

**Supplemental Information for:**

**CLASSIFICATION OF PEDIATRIC ACUTE LYMPHOBLASTIC  
LEUKEMIA BY GENE EXPRESSION PROFILING**

Mary E. Ross<sup>1</sup>, Xiaodong Zhou<sup>2</sup>, Guangchun Song<sup>2</sup>, Sheila A. Shurtleff<sup>2</sup>, Kevin Girtman<sup>2</sup>, W.  
Kent Williams<sup>2</sup>, Hsi-Che Liu<sup>2</sup>, Rami Mahfouz<sup>2</sup>, Susana C. Raimondi<sup>2</sup>, Noel Lenny<sup>2</sup>, Anami  
Patel<sup>2</sup>, & James R. Downing<sup>2,\*</sup>

## Table of Contents

### Section I: Patient Dataset

- Diagnostic ALL samples used for class prediction
- Subgroup distribution of ALL cases

### Section II: Methods

- Hybridization of microarrays
- Statistical methods

### Section III: Genetic Subtype Discriminating Genes

- Top 100 chi-square probe sets selected for *BCR-ABL* decision tree format
- Top 100 chi-square probe sets selected for *E2A-PBX1* decision tree format
- Top 100 chi-square probe sets selected for Hyperdiploid >50 decision tree format
- Top 100 chi-square probe sets selected for *MLL* decision tree format
- Top 100 chi-square probe sets selected for T-ALL decision tree format
- Top 100 chi-square probe sets selected for *TEL-AML1* decision tree format
  
- Top 100 chi-square probe sets selected for *BCR-ABL* parallel format
- Top 100 chi-square probe sets selected for *E2A-PBX1* parallel format
- Top 100 chi-square probe sets selected for Hyperdiploid >50 parallel format
- Top 100 chi-square probe sets selected for *MLL* parallel format
- Top 100 chi-square probe sets selected for T-ALL parallel format
- Top 100 chi-square probe sets selected for *TEL-AML1* parallel format

### Section IV: Diagnostic Accuracy

- Training and test set results
- Cross comparison of supervised learning algorithms

### Section V: Comparison of Expression Profiles and Real-time PCR (Taqman)

### Section VI: References

## I: Patient Dataset

132 cases of pediatric ALL were selected from the original 327 diagnostic bone marrow aspirates<sup>1</sup> to reanalyze on the higher density U133A and B microarrays. The selection of cases was based on having sufficient numbers of each subtype to build accurate class predictions, rather than reflecting the actual frequency of these groups in the pediatric population. The list of samples that were used in this reanalysis (Table S1), as well as the subtype distribution (Table S2) are shown below.

BCR-ABL-#1	Hyperdip>50-C18	Pseudodip-#6
BCR-ABL-#2	Hyperdip>50-C21	Pseudodip-C2-N
BCR-ABL-#3	Hyperdip>50-C22	Pseudodip-C3
BCR-ABL-#4	Hyperdip>50-C23	Pseudodip-C5
BCR-ABL-#5	Hyperdip>50-C27-N	Pseudodip-C6
BCR-ABL-#6	Hyperdip>50-C32	Pseudodip-C7
BCR-ABL-#7	Hyperdip>50-R4	Pseudodip-C9
BCR-ABL-#8	Hyperdip47-50-C14-N	Pseudodip-C14
BCR-ABL-#9	Hyperdip47-50-C3-N	Pseudodip-C16-N
BCR-ABL-Hyperdip-#10	Hypodip-#2	Pseudodip-R1-N
BCR-ABL-C1	Hypodip-2M#1	T-ALL-#5
BCR-ABL-R1	Hypodip-C2	T-ALL-#6
BCR-ABL-R2	Hypodip-C5	T-ALL-#7
BCR-ABL-R3	MLL-#1	T-ALL-#8
BCR-ABL-Hyperdip-R5	MLL-#2	T-ALL-#10
E2A-PBX1-#5	MLL-#3	T-ALL-C2
E2A-PBX1-#6	MLL-#4	T-ALL-C6
E2A-PBX1-#9	MLL-#5	T-ALL-C7
E2A-PBX1-#10	MLL-#6	T-ALL-C11
E2A-PBX1-#12	MLL-#7	T-ALL-C15
E2A-PBX1-#13	MLL-#8	T-ALL-C19
E2A-PBX1-2M#1	MLL-2M#1	T-ALL-C21
E2A-PBX1-C2	MLL-2M#2	T-ALL-R5
E2A-PBX1-C3	MLL-C1	T-ALL-R6
E2A-PBX1-C4	MLL-C2	TEL-AML1-#6
E2A-PBX1-C5	MLL-C3	TEL-AML1-#9
E2A-PBX1-C6	MLL-C4	TEL-AML1-#10
E2A-PBX1-C7	MLL-C5	TEL-AML1-#14
E2A-PBX1-C9	MLL-C6	TEL-AML1-2M#1
E2A-PBX1-C10	MLL-R1	TEL-AML1-2M#2

E2A-PBX1-C11	MLL-R2	TEL-AML1-C4
E2A-PBX1-C12	MLL-R3	TEL-AML1-C5
E2A-PBX1-R1	MLL-R4	TEL-AML1-C6
Hyperdip>50-#8	Normal-C1-N	TEL-AML1-C26
Hyperdip>50-#12	Normal-C2-N	TEL-AML1-C28
Hyperdip>50-#14	Normal-C3-N	TEL-AML1-C30
Hyperdip>50-C1	Normal-C4-N	TEL-AML1-C31
Hyperdip>50-C4	Normal-C7-N	TEL-AML1-C32
Hyperdip>50-C6	Normal-C8	TEL-AML1-C33
Hyperdip>50-C8	Normal-C9	TEL-AML1-C34
Hyperdip>50-C11	Normal-C11-N	TEL-AML1-C37
Hyperdip>50-C13	Normal-R1	TEL-AML1-C38
Hyperdip>50-C15	Normal-R2-N	TEL-AML1-C40
Hyperdip>50-C16	Pseudodip-#5	TEL-AML1-R3

Table Key: The nomenclature used in this paper is identical to that used in Yeoh et. al.,<sup>1</sup> and thus should facilitate cross comparisons between the datasets. The nomenclature indicates disease status at the time of the initial study and has not been updated as this dataset was not selected to address the issue of outcome. No analysis has been performed in this study to identify expression profiles associated with outcome.

Subtype Name-C# Dx Sample of patient in CCR

Subtype Name-R# Dx Sample of patient who developed a hematologic relapse

Subtype Name-# Dx Sample used for subgroup classification only

Subtype Name-2M# Dx Sample of patient who later developed 2nd AML

Subtype Name-N Dx Sample in novel group

**Table S2. Subgroup distribution of ALL cases**

Subgroup	Training Set	Test Set
<i>BCR-ABL</i>	11	4
<i>E2A-PBX1</i>	13	5
Hyperdiploid >50	13	4
<i>MLL</i>	15	5
T-ALL	12	2
<i>TEL-AML1</i>	15	5
Other	21	7
Total	100	32

## II: Methods

### Hybridization of microarrays

Hybridization solutions from our previous U95A study had been stored at -80°C since their initial use. These solutions were thawed at 45°C, then microcentrifuged for 2 minutes to remove

any insoluble material from the mixture. The hybridization solutions were added to U133A chips and allowed to hybridize for 16 hours at 45°C. At the end of the incubation period, the hybridization solution was removed from each U133A chip and refrozen. Subsequently, the hybridizations were thawed and hybridized to the U133B chip.

A non-stringent wash buffer (6X SSPE, 0.01% Tween 20) was added to each chip cassette after the hybridization solution was removed and the cassette allowed to equilibrate to room temperature. The microarray cassettes were then placed on the fluidics station and the antibody amplification protocol performed. The arrays were washed at 25°C with the non-stringent buffer followed by a more stringent wash at 50°C with 100 mM MES, 0.1M NaCl<sub>2</sub>, 0.01% Tween 20. The arrays were then stained with Streptavidin Phycoerythrin (SAPE, Molecular Probes, Eugene, OR) for 10 minutes at 25°C. Following another non-stringent wash, the arrays were hybridized for 10 minutes at 25°C with an antibody solution (100 mM MES, 1 M [Na<sup>+</sup>], 0.05% Tween 20, 2 mg/ml BSA, 0.1 mg/ml goat IgG, and 3 µg/ml biotinylated antibody). This solution was removed and the cassettes restained with the SAPE solution.

Arrays were scanned on a laser confocal scanner (Agilent, Palo Alto, CA) and then analyzed with Affymetrix Microarray Suite 5.0 (MAS 5.0). Detection values (present, marginal or absent) were determined by default parameters, and signal values were scaled by global methods to a target value of 500. After completing the scans, the arrays were visually inspected for defects and Affymetrix internal controls were utilized to monitor the success of hybridization, washing, and staining procedures.

### **Statistical methods**

The chi-square metric and the *k*-NN and ANN supervised learning algorithms have been previously described. For more information see <http://www.stjuderresearch.org/data/ALL1/>. The

SVM supervised learning algorithm that was used in this study is available as part of the software package Rv 1.6.0.

To determine the performance of each model using ANN, a confidence threshold was built for each diagnostic subtype utilizing a modification of the method described by Khan et al.<sup>2</sup> Models were built based on a decision tree format where each level of the decision tree contains only two possible distinctions – class and non-class (for example, T verses non-T). At each level, using only samples in the training set, 3 ANN models were built by 3-fold cross validation. The training set samples were then shuffled and 3 additional ANN models were built. This model building process was repeated for a total of 100 times at each step of the decision tree. Then an empirical probability distribution for the ANN output node value was built only for subtype under study, for example, T-ALL at the first step of the decision tree. Only nodal values greater than 0.5 for each subtype were included. For each individual sample in the training set, the 100 validation subtype node values were averaged and compared to threshold. Individual samples were assigned to the subtype under study only when its average subtype nodal value was greater than the 95% confidence threshold. For samples in the test set, subtype nodal values are averaged from all models generated in the 3-fold cross validation. A sample is assigned to the class under study when the average subtype nodal value is greater than the 95% confidence level defined on the training set. A sample not assigned to the subtype will progress to the next level of the decision tree, where the entire process is repeated.

### III: Genetic Subtype Discriminating Genes

The following tables contain a listing of the top 100 probe sets for each diagnostic subtypes ranked by their chi-square value (Tables S3-S8). Each table contains the Affymetrix U133 series probe set number, a gene description, gene symbol, chromosomal location, and primary GenBank reference. Chi-square values were calculated utilizing only the samples in the training set in a differential diagnosis decision tree format as discussed in the text and illustrated in Figure 2 (Tables S3-S8) or by a parallel approach (Tables S9-S14). The calculation of the fold change was done in a parallel format using the total data set and comparing the mean signal value in the class versus the mean signal value in the non-class. The last column indicates whether this gene had previously been identified as a class discriminator using the U95Av2 data (old) or identified as a class discriminator only using the U133 data (new) (Tables S3-S8).

**Table S3. Top 100 chi-square probe sets selected for *BCR-ABL* in decision tree format**

	<b>U133 probe set</b>	<b>Gene description</b>	<b>Gene symbol</b>	<b>Location</b>	<b>GenBank Reference</b>	<b>Chi-square value</b>	<b>BCR-ABL above/below mean</b>	<b>Fold change</b>	<b>old or new</b>
1	241812_at	EST FLJ39877	FLJ39877	2	AV648669	47.4	Above	5.2	new
2	201876_at	Paraoxonase 2	PON2	7q21.3	NM_000305.1	47.2	Above	18.7	old
3	201028_s_at	Antigen identified by monoclonal antibodies 12E7, F21 and O13	MIC2	Xp22.32	U82164.1	44.3	Above	2.6	old
4	200953_s_at	Cyclin D2	CCND2	12p13	NM_001759.1	42.3	Above	3.5	old
5	202947_s_at	glycophorin C (Gerbich blood group)	GYPC	2q14-q21	NM_002101.2	42.3	Above	3.1	old
6	223449_at	Semaphorin 6A	SEMA6A	5q23.1	AF225425.1	42.3	Above	4.3	new
7	201029_s_at	Antigen identified by monoclonal antibodies 12E7, F21 and O13	MIC2	Xp22.32	NM_002414.1	41.2	Above	2.4	old

8	204429_s_at	Solute carrier family 2 (facilitated glucose/fructose transporter), member 5	SLC2A5	1p36.2	BE560461	41.2	Above	5	old
9	210830_s_at	Paraoxonase 2	PON2	7q21.3	AF001602.1	41.2	Above	23.6	old
10	215028_at	Semaphorin 6A	SEMA6A	5	AB002438.1	41.2	Above	4.5	new
11	220024_s_at	Periaxin	PRX	19q13.13-q13.2	NM_020956.1	41.2	Above	8.2	new
12	201906_s_at	HYA22 protein	HYA22	3p21.3	NM_005808.1	41.1	Above	43.4	old
13	209365_s_at	Extracellular matrix protein 1	ECM1	1q21	U65932.1	41.1	Above	6	old
14	238689_at	GPR110 G protein-coupled receptor 110	GPR110	6	BG426455	41.1	Above	10.9	new
15	222154_s_at	DKFZP564A2416 unknown protein with a histone H5 signature.	DKFZP564A2416	2q33.1	AK002064.1	40.4	Above	12.4	new
16	218084_x_at	FXYP domain-containing ion transport regulator 5	FXYP5	19q12-q13.1	NM_014164.2	38	Above	1.5	new
17	212242_at	Tubulin, alpha 1 (testis specific)	TUBA1	2q36.2	AL565074	37	Above	3.2	old
18	201445_at	Calponin 3, acidic	CNN3	1p22-p21	NM_001839.1	36.3	Above	10.8	old
19	202771_at	KIAA0233 gene product	KIAA0233	16q24.3	NM_014745.1	36.3	Above	1.9	old
20	212298_at	Neuropilin 1	NRP1	10p12	BE620457	36.3	Above	13.8	new
21	212458_at	FLJ21897	FLJ21897	2	AW138902	36.3	Above	2.4	new
22	222488_s_at	Dynactin 4 (p62)	DCTN4	5q31-q32	BE218028	36.3	Above	3.6	new
23	222762_x_at	LIM domains containing 1	LIMD1	3p21.3	AU144259	36.3	Above	2.6	new
24	200951_s_at	Cyclin D2	CCND2	12p13	NM_001759.1	35.3	Above	12.7	old
25	204430_s_at	Solute carrier family 2 (facilitated glucose/fructose transporter), member 5	SLC2A5	1p36.2	NM_003039.1	35.3	Above	5.1	old
26	205467_at	Caspase 10, apoptosis -related cysteine protease	CASP10	2q33-q34	NM_001230.1	35.3	Above	3.6	old
27	225660_at	Semaphorin 6A	SEMA6A	5q23.1	W92748	35.3	Above	3.3	new
28	225913_at	FLJ21140 (Ser/Thr protein kinase)	FLJ21140	15	AK025943.1	35.3	Above	2.9	new
29	236489_at	EST		6	AI282097	35.3	Above	16.7	new
30	240173_at	EST		4	AI732969	35.3	Above	10.3	new
31	240499_at	EST		10	AA482221	35.3	Above	1.3	new
32	201310_s_at	P311 protein. Similar to gastrin/cholecystokinin type B receptor.	P311	5q21.3	NM_004772.1	35.2	Below	2.2	new
33	215617_at	FLJ11754	FLJ11754	2	AU145711	35.2	Above	14.4	new
34	242579_at	EST		4	AA935461	35.2	Above	10.2	new
35	202717_s_at	CDC16 cell division cycle 16 homolog	CDC16	13q34	NM_003903.1	34.4	Above	1.1	new
36	205055_at	Integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1)	ITGAE	17p13	NM_002208.3	34.4	Below	2.1	new
37	217967_s_at	Chromosome 1 ORF 24	C1orf24	1q25	AF288391.1	34.4	Above	3.2	new
38	201656_at	Integrin, alpha 6	ITGA6	2q31.1	NM_000210.1	33.9	Above	2.8	new
39	207196_s_at	Nef-associated factor 1	NAF1	5q32-q33.1	NM_006058.1	32.2	Above	1.4	new
40	219315_s_at	hypothetical protein FLJ23058	FLJ20898	16p13.12	NM_024600.1	32.2	Above	5.3	new
41	202123_s_at	V-abl Abelson murine leukemia viral oncogene	ABL1	9q34.1	NM_005157.2	31.4	Above	1.8	old

