Applying Multivariate Adaptive Splines to Identify Genes With Expressions Varying After Diagnosis in Microarray Experiments

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ABSTRACT:

PURPOSE: To analyze a microarray experiment to identify the genes with expressions varying after the diagnosis of breast cancer.

METHODS: A total of 44 928 probe sets in an Affymetrix microarray data publicly available on Gene Expression Omnibus from 249 patients with breast cancer were analyzed by the nonparametric multivariate adaptive splines. Then, the identified genes with turning points were grouped by K-means clustering, and their network relationship was subsequently analyzed by the Ingenuity Pathway Analysis.

RESULTS: In total, 1640 probe sets (genes) were reliably identified to have turning points along with the age at diagnosis in their expression profiling, of which 927 expressed lower after turning points and 713 expressed higher after the turning points. K-means clustered them into 3 groups with turning points centering at 54, 62.5, and 72, respectively. The pathway analysis showed that the identified genes were actively involved in various cancer-related functions or networks.

CONCLUSIONS: In this article, we applied the nonparametric multivariate adaptive splines method to a publicly available gene expression data and successfully identified genes with expressions varying before and after breast cancer diagnosis.

KEYWORDS: MASAL, breast cancer, turning point, microarray, Ingenuity

Introduction

Since the development of microarray for high-throughput analysis of gene expressions,[1] this technology has been widely used in many biomedical studies.[2–8] Cancer research is one of the main areas that apply this technology.[2,9–14] Among this, breast cancer research is the most common one.[15–19]

Although the development of microarrays and the ability to perform massively parallel gene expression analysis of human tumors has been shown great contribution to breast cancer classification, prognostication, and prediction during the last decade,[20] the heterogeneous nature of breast cancer and the lack of reliable pathological or molecular markers still reflects the complexity of the molecular alterations that underlie the development and progression of this disease and poses serious problems to clinical management.[21] Some studies proposed methods to identify genes consistently expressed at different levels in diseased and normal cases, which is useful to elucidate pathways in breast cancer progression.[21,22] Other studies have explored the gene expression changes that are associated with the various stages of breast cancer progression.[23] However, the genes with changing expression associated with diagnostic age are still poorly understood, although the risk of breast cancer is highly age related.

Multivariate adaptive regression splines (MARS) is a nonparametric regression procedure that fits the model with a number of piecewise linear functions (ie, truncated functions with knots).[24] Zhang[25] further extended this method to be capable of analyzing the data under longitudinal settings. By applying this method to a publicly available microarray data set,[26] this study intends to identify a novel set of genes that vary expressions along with the diagnosis of breast cancer. One of our aims is to improve our understanding of biological mechanism in disease progression at different stages of age and provide novel potential drug targets for breast cancer. The other aim is to demonstrate that the method developed in this study can be generalized to studies with the similar problems for other diseases (eg, lung cancer). The outline of the article is as follows.

Section "Method" describes the methods used in the study. Section "Results" presents the results. In section "Discussion," we discussed the findings identified by our method and study limitations, as well as the future work. The last section presents the conclusions.

Method

Microarray data set

We studied 44 928 probe sets in an Affymetrix microarray data publicly available on Gene Expression Omnibus (www.ncbi.nlm.nih.gov/geo/) (series number: GSE4922) from 249 patients with breast cancer, who were aged between 28 and 93 years old

and enrolled in a cohort at Uppsala.[26] The tumor specimens were assessed on Affymetrix U133 A and B arrays. Of 249 samples, 68 were grade 1 tumors, 126 were grade 2 tumors, and 55 were grade 3 tumors.

Processing microarray data through Robust Multichip Average

Robust Multichip Average (RMA) is an algorithm developed to extract the expression matrix from Affymetrix data.[27] Through RMA, the raw probe-level intensity values from the Affymetrix data are background corrected, $\log_2$ transformed, quantile normalized, and then summarized via a linear model to obtain an expression measure for each probe set. In this step, the raw Affymetrix data (GSE4922) are transformed to a normalized expression value matrix (44 928 probe sets × 249 patients) via RMA in *R 2.13.0* (www.bioconductor.org).

Identifying genes with expressions varying after diagnosis via multivariate adaptive splines

Compared with MARS,[24] Multivariate Adaptive Splines of Analysis for longitudinal data not only can analyze data under the longitudinal settings but also has the advantage of defining several interesting phases when the velocity of increased (or decreased) outcome changes.[25] Below is a brief description of the model and algorithm in MASAL.

Assume that the outcomes are repeatedly measured at q different time points for each of the N units. The outcome of unit i at jth observation ($i = 1 \ldots N, j = 1 \ldots q$), Y_{ij}, is equal to the following:

$$Y_{ij} = f(t_{ij}, x_{1,ij}, \ldots, x_{p,ij}) + e_i(x_{*,ij}, t_{ij}) \qquad (1)$$

where f is a smooth function, t_{ij} is the time of measurements, $x_{k,ij}(k = 1 \ldots p)$ is the kth covariate, e_i is an error term, and x_* is some covariates which the error term depends on.

Here, MASAL is used to regress gene expressions on age at diagnosis through R-package MASAL[25,28–30] and in so doing identify changing points for genes with age-varying expressions.

In this study, we mainly focus on the changes of gene expressions along with age (t), and only single measurement for each unit is available. Hence, in the absence of covariates and multiple measurements, the function (1) can be deduced as follows:

$$Y_i = f(t_i) + e_i(t_i) = \beta_0 + \sum_{m=1}^{M} \beta_m h_m(t_i) + e_i(t_i)$$

where β_0 is an intercept parameter, M is some unknown number of nonconstant terms, $h_m(t)$ is a basis function in a function set $\Gamma = \{(t-\tau)^+, t\}_{\tau \in (-\infty, +\infty)}$ $((t-\tau)^+ = \max(0, t-\tau)),$[25] or a product of 2 or more such functions. For each gene, β_0, β_m, M, and $h_m(t)$ are estimated from the data using R-package MASAL.

Another advantage of using MASAL is that MARS[24] searched for the knot $\tau*$ over all observed values of t_i only, and this restriction has been removed without computational cost by MASAL.[25]

Grouping the genes with the similar turning points by K-means clustering

K-means clustering is a method for finding clusters and cluster centers in a set of unlabeled data (ie, unsupervised machine learning).[31] Given a number of cluster centers of genes' turning points, the K-means procedure iteratively moves the center to minimize the total within-cluster variance. The desired number of cluster centers is a minimum cluster number which satisfies that the ratio of within-cluster variance to the total variance is larger than 90%. The goal of clustering analysis in this study is to group the genes with the similar expression turning points and then conduct the subsequent pathway analysis for their associations.

Modeling the biological systems for the clustered genes with Ingenuity Pathway Analysis

Ingenuity Pathway Analysis (IPA) is applied to understand the molecular and chemical interactions, cellular phenotypes, and disease processes within a system from RNA expression microarrays or single-nucleotide polymorphism microarrays. Ingenuity Pathway Analysis also provides insight into the causes of observed gene expression changes and into the predicted downstream biological effects of those changes. The main transcription factors and biological functions for each cluster will be analyzed by IPA (Ingenuity Systems, www.ingenuity.com).

Results

Out of 44 928 probe sets, 5765 (12.8%) were identified by MASAL to change expressions after diagnosis. However, due to the high variation at the tails, we only focused on the 1640 probe sets with age ranging from 49 to 75, which are close to the 20% and 80% quartiles of the diagnostic age. Out of these 1640 probe sets, 927 expressed lower after turning points and 713 expressed higher after the turning points. Table 1 listed the first 20 probe sets in the order of Affymetrix GeneChip with turning points at diagnosis. The full list can be found in Appendix 1. Figure 1 shows the example of 2 probe sets selected from Table 1.

K-means clustered the identified turning points into 3 major groups, and the corresponding centers are 54 (group 1), 62.5 (group 2), and 72 (group 3) (unit: year) (Figure 2).

The pathway analysis was first applied to all probe sets identified by MASAL (named "group all") and then followed by the 3 groups clustered by K-means (named "group 1," "group 2," and "group 3").

Table 1. Top 20 probe sets with expressions changing after diagnosis.

NO.	PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT	CLASS[B]
1	1053_at	RFC2	1	0.02068128	72.3	3
2	1598_g_at	GAS6	–1	–0.00805394	54	1
3	160020_at	MMP14	–1	–0.01132246	55	1
4	1773_at	FNTB	–1	–0.00219325	55	1
5	1861_at	BAD	1	0.01079149	70.4	3
6	200028_s_at	STARD7	1	0.00518349	58	2
7	200036_s_at	RPL10A	1	0.0037056	63	2
8	200037_s_at	CBX3	1	0.00358799	50	1
9	200044_at	SRSF9	1	0.01270005	73	3
10	200052_s_at	ILF2	1	0.04336231	52	1
11	200056_s_at	C1D	1	0.00218105	52	1
12	200073_s_at	HNRNPD	1	0.02292864	51	1
13	200093_s_at	HINT1	1	0.0104039	66	2
14	200602_at	APP	1	0.01021256	65	2
15	200635_s_at	PTPRF	1	0.0069691	60	2
16	200636_s_at	PTPRF	1	0.00784896	63	2
17	200657_at	SLC25A5	1	0.03717327	55	1
18	200666_s_at	DNAJB1	1	0.01246004	73	3
19	200689_x_at	EEF1G	1	0.01478889	57	1
20	200695_at	PPP2R1A	–1	–0.00494418	65	2

[a]1 indicates the expression of the gene increases after the turning point, whereas –1 indicates the expression of the gene decrease after the turning point.
[b]Grouping number in K-means clustering.

For the top canonical pathways, IPA shows that gonadotropin-releasing hormone (*GnRH*) signaling, inhibition of matrix metalloproteinases, and T-cell receptor signaling are the top-ranked pathways for these 4 groups (including group all, group 1, group 2, and group 3) (Table 2).

For the disease and disorder function, the cancer-related function is among the top 5 functions for group all, group 1, and group 3 (Table 3). The inflammatory response function is the top disease and disorder function for group 2.

For the molecular and cellular function, cellular growth and proliferation function is the no. 1 function for group all, group 1, group 3 and no. 2 for group 2. The function related to cell death and survival appears among the top 5 for 3 out of 4 groups (Table 4).

Interestingly, for the top 5 networks identified by IPA (Table 5), the overlaps among these 4 groups are very rare. In particular, RNA posttranscriptional modification, protein synthesis, and gene expression is the no. 1 network identified for group all. Developmental disorder, hereditary disorder, and ophthalmic disease is the no. 1 network for group 1. For group

2, hereditary disorder, respiratory disease, and cell cycle is the no. 1 network, and for group 3, the no. 1 network is amino acid metabolism, drug metabolism, and molecular transport.

For the upstream regulators analysis (Table 6), IPA found that the tumor protein *p53* (*TP53*), which is a tumor suppressor protein encoded by the *TP53* genes in humans, is the no. 1 transcription regulator in group 1. *TGFB1*, a secreted protein that performs many cellular functions (eg, control of cell growth, cell proliferation, and apoptosis), appears as one of the top 5 regulators among all 4 groups.

Discussion

In cancer research, it is natural to envision that there are genes that change expressions before and after the onset of cancer. Developing methods to identify these genes can assist us to further understand the process of carcinogenesis and provide potential drug targets for cancer treatment. In this article, we implemented a method developed by Zhang et al[29] to a publicly available gene expression data collected using the microarray technology, which has been widely used to study the
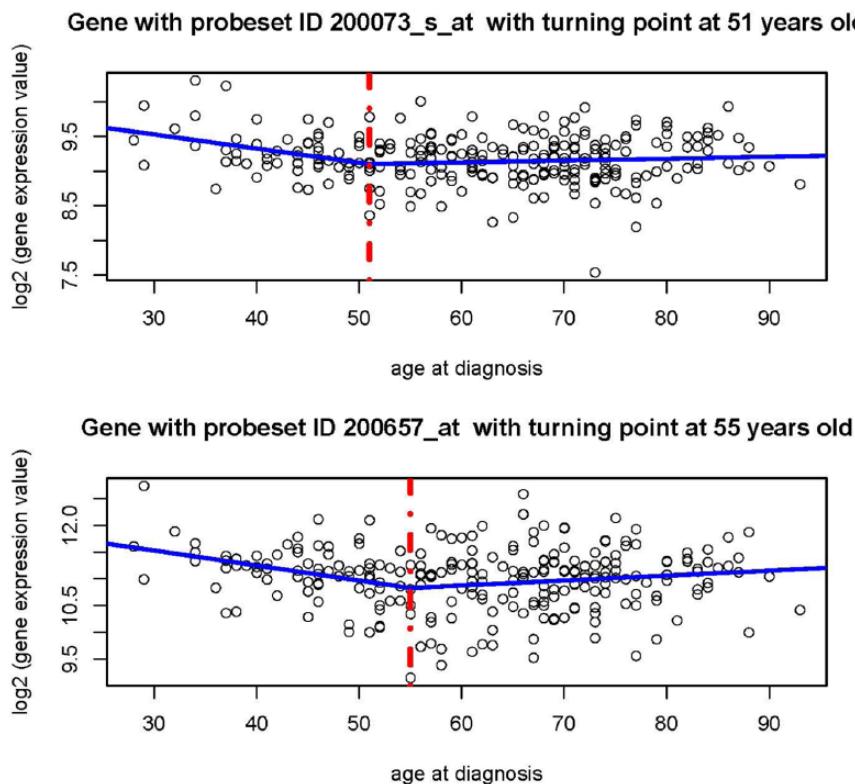
Figure 1. Examples of genes (probe sets) with expressions changing after diagnosis.
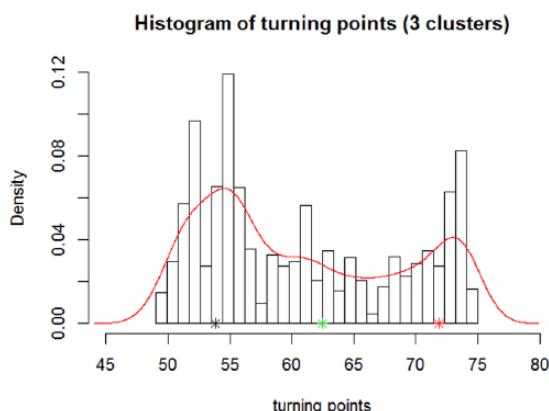
Figure 2. Distribution of the identified turning points and the grouping results from K-means clustering.

biomedical problems, particularly in cancer research in the past 20 years.

Our approach successfully identified genes that vary expressions before and after the diagnosis of breast cancer. The networks analysis by IPA shows that many of the identified or associated genes play important roles in the process of cancer development and progression. For instance, the tumor suppressor gene *p53* and the transforming growth factor *TGFB1* have been demonstrated to be associated with breast cancer risk in many studies.[32-36] Figures 3 and 4 show the regulator networks of these 2 factors from Ingenuity.

In addition to the genes, our approach can also identify networks or functions that are associated with breast cancer risk. For instance, we found that "Cancer" is among the top 5 disease and disorder functions, and *GnRH* signaling is among the top 5 canonical pathways for many clustered groups (Tables 2 and 3), whereas there is evidence showing that *GnRH* signaling is associated with risks of many types of cancers.[37–39]

For comparisons, we also separated the genes according to the sign of their turning points after clustering analysis and then re-ran the IPA. The results are uploaded as supplemental data.

The ideal data set to study this kind of problems is the one that collects longitudinal measurements for each gene from the same patient and the time spectrum should cover disease diagnosis. In addition, to have enough power, the study must have adequate sample size (eg, in the minimal range of several hundreds). However, this kind of data set is difficult to be obtained even though the cost for each array (or gene chip) has been greatly reduced nowadays. Our study findings show that the measurements of a gene expression from different patients can be pooled together to study the change of expression before and after disease diagnosis.

One of the study limitations is the lack of modeling covariates in the discovery of turning points, which will be one of our future research areas. In addition, we plan to apply the approaches demonstrated in this study to the data sets of other

Table 2. Top 5 canonical pathways identified by Ingenuity Pathway Analysis.

