL Samples Based on Bayesian Analysis of Gene Expression Data from the Lymphochip Microarray

[0198] A statistical method to classify DLBCL samples based on Bayesian analysis was developed using gene expression data obtained using the Lymphochip cDNA microarray (Rosenwald 2002). This data is available at http://llmpp.nih.gov/DLBCL. The data was divided into two sets: a training set used to create and optimize the prediction model, and a validation set to evaluate the performance of the model. The training set consisted of 42 ABC DLBCL samples and 67 GCB DLBCL samples, while the validation set consisted of 41 ABC DLBCL samples, 67 GCB DLBCL samples, and 57 type 3 DLBCL samples (Shipp 2002).

[0199] Genes that were listed as present on >50% of the samples were identified, and the signal value for these genes on each microarray was normalized to 1,000. After normalization, all signal values under 50 were set to 50. A $\log_2$ transformation was then performed on all the signal values.

[0200] An LPS for distinguishing between two lymphoma types was calculated for each sample X in the training set using an equation:

$$LPS(X) = \sum_j t_j X_j,$$

where X_j represents the expression level of gene j and t_j is a scaling factor whose value depends on the difference in expression of gene j between the two lymphoma types. The scaling factor used in this example was the t-statistic generated by at test of the difference in gene j expression between two lymphoma types. Only those genes with the largest t-statistics were included when calculating the LPS for each sample. The list of genes used to generate the LPS was narrowed further by including only those genes that were most variably expressed within the training set. Only genes in the top third with respect to variance were included. Genes that displayed a correlation with proliferation or lymph node signatures (Shaffer 2001; Rosenwald 2002) were eliminated from consideration, because these genes are often variably expressed within samples from a single lymphoma type (Rosenwald 2002).

[0201] Since the LPS is a linear combination of gene expression values, its distribution within each lymphoma type should be approximately normal, provided that it includes a sufficient number of genes and the correlation structure of those genes is not extreme. The mean and variance of these normal distributions within a lymphoma type can then be estimated from the combined LPS's of all samples within the type. The LPS distribution of two lymphoma types can be used to estimate the probability that a new sample belongs to one of the types using Bayes' rule. The probability q that a sample Y belongs to lymphoma type 1 can be determined by an equation:

$$q(Y \text{ is subtype } 1) = \frac{\phi(LPS(X); \hat{\mu}_1, \hat{\sigma}_1)}{\phi(LPS(Y); \hat{\mu}_1, \hat{\sigma}_1) + \phi(LPS(Y); \hat{\mu}_2, \hat{\sigma}_2)}$$

where $\phi(x; \mu,\sigma)$ is the normal density function with mean μ and standard deviation σ, $\hat{\mu}_1$ and $\hat{\sigma}_1$ are the sample mean and variance of the LPS values for lymphoma type 1, and $\hat{\mu}_2$ and $\hat{\sigma}_2$ are the sample mean and variance of the LPS values for lymphoma type 2. This calculation was used to determine the probability that each sample in the training set belonged to GCB or ABC. A sample was classified as a particular type if it had a 90% or greater probability of belonging to that type. The number of genes in the predictor model was optimized based on the accuracy with which the predictor classified samples into the ABC or GCB subtypes defined previously by hierarchical clustering (Rosenwald 2002). The final predictor incorporated 27 genes, and correctly classified 87% of the training set samples into the subtype to which they had been assigned by hierarchical clustering (FIG. **17**). The genes included in the predictor are listed in Table 2391.

TABLE 2391

UNIQID	Unigene ID Build 167	Gene symbol
19375	235860	FOXP1
19346	109150	SH3BP5
19227	193857	LOC96597
16049	439852	IGHM
32529	55098	C3orf6
24729	127686	IRF4
24899	81170	PIM1
19348	NA	NA
27565	444105	ENTPD1
17227	170359	IL16
26919	118722	FUT8
24321	171262	ETV6
29385	167746	BLNK
16858	376071	CCND2
31801	386140	BMF
19234	418004	PTPN1
26385	307734	MME
24361	388737	NA
24570	446198	NA
24904	18166	KIAA0870
24429	155024	BCL6
28224	387222	NEK6
27673	124922	LRMP
24376	317970	SERPINA11
17496	300592	MYBL1

TABLE 2391-continued

UNIQID	Unigene ID Build 167	Gene symbol
17218	283063	LMO2
28338	78877	ITPKB

[0202] Since the samples used to estimate the distribution of the LPS's were the same samples used to generate the model, there was a possibility of overfitting. Overfitting would result in a model that indicates a larger separation between the LPS's of two lymphoma types than would be found in independent data. To ensure that overfitting was not taking place, the model was tested on the validation set. The reproducibility of the predictor model was verified by its ability to correctly classify 88% of the samples in the validation set (FIG. **18**). Interestingly, 56% of the DLBCL samples that had been placed in the type 3 subtype by hierarchical clustering were classified as either ABC or GCB using this Bayesian model.

[0203] In previous experiments, the genes that were used to distinguish GCB and ABC were deliberately selected to include those that were preferentially expressed in normal GC B cells (Alizadeh 2000; Rosenwald 2002). In the present analysis, the predictor model was not biased a priori to include such genes. The ABC and GCB lymphoma types as defined by the Bayesian model were analyzed for differential expression of GC B cell restricted genes. Thirty seven genes were found to be both more highly expressed in GC B cells than at other stages of differentiation ($p<0.001$) and differentially expressed between DLBCL subtypes ($p<0.001$) (FIG. **19**A). These 37 genes are listed in Table 2392.

TABLE 2392

UNIQID	Unigene ID Build 167	Gene symbol
28014	300592	MYBL1
24376	317970	SERPINA11
24429	155024	BCL6
16886	124922	LRMP
27374	283063	LMO2
29912	446198	
24510	266175	PAG
24854	439767	TOX
32171	307734	MME
24361	388737	
19365	171857	Cyorf15a
27292	272251	KLHL5
24822	283794	PCDHGC3
30923	446195	
24825	88556	HDAC1
31696	91139	SLC1A1
26976	434281	PTK2
19279	49614	GCET2
17866	1765	LCK
24386	437459	MYO1E
33013	293130	VNN2
25126		
30498	157441	SPI1
26512	379414	MFHAS1
26582	153260	SH3KBP1
17840	132311	MAP2K1
26000	25155	NET1
24323	149342	AICDA
30922	435904	C21orf107
30641	79299	LHFPL2
19308	179608	DHRS9

TABLE 2392-continued

UNIQID	Unigene ID Build 167	Gene symbol
24455	405387	
30034	300208	SEC23IP
24977	169939	HS2ST1
24449	206097	RRAS2
30763	446198	
27987	73792	CR2

All but two (AICDA and DHRS9) of these 37 genes were more highly expressed in GCB than in ABC. This demonstrates that the DLBCL subtypes defined by the Bayesian predictor seem to differ with respect to their cell of origin, with GCB retaining the gene expression program of normal GC B cells.

[0204] ABC, on the other hand, displayed higher expression of genes characteristic of plasma cells (FIG. **19**B). Twenty four genes were found to be both more highly expressed in plasma cells than in B cells at earlier developmental stages ($p<0.001$) and differentially expressed between the DLBCL subtypes ($p<0.001$). These 24 genes are listed in Table 2393.

TABLE 2393

UNIQID	Unigene ID Build 167	Gene symbol
16614	127686	IRF4
26907	118722	FUT8
31104	313544	NS
19219	355724	CFLAR
26174	28707	SSR3
24566	169948	KCNA3
34500	442808	B4GALT2
26991	314828	UPP1
30191	438695	FKBP11
27402	259855	EEF2K
26096	434937	PPIB
15887	2128	DUSP5
32440	512686	C20orf59
34827	429975	PM5
29232	437638	XBP1
17763	76640	RGC32
32163	445862	RAB30
17814	5353	CASP10
31460	409223	SSR4
26693	83919	GCS1
25130	409563	PACAP
16436	267819	PPP1R2
31610	76901	PDIR
28961	212296	ITGA6

The majority of these plasma cell-restricted genes were more highly expressed in ABC than in GCB. Eight of the 32 genes encode proteins that reside and function in the endoplasmic reticulum (ER) or Golgi apparatus, suggesting that ABCs have increased the intracellular machinery for protein secretion. These eight genes are denoted in the above list by the designation "ER" or "golgi" in parentheses. Another gene on this list, XBP-1 transcription factor, encodes a protein that is required for plasma cell differentiation (Reimold 2001) and is involved in the response to unfolded proteins in the ER (Calfon 2002). ABCs have not undergone full plasmacytic differentiation, however, because other key plasma cell genes such as Blimp-1 were not more highly expressed in ABC.

Example 14

Classification of DLBCL Samples Based on Bayesian Analysis of Gene Expression Data from the Affymetrix HU6800 Microarray

[0205] The prediction method described in Example 14 above was applied to gene expression data from 58 DLBCL samples obtained using an Affymetrix HU6800 oligonucleotide microarray (Shipp 2002). This data is available at www.genome.wi.mit.edu/MPR/lymphoma. The first step in analyzing this data was to exclude all microarray features with a median signal value of <200 across the samples. Multiple microarray features representing the same gene were then averaged. Of the 27 genes in the DLBCL subtype predictor developed using the Lymphochip data (above), only 14 were represented on the Affymetrix array and passed this filtering process. These 14 genes are listed in Table 2394.

TABLE 2394

UNIQID	Unigene ID Build 167	Gene symbol
24729	127686	IRF4
17227	170359	IL16
26907	118722	FUT8
27565	444105	ENTPD1
16858	376071	CCND2
24899	81170	PIM1
16947	418004	PTPN1
16049	439852	IGHM
26385	307734	MME
27673	124922	LRMP
24429	155024	BCL6
17218	283063	LMO2
28338	78877	ITPKB
17496	300592	MYBL1

These 14 genes were used to create a new DLBCL subtype predictor in which the LPS scaling coefficients were again calculated based on the DLBCL subtype distinction in the Lymphochip data set (Rosenwald 2002). To account for systematic measuring differences between the Affymetrix and Lymphochip microarrays, the expression value of each gene on the Affymetrix microarray was shifted and scaled to match the mean and variance of the corresponding expression values on the Lymphochip. The adjusted expression values for each of the 14 genes were then used to calculate LPS's for each sample. DLBCL subtype membership was again assigned on a cut-off of 90% certainty. Several observations suggested that the predictor identified ABC and GCB samples within the Affymetrix data set that were comparable to those found in the Lymphochip data set. First, the relative proportions of ABC (29%) and GCB (53%) were very similar to the corresponding proportions in the Lymphochip data set (34% and 49%, respectively). Second, 43 genes were found to be differentially expressed between the two DLBCL subtypes with high significance ($p<0.001$) in the Affymetrix data. This number is substantially higher than would be expected by chance, given that the Affymetrix microarray measures the expression of approximately 5,720 genes. The symbols for these 43 genes were: IGHM; TCF4; IRF4; CCND2; SLA; BATF; KIAA0171; PRKCB1; P2RX5; GOT2; SPIB; CSNK1E; PIM2; MARCKS; PIM1; TPM2; FUT8; CXCR4; SP140; BCL2; PTPN1; KIAA0084; HLA-DMB; ACP1; HLA-DQA1; RTVP1; VCL; RPL21; ITPKB; SLAM; KRT8; DCK; PLEK; SCA1; PSIP2; FAM3C; GPR18; HMG14; CSTB; SPINK2; LRMP; MYBL1; and LMO2. Third, the 43 genes differentially expressed between the types included 22 genes that were not used in the predictor but were represented on Lymphochip arrays. Fourteen of these 22 genes were differentially expressed on the Lymphochip array with high statistical significance ($p<0.001$). Finally, the expression of the c-rel gene was previously found to correspond to amplification of the c-rel genomic locus in DLBCL tumor cells, and oncogenic event occurring in GCB but not ABC (Rosenwald 2002). In the Affymetrix data set, c-rel was differentially expressed between the two subtypes ($p=0.0025$), and was highly expressed only in a subset of GCB's.

Example 15

Identification of DLBCL Samples as PMBL Based on Bayesian Analysis of Gene Expression Data from the Lymphochip Microarray

[0206] 310 lymphoma biopsy samples identified as DLBCL by a panel of hematopathologists were divided into a 36 sample training set and a 274 sample validation set, with the validation set consisting of the DLBCL samples classified previously in Example 14. All patients from whom the samples were derived had been treated with anthracycline-containing multiagent chemotherapy protocols, with some patients additionally receiving radiation therapy. The training set was profiled for gene expression using Lymphochip microarrays comprising 15,133 cDNA elements as described previously (Alizadeh 2000). This data is available at the web site companion for Rosenwald et al., *J. Exp. Med.*, 198: 851-862 (2003), which is referenced therein at page 852 and which is hosted by Lymphoma/Leukemia Molecular Profiling Project Gateway at the National Institute of Health web site. The validation set had previously been profiled using Lymphochip microarrays comprising 12,196 cDNA elements (Rosenwald 2002). This data is available at the web site companion for Rosenwald et al., *New Eng. J. Med.*, 346: 1937-1947 (2002), which is referenced therein at page 1938 and which is hosted by the Lymphoma/Leukemia Molecular Profiling Project Gateway at the National Institute of Health web site.

[0207] A hierarchical clustering algorithm (Eisen 1998) was used to organize the genes by their expression patterns across the 36 samples in the training set. A large group of genes that were more highly expressed in lymphomas with mediastinal involvement than in other DLBCLs was shown to be tightly clustered in the resulting dendrogram (FIG. **20**A). This cluster of genes included two genes, MAL and FIG. **1**, previously shown to be highly expressed in PMBL (Copie-Bergman 2002; Copie-Bergman 2003). Several of the lymphomas with mediastinal involvement did not express this set of putative PMBL signature genes, and it was suspected that these samples were more likely to be conventional DLBCL than PMBL. Hierarchical clustering was used to organize the samples according to their expression of the PMBL signature genes, resulting in two major clusters of cases (FIG. **20**B). One cluster contained 21 samples designated "PMBL core" samples by virtue of their higher expression of PMBL signature genes. The other cluster contained some samples that had virtually no expression of these genes, and other samples that did express these genes but at lower levels than the PMBL core samples.

[0208] A gene expression-based method for distinguishing PMBL core cases from GCB and ABC DLBCL cases based

on Bayesian analysis was developed using the methods described in Examples 14 and 15. A set of genes were selected that were differentially expressed between the PMBL core samples and both GCB and ABC ($p<0.001$). This set of genes included all of the PMBL signature genes identified by hierarchical clustering (FIG. **20**A), as well as a large number of additional genes. Many of the genes in this set belonged to the lymph node gene expression signature (Alizadeh 2000; Rosenwald 2002). These genes were excluded from the final predictor because they might cause some DLBCL samples with higher expression of lymph node gene expression signature genes to be misclassified as PMBL. The list of PMBL distinction genes was refined by adding a requirement that they also be differentially expressed between the PMBL core samples and a subgroup of six DLBCL samples with higher expression of lymph node gene expression signature genes ($p<0.001$). The resulting set of 46 genes included 35 genes that were more highly expressed in PMBL and 11 genes that were more highly expressed in DLBCL (FIG. **21**A). The 46 genes in this set were PDL2, SNFT, ILI 3RA1, FGFR1, FLJ10420, CCL17/TARC, TNFRSF8/CD30, E2F2, MAL, TNFSF4/OX40 ligand, IL411/FIG. **1**, IMAGE:686580, BST2, FLJ31131, FCER2/CD23, SAMSN1, JAK2, FLJ00066, MST1R, TRAF1, SLAM, LY75, TNFRSF6/Fas, FNBP1, TLR7, TNFRSF17/BCMA, CDKN1A/p21CIP1, RGS9, IMAGE:1340506, NFKB2, KIAA0339, ITGAM, IL23A, SPINT2, MEF2A, PFDN5, ZNF141, IMAGE:4154313, IMAGE:825382, DLEU1, ITGAE, SH3BP5, BANK, TCL1A, PRKAR1B, and CARD11. A series of linear predictor scores were generated based on the expression of this gene set. Based on the distribution of linear predictor scores within a particular lymphoma type, Bayes' rule can be used to estimate the probability that a particular sample belongs to either of the two types. An arbitrary probability cut-off of 90% or greater was used to classify a sample as a particular lymphoma type. All of the PMBL core samples were classified as PMBL using this method, as were six of the other lymphoma samples with mediastinal involvement. However, nine of the lymphoma samples with mediastinal involvement were classified as a DLBCL, as were all of the GCB and ABC samples.

[0209] In the validation set, 11 samples were identified on clinical grounds as being consistent with a diagnosis of PMBL, and the Bayesian model classified nine of these as PMBL (FIG. **21**B). Interestingly, 12 of the remaining 263 DLBCL samples were classified as PMBL by the predictor. FIG. **21**B shows that these cases were indistinguishable by gene expression from the nine cases diagnosed as PMBL on clinical grounds. As expected, the average expression of the PMBL predictor genes in the 249 samples classified as DLBCL was notably lower than in the 22 PMBL cases. Thus, PMBL represents a third subgroup of DLBCL than can be distinguished from ABC and GCB by gene expression profiling.

[0210] Table 2395 compares the clinical parameters of patients assigned to the PMBL, ABC, and GCB subgroups of DLBCL using this prediction method.

TABLE 2395

	ABC DLBCL	GCB DLBCL	PMBL Training set	PMBL Validation set	PMBL All cases	P value
Median age	66	61	33	33	33	4.4E−16
Age <35	5%	10%	52%	56%	53%	7.2E−14
Age 35-60	29%	38%	44%	28%	37%	
Age >60	66%	52%	4%	17%	9%	
Gender = male	59%	53%	44%	50%	47%	0.38
Female <35	2%	3%	32%	39%	35%	1.1E−12
Male <35	2%	7%	20%	17%	19%	
Female 35-60	6%	18%	24%	6%	16%	
Male 35-60	23%	19%	20%	22%	21%	
Female >60	33%	25%	0%	6%	2%	
Male >60	34%	27%	4%	11%	7%	

PMBL patients were significantly younger than other DLBCL patients, with a median age at diagnosis of 33 years compared with a median age of 66 and 61 years for ABC and GCB patients, respectively. Although there was no significant difference in gender distribution among the DLBCL subgroups, young women (<35 years) accounted for 35% of PMBL patients, more than any other DLBCL subgroup. Young men (<35 years) were also more frequently represented in the PMBL subgroup, accounting for 19% of the patients. Correspondingly, older men and women (age >60) were significantly underrepresented in the PMBL subgroup. These clinical characteristics were observed in both the training set and the validation set of PMBL cases, demonstrating that the PMBL predictor reproducibly identified a clinically distinct subgroup of DLBCL patients.

[0211] The PMBL subgroup defined by the PMBL predictor had a relatively favorable overall survival rate after therapy (FIG. **22**). PMBL patients had a five-year survival rate of 64%, superior to the 46% rate seen in DLBCL patients as a whole ($p=0.0067$). The survival of the PMBL subgroup was significantly better than the 30% five-year survival rate of the ABC subgroup (FIG. **22**; $p=5.8E-5$), but only marginally better than the 59% five-year survival rate of the GCB subgroup ($p=0.18$).

Example 16

Classification of Lymphomas into Types Based on Bayesian Analysis of Gene Expression Data from the Lymph Dx Microarray

[0212] Based on the clustering of the Lymph Dx microarray signals for the DLBCL samples, a cluster of "proliferation signature" genes and a cluster of "lymph node signature" genes were identified. The expression of these genes was averaged to form a proliferation signature and a lymph node

signature. Each gene represented on the Lymph Dx microarray was placed into one of three "gene-list categories" based on its correlation with the proliferation or lymph node gene signatures. "Proliferation" genes were defined as those genes for which the correlation between their expression and the proliferation signature was greater than 0.35. Lymph node genes were defined as those genes for which the correlation between their expression and the lymph node signature was greater than 0.35. The remaining genes on the array were classified as standard genes. This classification resulted in 323 proliferation genes and 375 lymph node genes.

[0213] Two stages of lymphoma classification were performed using the gene expression data obtained for the above samples using the Lymph Dx microarray. The general procedure used to classify the samples is presented in flow chart form in FIG. **1**.

[0214] For the first stage of expression analysis, the samples were divided into five types: FL, MCL, SLL, FH, and a class of aggressive lymphomas that included DLBCL and BL. Samples obtained from subjects with other diagnoses (e.g., MALT, LPC) were omitted from this analysis. Data from the Lymph Dx microarray was then used to compare gene expression in each possible lymphoma type pair (e.g., FH vs. FL, MCL vs. SLL, etc.). This resulted in the creation of ten "pair-wise models" (one for each possible lymphoma type pair) for predicting whether a sample fell into a particular lymphoma type.

[0215] For each lymphoma type pair, the difference in expression between the two types for every gene on the microarray was calculated, and a t-statistic was generated to represent this difference. Within each gene-list category (proliferation, lymph node, and standard), individual genes were ordered based on the absolute value of their t-statistic. Only those genes that displayed a statistically significant difference in expression between the two types were included in the model. Those genes with largest absolute t-statistics in each gene-list category were then used to generate a linear predictor score (LPS) for each sample. For a sample X and a set of genes G, the LPS was defined as:

$$LPS(X) = \sum_{j \in G} t_j X_j,$$

where X_j is the expression of gene j in the sample and t_j is the t-statistic representing the difference in expression of gene j between the two lymphoma types. This formulation of LPS, known as the compound covariate predictor, has previously been used successfully (Radmacher 2002; Rosenwald 2003a; Wright 2003). Other ways to formulate an LPS include Fisher linear discriminant analysis (Dudoit 2002), weighted voting (Golub 1999), linear support vector machines (Ramaswamy 2001), and nearest shrunken centroids (Tibshirani 2002).

[0216] In order to optimize the number of genes used to generate the LPS, a series of LPS's were generated for each sample using between five and 100 genes from each gene-list category. The optimal number of genes is that number which generates a maximum t-statistic when comparing the LPS of two samples from different lymphoma types (FIG. **23**). This optimization procedure was repeated for every gene-list category in every pair-wise model, meaning that 30 optimizations were performed in all.

[0217] It was recognized that for some pair-wise models, it would be useful to calculate LPS's using different combinations of gene-list categories. LPS's were calculated for each sample using four different combinations. In the first, LPS was calculated using the standard genes only. In the second, LPS's were calculated for both the standard and proliferation genes, but not the lymph node genes. In the third, LPS's were calculated for both the standard and lymph node genes, but not the proliferation genes. In the fourth, LPS's were calculated using all three gene-list categories.

[0218] Depending on the number of gene-list categories included, between one and three LPS's were calculated for each sample in the pair-wise models. Thus, each sample could be thought of as a vector in a space of between one and three dimensions. Since the LPS's were sums of individual expressions, it was reasonable to approximate the distributions as normal. Multivariate normal distributions are defined by two quantities: a mean vector, which indicates the average value of each of the models within a given lymphoma type, and a covariance matrix, which indicates the magnitude and orientation spread of points away from this center. Both of these quantities can be estimated empirically from the observed data. FIG. **24** shows the Standard and Proliferation LPS's for the FL vs. DLBCL/BL pair-wise model. The dotted lines indicate the standard deviations from the fitted multivariate normal distributions.

[0219] Once the multidimensional distributions have been estimated, Bayes' rule (Bayes 1763) can be used to estimate the probability that a given sample belongs to one lymphoma type or another. Bayesian analysis of an LPS has been successfully employed in the past to distinguish DLBCL subtypes (Rosenwald 2003a, Wright 2003). For a sample X, the probability q of the sample belonging to a first lymphoma type rather than a second lymphoma type can be calculated using the formula:

$$q = \frac{\phi(LPS(X); \hat{\mu}_1, \hat{\sigma}_1)}{\phi(LPS(X); \hat{\mu}_1, \hat{\sigma}_1) + \phi(LPS(X); \hat{\mu}_2, \hat{\sigma}_2)}$$

where LPS(X) is the linear predictor score for sample X, $\phi(x; \mu,\sigma)$ is the normal density function with mean μ and standard deviation σ, $\hat{\mu}_1$ and $\hat{\sigma}_1$ are the mean and variance of the LPS's for the first lymphoma type, and $\hat{\mu}_2$ and $\hat{\sigma}_2$ are the mean and variance of the LPS's for the second lymphoma type. Using this equation, a single probability q value can be developed for each sample and for each of the four LPS combinations. This q value can then be used to classify a sample as a first lymphoma type, a second lymphoma type, or unclassified. Samples with the highest q values are classified as the first lymphoma type, while samples with the lowest q values are classified as the second lymphoma type. Samples with middle range q values are deemed unclassified. Classifying the samples in this manner requires two cut-off points: a lower cut-off point between the second lymphoma type and unclassified, and an upper cut-off point between unclassified and the first lymphoma type. To develop these cut-off points, samples were ordered by their q values, and each possible cut-off point between adjacent samples was considered. To ensure that the cut-off points were reasonable, the lower cut-off point was restricted to between 0.01 and 0.5 and the upper cut-off point was restricted to between 0.5 and 0.99.

[0220] Every cut-off point and model combination was analyzed by the following equation:

3.99*[(% of type 1 misidentified as type 2)+(% of type 2 misidentified as type 1)]+[(% of type 1 unclassified)+(% of type 2 misidentified)].

Using this equation, the cut-off point would be adjusted to allow an additional error only if this adjustment resulted in four or more unclassified samples becoming correctly classified. The final model and cut-off point for a given pair-wise analysis was that which minimized this equation. The equation utilizes percentages rather than the actual number of cases in order to account for the different number of samples in each class.

[0221] All cut-off points between a given pair of adjacent q-values will produce the same division of data. Since cut-off point optimality is defined in terms of dividing the data into subtypes, all cut-off points between a pair of borderline cases will be equally optimal. In choosing where to place the actual cut-off point values, values were chosen that would lead to a larger unclassified region. When the lower cut-off point was being defined, a value would be chosen that was ⅕ of the way from the smallest borderline case to the largest. When the upper cut-off point was being defined, a value would be chosen that was ⅘ of the way from the smallest borderline case to the largest. FIG. **25** illustrates the q-results of optimizing the cut-point for the FL versus DLBCL/BL samples. The optimal lower cut-off point for these samples was found at q=0.49, while the optimal upper cut-off point was found at q=0.84. FIG. **26** indicates how this choice of cut-off points divided the space of LPS's.

[0222] The above procedures resulted in a series of pair-wise models for comparing every lymphoma type to every other lymphoma type. If there are n types, then there will be n−1 pair-wise models for each type. Since there were five lymphoma types in the stage 1 analysis, each type was involved in 4 pair-wise models. For instance, there were four different pair-wise models for MCL: MCL vs. FH, MCL vs. FL, MCL vs. SLL, and MCL vs. DLBCL/BL. For each sample tested, each pair-wise model will produce one of three possible results: 1) the sample belongs to the first lymphoma type of the pair-wise model, 2) the sample belongs to the second lymphoma type of the pair-wise model, or 3) the sample is unclassified. If each of the n−1 models agrees that the sample belongs to a particular lymphoma type, then the sample is designated as belonging to that type. If the n−1 models do not all agree that the sample belongs to a particular lymphoma type, the sample is designated as unclassified.

[0223] To ensure that the above methods did not result in overfitting (i.e., models that fit particular idiosyncrasies of the training set but fail when applied to independent data), the models were validated by leave-one-out cross-validation fashion (Hills 1966). Each sample was removed from the data one at a time, and a predictive model was developed as described above using the remaining data. This model was then used to predict the sample that was removed. Since the model being used to predict a given sample was generated from data that did not include that sample, this method provided an unbiased estimate of the accuracy of the model.

[0224] The results of the leave-one-out predictions are set forth in Tables 2396 and 2397, below. The rows in each table correspond to different sample groups, while the columns indicate the prediction results. The standard to which the prediction results were compared in this stage was the diagnoses of a panel of eight expert hematopathologists who used histological morphology and immunohistochemistry to classify the samples. Table 2396 provides classification results for the five lymphoma types tested (DLBCL/BL, FL, FH, MCL, SLL), while Table 2397 provides more specific results for classification of subtypes within these five lymphoma types. The results set forth in Table 2396 are also summarized in FIG. **27**.

TABLE 2396

	DLBCL/BL	FL	FH	MCL	SLL	Unclassified	Total	% Correct	% Unclassified	% Error
DLBCL/BL	249	6	0	0	0	7	262	95%	2%	3%
FL	5	154	0	0	0	14	173	89%	8%	3%
FH	0	0	17	0	0	0	17	100%	0%	0%
MCL	0	0	0	22	0	0	22	100%	0%	0%
SLL	0	0	0	0	14	0	14	100%	0%	0%

TABLE 2397

	DLBCL/BL	FL	FH	MCL	SLL	Unclassified	Total	% Correct	% Unclassified	% Error
ABC	78	0	0	0	0	0	78	100%	0%	0%
GCB	77	4	0	0	0	4	85	91%	5%	5%
PMBL	33	0	0	0	0	0	33	100%	0%	0%
Unclassified DLBCL	27	1	0	0	0	2	30	90%	7%	3%
DLBCL (not yet subclassed)	14	0	0	0	0	1	15	93%	7%	0%
BL	20	1	0	0	0	0	21	95%	0%	5%
FL grade 1	1	78	0	0	0	3	82	95%	4%	1%
FL grade 2	2	58	0	0	0	3	63	92%	5%	3%
FL grade 3A	2	18	0	0	0	8	28	64%	29%	7%
Combined FL grades 1, 2, 3A	5	154	0	0	0	14	173	89%	8%	3%
FL grade 3B	2	1	0	0	0	4	7	14%	57%	29%
FL unknown grade	3	11	0	0	0	0	14	79%	0%	21%
FH	0	0	17	0	0	0	17	100%	0%	0%
MCL	0	0	0	22	0	0	22	100%	0%	0%
SLL	0	0	0	0	14	0	14	100%	0%	0%

[0225] As seen in Table 2396, perfect prediction of SLL, MCL, and FH samples was obtained. The success rate for predicting FL and the aggressive lymphomas (DLBCL/BL) was also very good, with only 3% of the samples being classified incorrectly. As seen in Table 2397, perfect prediction was also obtained for ABC and PMBL samples within the DLBCL samples.

Example 17

Classification of DLBCL/BL Samples into Subtypes Based on Bayesian Analysis of Gene Expression Data from the Lymph Dx Microarray

[0226] Samples identified as DLBCL/BL in Example 17 were subdivided into four types: ABC, GCB, PMBL, and BL. These samples were then used to generate six pair-wise models using the same procedure described in Example 17. The results of the leave-one-out predictions using these pair-wise models are set forth in Table 2398, below. These results are also summarized in FIG. **28**. The rows in the table correspond to different sample groups, while the columns indicate the prediction results. In this stage, the ability of the prediction method to identify BL was again measured against the diagnoses of hematopathologists. The ability of the prediction method to identify the various DLBCL subtypes, on the other hand, was measured against previous studies in which this distinction between subtypes was based on gene expression data from a Lymphochip microarray (Alizadeh 2000, Rosenwald 2002, Rosenwald 2003a, Wright 2003).

TABLE 2398

	ABC	GCB	PMBL	BL	Unclassified	Total	% Correct	% Unclassified	% Error
ABC	76	0	0	0	2	78	97%	3%	0%
GCB	1	66	2	4	4	77	86%	9%	5%
PMBL	0	2	27	0	4	33	82%	12%	6%
Unclassified DLBCL	5	9	1	1	11	27	NA	41%	4%
DLBCL (not yet subclassed)	5	5	0	1	3	14	NA	21%	7%
BL	0	1	0	18	1	20	90%	5%	5%
FL grade 1	0	1	0	0	0	1			
FL grade 2	0	1	0	0	1	2			
FL grade 3A	0	2	0	0	0	2			
Combined FL grades 1, 2, 3A	0	4	0	0	1	5			
FL grade 3B	0	1	0	0	1	2			
FL unknown grade	0	1	0	1	1	3			

[0227] As seen in Table 2398, only 1 of the 20 BL lymphoma samples was classified incorrectly. The classification of DLBCL into subtypes was also quite effective. All previously identified ABC subtype samples were again assigned to the ABC subtype, while only 5% of the GCB samples and 6% of the PMBL samples were assigned to a different subtype than they were assigned to previously.

[0228] The above classification was implemented using S+ software and the S+ subtype predictor script contained in the file entitled "Subtype_Predictor.txt," located in the computer program listing appendix contained on CD number 22 of 22. This S+ script implements the lymphoma prediction algorithm. When this script is pasted into an S+ script window and run in a working directory containing the data set files discussed below, it will produce a text file entitled "PredictionResults.txt," which indicates the results of the predictive algorithm. The other files in the computer program listing appendix contain the required data sets, in their required format, for carrying out the lymphoma type identification described above. The file entitled "GeneData.txt" contains the gene expression values for each sample analyzed. This file is included in the working directory when the S+ subtype predictor script is run. The file entitled "GeneID.txt" contains information about the genes in the GeneData.txt file, and is also included in the working directory when the S+ subtype predictor script is run. This file indicates the UNIQID for each gene, as well as the extent to which the gene is associated with the lymph node and proliferation signatures ("LN.cor" and "pro.cor," respectively). The contents of "GeneID.txt" are also set forth in Table 2415 below. The file entitled "SampleID.txt" contains information about the samples included in the "GeneData.txt" file, specifically the original classification of all the samples. This file is also included in the working directory when the S+ subtype predictor script is run. The file entitled "PredictionResults.txt" is an example of the productive output of the prediction algorithm.

[0229] After the above model was validated using leave-one-out cross-validation, the model was re-fit using all of the data to generate a final predictor that could be applied to a new set of data. Tables 2399-2414 indicate for each of the pair wise models the list of genes used, the weight given to each of those genes, the signature with which each gene was associated, the mean values and covariance matrices associated with the subtypes being compared, and the q-value cut-points of the pair-wise model.

TABLE 2399

ABC vs. BL

Signature	Scale	UNIQID	Unigene ID Build 167	Probe set	Gene symbol
Standard	−18.87	1101149	517226	229437_at	BIC
Standard	−17.4	1121452	227817	205681_at	BCL2A1
Standard	−16.42	1123163	421342	208991_at	STAT3
Standard	−16.2	1121629	41691	205965_at	BATF
Standard	−15	1134095	89555	208018_s_at	HCK
Standard	−14.75	1132636	306278	204490_s_at	CD44
Standard	−14.33	1119939	170087	202820_at	AHR
Standard	−14.25	1100138	278391	228234_at	TIRP
Standard	−14.02	1128626	501452	219424_at	EB13
Standard	−13.89	1132883	432453	205027_s_at	MAP3K8
Standard	−13.88	1134991	444105	209474_s_at	ENTPD1
Standard	−13.37	1109913	355724	239629_at	CFLAR
Standard	−13.25	1120389	75367	203761_at	SLA
Standard	−12.99	1131497	114931	202295_s_at	CTSH
Standard	−12.71	1115071	390476	223218_s_at	MAIL
Standard	−12.46	1136329	132739	211675_s_at	HIC
Standard	−12.41	1128195	115325	218699_at	RAB7L1
Standard	−12.37	1124381	440808	212288_at	FNBP1
Standard	−12.30	1100562	26608	228737_at	C20orf100
Standard	−12.24	1101272	179089	229584_at	DKFZp434
Standard	−12.18	1128536	21126	219279_at	DOCK10
Standard	−11.64	1098271	300670	226056_at	CDGAP
Standard	−11.41	1119566	433506	201954_at	ARPC1B
Standard	−11.11	1120651	80205	204269_at	PIM2
Standard	−10.89	1098952	62264	226841_at	KIAA0937
Standard	−10.80	1099939	488173	227983_at	MGC7036
Standard	−10.67	1134270	352119	208284_x_at	GGT1
Standard	−10.44	1134145	4750	208091_s_at	DKFZP564
Standard	−10.39	1123437	73090	209636_at	NFKB2
Standard	−10.17	1119884	418004	202716_at	PTPM1
Standard	−10.14	1129269	62919	220358_at	SNFT
Standard	−10.13	1126293	504816	215346_at	TNFRSF5
Standard	−10.12	1112344	163242	242406_at	
Standard	−10.10	1135550	221811	210550_s_at	RASGRF1
Standard	−10.08	1135165	170359	209827_s_at	IL16
Standard	−10.05	1120808	127686	204562_at	IRF4
Standard	−10.01	1122087	72927	206693_at	IL7
Standard	−9.97	1132004	415117	203217_s_at	SIAT9
Standard	−9.88	1114824	193370	222762_x_at	LIMD1
Standard	−9.87	1132034	410455	203271_s_at	UNC119
Standard	−9.87	1099680	210387	227677_at	JAK3
Standard	−9.86	1132830	31210	204908_s_at	BCL3
Standard	−9.79	1099631	367639	227624_at	FLJ20032
Standard	−9.78	1120267	256278	203508_at	TNFRSF1B
Standard	−9.77	1124187	378738	211986_at	MGC5395
Standard	−9.73	1108970	140489	238604_at	
Standard	−9.71	1136216	512152	211528_x_at	HLA-G
Standard	−9.71	1120993	327	204912_at	IL10RA
Standard	−9.68	1100847	97411	229070_at	C6orf105
Standard	−9.64	1123413	418291	209575_at	IL10RB
Standard	−9.62	1115704	350268	224569_s_at	IRF2BP2
Standard	−9.58	1108237	126232	237753_at	
Standard	−9.55	1121695	511759	206082_at	HCP5
Standard	−9.48	1101905	170843	230345_at	
Standard	−9.42	1119243	440165	201171_at	ATP6V0E
Standard	−9.39	1140457	210546	221658_s_at	IL21R
Standard	−9.32	1098506	193400	226333_at	IL6R
Standard	−9.31	1139805	414362	220230_s_at	CYB5R2
Standard	−9.30	1139037	173380	218223_s_at	CKIP-1
Standard	−9.28	1130533	76507	200706_s_at	LITAF
Standard	−9.15	1098678	386140	226530_at	BMF
Standard	−9.04	1133210	434374	205842_s_at	JAK2
Standard	9.05	1116432	409362	229356_x_at	KIAA1259
Standard	9.17	1097281	7037	224892_at	PLDN
Standard	9.17	1140018	438482	220917_s_at	PWDMP
Standard	9.30	1119997	367811	202951_at	STK38
Standard	9.41	1119817	409194	202561_at	TNKS
Standard	9.55	1139842	133523	220367_s_at	SAP130
Standard	9.64	1132122	307734	203434_s_at	MME
Standard	9.77	1119258	88556	201209_at	HDAC1
Standard	9.80	1128248	234149	218802_at	FLJ20647

TABLE 2399-continued

ABC vs. BL					
Standard	10.38	1101211	287659	229513_at	STRBP
Standard	10.52	1123419	170195	209590_at	BMP7
Standard	10.71	1133755	404501	207318_s_at	CDC2L5
Standard	10.80	1128192	102506	218696_at	EIF2AK3
Standard	10.85	1124786	22370	212847_at	NEXN
Standard	10.92	1130114	445084	221965_at	MPHOSPH9
Standard	11.00	1126081	309763	215030_at	GRSF1
Standard	11.17	1118736	96731	38340_at	HIP1R
Standard	11.26	1124613	296720	212599_at	AUTS2
Standard	11.43	1125456	300592	213906_at	MYBL1
Standard	11.60	1097177	9691	224761_at	GNA13
Standard	12.11	1120400	152207	203787_at	SSBP2
Standard	12.12	1139266	76640	218723_s_at	RGC32
Standard	12.22	1100770	65578	228976_at	
Standard	12.73	1131246	153752	201853_s_at	CDC25B
Standard	13.48	1096503	21379	223522_at	C9orf45
Standard	14.50	1124920	6150	213039_at	ARHGEF1
Standard	15.03	1128360	445043	218988_at	SLC35E3
Standard	15.24	1099444	434489	227407_at	FLJ90013
Standard	21.03	1134582	78202	208794_s_at	SMARCA4

Standard			
Mean ABC	−4179.76	Cut 1	0.20
Mean BL	−1894.68	Cut 2	0.80
Covariance ABC	53707.58		
Covariance BL	194887.5		

TABLE 2400

ABC vs. GCB					
Signature	Scale	UNIQID	Unigene ID Build 167	Probe set	Gene symbol
Standard	−15.31	1122645	158341	207641_at	TNFRSF13B
Standard	−14.56	1120651	80205	204269_at	PIM2
Standard	−14.18	1120808	127686	204562_at	IRF4
Standard	−13.84	1114824	193370	222762_x_at	LIMD1
Standard	−13.44	1136687	59943	212345_s_at	CREB3L2
Standard	−13.12	1139805	414362	220230_s_at	CYB5R2
Standard	−12.23	1104552	193857	233483_at	LOC96597
Standard	−12.19	1097236	235860	224837_at	FOXP1
Standard	−12.06	1121629	41691	205965_at	BATF
Standard	−11.93	1128195	115325	218699_at	RAB7L1
Standard	−11.72	1111503	502910	241383_at	KBRAS2
Standard	−11.66	1134991	444105	209474_s_at	ENTPD1
Standard	−11.27	1098678	386140	226530_at	BMF
Standard	−10.9	1131074	76894	201572_x_at	DCTD
Standard	−10.82	1135165	170359	209827_s_at	IL16
Standard	−10.7	1132396	118722	203988_s_at	FUT8
Standard	−10.54	1131541	310230	202369_s_at	TRAM2
Standard	−10.47	1105759	171262	235056_at	ETV6
Standard	−10.38	1121564	437783	205865_at	ARID3A
Standard	−10.16	1130472	192374	200599_s_at	TRA1
Standard	−10.04	1132058	161999	203313_s_at	TGIF
Standard	−10.03	1105684	195155	234973_at	SLC38A5
Standard	−9.95	1097735	26765	225436_at	LOC58489
Standard	−9.94	1115071	390476	223218_s_at	MAIL
Standard	−9.85	1101149	517226	229437_at	BIC
Standard	−9.83	1119884	418004	202716_at	PTPN1
Standard	−9.71	1134095	89555	208018_s_at	HCK
Standard	−9.68	1135550	221811	210550_s_at	RASGRF1
Standard	−9.61	1098927	356216	226811_at	FLJ20202
Standard	−9.6	1120389	75367	203761_at	SLA
Standard	−9.58	1133910	167746	207655_s_at	BLNK
Standard	9.56	1118736	96731	38340_at	HIP1R
Standard	9.58	1128860	323634	219753_at	STAG3
Standard	9.68	1134582	78202	208794_s_at	SMARCA4
Standard	9.7	1121853	98243	206310_at	SPINK2
Standard	10.14	1119258	88556	201209_at	HDAC1

TABLE 2400-continued

ABC vs. GCB

Standard	10.19	1132122	307734	203434_s_at	MME
Standard	10.23	1120400	152207	203787_at	SSBP2
Standard	10.48	1529344	317970	Lymph_Dx_065_at	SERPINA11
Standard	10.64	1124613	296720	212599_at	AUTS2
Standard	10.72	1132159	147868	203521_s_at	ZNF318
Standard	10.98	1097901	266175	225626_at	PAG
Standard	11.1	1128287	300063	218862_at	ASB13
Standard	12.26	1099686	117721	227684_at	
Standard	12.45	1112674	310320	242794_at	MAML3
Standard	13.15	1120370	78877	203723_at	ITPKB
Standard	14.23	1125456	300592	213906_at	MYBL1
Lymph Node	6.8	1097202	386779	224796_at	DDEF1
Lymph Node	6.85	1131755	241257	202729_s_at	LTBP1
Lymph Node	7.27	1136273	13775	211597_s_at	HOP
Lymph Node	7.35	1119424	75485	201599_at	OAT
Lymph Node	7.86	1095985	83883	222450_at	TMEPAI
Lymph Node	8.02	1124875	18166	212975_at	KIAA0870
Lymph Node	8.32	1124655	79299	212658_at	LHFPL2
Lymph Node	8.62	1115034	387222	223158_s_at	NEK6
Proliferation	−9.11	1120583	153768	204133_at	RNU3IP2
Proliferation	−7.87	1135492	408615	210448_s_at	P2RX5
Proliferation	−7.68	1127756	313544	217850_at	NS
Proliferation	−7.57	1097195	149931	224785_at	MGC29814
Proliferation	−7.31	1127813	14317	217962_at	NOLA3
Proliferation	−7.24	1138944	84753	218051_s_at	FLJ12442
Proliferation	−6.99	1139226	266514	218633_x_at	FLJ11342
Proliferation	−6.7	1137486	441069	214442_s_at	MIZ1
Proliferation	−6.51	1133786	153591	207396_s_at	ALG3
Proliferation	−6.45	1131150	75514	201695_s_at	NP
Proliferation	−6.45	1119076	268849	200681_at	GLO1
Proliferation	−6.38	1115679	8345	224523_s_at	MGC4308
Proliferation	−6.34	1110223	212709	239973_at	
Proliferation	−6.3	1529338	284275	Lymph_Dx_058_s_at	PAK2
Proliferation	−6.24	1135164	458360	209825_s_at	UMPK
Proliferation	−6.24	1128738	335550	219581_at	MGC2776
Proliferation	−6.01	1099088	14355	226996_at	
Proliferation	−5.98	1123192	315177	209100_at	IFRD2
Proliferation	−5.83	1116073	146161	227103_s_at	MGC2408
Proliferation	5.79	1097388	278839	225024_at	C20orf77
Proliferation	6.13	1124563	249441	212533_at	WEE1

	Standard	Lymph Node	Proliferation		
Mean ABC	−2226.57	476.67	−1096.34	Cut 1	0.50
Mean GCB	−1352.02	547.18	−1005.72	Cut 2	0.74
Covariance ABC	33472.10	3418.91	4347.99		
	3418.91	1296.05	846.32		
	4347.99	846.32	1609.13		
Covariance GCB	53751.59	466.34	751.08		
	466.34	777.74	249.29		
	751.08	249.29	1708.67		

TABLE 2401

ABC vs. PMBL

Signature	Scale	UNIQID	Unigene ID Build 167	Probe set	Gene symbol
Standard	−14.61	1097236	235860	224837_at	FOXP1
Standard	−14.47	1104552	193857	233483_at	LOC96597
Standard	−13.62	1122645	158341	207641_at	TNFRSF13B
Standard	−12.05	1135102	349845	209685_s_at	PRKCB1
Standard	−11.65	1096499	293867	223514_at	CARD11
Standard	−11.26	1124770	153261	212827_at	IGHM
Standard	−11.25	1125010	43728	213170_at	GPX7
Standard	−11.13	1109545	63187	239231_at	
Standard	−10.99	1109220	445977	238880_at	GTF3A
Standard	−10.87	1131074	76894	201572_x_at	DCTD
Standard	−10.68	1134517	75807	208690_s_at	PDLIM1
Standard	−10.63	1098604	32793	226444_at	SLC39A10

TABLE 2401-continued

ABC vs. PMBL

Standard	−10.56	1131219	109150	201810_s_at	SH3BP5
Standard	−10.52	1120651	80205	204269_at	PIM2
Standard	−10.39	1133910	167746	207655_s_at	BLNK
Standard	−10.32	1099396	435949	227346_at	ZNFN1A1
Standard	−10.25	1529297	132335	Lymph_Dx_015_at	
Standard	−10.17	1107575	424589	237033_at	MGC52498
Standard	−10.11	1117211	356509	233955_x_at	HSPC195
Standard	10.06	1129517	−33	220712_at	
Standard	10.29	1139950	437385	220731_s_at	FLJ10420
Standard	10.35	1097553	197071	225214_at	PSMB7
Standard	10.41	1119516	6061	201834_at	PRKAB1
Standard	10.47	1122772	66742	207900_at	CCL17
Standard	10.55	1132762	80395	204777_s_at	MAL
Standard	10.77	1099265	375762	227193_at	
Standard	10.81	1095996	288801	222482_at	SSBP3
Standard	11.14	1100770	65578	228976_at	
Standard	11.19	1133801	181097	207426_s_at	TNFSF4
Standard	11.61	1099154	97927	227066_at	MOBKL2C
Standard	11.63	1120370	78877	203723_at	ITPKB
Standard	11.8	1112674	310320	242794_at	MAML3
Standard	12.57	1105178	283961	234284_at	GNG8
Standard	12.63	1124613	296720	212599_at	AUTS2
Standard	13.28	1106415	169071	235774_at	
Standard	13.3	1121762	32970	206181_at	SLAMF1
Standard	13.6	1121853	98243	206310_at	SPINK2
Lymph Node	10.91	1105838	129837	235142_at	ZBTB8
Lymph Node	10.99	1136273	13775	211597_s_at	HOP
Lymph Node	11.02	1099418	172792	227370_at	KIAA1946
Lymph Node	11.46	1124875	18166	212975_at	KIAA0870
Lymph Node	11.99	1120299	79334	203574_at	NFIL3
Lymph Node	12.49	1135871	104717	211031_s_at	CYLN2
Lymph Node	13.33	1121767	458324	206187_at	PTGIR
Proliferation	−13.17	1138944	84753	218051_s_at	FLJ12442
Proliferation	−11.61	1116122	42768	227408_s_at	DKFZp761O0113
Proliferation	−11.16	1110223	212709	239973_at	
Proliferation	−9.93	1120717	444159	204394_at	SLC43A1
Proliferation	−9.54	1110099	116665	239835_at	TA-KRP
Proliferation	−9.49	1130942	445977	201338_x_at	GTF3A
Proliferation	−9.28	1123192	315177	209100_at	IFRD2
Proliferation	−9.14	1135492	408615	210448_s_at	P2RX5
Proliferation	−9.03	1120011	3068	202983_at	SMARCA3
Proliferation	−9.01	1096738	87968	223903_at	TLR9
Proliferation	−8.91	1108961	292088	238593_at	FLJ22531

	Standard	Lymph Node	Proliferation		
Mean ABC	−849.47	531.79	−1027.48	Cut 1	0.20
Mean PMBL	27.99	750.84	−872.43	Cut 2	0.80
Covariance ABC	14028.46	3705.84	3118.60		
	3705.84	2326.91	1083.37		
	3118.60	1083.37	1589.42		
Covariance PMBL	19425.29	5109.98	2199.28		
	5109.98	2084.28	620.86		
	2199.28	620.86	1028.44		

TABLE 2402

BL vs. GCB

Signature	Scale	UNIQID	Unigene ID Build 167	Probe set	Gene symbol
Standard	−12.78	1131246	153752	201853_s_at	CDC25B
Standard	−11.35	1099444	434489	227407_at	FLJ90013
Standard	−10.4	1116432	409362	229356_x_at	KIAA1259
Standard	−10.3	1134582	78202	208794_s_at	SMARCA4
Standard	−10.01	1133998	76884	207826_s_at	ID3
Standard	−9.3	1126081	309763	215030_at	GRSF1
Standard	−9.19	1096503	21379	223522_at	C9orf45
Standard	−8.95	1529340	−99	Lymph_Dx_061_at	
Standard	−8.88	1138128	390428	216199_s_at	MAP3K4

TABLE 2402-continued

BL vs. GCB					
Standard	−8.8	1099152	351247	227064_at	MGC15396
Standard	−8.69	1133757	6113	207320_x_at	STAU
Standard	−8.54	1116593	422889	230329_s_at	NUDT6
Standard	−8.4	1130926	508741	201310_s_at	C5orf13
Standard	−8.39	1135685	371282	210776_x_at	TCF3
Standard	−8.39	1140520	11747	221741_s_at	C20orf21
Standard	−8.34	1119802	7370	202522_at	PITPNB
Standard	−8.31	1096149	410205	222824_at	NUDT5
Standard	−8.23	1124786	22370	212847_at	NEXN
Standard	−8.07	1098012	355669	225756_at	CSNK1E
Standard	−7.89	1116317	526415	228661_s_at	
Standard	−7.86	1109195	416155	238853_at	
Standard	−7.71	1134880	168799	209265_s_at	METTL3
Standard	−7.66	1529298	136707	Lymph_Dx_016_at	
Standard	−7.55	1128660	413071	219471_at	C13orf18
Standard	−7.55	1138973	11270	218097_s_at	C10orf66
Standard	−7.46	1127294	421986	217028_at	CXCR4
Standard	7.47	1134270	352119	208284_x_at	GGT1
Standard	7.48	1120743	79197	204440_at	CD83
Standard	7.5	1098179	163725	225956_at	LOC153222
Standard	7.55	1121400	223474	205599_at	TRAF1
Standard	7.59	1114967	7905	223028_s_at	SNX9
Standard	7.6	1122087	72927	206693_at	IL7
Standard	7.64	1101905	170843	230345_at	
Standard	7.77	1120700	410745	204362_at	SCAP2
Standard	7.8	1120572	84	204116_at	IL2RG
Standard	7.84	1098271	300670	226056_at	CDGAP
Standard	7.9	1115073	131315	223220_s_at	BAL
Standard	7.9	1133210	434374	205842_s_at	JAK2
Standard	8	1129269	62919	220358_at	SNFT
Standard	8.01	1131940	1103	203085_s_at	TGFB1
Standard	8.07	1098506	193400	226333_at	IL6R
Standard	8.13	1120601	441129	204166_at	KIAA0963
Standard	8.21	1102540	434881	231093_at	FCRH3
Standard	8.24	1121695	511759	206082_at	HCP5
Standard	8.33	1136877	409934	212998_x_at	HLA-DQB1
Standard	8.37	1100138	278391	228234_at	TIRP
Standard	8.46	1126293	504816	215346_at	TNFRSF5
Standard	8.46	1127805	380627	217947_at	CKLFSF6
Standard	8.59	1136573	914	211991_s_at	HLA-DPA1
Standard	8.62	1119111	35052	200804_at	TEGT
Standard	8.7	1136329	132739	211675_s_at	HIC
Standard	8.74	1123690	111805	210176_at	TLR1
Standard	8.81	1138677	390440	217436_x_at	
Standard	8.89	1113993	131811	244286_at	
Standard	8.89	1132651	439767	204529_s_at	TOX
Standard	8.91	1119566	433506	201954_at	ARPC1B
Standard	9.01	1128626	501452	219424_at	EBI3
Standard	9.17	1101272	179089	229584_at	DKFZp434H2111
Standard	9.33	1136777	387679	212671_s_at	HLA-DQA1
Standard	9.33	1109756	530304	239453_at	
Standard	9.4	1136216	512152	211528_x_at	HLA-G
Standard	9.4	1124381	440808	212288_at	FNBP1
Standard	9.46	1099680	210387	227677_at	JAK3
Standard	9.49	1109913	355724	239629_at	CFLAR
Standard	9.55	1132636	306278	204490_s_at	CD44
Standard	9.59	1119243	440165	201171_at	ATP6V0E
Standard	9.72	1101149	517226	229437_at	BIC
Standard	9.8	1130674	381008	200905_x_at	HLA-E
Standard	10.34	1119939	170087	202820_at	AHR
Standard	10.44	1132883	432453	205027_s_at	MAP3K8
Standard	10.74	1121452	227817	205681_at	BCL2A1
Standard	10.84	1137360	429658	214196_s_at	CLN2
Standard	12.08	1132520	283063	204249_s_at	LMO2
Standard	12.33	1131497	114931	202295_s_at	CTSH
Standard	13.58	1123163	421342	208991_at	STAT3
Lymph Node	−9.1	1138136	433574	216215_s_at	RBM9
Lymph Node	8.78	1130121	411958	221978_at	HLA-F
Lymph Node	9.22	1139830	221851	220330_s_at	SAMSN1
Lymph Node	9.23	1131705	386467	202638_s_at	ICAM1
Lymph Node	9.62	1130168	75626	222061_at	CD58
Lymph Node	9.66	1121844	83077	206295_at	IL18
Lymph Node	9.68	1121000	519033	204924_at	TLR2
Lymph Node	9.83	1102437	437023	230966_at	IL4I1

TABLE 2402-continued

BL vs. GCB

Lymph Node	10.71	1119475	296323	201739_at	SGK
Lymph Node	11.09	1131786	375957	202803_s_at	ITGB2
Proliferation	−11.07	1133141	344524	205677_s_at	DLEU1
Proliferation	−10.04	1138259	89525	216484_x_at	HDGF
Proliferation	−9.74	1131578	202453	202431_s_at	MYC
Proliferation	−9.45	1137449	223745	214363_s_at	MATR3
Proliferation	−9.43	1130468	166463	200594_x_at	HNRPU
Proliferation	−9.21	1138157	82563	216251_s_at	KIAA0153
Proliferation	−9.15	1127756	313544	217850_at	NS
Proliferation	−9	1130433	246112	200058_s_at	U5-200KD
Proliferation	−8.76	1123108	108112	208828_at	POLE3
Proliferation	−8.75	1128738	335550	219581_at	MGC2776
Proliferation	−8.74	1122400	439911	207199_at	TERT
Proliferation	−8.66	1097948	69476	225684_at	LOC348235
Proliferation	−8.6	1119460	76122	201696_at	SFRS4
Proliferation	−8.6	1136401	27258	211761_s_at	SIP
Proliferation	−8.58	1099088	14355	226996_at	
Proliferation	−8.51	1134653	253536	208901_s_at	TOP1
Proliferation	−8.49	1140584	294083	221932_s_at	C14orf87
Proliferation	−8.43	1121309	23642	205449_at	HSU79266
Proliferation	−8.43	1120385	36708	203755_at	BUB1B
Proliferation	−8.38	1136710	75782	212429_s_at	GTF3C2
Proliferation	−8.36	1136605	448398	212064_x_at	MAZ
Proliferation	−8.24	1120697	323462	204355_at	DHX30
Proliferation	−8.19	1127833	382044	218001_at	MRPS2
Proliferation	−8.11	1096903	437460	224185_at	FLJ10385
Proliferation	−8.1	1120596	4854	204159_at	CDKN2C
Proliferation	−8.1	1120779	28853	204510_at	CDC7

	Standard	Lymph Node	Proliferation		
Mean BL	1098.69	576.05	−2392.12	Cut 1	0.09
Mean GCB	2187.37	768.53	−2129.35	Cut 2	0.53
Covariance BL	75263.67	12684.43	15734.77		
	12684.43	2650.81	2358.05		
	15734.77	2358.05	4653.00		
Covariance GCB	50548.22	9301.12	14182.83		
	9301.12	2602.51	3028.21		
	14182.83	3028.21	5983.04		

TABLE 2403

BL vs. PMBL

Signature	Scale	UNIQID	Unigene ID Build 167	Probe set	Gene Symbol
Standard	−13.54	1099444	434489	227407_at	FLJ90013
Standard	−13.42	1096503	21379	223522_at	C9orf45
Standard	−13.36	1130114	445084	221965_at	MPHOSPH9
Standard	−13.27	1124786	22370	212847_at	NEXN
Standard	−13.27	1134582	78202	208794_s_at	SMARCA4
Standard	−12.37	1096149	410205	222824_at	NUDT5
Standard	−11.95	1130855	77515	201189_s_at	ITPR3
Standard	−11.66	1529298	136707	Lymph_Dx_016_at	
Standard	−11.35	1131246	153752	201853_s_at	CDC25B
Standard	−11.17	1136925	436939	213154_s_at	BICD2
Standard	−11.08	1124188	282346	211987_at	TOP2B
Standard	−11.06	1133998	76884	207826_s_at	ID3
Standard	−10.76	1139266	76640	218723_s_at	RGC32
Standard	−10.74	1134880	168799	209265_s_at	METTL3
Standard	−10.69	1140520	11747	221741_s_at	C20orf21
Standard	−10.6	1109545	63187	239231_at	
Standard	−10.55	1106043	266331	235372_at	FREB
Standard	−10.52	1110214	144519	239964_at	TCL6
Standard	−10.49	1098592	283707	226431_at	ALS2CR13
Standard	−10.45	1109220	445977	238880_at	GTF3A
Standard	−10.41	1131263	249955	201877_s_at	PPP2R5C
Standard	10.54	1122772	66742	207900_at	CCL17
Standard	10.59	1109913	355724	239629_at	CFLAR
Standard	10.82	1119884	418004	202716_at	PTPN1