42	219938_s_at	homolog 1 proline-serine-threonine phosphatase interacting protein 2	PSTPIP2	18q12	NM_024430.1	31.2	Above	5	new
43	228046_at	EST;DKFZp434P0235	DKFZp434P0235	4	AA741243	31.2	Above	1.1	new
44	64064_at	Immune associated nucleotide 4 like 1	IAN4L1	7q36	AI435089	30.9	Above	3.3	new
45	222729_at	F-box and WD-40 domain protein 7 (archipelago homolog, Drosophila)	FBXW7	4q31.23	BE551877	30.5	Above	2.4	new
46	229975_at	EST		4	AI826437	30.5	Above	9.1	new
47	200864_s_at	RAB11A, member RAS oncogene family	RAB11A	15q21.3-q22.31	NM_004663.1	29.7	Above	1.4	old
48	203089_s_at	Protease, serine, 25	PRSS25	2p12	NM_013247.1	29.7	Above	1.7	new
49	205376_at	Inositol polyphosphate-4-phosphatase, type II	INPP4B	4q31.1	NM_003866.1	29.7	Above	12.4	new
50	209229_s_at	KIAA1115 protein	KIAA1115	19q13.42	BC002799.1	29.7	Above	1.3	new
51	219871_at	Hypothetical protein FLJ13197	FLJ13197	4p14	NM_024614.1	29.7	Above	14.5	new
52	222868_s_at	Interleukin 18 binding protein	IL18BP	11q13	AI521549	29.7	Above	7.1	new
53	235988_at	GPR110 G protein-coupled receptor 110	GPR110	6p12.3	AA746038	29.7	Above	15.8	new
54	239273_s_at	Matrix metalloproteinase 28	MMP28	17q11-q21.1	AI927208	29.7	Above	90.5	new
55	206150_at	Tumor necrosis factor receptor superfamily, member 7	TNFRSF7	12p13	NM_001242.1	29.5	Above	3.2	old
56	212203_x_at	Interferon induced transmembrane protein 3 (I-8U)	IFITM3	8q13.1	BF338947	29.5	Above	2.3	old
57	217110_s_at	Mucin 4	MUC4	3q29	AJ242547.1	29.5	Above	47.5	new
58	223075_s_at	hypothetical protein FLJ12783	FLJ12783	9q34.13-q34.3	AL136566.1	29.5	Above	3.9	new
59	229139_at	EST		8	AI202201	29.5	Above	10.8	new
60	229367_s_at	Hypothetical proteins FLJ22690.	FLJ22690	7	AW130536	29.5	Above	3.6	new
61	213093_at	FLJ30869	FLJ30869	Xq28	AI471375	29.1	Above	2.5	new
62	216033_s_at	FYN oncogene related to SRC	FYN	6	S74774.1	29.1	Above	2.7	new
63	202369_s_at	TRAM-like protein	KIAA0057	6p21.1-p12	NM_012288.1	28.7	Above	3.3	new
64	212592_at	immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides	IGJ	4q21	AV733266	28.7	Above	7.9	old
65	219218_at	hypothetical protein FLJ23058	FLJ23058	17q25.3	NM_024696.1	28.7	Below	6.2	new
66	242051_at	EST		Y	AI695695	28.7	Above	2.2	new
67	200655_s_at	Calmodulin 1 (phosphorylase kinase, delta)	CALM1	14q24-q31	NM_006888.1	28.5	Above	1.3	new
68	202794_at	Inositol polyphosphate-1-phosphatase	INPP1	2q32	NM_002194.2	28.4	Above	1.6	new
69	218348_s_at	HSPC055 protein	HSPC055	16p13.3	NM_014153.1	27.7	Below	1.1	new
70	205269_at	Lymphocyte cytosolic protein 2	LCP2	5q33.1-qter	AI123251	26.9	Above	1.6	new
71	238488_at	Ran binding protein 11	LOC51194	5q12.2	BF511602	26.9	Above	2.7	new
72	202242_at	Transmembrane 4 superfamily member 2	TM4SF2	Xq11.4	NM_004615.1	26.6	Above	1.7	new
73	218764_at	Hypothetical protein MGC5363	MGC5363	14q22.1-q22.3	NM_024064.1	26.6	Above	1.7	new
74	224811_at	FLJ30652	FLJ30652	3	BF112093	26.6	Above	1.5	new

75	225799_at	Hypothetical protein MGC4677	MGC4677	2q12.3	BF209337	26.6	Above	2.2	new
76	228297_at	Calponin 3, acidic	CNN3	1p22-p21	AI807004	26.6	Above	4.7	old
77	203508_at	Tumor necrosis factor receptor superfamily, member 1B	TNFRSF1B	1p36.3-p36.2	NM_001066.1	26	Above	2.6	old
78	208071_s_at	Leukocyte-associated Ig-like receptor 1	LAIR1	19q13.4	NM_021708.1	26	Above	2	old
79	209321_s_at	Adenylate cyclase 3.	ADCY3	2p24-p22	AF033861.1	26	Above	2.1	old
80	226345_at	DKFZp434O1317	DKFZp434O1317	10	AW270158	26	Below	1.4	new
81	200863_s_at	RAB11A, member RAS oncogene family	RAB11A	15q21.3-q22.31	AI215102	25.8	Above	1.4	old
82	205270_s_at	Lymphocyte cytosolic protein 2	LCP2	5q33.1-qter	NM_005565.2	25.8	Above	1.6	new
83	208881_x_at	Isopenentenyl-diphosphate delta isomerase	IDI1	10p15.3	BC005247.1	25.8	Below	1.7	new
84	212862_at	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	CDS2	20p13	AL568982	25.8	Above	1.8	new
85	213385_at	Chimerin 2	CHN2	7	AK026415.1	25.8	Above	3	new
86	218013_x_at	Dynactin 4 (p62)	DCTN4	5q31-q32	NM_016221.1	25.8	Above	3.6	new
87	218966_at	Myosin 5C	MYO5C	15q21	NM_018728.1	25.8	Above	1.8	new
88	200742_s_at	Ceroid-lipofuscinosis, neuronal 2, late infantile (Jansky-Bielschowsky disease). A pepstatin-insensitive lysosomal peptidase.	CLN2	11p15	BG231932	25	Above	1.5	new
89	203217_s_at	Sialyltransferase 9	SIAT9	2p11.2	NM_003896.1	25	Above	1.8	new
90	205259_at	Nuclear receptor subfamily 3, group C, member 2	NR3C2	4q31.1	NM_000901.1	25	Above	1.9	new
91	220684_at	T-box 21	TBX21	17q21.2	NM_013351.1	25	Above	3.3	new
92	225244_at	IMAGE3451454: GRASP protein	IMAGE3451454	1q42.13	AA019893	25	Above	2	new
93	239519_at	EST		10	AA927670	25	Above	18.2	new
94	203005_at	Lymphotoxin beta receptor (TNFR superfamily, member 3)	LTBR	12p13	NM_002342.1	24.3	Above	10	new
95	200665_s_at	Secreted protein, acidic, cysteine-rich (osteonectin)	SPARC	5q31.3-q32	NM_003118.1	24.3	Above	9.8	new
96	204004_at	PRKC, apoptosis, WT1, regulator	PAWR	12q21	AI336206	24.3	Above	3	new
97	204576_s_at	KIAA0643 protein	KIAA0643	16p12.3	AA207013	24.3	Above	2	new
98	214255_at	ATPase, Class V, type 10C	ATP10C	15q11-q13	AB011138.1	24.3	Above	9.9	new
99	216985_s_at	Syntaxin 3A	STX3A	11q12.3	AJ002077.1	24.3	Above	12	new
100	48106_at	FLJ20489	FLJ20489	12p11.1	H14241	24.3	Above	2.8	new

**Table S4. Top 100 chi-square probe sets selected for *E2A-PBX1* in decision tree format**

	<b>U133 probe set</b>	<b>Gene description</b>	<b>Symbol</b>	<b>Location</b>	<b>GenBank Reference</b>	<b>Chi-square value</b>	<b>E2A – PBX1 above/below mean</b>	<b>Fold change</b>	<b>old or new</b>
1	201579_at	FAT tumor suppressor homolog 1 (Drosophila)	FAT	4q34-q35	NM_005245.1	88.0	Above	9.9	old
2	201695_s_at	nucleoside phosphorylase	NP	14q13.1	NM_000270.1	88.0	Above	3.8	old
3	204674_at	lymphoid-restricted membrane protein	LRMP	12p12.3	NM_006152.1	88.0	Above	5.8	old
4	205253_at	pre-B-cell leukemia transcription factor 1	PBX1	1q23	NM_002585.1	88.0	Above	3549.2	old
5	212148_at	pre-B-cell leukemia transcription factor 1, splice variant	PBX1	1q23	BF967998	88.0	Above	5283.5	old
6	212151_at	pre-B-cell leukemia transcription factor 1, splice variant	PBX1	1q23	BF967998	88.0	Above	7472.2	old
7	212371_at	DKFZp586C1019	DKFZp586C1019	1	AL049397.1	88.0	Above	2.5	old
8	219155_at	retinal degeneration B beta	RDGGB	17q24.2	NM_012417.1	88.0	Above	2.7	new
9	225483_at	hypothetical protein MGC10485	MGC10485	11q25	AI971602	88.0	Above	7.7	new
10	227439_at	E2a-Pbx1-associated protein	EB-1	12	AW005572	88.0	Above	269.8	new
11	227949_at	Q9H4T4 like	H17739	20q13.32	AL357503	88.0	Above	59.3	new
12	230306_at	hypothetical protein MGC10485	MGC10485	11q25	AA514326	88.0	Above	19.2	new
13	231095_at	retinal degeneration B beta	RDGGB	17q24.2	AW193811	88.0	Above	25.6	new
14	203372_s_at	STAT induced STAT inhibitor-2	SOCS2	12q	AB004903.1	80.6	Below	23.4	old
15	206028_s_at	c-mer proto-oncogene tyrosine kinase	MERTK	2q14.1	NM_006343.1	80.6	Above	23.7	old
16	206181_at	signaling lymphocytic activation molecule	SLAM	1q22-q23	NM_003037.1	80.6	Above	6.3	old
17	208788_at	homolog of yeast long chain polyunsaturated fatty acid elongation enzyme 2	HELO1	6p21.1-p12.1	AL136939.1	80.6	Above	2.2	old
18	209760_at	KIAA0922 protein	KIAA0922	4q31.23	AL136932.1	80.6	Above	2.9	old
19	35974_at	lymphoid-restricted membrane protein	LRMP	12p12.3	U10485	80.6	Above	6.2	old
20	38340_at	huntingtin interacting protein 12	HIP12	12q24	AB014555	80.6	Above	3.8	old
21	208644_at	ADP-ribosyltransferase (NAD <sup>+</sup> ; poly (ADP-ribose) polymerase)	ADPRT	1q41-q42	M32721.1	80.2	Above	3.0	old
22	212789_at	KIAA0056 protein	KIAA0056	11q25	AI796581	80.2	Above	3.9	old
23	221113_s_at	wingless-type MMTV integration site family, member 16	WNT16	7q31	NM_016087.1	80.2	Above	2547.6	new
24	224022_x_at	wingless-type MMTV integration site family, member 16	WNT16	7q31	AF169963.1	80.2	Above	569.1	new
25	231040_at	EST		9	AW512988	80.2	Above	16.4	new

26	232289_at	FLJ14167	FLJ14167	17	BF237871	80.2	Above	144.1	new
27	235666_at	EST	FLJ20489	10	AA903473	80.2	Above	654.6	new
28	203373_at	STAT induced STAT inhibitor-2	SOCS2	12q	NM_003877.1	74.2	Below	24.8	old
29	210785_s_at	basement membrane-induced gene	ICB-1	1p35.3	AB035482.1	74.2	Below	4.1	old
30	224733_at	chemokine-like factor super family 3	CKLFSF3	16q23.1	AL574900	74.2	Below	41.7	new
31	225235_at	hypothetical protein MGC14859	MGC14859	5q35.3	AW007710	74.2	Above	3.6	new
32	204114_at	nidogen 2 (osteonidogen)	NID2	14q21-q22	NM_007361.1	73.1	Above	15.1	old
33	211913_s_at	c-mer proto-oncogene tyrosine kinase	MERTK	2q14.1	L08961.1	72.8	Above	37.7	old
34	219551_at	uncharacterized bone marrow protein BM040	BM040	3q21.1	NM_018456.1	72.8	Above	3.0	New
35	223693_s_at	hypothetical protein FLJ10324	FLJ10324	7p22	AL136731.1	72.8	Above	65.6	New
36	200600_at	moesin	MSN	Xq11.2-q12	NM_002444.1	72.5	Below	2.2	Old
37	213909_at	FLJ12280	FLJ12280	3	AU147799	72.5	Above	12.5	New
38	221669_s_at	acyl-Coenzyme A dehydrogenase family, member 8	ACAD8	11q25	BC001964.1	72.5	Above	2.6	New
39	235911_at	ESTs, Weakly similar to PIHUB6 salivary proline-rich protein precursor PRB1 (large allele)		3	AI885815	72.5	Above	36.6	New
40	243533_x_at	ESTs			H09663	72.5	Above	23.2	New
41	202615_at	DKFZp686D0521	DKFZp686D0521	9	BF222895	68.6	Below	6.2	Old
42	204774_at	ecotropic viral integration site 2A	EVI2A	17q11.2	NM_014210.1	68.6	Below	3.0	New
43	218283_at	synovial sarcoma translocation gene on chromosome 18-like 2	SS18L2	3p21	NM_016305.1	68.6	Above	1.6	New
44	209130_at	synaptosomal-associated protein, 23kDa	SNAP23	15q14	BC003686.1	67.8	Below	1.9	New
45	228580_at	serine protease HTRA3	HTRA3	4p16.1	AI828007	66.6	Above	3.8	New
46	202796_at	synaptopodin	KIAA1029	5q33.1	NM_007286.1	66.5	Above	52.3	Old
47	218640_s_at	phafin 2	FLJ13187	8q21.3	NM_024613.1	66.5	Above	3.1	New
48	235099_at	ESTs, Weakly similar to PLLP_HUMAN Plasmolipin [H.sapiens]		3	AW080832	66.5	Above	6.7	New
49	201889_at	family with sequence similarity 3, member C	FAM3C	7q22.1-q31.1	NM_014888.1	65.3	Above	4.6	New
50	202106_at	golgi autoantigen, golgin subfamily a, 3	GOLGA3	12q24.33	NM_005895.1	65.3	Above	3.3	Old
51	202208_s_at	ADP-ribosylation factor-like 7	ARL7	2q37.2	BC001051.1	65.3	Above	3.2	Old
52	205173_x_at	CD58 antigen, (lymphocyte function-associated antigen 3)	CD58	1p13	NM_001779.1	65.3	Above	2.4	Old
53	211744_s_at	CD58 antigen, (lymphocyte function-associated antigen 3)	CD58	1p13	BC005930.1	65.3	Above	2.5	Old
54	212552_at	hippocalcin-like 1	HPCAL1	2p25.1	BE617588	65.3	Below	2.6	Old
55	213358_at	KIAA0802 protein	KIAA0802	18p11.21	AB018345.1	65.3	Above	12.7	Old
56	222699_s_at	phafin 2	FLJ13187	8q21.3	BF439250	65.3	Above	3.5	New
57	225618_at	EST		17	AI769587	65.3	Below	5.3	New
58	238778_at	DKFZp451L157	DKFZp451	10	AI244661	65.3	Above	23.5	New

			L157						
59	239427_at	ESTs		1	AA131524	65.3	Above	13.7	New
60	47069_at	Rho GTPase activating protein 8	ARHGAP8	22q13.31	AA533284	65.3	Above	3.3	New
61	205769_at	solute carrier family 27 (fatty acid transporter), member 2	SLC27A2	15q21.2	NM_003645.1	65.1	Above	56.0	Old
62	210786_s_at	Friend leukemia virus integration 1	FLI1	11q24.1-q24.3	M93255.1	65.1	Above	2.2	Old
63	212985_at	DKFZp434E033	DKFZp434E033	4	BF115739	65.1	Above	7.1	New
64	227441_s_at	E2a-Pbx1-associated protein	EB-1	12	AW005572	65.1	Above	1139.4	New
65	234261_at	DKFZp761M10121	DKFZp761M10121	12	AL137313.1	65.1	Above	960.8	New
66	244565_at	ESTs		10	AI685824	65.1	Above	7.6	New
67	202181_at	KIAA0247 gene product	KIAA0247	14q24.1	NM_014734.1	63.7	Above	1.8	Old
68	202207_at	ADP-ribosylation factor-like 7	ARL7	2q37.2	NM_005737.2	63.7	Above	3.2	Old
69	207571_x_at	basement membrane-induced gene	ICB-1	1p35.3	NM_004848.1	63.7	Below	4.4	Old
70	209558_s_at	huntingtin interacting protein 12	HIP12	12q24	AB013384.1	61.1	Above	23.8	Old
71	213005_s_at	KIAA0172 protein	KIAA0172	9p24.3	D79994.1	61.1	Above	8.3	Old
72	236854_at	cDNA DKFZp667F0617	DKFZp667F0617	20	AA743694	61.1	Above	12.6	New
73	226233_at	tubulin-specific chaperone e	TBCE	1q42.3	BG112197	60.0	Above	2.6	New
74	203435_s_at	membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)	MME	3q25.1-q25.2	NM_007287.1	59.9	Below	2.2	Old
75	202478_at	GS3955 protein	GS3955	2p25.1	NM_021643.1	59.3	Above	4.0	Old
76	202479_s_at	GS3955 protein	GS3955	2p25.1	BC002637.1	59.3	Above	3.3	Old
77	203999_at	synaptotagmin I	SYT1	12cen-q21	NM_005639.1	59.3	Above	3.9	Old
78	212149_at	KIAA0143 protein	KIAA0143	8q24.12	AA805651	59.3	Below	13.5	New
79	212873_at	minor histocompatibility antigen HA-1	HA-1	19p13.3	BE349017	59.3	Below	2.9	Old
80	218346_s_at	p53 regulated PA26 nuclear protein	PA26	6q21	NM_014454.1	59.3	Below	4.7	New
81	224856_at	FK506 binding protein 5	FKBP5	6p21.3-21.2	AL122066.1	59.3	Below	5.5	Old
82	200811_at	cold inducible RNA binding protein	CIRBP	19p13.3	NM_001280.1	59.1	Below	5.8	Old
83	201722_s_at	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)	GALNT1	18q12.1	NM_020474.2	59.1	Below	1.8	New
84	223711_s_at	HSPC144 protein	HSPC144	11q25	AF182413.1	59.1	Above	2.0	New
85	233273_at	cDNA FLJ12010 fis	FLJ12010	1	AU146834	59.1	Above	30.6	New
86	201460_at	mitogen-activated protein kinase-activated protein kinase 2	MAPKAPK2	1q32	AI141802	57.9	Above	2.1	Old
87	202421_at	immunoglobulin superfamily, member 3	IGSF3	1p13	AB007935.1	57.9	Above	4.4	New
88	217983_s_at	ribonuclease 6 precursor	RNASE6PL	6q27	NM_003730.2	57.9	Below	3.4	New
89	218087_s_at	sorbin and SH3 domain containing 1	SORBS1	10q23.3-q24.1	NM_015385.1	57.9	Above	25.1	New