CLUSTER	NAME	*P* VALUE[a]	RATIO[b]
All	*GnRH* signaling	1.03E–07	27/153 (0.176)
	RAR activation	6.78E–07	31/195 (0.159)
	Role of NFAT in regulation of the immune response	8.83E–06	28/200 (0.14)
	UVC-induced MAPK signaling	1.25E–05	12/44 (0.273)
	Aryl hydrocarbon receptor signaling	1.73E–05	24/171 (0.14)
Group 1	Inhibition of matrix metalloproteinases	2.56E–05	8/40 (0.2)
	PEDF signaling	4.01E–04	9/79 (0.114)
	VEGF signaling	6.77E–04	10/109 (0.092)
	HIF1a signaling	1.62E–03	10/112 (0.089)
	PI3K/AKT signaling	1.89E–03	11/152 (0.072)
Group 2	T-cell receptor signaling	4.31E–05	9/109 (0.083)
	PKCq signaling in T lymphocytes	1.73E–04	9/144 (0.062)
	Axonal guidance signaling	1.84E–04	19/487 (0.039)
	Acute myeloid leukemia signaling	3.48E–04	7/84 (0.083)
	Reelin signaling in neurons	4.08E–04	7/85 (0.082)
Group 3	*GnRH* signaling	5.61E–07	14/153 (0.092)
	CXCR4 signaling	1.96E–05	13/174 (0.075)
	Androgen signaling	2.22E–05	11/145 (0.076)
	Corticotropin-releasing hormone signaling	2.41E–05	11/145 (0.076)
	NRF2-mediated oxidative stress response	2.57E–05	14/195 (0.072)

[a]Associated *P* value, as calculated using the right-tailed Fisher exact test, is a measure of the likelihood that the association is due to random chance alone.
[b]In the ratio, the numerator is the number of genes in a given pathway that meet the cutoff criteria and the denominator is the total number of genes that make up that pathway and that are in the reference gene set (www.ingenuity.com).

Table 3. Top 5 disease and disorder functions identified by Ingenuity Pathway Analysis.

CLUSTER	NAME	*P* VALUE[a]	NO. OF MOLECULES[b]
All	Cardiovascular disease	2.60E–19-1.14E–05	234
	Cancer	3.88E–15-3.35E–05	1054
	Infections disease	1.13E–12-2.13E–05	225
	Gastrointestinal disease	1.54E–11-3.56E–05	463
	Inflammatory response	3.68E–11-1.91E–05	238
Group 1	Cancer	1.18E–08-4.40E–03	506
	Cardiovascular disease	3.29E–08-3.93E–03	110
	Gastrointestinal disease	5.31E–07-2.35E–03	230
	Infectious disease	1.33E–06-3.98E–03	107
	Organismal injury and abnormalities	3.14E–06-3.91E–03	291
Group 2	Inflammatory response	1.78E–12-2.05E–04	82

(Continued)

Table 3. (Continued)

CLUSTER	NAME	*P* VALUE[a]	NO. OF MOLECULES[b]
	Immunologic disease	6.11E–10-8.59E–05	77
	Endocrine system disorders	4.99E–09-1.68E–04	63
	Gastrointestinal disease	4.99E–09-2.04E–04	144
	Metabolic disease	4.99E–09-1.32E–04	62
Group 3	Cardiovascular disease	1.83E–09-4.15E–03	76
	Cancer	5.08E–08-5.64E–03	317
	Organismal injury and abnormalities	5.08E–08-5.48E–03	168
	Reproductive system disease	5.08E–08-5.48E–03	157
	Inflammatory response	1.34E–05-5.47E–03	45

[a]Associated *P* value, as calculated using the right-tailed Fisher exact test, is a measure of the likelihood that the association is due to random chance alone.
[b]Total number of genes that are known to be associated with that process in the selected reference set (www.ingenuity.com).

Table 4. Top 5 molecular and cellular functions identified by Ingenuity Pathway Analysis.

CLUSTER	NAME	*P* VALUE	NO. OF MOLECULES
All	Cellular growth and proliferation	1.20E–35-3.56E–05	519
	Cell death and survival	4.85E–26-3.03E–05	478
	Cellular movement	2.74E–23-3.32E–05	318
	Cell morphology	3.52E–20-3.37E–05	375
	Cellular development	3.52E–19-3.56E–05	459
Group 1	Cellular growth and proliferation	3.28E–15-4.47E–03	237
	Cell death and survival	5.06E–13-4.27E–03	229
	Cell morphology	2.49E–12-4.49E–03	180
	Cellular development	9.97E–11-4.47E–03	211
	Cellular movement	6.04E–10-3.99E–03	150
Group 2	Cellular function and maintenance	1.02E–14-2.02E–04	120
	Cellular growth and proliferation	1.78E–14-1.60E–04	150
	Cell death and survival	7.19E–14-2.13E–04	142
	Cellular development	3.04E–13-2.11E–04	124
	Cellular movement	6.16E–13-2.02E–04	95
Group 3	Cellular growth and proliferation	2.37E–11-4.72E–03	160
	Cellular development	1.54E–06-5.14E–03	141
	Gene expression	1.59E–06-4.80E–03	101
	Cellular movement	2.56E–06-5.47E–03	92
	Molecular transport	2.95E–06-5.41E–03	107

Table 5. Top 5 networks identified by Ingenuity Pathway Analysis.

CLUSTER	ASSOCIATED NETWORK FUNCTIONS	SCORE[a]
All	RNA posttranscriptional modification, protein synthesis, gene expression	43
	DNA replication, recombination, and repair, hereditary disorder, respiratory disease	42
	Hereditary disorder, skeletal and muscular disorders, connective tissue disorders	40
	Connective tissue disorders, developmental disorder, hereditary disorder	38
	Cell signaling, cardiac dysfunction, cardiovascular disease	36
Group 1	Developmental disorder, hereditary disorder, ophthalmic disease	53
	RNA posttranscriptional modification, molecular transport, RNA trafficking	51
	Cell morphology, cellular assembly and organization, hair and skin development and function	41
	Carbohydrate metabolism, lipid metabolism, posttranslational modification	41
	Nucleic acid metabolism, small molecule biochemistry, cell morphology	38
Group 2	Hereditary disorder, respiratory disease, cell cycle	46
	Cellular movement, hematological system development and function, immune cell trafficking	46
	Posttranslational modification, lymphoid tissue structure and development, organ morphology	37
	Cellular development, cellular growth and proliferation, hematological system development and function	34
	RNA damage and repair, developmental disorder, hereditary disorder	34
Group 3	Amino acid metabolism, drug metabolism, molecular transport	54
	Cell cycle, nervous system development and function, carbohydrate metabolism	48
	Cell-to-cell signaling and interaction, organismal injury and abnormalities, reproductive system disease	34
	Cellular compromise, neurological disease, organismal injury and abnormalities	33
	Cell signaling, molecular transport, nucleic acid metabolism	28

[a]Also called P score, equaling to $-\log_{10}(P$ value) (www.ingenuity.com).

Table 6. Identified top 5 upstream regulators via Ingenuity Pathway Analysis for the 3 clusters of genes with expressions after diagnosis.

Table 6. (Continued)

CLUSTER	NAME	P VALUE OF OVERLAP[a]
All	*TGFB1*	2.13E–25
	TP53	1.76E–24
	Dexamethasone	1.77E–19
	Lipopolysaccharide	5.78E–17
	Tretinoin	9.83E–17
Group 1	*TP53*	2.10E–16
	ERBB2	1.00E–13
	TGFB1	4.07E–13
	MYC	6.55E–12
	Tretinoin	9.87E–09

CLUSTER	NAME	P VALUE OF OVERLAP[a]
Group 2	*TGFB1*	1.08E–12
	Lipopolysaccharide	3.94E–11
	CTNNB1	2.95E–10
	CD40LG	3.12E–10
	IL4	5.16E–10
Group 3	Dexamethasone	8.03E–11
	GNRH1	6.45E–08
	Pentobarbital	9.70E–08
	U0126	1.28E–07
	TGFB1	2.27E–07

[a]Associated P value, as calculated using the right-tailed Fisher exact test, is a measure of the likelihood that the association is due to random chance alone.
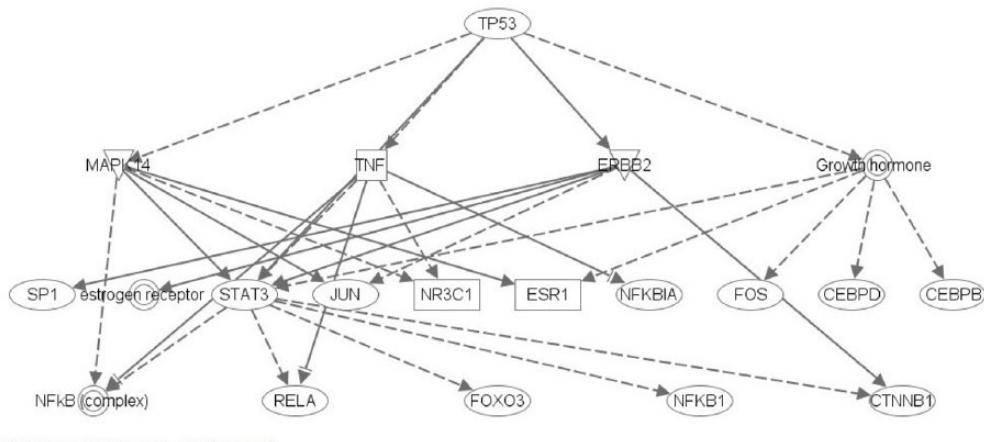
Figure 3. *P53*-mediated regulatory network via Ingenuity pathway analysis.
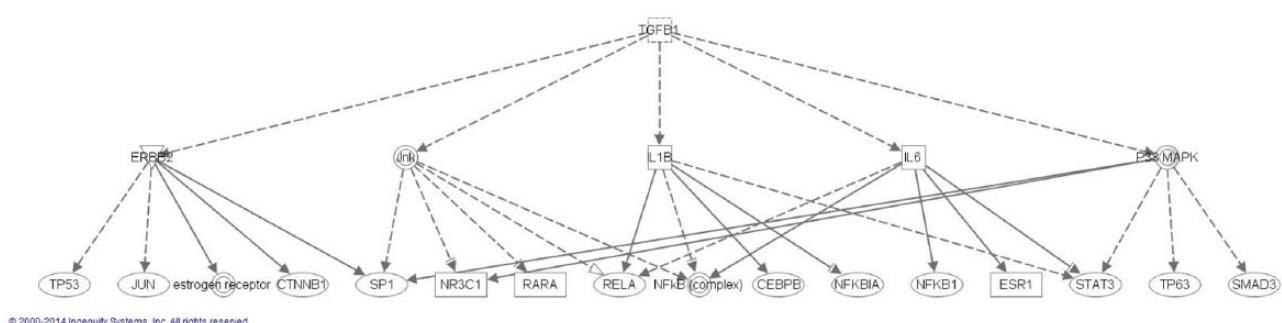
Figure 4. *TGFB1*-mediated regulatory network via Ingenuity pathway analysis.

cancer types, aiming at the search of common genes that vary expressions before and after diagnosis.

Conclusions

In this article, we implemented the nonparametric MASAL method to a publicly available gene expression data and successfully identified genes with expressions varying before and after breast cancer diagnosis.

Author Contributions

Both authors contributed to the conception and design; acquisition, analysis, and interpretation; drafting and review for important intellectual content; and final approval of the manuscript.

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Appendix 1. MASAL-identified Affymetrix probe sets with expressions varying after age at diagnosis.

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
1053_at	RFC2	1	0.020681276	72.3	3
1598_g_at	GAS6	−1	−0.008053943	55	1
160020_at	MMP14	−1	−0.011322456	55	1
1773_at	FNTB	−1	−0.002193251	54.9	1
1861_at	BAD	1	0.010791492	70.4	3
200028_s_at	STARD7	1	0.005183494	58	2
200036_s_at	RPL10A	1	0.003705597	63	2
200037_s_at	CBX3	1	0.003587988	50	1
200044_at	SRSF9	1	0.01270005	73	3
200052_s_at	ILF2	1	0.043362306	52	1
200056_s_at	C1D	1	0.002181049	52	1
200073_s_at	HNRNPD	1	0.02292864	51	1
200093_s_at	HINT1	1	0.0104039	66	2
200602_at	APP	1	0.010212558	65	2
200635_s_at	PTPRF	1	0.006969099	60	2
200636_s_at	PTPRF	1	0.007848957	63	2
200657_at	SLC25A5	1	0.037173266	55	1
200666_s_at	DNAJB1	1	0.012460043	73	3
200689_x_at	EEF1G	1	0.01478889	57	1
200695_at	PPP2R1A	−1	−0.004944177	65	2
200705_s_at	EEF1B2	1	0.020593807	57	1
200710_at	ACADVL	−1	−0.025771474	65	2
200736_s_at	GPX1	−1	−0.006516818	60	2
200738_s_at	PGK1	1	0.033401009	55	1
200750_s_at	RAN	1	0.041425598	55	1
200771_at	LAMC1	−1	−0.015436438	54	1
200783_s_at	STMN1	1	0.045718824	53.7	1
200784_s_at	LRP1	−1	−0.005880175	55.3	1
200785_s_at	LRP1	−1	−0.008523049	54	1
200786_at	PSMB7	1	0.029847546	51	1
200788_s_at	PEA15	−1	−0.007831258	70	3
200795_at	SPARCL1	−1	−0.041157133	74	3
200807_s_at	HSPD1	1	0.028066123	55	1
200808_s_at	ZYX	−1	−0.014372135	54	1
200818_at	ATP5O	1	0.003839639	52	1
200819_s_at	RPS15	1	0.007997715	74.5	3
200853_at	H2AFZ	1	0.05005612	52	1

Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
200875_s_at	NOP56	1	0.030448859	50.2	1
200877_at	CCT4	1	0.029883176	57	1
200889_s_at	SSR1	1	0.040855268	51.2	1
200890_s_at	SSR1	1	0.031121157	51	1
200896_x_at	HDGF	1	0.018880304	58	2
200897_s_at	PALLD	−1	−0.011491548	54	1
200902_at	15-Sep	1	0.027031625	63	2
200933_x_at	RPS4X	−1	−0.00555147	71	3
200970_s_at	SERP1	1	0.00857823	52.4	1
200971_s_at	SERP1	1	0.005917433	62	2
200988_s_at	PSME3	1	0.007179842	63	2
200992_at	IPO7	1	0.025406503	55	1
201006_at	PRDX2	1	0.002914926	54	1
201014_s_at	PAICS	1	0.051963932	54.5	1
201016_at	EIF1AX	1	0.031636083	52	1
201023_at	TAF7	1	0.011593772	68	3
201024_x_at	EIF5B	1	0.004750074	60.8	2
201029_s_at	CD99	−1	−0.009854727	54	1
201030_x_at	LDHB	1	0.053360252	52	1
201050_at	PLD3	−1	−0.005658197	65	2
201062_at	STOM	1	0.003262134	70	3
201086_x_at	SON	1	0.003419623	52	1
201104_x_at	NBPF10 (includes others)	−1	−0.011681326	72	3
201139_s_at	SSB	1	0.0184685	61	2
201141_at	GPNMB	−1	−0.021816381	61	2
201144_s_at	EIF2S1	1	0.022663874	55	1
201147_s_at	TIMP3	−1	−0.02833933	71.5	3
201148_s_at	TIMP3	−1	−0.002902471	54	1
201149_s_at	TIMP3	−1	−0.022775209	74	3
201150_s_at	TIMP3	−1	−0.049189245	54	1
201168_x_at	ARHGDIA	−1	−0.004970239	55	1
201175_at	TMX2	1	0.006777243	63	2
201177_s_at	UBA2	1	0.024407593	54.3	1
201196_s_at	AMD1	1	0.043963426	55	1
201197_at	AMD1	1	0.040959323	55	1
201201_at	CSTB	1	0.033261882	55	1

(Continued)

Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
201216_at	ERP29	1	0.011098955	70	3
201231_s_at	ENO1	1	0.031189763	55	1
201232_s_at	PSMD13	1	0.01111751	74	3
201234_at	ILK	−1	−0.003144894	55	1
201245_s_at	OTUB1	1	0.003820789	74	3
201260_s_at	SYPL1	1	0.009983251	68	3
201261_x_at	BGN	−1	−0.04932235	54	1
201263_at	TARS	1	0.028018948	55	1
201271_s_at	RALY	−1	−0.005714608	59	2
201272_at	AKR1B1	−1	−0.009412233	60	2
201273_s_at	SRP9	1	0.008086363	63	2
201279_s_at	DAB2	−1	−0.018470922	68	3
201283_s_at	TRAK1	−1	−0.016925341	52	1
201287_s_at	SDC1	−1	−0.014567094	54	1
201305_x_at	ANP32B	1	0.021924737	56.8	1
201306_s_at	ANP32B	1	0.024286511	54.7	1
201307_at	11-Sep	−1	−0.012429495	55	1
201316_at	PSMA2	1	0.003770473	52	1
201320_at	SMARCC2	−1	−0.015268803	52.2	1
201327_s_at	CCT6A	1	0.039685934	55	1
201341_at	ENC1	−1	−0.01665097	66	2
201354_s_at	BAZ2A	−1	−0.015447677	52	1
201360_at	CST3	−1	−0.03540076	64.4	2
201380_at	CRTAP	−1	−0.022269788	52	1
201407_s_at	PPP1CB	1	0.028433653	55	1
201408_at	PPP1CB	1	0.006901016	68	3
201410_at	PLEKHB2	1	0.012275124	67	3
201429_s_at	RPL37A	1	0.00104462	65	2
201432_at	CAT	−1	−0.011763311	70	3
201436_at	EIF4E	1	0.020840302	73.9	3
201439_at	GBF1	−1	−0.014192232	56	1
201447_at	TIA1	−1	−0.01124382	70	3
201458_s_at	BUB3	1	0.016891504	74	3
201466_s_at	JUN	−1	−0.022070725	72	3
201478_s_at	DKC1	1	0.02896628	56	1
201479_at	DKC1	1	0.02821084	56	1
201485_s_at	RCN2	1	0.03300275	55	1

Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
201486_at	RCN2	1	0.029454957	55.1	1
201501_s_at	GRSF1	1	0.008161561	51	1
201512_s_at	TOMM70A	1	0.02304052	55	1
201513_at	TSN	1	0.008621802	66	2
201519_at	TOMM70A	1	0.008739077	71	3
201520_s_at	GRSF1	1	0.003069883	54.9	1
201527_at	ATP6V1F	−1	−0.003527568	65	2
201554_x_at	GYG1	1	0.005254759	52	1
201569_s_at	SAMM50	1	0.01672354	73	3
201573_s_at	ETF1	1	0.030071188	51	1
201575_at	SNW1	1	0.00956705	73	3
201586_s_at	SFPQ	1	0.025422757	52	1
201595_s_at	ZC3H15	1	0.025020305	55	1
201626_at	INSIG1	1	0.007555377	52	1
201649_at	UBE2L6	−1	−0.004702133	65	2
201652_at	COPS5	1	0.0063026	58	2
201663_s_at	SMC4	1	0.055157191	52.5	1
201664_at	SMC4	1	0.050997144	52	1
201694_s_at	EGR1	−1	−0.031634756	74	3
201701_s_at	PGRMC2	1	0.011350691	63	2
201705_at	PSMD7	1	0.028654668	51.9	1
201712_s_at	RANBP2	1	0.004358294	58	2
201716_at	SNX1	−1	−0.019581259	67	3
201720_s_at	LAPTM5	−1	−0.00929031	60.1	2
201721_s_at	LAPTM5	−1	−0.010700759	61	2
201723_s_at	GALNT1	−1	−0.00497393	55	1
201724_s_at	GALNT1	−1	−0.007921046	55	1
201725_at	CDC123	1	0.027088483	52	1
201727_s_at	ELAVL1	1	0.023873692	52	1
201739_at	SGK1	−1	−0.02199339	74	3
201771_at	SCAMP3	1	0.007411346	69	3
201779_s_at	RNF13	1	0.00571518	57	1
201792_at	AEBP1	−1	−0.019001927	54	1
201816_s_at	GBAS	1	0.008609561	63	2
201839_s_at	EPCAM	1	0.051274578	56	1
201849_at	BNIP3	1	0.006017877	55	1

(Continued)

Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
201851_at	SH3GL1	−1	−0.003700253	61	2
201854_s_at	ATMIN	1	0.020638191	52.8	1
201857_at	ZFR	1	0.020526168	50	1
201895_at	ARAF	−1	−0.018518196	50.2	1
201917_s_at	SLC25A36	1	0.008480415	59	2
201934_at	WDR82	−1	−0.005217775	57.2	1
201938_at	CDK2AP1	1	0.024735476	59	2
201955_at	CCNC	1	0.031096128	53.7	1
201976_s_at	MYO10	1	0.051492329	50	1
201978_s_at	KIAA0141	−1	−0.020504566	73.9	3
201983_s_at	EGFR	1	0.064640163	59	2
201991_s_at	KIF5B	1	0.004574971	63	2
202006_at	PTPN12	1	0.025364075	56	1
202008_s_at	NID1	−1	−0.007412654	56	1
202025_x_at	ACAA1	−1	−0.019827358	51	1
202026_at	SDHD	1	0.02408305	52	1
202035_s_at	SFRP1	1	0.069799732	59	2
202036_s_at	SFRP1	1	0.076835281	59.4	2
202064_s_at	SEL1L	1	0.014944623	74	3
202144_s_at	ADSL	1	0.022940714	55.1	1
202156_s_at	CELF2	−1	−0.023192634	68	3
202157_s_at	CELF2	−1	−0.01738937	61	2
202159_at	FARSA	1	0.010567158	71	3
202175_at	CHPF	−1	−0.006782535	54	1
202177_at	GAS6	−1	−0.01195361	54	1
202192_s_at	GAS7	−1	−0.008056904	54	1
202196_s_at	DKK3	−1	−0.00751908	55	1
202212_at	PES1	1	0.0227084	50.6	1
202219_at	SLC6A8	−1	−0.00396909	66	2
202221_s_at	EP300	1	0.008326634	73	3
202230_s_at	CHERP	1	0.020205875	55	1
202231_at	EIF3M	1	0.025876084	52.5	1
202232_s_at	EIF3M	1	0.028191194	55.1	1
202233_s_at	UQCRH	1	0.036806018	53	1
202249_s_at	DCAF8	−1	−0.016618106	53	1
202266_at	TDP2	1	0.040634836	49.6	1
202273_at	PDGFRB	−1	−0.008631278	54	1

Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
202289_s_at	TACC2	1	0.015048026	60	2
202314_at	CYP51A1	1	0.00998947	58.4	2
202323_s_at	ACBD3	1	0.019312951	70	3
202325_s_at	ATP5J	1	0.012001615	73	3
202365_at	UNC119B	1	0.00585224	62	2
202376_at	SERPINA3	1	0.019952946	61	2
202380_s_at	NKTR	−1	−0.030480851	50.4	1
202383_at	KDM5C	−1	−0.0021561	56	1
202400_s_at	SRF	−1	−0.002250991	50.5	1
202406_s_at	TIAL1	1	0.007876885	71	3
202410_x_at	IGF2	−1	−0.025264003	74.7	3
202413_s_at	USP1	1	0.038263618	52.3	1
202435_s_at	CYP1B1	−1	−0.058406355	74	3
202436_s_at	CYP1B1	−1	−0.047302548	68	3
202461_at	EIF2B2	1	0.011629143	74	3
202465_at	PCOLCE	−1	−0.012421031	55	1
202483_s_at	RANBP1	1	0.032189106	52	1
202497_x_at	SLC2A3	−1	−0.006867739	65	2
202511_s_at	ATG5	1	0.032524818	51	1
202517_at	CRMP1	−1	−0.005307366	66.7	3
202518_at	BCL7B	1	0.002692604	61	2
202522_at	PITPNB	1	0.026613814	49.2	1
202539_s_at	HMGCR	1	0.008878005	63	2
202546_at	VAMP8	1	0.019204029	71	3
202550_s_at	VAPB	1	0.014858762	74.8	3
202614_at	SLC30A9	1	0.018151099	74.7	3
202615_at	GNAQ	−1	−0.011127099	72	3
202633_at	TOPBP1	1	0.025779434	52	1
202634_at	POLR2K	1	0.014849185	74	3
202658_at	PEX11B	1	0.015124819	73	3
202663_at	WIPF1	−1	−0.010005597	60.2	2
202664_at	WIPF1	−1	−0.019435935	60	2
202665_s_at	WIPF1	−1	−0.00708122	60	2
202666_s_at	ACTL6A	1	0.03678377	54.9	1
202685_s_at	AXL	−1	−0.0036812	55	1
202686_s_at	AXL	−1	−0.013042745	54	1

(Continued)

Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
202692_s_at	UBTF	–1	–0.016027066	56	1
202695_s_at	STK17A	–1	–0.003917617	62	2
202701_at	BMP1	–1	–0.004256096	55	1
202706_s_at	UMPS	1	0.008003631	63	2
202710_at	BET1	1	0.00597627	56	1
202723_s_at	FOXO1	–1	–0.00267881	54	1
202724_s_at	FOXO1	–1	–0.011039237	74	3
202741_at	PRKACB	–1	–0.012184324	56	1
202759_s_at	AKAP2	–1	–0.015570223	70.2	3
202765_s_at	FBN1	–1	–0.016645996	55	1
202779_s_at	UBE2S	1	0.05293612	53	1
202780_at	OXCT1	1	0.035030246	51	1
202790_at	CLDN7	1	0.01245907	61	2
202803_s_at	ITGB2	–1	–0.012046636	63	2
202810_at	DRG1	1	0.024958565	52	1
202812_at	GAA	–1	–0.033967722	59	2
202823_at	TCEB1	1	0.003544624	51	1
202826_at	SPINT1	1	0.02127197	68	3
202827_s_at	MMP14	–1	–0.014963159	55	1
202828_s_at	MMP14	–1	–0.013535144	55	1
202830_s_at	SLC37A4	1	0.067323779	71	3
202839_s_at	NDUFB7	1	0.016503055	74	3
202841_x_at	OGFR	–1	–0.002635186	60	2
202843_at	DNAJB9	1	0.006292606	55	1
202851_at	AAGAB	–1	–0.015764738	52	1
202854_at	HPRT1	1	0.032776864	54.7	1
202858_at	U2AF1	1	0.025979855	52.9	1
202880_s_at	CYTH1	–1	–0.004936756	61	2
202912_at	ADM	1	0.054801515	49.7	1
202918_s_at	MOB4	1	0.043684112	51.4	1
202928_s_at	PHF1	–1	–0.016699817	51.8	1
202932_at	YES1	1	0.040487247	56	1
202942_at	ETFB	1	0.021025408	73	3
202944_at	NAGA	–1	–0.006423669	60	2
202946_s_at	BTBD3	1	0.02923497	58	2
202952_s_at	ADAM12	–1	–0.022483138	55	1
202988_s_at	RGS1	–1	–0.015087562	58.9	2

Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
202993_at	ILVBL	1	0.012828406	70.7	3
202998_s_at	LOXL2	−1	−0.01592312	55	1
203003_at	MEF2D	−1	−0.021682388	52	1
203021_at	SLPI	1	0.077246027	55.7	1
203023_at	NOP16	1	0.024511096	56.6	1
203028_s_at	CYBA	−1	−0.011531753	61	2
203066_at	CHST15	−1	−0.043286927	52	1
203067_at	PDHX	1	0.027919956	51.8	1
203085_s_at	*TGFB1*	−1	−0.010198719	59	2
203095_at	MTIF2	1	0.013079616	73	3
203104_at	CSF1R	−1	−0.010145975	68	3
203114_at	SSSCA1	1	0.006800109	62.5	2
203122_at	TRAPPC12	−1	−0.017335373	52	1
203123_s_at	SLC11A2	1	0.005851758	59.9	2
203125_x_at	SLC11A2	1	0.003429626	61	2
203151_at	MAP1A	−1	−0.00473173	61.8	2
203164_at	SLC33A1	1	0.017903859	71	3
203165_s_at	SLC33A1	1	0.014156392	71	3
203167_at	TIMP2	−1	−0.011372948	60	2
203169_at	RGP1	1	0.005596311	62	2
203175_at	RHOG	−1	−0.004416996	61	2
203183_s_at	SMARCD1	−1	−0.005857874	73.3	3
203185_at	RASSF2	−1	−0.015539172	61	2
203211_s_at	MTMR2	1	0.031793613	51	1
203233_at	IL4R	−1	−0.005987249	61	2
203241_at	UVRAG	−1	−0.005431129	51	1
203246_s_at	NPRL2	−1	−0.020863073	59	2
203249_at	EZH1	−1	−0.027496446	74	3
203256_at	CDH3	1	0.065290872	57	1
203273_s_at	TUSC2	−1	−0.012857886	64.2	2
203305_at	F13A1	−1	−0.033861761	72.9	3
203316_s_at	SNRPE	1	0.028376987	55	1
203325_s_at	COL5A1	−1	−0.021093979	55	1
203329_at	PTPRM	−1	−0.021293105	54	1
203332_s_at	INPP5D	−1	−0.006304869	61	2
203345_s_at	MTF2	1	0.02395581	54	1

(Continued)

Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
203369_x_at	PDLIM7	−1	−0.002473961	55.4	1
203370_s_at	PDLIM7	−1	−0.012115468	54	1
203371_s_at	NDUFB3	1	0.004288782	51.8	1
203378_at	PCF11	−1	−0.022078939	69	3
203381_s_at	APOE	−1	−0.017348678	61	2
203382_s_at	APOE	−1	−0.013727972	61	2
203397_s_at	GALNT3	1	0.082726816	58	2
203405_at	PSMG1	1	0.036426414	52	1
203416_at	CD53	−1	−0.009114284	61	2
203417_at	MFAP2	−1	−0.022573531	55	1
203425_s_at	IGFBP5	−1	−0.016945826	66.3	2
203426_s_at	IGFBP5	−1	−0.011863312	67	3
203484_at	SEC61G	1	0.040485148	52	1
203490_at	ELF4	−1	−0.00428746	64.9	2
203497_at	MED1	1	0.047713564	55.6	1
203504_s_at	ABCA1	−1	−0.013581403	70.7	3
203512_at	TRAPPC3	1	0.009626303	71.1	3
203516_at	SNTA1	−1	−0.01160986	57.8	2
203523_at	LSP1	−1	−0.008050058	56	1
203530_s_at	STX4	−1	−0.021954827	58	2
203546_at	IPO13	−1	−0.00418376	67.9	3
203547_at	CD4	−1	−0.006834764	63.9	2
203560_at	GGH	1	0.072762433	55.9	1
203565_s_at	MNAT1	1	0.004915992	55	1
203570_at	LOXL1	−1	−0.074281526	55	1
203588_s_at	TFDP2	1	0.01222868	70.3	3
203592_s_at	FSTL3	−1	−0.021472533	54	1
203593_at	CD2AP	1	0.006463263	53	1
203621_at	NDUFB5	1	0.00666514	54.9	1
203631_s_at	GPRC5B	−1	−0.004342445	71	3
203640_at	MBNL2	1	0.032913613	51	1
203666_at	CXCL12	−1	−0.01316783	68	3
203670_at	TTLL3	−1	−0.020012099	52	1
203696_s_at	RFC2	1	0.023021779	72.7	3
203729_at	EMP3	−1	−0.009794283	59.1	2
203731_s_at	ZKSCAN5	1	0.00391593	72	3
203738_at	C5orf22	1	0.016038087	73	3

Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
203741_s_at	ADCY7	−1	−0.017102989	60.3	2
203751_x_at	JUND	−1	−0.010306135	66.9	3
203780_at	MPZL2	1	0.034637404	55	1
203824_at	TSPAN8	1	0.015091866	63	2
203835_at	LRRC32	−1	−0.031384497	55	1
203842_s_at	MAPRE3	−1	−0.017854778	51	1
203852_s_at	SMN1/SMN2	1	0.014562811	74	3
203856_at	VRK1	1	0.035498691	54	1
203858_s_at	COX10	1	0.002012455	54	1
203859_s_at	PALM	−1	-0.026880933	53	1
203876_s_at	MMP11	−1	−0.02418273	54	1
203878_s_at	MMP11	−1	−0.020555374	54	1
203892_at	WFDC2	1	0.029958032	61	2
203894_at	TUBG2	−1	−0.019421727	55.6	1
203895_at	PLCB4	1	0.039240914	56	1
203896_s_at	PLCB4	1	0.059136586	59	2
203920_at	NR1H3	1	0.004403759	51	1
203925_at	GCLM	1	0.028386172	54.5	1
203940_s_at	VASH1	−1	−0.026545699	52	1
203946_s_at	ARG2	1	0.053282953	49.6	1
203947_at	CSTF3	1	0.015024517	54	1
203956_at	MORC2	1	0.028832189	50	1
203980_at	FABP4	1	0.014723001	60.8	2
203994_s_at	C21orf2	−1	−0.018646531	50	1
203995_at	C21orf2	−1	−0.011477075	51.5	1
204005_s_at	PAWR	1	0.007326329	65.7	2
204023_at	RFC4	1	0.049080667	52.9	1
204036_at	LPAR1	−1	−0.018315819	72.4	3
204038_s_at	LPAR1	−1	−0.00269727	59	2
204040_at	RNF144A	−1	−0.010620366	54	1
204047_s_at	PHACTR2	−1	−0.008589811	65.9	2
204051_s_at	SFRP4	−1	−0.087964459	50	1
204052_s_at	SFRP4	−1	−0.010321952	53	1
204056_s_at	MVK	1	0.00677956	72	3
204067_at	SUOX	−1	−0.022609082	56	1
204084_s_at	CLN5	1	0.010766022	71	3

(Continued)

Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
204103_at	CCL4	−1	−0.013682571	68	3
204110_at	HNMT	1	0.004927683	65	2
204114_at	NID2	−1	−0.017726871	55	1
204122_at	TYROBP	−1	−0.01275846	60	2
204128_s_at	RFC3	1	0.027063344	52	1
204142_at	ENOSF1	−1	−0.013640237	73	3
204145_at	FRG1	1	0.010250574	67	3
204147_s_at	TFDP1	1	0.025717489	52	1
204163_at	EMILIN1	−1	−0.019245045	55	1
204165_at	WASF1	1	0.026926005	55.8	1
204192_at	CD37	−1	−0.009859158	61	2
204193_at	CHKB	−1	−0.015985753	58	2
204195_s_at	PKNOX1	1	0.010637274	74	3
204221_x_at	GLIPR1	−1	−0.007916199	55	1
204239_s_at	NNAT	1	0.001315846	70	3
204244_s_at	DBF4	1	0.055787962	53	1
204253_s_at	VDR	−1	−0.001229849	50	1
204269_at	PIM2	−1	−0.006865356	60	2
204276_at	TK2	−1	−0.019928758	61	2
204278_s_at	EBAG9	1	0.012655716	70	3
204293_at	SGSH	−1	−0.019661171	52.6	1
204302_s_at	CTIF	−1	−0.002116448	54.1	1
204310_s_at	NPR2	−1	−0.013159766	71	3
204348_s_at	AK4	1	0.041175708	61	2
204352_at	TRAF5	−1	−0.039993365	57	1
204357_s_at	LIMK1	−1	−0.005421023	56.5	1
204359_at	FLRT2	−1	−0.034865086	73.2	3
204400_at	EFS	1	0.053054257	61	2
204404_at	SLC12A2	1	0.01676106	64.2	2
204412_s_at	NEFH	−1	−0.01176867	55	1
204461_x_at	RAD1	1	0.008201298	64.4	2
204480_s_at	C9orf16	−1	−0.007424215	58	2
204552_at	INPP4A	−1	−0.003471195	51	1
204559_s_at	LSM7	1	0.032861527	74	3
204568_at	ATG14	−1	−0.024993447	54.9	1
204575_s_at	MMP19	−1	−0.013482207	72.1	3
204593_s_at	MIEF1	1	0.019548906	57	1

Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
204594_s_at	MIEF1	1	0.004021161	65	2
204610_s_at	CCDC85B	–1	–0.003713223	56	1
204619_s_at	VCAN	–1	–0.022266928	54.5	1
204632_at	RPS6KA4	–1	–0.00335559	64	2
204648_at	NPR1	–1	–0.013898033	56	1
204656_at	SHB	1	0.009468115	74	3
204672_s_at	ANKRD6	–1	–0.009739969	54	1
204675_at	SRD5A1	1	0.059084089	63.5	2
204682_at	LTBP2	–1	–0.011097065	53	1
204723_at	SCN3B	–1	–0.008140007	73	3
204726_at	CDH13	–1	–0.008206422	74	3
204734_at	KRT15	1	0.032873475	66	2
204737_s_at		1	0.004383352	73	3
204743_at	TAGLN3	–1	–0.010155455	73.8	3
204774_at	EVI2A	–1	–0.01309641	60	2
204789_at	FMNL1	–1	–0.005796731	63	2
204790_at	SMAD7	–1	–0.005279303	54	1
204793_at	GPRASP1	–1	–0.01086367	70	3
204796_at	EML1	–1	–0.007695864	68	3
204799_at	ZBED4	1	0.035767461	51.8	1
204807_at	TMEM5	1	0.006322376	57	1
204808_s_at	TMEM5	1	0.007146375	57	1
204845_s_at	ENPEP	–1	–0.004164623	59	2
204853_at	ORC2	1	0.00321615	61	2
204876_at	ZNF646	–1	–0.01330087	64	2
204878_s_at	TAOK2	–1	–0.015088459	51	1
204882_at	ARHGAP25	–1	–0.007492541	61	2
204884_s_at	HUS1	–1	–0.00273482	70	3
204887_s_at	PLK4	1	0.023379994	54	1
204900_x_at	SAP30	1	0.053853083	51	1
204904_at	GJA4	–1	–0.014305678	57	1
204905_s_at	EEF1E1	1	0.041595731	55	1
204907_s_at	BCL3	–1	–0.002416961	51	1
204927_at	RASSF7	–1	–0.019048362	55	1
204937_s_at	ZNF274	1	0.012169749	67	3
204939_s_at	PLN	–1	–0.041204082	54	1

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Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
204940_at	PLN	–1	–0.01995354	53	1
204948_s_at	FST	–1	–0.018351809	69	3
204958_at	PLK3	–1	–0.014227281	57	1
204966_at	BAI2	–1	–0.04039057	57	1
204977_at	DDX10	1	0.016448448	53.8	1
204986_s_at	TAOK2	–1	–0.02238088	56	1
205003_at	DOCK4	–1	–0.009100754	61	2
205028_at	TRO	–1	–0.003492832	72	3
205044_at	GABRP	1	0.096363905	57.2	1
205047_s_at	ASNS	1	0.003789336	56.9	1
205050_s_at	MAPK8IP2	–1	–0.01917578	51.8	1
205057_s_at	IDUA	–1	–0.018272163	56	1
205059_s_at	IDUA	–1	–0.038275109	56.8	1
205061_s_at	EXOSC9	1	0.005937668	72	3
205071_x_at	XRCC4	1	0.006418104	70.6	3
205081_at	CRIP1	–1	–0.088742985	49.7	1
205100_at	GFPT2	–1	–0.050080286	73	3
205118_at	FPR1	–1	–0.003457766	74	3
205119_s_at	FPR1	–1	–0.011216048	74	3
205126_at	VRK2	–1	–0.007702051	65	2
205139_s_at	UST	–1	–0.005955717	54	1
205147_x_at	NCF4	–1	–0.008111266	68	3
205161_s_at	PEX11A	1	0.003180745	60	2
205170_at	STAT2	–1	–0.003784776	59	2
205183_at	HNRNPD	1	0.003306205	69	3
205192_at	MAP3K14	–1	–0.014099759	61	2
205212_s_at	ACAP1	–1	–0.015177815	63	2
205219_s_at	GALK2	1	0.001407182	52	1
205222_at	EHHADH	1	0.00263417	49	1
205225_at	ESR1	–1	–0.107436091	59	2
205246_at	PEX13	1	0.023892625	54.3	1
205254_x_at	TCF7	–1	–0.003868772	65	2
205260_s_at	ACYP1	1	0.006477881	62.7	2
205270_s_at	LCP2	–1	-0.00671001	61	2
205277_at	PRDM2	–1	–0.019196922	52.3	1
205281_s_at	PIGA	1	0.020007124	55	1
205284_at	URB2	1	0.020585933	51	1

Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
205303_at	KCNJ8	–1	–0.00264586	73	3
205312_at	SPI1	–1	–0.004971932	61	2
205322_s_at	MTF1	1	0.003082259	62	2
205330_at	MN1	–1	–0.010889158	57	1
205335_s_at	SRP19	1	0.004744561	49.5	1
205346_at	ST3GAL2	–1	–0.002849848	56	1
205350_at	CRABP1	1	0.087149089	54.9	1
205362_s_at	PFDN4	–1	–0.006574282	74	3
205363_at	BBOX1	1	0.055754288	59	2
205369_x_at	DBT	1	0.005492961	71	3
205381_at	LRRC17	–1	–0.053482351	74	3
205407_at	RECK	–1	–0.018957962	55	1
205422_s_at	ITGBL1	–1	–0.097178462	55	1
205452_at	PIGB	–1	–0.021225892	49.7	1
205456_at	CD3E	–1	–0.005916496	61	2
205474_at	CRLF3	–1	–0.0081288	61	2
205480_s_at	UGP2	1	0.027712814	55	1
205505_at	GCNT1	1	0.028543924	55.9	1
205516_x_at	CIZ1	–1	–0.009904011	66	2
205520_at	STRN	1	0.001972291	57.6	1
205538_at	CORO2A	1	0.011461556	73	3
205574_x_at	BMP1	–1	–0.010194308	56	1
205576_at	SERPIND1	–1	–0.001550979	73.5	3
205578_at	ROR2	–1	–0.00502805	56	1
205611_at	TNFSF12	–1	–0.018472384	55	1
205624_at	CPA3	–1	–0.013270626	59	2
205628_at	PRIM2	1	0.011790884	65.4	2
205642_at	CNTRL	–1	–0.008798163	71	3
205644_s_at	SNRPG	1	0.032857013	51.8	1
205646_s_at	PAX6	1	0.015821847	71.9	3
205670_at	GAL3ST1	1	0.004625746	69	3
205677_s_at	DLEU1	1	0.003950744	51	1
205688_at	TFAP4	–1	–0.001631653	65	2
205695_at	SDS	–1	–0.008864128	61	2
205698_s_at	MAP2K6	1	0.015023882	74	3
205700_at	HSD17B6	–1	–0.005742163	59	2

(Continued)

Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
205712_at	PTPRD	−1	−0.005389445	62.1	2
205713_s_at	COMP	−1	−0.101897332	55	1
205721_at	GFRA2	−1	−0.007970229	74	3
205748_s_at	RNF126	1	0.009549439	74	3
205758_at	CD8A	−1	−0.009694084	61	2
205763_s_at	DDX18	1	0.021558314	55	1
205774_at	F12	1	0.021858818	67	3
205779_at	RAMP2	−1	−0.02679669	66	2
205783_at	KLK13	1	0.009974613	70	3
205801_s_at	RASGRP3	−1	−0.011199072	74	3
205821_at	KLRC4-KLRK1/KLRK1	−1	−0.006798137	61	2
205826_at	MYOM2	1	0.052941388	74	3
205878_at	POU6F1	−1	−0.01544202	53	1
205884_at	ITGA4	−1	−0.004121306	61	2
205886_at	REG1B	−1	−0.005250773	73	3
205894_at	ARSE	−1	−0.002588427	51	1
205967_at		1	0.041953197	52	1
205970_at	MT3	1	0.004317994	71	3
205978_at	KL	−1	−0.032470162	66	2
205981_s_at	ING2	1	0.023018873	74.4	3
205990_s_at	WNT5A	−1	−0.035124288	74	3
206007_at	PRG4	−1	−0.006369474	73	3
206025_s_at	TNFAIP6	−1	−0.023182271	54	1
206026_s_at	TNFAIP6	−1	−0.018898325	54	1
206055_s_at	SNRPA1	1	0.030645156	53	1
206060_s_at	PTPN22	−1	−0.004834074	61	2
206091_at	MATN3	−1	−0.008934241	57	1
206101_at	ECM2	−1	−0.020137827	69.7	3
206102_at	GINS1	1	0.064490516	49	1
206115_at	EGR3	−1	−0.021320385	67.9	3
206139_at	PI4KB	1	0.006046644	74	3
206150_at	CD27	−1	−0.007929597	60.2	2
206156_at	GJB5	1	0.004464139	71.9	3
206158_s_at	CNBP	1	0.005355839	66	2
206214_at	PLA2G7	−1	−0.016453404	68	3
206221_at	RASA3	−1	−0.001433115	51	1
206230_at	LHX1	−1	−0.002830329	66	2

Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
206248_at	PRKCE	–1	–0.013383418	73	3
206249_at	MAP3K13	1	0.004803658	63	2
206274_s_at	CROCC	–1	–0.001191974	51	1
206287_s_at	ITIH4	–1	–0.014810388	58	2
206314_at	ZKSCAN7	–1	–0.008470859	70	3
206323_x_at	OPHN1	–1	–0.004852682	66.1	2
206326_at	GRP	–1	–0.01099528	55	1
206357_at	OPA3	1	0.005899953	72	3
206368_at	CPLX2	1	0.000688179	61	2
206388_at	PDE3A	–1	–0.005149366	74	3
206461_x_at	MT1H	1	0.030533241	56	1
206471_s_at	PLXNC1	–1	–0.006363643	62.8	2
206480_at	LTC4S	–1	–0.012875851	56	1
206514_s_at	CYP4F3	–1	–0.001508475	57	1
206539_s_at	CYP4F12	–1	–0.015824049	52	1
206550_s_at	NUP155	1	0.02998634	55	1
206584_at	LY96	–1	–0.015634144	60	2
206601_s_at	HOXD3	–1	–0.014857177	73	3
206615_s_at	ADAM22	–1	–0.004051411	73.3	3
206628_at	SLC5A1	1	0.008937046	68.9	3
206629_at	ADAMTSL2	–1	–0.023316277	53	1
206637_at	P2RY14	–1	–0.010554565	70.5	3
206638_at	HTR2B	–1	–0.006709412	57	1
206639_x_at	HTN1	–1	–0.001871546	52	1
206646_at	GLI1	–1	–0.01935035	49.7	1
206725_x_at	BMP1	–1	–0.002960977	63	2
206786_at	HTN3	1	0.00274593	66	2
206808_at	HNRNPA3P1	–1	–0.001581345	64.9	2
206811_at	ADCY8	1	0.00953088	72.6	3
206823_at	L3MBTL1	–1	–0.005395062	73	3
206825_at	OXTR	–1	–0.020672042	70	3
206833_s_at	ACYP2	1	0.007135824	58	2
206868_at	STARD8	–1	–0.012487841	55.8	1
206932_at	CH25H	–1	–0.034558785	74	3
206960_at	LPAR4	–1	–0.003440098	67	3
207009_at	PHOX2B	1	0.001633269	53	1

(Continued)

Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
207014_at	GABRA2	−1	−0.069222173	74	3
207016_s_at	ALDH1A2	−1	−0.016066386	73	3
207053_at	SLC8A1	−1	−0.002304534	62	2
207062_at	IAPP	1	0.00225073	56.2	1
207092_at	LEP	−1	−0.058120996	72	3
207094_at	CXCR1	1	0.006913387	69	3
207100_s_at	VAMP1	−1	−0.016606556	51.3	1
207120_at	ZNF667	1	0.013535069	67.8	3
207155_at	TBX5	−1	−0.002712364	52	1
207173_x_at	CDH11	−1	−0.024564546	54.7	1
207181_s_at	CASP7	1	0.026029107	74.6	3
207188_at	CDK3	−1	−0.002590327	55	1
207191_s_at	ISLR	−1	−0.016965775	55	1
207192_at	DNASE1L2	−1	−0.012875917	56	1
207238_s_at	PTPRC	−1	−0.011404332	61	2
207286_at	CEP135	1	0.001843094	70.5	3
207300_s_at	F7	−1	−0.046076744	57	1
207338_s_at	ZNF200	1	0.017946576	74	3
207348_s_at	LIG3	−1	−0.003631545	60	2
207405_s_at	RAD17	1	0.012575516	66	2
207410_s_at	TLX2	1	0.003087143	70.8	3
207415_at	PLA2R1	−1	−0.007558278	74.9	3
207426_s_at	TNFSF4	−1	−0.008346775	62	2
207440_at	SLC35A2	−1	−0.003953841	62	2
207464_at	AHCYL1	−1	−0.001529741	55	1
207492_at	NGLY1	−1	−0.006476456	73	3
207496_at	MS4A2	−1	−0.033833968	49.1	1
207514_s_at	GNAT1	−1	−0.008053869	55.6	1
207522_s_at	ATP2A3	−1	−0.044014151	59	2
207574_s_at	GADD45B	−1	−0.0072881	57	1
207576_x_at	OXT	−1	−0.003881851	61	2
207595_s_at	BMP1	−1	−0.007438727	57.6	1
207607_at	ASCL2	1	0.006407305	74	3
207616_s_at	TANK	1	0.024556197	55.4	1
207625_s_at	CBFA2T2	−1	−0.016288182	50.9	1
207638_at	TMPRSS15	−1	−0.008312016	73	3
207643_s_at	TNFRSF1A	−1	−0.006428769	66	2

Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
207668_x_at	PDIA6	1	0.032045331	52.4	1
207671_s_at	BEST1	−1	−0.011261435	65	2
207677_s_at	NCF4	−1	−0.00832035	61	2
207681_at	CXCR3	−1	−0.004335797	61	2
207691_x_at	ENTPD1	−1	−0.00851196	55.6	1
207696_at	FUT9	−1	−0.001874256	67	3
207699_at	ZFHX2	−1	−0.000607455	51.5	1
207704_s_at	GAS7	−1	−0.006256607	55	1
207717_s_at	PKP2	1	0.009926896	65	2
207721_x_at	HINT1	1	0.007954825	63	2
207722_s_at	BTBD2	−1	−0.003551506	50	1
207795_s_at	KLRD1	−1	−0.003341938	61	2
207855_s_at	CLCC1	1	0.013393736	71	3
207926_at	GP5	−1	−0.010217327	61	2
207979_s_at	CD8B	−1	−0.005355289	61	2
207990_x_at	ACRV1	−1	−0.006665125	73	3
208010_s_at	PTPN22	−1	−0.002821009	67.7	3
208021_s_at	RFC1	1	0.010231101	73	3
208033_s_at	ZFHX3	−1	−0.009923495	66.8	3
208100_x_at	SEMA6C	−1	−0.00049193	51	1
208105_at	GIPR	−1	−0.000438796	52	1
208114_s_at	ISG20L2	1	0.00727387	73	3
208117_s_at	LAS1L	1	0.030182479	71	3
208130_s_at	TBXAS1	−1	−0.001401223	52	1
208131_s_at	PTGIS	−1	−0.029359086	73	3
208133_at	RFC1	1	0.003119399	69	3
208143_s_at	EDDM3A	−1	−0.003432941	73	3
208144_s_at		1	0.001626296	64	2
208154_at		−1	−0.00139524	52	1
208165_s_at	PRSS16	1	0.013632485	60	2
208169_s_at	PTGER3	−1	−0.005768259	73.4	3
208175_s_at	DMP1	−1	−0.004354438	73	3
208190_s_at	LSR	1	0.029025324	60	2
208194_s_at	STAM2	1	0.002881214	68.2	3
208199_s_at	ZBTB14	−1	−0.000895816	56	1
208213_s_at	KCNAB1	−1	−0.004891889	74	3

(Continued)

Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
208215_x_at	DRD4	–1	–0.002361482	54	1
208250_s_at	DMBT1	1	0.001444092	52	1
208345_s_at	POU3F1	–1	–0.004731524	65.7	2
208364_at	INPP4A	–1	–0.009000459	73	3
208370_s_at	RCAN1	1	0.062837739	50.5	1
208372_s_at	LIMK1	–1	–0.002858123	51	1
208414_s_at	HOXB3	–1	–0.012479798	63.4	2
208452_x_at	MYO9B	–1	–0.001777873	50	1
208456_s_at	RRAS2	1	0.046101394	50.5	1
208457_at	GABRD	–1	–0.010035931	56	1
208458_at	SCNN1D	–1	–0.011581022	55	1
208461_at	HIC1	–1	–0.003349625	55	1
208467_at	KLF12	–1	–0.002678688	65	2
208476_s_at	FRMD4A	–1	–0.016168686	73	3
208499_s_at	DNAJC3	1	0.005225892	58	2
208592_s_at	CD1E	–1	–0.007666086	74	3
208611_s_at	SPTAN1	–1	–0.02172147	56	1
208657_s_at	09-Sep	–1	–0.007641817	63	2
208672_s_at	SRSF3	1	0.013317061	55	1
208691_at	TFRC	1	0.04033919	55.5	1
208697_s_at	EIF3E	1	0.023686075	58.5	2
208705_s_at	EIF5	1	0.003653447	51	1
208706_s_at	EIF5	1	0.007931368	61.8	2
208708_x_at	EIF5	1	0.033488942	52	1
208720_s_at	RBM39	–1	–0.019522744	51	1
208761_s_at	SUMO1	1	0.022832397	55	1
208762_at	SUMO1	1	0.004750856	67	3
208773_s_at	ANKHD1	1	0.007523255	63	2
208787_at	MRPL3	1	0.022763244	55	1
208794_s_at	SMARCA4	1	0.032681844	51.8	1
208795_s_at	MCM7	1	0.036632162	53.9	1
208800_at	SRP72	1	0.002451576	52	1
208813_at	GOT1	1	0.007617568	55	1
208826_x_at	HINT1	1	0.005648649	56	1
208828_at	POLE3	1	0.023295207	55	1
208850_s_at	THY1	–1	–0.012288702	55	1
208851_s_at	THY1	–1	–0.012651615	55	1

Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
208864_s_at	TXN	1	0.028753944	55	1
208898_at	ATP6V1D	1	0.012541307	73	3
208899_x_at	ATP6V1D	1	0.015272363	73.3	3
208951_at	ALDH7A1	1	0.024999133	58	2
208967_s_at	AK2	1	0.004338227	52	1
208985_s_at	EIF3J	1	0.026684865	52	1
208993_s_at	PPIG	1	0.007319788	61	2
208995_s_at	PPIG	1	0.008003221	68	3
209012_at	TRIO	–1	–0.003744283	55	1
209019_s_at	PINK1	–1	–0.019754583	52	1
209025_s_at	SYNCRIP	1	0.04405723	51	1
209030_s_at	CADM1	–1	–0.017108151	69	3
209031_at	CADM1	–1	–0.02736402	69	3
209036_s_at	MDH2	1	0.006879143	55	1
209063_x_at	PAIP1	1	0.023892845	55	1
209070_s_at	RGS5	–1	–0.046263402	70	3
209071_s_at	RGS5	–1	–0.052789333	55	1
209080_x_at	GLRX3	1	0.028263897	52	1
209082_s_at	COL18A1	–1	–0.010733526	54	1
209083_at	CORO1A	–1	–0.010553297	61	2
209085_x_at	RFC1	1	0.008051056	73	3
209096_at	UBE2V2	1	0.036472239	71	3
209107_x_at	NCOA1	–1	–0.016644864	69.2	3
209121_x_at	NR2F2	–1	–0.054074605	51	1
209135_at	ASPH	1	0.018551371	60.1	2
209146_at	MSMO1	1	0.008272903	51	1
209156_s_at	COL6A2	–1	–0.028955898	54.9	1
209166_s_at	MAN2B1	–1	–0.008978846	61	2
209168_at	GPM6B	1	0.02187284	57	1
209188_x_at	DR1	1	0.025302611	52	1
209189_at	FOS	–1	–0.037035686	72.8	3
209193_at	PIM1	–1	–0.008588493	61	2
209201_x_at	CXCR4	–1	–0.017415947	61	2
209202_s_at	EXTL3	–1	–0.004717695	68	3
209242_at	PEG3	1	0.024486225	65	2
209244_s_at	KIF1C	–1	–0.001769296	51	1
209253_at	SORBS3	–1	–0.021280929	53	1

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Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
209255_at	KLHDC10	1	0.006983006	56	1
209262_s_at	NR2F6	1	0.006432974	52	1
209277_at	TFPI2	−1	−0.017524779	73	3
209278_s_at	TFPI2	−1	−0.026696507	70	3
209280_at	MRC2	−1	−0.005726504	55	1
209304_x_at	GADD45B	−1	−0.00640746	57	1
209306_s_at	SWAP70	1	0.009288531	62.5	2
209325_s_at	RGS16	−1	−0.010130661	67	3
209326_at	SLC35A2	1	0.017461654	74.2	3
209330_s_at	HNRNPD	1	0.027393825	52	1
209342_s_at	IKBKB	−1	−0.02925191	56	1
209348_s_at	MAF	−1	−0.012494096	58	2
209356_x_at	EFEMP2	−1	−0.013382438	54	1
209358_at	TAF11	1	0.028624666	51	1
209359_x_at	LOC100506403	−1	−0.003972161	65	2
209369_at	ANXA3	1	0.059580301	61	2
209386_at	TM4SF1	1	0.013802012	63	2
209392_at	ENPP2	−1	−0.034516294	74	3
209402_s_at	SLC12A4	−1	−0.002661332	55	1
209432_s_at	CREB3	1	0.010306369	74	3
209445_x_at	COA1	1	0.002337002	50	1
209447_at	SYNE1	−1	−0.006870076	60	2
209451_at	TANK	1	0.03210213	50	1
209461_x_at	WDR18	1	0.01027931	71	3
209467_s_at	MKNK1	−1	−0.00499646	68.2	3
209473_at	ENTPD1	−1	−0.007459188	55	1
209479_at	CCDC28A	1	0.003796492	51.9	1
209495_at	CEP250	−1	−0.003282115	63	2
209496_at	RARRES2	−1	−0.010705868	57	1
209498_at	CEACAM1	1	0.056243071	53.4	1
209507_at	RPA3	1	0.014078532	74	3
209513_s_at	HSDL2	1	0.008055285	54	1
209529_at	PPAP2C	1	0.014907304	68	3
209533_s_at	PLAA	1	0.023971334	52.1	1
209534_x_at	AKAP13	−1	−0.004006214	54	1
209559_at	HIP1R	−1	−0.01261672	51	1
209579_s_at	MBD4	1	0.014264271	73	3

Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
209588_at	EPHB2	–1	–0.003574688	61	2
209619_at	CD74	–1	–0.013878358	68	3
209632_at	PPP2R3A	1	0.002493209	50	1
209652_s_at	PGF	–1	–0.017135891	56	1
209670_at	TRAC	–1	–0.01326054	61	2
209671_x_at	TRAC	–1	–0.010355958	64	2
209687_at	CXCL12	–1	–0.028486888	68	3
209690_s_at	DOK4	–1	–0.002087092	55	1
209691_s_at	DOK4	–1	–0.004956545	56	1
209694_at	PTS	1	0.026414648	55	1
209696_at	FBP1	–1	–0.044899243	64	2
209721_s_at	IFFO1	–1	–0.005467695	61	2
209741_x_at	SCAPER	1	0.004190535	58	2
209758_s_at	MFAP5	–1	–0.016007596	60	2
209765_at	ADAM19	–1	–0.010695588	60	2
209773_s_at	RRM2	1	0.065024293	52	1
209775_x_at	SLC19A1	1	0.004778167	71	3
209786_at	HMGN4	1	0.03699426	52	1
209789_at	CORO2B	–1	–0.006275761	55	1
209795_at	CD69	–1	–0.016825007	61	2
209796_s_at	CNPY2	1	0.005805676	55	1
209807_s_at	NFIX	1	0.005837316	53	1
209822_s_at	VLDLR	1	0.043024834	49.3	1
209827_s_at	IL16	–1	–0.00830373	63	2
209842_at	SOX10	1	0.057036791	56.9	1
209879_at	SELPLG	–1	–0.006582818	61	2
209901_x_at	AIF1	–1	–0.008868075	68	3
209903_s_at	ATR	1	0.004761668	50.3	1
209923_s_at	BRAP	1	0.005921927	72	3
209928_s_at	MSC	–1	–0.003465764	54	1
209933_s_at	CD300A	–1	–0.007951109	68	3
209943_at	FBXL4	1	0.01876293	57.3	1
209981_at	CSDC2	–1	–0.003032245	50.5	1
209988_s_at	ASCL1	1	0.00618552	58	2
210004_at	OLR1	–1	–0.008388745	58	2
210039_s_at	PRKCQ	–1	–0.008385406	74.1	3

(Continued)

Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
210044_s_at	LYL1	−1	−0.012756805	62.9	2
210062_s_at	ZNF589	−1	−0.014861534	52	1
210068_s_at	AQP4	1	0.003142272	66.3	2
210072_at	CCL19	−1	−0.049166772	74	3
210078_s_at	KCNAB1	−1	−0.005914121	74	3
210079_x_at	KCNAB1	−1	−0.005771915	73	3
210080_x_at	CELA3A	1	0.005610879	70	3
210089_s_at	LAMA4	−1	−0.003865885	58.7	2
210092_at	MAGOH	1	0.043408119	51.8	1
210104_at	MED6	1	0.019215821	73.4	3
210105_s_at	FYN	−1	−0.015471332	61	2
210115_at	RPL39L	1	0.029804697	55.9	1
210135_s_at	SHOX2	−1	−0.0126403	55	1
210184_at	ITGAX	−1	−0.017269527	61	2
210211_s_at	HSP90AA1	1	0.024342888	58	2
210216_x_at	RAD1	1	0.023888463	49.3	1
210249_s_at	NCOA1	−1	−0.016615135	69	3
210250_x_at	ADSL	1	0.023609115	57	1
210269_s_at	AKAP17A	−1	−0.006282616	54.9	1
210273_at	PCDH7	−1	−0.006754223	54.9	1
210283_x_at	PAIP1	1	0.032059007	55	1
210325_at	CD1A	−1	−0.014495126	74.6	3
210344_at	OSBPL7	−1	−0.008739886	62	2
210365_at	LOC100506403	−1	−0.020282377	73	3
210374_x_at	PTGER3	−1	−0.016392856	74	3
210379_s_at	TLK1	1	0.005219704	67	3
210386_s_at	MTX1	1	0.017618042	74	3
210397_at	DEFB1	1	0.065729279	59.9	2
210421_s_at	SLC24A1	1	0.006264454	70	3
210428_s_at	HGS	−1	−0.003381613	54	1
210443_x_at	OGFR	−1	−0.003040057	62	2
210458_s_at	TANK	1	0.01838736	51	1
210466_s_at	SERBP1	1	0.02631014	51	1
210471_s_at	KCNAB1	1	0.002701012	66	2
210484_s_at	LOC254896	−1	−0.013874527	62.4	2
210486_at	ANKMY1	−1	−0.016221178	50	1
210487_at	DNTT	1	0.003205134	70	3

Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
210495_x_at	FN1	−1	−0.014392289	54	1
210511_s_at	INHBA	−1	−0.017743823	54	1
210520_at	FETUB	1	0.00278198	65	2
210561_s_at	WSB1	−1	−0.004654024	54	1
210573_s_at	POLR3C	1	0.004389308	63.5	2
210615_at	NRP1	−1	−0.00172473	60	2
210622_x_at	CDK10	−1	−0.001715645	50	1
210630_s_at	RAD52	−1	−0.00711312	74	3
210656_at	EED	−1	−0.008473005	67	3
210657_s_at	04-Sep	−1	−0.002303866	55	1
210684_s_at	DLG4	−1	−0.015342255	51	1
210695_s_at	WWOX	−1	−0.025017257	66	2
210697_at	ZNF257	−1	−0.00239865	66	2
210704_at	FEZ2	1	0.003166979	59.1	2
210713_at	ITSN1	−1	−0.000473134	51	1
210720_s_at	NECAB3	−1	−0.033025654	57.1	1
210723_x_at		1	0.002191919	54	1
210757_x_at	DAB2	−1	−0.027956016	68	3
210762_s_at	DLC1	−1	−0.02476512	74	3
210786_s_at	FLI1	−1	−0.008441657	73	3
210817_s_at	CALCOCO2	−1	−0.007626016	67	3
210839_s_at	ENPP2	−1	−0.026938799	74.7	3
210868_s_at	ELOVL6	1	0.01167143	74	3
210872_x_at	GAS7	−1	−0.008580073	73	3
210887_s_at	EVC	−1	−0.004225398	73	3
210888_s_at	ITIH1	1	0.003453366	71	3
210893_at		−1	−0.003519419	73	3
210907_s_at	PDCD10	1	0.003728466	54.6	1
210915_x_at		−1	−0.019336906	61	2
210947_s_at	MSH3	1	0.007550419	68	3
210948_s_at	LEF1	−1	−0.01089517	65	2
210969_at	PKN2	−1	−0.004379973	74.9	3
210972_x_at	TRAC	−1	−0.010779128	61	2
210977_s_at	HSF4	−1	−0.01342623	52	1
210982_s_at	HLA-DRA	−1	−0.018328412	68	3
210983_s_at	MCM7	1	0.044511272	52.8	1