TABLE 2403-continued

BL vs. PMBL					
Standard	10.83	1135189	137569	209863_s_at	TP73L
Standard	10.89	1123437	73090	209636_at	NFKB2
Standard	11.15	1124381	440808	212288_at	FNBP1
Standard	11.26	1108237	126232	237753_at	
Standard	11.34	1101149	517226	229437_at	BIC
Standard	11.77	1139774	15827	220140_s_at	SNX11
Standard	11.87	1123163	421342	208991_at	STAT3
Standard	11.93	1129269	62919	220358_at	SNFT
Standard	12.03	1132636	306278	204490_s_at	CD44
Standard	12.1	1138677	390440	217436_x_at	
Standard	12.2	1139950	437385	220731_s_at	FLJ10420
Standard	12.25	1134270	352119	208284_x_at	GGT1
Standard	12.27	1136216	512152	211528_x_at	HLA-G
Standard	12.79	1121400	223474	205599_at	TRAF1
Standard	12.82	1119939	170087	202820_at	AHR
Standard	13.12	1126293	504816	215346_at	TNFRSF5
Standard	13.44	1100138	278391	228234_at	TIRP
Standard	13.74	1132883	432453	205027_s_at	MAP3K8
Standard	13.94	1131497	114931	202295_s_at	CTSH
Standard	14.15	1121762	32970	206181_at	SLAMF1
Standard	14.51	1132520	283063	204249_s_at	LMO2
Standard	14.68	1121452	227817	205681_at	BCL2A1
Standard	15.24	1105178	283961	234284_at	GNG8
Lymph Node	10.95	1121205	2488	205269_at	LCP2
Lymph Node	11.22	1140845	21486	AFFX-HUMISGF3A/M97935_3_at	STAT1
Lymph Node	11.45	1131068	118400	201564_s_at	FSCN1
Lymph Node	11.92	1131705	386467	202638_s_at	ICAM1
Lymph Node	12.06	1131038	81328	201502_s_at	NFKBIA
Lymph Node	12.49	1121444	153563	205668_at	LY75
Lymph Node	13.01	1123457	446304	209684_at	RIN2
Lymph Node	13.19	1140404	354740	221584_s_at	KCNMA1
Lymph Node	13.26	1124875	18166	212975_at	KIAA0870
Lymph Node	14.06	1102437	437023	230966_at	IL4I1
Lymph Node	14.11	1132766	82359	204781_s_at	TNFRSF6
Lymph Node	15.31	1121767	458324	206187_at	PTGIR
Lymph Node	15.32	1135871	104717	211031_s_at	CYLN2
Lymph Node	15.34	1138652	444471	217388_s_at	KYNU
Lymph Node	16.01	1139830	221851	220330_s_at	SAMSN1

	Standard	Lymph Node		
Mean BL	−66.97	1445.63	Cut 1	0.20
Mean PMBL	1205.38	2041.25	Cut 2	0.80
Covariance BL	35263.67	13424.88		
	13424.88	7458.56		
Covariance PMBL	12064.38	5113.74		
	5113.74	3216.53		

TABLE 2404

FH vs. DLBCL-BL					
Signature	Scale	UNIQID	Unigene ID Build 167	Probe set	Gene Symbol
Standard	−12.81	1104910	458262	233969_at	IGL@
Standard	−11.54	1102898	145519	231496_at	FKSG87
Standard	−11.46	1117298	449586	234366_x_at	
Standard	−11.46	1132973	169294	205255_x_at	TCF7
Standard	−11.22	1133099	88646	205554_s_at	DNASE1L3
Standard	−10.76	1131531	153647	202350_s_at	MATN2
Standard	−10.59	1124283	406612	212144_at	UNC84B
Standard	−10.35	1099847	36723	227867_at	LOC129293
Standard	−10.22	1136430	102950	211798_x_at	IGLJ3
Standard	−10.05	1117394	−13	234792_x_at	
Standard	−9.95	1133047	528338	205434_s_at	AAK1
Standard	−9.95	1098865	250905	226741_at	LOC51234
Standard	−9.82	1108515	98132	238071_at	LCN6
Standard	−9.8	1131407	154248	202125_s_at	ALS2CR3
Standard	−9.77	1128469	390817	219173_at	FLJ22686

TABLE 2404-continued

FH vs. DLBCL-BL

Standard	−9.7	1123875	428	210607_at	FLT3LG
Standard	−9.69	1131875	169172	202965_s_at	CAPN6
Standard	−9.69	1135173	3781	209841_s_at	LRRN3
Standard	−9.48	1099798	411081	227811_at	FGD3
Standard	−9.41	1119046	349499	200606_at	DSP
Standard	−9.36	1122449	278694	207277_at	CD209
Standard	−9.34	1114017	133255	244313_at	
Standard	−9.34	1122767	652	207892_at	TNFSF5
Standard	−9.24	1123369	79025	209481_at	SNRK
Standard	−9.16	1098954	128905	226844_at	MOBKL2B
Standard	−9.14	1135513	421437	210481_s_at	CD209L
Standard	−9.08	1100904	426296	229145_at	LOC119504
Standard	−8.99	1122738	81743	207840_at	CD160
Standard	−8.94	1120925	204891	204773_at	IL11RA
Standard	9.09	1123055	185726	208691_at	TFRC
Standard	9.62	1134858	405954	209226_s_at	TNPO1
Standard	10.19	1123052	180909	208680_at	PRDX1
Standard	10.81	1124178	446579	211969_at	HSPCA
Lymph Node	−10.59	1137597	3903	214721_x_at	CDC42EP4
Lymph Node	−9.69	1119684	439586	202242_at	TM4SF2
Lymph Node	−9.25	1125593	8910	214180_at	MAN1C1
Lymph Node	−8.44	1124318	21858	212190_at	SERPINE2
Lymph Node	−8.09	1119448	212296	201656_at	ITGA6
Lymph Node	−8.07	1125546	125036	214081_at	PLXDC1
Lymph Node	−7.7	1097683	132569	225373_at	PP2135
Lymph Node	−7.56	1101305	112742	229623_at	
Lymph Node	7.45	1135240	436852	209955_s_at	FAP
Proliferation	6.97	1135101	20830	209680_s_at	KIFC1
Proliferation	7.03	1130426	432607	200039_s_at	PSMB2
Proliferation	7.04	1130501	2795	200650_s_at	LDHA
Proliferation	7.08	1130744	158688	201027_s_at	EIF5B
Proliferation	7.23	1137506	75258	214501_s_at	H2AFY
Proliferation	7.32	1131474	95577	202246_s_at	CDK4
Proliferation	7.39	1130871	159087	201222_s_at	RAD23B
Proliferation	7.42	1119375	381072	201489_at	PPIF
Proliferation	7.47	1136595	404814	212038_s_at	VDAC1
Proliferation	7.7	1135858	90093	211015_s_at	HSPA4
Proliferation	7.78	1130527	184233	200692_s_at	HSPA9B
Proliferation	7.78	1130820	151777	201144_s_at	EIF2S1
Proliferation	7.83	1115829	433213	225253_s_at	METTL2
Proliferation	7.84	1134699	439683	208974_x_at	KPNB1
Proliferation	7.87	1120274	31584	203517_at	MTX2
Proliferation	7.92	1136786	63788	212694_s_at	PCCB
Proliferation	7.95	1097172	434886	224753_at	CDCA5
Proliferation	8.4	1138537	−12	217140_s_at	
Proliferation	8.53	1119488	154672	201761_at	MTHFD2
Proliferation	8.58	1130799	233952	201114_x_at	PSMA7
Proliferation	8.72	1135673	82159	210759_s_at	PSMA1
Proliferation	9.4	1114679	16470	222503_s_at	FLJ10904

	Standard	Lymph Node	Proliferation		
Mean FH	−2193.59	−588.21	1571.78	Cut 1	0.50
Mean DLBCL-BL	−1448.27	−441.91	1735.00	Cut 2	0.92
Covariance FH	6729.73	1223.99	2541.22		
	1223.99	405.22	293.72		
	2541.22	293.72	1797.58		
Covariance DLBCL-BL	17675.23	3642.41	4158.43		
	3642.41	1379.81	1066.48		
	4158.43	1066.48	2858.21		

TABLE 2405

FH vs. FL

Signature	Scale	UNIQID	Unigene ID Build 167	Probe set	Gene Symbol
Standard	−11.23	1117298	449586	234366_x_at	
Standard	−10.62	1121953	38365	206478_at	KIAA0125
Standard	−10.6	1104910	458262	233969_at	IGL@

TABLE 2405-continued

FH vs. FL					
Standard	−10.39	1136430	102950	211798_x_at	IGLJ3
Standard	−9.96	1129281	395486	220377_at	C14orf110
Standard	−9.73	1118835	102336	47069_at	ARHGAP8
Standard	−9.21	1127807	7236	217950_at	NOSIP
Standard	−9.05	1128377	371003	219014_at	PLAC8
Standard	−8.85	1101004	2969	229265_at	SKI
Standard	9.06	1139411	368238	219073_s_at	OSBPL10
Standard	9.07	1120789	154729	204524_at	PDPK1
Standard	9.21	1136464	159428	211833_s_at	BAX
Standard	9.29	1125279	445652	213575_at	TRA2A
Standard	9.45	1529390	79241	Lymph_Dx_120_at	BCL2
Standard	9.52	1132022	173911	203247_s_at	ZNF24
Standard	9.57	1139645	134051	219757_s_at	C14orf101
Standard	9.64	1137561	67397	214639_s_at	HOXA1
Standard	9.66	1114893	314623	222891_s_at	BCL11A
Standard	10.38	1098095	131059	225852_at	ANKRD17
Standard	10.4	1134858	405954	209226_s_at	TNPO1
Standard	12.65	1101054	173328	229322_at	PPP2R5E
Standard	12.79	1124178	446579	211969_at	HSPCA
Standard	13.34	1135489	288178	210438_x_at	SSA2

	Standard		
Mean FH	136.43	Cut 1	0.50
Mean FL	640.38	Cut 2	0.99
Covariance FH	10719.40		
Covariance FL	9373.11		

TABLE 2406

FH vs. MCL					
Signature	Scale	UNIQID	Unigene ID Build 167	Probe set	Gene Symbol
Standard	13.05	1100258	88442	228377_at	KIAA1384
Standard	13.43	1529382	371468	Lymph_Dx_111_at	CCND1
Standard	13.54	1106855	455101	236255_at	KIAA1909
Standard	13.73	1529308	193014	Lymph_Dx_027_x_at	
Standard	14.56	1100873	445884	229103_at	
Standard	21.12	1132834	432638	204914_s_at	SOX11
Lymph Node	−8.44	1130378	234434	44783_s_at	HEY1
Lymph Node	−7.92	1123552	423077	209879_at	SELPLG
Lymph Node	−7.7	1131218	76753	201809_s_at	ENG
Lymph Node	−7.4	1097683	132569	225373_at	PP2135
Lymph Node	−7.15	1136273	13775	211597_s_at	HOP
Lymph Node	14.16	1134532	371468	208711_s_at	CCND1

	Standard	Lymph Node		
Mean FH	451.68	−282.65	Cut 1	0.20
Mean MCFL	863.16	−156.82	Cut 2	0.80
Covariance FH	1617.92	222.89		
	222.89	271.65		
Covariance MCL	3154.38	917.30		
	917.30	659.94		

TABLE 2407

FH vs. SLL					
Signature	Scale	UNIQID	Unigene ID Build 167	Probe set	Gene Symbol
Standard	−13.14	1120765	343329	204484_at	PIK3C2B
Standard	−12.9	1097897	266175	225622_at	PAG
Standard	12.72	1133195	274243	205805_s_at	ROR1
Standard	12.74	1140416	58831	221601_s_at	TOSO
Standard	13.53	1131687	369280	202606_s_at	TLK1
Standard	13.57	1107044	163426	236458_at	

TABLE 2407-continued

FH vs. SLL

Standard	14.43	1529389	79241	Lymph_Dx_119_at	BCL2
Standard	14.51	1129026	135146	220007_at	FLJ13984
Standard	14.77	1136987	21695	213370_s_at	SFMBT1
Standard	14.79	1137109	469653	213689_x_at	RPL5
Standard	15.37	1529308	193014	Lymph_Dx_027_x_at	
Standard	15.82	1120832	57856	204604_at	PFTK1
Standard	17.37	1135550	221811	210550_s_at	RASGRF1
Standard	18.98	1122864	434384	208195_at	TTN
Lymph Node	−12.89	1123038	119000	208636_at	ACTN1
Lymph Node	−12.8	1130378	234434	44783_s_at	HEY1
Lymph Node	−11.59	1124875	18166	212975_at	KIAA0870
Lymph Node	−11.47	1103497	50115	232231_at	
Lymph Node	−10.31	1099358	93135	227300_at	
Lymph Node	−10.27	1121129	285401	205159_at	CSF2RB
Lymph Node	−10.23	1100249	388674	228367_at	HAK
Lymph Node	−10.05	1132345	109225	203868_s_at	VCAM1
Lymph Node	−9.93	1123401	50130	209550_at	NDN
Lymph Node	−9.75	1120500	82568	203979_at	CYP27A1
Lymph Node	−9.57	1124318	21858	212190_at	SERPINE2
Lymph Node	−9.48	1120288	17483	203547_at	CD4
Lymph Node	−9.45	1123372	195825	209487_at	RBPMS
Lymph Node	−9.39	1123376	37682	209496_at	RARRES2
Lymph Node	−9.29	1123213	12956	209154_at	TIP-1
Lymph Node	−9.23	1098412	409515	226225_at	MCC
Lymph Node	−9.23	1125593	8910	214180_at	MAN1C1
Lymph Node	−9.17	1131786	375957	202803_s_at	ITGB2
Lymph Node	−9.04	1097683	132569	225373_at	PP2135
Lymph Node	−8.91	1097255	380144	224861_at	
Lymph Node	−8.76	1131068	118400	201564_s_at	FSCN1
Lymph Node	−8.7	1119074	54457	200675_at	CD81
Lymph Node	−8.68	1125130	35861	213338_at	RIS1
Lymph Node	−8.59	1139661	416456	219806_s_at	FN5

	Standard	Lymph Node		
Mean FH	1144.02	−2223.71	Cut 1	0.20
Mean SLL	1592.27	−1798.11	Cut 2	0.80
Covariance FH	902.56	442.69		
	442.69	809.90		
Covariance SLL	2426.26	2938.58		
	2938.58	9435.72		

TABLE 2408

FL vs. DLBCL-BL

Signature	Scale	UNIQID	Unigene ID Build 167	Probe set	Gene Symbol
Standard	−23.03	1124833	356416	212914_at	CBX7
Standard	−22.25	1099204	193784	227121_at	
Standard	−22.2	1119766	93231	202423_at	MYST3
Standard	−22.04	1099798	411081	227811_at	FGD3
Standard	−22.01	1102898	145519	231496_at	FKSG87
Standard	−21.79	1131197	269902	201778_s_at	KIAA0494
Standard	−21.69	1098415	130900	226230_at	KIAA1387
Standard	−21.57	1120834	57907	204606_at	CCL21
Standard	−21.39	1130155	436657	222043_at	CLU
Standard	−20.98	1100904	426296	229145_at	LOC119504
Standard	−20.8	1131531	153647	202350_s_at	MATN2
Standard	−20.72	1137582	433732	214683_s_at	CLK1
Standard	−20.66	1119782	155418	202478_at	TRB2
Standard	−20.59	1122767	652	207892_at	TNFSF5
Standard	−20.58	1125001	16193	213158_at	
Standard	−20.56	1134921	413513	209341_s_at	IKBKB
Standard	−20.56	1132973	169294	205255_x_at	TCF7
Standard	−20.53	1136984	498154	213364_s_at	SNX1
Standard	−20.41	1115888	35096	225629_s_at	ZBTB4
Standard	−20.37	1120160	436976	203288_at	KIAA0355
Standard	−20.36	1139054	25726	218263_s_at	LOC58486
Standard	−20.31	1130030	301872	221834_at	LONP
Standard	−20.08	1133024	436987	205383_s_at	ZNF288

TABLE 2408-continued

FL vs. DLBCL-BL					
Standard	−20.05	1124666	526394	212672_at	ATM
Standard	−19.3	1529397	406557	Lymph_Dx_127_s_at	CLK4
Standard	−19.16	1116056	243678	226913_s_at	SOX8
Standard	−19.14	1098433	202577	226250_at	
Standard	−19.1	1123635	408614	210073_at	SIAT8A
Standard	−18.95	1138920	24395	218002_s_at	CXCL14
Standard	−18.84	1133099	88646	205554_s_at	DNASE1L3
Standard	−18.83	1098495	443668	226318_at	TBRG1
Standard	−18.64	1100879	119983	229111_at	MASP2
Standard	−18.59	1120695	385685	204352_at	TRAF5
Standard	−18.55	1119983	409783	202920_at	ANK2
Standard	−18.5	1101276	1098	229588_at	ERdj5
Standard	−18.47	1099140	500350	227052_at	
Standard	−18.46	1529331	374126	Lymph_Dx_051_s_at	
Standard	−18.45	1131752	170133	202724_s_at	FOXO1A
Standard	−18.45	1099265	375762	227193_at	
Standard	−18.32	1098179	163725	225956_at	LOC153222
Standard	−18.29	1119568	269777	201957_at	PPP1R12B
Standard	−18.19	1099900	444508	227934_at	
Standard	−18.17	1119361	391858	201448_at	TIA1
Standard	−18.02	1121650	421137	206002_at	GPR64
Standard	−17.91	1100911	320147	229152_at	C4orf7
Standard	−17.86	1529285	348929	Lymph_Dx_002_at	KIAA1219
Standard	−17.47	1529357	444651	Lymph_Dx_081_at	
Standard	−17.42	1131863	2316	202936_s_at	SOX9
Standard	−17.16	1129943	512828	221626_at	ZNF506
Standard	−17.12	1121301	449971	205437_at	ZNF134
Standard	−17.11	1131340	437457	202018_s_at	LTF
Standard	−17.1	1124606	444324	212588_at	PTPRC
Standard	−17.08	1131407	154248	202125_s_at	ALS2CR3
Standard	−16.97	1118939	198161	60528_at	PLA2G4B
Standard	−16.91	1134738	75842	209033_s_at	DYRK1A
Standard	−16.9	1134083	285091	207996_s_at	C18orf1
Standard	−16.89	1120925	204891	204773_at	IL11RA
Standard	−16.86	1110070	−101	239803_at	
Standard	−16.83	1100042	351413	228113_at	RAB37
Standard	−16.82	1120134	75545	203233_at	IL4R
Standard	−16.75	1124283	406612	212144_at	UNC84B
Standard	−16.72	1109603	−100	239292_at	
Standard	−16.71	1120509	155090	204000_at	GNB5
Standard	−16.65	1133538	1416	206760_s_at	FCER2
Standard	−16.64	1130735	179526	201009_s_at	TXNIP
Standard	−16.59	1100150	9343	228248_at	MGC39830
Standard	−16.54	1124237	258855	212080_at	MLL
Standard	−16.51	1124416	283604	212331_at	RBL2
Standard	−16.48	1133091	73792	205544_s_at	CR2
Standard	−16.46	1131263	249955	201877_s_at	PPP2R5C
Standard	−16.44	1118347	528404	243366_s_at	ITGA4
Standard	−16.43	1529343	521948	Lymph_Dx_064_at	
Standard	−16.43	1099549	446665	227533_at	
Standard	17.05	1529453	372679	Lymph_Dx_085_at	FCGR3A
Standard	17.41	1097540	388087	225195_at	
Standard	18.47	1140473	17377	221676_s_at	CORO1C
Standard	18.55	1121100	301921	205098_at	CCR1
Standard	20.07	1124254	301743	212110_at	SLC39A14
Standard	20.2	1130771	61153	201068_s_at	PSMC2
Standard	21.46	1137583	273415	214687_x_at	ALDOA
Standard	21.55	1098168	22151	225943_at	NLN
Standard	24.07	1123055	185726	208691_at	TFRC
Standard	24.09	1123052	180909	208680_at	PRDX1
Lymph Node	−20.5	1137597	3903	214721_x_at	CDC42EP4
Lymph Node	−18.52	1124318	21858	212190_at	SERPINE2
Lymph Node	−18.5	1136762	380138	212624_s_at	CHN1
Lymph Node	−18.07	1101305	112742	229623_at	
Lymph Node	−17.75	1100249	388674	228367_at	HAK
Lymph Node	−16.1	1098412	409515	226225_at	MCC
Lymph Node	−15.51	1140464	111676	221667_s_at	HSPB8
Lymph Node	−15.43	1136832	434959	212842_x_at	RANBP2L1
Lymph Node	−15.37	1119684	439586	202242_at	TM4SF2
Lymph Node	−15.02	1097448	250607	225093_at	UTRN
Lymph Node	−14.83	1136844	16007	212875_s_at	C21orf25
Lymph Node	−14.73	1135056	169946	209604_s_at	GATA3
Lymph Node	−14.48	1097202	386779	224796_at	DDEF1

TABLE 2408-continued

FL vs. DLBCL-BL					
Lymph Node	−14.44	1121278	21355	205399_at	DCAMKL1
Lymph Node	−14.22	1125009	27621	213169_at	
Lymph Node	−13.97	1100288	26981	228411_at	ALS2CR19
Lymph Node	−13.51	1132462	14845	204131_s_at	FOXO3A
Lymph Node	−13.37	1135322	450230	210095_s_at	IGFBP3
Lymph Node	−13.35	1097280	423523	224891_at	
Lymph Node	−12.86	1137097	20107	213656_s_at	KNS2
Lymph Node	−12.85	1098809	359394	226682_at	
Lymph Node	−12.28	1124875	18166	212975_at	KIAA0870
Lymph Node	−12.18	1132345	109225	203868_s_at	VCAM1
Lymph Node	−12	1097561	19221	225224_at	DKFZP566G1424
Lymph Node	−11.71	1123401	50130	209550_at	NDN
Lymph Node	−11.04	1136996	283749	213397_x_at	RNASE4
Lymph Node	−10.77	1136788	355455	212698_s_at	36778
Lymph Node	−10.71	1098822	443452	226695_at	PRRX1
Lymph Node	−10.63	1134200	90786	208161_s_at	ABCC3
Lymph Node	−10.47	1136427	276506	211795_s_at	FYB
Lymph Node	−10.46	1121186	100431	205242_at	CXCL13
Lymph Node	−10.39	1099332	32433	227272_at	
Lymph Node	−10.39	1098978	124863	226869_at	
Lymph Node	−10.22	1103303	49605	232000_at	C9orf52
Lymph Node	−10.16	1131325	13313	201990_s_at	CREBL2
Lymph Node	−10.16	1098174	274401	225949_at	LOC340371
Lymph Node	−9.93	1124733	66762	212771_at	LOC221061
Lymph Node	−9.42	1123372	195825	209487_at	RBPMS
Lymph Node	−9.36	1132220	448805	203632_s_at	GPRC5B
Lymph Node	−9.29	1120703	83974	204368_at	SLCO2A1
Lymph Node	−9.26	1132013	434961	203232_s_at	SCA1
Lymph Node	−9.25	1097307	379754	224929_at	LOC340061
Lymph Node	−9.18	1119251	433941	201194_at	SEPW1
Lymph Node	−9.08	1097609	6093	225283_at	ARRDC4
Lymph Node	−9.07	1136459	252550	211828_s_at	KIAA0551
Lymph Node	−8.86	1132775	1027	204803_s_at	RRAD
Lymph Node	−8.78	1098946	135121	226834_at	ASAM
Lymph Node	−8.68	1140589	433488	221942_s_at	GUCY1A3
Lymph Node	−8.44	1116966	301124	232744_x_at	
Lymph Node	−8.39	1100130	76494	228224_at	PRELP
Lymph Node	−8.36	1110019	−94	239744_at	
Lymph Node	−8.3	1134647	298654	208892_s_at	DUSP6
Lymph Node	−8.28	1125593	8910	214180_at	MAN1C1
Lymph Node	7.97	1134370	1422	208438_s_at	FGR
Lymph Node	8.05	1123566	155935	209906_at	C3AR1
Lymph Node	8.09	1131119	349656	201647_s_at	SCARB2
Lymph Node	8.11	1123586	93841	209948_at	KCNMB1
Lymph Node	8.13	1128615	104800	219410_at	FLJ10134
Lymph Node	8.21	1097297	166254	224917_at	VMP1
Lymph Node	8.23	1120299	79334	203574_at	NFIL3
Lymph Node	8.37	1128157	23918	218631_at	VIP32
Lymph Node	8.4	1130054	82547	221872_at	RARRES1
Lymph Node	8.41	1098152	377588	225922_at	KIAA1450
Lymph Node	8.53	1101566	98558	229947_at	
Lymph Node	8.59	1135251	21486	209969_s_at	STAT1
Lymph Node	8.84	1099167	381105	227080_at	MGC45731
Lymph Node	9.01	1132920	753	205119_s_at	FPR1
Lymph Node	9.26	1097253	77873	224859_at	B7H3
Lymph Node	9.29	1120500	82568	203979_at	CYP27A1
Lymph Node	9.36	1131507	172928	202311_s_at	COL1A1
Lymph Node	9.38	1096456	82407	223454_at	CXCL16
Lymph Node	9.49	1136172	38084	211470_s_at	SULT1C1
Lymph Node	10.03	1138244	418138	216442_x_at	FN1
Lymph Node	10.34	1134424	−17	208540_x_at	S100A14
Lymph Node	10.48	1136152	458436	211434_s_at	CCRL2
Lymph Node	10.51	1118708	7835	37408_at	MRC2
Lymph Node	10.6	1136540	179657	211924_s_at	PLAUR
Lymph Node	10.63	1098278	166017	226066_at	MITF
Lymph Node	10.76	1119477	163867	201743_at	CD14
Lymph Node	10.81	1096429	64896	223405_at	NPL
Lymph Node	11.58	1123672	67846	210152_at	LILRB4
Lymph Node	12	1096364	29444	223276_at	NID67
Lymph Node	12.16	1119070	445570	200663_at	CD63
Lymph Node	12.3	1133065	77274	205479_s_at	PLAU
Lymph Node	12.5	1135240	436852	209955_s_at	FAP
Lymph Node	13.09	1116826	26204	231823_s_at	KIAA1295
Lymph Node	13.32	1119068	417004	200660_at	S100A11

TABLE 2408-continued

FL vs. DLBCL-BL

Lymph Node	13.45	1120266	246381	203507_at	CD68
Lymph Node	13.63	1133216	502577	205872_x_at	PDE4DIP
Lymph Node	13.67	1131815	386678	202856_s_at	SLC16A3
Lymph Node	14.38	1132132	279910	203454_s_at	ATOX1
Lymph Node	15.25	1134682	411701	208949_s_at	LGALS3
Lymph Node	15.46	1119237	389964	201141_at	GPNMB
Lymph Node	15.89	1137698	442669	215001_s_at	GLUL
Lymph Node	17.8	1137782	384944	215223_s_at	SOD2
Lymph Node	20.11	1130629	135226	200839_s_at	CTSB
Proliferation	21.02	1119375	381072	201489_at	PPIF
Proliferation	21.24	1119488	154672	201761_at	MTHFD2
Proliferation	21.31	1119467	21635	201714_at	TUBG1
Proliferation	21.68	1130820	151777	201144_s_at	EIF2S1
Proliferation	21.69	1131474	95577	202246_s_at	CDK4
Proliferation	22.2	1125249	244723	213523_at	CCNE1
Proliferation	22.97	1130501	2795	200650_s_at	LDHA
Proliferation	23.12	1136913	99962	213113_s_at	SLC43A3
Proliferation	24.05	1130426	432607	200039_s_at	PSMB2

	Standard	Lymph Node	Proliferation		
Mean FL	−11121.51	−1603.39	1890.60	Cut 1	0.34
Mean DLBCL-BL	−8760.65	−460.71	2101.10	Cut 2	0.94
Covariance FL	246359.77	111505.42	28908.20		
	111505.42	67036.17	13130.59		
	28908.20	13130.59	4617.24		
Covariance DLBCL-BL	413069.12	178811.32	30151.89		
	178811.32	106324.53	10877.26		
	30151.89	10877.26	5180.68		

TABLE 2409

FL vs. MCL

Signature	Scale	UNIQID	Unigene ID Build 167	Probe set	Gene Symbol
Standard	−24.56	1123731	17165	210258_at	RGS13
Standard	−22.56	1133192	24024	205801_s_at	RASGRP3
Standard	−21.12	1114543	156189	244887_at	
Standard	−18.49	1120090	155024	203140_at	BCL6
Standard	−18.07	1124646	436432	212646_at	RAFTLIN
Standard	−17.24	1132122	307734	203434_s_at	MME
Standard	−16.63	1105986	49614	235310_at	GCET2
Standard	−15.09	1120134	75545	203233_at	IL4R
Standard	−14.05	1132651	439767	204529_s_at	TOX
Standard	13.8	1098277	6786	226065_at	PRICKLE1
Standard	13.85	1109560	207428	239246_at	FARP1
Standard	13.86	1103504	142517	232239_at	
Standard	13.88	1132734	126248	204724_s_at	COL9A3
Standard	13.91	1115905	301478	225757_s_at	CLMN
Standard	14.89	1098840	55098	226713_at	C3orf6
Standard	14.97	1100873	445884	229103_at	
Standard	14.99	1139393	170129	219032_x_at	OPN3
Standard	16.13	1124864	411317	212960_at	KIAA0882
Standard	16.36	1106855	455101	236255_at	KIAA1909
Standard	16.43	1120858	410683	204647_at	HOMER3
Standard	17.38	1130926	508741	201310_s_at	C5orf13
Standard	18.3	1103711	288718	232478_at	
Standard	18.62	1109505	8162	239186_at	MGC39372
Standard	20.31	1132834	432638	204914_s_at	SOX11
Standard	22.61	1096070	241565	222640_at	DNMT3A
Standard	28.66	1529382	371468	Lymph_Dx_111_at	CCND1
Lymph Node	−10.77	1097202	386779	224796_at	DDEF1
Lymph Node	−10.22	1119546	433898	201921_at	GNG10
Lymph Node	−9.89	1132766	82359	204781_s_at	TNFRSF6
Lymph Node	−9.4	1138867	10706	217892_s_at	EPLIN
Lymph Node	9.65	1125025	301094	213196_at	
Lymph Node	10.44	1134797	433394	209118_s_at	TUBA3
Lymph Node	22.6	1529456	371468	Lymph_Dx_113_at	CCND1
Proliferation	−7.36	1097948	69476	225684_at	LOC348235
Proliferation	−7.31	1130747	234489	201030_x_at	LDHB

TABLE 2409-continued

FL vs. MCL

Proliferation	−6.95	1130923	459987	201306_s_at	ANP32B
Proliferation	−6.87	1120205	5198	203405_at	DSCR2
Proliferation	−6.64	1132468	79353	204147_s_at	TFDP1
Proliferation	−6.1	1119916	177584	202780_at	OXCT
Proliferation	−6.08	1119873	446393	202697_at	CPSF5
Proliferation	−6.08	1119488	154672	201761_at	MTHFD2
Proliferation	−6.04	1130658	447492	200886_s_at	PGAM1
Proliferation	−5.82	1132825	512813	204900_x_at	SAP30
Proliferation	−5.53	1115607	435733	224428_s_at	CDCA7
Proliferation	−5.44	1120316	63335	203611_at	TERF2
Proliferation	−5.34	1114970	279529	223032_x_at	PX19
Proliferation	−5.32	1140843	169476	AFFX-HUMGAPDH/M33197_5_at	GAPD
Proliferation	−5.28	1131081	180610	201586_s_at	SFPQ
Proliferation	−5.15	1121062	408658	205034_at	CCNE2
Proliferation	5.15	1120986	172052	204886_at	PLK4
Proliferation	5.16	1097195	149931	224785_at	MGC29814
Proliferation	5.2	1120011	3068	202983_at	SMARCA3
Proliferation	5.47	1100183	180582	228286_at	FLJ40869
Proliferation	5.67	1121012	96055	204947_at	E2F1
Proliferation	5.84	1115679	8345	224523_s_at	MGC4308
Proliferation	5.88	1135285	449501	210024_s_at	UBE2E3
Proliferation	5.92	1120520	35120	204023_at	RFC4
Proliferation	6.16	1529361	388681	Lymph_Dx_086_s_at	HDAC3
Proliferation	6.45	1096054	21331	222606_at	FLJ10036
Proliferation	6.45	1096738	87968	223903_at	TLR9
Proliferation	6.51	1136781	120197	212680_x_at	PPP1R14B
Proliferation	6.63	1119466	179718	201710_at	MYBL2
Proliferation	6.65	1136285	182490	211615_s_at	LRPPRC
Proliferation	6.67	1136853	66170	212922_s_at	SMYD2
Proliferation	7.45	1119390	77254	201518_at	CBX1
Proliferation	8.87	1116122	42768	227408_s_at	DKFZp761O0113
Proliferation	10.12	1119515	3352	201833_at	HDAC2

	Standard	Lymph Node	Proliferation		
Mean FL	−18.82	−33.90	23.53	Cut 1	0.14
Mean MCL	1558.10	113.95	165.48	Cut 2	0.58
Covariance FL	21302.14	1098.24	678.04		
	1098.24	226.29	75.99		
	678.04	75.99	315.67		
Covariance MCL	81008.29	5261.37	9185.20		
	5261.37	2047.34	875.56		
	9185.20	875.56	1447.43		

TABLE 2410

FL vs. SLL

Signature	Scale	UNIQID	Unigene ID Build 167	Probe set	Gene Symbol
Standard	−21.04	1123731	17165	210258_at	RGS13
Standard	−20.91	1124646	436432	212646_at	RAFTLIN
Standard	−18.82	1099651	120785	227646_at	EBF
Standard	−18.12	1114543	156189	244887_at	
Standard	−17.85	1105986	49614	235310_at	GCET2
Standard	−16.73	1100911	320147	229152_at	C4orf7
Standard	−15.77	1132122	307734	203434_s_at	MME
Standard	−15.12	1120090	155024	203140_at	BCL6
Standard	−14.89	1097897	266175	225622_at	PAG
Standard	−14.36	1529343	521948	Lymph_Dx_064_at	
Standard	−14.32	1529318	291954	Lymph_Dx_038_at	
Standard	−14.06	1128694	171466	219517_at	ELL3
Standard	−13.61	1101586	187884	229971_at	GPR114
Standard	−13.57	1119752	511745	202391_at	BASP1
Standard	−13.13	1137561	67397	214639_s_at	HOXA1
Standard	−12.85	1097247	388761	224851_at	CDK6
Standard	−12.43	1529344	317970	Lymph_Dx_065_at	SERPINA11
Standard	−12.4	1120765	343329	204484_at	PIK3C2B
Standard	−12.33	1130155	436657	222043_at	CLU
Standard	−12.07	1529292	−92	Lymph_Dx_010_at	

TABLE 2410-continued

FL vs. SLL					
Standard	−12.01	1119939	170087	202820_at	AHR
Standard	−11.82	1119919	199263	202786_at	STK39
Standard	−11.77	1099686	117721	227684_at	
Standard	−11.63	1119782	155418	202478_at	TRB2
Standard	10.97	1529309	512797	Lymph_Dx_028_at	HSH2
Standard	10.97	1139393	170129	219032_x_at	OPN3
Standard	11.04	1131246	153752	201853_s_at	CDC25B
Standard	11.07	1140391	44865	221558_s_at	LEF1
Standard	11.16	1140416	58831	221601_s_at	TOSO
Standard	11.35	1127807	7236	217950_at	NOSIP
Standard	11.67	1529317	−98	Lymph_Dx_037_at	
Standard	11.81	1117343	306812	234643_x_at	BUCS1
Standard	11.82	1102081	506977	230551_at	
Standard	11.82	1135042	79015	209582_s_at	MOX2
Standard	11.96	1132734	126248	204724_s_at	COL9A3
Standard	12.09	1137109	469653	213689_x_at	RPL5
Standard	12.14	1099939	488173	227983_at	MGC7036
Standard	12.19	1129103	99430	220118_at	TZFP
Standard	12.47	1135592	758	210621_s_at	RASA1
Standard	12.78	1108970	140489	238604_at	
Standard	12.92	1097143	74335	224716_at	HSPCB
Standard	13.18	1136865	412128	212959_s_at	MGC4170
Standard	13.96	1098220	80720	226002_at	GAB1
Standard	14.06	1100847	97411	229070_at	C6orf105
Standard	14.39	1098865	250905	226741_at	LOC51234
Standard	15.57	1136687	59943	212345_s_at	CREB3L2
Standard	15.75	1107044	163426	236458_at	
Standard	16.52	1123622	8578	210051_at	EPAC
Standard	17.74	1136987	21695	213370_s_at	SFMBT1
Standard	19.15	1129026	135146	220007_at	FLJ13984
Standard	19.65	1131854	414985	202923_s_at	GCLC
Lymph Node	−14.99	1124875	18166	212975_at	KIAA0870
Lymph Node	−14.33	1099358	93135	227300_at	
Lymph Node	−13.26	1121129	285401	205159_at	CSF2RB
Lymph Node	−12.61	1119074	54457	200675_at	CD81
Lymph Node	−12.52	1121029	412999	204971_at	CSTA
Lymph Node	−11.48	1137247	234734	213975_s_at	LYZ
Lymph Node	−10.97	1128781	79741	219648_at	FLJ10116
Lymph Node	11.79	1119880	442844	202709_at	FMOD
Lymph Node	14.4	1134370	1422	208438_s_at	FGR

	Standard	Lymph Node		
Mean FL	−663.95	−730.08	Cut 1	0.20
Mean SLL	1332.84	−484.93	Cut 2	0.80
Covariance FL	37097.15	1710.73		
	1710.73	663.78		
Covariance SLL	85989.25	17661.52		
	17661.52	4555.06		

TABLE 2411

GCB vs. PMBL					
Signature	Scale	UNIQID	Unigene ID Build 167	Probe set	Gene Symbol
Standard	−8.39	1096440	231320	223423_at	GPR160
Standard	−8.13	1096108	292871	222731_at	ZDHHC2
Standard	−8.12	1125231	446375	213489_at	MAPRE2
Standard	−8.02	1136759	188882	212605_s_at	
Standard	−7.91	1096499	293867	223514_at	CARD11
Standard	−7.8	1099388	124024	227336_at	DTX1
Standard	−7.71	1139623	193736	219667_s_at	BANK1
Standard	−7.68	1098592	283707	226431_at	ALS2CR13
Standard	−7.67	1107575	424589	237033_at	MGC52498
Standard	−7.63	1116829	115467	231840_x_at	LOC90624
Standard	−7.42	1130114	445084	221965_at	MPHOSPH9
Standard	−7.27	1098909	446408	226789_at	

TABLE 2411-continued

GCB vs. PMBL					
Standard	7.34	1138759	396404	217707_x_at	SMARCA2
Standard	7.37	1120355	80420	203687_at	CX3CL1
Standard	7.4	1134270	352119	208284_x_at	GGT1
Standard	7.44	1115441	5470	224156_x_at	IL17RB
Standard	7.78	1103054	341531	231690_at	
Standard	7.91	1119765	81234	202421_at	IGSF3
Standard	7.92	1119438	118110	201641_at	BST2
Standard	8.09	1135645	31439	210715_s_at	SPINT2
Standard	8.15	1106015	96885	235343_at	FLJ12505
Standard	8.18	1121400	223474	205599_at	TRAF1
Standard	8.38	1139950	437385	220731_s_at	FLJ10420
Standard	8.73	1122112	1314	206729_at	TNFRSF8

TABLE 2411-continued

GCB vs. PMBL					
Standard	8.77	1122772	66742	207900_at	CCL17
Standard	8.84	1132762	80395	204777_s_at	MAL
Standard	9.64	1139774	15827	220140_s_at	SNX11
Standard	10.53	1133801	181097	207426_s_at	TNFSF4
Standard	11.52	1106415	169071	235774_at	
Standard	12.09	1129269	62919	220358_at	SNFT

TABLE 2411-continued

GCB vs. PMBL			
	Standard		
Mean GCB	292.76	Cut 1	0.16
Mean PMBL	725.28	Cut 2	0.50
Covariance GCB	8538.86		
Covariance PMBL	11405.23		

TABLE 2412

MCL vs. DLBCL-BL

Signature	Scale	UNIQID	Unigene ID Build 167	Probe set	Gene Symbol
Standard	−26.11	1529382	371468	Lymph_Dx_111_at	CCND1
Standard	−18.35	1103711	288718	232478_at	
Standard	−17.03	1106855	455101	236255_at	KIAA1909
Standard	−16.49	1098840	55098	226713_at	C3orf6
Standard	−15.41	1109505	8162	239186_at	MGC39372
Standard	−15.11	1098954	128905	226844_at	MOBKL2B
Standard	−14.96	1103504	142517	232239_at	
Standard	−14.74	1096070	241565	222640_at	DNMT3A
Standard	−13.81	1137663	247362	214909_s_at	DDAH2
Standard	−13.8	1124864	411317	212960_at	KIAA0882
Standard	−13.62	1140127	125300	221044_s_at	TRIM34
Standard	−13.62	1119361	391858	201448_at	TIA1
Standard	−13.37	1127849	76691	218032_at	SNN
Standard	13.72	1133192	24024	205801_s_at	RASGRP3
Standard	13.85	1137583	273415	214687_x_at	ALDOA
Standard	15.02	1123052	180909	208680_at	PRDX1
Standard	16.21	1097611	438993	225285_at	BCAT1
Lymph Node	−19.18	1529456	371468	Lymph_Dx_113_at	CCND1
Lymph Node	−10.71	1098978	124863	226869_at	
Lymph Node	−9.17	1097448	250607	225093_at	UTRN
Lymph Node	8.84	1135240	436852	209955_s_at	FAP
Lymph Node	9.11	1119475	296323	201739_at	SGK
Lymph Node	9.22	1119237	389964	201141_at	GPNMB
Lymph Node	9.46	1130629	135226	200839_s_at	CTSB
Lymph Node	10.1	1130054	82547	221872_at	RARRES1

	Standard	Lymph Node		
Mean MCL	−1417.55	−25.58	Cut 1	0.50
Mean DLBCL-BL	−756.07	202.29	Cut 2	0.88
Covariance MCL	15347.98	3525.48		
	3525.48	5420.31		
Covariance DLBCL-BL	5132.06	1007.64		
	1007.64	991.38		

TABLE 2413

MCL vs. SLL

Signature	Scale	UNIQID	Unigene ID Build 167	Probe set	Gene Symbol
Standard	−20.18	1132834	432638	204914_s_at	SOX11
Standard	−15.17	1130926	508741	201310_s_at	C5orf13
Standard	13.44	1116150	16229	227606_s_at	AMSH-LP
Standard	14.44	1120134	75545	203233_at	IL4R
Standard	15.18	1529437	445162	Lymph_Dx_175_at	BTLA
Standard	15.19	1529317	−98	Lymph_Dx_037_at	
Standard	16.2	1135042	79015	209582_s_at	MOX2

	Standard		
Mean MCL	181.38	Cut 1	0.20
Mean SLL	564.92	Cut 2	0.80
Covariance MCL	1734.42		
Covariance SLL	910.75		

TABLE 2414

SLL vs. DLBCL-BL

Signature	Scale	UNIQID	Unigene ID Build 167	Probe set	Gene Symbol
Standard	−16.014498	1123622	8578	210051_at	EPAC
Standard	−15.26356533	1102081	506977	230551_at	
Standard	−14.82150028	1107044	163426	236458_at	
Standard	−14.17813266	1098865	250905	226741_at	LOC51234
Standard	−12.92844719	1110740	416810	240538_at	
Standard	−12.86520757	1129026	135146	220007_at	FLJ13984
Standard	−12.2702748	1135592	758	210621_s_at	RASA1
Standard	−11.87309449	1117343	306812	234643_x_at	BUCS1
Standard	−11.81789137	1136987	21695	213370_s_at	SFMBT1
Standard	−11.78631706	1124830	9059	212911_at	KIAA0962
Standard	−11.39454435	1133538	1416	206760_s_at	FCER2
Standard	−11.39050362	1135802	439343	210944_s_at	CAPN3
Standard	11.72928644	1120770	300825	204493_at	BID
Lymph Node	−12.21593247	1119880	442844	202709_at	FMOD
Lymph Node	9.514704847	1135240	436852	209955_s_at	FAP
Lymph Node	9.739298877	1096429	64896	223405_at	NPL
Lymph Node	10.05087645	1119475	296323	201739_at	SGK
Lymph Node	13.11985922	1119237	389964	201141_at	GPNMB
Proliferation	10.47525875	1128106	14559	218542_at	C10orf3
Proliferation	10.53295782	1132825	512813	204900_x_at	SAP30
Proliferation	11.93918891	1130501	2795	200650_s_at	LDHA
Proliferation	11.98738778	1123439	287472	209642_at	BUB1
Proliferation	11.99741644	1115607	435733	224428_s_at	CDCA7

	Standard	Lymph Node	Proliferation		
Mean SLL	−1383.640809	177.4452398	467.2463569	Cut 1	0.201266305
Mean DLBCL-BL	−926.7275468	329.6795845	582.9070266	Cut 2	0.799816116
Covariance SLL	3591.384775	1789.7516	856.0703202		
	1789.7516	1421.869535	663.4782048		
	856.0703202	663.4782048	965.6470151		
Covariance DLBCL-BL	2922.643347	473.543487	634.3258773		
	473.543487	931.9845277	−53.85584619		
	634.3258773	−53.85584619	767.3545404		

[0230] As stated above, the foregoing is merely intended to illustrate various embodiments of the present invention. The specific modifications discussed above are not to be construed as limitations on the scope of the invention. It will be apparent to one skilled in the art that various equivalents, changes, and modifications may be made without departing from the scope of the invention, and it is understood that such equivalent embodiments are to be included herein. All references cited herein are incorporated by reference as if fully set forth herein.

[0231] Abbreviations used herein: ABC, activated B-cell-like diffuse large B cell lymphoma; BL, Burkitt lymphoma; CHOP, cyclophosphamide, doxorubicine, vincristine, and prednisone; CI, confidence interval; CNS, central nervous system; DLBCL, diffuse large B-cell lymphoma; ECOG, Eastern Cooperative Oncology Group; EST, expressed sequence tag; FACS, fluorescence-activated cell sorting; FH, follicular hyperplasia; FL, follicular lymphoma; GCB, germinal center B-cell-like diffuse large B cell lymphoma; GI, gastrointestinal; IPI, International Prognostic Index; LPC, lymphoplasmacytic lymphoma; LPS, linear predictor score; MALT, mucosa-associated lymphoid tissue lymphomas; MCL, mantle cell lymphoma; MHC, major histocompatibility complex; NA, not available or not applicable; NK, natural killer; NMZ, nodal marginal zone lymphoma; PCR, polymerase chain reaction; PMBL, primary mediastinal B-cell lymphoma; PTLD, post-transplant lymphoproliferative disorder; REAL, Revised European-American Lymphoma; RPA, RNase protection assay; RR, relative risk of death; RT-PCR, reverse transcriptase polymerase chain reaction; SAGE, serial analysis of gene expression; SLL, small lymphocytic lymphoma; WHO, World Health Organization.

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TABLE 2415

GeneID.txt

Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
1	1095985	1095985: TMEPAI :: transmembrane, prostate androgen induced RNA	83883	0.765572912605858	−0.305829906881871
2	1095996	1095996: SSBP3 :: single stranded DNA binding protein 3	288801	0.337878824571224	−0.246570833627667
3	1096028	1096028: STMN3 :: stathmin-like 3	285753	0.247291930603322	−0.512359910432692
4	1096035	1096035: UGCGL1 :: UDP-glucose ceramide glucosyltransferase-like 1	105794	−0.044857707563452	0.126915353662946
5	1096038	1096038: PPM2C :: protein phosphatase 2C, magnesium-dependent, catalytic subunit	22265	0.059429204462921	−0.188473830832503
6	1096054	1096054: FLJ10036 :: hypothetical protein FLJ10036	21331	−0.371427712016433	0.730940143905553
7	1096070	1096070: DNMT3A :: DNA (cytosine-5-)-methyltransferase 3 alpha	241565	0.065715669272673	−0.156420432074750
8	1096077	1096077: IPO11 :: importin 11	441043	−0.272220885257140	0.497353016437345
9	1096078	1096078: HSU84971 :: fetal hypothetical protein	284216	−0.414916213421669	0.418061447763775
10	1096085	1096085: HSPC109 :: hypothetical protein HSPC109	224137	−0.293990882168277	0.238351282285725
11	1096108	1096108: ZDHHC2 :: zinc finger, DHHC domain containing 2	292871	−0.051768610245872	0.113517147008026
12	1096149	1096149: NUDT5 :: nudix (nucleoside diphosphate linked moiety X)-type motif 5	410205	−0.328630578583663	0.210623718410482
13	1096152	1096152: IL20RA :: interleukin 20 receptor, alpha	288240	−0.082760468199485	−0.000212236348592
14	1096158	1096158: SLAMF7 :: SLAM family member 7	132906	0.141965675898601	−0.400637349397057
15	1096163	1096163: FKSG14 :: leucine zipper protein FKSG14	164018	−0.302881859478226	0.709798806284115
16	1096172	1096172: AKT3 :: v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	300642	0.079018970053188	−0.070815586824077
17	1096180	1096180: HSPC065 :: HSPC065 protein	11614	−0.248427935178953	0.244895501152730
18	1096182	1096182: ITGA11 :: integrin, alpha 11	256297	0.484784321132005	−0.141574493942455
19	1096220	1096220: IL22 :: interleukin 22	287369	−0.012202602288250	0.102513778017030
20	1096248	1096248: NAT5 :: N-acetyltransferase 5 (ARD1 homolog, *S. cerevisiae*)	109253	−0.179981414304964	0.304665808254639
21	1096251	1096251: SLC40A1 :: solute carrier family 40 (iron-regulated transporter), member 1	409875	−0.350169148476026	−0.039724364810070
22	1096297	1096297: UCK1 :: uridine-cytidine kinase 1	9597	0.107276488247798	−0.131638659028410
23	1096300	1096300: MGC2714 :: hypothetical protein MGC2714	74284	−0.293976225239911	0.702711029782148
24	1096341	1096341: SNX8 :: sorting nexin 8	12169	0.143322315228953	−0.018039018612117
25	1096356	1096356: ALS2CR2 :: amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 2	259230	0.110280642995490	−0.020357388828095
26	1096357	1096357: FLJ20432 :: hypothetical protein FLJ20432	57898	−0.498064299913012	0.547207859146077
27	1096362	1096362: TCF19 :: transcription factor 19 (SC1)	512706	−0.399070415427405	0.449227205058841
28	1096364	1096364: NID67 :: putative small membrane protein NID67	29444	0.683874750520760	−0.414039064356815
29	1096369	1096369: DERP6 :: S-phase 2 protein	417029	−0.344757531355776	0.376048402134116
30	1096378	1096378: URP2 :: UNC-112 related protein 2	180535	0.201631483396441	−0.176115831847333
31	1096379	1096379: SLC37A3 :: solute carrier family 37 (glycerol-3-phosphate transporter), member 3	439590	0.381537720604309	−0.447728614022874
32	1096406	1096406: C6orf115 :: chromosome 6 open reading frame 115	238205	0.165024207205827	−0.097834654666083
33	1096429	1096429: NPL :: N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)	64896	0.521727444062009	−0.359471289677876
34	1096440	1096440: GPR160 :: G protein-coupled receptor 160	231320	−0.270973814036627	0.306462668135112
35	1096442	1096442: SIK2 :: salt-inducible serine/threonine kinase 2	306864	−0.062856819831174	0.170832425890252
36	1096446	1096446: GBP3 :: guanylate binding protein 3	92287	0.386684402604806	−0.494981443515261
37	1096456	1096456: CXCL16 :: chemokine (C—X—C motif) ligand 16	82407	0.534265409104252	−0.494680174142867
38	1096460	1096460: CAMKK1 :: calcium/calmodulin-dependent protein kinase kinase 1, alpha	8417	0.063944985869638	−0.228128654986856
39	1096466	1096466: RASD1 :: RAS, dexamethasone-induced 1	25829	0.289870036740434	−0.219151800055010
40	1096469	1096469: RAB3IP :: RAB3A interacting protein (rabin3)	103267	−0.332016102837598	0.464149286520712
41	1096499	1096499: CARD11 :: caspase recruitment domain family, member 11	293867	−0.436883733442666	0.265844768784079
42	1096503	1096503: C9orf45 :: chromosome 9 open reading frame 45	21379	−0.298819325021361	−0.023184197355755
43	1096530	1096530: PACAP :: proapoptotic caspase adaptor protein	409563	−0.314448231660953	0.248763567467872
44	1096570	1096570: ANUBL1 :: AN1, ubiquitin-like, homolog (*Xenopus laevis*)	409813	0.087244086284512	−0.114499206537960
45	1096579	1096579: HCST :: hematopoietic cell signal transducer	117339	0.191275472761633	−0.323814264064461
46	1096609	1096609: ARSD :: arylsulfatase D	−35	0.501162661333468	−0.492064259946528
47	1096615	1096615: RPL27A :: ribosomal protein L27a	356342	−0.284923968217501	0.414116756593771
48	1096616	1096616: C1QTNF4 :: C1q and tumor necrosis factor related protein 4	119302	0.245717528496956	−0.066211741589717
49	1096617	1096617: CCL26 :: chemokine (C-C motif) ligand 26	131342	0.139107804989950	−0.111244751036349
50	1096621	1096621: STK29 :: serine/threonine kinase 29	170819	0.121643230282416	0.000022906837176
51	1096690	1096690: TNFRSF19 :: tumor necrosis factor receptor superfamily, member 19	334174	0.046446130012764	−0.106555400562260
52	1096693	1096693: PDCDILG1 :: programmed cell death 1 ligand 1	443271	0.256067109408327	−0.178200268373170
53	1096719	1096719: ARP3BETA :: actin-related protein 3-beta	250153	0.245831877624803	−0.006615297551808

TABLE 2415-continued

GeneID.txt

Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
54	1096738	1096738: TLR9 :: toll-like receptor 9	87968	−0.454086982168439	0.435099752153320
55	1096742	1096742: ERN2 :: *Homo sapiens* hypothetical gene supported by NM_033266 (LOC374284), mRNA	114905	−0.020800763316815	0.082977324102791
56	1096805	1096805: CCL28 :: chemokine (C-C motif) ligand 28	334633	−0.119965557753727	−0.076751767859586
57	1096829	1096829: IL20 :: interleukin 20	272373	0.000592650321134	0.142312268819410
58	1096834	1096834: IL17C :: interleukin 17C	278911	−0.085306904722356	−0.026275991743137
59	1096877	1096877: MGC13008 :: hypothetical protein MGC13008	326732	−0.152752641907604	0.133576812781343
60	1096903	1096903: FLJ10385 :: hypothetical protein FLJ10385	437460	−0.363962088997560	0.386488614725012
61	1096936	1096936: IL1F10 :: interleukin 1 family, member 10 (theta)	306974	−0.088807796915772	0.147815256172852
62	1096965	1096965: PRO1853 :: hypothetical protein PRO1853	433466	0.234905061259092	−0.151522525032889
63	1096981	1096981: PDCD1LG2 :: programmed cell death 1 ligand 2	61929	0.411512700132525	−0.339724398106172
64	1097030	1097030: :: *Homo sapiens* transcribed sequence with moderate similarity to protein pir: I60307 (*E. coli*) 160307 beta-galactosidase, alpha peptide - *Escherichia coli*	511801	0.084096291164457	−0.211349577111875
65	1097065	1097065: MAPK1 :: mitogen-activated protein kinase 1	324473	−0.067419611001008	−0.077605763020246
66	1097096	1097096: SEPN1 :: selenoprotein N, 1	8518	0.486311887679975	−0.324166091574385
67	1097107	1097107: LENG8 :: leukocyte receptor cluster (LRC) member 8	−27	−0.367283482545225	0.117896751606288
68	1097109	1097109: MESDC2 :: mesoderm development candidate 2	−23	−0.084057602411658	0.123691273481405
69	1097126	1097126: ANTXR1 :: anthrax toxin receptor 1	274520	0.872281447063434	−0.360699565338566
70	1097143	1097143: HSPCB :: heat shock 90 kDa protein 1, beta	74335	−0.329763699311407	0.161353868658910
71	1097156	1097156: CKLFSF3 :: chemokine-like factor super family 3	298198	0.356521698413820	−0.224978670328984
72	1097161	1097161: :: *Homo sapiens* cDNA clone IMAGE: 5270526, partial cds	5064	−0.283918984792974	0.245645271796048
73	1097172	1097172: CDCA5 :: cell division cycle associated 5	434886	−0.327278444996126	0.823349285555297
74	1097177	1097177: GNA13 :: guanine nucleotide binding protein (G protein), alpha 13	9691	−0.037330227523842	0.164092697479536
75	1097195	1097195: MGC29814 :: hypothetical protein MGC29814	−22	−0.311093569811657	0.387394625596569
76	1097202	1097202: DDEF1 :: development and differentiation enhancing factor 1	−33	0.404219688288097	−0.239957287582709
77	1097229	1097229: CPSF5 :: cleavage and polyadenylation specific factor 5, 25 kDa	446393	−0.364448004904438	0.618328935053735
78	1097236	1097236: FOXP1 :: forkhead box P1	235860	−0.374613701666339	0.219940106264499
79	1097247	1097247: :: *Homo sapiens* cDNA clone IMAGE: 4520413, partial cds	388761	0.078706536819919	0.079845030074853
80	1097253	1097253: B7H3 :: B7 homolog 3	77873	0.509686941959052	−0.300155823803531
81	1097255	1097255: :: *Homo sapiens*, clone IMAGE: 5289004, mRNA	380144	0.655182909405963	−0.480162974610710
82	1097271	1097271: RALA :: v-ral simian leukemia viral oncogene homolog A (ras related)	6906	0.233158496732894	0.116175646014776
83	1097280	1097280: :: *Homo sapiens* cDNA clone IMAGE: 4814010, partial cds	423523	0.425384591076580	−0.493447794310351
84	1097281	1097281: PLDN :: pallidin homolog (mouse)	7037	0.173437680009131	−0.194314449880568
85	1097282	1097282: LOC283241 :: hypothetical protein LOC283241	356719	−0.025407453597505	−0.131750092303776
86	1097290	1097290: CIRH1A :: cirrhosis, autosomal recessive 1A (cirhin)	151001	−0.492530933582546	0.676549644346020
87	1097297	1097297: VMP1 :: likely ortholog of rat vacuole membrane protein 1	166254	0.453085943117571	−0.244926367026450
88	1097307	1097307: LOC340061 :: hypothetical protein LOC340061	379754	0.677089831326282	−0.583057243877707
89	1097310	1097310: SMAP-5 :: golgi membrane protein SB140	5672	0.264429734648259	−0.148300598780685
90	1097325	1097325: LASS5 :: LAG1 longevity assurance homolog 5 (*S. cerevisiae*)	458450	0.077585149886997	−0.030530283585439
91	1097329	1097329: TEAD1 :: TEA domain family member 1 (SV40 transcriptional enhancer factor)	153408	0.609915504509915	−0.330588741531368
92	1097334	1097334: FLJ10074 :: hypothetical protein FLJ10074	71573	0.148822099251370	−0.036195940379043
93	1097359	1097359: :: *Homo sapiens* transcribed sequence with weak similarity to protein ref: NP_060312.1 (*H. sapiens*) hypothetical protein FLJ20489 [*Homo sapiens*]	518723	0.053800334461785	−0.154524230021900
94	1097365	1097365: CKLFSF4 :: chemokine-like factor super family 4	325825	0.519294317954343	−0.216309380198487
95	1097371	1097371: PHF13 :: PHD finger protein 13	7299	−0.321720660373057	0.340367027876139
96	1097383	1097383: CAMK2D :: calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	111460	−0.290642761065368	0.133360053100389
97	1097388	1097388: C20orf77 :: chromosome 20 open reading frame 77	278839	−0.197775027946280	0.376751974725969
98	1097395	1097395: FAD104 :: FAD104	299883	0.736100200479402	−0.373635154671711
99	1097424	1097424: DKFZP434C131 :: DKFZP434C131 protein	7978	−0.134018331816916	−0.109225857504428
100	1097441	1097441: FLJ38426 :: hypothetical protein FLJ38426	6799	−0.402273189776746	0.543694221269586
101	1097448	1097448: UTRN :: utrophin (homologous to dystrophin)	250607	0.360883799114271	−0.584276143462886
102	1097540	1097540: :: *Homo sapiens* cDNA FLJ13141 fis, clone NT2RP3003210.	388087	−0.061066580853079	0.258721848569539
103	1097553	1097553: PSMB7 :: proteasome (prosome, macropain) subunit, beta type, 7	197071	0.311409341908515	−0.205155556831752
104	1097561	1097561: C20orf112 :: chromosome 20 open reading frame 112	19221	0.527162504741833	−0.440301485246365
105	1097563	1097563: FLJ14743 :: hypothetical protein FLJ14743	169577	−0.168921612398568	−0.030167777542399
106	1097564	1097564: SKIL :: SKI-like	272108	−0.048959117197389	0.045546934477234
107	1097600	1097600: SAT2 :: spermidine/spermine N1-acetyltransferase 2	10846	0.349508117260322	−0.551195374259974
108	1097609	1097609: LOC91947 :: hypothetical protein LOC91947	6093	0.698019824770373	−0.413944744306518
109	1097610	1097610: DNAJC3 :: DnaJ (Hsp40) homolog, subfamily C, member 3	6019	0.354942495910287	−0.301478249730580
110	1097611	1097611: BCAT1 :: branched chain aminotransferase 1, cytosolic	438993	0.231503275940178	0.054391439403167
111	1097614	1097614: MGC16063 :: hypothetical protein MGC16063	410491	0.046334195779423	−0.052886978168640
112	1097637	1097637: ACBD6 :: acyl-Coenzyme A binding domain containing 6	63220	−0.455371733025381	0.588517058172155
113	1097665	1097665: HT011 :: uncharacterized hypothalamus protein HT011	434241	0.302114923194357	−0.218617058012615