90	218491_s_at	HSPC144 protein	HSPC144	11q25	NM_014174.1	57.9	Above	1.4	New
91	201825_s_at	CGI-49 protein	LOC51097	1q44	AL572542	57.8	Above	2.2	Old
92	202206_at	ADP-ribosylation factor-like 7	ARL7	2q37.2	NM_005737.2	57.8	Above	3.9	Old
93	218683_at	polypyrimidine tract binding protein 2	PTBP2	1p22.11-p21.3	NM_021190.1	57.8	Above	1.8	New
94	226590_at	cDNA clone EUROIMAGE 1517766		9	AA031404	57.8	Above	3.1	New
95	227440_at	E2a-Pbx1-associated protein	EB-1	12	AW005572	57.8	Above	1168.9	New
96	229770_at	hypothetical protein FLJ31978	FLJ31978	12q24.33	AI041543	57.8	Above	51.8	New
97	40148_at	amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like)	APBB2	4p14	U62325	57.8	Above	6.2	Old
98	212959_s_at	MGC4170 protein	MGC4170	12q23.1	AK001821.1	57.2	Below	3.0	New
99	203143_s_at	KIAA0040 gene product	KIAA0040	1q24-25	T79953	56.3	Above	2.4	New
100	209683_at	hypothetical protein DKFZp566A1524	DKFZP566A1524	2p24.2	AA243659	56.3	Below	10.0	New

**Table S5. Top 100 chi-square probe sets selected for Hyperdiploid >50 in decision tree format**

	<b>U133 probe set</b>	<b>Gene description</b>	<b>Symbol</b>	<b>Location</b>	<b>GenBank Reference</b>	<b>Chi-square value</b>	<b>HD&gt;50 above/below mean</b>	<b>Fold change</b>	<b>old or new</b>
1	200600_at	Moesin (membrane-organizing extensio spike protein)	MSN	Xq11.2-q12	NM_002444.1	34.0	Above	1.9	old
2	200737_at	Phosphoglycerate kinase 1	PGK1	Xq13	NM_000291.1	34.0	Above	1.8	old
3	200980_s_at	Pyruvate dehydrogenase (lipoamide) alpha 1	PDHA1	Xp22.2-p22.1	NM_000284.1	34.0	Above	1.7	new
4	201136_at	Proteolipid protein 2 (colonic epithelium-enriched)	PLP2	Xp11.23	NM_002668.1	34.0	Above	3.3	old
5	201807_at	Vacuolar protein sorting 26 (yeast)	VPS26	10q21.1	NM_004896.1	34.0	Above	1.7	old
6	202214_s_at	Cullin 4B	CUL4B	Xq23	NM_003588.1	34.0	Above	1.9	new
7	202557_at	Stress 70 protein chaperone, microsome associated, 60 kD	STCH	21q11	AI718418	34.0	Above	2.0	new
8	202593_s_at	membrane interacting protein of RGS16	MIR16	16p12-p11.2	NM_016641.1	34.0	Below	1.6	new
9	203680_at	Protein kinase, cAMP-dependent, regulatory, type II, beta	PRKAR2B	7q22-q31.1	NM_002736.1	34.0	Above	3.3	new
10	204194_at	BTB and CNC homology 1, basic leucine zipper transcription factor 1	BACH1	21q22.11	NM_001186.1	34.0	Above	1.8	new
11	205324_s_at	FtsJ homolog 1 (E. coli)	FTSJ1	Xp11.23	NM_012280.1	34.0	Above	2.1	old
12	208598_s_at	Upstream regulatory element binding protein 1	UREB1	Xp11.22	NM_005703.2	34.0	Above	1.6	old
13	208861_s_at	Alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)	ATRX	Xq13.1-q21.1	U72937.2	34.0	Above	1.7	old

14	211342_x_at	trinucleotide repeat containing 11 (THR-associated protein, 230 kDa subunit)	TNRC11	Xq13	BC004354.1	34.0	Above	1.8	new
15	216071_x_at	Trinucleotide repeat containing 11	TNRC11	Xq13	AF132033	34.0	Above	1.8	new
16	218573_at	APR-1 protein/melanoma-associated antigen	MAGEH1	Xp11.22	NM_014061.1	34.0	Above	3.0	new
17	219485_s_at	proteasome (prosome, macropain) 26S subunit, non-ATPase, 10	PSMD10	Xq22.3	NM_002814.1	34.0	Above	2.4	old
18	200655_s_at	Calmodulin 1 (phosphorylase kinase, delta)	CALM1	14q24-q31	NM_006888.1	30.1	Above	1.7	old
19	200738_s_at	Phosphoglycerate kinase 1	PGK1	Xq13	NM_000291.1	30.1	Above	1.8	old
20	200944_s_at	High-mobility group (nonhistone chromosomal) protein 14; member of the HMG 14/17 family	HMG14	21q22.2	NM_004965.1	30.1	Above	1.7	old
21	201092_at	Retinoblastoma binding protein 7	RBBP7	Xp22.31	NM_002893.2	30.1	Above	1.6	new
22	201100_s_at	Ubiquitin specific protease 9	USP9X	Xp11.4	NM_004652.2	30.1	Above	1.7	old
23	201688_s_at	Tumor protein D52	TPD52	8q21	BE974098	30.1	Below	4.1	new
24	201899_s_at	Ubiquitin-conjugating enzyme E2A (RAD6 homolog)	UBE2A	Xq24-q25	NM_003336.1	30.1	Above	1.8	old
25	202325_s_at	ATP synthase, H <sup>+</sup> transporting, mitochondrial F0 complex, subunit F6	ATP5J	21q21.1	NM_001685.1	30.1	Above	1.6	old
26	202829_s_at	Synaptobrevin-like 1	SYBL1	Xq28	NM_005638.1	30.1	Above	1.5	old
27	202854_at	Hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)	HPRT1	Xq26.1	NM_000194.1	30.1	Above	1.4	old
28	206846_s_at	Histone deacetylase 6	HDAC6	Xp11.23	NM_006044.2	30.1	Above	1.5	new
29	209370_s_at	SH3-domain binding protein 2	SH3BP2	4p16.3	AB000462.1	30.1	Above	3.1	new
30	209565_at	zinc finger protein 183 (RING finger, C3HC4 type)	ZNF183	Xq25-q26	BC000832.1	30.1	Above	2.2	new
31	212846_at	KIAA0179 protein.	KIAA0179	21q22.3	D80001.1	30.1	Above	2.0	old
32	217356_s_at	Phosphoglycerate kinase	PGK1	Xq13	S81916.1	30.1	Above	1.8	new
33	218163_at	MCT-1 protein	MCT-1	Xq22-24	NM_014060.1	30.1	Above	1.8	new
34	218386_x_at	Ubiquitin specific protease 16; de-ubiquitinates histone H2A; ubiquitous expression.	USP16	21q22.11	NM_006447.1	30.1	Above	1.7	new
35	218402_s_at	Hermansky-Pudlak syndrome 4	HPS4		NM_022081.1	30.1	Below	3.4	new
36	218495_at	Ubiquitously-expressed transcript	UXT	Xp11.23-p11.22	NM_004182.1	30.1	Above	1.5	new
37	218499_at	Mst3 and SOK1-related kinase/STE20-like kinase; contains a Ser/Thr protein kinase domain	MST4	Xq26.1	NM_016542.1	30.1	Above	2.5	new
38	218757_s_at	Similar to yeast Upf3, variant B	UPF3B	Xq25-q26	NM_023010.1	30.1	Above	2.3	new
39	219038_at	Hypothetical protein FLJ11565	FLJ11565	Xq22.2	NM_024657.1	30.1	Above	6.9	new
40	229967_at	Chemokine-like factor super family 2.	CKLFSF2	16q23.1	AA778552	30.1	Above	4.3	new
41	242794_at	EST		4q31.1	AI569476	30.1	Above	3.2	new
42	201132_at	Heterogeneous nuclear ribonucleoprotein H2 (H')	HNRPH2	Xq22	NM_019597.1	30.0	Above	2.0	old
43	201312_s_at	SH3 domain binding glutamic acid-rich protein like	SH3BGRL	Xq13.3	NM_003022.1	30.0	Above	1.6	old

44	201894_s_at	Decorin; glycoprotein that binds to type I collagen fibrils & plays a role in matrix assembly.	DCN	12q13.2	NM_001920.1	30.0	Above	1.5	new
45	201923_at	Peroxiredoxin 4	PRDX4	Xp22.13	NM_006406.1	30.0	Above	1.9	old
46	202371_at	Hypothetical protein FLJ21174	FLJ21174	Xq22.1	NM_024863.1	30.0	Above	3.6	old
47	203126_at	Inositol(myo)-1(or 4)-monophosphatase 2	IMPA2	18p11.2	NM_014214.1	30.0	Above	4.1	old
48	204219_s_at	proteasome (prosome, macropain) 26S subunit, ATPase, 1	PSMC1	19p13.3	NM_002802.1	30.0	Above	1.3	old
49	204835_at	polymerase (DNA directed), alpha	POLA	Xp22.1-p21.3	NM_016937.1	30.0	Above	2.0	old
50	212071_s_at	Spectrin, beta, non-erythrocytic 1	SPTBN1	2p21	BE968833	30.0	Below	1.7	new
51	212419_at	EST		10q22.3	AL049949.1	30.0	Above	13.1	new
52	212718_at	Hypothetical protein MGC5370	MGC5378	14q32.2	BG110231	30.0	Above	1.5	new
53	213502_x_at	Homo sapiens cDNA FLJ32313 fis, clone PROST2003232, weakly similar to BETA-GLUCURONIDASE PRECURSOR (EC 3.2.1.31)	FLJ32313	22q11.23	X03529	30.0	Below	1.8	old
54	214051_at	Thymosin, beta	TMSNB	Xq21.33-q22.3	BF677486	30.0	Above	3.1	new
55	226039_at	Mannosyl (alpha-1,3)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase	MGAT4A	2q11.2	AW006441	30.0	Above	3.0	new
56	227279_at	hypothetical protein MGC15737	MGC15737	Xq22.1	AA847654	30.0	Above	5.6	new
57	200642_at	Superoxide dismutase 1, soluble	SOD1	21q22.11	NM_000454.1	26.7	Above	2.3	old
58	200799_at	Heat shock 70kD protein 1A	HSPA1A	6p21.3	NM_005345.3	26.7	Above	2.7	old
59	200943_at	High-mobility group (nonhistone chromosomal) protein 14; member of the HMG 14/17 family	HMG14	21q22.2	NM_004965.1	26.7	Above	1.6	old
60	201018_at	Eukaryotic translation initiation factor 1A	EIF1A	Xp22.12	BE542684	26.7	Above	1.8	new
61	201311_s_at	SH3 domain binding glutamic acid-rich protein like	SH3BGRL	Xq13.3	AL515318	26.7	Above	1.6	old
62	201443_s_at	ATPase, H+ transporting, lysosomal interacting protein 2	ATP6IP2	Xq21	AF248966.1	26.7	Above	1.9	old
63	201472_at	Von Hippel-Lindau binding protein 1	VBP1	Xq28	NM_003372.2	26.7	Above	1.7	old
64	201689_s_at	Tumor protein D52	TPD52	8q21	BE974098	26.7	Below	4.3	new
65	202602_s_at	HIV TAT specific factor 1	HTATSF1	Xq26.1-q27.2	NM_014500.1	26.7	Above	1.5	old
66	203041_s_at	Lysosomal-associated membrane protein 2	LAMP2	Xq24	J04183.1	26.7	Above	3.1	old
67	203102_s_at	Mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	MGAT2	14q21	NM_002408.2	26.7	Above	1.6	new
68	203744_at	High-mobility group (nonhistone chromosomal) protein 4	HMG4	Xq28	NM_005342.1	26.7	Above	1.9	new
69	205518_s_at	Cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminic acid monooxygenase)	CMAH	6p22-p23	NM_003570.1	26.7	Below	2.9	new
70	208683_at	Calpain 2, (m/II) large subunit; calcium-	CAPN2	1q41-q42	M23254.1	26.7	Above	2.2	old

71	209440_at	dependent Cys protease. Phosphoribosyl pyrophosphate synthetase 1; purine biosynthesis.	PRPS1	Xq21-q27	BC001605.1	26.7	Above	1.4	old
72	210786_s_at	Friend leukemia virus integration 1	FLI1	11q24.1-q24.3	M93255.1	26.7	Below	2.5	old
73	212070_at	G protein-coupled receptor 56	GPR56	16q13	AL554008	26.7	Above	2.4	new
74	213334_x_at	Three prime repair exonuclease 2	TREX2	Xq28	BE676218	26.7	Above	1.7	old
75	215117_at	Recombination activating gene 2; V(D)J recombinase.	RAG2	11p13	AW058148	26.7	Below	27.2	old
76	218694_at	ALEX1 protein	ALEX1	Xq21.33-q22.2	NM_016608.1	26.7	Above	2.8	new
77	222741_s_at	hypothetical protein FLJ11101	FLJ11101	6p21.1	AI761426	26.7	Above	1.5	new
78	223082_at	SH3-domain kinase binding protein 1	SH3KBP1	Xp22.1-p21.3	AF230904.1	26.7	Above	2.0	new
79	225105_at	clone MGC:23936 IMAGE:3838595, mRNA, complete cds		12q23.3	BF969397	26.7	Above	2.1	new
80	225406_at	Twisted gastrulation	TSG	18p11.3	AA195009	26.7	Above	1.9	new
81	225553_at	Homo sapiens cDNA FLJ12874 fis		14q22.2	AL042817	26.7	Above	1.6	new
82	226199_at	Hypothetical protein MGC23937	MGC23937	Xq13.1	AL563795	26.7	Above	2.1	new
83	226875_at	Hypothetical protein FLJ32122	FLJ32122	Xq24	AI742838	26.7	Above	2.3	new
84	232974_at	cDNA FLJ12417 fis		Xp22.31	AU148256	26.7	Above	3.1	new
85	46323_at	Ca <sup>2+</sup> -dependent endoplasmic reticulum nucleoside diphosphatase	SHAPY	17q25.3	AL120741	26.7	Above	1.7	new
86	203694_s_at	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 16	DDX16	6p21.3	NM_003587.2	26.3	Above	1.3	old
87	200658_s_at	Prohibitin	PHB	17q21	AL560017	26.3	Above	2.0	old
88	201898_s_at	ubiquitin-conjugating enzyme E2A (RAD6 homolog)	UBE2A	Xq24-q25	AI126625	26.3	Above	1.6	old
89	203556_at	KIAA0854 protein	KIAA0854	8q24.13	NM_014943.1	26.3	Below	1.6	old
90	203745_at	Holocytochrome c synthase (cytochrome c heme- lyase)	HCCS	Xp22.3	AI801013	26.3	Above	2.1	new
91	203909_at	Solute carrier family 9 (sodium/hydrogen exchanger), isoform 6	SLC9A6	Xq26.3	NM_006359.1	26.3	Above	1.9	old
92	204446_s_at	Arachidonate 5-lipoxygenase	ALOX5	10q11.2	NM_000698.1	26.3	Above	4.2	old
93	205191_at	Retinitis pigmentosa 2 (X-linked recessive)	RP2	Xp11.4-p11.21	NM_006915.1	26.3	Above	2.1	old
94	206874_s_at	Ste20-related serine/threonine kinase	SLK	10q25.1	AL138761	26.3	Above	1.6	new
95	208073_x_at	Tetratricopeptide repeat domain 3	TTC3	21q22.2	NM_003316.1	26.3	Above	1.9	old
96	209056_s_at	CDC5 cell division cycle 5-like ( <i>S. pombe</i> )	CDC5L	6p21	AW268817	26.3	Above	1.4	new
97	210645_s_at	Tetratricopeptide repeat domain 3	TTC3	21q22.2	D83077.1	26.3	Above	2.2	old
98	215773_x_at	ADP-ribosyltransferase (NAD <sup>+</sup> ; poly(ADP- ribose) polymerase)-like 2	ADPRTL2	14q11.2-q12	AJ236912.1	26.3	Above	1.6	old
99	215884_s_at	Ubiquilin 2	UBQLN2	Xp11.23-p11.1	AK001029.1	26.3	Above	1.9	new
100	217954_s_at	PHD finger protein 3	PHF3	6	NM_015153.1	26.3	Above	1.5	new