(Continued)

Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
211014_s_at	PML	−1	−0.003233904	65	2
211031_s_at	CLIP2	−1	−0.008191188	54	1
211038_s_at	CROCCP2	−1	−0.01612608	71	3
211056_s_at	SRD5A1	1	0.027688361	56	1
211062_s_at	CPZ	−1	−0.008061463	55	1
211069_s_at	SUMO1	1	0.024293662	51	1
211075_s_at	CD47	1	0.049216445	55.9	1
211101_x_at	LILRA2	−1	−0.01371497	55	1
211156_at	CDKN2A	−1	−0.009984758	66	2
211180_x_at	LOC100506403	−1	−0.004030121	64	2
211213_at	ORC5	−1	−0.003367278	74	3
211225_at	FUT5	1	0.003674053	69.6	3
211275_s_at	GYG1	1	0.005962622	52	1
211325_x_at	DSTNP2	1	0.007453647	62.7	2
211326_x_at	HFE	1	0.005728105	68	3
211327_x_at	HFE	1	0.004652094	70	3
211338_at	IFNA2	−1	−0.004512483	73	3
211339_s_at	ITK	−1	−0.011021042	61	2
211375_s_at	ILF3	1	0.026406653	52	1
211379_x_at	B3GALNT1	1	0.022563132	67.2	3
211382_s_at	TACC2	1	0.012186082	60	2
211411_at		−1	−0.009049674	52	1
211432_s_at	TYRO3	−1	−0.008207197	74	3
211461_at	CSPG4P1Y	−1	−0.001073265	51	1
211499_s_at	MAPK11	−1	−0.015811833	55.1	1
211522_s_at	GNRHR	−1	−0.006160528	74.1	3
211538_s_at	HSPA2	1	0.021762761	62.9	2
211552_s_at	ALDH4A1	−1	−0.002294496	51	1
211591_s_at	PDE4A	−1	−0.008794607	56	1
211623_s_at	FBL	1	0.026764762	52	1
211636_at	IGHM	−1	−0.003018704	64.9	2
211649_x_at	IGHM	−1	−0.00573693	55	1
211654_x_at	HLA-DQB1	−1	−0.013606308	56	1
211668_s_at	PLAU	−1	−0.014584021	60	2
211678_s_at	RNF114	1	0.003562084	74	3
211692_s_at	BBC3	−1	−0.018726492	52	1
211716_x_at	ARHGDIA	−1	−0.004523535	54.5	1

Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
211719_x_at	FN1	−1	−0.013954101	54	1
211747_s_at	LSM5	1	0.036818655	52	1
211754_s_at	SLC25A17	1	0.013215734	74	3
211755_s_at	ATP5F1	1	0.006225798	63	2
211766_s_at	PNLIPRP2	1	0.019987781	70	3
211774_s_at	MMACHC	1	0.00165358	51	1
211796_s_at		−1	−0.018476619	61	2
211813_x_at	DCN	−1	−0.013028591	54.5	1
211835_at	IGKC	−1	−0.003385566	55.4	1
211837_s_at	PTCRA	−1	−0.012116821	56	1
211844_s_at	NRP2	−1	−0.002228732	50	1
211902_x_at	YME1L1	−1	−0.009152665	65	2
211915_s_at		−1	−0.003486376	65	2
211919_s_at	CXCR4	−1	−0.017283194	61	2
211925_s_at	PLCB1	1	0.003951515	69	3
211931_s_at		1	0.026926457	51.1	1
211953_s_at	IPO5	1	0.033498949	51	1
211954_s_at	IPO5	1	0.039625924	52	1
211955_at	IPO5	1	0.034729364	52	1
211958_at	IGFBP5	−1	−0.025158983	65	2
211959_at	IGFBP5	−1	−0.025432438	65	2
211967_at	TMEM123	1	0.040693832	64	2
211969_at	HSP90AA1	1	0.02270214	58	2
211980_at	COL4A1	−1	−0.017478805	74	3
211990_at	HLA-DPA1	−1	−0.012934206	58.6	2
211991_s_at	HLA-DPA1	−1	−0.014401253	64	2
212026_s_at	EXOC7	−1	−0.014108513	59	2
212070_at	GPR56	1	0.043006909	55	1
212081_x_at	PRRC2A	−1	−0.003492793	55	1
212135_s_at	ATP2B4	−1	−0.01678209	72	3
212143_s_at	IGFBP3	−1	−0.038474297	74	3
212146_at	PLEKHM2	−1	−0.004399844	54	1
212160_at	XPOT	1	0.039124699	52	1
212175_s_at	AK2	1	0.026459622	54.3	1
212188_at	KCTD12	−1	−0.021067158	73.4	3
212192_at	KCTD12	−1	−0.025523622	74	3

(Continued)

Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
212223_at	IDS	−1	−0.005250174	53	1
212229_s_at	FBXO21	1	0.012466826	73.8	3
212247_at	NUP205	1	0.02534489	55	1
212271_at	MAPK1	1	0.033518335	52	1
212273_x_at	GNAS	1	0.046939113	74.6	3
212319_at	SGSM2	−1	−0.027089109	53	1
212320_at	TUBB	1	0.024820549	52	1
212325_at	LIMCH1	1	0.012400338	63	2
212330_at	TFDP1	1	0.035072731	52	1
212337_at	TUG1	1	0.019800715	52	1
212340_at	YIPF6	1	0.009547606	69.2	3
212342_at	YIPF6	1	0.006416162	49.6	1
212369_at	ZNF384	−1	−0.002911425	63	2
212378_at	GART	1	0.019685174	54.8	1
212397_at	RDX	1	0.043514985	51.9	1
212398_at	RDX	1	0.029902082	51	1
212413_at	06-Sep	−1	−0.005183082	58	2
212414_s_at	06-Sep	−1	−0.012807475	59.6	2
212432_at	GRPEL1	1	0.014785809	74	3
212434_at	GRPEL1	1	0.018596993	74	3
212457_at	TFE3	−1	−0.003789553	57.3	1
212463_at	CD59	1	0.033150244	58.3	2
212464_s_at	FN1	−1	−0.01583985	54	1
212472_at	MICAL2	−1	−0.010920091	54	1
212473_s_at	MICAL2	−1	−0.01091531	54	1
212477_at	ACAP2	1	0.001264708	58	2
212479_s_at	RMND5A	1	0.021025709	52	1
212486_s_at	FYN	−1	−0.009645805	70	3
212488_at	COL5A1	−1	−0.022952342	54	1
212489_at	COL5A1	−1	−0.022588589	54.2	1
212497_at	MAPK1IP1L	−1	−0.003123877	64.4	2
212499_s_at	MAPK1IP1L	1	0.018427392	63	2
212503_s_at	DIP2C	−1	−0.005173235	55	1
212508_at	MOAP1	1	0.011490513	62	2
212509_s_at	MXRA7	−1	−0.00854846	54	1
212538_at	DOCK9	−1	−0.087989451	69	3
212540_at	CDC34	1	0.013396132	74	3

Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
212568_s_at	DLAT	1	0.030264005	52.1	1
212590_at	RRAS2	1	0.048346164	50.3	1
212599_at	AUTS2	1	0.013600845	52	1
212601_at	ZZEF1	−1	−0.016176772	56.1	1
212610_at	PTPN11	1	0.001710008	51	1
212618_at	ZNF609	−1	−0.005204659	65.3	2
212653_s_at	EHBP1	1	0.02196635	56	1
212670_at	ELN	−1	−0.018679206	55	1
212684_at	ZNF3	1	0.012316804	74	3
212685_s_at	TBL2	1	0.004004428	52	1
212695_at	CRY2	−1	−0.018082692	51.7	1
212701_at	TLN2	−1	−0.010390816	73	3
212703_at	TLN2	−1	−0.006947667	68	3
212713_at	MFAP4	−1	−0.035799844	74	3
212725_s_at	TUG1	1	0.027328819	50.3	1
212730_at	SYNM	1	0.060536725	56.2	1
212747_at	ANKS1A	1	0.019506305	55.5	1
212758_s_at	ZEB1	−1	−0.025542529	74	3
212764_at	ZEB1	−1	−0.013986873	54.5	1
212778_at	PACS2	−1	−0.005260583	55.4	1
212796_s_at	TBC1D2B	−1	−0.006861654	59.8	2
212813_at	JAM3	−1	−0.023007054	74	3
212817_at	DNAJB5	−1	−0.007444418	68	3
212822_at	HEG1	−1	−0.003213803	55.1	1
212854_x_at	NBPF10 (includes others)	−1	−0.008928695	71	3
212880_at	WDR7	−1	−0.025633285	53	1
212884_x_at	APOE	−1	−0.009349407	60	2
212946_at	VWA8	−1	−0.033521291	73.7	3
212948_at	CAMTA2	−1	−0.017933965	53	1
212977_at	ACKR3	−1	−0.014793957	68.3	3
212989_at	SGMS1	−1	−0.007101736	60	2
212998_x_at	HLA-DQB1	−1	−0.014903473	59.9	2
212999_x_at	HLA-DQB1	−1	−0.009265122	61	2
213015_at	BBX	1	0.005627024	59	2
213036_x_at	ATP2A3	−1	−0.036218266	59	2
213042_s_at	ATP2A3	−1	−0.028066718	59	2

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Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
213045_at	MAST3	−1	−0.015860931	60.6	2
213048_s_at	SET	1	0.017862127	58	2
213063_at	ZC3H14	1	0.005713643	65	2
213064_at	ZC3H14	1	0.008284777	65	2
213068_at	DPT	−1	−0.024251781	71	3
213071_at	DPT	−1	−0.029113565	72.2	3
213083_at	SLC35D2	1	0.004320656	67	3
213085_s_at	WWC1	1	0.006220128	61	2
213086_s_at	CSNK1A1	1	0.006594004	55	1
213095_x_at	AIF1	−1	−0.008195471	68	3
213100_at	UNC5B	−1	−0.033320512	56	1
213125_at	OLFML2B	−1	−0.052334516	56.3	1
213129_s_at	GCSH	1	0.039736361	55.4	1
213133_s_at	GCSH	1	0.027856843	55	1
213149_at	DLAT	1	0.029934037	53.7	1
213193_x_at		−1	−0.015360874	61	2
213211_s_at	TAF6L	1	0.006706113	74	3
213241_at	PLXNC1	−1	−0.017773764	56.2	1
213242_x_at	CEP170B	−1	−0.002507612	50	1
213252_at	SH3PXD2A	−1	−0.005284787	54	1
213261_at	TRANK1	−1	−0.007968099	61	2
213273_at	TENM4	−1	−0.020216241	71	3
213295_at	CYLD	−1	−0.02413876	64	2
213310_at		1	0.033057357	55.3	1
213316_at	KIAA1462	−1	−0.031928004	55	1
213324_at	SRC	−1	−0.004419454	62	2
213342_at	YAP1	1	0.025121912	61	2
213404_s_at	RHEB	1	0.029507589	55	1
213406_at	WSB1	−1	−0.001725802	52	1
213416_at	ITGA4	−1	−0.010650963	60	2
213422_s_at	MXRA8	−1	−0.010531186	54	1
213425_at	WNT5A	−1	−0.02238513	73	3
213426_s_at	CAV2	−1	−0.013222911	52	1
213452_at	ZNF184	1	0.023511069	52	1
213504_at	COPS6	1	0.008271966	71	3
213512_at	C14orf79	−1	−0.025919671	50.9	1
213527_s_at	ZNF688	−1	−0.023904557	56	1

Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
213537_at	HLA-DPA1	−1	−0.014591542	64	2
213543_at	SGCD	−1	−0.00993916	58	2
213549_at	PDZD8	1	0.023497436	73	3
213556_at	PINLYP	−1	−0.002759443	61	2
213594_x_at	SRSF10	1	0.021965374	52	1
213612_x_at	NBPF10 (includes others)	−1	−0.008525988	72	3
213652_at	PCSK5	−1	−0.015029506	74	3
213699_s_at	YWHAQ	1	0.022407958	56	1
213701_at	C12orf29	1	0.00693861	56.9	1
213725_x_at	XYLT1	−1	−0.016970277	72	3
213733_at	MYO1F	−1	−0.005760766	63.9	2
213741_s_at	KPNA1	1	0.015642666	71.4	3
213751_at	PPP1R37	−1	−0.002972645	63	2
213754_s_at	PAIP1	1	0.024015176	55	1
213762_x_at	RBMX	1	0.024113096	52	1
213764_s_at	MFAP5	−1	−0.021030174	68.1	3
213765_at	MFAP5	−1	−0.022435507	68	3
213766_x_at	GNA11	1	0.007170277	67	3
213779_at	EMID1	−1	−0.045281954	66	2
213786_at	TAX1BP1	1	0.004693732	50	1
213808_at	ADAM23	−1	−0.004357652	71	3
213831_at	HLA-DQA1	−1	−0.019162046	56	1
213851_at	TMEM110	1	0.007591389	71	3
213852_at	RBM8A	1	0.012281256	62	2
213853_at	DNAJC24	−1	−0.00412684	69	3
213860_x_at	CSNK1A1	1	0.005407885	55	1
213867_x_at	ACTB	−1	−0.002254971	57	1
213868_s_at	DHRS7	1	0.003579356	69	3
213869_x_at	THY1	−1	−0.010362775	55	1
213884_s_at	TRIM3	−1	−0.021433023	53	1
213885_at	TRIM3	−1	−0.028625141	52	1
213891_s_at	TCF4	−1	−0.012765379	55	1
213894_at	THSD7A	−1	−0.027349763	73	3
213905_x_at	BGN	−1	−0.050782441	54	1
213909_at	LRRC15	−1	−0.077983649	54	1
213910_at	IGFBP7	−1	−0.020090519	55	1

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Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
213911_s_at	H2AFZ	1	0.047513134	52	1
213920_at	CUX2	−1	−0.00834383	66	2
213927_at	MAP3K9	1	0.005920611	59	2
213929_at	EXPH5	1	0.006797129	65	2
213931_at	ID2	−1	−0.012538546	52	1
213982_s_at	RABGAP1L	−1	−0.00701747	58	2
213991_s_at	HS3ST1	1	0.002402922	53.6	1
213993_at	SPON1	−1	−0.00915685	54	1
214043_at	PTPRD	−1	−0.007690197	54	1
214045_at	LIAS	1	0.005196844	66	2
214051_at	TMSB15A	1	0.043259178	56	1
214066_x_at	NPR2	−1	−0.007757946	74.7	3
214068_at	BEAN1	−1	−0.003626639	62	2
214085_x_at	GLIPR1	−1	−0.011918309	54.8	1
214102_at		1	0.016612682	65	2
214113_s_at	RBM8A	1	0.015055059	73	3
214123_s_at	NOP14-AS1	−1	−0.014895538	54	1
214173_x_at	URI1	1	0.032902034	55	1
214180_at	MAN1C1	−1	−0.022400037	64	2
214198_s_at	DGCR2	1	0.01155344	73	3
214213_x_at	LMNA	−1	−0.015999996	52	1
214244_s_at	ATP6V0E1	1	0.004683346	66	2
214266_s_at	PDLIM7	−1	−0.005328151	56	1
214274_s_at	ACAA1	−1	−0.02978985	55.8	1
214282_at	CP	1	0.024411577	49.2	1
214286_at	GNAT1	1	0.004546581	69	3
214293_at	11-Sep	−1	−0.005046203	55	1
214298_x_at	06-Sep	−1	−0.011971268	68	3
214304_x_at	SYNM	1	0.003230226	71	3
214317_x_at	RPS9	−1	−0.006120938	74	3
214319_at	FRY	−1	−0.020957681	52	1
214352_s_at	KRAS	1	0.006368268	59	2
214389_at	SLC5A12	−1	−0.001133745	52	1
214391_x_at	PTGER1	−1	−0.003604045	73.2	3
214398_s_at	IKBKE	1	0.004710827	71	3
214418_at	CT62	−1	−0.009292685	64.7	2
214436_at	FBXL2	−1	−0.027305598	49.1	1

Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
214437_s_at	SHMT2	1	0.027548528	53.1	1
214454_at	ADAMTS2	−1	−0.008072743	58	2
214460_at	LSAMP	−1	−0.012128949	74	3
214461_at	LBP	1	0.052680006	52.7	1
214505_s_at	FHL1	−1	−0.014689093	74.9	3
214578_s_at	ROCK1	−1	−0.017127642	74	3
214611_at	GRIK1	1	0.003524213	65	2
214625_s_at	MINK1	−1	−0.001987516	56.8	1
214631_at	ZBTB33	−1	−0.003612663	74	3
214632_at	NRP2	−1	−0.00692042	50	1
214638_s_at	CCNT2	−1	−0.003724041	71	3
214674_at	USP19	−1	−0.014460171	51	1
214700_x_at	RIF1	1	0.025553765	49.3	1
214701_s_at	FN1	−1	−0.012516833	56	1
214710_s_at	CCNB1	1	0.077450716	51.7	1
214755_at	UAP1L1	−1	−0.00465394	56	1
214780_s_at	MYO9B	−1	−0.007012814	67	3
214800_x_at	BTF3	1	0.00772681	62	2
214803_at	CDH6	−1	−0.021533935	57	1
214807_at	PLXDC2	−1	−0.018668324	71.5	3
214812_s_at	MOB1A	−1	−0.003320677	71	3
214816_x_at	C19orf40	1	0.004683365	70	3
214818_at	CCDC57	−1	−0.010056955	52	1
214841_at	CNIH3	−1	−0.005447183	54	1
214918_at	HNRNPM	−1	−0.004664526	73	3
214927_at	ITGBL1	−1	−0.067630171	54.2	1
214953_s_at	APP	1	0.010295245	68	3
214963_at	NUP160	1	0.003745019	68	3
214981_at	POSTN	−1	−0.00868692	54	1
214994_at	APOBEC3F	1	0.006095685	73	3
215009_s_at	THAP9-AS1	1	0.007619789	61.3	2
215030_at	GRSF1	1	0.005114809	56.6	1
215051_x_at	AIF1	−1	−0.010127238	68	3
215064_at	SC5D	−1	−0.009580163	73	3
215077_at	COL3A1	−1	−0.003042343	55	1
215085_x_at	DLEC1	−1	−0.006060785	73	3

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Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
215116_s_at	DNM1	−1	−0.012645746	55	1
215165_x_at	UMPS	1	0.010607779	71.7	3
215175_at	PCNX	−1	−0.009826168	74.8	3
215207_x_at	NUS1	1	0.021447334	52	1
215235_at	SPTAN1	−1	−0.020310924	56	1
215248_at	GRB10	1	0.00513512	63	2
215256_x_at	ARHGAP33	−1	−0.013728325	51	1
215279_at		−1	−0.001055185	52	1
215287_at	STRN	1	0.008442385	62.6	2
215301_at	SYCE1L	−1	−0.007314521	73	3
215329_s_at	CDK11A/CDK11B	−1	−0.004647251	66	2
215332_s_at	CD8B	−1	−0.00507402	68	3
215333_x_at	GSTM1	1	0.015635534	71	3
215351_at	RTCA	−1	−0.001848563	52	1
215358_x_at	ZNF37BP	−1	−0.022009839	52	1
215371_at	MED27	−1	−0.007581119	56	1
215446_s_at	LOX	−1	−0.026444147	57	1
215462_at	PLK3	−1	−0.001137683	51.4	1
215468_at		−1	−0.002527967	70	3
215524_x_at		−1	−0.003066025	61	2
215536_at	HLA-DQB2	−1	−0.033618702	73	3
215572_at		1	0.005176282	72	3
215617_at	SPATS2L	−1	−0.015170777	74	3
215623_x_at	SMC4	1	0.002770016	59	2
215655_at	GRIK2	−1	−0.002499608	73	3
215660_s_at	MAST2	−1	−0.004042937	67	3
215706_x_at	ZYX	−1	−0.008831883	54	1
215728_s_at	ACOT7	1	0.006929538	72	3
215751_at		1	0.000754632	52	1
215768_at		−1	−0.050156605	73	3
215784_at	CD1E	−1	−0.014924132	74	3
215872_at		−1	−0.001370956	73	3
215920_s_at	NPIPB4 (includes others)	−1	−0.004639767	64	2
215927_at	ARFGEF2	1	0.004411749	69	3
215993_at		−1	−0.002529345	71	3
216004_s_at	PKNOX1	−1	−0.00467703	74	3
216033_s_at	FYN	−1	−0.013874183	61	2

Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
216074_x_at	WWC1	1	0.005260519	61	2
216090_x_at		−1	−0.005166272	73	3
216099_at	HTR7P1	−1	−0.009925502	51	1
216119_s_at	SPEF1	−1	−0.017872635	51	1
216149_at	LRRC37BP1	−1	−0.005726623	73	3
216153_x_at	RECK	−1	−0.004341952	62	2
216155_at		−1	−0.007284741	58	2
216180_s_at	SYNJ2	−1	−0.014521411	52	1
216198_at	ATF7IP	−1	−0.009248851	52	1
216200_at	PLEKHM1	−1	−0.001762964	62	2
216254_at	PARVB	−1	−0.001637399	52	1
216272_x_at	SYDE1	−1	−0.002873955	54.1	1
216278_at		−1	−0.003260127	69	3
216300_x_at	RARA	−1	−0.018485268	55	1
216322_at	CD58	−1	−0.004514957	71	3
216338_s_at	YIPF3	1	0.014268943	74	3
216399_s_at	SCAPER	1	0.003181993	58.7	2
216441_at		−1	−0.003982924	73	3
216468_s_at	ZNF682	−1	−0.008991908	74	3
216484_x_at	HDGF	1	0.016702552	69.3	3
216497_at	GSX1	−1	−0.002537367	72	3
216515_x_at		1	0.006316218	73	3
216555_at	PRR14L	1	0.002772094	61	2
216558_x_at		−1	−0.004745949	60	2
216600_x_at	ALDOB	1	0.005729381	70	3
216627_s_at	B4GALT1	1	0.009220322	69	3
216652_s_at	DR1	1	0.029856299	52	1
216683_at		−1	−0.002416538	69	3
216736_at	TM6SF2	−1	−0.013484337	52	1
216741_at		−1	−0.011242339	52	1
216788_at	ZNF443	−1	−0.009792006	67	3
216795_at		−1	−0.005007294	73	3
216798_at	RNH1	1	0.004546005	69	3
216834_at	RGS1	−1	−0.010778235	56.4	1
216835_s_at	DOK1	−1	−0.027201979	52	1
216845_x_at	KMT2D	1	0.005572702	69	3

(Continued)

Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
216860_s_at	GDF11	–1	–0.003671584	63	2
216902_s_at	RRN3P1	–1	–0.008524991	71.5	3
216903_s_at	MICU1	–1	–0.003487697	55	1
216945_x_at	PASK	–1	–0.002674892	61	2
216949_s_at	PKD1	–1	–0.00242239	56	1
216954_x_at	ATP5O	1	0.001796284	51	1
216973_s_at	HOXB7	–1	–0.01149701	68	3
216979_at	NR4A3	–1	–0.012569389	74	3
216987_at	IRF4	1	0.001431595	57	1
217027_x_at		1	0.007717889	74	3
217039_x_at		–1	–0.0024025	63	2
217043_s_at	MFN1	1	0.022380514	55	1
217063_x_at	YME1L1	–1	–0.004053451	73.1	3
217071_s_at	MTHFR	1	0.003243419	71	3
217072_at	CD300A	1	0.004361404	70	3
217076_s_at	HOXD3	–1	–0.002091584	63	2
217092_x_at		1	0.002502026	57	1
217106_x_at	DIMT1	1	0.019899387	56	1
217144_at		1	0.008857692	68.3	3
217165_x_at	MT1F	1	0.033386095	56	1
217178_at	RARG	1	0.004304661	71.8	3
217192_s_at	PRDM1	–1	–0.003283113	55	1
217203_at		–1	–0.011305684	51	1
217220_at	LOC100287387	–1	–0.005528919	73	3
217221_x_at	RBM10	–1	–0.004453757	53.4	1
217229_at	ASB4	–1	–0.007368188	63	2
217256_x_at		–1	–0.008212555	74.7	3
217321_x_at	ATXN3	–1	–0.00092443	51	1
217325_at	KRT3	1	0.006473752	69.9	3
217364_x_at		1	0.010219724	57.5	1
217369_at	IGHG1	–1	–0.013301511	56	1
217386_at		1	0.002773704	69	3
217454_at		–1	–0.001418017	56	1
217461_x_at		1	0.004622861	64	2
217467_at		–1	–0.031537321	73	3
217525_at	OLFML1	–1	–0.010474838	55	1
217549_at		–1	–0.016902963	51	1

Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
217608_at	SREK1IP1	1	0.007319422	63	2
217649_at	ZFAND5	−1	−0.00943295	70.3	3
217680_x_at	RPL10	−1	−0.004440191	74	3
217685_at	SLC16A3	1	0.006519198	69	3
217720_at	CHCHD2	1	0.030229312	52	1
217724_at	SERBP1	1	0.021647058	55	1
217725_x_at	SERBP1	1	0.036447166	52	1
217738_at	NAMPT	1	0.039508234	58.5	2
217739_s_at	NAMPT	1	0.039746814	59	2
217744_s_at	PERP	1	0.045645851	61	2
217761_at	ADI1	1	0.023260139	74	3
217772_s_at	MTCH2	1	0.036122462	52	1
217776_at	RDH11	1	0.008477852	65	2
217817_at	ARPC4	−1	−0.004800569	63.9	2
217820_s_at	ENAH	1	0.079180065	65	2
217848_s_at	PPA1	1	0.028833718	52	1
217870_s_at	CMPK1	1	0.028146503	52	1
217874_at	SUCLG1	1	0.003974768	58	2
217878_s_at	CDC27	1	0.012128334	74	3
217883_at	MMADHC	1	0.012684221	68	3
217890_s_at	PARVA	−1	−0.009141227	70	3
217905_at	MCMBP	1	0.009765596	74.2	3
217938_s_at	KCMF1	1	0.022712468	55.1	1
217968_at	TSSC1	1	0.024243086	74.5	3
217977_at	MSRB1	1	0.006665599	71.6	3
217991_x_at	SSBP3	−1	−0.007457582	70	3
218012_at	TSPYL2	−1	−0.015694457	65.9	2
218027_at	MRPL15	1	0.037496409	54.3	1
218029_at	FAM65A	−1	−0.0014132	55.1	1
218042_at	COPS4	1	0.009346104	63	2
218044_x_at	PTMS	1	0.00585304	72	3
218058_at	CXXC1	−1	−0.001074477	51	1
218073_s_at	NDC1	1	0.046855099	51	1
218092_s_at	AGFG1	1	0.042297542	51	1
218106_s_at	MRPS10	1	0.009629982	67.2	3
218133_s_at	NIF3L1	1	0.008512775	68	3

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Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
218138_at	MKKS	1	0.004356445	50	1
218140_x_at	SRPRB	1	0.00529983	51.6	1
218145_at	TRIB3	1	0.013147311	69	3
218146_at	GLT8D1	−1	−0.020214214	53	1
218148_at	CENPT	−1	−0.003881519	55	1
218162_at	OLFML3	−1	−0.012616076	55.1	1
218163_at	MCTS1	1	0.003338348	51	1
218176_at	MAGEF1	1	0.005682727	53.8	1
218202_x_at	MRPL44	1	0.009052642	74	3
218209_s_at	RPRD1A	1	0.033334819	54	1
218213_s_at	TMEM258	1	0.027850461	51.6	1
218214_at	C12orf44	1	0.013850886	73.5	3
218223_s_at	PLEKHO1	−1	−0.015369652	61	2
218235_s_at	UTP11L	1	0.021948495	51	1
218237_s_at	SLC38A1	1	0.017049255	58	2
218238_at	GTPBP4	1	0.039206443	55	1
218239_s_at	GTPBP4	1	0.033764518	52.5	1
218256_s_at	NUP54	1	0.021777449	62.7	2
218289_s_at	UBA5	1	0.006360044	52	1
218295_s_at	NUP50	1	0.025510519	52	1
218299_at	C11orf24	−1	−0.004693826	56.1	1
218306_s_at	HERC1	−1	−0.010768897	70	3
218324_s_at	SPATS2	1	0.009107394	74	3
218339_at	MRPL22	1	0.003452992	50	1
218349_s_at	ZWILCH	1	0.028963842	52.8	1
218350_s_at	GMNN	1	0.090539674	49.7	1
218353_at	RGS5	−1	−0.06849908	53	1
218375_at	NUDT9	1	0.008292087	62	2
218376_s_at	MICAL1	−1	−0.005680092	60.6	2
218403_at	TRIAP1	1	0.00876893	73	3
218415_at	VPS33B	−1	−0.004468988	69	3
218423_x_at	VPS54	1	0.025069186	51	1
218434_s_at	AACS	1	0.005925656	51	1
218466_at	TBC1D17	−1	−0.022572925	49.4	1
218480_at	AGBL5	1	0.006469892	68.5	3
218482_at	ENY2	1	0.031184219	56	1
218496_at	RNASEH1	1	0.006024942	63.8	2

Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
218497_s_at	RNASEH1	1	0.023449842	55	1
218504_at	FAHD2A	1	0.005433492	58	2
218509_at	LPPR2	−1	−0.015756779	56	1
218527_at	APTX	1	0.030407602	74	3
218530_at	FHOD1	−1	−0.004637787	58	2
218538_s_at	MRS2	1	0.054854641	51	1
218547_at	DHDDS	1	0.003682818	67	3
218581_at	ABHD4	−1	−0.003103683	62	2
218605_at	TFB2M	1	0.006608795	55	1
218622_at	NUP37	1	0.033272889	52	1
218630_at	MKS1	−1	−0.00287743	50	1
218646_at	C4orf27	1	0.004400239	63	2
218648_at	CRTC3	−1	−0.018008062	73.3	3
218656_s_at	LHFP	−1	−0.030250928	74	3
218680_x_at	HYPK	1	0.01651961	74	3
218703_at	SEC22A	1	0.004967959	61	2
218723_s_at	RGCC	−1	−0.033508382	74	3
218735_s_at	ZNF544	1	0.013468712	73	3
218740_s_at	CDK5RAP3	−1	−0.035942024	53	1
218745_x_at	TMEM161A	1	0.013490532	52	1
218759_at	DVL2	−1	−0.013335176	51	1
218772_x_at	TMEM38B	1	0.036635769	58	2
218773_s_at	MSRB2	−1	−0.006449346	62	2
218782_s_at	ATAD2	1	0.062133217	52	1
218811_at	ORAI2	1	0.004203993	70	3
218818_at	FHL3	−1	−0.003678097	54.5	1
218828_at	PLSCR3	−1	−0.004054141	55	1
218833_at	ZAK	1	0.001847066	53.9	1
218868_at	ACTR3B	1	0.034931532	54.9	1
218881_s_at	FOSL2	−1	−0.00341146	65	2
218884_s_at	GUF1	1	0.00875807	73	3
218892_at	DCHS1	−1	−0.015751924	74	3
218897_at	TMEM177	1	0.010832966	71.6	3
218921_at	SIGIRR	−1	−0.031246483	56	1
218934_s_at	HSPB7	−1	−0.018125263	72	3
218936_s_at	CCDC59	1	0.030776075	51	1