TABLE 2415-continued

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Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
114	1097676	1097676: PGM2 :: phosphoglucomutase 2	23363	−0.105211493496590	0.411367274902218
115	1097683	1097683: PP2135 :: PP2135 protein	132569	0.438652292433518	−0.531837589765522
116	1097684	1097684: MGC45714 :: hypothetical protein MGC45714	368878	−0.262573752576479	0.186215149748326
117	1097704	1097704: C1orf19 :: chromosome 1 open reading frame 19	440663	−0.299851016612681	0.328280021104323
118	1097707	1097707: C20orf64 :: chromosome 20 open reading frame 64	440263	−0.208966762154304	0.237923731267286
119	1097717	1097717: FLJ14681 :: hypothetical protein FLJ14681	23317	0.125057120164488	−0.094075705262804
120	1097735	1097735: LOC58489 :: hypothetical protein from EUROIMAGE 588495	26765	−0.152766753795439	0.150760192399265
121	1097804	1097804: FLJ10213 :: hypothetical protein FLJ10213	446590	−0.232974145960649	0.385796656610468
122	1097814	1097814: CENTB5 :: centaurin, beta 5	21446	0.025599591925261	−0.077279249251246
123	1097824	1097824: MAP2 :: microtubule-associated protein 2	167	0.117548992931937	−0.120439543060478
124	1097887	1097887: KIAA0303 :: KIAA0303 protein	212787	0.092960318117084	−0.116573446206172
125	1097897	1097897: PAG :: phosphoprotein associated with glycosphingolipid-enriched microdomains	266175	0.191577241800621	−0.085455707264803
126	1097899	1097899: LOC92017 :: similar to RIKEN cDNA 4933437K13	145047	0.096634326522832	−0.342206059804613
127	1097901	1097901: PAG :: phosphoprotein associated with glycosphingolipid-enriched microdomains	266175	0.204617854117621	−0.117013400778641
128	1097902	1097902: KIAA1706 :: KIAA1706 protein	412318	0.203615260815970	−0.140541494164973
129	1097918	1097918: LOC90378 :: atherin	140309	−0.379406336299933	0.520098002520735
130	1097928	1097928: SEMA6A :: sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	443012	0.234759397668220	−0.219646366867697
131	1097930	1097930: ZAK :: sterile alpha motif and leucine zipper containing kinase AZK	115175	0.108699289989043	0.073998196964394
132	1097940	1097940: LOC91663 :: hypothetical protein BC013995	380906	0.706870503069227	−0.502093351185603
133	1097948	1097948: LOC348235 :: hypothetical protein LOC348235	69476	−0.269699076470008	0.529419096597393
134	1097961	1097961: :: *Homo sapiens* ACA9 snoRNA gene	25892	−0.429719438748216	0.625988904538759
135	1097966	1097966: KIAA1545 :: KIAA1545 protein	127270	0.027173493843938	−0.400522062454424
136	1097976	1097976: raptor :: raptor	218017	−0.148308861940539	0.120470330039901
137	1098012	1098012: CSNK1E :: casein kinase 1, epsilon	355669	−0.342068884130279	0.262100628123216
138	1098023	1098023: KIAA1972 :: KIAA1972 protein	181161	−0.129150683371564	0.086536959397880
139	1098065	1098065: FLJ14957 :: hypothetical protein FLJ14957	10119	0.609772948330722	−0.373661396100191
140	1098069	1098069: :: *Homo sapiens* mRNA similar to QIL1 (cDNA clone MGC: 57483 IMAGE: 5288954), complete cds	356626	−0.282366680428328	0.222535690878294
141	1098095	1098095: ANKRD17 :: ankyrin repeat domain 17	131059	−0.102008011290600	0.114467644297043
142	1098103	1098103: NSE2 :: breast cancer membrane protein 101	124951	0.223410146111536	−0.418382440606729
143	1098145	1098145: KIAA2002 :: KIAA2002 protein	9587	−0.043305517146293	−0.071453322767335
144	1098152	1098152: KIAA1450 :: KIAA1450 protein	377588	0.582609629394882	−0.401088162485662
145	1098156	1098156: MAP3K1 :: mitogen-activated protein kinase kinase kinase 1	170610	−0.393164723370577	0.064183682917463
146	1098168	1098168: NLN :: neurolysin (metallopeptidase M3 family)	22151	−0.086110889605484	0.266365022083743
147	1098174	1098174: LOC340371 :: hypothetical protein LOC340371	274401	0.371605420749830	−0.378069656516585
148	1098179	1098179: LOC153222 :: adult retina protein	163725	0.113653935807107	−0.578870218791412
149	1098186	1098186: MGC11349 :: hypothetical protein MGC11349	288697	−0.411774761515353	0.252798351125526
150	1098195	1098195: DKFZp762C1112 :: hypothetical protein DKFZp762C1112	88594	−0.162948668373984	0.064023508939311
151	1098204	1098204: PRKAA1 :: protein kinase, AMP-activated, alpha 1 catalytic subunit	43322	0.082481444229336	−0.126559120661099
152	1098220	1098220: GAB1 :: GRB2-associated binding protein 1	80720	−0.270353808866967	0.129171526797500
153	1098234	1098234: CD47 :: CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	446414	−0.204808859254960	−0.130670945404961
154	1098235	1098235: CKLFSF7 :: chemokine-like factor super family 7	440494	−0.003820637227097	−0.213943192132446
155	1098242	1098242: KIAA0379 :: KIAA0379 protein	273104	−0.146990537817309	0.382995758727720
156	1098252	1098252: KIAA1203 :: ubiquitin-specific protease KIAA1203	16953	−0.006618002834239	0.046833591332181
157	1098256	1098256: SVH :: SVH protein	431871	−0.452504903187901	0.363026813249536
158	1098258	1098258: AGS3 :: activator of G-protein signaling 3	239370	0.310744715383991	−0.322355508448668
159	1098268	1098268: MAP2K7 :: mitogen-activated protein kinase kinase 7	110299	−0.298346850539865	0.241278514570550
160	1098271	1098271: CDGAP :: KIAA1204 protein	300670	0.173495129742519	−0.257241770812174
161	1098277	1098277: PRICKLE1 :: prickle-like 1 (*Drosophila*)	6786	−0.273817683372350	0.064132444418075
162	1098278	1098278: MITF :: microphthalmia-associated transcription factor	166017	0.618314859385319	−0.387872278743441
163	1098303	1098303: FRCP2 :: likely ortholog of mouse fibronectin type III repeat containing protein 2	15463	0.010448057045878	−0.100537311719435
164	1098338	1098338: HRB2 :: HIV-1 rev binding protein 2	269857	0.310283160362659	−0.307858826824513
165	1098405	1098405: IL7R :: interleukin 7 receptor	362807	0.549494110248763	−0.263717657392419
166	1098412	1098412: MCC :: mutated in colorectal cancers	−24	0.454236696826577	−0.310591183271143
167	1098415	1098415: KIAA1387 :: KIAA1387 protein	130900	−0.116869481419355	−0.122838250620999
168	1098433	1098433: :: *Homo sapiens* cDNA FLJ10158 fis, clone HEMBA1003463.	202577	0.136410689468839	−0.299039669796789
169	1098447	1098447: JDP2 :: jun dimerization protein 2	154095	−0.141461142027089	0.099602291803127
170	1098459	1098459: SPUVE :: protease, serine, 23	25338	0.737264124009213	−0.334058738986943
171	1098461	1098461: DNER :: delta-notch-like EGF repeat-containing transmembrane	234074	0.041020174413569	−0.067455662571597
172	1098476	1098476: pknbeta :: protein kinase PKNbeta	300485	−0.194588649952929	0.049490469697965
173	1098495	1098495: TBRG1 :: likely ortholog of mouse transforming growth factor beta regulated gene 1	443668	0.052385916360886	−0.306318481977251

TABLE 2415-continued

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Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
174	1098506	1098506: IL6R :: interleukin 6 receptor	193400	0.299704358316571	−0.483797688597999
175	1098521	1098521: OPN3 :: opsin 3 (encephalopsin, panopsin)	170129	−0.309674653956075	0.290933486492843
176	1098548	1098548: NFIC :: nuclear factor I/C (CCAAT-binding transcription factor)	436639	0.577838108495008	−0.573059285395985
177	1098550	1098550: :: *Homo sapiens* cDNA FLJ36584 fis, clone TRACH2013450.	355655	−0.090479408634668	−0.005454207841183
178	1098553	1098553: HTPAP :: HTPAP protein	437179	0.172952993194321	−0.447010228881662
179	1098574	1098574: KIAA0233 :: KIAA0233 gene product	79077	−0.341045883809633	0.355913888061517
180	1098592	1098592: FLJ38771 :: hypothetical protein FLJ38771	283707	−0.370411569171726	0.240153206136564
181	1098604	1098604: SLC39A10 :: solute carrier family 39 (zinc transporter), member 10	32793	−0.356817082601293	0.039590884115228
182	1098607	1098607: MGC15887 :: hypothetical gene supported by BC009447	38516	−0.202635383865497	0.273499931529896
183	1098611	1098611: PDK1 :: pyruvate dehydrogenase kinase, isoenzyme 1	433611	0.011464972668250	0.218494255827149
184	1098613	1098613: RENT1 :: regulator of nonsense transcripts 1	388125	−0.409061726498054	0.340688285828164
185	1098618	1098618: PIK3AP1 :: phosphoinositide-3-kinase adaptor protein 1	374836	−0.256727551852790	0.025741438982940
186	1098629	1098629: :: *Homo sapiens* mRNA; cDNA DKFZp434B0425 (from clone DKFZp434B0425)	103305	−0.188649329326843	0.425239786821600
187	1098658	1098658: PAK1 :: p21/Cdc42/Rac1-activated kinase 1 (STE20 homolog, yeast)	64056	0.012658587060208	−0.114254490164613
188	1098668	1098668: BCAT1 :: branched chain aminotransferase 1, cytosolic	438993	0.198467154785237	0.101188582172517
189	1098669	1098669: KCTD10 :: potassium channel tetramerisation domain containing 10	302746	−0.054505167679050	0.005953626629536
190	1098678	1098678: BMF :: Bcl-2 modifying factor	386140	−0.340027764754526	0.107012841951926
191	1098683	1098683: ITGB6 :: integrin, beta 6	57664	0.254592203414043	−0.200152902993317
192	1098694	1098694: :: *Homo sapiens* mRNA; cDNA DKFZp547J047 (from clone DKFZp547J047)	97837	0.128247191609226	−0.269181101036406
193	1098718	1098718: PSPC1 :: paraspeckle component 1	16364	−0.320538780285753	0.522732450579130
194	1098771	1098771: KIAA1501 :: KIAA1501 protein	374446	0.328061924477626	−0.168759177690866
195	1098784	1098784: MARK1 :: MAP/microtubule affinity-regulating kinase 1	12808	0.088534795440517	−0.093360079546100
196	1098809	1098809: :: *Homo sapiens* hypothetical protein LOC283666, mRNA (cDNA clone IMAGE: 4415549), partial cds	359394	0.447370410855574	−0.496179620225829
197	1098821	1098821: PALM2 :: paralemmin 2	42322	0.179862598270706	−0.187856000103763
198	1098822	1098822: PRRX1 :: paired related homeobox 1	443452	0.774883481649142	−0.543483135789053
199	1098832	1098832: FGFR1 :: fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)	748	0.543603649322806	−0.330357417669066
200	1098840	1098840: C3orf6 :: chromosome 3 open reading frame 6	55098	−0.146221260881764	−0.090592943233251
201	1098862	1098862: MGC26694 :: hypothetical protein MGC26694	303669	−0.034863463975044	−0.146817360127211
202	1098865	1098865: LOC51234 :: hypothetical protein LOC51234	250905	0.159594910624286	−0.309933221730095
203	1098883	1098883: MBTPS2 :: membrane-bound transcription factor protease, site 2	412014	0.360729355144278	0.015238352387109
204	1098893	1098893: ATP8B2 :: ATPase, Class I, type 8B, member 2	43577	0.159404272308497	−0.298738852653094
205	1098898	1098898: ADAM12 :: a disintegrin and metalloproteinase domain 12 (meltrin alpha)	−36	0.763097942064200	−0.294746482348485
206	1098909	1098909: MGC71745 :: similar to embigin	446408	−0.262428029790519	−0.053305715167356
207	1098918	1098918: FGD6 :: FYVE, RhoGEF and PH domain containing 6	170623	0.156113760591959	0.048524812619013
208	1098927	1098927: FLJ20202 :: FLJ20202 protein	356216	−0.081190091806277	−0.118355192853442
209	1098946	1098946: :: *Homo sapiens* transcribed sequence with moderate similarity to protein sp: P39195 (*H. sapiens*) ALU8_HUMAN Alu subfamily SX sequence contamination warning entry	135121	0.645970747276803	−0.478233290280070
210	1098951	1098951: H2AFY :: H2A histone family, member Y	75258	−0.105148799565054	0.000183905271443
211	1098952	1098952: KIAA0937 :: KIAA0937 protein	62264	−0.155610228904124	−0.112321975971408
212	1098954	1098954: MOB3B :: MOB3B protein	128905	0.141136508773827	−0.149504432709389
213	1098962	1098962: BMP2K :: BMP2 inducible kinase	20137	0.286170948451110	−0.181990310332082
214	1098978	1098978: :: *Homo sapiens* full length insert cDNA clone ZD77F06	124863	0.619336132796843	−0.505050387984609
215	1098987	1098987: FLJ21127 :: hypothetical protein FLJ21127	412559	0.062127070347666	−0.441644144559995
216	1098991	1098991: LRRN1 :: leucine rich repeat neuronal 1	126085	0.069832672264346	−0.114738890765678
217	1099028	1099028: FNDC1 :: fibronectin type III domain containing 1	334838	0.631435118754401	−0.300213120295103
218	1099032	1099032: :: *Homo sapiens* cDNA clone IMAGE: 4448513, partial cds	35962	−0.258137643029524	0.696628339145868
219	1099040	1099040: HTRA3 :: serine protease HTRA3	390421	0.507829674693844	−0.252934339568439
220	1099053	1099053: :: *Homo sapiens* mRNA; cDNA DKFZp761D1624 (from clone DKFZp761D1624)	376041	−0.147877893008140	−0.132787590083425
221	1099058	1099058: :: *Homo sapiens*, clone IMAGE: 5267224, mRNA	425116	−0.152727193720123	0.086705174421553
222	1099072	1099072: MAP3K2 :: mitogen-activated protein kinase kinase kinase 2	28827	0.326012687586492	−0.341129976548376
223	1099088	1099088: :: *Homo sapiens* mRNA; cDNA DKFZp686N20218 (from clone DKFZp686N20218)	14355	−0.339066628811356	0.384877728106452
224	1099105	1099105: LATS2 :: LATS, large tumor suppressor, homolog 2 (*Drosophila*)	78960	0.495842158034742	−0.343366651347192
225	1099112	1099112: :: *Homo sapiens* cDNA FLJ39934 fis, clone SPLEN2021458, weakly similar to *Mus musculus* mdgl-1 mRNA.	368672	0.271313775607110	−0.552177849009380
226	1099120	1099120: :: *Homo sapiens* cDNA FLJ46579 fis, clone THYMU3042758	371680	−0.188611271416496	0.122311426949034
227	1099124	1099124: FLJ21870 :: hypothetical protein FLJ21870	396161	0.519619700424312	−0.453311608748159
228	1099128	1099128: AKAP13 :: A kinase (PRKA) anchor protein 13	350631	−0.013033876971250	−0.132909940435626

TABLE 2415-continued

GeneID.txt

Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
229	1099135	1099135: SLC39A11 :: solute carrier family 39 (metal ion transporter), member 11	3402	0.326183693547397	−0.243872317095855
230	1099140	1099140: :: *Homo sapiens* cDNA FLJ26764 fis, clone PRS02668	500350	0.065600037256185	−0.226915577288523
231	1099148	1099148: TNFRSF19L :: tumor necrosis factor receptor superfamily, member 19-like	434975	0.188804128027844	−0.086049656003445
232	1099150	1099150: :: *Homo sapiens* mRNA; cDNA DKFZp686L01105 (from clone DKFZp686L01105	240443	0.440961016035862	−0.370874002114838
233	1099152	1099152: MGC15396 :: hypothetical protein MGC15396	351247	−0.310898020091843	0.293673968871125
234	1099154	1099154: MOB3C :: MOB3C protein	97927	0.205447190901989	−0.397428894897845
235	1099167	1099167: MGC45731 :: hypothetical protein MGC45731	381105	0.510485627999948	−0.199429872177220
236	1099204	1099204: :: *Homo sapiens* mRNA; cDNA DKFZp586K1922 (from clone DKFZp586K1922)	193784	0.208527885951095	−0.331184935715711
237	1099265	1099265: :: *Homo sapiens*,clone IMAGE: 4828750, mRNA	375762	0.191460172021332	−0.292819027251602
238	1099291	1099291: FBXO10 :: F-box only protein 10	130774	−0.241213003745553	0.140643790486120
239	1099292	1099292: RNPC2 :: RNA-binding region (RNP1, RRM) containing 2	282901	−0.011512027826638	−0.146104933503048
240	1099299	1099299: EVL :: Enah/Vasp-like	241471	0.217471121189110	−0.497486588999731
241	1099318	1099318: LOC149420 :: casein kinase	29911	−0.031451620931163	0.032273607550190
242	1099328	1099328: FLJ35779 :: hypothetical protein FLJ35779	432726	−0.254822688277176	0.160319358394402
243	1099332	1099332: :: *Homo sapiens* cDNA FLJ44521 fis, clone UTERU3002786	32433	0.353038975004276	−0.376426689684681
244	1099358	1099358: LOC338773 :: hypothetical protein LOC338773	449718	0.813232650418064	−0.319504511328730
245	1099377	1099377: ADCK4 :: aarF domain containing kinase 4	130712	−0.050763139906985	0.004763238452783
246	1099388	1099388: DTX1 :: deltex homolog 1 (*Drosophila*)	124024	−0.194780161074778	0.313061833581174
247	1099396	1099396: ZNFN1A1 :: zinc finger protein, subfamily 1A, 1 (Ikaros)	435949	−0.480396437660557	0.241771812595989
248	1099403	1099403: PAG :: phosphoprotein associated with glycosphingolipid-enriched microdomains	266175	0.157815263023168	−0.138144351639275
249	1099418	1099418: KIAA1946 :: KIAA1946 protein	172792	0.352518727172842	−0.221041836869096
250	1099444	1099444: FLJ90013 :: hypothetical protein FLJ90013	434489	−0.154725204627076	0.144181046064220
251	1099510	1099510: ADCK1 :: aarF domain containing kinase 1	15251	0.036823049790738	−0.189535081209326
252	1099526	1099526: LCHN :: LCHN protein	521240	0.059814201915876	−0.318229548955097
253	1099539	1099539: CXorf15 :: chromosome X open reading frame 15	201624	−0.159971879950874	0.335150972693171
254	1099549	1099549: :: *Homo sapiens* transcribed sequences	−45	−0.384484470966513	0.213030278389421
255	1099563	1099563: :: *Homo sapiens* mRNA; cDNA DKFZp686J0156 (from clone DKFZp686J0156)	388347	0.091030785211341	−0.163765026275539
256	1099598	1099598: MGC2452 :: hypothetical protein MGC2452	275711	−0.347670787807501	0.173371242361433
257	1099631	1099631: FLJ20032 :: hypothetical protein FLJ20032	367639	−0.105513306302497	−0.093592194250014
258	1099633	1099633: SGKL :: serum/glucocorticoid regulated kinase-like	380877	0.366469483816619	−0.401250676057012
259	1099651	1099651: EBF :: early B-cell factor	−31	−0.137184837781477	0.247346085114095
260	1099669	1099669: MGC45428 :: hypothetical protein MGC45428	45057	−0.094311296476672	−0.134670571453547
261	1099680	1099680: JAK3 :: Janus kinase 3 (a protein tyrosine kinase, leukocyte)	210387	0.158713315773940	−0.344236607885679
262	1099686	1099686: :: *Homo sapiens* transcribed sequence with weak similarity to protein ref: NP_060312.1 (*H. sapiens*) hypothetical protein FLJ20489 [*Homo sapiens*]	117721	0.339760641299220	−0.126834793111279
263	1099699	1099699: SOCS3 :: suppressor of cytokine signaling 3	436943	0.458674229868194	−0.269705172389045
264	1099711	1099711: :: *Homo sapiens* mRNA; cDNA DKFZp686I21166 (from clone DKFZp686I21166)	243596	0.139055481628475	0.201358145780389
265	1099734	1099734: KIS :: kinase interacting with leukemia-associated gene (stathmin)	127310	0.002341421127241	−0.061937188018310
266	1099743	1099743: TRAD :: serine/threonine kinase with Dbl- and pleckstrin homology domains	162189	0.130663684870377	−0.073102099734362
267	1099748	1099748: :: *Homo sapiens* cDNA FLJ42435 fis, clone BLADE2006849	356481	0.085730011981031	−0.405219346399157
268	1099760	1099760: CSNK1G3 :: casein kinase 1, gamma 3	129206	−0.007660349798916	−0.109292619399866
269	1099798	1099798: FGD3 :: FGD1 family, member 3	411081	−0.015909131360829	−0.501064586770852
270	1099826	1099826: RAB30 :: RAB30, member RAS oncogene family	445862	−0.294473360458321	0.412965834268278
271	1099830	1099830: EPM2AIP1 :: EPM2A (laforin) interacting protein 1	28020	−0.358690409532099	0.237419003752701
272	1099847	1099847: LOC129293 :: hypothetical protein LOC129293	36723	−0.029109229364516	−0.268448964730217
273	1099857	1099857: :: *Homo sapiens* annexin II receptor mRNA, complete cds	119768	0.049788466833904	−0.291863614075693
274	1099886	1099886: :: *Homo sapiens* mRNA; cDNA DKFZp434N2116 (from clone DKFZp434N2116)	−49	0.148774754361664	−0.263395075051385
275	1099900	1099900: :: *Homo sapiens* transcribed sequences	444508	−0.104446381462296	−0.145223660017070
276	1099939	1099939: MGC7036 :: hypothetical protein MGC7036	488173	−0.099560227175285	−0.171318365358415
277	1099951	1099951: LOC170394 :: hypothetical protein BC011630	157728	0.274596536409081	−0.347843922255294
278	1099953	1099953: C21orf4 :: chromosome 21 open reading frame 4	433668	0.047645355151766	−0.294401060293225
279	1099960	1099960: :: *Homo sapiens* cDNA clone IMAGE: 3462401, partial cds	144583	−0.127871935602877	−0.010821560153853
280	1099965	1099965: LOC138428 :: hypothetical protein LOC138428	71962	0.091962882474027	−0.091249651864211
281	1099978	1099978: STK33 :: serine/threonine kinase 33	148135	−0.179708365440309	0.235587009064294
282	1099995	1099995: LOC115265 :: similar to Smhs1 protein	107515	0.007329815357109	−0.132004117518270
283	1100005	1100005: DUFD1 :: DUF729 domain containing 1	121536	−0.135976170321747	0.601059023563389
284	1100027	1100027: AMICA :: adhesion molecule AMICA	16291	0.300925302822323	−0.551597607471469
285	1100040	1100040: RASGRF2 :: Ras protein-specific guanine nucleotide-releasing factor 2	410953	0.147596960954750	−0.215628806283083
286	1100042	1100042: RAB37 :: RAB37, member of RAS oncogene family	351413	0.165978306204715	−0.447611162228477
287	1100054	1100054: :: *Homo sapiens* cDNA FLJ10641 fis, clone NT2RP2005748.	125353	−0.093387430515190	−0.046922285279186

TABLE 2415-continued

GeneID.txt

Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
288	1100060	1100060: RIPK3 :: receptor-interacting serine-threonine kinase 3	268551	−0.080673891292211	−0.183740301156722
289	1100071	1100071: IBRDC2 :: IBR domain containing 2	432653	−0.096139559105640	0.021910530191750
290	1100130	1100130: PRELP :: proline arginine-rich end leucine-rich repeat protein	76494	0.448903531773197	−0.427716260301673
291	1100136	1100136: NUDT1 :: nudix (nucleoside diphosphate linked moiety X)-type motif 1	413078	0.056972383642216	−0.056702588166804
292	1100138	1100138: CGI-109 :: CGI-109 protein	278391	0.075525386230414	−0.015196240931810
293	1100144	1100144: :: *Homo sapiens* transcribed sequence with moderate similarity to protein ref: NP_004563.1 (*H. sapiens*) plakophilin 2 [*Homo sapiens*]	436379	0.342120616958852	−0.305881511542112
294	1100150	1100150: KIAA1999 :: KIAA1999 protein	9343	0.043922323292873	−0.262547992538478
295	1100159	1100159: FLJ00332 :: FLJ00332 protein	123164	−0.175114276904071	−0.151251745398630
296	1100161	1100161: LOC142678 :: skeletrophin	135805	−0.268803408286193	0.043074199399014
297	1100171	1100171: FLJ11029 :: hypothetical protein FLJ11029	274448	−0.315599369534162	0.776632148727844
298	1100183	1100183: FLJ40869 :: hypothetical protein FLJ40869	180582	−0.319113707524938	0.407258049070190
299	1100249	1100249: HAK :: heart alpha-kinase	388674	0.405202029528982	−0.422914576572978
300	1100258	1100258: KIAA1384 :: KIAA1384 protein	88442	−0.482927417502683	0.245462430738922
301	1100263	1100263: LOC90268 :: hypothetical protein BC007706	406335	0.061549164584574	0.052439579303132
302	1100288	1100288: ALS2CR19 :: amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 19	26981	0.428889792428239	−0.320712838583390
303	1100290	1100290: :: *Homo sapiens* cDNA FLJ30800 fis, clone FEBRA2001197.	4241	0.136196171503417	−0.229576669665241
304	1100301	1100301: LLT1 :: lectin-like NK cell receptor	356250	−0.001129259036374	−0.099966890057848
305	1100311	1100311: HSPC163 :: HSPC163 protein	445890	0.105307377070741	−0.165266726365081
306	1100335	1100335: :: *Homo sapiens* transcribed sequence with moderate similarity to protein pir: I60307 (*E. coli*) I60307 beta-galactosidase, alpha peptide - *Escherichia coli*	268474	−0.125278649387652	0.316598617445776
307	1100339	1100339: FLJ14813 :: hypothetical protein FLJ14813	276905	−0.222316026912740	0.607673448698899
308	1100384	1100384: ADCK5 :: aarF domain containing kinase 5	283374	0.020059370587246	0.007329091610762
309	1100405	1100405: KIAA0792 :: KIAA0792 gene product	119387	0.252199782581926	−0.442247983365885
310	1100420	1100420: KIAA1804 :: mixed lineage kinase 4	50883	−0.165851676757938	0.231232139369928
311	1100423	1100423: FLJ30973 :: hypothetical protein FLJ30973	50841	0.159003371714792	−0.138588437250525
312	1100433	1100433: HTRA3 :: serine protease HTRA3	390421	0.163178704381462	−0.118871240794897
313	1100443	1100443: MS4A1 :: membrane-spanning 4-domains, subfamily A, member 1	438040	−0.105067576170844	0.035186610667903
314	1100496	1100496: LOC139886 :: hypothetical protein LOC139886	111496	−0.124735215994899	0.440981805278388
315	1100538	1100538: PRG4 :: proteoglycan 4, (megakaryocyte stimulating factor, articular superficial zone protein, camptodactyly, arthropathy, coxa vara, pericarditis syndrome)	432458	−0.021487630294264	−0.194800347586334
316	1100561	1100561: HEL308 :: DNA helicase HEL308	194109	−0.185491511987517	0.129409778871118
317	1100562	1100562: C20orf100 :: chromosome 20 open reading frame 100	26608	0.059305525501118	−0.237095028247775
318	1100581	1100581: :: *Homo sapiens* mRNA; cDNA DKFZp667A1115 (from clone DKFZp667A1115)	356307	0.165135933716527	0.026126858437344
319	1100585	1100585: LFNG :: lunatic fringe homolog (*Drosophila*)	159142	0.308152082775067	−0.295830383149056
320	1100591	1100591: HKR2 :: GLI-Kruppel family member HKR2	388162	−0.281373260470838	0.142310651962664
321	1100598	1100598: :: *Homo sapiens* cDNA FLJ40955 fis, clone UTERU2011199.	438749	−0.081272856483147	0.389541653250864
322	1100609	1100609: PPIL2 :: peptidylprolyl isomerase (cyclophilin)-like 2	447045	−0.010033297668578	−0.251624647902145
323	1100625	1100625: RORC :: RAR-related orphan receptor C	232803	−0.017550954843166	−0.115801492903445
324	1100721	1100721: :: *Homo sapiens* cDNA FLJ32207 fis, clone PLACE6003204.	18713	0.320178262906959	−0.294600821446125
325	1100750	1100750: :: *Homo sapiens*,clone IMAGE: 4753714, mRNA	280387	−0.220418967314602	0.334098240571130
326	1100753	1100753: ZNF19 :: zinc finger protein 19 (KOX 12)	512717	−0.096315574634547	−0.073564313338261
327	1100770	1100770: :: *Homo sapiens* transcribed sequences	65578	0.126400491381177	−0.124140490500188
328	1100847	1100847: C6orf105 :: chromosome 6 open reading frame 105	97411	0.101671461597607	−0.160154386139487
329	1100849	1100849: :: *Homo sapiens* cDNA FLJ34866 fis, clone NT2NE2014113.	184430	−0.409355182450365	0.352909174326550
330	1100851	1100851: EHD4 :: EH-domain containing 4	55058	0.321339038108403	−0.287001767216924
331	1100871	1100871: :: *Homo sapiens* cDNA FLJ32274 fis, clone PROST2000036.	48353	0.435206681695438	−0.544521387799030
332	1100873	1100873: :: *Homo sapiens* transcribed sequences	445884	−0.204883351763766	0.157721916475158
333	1100879	1100879: MASP2 :: mannan-binding lectin serine protease 2	119983	−0.112831783867775	−0.290649076935063
334	1100904	1100904: LOC119504 :: hypothetical protein LOC119504	−25	−0.099036342262842	−0.256431195474163
335	1100911	1100911: C4orf7 :: chromosome 4 open reading frame 7	320147	0.060001350276090	−0.084108354010684
336	1100916	1100916: PRKWNK4 :: protein kinase, lysine deficient 4	105448	0.108814731820795	−0.011505711122245
337	1100977	1100977: NRG3 :: neuregulin 3	−8	0.107540349948529	−0.052860133552450
338	1100995	1100995: FLJ32029 :: hypothetical protein FLJ32029	26612	0.222494929393081	−0.247794549127664
339	1101004	1101004: SKI :: v-ski sarcoma viral oncogene homolog (avian)	2969	0.300578623845209	−0.357871271240017
340	1101023	1101023: EPHA7 :: EphA7	73962	−0.081992625701500	−0.012091224764700
341	1101054	1101054: PPP2R5E :: protein phosphatase 2, regulatory subunit B (B56), epsilon isoform	173328	−0.142239905250465	0.091911875646825
342	1101096	1101096: :: *Homo sapiens* transcribed sequences	457403	0.393655668577862	−0.355743747889559
343	1101119	1101119: IL17RE :: interleukin 17 receptor E	390823	0.039586216405584	0.044022252281821
344	1101128	1101128: MGC45419 :: Similar to calcium/calmodulin-dependent protein kinase 1, beta	436667	−0.241815550224320	0.169113348318235
345	1101149	1101149: :: *Homo sapiens* BIC noncoding mRNA, complete sequence	517226	0.029858079836277	−0.090026984564981
346	1101211	1101211: STRBP :: spermatid perinuclear RNA binding protein	287659	−0.250696465092268	0.025159511937388
347	1101272	1101272: DKFZp434H2111 :: hypothetical protein DKFZp434H2111	179089	0.009706674301822	−0.269133228709153

TABLE 2415-continued

GeneID.txt

Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
348	1101276	1101276: ERdj5 :: ER-resident protein ERdj5	1098	0.006940542351402	0.036655849606570
349	1101291	1101291: PPP3CA :: protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha)	272458	−0.133666602302100	0.284183973397199
350	1101295	1101295: FLJ40629 :: hypothetical protein FLJ40629	99807	−0.205479511626541	0.628330940348730
351	1101305	1101305: :: *Homo sapiens* cDNA clone IMAGE: 6301163, containing frame- shift errors	112742	0.473043674581829	−0.340194063635630
352	1101322	1101322: :: *Homo sapiens* similar to RIKEN cDNA 2900024C23 (LOC125704), mRNA	227699	−0.115836732640888	0.157977457392334
353	1101354	1101354: P2RY8 :: purinergic receptor P2Y, G-protein coupled, 8	111377	0.121615764539941	−0.111489709331474
354	1101416	1101416: FLJ41238 :: FLJ41238 protein	338851	0.215337920108734	−0.112373898517407
355	1101430	1101430: :: *Homo sapiens* transcribed sequences	418040	0.232052953728175	−0.060942343084998
356	1101439	1101439: TERF2 :: telomeric repeat binding factor 2	63335	−0.043553911594881	0.235168237858145
357	1101477	1101477: NUCB2 :: nucleobindin 2	423095	0.160097042319521	−0.161034301134445
358	1101478	1101478: MGC45780 :: hypothetical protein MGC45780	146246	0.560131166008654	−0.244033724256484
359	1101514	1101514: FLJ32363 :: FLJ32363 protein	88801	−0.213358324410450	0.584456949856772
360	1101566	1101566: :: *Homo sapiens* cDNA FLJ26876 fis, clone PRS09003	98558	0.547923586173589	−0.120576676385804
361	1101582	1101582: CKLFSF2 :: chemokine-like factor super family 2	195685	−0.164617883959410	0.163800631985653
362	1101586	1101586: GPR114 :: G protein-coupled receptor 114	187884	0.106771558157668	−0.040640551768368
363	1101628	1101628: LOC374654 :: similar to kinesin family member 21A; N-5 kinesin	441708	−0.330140484955472	0.649432137236986
364	1101634	1101634: :: *Homo sapiens* transcribed sequences	510588	−0.187767924798762	0.150456533036268
365	1101687	1101687: FNBP1 :: formin binding protein 1	440808	0.094301262952051	−0.183143704416937
366	1101708	1101708: MCOLN2 :: mucolipin 2	459526	−0.206286880737142	0.089733971257195
367	1101758	1101758: OSM :: oncostatin M	248156	0.427679944948121	−0.134414873641202
368	1101775	1101775: TTBK1 :: tau tubulin kinase 1	343820	−0.106506268653088	0.070427043729278
369	1101777	1101777: MGC33630 :: hypothetical protein MGC33630	359981	0.095553061289930	0.052525796095336
370	1101829	1101829: GPR92 :: G protein-coupled receptor 92	155538	−0.170716626765422	0.053271309080346
371	1101892	1101892: CCL27 :: chemokine (C-C motif) ligand 27	225948	0.090149523471370	0.082897675676425
372	1101905	1101905: :: *Homo sapiens* transcribed sequence with weak similarity to protein pir: I60307 (*E. coli*) I60307 beta-galactosidase, alpha peptide - *Escherichia coli*	170843	0.191141074226577	−0.112946854380485
373	1101944	1101944: :: *Homo sapiens* transcribed sequences	439064	0.511312767121963	−0.502590781948196
374	1101948	1101948: :: *Homo sapiens* mRNA full length insert cDNA clone EUROIMAGE 2138357	14411	0.109781853161187	−0.205413488978966
375	1101974	1101974: EPHB1 :: EphB1	272311	−0.151333397001395	−0.109778957757325
376	1102027	1102027: CD5 :: CD5 antigen (p56-62)	58685	0.051477533952002	−0.356234543694019
377	1102030	1102030: SLC20A1 :: solute carrier family 20 (phosphate transporter), member 1	110855	0.320766322780251	−0.218010866476956
378	1102081	1102081: :: *Homo sapiens* mRNA; cDNA DKFZp686L0948 (from clone DKFZp686L0948)	506977	−0.014999088235277	−0.142774708354838
379	1102165	1102165: :: *Homo sapiens* cDNA FLJ12909 fis, clone NT2RP2004400.	152460	0.286428236301455	−0.254747456654948
380	1102193	1102193: :: *Homo sapiens* transcribed sequences	22668	0.225058272151899	0.014961101827526
381	1102282	1102282: GCNT2 :: glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	934	0.048762986298498	−0.034020100922042
382	1102350	1102350: MGC42105 :: hypothetical protein MGC42105	25845	−0.026228919079674	−0.028985150162382
383	1102408	1102408: RAB3GAP :: RAB3 GTPase-ACTIVATING PROTEIN	306327	−0.084819962049070	0.075341563718927
384	1102415	1102415: CKLFSF5 :: chemokine-like factor super family 5	99272	0.082819335162941	−0.159143215400658
385	1102437	1102437: NUP62 :: nucleoporin 62 kDa	437023	0.418912844259920	−0.394203628829545
386	1102470	1102470: :: *Homo sapiens* transcribed sequence with weak similarity to protein ref: NP_060265.1 (*H. sapiens*) hypothetical protein FLJ20378 [*Homo sapiens*]	292915	0.105172178085776	−0.079629308072535
387	1102471	1102471: UNC5CL :: unc-5 homolog C (*C. elegans*)-like	158357	−0.094907736964586	−0.227754093321577
388	1102479	1102479: STK11 :: serine/threonine kinase 11 (Peutz-Jeghers syndrome)	301772	0.037690452961669	−0.137459558533489
389	1102537	1102537: :: *Homo sapiens* transcribed sequences	202151	0.108853907619606	−0.170270299488847
390	1102540	1102540: FCRH3 :: Fc receptor-like protein 3	434881	−0.153114207986084	0.059006826674309
391	1102633	1102633: :: *Homo sapiens* transcribed sequences	511124	−0.038532708435624	0.067743723935813
392	1102652	1102652: CKLFSF1 :: chemokine-like factor super family 1	343717	0.147463476236581	−0.107172237917063
393	1102654	1102654: KIAA0350 :: KIAA0350 protein	380599	−0.099657744074508	0.234041359355527
394	1102725	1102725: C21orf42 :: chromosome 21 open reading frame 42	234016	0.122651922822787	−0.047341180286403
395	1102744	1102744: :: *Homo sapiens* transcribed sequences	198671	−0.161033129852380	0.020948786809089
396	1102821	1102821: :: *Homo sapiens* mRNA; cDNA DKFZp686L14188 (from clone DKFZp686L14188)	202024	0.118625008373993	0.023472946360875
397	1102859	1102859: :: *Homo sapiens* cDNA FLJ42418 fis, clone BLADE2001987	446195	−0.065690917989146	0.168415178725098
398	1102885	1102885: CCNB3 :: cyclin B3	130310	−0.092278455245970	0.067527659533562
399	1102898	1102898: FKSG87 :: FKSG87 protein	145519	−0.013747221559531	−0.070588363385651
400	1102912	1102912: MGC15882 :: hypothetical protein MGC15882	194610	−0.011672180281967	0.144165981071462
401	1103054	1103054: :: *Homo sapiens* transcribed sequences	341531	0.223445105771884	−0.188710045144392
402	1103107	1103107: TAL2 :: T-cell acute lymphocytic leukemia 2	247978	−0.092171941247663	0.081590292816983
403	1103111	1103111: RPC155 :: polymerase (RNA) III (DNA directed) (155 kD)	436896	−0.300266776102017	0.238379729664432
404	1103120	1103120: TNFRSF10A :: tumor necrosis factor receptor superfamily, member 10a	401745	−0.021792053857555	0.031738694361568

TABLE 2415-continued

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Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
405	1103124	1103124: IRAK2 :: interleukin-1 receptor-associated kinase 2	424542	0.339830393625871	−0.235298214260479
406	1103134	1103134: MYLK2 :: myosin light chain kinase 2, skeletal muscle	86092	0.018064833082290	−0.026257429266506
407	1103137	1103137: EPHA8 :: EphA8	283613	−0.127428747463846	0.109096457119722
408	1103139	1103139: NOG :: noggin	248201	0.112737761541130	−0.019607674631529
409	1103224	1103224: HOXD8 :: homeo box D8	301963	0.288364072940970	−0.201074068135796
410	1103264	1103264: DKFZP434I0714 :: hypothetical protein DKFZP434I0714	142307	−0.322975964968122	0.264079373684896
411	1103272	1103272: :: *Homo sapiens*,clone IMAGE: 5312754, mRNA	137206	−0.100994707504263	0.025377105393344
412	1103284	1103284: TPCN2 :: two pore segment channel 2	186655	0.345601083093747	−0.227937096818758
413	1103303	1103303: C9orf52 :: chromosome 9 open reading frame 52	49605	0.399198468444216	−0.466790651317946
414	1103304	1103304: :: *Homo sapiens* clone CDABP0095 mRNA sequence	46919	0.065720206673849	−0.204868670295576
415	1103390	1103390: BPNT1 :: 3'(2'), 5'-bisphosphate nucleotidase 1	271752	0.136442060214909	0.191250282764510
416	1103398	1103398: FLJ10244 :: Ral-A exchange factor RalGPS2	220745	−0.361204561848680	0.406852093691962
417	1103420	1103420: MBNL2 :: muscleblind-like 2 (Drosophila)	372571	0.124346374266239	−0.191222651743482
418	1103475	1103475: EBF :: early B-cell factor	120785	−0.141391424615001	0.266048426373043
419	1103497	1103497: :: *Homo sapiens* mRNA; cDNA DKFZp761J1112 (from clone DKFZp761J1112)	50115	0.602843374034205	−0.450380110586192
420	1103504	1103504: :: *Homo sapiens* mRNA; cDNA DKFZp434P0810 (from clone DKFZp434P0810)	142517	0.038565684752532	−0.192091997201980
421	1103540	1103540: PRKWNK3 :: protein kinase, lysine deficient 3	92423	0.079917307313713	−0.146365124023944
422	1103639	1103639: KIAA1765 :: KIAA1765 protein	388304	−0.021903689889921	−0.015706254591252
423	1103711	1103711: :: *Homo sapiens* cDNA FLJ11833 fis, clone HEMBA1006579.	288718	−0.117756771697465	0.060550901815652
424	1103766	1103766: TP73 :: tumor protein p73	192132	−0.202367662929968	0.151460270224789
425	1103855	1103855: LOC153684 :: hypothetical protein LOC153684	259625	0.089916530004118	−0.401249389389032
426	1103858	1103858: PSMA3 :: proteasome (prosome, macropain) subunit, alpha type, 3	246240	0.036320631564259	−0.110232856407265
427	1103921	1103921: MS4A6A :: membrane-spanning 4-domains, subfamily A, member 6A	371612	0.079553258539825	−0.373450772906280
428	1103932	1103932: :: *Homo sapiens* clone HQ0319	31330	0.132220773211356	−0.148815074748484
429	1103982	1103982: MGC26226 :: beta cysteine string protein	142926	0.343337538439363	−0.063435983118753
430	1104072	1104072: :: *Homo sapiens* cDNA FLJ11586 fis, clone HEMBA1003720.	287429	−0.084275585872729	−0.086488630731059
431	1104175	1104175: KIAA1639 :: KIAA1639 protein	287383	0.240417880903839	−0.271486553982473
432	1104195	1104195: DNAH8 :: dynein, axonemal, heavy polypeptide 8	172101	0.125358396983583	−0.167980969699610
433	1104254	1104254: :: *Homo sapiens* cDNA FLJ12299 fis, clone MAMMA1001851.	492700	−0.151297255208119	0.081019729886145
434	1104373	1104373: :: *Homo sapiens* cDNA FLJ11709 fis, clone HEMBA1005133.	295633	−0.005756063382418	−0.123990346935139
435	1104545	1104545: :: *Homo sapiens* cDNA FLJ20182 fis, clone COLF0190	254477	−0.180198148895551	0.014637656197947
436	1104552	1104552: LOC96597 :: hypothetical protein LOC96597	193857	−0.294998056306420	0.136359195898485
437	1104840	1104840: :: *Homo sapiens* cDNA FLJ20112 fis, clone COL05405	482250	−0.057537557429858	−0.243362980194851
438	1104870	1104870: KIAA1486 :: KIAA1486 protein	210958	−0.077488245043722	−0.071174044111354
439	1104905	1104905: FLJ14753 :: hypothetical protein F1114753	13453	0.046259333205597	−0.072272236986864
440	1104910	1104910: IGL@ :: immunoglobulin lambda locus	−28	−0.021591390579858	0.046363051743828
441	1105001	1105001: :: *Homo sapiens* transcribed sequence with moderate similarity to protein sp: P39193 (*H. sapiens*) ALU6_HUMAN Alu subfamily SP sequence contamination warning entry	296695	−0.014192107773996	−0.089068020278894
442	1105178	1105178: GNG8 :: guanine nucleotide binding protein (G protein), gamma 8	283961	0.242480929979626	−0.272541916184894
443	1105248	1105248: :: *Homo sapiens* similar to Olfactory receptor 111 (Olfactory receptor 19-20) (OR19-20) (LOC126370), mRNA	−47	0.105352411032661	−0.084585315483932
444	1105668	1105668: :: Genomic sequence on chromosome 6q23	−62	−0.123114691799488	0.460907242218706
445	1105684	1105684: SLC38A5 :: solute carrier family 38, member 5	195155	−0.215379417617045	0.165637048268766
446	1105728	1105728: MGC24180 :: hypothetical protein MGC24180	13034	−0.273706962285229	0.476949972442765
447	1105732	1105732: FLJ32549 :: hypothetical protein FLJ32549	396626	−0.185773660713166	0.331821807671563
448	1105751	1105751: :: *Homo sapiens* transcribed sequences	176376	0.282674447127367	−0.540879875488500
449	1105759	1105759: ETV6 :: ets variant gene 6 (TEL oncogene)	171262	−0.063219469536356	−0.109967146172245
450	1105798	1105798: CKLFSF8 :: chemokine-like factor super family 8	154986	−0.226202356526156	0.078083683806646
451	1105814	1105814: :: *Homo sapiens* cDNA clone MGC: 61554 IMAGE: 6174351, complete cds	105223	−0.299247057499614	0.681904708275970
452	1105832	1105832: GSDML :: gasdermin-like	306777	−0.030059243970236	−0.173576690137134
453	1105838	1105838: ZBTB8 :: zinc finger and BTB domain containing 8	129837	0.350149587738349	−0.241921665436000
454	1105842	1105842: KIAA1145 :: KIAA1145 protein	173392	0.181381965671083	−0.293334666502675
455	1105854	1105854: FLJ14803 :: hypothetical protein FLJ14803	267245	−0.289009334412393	0.391432538881942
456	1105866	1105866: ZNF92 :: zinc finger protein 92 (HTF12)	9521	−0.217503504116412	0.242431438313012
457	1105900	1105900: :: *Homo sapiens* transcribed sequence with weak similarity to protein ref: NP_060312.1 (*H. sapiens*) hypothetical protein FLJ20489 [*Homo sapiens*]	525015	−0.039954870700039	0.063846335693864
458	1105915	1105915: :: *Homo sapiens* similar to seven transmembrane helix receptor (LOC346170), mRNA	332649	0.355873471451831	−0.549616497728459
459	1105935	1105935: :: *Homo sapiens* cDNA FLJ42786 fis, clone BRAWH3006761	444290	−0.004981640577809	0.009313018150590
460	1105936	1105936: KSR :: kinase suppressor of ras	276238	0.402034241649637	−0.508523150659365

TABLE 2415-continued

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Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
461	1105959	1105959: :: *Homo sapiens* cDNA FLJ43911 fis, clone TEST14010928	−52	0.045923922873497	−0.170316061302771
462	1105986	1105986: GCET2 :: germinal center expressed transcript 2	49614	−0.086493932869463	0.206833859689091
463	1106013	1106013: DNAJC3 :: DnaJ (Hsp40) homolog, subfamily C, member 3	6019	0.151020336613047	−0.095724381670206
464	1106015	1106015: FLJ12505 :: hypothetical protein FLJ12505	96885	0.003443352514749	−0.152871957172409
465	1106025	1106025: KIAA0746 :: KIAA0746 protein	49500	0.096092302067900	0.172477760689875
466	1106030	1106030: UNQ3030 :: ELLP3030	162185	−0.141195502114527	−0.119993933340636
467	1106043	1106043: FREB :: Fc receptor homolog expressed in B cells	266331	−0.332541268340366	0.343043552564271
468	1106053	1106053: MYO7B :: myosin VIIB	154578	0.020701117764110	−0.030706574277501
469	1106088	1106088: :: *Homo sapiens*, clone IMAGE: 4689481, mRNA	499235	0.232626061986162	−0.237498779839844
470	1106110	1106110: FOXP1 :: forkhead box P1	235860	−0.337961967073500	0.177654717311019
471	1106124	1106124: HAVCR2 :: hepatitis A virus cellular receptor 2	155111	0.433718618157491	−0.387490674695267
472	1106126	1106126: PPIB :: peptidylprolyl isomerase B (cyclophilin B)	434937	0.089296594603901	−0.151245276102718
473	1106159	1106159: :: *Homo sapiens* clone DNA49141 LGLL338 (UNQ338) mRNA, complete cds	208081	0.175796277722861	−0.190528520520377
474	1106196	1106196: :: *Homo sapiens* cDNA FLJ44273 fis, clone TOVAR2001281	142074	0.260032888023746	−0.248582710869995
475	1106204	1106204: SDP35 :: cell cycle control protein SDP35	445098	−0.281476076882118	0.762743730546786
476	1106230	1106230: FLJ90806 :: hypothetical protein FLJ90806	381225	−0.344498084563556	0.748294017497618
477	1106279	1106279: CAMK1D :: calcium/calmodulin-dependent protein kinase ID	130065	−0.131837900700824	−0.026370539273523
478	1106306	1106306: :: *Homo sapiens* transcribed sequence with weak similarity to protein pir: JC1405 (*H. sapiens*) JC1405 6-pyruvoyltetrahydropterin synthase - human	14204	0.222510499735753	−0.057963784683797
479	1106317	1106317: PRDM1 :: PR domain containing 1, with ZNF domain	381140	0.202422907441878	−0.278012993914435
480	1106323	1106323: :: *Homo sapiens* transcribed sequence with moderate similarity to protein ref: NP_056011.1 (*H. sapiens*) KIAA0922 protein [*Homo sapiens*]	442690	−0.316314328384987	0.085395654673848
481	1106394	1106394: :: *Homo sapiens* transcribed sequence with moderate similarity to protein ref: NP_060265.1 (*H. sapiens*) hypothetical protein FLJ20378 [*Homo sapiens*]	126932	0.022214815501423	−0.037232237149913
482	1106401	1106401: MGC15827 :: hypothetical protein MGC15827	11849	−0.187511903901925	0.040102924392511
483	1106415	1106415: :: *Homo sapiens* cDNA FLJ42409 fis, clone BLADE2000866	169071	0.211976489947730	−0.154318192993322
484	1106478	1106478: :: *Homo sapiens* transcribed sequences	119898	−0.094232371717217	0.225662520964665
485	1106522	1106522: :: *Homo sapiens* transcribed sequences	31903	−0.283587160786216	0.127680579514931
486	1106589	1106589: MIST1 :: class II bHLH protein MIST1	22627	−0.047877525130132	−0.002404261340158
487	1106722	1106722: FLJ14494 :: hypothetical protein FLJ14494	150458	−0.060926027646147	−0.002462635331184
488	1106781	1106781: LTB4R :: leukotriene B4 receptor	445013	0.007134788675039	−0.190509701181572
489	1106855	1106855: KIAA1909 :: KIAA1909 protein inhibits CDK4)	455101	−0.112998501100632	−0.036068093105841
490	1106908	1106908: CDKN2B :: cyclin-dependent kinase inhibitor 2B (p15,	72901	0.338895194330555	−0.124572813650838
491	1106935	1106935: CTLA4 :: cytotoxic T-lymphocyte-associated protein 4	247824	0.242155855304133	−0.478880430951650
492	1106990	1106990: :: *Homo sapiens* transcribed sequences	369561	0.325855303432119	−0.572765753817467
493	1107044	1107044: :: *Homo sapiens* transcribed sequences	163426	−0.248956419132601	−0.074083786735442
494	1107076	1107076: BCL2L10 :: BCL2-like 10 (apoptosis facilitator)	283672	−0.174263409358457	0.142807702201562
495	1107124	1107124: :: *Homo sapiens* transcribed sequences	130203	0.032157877924701	−0.055754120038729
496	1107190	1107190: MGC10986 :: hypothetical protein MGC10986	50601	−0.227953163675436	0.145694856605193
497	1107197	1107197: :: *Homo sapiens* transcribed sequence with strong similarity to protein pir: A48045 (*H. sapiens*) A48045 ribosomal protein S27, cytosolic - (reprolysin type) human	40838	0.001673335706470	−0.094560326284670
498	1107329	1107329: LHFPL3 :: lipoma HMGIC fusion partner-like 3	439124	0.049458571639358	0.016357240588240
499	1107348	1107348: SAMD3 :: sterile alpha motif domain containing 3	440508	0.383635070918944	−0.539687643012946
500	1107369	1107369: :: *Homo sapiens* similar to kinase, Germline helicase-Binding, mitogen/stress activated protein kinase, c-jun N-terminal kinase (kgb-2) (LOC375783), mRNA	512466	−0.113783226530150	0.145555603342058
501	1107457	1107457: ADAMTS2 :: a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 2	120330	0.311369108148620	−0.287615459819004
502	1107527	1107527: :: *Homo sapiens* clone DNA57836 GLPG464 (UNQ464) mRNA, complete cds	14706	0.214235142595632	−0.115893542930530
503	1107575	1107575: MGC52498 :: hypothetical protein MGC52498	424589	−0.256404584752245	0.133592527736628
504	1107637	1107637: :: *Homo sapiens* transcribed sequences	135491	0.216865140113354	−0.301114146422204
505	1107762	1107762: :: *Homo sapiens* transcribed sequences	58597	−0.026249400695137	0.105000264860588
506	1107838	1107838: :: *Homo sapiens* cDNA FLJ45323 fis, clone BRHIP3006390	−51	0.259677601688845	−0.248521794709865
507	1107997	1107997: IL22RA2 :: interleukin 22 receptor, alpha 2	126891	0.425997734470218	−0.065713810429864
508	1108088	1108088: :: *Homo sapiens* cDNA FLJ42957 fis, clone BRSTN2010500	441601	0.224696354704615	−0.357079341494018
509	1108200	1108200: :: *Homo sapiens* transcribed sequences	156135	0.122650831349266	−0.127800809316600
510	1108237	1108237: :: *Homo sapiens* transcribed sequence with weak similarity to protein sp: P39189 (*H. sapiens*) ALU2_HUMAN Alu subfamily SB sequence contamination warning entry	126232	0.150006719613133	−0.176773524991788
511	1108323	1108323: :: *Homo sapiens* transcribed sequence with moderate similarity to protein ref: NP_005898.1	520353	−0.056559071242791	−0.017831032028604