**Table S6. Top 100 chi-square probe sets selected for *MLL* in decision tree format**

	<b>U133 probe set</b>	<b>Gene description</b>	<b>Symbol</b>	<b>Location</b>	<b>GenBank Reference</b>	<b>Chi-square value</b>	<b>MLL above/below mean</b>	<b>Fold change</b>	<b>old or new</b>
1	202603_at	a disintegrin and metalloproteinase domain 10	ADAM10	15q22	N51370	44.6	Above	1.8	old
2	219463_at	chromosome 20 open reading frame 103	C20orf103	20p12	NM_012261.1	44.6	Above	24.7	new
3	224772_at	neuron navigator 1	NAV1		AB032977.1	44.6	Below	3.8	new
4	204069_at	Meis1, myeloid ecotropic viral integration site 1 homolog	MEIS1	2p14-p13	NM_002398.1	44.4	Above	73.7	old
5	218966_at	myosin 5C	MYO5C	15q21	NM_018728.1	44.4	Below	4.5	new
6	226939_at	cDNA FLJ37247 fis	FLJ37247		AI202327	44.4	Above	6.9	new
7	204446_s_at	arachidonate 5-lipoxygenase	ALOX5	10q11.2	NM_000698.1	40.7	Below	66.8	old
8	206492_at	fragile histidine triad gene	FHIT	3p14.2	NM_002012.1	40.7	Below	36.6	old
9	212588_at	protein tyrosine phosphatase, receptor type, C	PTPRC	1q31-q32	AI809341	40.7	Above	2.3	old
10	215925_s_at	CD72 antigen	CD72	9p11.2	AF283777.2	40.7	Above	3.0	old
11	211733_x_at	sterol carrier protein 2	SCP2	1p32	BC005911.1	40.1	Above	1.5	old
12	212386_at	cDNA FLJ11918 fis	FLJ11918		AK021980.1	40.1	Below	3.1	new
13	218764_at	Protein Kinase C eta isoform.	PRKCH	14q22.1-q22.3	NM_024064.1	40.1	Below	7.6	new
14	218847_at	IGF-II mRNA-binding protein 2	IMP-2	3q28	NM_006548.1	40.1	Above	23.2	new
15	222409_at	coronin, actin binding protein, 1C	CORO1C	12q24.1	AL162070.1	40.1	Above	4.8	new
16	242172_at	ESTs			N50406	40.1	Above	33.6	new
17	201153_s_at	muscleblind-like (Drosophila)	MBNL	3q25	NM_021038.1	40.0	Above	2.1	old
18	210487_at	deoxynucleotidyltransferase, terminal	DNTT	10q23-q24	M11722.1	40.0	Below	2.9	old
19	219686_at	gene for serine/threonine protein kinase	HSA250839	4p16.2	NM_018401.1	40.0	Below	28.3	new
20	226981_at	Homo sapiens, clone IMAGE:4401491, mRNA			AW002079	37.4	Below	1.0	new
21	203375_s_at	tripeptidyl peptidase II	TPP2	13q32-q33	NM_003291.1	37.2	Above	1.6	new
22	221676_s_at	coronin, actin binding protein, 1C	CORO1C	12q24.1	BC002342.1	37.2	Above	3.5	new
23	201152_s_at	muscleblind-like (Drosophila)	MBNL	3q25	NM_021038.1	36.2	Above	2.2	old
24	221773_at	ELK3, ETS-domain protein (SRF accessory protein 2)	ELK3	12q23	AW575374	36.2	Below	8.2	new
25	201162_at	insulin-like growth factor binding protein 7	IGFBP7	4q12	NM_001553.1	36.0	Above	4.3	old
26	201163_s_at	insulin-like growth factor binding protein 7	IGFBP7	4q12	NM_001553.1	36.0	Above	4.0	old
27	203836_s_at	mitogen-activated protein kinase kinase kinase 5	MAP3K5	6q22.33	D84476.1	36.0	Above	13.9	old
28	203837_at	mitogen-activated protein kinase kinase kinase 5	MAP3K5	6q22.33	NM_005923.2	36.0	Above	4.2	old
29	213891_s_at	cDNA FLJ11918 fis	FLJ11918		AI927067	36.0	Below	3.2	new
30	214895_s_at	a disintegrin and metalloproteinase domain 10	ADAM10	15q22	AU135154	36.0	Above	1.9	old

31	226415_at	KIAA1576 protein	KIAA1576	16q22.1	AA156723	36.0	Above	40.7	new
32	235879_at	ESTs			AI697540	36.0	Above	3.8	new
33	212387_at	cDNA FLJ11918 fis	FLJ11918		AK021980.1	35.8	Below	3.3	new
34	218988_at	bladder cancer over expressed protein	BLOV1	12q15	NM_018656.1	35.8	Below	16.3	new
35	228555_at	EST; by BLAT calcium/calmodulin-dependent Protine Kinase type II Delta chain (CAMK GROUP I)	CAMK2D		AA029441	35.8	Above	3.1	new
36	202975_s_at	Rho-related BTB domain containing 3	RHOBTB3	5q21.2	N21138	35.3	Above	5.5	old
37	201105_at	lectin, galactoside-binding, soluble, 1 (galectin 1)	LGALS1	22q13.1	NM_002305.2	34.5	Above	14.5	old
38	203434_s_at	membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)	MME	3q25.1-q25.2	AI433463	34.1	Below	31.2	old
39	212135_s_at	calcium transporting ATPase plasma membrane protein.	ATP2B4		AW517686	34.1	Below	2.4	new
40	212136_at	calcium transporting ATPase plasma membrane protein.	ATP2B4		AW517686	34.1	Below	2.1	new
41	230179_at	cDNA DKFZp547P158	DKFZp547 P158		N52572	34.1	Below	6.4	new
42	218217_at	likely homolog of rat and mouse retinoid- inducible serine carboxypeptidase	RISC	17q23.2	NM_021626.1	32.8	Above	3.4	new
43	225841_at	hypothetical protein FLJ30525	FLJ30525	1p13.2	BE502436	32.8	Above	1.8	new
44	226668_at	hypothetical protein FLJ36175	FLJ36175		W80623	32.8	Above	2.4	new
45	200989_at	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	HIF1A	14q21-q24	NM_001530.1	32.2	Below	1.8	old
46	201151_s_at	muscleblind-like (Drosophila)	MBNL	3q25	NM_021038.1	32.2	Above	2.6	old
47	201563_at	sorbitol dehydrogenase	SORD	15q15.3	L29008.1	32.2	Above	1.8	new
48	203753_at	transcription factor 4	TCF4	18q21.1	NM_003199.1	32.2	Below	2.9	new
49	205668_at	lymphocyte antigen 75	LY75	2q24	NM_002349.1	32.2	Above	2.1	new
50	206471_s_at	plexin C1	PLXNC1	12q23.3	NM_005761.1	32.2	Above	7.7	old
51	211302_s_at	phosphodiesterase 4B, cAMP-specific	PDE4B	1p31	L20966.1	32.2	Below	3.0	old
52	212012_at	Melanoma associated gene	D2S448	2pter-p25.1	AF200348.1	32.2	Below	2.4	old
53	212063_at	CD44 antigen	CD44	11p13	BE903880	32.2	Above	3.1	new
54	213241_at	plexin C1	PLXNC1		AF035307.1	32.2	Above	2.5	old
55	214651_s_at	homeo box A9	HOXA9	7p15-p14	U41813.1	32.2	Above	28.5	old
56	218140_x_at	APMCF1 protein	APMCF1	3q22.2	NM_021203.1	32.2	Above	1.4	new
57	219988_s_at	hypothetical protein FLJ10597	FLJ10597	1p34.1	NM_018150.1	32.2	Above	1.9	new
58	223046_at	egl nine homolog 1 (C. elegans)	EGLN1	1q42.1	NM_022051.1	32.2	Below	4.2	new
59	224150_s_at	p10-binding protein	BITE	3q22-q23	AF289495.1	32.2	Above	2.1	new
60	224933_s_at	hypothetical protein DKFZp761F0118	DKFZp761 F0118	10q22.1	AB037801.1	32.2	Above	1.9	new
61	201078_at	transmembrane 9 superfamily member 2	TM9SF2	13q32.3	NM_004800.1	32.0	Above	1.5	new

62	205550_s_at	brain and reproductive organ-expressed (TNFRSF1A modulator)	BRE	2p23.3	NM_004899.1	32.0	Above	2.0	new
63	212382_at	cDNA FLJ11918 fis	FLJ11918		AK021980.1	32.0	Below	2.7	new
64	225019_at	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	CAMK2D	4q25	AA777512	32.0	Above	3.6	new
65	225202_at	Rho-related BTB domain containing 3	RHOBTB3	5q21.2	BE620739	32.0	Above	5.5	old
66	228855_at	nudix (nucleoside diphosphate linked moiety X)-type motif 7	NUDT7		AI927964	32.0	Above	5.6	new
67	231899_at	KIAA1726 protein	KIAA1726	11q23.1	AB051513.1	32.0	Above	33.0	new
68	52164_at	chromosome 11 open reading frame 24	C11orf24	11q13	AA065185	32.0	Above	2.3	new
69	212660_at	KIAA0239 protein	KIAA0239	5q31.1	AI735639	31.7	Below	1.7	old
70	213513_x_at	actin related protein 2/3 complex, subunit 2, 34kDa	ARPC2	2q36.1	BG034239	31.7	Above	1.3	old
71	222603_at	hypothetical protein FLJ23309	FLJ23309	9p24	AL136980	31.7	Above	3.6	new
72	238558_at	ESTs			AI445833	31.7	Above	3.8	new
73	202391_at	brain abundant, membrane attached signal protein 1	BASP1	5p15.1-p14	NM_006317.1	31.3	Above	2.1	old
74	202604_x_at	a disintegrin and metalloproteinase domain 10	ADAM10	15q22	NM_001110.1	31.3	Above	1.8	old
75	203435_s_at	membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)	MME	3q25.1-q25.2	NM_007287.1	31.3	Below	54.8	old
76	204445_s_at	arachidonate 5-lipoxygenase	ALOX5	10q11.2	AI361850	31.3	Below	687.0	old
77	209705_at	likely ortholog of mouse metal response element binding transcription factor 2	M96	1p22.1	AF073293.1	31.3	Below	1.5	old
78	214366_s_at	arachidonate 5-lipoxygenase	ALOX5	10q11.2	AA995910	31.3	Below	54.7	old
79	215000_s_at	fasciculation and elongation protein zeta 2 (zygin II)	FEZ2	2p21	AL117593.1	31.3	Above	1.7	new
80	220643_s_at	Fas apoptotic inhibitory molecule	FAIM	3q23	NM_018147.1	31.3	Above	2.9	new
81	226459_at	Homo sapiens gastric cancer-related protein GCYS-20 (gcys-20) mRNA, complete cds			AW575754	31.3	Above	1.6	new
82	238712_at	ESTs			BF801735	31.3	Above	2.7	new
83	229686_at	cDNA FLJ35637 fis	FLJ35637		AI436587	31.0	Below	1.5	new
84	222620_s_at	hypothetical protein similar to mouse Dnajl1	DNAJL1	10p11.23	BF591419	29.8	Above	2.4	new
85	224516_s_at	hypothetical protein HSPC195	HSPC195	5q31.3	BC006428.1	29.8	Above	2.7	new
86	203217_s_at	sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase)	SIAT9	2p11.2	NM_003896.1	28.8	Below	2.1	new
87	204030_s_at	schwannomin interacting protein 1	SCHIP1	3q25.32	NM_014575.1	28.8	Below	17.6	old
88	209191_at	tubulin beta-5	TUBB-5		BC002654.1	28.8	Above	6.4	new
89	213541_s_at	v-ets erythroblastosis virus E26 oncogene like (avian)	ERG	21q22.3	AI351043	28.8	Below	2.8	old
90	213773_x_at	Williams Beuren syndrome chromosome region	WBSCR20	7q11.23	AW248552	28.8	Above	1.3	new

		20A	A						
91	219243_at	immunity associated protein 4	HIMAP4	7q35	NM_018326.1	28.8	Below	13.4	new
92	219256_s_at	hypothetical protein FLJ20356	FLJ20356	4p16.1	NM_018986.1	28.8	Below	2.6	new
93	223358_s_at	phosphodiesterase 7A	PDE7A	8q13	AW269834	28.8	Above	1.5	new
94	224796_at	development and differentiation enhancing factor 1	DDEF1	8q24.1-q24.2	W03103	28.8	Below	1.8	new
95	203076_s_at	MAD, mothers against decapentaplegic homolog 2 (Drosophila)	MADH2	18q21.1	U65019.1	28.7	Below	2.0	new
96	212385_at	cDNA FLJ11918 fis	FLJ11918		AK021980.1	28.7	Below	3.2	new
97	216026_s_at	polymerase (DNA directed), epsilon	POLE	12q24.3	AL080203.1	28.7	Below	3.0	old
98	217118_s_at	KIAA0930 protein	KIAA0930	22q13.31	AK025608.1	28.7	Above	1.9	new
99	219821_s_at	hypothetical protein FLJ20330	FLJ20330	6pter-p22.1	NM_018988.1	28.7	Below	5.5	new
100	201875_s_at	hypothetical protein FLJ21047	FLJ21047	1q23.2	NM_024569.1	28.5	Above	2.0	new

**Table S7. Top 100 chi-square probe sets selected for T-ALL in decision tree format**

	U133 probe set	Gene description	Symbol	Location	GenBank Reference	Chi-square	T-ALL above/below mean	Fold change	old or new
1	201137_s_at	major histocompatibility complex, class II, DP beta 1	HLA-DPB1	6p21.3	NM_002121.1	100.0	Below	21.0	old
2	202113_s_at	sorting nexin 2	SNX2	5q23	AF043453.1	100.0	Below	4.2	old
3	202114_at	sorting nexin 2	SNX2	5q23	NM_003100.1	100.0	Below	4.6	old
4	203675_at	nucleobindin 2	NUCB2	11p15.1-p14	NM_005013.1	100.0	Above	3.6	old
5	204670_x_at	major histocompatibility complex, class II, DR beta 3	HLA-DRB3	6p21.3	NM_002125.1	100.0	Below	13.4	old
6	205297_s_at	CD79B antigen (immunoglobulin-associated beta)	CD79B	17q23	NM_000626.1	100.0	Below	23.3	old
7	205456_at	CD3E antigen, epsilon polypeptide (TiT3 complex)	CD3E	11q23	NM_000733.1	100.0	Above	20.7	old
8	206398_s_at	CD19 antigen	CD19	16p11.2	NM_001770.1	100.0	Below	5693.6	old
9	208306_x_at	major histocompatibility complex, class II, DR beta 4	HLA-DRB4	6p21.3	NM_021983.2	100.0	Below	8.3	old
10	208894_at	major histocompatibility complex, class II, DR alpha	HLA-DRA	6p21.3	M60334.1	100.0	Below	20.9	old
11	209312_x_at	major histocompatibility complex, class II, DR beta 1	HLA-DRB1	6p21.3	U65585.1	100.0	Below	12.6	old
12	209619_at	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-	CD74	5q32	K01144.1	100.0	Below	15.1	old

associated)