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Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
218946_at	NFU1	1	0.005732377	52	1
218963_s_at	KRT23	1	0.019782358	61	2
218980_at	FHOD3	−1	−0.016019284	54	1
218981_at	ACN9	1	0.024026946	56	1
218982_s_at	MRPS17	1	0.042228095	52.4	1
219016_at	FASTKD5	1	0.018950613	52	1
219022_at	C12orf43	1	0.010178248	74	3
219024_at	PLEKHA1	1	0.00611299	55.4	1
219025_at	CD248	−1	−0.009821163	57.2	1
219036_at	CEP70	1	0.014502413	72	3
219039_at	SEMA4C	−1	−0.002269247	51	1
219057_at	RABEP2	−1	−0.015402577	55	1
219070_s_at	MOSPD3	−1	−0.002253036	58	2
219072_at	BCL7C	−1	−0.004537439	59	2
219076_s_at	PXMP2	1	0.00865207	71	3
219077_s_at	WWOX	−1	−0.04927174	69	3
219087_at	ASPN	−1	−0.015292807	50	1
219102_at	RCN3	−1	−0.007567948	54.7	1
219110_at	GAR1	1	0.02889491	56.1	1
219114_at	C3orf18	−1	−0.020362248	49.4	1
219132_at	PELI2	−1	−0.015647912	72.6	3
219135_s_at	LMF1	−1	−0.018075783	55.6	1
219142_at	RASL11B	−1	−0.005031472	50	1
219165_at	PDLIM2	−1	−0.011909653	55	1
219179_at	DACT1	−1	−0.015338324	54	1
219184_x_at	TIMM22	1	0.002780772	50	1
219191_s_at	BIN2	−1	−0.006882356	63	2
219212_at	HSPA14	1	0.027232044	54.4	1
219213_at	JAM2	−1	−0.020671924	73.6	3
219226_at	CDK12	1	0.023315659	55.6	1
219275_at	PDCD5	1	0.028700287	55.1	1
219304_s_at	PDGFD	−1	−0.010084957	58	2
219310_at	SYNDIG1	−1	−0.008880221	58	2
219334_s_at	NABP1	−1	−0.003996031	68	3
219336_s_at	ASCC1	1	0.009693331	73	3
219384_s_at	ADAT1	1	0.011628432	74.1	3
219393_s_at	AKT3	−1	−0.001968733	50	1

Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
219396_s_at	NEIL1	–1	–0.023386427	52	1
219413_at	ACBD4	–1	–0.018733689	52	1
219421_at	TTC33	1	0.017623997	56	1
219433_at	BCOR	–1	–0.021183648	72	3
219458_s_at	NSUN3	1	0.006861184	74.1	3
219463_at	LAMP5	–1	–0.012530418	57	1
219483_s_at	PORCN	–1	–0.014990087	55	1
219494_at	RAD54B	1	0.035470678	50.5	1
219505_at	CECR1	–1	–0.01201401	63.1	2
219513_s_at	SH2D3A	1	0.01535505	74	3
219516_at	TRPV4	1	0.00388411	68	3
219539_at	GEMIN6	1	0.011471613	73	3
219561_at	COPZ2	–1	–0.005679486	55	1
219563_at	LINC00341	–1	–0.025291232	74	3
219593_at	SLC15A3	–1	–0.005564485	60	2
219594_at	NINJ2	–1	–0.014642496	58	2
219612_s_at	FGG	1	0.031005644	72.4	3
219636_s_at	ARMC9	–1	–0.019348722	54	1
219637_at	ARMC9	–1	–0.003525923	57	1
219654_at	PTPLA	1	0.044216126	50.5	1
219655_at	SUGCT	–1	–0.004809382	54	1
219656_at	PCDH12	–1	–0.012750319	55.5	1
219665_at	NUDT18	–1	–0.017568705	56	1
219673_at	MCM9	1	0.001363628	52	1
219676_at	ZSCAN16	1	0.003971955	55	1
219677_at	SPSB1	–1	–0.010878403	54	1
219719_at	HIGD1B	–1	–0.013604533	55	1
219733_s_at	SLC27A5	1	0.009653394	70	3
219773_at	NOX4	–1	–0.007774889	55	1
219778_at	ZFPM2	–1	–0.050650091	55	1
219779_at	ZFHX4	–1	–0.036048877	54	1
219787_s_at	ECT2	1	0.069804572	53.5	1
219795_at	SLC6A14	1	0.059451544	56	1
219817_at	MAPKAPK5-AS1	1	0.002256037	57	1
219833_s_at	EFHC1	–1	–0.039573145	53	1
219842_at	ARL15	–1	–0.017210659	70	3

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Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
219858_s_at	MFSD6	1	0.008366281	67	3
219895_at	TMEM255A	−1	−0.004591626	52	1
219909_at	MMP28	−1	−0.009834701	56	1
219966_x_at	BANP	1	0.009996788	72	3
219978_s_at	NUSAP1	1	0.044934588	52.9	1
219984_s_at	HRASLS	1	0.027322355	54.6	1
220036_s_at	LMBR1L	−1	−0.018847045	51.1	1
220065_at	TNMD	−1	−0.013979848	73	3
220079_s_at	USP48	1	0.002444618	66	2
220084_at	C14orf105	−1	−0.003512562	73	3
220092_s_at	ANTXR1	−1	−0.006140121	55.6	1
220122_at	MCTP1	−1	−0.037684577	71	3
220141_at	C11orf63	−1	−0.007802353	70	3
220145_at	MAP9	1	0.033368677	74	3
220180_at	CCDC68	−1	−0.007915402	71	3
220203_at	BMP8A	−1	−0.002645474	56	1
220232_at	SCD5	−1	−0.006300751	49.8	1
220264_s_at	GPR107	1	0.003458903	65	2
220272_at	BNC2	−1	−0.005688277	54	1
220302_at	MAK	−1	−0.010569391	71	3
220326_s_at	ARHGEF40	−1	−0.005790566	54.5	1
220334_at	RGS17	−1	−0.007677622	73	3
220341_s_at	C5orf45	−1	−0.016726551	50	1
220356_at	CORIN	−1	−0.021207523	72.2	3
220363_s_at	ELMO2	−1	−0.004962166	62	2
220384_at	NME8	−1	−0.004075125	60	2
220425_x_at	ROPN1B	1	0.056350304	56	1
220428_at	CD207	−1	−0.017503513	74	3
220504_at	KERA	−1	−0.003344542	53	1
220560_at	C11orf21	−1	−0.003338083	61	2
220574_at	SEMA6D	−1	−0.012292691	73	3
220608_s_at	ZNF770	−1	−0.004928718	74.2	3
220615_s_at	FAR2	1	0.0222938	73	3
220631_at	OSGEPL1	1	0.004971225	67	3
220639_at	TM4SF20	−1	−0.009180871	67	3
220682_s_at	KLHL5	1	0.002566725	66	2
220702_at	TLK1	−1	−0.006415514	73	3

Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
220725_x_at	DNAH3	–1	–0.003440253	63	2
220732_at	PREX2	–1	–0.007275961	74	3
220750_s_at	LEPRE1	–1	–0.009608172	57	1
220772_at	BPESC1	–1	–0.014933516	73	3
220784_s_at	UTS2	–1	–0.004480871	74	3
220809_at		–1	–0.001255103	59.8	2
220838_at	EXD3	1	0.007755821	74	3
220842_at	AHI1	–1	–0.005004183	71	3
220876_at		–1	–0.00456493	72	3
220892_s_at	PSAT1	1	0.022322764	54	1
220909_at	TRIM46	1	0.00643895	74.1	3
220925_at	NAA35	1	0.005422738	61	2
220990_s_at	VMP1	–1	–0.006327222	59	2
221002_s_at	TSPAN14	–1	–0.004303436	51	1
221011_s_at	LBH	–1	–0.013825576	60	2
221058_s_at	CKLF	–1	–0.004959861	62	2
221145_at		1	0.00295299	69	3
221152_at	COL8A1	–1	–0.004324977	71	3
221163_s_at	MLXIPL	–1	–0.014652863	51.9	1
221182_at	MROH9	–1	–0.007188594	52.5	1
221185_s_at	IQCG	1	0.031648664	55	1
221195_at	RNFT1	–1	–0.002343366	59	2
221205_at		–1	–0.004147991	73	3
221222_s_at	C1orf56	1	0.010273033	74.5	3
221233_s_at	FAM135A	–1	–0.001253822	73	3
221234_s_at	BACH2	–1	–0.01132088	54	1
221246_x_at	TNS1	–1	–0.01575234	75	3
221249_s_at	FAM117A	–1	–0.007472503	65	2
221265_s_at	VWA9	1	0.004431277	71	3
221269_s_at	SH3BGRL3	–1	–0.006585564	58	2
221288_at	GPR22	–1	–0.006422248	74	3
221335_x_at	SMG9	–1	–0.002252513	59	2
221348_at	NPPC	1	0.006625491	73	3
221363_x_at	GPR25	–1	–0.000668896	51	1
221452_s_at	TMEM14B	1	0.041376675	52	1
221461_at	TAS2R9	–1	–0.005278705	73	3

(Continued)

Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
221472_at	SERINC3	–1	–0.020508075	53	1
221509_at	DENR	1	0.017451045	73.7	3
221528_s_at	ELMO2	–1	–0.006116782	62	2
221529_s_at	PLVAP	–1	–0.032433033	56.5	1
221541_at	CRISPLD2	–1	–0.052538828	74	3
221558_s_at	LEF1	–1	–0.018969246	59	2
221570_s_at	METTL5	1	0.027904931	55	1
221587_s_at	C19orf24	1	0.010876699	74	3
221596_s_at	RBM48	1	0.017635231	64.5	2
221646_s_at	ZDHHC11	1	0.041453758	74	3
221660_at	MYL10	–1	–0.011200609	61	2
221666_s_at	PYCARD	–1	–0.048491301	59	2
221667_s_at	HSPB8	1	0.024112897	50	1
221705_s_at	SIKE1	1	0.02348753	57.4	1
221728_x_at	XIST	–1	–0.020766004	73	3
221729_at	COL5A2	–1	–0.023679154	54.1	1
221747_at	TNS1	–1	–0.018001103	72	3
221760_at	MAN1A1	–1	–0.024389119	72	3
221764_at	R3HDM4	–1	–0.003052223	56	1
221769_at	SPSB3	–1	–0.023125999	50	1
221783_at	WIZ	–1	–0.005531713	65	2
221843_s_at	TLDC1	1	0.027168318	56	1
221864_at	ORAI3	–1	–0.022177749	53	1
221866_at	TFEB	1	0.004927553	71	3
221870_at	EHD2	–1	–0.020098833	55	1
221883_at	PKNOX1	1	0.004726421	57.6	1
221887_s_at	DFNB31	–1	–0.018998929	52	1
221900_at	COL8A2	–1	–0.020483792	54	1
221901_at	KIAA1644	–1	–0.002018809	55	1
221909_at	RNFT2	1	0.019203476	74	3
221912_s_at	CCDC28B	–1	–0.006025838	68	3
221915_s_at	RANBP1	1	0.003675824	70	3
221931_s_at	SEH1L	1	0.041303016	51	1
221941_at	PAOX	–1	–0.014487136	51.7	1
221950_at	EMX2	–1	–0.00648209	57.9	2
221988_at	SMIM7	1	0.003813623	57	1
221989_at	RPL10	–1	–0.007752286	50	1

Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
222000_at	C1orf174	1	0.016045832	63	2
222004_s_at	DOCK6	1	0.004087882	69	3
222020_s_at	NTM	−1	−0.006401421	55	1
222059_at	ZNF335	−1	−0.01510821	52	1
222063_s_at	CDS1	−1	−0.003003453	65	2
222106_at	PRND	−1	−0.024655104	58	2
222120_at	ZNF764	−1	−0.012648532	59	2
222135_at	ZNF814	−1	−0.001316715	51.5	1
222146_s_at	TCF4	−1	−0.013213214	54.9	1
222165_x_at	C9orf16	−1	−0.003827897	58	2
222175_s_at	MED15	−1	−0.003114704	57	1
222203_s_at	RDH14	1	0.006846477	63	2
222206_s_at	NCLN	1	0.009297396	74	3
222238_s_at	POLM	−1	−0.019229499	51	1
222249_at		−1	−0.006766395	73.6	3
222255_at	PRX	1	0.00277732	59	2
222295_x_at		1	0.002433314	62	2
222314_x_at	EGOT	−1	−0.039773083	49.3	1
243_g_at	MAP4	−1	−0.006269449	62	2
32402_s_at	SYMPK	1	0.007610969	74	3
32723_at	CSTF1	1	0.013340703	74.1	3
33778_at	TBC1D22A	1	0.010345711	71.2	3
33850_at	MAP4	−1	−0.017267838	51	1
34206_at	ARAP1	−1	−0.013094839	72	3
34210_at	CD52	−1	−0.019592968	62.8	2
34406_at	PACS2	−1	−0.00368313	54.5	1
35626_at	SGSH	−1	−0.029827695	54	1
35776_at	ITSN1	−1	−0.013456537	72.2	3
36004_at	IKBKG	−1	−0.010889908	51	1
36030_at	IFFO1	−1	−0.005529727	60	2
36566_at	CTNS	−1	−0.011971802	59	2
37028_at	PPP1R15A	−1	−0.00855461	72	3
37408_at	MRC2	−1	−0.011140824	55	1
37996_s_at	DMPK	−1	−0.00446131	57	1
38398_at	MADD	−1	−0.010930894	51	1
39582_at	CYLD	−1	−0.021072163	64	2

(Continued)

Appendix 1. (Continued)

PROBE SET	GENE SYMBOL	SIGN[a]	SLOPE	TURNING POINT[b]	GROUP[c]
40465_at	DDX23	1	0.008202074	73	3
41047_at	C9orf16	−1	−0.005828861	59.2	2
41856_at	UNC5B	−1	−0.018779625	58	2
44702_at	SYDE1	−1	−0.00404712	55	1
45297_at	EHD2	−1	−0.02439951	54	1
45749_at	FAM65A	−1	−0.013589662	57	1
45828_at	ATP5SL	1	0.005539981	57	1
46142_at	LMF1	−1	−0.016686081	57.2	1
47069_at	PRR5	−1	−0.004110347	54.8	1
47530_at	C9orf156	1	0.004283289	58.2	2
47553_at	DFNB31	−1	−0.022621359	52	1
48580_at	CXXC1	−1	−0.014208177	52.4	1
51200_at	C19orf60	−1	−0.006060668	66	2
52078_at	TMEM222	−1	−0.013404356	50	1
52169_at	STRADA	−1	−0.010991144	57.2	1
52255_s_at	COL5A3	−1	−0.005362448	57	1
52651_at	COL8A2	−1	−0.013578606	54	1
52837_at	KIAA1644	−1	−0.003742206	54.4	1
52940_at	SIGIRR	−1	−0.025554438	56	1
56197_at	PLSCR3	−1	−0.004310889	58	2
57703_at	SENP5	1	0.016306073	53	1
58780_s_at	ARHGEF40	−1	−0.018234272	69	3
59375_at	MYO15B	−1	−0.027885011	53	1
61734_at	RCN3	−1	−0.014575956	55	1
64408_s_at	CALML4	1	0.007170577	70	3
64899_at	LPPR2	−1	−0.014807756	55	1
65718_at	GPR124	−1	−0.004574818	54.2	1
74694_s_at	RABEP2	−1	−0.031131939	56.4	1
77508_r_at	RABEP2	−1	−0.011363256	55.3	1
89476_r_at	NPEPL1	−1	−0.01217998	62	2
91816_f_at	MEX3D	1	0.034822051	65	2
AFFX-HUMGAPDH/ M33197_5_at	GAPDH	1	0.0413017	52	1
AFFX-r2-Bs-dap-3_at		−1	−0.002687966	73	3

Ages at the tails were excluded to reduce the variations.
[a]Positive indicates the expression is up after diagnosis and negative is the opposite.
[b]Turning point identified by MASAL.
[c]Group identified by K-means.