TABLE 2415-continued

GeneID.txt

Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
		(*H. sapiens*) mannosidase, alpha, class 1A, member 1; Man9-mannosidase [*Homo sapiens*]			
512	1108347	1108347: :: *Homo sapiens* transcribed sequences	121476	0.042929515389297	0.180791027467577
513	1108467	1108467: LOC285016 :: hypothetical protein LOC285016	346333	0.077616196801139	−0.053502666868708
514	1108473	1108473: FLJ34389 :: hypothetical protein FLJ34389	119878	0.154316813062797	−0.310176893404700
515	1108515	1108515: LCN6 :: lipocalin 6	98132	−0.052695347232417	−0.116970698134434
516	1108745	1108745: TEAD2 :: TEA domain family member 2	166556	−0.076084681856776	0.034540377111740
517	1108776	1108776: :: *Homo sapiens* cDNA FLJ30967 fis, clone HEART2000309, weakly similar to PTB-ASSOCIATED SPLICING FACTOR.	513346	0.008924647334006	−0.176389651304266
518	1108910	1108910: :: *Homo sapiens* transcribed sequence with strong similarity to protein ref: NP_542398.1 (*H. sapiens*) hypothetical protein MGC15407 [*Homo sapiens*]	351848	0.098503999737852	−0.107340932053734
519	1108925	1108925: KIAA0853 :: KIAA0853	136102	−0.067377606440520	−0.082618534020208
520	1108961	1108961: FLJ22531 :: hypothetical protein FLJ22531	292088	−0.420239196092467	0.357243765247241
521	1108970	1108970: :: *Homo sapiens* cDNA FLJ25559 fis, clone JTH02834	140489	−0.190988477846490	−0.089199166803974
522	1108988	1108988: NLK :: nemo-like kinase	3532	−0.030608793253581	0.089882597947955
523	1109058	1109058: FLJ38499 :: hypothetical protein FLJ38499	220277	−0.089335338277617	−0.065610169727742
524	1109107	1109107: FLJ10392 :: hypothetical protein FLJ10392	292925	−0.222666311239519	0.361324446901530
525	1109188	1109188: TNFRSF11A :: tumor necrosis factor receptor superfamily, member 11a, activator of NFKB	204044	0.280812133971682	−0.079369288251375
526	1109195	1109195: :: *Homo sapiens* cDNA FLJ41734 fis, clone HLUNG2018029	416155	−0.397342842842403	0.280143126653589
527	1109210	1109210: KCNK9 :: potassium channel, subfamily K, member 9	117010	−0.017281359417599	−0.083690216430606
528	1109220	1109220: GTF3A :: general transcription factor IIIA	445977	−0.429250063896662	0.332595945727056
529	1109505	1109505: MGC39372 :: hypothetical protein MGC39372	8162	0.075357807105408	−0.258052753389713
530	1109519	1109519: ALS2CR7 :: amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 7	348711	0.119836847940248	−0.019289786238779
531	1109530	1109530: :: *Homo sapiens* transcribed sequences	123244	−0.393536865160815	0.467473280881231
532	1109545	1109545: :: *Homo sapiens* cDNA FLJ41910 fis, clone PEBLM2007834	63187	−0.397583692461428	0.257403431395117
533	1109557	1109557: NP220 :: NP220 nuclear protein	444548	−0.135367039008095	−0.087433086257880
534	1109560	1109560: FARP1 :: FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	207428	0.033336743092972	−0.086075002105908
535	1109603	1109603: :: *Homo sapiens* transcribed sequences	317740	−0.351537059310986	0.129233831238711
536	1109732	1109732: :: *Homo sapiens* transcribed sequences	374124	0.300165387297213	−0.442390304962831
537	1109756	1109756: FNBP1 :: formin binding protein 1	191534	0.061372936344349	−0.209804169980805
538	1109827	1109827: GPR155 :: G protein-coupled receptor 154	127196	0.242983476822492	−0.418280288872407
539	1109913	1109913: CFLAR :: CASP8 and FADD-like apoptosis regulator	355724	0.207532726896619	−0.403624127184567
540	1110019	1110019: :: *Homo sapiens* transcribed sequences	31444	0.360190305256616	−0.350732887975507
541	1110070	1110070: :: *Homo sapiens* transcribed sequences	122464	0.271451755158904	−0.436226517954694
542	1110099	1110099: TA-KRP :: T-cell activation ketch repeat protein	116665	−0.445325720625770	0.477608651819287
543	1110198	1110198: :: *Homo sapiens* transcribed sequences	189046	−0.298393216431026	0.206436758539511
544	1110214	1110214: TCL6 :: T-cell leukemia/lymphoma 6	144519	−0.228315826191486	0.241502528970347
545	1110223	1110223: :: *Homo sapiens* transcribed sequence with moderate similarity to protein ref: NP_060265.1 (*H. sapiens*) hypothetical protein FLJ20378 [*Homo sapiens*]	212709	−0.430615107958902	0.454780809992101
546	1110284	1110284: ELL2 :: elongation factor, RNA polymerase II, 2	192221	0.191540498442880	−0.196150765305570
547	1110309	1110309: :: *Homo sapiens* transcribed sequences	105623	−0.215474752721580	0.156976932842674
548	1110313	1110313: FLJ39873 :: hypothetical protein FLJ39873	421750	0.069702715608045	−0.402411470521682
549	1110486	1110486: :: *Homo sapiens* transcribed sequences	445054	0.041319461801742	−0.116877614471182
550	1110608	1110608: CARD14 :: caspase recruitment domain family, member 14	306227	0.331483074884149	−0.441101824343302
551	1110610	1110610: :: *Homo sapiens* transcribed sequences	436906	0.028013446240267	−0.137363692502881
552	1110740	1110740: :: *Homo sapiens* transcribed sequences	416810	−0.195991680240688	0.007835013134266
553	1110852	1110852: :: *Homo sapiens* cDNA FLJ44885 fis, clone BRAMY2039630	196026	0.195262191447797	−0.125057253667954
554	1110871	1110871: :: *Homo sapiens* transcribed sequences	431753	0.138463783532811	−0.121059247114496
555	1111070	1111070: :: *Homo sapiens* transcribed sequence with moderate similarity to protein sp: P39192 (*H. sapiens*) ALU5_HUMAN Alu subfamily SC sequence contamination warning entry	202201	−0.050110477343771	−0.034250369213883
556	1111478	1111478: ERK8 :: extracellular signal-regulated kinase 8	133017	−0.120955857697857	−0.022637205903073
557	1111486	1111486: :: *Homo sapiens* cDNA FLJ42259 fis, clone TKIDN2011289	33024	0.187010000009634	−0.440447209346948
558	1111494	1111494: IMPDH2 :: IMP (inosine monophosphate) dehydrogenase 2	75432	−0.153973066560439	0.069775805472499
559	1111503	1111503: KBRAS2 :: I-kappa-B-interacting Ras-like protein 2	502910	−0.291172996398988	0.201225423261566
560	1111694	1111694: :: *Homo sapiens* transcribed sequences	157302	0.134965621816156	−0.064733017359634
561	1111807	1111807: OFD1 :: oral-facial-digital syndrome 1	6483	0.150829248997032	−0.253651952300585
562	1111946	1111946: :: *Homo sapiens* transcribed sequences	280881	−0.159828571994911	−0.162813334629172
563	1112019	1112019: :: *Homo sapiens* hypothetical LOC148280 (LOC148280), mRNA	196484	0.071877889993013	−0.048827289854263
564	1112052	1112052: :: *Homo sapiens* cDNA FLJ31445 fis, clone NT2NE2000864.	525361	−0.072204408405921	0.020806399380158
565	1112061	1112061: :: *Homo sapiens* cDNA FLJ90513 fis, clone NT2RP3004355.	43410	0.261039034660754	−0.299416343840340
566	1112256	1112256: ING3 :: inhibitor of growth family, member 3	143198	−0.125562046082355	0.143701534203396
567	1112344	1112344: :: *Homo sapiens* transcribed sequences	163242	−0.146713182348301	0.093803692880128

TABLE 2415-continued

GeneID.txt

Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
568	1112510	1112510: C14orf20 :: chromosome 14 open reading frame 20	314432	0.104763882180010	−0.081623532083441
569	1112521	1112521: :: *Homo sapiens* transcribed sequence with weak similarity to protein ref: NP_009032.1 (*H. sapiens*) sarcosine dehydrogenase; dimethylglycine dehydrogenase-like 1 [*Homo sapiens*]	244818	0.186313001167652	−0.195394559688516
570	1112552	1112552: :: *Homo sapiens* transcribed sequences	89029	0.113342903534869	−0.150103125377604
571	1112674	1112674: MAML3 :: mastermind-like 3 (*Drosophila*)	310320	0.342597737627672	−0.164070058630283
572	1112689	1112689: SERPINB9 :: serine (or cysteine) proteinase inhibitor, Glade B (ovalbumin), member 9	104879	0.143780170116893	−0.201560350725374
573	1112762	1112762: :: *Homo sapiens* mRNA; cDNA DKFZp686G24244 (from clone DKFZp686G24244)	208179	0.150233483486388	−0.257040066964479
574	1112764	1112764: IFNGR1 :: interferon gamma receptor 1	180866	0.374189546225726	−0.308519391383641
575	1112837	1112837: NRD1 :: nardilysin (N-arginine dibasic convertase)	4099	−0.128229223629686	0.093232911170115
576	1112849	1112849: :: *Homo sapiens* cDNA FLJ30333 fis, clone BRACE2007262.	208965	0.195240136859781	−0.389576368956041
577	1112871	1112871: :: *Homo sapiens* transcribed sequences	269493	−0.168246902555918	−0.116751272574924
578	1112935	1112935: NFAM1 :: NFAT activation molecule 1	436677	0.349529061115025	−0.429878706483203
579	1112981	1112981: :: *Homo sapiens* transcribed sequences	86650	−0.347953389898022	0.075874931243046
580	1113020	1113020: LOC161577 :: LOC161577 protein	373484	0.135613302187717	0.036736840045959
581	1113263	1113263: :: *Homo sapiens* cDNA FLJ46553 fis, clone THYMU3038879	435736	−0.148749974226581	0.101621280353679
582	1113435	1113435: :: *Homo sapiens* cDNA F1136210 fis, clone THYMU2000155	100636	0.034825029929201	−0.041626982844820
583	1113488	1113488: :: *Homo sapiens*, Similar to Eph receptor A7, clone IMAGE: 5273054, mRNA	129435	0.009080742764582	0.044988996497229
584	1113500	1113500: :: *Homo sapiens* cDNA FLJ37931 fis, clone CTONG2004397.	165900	0.272078126902990	−0.472804242511080
585	1113545	1113545: :: *Homo sapiens* cDNA FLJ46553 fis, clone THYMU3038879	435736	−0.008456873734778	0.007667610676891
586	1113555	1113555: :: *Homo sapiens* transcribed sequences	291993	−0.139176879567708	−0.125987425138451
587	1113589	1113589: BRAF :: v-raf murine sarcoma viral oncogene homolog B1	162967	−0.121772870570279	0.253077019731888
588	1113730	1113730: :: *Homo sapiens* transcribed sequences	293771	0.114063697377525	−0.237457649248006
589	1113769	1113769: :: *Homo sapiens* full length insert cDNA clone YZ11B11	46996	−0.393658244074914	0.080473352209481
590	1113783	1113783: FLJ14431 :: hypothetical protein FLJ14431	512793	−0.222799826904987	0.358817889836136
591	1113930	1113930: MGC35521 :: pellino 3 alpha lambda receptor)	24725	−0.055846303583161	0.210056043718661
592	1113972	1113972: IL28RA :: interleukin 28 receptor, alpha (interferon,	386334	−0.185314697287965	0.230148638275733
593	1113993	1113993: :: *Homo sapiens* transcribed sequence with moderate similarity to protein ref: NP_060265.1 (*H. sapiens*) hypothetical protein FLJ20378 [*Homo sapiens*]	131811	0.173371210700442	−0.239300750059210
594	1114017	1114017: :: *Homo sapiens* transcribed sequences	133255	0.308724526786620	−0.310188543930668
595	1114064	1114064: MYO3A :: myosin IIIA	148228	−0.300520026473458	0.088707148385397
596	1114109	1114109: DCAL1 :: dendritic cell-associated lectin-1	203041	−0.191231948777420	0.183023497372357
597	1114162	1114162: :: *Homo sapiens* transcribed sequences	435736	0.258730255563098	−0.182285726467478
598	1114351	1114351: PER1 :: period homolog 1 (*Drosophila*)	514664	0.065700609177559	−0.158512640752179
599	1114503	1114503: :: *Homo sapiens* transcribed sequences	170577	−0.049779313136241	−0.022799815868667
600	1114543	1114543: :: *Homo sapiens* transcribed sequences	156189	0.089727575328993	0.087415478817855
601	1114679	1114679: FLJ10904 :: hypothetical protein FLJ10904	16470	−0.313418247196259	0.568840722644661
602	1114715	1114715: PRKCN :: protein kinase C, nu	434387	−0.130103404630746	0.271352489418930
603	1114726	1114726: NLK :: nemo-like kinase	3532	−0.003199898057120	0.151365565219048
604	1114766	1114766: RCL1 :: RNA terminal phosphate cyclase-like 1	113052	−0.087555464003998	0.217546838114269
605	1114824	1114824: LIMD1 :: LIM domains containing 1	193370	−0.148463864832943	−0.033916294109501
606	1114853	1114853: ARHF :: ras homolog gene family, member F (in filopodia)	512618	0.016180684058318	0.014510688794040
607	1114877	1114877: AK5 :: adenylate kinase 5	18268	0.232192378472237	−0.050181060405945
608	1114893	1114893: BCL11A :: B-cell CLL/lymphoma 11A (zinc finger protein)	314623	−0.285216070613527	0.316813819176734
609	1114913	1114913: KIAA0748 :: KIAA0748 gene product	33187	−0.210416126426711	−0.027114426717208
610	1114967	1114967: SNX9 :: sorting nexin 9	7905	0.297577356714608	−0.280214852748554
611	1114970	1114970: PX19 :: px19-like protein	279529	−0.259951401409926	0.398931866897413
612	1114977	1114977: HSPC182 :: HSPC182 protein	30026	−0.026093693057321	0.046619049116212
613	1114981	1114981: XPO5 :: exportin 5	203206	−0.414069207073602	0.452995936587216
614	1114988	1114988: IBA2 :: ionized calcium binding adapter molecule 2	4944	0.122190372505081	−0.254155885467689
615	1115008	1115008: USP47 :: ubiquitin specific protease 47	441028	0.061008496955961	−0.051040281866044
616	1115012	1115012: SFRP2 :: secreted frizzled-related protein 2	31386	0.562213196556748	−0.283291904250779
617	1115034	1115034: NEK6 :: NIMA (never in mitosis gene a)-related kinase 6	387222	0.387672292810071	−0.139523546421676
618	1115052	1115052: MLL5 :: myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, *Drosophila*)	380021	0.039758974918423	−0.107953085916089
619	1115071	1115071: MAIL :: molecule possessing ankyrin repeats induced by lipopolysaccharide (MAIL), homolog of mouse	390476	−0.110817987747237	−0.026034205682165
620	1115073	1115073: BAL :: B aggressive lymphoma gene	131315	0.175136379072991	−0.372997453296061
621	1115128	1115128: BOK :: BCL2-related ovarian killer	293753	0.453574167307278	−0.255947563977460
622	1115160	1115160: LYAR :: hypothetical protein FLJ20425	425427	−0.406888533093173	0.586797819139025
623	1115176	1115176: CKLF :: chemokine-like factor	15159	0.192788341170135	0.046619194874123
624	1115186	1115186: MRPL47 :: mitochondrial ribosomal protein L47	283734	−0.420230779755538	0.571199396674772
625	1115194	1115194: TNFSF13B :: tumor necrosis factor (ligand) superfamily, member 13b	270737	0.475174704917625	−0.577483430130737
626	1115203	1115203: RPS6KL1 :: ribosomal protein S6 kinase-like 1	414481	0.015390697806082	0.003703623518892
627	1115226	1115226: KIAA1683 :: KIAA1683 protein	279718	−0.006255737442234	−0.282909576455325

TABLE 2415-continued

GeneID.txt

Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
628	1115253	1115253: BCL2L13 :: BCL2-like 13 (apoptosis facilitator)	310922	−0.183634412043605	0.327528714656041
629	1115271	1115271: DKFZp761C169 :: vasculin	71252	−0.368758470490713	0.067050568022970
630	1115286	1115286: TLR10 :: toll-like receptor 10	120551	−0.259024464746980	0.325663372291740
631	1115290	1115290: GSG2 :: haspin	193666	−0.482306139325171	0.619212145708754
632	1115303	1115303: LOC51244 :: hypothetical protein LOC51244	236257	−0.249657257281461	0.132172351643750
633	1115309	1115309: DKFZP434F091 :: DKFZP434F091 protein	443081	−0.240319754851193	0.324212477679077
634	1115329	1115329: MGC4796 :: Ser/Thr-like kinase	439658	0.040208198815129	−0.018704127839472
635	1115338	1115338: STK31 :: serine/threonine kinase 31	224355	−0.053536185139454	−0.107899047198573
636	1115347	1115347: HDAC8 :: histone deacetylase 8	112272	−0.028339713769977	0.390069214505358
637	1115360	1115360: PRO1073 :: PRO1073 protein	187199	0.015150578049290	−0.241074918363573
638	1115441	1115441: IL17RB :: interleukin 17 receptor B	5470	−0.063434193422993	−0.014102884885889
639	1115519	1115519: MRPS36 :: mitochondrial ribosomal protein S36	408914	−0.297069852346310	0.396251982430131
640	1115566	1115566: SP329 :: hypothetical protein SP329	−5	−0.118697538219683	−0.012110621854279
641	1115587	1115587: IRTA1 :: immunoglobulin superfamily receptor translocation associated 1	120260	−0.052595986636235	0.142155752703307
642	1115589	1115589: IRTA2 :: immunoglobulin superfamily receptor translocation associated 2	415950	−0.265747517495947	0.086115378248171
643	1115591	1115591: SSTK :: serine/threonine protein kinase SSTK	367871	−0.128216622193601	0.059300320623737
644	1115607	1115607: CDCA7 :: cell division cycle associated 7	435733	−0.262295427951373	0.573434589773844
645	1115621	1115621: RIOK1 :: RIO kinase 1 (yeast)	437474	−0.229738976454067	0.447251600358189
646	1115646	1115646: HECTD1 :: HECT domain containing 1	210850	−0.167037011541555	0.128780114293504
647	1115668	1115668: RTN4IP1 :: reticulon 4 interacting protein 1	155839	−0.320652767737175	0.306593126968738
648	1115673	1115673: IL17RC :: interleukin 17 receptor C	129959	0.311147392581012	−0.307735752432534
649	1115679	1115679: MGC4308 :: hypothetical protein MGC4308	8345	−0.482150529158383	0.656200427232135
650	1115695	1115695: TNFRSF18 :: tumor necrosis factor receptor superfamily, member 18	212680	0.126824051069217	−0.342995126764104
651	1115696	1115696: IL1F7 :: interleukin 1 family, member 7 (zeta)	166371	0.135412621405814	−0.163355627129065
652	1115704	1115704: IRF2BP2 :: interferon regulatory factor 2 binding protein 2	350268	0.258469364814320	−0.344047490615961
653	1115763	1115763: GPT2 :: glutamic pyruvate transaminase (alanine aminotransferase) 2	355862	−0.262333353369976	0.306381008609851
654	1115800	1115800: RPE :: ribulose-5-phosphate-3-epimerase	282260	−0.040365629363253	0.244729456838177
655	1115812	1115812: EIF2AK4 :: eukaryotic translation initiation factor 2 alpha kinase 4	412102	0.045588510962448	−0.074238327120572
656	1115813	1115813: CTL2 :: CTL2 gene	105509	−0.221292272952100	−0.028168066606459
657	1115829	1115829: FLJ12760 :: hypothetical protein FLJ12760	381204	−0.369293215780449	0.627808556684385
658	1115840	1115840: KIAA1728 :: KIAA1728 protein	437362	0.589217883938435	−0.416684777312541
659	1115876	1115876: TIMM23 :: translocase of inner mitochondrial membrane 23 homolog (yeast)	11866	−0.381689052923779	0.668903617669604
660	1115877	1115877: AKIP :: aurora-A kinase interacting protein	76239	−0.207980996336103	0.344080166383221
661	1115888	1115888: ZBTB4 :: zinc finger and BTB domain containing 4	35096	0.298080578428648	−0.657393520135917
662	1115892	1115892: STK35 :: serine/threonine kinase 35	100057	0.153696425328605	−0.057444650366930
663	1115895	1115895: RPC8 :: RNA polymerase III subunit RPC8	202505	−0.354708569266870	0.493832792496113
664	1115905	1115905: CLMN :: calmin (calponin-like, transmembrane)	301478	0.091056873434158	−0.184176927851473
665	1115916	1115916: MGC13204 :: hypothetical protein MGC13204	157148	−0.291511838717354	0.401615662719805
666	1115917	1115917: C6orf83 :: chromosome 6 open reading frame 83	284265	0.270658416402021	−0.224326090174219
667	1115953	1115953: ZNF385 :: zinc finger protein 385	278422	0.309580141662476	−0.371867309369219
668	1115955	1115955: FLJ31434 :: hypothetical protein FLJ31434	7988	−0.153394088626576	0.245407623813638
669	1115960	1115960: FRAS1 :: Fraser syndrome 1 (fused homolog, *Drosophila*)	15420	0.273562188785241	−0.206947496325428
670	1115965	1115965: STK36 :: serine/threonine kinase 36	26996	0.076460376343936	−0.120715477463443
671	1116001	1116001: SON :: SON DNA binding protein	430541	−0.038000317919225	−0.084548879882143
672	1116006	1116006: PTBP1 :: polypyrimidine tract binding protein 1	172550	−0.116461984704372	0.168668607063908
673	1116022	1116022: p30 :: nuclear protein p30 with YRPW motif-like	433422	−0.040984109576481	0.089035758253502
674	1116045	1116045: HEYL :: hairy/enhancer-of-split related	23823	0.298715739339798	−0.119650232859985
675	1116056	1116056: SOX8 :: SRY (sex determining region Y)-box 8	243678	0.060190043795450	−0.181079858440255
676	1116063	1116063: RALBP1 :: ralA binding protein 1	75447	−0.325857678019344	0.201375045992707
677	1116071	1116071: :: *Homo sapiens* mRNA; cDNA DKFZp586O031 (from clone DKFZp586O031)	502564	0.326268800212765	−0.248774088633798
678	1116073	1116073: MGC2408 :: hypothetical protein MGC2408	146161	−0.367109495613606	0.473361274829460
679	1116085	1116085: BACH2 :: BTB and CNC homology 1, basic leucine zipper transcription factor 2	88414	−0.246093347541336	0.093569752151740
680	1116103	1116103: LTBP3 :: latent transforming growth factor beta binding protein 3	289019	0.342939273133271	−0.369780572465803
681	1116122	1116122: DKFZp761O0113 :: hypothetical protein DKFZp761O0113	42768	−0.426616095442673	0.454893774014263
682	1116126	1116126: INSR :: insulin receptor	438669	0.454459408301310	−0.265298709888399
683	1116150	1116150: AMSH-LP :: associated molecule with the SH3 domain of STAM (AMSH) like protein	16229	−0.266185991205955	0.083378166105849
684	1116181	1116181: TAF15 :: TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68 kDa	402752	−0.062544122751392	0.006142039132744
685	1116219	1116219: NAP1L :: napsin B pseudogene	322854	−0.189162359230305	0.087037800792380
686	1116233	1116233: PAPPA :: pregnancy-associated plasma protein A	455350	0.251466587847966	−0.234146528669534

TABLE 2415-continued

GeneID.txt

Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
687	1116277	1116277: C10orf33 :: chromosome 10 open reading frame 33	118210	0.094135933623219	−0.201399654874422
688	1116317	1116317: :: *Homo sapiens* cDNA clone IMAGE: 4821863, partial cds	440776	−0.349847858207637	0.196451295358354
689	1116432	1116432: KIAA1259 :: hypothetical protein KIAA1259	525807	−0.153668990852911	−0.021062212586290
690	1116445	1116445: C6.1A :: c6.1A	301927	−0.091951874829546	0.312024877401937
691	1116593	1116593: NUDT6 :: nudix (nucleoside diphosphate linked moiety X)-type motif 6	422889	−0.159193962550566	0.195466499750992
692	1116666	1116666: DKFZP564B1162 :: hypothetical protein DKFZp564B1162	442801	−0.383182496994710	0.271520439423627
693	1116676	1116676: MSI2 :: musashi homolog 2 (*Drosophila*)	185084	−0.282699630935485	0.106190364019197
694	1116715	1116715: FLJ20574 :: hypothetical protein FLJ20574	123427	−0.193791635217953	0.316655728293102
695	1116826	1116826: KIAA1295 :: KIAA1295 protein	26204	0.721314629392213	−0.377963323366938
696	1116829	1116829: LOC90624 :: hypothetical protein LOC90624	115467	−0.335027077607960	0.336788815470870
697	1116844	1116844: CSNK1G1 :: casein kinase 1, gamma 1	405789	−0.058317444499632	0.048781994752368
698	1116854	1116854: :: *Homo sapiens* cDNA FLJ14309 fis, clone PLACE3000221.	438623	−0.043460166463994	−0.054723733397946
699	1116863	1116863: TLR4 :: toll-like receptor 4	174312	0.475472475469738	−0.300348466739063
700	1116879	1116879: TNIP2 :: TNFAIP3 interacting protein 2	325630	0.312285624448172	−0.214671720019409
701	1116958	1116958: PBF :: papillomavirus regulatory factor PRF-1	27410	−0.229333149413005	0.297027698820665
702	1116966	1116966: :: *Homo sapiens* cDNA FLJ11681 fis, clone HEMBA1004865.	301124	0.430855116758033	−0.468612200509693
703	1117023	1117023: BCL2L12 :: BCL2-like 12 (proline rich)	289052	−0.470242230711918	0.673594400951872
704	1117211	1117211: HSPC195 :: hypothetical protein HSPC195	356509	−0.350305805203319	0.246811696581929
705	1117245	1117245: HARS2 :: histidyl-tRNA synthetase 2	444706	−0.175279674549348	0.324254247578305
706	1117278	1117278: ACAS2 :: acetyl-Coenzyme A synthetase 2 (ADP forming)	14779	0.360381976214154	−0.450784610189096
707	1117298	1117298: :: *Homo sapiens* clone H3 anti-mucin1 light chain variable region mRNA, partial cds	449586	0.190383103967389	−0.163373239822681
708	1117343	1117343: BUCS1 :: butyryl Coenzyme A synthetase 1	306812	0.002627195859024	−0.128596603481639
709	1117350	1117350: FLJ10407 :: hypothetical protein FLJ10407	435982	−0.321428599824394	0.748139228339341
710	1117373	1117373: SEMA4B :: sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B	416077	0.070054264582924	−0.127801110560990
711	1117394	1117394: :: immunoglobulin heavy chain V region	−37	0.077318881358942	0.037375816090329
712	1117403	1117403: FBXO5 :: F-box only protein 5	272027	−0.270275521248700	0.472830182511296
713	1117517	1117517: Rgr :: Ral-GDS related protein Rgr	148656	0.085023272566783	−0.339585977561694
714	1117555	1117555: NOD3 :: NOD3 protein	128357	0.017413352126443	−0.259854083394416
715	1117599	1117599: MGC27085 :: hypothetical protein MGC27085	120277	−0.297300511558719	0.294857589419262
716	1117644	1117644: :: *Homo sapiens* transcribed sequence with moderate similarity to protein ref: NP_060312.1 (*H. sapiens*) hypothetical protein FLJ20489 [*Homo sapiens*]	34174	−0.043891472376770	−0.046176754319814
717	1117747	1117747: :: *Homo sapiens* hypothetical LOC256686 (LOC256686), mRNA	158272	−0.156604323316062	−0.033451106438867
718	1117800	1117800: :: *Homo sapiens* LOH11CR1F gene, loss of heterozygosity, 11, chromosomal region 1 gene F product	125166	−0.265166847772953	−0.035683423757495
719	1117835	1117835: CR1L :: complement component (3b/4b) receptor 1-like	89688	0.276367621813185	−0.053572671658412
720	1117853	1117853: :: *Homo sapiens* transcribed sequence with strong similarity to protein pdb: 1BGM (*E. coli*) O Chain O, Beta-Galactosidase (Chains I-P)	268724	−0.098130731820168	−0.212694005004947
721	1117977	1117977: :: Unknown	−40	−0.092034285015709	−0.087991577681170
722	1118148	1118148: ZBP1 :: Z-DNA binding protein 1	−2	0.152802746225995	−0.384059831029427
723	1118228	1118228: :: *Homo sapiens* hypothetical LOC339541 (LOC339541), mRNA	173679	−0.201134297495305	−0.035774496444703
724	1118286	1118286: :: *Homo sapiens* transcribed sequences	147381	−0.379333390537201	0.451787557640792
725	1118347	1118347: ITGA4 :: integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)	145140	0.055639362171438	−0.253900279097663
726	1118414	1118414: FCRH1 :: Fc receptor-like protein 1	415473	−0.092952084806830	0.080500778588061
727	1118573	1118573: GSK3A :: glycogen synthase kinase 3 alpha	435970	−0.351134088845212	0.325972671457629
728	1118612	1118612: NPR1 :: natriuretic peptide receptor A/guanylate cyclase A (atrionatriuretic peptide receptor A)	438864	0.155477087321411	−0.159267282520294
729	1118621	1118621: CGI-96 :: CGI-96 protein	239934	−0.292642395717393	0.473939710525280
730	1118659	1118659: MAPK7 :: mitogen-activated protein kinase 7	150136	−0.051883863404460	−0.141266790241099
731	1118681	1118681: MAFF :: v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	460889	0.647665560383226	−0.362054883818999
732	1118684	1118684: MIPEP :: mitochondrial intermediate peptidase	68583	−0.328213532979876	0.407014917128267
733	1118708	1118708: MRC2 :: mannose receptor, C type 2	7835	0.754467580767100	−0.424450710158145
734	1118736	1118736: HIP1R :: huntingtin interacting protein-1-related	96731	0.039974764124592	0.066130790515351
735	1118772	1118772: STK10 :: serine/threonine kinase 10	16134	0.030402652799298	−0.421006508321850
736	1118835	1118835: ARHGAP8 :: Rho GTPase activating protein 8	102336	0.311235535095650	−0.396387124788783
737	1118861	1118861: PEX16 :: peroxisomal biogenesis factor 16	100915	0.029858540970158	−0.043179604561765
738	1118939	1118939: PLA2G4B :: phospholipase A2, group IVB (cytosolic)	198161	0.217116959349918	−0.409971040705761
739	1118949	1118949: IAN4L1 :: immune associated nucleotide 4 like 1 (mouse)	412331	0.142206792172366	−0.512656283348152
740	1118963	1118963: :: *Homo sapiens* cDNA FLJ42818 fis, clone BRCAN2015371	−53	−0.064431805022853	−0.171638599308421
741	1119003	1119003: EIF4G2 :: eukaryotic translation initiation factor 4 gamma, 2	183684	−0.133347112654528	0.112848239923822
742	1119007	1119007: GDI2 :: GDP dissociation inhibitor 2	56845	−0.382242002371530	0.470849494659261
743	1119015	1119015: RPS5 :: ribosomal protein S5	378103	−0.384887386329798	0.343492082296666

TABLE 2415-continued

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Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
744	1119039	1119039: SMAP :: small acidic protein	447513	−0.301459283715944	0.321366636007445
745	1119046	1119046: DSP :: desmoplakin	349499	0.323961715872806	−0.285977303076169
746	1119056	1119056: UBB :: ubiquitin B	356190	0.028334739217252	−0.196600028796086
747	1119061	1119061: MLP :: MARCKS-like protein	75061	0.003502916223950	0.225174791526797
748	1119068	1119068: S100A11 :: S100 calcium binding protein A11 (calgizzarin)	417004	0.629923256421890	−0.515428592835300
749	1119070	1119070: CD63 :: CD63 antigen (melanoma 1 antigen)	445570	0.600681920968223	−0.477615687123999
750	1119071	1119071: UBE2D3 :: ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	411826	−0.152909102348063	0.188214633454210
751	1119072	1119072: XBP1 :: X-box binding protein 1	437638	−0.073072023747563	0.071992250474592
752	1119074	1119074: CD81 :: CD81 antigen (target of antiproliferative antibody 1)	54457	0.460590309714153	−0.316306331329744
753	1119076	1119076: GLO1 :: glyoxalase I	268849	−0.485600996113581	0.560563431563709
754	1119090	1119090: FKBP1A :: FK506 binding protein 1A, 12 kDa	374638	−0.167154087365112	0.256238003053443
755	1119111	1119111: TEGT :: testis enhanced gene transcript (BAX inhibitor 1)	35052	0.117050432650685	−0.195242199439661
756	1119139	1119139: DNAJA1 :: DnaJ (Hsp40) homolog, subfamily A, member 1	388392	−0.106484916885441	0.145147017992332
757	1119155	1119155: DEK :: DEK oncogene (DNA binding)	110713	−0.246967603602159	0.515244500061071
758	1119171	1119171: ACTA2 :: actin, alpha 2, smooth muscle, aorta	208641	0.761340632898360	−0.452825423217664
759	1119173	1119173: MDH1 :: malate dehydrogenase 1, NAD (soluble)	75375	−0.127094708879037	0.258023826328223
760	1119183	1119183: RBM4 :: RNA binding motif protein 4	211203	−0.428472864406565	0.396021571030955
761	1119186	1119186: CD9 :: CD9 antigen (p24)	387579	0.381081618660027	−0.168246859132740
762	1119202	1119202: TGM2 :: transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)	512708	0.435342892077885	−0.323641082136671
763	1119209	1119209: RCN1 :: reticulocalbin 1, EF-hand calcium binding domain	167791	0.571093261465677	−0.388503774716019
764	1119212	1119212: MMP2 :: matrix metalloproteinase 2 (gelatinase A, 72 kDa gelatinase, 72 kDa type IV collagenase)	367877	0.910359724823026	−0.353773466993166
765	1119237	1119237: GPNMB :: glycoprotein (transmembrane) nmb	389964	0.610412926960347	−0.312611665779815
766	1119239	1119239: HAX1 :: HS1 binding protein	199625	−0.465663098537398	0.508445219571895
767	1119243	1119243: ATP6V0E :: ATPase, H+ transporting, lysosomal 9 kDa, V0 subunit e	440165	0.250369153999525	−0.272868162874347
768	1119245	1119245: FBXO7 :: F-box only protein 7	5912	−0.231979379939439	0.094393580671121
769	1119251	1119251: SEPW1 :: selenoprotein W, 1	433941	0.410533826180220	−0.461863162528100
770	1119258	1119258: HDAC1 :: histone deacetylase 1	88556	−0.067200590610105	0.310238210060964
771	1119260	1119260: LGMN :: legumain	18069	−0.000745128042019	−0.229008754509885
772	1119263	1119263: C12orf8 :: chromosome 12 open reading frame 8	511762	−0.476397099487274	0.260114831651188
773	1119268	1119268: ILK :: integrin-linked kinase	6196	0.333491562996737	−0.117810222588527
774	1119294	1119294: TOP2A :: topoisomerase (DNA) II alpha 170 kDa	156346	−0.344066595023870	0.821915015867740
775	1119300	1119300: STK25 :: serine/threonine kinase 25 (STE20 homolog, yeast)	155206	−0.283256434250802	0.270411211177143
776	1119311	1119311: ENC1 :: ectodermal-neural cortex (with BTB-like domain)	104925	0.258463564894777	−0.221825498871520
777	1119317	1119317: SLC9A3R1 :: solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 1	396783	−0.014658638115010	−0.191639458116196
778	1119325	1119325: OAZ2 :: ornithine decarboxylase antizyme 2	74563	0.242847106449200	−0.195053295490539
779	1119334	1119334: ITGA5 :: integrin, alpha 5 (fibronectin receptor, alpha polypeptide)	149609	0.742369051797669	−0.374025974512821
780	1119350	1119350: ALDH2 :: aldehyde dehydrogenase 2 family (mitochondrial)	331141	0.608086049431527	−0.390151454914606
781	1119361	1119361: TIA1 :: TIA1 cytotoxic granule-associated RNA binding protein	391858	−0.026668805173817	−0.189784545154414
782	1119365	1119365: MAPKAPK2 :: mitogen-activated protein kinase-activated protein kinase 2	75074	−0.059278973835078	−0.035574775797084
783	1119369	1119369: JUNB :: jun B proto-oncogene	400124	0.460486004055358	−0.369644781391790
784	1119375	1119375: PPIF :: peptidylprolyl isomerase F (cyclophilin F)	381072	−0.116077021105342	0.359654077539207
785	1119383	1119383: IGFBP4 :: insulin-like growth factor binding protein 4	1516	0.627827304350395	−0.357001758702634
786	1119390	1119390: CBX1 :: chromobox homolog 1 (HP1 beta homolog *Drosophila*)	77254	−0.286085532090585	0.535476131212779
787	1119400	1119400: DUSP3 :: dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	181046	0.384346199622817	−0.392842766782088
788	1119401	1119401: FHL1 :: four and a half LIM domains 1	421383	0.342758824589712	−0.226789376446408
789	1119417	1119417: FAT :: FAT tumor suppressor homolog 1 (*Drosophila*)	166994	0.742466957569965	−0.454543207590739
790	1119424	1119424: OAT :: ornithine aminotransferase (gyrate atrophy)	75485	0.460491519833347	−0.147080268886920
791	1119438	1119438: BST2 :: bone marrow stromal cell antigen 2	118110	0.327211434111655	−0.338002355723367
792	1119443	1119443: JAK1 :: Janus kinase 1 (a protein tyrosine kinase)	436004	−0.025586939182056	0.025836310250933
793	1119445	1119445: KRT19 :: keratin 19	309517	0.265474647684479	−0.137484590496784
794	1119448	1119448: ITGA6 :: integrin, alpha 6	212296	0.412797513436557	−0.255244929698541
795	1119460	1119460: SFRS4 :: splicing factor, arginine/serine-rich 4	76122	−0.219899785493274	0.375669306197949
796	1119462	1119462: CCND3 :: cyclin D3	83173	0.050395367966880	0.143613724160422
797	1119466	1119466: MYBL2 :: v-myb myeloblastosis viral oncogene homolog (avian)-like 2	179718	−0.410801274991122	0.741902823834935
798	1119467	1119467: TUBG1 :: tubulin, gamma 1	21635	−0.430720113786154	0.761998646900583
799	1119475	1119475: SGK :: serum/glucocorticoid regulated kinase	296323	0.458464756569231	−0.179908409244619
800	1119477	1119477: CD14 :: CD14 antigen	75627	0.374658686322277	−0.449833721869226
801	1119479	1119479: TP53 :: tumor protein p53 (Li-Fraumeni syndrome)	426890	−0.273520348057380	0.189062886154923
802	1119488	1119488: MTHFD2 :: methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase	154672	−0.190082814208343	0.507122961206866

TABLE 2415-continued

GeneID.txt

Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
803	1119503	1119503: POLR2B :: polymerase (RNA) II (DNA directed) polypeptide B, 140 kDa	149353	−0.276147772083673	0.452575668664126
804	1119510	1119510: KRT5 :: keratin 5 (epidermolysis bullosa simplex, Dowling-Meara/Kobner/Weber-Cockayne types)	433845	0.173908847805493	−0.148894839466960
805	1119515	1119515: HDAC2 :: histone deacetylase 2	3352	−0.296163638102074	0.420133073064140
806	1119516	1119516: PRKAB1 :: protein kinase, AMP-activated, beta 1 non-catalytic subunit	6061	−0.032255323397443	0.048963236579424
807	1119519	1119519: BNIP3 :: BCL2/adenovirus E1B 19 kDa interacting protein 3	79428	0.070790959573082	0.034778072787655
808	1119533	1119533: WDR23 :: WD repeat domain 23	283976	−0.176058140462130	0.021248719822432
809	1119537	1119537: ARAF1 :: v-raf murine sarcoma 3611 viral oncogene homolog 1	423807	−0.080692792057249	0.107243029276800
810	1119541	1119541: FARP1 :: FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	207428	0.319164983800046	−0.239696774568353
811	1119546	1119546: GNG10 :: guanine nucleotide binding protein (G protein), gamma 10	433898	0.366292039811560	−0.247632394673373
812	1119557	1119557: SNK :: serum-inducible kinase	398157	0.703474357008969	−0.369781265328559
813	1119559	1119559: CPD :: carboxypeptidase D	5057	0.477567634089383	−0.484691652037264
814	1119561	1119561: FURIN :: furin (paired basic amino acid cleaving enzyme)	59242	0.203389107343861	−0.194260517260963
815	1119564	1119564: ALCAM :: activated leukocyte cell adhesion molecule	10247	−0.174212933203010	−0.033522636800175
816	1119565	1119565: CIB1 :: calcium and integrin binding 1 (calmyrin)	135471	0.077380378763426	−0.165969584136888
817	1119566	1119566: ARPC1B :: actin related protein 2/3 complex, subunit 1B, 41 kDa	433506	0.030123569365004	−0.044674445410727
818	1119568	1119568: PPP1R12B :: protein phosphatase 1, regulatory (inhibitor) subunit 12B	130760	0.031485901809650	−0.198501575206590
819	1119582	1119582: SIAT1 :: sialyltransferase 1 (beta-galactoside alpha-2,6-sialyltransferase)	2554	−0.494168402771241	0.205936873075801
820	1119611	1119611: BIRC2 :: baculoviral IAP repeat-containing 2	289107	0.153685965242011	−0.064993693037635
821	1119633	1119633: PRPF4B :: PRP4 pre-mRNA processing factor 4 homolog B (yeast)	198891	−0.349211363145953	0.381772530527532
822	1119636	1119636: RIOK3 :: RIO kinase 3 (yeast)	209061	0.081817545037163	−0.207039528628000
823	1119639	1119639: BS69 :: adenovirus 5 E1A binding protein	145894	0.220729171963144	−0.452502889318328
824	1119647	1119647: PRKCL1 :: protein kinase C-like 1	2499	−0.359787604971237	0.315822728005629
825	1119652	1119652: CHPF :: chondroitin polymerizing factor	458374	0.231475094432380	−0.103490870734691
826	1119655	1119655: :: *Homo sapiens* hypothetical gene supported by NM_018065 (LOC374293), mRNA	407181	0.271438641659253	−0.320546868315670
827	1119667	1119667: ARL7 :: ADP-ribosylation factor-like 7	111554	0.344025040053841	−0.364460171367448
828	1119680	1119680: NNMT :: nicotinamide N-methyltransferase	364345	0.849481601667150	−0.407473012706719
829	1119683	1119683: C8FW :: phosphoprotein regulated by mitogenic pathways	444947	0.175976631640823	−0.225708506051835
830	1119684	1119684: TM4SF2 :: transmembrane 4 superfamily member 2	439586	0.370013597929631	−0.285991368891065
831	1119694	1119694: BMI1 :: B lymphoma Mo-MLV insertion region (mouse)	380403	−0.051029087019197	−0.238731608205694
832	1119699	1119699: PDGFRB :: platelet-derived growth factor receptor, beta polypeptide	307783	0.727905513250235	−0.426870326630435
833	1119706	1119706: GAK :: cyclin G associated kinase	153227	0.047312310573583	−0.212371832168573
834	1119708	1119708: SERPINF1 :: serine (or cysteine) proteinase inhibitor, Clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1	173594	0.818127717962518	−0.494784353536062
835	1119709	1119709: FRAP1 :: FK506 binding protein 12-rapamycin associated protein 1	338207	−0.100924735319417	0.123840911452660
836	1119725	1119725: CSK :: c-src tyrosine kinase	77793	−0.342193698499374	0.386680662501259
837	1119729	1119729: TK1 :: thymidine kinase 1, soluble	164457	−0.178159168560846	0.621943500601026
838	1119734	1119734: ITGAV :: integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)	436873	0.880095069226405	−0.341583015797392
839	1119752	1119752: BASP1 :: brain abundant, membrane attached signal protein 1	511745	0.039736680045055	0.128939385773097
840	1119765	1119765: IGSF3 :: immunoglobulin superfamily, member 3	81234	0.043154074341915	−0.220966017200884
841	1119766	1119766: MYST3 :: MYST histone acetyltransferase (monocytic leukemia) 3	93231	−0.201625331472481	0.020169749212703
842	1119775	1119775: HDAC5 :: histone deacetylase 5	9028	−0.047258845589192	−0.144307812706093
843	1119780	1119780: MPI :: mannose phosphate isomerase	75694	−0.249376705561104	0.265128946611980
844	1119782	1119782: TRB2 :: tribbles homolog 2	155418	0.015840462162037	−0.057383709246075
845	1119799	1119799: BCL7B :: B-cell CLL/lymphoma 7B	408219	−0.301353371006817	0.333515975123573
846	1119802	1119802: PITPNB :: phosphotidylinositol transfer protein, beta	7370	−0.279346455254819	0.285255269810126
847	1119807	1119807: MAPK14 :: mitogen-activated protein kinase 14	79107	−0.103247521829532	0.086030304232384
848	1119808	1119808: IRF1 :: interferon regulatory factor 1	80645	0.214974139783435	−0.487005406874141
849	1119813	1119813: PRKCD :: protein kinase C, delta	155342	−0.095881893640700	0.021482940393706
850	1119817	1119817: TNKS :: tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase	409194	−0.047999395366169	0.021277604032916
851	1119820	1119820: CSNK1G2 :: casein kinase 1, gamma 2	181390	0.101155785845682	−0.029637775969762
852	1119826	1119826: TYMS :: thymidylate synthetase	87491	−0.371762638989175	0.732371010652222
853	1119838	1119838: GNAQ :: guanine nucleotide binding protein (G protein), q polypeptide	469951	0.608858917985059	−0.451610474749559
854	1119841	1119841: LYN :: v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	80887	−0.385987016514418	0.241969623986561

TABLE 2415-continued

GeneID.txt

Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
855	1119846	1119846: POLR2K :: polymerase (RNA) II (DNA directed) polypeptide K, 7.0 kDa	351475	−0.144645595994654	0.345426430436713
856	1119860	1119860: MAP2K1 :: mitogen-activated protein kinase kinase 1	132311	0.081523729635758	0.107249499092262
857	1119868	1119868: TNFSF10 :: tumor necrosis factor (ligand) superfamily, member 10	387871	0.361597221904698	−0.553123293632563
858	1119872	1119872: OSR1 :: oxidative-stress responsive 1	95220	−0.348692541889615	0.471254203040539
859	1119873	1119873: CPSF5 :: cleavage and polyadenylation specific factor 5, 25 kDa	446393	−0.235700347405962	0.584626529399289
860	1119876	1119876: DUSP11 :: dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)	14611	−0.190844618983350	0.299994415193974
861	1119878	1119878: CCNB2 :: cyclin B2	194698	−0.291964604694904	0.784720009084587
862	1119880	1119880: FMOD :: fibromodulin	442844	0.561780493586553	−0.548252797794380
863	1119884	1119884: PTPN1 :: protein tyrosine phosphatase, non-receptor type 1	418004	−0.007199191487470	0.033799420525184
864	1119889	1119889: PDCD4 :: programmed cell death 4 (neoplastic transformation inhibitor)	257697	−0.387457805191161	0.042363269173874
865	1119894	1119894: ACY1 :: aminoacylase 1	334707	−0.350776535174252	0.264656076550105
866	1119895	1119895: PRKACB :: protein kinase, cAMP-dependent, catalytic, beta	156324	−0.005364457034190	−0.120396590491985
867	1119903	1119903: p44S10 :: proteasome regulatory particle subunit p44S10	350939	−0.492672600495662	0.540375320876622
868	1119906	1119906: ROCK2 :: Rho-associated, coiled-coil containing protein kinase 2	58617	−0.037457516068621	0.095524196892679
869	1119907	1119907: CASP3 :: caspase 3, apoptosis-related cysteine protease	141125	−0.261343210354826	0.147838406405152
870	1119916	1119916: OXCT :: 3-oxoacid CoA transferase	177584	−0.420512115118106	0.570427247250647
871	1119919	1119919: STK39 :: serine threonine kinase 39 (STE20/SPS1 homolog, yeast)	199263	0.036380914794334	0.137316042469944
872	1119920	1119920: MAPKAPK3 :: mitogen-activated protein kinase-activated protein kinase 3	234521	0.033224901009291	−0.290845134954234
873	1119924	1119924: INPP1 :: inositol polyphosphate-1-phosphatase	32309	0.323225977540793	−0.354327057539113
874	1119928	1119928: CLPP :: ClpP caseinolytic protease, ATP-dependent, proteolytic subunit homolog (*E. coli*)	317335	−0.383473848217803	0.493264263215279
875	1119936	1119936: AMSH :: associated molecule with the SH3 domain of STAM	12479	−0.212970492666360	0.177745673538672
876	1119939	1119939: AHR :: aryl hydrocarbon receptor	170087	0.256970446704131	−0.173340326402877
877	1119946	1119946: AGT :: angiotensinogen (serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 8)	19383	−0.083357114527211	0.115295274530192
878	1119950	1119950: TAF15 :: TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68 kDa	402752	−0.306440406993752	0.338606484125856
879	1119972	1119972: EPHB4 :: EphB4	437008	0.213883588482106	−0.276537887742675
880	1119979	1119979: MSH6 :: mutS homolog 6 (*E. coli*)	445052	−0.210797269834120	0.563006959737033
881	1119983	1119983: ANK2 :: ankyrin 2, neuronal	409783	0.239718352750997	−0.362446515998409
882	1119995	1119995: IL1R1 :: interleukin 1 receptor, type I	82112	0.880259393296759	−0.523750968501772
883	1119997	1119997: STK38 :: serine/threonine kinase 38	367811	0.116255029911486	−0.270963700598019
884	1119998	1119998: C1QB :: complement component 1, q subcomponent, beta polypeptide	8986	−0.064997812238848	−0.308036422540148
885	1120008	1120008: DYRK2 :: dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	173135	0.139680495957613	−0.138798127049231
886	1120011	1120011: SMARCA3 :: SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3	3068	−0.393821573018423	0.440572225264925
887	1120016	1120016: STARD3 :: START domain containing 3	77628	0.197666440603128	−0.216926094278756
888	1120023	1120023: LTBR :: lymphotoxin beta receptor (TNFR superfamily, member 3)	1116	0.449547762265972	−0.391678588451956
889	1120024	1120024: INPP5A :: inositol polyphosphate-5-phosphatase, 40 kDa	408063	0.343186933129608	−0.211635679580085
890	1120026	1120026: STAT5A :: signal transducer and activator of transcription 5A	437058	0.233594777682906	−0.490211434372936
891	1120038	1120038: CHSY1 :: carbohydrate (chondroitin) synthase 1	110488	0.469412842283311	−0.278608622720236
892	1120044	1120044: BCAS2 :: breast carcinoma amplified sequence 2	22960	−0.118171434304281	0.380613118455193
893	1120053	1120053: COG2 :: component of oligomeric golgi complex 2	82399	−0.322127622203961	0.285853667630216
894	1120055	1120055: MADH2 :: MAD, mothers against decapentaplegic homolog 2 (*Drosophila*)	110741	−0.198373862314482	0.151233465555872
895	1120059	1120059: THBS2 :: thrombospondin 2	458354	0.823561522648464	−0.307597847291106
896	1120063	1120063: SDF2 :: stromal cell-derived factor 2	118684	−0.151141188451317	0.205246091448918
897	1120069	1120069: CSF1R :: colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog	174142	0.586483471012455	−0.538330757879298
898	1120072	1120072: PTK2B :: PTK2B protein tyrosine kinase 2 beta	405474	0.025565694638970	−0.081698039331191
899	1120079	1120079: IMPA2 :: inositol(myo)-1(or 4)-monophosphatase 2	5753	−0.142422649698462	0.380777710316534
900	1120081	1120081: PDGFRA :: platelet-derived growth factor receptor, alpha polypeptide	74615	0.801797080306997	−0.363577157808831
901	1120082	1120082: RB1 :: retinoblastoma 1 (including osteosarcoma)	408528	−0.092716888870664	0.307873154083231
902	1120088	1120088: HAT1 :: histone acetyltransferase 1	13340	−0.233187350154903	0.685057151008412
903	1120089	1120089: DAPK1 :: death-associated protein kinase 1	244318	0.466586398338559	−0.514289733675279
904	1120090	1120090: BCL6 :: B-cell CLL/lymphoma 6 (zinc finger protein 51)	155024	0.144941230662303	0.048693731993595
905	1120108	1120108: ARHG :: ras homolog gene family, member G (rho G)	75082	0.190899333887631	−0.071434473852746

TABLE 2415-continued

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Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
906	1120120	1120120: ABCC4 :: ATP-binding cassette, sub-family C (CFTR/MRP), member 4	307915	0.227392907322269	−0.077875606978302
907	1120121	1120121: CDK9 :: cyclin-dependent kinase 9 (CDC2-related kinase)	150423	0.045051374703949	−0.071571722929467
908	1120127	1120127: CDC2 :: cell division cycle 2, G1 to S and G2 to M	334562	−0.356711902630063	0.859586003083525
909	1120128	1120128: MAPK9 :: mitogen-activated protein kinase 9	348446	0.053836424867107	0.050716859954676
910	1120129	1120129: TLE1 :: transducin-like enhancer of split 1 (E(sp1) homolog, *Drosophila*)	406491	−0.147138605178005	0.004837891616427
911	1120134	1120134: IL4R :: interleukin 4 receptor	75545	−0.046782309391954	−0.158009856362830
912	1120137	1120137: FCGBP :: Fc fragment of IgG binding protein	111732	−0.021179847554413	0.084901186125138
913	1120145	1120145: CDH3 :: cadherin 3, type 1, P-cadherin (placental)	191842	0.208811388283192	−0.196206998994574
914	1120152	1120152: IRF2 :: interferon regulatory factor 2	83795	−0.245349312777798	−0.021862320330082
915	1120153	1120153: LMNB1 :: lamin B1	89497	−0.349360475211000	0.567523295277270
916	1120160	1120160: KIAA0355 :: KIAA0355 gene product	436976	−0.006389482890844	−0.147844881582699
917	1120163	1120163: DCK :: deoxycytidine kinase	709	−0.262602853143119	0.474753625341165
918	1120191	1120191: SOCS2 :: suppressor of cytokine signaling 2	405946	0.205081336164991	−0.120603880465586
919	1120194	1120194: RPS6KA1 :: ribosomal protein S6 kinase, 90 kDa, polypeptide 1	149957	−0.172834971698563	0.110172857246101
920	1120196	1120196: TBC1D4 :: TBC1 domain family, member 4	173802	0.252268611353589	−0.365300630429192
921	1120205	1120205: DSCR2 :: Down syndrome critical region gene 2	5198	−0.341638325826115	0.713407022486365
922	1120214	1120214: CD53 :: CD53 antigen	443057	−0.152751764379210	−0.049590054715558
923	1120216	1120216: CCNA2 :: cyclin A2	85137	−0.324160296081840	0.777319506164410
924	1120254	1120254: RTN1 :: reticulon 1	99947	0.612541977651677	−0.539497884538483
925	1120261	1120261: EPHA2 :: EphA2	171596	0.217934786713959	−0.365366022247552
926	1120266	1120266: CD68 :: CD68 antigen	246381	0.451189190580461	−0.397687894156014
927	1120267	1120267: TNFRSF1B :: tumor necrosis factor receptor superfamily, member 1B	256278	0.233418379708817	−0.357196376724822
928	1120269	1120269: MET :: met proto-oncogene (hepatocyte growth factor receptor)	419124	0.095532546067821	0.070544177910803
929	1120272	1120272: MAP3K3 :: mitogen-activated protein kinase kinase kinase 3	29282	0.044758338920690	−0.191842282997896
930	1120274	1120274: MTX2 :: metaxin 2	31584	−0.329576839455756	0.527764199207566
931	1120278	1120278: SEMA4D :: sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D	511748	0.224371642866400	−0.290878044536958
932	1120288	1120288: CD4 :: CD4 antigen (p55)	17483	0.453027496725459	−0.493671880192508
933	1120289	1120289: MAP4K5 :: mitogen-activated protein kinase kinase kinase kinase 5	246970	−0.101195827454930	0.110280186060386
934	1120299	1120299: NFIL3 :: nuclear factor, interleukin 3 regulated	79334	0.418150198365747	−0.353861915577026
935	1120300	1120300: CSNK2A2 :: casein kinase 2, alpha prime polypeptide	82201	−0.447144828589450	0.441822317864757
936	1120316	1120316: TERF2 :: telomeric repeat binding factor 2	63335	−0.223834288936832	0.378657341977871
937	1120317	1120317: BYSL :: bystin-like	106880	−0.480611242448932	0.673114888210520
938	1120324	1120324: IGF1R :: insulin-like growth factor 1 receptor	239176	0.486016697137607	−0.246282140833788
939	1120335	1120335: MAP3K11 :: mitogen-activated protein kinase kinase kinase 11	432787	0.167553983611871	−0.337924652268674
940	1120350	1120350: IL1RL1LG :: interleukin 1 receptor-like 1 ligand	446686	0.073526468292361	−0.142883449531743
941	1120353	1120353: BCL2 :: B-cell CLL/lymphoma 2	79241	−0.350722162941236	−0.216689018753782
942	1120355	1120355: CX3CL1 :: chemokine (C—X3—C motif) ligand 1	80420	0.096212197388840	−0.260021878158517
943	1120356	1120356: PKD2 :: polycystic kidney disease 2 (autosomal dominant)	458291	0.604711621900698	−0.246336208434929
944	1120359	1120359: FRZB :: frizzled-related protein	128453	0.089133553635861	−0.257184446624874
945	1120361	1120361: PDE4B :: phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)	188	−0.084837939596466	−0.104428923019524
946	1120362	1120362: PHKG2 :: phosphorylase kinase, gamma 2 (testis)	196177	−0.077059000678308	−0.191291041020843
947	1120366	1120366: DPP4 :: dipeptidylpeptidase 4 (CD26, adenosine deaminase complexing protein 2)	44926	0.297035769550426	−0.200947213073117
948	1120370	1120370: ITPKB :: inositol 1,4,5-trisphosphate 3-kinase B	78877	0.190360802060295	−0.169751144548655
949	1120373	1120373: BAK1 :: BCL2-antagonist/killer 1	93213	−0.200140816613802	0.113338862865570
950	1120378	1120378: FLJ11193 :: hypothetical protein FLJ11193	151046	−0.272022865326159	0.234783123016162
951	1120385	1120385: BUB1B :: BUB1 budding uninhibited by benzimidazoles 1 homolog beta (yeast)	36708	−0.428733600165811	0.833405557024467
952	1120387	1120387: CTSO :: cathepsin O	75262	0.374520964899448	−0.580832415098230
953	1120389	1120389: SLA :: Src-like-adaptor	75367	−0.172426216404282	−0.127234467000589
954	1120400	1120400: SSBP2 :: single-stranded DNA binding protein 2	152207	0.138133470457960	0.041953623299176
955	1120402	1120402: CDC42BPA :: CDC42 binding protein kinase alpha (DMPK-like)	18586	0.342860793681219	−0.308950300777485
956	1120417	1120417: FLJ10055 :: hypothetical protein FLJ10055	9398	0.458712245189916	−0.309562635887674
957	1120419	1120419: NJMU-R1 :: protein kinase Njmu-R1	9800	−0.188537102796126	0.435261002773401
958	1120422	1120422: GARP :: glycoprotein A repetitions predominant	151641	0.210134245590657	0.098618718300581
959	1120423	1120423: MAP3K5 :: mitogen-activated protein kinase kinase kinase 5	151988	0.128014378546006	−0.414691971823296
960	1120425	1120425: RPS6KA3 :: ribosomal protein S6 kinase, 90 kDa, polypeptide 3	188361	0.280819408584904	−0.003327617440558
961	1120433	1120433: VRK1 :: vaccinia related kinase 1	422662	−0.298915556379366	0.717298406899907
962	1120438	1120438: USP46 :: ubiquitin specific protease 46	109268	−0.301682893848221	0.251115921079262
963	1120465	1120465: CXCL9 :: chemokine (C—X—C motif) ligand 9	77367	0.091216036037422	−0.424535324487160