13	210116_at	SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome)	SH2D1A	Xq25-q26	AF072930.1	100.0	Above	150.7	old
14	210982_s_at	major histocompatibility complex, class II, DR alpha	HLA-DRA	6p21.3	M60333.1	100.0	Below	23.4	old
15	211990_at	major histocompatibility complex, class II, DP alpha 1	HLA-DPA1	6p21.3	M27487.1	100.0	Below	19.6	old
16	211991_s_at	major histocompatibility complex, class II, DP alpha 1	HLA-DPA1	6p21.3	M27487.1	100.0	Below	24.5	old
17	213539_at	CD3D antigen, delta polypeptide (TiT3 complex)	CD3D	11q23	NM_000732.1	100.0	Above	35.7	old
18	214049_x_at	CD7 antigen (p41)	CD7	17q25.2-q25.3	AI829961	100.0	Above	312.2	old
19	214551_s_at	CD7 antigen (p41)	CD7	17q25.2-q25.3	NM_006137.2	100.0	Above	228.1	old
20	217147_s_at	T-cell receptor interacting molecule	TRIM	3q13	AJ240085.1	100.0	Above	42.6	new
21	217478_s_at	MHC, class IIa, HLA-DMA	HLA-DMA		X76775	100.0	Below	11.9	old
22	221969_at	paired box gene 5 (B-cell lineage specific activator protein)	PAX5	9p13	BF510692	100.0	Below	3922.0	new
23	227646_at	early B-cell factor	EBF	5q34	BG435302	100.0	Below	85.0	new
24	229487_at	cDNA FLJ39389 fis	FLJ39389	5	W73890	100.0	Below	7685.7	new
25	229838_at	cDNA FLJ39156 fis	FLJ39156		A1377271	100.0	Above	12.7	old
26	232204_at	early B-cell factor	EBF	5q34	AF208502.1	100.0	Below	7129.1	new
27	203965_at	ubiquitin specific protease 20	USP20	9q34.12-q34.13	NM_006676.1	91.3	Above	9.0	old
28	204891_s_at	lymphocyte-specific protein tyrosine kinase	LCK	1p34.3	NM_005356.1	91.3	Above	13.8	old
29	205255_x_at	transcription factor 7 (T-cell specific, HMG-box)	TCF7	5q31.1	NM_003202.1	91.3	Above	8.4	old
30	207655_s_at	B-cell linker	BLNK	10q23.2-q23.33	NM_013314.1	91.3	Below	103.2	old
31	209771_x_at	CD24 antigen (small cell lung carcinoma cluster 4 antigen)	CD24	6q21	AA761181	91.3	Below	40.1	old
32	211796_s_at	T cell receptor beta locus	TRB	7q34	AF043179.1	91.3	Above	20.7	old
33	213792_s_at	insulin receptor	INSR	19p13.3-p13.2	AA485908	91.3	Below	8.0	old
34	215193_x_at	major histocompatibility complex, class II, DR beta 3	HLA-DRB3	6p21.3	AJ297586.1	91.3	Below	12.1	old
35	216379_x_at	KIAA1919 protein	KIAA1919	6q22.1	AK000168.1	91.3	Below	44.0	old
36	219191_s_at	bridging integrator 2	BIN2	12q13	NM_016293.1	91.3	Above	271.0	new
37	219563_at	hypothetical protein FLJ21276	FLJ21276	14q32.2	NM_024633.1	91.3	Below	5.8	new
38	219724_s_at	KIAA0748 gene product	KIAA0748	12q12	NM_014796.1	91.3	Above	11.6	new
39	221750_at	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	HMGCS1	5p14-p13	BG035985	91.3	Above	3.4	new
40	226157_at	cDNA FLJ39131 fis	FLJ39131	3	AI569747	91.3	Above	4.4	old
41	226496_at	hypothetical protein FLJ22611	FLJ22611	9p11.1	BG291039	91.3	Below	7.6	new
42	266_s_at	CD24 antigen (small cell lung carcinoma cluster 4	CD24	6q21	L33930	91.3	Below	69.7	old

		antigen)								
43	39318_at	T-cell leukemia/lymphoma 1A	TCL1A	14q32.1	X82240	91.3	Below	367.4	old	
44	204214_s_at	RAB32, member RAS oncogene family	RAB32	6q24.3	NM_006834.1	90.6	Above	127.9	new	
45	204777_s_at	mal, T-cell differentiation protein	MAL	2cen-q13	NM_002371.2	90.6	Above	96.8	old	
46	204890_s_at	lymphocyte-specific protein tyrosine kinase	LCK	1p34.3	U07236.1	90.6	Above	18.6	old	
47	205049_s_at	CD79A antigen (immunoglobulin-associated alpha)	CD79A	19q13.2	NM_001783.1	90.6	Below	11.4	old	
48	205254_x_at	transcription factor 7 (T-cell specific, HMG-box)	TCF7	5q31.1	AW027359	90.6	Above	352.0	old	
49	205504_at	Bruton agammaglobulinemia tyrosine kinase	BTK	Xq21.33-q22	NM_000061.1	90.6	Below	6.6	old	
50	210915_x_at	T cell receptor beta locus	TRB	7q34	M15564.1	90.6	Above	15.9	old	
51	211211_x_at	SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome)	SH2D1A	Xq25-q26	AF100542.1	90.6	Above	1963.5	old	
52	213830_at	T cell receptor delta locus	TRD	14q11.2	AW007751	90.6	Above	7411.2	old	
53	216191_s_at	T cell receptor delta locus	TRD	14q11.2	X72501.1	90.6	Above	253.7	old	
54	217143_s_at	T cell receptor delta locus	TRD	14q11.2	X06557.1	90.6	Above	151.9	old	
55	219528_s_at	B-cell CLL/lymphoma 11B (zinc finger protein)	BCL11B	14q32.31-q32.32	NM_022898.1	90.6	Above	11.6	new	
56	220418_at	ubiquitin associated and SH3 domain containing, A	UBASH3A	21q22.3	NM_018961.1	90.6	Above	759.3	new	
57	222895_s_at	B-cell CLL/lymphoma 11B (zinc finger protein)	BCL11B	14q32.31-q32.32	AA918317	90.6	Above	11.7	new	
58	223553_s_at	hypothetical protein FLJ22570	FLJ22570	5q35.3	BC004564.1	90.6	Below	6.1	new	
59	225090_at	HRD1 protein	HRD1	11q12	AA844682	90.6	Below	3.6	new	
60	226459_at	Homo sapiens gastric cancer-related protein GCYS-20 (gcys-20) mRNA, complete cds			AW575754	90.6	Below	10.7	new	
61	228314_at	cDNA FLJ37485 fis	FLJ37485		BE877357	90.6	Below	4.7	new	
62	201384_s_at	membrane component, chromosome 17, surface marker 2 (ovarian carcinoma antigen CA125)	M17S2	17q21.1	NM_005899.1	83.8	Above	3.3	new	
63	202540_s_at	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	HMGCR	5q13.3-q14	NM_000859.1	83.8	Above	4.4	old	
64	203198_at	cyclin-dependent kinase 9 (CDC2-related kinase)	CDK9	9q34.1	NM_001261.1	83.8	Below	4.8	old	
65	203932_at	major histocompatibility complex, class II, DM beta	HLA-DMB	6p21.3	NM_002118.1	83.8	Below	7.9	old	
66	204613_at	phospholipase C, gamma 2 (phosphatidylinositol-specific)	PLCG2	16q24.1	NM_002661.1	83.8	Below	3.9	old	
67	205267_at	POU domain, class 2, associating factor 1	POU2AF1	11q23.1	NM_006235.1	83.8	Below	11.2	old	
68	208650_s_at	CD24 antigen (small cell lung carcinoma cluster 4 antigen)	CD24	6q21	BG327863	83.8	Below	74.7	old	
69	208651_x_at	CD24 antigen (small cell lung carcinoma cluster 4 antigen)	CD24	6q21	M58664.1	83.8	Below	52.7	old	
70	209995_s_at	T-cell leukemia/lymphoma 1A	TCL1A	14q32.1	BC003574.1	83.8	Below	20166.	old 2	
71	210038_at	protein kinase C, theta	PRKCQ	10p15	AL137145	83.8	Above	12.7	old	
72	211126_s_at	cysteine and glycine-rich protein 2	CSRP2	12q21.1	U46006.1	83.8	Below	18.0	old	
73	220068_at	pre-B lymphocyte gene 3	VPREB3	22q11.23	NM_013378.1	83.8	Below	6559.8	new	

74	226245_at	cDNA DKFZp451C132	DKFZp451C132		U55984	83.8	Above	8.7	new
75	202615_at	cDNA DKFZp686D0521	DKFZp686D0521		BF222895	82.2	Above	3.1	old
76	224861_at	cDNA FLJ31057 fis	FLJ31057		BF477658	82.2	Above	3.5	new
77	201194_at	selenoprotein W, 1	SEPW1	19q13.3	NM_003009.1	82.0	Above	3.8	old
78	201349_at	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 1	SLC9A3R1	17q25.2	NM_004252.1	82.0	Above	2.9	old
79	202539_s_at	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	HMGCR	5q13.3-q14	AL518627	82.0	Above	3.5	old
80	203588_s_at	transcription factor Dp-2 (E2F dimerization partner 2)	TFDP2	3q23	BG034328	82.0	Above	17.5	old
81	204852_s_at	protein tyrosine phosphatase, non-receptor type 7	PTPN7	1q32.1	NM_002832.1	82.0	Above	9.5	old
82	207434_s_at	FXVD domain containing ion transport regulator 2	FXVD2	11q23	NM_021603.1	82.0	Above	14.6	old
83	208872_s_at	DNA segment, single copy probe LNS-CAI/LNS-CAII	D5S346	5q22-q23	AA814140	82.0	Below	2.6	old
84	209200_at	MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C)	MEF2C	5q14	N22468	82.0	Below	7.5	old
85	212795_at	KIAA1033 protein	KIAA1033	12q24.11	AL137753.1	82.0	Below	2.4	old
86	212827_at	immunoglobulin heavy constant mu	IGHM	14q32.33	X17115.1	82.0	Below	13.1	old
87	213193_x_at	T cell receptor beta locus	TRB	7q34	AL559122	82.0	Above	10.9	old
88	221002_s_at	tetraspanin similar to TM4SF9	DC-TM4F2	10q23.2	NM_030927.1	82.0	Below	2.1	new
89	225314_at	hypothetical protein MGC45416	MGC45416	4p12	BG291649	82.0	Above	5.5	new
90	227432_s_at	insulin receptor	INSR	19p13.3-p13.2	AI215106	82.0	Below	6.0	old
91	203332_s_at	inositol polyphosphate-5-phosphatase, 145kDa	INPP5D	2q36-q37	NM_005541.1	81.5	Below	2.2	old
92	203589_s_at	transcription factor Dp-2 (E2F dimerization partner 2)	TFDP2	3q23	NM_006286.1	81.5	Above	35.1	old
93	205674_x_at	FXVD domain containing ion transport regulator 2	FXVD2	11q23	NM_001680.2	81.5	Above	12.2	old
94	209881_s_at	Linker for activation of T cells	LAT	16q13	AF036905.1	81.5	Above	1823.4	old
95	211005_at	Linker for activation of T cells	LAT	16q13	AF036906.1	81.5	Above	67.8	old
96	211075_s_at	CD47	CD47		Z25521.1	81.5	Above	2.1	old
97	211210_x_at	SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome)	SH2D1A	Xq25-q26	AF100539.1	81.5	Above	300.2	old
98	213601_at	slit homolog 1 (Drosophila)	SLIT1	10q23.3-q24	AB011537.2	81.5	Above	1752.1	old
99	213857_s_at	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	CD47	3q13.1-q13.2	BG230614	81.5	Above	2.2	old
100	214924_s_at	KIAA1042 protein	KIAA1042	3p25.3-p24.1	AK000754.1	81.5	Below	2.3	old

**Table S8. Top 100 chi-square probe sets selected for *TEL-AML1* in decision tree format**

	<b>U133 probe set</b>	<b>Gene description</b>	<b>Symbol</b>	<b>Location</b>	<b>GenBank Reference</b>	<b>Chi-square value</b>	<b>TEL-AML above/below mean</b>	<b>Fold change</b>	<b>old or new</b>
1	224722_at	KIAA1323	KIAA1323	18q11.1	W80418	75	Above	7.6	new
2	227377_at	FLJ12722	FLJ12722	17q21.32	AK022784.1	75	Above	2446.3	new
3	237206_at	Homo sapiens cDNA FLJ39434	FLJ39434	17p12	AI452798	75	Above	23.7	new
4	241505_at	EST			BF513468	75	Above	13.4	new
5	203184_at	Fibrillin 2 (congenital contractural arachnodactyly)	FBN2	5q23.2	NM_001999.2	69.1	Above	14.4	new
6	205109_s_at	Rho guanine nucleotide exchange factor (GEF) 4	ARHGEF4	2q22	NM_015320.1	69.1	Above	148.1	old
7	210650_s_at	Piccolo (presynaptic cytomatrix protein)	PCLO	7q21.11	BC001304.1	69.1	Above	101.2	old
8	213558_at	Piccolo (presynaptic cytomatrix protein)	PCLO	7q21.11	AB011131.1	69.1	Above	77.5	old
9	220451_s_at	baculoviral IAP repeat-containing 7 (livin)	BIRC7	20q13.3	NM_022161.1	69.1	Above	25.4	new
10	224720_at	KIAA1323	KIAA1323	18q11.1	W80418	69.1	Above	4.3	new
11	235694_at	Homo sapiens, clone IMAGE:4661943, mRNA, partial cds		20q13.33	N49233	69.1	Above	9.3	new
12	202808_at	Hypothetical protein FLJ20154	FLJ20154	10q24.32	AK000161.1	68.9	Above	3.7	old
13	206032_at	Desmocollin 3	DSC3	18q12.1	AI797281	68.9	Above	54.1	new
14	206033_s_at	Desmocollin 3	DSC3	18q12.1	NM_001941.2	68.9	Above	357.1	new
15	209228_x_at	Putative prostate cancer tumor suppressor gene	N33	8p22	U42349.1	68.9	Above	20.8	new
16	224725_at	KIAA1323	KIAA1323	18q11.1	W80418	68.9	Above	3.6	new
17	203910_at	PTPL1-associated RhoGAP 1	PARG1	1p22.1	NM_004815.1	64	Above	7.1	new
18	204849_at	Transcription factor-like 5 (basic helix-loop-helix)	TCFL5	20q13.33	NM_006602.1	64	Above	8.9	old
19	206231_at	Potassium intermediate/small conductance calcium-activated channel, subfamily N, member 1	KCNN1	19p13.1	NM_002248.2	64	Above	72.7	old
20	208056_s_at	Core-binding factor, runt domain, alpha subunit 2; translocated to, 3	CBFA2T3	16q24	NM_005187.2	63	Above	2.5	old
21	211222_s_at	Huntingtin-associated protein 1 (neuroan 1)	HAP1	17q21.2	AF040723.1	63	Above	80.8	new
22	223468_s_at	hypothetical protein from EUROIMAGE 363668 RGM: likely ortholog of chicken repulsive guidance molecule	RGM	15q26.1	AL136826.1	63	Above	10.6	new
23	227266_s_at	FYN-binding protein	FYB	5p13.1	BF679849	63	Above	3.1	old

24	228158_at	ESTs, Highly similar to A43542 lymphocyte-specific protein 1 - human		2p11.1	AI623211	63	Above	7.9	new
25	37986_at	Eerythropoietin receptor	EPOR	19p13.2	M60459	63	Above	15.5	old
26	203464_s_at	Epsin 2	EPN2	17p11.1	NM_014964.1	62.9	Above	43.3	new
27	213317_at	chloride intracellular channel 5	CLIC5	6p21.1	AL049313.1	62.9	Above	99.3	old
28	213423_x_at	Putative prostate cancer tumor suppressor	N33	8p22	AI884858	62.9	Above	15.7	new
29	226817_at	Desmocollin 2	DSC2	18q12.1	AU154691	62.9	Above	48.3	new
30	227862_at	ESTs, Weakly similar to hypothetical protein FLJ22184		1p35.1	AA037766	62.9	Above	14.7	new
31	229339_at	EST			AI093327	62.9	Above	31.1	new
32	211795_s_at	FYN binding protein	FYB	5p13.1	AF198052.1	59.4	Above	4.1	old
33	218627_at	Hypothetical protein FLJ11259	FLJ11259	12q23.1	NM_018370.1	57.9	Above	4.6	new
34	221748_s_at	Tensin	TNS	2q35	AL046979	57.9	Above	6.6	new
35	200709_at	FK506 binding protein 1A (12kD)	FKBP1A	20p13	NM_000801.1	57.1	Above	1.8	old
36	204615_x_at	Isopentenyl-diphosphate delta isomerase	IDI1	10p15.3	NM_004508.1	57.1	Above	2.6	old
37	208881_x_at	Isopentenyl-diphosphate delta isomerase	IDI1	10p15.3	BC005247.1	57.1	Above	2.6	old
38	213301_x_at	Transcriptional intermediary factor 1	TIF1	7q34	AL538264	57.1	Above	2.0	new
39	221747_at	Tensin	TNS	2q35	AL046979	57.1	Above	49.2	new
40	224726_at	KIAA1323	KIAA1323	18q11.1	W80418	57.1	Above	26.1	new
41	231455_at	ESTs		2p25.2	AA768888	57.1	Above	7.7	new
42	232750_at	Homo sapiens cDNA FLJ13750	FLJ13750	2q35	AU158570	57.1	Above	35.0	new
43	209685_s_at	Protein kinase C, beta 1	PRKCB1	16p11.2	M13975.1	53.6	Above	1.9	old
44	204404_at	solute carrier family 12 (sodium/potassium/chloride transporters), member 2	SLC12A2	5q23.3	NM_001046.1	53.4	Above	2.0	new
45	239673_at	ESTs		4q31.23	AW080999	53.4	Above	9.0	new
46	240950_s_at	Homo sapiens cDNA FLJ32658	FLJ32658	19q13.33	AA400740	53.4	Above	9.9	new
47	204297_at	Phosphoinositide-3-kinase, class 3	PIK3C3	18q12.3	NM_002647.1	52.5	Above	4.5	old
48	206591_at	Recombination activating gene 1	RAG1	11p13	NM_000448.1	52.1	Above	5.4	old
49	209962_at	Erythropoietin receptor	EPOR	19p13.2	M34986.1	52.1	Above	17.0	old
50	209963_s_at	Erythropoietin receptor	EPOR	19p13.2	M34986.1	52.1	Above	7.6	old
51	210186_s_at	FK506 binding protein 1A (12kD)	FKBP1A	20p13	BC005147.1	52.1	Above	1.8	old
52	219866_at	Chloride intracellular channel 5	CLIC5	6p21.1	NM_016929.1	52.1	Above	60.3	old
53	203474_at	IQ motif containing GTPase activating protein 2	IQGAP2	5q13.2	NM_006633.1	51.6	Below	2.8	old
54	210058_at	Mitogen-activated protein kinase 13	MAPK13	6p21.1	BC000433.1	51.6	Above	2.3	new
55	211891_s_at	Rho guanine nucleotide exchange factor (GEF) 4	ARHGEF4	2q22	AB042199.1	51.6	Above	452.6	old
56	214214_s_at	Complement component 1, q subcomponent binding protein	C1QBP	17p13.3	AU151801	51.6	Below	2.0	old
57	218152_at	High-mobility group 20A	HMG20A	15q24	NM_018200.1	51.6	Above	1.7	new
58	234983_at	ESTs	FLJ21415	12q24.22	BE893995	51.6	Above	2.4	new

59	240446_at	KIAA1323	KIAA1323	18q11.2	AI798164	51.6	Above	102.2	new
60	244107_at	ESTs		18q12.1	AW189097	51.6	Above	518.9	new
61	205794_s_at	Neuro-oncological ventral antigen 1	NOVA1	14q12	NM_002515.1	51.4	Above	40.4	new
62	217628_at	chloride intracellular channel 5	CLIC5	6p21.1	BF032808	51.4	Above	87.4	old
63	218804_at	Hypothetical protein FLJ10261	FLJ10261	11q13.3	NM_018043.1	51.4	Above	41.6	new
64	230698_at	Homo sapiens mRNA; cDNA DKFZp434H205		7q11.22	AW072102	51.4	Above	8.7	new
65	225129_at	cDNA FLJ37548 fis	FLJ37548	16q13	AW170571	49.4	Above	3.0	new
66	201266_at	Thioredoxin reductase 1	TXNRD1	12q23-q24.1	NM_003330.1	48.2	Above	1.7	old
67	203611_at	Telomeric repeat binding factor 2	TERF2	16q22.1	NM_005652.1	48.2	Above	5.3	old
68	213017_at	abhydrolase domain containing 3	ABHD3	18q11.1	AL534702	48.2	Above	4.0	new
69	236430_at	hypothetical protein MGC23911	MGC23911	16q22.1	AA708152	48.2	Above	16.8	new
70	209035_at	Midkine (neurite growth-promoting factor 2).	MDK	11p11.2	M69148.1	47.7	Above	4.6	old
71	209193_at	Pim-1 oncogene	PIM1	6p21.2	M24779.1	47.7	Above	2.0	old
72	218625_at	Neuritin 1	NRN1	6p24.1	NM_016588.1	47.7	Above	5.1	new
73	226038_at	Hypothetical protein FLJ23749	FLJ23749	8p23.1	BF680438	47.7	Above	5.2	new
74	232227_at	ESTs, Moderately similar to AF161442_1 HSPC324		9q34.3	AV736391	47.7	Above	14.7	new
75	204160_s_at	Ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)	ENPP4	6p12.3	AW194947	46.5	Above	7.2	new
76	206233_at	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6	B4GALT6	18q11	AF097159.1	46.5	Above	2.6	new
77	218813_s_at	SH3-domain GRB2-like endophilin B2	SH3GLB2	9q34.11	NM_020145.1	46.5	Above	6.2	new
78	227111_at	Homo sapiens cDNA FLJ31099 fis, clone IMR321000230	FLJ31099	9q33	BG179317	46.5	Above	2.7	new
79	202382_s_at	Glucosamine-6-phosphate isomerase	GNPI	5q21	NM_005471.1	46.2	Above	5.6	new
80	202838_at	Fucosidase, alpha-L- 1, tissue	FUCA1	1p34	NM_000147.1	46.2	Above	4.8	old
81	225731_at	Hypothetical protein KIAA1223	KIAA1223	4q26	AB033049.1	46.2	Above	2.8	new
82	225835_at	Homo sapiens cDNA: FLJ21409 fis, clone COL03924		5q23.2	AK025062.1	46.2	Above	3.6	new
83	229790_at	Telomeric repeat binding factor 2	TERF2	16q22.1	AW006832	46.2	Above	7.4	old
84	230069_at	Hypothetical protein FLJ12876	FLJ12876	5q35.3	BF593817	46.2	Above	9.4	new
85	235872_at	ESTs			BE408975	46.2	Above	17.7	new
86	239300_at	EST		18q12.3	AI632214	46.2	Above	3.0	new
87	241940_at	EST		18q11.2	BF477544	46.2	Above	2.9	new
88	203370_s_at	Enigma (LIM domain protein)	ENIGMA	5q35.3	NM_005451.2	45.9	Above	8.1	new
89	215149_at	LOC149153:	LOC149153	1p36.32	AF052109.1	45.9	Above	9.2	new
90	217901_at	Desmoglein 2 desmosomal cadherin	DSG2	18q12.1	BF031829	45.9	Above	6.7	new
91	235333_at	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6	B4GALT6	18q12.1	BG503479	45.9	Above	2.0	new

92	242881_x_at	EST			BG285837	45.9	Above	11.8	new
93	200783_s_at	Stathmin 1/oncoprotein 18 leukemia-associated phosphoprotein	STMN1	1p35.1	NM_005563.2	45.8	Above	1.5	old
94	201334_s_at	Rho guanine nucleotide exchange factor (GEF) 12	ARHGEF12	11q23.3	NM_015313.1	45.8	Above	6.1	new
95	203038_at	Protein tyrosine phosphatase, receptor type, K	PTPRK	6q22.33	NM_002844.1	45.8	Above	9.1	old
96	209735_at	ATP-binding cassette, sub-family G (WHITE), member 2	ABCG2	4q22	AF098951.2	45.8	Above	4.5	new
97	212063_at	Unactive progesterone receptor, 23 kD	P23	12q12	BE903880	45.8	Below	7.4	new
98	212399_s_at	KIAA0121 gene product	KIAA0121	3p25.2	D50911.2	45.8	Above	1.8	old
99	212438_at	Putative nucleic acid binding protein RY-1	RY1	2p13.1	BG252325	45.2	Above	1.7	old
100	214761_at	OLF-1/early B-cell factor associated zinc finger protein	OAZ	16q12	AW149417	45.2	Above	2.1	old

**Table S9. Top 100 chi-square probe sets selected for *BCR-ABL* in parallel format**

	<b>U133 probe set</b>	<b>Gene description</b>	<b>Symbol</b>	<b>Location</b>	<b>GenBank Reference</b>	<b>Unigene Reference</b>	<b>Chi-square value</b>	<b>BCR-ABL above/below mean</b>	<b>Fold change</b>
1	201876_at	paraoxonase 2	PON2	7q21.3	NM_000305.1	Hs.169857	70.8	Above	18.6
2	210830_s_at	paraoxonase 2	PON2	7q21.3	AF001602.1	Hs.169857	70.8	Above	23.4
3	209365_s_at	extracellular matrix protein 1	ECM1	1q21	U65932.1	Hs.81071	70.4	Above	6.0
4	209238_at	syntaxin 3A	STX3A	11q12.3	BE966922	Hs.82240	66.5	Above	2.2
5	212242_at	tubulin, alpha 1 (testis specific)	TUBA1	2q36.2	AL565074	Hs.75318	64.9	Above	3.2
6	222488_s_at	dynactin 4 (p62)	DCTN4	5q31-q32	BE218028	Hs.180952	63.3	Above	3.6
7	222762_x_at	LIM domains containing 1	LIMD1	3p21.3	AU144259	Hs.48469	63.3	Above	2.6
8	201310_s_at	P311 protein. Similar to gastrin/cholecystokinin type B receptor	P311	5q21.3	NM_004772.1	Hs.142827	61.3	Below	2.2
9	215617_at	Homo sapiens cDNA FLJ11754 fis, clone HEMBA1005588			AU145711	Hs.301006	61.3	Above	15.8
10	200951_s_at	cyclin D2	CCND2	12p13	NM_001759.1	Hs.75586	60.9	Above	12.6
11	204430_s_at	solute carrier family 2 (facilitated glucose/fructose transporter), member 5	SLC2A5	1p36.2	NM_003039.1	Hs.33084	60.9	Above	5.1
12	200953_s_at	cyclin D2	CCND2	12p13	NM_001759.1	Hs.75586	60.7	Above	3.6
13	222154_s_at	DKFZP564A2416 protein	DKFZP564A2416	2q33.1	AK002064.1	Hs.5297	60.3	Above	12.3
14	204429_s_at	solute carrier family 2 (facilitated glucose/fructose transporter), member 5	SLC2A5	1p36.2	BE560461	Hs.33084	57.1	Above	5.0

15	219315_s_at	hypothetical protein FLJ20898	FLJ20898	16p13.12	NM_024600.1	Hs.25549	57.1	Above	5.4
16	241812_at	Homo sapiens cDNA FLJ35598 fis, clone SPLEN2008317			AV648669	Hs.199438	55.9	Above	5.2
17	201906_s_at	HYA22 protein	HYA22	3p21.3	NM_005808.1	Hs.147189	54.0	Above	43.1
18	202947_s_at	glycophorin C (Gerbich blood group)	GYPC	2q14-q21	NM_002101.2	Hs.81994	54.0	Above	3.1
19	242579_at	ESTs			AA935461	Hs.161712	54.0	Above	10.1
20	212203_x_at	interferon induced transmembrane protein 3 (1-8U)	IFITM3	11	BF338947	Hs.182241	52.0	Above	2.3
21	240173_at	ESTs			AI732969	Hs.126245	52.0	Above	10.2
22	212298_at	neuropilin 1	NRP1	10p12	BE620457	Hs.69285	51.8	Above	13.7
23	212592_at	immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides	IGJ	4q21	AV733266	Hs.76325	51.8	Above	8.0
24	222868_s_at	interleukin 18 binding protein	IL18BP	11q13	AI521549	Hs.325978	51.6	Above	7.1
25	235988_at	ESTs			AA746038	Hs.125343	51.6	Above	15.6
26	239273_s_at	matrix metalloproteinase 28	MMP28	17q11-q21.1	AI927208	Hs.231958	51.6	Above	89.8
27	219938_s_at	proline-serine-threonine phosphatase interacting protein 2	PSTPIP2	18q12	NM_024430.1	Hs.69149	51.6	Above	5.2
28	207196_s_at	Nef-associated factor 1	NAF1	5q32-q33.1	NM_006058.1	Hs.109281	47.2	Above	1.4
29	227533_at	ESTs			AA732944	Hs.5415	47.1	Below	2.7
30	217110_s_at	mucin 4	MUC4	3q29	AJ242547.1	Hs.198267	45.0	Above	47.2
31	220684_at	T-box 21	TBX21	17q21.2	NM_013351.1	Hs.272409	45.0	Above	3.3
32	227182_at	hypothetical protein MGC26847	MGC26847	9q22.2	AW966474	Hs.88417	45.0	Above	7.2
33	223075_s_at	hypothetical protein FLJ12783	FLJ12783	9q34.13-q34.3	AL136566.1	Hs.4944	45.0	Above	3.9
34	202748_at	guanylate binding protein 2, interferon-inducible	GBP2	1p22.1	NM_004120.2	Hs.171862	44.5	Above	3.9
35	214657_s_at	multiple endocrine neoplasia I	MEN1	11q13	AU134977	Hs.240443	43.3	Above	2.3
36	202771_at	KIAA0233 gene product	KIAA0233	16q24.3	NM_014745.1	Hs.79077	43.3	Above	1.9
37	217967_s_at	chromosome 1 open reading frame 24	C1orf24	1q25	AF288391.1	Hs.48778	43.3	Above	3.3
38	220024_s_at	Periaxin	PRX	19q13.13-q13.2	NM_020956.1	Hs.205457	43.3	Above	8.1
39	203217_s_at	sialyltransferase 9	SIAT9	2p11.2	NM_003896.1	Hs.225939	43.2	Above	1.8
40	238689_at	Homo sapiens cDNA FLJ30646 fis, clone CTONG2004716, weakly similar to Rattus norvegicus mRNA for seven transmembrane receptor			BG426455	Hs.256897	43.2	Above	10.8
41	200665_s_at	secreted protein, acidic, cysteine-rich (osteonectin)	SPARC	5q31.3-q32	NM_003118.1	Hs.111779	42.9	Above	10.5
42	200864_s_at	RAB11A, member RAS oncogene family	RAB11A	15q21.3-q22.31	NM_004663.1	Hs.75618	42.9	Above	1.4
43	213075_at	Homo sapiens, clone IMAGE:3140802, mRNA			AL050002.1	Hs.94795	42.9	Above	26.4
44	236489_at	ESTs			AI282097	Hs.72307	42.9	Above	16.6
45	48106_at	hypothetical protein FLJ20489	FLJ20489	12p11.1	H14241	Hs.306989	42.6	Above	2.8

46	203005_at	lymphotoxin beta receptor (TNFR superfamily, member 3)	LTBR	12p13	NM_002342.1	Hs.1116	42.6	Above	9.9
47	205467_at	caspase 10, apoptosis-related cysteine protease	CASP10	2q33-q34	NM_001230.1	Hs.5353	42.6	Above	3.6
48	220454_s_at	semaphorin 6A	SEMA6A	5q23.1	NM_020796.1	Hs.263395	42.6	Above	3.3
49	228696_at	prostein protein	LOC85414	1q31.1	AA631143	Hs.278695	42.6	Above	95.9
50	235306_at	hypothetical protein DKFZp667I133	DKFZp667I133	7q35	AI611648	Hs.95834	42.6	Above	3.5
51	239272_at	matrix metalloproteinase 28	MMP28	17q11-q21.1	AI927208	Hs.231958	42.6	Above	14.2
52	242572_at	ESTs			BF435438	Hs.269924	42.6	Above	4.9
53	242677_at	ESTs			AI088099	Hs.173548	42.6	Above	469.2
54	244597_at	ESTs			AA701247	Hs.269548	42.6	Above	11.7
55	218013_x_at	dynactin 4 (p62)	DCTN4	5q31-q32	NM_016221.1	Hs.180952	41.5	Above	3.6
56	218084_x_at	FXYD domain containing ion transport regulator 5	FXYD5	19q12-q13.1	NM_014164.2	Hs.333418	41.5	Above	1.5
57	221790_s_at	LDL receptor adaptor protein	ARH	1p36-p35	AL545035	Hs.184482	41.5	Above	3.5
58	201028_s_at	antigen identified by monoclonal antibodies 12E7, F21 and O13	MIC2	Xp22.32	U82164.1	Hs.177543	41.4	Above	2.6
59	210105_s_at	FYN oncogene related to SRC, FGR, YES	FYN	6q21	M14333.1	Hs.169370	40.7	Above	1.8
60	201445_at	calponin 3, acidic	CNN3	1p22-p21	NM_001839.1	Hs.194662	39.8	Above	10.7
61	229139_at	Homo sapiens, clone IMAGE:4245141, mRNA			AI202201	Hs.293836	39.5	Above	10.7
62	229975_at	ESTs			AI826437	Hs.72472	39.0	Above	9.0
63	205055_at	integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha polypeptide)	ITGAE	17p13	NM_002208.3	Hs.851	38.8	Below	2.1
64	226190_at	glucose phosphate isomerase	GPI	19q13.1	BG029496	Hs.279789	38.8	Above	3.5
65	209732_at	C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 2 (activation-induced)	CLECSF2	12p13-p12	BC005254.1	Hs.85201	37.1	Above	2.3
66	210487_at	deoxynucleotidyltransferase, terminal	DNTT	10q23-q24	M11722.1	Hs.272537	37.1	Above	2.0
67	203508_at	tumor necrosis factor receptor superfamily, member 1B	TNFRSF1B	1p36.3-p36.2	NM_001066.1	Hs.256278	36.4	Above	2.6
68	209321_s_at	adenylate cyclase 3	ADCY3	2p24-p22	AF033861.1	Hs.8402	36.4	Above	2.0
69	212552_at	hippocalcin-like 1	HPCAL1	2p25.1	BE617588	Hs.3618	36.4	Above	2.0
70	219871_at	hypothetical protein FLJ13197	FLJ13197	4p14	NM_024614.1	Hs.29725	36.4	Above	14.4
71	203159_at	glutaminase	GLS	2q32-q34	NM_014905.1	Hs.239189	36.4	Above	1.5
72	203725_at	growth arrest and DNA-damage-inducible, alpha	GADD45A	1p31.2-p31.1	NM_001924.2	Hs.80409	36.4	Above	3.1
73	208893_s_at	dual specificity phosphatase 6	DUSP6	12q22-q23	BC005047.1	Hs.180383	36.4	Above	3.6
74	228297_at	calponin 3, acidic	CNN3	1p22-p21	AI807004	Hs.194662	36.4	Above	4.9
75	231055_at	ESTs			BF432941	Hs.263462	36.4	Above	3.4
76	202123_s_at	v-abl Abelson murine leukemia viral oncogene homolog 1	ABL1	9q34.1	NM_005157.2	Hs.146355	35.2	Above	1.8