TABLE 2415-continued

GeneID.txt

Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
964	1120477	1120477: KDR :: kinase insert domain receptor (a type III receptor tyrosine kinase)	12337	0.473056670592013	−0.203310434691520
965	1120478	1120478: ACVR1 :: activin A receptor, type I	150402	0.691949086102474	−0.523920470761015
966	1120483	1120483: CSTF3 :: cleavage stimulation factor, 3' pre-RNA, subunit 3, 77 kDa	180034	−0.518586670460773	0.446316197113926
967	1120484	1120484: MPO :: myeloperoxidase	458272	0.101960994023863	−0.054587543757020
968	1120494	1120494: CDC6 :: CDC6 cell division cycle 6 homolog (*S. cerevisiae*)	405958	−0.416635429243115	0.842295577203676
969	1120500	1120500: CYP27A1 :: cytochrome P450, family 27, subfamily A, polypeptide 1	82568	0.653610023886872	−0.304787134639314
970	1120509	1120509: GNB5 :: guanine nucleotide binding protein (G protein), beta 5	155090	−0.267362638918031	0.200244247175214
971	1120520	1120520: RFC4 :: replication factor C (activator 1) 4, 37 kDa	35120	−0.501231595987143	0.789659303959865
972	1120524	1120524: TRIP13 :: thyroid hormone receptor interactor 13	436187	−0.368479048817546	0.832946538281856
973	1120529	1120529: CEBPA :: CCAAT/enhancer binding protein (C/EBP), alpha	76171	0.603459145525783	−0.430431783000636
974	1120538	1120538: ICSBP1 :: interferon consensus sequence binding protein 1	14453	−0.202713033551771	0.034802475287723
975	1120544	1120544: STK3 :: serine/threonine kinase 3 (STE20 homolog, yeast)	166684	0.085584173231200	−0.034463191343131
976	1120553	1120553: PRAME :: preferentially expressed antigen in melanoma	30743	0.096253753354037	0.013328837460755
977	1120555	1120555: STK19 :: serine/threonine kinase 19	444	0.168786958397468	−0.247788203132821
978	1120562	1120562: CCL4 :: chemokine (C-C motif) ligand 4	75703	0.281322248691298	−0.465719953116774
979	1120564	1120564: TESK1 :: testis-specific kinase 1	79358	0.100723203368127	−0.228465660577298
980	1120572	1120572: IL2RG :: interleukin 2 receptor, gamma (severe combined immunodeficiency)	84	0.235330936351446	−0.396807810508209
981	1120574	1120574: CD48 :: CD48 antigen (B-cell membrane protein)	901	−0.194668752468389	−0.098819351341990
982	1120580	1120580: RFC3 :: replication factor C (activator 1) 3, 38 kDa	115474	−0.307682737839499	0.789291151763360
983	1120581	1120581: BCL9 :: B-cell CLL/lymphoma 9	415209	−0.190510681098454	0.148503187654638
984	1120583	1120583: RNU3IP2 :: RNA, U3 small nucleolar interacting protein 2	153768	−0.526724070424994	0.500938051852095
985	1120588	1120588: TPST1 :: tyrosylprotein sulfotransferase 1	421194	0.700554999280495	−0.302446735476920
986	1120593	1120593: STAB1 :: stabilin 1	301989	0.315207523101052	−0.361469709646652
987	1120594	1120594: CDO1 :: cysteine dioxygenase, type I	442378	0.096654329449506	−0.131902879792736
988	1120595	1120595: KIAA0999 :: KIAA0999 protein	444909	−0.158743720518346	0.006339680783502
989	1120596	1120596: CDKN2C :: cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	4854	−0.277992134637003	0.464801755714349
990	1120601	1120601: KIAA0963 :: KIAA0963 protein	441129	0.115377312801900	−0.173467001738638
991	1120605	1120605: RPS6KB1 :: ribosomal protein S6 kinase, 70 kDa, polypeptide 1	86858	−0.049333332738750	0.272123372076907
992	1120615	1120615: IFNAR1 :: interferon (alpha, beta and omega) receptor 1	181315	0.109452635758577	−0.098788842929034
993	1120616	1120616: CD37 :: CD37 antigen	153053	−0.532314280274716	0.308291940284235
994	1120617	1120617: CPT1B :: carnitine palmitoyltransferase 1B (muscle)	439777	0.229122288389948	−0.467225308462803
995	1120625	1120625: RNGTT :: RNA guanylyltransferase and 5'-phosphatase	27345	−0.060185273034959	−0.030566655399450
996	1120630	1120630: DKFZP564M082 :: DKFZP564M082 protein	38044	−0.185687083825884	0.335258295065521
997	1120633	1120633: HDAC4 :: histone deacetylase 4	222874	0.268465157579931	−0.393330515146740
998	1120637	1120637: FCER1G :: Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide	433300	0.331513918783418	−0.400800744737435
999	1120643	1120643: CDK2 :: cyclin-dependent kinase 2	19192	−0.293669215593932	0.661617674173487
1000	1120645	1120645: FADS3 :: fatty acid desaturase 3	21765	0.055507218063663	0.088445892207464
1001	1120651	1120651: PIM2 :: pim-2 oncogene	80205	−0.281220927786929	0.185187824043508
1002	1120673	1120673: KIAA0711 :: KIAA0711 gene product	5333	0.068811665106344	0.005641795833107
1003	1120695	1120695: TRAF5 :: TNF receptor-associated factor 5	385685	−0.019131171585834	−0.161636874402010
1004	1120697	1120697: DHX30 :: DEAN (Asp-Glu-Ala-His) box polypeptide 30	323462	−0.471181063703452	0.425078805218812
1005	1120700	1120700: SCAP2 :: src family associated phosphoprotein 2	410745	−0.186747761610340	0.225356576750172
1006	1120703	1120703: SLCO2A1 :: solute carrier organic anion transporter family, member 2A1	83974	0.364711626940315	−0.247170134183657
1007	1120716	1120716: CAMK1 :: calcium/calmodulin-dependent protein kinase I	512804	0.168875956443599	−0.200055505150205
1008	1120717	1120717: SLC43A1 :: solute carrier family 43, member 1	444159	−0.376807044586730	0.520626875405123
1009	1120720	1120720: KCNN4 :: potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4	10082	0.136091693845411	−0.076690223326382
1010	1120730	1120730: G1P3 :: interferon, alpha-inducible protein (clone IFI-6-16)	287721	0.310445834508628	−0.358938894023986
1011	1120743	1120743: CD83 :: CD83 antigen (activated B lymphocytes, immunoglobulin superfamily)	79197	0.016342520267471	−0.056434824824793
1012	1120750	1120750: LDOC1 :: leucine zipper, down-regulated in cancer 1	45231	0.348398089655945	−0.373744732997425
1013	1120755	1120755: CXCL1 :: chemokine (C—X—C motif) ligand 1 (melanoma growth stimulating activity, alpha)	789	0.239712817378015	−0.227377568731226
1014	1120765	1120765: PIK3C2B :: phosphoinositide-3-kinase, class 2, beta polypeptide	343329	0.099676443902521	−0.033239919662244
1015	1120770	1120770: BID :: BH3 interacting domain death agonist	300825	−0.168931051298000	0.231696940935265
1016	1120779	1120779: CDC7 :: CDC7 cell division cycle 7 (*S. cerevisiae*)	28853	−0.364719870070187	0.702890401522440
1017	1120780	1120780: FARP2 :: FERM, RhoGEF and pleckstrin domain protein 2	301283	0.218332541521728	−0.357639798743606
1018	1120785	1120785: PPIC :: peptidylprolyl isomerase C (cyclophilin C)	110364	0.833250100411904	−0.364870410416830
1019	1120789	1120789: PDPK1 :: 3-phosphoinositide dependent protein kinase-1	154729	0.036213766133773	−0.055311931358302
1020	1120792	1120792: CXCL10 :: chemokine (C—X—C motif) ligand 10	413924	0.166606940060415	−0.407303162829402
1021	1120803	1120803: IKBKE :: inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon	321045	0.173038590863187	−0.262684854061046

TABLE 2415-continued

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Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
1022	1120808	1120808: IRF4 :: interferon regulatory factor 4	127686	−0.274522690905631	0.214443660765563
1023	1120809	1120809: SELL :: selectin L (lymphocyte adhesion molecule 1)	82848	−0.034467098542711	−0.232667176371041
1024	1120813	1120813: KIAA0831 :: KIAA0831	414809	0.140198507173410	−0.440539960257267
1025	1120814	1120814: ICK :: intestinal cell (MAK-like) kinase	417022	0.185512034005136	−0.254094458847882
1026	1120818	1120818: FGFR4 :: fibroblast growth factor receptor 4	165950	−0.173305192411460	0.170225481596070
1027	1120824	1120824: ARK5 :: KIAA0537 gene product	200598	0.639988433549215	−0.342249782851512
1028	1120825	1120825: CHL1 :: cell adhesion molecule with homology to L1CAM (close homolog of L1)	388344	0.116148782379396	−0.093424425417522
1029	1120828	1120828: EPHB3 :: EphB3	2913	0.273313344428643	−0.065126563411831
1030	1120832	1120832: PFTK1 :: PFTAIRE protein kinase 1	57856	0.168005950948601	−0.028716212628633
1031	1120834	1120834: CCL21 :: chemokine (C-C motif) ligand 21	57907	−0.035804408078127	−0.204294856872407
1032	1120838	1120838: PKIA :: protein kinase (cAMP-dependent, catalytic) inhibitor alpha	433700	−0.146391280990281	0.187655861583021
1033	1120839	1120839: PLCG2 :: phospholipase C, gamma 2 (phosphatidylinositol-specific)	512298	−0.460928399830360	0.522088964678862
1034	1120846	1120846: RPS6KA4 :: ribosomal protein S6 kinase, 90 kDa, polypeptide 4	105584	0.045791529310886	−0.164030593362306
1035	1120847	1120847: NEK4 :: NIMA (never in mitosis gene a)-related kinase 4	433008	−0.162080158681806	0.363435471138679
1036	1120853	1120853: NEK2 :: NIMA (never in mitosis gene a)-related kinase 2	153704	−0.257915260526437	0.773686557142882
1037	1120854	1120854: EDG1 :: endothelial differentiation, sphingolipid G-protein-coupled receptor, 1	154210	−0.122104475497316	−0.071633341557146
1038	1120858	1120858: HOMER3 :: homer homolog 3 (*Drosophila*)	410683	0.335496794625231	−0.271528013190748
1039	1120863	1120863: CCL5 :: chemokine (C-C motif) ligand 5	489044	0.542336364272824	−0.582181977929694
1040	1120875	1120875: LRMP :: lymphoid-restricted membrane protein	124922	0.003183268254248	0.168887881459636
1041	1120880	1120880: LTBP2 :: latent transforming growth factor beta binding protein 2	105689	0.826255058669113	−0.434328882440352
1042	1120881	1120881: ICAM2 :: intercellular adhesion molecule 2	433303	−0.213253074312284	−0.041517977663047
1043	1120900	1120900: EPHB6 :: EphB6	380089	0.013945388707104	−0.198607193449715
1044	1120918	1120918: HLF :: hepatic leukemia factor	250692	0.013775304997262	−0.055242216674679
1045	1120923	1120923: ARHGEF5 :: Rho guanine nucleotide exchange factor (GEF) 5	334	0.209882084442928	−0.150683350886678
1046	1120925	1120925: IL11RA :: interleukin 11 receptor, alpha	204891	0.273246691313366	−0.470149289804446
1047	1120946	1120946: MAPK10 :: mitogen-activated protein kinase 10	25209	−0.002920323341900	0.154019887369059
1048	1120952	1120952: TTK :: TTK protein kinase	169840	−0.236416169728487	0.593602839749024
1049	1120955	1120955: MELK :: maternal embryonic leucine zipper kinase	184339	−0.208951798652608	0.724555523338905
1050	1120958	1120958: CDK8 :: cyclin-dependent kinase 8	397734	−0.039317157762445	0.224625838601688
1051	1120976	1120976: GCHFR :: GTP cyclohydrolase I feedback regulatory protein	245644	−0.035026457160826	0.213041780115649
1052	1120980	1120980: TLE4 :: transducin-like enhancer of split 4 (E(sp1) homolog, *Drosophila*)	99824	−0.030677104931693	−0.067870579035081
1053	1120986	1120986: STK18 :: serine/threonine kinase 18	172052	−0.272148311899732	0.739975084000157
1054	1120993	1120993: IL10RA :: interleukin 10 receptor, alpha	327	0.047545601645909	−0.184922274295712
1055	1121000	1121000: TLR2 :: toll-like receptor 2	519033	0.429492421868063	−0.480462743962837
1056	1121005	1121005: TNFRSF11B :: tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)	81791	0.322049857523582	−0.151124812823603
1057	1121007	1121007: MAP4K2 :: mitogen-activated protein kinase kinase kinase kinase 2	512671	−0.234244240729329	0.375556542684312
1058	1121012	1121012: E2F1 :: E2F transcription factor 1	96055	−0.334386168154563	0.678410948823103
1059	1121013	1121013: ICAM3 :: intercellular adhesion molecule 3	353214	−0.297026833246660	−0.013311917844355
1060	1121021	1121021: CNK :: cytokine-inducible kinase	153640	−0.019398263377201	−0.088470692615038
1061	1121028	1121028: APOM :: apolipoprotein M	247323	0.080461690727297	−0.173511617318374
1062	1121029	1121029: CSTA :: cystatin A (stefin A)	412999	0.725032558235074	−0.312936257878748
1063	1121033	1121033: EMP2 :: epithelial membrane protein 2	511911	0.712789461038450	−0.289956290195573
1064	1121054	1121054: TGFA :: transforming growth factor, alpha	170009	0.070989900125764	−0.072416748854938
1065	1121057	1121057: STAT5B :: signal transducer and activator of transcription 5B	434992	0.014885551405709	−0.076250115454824
1066	1121061	1121061: ITGA2 :: integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	387725	−0.029030779750270	0.035897612258061
1067	1121062	1121062: CCNE2 :: cyclin E2	408658	−0.210155943554150	0.646944545337192
1068	1121073	1121073: AUH :: AU RNA binding protein/enoyl-Coenzyme A hydratase	81886	0.171546279035464	−0.332955161867336
1069	1121076	1121076: ITGAE :: integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha polypeptide)	389133	−0.413199084125475	0.301133545375388
1070	1121082	1121082: IL1B :: interleukin 1, beta	126256	0.253565351329184	−0.274936908342392
1071	1121100	1121100: CCR1 :: chemokine (C-C motif) receptor 1	301921	0.341955874946600	−0.274774576684184
1072	1121102	1121102: MHC2TA :: MHC class II transactivator	126714	0.094969874201105	−0.250509581424846
1073	1121115	1121115: MEF2B :: MADS box transcription enhancer factor 2, polypeptide B (myocyte enhancer factor 2B)	78881	−0.260397502438443	0.457668819142024
1074	1121117	1121117: VRK2 :: vaccinia related kinase 2	82771	0.105930454706077	−0.045187449295500
1075	1121120	1121120: RAGE :: renal tumor antigen	104119	0.011704601675353	−0.003336985459853
1076	1121129	1121129: CSF2RB :: colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)	285401	0.473407369637606	−0.474705087565604

TABLE 2415-continued

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Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
1077	1121136	1121136: DDR2 :: discoidin domain receptor family, member 2	440905	0.497410432793414	−0.341535633908894
1078	1121143	1121143: GNG4 :: guanine nucleotide binding protein (G protein), gamma 4	447973	0.065124580945373	−0.114186071226629
1079	1121149	1121149: MAP3K14 :: mitogen-activated protein kinase kinase kinase 14	440315	−0.045622884625820	−0.157979391580511
1080	1121159	1121159: RELB :: v-rel reticuloendotheliosis viral oncogene homolog B, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (avian)	307905	−0.014117999369713	0.054575676509177
1081	1121161	1121161: IL6 :: interleukin 6 (interferon, beta 2)	512234	0.270707514058880	−0.160285802317573
1082	1121166	1121166: STK17B :: serine/threonine kinase 17b (apoptosis-inducing)	88297	0.135353436195562	0.076356575160992
1083	1121170	1121170: HM74 :: putative chemokine receptor	458425	0.109820599871215	−0.169065883762500
1084	1121186	1121186: CXCL13 :: chemokine (C—X—C motif) ligand 13 (B-cell chemoattractant)	100431	0.378549805355286	−0.294764973487508
1085	1121190	1121190: NOTCH4 :: Notch homolog 4 (*Drosophila*)	436100	0.101751050016826	−0.006262723965488
1086	1121195	1121195: PBX1 :: pre-B-cell leukemia transcription factor 1	408222	−0.059508030808216	−0.012690445881844
1087	1121201	1121201: BCL10 :: B-cell CLL/ lymphoma 10	193516	−0.097298819688125	0.262527744599808
1088	1121203	1121203: LIF :: leukemia inhibitory factor (cholinergic differentiation factor)	2250	0.227708415345235	−0.237257236108422
1089	1121205	1121205: LCP2 :: lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76 kDa)	2488	0.509256290000162	−0.616098101683677
1090	1121217	1121217: IL2RB :: interleukin 2 receptor, beta	75596	0.233728921730338	−0.367351838583743
1091	1121220	1121220: RBL1 :: retinoblastoma-like 1 (p107)	87	−0.254718182068782	0.437740141713836
1092	1121228	1121228: SPI1 :: spleen focus forming virus (SFFV) proviral integration oncogene spi1	157441	0.101862646966026	−0.078795355216853
1093	1121248	1121248: BARD1 :: BRCA1 associated RING domain 1	54089	−0.332520033583970	0.540409719004797
1094	1121265	1121265: PLAG1 :: pleiomorphic adenoma gene 1	14968	−0.055939614174796	0.094487218739530
1095	1121276	1121276: CHEK1 :: CHK1 checkpoint homolog (*S. pombe*)	24529	−0.352853420627079	0.836388056331936
1096	1121278	1121278: DCAMKL1 :: doublecortin and CaM kinase-like 1	21355	0.412883143697658	−0.298495227861876
1097	1121281	1121281: IL1R2 :: interleukin 1 receptor, type II	25333	0.142459721447506	−0.302261496758997
1098	1121287	1121287: STK4 :: serine/threonine kinase 4	35140	−0.141211379313466	0.140410355369261
1099	1121290	1121290: FES :: feline sarcoma oncogene	7636	0.126479905402088	−0.115090374078902
1100	1121291	1121291: EBI2 :: Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor)	784	0.235439422364981	−0.105451694013327
1101	1121301	1121301: ZNF211 :: zinc finger protein 211	511749	−0.256995974326506	−0.116130479767648
1102	1121306	1121306: SNAPC1 :: small nuclear RNA activating complex, polypeptide 1, 43 kDa	179312	−0.111148822811151	0.479702938197036
1103	1121309	1121309: HSU79266 :: protein predicted by clone 23627	23642	−0.229837789455481	0.499904248128160
1104	1121315	1121315: MST1R :: macrophage stimulating 1 receptor (c-met-related tyrosine kinase)	2942	0.207517198765213	−0.192186835039801
1105	1121316	1121316: CD3E :: CD3E antigen, epsilon polypeptide (TiT3 complex)	3003	0.224738515046276	−0.499493301566731
1106	1121322	1121322: CASP10 :: caspase 10, apoptosis-related cysteine protease	5353	0.089986731593722	−0.314526392551084
1107	1121326	1121326: CCL20 :: chemokine (C-C motif) ligand 20	75498	0.215322214165972	−0.132606733260028
1108	1121329	1121329: SIT :: SHP2 interacting transmembrane adaptor	88012	−0.210345828377640	0.102148279065859
1109	1121331	1121331: TESK2 :: testis-specific kinase 2	8980	−0.039483229481418	0.033775496434037
1110	1121343	1121343: BTK :: Bruton agammaglobulinemia tyrosine kinase	159494	−0.264292738475593	0.221493414593700
1111	1121368	1121368: SV2B :: synaptic vesicle glycoprotein 2B	8071	0.141032356631520	−0.147797431288585
1112	1121371	1121371: TRAF6 :: TNF receptor-associated factor 6	90957	0.075399751558709	−0.168875636897418
1113	1121380	1121380: LAMP3 :: lysosomal-associated membrane protein 3	10887	0.570357891518240	−0.407916378045071
1114	1121383	1121383: ANGPT2 :: angiopoietin 2	115181	0.217195685938879	−0.123710120323309
1115	1121387	1121387: ROR2 :: receptor tyrosine kinase-like orphan receptor 2	208080	0.489331037769812	−0.053435946072310
1116	1121400	1121400: TRAF1 :: TNF receptor-associated factor 1	438253	0.142917780292670	−0.296365843618807
1117	1121404	1121404: ANGPT1 :: angiopoietin 1	2463	0.374587616111693	−0.287681985161262
1118	1121406	1121406: TNFSF12 :: tumor necrosis factor (ligand) superfamily, member 12	−4	0.458155673630534	−0.447921783667761
1119	1121408	1121408: LOC51760 :: B/K protein	258326	0.108520226350273	−0.337094362419053
1120	1121414	1121414: ALKBH :: alkB, alkylation repair homolog (*E. coli*)	94542	−0.519450896479011	0.507278510441829
1121	1121436	1121436: HDAC9 :: histone deacetylase 9	116753	−0.062542813471143	0.051528289785797
1122	1121444	1121444: LY75 :: lymphocyte antigen 75	153563	0.467870413003146	−0.334208325739869
1123	1121452	1121452: BCL2A1 :: BCL2-related protein A1	227817	0.047073151548673	0.008784276860166
1124	1121468	1121468: IL17R :: interleukin 17 receptor	129751	0.254701924480632	−0.250835608176983
1125	1121473	1121473: ITGB7 :: integrin, beta 7	1741	0.050306964647293	−0.260994122489540
1126	1121482	1121482: OSMR :: oncostatin M receptor	238648	0.287543499924824	−0.061525651754073
1127	1121497	1121497: CD8A :: CD8 antigen, alpha polypeptide (p32)	85258	0.254383170803894	−0.508843134467300
1128	1121511	1121511: BIK :: BCL2-interacting killer (apoptosis-inducing)	155419	−0.211383209660163	0.261057336302683
1129	1121516	1121516: CD1D :: CD1D antigen, d polypeptide	1799	−0.172683395640843	0.187984153848567
1130	1121518	1121518: WISP2 :: WNT1 inducible signaling pathway protein 2	194679	0.333528312498693	−0.211973809992181
1131	1121533	1121533: KLRK1 :: killer cell lectin-like receptor subfamily K, member 1	387787	0.170707791965083	−0.181208812511698
1132	1121542	1121542: CD2 :: CD2 antigen (p50), sheep red blood cell receptor	89476	0.302548346747810	−0.578942684928591
1133	1121546	1121546: VNN1 :: vanin 1	12114	0.567093184662778	−0.186561364898219
1134	1121554	1121554: TULP3 :: tubby like protein 3	437046	−0.056650771210584	0.127766542380693

TABLE 2415-continued

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Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
1135	1121558	1121558: NGFR :: nerve growth factor receptor (TNFR superfamily, member 16)	415768	0.195753701211791	−0.227262553501829
1136	1121559	1121559: LY86 :: lymphocyte antigen 86	184018	−0.155376905904987	0.017075510540213
1137	1121560	1121560: SPIB :: Spi-B transcription factor (Spi-1/PU.1 related)	437905	−0.289957995332695	0.340996439336590
1138	1121564	1121564: DRIL1 :: dead ringer-like 1 (*Drosophila*)	437783	−0.163786854286590	0.046472888560482
1139	1121572	1121572: LIFR :: leukemia inhibitory factor receptor	446501	0.067083275968437	−0.093351915656365
1140	1121573	1121573: POU6F1 :: POU domain, class 6, transcription factor 1	2815	0.254499733231130	−0.448893257238791
1141	1121574	1121574: PRKCM :: protein kinase C, mu	2891	0.439535360328520	−0.205359630656177
1142	1121584	1121584: CX3CR1 :: chemokine (C—X3—C motif) receptor 1	78913	0.056642673180032	−0.293821160742612
1143	1121585	1121585: CCNA1 :: cyclin A1	417050	0.132967965511067	−0.090551131678455
1144	1121587	1121587: PNOC :: prepronociceptin	371809	−0.282566914984081	0.053468907476172
1145	1121589	1121589: MICA :: MHC class I polypeptide-related sequence A	90598	0.099729225201395	−0.121123956711348
1146	1121629	1121629: BATF :: basic leucine zipper transcription factor, ATF-like	41691	−0.163961627042657	0.058949273380032
1147	1121643	1121643: AATK :: apoptosis-associated tyrosine kinase	514575	0.235022117248436	−0.174404212348862
1148	1121645	1121645: CD84 :: CD84 antigen (leukocyte antigen)	398093	0.461177430829423	−0.431475417777315
1149	1121650	1121650: GPR64 :: G protein-coupled receptor 64	421137	0.107743443918073	−0.167252293860867
1150	1121655	1121655: ITGA9 :: integrin, alpha 9	222	−0.003296977642853	−0.030819207041264
1151	1121680	1121680: SELP :: selectin P (granule membrane protein 140 kDa, antigen CD62)	73800	0.185759516369856	−0.431934182574265
1152	1121689	1121689: B7 :: B7 gene	155586	0.026543717156240	−0.054949053008795
1153	1121693	1121693: KIAA0450 :: KIAA0450 gene product	170156	0.196900710769728	−0.124900645118200
1154	1121695	1121695: HCP5 :: HLA complex P5	511759	0.195273337988109	−0.381571715087991
1155	1121711	1121711: MAPK12 :: mitogen-activated protein kinase 12	432642	−0.187453008816577	0.315641675037325
1156	1121717	1121717: EPHA4 :: EphA4	73964	−0.095018154579005	0.154787074255348
1157	1121720	1121720: STAT4 :: signal transducer and activator of transcription 4	80642	0.218763690606469	−0.502198054702293
1158	1121722	1121722: CD33 :: CD33 antigen (gp67)	83731	0.276204494664653	−0.362551394460205
1159	1121726	1121726: BLR1 :: Burkitt lymphoma receptor 1, GTP binding protein (chemokine (C—X—C motif) receptor 5)	113916	−0.189249439889998	0.258207310335521
1160	1121739	1121739: ZNF135 :: zinc finger protein 135 (clone pHZ-17)	85863	0.068019769137243	−0.110406382804294
1161	1121743	1121743: IL3RA :: interleukin 3 receptor, alpha (low affinity)	460433	0.418128176852651	−0.393074905406381
1162	1121745	1121745: TNFRSF7 :: tumor necrosis factor receptor superfamily, member 7	355307	−0.049393561288948	−0.199094753107042
1163	1121757	1121757: ADRB2 :: adrenergic, beta-2-, receptor, surface	2551	−0.123856836471263	−0.066380767065075
1164	1121759	1121759: IL13RA2 :: interleukin 13 receptor, alpha 2	336046	0.096030075479116	−0.004610449857012
1165	1121760	1121760: BMP6 :: bone morphogenetic protein 6	285671	−0.053975160456425	−0.004161001141957
1166	1121762	1121762: SLAMF1 :: signaling lymphocytic activation molecule family member 1	32970	0.321497941850406	−0.439833541268522
1167	1121767	1121767: PTGIR :: prostaglandin I2 (prostacyclin) receptor (IP)	458324	0.401404596559871	−0.371573726069884
1168	1121780	1121780: LY64 :: lymphocyte antigen 64 homolog, radioprotective 105 kDa (mouse)	87205	−0.166019615235407	0.174712903525339
1169	1121783	1121783: SELE :: selectin E (endothelial adhesion molecule 1)	89546	0.501259144636438	−0.323622231877747
1170	1121788	1121788: STK23 :: serine/threonine kinase 23	104865	0.096615237663810	−0.087773525250173
1171	1121792	1121792: TNFRSF10C :: tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular domain	119684	0.015465407320874	−0.016309866660398
1172	1121793	1121793: KPI2 :: kinase phosphatase inhibitor 2	122708	0.010013315668082	−0.019382995908031
1173	1121809	1121809: MICB :: MHC class I polypeptide-related sequence B	211580	−0.140424139371804	0.239690343077825
1174	1121814	1121814: BLK :: B lymphoid tyrosine kinase	389900	−0.311965481456666	0.229138774463185
1175	1121828	1121828: TLR3 :: toll-like receptor 3	29499	0.342320705636510	−0.203784020011193
1176	1121834	1121834: PRKY :: protein kinase, Y-linked	183165	0.060119302404676	−0.023441991964129
1177	1121841	1121841: NTS :: neurotensin	80962	−0.147437100102581	0.037573389779696
1178	1121844	1121844: IL18 :: interleukin 18 (interferon-gamma-inducing factor)	83077	0.681064645596460	−0.401312565491562
1179	1121848	1121848: TEC :: tec protein tyrosine kinase	278005	0.007139144026899	0.077786277898995
1180	1121853	1121853: SPINK2 :: serine protease inhibitor, Kazal type, 2 (acrosin-trypsin inhibitor)	98243	0.231340981766496	−0.118178578456530
1181	1121854	1121854: GUCY2C :: guanylate cyclase 2C (heat stable enterotoxin receptor)	171470	−0.166410484543226	0.015691903143909
1182	1121857	1121857: CRLF1 :: cytokine receptor-like factor 1	114948	0.069617938465999	0.053913442948466
1183	1121869	1121869: CXCL6 :: chemokine (C—X—C motif) ligand 6 (granulocyte chemotactic protein 2)	164021	0.144226064872636	−0.051053576857340
1184	1121870	1121870: CCR7 :: chemokine (C-C motif) receptor 7	1652	−0.067933367028353	−0.306029747322952
1185	1121874	1121874: IL2RA :: interleukin 2 receptor, alpha	130058	−0.051302661595226	0.043326548605735
1186	1121887	1121887: MAF :: v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	134859	0.291531644291303	−0.423330770602855
1187	1121918	1121918: FER :: fer (fps/fes related) tyrosine kinase (phosphoprotein NCP94)	121558	−0.081261198422925	−0.022672401143613
1188	1121947	1121947: BMX :: BMX non-receptor tyrosine kinase	27372	−0.045807586018934	−0.042093914097017
1189	1121953	1121953: KIAA0125 :: KIAA0125	38365	−0.074164934794289	0.093942617186532
1190	1121956	1121956: PTK6 :: PTK6 protein tyrosine kinase 6	51133	−0.017027139910115	−0.158651344799207
1191	1121959	1121959: LAG3 :: lymphocyte-activation gene 3	409523	0.193959621692431	−0.437806691232694
1192	1121963	1121963: ITGA2B :: integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41B)	411312	−0.279619286050182	0.284911304714724

TABLE 2415-continued

GeneID.txt

Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
1193	1121966	1121966: OCA2 :: oculocutaneous albinism II (pink-eye dilution homolog, mouse)	82027	−0.126556699537153	−0.138777934994851
1194	1121970	1121970: TNFSF7 :: tumor necrosis factor (ligand) superfamily, member 7	99899	−0.052884033648974	0.076289357833760
1195	1121996	1121996: CD28 :: CD28 antigen (Tp44)	1987	0.189150158821898	−0.444718988396679
1196	1122007	1122007: IL24 :: interleukin 24	411311	−0.043959538709898	−0.038229511247943
1197	1122009	1122009: CDKL5 :: cyclin-dependent kinase-like 5	50905	−0.110217563326053	0.038629974027743
1198	1122021	1122021: RAG1 :: recombination activating gene 1	73958	0.003594546430902	−0.000989138304343
1199	1122036	1122036: IL18R1 :: interleukin 18 receptor 1	159301	0.022775763687888	−0.206454025052186
1200	1122051	1122051: GPR105 :: G protein-coupled receptor 105	2465	0.059326766092437	−0.376983837880304
1201	1122053	1122053: TNFRSF17 :: tumor necrosis factor receptor superfamily, member 17	2556	−0.118896791192488	−0.141169001959615
1202	1122065	1122065: IGLL1 :: immunoglobulin lambda-like polypeptide 1	348935	−0.101518631934236	0.138252188755721
1203	1122075	1122075: FLT3 :: fms-related tyrosine kinase 3	385	−0.023290399924544	−0.134479118790636
1204	1122087	1122087: IL7 :: interleukin 7	72927	−0.054663149358440	0.163686002792952
1205	1122091	1122091: TEK :: TEK tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal)	89640	0.405019112365656	−0.229314036859117
1206	1122104	1122104: LMO1 :: LIM domain only 1 (rhombotin 1)	1149	−0.088512856329657	0.001423124698225
1207	1122112	1122112: TNFRSF8 :: tumor necrosis factor receptor superfamily, member 8	1314	0.306311232422199	−0.257781706042048
1208	1122131	1122131: CHST7 :: carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7	138155	0.017714188893945	−0.187857053179300
1209	1122139	1122139: ITGA10 :: integrin, alpha 10	158237	−0.126540289117975	−0.102013873270510
1210	1122156	1122156: ERBB4 :: v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	1939	−0.201573406555134	0.167789413767230
1211	1122165	1122165: CD3G :: CD3G antigen, gamma polypeptide (TiT3 complex)	2259	0.255114685310457	−0.501702664933897
1212	1122181	1122181: TXK :: TXK tyrosine kinase	29877	0.116717796088994	−0.338924617001779
1213	1122215	1122215: CCBP2 :: chemokine binding protein 2	24286	−0.095047926225869	0.017068598097254
1214	1122217	1122217: IL12RB1 :: interleukin 12 receptor, beta 1	223894	−0.057505725481306	0.035649057057820
1215	1122219	1122219: AMHR2 :: anti-Mullerian hormone receptor, type II	437877	−0.056887826816452	−0.019958969581757
1216	1122230	1122230: TNFSF9 :: tumor necrosis factor (ligand) superfamily, member 9	1524	−0.225333682313531	0.214293634736012
1217	1122241	1122241: PRKCA :: protein kinase C, alpha	349611	−0.004779534344590	0.129090253603676
1218	1122253	1122253: TGFBR1 :: transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53 kDa)	28005	0.014232227032144	0.012676202549217
1219	1122274	1122274: CXCR6 :: chemokine (C—X—C motif) receptor 6	34526	0.291116004542739	−0.538726060188242
1220	1122275	1122275: LTA :: lymphotoxin alpha (TNF superfamily, member 1)	36	0.272859492127863	−0.052120311047222
1221	1122277	1122277: CCR2 :: chemokine (C-C motif) receptor 2	511794	0.312042067191461	−0.414949503001742
1222	1122281	1122281: CCR6 :: chemokine (C-C motif) receptor 6	46468	−0.003994610054083	−0.285880226053799
1223	1122284	1122284: CCL25 :: chemokine (C-C motif) ligand 25	310511	−0.011468124459718	0.021672293312355
1224	1122288	1122288: IL12RB2 :: interleukin 12 receptor, beta 2	413608	0.126082647687914	−0.226273945847826
1225	1122292	1122292: IL8RB :: interleukin 8 receptor, beta	846	−0.024711905520565	−0.102623869064591
1226	1122304	1122304: KITLG :: KIT ligand	1048	−0.055609736205835	0.138263983925332
1227	1122327	1122327: ERN1 :: ER to nucleus signalling 1	137575	−0.081788789340055	0.000256455518645
1228	1122335	1122335: CDKL2 :: cyclin-dependent kinase-like 2 (CDC2-related kinase)	143241	−0.064687268142039	−0.099486553801662
1229	1122344	1122344: IL8RA :: interleukin 8 receptor, alpha	194778	0.010181353539432	−0.043034622453406
1230	1122353	1122353: EMR1 :: egf-like module containing, mucin-like, hormone receptor-like 1	2375	0.070191511848735	−0.358463771479546
1231	1122380	1122380: IL12A :: interleukin 12A (natural killer cell stimulatory factor 1, cytotoxic lymphocyte maturation factor 1, p35)	673	−0.156980730012675	0.067544361254343
1232	1122382	1122382: HMMR :: hyaluronan-mediated motility receptor (RHAMM)	72550	−0.364008235773999	0.783745372336510
1233	1122388	1122388: TLX1 :: T-cell leukemia, homeobox 1	89583	−0.006028747857682	0.090819031432347
1234	1122394	1122394: CDK3 :: cyclin-dependent kinase 3	100009	−0.109434076904651	0.005235741268251
1235	1122400	1122400: TERT :: telomerase reverse transcriptase	439911	−0.305125651996366	0.360989824065773
1236	1122412	1122412: TNFSF8 :: tumor necrosis factor (ligand) superfamily, member 8	177136	−0.173470362237192	0.039366962226564
1237	1122420	1122420: PRKACG :: protein kinase, cAMP-dependent, catalytic, gamma	158029	−0.042291694825976	0.107568347535975
1238	1122428	1122428: UGT2B17 :: UDP glycosyltransferase 2 family, polypeptide B17	183596	−0.009708775277058	−0.154853580284755
1239	1122449	1122449: CD209 :: CD209 antigen	278694	−0.054065050435346	−0.148476591045507
1240	1122471	1122471: PHKG1 :: phosphorylase kinase, gamma 1 (muscle)	512612	0.079932856062166	−0.081039280982416
1241	1122491	1122491: CCL16 :: chemokine (C-C motif) ligand 16	10458	−0.182443367350429	0.080347048721680
1242	1122537	1122537: IL10 :: interleukin 10	193717	0.084051369998383	−0.014477195723495
1243	1122541	1122541: CSF3 :: colony stimulating factor 3 (granulocyte)	2233	0.023378070359723	−0.012578972648323
1244	1122544	1122544: TLR6 :: toll-like receptor 6	366986	−0.034908792550942	−0.117727856389484
1245	1122581	1122581: PRKG2 :: protein kinase, cGMP-dependent, type II	41749	0.032701567417012	0.012446649249384
1246	1122596	1122596: CCL1 :: chemokine (C-C motif) ligand 1	72918	0.016785310093019	−0.118957054913180
1247	1122599	1122599: IL4 :: interleukin 4	73917	0.018527418005221	−0.024997209419818
1248	1122602	1122602: MPL :: myeloproliferative leukemia virus oncogene	84171	−0.028592483197097	0.035730086206858

TABLE 2415-continued

GeneID.txt

Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
1249	1122609	1122609: CHRNA6 :: cholinergic receptor, nicotinic, alpha polypeptide 6	103128	0.140757431162138	−0.089510942877138
1250	1122610	1122610: ROS1 :: v-ros UR2 sarcoma virus oncogene homolog 1 (avian)	1041	0.052118846272900	−0.039273113315543
1251	1122640	1122640: PDCD1 :: programmed cell death 1	158297	0.037884799709331	−0.335541082139966
1252	1122645	1122645: TNFRSF13B :: tumor necrosis factor receptor superfamily, member 13B	158341	−0.357072434096211	0.193042174649931
1253	1122664	1122664: CXCR3 :: chemokine (C—X—C motif) receptor 3	198252	0.247485780222157	−0.455289533280340
1254	1122680	1122680: PRKAA2 :: protein kinase, AMP-activated, alpha 2 catalytic subunit	256067	0.129427414307946	−0.021680077911729
1255	1122710	1122710: CDKL1 :: cyclin-dependent kinase-like 1 (CDC2-related kinase)	380788	−0.130816816182024	0.037546570109463
1256	1122738	1122738: CD160 :: CD160 antigen	81743	−0.080492304819797	−0.166670719053082
1257	1122740	1122740: IL13 :: interleukin 13	845	−0.045698316016691	0.035475880600793
1258	1122743	1122743: IL2 :: interleukin 2	89679	−0.018591226450345	−0.082394388827525
1259	1122744	1122744: CXCL3 :: chemokine (C—X—C motif) ligand 3	89690	0.201982112102107	−0.162220923472979
1260	1122749	1122749: CCL22 :: chemokine (C-C motif) ligand 22	97203	0.126129955425322	−0.113302826242635
1261	1122763	1122763: GUCY2D :: guanylate cyclase 2D, membrane (retina-specific)	309958	0.092659149259446	−0.222285418267571
1262	1122767	1122767: TNFSF5 :: tumor necrosis factor (ligand) superfamily, member 5 (hyper-IgM syndrome)	652	0.094318123549143	−0.250910889088908
1263	1122772	1122772: CCL17 :: chemokine (C-C motif) ligand 17	66742	0.224016681721616	−0.157484933905442
1264	1122773	1122773: IL12B :: interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40)	674	0.157191653410742	−0.031305411933949
1265	1122774	1122774: IL5RA :: interleukin 5 receptor, alpha	68876	0.033919120198367	0.031505076254719
1266	1122775	1122775: IL3 :: interleukin 3 (colony-stimulating factor, multiple)	694	0.027509333831645	0.004526584546124
1267	1122776	1122776: TNFSF14 :: tumor necrosis factor (ligand) superfamily, member 14	129708	0.086682929814505	−0.077782141454216
1268	1122796	1122796: IL5 :: interleukin 5 (colony-stimulating factor, eosinophil)	2247	0.031894751519528	0.038555120526004
1269	1122824	1122824: IL1RL2 :: interleukin 1 receptor-like 2	416814	0.150407278683836	−0.109242280419714
1270	1122834	1122834: CCR8 :: chemokine (C-C motif) receptor 8	113222	−0.076673872782458	−0.054598693128587
1271	1122863	1122863: IL9 :: interleukin 9	960	0.063436658685755	−0.069964371344722
1272	1122864	1122864: TTN :: titin	434384	−0.079878461568367	0.057803856684836
1273	1122865	1122865: IL1A :: interleukin 1, alpha	1722	−0.053194597179340	0.097988885553944
1274	1122914	1122914: CCR3 :: chemokine (C-C motif) receptor 3	506190	0.067137799577373	−0.079789679856537
1275	1122939	1122939: CCR4 :: chemokine (C-C motif) receptor 4	184926	0.000316877107091	−0.040959986051264
1276	1122956	1122956: LGALS2 :: lectin, galactoside-binding, soluble, 2 (galectin 2)	113987	0.418472381199476	−0.449328556890785
1277	1122983	1122983: TLX3 :: T-cell leukemia, homeobox 3	249125	−0.003266906586252	−0.023843091659097
1278	1122994	1122994: GPR15 :: G protein-coupled receptor 15	159900	−0.062091251933203	−0.043311935732794
1279	1123026	1123026: SCN10A :: sodium channel, voltage-gated, type X, alpha	250443	−0.116973597586132	0.070503156564898
1280	1123038	1123038: ACTN1 :: actinin, alpha 1	119000	0.873550797366042	−0.478675322021290
1281	1123039	1123039: P5 :: protein disulfide isomerase-related protein	212102	−0.033833903377211	0.140785743381923
1282	1123052	1123052: PRDX1 :: peroxiredoxin 1	180909	0.191988590052824	0.162925830590233
1283	1123053	1123053: CAPN2 :: calpain 2, (m/II) large subunit	350899	0.421280597945986	−0.436423248559518
1284	1123055	1123055: TFRC :: transferrin receptor (p90, CD71)	185726	0.040046865678309	0.144813077262144
1285	1123086	1123086: CSNK1D :: casein kinase 1, delta	378918	−0.155933500932564	−0.190171534622886
1286	1123105	1123105: PTK2 :: PTK2 protein tyrosine kinase 2	434281	0.288913388096928	−0.065583389930882
1287	1123108	1123108: POLE3 :: polymerase (DNA directed), epsilon 3 (p17 subunit)	108112	−0.436072096527712	0.682902758497920
1288	1123127	1123127: HLA-DRA :: major histocompatibility complex, class II, DR alpha	409805	0.047143225726272	−0.242770437918495
1289	1123148	1123148: TGFBR2 :: transforming growth factor, beta receptor II (70/80 kDa)	82028	0.010273158752569	−0.246551848934111
1290	1123160	1123160: PECAM1 :: platelet/endothelial cell adhesion molecule (CD31 antigen)	78146	0.369552095411465	−0.455742171741395
1291	1123163	1123163: STAT3 :: signal transducer and activator of transcription 3 (acute-phase response factor)	421342	0.088647677138997	−0.076284629745413
1292	1123188	1123188: RAB5A :: RAB5A, member RAS oncogene family	73957	0.023479248710834	−0.110193635053030
1293	1123192	1123192: IFRD2 :: interferon-related developmental regulator 2	315177	−0.486021348173979	0.488527458940548
1294	1123193	1123193: CTGF :: connective tissue growth factor	410037	0.729609445971057	−0.281419391890177
1295	1123198	1123198: CDKN1B :: cyclin-dependent kinase inhibitor 1B (p27, Kip1)	238990	0.042312425837938	−0.254204935247715
1296	1123213	1123213: TIP-1 :: Tax interaction protein 1	12956	0.478214019444825	−0.210865933337574
1297	1123223	1123223: AGR2 :: anterior gradient 2 homolog (*Xenopus laevis*)	226391	0.144465715233955	−0.064593480852986
1298	1123231	1123231: FOS :: v-fos FBJ murine osteosarcoma viral oncogene homolog	25647	0.457477092929620	−0.327994685230221
1299	1123233	1123233: PIM1 :: pim-1 oncogene	81170	−0.260781292717673	0.122887357920644
1300	1123235	1123235: C6orf11 :: chromosome 6 open reading frame 11	436930	−0.301325588310411	0.312607703475414
1301	1123250	1123250: C2F :: C2f protein	135643	−0.408607477799746	0.542558649958536
1302	1123255	1123255: NFKB1 :: nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	160557	−0.247639376875525	0.307813059694491
1303	1123278	1123278: TNFRSF10B :: tumor necrosis factor receptor superfamily, member 10b	51233	0.231916404010982	−0.133446996009752
1304	1123286	1123286: BCL2L2 :: BCL2-like 2	410026	0.430813129995590	−0.256934797251460
1305	1123289	1123289: POLR1C :: polymerase (RNA) I polypeptide C, 30 kDa	5409	−0.439470276015570	0.558476803814871

TABLE 2415-continued

GeneID.txt

Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
1306	1123293	1123293: ULK1 :: unc-51-like kinase 1 (*C. elegans*)	47061	0.234598147527924	−0.243014710846460
1307	1123298	1123298: SIAH2 :: seven in absentia homolog 2 (*Drosophila*)	20191	−0.020735974007859	0.251511790730967
1308	1123304	1123304: TNFRSF14 :: tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator)	279899	0.406281787477635	−0.640800528626002
1309	1123308	1123308: BAD :: BCL2-antagonist of cell death	76366	−0.055804103966625	0.200577209644432
1310	1123310	1123310: EPHX2 :: epoxide hydrolase 2, cytoplasmic	212088	0.032733558863813	−0.191468518846761
1311	1123317	1123317: TM4SF1 :: transmembrane 4 superfamily member 1	351316	0.511955936150185	−0.296195607797757
1312	1123321	1123321: ENPP2 :: ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	23719	0.354323804583203	−0.253537585629660
1313	1123331	1123331: GRB10 :: growth factor receptor-bound protein 10	512118	0.546048470195960	−0.318504437702318
1314	1123346	1123346: SERPINA3 :: serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3	76353	0.043287278241036	0.026601557579208
1315	1123358	1123358: AURKB :: aurora kinase B	442658	−0.383920119898266	0.752032680493908
1316	1123369	1123369: SNRK :: SNF-1 related kinase	79025	0.063554265111443	−0.312500317456464
1317	1123372	1123372: RBPMS :: RNA binding protein with multiple splicing	195825	0.729190743697357	−0.416042636778450
1318	1123376	1123376: RARRES2 :: retinoic acid receptor responder (tazarotene induced) 2	37682	0.767753207447146	−0.419368115432137
1319	1123399	1123399: IGF1 :: insulin-like growth factor 1 (somatomedin C)	308053	0.351339548125761	−0.181596238406175
1320	1123401	1123401: NDN :: necdin homolog (mouse)	50130	0.666813744865187	−0.449821627439369
1321	1123413	1123413: IL10RB :: interleukin 10 receptor, beta	418291	0.143751576129052	−0.265149372827460
1322	1123419	1123419: BMP7 :: bone morphogenetic protein 7 (osteogenic protein 1)	170195	−0.025788274570143	0.099776284015714
1323	1123429	1123429: CD74 :: CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)	446471	−0.002859916045464	−0.296446042702963
1324	1123430	1123430: STK16 :: serine/threonine kinase 16	153003	−0.161361543731864	0.064323356701808
1325	1123437	1123437: NFKB2 :: nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	73090	0.219171220578543	−0.215739729198764
1326	1123439	1123439: BUB1 :: BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)	287472	−0.257755664849282	0.734307550843963
1327	1123455	1123455: CBLB :: Cas-Br-M (murine) ecotropic retroviral transforming sequence b	436986	−0.033290616456071	−0.205794640235363
1328	1123457	1123457: RIN2 :: Ras and Rab interactor 2	446304	0.795227551186921	−0.522963551553488
1329	1123459	1123459: CXCL12 :: chemokine (C—X—C motif) ligand 12 (stromal cell-derived factor 1)	436042	0.338116509418455	−0.536175354841238
1330	1123470	1123470: M96 :: likely ortholog of mouse metal response element binding transcription factor 2	31016	−0.246647928566614	0.509698649157703
1331	1123476	1123476: SLC35D1 :: solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1	82635	0.038691099915535	0.137047545122540
1332	1123479	1123479: CSF1 :: colony stimulating factor 1 (macrophage)	173894	0.565439363613831	−0.571152588046333
1333	1123490	1123490: CLECSF2 :: C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 2 (activation-induced)	85201	0.437423695658292	−0.418715249984207
1334	1123497	1123497: TGFB3 :: transforming growth factor, beta 3	2025	0.419181791755442	−0.341070014629490
1335	1123502	1123502: KIAA0922 :: KIAA0922 protein	511944	−0.430991697827225	0.463134135573600
1336	1123507	1123507: BTN3A1 :: butyrophilin, subfamily 3, member A1	284283	0.198254555831932	−0.590128827200630
1337	1123529	1123529: PTCH :: patched homolog (*Drosophila*)	159526	−0.162582198261289	0.118247234101131
1338	1123535	1123535: C6orf32 :: chromosome 6 open reading frame 32	389488	−0.248332319157757	0.033447287747404
1339	1123552	1123552: SELPLG :: selectin P ligand	423077	0.480246751583851	−0.619068427619529
1340	1123566	1123566: C3AR1 :: complement component 3a receptor 1	155935	0.371658703605566	−0.442232534412039
1341	1123573	1123573: CCL18 :: chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)	16530	−0.014202367476697	−0.100068061738832
1342	1123581	1123581: RIPK1 :: receptor (TNFRSF)-interacting serine-threonine kinase 1	390758	0.136323407164192	−0.285283218731897
1343	1123584	1123584: VEGFC :: vascular endothelial growth factor C	79141	0.472324986740103	−0.294475802861250
1344	1123586	1123586: KCNMB1 :: potassium large conductance calcium-activated channel, subfamily M, beta member 1	93841	0.508193311461163	−0.344403736032782
1345	1123587	1123587: NCF2 :: neutrophil cytosolic factor 2 (65 kDa, chronic granulomatous disease, autosomal 2)	949	0.283365445260573	−0.264421095224310
1346	1123608	1123608: MALT1 :: mucosa associated lymphoid tissue lymphoma translocation gene 1	180566	0.047487079344585	−0.196154131449671
1347	1123611	1123611: INDO :: indoleamine-pyrrole 2,3 dioxygenase	840	0.253222128158468	−0.456068797135009
1348	1123613	1123613: CD3Z :: CD3Z antigen, zeta polypeptide (TiT3 complex)	97087	0.153062526309775	−0.337757592132146
1349	1123614	1123614: PRKCQ :: protein kinase C, theta	408049	0.305157145865210	−0.562196305322430
1350	1123622	1123622: EPAC :: Rap1 guanine-nucleotide-exchange factor directly activated by cAMP	8578	0.023864373661857	−0.205096809629451
1351	1123628	1123628: MAPK13 :: mitogen-activated protein kinase 13	178695	0.033235172641225	−0.074571795620075
1352	1123634	1123634: CCL19 :: chemokine (C-C motif) ligand 19	50002	0.237018077209330	−0.370272180731036
1353	1123635	1123635: SIAT8A :: sialyltransferase 8A (alpha-N-acetylneuraminate: alpha-2,8-sialyltransferase, GD3 synthase)	408614	0.199110330196979	−0.415743690175678
1354	1123643	1123643: MAGOH :: mago-nashi homolog, proliferation-associated (*Drosophila*)	421576	−0.355879676099144	0.581734359749056
1355	1123663	1123663: CCL11 :: chemokine (C-C motif) ligand 11	54460	0.264138545851733	−0.204563118558087
1356	1123671	1123671: HIPK3 :: homeodomain interacting protein kinase 3	30148	0.047603483230918	0.055945015733371

TABLE 2415-continued

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Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
1357	1123672	1123672: LILRB4 :: leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4	67846	0.478261377044532	−0.316050786052444
1358	1123679	1123679: CXCL11 :: chemokine (C—X—C motif) ligand 11	103982	0.103429322264231	−0.363739751119532
1359	1123680	1123680: GZMB :: granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	1051	0.089403932441954	−0.206108503310258
1360	1123682	1123682: TLR5 :: toll-like receptor 5	114408	0.339045664045358	−0.420163322335381
1361	1123690	1123690: TLR1 :: toll-like receptor 1	111805	0.315917942895492	−0.331871994933504
1362	1123694	1123694: ITGAX :: integrin, alpha X (antigen CD11C (p150), alpha polypeptide)	385521	0.624065221290532	−0.401652202104813
1363	1123731	1123731: RGS13 :: regulator of G-protein signalling 13	17165	0.094370061595793	0.059059084280978
1364	1123744	1123744: GPR18 :: G protein-coupled receptor 18	88269	−0.051853832062774	−0.095369670056525
1365	1123760	1123760: ILT7 :: leukocyte immunoglobulin-like receptor, subfamily A (without TM domain), member 4	406708	−0.202312173039078	−0.048154927899969
1366	1123762	1123762: FLT4 :: fms-related tyrosine kinase 4	415048	0.007820470422523	0.029361292237663
1367	1123778	1123778: CAMK4 :: calcium/calmodulin-dependent protein kinase IV	440638	−0.092561842977911	0.158012560576592
1368	1123780	1123780: IFNG :: interferon, gamma	856	0.123476147166574	−0.362163213194207
1369	1123814	1123814: ICOS :: inducible T-cell co-stimulator	56247	0.192515826351840	−0.464793820617578
1370	1123816	1123816: IL1RL1 :: interleukin 1 receptor-like 1	66	0.186852010516034	−0.130615795169223
1371	1123833	1123833: DNTT :: deoxynucleotidyltransferase, terminal	−32	−0.056799193445582	−0.009669825386535
1372	1123842	1123842: FUT7 :: fucosyltransferase 7 (alpha (1,3) fucosyltransferase)	457	0.137471775731450	−0.222998236604638
1373	1123847	1123847: BMPR1B :: bone morphogenetic protein receptor, type IB	87223	0.025637318140648	−0.036872289193971
1374	1123875	1123875: FLT3LG :: fms-related tyrosine kinase 3 ligand	428	0.156345539863462	−0.365585933772951
1375	1123889	1123889: TNFSF11 :: tumor necrosis factor (ligand) superfamily, member 11	333791	−0.074241864883289	−0.115086529686344
1376	1123890	1123890: TNFRSF10D :: tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain	129844	−0.031223526539161	−0.058937352170284
1377	1123892	1123892: CMKLR1 :: chemokine-like receptor 1	159553	0.322809856731336	−0.382060391333891
1378	1123938	1123938: FPRL1 :: formyl peptide receptor-like 1	99855	0.137586060931396	−0.155416553108998
1379	1123954	1123954: TNFSF6 :: tumor necrosis factor (ligand) superfamily, member 6	2007	0.182530654744065	−0.397622965632797
1380	1123988	1123988: LAT :: linker for activation of T cells	498997	0.229116696368979	−0.579887127104931
1381	1124049	1124049: my048 :: my048 protein	−1	−0.037955390490940	−0.086367167725680
1382	1124132	1124132: PRDX2 :: peroxiredoxin 2	432121	−0.125199234865877	0.288816173026307
1383	1124137	1124137: MGC27165 :: hypothetical protein MGC27165	366	−0.128484811098311	0.100510215963241
1384	1124176	1124176: COL4A2 :: collagen, type IV, alpha 2	407912	0.536118179940743	−0.067710785250196
1385	1124177	1124177: PORIMIN :: pro-oncosis receptor inducing membrane injury gene	172089	0.018031256600808	0.028546874924655
1386	1124178	1124178: HSPCA :: heat shock 90 kDa protein 1, alpha	446579	−0.115263936938935	0.214973051423235
1387	1124187	1124187: MGC5395 :: hypothetical protein MGC5395	378738	0.349346778708932	−0.417635861357430
1388	1124188	1124188: TOP2B :: topoisomerase (DNA) II beta 180 kDa	282346	−0.195346249007339	0.155878107050520
1389	1124192	1124192: PRKWNK1 :: protein kinase, lysine deficient 1	275999	0.004140487461706	−0.055577533920845
1390	1124195	1124195: H3F3B :: H3 histone, family 3B (H3.3B)	180877	0.095080814992035	−0.280306583417667
1391	1124215	1124215: PNN :: pinin, desmosome associated protein	409965	−0.441382373300142	0.501531516295816
1392	1124237	1124237: MLL :: myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, *Drosophila*)	258855	−0.016966825088812	−0.249537844930093
1393	1124254	1124254: SLC39A14 :: solute carrier family 39 (zinc transporter), member 14	301743	0.321139013957588	0.167246613564032
1394	1124266	1124266: DKFZP564D116 :: DKFZP564D116 protein	438991	−0.280125370200864	0.287120197674624
1395	1124283	1124283: UNC84B :: unc-84 homolog B (*C. elegans*)	406612	0.315002331643639	−0.548815227035707
1396	1124296	1124296: SDC2 :: syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan)	1501	0.693813172081440	−0.342258189120497
1397	1124304	1124304: CPNE1 :: copine I	166887	−0.504868086841360	0.680830591678959
1398	1124316	1124316: ACACA :: acetyl-Coenzyme A carboxylase alpha	449863	−0.181134877886522	0.274185965541523
1399	1124318	1124318: SERPINE2 :: serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2	21858	0.370324342365429	−0.211095115024570
1400	1124321	1124321: IL6ST :: interleukin 6 signal transducer (gp130, oncostatin M receptor)	71968	0.278059468191875	−0.396320310680725
1401	1124342	1124342: PPAP2B :: phosphatidic acid phosphatase type 2B	432840	0.745344693498752	−0.321206737384094
1402	1124357	1124357: C7orf14 :: chromosome 7 open reading frame 14	413636	−0.402085858524422	0.657812900111462
1403	1124362	1124362: CAMKK2 :: calcium/calmodulin-dependent protein kinase kinase 2, beta	297343	0.082047941910144	0.012170322660202
1404	1124365	1124365: TNRC15 :: trinucleotide repeat containing 15	334871	−0.146171232833643	0.129612912259863
1405	1124377	1124377: MAC30 :: hypothetical protein MAC30	199695	−0.473824954763453	0.767955627108751
1406	1124381	1124381: FNBP1 :: formin binding protein 1	440808	0.019230980336461	−0.207117033691842
1407	1124384	1124384: HIPK1 :: homeodomain interacting protein kinase 1	12259	0.038569082287500	−0.073989736759850
1408	1124391	1124391: NEK9 :: NIMA (never in mitosis gene a)-related kinase 9	7200	−0.285215409926676	0.158971093711156
1409	1124400	1124400: BCL2L1 :: BCL2-like 1	305890	0.023976484721047	−0.056514291309960
1410	1124411	1124411: FLJ10619 :: hypothetical protein FLJ10619	194737	−0.018902760490884	−0.337181044074577
1411	1124416	1124416: RBL2 :: retinoblastoma-like 2 (p130)	283604	0.043711845509004	−0.322756914235943
1412	1124429	1124429: SULF1 :: sulfatase 1	409602	0.756874827644649	−0.200326821232171
1413	1124438	1124438: CLIPR-59 :: CLIP-170-related protein	7357	0.348844827581408	−0.173908788877715
1414	1124456	1124456: TCF4 :: transcription factor 4	359289	−0.184783079390691	0.173790437828407