77	225108_at	ESTs			BF111719	Hs.356237	35.0	Above	3.0
78	239519_at	ESTs			AA927670	Hs.131704	35.0	Above	18.1
79	64064_at	immune associated nucleotide 4 like 1 (mouse)	IAN4L1	7q36	AI435089	Hs.26194	34.1	Above	3.4
80	204576_s_at	KIAA0643 protein	KIAA0643	16p12.3	AA207013	Hs.155995	34.1	Above	1.9
81	205376_at	inositol polyphosphate-4-phosphatase, type II, 105kDa	INPP4B	4q31.1	NM_003866.1	Hs.153687	34.1	Above	16.7
82	218693_at	transmembrane 4 superfamily member tetraspan NET-7	NET-7	10q22.3	NM_012339.1	Hs.95583	34.1	Above	21.9
83	219073_s_at	oxysterol binding protein-like 10	OSBPL10	3p22.3	NM_017784.1	Hs.321622	34.1	Above	4.9
84	222126_at	insulin receptor substrate 3-like	IRS3L	7q22	AI247494	Hs.30827	34.1	Above	7.4
85	216985_s_at	syntaxin 3A	STX3A	11q12.3	AJ002077.1	Hs.82240	34.1	Above	11.9
86	201809_s_at	endoglin (Osler-Rendu-Weber syndrome 1)	ENG	9q33-q34.1	NM_000118.1	Hs.76753	34.1	Above	6.0
87	201204_s_at	ribosome binding protein 1 homolog 180kDa	RRBP1	20p12	AI921320	Hs.98614	33.7	Above	2.6
88	201743_at	CD14 antigen	CD14	5q31.1	NM_000591.1	Hs.75627	33.7	Above	3.6
89	202180_s_at	major vault protein	MVP	16p13.1-p11.2	NM_017458.1	Hs.80680	33.7	Above	4.3
90	203253_s_at	KIAA0433 protein	KIAA0433	5q15	NM_015216.1	Hs.26179	33.7	Above	1.5
91	209030_s_at	immunoglobulin superfamily, member 4	IGSF4	11q23.2	NM_014333.1	Hs.70337	33.7	Above	10.8
92	209829_at	chromosome 6 open reading frame 32	C6orf32	6p22.3-p21.32	AB002384.1	Hs.101359	33.7	Above	2.1
93	212365_at	myosin IB	MYO1B	2q12-q34	AK000160.1	Hs.121576	33.7	Above	3.0
94	214255_at	ATPase, Class V, type 10C	ATP10C	15q11-q13	AB011138.1	Hs.44697	33.7	Above	9.8
95	214321_at	nephroblastoma over expressed gene	NOV	8q24.1	BF440025	Hs.235935	33.7	Above	49.2
96	218086_at	neural proliferation, differentiation and control, 1	NPDC1	9q34.3	NM_015392.1	Hs.105547	33.7	Above	28.8
97	222937_s_at	matrix metalloproteinase 28	MMP28	17q11-q21.1	AF219624.1	Hs.231958	33.7	Above	70.2
98	225113_at	Homo sapiens mRNA; cDNA DKFZp762O2215 (from clone DKFZp762O2215)			BF111719	Hs.331666	33.7	Above	7.2
99	225244_at	IMAGE3451454: GRASP protein	IMAGE345 1454	1q42.13	AA019893	Hs.325081	33.7	Above	2.0
100	228573_at	capillary morphogenesis protein 2	CMG2	4q21.21	BE673665	Hs.5897	33.7	Above	2.2

**Table S10. Top 100 chi-square probe sets selected for *E2A-PBX1* in parallel format**

	U133 probe set	Gene description	Symbol	Location	GenBank Reference	Unigene Reference	Chi-square value	E2A-PBX Above/below mean	Fold change
1	201695_s_at	nucleoside phosphorylase	NP	14q13.1	NM_000270.1	Hs.75514	100.0	Above	3.8
2	204674_at	lymphoid-restricted membrane protein	LRMP	12p12.3	NM_006152.1	Hs.40202	100.0	Above	5.8
3	205253_at	pre-B-cell leukemia transcription factor 1	PBX1	1q23	NM_002585.1	Hs.155691	100.0	Above	3549.2

4	212148_at	pre-B-cell leukemia transcription factor 1, splice variant	PBX1				100.0	Above	5283.5
5	212151_at	pre-B-cell leukemia transcription factor 1, splice variant	PBX1				100.0	Above	7472.2
6	212371_at	Homo sapiens mRNA; cDNA DKFZp586C1019 (from clone DKFZp586C1019)			AL049397.1	Hs.12314	100.0	Above	2.5
7	219155_at	retinal degeneration B beta	RDGBB	17q24.2	NM_012417.1	Hs.333212	100.0	Above	2.7
8	225483_at	hypothetical protein MGC10485	MGC10485	11q25	AI971602	Hs.334684	100.0	Above	7.7
9	227439_at	E2a-Pbx1-associated protein	EB-1	12	AW005572	Hs.372732	100.0	Above	267.7
10	227949_at	Q9H4T4 like	H17739	20q13.32	AL357503	Hs.288513	100.0	Above	59.8
11	230306_at	hypothetical protein MGC10485	MGC10485	11q25	AA514326	Hs.334684	100.0	Above	19.1
12	231095_at	ESTs, Moderately similar to retinal degeneration B beta [Homo sapiens] [H.sapiens]			AW193811	Hs.112703	100.0	Above	26.7
13	35974_at	lymphoid-restricted membrane protein	LRMP	12p12.3	U10485	Hs.40202	91.8	Above	6.1
14	38340_at	huntingtin interacting protein 12	HIP12	12q24	AB014555	Hs.96731	91.8	Above	3.8
15	206028_s_at	c-mer proto-oncogene tyrosine kinase	MERTK	2q14.1	NM_006343.1	Hs.306178	91.8	Above	24.2
16	206181_at	signaling lymphocytic activation molecule	SLAM	1q22-q23	NM_003037.1	Hs.32970	91.8	Above	6.4
17	208644_at	ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)	ADPRT	1q41-q42	M32721.1	Hs.177766	91.3	Above	3.0
18	221113_s_at	wingless-type MMTV integration site family, member 16	WNT16	7q31	NM_016087.1	Hs.272375	91.3	Above	2547.6
19	232289_at	Homo sapiens cDNA FLJ14167 fis, clone NT2RP2001214			BF237871	Hs.200629	91.3	Above	143.0
20	224022_x_at	wingless-type MMTV integration site family, member 16	WNT16	7q31	AF169963.1	Hs.272375	91.3	Above	565.4
21	235666_at	ESTs, Weakly similar to hypothetical protein FLJ20489 [Homo sapiens] [H.sapiens]			AA903473	Hs.153717	91.3	Above	649.9
22	225235_at	hypothetical protein MGC14859	MGC14859	5q35.3	AW007710	Hs.57100	84.7	Above	3.7
23	224733_at	chemokine-like factor super family 3	CKLFSF3	16q23.1	AL574900	Hs.7773	84.7	Below	41.6
24	211913_s_at				L08961.1		83.1	Above	42.3
25	219551_at	uncharacterized bone marrow protein BM040	BM040	3q21.1	NM_018456.1	Hs.26892	83.1	Above	3.0
26	223693_s_at	hypothetical protein FLJ10324	FLJ10324	7p22	AL136731.1	Hs.157158	83.1	Above	65.0
27	200600_at	moesin	MSN	Xq11.2-q12	NM_002444.1	Hs.170328	82.7	Below	2.2
28	213909_at	Homo sapiens cDNA FLJ12280			AU147799	Hs.288467	82.7	Above	12.4
29	235911_at	ESTs, Weakly similar to PIHUB6 salivary proline-rich protein precursor PRB1 (large allele) - human [H.sapiens]			AI885815	Hs.184727	82.7	Above	36.3
30	243533_x_at	ESTs			H09663	Hs.106490	82.7	Above	24.4
31	204114_at	nidogen 2 (osteonidogen)	NID2	14q21-q22	NM_007361.1	Hs.82733	82.3	Above	15.1

32	202615_at	Homo sapiens mRNA; cDNA DKFZp686D0521 (from clone DKFZp686D0521)			BF222895	Hs.356786	78.4	Below	6.1
33	212789_at	KIAA0056 protein	KIAA0056	11q25	AI796581	Hs.13421	78.4	Above	3.9
34	228580_at	serine protease HTRA3	HTRA3	4p16.1	AI828007	Hs.60440	76.1	Above	3.7
35	202796_at	synaptopodin	KIAA1029	5q33.1	NM_007286.1	Hs.5307	76.1	Above	51.9
36	218640_s_at	phafin 2	FLJ13187	8q21.3	NM_024613.1	Hs.29724	76.1	Above	3.1
37	231040_at	ESTs			AW512988	Hs.184780	76.1	Above	16.3
38	235099_at	ESTs, Weakly similar to PLLP_HUMAN Plasmolipin [H.sapiens]			AW080832	Hs.154986	76.1	Above	6.7
39	205173_x_at	CD58 antigen, (lymphocyte function-associated antigen 3)	CD58	1p13	NM_001779.1	Hs.75626	74.6	Above	2.4
40	211744_s_at	CD58 antigen, (lymphocyte function-associated antigen 3)	CD58	1p13	BC005930.1	Hs.75626	74.6	Above	2.4
41	213358_at	KIAA0802 protein	KIAA0802	18p11.21	AB018345.1	Hs.27657	74.6	Above	12.6
42	201889_at	family with sequence similarity 3, member C	FAM3C	7q22.1-q31.1	NM_014888.1	Hs.29882	74.6	Above	4.6
43	222699_s_at	phafin 2	FLJ13187	8q21.3	BF439250	Hs.29724	74.6	Above	3.5
44	238778_at	Homo sapiens mRNA; cDNA DKFZp451L157 (from clone DKFZp451L157)			AI244661	Hs.350684	74.6	Above	23.3
45	205769_at	solute carrier family 27 (fatty acid transporter), member 2	SLC27A2	15q21.2	NM_003645.1	Hs.11729	74.4	Above	80.6
46	210786_s_at	Friend leukemia virus integration 1	FLI1	11q24.1-q24.3	M93255.1	Hs.108043	74.4	Above	2.2
47	212985_at	cDNA DKFZp434E033	DKFZp434E033		BF115739	Hs.15740	74.4	Above	7.0
48	221669_s_at	acyl-Coenzyme A dehydrogenase family, member 8	ACAD8	11q25	BC001964.1	Hs.14791	74.4	Above	2.6
49	227441_s_at	E2a-Pbx1-associated protein	EB-1	12	AW005572	Hs.372732	74.4	Above	1139.4
50	234261_at	Homo sapiens mRNA; cDNA DKFZp761M10121 (from clone DKFZp761M10121)			AL137313.1	Hs.306449	74.4	Above	960.8
51	244565_at	ESTs			AI685824	Hs.171068	74.4	Above	7.4
52	209760_at	KIAA0922 protein	KIAA0922	4q31.23	AL136932.1	Hs.37892	73.0	Above	2.9
53	218283_at	synovial sarcoma translocation gene on chromosome 18-like 2	SS18L2	3p21	NM_016305.1	Hs.9774	72.8	Above	1.6
54	209558_s_at	huntingtin interacting protein 12	HIP12	12q24	AB013384.1	Hs.96731	70.0	Above	23.6
55	213005_s_at	KIAA0172 protein	KIAA0172	9p24.3	D79994.1	Hs.77546	70.0	Above	8.3
56	236854_at	Homo sapiens mRNA; cDNA DKFZp667F0617 (from clone DKFZp667F0617)			AA743694	Hs.48984	70.0	Above	12.5
57	203435_s_at	membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)	MME	3q25.1-q25.2	NM_007287.1	Hs.1298	68.3	Below	2.2

58	204774_at	ecotropic viral integration site 2A	EVI2A	17q11.2	NM_014210.1	Hs.70499	68.1	Below	3.0
59	201579_at	FAT tumor suppressor homolog 1 (Drosophila)	FAT	4q34-q35	NM_005245.1	Hs.166994	68.1	Above	9.8
60	203999_at	synaptotagmin I	SYT1	12cen-q21	NM_005639.1	Hs.154679	68.1	Above	3.9
61	200811_at	cold inducible RNA binding protein	CIRBP	19p13.3	NM_001280.1	Hs.119475	67.8	Below	5.8
62	202106_at	golgi autoantigen, golgin subfamily a, 3	GOLGA3	12q24.33	NM_005895.1	Hs.4953	67.8	Above	3.2
63	233273_at	Homo sapiens cDNA FLJ12010 fis, clone HEMBB1001635			AU146834	Hs.296684	67.8	Above	30.4
64	239427_at	ESTs			AA131524	Hs.374124	67.8	Above	13.6
65	218087_s_at	sorbin and SH3 domain containing 1	SORBS1	10q23.3-q24.1	NM_015385.1	Hs.108924	66.3	Above	24.9
66	201460_at	mitogen-activated protein kinase-activated protein kinase 2	MAPKAPK2	1q32	AI141802	Hs.75074	66.3	Above	2.1
67	202421_at	immunoglobulin superfamily, member 3	IGSF3	1p13	AB007935.1	Hs.81234	66.3	Above	4.3
68	40148_at	amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like)	APBB2	4p14	U62325	Hs.324125	66.2	Above	6.2
69	212165_at	hypothetical protein BC013073	LOC92703	1q31.1	AL133052.1	Hs.17481	66.2	Above	1.9
70	226590_at	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1517766			AA031404	Hs.349208	66.2	Above	3.1
71	227440_at	E2a-Pbx1-associated protein	EB-1	12	AW005572	Hs.372732	66.2	Above	1168.9
72	203143_s_at	KIAA0040 gene product	KIAA0040	1q24-25	T79953	Hs.158282	64.7	Above	2.4
73	228153_at	Homo sapiens mRNA; cDNA DKFZp451E085 (from clone DKFZp451E085)			AI953847	Hs.294092	64.7	Above	4.1
74	212959_s_at	MGC4170 protein	MGC4170	12q23.1	AK001821.1	Hs.7041	64.6	Below	3.0
75	202181_at	KIAA0247 gene product	KIAA0247	14q24.1	NM_014734.1	Hs.82426	63.7	Above	1.8
76	204562_at	interferon regulatory factor 4	IRF4	6p25-p23	NM_002460.1	Hs.82132	63.7	Above	4.9
77	218949_s_at	hypothetical protein FLJ10989	FLJ10989	6q21	NM_018292.1	Hs.210778	63.7	Above	3.2
78	219517_at	hypothetical protein FLJ22637	FLJ22637	15q14	NM_025165.1	Hs.296178	63.7	Above	3.4
79	224856_at	FK506 binding protein 5	FKBP5	6p21.3-21.2	AL122066.1	Hs.7557	63.7	Below	5.5
80	225389_at	BTB domain protein BDPL	BDPL	14q32	AW149498	Hs.7367	63.7	Above	3.2
81	226392_at	Homo sapiens cDNA: FLJ21652 fis, clone COL08582			AI888503	Hs.98445	63.7	Below	3.4
82	219667_s_at	hypothetical protein FLJ20706	BANK	4q22.2	NM_017935.1	Hs.193736	62.9	Below	5.6
83	212845_at	KIAA1053 protein	KIAA1053	14q22.1	AB028976.1	Hs.173571	61.9	Above	14.6
84	213940_s_at	formin-binding protein 17	FBP17	9q34	AU145053	Hs.301763	61.9	Below	12.3
85	219111_s_at	ATP-dependent RNA helicase	MGC2835	12q24.11	NM_024072.1	Hs.70582	61.9	Above	1.9
86	219518_s_at	hypothetical protein FLJ22637	FLJ22637	15q14	NM_025165.1	Hs.296178	61.9	Above	5.7
87	220389_at	hypothetical protein FLJ23514	FLJ23514	11q14.1	NM_021827.1	Hs.144913	61.9	Above	6.5
88	47069_at	Rho GTPase activating protein 8	ARHGAP8	22q13.31	AA533284	Hs.102336	61.9	Above	3.4
89	212774_at	zinc finger protein 238	ZNF238	1q44-qter	AJ223321	Hs.69997	61.9	Above	1.8
90	201443_s_at	ATPase, H <sup>+</sup> transporting, lysosomal interacting protein 2	ATP6IP2	Xq21	AF248966.1	Hs.183434	60.9	Below	1.9