TABLE 2415-continued

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Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
1415	1124539	1124539: TENC1 :: tensin like C1 domain-containing phosphatase	6147	0.403712878533374	−0.395953899027013
1416	1124543	1124543: C10orf22 :: chromosome 10 open reading frame 22	99821	−0.016931232646163	−0.133800710298489
1417	1124549	1124549: MOAP1 :: modulator of apoptosis 1	24719	−0.176013780064857	0.084745406142491
1418	1124561	1124561: NEK7 :: NIMA (never in mitosis gene a)-related kinase 7	24119	0.122442978195907	−0.209971856127309
1419	1124563	1124563: WEE1 :: WEE1 homolog (*S. pombe*)	249441	−0.173056305348263	0.447075281308176
1420	1124577	1124577: HPCAL1 :: hippocalcin-like 1	3618	0.135165512513168	−0.299780255879962
1421	1124583	1124583: GDAP1L1 :: ganglioside-induced differentiation-associated protein 1-like 1	20977	0.367602161929472	−0.305814749065091
1422	1124594	1124594: STK38L :: serine/threonine kinase 38 like	184523	0.019320900966301	0.207490282567835
1423	1124606	1124606: PTPRC :: protein tyrosine phosphatase, receptor type, C	444324	0.045317285693567	−0.221810375999856
1424	1124610	1124610: IGJ :: immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides	381568	0.056282104720538	−0.080088230864314
1425	1124613	1124613: AUTS2 :: autism susceptibility candidate 2	296720	0.290104164160183	−0.197864543648102
1426	1124616	1124616: MRPS31 :: mitochondrial ribosomal protein S31	154655	−0.254775558867050	0.431147918074326
1427	1124620	1124620: PTPN11 :: protein tyrosine phosphatase, non-receptor type 11 (Noonan syndrome 1)	83572	−0.287606650758719	0.434137390616062
1428	1124646	1124646: RAFTLIN :: raft-linking protein	436432	0.219635297170966	−0.099887736967582
1429	1124655	1124655: LHFPL2 :: lipoma HMGIC fusion partner-like 2	79299	0.364628032686042	−0.274907028091758
1430	1124658	1124658: KIAA0674 :: KIAA0674 protein	522351	0.289946684284484	−0.325443854542448
1431	1124666	1124666: ATM :: ataxia telangiectasia mutated (includes complementation groups A, C and D)	504644	−0.214240439565213	−0.133443390905161
1432	1124692	1124692: MFAP4 :: microfibrillar-associated protein 4	296049	0.330287096674728	−0.408382477540657
1433	1124705	1124705: DMN :: desmuslin	381347	0.311462686240068	−0.392006888364421
1434	1124712	1124712: ARHGAP19 :: Rho GTPase activating protein 19	80305	−0.446305815524552	0.650257768410998
1435	1124713	1124713: PIK3R4 :: phosphoinositide-3-kinase, regulatory subunit 4, p150	306747	−0.340750199021012	0.190039732116352
1436	1124723	1124723: RNF3 :: ring finger protein 3	435065	0.226995185267053	−0.232885578590650
1437	1124733	1124733: LOC221061 :: hypothetical protein LOC221061	66762	0.444250988609368	−0.296397457839185
1438	1124734	1124734: ZNF238 :: zinc finger protein 238	446677	−0.344114190160318	0.037963727929040
1439	1124745	1124745: KIAA0056 :: KIAA0056 protein	438550	−0.367377449201276	0.681944184031488
1440	1124753	1124753: CIT :: citron (rho-interacting, serine/threonine kinase 21)	405932	−0.266684914532091	0.597601592399224
1441	1124755	1124755: KIAA0367 :: KIAA0367 protein	23311	0.175438520231790	−0.161328615677927
1442	1124760	1124760: JAM3 :: junctional adhesion molecule 3	419149	0.502500585815783	−0.322402807479759
1443	1124768	1124768: FUBP3 :: far upstream element (FUSE) binding protein 3	98751	0.043553346616365	0.132673344353371
1444	1124770	1124770: IGHM :: *Homo sapiens* transcribed sequence with moderate similarity to protein sp: P01871 (*H. sapiens*) MUC_HUMAN Ig MU chain C region	439852	−0.264170929427200	0.171558583437037
1445	1124782	1124782: NCAM1 :: neural cell adhesion molecule 1	78792	0.067740345913373	−0.116287844761153
1446	1124786	1124786: nexilin :: likely ortholog of rat F-actin binding protein nexilin	22370	−0.363619385660829	0.232945437352754
1447	1124798	1124798: NCOA2 :: nuclear receptor coactivator 2	446678	0.236699642816994	−0.309047597110174
1448	1124800	1124800: MAPKAPK5 :: mitogen-activated protein kinase-activated protein kinase 5	413901	−0.193391449305070	0.467024572248984
1449	1124806	1124806: PIASY :: protein inhibitor of activated STAT protein PIASy	105779	−0.249365264160332	0.182499663961299
1450	1124820	1124820: CDK11 :: cyclin-dependent kinase (CDC2-like) 11	129836	0.171715198585524	−0.189801012482926
1451	1124830	1124830: KIAA0962 :: KIAA0962 protein	9059	−0.239108218809974	−0.071631456643250
1452	1124831	1124831: RPS6KA2 :: ribosomal protein S6 kinase, 90 kDa, polypeptide 2	301664	0.542423703800096	−0.359666198197007
1453	1124833	1124833: CBX7 :: chromobox homolog 7	356416	0.200522108417050	−0.597074769576343
1454	1124862	1124862: DYRK4 :: dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4	439530	−0.185930582424260	0.107350511374489
1455	1124864	1124864: KIAA0882 :: KIAA0882 protein	411317	0.230195362925492	−0.120226438072572
1456	1124875	1124875: KIAA0870 :: KIAA0870 protein	18166	0.381004144174920	−0.317090511411673
1457	1124889	1124889: BTBD14A :: BTB (POZ) domain containing 14A	244847	0.322548142484688	−0.483195482115568
1458	1124893	1124893: MARCKS :: myristoylated alanine-rich protein kinase C substrate	318603	0.220998638177546	−0.233172073523505
1459	1124913	1124913: SSA2 :: Sjogren syndrome antigen A2 (60 kDa, ribonucleoprotein autoantigen SS-A/Ro)	288178	−0.317060278822500	0.353157816804561
1460	1124920	1124920: P114-RHO-GEF :: Rho-specific guanine nucleotide exchange factor p114	6150	−0.017421135592496	−0.142182975239113
1461	1124921	1124921: ROCK1 :: Rho-associated, coiled-coil containing protein kinase 1	306307	−0.219106199756838	0.167252552911467
1462	1124922	1124922: KIAA0561 :: KIAA0561 protein	173864	0.154513049267643	−0.226411686845406
1463	1124941	1124941: DPT :: dermatopontin	80552	0.606288990238186	−0.334437688929020
1464	1124942	1124942: KIAA1237 :: KIAA1237 protein	433452	0.544385475743196	−0.326311080060450
1465	1124948	1124948: LOC169611 :: hypothetical protein LOC169611	357004	0.159693541113982	−0.213898050682879
1466	1124953	1124953: SLC35D2 :: solute carrier family 35, member D2	386278	0.302215615930412	−0.532374546381988
1467	1124967	1124967: CAMK2A :: calcium/calmodulin-dependent protein kinase (CaM kinase) II alpha	143535	−0.044227814406713	0.135835028117236
1468	1124972	1124972: NEK3 :: NIMA (never in mitosis gene a)-related kinase 3	2236	−0.004668815670307	−0.018473350732855
1469	1125001	1125001: :: *Homo sapiens* mRNA; cDNA DKFZp586B211 (from clone DKFZp586B211)	16193	0.309877128137494	−0.394819111003227

TABLE 2415-continued

GeneID.txt

Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
1470	1125009	1125009: SEMA5A :: sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A	27621	0.570335387773131	−0.238333322497496
1471	1125010	1125010: GPX6 :: glutathione peroxidase 6	43728	−0.406180476172999	0.329256599051926
1472	1125013	1125013: TTC9 :: tetratricopeptide repeat domain 9	79170	0.203290284926991	−0.070305427994692
1473	1125025	1125025: :: *Homo sapiens*, clone IMAGE: 5402962, mRNA	301094	0.373028589705817	−0.358455467318352
1474	1125027	1125027: ACVR1B :: activin A receptor, type IB	371974	0.452094421087183	−0.406256554874994
1475	1125058	1125058: ATP10D :: ATPase, Class V, type 10D	437241	0.239777925038262	−0.208589626023053
1476	1125079	1125079: MAP3K12 :: mitogen-activated protein kinase kinase kinase 12	211601	−0.023529974489696	0.097742384028628
1477	1125122	1125122: SRC :: v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	436015	0.325821834875497	−0.281566755677791
1478	1125124	1125124: VAMP1 :: vesicle-associated membrane protein 1 (synaptobrevin 1)	20021	0.028033847060342	−0.030330298910767
1479	1125130	1125130: RIS1 :: Ras-induced senescence 1	35861	0.707291900474651	−0.304594771554232
1480	1125132	1125132: FEM1C :: fem-1 homolog c (*C. elegans*)	47367	−0.178267778288773	0.251919721452546
1481	1125136	1125136: CDKN1C :: cyclin-dependent kinase inhibitor 1C (p57, Kip2)	106070	0.205535321358345	−0.417689553546756
1482	1125181	1125181: HSPA6 :: heat shock 70 kDa protein 6 (HSP70B')	3268	0.218052146790839	−0.175456230712095
1483	1125195	1125195: :: *Homo sapiens* cDNA FLJ34019 fis, clone FCBBF2002898.	7309	0.062351973383136	−0.242830127018530
1484	1125231	1125231: MAPRE2 :: microtubule-associated protein, RP/EB family, member 2	446375	−0.258250546492020	0.146207410520459
1485	1125245	1125245: DKFZP564J157 :: DKFZp564J157 protein	132977	−0.084163299925425	0.043797186647820
1486	1125246	1125246: PRKCI :: protein kinase C, iota	496511	0.149649650776333	−0.029379048720556
1487	1125249	1125249: CCNE1 :: cyclin E1	244723	−0.378533610256387	0.582611267644762
1488	1125279	1125279: TRA2A :: transformer-2 alpha	445652	−0.039745460274163	−0.006496641958592
1489	1125305	1125305: MAGED2 :: melanoma antigen, family D, 2	376719	0.279186046231037	−0.229412259186242
1490	1125377	1125377: KIAA0298 :: KIAA0298 gene product	196966	0.043538773140655	−0.083535310053914
1491	1125397	1125397: RABL4 :: RAB, member of RAS oncogene family-like 4	415172	−0.076074155660607	−0.152334780877398
1492	1125456	1125456: MYBL1 :: v-myb myeloblastosis viral oncogene homolog (avian)-like 1	300592	0.085358543549403	0.119727077539206
1493	1125459	1125459: CPN2 :: carboxypeptidase N, polypeptide 2, 83 kD	288467	0.753834612101326	−0.275359926533248
1494	1125462	1125462: NKG7 :: natural killer cell group 7 sequence	10306	0.376390754863940	−0.440135617189111
1495	1125485	1125485: CD6 :: CD6 antigen	436949	0.336912237115247	−0.602384838687388
1496	1125516	1125516: ZAP70 :: zeta-chain (TCR) associated protein kinase 70 kDa	234569	0.095543492046246	−0.451426018665455
1497	1125520	1125520: CCL8 :: chemokine (C-C motif) ligand 8	271387	0.121752040709514	−0.288077095465458
1498	1125527	1125527: MGC39900 :: hypothetical protein MGC39900	422848	−0.180192646407023	0.262739415756805
1499	1125532	1125532: MYCL1 :: v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avian)	−20	0.466507304726902	−0.557697249345758
1500	1125546	1125546: PLXDC1 :: plexin domain containing 1	125036	0.495153683434132	−0.378145766567478
1501	1125593	1125593: MAN1C1 :: mannosidase, alpha, class 1C, member 1	8736	0.401795734231727	−0.364401736769574
1502	1125634	1125634: ITGA8 :: integrin, alpha 8	171025	0.075527959445201	0.079267924222490
1503	1125658	1125658: CAMK2G :: calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	12436	−0.135367047257270	−0.093006589024883
1504	1125685	1125685: STK22B :: serine/threonine kinase 22B (spermiogenesis associated)	103978	0.044261258588761	−0.051415134140489
1505	1125742	1125742: KLRB1 :: killer cell lectin-like receptor subfamily B, member 1	169824	0.079711384000230	−0.301963846541283
1506	1125789	1125789: FPRL2 :: formyl peptide receptor-like 2	511953	0.380389682365687	−0.166148068940340
1507	1125818	1125818: PAK3 :: p21 (CDKN1A)-activated kinase 3	152663	0.225596497818733	−0.244616982595961
1508	1125826	1125826: PRF1 :: perforin 1 (pore forming protein)	2200	0.124824075540851	−0.389188823848422
1509	1125852	1125852: ITGA1 :: integrin, alpha 1	439320	0.180842213274704	−0.117040332953727
1510	1125854	1125854: KIAA0472 :: KIAA0472 protein	6874	0.110910134647931	−0.172998818690132
1511	1125872	1125872: MGC14376 :: hypothetical protein MGC14376	417157	0.612329640905422	−0.552935361435317
1512	1125901	1125901: KIAA1069 :: KIAA1069 protein	193143	−0.056011672384808	0.098707635358308
1513	1125916	1125916: :: *Homo sapiens* mRNA, chromosome 1 specific transcript KIAA0507.	497770	−0.163266668946423	0.152187955657425
1514	1125917	1125917: CLCN4 :: chloride channel 4	417091	−0.081086279636081	−0.031095539270792
1515	1125919	1125919: G2 :: G2 protein	432369	0.118135844564772	−0.183475617606038
1516	1125921	1125921: :: *Homo sapiens* immunoglobulin kappa light chain VKJ region mRNA, partial cds	512124	0.054181904837014	−0.063477080905441
1517	1125927	1125927: IRLB :: c-myc promoter-binding protein	511742	0.007967940915944	0.004344525393029
1518	1125928	1125928: SUSP1 :: SUMO-1-specific protease	435628	0.126140052656316	−0.187357956669395
1519	1126047	1126047: MAP3K9 :: mitogen-activated protein kinase kinase kinase 9	437214	−0.123477928740905	0.090270515939190
1520	1126081	1126081: GRSF1 :: G-rich RNA sequence binding factor 1	309763	−0.195427410459479	0.297879353203236
1521	1126131	1126131: RAG2 :: recombination activating gene 2	159376	0.018198564132967	0.095689042169220
1522	1126148	1126148: FLJ36166 :: hypothetical protein FLJ36166	408264	−0.341178035851254	0.550186976150584
1523	1126293	1126293: TNFRSF5 :: tumor necrosis factor receptor superfamily, member 5	504816	0.123994547059363	−0.098192969696021
1524	1126387	1126387: MAP2K3 :: mitogen-activated protein kinase kinase 3	180533	0.157473211343872	−0.097765784491014
1525	1126408	1126408: :: *Homo sapiens* mRNA; cDNA DKFZp586O1318 (from clone DKFZp586O1318)	22689	−0.068959872372587	0.053238627545519

TABLE 2415-continued

GeneID.txt

Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
1526	1126540	1126540: KIAA1659 :: KIAA1659 protein	474916	0.081108591309987	−0.038577312232724
1527	1126554	1126554: LOC91752 :: similar to C630007C17Rik protein	159528	−0.268188912986088	0.246488536495623
1528	1126559	1126559: INSRR :: insulin receptor-related receptor	248138	−0.098379843482530	0.105773648371041
1529	1126858	1126858: ITGB3 :: integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	87149	0.042983325871373	−0.144497681552225
1530	1126892	1126892: ITGA7 :: integrin, alpha 7	74369	0.083341738800239	−0.203924509390271
1531	1127214	1127214: EPHA5 :: EphA5	201920	−0.013824470163245	−0.036690220251078
1532	1127290	1127290: :: *Homo sapiens* ribosomal protein S4-like (RPS4L), mRNA	−48	−0.144124961156077	0.225161668972163
1533	1127294	1127294: CXCR4 :: chemokine (C—X—C motif) receptor 4	421986	−0.089364882672779	−0.133650582979350
1534	1127371	1127371: TIA1 :: TIA1 cytotoxic granule-associated RNA binding protein	444689	−0.170709900312428	−0.069039973369378
1535	1127567	1127567: FLJ20013 :: hypothetical protein FLJ20013	−29	−0.192452771538394	0.083618644652907
1536	1127576	1127576: :: *Homo sapiens*, clone IMAGE: 4794941, mRNA	172998	0.025947000616036	−0.064411420957178
1537	1127720	1127720: NRBP :: nuclear receptor binding protein	272736	0.242411931589308	−0.319823036043122
1538	1127742	1127742: GK001 :: GK001 protein	8207	−0.175524415712497	0.253654275070550
1539	1127744	1127744: ARPC4 :: actin related protein 2/3 complex, subunit 4, 20 kDa	323342	0.037191497103242	−0.033346100698264
1540	1127756	1127756: NS :: nucleostemin	313544	−0.515885407863687	0.598986978423638
1541	1127761	1127761: PIAS1 :: protein inhibitor of activated STAT, 1	75251	0.042686201903289	−0.222289998859397
1542	1127775	1127775: EPS15 :: epidermal growth factor receptor pathway substrate 15	79095	0.189507964126997	−0.127894991253663
1543	1127805	1127805: CKLFSF6 :: chemokine-like factor super family 6	380627	0.228996715729709	−0.226964695189832
1544	1127807	1127807: NOSIP :: nitric oxide synthase interacting protein	7236	−0.247563970229520	0.168975022386913
1545	1127813	1127813: NOLA3 :: nucleolar protein family A, member 3 (H/ACA small nucleolar RNPs)	14317	−0.267329642981471	0.382544204532760
1546	1127822	1127822: SEPX1 :: selenoprotein X, 1	279623	−0.043578471725612	−0.020427563338161
1547	1127833	1127833: MRPS2 :: mitochondrial ribosomal protein S2	382044	−0.470025507537828	0.585205355806807
1548	1127838	1127838: SE20-4 :: cutaneous T-cell lymphoma-associated tumor antigen se20-4	136164	−0.103258781815064	−0.031095347592986
1549	1127849	1127849: SNN :: stannin	76691	0.021266526827127	−0.236719002607138
1550	1127864	1127864: SLC12A7 :: solute carrier family 12 (potassium/chloride transporters), member 7	172613	0.368860530480438	−0.359243502019673
1551	1127873	1127873: C20orf4 :: chromosome 20 open reading frame 4	11314	−0.275330975017113	0.241185315693476
1552	1127885	1127885: TMEM2 :: transmembrane protein 2	160417	0.268288787080805	−0.265983709098421
1553	1127901	1127901: C20orf97 :: chromosome 20 open reading frame 97	344378	−0.391732683018817	0.394691280966108
1554	1127931	1127931: FLJ22378 :: hypothetical protein FLJ22378	288284	0.149298653587153	−0.194275386943659
1555	1127940	1127940: NUBP2 :: nucleotide binding protein 2 (MinD homolog, *E. coli*)	256549	−0.300885491703953	0.428992853698371
1556	1127943	1127943: C1QA :: complement component 1, q subcomponent, alpha polypeptide	9641	−0.026333557586648	−0.341150779315542
1557	1128042	1128042: SIL1 :: endoplasmic reticulum chaperone SIL1, homolog of yeast	297875	0.393325385452913	−0.355463933112278
1558	1128066	1128066: HTF9C :: Hpall tiny fragments locus 9C	63609	−0.338428568018676	0.192274782223654
1559	1128070	1128070: RRP46 :: exosome component Rrp46	283741	−0.554229516123466	0.607715184909214
1560	1128079	1128079: MST4 :: Mst3 and SOK1-related kinase	23643	−0.195204488353103	0.431778599814938
1561	1128095	1128095: TBK1 :: TANK-binding kinase 1	432466	−0.035307688412218	0.050927269206120
1562	1128099	1128099: 8D6A :: 8D6 antigen	333427	−0.338346262971788	0.398554942958158
1563	1128100	1128100: FHOD1 :: formin homology 2 domain containing 1	95231	0.069172504045891	0.055506953252559
1564	1128106	1128106: C10orf3 :: chromosome 10 open reading frame 3	14559	−0.301849657377729	0.772091150877424
1565	1128111	1128111: FLJ10948 :: hypothetical protein FLJ10948	170915	0.136309727475261	−0.496737872614298
1566	1128125	1128125: ABHD4 :: abhydrolase domain containing 4	445665	0.361732950699424	−0.356070410710610
1567	1128144	1128144: DKFZp761K1423 :: hypothetical protein DKFZp761K1423	236438	0.320671799542360	−0.191688492385100
1568	1128151	1128151: NRN1 :: neuritin 1	103291	−0.053655137752169	−0.122190847084027
1569	1128157	1128157: VIP32 :: vasopressin-induced transcript	23918	0.450125317312805	−0.335255101074634
1570	1128164	1128164: FLJ20534 :: hypothetical protein FLJ20534	44344	−0.136223990395658	0.499752179475021
1571	1128167	1128167: SLC25A15 :: solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15	78457	−0.292180964755755	0.464300618499445
1572	1128174	1128174: FZD4 :: frizzled homolog 4 (*Drosophila*)	19545	0.417791773620202	−0.227574007070855
1573	1128192	1128192: EIF2AK3 :: eukaryotic translation initiation factor 2-alpha kinase 3	102506	0.030022657950088	−0.105794931461638
1574	1128195	1128195: RAB7L1 :: RAB7, member RAS oncogene family-like 1	115325	−0.071449934839951	0.001712965210567
1575	1128214	1128214: FLJ13848 :: hypothetical protein FLJ13848	408443	−0.389491187946975	0.393766423852120
1576	1128223	1128223: FLJ10307 :: hypothetical protein FLJ10307	55024	−0.231713872811175	−0.036428732445300
1577	1128231	1128231: PRKCH :: protein kinase C, eta	315366	0.291069538767355	−0.571782301191371
1578	1128248	1128248: FLJ20647 :: hypothetical protein FLJ20647	234149	−0.131530675006671	0.267271954474071
1579	1128283	1128283: TNFRSF21 :: tumor necrosis factor receptor superfamily, member21	159651	0.338287130511519	−0.244101265027556
1580	1128287	1128287: ASB13 :: ankyrin repeat and SOCS box-containing 13	300063	0.278584506324044	−0.103554299642182
1581	1128298	1128298: MRPL2 :: mitochondrial ribosomal protein L2	55041	−0.385624463595324	0.416247769862519
1582	1128311	1128311: RPS6KC1 :: ribosomal protein S6 kinase, 52 kDa, polypeptide 1	30352	0.017290660641073	−0.083949026713284

TABLE 2415-continued

GeneID.txt

Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
1583	1128321	1128321: SIGIRR :: single Ig IL-1R-related molecule	433036	0.155437434081317	−0.312639809674620
1584	1128341	1128341: BRF2 :: BRF2, subunit of RNA polymerase III transcription initiation factor, BRF1-like	274136	−0.202955230211738	0.332040507811259
1585	1128356	1128356: C1RL :: complement component 1, r subcomponent-like	415792	0.680615686054409	−0.570295986072283
1586	1128360	1128360: SLC35E3 :: solute carrier family 35, member E2	445043	−0.080000685186761	0.123127675676569
1587	1128377	1128377: PLAC8 :: placenta-specific 8	371003	−0.177981381447672	−0.090435241558140
1588	1128386	1128386: CD164L1 :: CD164 sialomucin-like 1	195727	0.578953125706333	−0.242872939295295
1589	1128387	1128387: HIPK2 :: homeodomain interacting protein kinase 2	397465	0.118459663415695	−0.299358008807702
1590	1128395	1128395: SEMA4C :: sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C	7188	0.385224538166251	−0.358632797373520
1591	1128401	1128401: ChGn :: chondroitin beta1,4 N-acetylgalactosaminyltransferase	341073	0.528070744382773	−0.289776027652708
1592	1128418	1128418: CGI-14 :: CGI-14 protein	433499	−0.127373034363878	0.114200478146125
1593	1128435	1128435: PF20 :: PF20	6783	0.092087102441032	0.063200995954978
1594	1128439	1128439: FKBP11 :: FK506 binding protein 11, 19 kDa	438695	−0.246180835487664	0.168972167224322
1595	1128447	1128447: FLJ10287 :: hypothetical protein FLJ10287	40337	−0.367947704342123	0.323692416170365
1596	1128457	1128457: TOPK :: T-LAK cell-originated protein kinase	104741	−0.286232290714309	0.809770422276984
1597	1128469	1128469: :: *Homo sapiens* similar to hypothetical protein FLJ22686 (LOC374825), mRNA	−46	0.317659021852908	−0.443676848604039
1598	1128471	1128471: FLJ22555 :: hypothetical protein FLJ22555	3592	−0.214459966486640	0.459159303116971
1599	1128494	1128494: MDA5 :: melanoma differentiation associated protein-5	389539	0.381564813967180	−0.464350966920936
1600	1128506	1128506: CRK7 :: CDC2-related protein kinase 7	416108	−0.171991120566355	0.362497043497882
1601	1128535	1128535: MAP3K6 :: mitogen-activated protein kinase kinase kinase 6	194694	0.409909576040118	−0.416460864199563
1602	1128536	1128536: DOCK10 :: dedicator of cytokinesis 10	21126	−0.091474581348913	−0.246286876471628
1603	1128585	1128585: AVEN :: apoptosis, caspase activation inhibitor	63168	−0.185978318974428	0.287881726289107
1604	1128615	1128615: FLJ10134 :: hypothetical protein FLJ10134	104800	0.750296824306779	−0.281205969297433
1605	1128626	1128626: EBI3 :: Epstein-Barr virus induced gene 3	501452	0.153228999312480	−0.034410934349004
1606	1128648	1128648: DPEP2 :: dipeptidase 2	499331	0.129320687206103	−0.345950212590144
1607	1128653	1128653: PAK6 :: p21(CDKN1A)-activated kinase 6	21420	−0.267089728890750	0.211427597958234
1608	1128655	1128655: C20orf103 :: chromosome 20 open reading frame 103	22920	−0.036922789176067	−0.017091313081673
1609	1128660	1128660: C13orf18 :: chromosome 13 open reading frame 18	413071	−0.329977691323448	0.232152112413912
1610	1128681	1128681: CLC :: cardiotrophin-like cytokine	191548	0.143956240585398	−0.053287848623373
1611	1128688	1128688: MYOZ1 :: myozenin 1	238756	−0.032274730636254	0.068290273280881
1612	1128694	1128694: ELL3 :: elongation factor RNA polymerase II-like 3	171466	−0.107780233344866	0.274777673936412
1613	1128705	1128705: HUNK :: hormonally upregulated Neu-associated kinase	109437	−0.156244532976336	0.084177298832988
1614	1128710	1128710: NEK11 :: NIMA (never in mitosis gene a)-related kinase 11	159146	−0.014339677064164	−0.057185262323488
1615	1128713	1128713: KCTD14 :: potassium channel tetramerisation domain containing 14	17296	0.153126487439279	−0.305451178240051
1616	1128733	1128733: CADPS2 :: Ca2+-dependent activator protein for secretion 2	489847	0.517597656273347	−0.367879062028602
1617	1128738	1128738: MGC2776 :: hypothetical protein MGC2776	335550	−0.441569943886905	0.397227563725956
1618	1128757	1128757: IRAK4 :: interleukin-1 receptor-associated kinase 4	142295	0.005480770877186	−0.089519474289808
1619	1128781	1128781: FLJ10116 :: hypothetical protein FLJ10116	79741	0.593995376539243	−0.326248755475982
1620	1128786	1128786: PTPLA :: protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a	114062	−0.173989199888605	0.042407369155574
1621	1128787	1128787: C7orf10 :: chromosome 7 open reading frame 10	114611	0.066883608916300	0.135633101298342
1622	1128801	1128801: ZNF435 :: zinc finger protein 435	288539	0.095389848084550	−0.186965157005102
1623	1128807	1128807: HSA250839 :: gene for serine/threonine protein kinase	58241	0.148179807102335	−0.027164856808638
1624	1128845	1128845: FLJ20174 :: hypothetical protein FLJ20174	272416	−0.252855787139230	−0.168029598476545
1625	1128860	1128860: STAG3 :: stromal antigen 3	323634	0.166435463482480	−0.080903410843672
1626	1128900	1128900: STAG3 :: stromal antigen 3	323634	−0.126310620816102	−0.004486849116136
1627	1128901	1128901: LATS1 :: LATS, large tumor suppressor, homolog 1 (*Drosophila*)	487239	0.009763439382962	−0.024911702773039
1628	1128915	1128915: CDKL3 :: cyclin-dependent kinase-like 3	105818	−0.132291718442723	0.219964373254252
1629	1128965	1128965: FGD6 :: FYVE, RhoGEF and PH domain containing 6	170623	0.109709621274018	0.168419208192988
1630	1128969	1128969: FLJ10213 :: hypothetical protein FLJ10213	446590	−0.234154512640439	0.026794437866472
1631	1129024	1129024: GPR86 :: G protein-coupled receptor 86	13040	0.305292619286846	−0.457485905772554
1632	1129026	1129026: FLJ13984 :: hypothetical protein FLJ13984	135146	−0.309743417499126	−0.013237106043976
1633	1129043	1129043: ACVR2B :: activin A receptor, type IIB	23994	0.068257334337018	−0.078869667492364
1634	1129049	1129049: IRAK3 :: interleukin-1 receptor-associated kinase 3	268552	0.295844788432385	−0.096238995458166
1635	1129059	1129059: IL23A :: interleukin 23, alpha subunit p19	98309	0.110558754830653	−0.172783710046595
1636	1129061	1129061: IL22RA1 :: interleukin 22 receptor, alpha 1	110915	−0.049741735912372	0.102523209371207
1637	1129064	1129064: BRDG1 :: BCR downstream signaling 1	121128	−0.052914098023446	0.083226377510035
1638	1129071	1129071: VPREB3 :: pre-B lymphocyte gene 3	136713	−0.116559035957489	0.155319891626767
1639	1129085	1129085: C5R1 :: complement component 5 receptor 1 (C5a ligand)	2161	0.431190714150359	−0.091961719019167
1640	1129103	1129103: TZFP :: testis zinc finger protein	99430	−0.084913089830395	0.006324170944062
1641	1129120	1129120: TLR7 :: toll-like receptor 7	179152	0.189943623624734	−0.353578222257396
1642	1129151	1129151: MUC16 :: mucin 16	−21	0.088376628477854	−0.269336853755411
1643	1129203	1129203: IL17B :: interleukin 17B	110040	−0.004171272880353	−0.001612024722616
1644	1129223	1129223: GALNT10 :: UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (GalNAc-T10)	512728	−0.024712521451973	−0.316144966589372

TABLE 2415-continued

GeneID.txt

Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
1645	1129228	1129228: MAK :: male germ cell-associated kinase	148496	0.079167291478789	0.015734627365448
1646	1129232	1129232: CD244 :: CD244 natural killer cell receptor 2B4	157872	0.073453493038786	−0.377710109106282
1647	1129245	1129245: IL1F9 :: interleukin 1 family, member 9	211238	−0.094915764294385	−0.121817602131821
1648	1129265	1129265: CCRL1 :: chemokine (C-C motif) receptor-like 1	310512	−0.148880028528658	0.181608150889073
1649	1129269	1129269: SNFT :: Jun dimerization protein p21SNFT	62919	0.196502835728553	−0.241893188568789
1650	1129281	1129281: C14orf110 :: chromosome 14 open reading frame 110	395486	−0.027842501648286	0.029163772973386
1651	1129310	1129310: CARK :: cardiac ankyrin repeat kinase	414091	−0.106755206423672	0.156920333732655
1652	1129336	1129336: KCNK12 :: potassium channel, subfamily K, member 12	252617	0.256164419250147	−0.076661906553981
1653	1129419	1129419: GPR2 :: G protein-coupled receptor 2	278446	−0.153560376153935	0.073266711206152
1654	1129495	1129495: TBX21 :: T-box 21	272409	0.099926962762925	−0.206774112272127
1655	1129517	1129517: :: FLJ12193	−63	0.268548338773064	−0.234272075916895
1656	1129535	1129535: RPS6KA6 :: ribosomal protein S6 kinase, 90 kDa, polypeptide 6	368153	−0.060691156845818	−0.112486779113327
1657	1129537	1129537: IL19 :: interleukin 19	71979	0.042032462904672	−0.082637131351126
1658	1129661	1129661: IL17E :: interleukin 17E	302036	0.015759941561729	−0.147728639632796
1659	1129681	1129681: TNFSF15 :: tumor necrosis factor (ligand) superfamily, member 15	241382	0.003868440543706	−0.085807864212777
1660	1129694	1129694: IL26 :: interleukin 26	272350	0.014873438384474	−0.150408790090459
1661	1129743	1129743: DKFZP434A0131 :: DKFZp434A0131 protein	429531	−0.053337181033571	−0.096738574513564
1662	1129754	1129754: IL21 :: interleukin 21	302014	0.101034557454981	−0.028904887858268
1663	1129760	1129760: RNASEL :: ribonuclease L (2',5'-oligoisoadenylate synthetase-dependent)	404277	−0.076744614539946	0.041338871532864
1664	1129812	1129812: CHRNG :: cholinergic receptor, nicotinic, gamma polypeptide	248101	−0.094659546499748	0.198887933475047
1665	1129821	1129821: MOS :: v-mos Moloney murine sarcoma viral oncogene homolog	248146	−0.077862620804062	0.125245212560540
1666	1129825	1129825: TNFSF18 :: tumor necrosis factor (ligand) superfamily, member 18	248197	−0.075226623664457	0.081966056961447
1667	1129874	1129874: CCL24 :: chemokine (C-C motif) ligand 24	247838	−0.009869595016579	0.024069346953711
1668	1129879	1129879: XCR1 :: chemokine (C motif) receptor 1	248116	−0.036265621695120	0.105554164155718
1669	1129887	1129887: B4GALT5 :: UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5	107526	0.380271891913627	−0.303897639472657
1670	1129907	1129907: EIF4EBP1 :: eukaryotic translation initiation factor 4E binding protein 1	406408	0.036754064214461	0.115319060732266
1671	1129911	1129911: GRWD1 :: glutamate-rich WD repeat containing 1	400625	−0.439357897736726	0.474210086029623
1672	1129917	1129917: MARK4 :: MAP/microtubule affinity-regulating kinase 4	118843	−0.170633612286300	−0.010230271789505
1673	1129923	1129923: TRAF3 :: TNF receptor-associated factor 3	297660	0.028090348976765	−0.086664596169330
1674	1129943	1129943: ZNF506 :: zinc finger protein 506	512828	−0.101116534668903	−0.220361168950301
1675	1129967	1129967: C19orf10 :: chromosome 19 open reading frame 10	10927	0.049070512080832	−0.032487526942485
1676	1129978	1129978: SSH1 :: slingshot 1	60377	0.219169062430177	−0.289189938099277
1677	1129993	1129993: FLJ14827 :: hypothetical protein FLJ14827	412981	−0.480749758772810	0.554011664313080
1678	1130007	1130007: NTRK2 :: neurotrophic tyrosine kinase, receptor, type 2	494313	0.120279477549603	−0.243907629075211
1679	1130030	1130030: LONP :: peroxisomal lon protease	301872	−0.072061292782188	−0.319264601727642
1680	1130040	1130040: :: *Homo sapiens*, clone IMAGE: 3626627, mRNA	356460	−0.322229909790390	0.205828937779337
1681	1130054	1130054: RARRES1 :: retinoic acid receptor responder (tazarotene induced) 1	82547	0.685839603413505	−0.362689495840938
1682	1130072	1130072: T1A-2 :: lung type-I cell membrane-associated glycoprotein	468675	0.818831553703874	−0.294460779566936
1683	1130078	1130078: CYLD :: cylindromatosis (turban tumor syndrome)	386952	0.183694775256214	−0.419576263991755
1684	1130088	1130088: PCTK2 :: PCTAIRE protein kinase 2	258536	0.072152820235518	−0.107600969822367
1685	1130090	1130090: LGN :: LGN protein	278338	0.004272301688512	0.479039312613795
1686	1130114	1130114: MPHOSPH9 :: M-phase phosphoprotein 9	445084	−0.379537586983120	0.341620894714238
1687	1130117	1130117: PAX5 :: paired box gene 5 (B-cell lineage specific activator protein)	22030	−0.246528946838740	0.352341177052491
1688	1130121	1130121: HLA-F :: major histocompatibility complex, class I, F	411958	0.377839466682894	−0.570631345032229
1689	1130155	1130155: CLU :: clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J)	436657	0.161844555045734	−0.283244372504117
1690	1130168	1130168: CD58 :: CD58 antigen, (lymphocyte function-associated antigen 3)	75626	0.364492432723028	−0.362266715730823
1691	1130169	1130169: WSX1 :: class I cytokine receptor	132781	0.184454748443662	−0.424999376453384
1692	1130201	1130201: HRBL :: HIV-1 Rev binding protein-like	278502	−0.075697663993041	−0.039821664399179
1693	1130293	1130293: :: *Homo sapiens* partial mRNA, clone c4-1c6	292853	−0.155443177799334	0.095843890123974
1694	1130337	1130337: :: *Homo sapiens* cDNA FLJ39459 fis, clone PROST2011439.	491069	−0.023896848401736	−0.224046963581455
1695	1130354	1130354: SFN :: stratifin	184510	0.018070370867865	0.079139608113699
1696	1130378	1130378: HEY1 :: hairy/enhancer-of-split related with YRPW motif 1	234434	0.395156586940864	−0.286377579116489
1697	1130387	1130387: C20orf27 :: chromosome 20 open reading frame 27	274422	−0.419033206665522	0.532077072330916
1698	1130393	1130393: FLJ10357 :: hypothetical protein FLJ10357	22451	0.634166877712643	−0.441880136419289
1699	1130400	1130400: FRA :: Fos-related antigen	170253	−0.094009668900306	−0.063800779529085
1700	1130426	1130426: PSMB2 :: proteasome (prosome, macropain) subunit, beta type, 2	432607	−0.206477681739062	0.544052744959488
1701	1130429	1130429: JTB :: jumping translocation breakpoint	6396	−0.414145041883499	0.347678891334252
1702	1130430	1130430: ILF2 :: interleukin enhancer binding factor 2, 45 kDa	75117	−0.551604865259108	0.730255055075483
1703	1130433	1130433: U5-200KD :: U5 snRNP-specific protein, 200-KD	246112	−0.366436179521191	0.365690965936921

TABLE 2415-continued

GeneID.txt

Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
1704	1130446	1130446: MGC2749 :: hypothetical protein MGC2749	369785	−0.162045856993512	0.204027835507349
1705	1130447	1130447: OAZ1 :: ornithine decarboxylase antizyme 1	446427	−0.027334049396156	−0.125481385009298
1706	1130465	1130465: ANAPC5 :: anaphase promoting complex subunit 5	7101	−0.188040952374909	0.335759442290327
1707	1130468	1130468: HNRPU :: heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	166463	−0.414228315104379	0.449595813895559
1708	1130472	1130472: TRA1 :: tumor rejection antigen (gp96) 1	192374	−0.058770406781845	0.008454200316347
1709	1130482	1130482: KIAA0152 :: KIAA0152 gene product	181418	−0.013046088161047	0.140884826685794
1710	1130483	1130483: CALM3 :: calmodulin 3 (phosphorylase kinase, delta)	334330	0.034506605516631	0.070747117402494
1711	1130501	1130501: LDHA :: lactate dehydrogenase A	2795	−0.113416716689169	0.557153040616862
1712	1130509	1130509: SPARC :: secreted protein, acidic, cysteine-rich (osteonectin)	111779	0.837304026622357	−0.223436112872554
1713	1130518	1130518: HMGB1 :: high-mobility group box 1	434102	−0.304610144944285	0.589052869603598
1714	1130527	1130527: HSPA9B :: heat shock 70 kDa protein 9B (mortalin-2)	184233	−0.405952252455406	0.580488234077170
1715	1130533	1130533: LITAF :: lipopolysaccharide-induced TNF factor	76507	0.223648867635184	−0.307782200282530
1716	1130588	1130588: HNRPK :: heterogeneous nuclear ribonucleoprotein K	307544	−0.404667709940553	0.444695456954984
1717	1130603	1130603: MCL1 :: myeloid cell leukemia sequence 1 (BCL2-related)	86386	0.116326408892859	−0.411472574543256
1718	1130618	1130618: GRCC9 :: likely ortholog of mouse gene rich cluster, C9 gene	83848	−0.105851503751508	0.515020841340678
1719	1130622	1130622: ZNF207 :: zinc finger protein 207	97128	−0.352374085161843	0.668735280109416
1720	1130624	1130624: SCD :: stearoyl-CoA desaturase (delta-9-desaturase)	119597	0.068466925131898	0.042110137344519
1721	1130629	1130629: CTSB :: cathepsin B	135226	0.463103175029523	−0.332067792414087
1722	1130631	1130631: EPRS :: glutamyl-prolyl-tRNA synthetase	171292	−0.242075805489007	0.343011789857582
1723	1130645	1130645: KIAA1007 :: KIAA1007 protein	279949	−0.508883745098830	0.647834071617021
1724	1130653	1130653: NOL5A :: nucleolar protein 5A (56 kDa with KKE/D repeat)	376064	−0.491441299595535	0.618358768431825
1725	1130658	1130658: PGAM1 :: phosphoglycerate mutase 1 (brain)	447492	−0.225449863013289	0.594965205536490
1726	1130668	1130668: KIAA0992 :: palladin	194431	0.738444323208338	−0.353184585890758
1727	1130674	1130674: HLA-E :: major histocompatibility complex, class I, E	381008	0.316878271078233	−0.616553306253961
1728	1130676	1130676: KIAA0992 :: palladin	194431	0.571670265195923	−0.239239604892387
1729	1130680	1130680: EIF4A2 :: eukaryotic translation initiation factor 4A, isoform 2	511904	−0.406851760364394	0.031928463084035
1730	1130687	1130687: SLC3A2 :: solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	79748	0.005620687941009	0.221535198891908
1731	1130704	1130704: CCND2 :: cyclin D2	376071	−0.086227213019376	−0.105185207044404
1732	1130707	1130707: SSRP1 :: structure specific recognition protein 1	79162	−0.478812788644878	0.723198294147642
1733	1130712	1130712: ABLIM1 :: actin binding LIM protein 1	442540	0.028989108097744	−0.024740365180999
1734	1130732	1130732: UBE2V1 :: ubiquitin-conjugating enzyme E2 variant 1	381025	−0.365959820864458	0.273619600177731
1735	1130735	1130735: TXNIP :: thioredoxin interacting protein	179526	0.147134141082822	−0.423880593075217
1736	1130744	1130744: IF2 :: translation initiation factor IF2	158688	−0.436040464525393	0.549498651391074
1737	1130746	1130746: CD99 :: CD99 antigen	283477	0.491775584257276	−0.301267508834440
1738	1130747	1130747: LDHB :: lactate dehydrogenase B	234489	−0.474279747751518	0.634264298790119
1739	1130755	1130755: ANP32A :: acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	356089	−0.531594087149504	0.564703678975089
1740	1130771	1130771: PSMC2 :: proteasome (prosome, macropain) 26S subunit, ATPase, 2	61153	−0.076342918509587	0.303662557781198
1741	1130799	1130799: PSMA7 :: proteasome (prosome, macropain) subunit, alpha type, 7	233952	−0.183548593771997	0.433457258460047
1742	1130812	1130812: CDH1 :: cadherin 1, type 1, E-cadherin (epithelial)	194657	0.150350262021869	−0.310581185010029
1743	1130820	1130820: EIF2S1 :: eukaryotic translation initiation factor 2, subunit 1 alpha, 35 kDa	151777	−0.248919180836398	0.645496589136077
1744	1130835	1130835: IGFBP7 :: insulin-like growth factor binding protein 7	435795	0.694869060684746	−0.451635497409526
1745	1130839	1130839: ARHGDIA :: Rho GDP dissociation inhibitor (GDI) alpha	159161	−0.287041819068728	0.319746037482479
1746	1130852	1130852: CHD4 :: chromodomain helicase DNA binding protein 4	74441	−0.227607885519199	0.309877252850406
1747	1130855	1130855: ITPR3 :: inositol 1,4,5-triphosphate receptor, type 3	77515	−0.090037163752447	0.246241985491480
1748	1130871	1130871: RAD23B :: RAD23 homolog B (*S. cerevisiae*)	159087	−0.155432198525978	0.354647062606468
1749	1130879	1130879: ENO1 :: enolase 1, (alpha)	433455	−0.103238523231766	0.472120612291936
1750	1130882	1130882: BTG2 :: BTG family, member 2	75462	−0.401612459640219	0.215056573193418
1751	1130888	1130888: RAF1 :: v-raf-1 murine leukemia viral oncogene homolog 1	257266	−0.316699264696602	0.210654762972939
1752	1130898	1130898: SYPL :: synaptophysin-like protein	80919	−0.020322791403430	0.180749968332613
1753	1130900	1130900: BGN :: biglycan	821	0.433491624346225	−0.034657560783871
1754	1130906	1130906: HNRPAB :: heterogeneous nuclear ribonucleoprotein A/B	81361	−0.530041416930423	0.790305469314572
1755	1130910	1130910: APEH :: N-acylaminoacyl-peptide hydrolase	221589	−0.396613250677159	0.314489748130245
1756	1130911	1130911: SDC1 :: syndecan 1	82109	0.257574142041331	−0.110610745819271
1757	1130914	1130914: WSB1 :: SOCS box-containing WD protein SWiP-1	315379	0.152566035413182	−0.130582325128830
1758	1130922	1130922: ANP32B :: acidic (leucine-rich) nuclear phosphoprotein 32 family, member B	459987	−0.268323023580090	0.586480999073766
1759	1130923	1130923: ANP32B :: acidic (leucine-rich) nuclear phosphoprotein 32 family, member B	459987	−0.356618082166821	0.545047027556475
1760	1130926	1130926: C5orf13 :: chromosome 5 open reading frame 13	508741	−0.066893451027013	0.226117239200541
1761	1130936	1130936: STAT6 :: signal transducer and activator of transcription 6, interleukin-4 induced	437475	−0.187297336007257	0.021013107700686
1762	1130942	1130942: GTF3A :: general transcription factor IIIA	445977	−0.468852559402542	0.503393496496502
1763	1130972	1130972: IGF2R :: insulin-like growth factor 2 receptor	76473	0.214658478470718	−0.361049786465530
1764	1130977	1130977: ADRBK1 :: adrenergic, beta, receptor kinase 1	83636	−0.099523373504707	0.102662710355176
1765	1130994	1130994: DPYSL3 :: dihydropyrimidinase-like 3	150358	0.809042808419035	−0.446523381134851

TABLE 2415-continued

GeneID.txt

Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
1766	1131012	1131012: JUN :: v-jun sarcoma virus 17 oncogene homolog (avian)	78465	0.457086129845903	−0.354589691205210
1767	1131019	1131019: ITGA3 :: integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)	265829	0.053523581836060	−0.199397777676044
1768	1131038	1131038: NFKBIA :: nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	81328	0.462390024451032	−0.318458395207705
1769	1131068	1131068: FSCN1 :: fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)	118400	0.536725531023657	−0.251210253863877
1770	1131069	1131069: ID2 :: inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	180919	0.247341922577442	−0.202808821943620
1771	1131074	1131074: DCTD :: dCMP deaminase	76894	−0.248202975835252	0.038410672144689
1772	1131081	1131081: SFPQ :: splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	180610	−0.473453393950819	0.738837614730302
1773	1131082	1131082: IRAK1 :: interleukin-1 receptor-associated kinase 1	182018	−0.020262248068331	0.232370997542063
1774	1131107	1131107: RRAGA :: Ras-related GTP binding A	432330	0.325855382913029	−0.128821612464194
1775	1131110	1131110: IER3 :: immediate early response 3	76095	0.516595624226035	−0.400848458725700
1776	1131119	1131119: SCARB2 :: scavenger receptor class B, member 2	323567	0.355068180876334	−0.357222941974828
1777	1131140	1131140: C14orf92 :: chromosome 14 open reading frame 92	194035	−0.175581522276715	0.264736273192001
1778	1131149	1131149: EGR1 :: early growth response 1	326035	0.334773228743566	−0.223509421726847
1779	1131150	1131150: NP :: nucleoside phosphorylase	75514	−0.354544451710958	0.542011939879683
1780	1131181	1131181: LUM :: lumican	406475	0.892642895727236	−0.356076175533182
1781	1131197	1131197: KIAA0494 :: KIAA0494 gene product	269902	0.137090820104737	−0.390038678127149
1782	1131218	1131218: ENG :: endoglin (Osler-Rendu-Weber syndrome 1)	76753	0.656737413741246	−0.520955702540722
1783	1131219	1131219: SH3BP5 :: SH3-domain binding protein 5 (BTK-associated)	109150	−0.312938579490861	0.164418197287064
1784	1131246	1131246: CDC25B :: cell division cycle 25B	153752	−0.153291439533977	0.090249162613185
1785	1131260	1131260: ABCE1 :: ATP-binding cassette, sub-family E (OABP), member 1	12013	−0.388231075478314	0.595908004595403
1786	1131263	1131263: PPP2R5C :: protein phosphatase 2, regulatory subunit B (B56), gamma isoform	249955	−0.278824832021527	−0.010546616087432
1787	1131268	1131268: IL13RA1 :: interleukin 13 receptor, alpha 1	285115	0.603655816737742	−0.426475715000783
1788	1131274	1131274: CKS1B :: CDC28 protein kinase regulatory subunit 1B	374378	−0.472115050926466	0.804871568180769
1789	1131290	1131290: DAF :: decay accelerating factor for complement (CD55, Cromer blood group system)	408864	−0.021713657405561	−0.031992085263801
1790	1131321	1131321: EGFR :: epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	77432	0.260851077631343	−0.225904558910021
1791	1131325	1131325: CREBL2 :: cAMP responsive element binding protein-like 2	13313	0.554796719681771	−0.648770892709224
1792	1131336	1131336: ZNF410 :: zinc finger protein 410	405945	−0.192207934621065	0.122792077578381
1793	1131340	1131340: LTF :: lactotransferrin	437457	0.235576626054540	−0.261846903756942
1794	1131342	1131342: LANCL1 :: LanC lantibiotic synthetase component C-like 1 (bacterial)	13351	−0.017539774281155	0.118963845188131
1795	1131379	1131379: PLTP :: phospholipid transfer protein	439312	0.233879501502951	−0.271204990365974
1796	1131395	1131395: BRD4 :: bromodomain containing 4	278675	−0.010421483777346	0.015984797307132
1797	1131401	1131401: CPNE3 :: copine III	14158	0.041142882609723	−0.055081905354774
1798	1131405	1131405: ABL1 :: v-abl Abelson murine leukemia viral oncogene homolog 1	446504	−0.221476283909564	0.182435762966943
1799	1131407	1131407: ALS2CR3 :: amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3	154248	0.338869376678187	−0.439596598652341
1800	1131411	1131411: ACTR1B :: ARP1 actin-related protein 1 homolog B, centractin beta (yeast)	2477	0.077923077119751	−0.079428496373113
1801	1131414	1131414: CLK3 :: CDC-like kinase 3	511790	−0.269988760385229	0.082665928562320
1802	1131450	1131450: SRPK1 :: SFRS protein kinase 1	369358	−0.461499682598341	0.660300221952223
1803	1131473	1131473: PSMB4 :: proteasome (prosome, macropain) subunit, beta type, 4	89545	−0.520434353958541	0.484814019338330
1804	1131474	1131474: CDK4 :: cyclin-dependent kinase 4	95577	−0.439683564755247	0.779895489372238
1805	1131490	1131490: CDKN1A :: cyclin-dependent kinase inhibitor 1A (p21, Cip1)	370771	0.385643552030945	−0.301994028596566
1806	1131497	1131497: CTSH :: cathepsin H	114931	0.330713175489614	−0.355002555291128
1807	1131503	1131503: SMARCA5 :: SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	135705	−0.387527664547821	0.543569727624998
1808	1131507	1131507: COL1A1 :: collagen, type I, alpha 1	172928	0.748114290829864	−0.207748584834290
1809	1131531	1131531: MATN2 :: matrilin 2	153647	0.325141676021648	−0.307381647293302
1810	1131541	1131541: TRAM2 :: translocation associated membrane protein 2	310230	−0.109763921862653	0.121260099038360
1811	1131561	1131561: COL1A2 :: collagen, type I, alpha 2	232115	0.874692627775946	−0.334576284522396
1812	1131578	1131578: MYC :: v-myc myelocytomatosis viral oncogene homolog (avian)	202453	−0.473650493201987	0.439091538893661
1813	1131584	1131584: IDS :: iduronate 2-sulfatase (Hunter syndrome)	303154	0.409153834815565	−0.206704914490955
1814	1131592	1131592: CTSK :: cathepsin K (pycnodysostosis)	83942	0.848850881019183	−0.369116963340649
1815	1131594	1131594: ERBB3 :: v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	306251	−0.037028165004209	0.014125470226058
1816	1131614	1131614: RANBP1 :: RAN binding protein 1	24763	−0.497718394256005	0.861673208863039
1817	1131636	1131636: SPOCK2 :: sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2	436193	0.163651135120878	−0.586216415254260
1818	1131637	1131637: MADH4 :: MAD, mothers against decapentaplegic homolog 4 (*Drosophila*)	75862	−0.296122555295810	0.254301505485065

TABLE 2415-continued

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Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
1819	1131640	1131640: DHFR :: dihydrofolate reductase	83765	−0.318925662013329	0.697984260974183
1820	1131645	1131645: SCYE1 :: small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating)	105656	−0.408590686241245	0.435284600019574
1821	1131654	1131654: MYLK :: myosin, light polypeptide kinase	506692	0.651782538418739	−0.499306112068076
1822	1131663	1131663: MARK3 :: MAP/microtubule affinity-regulating kinase 3	437625	−0.127947033428119	0.128365431201822
1823	1131687	1131687: TLK1 :: tousled-like kinase 1	369280	−0.479727631283518	0.180410183690407
1824	1131705	1131705: ICAM1 :: intercellular adhesion molecule 1 (CD54), human rhinovirus receptor	386467	0.378982406710592	−0.337971803564004
1825	1131710	1131710: TNFAIP3 :: tumor necrosis factor, alpha-induced protein 3	211600	0.463815458286967	−0.506090111158935
1826	1131733	1131733: AXL :: AXL receptor tyrosine kinase	83341	0.378282997894475	−0.403851757655397
1827	1131737	1131737: STK17A :: serine/threonine kinase 17a (apoptosis-inducing)	9075	0.130652258117317	−0.103978746190248
1828	1131752	1131752: FOXO1A :: forkhead box O1A (rhabdomyosarcoma)	170133	−0.122578273317010	0.040350502997271
1829	1131753	1131753: IFNGR1 :: interferon gamma receptor 1	180866	0.618517741082226	−0.417914352213948
1830	1131755	1131755: LTBP1 :: latent transforming growth factor beta binding protein 1	241257	0.502355072705751	−0.139333692684381
1831	1131757	1131757: LSM4 :: LSM4 homolog, U6 small nuclear RNA associated (*S. cerevisiae*)	76719	−0.338083430713762	0.555861490784508
1832	1131767	1131767: RFXANK :: regulatory factor X-associated ankyrin-containing protein	296776	−0.298195363108909	0.396266516850386
1833	1131778	1131778: E2-EPF :: ubiquitin carrier protein	396393	−0.444812770066341	0.811955135837133
1834	1131786	1131786: ITGB2 :: integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit)	375957	0.558038370974376	−0.444583848022385
1835	1131806	1131806: DNAJB9 :: DnaJ (Hsp40) homolog, subfamily B, member 9	6790	0.130968076956592	−0.292357967581071
1836	1131808	1131808: RALBP1 :: ralA binding protein 1	75447	−0.431671598650297	0.449909231902008
1837	1131813	1131813: RYK :: RYK receptor-like tyrosine kinase	285346	0.032808356450494	−0.176195154516543
1838	1131815	1131815: SLC16A3 :: solute carrier family 16 (monocarboxylic acid transporters), member 3	386678	0.595720282107956	−0.261951094065078
1839	1131816	1131816: IL8 :: interleukin 8	624	0.140264002040061	−0.022197751307439
1840	1131827	1131827: PSCD1 :: pleckstrin homology, Sec7 and coiled-coil domains 1(cytohesin 1)	1050	0.009086209334830	−0.326598876849318
1841	1131835	1131835: ANPEP :: alanyl (membrane) aminopeptidase (aminopeptidase N, aminopeptidase M, microsomal aminopeptidase, CD13, p150)	1239	0.560675531752289	−0.319995337520616
1842	1131839	1131839: SFRS3 :: splicing factor, arginine/serine-rich 3	405144	−0.462771409363554	0.757901723793864
1843	1131845	1131845: NBS1 :: Nijmegen breakage syndrome 1 (nibrin)	25812	0.187739986384909	−0.055487351990348
1844	1131847	1131847: CD97 :: CD97 antigen	3107	0.470642638940702	−0.594528313613836
1845	1131854	1131854: GCLC :: glutamate-cysteine ligase, catalytic subunit	414985	−0.229812122262907	0.033652611178791
1846	1131861	1131861: YES1 :: v-yes-1 *Yamaguchi sarcoma* viral oncogene homolog 1	194148	0.404068940647571	−0.352614969792935
1847	1131863	1131863: SOX9 :: SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal)	2316	0.023548359459035	0.008979903745464
1848	1131868	1131868: GYPC :: glycophorin C (Gerbich blood group)	81994	0.068679003500084	−0.169866880145741
1849	1131870	1131870: ADAM12 :: a disintegrin and metalloproteinase domain 12 (meltrin alpha)	8850	0.672171616380497	−0.290298904712172
1850	1131875	1131875: CAPN6 :: calpain 6	169172	0.053625471376072	−0.113317658717737
1851	1131916	1131916: PIAS3 :: protein inhibitor of activated STAT3	435761	0.060317360202652	−0.119267354100978
1852	1131918	1131918: MTSS1 :: metastasis suppressor 1	77694	0.126594607748513	−0.215833828228631
1853	1131925	1131925: TCTA :: T-cell leukemia translocation altered gene	250894	−0.140634086253037	−0.084263934757262
1854	1131940	1131940: TGFB1 :: transforming growth factor, beta 1 (Camurati-Engelmann disease)	1103	0.077307306507790	−0.219635532756303
1855	1131955	1131955: WHSC2 :: Wolf-Hirschhorn syndrome candidate 2	21771	−0.428553483194901	0.522335335717293
1856	1131964	1131964: KIF5C :: kinesin family member 5C	6641	0.178798859283669	−0.000776060927303
1857	1131972	1131972: PAK4 :: p21(CDKN1A)-activated kinase 4	20447	−0.184120285169395	0.182353309770624
1858	1131975	1131975: RNF8 :: ring finger protein (C3HC4 type) 8	24439	−0.246051078343186	0.456159857346887
1859	1131998	1131998: RFC5 :: replication factor C (activator 1) 5, 36.5 kDa	443227	−0.304105043276485	0.580015219267383
1860	1132004	1132004: SIAT9 :: sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase)	415117	0.131829639089957	−0.357953062221225
1861	1132011	1132011: CLK2 :: CDC-like kinase 2	73986	−0.433221154262639	0.333142142452891
1862	1132013	1132013: SCA1 :: spinocerebellar ataxia 1 (olivopontocerebellar ataxia 1, autosomal dominant, ataxin 1)	434961	0.573011124237002	−0.558158560945881
1863	1132016	1132016: NOTCH3 :: Notch homolog 3 (*Drosophila*)	8546	0.516342851051717	−0.283665731808773
1864	1132022	1132022: ZNF24 :: zinc finger protein 24 (KOX 17)	173911	−0.132362253139443	0.019939787690243
1865	1132031	1132031: MAP2K4 :: mitogen-activated protein kinase kinase 4	134106	−0.044326630951000	0.077057186977509
1866	1132034	1132034: UNC119 :: unc-119 homolog (*C. elegans*)	410455	0.162674778479055	−0.152850646527214
1867	1132035	1132035: PDAP2 :: PDGFA associated protein 2	8186	−0.351063634678681	0.341148418065009
1868	1132058	1132058: TGIF :: TGFB-induced factor (TALE family homeobox)	161999	−0.089955439319608	0.012983428575114
1869	1132104	1132104: TBC1D4 :: TBC1 domain family, member 4	173802	0.174716497125486	−0.303331906685459
1870	1132122	1132122: MME :: membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)	307734	0.091058727833380	0.213585135607787
1871	1132132	1132132: ATOX1 :: ATX1 antioxidant protein 1 homolog (yeast)	279910	0.371746754962258	−0.235388977702808
1872	1132159	1132159: ZNF318 :: zinc finger protein 318	147868	0.039152606400365	0.161742423454252

TABLE 2415-continued

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Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
1873	1132178	1132178: PTTG1 :: pituitary tumor-transforming 1	350966	−0.258893293711822	0.666347157955608
1874	1132196	1132196: CSF3R :: colony stimulating factor 3 receptor (granulocyte)	381027	0.438613330885891	−0.418452605605811
1875	1132220	1132220: GPRC5B :: G protein-coupled receptor, family C, group 5, member B	448805	0.366763832566919	−0.427970742931399
1876	1132223	1132223: FGFR2 :: fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome)	404081	0.317558427639917	−0.241289886185299
1877	1132230	1132230: PLA2G2A :: phospholipase A2, group IIA (platelets, synovial fluid)	76422	0.279193056674363	−0.160817405939559
1878	1132236	1132236: TMOD1 :: tropomodulin 1	374849	0.324423040844218	−0.350644740562922
1879	1132256	1132256: KIAA0173 :: KIAA0173 gene product	169910	0.031123896338403	0.336046918386896
1880	1132260	1132260: FZD7 :: frizzled homolog 7 (*Drosophila*)	173859	0.462892817101932	−0.413817554150429
1881	1132288	1132288: STS :: steroid sulfatase (microsomal), arylsulfatase C, isozyme S	79876	0.134794043837710	0.081300346040601
1882	1132292	1132292: BLVRA :: biliverdin reductase A	435726	0.307210356182809	−0.329095748235412
1883	1132294	1132294: RPS6KB2 :: ribosomal protein S6 kinase, 70 kDa, polypeptide 2	103081	0.046867241876797	−0.031492411847754
1884	1132306	1132306: BCL7A :: B-cell CLL/lymphoma 7A	−34	−0.145765239332859	0.288878301794857
1885	1132329	1132329: ACK1 :: activated p21cdc42Hs kinase	128392	0.015481843347622	−0.205600218015162
1886	1132336	1132336: GAB2 :: GRB2-associated binding protein 2	30687	0.279420865222956	−0.316921655907721
1887	1132345	1132345: VCAM1 :: vascular cell adhesion molecule 1	109225	0.423122552434272	−0.521238250710401
1888	1132349	1132349: DMD :: dystrophin (muscular dystrophy, Duchenne and Becker types)	169470	0.015601524791194	0.155636775212336
1889	1132353	1132353: THBD :: thrombomodulin	2030	0.319336617488327	−0.304072866702818
1890	1132354	1132354: DAPK3 :: death-associated protein kinase 3	153908	−0.087408304874834	0.165959747878693
1891	1132375	1132375: MARK2 :: MAP/microtubule affinity-regulating kinase 2	157199	0.003817055906942	−0.029439031931299
1892	1132376	1132376: BTN2A1 :: butyrophilin, subfamily 2, member A1	169963	0.269826752423953	−0.381922260724480
1893	1132396	1132396: FUT8 :: fucosyltransferase 8 (alpha (1,6) fucosyltransferase)	118722	−0.244646243998852	0.231749952936851
1894	1132407	1132407: PAWR :: PRKC, apoptosis, WT1, regulator	406074	−0.256402843713444	0.392482360907927
1895	1132426	1132426: C6orf56 :: chromosome 6 open reading frame 56	102471	0.075623143391260	−0.263519720550745
1896	1132428	1132428: SFRP4 :: secreted frizzled-related protein 4	105700	0.470112484475708	−0.289073301793498
1897	1132433	1132433: ME1 :: malic enzyme 1, NADP(+)-dependent, cytosolic	14732	0.235924704818424	−0.341006938347295
1898	1132434	1132434: PRKX :: protein kinase, X-linked	147996	0.082516439464899	−0.203822460383043
1899	1132435	1132435: ULK2 :: unc-51-like kinase 2 (*C. elegans*)	168762	0.025216376306500	−0.043076970364662
1900	1132449	1132449: STK6 :: serine/threonine kinase 6	250822	−0.342484271052208	0.854223977659442
1901	1132460	1132460: CDC45L :: CDC45 cell division cycle 45-like (*S. cerevisiae*)	114311	−0.392694067278240	0.786127341984203
1902	1132462	1132462: FOXO3A :: forkhead box O3A	14845	0.368591254754925	−0.433764383288663
1903	1132468	1132468: TFDP1 :: transcription factor Dp-1	79353	−0.281111016450068	0.587665041868591
1904	1132479	1132479: CKS2 :: CDC28 protein kinase regulatory subunit 2	83758	−0.336131034183213	0.776594329768994
1905	1132485	1132485: ADRBK2 :: adrenergic, beta, receptor kinase 2	445563	0.026350082372157	0.212105726957152
1906	1132498	1132498: PRKR :: protein kinase, interferon-inducible double stranded RNA dependent	439523	0.066840579394694	−0.087904249908943
1907	1132504	1132504: GLIPR1 :: GLI pathogenesis-related 1 (glioma)	511765	0.332274083428259	−0.223315863333576
1908	1132519	1132519: CDK5 :: cyclin-dependent kinase 5	166071	−0.047271288760870	0.233374203627911
1909	1132520	1132520: LMO2 :: LIM domain only 2 (rhombotin-like 1)	283063	0.322555941970676	−0.133225258835905
1910	1132525	1132525: VDR :: vitamin D (1,25-dihydroxyvitamin D3) receptor	2062	0.433864275074134	−0.287514297938507
1911	1132529	1132529: C6orf9 :: chromosome 6 open reading frame 9	288316	0.020696537691352	−0.351700071982180
1912	1132531	1132531: PKMYT1 :: membrane-associated tyrosine- and threonine-specific cdc2-inhibitory kinase	77783	−0.326448359051311	0.770085323613511
1913	1132536	1132536: PMAIP1 :: phorbol-12-myristate-13-acetate-induced protein 1	96	−0.264821671020407	0.140274139633261
1914	1132545	1132545: CD151 :: CD151 antigen	512857	0.484034201302057	−0.267724272339692
1915	1132547	1132547: NPR2 :: natriuretic peptide receptor B/guanylate cyclase B (atrionatriuretic peptide receptor B)	78518	0.146399574004803	−0.263444587844550
1916	1132572	1132572: LIMK1 :: LIM domain kinase 1	36566	0.134056222788714	0.042055189501082
1917	1132584	1132584: FGFR3 :: fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)	1420	0.147516952526905	−0.119140751786612
1918	1132592	1132592: GPRK5 :: G protein-coupled receptor kinase 5	211569	0.177329362173847	−0.033025403899686
1919	1132614	1132614: ALOX5 :: arachidonate 5-lipoxygenase	89499	0.253272865281527	−0.158095339023624
1920	1132628	1132628: TIE :: tyrosine kinase with immunoglobulin and epidermal growth factor homology domains	78824	0.235417471722526	−0.055952441856724
1921	1132636	1132636: CD44 :: CD44 antigen (homing function and Indian blood group system)	306278	0.170483625093136	−0.070535279463917
1922	1132651	1132651: TOX :: thymus high mobility group box protein TOX	439767	0.118932638076210	−0.079565463918791
1923	1132700	1132700: RPS6KA5 :: ribosomal protein S6 kinase, 90 kDa, polypeptide 5	109058	−0.017334567062377	−0.166266633063264
1924	1132726	1132726: MAPK4 :: mitogen-activated protein kinase 4	433728	0.009521048919827	−0.084175684705991
1925	1132734	1132734: COL9A3 :: collagen, type IX, alpha 3	126248	−0.101320116382731	0.079697319215094
1926	1132762	1132762: MAL :: mal, T-cell differentiation protein	80395	0.252541285182322	−0.443739008537555
1927	1132766	1132766: TNFRSF6 :: tumor necrosis factor receptor superfamily, member 6	82359	0.439880140313859	−0.246840312593953

TABLE 2415-continued

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Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
1928	1132768	1132768: IFNAR2 :: interferon (alpha, beta and omega) receptor 2	512211	0.004319875316505	−0.106811200549353
1929	1132775	1132775: RRAD :: Ras-related associated with diabetes	1027	0.382640243706838	−0.245069256965701
1930	1132780	1132780: CACNA2D2 :: calcium channel, voltage-dependent, alpha 2/delta subunit 2	389415	−0.008811475360416	−0.089903821942477
1931	1132787	1132787: BMPR1A :: bone morphogenetic protein receptor, type IA	2534	−0.115173969757864	0.228241887165543
1932	1132799	1132799: APAF1 :: apoptotic protease activating factor	373575	0.108985290832645	0.033820592215645
1933	1132809	1132809: PSK :: prostate derived STE20-like kinase PSK	122823	−0.084370387981083	0.063316707183397
1934	1132818	1132818: LCK :: lymphocyte-specific protein tyrosine kinase	1765	0.166418049475020	−0.319367837467735
1935	1132825	1132825: SAP30 :: sin3-associated polypeptide, 30 kDa	512813	0.064474665431520	0.408174220850057
1936	1132830	1132830: BCL3 :: B-cell CLL/lymphoma 3	31210	0.012241396097884	−0.005770899349080
1937	1132834	1132834: SOX11 :: SRY (sex determining region Y)-box 11	432638	−0.130130852086878	0.008934439925760
1938	1132850	1132850: DYRK1B :: dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1B	130988	−0.150245711405737	−0.064037848783788
1939	1132851	1132851: :: *Homo sapiens* cDNA FLJ46012 fis, clone SPLEN2007689, highly similar to Neutrophil cytosol factor 1	1583	−0.105077219223237	−0.185727977850533
1940	1132852	1132852: CENPA :: centromere protein A, 17 kDa	1594	−0.330307054028778	0.834198009135619
1941	1132860	1132860: PSK :: prostate derived STE20-like kinase PSK	122823	−0.140238455355596	0.075742960594935
1942	1132862	1132862: ITGB4 :: integrin, beta 4	85266	−0.001397803543690	−0.006702616683621
1943	1132866	1132866: ATF5 :: activating transcription factor 5	9754	−0.083740507309572	−0.030416622263988
1944	1132874	1132874: ADORA2A :: adenosine A2a receptor	197029	−0.171103874940728	0.175530614350310
1945	1132883	1132883: MAP3K8 :: mitogen-activated protein kinase kinase kinase 8	432453	0.220120953209822	−0.207562161908588
1946	1132890	1132890: CD79A :: CD79A antigen (immunoglobulin-associated alpha)	79630	−0.337177451882671	0.299810735012318
1947	1132892	1132892: KIT :: v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	81665	0.346843052155709	−0.287525269110642
1948	1132918	1132918: CCL3 :: chemokine (C-C motif) ligand 3	73817	0.210200763463909	−0.379856191443791
1949	1132920	1132920: FPR1 :: formyl peptide receptor 1	753	0.450668752553231	−0.271074665943058
1950	1132953	1132953: ADAM8 :: a disintegrin and metalloproteinase domain 8	86947	0.090679204456041	−0.122432730144956
1951	1132959	1132959: ATP7A :: ATPase, Cu++ transporting, alpha polypeptide (Menkes syndrome)	606	0.366616137158226	−0.278472771716937
1952	1132961	1132961: CENTB1 :: centaurin, beta 1	337242	0.059851837494540	−0.386761070675942
1953	1132973	1132973: TCF7 :: transcription factor 7 (T-cell specific, HMG-box)	169294	0.123121096136518	−0.447164392087382
1954	1132979	1132979: CCRK :: cell cycle related kinase	26322	0.207844813354062	−0.131701392184582
1955	1132990	1132990: CD79B :: CD79B antigen (immunoglobulin-associated beta)	89575	−0.344622456167376	0.358039114087407
1956	1132994	1132994: OGG1 :: 8-oxoguanine DNA glycosylase	380271	−0.137099966252423	0.320169119840156
1957	1132996	1132996: KMO :: kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	409081	0.211990018555365	−0.291776582897728
1958	1133004	1133004: ACVR2 :: activin A receptor, type II	389846	0.279599795179747	−0.239731396808758
1959	1133011	1133011: TMSNB :: thymosin, beta, identified in neuroblastoma cells	56145	−0.002520060395082	0.071841149776115
1960	1133021	1133021: ACHE :: acetylcholinesterase (YT blood group)	154495	0.402482778770336	−0.155787254777042
1961	1133024	1133024: ZNF288 :: zinc finger protein 288	436987	0.265865101259661	−0.396721785363083
1962	1133030	1133030: CCL15 :: chemokine (C-C motif) ligand 15	272493	0.057379944824827	−0.281520577334817
1963	1133042	1133042: ITGBL1 :: integrin, beta-like 1 (with EGF-like repeat domains)	311054	0.622932591813418	−0.328959959392322
1964	1133047	1133047: AAK1 :: AP2 associated kinase 1	135941	0.348101012819978	−0.519349741936085
1965	1133049	1133049: H2AFX :: H2A histone family, member X	147097	−0.194779401220227	0.611672944781315
1966	1133065	1133065: PLAU :: plasminogen activator, urokinase	77274	0.783707351172337	−0.379451893760215
1967	1133068	1133068: G1P2 :: interferon, alpha-inducible protein (clone IFI-15K)	458485	0.224134143117873	−0.313126229936884
1968	1133076	1133076: PDCD8 :: programmed cell death 8 (apoptosis-inducing factor)	18720	−0.157569526709521	0.402184728488840
1969	1133080	1133080: KATNA1 :: katanin p60 (ATPase-containing) subunit A 1	440341	−0.165970006007139	0.181023125522753
1970	1133091	1133091: CR2 :: complement component (3d/Epstein Barr virus) receptor 2	73792	0.030214844042362	0.092058217437685
1971	1133093	1133093: TYK2 :: tyrosine kinase 2	75516	−0.217551973397616	−0.002422536201704
1972	1133099	1133099: DNASE1L3 :: deoxyribonuclease I-like 3	88646	−0.257980874817348	−0.166979927446227
1973	1133102	1133102: FRDA :: Friedreich ataxia	360041	−0.335514224531287	0.492486823001609
1974	1133111	1133111: PDE9A :: phosphodiesterase 9A	389777	0.133104476615309	−0.019862978252224
1975	1133117	1133117: PACE-1 :: ezrin-binding partner PACE-1	435560	−0.016659594094386	−0.002954180593273
1976	1133119	1133119: MST1 :: macrophage stimulating 1 (hepatocyte growth factor-like)	512587	0.017059225812341	−0.167280765698926
1977	1133138	1133138: HLA-DOB :: major histocompatibility complex, class II, DO beta	1802	−0.150884123016589	−0.047034927110652
1978	1133141	1133141: DLEU1 :: deleted in lymphocytic leukemia, 1	344524	−0.476295741441405	0.564225564362615
1979	1133148	1133148: CD38 :: CD38 antigen (p45)	174944	−0.086274304083668	−0.258405804308845
1980	1133150	1133150: MAP2K6 :: mitogen-activated protein kinase kinase 6	256924	−0.060625002575886	0.143053623586413
1981	1133156	1133156: COMP :: cartilage oligomeric matrix protein	1584	0.441890669117056	−0.195814414026257
1982	1133184	1133184: ITGAM :: integrin, alpha M (complement component receptor 3, alpha; also known as CD11b (p170), macrophage antigen alpha polypeptide)	172631	0.753289632173116	−0.438207938207401
1983	1133192	1133192: RASGRP3 :: RAS guanyl releasing protein 3 (calcium and DAG-regulated)	24024	−0.227545188050837	0.110767187589711
1984	1133195	1133195: ROR1 :: receptor tyrosine kinase-like orphan receptor 1	274243	0.211583482691962	−0.095352844765974
1985	1133210	1133210: JAK2 :: Janus kinase 2 (a protein tyrosine kinase)	434374	0.211723154336484	−0.309565714170364

TABLE 2415-continued

GeneID.txt

Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
1986	1133216	1133216: PDE4DIP :: phosphodiesterase 4D interacting protein (myomegalin)	390449	0.469859143755927	−0.270025422668526
1987	1133219	1133219: RET :: ret proto-oncogene (multiple endocrine neoplasia and medullary thyroid carcinoma 1, Hirschsprung disease)	350321	0.039216692256241	−0.113466892491905
1988	1133227	1133227: NOLC1 :: nucleolar and coiled-body phosphoprotein 1	75337	−0.467836599715920	0.605412542908700
1989	1133232	1133232: CEL :: carboxyl ester lipase (bile salt-stimulated lipase)	406160	−0.047643754334538	0.004264213209241
1990	1133252	1133252: EPHA1 :: EphA1	89839	0.291635532708424	−0.334277608203048
1991	1133260	1133260: IL15 :: interleukin 15	168132	0.477661261402447	−0.545949137402680
1992	1133272	1133272: MERTK :: c-mer proto-oncogene tyrosine kinase	306178	0.252944775766872	−0.308345262733304
1993	1133275	1133275: REL :: v-rel reticuloendotheliosis viral oncogene homolog (avian)	44313	−0.085309557979979	0.156958739161487
1994	1133296	1133296: EPHA3 :: EphA3	123642	0.158232174391835	−0.146669730921844
1995	1133299	1133299: CSNK2A1 :: casein kinase 2, alpha 1 polypeptide	446484	−0.402393962409281	0.443591691051582
1996	1133300	1133300: CTH :: cystathionase (cystathionine gamma-lyase)	19904	−0.174763128546197	0.309368945386643
1997	1133355	1133355: MATK :: megakaryocyte-associated tyrosine kinase	437808	0.209013931316900	−0.223912921475326
1998	1133358	1133358: TAL1 :: T-cell acute lymphocytic leukemia 1	73828	0.099663664736123	−0.092238236560719
1999	1133376	1133376: DAPK2 :: death-associated protein kinase 2	129208	0.312209231371153	−0.375817373135772
2000	1133388	1133388: MAP3K10 :: mitogen-activated protein kinase kinase kinase 10	435014	−0.085980697049518	−0.084119677925152
2001	1133389	1133389: XCL1 :: chemokine (C motif) ligand 1	174228	−0.035790980270872	−0.263917654207473
2002	1133392	1133392: PFC :: properdin P factor, complement	53155	0.101600551414248	−0.305806420968560
2003	1133397	1133397: PF4 :: platelet factor 4 (chemokine (C—X—C motif) ligand 4)	81564	0.138980500020639	−0.024818220159783
2004	1133400	1133400: CD19 :: CD19 antigen	96023	−0.142433949967589	0.163988190753814
2005	1133405	1133405: CCL13 :: chemokine (C-C motif) ligand 13	414629	−0.083416470126778	−0.088402738547819
2006	1133406	1133406: ABL2 :: v-abl Abelson murine leukemia viral oncogene homolog 2 (arg, Abelson-related gene)	159472	0.022813711233182	0.032696347502914
2007	1133407	1133407: TCL1B :: T-cell leukemia/lymphoma 1B	512850	−0.174317478777086	0.242190379023676
2008	1133408	1133408: DDEF2 :: development and differentiation enhancing factor 2	12802	0.540194218430208	−0.416938590146850
2009	1133430	1133430: TNFRSF6B :: tumor necrosis factor receptor superfamily, member 6b, decoy	348183	0.269171054691013	−0.078298763058308
2010	1133445	1133445: CHC1 :: chromosome condensation 1	196769	−0.388958919390715	0.590137912621854
2011	1133453	1133453: RGS9 :: regulator of G-protein signalling 9	117149	0.120525989789610	−0.176381127128455
2012	1133476	1133476: MAP4K4 :: mitogen-activated protein kinase kinase kinase kinase 4	3628	0.186100449709661	0.138800618028371
2013	1133515	1133515: PTPN6 :: protein tyrosine phosphatase, non-receptor type 6	63489	0.012603181388466	−0.102763121939913
2014	1133538	1133538: FCER2 :: Fc fragment of IgE, low affinity II, receptor for (CD23A)	1416	0.106023153171250	−0.252188795472937
2015	1133565	1133565: HDAC6 :: histone deacetylase 6	6764	−0.192135925793860	0.026151793306868
2016	1133568	1133568: MAP3K7 :: mitogen-activated protein kinase kinase kinase 7	290346	−0.068454670946960	0.068695359831212
2017	1133569	1133569: HYAL2 :: hyaluronoglucosaminidase 2	76873	0.266854829641114	−0.217178690680440
2018	1133576	1133576: HRK :: harakiri, BCL2 interacting protein (contains only BH3 domain)	87247	−0.136002276499443	0.126882867488172
2019	1133577	1133577: SLK :: Ste20-related serine/threonine kinase	105751	0.130411355792943	−0.076955906871234
2020	1133580	1133580: LILRA3 :: leukocyte immunoglobulin-like receptor, subfamily A (without TM domain), member 3	113277	−0.251926329094464	−0.009994293775648
2021	1133595	1133595: IL11 :: interleukin 11	1721	0.030444042014686	−0.107584215640277
2022	1133618	1133618: CCR5 :: chemokine (C-C motif) receptor 5	511796	0.412073449175704	−0.559429116658751
2023	1133629	1133629: PTK7 :: PTK7 protein tyrosine kinase 7	90572	0.437358321386405	−0.235325422507285
2024	1133652	1133652: ASS :: argininosuccinate synthetase	160786	0.299982247486773	−0.281306420532693
2025	1133672	1133672: TNF :: tumor necrosis factor (TNF superfamily, member 2)	241570	0.229157733455114	−0.039984679710739
2026	1133676	1133676: MAPK6 :: mitogen-activated protein kinase 6	271980	−0.053402388955127	0.156113673288142
2027	1133694	1133694: AKT1 :: v-akt murine thymoma viral oncogene homolog 1	368861	−0.098441215455632	0.210637913631811
2028	1133700	1133700: CDH11 :: cadherin 11, type 2, OB-cadherin (osteoblast)	443435	0.910273241078143	−0.447714717232453
2029	1133701	1133701: CD80 :: CD80 antigen (CD28 antigen ligand 1, B7-1 antigen)	838	0.234271452338870	−0.123295283109379
2030	1133702	1133702: FRK :: fyn-related kinase	89426	−0.088749786570166	0.145490673392961
2031	1133704	1133704: CASP7 :: caspase 7, apoptosis-related cysteine protease	9216	0.150284681291938	−0.040276646079796
2032	1133708	1133708: ICAM4 :: intercellular adhesion molecule 4, Landsteiner-Wiener blood group	512159	0.072389666323349	−0.128178472781610
2033	1133724	1133724: PCTK1 :: PCTAIRE protein kinase 1	171834	−0.039172844280366	0.183412682054809
2034	1133731	1133731: UBN1 :: ubinuclein 1	21479	−0.233103646285480	0.126011351317026
2035	1133753	1133753: KIR3DL2 :: killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 2	56328	0.057615719536991	0.021322335954838
2036	1133755	1133755: CDC2L5 :: cell division cycle 2-like 5 (cholinesterase-related cell division controller)	404501	−0.171682635768532	−0.003512231465868
2037	1133757	1133757: STAU :: staufen, RNA binding protein (*Drosophila*)	6113	−0.285814369623812	0.192008922806710
2038	1133766	1133766: LTB :: lymphotoxin beta (TNF superfamily, member 3)	376208	0.229636210128755	−0.178027816423099
2039	1133778	1133778: IL15RA :: interleukin 15 receptor, alpha	12503	0.411529350916578	−0.384522006576836
2040	1133786	1133786: ALG3 :: asparagine-linked glycosylation 3 homolog (yeast, alpha-1,3-mannosyltransferase)	153591	−0.379755131485044	0.383219707931730

TABLE 2415-continued

GeneID.txt

Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
2041	1133801	1133801: TNFSF4 :: tumor necrosis factor (ligand) superfamily, member 4 (tax-transcriptionally activated glycoprotein 1, 34 kDa)	181097	0.137229819751181	−0.275883435383981
2042	1133802	1133802: CDC2L2 :: cell division cycle 2-like 2	402748	−0.137802379411402	0.057863977677410
2043	1133810	1133810: CCR9 :: chemokine (C-C motif) receptor 9	225946	−0.117781028827656	0.124533083271088
2044	1133829	1133829: MS4A2 :: membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for; beta polypeptide)	386748	0.177404858682871	−0.054031419783302
2045	1133834	1133834: LAIR2 :: leukocyte-associated Ig-like receptor 2	43803	0.226784659149121	−0.267608718674007
2046	1133846	1133846: TNFRSF9 :: tumor necrosis factor receptor superfamily, member 9	193418	0.533030357422095	−0.338024239621130
2047	1133848	1133848: SYK :: spleen tyrosine kinase	192182	−0.311059247048826	0.343785891142310
2048	1133867	1133867: C1orf38 :: chromosome 1 open reading frame 38	10649	0.307862904192117	−0.388823072767907
2049	1133869	1133869: GADD45B :: growth arrest and DNA-damage-inducible, beta	110571	0.223306853942758	−0.339610292113472
2050	1133901	1133901: MUSK :: muscle, skeletal, receptor tyrosine kinase	156465	0.045285571984218	0.076108036762733
2051	1133904	1133904: TNFRSF1A :: tumor necrosis factor receptor superfamily, member 1A	159	0.643710808786366	−0.596010985742485
2052	1133910	1133910: BLNK :: B-cell linker	167746	−0.446169388331319	0.329125198490164
2053	1133931	1133931: LILRB2 :: leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2	306230	0.189896565915764	−0.333536831009256
2054	1133998	1133998: ID3 :: inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	76884	−0.231618348471321	0.102308599561213
2055	1134069	1134069: CD8B1 :: CD8 antigen, beta polypeptide 1 (p37)	405667	0.225901023201953	−0.484596706630053
2056	1134076	1134076: ARPC2 :: actin related protein 2/3 complex, subunit 2, 34 kDa	83583	0.136046734918812	−0.005298188257533
2057	1134083	1134083: C18orf1 :: chromosome 18 open reading frame 1	285091	0.346451715122800	−0.373477515568528
2058	1134095	1134095: HCK :: hemopoietic cell kinase	89555	−0.014720188541950	0.038451469448641
2059	1134109	1134109: MADCAM1 :: mucosal vascular addressin cell adhesion molecule 1	102598	0.147538030038399	−0.064881411838308
2060	1134133	1134133: CCL7 :: chemokine (C-C motif) ligand 7	251526	0.166588295892007	−0.023081827233061
2061	1134145	1134145: DKFZP564K0822 :: hypothetical protein DKFZp564K0822	4750	−0.071386477041643	−0.062712005236753
2062	1134200	1134200: ABCC3 :: ATP-binding cassette, sub-family C (CFTR/MRP), member 3	90786	0.559310932835367	−0.393423898786516
2063	1134212	1134212: TRIO :: triple functional domain (PTPRF interacting)	367689	0.207746847343388	−0.222959913655619
2064	1134220	1134220: MYO7A :: myosin VIIA (Usher syndrome 1B (autosomal recessive, severe))	370421	−0.017653358783537	−0.192603530737153
2065	1134230	1134230: RASGRP2 :: RAS guanyl releasing protein 2 (calcium and DAG-regulated)	99491	−0.154642991810068	0.051124540138756
2066	1134233	1134233: ALK :: anaplastic lymphoma kinase (Ki-1)	410680	0.186575254434794	−0.189026699772156
2067	1134270	1134270: GGT1 :: gamma-glutamyltransferase 1	352119	0.251750587831380	−0.349120537758305
2068	1134271	1134271: POU5F1 :: POU domain, class 5, transcription factor 1	249184	−0.156623761238959	0.029995443126806
2069	1134280	1134280: CRLF2 :: cytokine receptor-like factor 2	287729	−0.035287889475792	−0.057636116646176
2070	1134296	1134296: FY :: Duffy blood group	183	0.217642615578632	−0.364345371369456
2071	1134316	1134316: GPRK2L :: G protein-coupled receptor kinase 2-like (*Drosophila*)	32959	0.033589097434719	−0.026724476713475
2072	1134361	1134361: KIR2DL4 :: killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 4	515605	−0.064371839816714	−0.027523138295799
2073	1134370	1134370: FGR :: Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog	1422	0.469900254155040	−0.371138296962091
2074	1134379	1134379: C4A :: complement component 4A	150833	0.153921754790563	−0.492982998610867
2075	1134422	1134422: BCL2L11 :: BCL2-like 11 (apoptosis facilitator)	84063	−0.167169905260362	0.312275568218554
2076	1134424	1134424: S100A14 :: LOC392086: similar to Putative S100 calcium-binding protein A11 pseudogene	−6	0.577071499097494	−0.451549726315866
2077	1134457	1134457: NTRK1 :: neurotrophic tyrosine kinase, receptor, type 1	406293	−0.051929755731206	−0.076605673516509
2078	1134480	1134480: MACF1 :: microtubule-actin crosslinking factor 1	372463	0.385302560920052	−0.489132821439022
2079	1134494	1134494: MSF :: MLL septin-like fusion	288094	−0.158164582532209	0.094745859172743
2080	1134517	1134517: PDLIM1 :: PDZ and LIM domain 1 (elfin)	75807	−0.318932656287507	0.232330090652600
2081	1134523	1134523: TKT :: transketolase (Wernicke-Korsakoff syndrome)	89643	−0.157519567091726	0.331118833432058
2082	1134532	1134532: CCND1 :: cyclin D1 (PRAD1: parathyroid adenomatosis 1)	371468	0.357568571752350	−0.289354652996340
2083	1134533	1134533: LOC54499 :: putative membrane protein	93832	0.027985409927586	0.065539358200285
2084	1134542	1134542: HLA-B :: major histocompatibility complex, class I, B	77961	0.252413302304409	−0.486244623630763
2085	1134582	1134582: SMARCA4 :: SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	78202	−0.042161334059780	0.201113183134652
2086	1134593	1134593: HLA-C :: major histocompatibility complex, class I, C	274485	0.150604563084478	−0.372850743553715
2087	1134615	1134615: THY1 :: Thy-1 cell surface antigen	134643	0.740295008324578	−0.289362396064258
2088	1134618	1134618: STK24 :: serine/threonine kinase 24 (STE20 homolog, yeast)	168913	−0.302773915211256	0.366245931868612
2089	1134647	1134647: DUSP6 :: dual specificity phosphatase 6	298654	0.506041172080515	−0.442864261312140
2090	1134653	1134653: TOP1 :: topoisomerase (DNA) I	253536	−0.386004901157803	0.578538864529316
2091	1134665	1134665: SRI :: sorcin	422340	0.070635339781393	0.014029892560073
2092	1134674	1134674: ID1 :: inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	410900	0.315979164228629	−0.295857070867065

TABLE 2415-continued

GeneID.txt

Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
2093	1134676	1134676: TLOC1 :: translocation protein 1	158193	−0.382787060158885	0.187687539924563
2094	1134679	1134679: BECN1 :: beclin 1 (coiled-coil, myosin-like BCL2 interacting protein)	12272	0.105603493319489	−0.102323703391318
2095	1134682	1134682: LGALS3 :: lectin, galactoside-binding, soluble, 3 (galectin 3)	411701	0.499705085052146	−0.365258666150658
2096	1134687	1134687: TXNDC4 :: thioredoxin domain containing 4 (endoplasmic reticulum)	154023	0.223571308720130	−0.241073271383677
2097	1134699	1134699: KPNB1 :: karyopherin (importin) beta 1	439683	−0.284720382004117	0.534018688023989
2098	1134706	1134706: FBXL11 :: F-box and leucine-rich repeat protein 11	219614	0.044440338914973	−0.202122236667693
2099	1134710	1134710: PPIG :: peptidyl-prolyl isomerase G (cyclophilin G)	77965	0.018281322001863	−0.014383939906630
2100	1134727	1134727: PINK1 :: PTEN induced putative kinase 1	439600	0.312058012057399	−0.245134769222099
2101	1134738	1134738: DYRK1A :: dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A	75842	−0.064568512991221	−0.100866986311723
2102	1134753	1134753: WHSC1 :: Wolf-Hirschhorn syndrome candidate 1	110457	−0.341151329387829	0.729975148861719
2103	1134778	1134778: RFC1 :: replication factor C (activator 1) 1, 145 kDa	166563	−0.336733099289826	0.528235750344208
2104	1134797	1134797: TUBA3 :: tubulin, alpha 3	433394	0.405096128352181	−0.125508822982315
2105	1134837	1134837: IRS2 :: insulin receptor substrate 2	143648	0.449386774571679	−0.337887011456020
2106	1134843	1134843: MEF2C :: MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C)	368950	0.073971584405973	0.121033219047677
2107	1134850	1134850: PLEKHC1 :: pleckstrin homology domain containing, family C (with FERM domain) member 1	270411	0.727857421507228	−0.375542340871581
2108	1134852	1134852: EWSR1 :: Ewing sarcoma breakpoint region 1	374477	−0.370094949141491	0.556503015981440
2109	1134858	1134858: KPNB2 :: karyopherin (importin) beta 2	405954	−0.133123256535390	0.344301361055445
2110	1134865	1134865: MINK :: misshapen/NIK-related kinase	112028	−0.014360239308387	−0.031348981802659
2111	1134880	1134880: METTL3 :: methyltransferase like 3	168799	−0.501356501976032	0.326720755408380
2112	1134888	1134888: TFPI2 :: tissue factor pathway inhibitor 2	438231	0.308231647753657	−0.273918942666535
2113	1134903	1134903: SWAP70 :: SWAP-70 protein	153026	0.029725397316418	0.226883023659028
2114	1134921	1134921: IKBKB :: inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta	413513	0.101776675617754	−0.509485574811757
2115	1134928	1134928: SIN3B :: SIN3 homolog B, transcriptional regulator (yeast)	13999	−0.095326097028722	−0.220883061797362
2116	1134933	1134933: RUNX1 :: runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene)	410774	0.136721482617340	−0.286235830963271
2117	1134945	1134945: KIAA1128 :: KIAA1128 protein	81897	0.307874711629927	−0.456973877209662
2118	1134961	1134961: IFI35 :: interferon-induced protein 35	50842	0.138043455897837	−0.401306837995058
2119	1134988	1134988: MKNK1 :: MAP kinase-interacting serine/threonine kinase 1	79516	0.226240988283301	−0.360081299039555
2120	1134991	1134991: ENTPD1 :: ectonucleoside triphosphate diphosphohydrolase 1	444105	−0.067132377128918	0.006527793482675
2121	1135002	1135002: TNFSF13 :: tumor necrosis factor (ligand) superfamily, member 13	54673	0.660500070596942	−0.623176642780856
2122	1135023	1135023: CD34 :: CD34 antigen	374990	0.253442729839205	−0.043705876432332
2123	1135024	1135024: RIPK2 :: receptor-interacting serine-threonine kinase 2	103755	0.283145198315740	−0.016099665131011
2124	1135028	1135028: CD36 :: CD36 antigen (collagen type I receptor, thrombospondin receptor)	443120	0.021104930817611	0.007796830614863
2125	1135042	1135042: MOX2 :: antigen identified by monoclonal antibody MRC OX-2	79015	0.083289319982643	−0.213987775490654
2126	1135047	1135047: EPHB2 :: EphB2	125124	0.381665736064432	−0.280685437494666
2127	1135056	1135056: GATA3 :: GATA binding protein 3	169946	0.372973462657120	−0.616704878063501
2128	1135068	1135068: ALP :: alpha-actinin-2-associated LIM protein	71719	0.718732925951149	−0.283895978541139
2129	1135080	1135080: CDKN2A :: cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	421349	0.078828027642853	0.161587695324233
2130	1135085	1135085: C22orf4 :: chromosome 22 open reading frame 4	505862	−0.026573621098559	0.016415427963998
2131	1135088	1135088: TM4SF10 :: transmembrane 4 superfamily member 10	8769	0.788275799148947	−0.406065038614432
2132	1135093	1135093: CHUK :: conserved helix-loop-helix ubiquitous kinase	198998	0.109586518187874	0.124991404895728
2133	1135101	1135101: KIFC1 :: kinesin family member C1	20830	−0.215761248668721	0.596798091443639
2134	1135102	1135102: PRKCB1 :: protein kinase C, beta 1	349845	−0.441119819917753	0.127447919616108
2135	1135130	1135130: MYCN :: v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	25960	0.205396780967846	−0.132247221716585
2136	1135138	1135138: CD24 :: CD24 antigen (small cell lung carcinoma cluster 4 antigen)	375108	−0.224445750701083	0.047897690312253
2137	1135141	1135141: CXCL2 :: chemokine (C—X—C motif) ligand 2	75765	0.216024020910474	−0.301155542846476
2138	1135151	1135151: CASP6 :: caspase 6, apoptosis-related cysteine protease	3280	−0.029027422712854	0.022459532296497
2139	1135164	1135164: UMPK :: uridine monophosphate kinase	458360	−0.281270374505862	0.508366629782454
2140	1135165	1135165: IL16 :: interleukin 16 (lymphocyte chemoattractant factor)	170359	−0.352018704696172	0.134294035068052
2141	1135168	1135168: DNASE2 :: deoxyribonuclease II, lysosomal	118243	0.356638133348548	−0.424972558101864
2142	1135173	1135173: LRRN3 :: leucine rich repeat neuronal 3	3781	0.011132687277529	−0.007027834231566
2143	1135186	1135186: ANXA7 :: annexin A7	386741	0.230842216449984	−0.125584578249155
2144	1135189	1135189: TP73L :: tumor protein p73-like	137569	0.032938699487530	−0.029874965045244
2145	1135209	1135209: SIAHBP1 :: fuse-binding protein-interacting repressor	74562	−0.298973092029240	0.426608855649514
2146	1135214	1135214: TGFB2 :: transforming growth factor, beta 2	169300	−0.003837754874404	0.033518502051147
2147	1135226	1135226: IKBKG :: inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma	43505	0.063215168889229	−0.006415810511503
2148	1135227	1135227: NFE2 :: nuclear factor (erythroid-derived 2), 45 kDa	75643	0.023578319912982	−0.069183481854815
2149	1135229	1135229: DUT :: dUTP pyrophosphatase	367676	−0.383694472826659	0.644465225193040
2150	1135234	1135234: GSK3B :: glycogen synthase kinase 3 beta	282359	0.025939798183179	0.093409732601449

TABLE 2415-continued

GeneID.txt

Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
2151	1135240	1135240: FAP :: fibroblast activation protein, alpha	436852	0.815662355251253	−0.281574290766028
2152	1135251	1135251: STAT1 :: signal transducer and activator of transcription 1, 91 kDa	21486	0.378465896040287	−0.526929553625389
2153	1135253	1135253: JTV1 :: JTV1 gene	301613	−0.464197830009685	0.642155481384349
2154	1135267	1135267: TCL1A :: T-cell leukemia/lymphoma 1A	2484	−0.422456471874368	0.350212964400887
2155	1135270	1135270: SOCS1 :: suppressor of cytokine signaling 1	50640	0.096514479095770	−0.088097434161321
2156	1135285	1135285: UBE2E3 :: ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast)	449501	−0.299207238123007	0.432887460519918
2157	1135299	1135299: LYL1 :: lymphoblastic leukemia derived sequence 1	46446	−0.060409506735203	0.127799805000889
2158	1135322	1135322: IGFBP3 :: insulin-like growth factor binding protein 3	450230	0.451581199548195	−0.038586544922136
2159	1135328	1135328: FYN :: FYN oncogene related to SRC, FGR, YES	390567	0.246626834451783	−0.483001893866662
2160	1135350	1135350: DYRK3 :: dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	164267	−0.130079797899979	0.204564836502494
2161	1135374	1135374: BMPR2 :: bone morphogenetic protein receptor, type II (serine/threonine kinase)	53250	0.021907823889001	−0.049583428001536
2162	1135379	1135379: LILRB3 :: leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	−26	0.242300305886075	−0.328430462600683
2163	1135380	1135380: CSF2 :: colony stimulating factor 2 (granulocyte-macrophage)	1349	0.067243088208555	−0.044335581523926
2164	1135383	1135383: CDKN2D :: cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)	435051	−0.124512964427258	0.064707859522555
2165	1135395	1135395: GG2-1 :: TNF-induced protein	17839	−0.287358473815222	0.057585874019656
2166	1135399	1135399: ZNF216 :: zinc finger protein 216	406096	0.562730843915336	−0.447012756023576
2167	1135467	1135467: CAMK2B :: calcium/calmodulin-dependent protein kinase (CaM kinase) II beta	321572	0.134875231463102	0.065771849282309
2168	1135475	1135475: CHEK2 :: CHK2 checkpoint homolog (*S. pombe*)	146329	−0.397443511905394	0.548880091150802
2169	1135487	1135487: SCN3A :: sodium channel, voltage-gated, type III, alpha	300717	0.035229423784445	−0.077879014673317
2170	1135489	1135489: SSA2 :: Sjogren syndrome antigen A2 (60 kDa, ribonucleoprotein autoantigen SS-A/Ro)	288178	−0.213090090407771	0.262043380399309
2171	1135492	1135492: P2RX5 :: purinergic receptor P2X, ligand-gated ion channel, 5	408615	−0.492212038510146	0.364853473313676
2172	1135513	1135513: CD209L :: CD209 antigen-like	421437	−0.269435883536644	0.024441295489601
2173	1135526	1135526: VEGF :: vascular endothelial growth factor	73793	0.325113508581393	−0.029534731933042
2174	1135529	1135529: AKAP12 :: A kinase (PRKA) anchor protein (gravin) 12	197081	0.327798628207461	−0.280667211293206
2175	1135541	1135541: BIRC3 :: baculoviral IAP repeat-containing 3	127799	0.215026966456852	−0.008057017397116
2176	1135549	1135549: CCL23 :: chemokine (C-C motif) ligand 23	169191	0.169612975596130	−0.255583009309114
2177	1135550	1135550: RASGRF1 :: Ras protein-specific guanine nucleotide-releasing factor 1	221811	−0.174032798373146	0.109815766607271
2178	1135571	1135571: LIMK2 :: LIM domain kinase 2	278027	0.228969728759419	−0.179979819712335
2179	1135583	1135583: KLRD1 :: killer cell lectin-like receptor subfamily D, member 1	41682	0.154767088293625	−0.291292436228335
2180	1135592	1135592: RASA1 :: RAS p21 protein activator (GTPase activating protein) 1	758	−0.128504626836331	0.005951003511595
2181	1135593	1135593: CDK10 :: cyclin-dependent kinase (CDC2-like) 10	77313	−0.262720735278780	0.116299156451995
2182	1135606	1135606: LAIR1 :: leukocyte-associated Ig-like receptor 1	407964	0.367419923397012	−0.504520192225527
2183	1135622	1135622: MAPK8 :: mitogen-activated protein kinase 8	445864	−0.115106896338892	0.066131476924408
2184	1135645	1135645: SPINT2 :: serine protease inhibitor, Kunitz type, 2	31439	0.037566720623906	−0.249380484239846
2185	1135665	1135665: DDR1 :: discoidin domain receptor family, member 1	423573	0.230146680281770	−0.299775043520402
2186	1135673	1135673: PSMA1 :: proteasome (prosome, macropain) subunit, alpha type, 1	82159	−0.281720666174377	0.513064897309524
2187	1135684	1135684: CASP9 :: caspase 9, apoptosis-related cysteine protease	329502	−0.211300862040939	0.245352650816304
2188	1135685	1135685: TCF3 :: transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	371282	−0.132625532853511	0.339380670215153
2189	1135735	1135735: ACVRL1 :: activin A receptor type II-like 1	410104	0.299065710574511	−0.308189802383384
2190	1135743	1135743: TNFRSF25 :: tumor necrosis factor receptor superfamily, member 25	299558	0.234872487618209	−0.471595034051215
2191	1135755	1135755: MCAM :: melanoma cell adhesion molecule	511397	0.269827609205101	0.050442231517023
2192	1135773	1135773: FCGR2B :: Fc fragment of IgG, low affinity IIb, receptor for (CD32)	126384	−0.094710034742556	0.074929655761349
2193	1135778	1135778: CD86 :: CD86 antigen (CD28 antigen ligand 2, B7-2 antigen)	27954	0.168916871462908	−0.289281311109271
2194	1135795	1135795: Lin10 :: lin-10 protein homolog	55923	0.528293814614649	−0.217959944059237
2195	1135801	1135801: CHS1 :: Chediak-Higashi syndrome 1	130188	0.115318364998609	−0.224257398564241
2196	1135802	1135802: CAPN3 :: calpain 3, (p94)	439343	0.164155251202988	−0.418087129363220
2197	1135826	1135826: PFKM :: phosphofructokinase, muscle	75160	−0.358643155033839	0.498879090538368
2198	1135830	1135830: GPRK6 :: G protein-coupled receptor kinase 6	235116	−0.137147395547579	−0.066956658835406
2199	1135835	1135835: TPM1 :: tropomyosin 1 (alpha)	133892	0.844500075257288	−0.400650137852855
2200	1135852	1135852: UBE2I :: ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast)	302903	−0.055021621102330	0.012335299075447
2201	1135858	1135858: HSPA4 :: heat shock 70 kDa protein 4	90093	−0.273737239778974	0.470740053479600
2202	1135866	1135866: MGLL :: monoglyceride lipase	409826	−0.105545203381370	−0.152401403416860
2203	1135871	1135871: CYLN2 :: cytoplasmic linker 2	104717	0.492247783576989	−0.405561899962111
2204	1135899	1135899: DBI :: diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein)	78888	0.106730411631004	0.010913990066277

TABLE 2415-continued

GeneID.txt

Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
2205	1135925	1135925: LILRB1 :: leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1	149924	−0.022827469254302	−0.121870105927558
2206	1135929	1135929: NFATC1 :: nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1	512591	−0.230076225407584	0.015263924708268
2207	1135930	1135930: AURKC :: aurora kinase C	98338	−0.015602552109567	−0.050852618143140
2208	1135966	1135966: THPO :: thrombopoietin (myeloproliferative leukemia virus oncogene ligand, megakaryocyte growth and development factor)	1166	−0.070240091216135	0.060929707028526
2209	1135968	1135968: ACTN1 :: actinin, alpha 1	119000	0.803045210914051	−0.443427303702404
2210	1135974	1135974: RENT1 :: regulator of nonsense transcripts 1	388125	−0.277013571071871	0.271498553157074
2211	1135982	1135982: PSTPIP1 :: proline-serine-threonine phosphatase interacting protein 1	129758	0.263915152962747	−0.498016545266176
2212	1135994	1135994: ICOSL :: inducible T-cell co-stimulator ligand	14155	0.095990130380820	−0.112046453556527
2213	1136002	1136002: CASK :: calcium/calmodulin-dependent serine protein kinase (MAGUK family)	288196	0.101320852559842	−0.096367400453437
2214	1136048	1136048: TNFRSF25 :: tumor necrosis factor receptor superfamily, member 25	299558	0.124716682297827	−0.408102750362765
2215	1136051	1136051: CSF2RA :: colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	520937	0.614522954701183	−0.281145422492197
2216	1136055	1136055: UBC :: ubiquitin C	183704	−0.017390939478490	−0.243810714198309
2217	1136056	1136056: CDK7 :: cyclin-dependent kinase 7 (MO15 homolog, Xenopus laevis, cdk-activating kinase)	184298	−0.204830293446290	0.441840876555980
2218	1136087	1136087: ITK :: IL2-inducible T-cell kinase	211576	0.211045649761843	−0.423904231475203
2219	1136109	1136109: MAP2K5 :: mitogen-activated protein kinase kinase 5	436145	−0.270995770271572	0.045366180573479
2220	1136150	1136150: TYRO3 :: TYRO3 protein tyrosine kinase	381282	0.069212714183531	−0.029671317117098
2221	1136152	1136152: CCRL2 :: chemokine (C-C motif) receptor-like 2	458436	0.360883312741600	−0.375561473188188
2222	1136162	1136162: AKT2 :: v-akt murine thymoma viral oncogene homolog 2	326445	−0.208297523200300	0.174642196469647
2223	1136172	1136172: SULT1C1 :: sulfotransferase family, cytosolic, 1C, member 1	38084	0.650163073768228	−0.258621533863630
2224	1136185	1136185: ITGB8 :: integrin, beta 8	355722	−0.039929578583942	−0.041458162075154
2225	1136193	1136193: MAPK11 :: mitogen-activated protein kinase 11	57732	0.306565774763432	−0.328494812564979
2226	1136216	1136216: HLA-G :: HLA-G histocompatibility antigen, class I, G	512152	0.332885800453946	−0.553560222998666
2227	1136269	1136269: MAST205 :: microtubule associated testis specific serine/threonine protein kinase	101474	0.223412342428654	0.138958768884101
2228	1136273	1136273: HOP :: homeodomain-only protein	13775	0.476703362822473	−0.307711782501049
2229	1136285	1136285: LRPPRC :: leucine-rich PPR-motif containing	182490	−0.435679656870025	0.601290247138512
2230	1136329	1136329: HIC :: I-mfa domain-containing protein	132739	−0.027288699750570	−0.117406065312260
2231	1136337	1136337: NCALD :: neurocalcin delta	90063	0.338984738958917	−0.245462539985130
2232	1136343	1136343: BBC3 :: BCL2 binding component 3	87246	−0.050405192310055	−0.036901688934723
2233	1136357	1136357: SCGF :: stem cell growth factor; lymphocyte secreted C-type lectin	512680	0.677947187540831	−0.298730690287187
2234	1136362	1136362: OK/SW-cl.56 :: beta 5-tubulin	356729	−0.408563420151110	0.742172430214216
2235	1136369	1136369: FLJ20323 :: hypothetical protein FLJ20323	387140	−0.262683063661753	0.404486726869442
2236	1136371	1136371: FMO2 :: flavin containing monooxygenase 2	361155	0.052259965061053	−0.122705355848300
2237	1136379	1136379: FCER1A :: Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide	897	0.013936619697511	−0.013197557598909
2238	1136391	1136391: PTGDS :: prostaglandin D2 synthase 21 kDa (brain)	446429	0.511480233544877	−0.435655362037836
2239	1136393	1136393: TUBA6 :: tubulin alpha 6	406578	−0.179227481381745	0.374710668827628
2240	1136401	1136401: SIP :: Siah-interacting protein	27258	−0.379183284208103	0.535722487344917
2241	1136408	1136408: POU2F2 :: POU domain, class 2, transcription factor 2	1101	−0.354137582792841	0.429728063769577
2242	1136427	1136427: FYB :: FYN binding protein (FYB-120/130)	276506	0.357796609387918	−0.441555304919001
2243	1136430	1136430: IGLJ3 :: immunoglobulin lambda joining 3	102950	0.109778160374844	−0.098831871658468
2244	1136459	1136459: KIAA0551 :: Traf2 and NCK interacting kinase	252550	0.365508689849397	−0.430643879731062
2245	1136464	1136464: BAX :: BCL2-associated X protein	159428	−0.106116191477644	0.042671340080830
2246	1136540	1136540: PLAUR :: plasminogen activator, urokinase receptor	179657	0.666710687865820	−0.301093054608278
2247	1136573	1136573: HLA-DPA1 :: major histocompatibility complex, class II, DP alpha 1	914	0.093919078766697	−0.282244466739273
2248	1136585	1136585: MKI67 :: antigen identified by monoclonal antibody Ki-67	80976	−0.322784784394788	0.786209797714773
2249	1136595	1136595: VDAC1 :: voltage-dependent anion channel 1	404814	−0.329398024691907	0.585972473136041
2250	1136599	1136599: MAPK3 :: mitogen-activated protein kinase 3	861	0.079560238680393	0.110483410795923
2251	1136601	1136601: KIAA1522 :: KIAA1522 protein	322735	−0.282563015525018	0.476574635966113
2252	1136605	1136605: MAZ :: MYC-associated zinc finger protein (purine-binding transcription factor)	448398	−0.375211792940038	0.462155982376696
2253	1136620	1136620: COL6A1 :: collagen, type VI, alpha 1	415997	0.752399713314935	−0.294498892879228
2254	1136655	1136655: FBXO9 :: F-box only protein 9	388387	−0.340363407814236	0.444483352898254
2255	1136662	1136662: PIK3R1 :: phosphoinositide-3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)	6241	0.238423381122479	−0.289911768148796
2256	1136681	1136681: KHSRP :: KH-type splicing regulatory protein (FUSE binding protein 2)	91142	−0.176274134948602	0.237953667245025
2257	1136687	1136687: CREB3L2 :: cAMP responsive element binding protein 3-like 2	59943	−0.194398113086998	−0.060634386685776
2258	1136692	1136692: KIAA0913 :: KIAA0913 protein	65135	0.157495567129249	−0.509878413292112
2259	1136702	1136702: KIAA0121 :: KIAA0121 gene product	155584	0.054990929492512	0.085009319320804

TABLE 2415-continued

GeneID.txt

Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
2260	1136710	1136710: GTF3C2 :: general transcription factor IIIC, polypeptide 2, beta 110 kDa	75782	−0.396439011974729	0.384390673177142
2261	1136712	1136712: LOC253782 :: hypothetical protein LOC253782	503941	0.206133682187914	−0.355144643398998
2262	1136718	1136718: SUCLG2 :: succinate-CoA ligase, GDP-forming, beta subunit	446476	−0.367316089248735	0.168181491783958
2263	1136722	1136722: TPM4 :: tropomyosin 4	250641	0.032764759626493	0.117199289648095
2264	1136724	1136724: DNAJC8 :: DnaJ (Hsp40) homolog, subfamily C, member 8	433540	−0.227564371595965	0.384799422123307
2265	1136759	1136759: :: *Homo sapiens* clone 23872 mRNA sequence	188882	−0.246541834783006	0.118058054542888
2266	1136762	1136762: CHN1 :: chimerin (chimaerin) 1	380138	0.531781776267429	−0.309684138139920
2267	1136765	1136765: PRKCL2 :: protein kinase C-like 2	69171	−0.052449761989885	0.002703484644613
2268	1136774	1136774: IL1RN :: interleukin 1 receptor antagonist	81134	0.198165705307058	−0.271282824734418
2269	1136777	1136777: HLA-DQA1 :: major histocompatibility complex, class II, DQ alpha 1	387679	0.095000643669076	−0.192356554908310
2270	1136781	1136781: PPP1R14B :: protein phosphatase 1, regulatory (inhibitor) subunit 14B	120197	−0.350667785791036	0.599063986397151
2271	1136784	1136784: JMJD1 :: jumonji domain containing 1	321707	0.037507681795198	0.042300448176934
2272	1136786	1136786: PCCB :: propionyl Coenzyme A carboxylase, beta polypeptide	63788	−0.589479064855973	0.500462229668922
2273	1136788	1136788: SEPT10 :: septin 10	355455	0.743385086666469	−0.472469825174593
2274	1136819	1136819: DKFZP564O043 :: hypothetical protein DKFZp564O043	112605	−0.108061343689995	0.015483574748141
2275	1136831	1136831: PPFIBP2 :: PTPRF interacting protein, binding protein 2 (liprin beta 2)	12953	0.029792915483790	−0.007676278659483
2276	1136832	1136832: RANBP2L1 :: RAN binding protein 2-like 1	434959	0.482289022689679	−0.582659344585077
2277	1136844	1136844: C21orf25 :: chromosome 21 open reading frame 25	16007	0.360004946699269	−0.421664849812932
2278	1136853	1136853: SMYD2 :: SET and MYND domain containing 2	66170	−0.372211589853700	0.355510218953968
2279	1136859	1136859: KIAA1199 :: KIAA1199 protein	212584	0.436417109927428	−0.218192786328106
2280	1136865	1136865: MGC4170 :: MGC4170 protein	412128	0.282712755201433	−0.388421252788627
2281	1136876	1136876: TLK2 :: tousled-like kinase 2	445078	−0.155319085898057	0.204103146968723
2282	1136877	1136877: HLA-DQB2 :: major histocompatibility complex, class II, DQ beta 2	375115	0.192335314451624	−0.319281345548139
2283	1136902	1136902: :: *Homo sapiens* mRNA; cDNA DKFZp779B1535 (from clone DKFZp779B1535)	442592	0.037180838679762	0.027204468801935
2284	1136903	1136903: EEF1D :: eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	334798	−0.169515366664499	0.121701880331947
2285	1136913	1136913: EEG1 :: likely ortholog of mouse embryonic epithelial gene 1	99962	−0.120301577698138	0.418446911641021
2286	1136925	1136925: BICD2 :: bicaudal D homolog 2 (*Drosophila*)	436939	−0.290814207335427	0.194781442202637
2287	1136938	1136938: MINA53 :: myc-induced nuclear antigen, 53 kDa	23294	−0.417163002239899	0.308929563321094
2288	1136939	1136939: :: *Homo sapiens* T cell receptor beta chain BV20S1 BJ1-5 BC1 mRNA, complete cds	419777	0.254956828947675	−0.564468551099593
2289	1136971	1136971: STIP1 :: stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein)	257827	−0.246439382578630	0.490417223621355
2290	1136972	1136972: NEK1 :: NIMA (never in mitosis gene a)-related kinase 1	414410	−0.231210263189500	0.204963384701897
2291	1136983	1136983: :: *Homo sapiens* similar to Nuclear envelope pore membrane protein	450237	−0.388641220178648	0.487819551534725
2292	1136984	1136984: SNX1 :: sorting nexin 1	498154	−0.040880352409561	−0.263364454525231
2293	1136987	1136987: SFMBT1 :: Scm-like with four mbt domains 1	21695	−0.302266892109625	0.163781928286487
2294	1136988	1136988: CASP8 :: caspase 8, apoptosis-related cysteine protease	243491	0.135637824443728	−0.336196763757261
2295	1136996	1136996: RNASE4 :: ribonuclease, RNase A family, 4	283749	0.530666527925623	−0.397210146260416
2296	1137022	1137022: ITGAL :: integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide)	174103	0.205038646441539	−0.397020451104670
2297	1137026	1137026: MAP2K2 :: mitogen-activated protein kinase kinase 2	366546	−0.262905023273146	0.252101699347407
2298	1137042	1137042: G0S2 :: putative lymphocyte G0/G1 switch gene	432132	0.538116332321084	−0.276091529850567
2299	1137097	1137097: KNS2 :: kinesin 2 60/70 kDa	512578	0.399642064990379	−0.453052638372648
2300	1137109	1137109: RPL5 :: ribosomal protein L5	469653	−0.122252811851800	0.006080037924381
2301	1137112	1137112: MUC1 :: mucin 1, transmembrane	89603	0.317119298256267	−0.312275797088170
2302	1137137	1137137: FLNA :: filamin A, alpha (actin binding protein 280)	195464	0.567136331652304	−0.391193497147128
2303	1137158	1137158: C14orf120 :: chromosome 14 open reading frame 120	9043	−0.282866289386583	0.413058262482048
2304	1137201	1137201: SRRM2 :: serine/arginine repetitive matrix 2	433343	−0.272530261309250	0.320630860600962
2305	1137202	1137202: SMT3H2 :: SMT3 suppressor of mif two 3 homolog 2 (yeast)	380973	−0.234617743279140	0.241957518841459
2306	1137247	1137247: LYZ :: lysozyme (renal amyloidosis)	234734	0.608426386367492	−0.450067626480979
2307	1137273	1137273: ITGB5 :: integrin, beta 5	149846	0.649262426877578	−0.271621269006555
2308	1137289	1137289: CD7 :: CD7 antigen (p41)	36972	0.165984784499907	−0.465353463451909
2309	1137291	1137291: XTP2 :: HBxAg transactivated protein 2	446197	0.078785114363620	−0.149442218814294
2310	1137308	1137308: FUBP1 :: far upstream element (FUSE) binding protein 1	118962	−0.421138601237465	0.248985090248871
2311	1137328	1137328: PDE4DIP :: phosphodiesterase 4D interacting protein (myomegalin)	502577	0.240910452929125	−0.201889801334610
2312	1137332	1137332: PPBP :: pro-platelet basic protein (chemokine (C—X—C motif) ligand 7)	2164	0.006793019489238	−0.121914777496122
2313	1137343	1137343: FH :: fumarate hydratase	391168	−0.259855496056412	0.452895074131933
2314	1137360	1137360: CLN2 :: ceroid-lipofuscinosis, neuronal 2, late infantile (Jansky-Bielschowsky disease)	429658	0.086740222842950	−0.125808364812224
2315	1137378	1137378: TNFRSF4 :: tumor necrosis factor receptor superfamily, member 4	129780	0.371458297794605	−0.397187816049941

TABLE 2415-continued

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Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
2316	1137439	1137439: MAP4K1 :: mitogen-activated protein kinase kinase kinase kinase 1	95424	−0.303418341057957	0.261214531356896
2317	1137447	1137447: HSPCB :: heat shock 90 kDa protein 1, beta	74335	−0.458725739759769	0.604001646900960
2318	1137449	1137449: MATR3 :: matrin 3	223745	−0.387281340518201	0.358637187063220
2319	1137481	1137481: C4A :: complement component 4A	150833	0.182892012520496	−0.507231719813946
2320	1137486	1137486: MIZ1 :: Msx-interacting-zinc finger	441069	−0.443002780855262	0.498631456766930
2321	1137488	1137488: NFKBIB :: nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, beta	9731	−0.222344495661454	0.244641154107860
2322	1137492	1137492: HLA-C :: major histocompatibility complex, class I, C	274485	0.197365260701921	−0.407821263356476
2323	1137506	1137506: H2AFY :: H2A histone family, member Y	75258	−0.149835935606420	0.445133707052547
2324	1137512	1137512: PC4 :: activated RNA polymerase II transcription cofactor 4	229641	−0.082525052793081	−0.145075136097169
2325	1137534	1137534: CD7 :: CD7 antigen (p41)	36972	0.107180183166121	−0.365438064689284
2326	1137539	1137539: XCL2 :: chemokine (C motif) ligand 2	458346	−0.053308591493161	−0.246840014028833
2327	1137561	1137561: HOXA1 :: homeo box A1	67397	−0.150079735454765	0.253920313043797
2328	1137582	1137582: CLK1 :: CDC-like kinase 1	433732	0.093677520704906	−0.366781439753622
2329	1137583	1137583: ALDOA :: aldolase A, fructose-bisphosphate	273415	0.018724212498213	0.324301589252045
2330	1137594	1137594: CCNB1 :: cyclin B1	23960	−0.375043781726022	0.836819695371722
2331	1137597	1137597: CDC42EP4 :: CDC42 effector protein (Rho GTPase binding) 4	3903	0.425898445808089	−0.369669790160663
2332	1137601	1137601: GLG1 :: golgi apparatus protein 1	78979	−0.035094612373837	0.009288993829497
2333	1137626	1137626: PCTK3 :: PCTAIRE protein kinase 3	445402	0.603150172723823	−0.262769906333315
2334	1137643	1137643: GRHPR :: glyoxylate reductase/hydroxypyruvate reductase	155742	−0.295435375518062	0.291585562608132
2335	1137663	1137663: DDAH2 :: dimethylarginine dimethylaminohydrolase 2	247362	0.202876395419915	−0.290851646277916
2336	1137687	1137687: CXCL5 :: chemokine (C—X—C motif) ligand 5	89714	0.150406826331083	0.017128841867423
2337	1137698	1137698: GLUL :: glutamate-ammonia ligase (glutamine synthase)	442669	0.408287031744038	−0.261412315186599
2338	1137742	1137742: TSC22 :: transforming growth factor beta-stimulated protein TSC-22	433796	0.564778777615456	−0.406101020606446
2339	1137751	1137751: RBMS1 :: RNA binding motif, single stranded interacting protein 1	241567	0.433483960928137	−0.410155449387123
2340	1137760	1137760: DEDD :: death effector domain containing	169681	−0.230491915465838	0.225693647285405
2341	1137771	1137771: HLA-DRB3 :: major histocompatibility complex, class II, DR beta 3	308026	0.206113521293342	−0.346477434254079
2342	1137782	1137782: SOD2 :: superoxide dismutase 2, mitochondrial	384944	0.418904407792592	−0.306800309295515
2343	1137806	1137806: HLA-A :: major histocompatibility complex, class I, A	181244	0.201083967413937	−0.433287362783418
2344	1137809	1137809: CD8B1 :: CD8 antigen, beta polypeptide 1 (p37)	405667	0.185618649145311	−0.524929307636060
2345	1137838	1137838: C6orf4 :: chromosome 6 open reading frame 4	437508	−0.011993611215563	0.009969912053544
2346	1137868	1137868: BTN2A1 :: butyrophilin, subfamily 2, member A1	169963	0.262408129037849	−0.396710767904983
2347	1137908	1137908: :: *Homo sapiens* similar to Gamma-glutamyltranspeptidase 1 precursor (Gamma-glutamyltransferase 1) (CD224 antigen) (LOC376813), mRNA	454906	0.210979969677693	−0.256296439980480
2348	1137955	1137955: SNRPA1 :: small nuclear ribonucleoprotein polypeptide A'	434901	−0.369156412146049	0.608254320273560
2349	1138030	1138030: CD72 :: CD72 antigen	116481	−0.294390921816877	0.100908549519153
2350	1138048	1138048: LY9 :: lymphocyte antigen 9	403857	0.073607730059501	−0.263186409754900
2351	1138120	1138120: ITGB1 :: integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	287797	0.160065610900893	−0.075596946134885
2352	1138128	1138128: MAP3K4 :: mitogen-activated protein kinase kinase kinase 4	390428	−0.049185143371545	−0.087852800223420
2353	1138132	1138132: IGKV1D-13 :: immunoglobulin kappa variable 1D-13	390427	0.037120917614071	−0.136065857206246
2354	1138136	1138136: RBM9 :: RNA binding motif protein 9	351478	0.378938518577512	−0.126082972595542
2355	1138147	1138147: PRKACA :: protein kinase, cAMP-dependent, catalytic, alpha	194350	−0.053368491488809	0.041644135318140
2356	1138150	1138150: MCM5 :: MCM5 minichromosome maintenance deficient 5, cell division cycle 46 (*S. cerevisiae*)	77171	−0.444102278229523	0.638269533484216
2357	1138157	1138157: KIAA0153 :: KIAA0153 protein	82563	−0.391835266746382	0.547098931278669
2358	1138192	1138192: NR3C1 :: nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	512414	0.118279477753652	−0.092009520189905
2359	1138244	1138244: FN1 :: fibronectin 1	418138	0.813782327518728	−0.313203946687403
2360	1138259	1138259: HDGF :: hepatoma-derived growth factor (high-mobility group protein 1-like)	89525	−0.214962450182430	0.470812643332632
2361	1138279	1138279: TPT1 :: tumor protein, translationally-controlled 1	374596	−0.064219389358256	−0.167378055599220
2362	1138312	1138312: CCL2 :: chemokine (C-C motif) ligand 2	303649	0.221948111535212	−0.350981175150463
2363	1138331	1138331: P5 :: protein disulfide isomerase-related protein	−7	−0.107207026289785	0.265506953156497
2364	1138355	1138355: ADA :: adenosine deaminase	407135	0.040541203021177	−0.080197093953995
2365	1138379	1138379: ERBB2 :: v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	446352	0.283250039386084	−0.286769120359251
2366	1138392	1138392: MTCP1 :: mature T-cell proliferation 1	3548	−0.004895350279116	0.276483111443163
2367	1138400	1138400: IL17 :: interleukin 17 (cytotoxic T-lymphocyte-associated serine esterase 8)	41724	−0.032075332580235	−0.038773611235492
2368	1138417	1138417: ST14 :: suppression of tumorigenicity 14 (colon carcinoma, matriptase, epithin)	56937	−0.230448449478436	0.279346957925828
2369	1138421	1138421: KIAA0690 :: KIAA0690 protein	434251	−0.309133083322402	0.403967809571089
2370	1138441	1138441: PASK :: PAS domain containing serine/threonine kinase	397891	0.144733774920620	−0.188242721745811
2371	1138443	1138443: FCGR1A :: Fc fragment of IgG, high affinity Ia, receptor for (CD64)	77424	0.207475205893738	−0.341850921762133

TABLE 2415-continued

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Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
2372	1138507	1138507: DMPK :: dystrophia myotonica-protein kinase	898	0.021947645562805	−0.046183891035291
2373	1138515	1138515: HOMER2 :: homer homolog 2 (*Drosophila*)	93564	−0.020645296163426	−0.133209561135918
2374	1138532	1138532: CAMK1G :: calcium/calmodulin-dependent protein kinase IG	199068	−0.012177377955444	0.053516560538452
2375	1138537	1138537: VDAC1P :: voltage-dependent anion channel 1 pseudogene	−3	−0.324102650163308	0.516292454706352
2376	1138538	1138538: TRD@ :: T cell receptor delta locus	2014	0.236980853252771	−0.340030980985647
2377	1138541	1138541: TNK1 :: tyrosine kinase, non-receptor, 1	203420	−0.149408449223409	−0.017420119646561
2378	1138555	1138555: LTK :: leukocyte tyrosine kinase	434481	−0.192632421203761	0.079999448729701
2379	1138567	1138567: CYB561 :: cytochrome b-561	355264	0.218450857044390	−0.352832586952820
2380	1138645	1138645: MDM2 :: Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse)	212217	−0.068650083946957	0.108796027856608
2381	1138647	1138647: ETV6 :: ets variant gene 6 (TEL oncogene)	171262	−0.010676070319985	−0.013258155419776
2382	1138652	1138652: KYNU :: kynureninase (L-kynurenine hydrolase)	444471	0.465037916013166	−0.350613895243343
2383	1138670	1138670: CD22 :: CD22 antigen	262150	−0.303837324203375	0.291639786954158
2384	1138671	1138671: HIRA :: HIR histone cell cycle regulation defective homolog A (*S. cerevisiae*)	415735	−0.234356236620965	0.181811279669565
2385	1138677	1138677: :: *Homo sapiens* cDNA clone MGC: 71446 IMAGE: 5420082, complete cds	−50	0.334871522054608	−0.565143538142995
2386	1138721	1138721: CR1 :: complement component (3b/4b) receptor 1, including Knops blood group system	334019	0.213185633461993	−0.167181676121616
2387	1138759	1138759: SMARCA2 :: SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	396404	0.239912669361491	−0.356112384377712
2388	1138765	1138765: SEC61A1 :: Sec61 alpha 1 subunit (*S. cerevisiae*)	306079	−0.173564213544419	0.042950263600793
2389	1138778	1138778: HRI :: heme-regulated initiation factor 2-alpha kinase	434986	−0.436150698025647	0.461973052646480
2390	1138780	1138780: PBEF :: pre-B-cell colony-enhancing factor	293464	0.089301913080073	0.030231044097990
2391	1138783	1138783: WAC :: WW domain-containing adapter with a coiled-coil region	370152	−0.309940954918134	0.313859449051489
2392	1138789	1138789: FLJ13855 :: hypothetical protein FLJ13855	369120	0.086491087161513	−0.352846239711779
2393	1138801	1138801: HSPC152 :: hypothetical protein HSPC152	333579	−0.483341541739176	0.490594109811054
2394	1138832	1138832: USP39 :: ubiquitin specific protease 39	12820	−0.352268143901638	0.421581995099915
2395	1138845	1138845: CDC42BPB :: CDC42 binding protein kinase beta (DMPK-like)	436985	0.425134584059284	−0.387183184478298
2396	1138858	1138858: MIF :: macrophage migration inhibitory factor (glycosylation-inhibiting factor)	407995	−0.407665306199589	0.682825403279751
2397	1138867	1138867: EPLIN :: epithelial protein lost in neoplasm beta	10706	0.464814747439025	−0.363469285796447
2398	1138874	1138874: TCFL4 :: transcription factor-like 4	383019	−0.314256250926088	0.306346209499633
2399	1138878	1138878: DNCL2A :: dynein, cytoplasmic, light polypeptide 2A	100002	−0.153830377554263	−0.051030556926909
2400	1138887	1138887: HDAC7A :: histone deacetylase 7A	200063	−0.078208993612420	0.074601964005980
2401	1138905	1138905: KIAA1194 :: KIAA1194	437844	−0.281406606938181	0.481911861505412
2402	1138910	1138910: MORF4L1 :: mortality factor 4 like 1	374503	0.034752735498991	−0.015115740634790
2403	1138920	1138920: CXCL14 :: chemokine (C—X—C motif) ligand 14	24395	0.272782188852422	−0.301011805560417
2404	1138944	1138944: FLJ12442 :: hypothetical protein FLJ12442	84753	−0.388324622909977	0.572404037246780
2405	1138959	1138959: RICH1 :: RhoGAP interacting with CIP4 homologs 1	203605	−0.433959401052288	0.126101372366550
2406	1138973	1138973: MGC2491 :: hypothetical protein MGC2491	11270	−0.252406521349047	0.318256960904562
2407	1138994	1138994: SCAMP2 :: secretory carrier membrane protein 2	238030	−0.048843627249750	−0.056347071925834
2408	1138995	1138995: FLJ22056 :: hypothetical protein FLJ22056	24956	0.312239840661249	−0.155950823692214
2409	1139005	1139005: CABC1 :: chaperone, ABC1 activity of bc1 complex like (*S. pombe*)	273186	−0.132100329795946	−0.079271294569867
2410	1139017	1139017: NANS :: N-acetylneuraminic acid synthase (sialic acid synthase)	274424	0.139351446215690	0.183979506976574
2411	1139026	1139026: MKNK2 :: MAP kinase-interacting serine/threonine kinase 2	512094	−0.060610570736422	0.129185990473453
2412	1139037	1139037: CKIP-1 :: CK2 interacting protein 1; HQ0024c protein	173380	0.184289444061499	−0.394499906002833
2413	1139039	1139039: TNKS2 :: tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	280776	−0.153598065351604	0.099989367851187
2414	1139048	1139048: CNOT7 :: CCR4-NOT transcription complex, subunit 7	170553	−0.298252308752349	0.459920880578746
2415	1139054	1139054: LOC58486 :: transposon-derived Buster1 transposase-like protein	25726	−0.222878320242169	−0.007560363161300
2416	1139076	1139076: HERC1 :: hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1	133411	0.337597568585952	−0.434587953268159
2417	1139100	1139100: GMNN :: geminin, DNA replication inhibitor	234896	−0.318640932117085	0.797462309697701
2418	1139105	1139105: USP21 :: ubiquitin specific protease 21	8015	−0.434624771827016	0.226787372995122
2419	1139106	1139106: TNFRSF12A :: tumor necrosis factor receptor superfamily, member 12A	355899	0.499326017992532	−0.272857576593047
2420	1139127	1139127: DNAJC1 :: DnaJ (Hsp40) homolog, subfamily C, member 1	13015	0.333008884215991	−0.255813893496613
2421	1139185	1139185: RIOK2 :: RIO kinase 2 (yeast)	27021	−0.394717490147720	0.430516797716350
2422	1139196	1139196: MAFB :: v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	169487	0.439789287104131	−0.478712508849918
2423	1139202	1139202: KBTBD4 :: kelch repeat and BTB (POZ) domain containing 4	440695	−0.139779161280927	0.186642624167192
2424	1139215	1139215: MDS029 :: uncharacterized hematopoietic stem/progenitor cells protein MDS029	43549	−0.231448151224285	0.519061887050639
2425	1139226	1139226: FLJ11342 :: hypothetical protein FLJ11342	266514	−0.505040308522747	0.354962950374504
2426	1139230	1139230: PLEKHF2 :: pleckstrin homology domain containing, family F (with FYVE domain) member 2	29724	0.047925608046581	0.167450282579172

TABLE 2415-continued

GeneID.txt

Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
2427	1139235	1139235: FLJ11196 :: acheron	416755	0.518138878363181	−0.428622150654900
2428	1139265	1139265: FLJ12436 :: hypothetical protein FLJ12436	187657	−0.499034983187793	0.623313352401062
2429	1139266	1139266: RGC32 :: RGC32 protein	76640	0.159027989824428	−0.087571314039428
2430	1139274	1139274: CDK5RAP3 :: CDK5 regulatory subunit associated protein 3	20157	−0.323524477001354	−0.008936362298060
2431	1139277	1139277: TAPBP-R :: TAP binding protein related	267993	0.175034517314223	−0.361681139356850
2432	1139280	1139280: FBXW7 :: F-box and WD-40 domain protein 7 (archipelago homolog, *Drosophila*)	312503	−0.256428453680362	0.231741417406240
2433	1139301	1139301: BSPRY :: B-box and SPRY domain containing	108502	−0.193830915039114	−0.024241326240483
2434	1139303	1139303: FLJ20511 :: hypothetical protein FLJ20511	134406	−0.307110727683744	0.247243898936555
2435	1139314	1139314: FCGRT :: Fc fragment of IgG, receptor, transporter, alpha	111903	0.263924260656374	−0.500814050113789
2436	1139360	1139360: FLJ10486 :: hypothetical protein FLJ10486	173946	−0.403868709065567	0.512692327611680
2437	1139393	1139393: OPN3 :: opsin 3 (encephalopsin, panopsin)	170129	0.076789396477269	−0.141913398593755
2438	1139411	1139411: OSBPL10 :: oxysterol binding protein-like 10	368238	−0.417496181839488	0.261396462305931
2439	1139444	1139444: RABL2B :: RAB, member of RAS oncogene family-like 2B	355874	0.063409117787863	−0.166237878791748
2440	1139461	1139461: BIN2 :: bridging integrator 2	14770	0.256527759821467	−0.339692650263970
2441	1139466	1139466: LOC51762 :: RAB-8b protein	365655	0.231557760181664	−0.095180733736222
2442	1139483	1139483: FKBP10 :: FK506 binding protein 10, 65 kDa	3849	0.674153797219952	−0.221743793245193
2443	1139526	1139526: HSPC177 :: hypothetical protein HSPC177	415534	0.163735980619122	−0.137102206317660
2444	1139528	1139528: TRPM4 :: transient receptor potential cation channel, subfamily M, member 4	31608	0.131053770432532	−0.044594419561590
2445	1139531	1139531: MGC8407 :: hypothetical protein MGC8407	145156	−0.078540256164261	0.151455641167260
2446	1139542	1139542: NEIL1 :: nei endonuclease VIII-like 1 (E. coli)	512732	0.026893739120928	0.051569026919496
2447	1139552	1139552: FLJ23119 :: hypothetical protein FLJ23119	413386	−0.003018803127220	−0.058250007576066
2448	1139556	1139556: RIN3 :: Ras and Rab interactor 3	413374	0.295487317472535	−0.531059799897965
2449	1139572	1139572: SNCAIP :: synuclein, alpha interacting protein (synphilin)	24948	0.148663268443581	−0.169804663179603
2450	1139575	1139575: SN :: sialoadhesin	31869	−0.010823611694524	−0.347990816689990
2451	1139579	1139579: BCL11B :: B-cell CLL/lymphoma 11B (zinc finger protein)	57987	0.269001973086771	−0.570933632618085
2452	1139603	1139603: ZNF226 :: zinc finger protein 226	145956	0.112382635429707	−0.194688343434095
2453	1139623	1139623: BANK1 :: B-cell scaffold protein with ankyrin repeats 1	193736	−0.166958172604313	0.185243160384443
2454	1139645	1139645: C14orf101 :: chromosome 14 open reading frame 101	134051	−0.193861410475501	0.089892119649755
2455	1139654	1139654: ECT2 :: epithelial cell transforming sequence 2 oncogene	293257	−0.204095198089242	0.656075928375559
2456	1139661	1139661: FN5 :: FN5 protein	416456	0.567268031407027	−0.473817226590911
2457	1139663	1139663: RNPC4 :: RNA-binding region (RNP1, RRM) containing 4	4997	−0.312001381814897	0.310598617201023
2458	1139669	1139669: C17 :: cytokine-like protein C17	13872	0.224259916127251	−0.255436447025748
2459	1139767	1139767: FBXL12 :: F-box and leucine-rich repeat protein 12	12439	−0.175973426526743	0.041273627872276
2460	1139774	1139774: SNX11 :: sorting nexin 11	15827	0.021233224776666	−0.069044004608862
2461	1139805	1139805: CYB5R2 :: cytochrome b5 reductase b5R.2	414362	−0.255806993410501	0.209851938563531
2462	1139830	1139830: SAMSN1 :: SAM domain, SH3 domain and nuclear localisation signals, 1	221851	0.370981356457398	−0.381164453290482
2463	1139831	1139831: FLJ21736 :: esterase 31	268700	−0.011968075306893	−0.016434297612474
2464	1139839	1139839: SGK2 :: serum/glucocorticoid regulated kinase 2	62863	0.024109656506769	0.032626900537836
2465	1139842	1139842: SAP130 :: mSin3A-associated protein 130	133523	−0.097742321655318	0.266312994370097
2466	1139925	1139925: FAIM :: Fas apoptotic inhibitory molecule	173438	−0.124987151146701	0.328309523235883
2467	1139949	1139949: DNAH3 :: dynein, axonemal, heavy polypeptide 3	375739	−0.169731374035577	0.074225125499242
2468	1139950	1139950: FLJ10420 :: hypothetical protein FLJ10420	437385	0.236816945983053	−0.335727361898558
2469	1139955	1139955: SLC12A6 :: solute carrier family 12 (potassium/chloride transporters), member 6	4876	−0.020487054568829	−0.037480624844835
2470	1139957	1139957: NGLY1 :: N-glycanase 1	63657	−0.525638023143142	0.363478080938368
2471	1139962	1139962: C5orf4 :: chromosome 5 open reading frame 4	10235	0.230250368247300	−0.233149594377572
2472	1139969	1139969: JIK :: STE20-like kinase	12040	−0.197720240185810	0.063503215792743
2473	1139971	1139971: LIMS2 :: LIM and senescent cell antigen-like domains 2	127273	−0.023501693605426	−0.081611153834008
2474	1140007	1140007: TPT :: trans-prenyltransferase	279865	−0.267154068193449	0.678834620628513
2475	1140018	1140018: PWDMP :: WD repeat membrane protein PWDMP	438482	−0.133214603635881	0.120024613326089
2476	1140027	1140027: FLJ13409 :: hypothetical protein FLJ13409	−30	0.032352790493303	−0.421061800596014
2477	1140031	1140031: SIAT7D :: sialyltransferase 7D ((alpha-N-acetylneuraminyl-2,3-betagalactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltransferase)	3972	−0.255702042856147	0.129661591849210
2478	1140072	1140072: SLCO5A1 :: solute carrier organic anion transporter family, member 5A1	199750	0.242253459635359	−0.221156982559850
2479	1140075	1140075: SNARK :: likely ortholog of rat SNF1/AMP-activated protein kinase	172012	−0.047490349579645	−0.277054802560530
2480	1140088	1140088: DC-TM4F2 :: tetraspanin similar to TM4SF9	509050	0.226500769788379	−0.262234704475871
2481	1140127	1140127: TRIM34 :: tripartite motif-containing 34	125300	−0.165828521151955	0.102914713660907
2482	1140151	1140151: FLJ22757 :: hypothetical protein FLJ22757	236449	−0.089956291622834	−0.171243944377416
2483	1140214	1140214: ANKRD3 :: ankyrin repeat domain 3	55565	−0.135384096304679	0.090538047157569
2484	1140236	1140236: SPAP1 :: SH2 domain containing phosphatase anchor protein 1	194976	−0.437940303418959	0.326018914273141
2485	1140238	1140238: BCLG :: apoptosis regulator BCL-G	11962	−0.042826609936427	−0.286603480568969
2486	1140344	1140344: BNIP3L :: BCL2/adenovirus E1B 19 kDa interacting protein 3-like	132955	0.217814730487477	0.049767573763502

TABLE 2415-continued

GeneID.txt

Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
2487	1140370	1140370: CDCA8 :: cell division cycle associated 8	48855	−0.413518820286071	0.851402787359892
2488	1140378	1140378: BHLHB3 :: basic helix-loop-helix domain containing, class B, 3	437282	0.441953829397093	−0.128845498205439
2489	1140391	1140391: LEF1 :: lymphoid enhancer-binding factor 1	44865	−0.102669812122025	−0.218911457849257
2490	1140399	1140399: PLAB :: prostate differentiation factor	296638	0.096863129825544	−0.118898412519241
2491	1140404	1140404: KCNMA1 :: potassium large conductance calcium-activated channel, subfamily M, alpha member 1	354740	0.587653373643620	−0.452387471739584
2492	1140416	1140416: TOSO :: regulator of Fas-induced apoptosis	58831	−0.227010373770165	−0.159494002878968
2493	1140457	1140457: IL21R :: interleukin 21 receptor	210546	0.212002655160102	−0.176888063733686
2494	1140464	1140464: H11 :: protein kinase H11	111676	0.562080363557665	−0.327453925079561
2495	1140473	1140473: CORO1C :: coronin, actin binding protein, 1C	17377	0.173358377940601	−0.047338136392363
2496	1140491	1140491: DKFZp761P1010 :: hypothetical protein DKFZp761P1010	24979	0.101756726051739	−0.183027999855880
2497	1140497	1140497: FLJ12750 :: hypothetical protein FLJ12750	77870	0.339043501264461	−0.382487661946037
2498	1140520	1140520: C20orf21 :: chromosome 20 open reading frame 21	11747	−0.439383490087482	0.339299186966798
2499	1140524	1140524: C6orf37 :: chromosome 6 open reading frame 37	10784	0.464548931082200	−0.451242812457036
2500	1140534	1140534: ARH :: LDL receptor adaptor protein	184482	0.219197513436446	−0.333907644050982
2501	1140565	1140565: HLA-F :: major histocompatibility complex, class I, F	411958	0.384933870287039	−0.597355642875244
2502	1140567	1140567: CLIC4 :: chloride intracellular channel 4	25035	0.087366213877805	0.196012165859917
2503	1140570	1140570: HSPA8 :: heat shock 70 kDa protein 8	180414	−0.023139381570294	0.050939786779129
2504	1140571	1140571: ADCK2 :: aarF domain containing kinase 2	210397	0.029868578992176	0.158934520479412
2505	1140574	1140574: MGC1203 :: hypothetical protein MGC1203	17987	0.086226740004958	0.127077044778373
2506	1140584	1140584: C14orf87 :: chromosome 14 open reading frame 87	294083	−0.335638395822406	0.547973957918325
2507	1140589	1140589: GUCY1A3 :: guanylate cyclase 1, soluble, alpha 3	433488	0.456463431988372	−0.374874498826929
2508	1140613	1140613: VRK3 :: vaccinia related kinase 3	443330	−0.380702233123925	0.211440380539557
2509	1140630	1140630: FLT1 :: fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)	347713	0.192942882655688	−0.123277559696215
2510	1140632	1140632: MCM4 :: MCM4 minichromosome maintenance deficient 4 (*S. cerevisiae*)	460184	−0.376728198824448	0.850172826162782
2511	1140729	1140729: IL1F5 :: interleukin 1 family, member 5 (delta)	207224	−0.011674717854802	0.027823140475085
2512	1140745	1140745: FER1L4 :: fer-1-like 4 (*C. elegans*)	72222	−0.172974560266972	0.044998775095322
2513	1140781	1140781: NA	−9	0.014530846048607	−0.103093007369487
2514	1140782	1140782: NA	−10	0.006268837628174	−0.083328907951826
2515	1140783	1140783: NA	−11	0.058336388513323	−0.094737922344377
2516	1140784	1140784: NA	−12	0.009386086273623	−0.065007336367840
2517	1140785	1140785: NA	−13	0.047643577567512	−0.140278204847852
2518	1140786	1140786: NA	−14	0.016786919443948	−0.174405991353998
2519	1140787	1140787: NA	−15	0.022891073012834	−0.155713264657076
2520	1140788	1140788: :: Affy control	−76	−0.117884908267157	0.200102966609546
2521	1140789	1140789: NA	−16	−0.053745102351612	0.056855755515683
2522	1140790	1140790: NA	−17	−0.002474950353002	0.146778154626489
2523	1140791	1140791: :: Affy control	−77	−0.044010031551127	0.103181030663411
2524	1140792	1140792: :: Affy control	−78	−0.170357382284597	0.155867721321911
2525	1140793	1140793: :: Affy control	−79	−0.094085257903303	0.015739455221676
2526	1140794	1140794: :: Affy control	−80	0.072047623150024	0.031475688587574
2527	1140795	1140795: :: Affy control	−81	0.019559904867390	−0.028763995255638
2528	1140796	1140796: :: Affy control	−82	−0.002597758314342	0.056810099843959
2529	1140797	1140797: :: Affy control	−83	−0.083637785960315	0.013226984835784
2530	1140798	1140798: :: Affy control	−84	−0.149412058607628	0.063774018243496
2531	1140799	1140799: :: Affy control	−85	−0.067949626733013	0.067189679174101
2532	1140800	1140800: NA	−18	0.004654423406066	−0.073603651584715
2533	1140801	1140801: NA	−19	0.007232174980560	−0.083719225734612
2534	1140802	1140802: :: Affy control	−86	−0.041429693151471	0.043909563253514
2535	1140803	1140803: :: Affy control	−87	−0.016514640117280	0.026369412380536
2536	1140804	1140804: :: Affy control	−88	−0.031829051168426	0.077781369765560
2537	1140805	1140805: :: Affy control	−89	0.020865760367817	−0.204408613047135
2538	1140806	1140806: :: Affy control	−90	−0.023926340232166	0.208878284785108
2539	1140807	1140807: :: Affy control	−91	0.113490613013508	−0.030826444609494
2540	1140808	1140808: :: Affy control	−92	0.012514982361291	0.075200735866390
2541	1140809	1140809: :: Affy control	−93	0.136504292454269	−0.119517051436108
2542	1140810	1140810: :: Affy control	−94	−0.057422781927538	0.086665252476037
2543	1140811	1140811: :: Affy control	−95	0.133189510202426	−0.101012852018164
2544	1140812	1140812: :: Affy control	−96	0.001223309520009	0.095793180622117
2545	1140813	1140813: :: Affy control	−97	−0.009371369059179	0.052514206556146
2546	1140814	1140814: :: Affy control	−98	−0.027062251510449	−0.029446918626741
2547	1140815	1140815: :: Affy control	−99	−0.019326891464828	0.082329569464007
2548	1140816	1140816: :: Affy control	−100	−0.016568107211094	0.097017805392993
2549	1140817	1140817: :: Affy control	−101	−0.006509426539146	0.128549591393422
2550	1140818	1140818: :: Affy control	−102	0.027938036404715	−0.189543315055064
2551	1140819	1140819: :: Affy control	−103	−0.021413730370109	−0.133918701719173
2552	1140820	1140820: :: Affy control	−104	0.001578324636409	−0.072457711989475
2553	1140821	1140821: :: Affy control	−105	−0.006400037365219	−0.059009456108435
2554	1140822	1140822: :: Affy control	−106	−0.023396144647357	−0.065693911773797

TABLE 2415-continued

GeneID.txt

Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
2555	1140823	1140823: :: Affy control	−107	0.011662567339774	−0.073288829281112
2556	1140824	1140824: :: Affy control	−108	0.012768276145964	−0.117644303599034
2557	1140825	1140825: :: Affy control	−109	−0.009563443665290	−0.042035406725848
2558	1140826	1140826: :: Affy control	−110	−0.000777025451842	−0.095436504049974
2559	1140827	1140827: :: Affy control	−111	−0.019671268603360	0.017149224395412
2560	1140828	1140828: :: Affy control	−112	−0.001327627906192	0.024569651878159
2561	1140829	1140829: :: Affy control	−113	−0.166625799047804	0.056909535950037
2562	1140834	1140834: ACTB :: Affy control actin, beta	426930	0.036626782020363	−0.206629607105101
2563	1140835	1140835: ACTB :: Affy control actin, beta	426930	−0.149602339907586	0.129812469536959
2564	1140836	1140836: ACTB :: Affy control actin, beta	426930	−0.091647722342469	0.000432322929413
2565	1140837	1140837: :: Affy control	−114	0.094646356888252	0.037746051614047
2566	1140838	1140838: :: Affy control	−115	0.117242895542767	0.062821055865340
2567	1140839	1140839: :: Affy control	−116	0.089772638224071	0.092598810615234
2568	1140842	1140842: GAPD :: Affy control glyceraldehyde-3-phosphate dehydrogenase	169476	−0.081770293481056	0.122359836917701
2569	1140843	1140843: GAPD :: Affy control glyceraldehyde-3-phosphate dehydrogenase	169476	−0.243924592429084	0.422918916154454
2570	1140844	1140844: GAPD :: Affy control glyceraldehyde-3-phosphate dehydrogenase	169476	−0.205317596747236	0.311010631943087
2571	1140845	1140845: STAT1 :: Affy control signal transducer and activator of transcription 1, 91 kDa	21486	0.377358722885690	−0.541349128751760
2572	1140846	1140846: STAT1 :: Affy control signal transducer and activator of transcription 1, 91 kDa	21486	0.097287175817027	−0.226153881821370
2573	1140847	1140847: STAT1 :: Affy control signal transducer and activator of transcription 1, 91 kDa	21486	0.216947517172567	−0.391088029796798
2574	1140848	1140848: STAT1 :: Affy control signal transducer and activator of transcription 1, 91 kDa	21486	0.222030839773439	−0.348450525763477
2575	1529284	1529284: MCC :: mutated in colorectal cancers	409515	0.110972159568218	−0.072345229884740
2576	1529285	1529285: KIAA1219 :: KIAA1219 protein	348929	−0.184556459472403	−0.049692544277234
2577	1529286	1529286: MADH5 :: MAD, mothers against decapentaplegic homolog 5 (*Drosophila*)	167700	0.031685751568576	0.146378764529449
2578	1529287	1529287: KIAA0303 :: KIAA0303 protein	212787	0.051481011707667	0.042849436971698
2579	1529288	1529288: CCNG2 :: cyclin G2	13291	0.077063799482395	0.059768352114886
2580	1529289	1529289: :: *Homo sapiens* cDNA FLJ12727 fis, clone NT2RP2000027.	96557	−0.021365736556446	−0.015983700308380
2581	1529290	1529290: N4BP3 :: Nedd4 binding protein 3	101761	−0.098254325850797	0.157368217757306
2582	1529291	1529291: :: *Homo sapiens* transcribed sequences	104450	−0.076267577354527	−0.040509704775555
2583	1529292	1529292: :: *Homo sapiens* transcribed sequences	105261	0.033769033555145	0.129433981816277
2584	1529293	1529293: :: *Homo sapiens* hypothetical LOC284134 (LOC284134), mRNA	113117	0.156492425740869	−0.366194468589873
2585	1529294	1529294: :: *Homo sapiens* hypothetical LOC284134 (LOC284134), mRNA	113117	0.182603122401687	−0.404979176023783
2586	1529295	1529295: :: *Homo sapiens* transcribed sequences	116441	0.033705717151087	0.117633519020541
2587	1529296	1529296: :: *Homo sapiens* transcribed sequences	122428	0.139091174867969	0.107806582080154
2588	1529297	1529297: :: *Homo sapiens* mRNA; cDNA DKFZp686F08109 (from clone DKFZp686F08109)	132335	−0.297312324845849	0.119929613672577
2589	1529298	1529298: :: *Homo sapiens* mRNA; cDNA DKFZp667B1520 (from clone DKFZp667B1520)	136707	−0.314207665564666	0.198327056016028
2590	1529299	1529299: :: *Homo sapiens* cDNA FLJ42786 fis, clone	444290	−0.064690184926136	0.011327312833764
2591	1529300	1529300: :: *H. sapiens* mRNA for immunoglobulin kappa light chain BRAWH3006761 VJ region (ID POM433)	449608	−0.204293297723690	0.145878170957971
2592	1529301	1529301: :: AI281566	−117	0.071716279105228	−0.042503405899593
2593	1529302	1529302: ELF3 :: E74-like factor 3 (ets domain transcription factor, epithelial-specific)	67928	0.029898524927091	0.032305158454658
2594	1529303	1529303: :: W22811	−38	−0.128640352347951	−0.034389181844250
2595	1529304	1529304: :: W22811	−38	−0.018858926497905	−0.156662687401548
2596	1529305	1529305: :: *Homo sapiens* transcribed sequence with moderate similarity to protein ref: NP_060312.1 (*H. sapiens*) hypothetical protein FLJ20489 [*Homo sapiens*]	173957	0.045101000387545	−0.125823818297820
2597	1529306	1529306: MGC26706 :: hypothetical protein MGC26706	190043	0.022863081364640	0.090864014434462
2598	1529307	1529307: :: *Homo sapiens* cDNA FLJ46553 fis, clone THYMU3038879	435736	−0.117004056094557	0.108321654537967
2599	1529308	1529308: :: *Homo sapiens* transcribed sequences	193014	−0.194608455512361	0.159131057131648
2600	1529309	1529309: HSH2 :: hematopoietic SH2 protein	512797	−0.284514425855296	−0.009187563040830
2601	1529310	1529310: PRKAG1 :: protein kinase, AMP-activated, gamma 1 non-catalytic subunit	3136	0.084646768018470	−0.094185610330221
2602	1529311	1529311: :: *Homo sapiens* transcribed sequences	251214	−0.008562152181595	0.207360519494227
2603	1529312	1529312: :: *Homo sapiens* cDNA FLJ34500 fis, clone HLUNG2005479.	255809	−0.072056295484426	−0.259485982293033
2604	1529313	1529313: :: *Homo sapiens* transcribed sequences	271998	0.004383347722577	0.265566854529143
2605	1529314	1529314: :: *Homo sapiens* transcribed sequences	276342	−0.006227323367580	0.045472523730890

TABLE 2415-continued

GeneID.txt

Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
2606	1529315	1529315: :: *Homo sapiens* transcribed sequence with weak similarity to protein ref: NP_062553.1 (*H. sapiens*) hypothetical protein FLJ11267 [*Homo sapiens*]	445718	−0.084112604384647	0.019415177758716
2607	1529316	1529316: ZNF198 :: zinc finger protein 198	315241	−0.086336901114135	0.076958490701384
2608	1529317	1529317: :: AA828425	−118	−0.224014424936674	−0.223856158514235
2609	1529318	1529318: :: *Homo sapiens* transcribed sequences	291954	0.073854603491552	0.079840492528659
2610	1529319	1529319: KIAA0970 :: KIAA0970 protein	103329	−0.004662599096684	0.007648241002329
2611	1529320	1529320: :: *Homo sapiens* , clone IMAGE: 5222345, mRNA	309149	−0.023029642379006	−0.010624843950025
2612	1529321	1529321: IL24 :: interleukin 24	411311	−0.109990803451750	0.025765040861020
2613	1529322	1529322: :: *Homo sapiens* transcribed sequence with weak similarity to protein ref: NP_038605.1 (*M. musculus*) L1 repeat, Tf subfamily, member 30 [*Mus musculus*]	514291	0.030436007092166	−0.175347477632027
2614	1529323	1529323: :: *Homo sapiens* transcribed sequences	345834	0.336779571590933	−0.359684409503434
2615	1529324	1529324: GZMH :: granzyme H (cathepsin G-like 2, protein h-CCPX)	348264	0.239243227392061	−0.419048485474577
2616	1529325	1529325: :: BQ003404	−75	−0.140464406043795	−0.021462938104706
2617	1529326	1529326: HDAC7A :: histone deacetylase 7A	200063	−0.109850414890401	0.080269797544815
2618	1529327	1529327: SMN2 :: survival of motor neuron 2, centromeric	288986	−0.042384278985820	0.248777434604123
2619	1529328	1529328: :: *Homo sapiens* transcribed sequences	369056	0.056981262751925	−0.112051222335899
2620	1529329	1529329: :: *Homo sapiens* transcribed sequences	369101	−0.135338205033608	0.159470087740367
2621	1529330	1529330: LOC153684 :: hypothetical protein LOC153684	259625	−0.105755172392999	0.046487888216411
2622	1529331	1529331: :: *Homo sapiens* transcribed sequence with weak similarity to protein ref: NP_060312.1 (*H. sapiens*) hypothetical protein FLJ20489 [*Homo sapiens*]	374126	−0.201436415316463	0.127028345378989
2623	1529332	1529332: LOC134492 :: similar to RIKEN cDNA 2700047N05	140443	−0.300773106127023	0.228609503612335
2624	1529333	1529333: :: *Homo sapiens* cDNA FLJ40549 fis, clone THYMU2001916	378849	−0.016962900796743	0.032654218738799
2625	1529334	1529334: :: *Homo sapiens* transcribed sequence with moderate similarity to protein ref: NP_071431.1 (*H. sapiens*) cytokine receptor-like factor 2; cytokine receptor CRL2 precusor [*Homo sapiens*]	380255	−0.073135831632244	−0.084277957239007
2626	1529335	1529335: :: *Homo sapiens* mRNA; cDNA DKFZp586L141 (from clone DKFZp586L141)	400872	−0.379618839813305	0.435859102100720
2627	1529336	1529336: PTK2B :: PTK2B protein tyrosine kinase 2 beta	405474	0.064169101462340	−0.102556747779252
2628	1529337	1529337: C6orf166 :: chromosome 6 open reading frame 166	201864	−0.018977987327815	0.016953866594291
2629	1529338	1529338: PAK2 :: p21 (CDKN1A)-activated kinase 2	284275	−0.396911297097266	0.365705541778953
2630	1529339	1529339: :: *Homo sapiens* transcribed sequences	427710	−0.126611681377431	0.072949549681158
2631	1529340	1529340: :: AA827872	−119	−0.119915444623348	0.179233924660731
2632	1529341	1529341: LY75 :: lymphocyte antigen 75	153563	0.188892498067345	0.001326615372681
2633	1529342	1529342: :: BQ026237	−74	0.158306373307698	−0.426400997795195
2634	1529343	1529343: :: *Homo sapiens* transcribed sequence	521948	−0.039648581482154	0.106009965624923
2635	1529344	1529344: SERPINA11 :: serine proteinase inhibitor A11	317970	0.238830242521113	0.051394835638056
2636	1529345	1529345: :: *Homo sapiens* transcribed sequences	443475	−0.098204977598259	0.032635938575475
2637	1529346	1529346: :: *Homo sapiens* transcribed sequences	443935	−0.133480744808980	−0.138767694000192
2638	1529347	1529347: :: *Homo sapiens* transcribed sequences	444019	−0.261867960347880	0.063087517442791
2639	1529348	1529348: SOS1 :: son of sevenless homolog 1 (*Drosophila*)	326392	−0.112147722903032	−0.017345761915274
2640	1529349	1529349: :: *Homo sapiens* transcribed sequences	445500	0.004876940094089	−0.293504921159920
2641	1529350	1529350: :: *Homo sapiens* transcribed sequences	445884	−0.196163065913620	0.239480017540847
2642	1529351	1529351: :: *Homo sapiens* transcribed sequences	445898	−0.072117447206842	0.178173670478469
2643	1529352	1529352: :: *Homo sapiens* cDNA FLJ42418 fis, clone BLADE2001987	446195	−0.006498231102315	0.089100493304306
2644	1529353	1529353: :: *Homo sapiens* transcribed sequences	446198	−0.054986078590614	−0.011114342560876
2645	1529354	1529354: BCL11A :: B-cell CLL/lymphoma 11A (zinc finger protein)	314623	−0.275920246770634	0.357053851248126
2646	1529355	1529355: :: *Homo sapiens* transcribed sequences	370675	0.107276183111680	−0.141870873747761
2647	1529356	1529356: C14orf170 :: chromosome 14 open reading frame 170	303775	−0.058235352127145	−0.001935868254300
2648	1529357	1529357: :: *Homo sapiens* transcribed sequences	444651	−0.169332893572493	0.118609634840753
2649	1529358	1529358: :: *Homo sapiens* transcribed sequence with moderate similarity to protein sp: P39195 (*H. sapiens*) ALU8_HUMAN Alu subfamily SX sequence contamination warning entry	127178	0.185280771017017	−0.002341003747225
2650	1529359	1529359: :: AA832388	326173	0.185128908116345	−0.201485649206219
2651	1529360	1529360: :: *Homo sapiens* transcribed sequences	443036	0.156862502241191	−0.359190734129611
2652	1529361	1529361: HDAC3 :: histone deacetylase 3	388681	−0.361732180141791	0.391019787446920
2653	1529362	1529362: PLK :: polo-like kinase (*Drosophila*)	329989	−0.388320346854452	0.833332607616786
2654	1529363	1529363: NOTCH1 :: Notch homolog 1, translocation-associated (*Drosophila*)	311559	0.259233913232295	−0.421434088005552
2655	1529364	1529364: ATM :: ataxia telangiectasia mutated (includes complementation groups A, C and D)	504644	−0.118986043194098	−0.148365556666337
2656	1529365	1529365: TNFRSF13C :: tumor necrosis factor receptor superfamily, member 13C	344088	−0.057992715606171	0.052741212228336
2657	1529366	1529366: :: EBV LMP1 unique	−65	−0.082164264138660	0.018369754127342
2658	1529367	1529367: :: EBV LMP1 3' end	−66	−0.064572311852911	−0.069680793133709
2659	1529368	1529368: :: EBV EBNA2 3' end	−70	−0.173445974852027	0.205542104461719
2660	1529369	1529369: :: EBV EBNA1 CDS	−71	−0.071747968325640	0.065345583125480
2661	1529370	1529370: :: EBV LPM2A	−64	−0.001163089708170	−0.110956119752116
2662	1529371	1529371: :: EBV BHRFA	−73	−0.010090518075703	−0.076381918817641

TABLE 2415-continued

GeneID.txt

Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
2663	1529372	1529372: :: EBV BZLF1	−72	−0.221272834194238	0.120180577006682
2664	1529373	1529373: :: EBV EBNA3A	−69	−0.161072632651006	0.055854607395513
2665	1529374	1529374: :: EBV EBNA3C	−67	0.059031065592265	−0.071187244369590
2666	1529375	1529375: :: HHV8 K13	−59	−0.013666002623568	−0.085249642533594
2667	1529376	1529376: :: HHV8 T0.7/P6	−57	−0.038217131973910	−0.030850737271204
2668	1529377	1529377: :: HHV8 T1.1	−56	0.032597223400267	−0.067543040593593
2669	1529378	1529378: :: HHV8 ORF73/LANA	−58	−0.015664193006648	0.006139430844953
2670	1529379	1529379: :: HHV8 vMIP1b ORFK4.2 KIE-3	−54	−0.015626336025217	−0.056403407873870
2671	1529380	1529380: :: HHV8 vIL6	−55	−0.115982682592600	0.085106875588196
2672	1529381	1529381: :: HHV8 K1-32 Bcb K1 protein	−60	0.046823898274642	0.001406007567692
2673	1529382	1529382: CCND1 :: Cyclin D1 coding region; by 498-1097 of NM_053056	371468	0.094277437820395	−0.132713478377930
2674	1529383	1529383: CCND1 :: Cyclin D1 3' end; by 3691-4290 of NM_053056	371468	0.555196850752576	−0.483293591801984
2675	1529384	1529384: CCND1 :: Cyclin D1; bp 2491-3090 of NM_053056	371468	0.365173665475046	−0.261555570413604
2676	1529385	1529385: CCND1 :: Cyclin D1; bp 1891-2490 of NM_054056	371468	0.281719638953775	−0.208410405004593
2677	1529386	1529386: CCND1 :: Cyclin D1; bp 1291-1890 of NM_054056	371468	0.429543765430906	−0.281718193371932
2678	1529387	1529387: BCL2 :: BCL-2 MBR by 2409-3009 of NM_000633	79241	−0.293554931269457	−0.116661021933823
2679	1529388	1529388: BCL2 :: BCL-2 coding region end; bp 152-751 of NM_000633	79241	−0.141729791902808	−0.017721784560266
2680	1529389	1529389: BCL2 :: BCL-2 3' end; bp 5431-6030 of NM_000633	79241	−0.344617915920712	−0.207115780844928
2681	1529390	1529390: BCL2 :: BCL-2; bp 1401-2000 of NM_000633	79241	−0.219032917773749	0.010350953136667
2682	1529391	1529391: BCL2 :: BCL-2; bp 4431-5030 of NM_000633	79241	−0.403717253508751	−0.020031412999953
2683	1529392	1529392: ACVR1C :: activin A receptor, type IC	352338	0.054521329510957	−0.065435713301877
2684	1529393	1529393: KIAA1811 :: KIAA1811 protein	182081	0.333009117195884	−0.304901694858517
2685	1529394	1529394: LOC91807 :: myosin light chain kinase (MLCK)	339846	−0.123907032755405	0.183602253317435
2686	1529395	1529395: :: *Homo sapiens* similar to Serine/threonine-protein kinase KKIALRE (Cyclin-dependent kinase-like 1) (LOC344387), mRNA	403201	0.028612792038585	0.028966275624666
2687	1529396	1529396: MGC33182 :: casein kinase I alpha S-like	512897	−0.038017413092940	−0.004616315101532
2688	1529397	1529397: CLK4 :: CDC-like kinase 4	406557	0.086234150880245	−0.366605829522404
2689	1529398	1529398: HSMDPKIN :: myotonic dystrophy protein kinase like protein	293590	−0.079557360480167	0.120197897136261
2690	1529399	1529399: LOC203806 :: hypothetical protein LOC203806	256916	0.035952284333729	−0.030481696710319
2691	1529400	1529400: FLJ32818 :: hypothetical protein FLJ32818	210697	−0.124775961566475	0.094567535746030
2692	1529401	1529401: MAP4K3 :: mitogen-activated protein kinase kinase kinase kinase 3	399752	0.277778965134787	−0.259253792231314
2693	1529402	1529402: KSR2 :: kinase suppressor of Ras-2	375836	−0.043546893836039	−0.006972792768919
2694	1529403	1529403: KIAA1883 :: KIAA1883 protein	511780	−0.131034308134048	0.103925962598284
2695	1529404	1529404: MAP3K1 :: mitogen-activated protein kinase kinase kinase 1	170610	−0.109948582091028	0.087977859649393
2696	1529405	1529405: SAST :: syntrophin associated serine/threonine kinase	227489	0.126274276066276	−0.071352270643548
2697	1529406	1529406: MYO3B :: myosin IIIB	409066	0.155629369566744	−0.026270257889408
2698	1529407	1529407: PAK2 :: p21 (CDKN1A)-activated kinase 2	284275	−0.372590149141074	0.355639782047009
2699	1529408	1529408: PSKH2 :: serine/threonine kinase PSKH2	336929	0.039376351837621	−0.003523691344492
2700	1529409	1529409: FLJ25006 :: hypothetical protein FLJ25006	351173	−0.185470415631171	0.355295627732664
2701	1529410	1529410: SNF1LK :: SNF1-like kinase	380991	0.310744319100462	−0.191354110343142
2702	1529411	1529411: APEG1 :: aortic preferentially expressed protein 1	80181	−0.015090155827916	0.049326921582975
2703	1529412	1529412: STK22C :: serine/threonine kinase 22C (spermiogenesis associated)	512763	−0.152113151357401	0.144006256228092
2704	1529413	1529413: PRKWNK2 :: protein kinase, lysine deficient 2	232116	0.043707511124126	−0.024587852541792
2705	1529414	1529414: MGC22688 :: hypothetical protein MGC22688	352370	0.129203581496830	−0.037058867228545
2706	1529415	1529415: DKFZp686A17109 :: hypothetical protein DKFZp686A17109	369523	−0.148462736251386	0.034953320101641
2707	1529416	1529416: CDKN2A :: p14ARF; unique 5O region from INK4a locus	421349	0.054323363043638	0.129218335773114
2708	1529417	1529417: CDKN2A :: INK4a locus common sequence shared by p14ARF and all p16 mRNA isoforms	421349	0.042141777381482	0.177690611245249
2709	1529418	1529418: CDKN2A :: p16INK4a; p16 unique sequence shared by p16INK4a transcript variants 1 and 3 but not p16INK4a transcript variant 2 and variant 4 (p14ARF)	421349	−0.067908769750351	0.020087857642895
2710	1529419	1529419: :: *Homo sapiens* transcribed sequences	104182	−0.097146163320226	0.131715317478596
2711	1529420	1529420: IL17F :: interleukin 17F	272295	0.045525457266783	−0.009988757123239
2712	1529421	1529421: IL27 :: interleukin 27	375043	−0.004883677033980	−0.115384956701855
2713	1529422	1529422: IL23R :: interleukin-23 receptor	375184	0.094119854675173	0.044609962750620
2714	1529423	1529423: ITGAD :: integrin, alpha D	381264	0.148605834731398	−0.198509767943520
2715	1529424	1529424: CCL3L1 :: chemokine (C-C motif) ligand 3-like 1	512683	0.205301608020911	−0.340808318654676
2716	1529425	1529425: IL9R :: interleukin 9 receptor	406228	−0.045519588598842	0.085600863168274
2717	1529426	1529426: IL28B :: interleukin 28B (interferon, lambda 3)	406744	0.189355610681505	−0.165534213809855
2718	1529427	1529427: IL29 :: interleukin 29 (interferon, lambda 1)	406745	−0.014392642430728	−0.070805657034640
2719	1529428	1529428: NGFR :: nerve growth factor receptor (TNFR superfamily, member 16)	415768	0.035324253127484	−0.128267249447899
2720	1529429	1529429: IL17D :: interleukin 17D	434103	−0.069810691656676	0.069997307160626
2721	1529430	1529430: SPHK2 :: sphingosine kinase 2	444484	−0.321834026215950	0.170461543915022
2722	1529431	1529431: :: *Homo sapiens* transcribed sequences	446193	−0.168353154209300	0.128224145113833
2723	1529432	1529432: :: IgG1 constant region	−41	0.076813190211455	−0.105760779150212
2724	1529433	1529433: :: IgG1 constant region	−41	0.070417647231205	−0.075267225590524
2725	1529434	1529434: FLJ27099 :: IgG4 constant region	103995	0.018230596259647	−0.077214639544862

TABLE 2415-continued

GeneID.txt

Order	UNIQID	NAME	GENEID	LN.cor	Pro.cor
2726	1529435	1529435: :: IgA1 constant region	−44	0.186737460085977	−0.317208744354907
2727	1529436	1529436: :: IgE constant region	−43	0.101726014546358	−0.187640538570034
2728	1529437	1529437: BTLA :: B and T lymphocyte associated	445162	−0.318763487600451	0.010989475889237
2729	1529443	1529443: :: *Homo sapiens* transcribed sequences	88886	−0.026012720914063	0.076787080847203
2730	1529444	1529444: :: *Homo sapiens* transcribed sequences	126905	0.010228055161144	0.032713206278291
2731	1529445	1529445: :: BE675157	159050	−0.262325467861960	0.149553276873531
2732	1529446	1529446: :: *Homo sapiens* transcribed sequences	190626	−0.025863059671753	−0.065797375687666
2733	1529447	1529447: :: *Homo sapiens* transcribed sequences	291886	−0.035807248922759	0.126157477853033
2734	1529448	1529448: :: *Homo sapiens* transcribed sequences	369101	−0.122448573444494	0.135610608469673
2735	1529449	1529449: :: BQ710740	428762	−0.140372978110498	0.061475408728652
2736	1529450	1529450: :: AA255658	−120	−0.077793575103323	−0.096601745707301
2737	1529451	1529451: JMY :: junction-mediating and regulatory protein	396853	−0.070253972528956	0.001481500267825
2738	1529452	1529452: AIM1 :: absent in melanoma 1	422550	−0.047576787628458	0.022144076488709
2739	1529453	1529453: FCGR3A :: Fc fragment of IgG, low affinity IIIa, receptor for (CD16)	372679	0.105750028795122	−0.221420850072347
2740	1529454	1529454: :: EBV EBNA3B	−68	0.025237645629957	−0.049752634590638
2741	1529455	1529455: :: HHV8 BCL2 homologue	−61	−0.053831710598311	0.124768914047081
2742	1529456	1529456: CCND1 :: Cyclin D1; bp 3091-3690 of NM_053056	371468	0.563476075442490	−0.453521864341999
2743	1529457	1529457: GPRK7 :: G protein-coupled receptor kinase 7	351818	−0.113143362958157	0.050092066170263
2744	1529458	1529458: NEK8 :: NIMA (never in mitosis gene a)-related kinase 8	448468	−0.258903564937414	0.040064079685056
2745	1529459	1529459: SRMS :: src-related kinase lacking C-terminal regulatory tyrosine and N-terminal myristylation sites	411061	−0.038227711901371	0.147063354283128

1. A method for predicting survival in a follicular lymphoma (FL) subject comprising the steps of

a) isolating gene expression product from a biopsy sample from a subject;

b) obtaining gene expression data from the isolated gene expression product, wherein the gene expression data comprises data for genes in an immune response-1 gene expression signature and genes in an immune response-2 gene expression signature;

c) obtaining an average gene expression level for the genes in the immune response-1 gene expression signature to thereby obtain an immune response-1 gene expression signature value;

d) obtaining an average gene expression level for the genes in the immune response-2 gene expression signature to thereby obtain an immune response-2 gene expression signature value; and

f) calculating a survival predictor score using an equation: [2.71*(immune response-2 gene expression signature value)]−[2.36*(immune response-1 gene expression signature value)]; wherein a higher survival predictor score is associated with worse survival.

2. The method of claim **1** wherein the step of obtaining gene expression data comprises use of a microarray.

3. The method of claim **1** wherein the immune response-1 gene expression signature comprises at least one gene selected from the group consisting of (listed by UNIQID): 1095985, 1096579, 1097255, 1097307, 1097329, 1097561, 1098152, 1098405, 1098548, 1098893, 1099053, 1100871, 1120196, 1101004, 1103303, 1107713, 1115194, 1119251, 1119838, 1119924, 1120267, 1121313, 1121406, 1121720, 1122956, 1123038, 1123092, 1123875, 1124760, 1128356, 1128395, 1132104, 1133408, 1134069, 1134751, 1134945, 1135743, 1135968, 1136048, 1136087, 1137137, 1137289, 1137534, 1139339, 1139461, 11400391, 140524, and 1140759.

4. The method of claim **1** wherein the immune response-2 gene expression signature comprises at least one gene selected from the group consisting of (listed by UNIQID): 1118755, 1118966, 1121053, 1121267, 1121331, 1121766, 1121852, 1122624, 1122679, 1122770, 1123767, 1123841, 1126097, 1126380, 1126628, 1126836, 1127277, 1127519, 1127648, 1128483, 1128818, 1129012, 1129582, 1129658, 1129705, 1129867, 1130003, 1130388, 1131837, 1133843, 1133949, 1134447, 1135117, 1136017, 1137478, 1137745, 1137768, 1138476, 1138529, 1138601, 1139862, 1140189, and 1140389.

5. A method for predicting survival in a diffuse large B cell lymphoma (DLBCL) subject comprising the steps of:

a) isolating gene expression product from a biopsy sample from a subject;

b) obtaining gene expression data from the isolated gene expression product, wherein the gene expression data comprises data for genes in an ABC DLBCL high gene expression signature, a lymph node gene expression signature, and an MHC class II gene expression signature;

c) obtaining an average gene expression level for the genes in the ABC DLBCL high gene expression signature to thereby obtain an ABC DLBCL high gene expression signature value;

d) obtaining an average gene expression level for the genes in the lymph node gene expression signature to thereby obtain a lymph node gene expression signature value;

e) obtaining an average gene expression level for the genes in the MHC class II gene expression signature to thereby obtain an MHC class II gene expression signature value;

f) calculating a survival predictor score using an equation: [0.586*(ABC DLBCL high gene expression signature value)]−[0.468*(lymph node gene expression signature value)]−[0.336*(MHC class II gene expression signature)]−[0.2006*(MHC class II gene expression signature value)]; wherein a higher survival predictor score is associated with worse survival.

6. The method of claim **5** wherein the step of obtaining gene expression data comprises use of a micro array.

7. The method of claim **5** wherein the ABC DLBCL gene expression signature comprises at least one gene selected from the group consisting of (listed by UNIQID): 1134271, 1121564, 1119889, 1133300, 1106030, 1139301, 1122131, 1114824, 1100161, and 1120129.

8. The method of claim **5** wherein the lymph node gene expression signature comprises at least one gene selected from the group consisting of (listed by UNIQID): 1097126, 1120880, 1098898, 1123376, 1128945, 1130994, 1124429, 1099358, 1130509, 1095985, 1123038, 1133700, 1122101, and 1124296.

9. The method of claim **5** wherein the MHC class II gene expression signature comprises at least one gene selected from the group consisting of (listed by UNIQID): 1123127, 1136777, 1137771, 1134281, 1136573, and 1132710.

10. A method for predicting survival in a mantle cell lymphoma (MCL) subject comprising the steps of:

a) isolating gene expression product from a biopsy sample from a subject;

b) obtaining gene expression data from the isolated gene expression product, wherein the gene expression data comprises data for genes in a proliferation gene expression signature;

c) averaging the gene expression level of genes from the proliferation gene expression signature to thereby obtain a proliferation gene expression signature value;

d) calculating a survival predictor score using an equation: [1.66*(proliferation gene expression signature value)]; wherein a higher survival predictor score is associated with worse survival.

11. The method of claim **10** wherein the step of obtaining gene expression data comprises use of a microarray.

12. The method of claim **10** wherein the proliferation gene expression signature comprises at least one gene selected from the group consisting of (listed by UNIQID): 1097290, 1101295, 1119729, 1120153, 1120494, 1124745, 1126148, 1130618, 1134753, 1139654, and 1140632.

13. The method of claim **10** wherein the proliferation gene expression signature comprises at least one gene selected from the group consisting of (listed by UNIQID): 1119294, 1119729, 1120153, 1121276, 1123358, 1124178, 1124563, 1130799, 1131274, 1131778, 1132449, 1135229, and 1136585.

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