91	204836_at	glycine dehydrogenase (decarboxylating; glycine decarboxylase, glycine cleavage system protein P)	GLDC	9p22	NM_000170.1	Hs.380791	60.1	Above	3.1
92	217732_s_at	integral membrane protein 2B	ITM2B	13q14.3	AF092128.1	Hs.239625	60.1	Below	2.0
93	201029_s_at	antigen identified by monoclonal antibodies 12E7, F21 and O13	MIC2	Xp22.32	NM_002414.1	Hs.177543	59.8	Below	5.7
94	204174_at	arachidonate 5-lipoxygenase-activating protein	ALOX5AP	13q12	NM_001629.1	Hs.100194	59.8	Below	48.1
95	206255_at	B lymphoid tyrosine kinase	BLK	8p23-p22	NM_001715.1	Hs.2243	59.8	Above	6.0
96	212873_at	minor histocompatibility antigen HA-1	HA-1	19p13.3	BE349017	Hs.196914	59.8	Below	2.9
97	211963_s_at	actin related protein 2/3 complex, subunit 5, 16kDa	ARPC5	1q24.3	AL516350	Hs.82425	59.6	Above	1.7
98	218683_at	polypyrimidine tract binding protein 2	PTBP2	1p22.11-p21.3	NM_021190.1	Hs.34956	59.6	Above	1.8
99	221234_s_at	BTB and CNC homology 1, basic leucine zipper transcription factor 2	BACH2	6q15	NM_021813.1	Hs.88414	59.6	Above	2.7
100	240718_at	ESTs, Highly similar to I38656 lymphoid-restricted membrane protein - human [H.sapiens]			AW303384	Hs.124922	59.6	Above	11.9

**Table S11. Top 100 chi-square probe sets selected for Hyperdiploid >50 in parallel format**

	U133 probe set	Gene description	Symbol	Location	GenBank Reference	Unigene Reference	Chi-square value	HD>50 above/below mean	Fold change
1	216071_x_at	trinucleotide repeat containing 11	TNRC11	Xq13	AF132033	Hs.211607	91.8	Above	1.8
2	218757_s_at	similar to yeast Upf3, variant B	UPF3B	Xq25-q26	NM_023010.1	Hs.103832	91.3	Above	2.3
3	208861_s_at	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)	ATRAX	Xq13.1-q21.1	U72937.2	Hs.96264	91.3	Above	1.7
4	200980_s_at	pyruvate dehydrogenase (lipoamide) alpha 1	PDHA1	Xp22.2-p22.1	NM_000284.1	Hs.1023	83.1	Above	1.7
5	202371_at	hypothetical protein FLJ21174	FLJ21174	Xq22.1	NM_024863.1	Hs.194329	83.1	Above	3.6
6	205324_s_at	FtsJ homolog 1 (E. coli)	FTSJ1	Xp11.23	NM_012280.1	Hs.23170	83.1	Above	2.2
7	201899_s_at	ubiquitin-conjugating enzyme E2A (RAD6 homolog)	UBE2A	Xq24-q25	NM_003336.1	Hs.80612	82.7	Above	1.8
8	212846_at	KIAA0179 protein	KIAA0179	21q22.3	D80001.1	Hs.152629	82.7	Above	2.0
9	218499_at	Mst3 and SOK1-related kinase	MST4	Xq26.1	NM_016542.1	Hs.23643	82.7	Above	2.5
10	221689_s_at	Down syndrome critical region gene 5	DSCR5	21q22.2	AB035745.1	Hs.66493	82.7	Above	2.2
11	219038_at	hypothetical protein FLJ11565	FLJ11565	Xq22.2	NM_024657.1	Hs.61763	78.8	Above	6.8
12	208598_s_at	Upstream regulatory element binding protein 1	UREB1	Xp11.22	NM_005703.2		78.4	Above	1.6

13	201100_s_at	ubiquitin specific protease 9, X chromosome (fat facets-like Drosophila)	USP9X	Xp11.4	NM_004652.2	Hs.77578	76.1	Above	1.7
14	201132_at	heterogeneous nuclear ribonucleoprotein H2 (H')	HNRPH2	Xq22	NM_019597.1	Hs.278857	74.6	Above	2.0
15	201898_s_at	ubiquitin-conjugating enzyme E2A (RAD6 homolog)	UBE2A	Xq24-q25	AI126625	Hs.80612	74.6	Above	1.6
16	213289_at	Homo sapiens cDNA FLJ39590 fis, clone SKNMC1000079			BE221922	Hs.356269	74.6	Above	3.8
17	219485_s_at	proteasome (prosome, macropain) 26S subunit, non-ATPase, 10	PSMD10	Xq22.3	NM_002814.1	Hs.7756	74.6	Above	2.4
18	218878_s_at	sirtuin silent mating type information regulation 2 homolog 1 (S. cerevisiae)	SIRT1	10q22.2	NM_012238.3	Hs.31176	74.4	Above	1.4
19	228005_at	ESTs, Weakly similar to T45117 hU1-70K protein (286 AA) [imported] - human (fragment) [H.sapiens]			BE677308	Hs.96716	74.4	Above	3.8
20	201136_at	proteolipid protein 2 (colonic epithelium-enriched)	PLP2	Xp11.23	NM_002668.1	Hs.77422	73.0	Above	3.4
21	202214_s_at	cullin 4B	CUL4B	Xq23	NM_003588.1	Hs.155976	73.0	Above	1.9
22	242794_at	ESTs			AI569476	Hs.177135	70.0	Above	3.2
23	211342_x_at	trinucleotide repeat containing 11 (THR-associated protein, 230 kDa subunit)	TNRC11	Xq13	BC004354.1		68.1	Above	1.8
24	212419_at	Homo sapiens, similar to Y43E12A.2.p, clone MGC:33537 IMAGE:4821347, mRNA, complete cds			AL049949.1	Hs.28264	68.1	Above	13.0
25	207785_s_at	H-2K binding factor-2	LOC51580	9	NM_015874.1	Hs.347340	67.8	Above	1.8
26	212460_at	hypothetical protein MGC24447	MGC24447	14	BE738425	Hs.353161	67.8	Above	2.2
27	203745_at	holocytochrome c synthase (cytochrome c heme-lyase)	HCCS	Xp22.3	AI801013	Hs.211571	67.8	Above	2.0
28	209565_at	zinc finger protein 183 (RING finger, C3HC4 type)	ZNF183	Xq25-q26	BC000832.1	Hs.64794	67.8	Above	2.2
29	201099_at	ubiquitin specific protease 9, X chromosome (fat facets-like Drosophila)	USP9X	Xp11.4	AA824386	Hs.77578	66.3	Above	1.6
30	203974_at	DNA segment, numerous copies, expressed probes (GS1 gene)	DXF68S1E	Xp22.32	NM_012080.1	Hs.78991	66.3	Above	4.0
31	215884_s_at	ubiquilin 2	UBQLN2	Xp11.23-p11.1	AK001029.1	Hs.4552	66.2	Above	1.9
32	200642_at	superoxide dismutase 1, soluble	SOD1	21q22.11	NM_000454.1	Hs.75428	64.7	Above	2.3
33	200738_s_at	phosphoglycerate kinase 1	PGK1	Xq13	NM_000291.1	Hs.78771	64.7	Above	1.8
34	201312_s_at	SH3 domain binding glutamic acid-rich protein like	SH3BGRL	Xq13.3	NM_003022.1	Hs.14368	64.7	Above	1.6
35	226875_at	hypothetical protein FLJ32122	FLJ32122	Xq24	AI742838	Hs.107513	64.6	Above	2.3
36	228057_at	similar to Smhs1 protein	LOC115265	4q22.1	AA528140	Hs.107515	63.7	Above	6.7

37	232974_at	Homo sapiens cDNA FLJ12417 fis, clone MAMMA1003039			AU148256	Hs.226469	63.7	Above	3.1
38	232034_at	Homo sapiens mRNA; cDNA DKFZp564N0763 (from clone DKFZp564N0763)			AL117607.1	Hs.175563	62.1	Above	6.1
39	200944_s_at	high-mobility group nucleosome binding domain 1	HMGN1	21q22.2	NM_004965.1	Hs.251064	61.9	Above	1.7
40	201443_s_at	ATPase, H <sup>+</sup> transporting, lysosomal interacting protein 2	ATP6IP2	Xq21	AF248966.1	Hs.183434	61.9	Above	1.9
41	226333_at	interleukin 6 receptor	IL6R	1q21	AV700030	Hs.193400	61.9	Above	8.7
42	203585_at	zinc finger protein 185 (LIM domain)	ZNF185	Xq28	NM_007150.1	Hs.16622	60.9	Above	10.7
43	206846_s_at	histone deacetylase 6	HDAC6	Xp11.23	NM_006044.2	Hs.6764	60.1	Above	1.5
44	216095_x_at	myotubularin related protein 1	MTMR1	Xq28	AF057354.1	Hs.372428	60.1	Above	1.8
45	226039_at	Mannosyl (alpha-1,3)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase	MGAT4A	2q11.2	AW006441	Hs.24210	60.1	Above	3.0
46	227210_at	Homo sapiens cDNA FLJ32568 fis, clone SPLEN2000098			T65020	Hs.12699	60.1	Above	3.6
47	236172_at	ESTs			AW206817	Hs.158186	60.1	Above	2.4
48	214735_at	phosphoinositide-binding protein PIP3-E	PIP3-E	6q25.2	AW166711	Hs.185140	59.8	Above	6.4
49	206147_x_at	sex comb on midleg-like 2 (Drosophila)	SCML2	Xp22	NM_006089.1	Hs.171558	59.6	Above	2.2
50	209022_at	stromal antigen 2	STAG2	Xq25	AK026678.1	Hs.8217	59.6	Above	1.7
51	213282_at	Homo sapiens cDNA FLJ39590 fis, clone SKNMC1000079			BE221922	Hs.356269	59.6	Above	2.2
52	218582_at	hypothetical protein FLJ20445	FLJ20445	10q23.33	NM_017824.1	Hs.343748	59.6	Above	1.6
53	218694_at	ALEX1 protein	ALEX1	Xq21.33-q22.2	NM_016608.1	Hs.9728	59.6	Above	2.8
54	226785_at	Homo sapiens cDNA FLJ36516 fis, clone TRACH2001898			BF475862	Hs.88252	59.6	Above	1.9
55	200655_s_at	calmodulin 1 (phosphorylase kinase, delta)	CALM1	14q24-q31	NM_006888.1	Hs.177656	58.7	Above	1.7
56	210176_at	toll-like receptor 1	TLR1	4p14	AL050262.1	Hs.2474	58.2	Above	2.1
57	202711_at	ephrin-B1	EFNB1	Xq12	NM_004429.1	Hs.144700	58.2	Above	14.9
58	204446_s_at	arachidonate 5-lipoxygenase	ALOX5	10q11.2	NM_000698.1	Hs.89499	58.2	Above	4.2
59	219297_at	similar to rab11-binding protein	FLJ11116	Xq24	NM_019045.1	Hs.98510	58.2	Above	2.4
60	201923_at	peroxiredoxin 4	PRDX4	Xp22.13	NM_006406.1	Hs.83383	58.2	Above	1.9
61	212929_s_at	KIAA0592 protein	KIAA0592	10q11.21	W68158	Hs.13273	58.2	Above	5.0
62	204045_at	transcription elongation factor A (SII)-like 1	TCEAL1	Xq22.1	NM_004780.1	Hs.95243	56.8	Above	2.1
63	208117_s_at	hypothetical protein FLJ12525	FLJ12525	Xq12-q13	NM_031206.1	Hs.321618	56.8	Above	2.2
64	209620_s_at	ATP-binding cassette, sub-family B (MDR/TAP), member 7	ABCB7	Xq12-q13	AB005289.1	Hs.125856	56.8	Above	2.1
65	209679_s_at	hypothetical protein from clone 643	LOC57228	12q11	BC003379.1	Hs.206501	56.8	Above	5.6
66	217954_s_at	PHD finger protein 3	PHF3		NM_015153.1	Hs.78893	56.8	Above	1.5
67	218414_s_at	LIS1-interacting protein NUDE1, rat homolog	NUDE1	16p13.11	NM_017668.1	Hs.263925	56.8	Above	2.0

68	226037_s_at	TAF9-like RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa	TAF9L	Xq13.1-q21.1	AL049589	Hs.171723	56.8	Above	1.9
69	227279_at	hypothetical protein MGC15737	MGC15737	Xq22.1	AA847654	Hs.39122	56.8	Above	5.6
70	200600_at	Moesin (membrane organizing extension spike protein)	MSN	Xq11.2-q12	NM_002444.1	Hs.170328	56.2	Above	1.9
71	200701_at	Niemann-Pick disease, type C2	NPC2	14q24.3	NM_006432.1	Hs.119529	55.9	Above	1.7
72	200737_at	phosphoglycerate kinase 1	PGK1	Xq13	NM_000291.1	Hs.78771	55.9	Above	1.8
73	201642_at	interferon gamma receptor 2 (interferon gamma transducer 1)	IFNGR2	21q22.11	NM_005534.1	Hs.177559	55.9	Above	2.5
74	214527_s_at	polyglutamine binding protein 1	PQBP1	Xp11.23	AB041836.1	Hs.30570	55.9	Above	1.7
75	223082_at	SH3-domain kinase binding protein 1	SH3KBP1	Xp22.1-p21.3	AF230904.1	Hs.153260	55.9	Above	2.0
76	225182_at	Homo sapiens EST from clone 491476, full insert			AL355685.1	Hs.9042	55.9	Above	2.1
77	226760_at	Homo sapiens cDNA FLJ32174 fis, clone PLACE6001064			BF666325	Hs.297007	55.9	Above	2.2
78	204572_s_at	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)	PIN4	Xq13	NM_006223.1	Hs.11774	54.8	Above	2.9
79	201092_at	retinoblastoma binding protein 7	RBBP7	Xp22.31	NM_002893.2	Hs.31314	54.0	Above	1.6
80	204690_at	syntaxin 8	STX8	17p12	NM_004853.1	Hs.380938	54.0	Above	1.4
81	206016_at	JM1 protein	JM1	Xp11.23	NM_014008.1	Hs.26333	54.0	Above	2.3
82	218021_at	peroxisomal short-chain alcohol dehydrogenase	humNRDR	14q11.2	NM_021004.1	Hs.6318	54.0	Above	4.0
83	221808_at	RAB9A, member RAS oncogene family	RAB9A	Xp22.2	NM_004251.1	Hs.330994	54.0	Above	1.8
84	223497_at	KIAA1411 protein	KIAA1411	6q12-q13	AL136820.1	Hs.107287	54.0	Above	3.8
85	226335_at	Homo sapiens cDNA FLJ12807 fis, clone NT2RP2002316			BG498334	Hs.188361	54.0	Above	2.0
86	201311_s_at	SH3 domain binding glutamic acid-rich protein like	SH3BGRL	Xq13.3	AL515318	Hs.14368	53.0	Above	1.6
87	202829_s_at	synaptobrevin-like 1	SYBL1	Xq28	NM_005638.1	Hs.24167	53.0	Above	1.5
88	209370_s_at	SH3-domain binding protein 2	SH3BP2	4p16.3	AB000462.1	Hs.167679	53.0	Above	3.2
89	46323_at	Ca <sup>2+</sup> -dependent endoplasmic reticulum nucleoside diphosphatase	SHAPY	17q25.3	AL120741	Hs.8859	52.3	Above	1.7
90	200658_s_at	prohibitin	PHB	17q21	AL560017	Hs.75323	52.3	Above	2.0
91	202974_at	membrane protein, palmitoylated 1, 55kDa	MPP1	Xq28	NM_002436.2	Hs.1861	52.3	Above	2.2
92	221188_s_at	cell death-inducing DFFA-like effector b	CIDEB	14q11.2	NM_014430.1	Hs.288835	52.3	Above	2.4
93	203776_at	T54 protein	T54	Xp11.23	NM_015698.1	Hs.100391	52.3	Above	2.0
94	211974_x_at	CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344)	CD59	11p13	AL513759	Hs.278573	52.3	Above	1.7
95	213000_at	nuclear matrix protein NXP-2	NXP-2	21q22.13	AP000693	Hs.70359	52.3	Above	1.9
96	225361_x_at	similar to hypothetical protein MGC17347	LOC159090	Xq26.2	AI341165	Hs.353200	52.3	Above	1.8
97	226905_at	Homo sapiens, clone IMAGE:4564684, mRNA, partial cds			BG036514	Hs.345588	52.3	Above	4.0

partial cds

98	223294_at	hypothetical protein LOC51260	LOC51260	Xq13.1	BC001220.1	Hs.128764	52.3	Above	1.8
99	226810_at	Homo sapiens mRNA; cDNA DKFZp761M0111 (from clone DKFZp761M0111)			BE500942	Hs.13299	52.2	Above	2.5
100	238469_at	hypothetical protein FLJ21079	FLJ21079	6q14.1	BE620374	Hs.16512	51.8	Above	2.2

**Table S12. Top 100 chi-square probe sets selected for *MLL* in parallel format**

	<b>U133 probe set</b>	<b>Gene description</b>	<b>Symbol</b>	<b>Location</b>	<b>GenBank Reference</b>	<b>Unigene Reference</b>	<b>Chi-square value</b>	<b>MLL above/below mean</b>	<b>Fold change</b>
1	226939_at	Homo sapiens cDNA FLJ37247 fis, clone BRAMY2006397			AI202327	Hs.44833	92.2	Above	7
2	219463_at	chromosome 20 open reading frame 103	C20orf103	20p12	NM_012261.1	Hs.22920	86.2	Above	24
3	204069_at	Meis1, myeloid ecotropic viral integration site 1 homolog	MEIS1	2p14-p13	NM_002398.1	Hs.170177	84.9	Above	73
4	203837_at	mitogen-activated protein kinase kinase kinase 5	MAP3K5	6q22.33	NM_005923.2	Hs.151988	77.3	Above	4
5	226415_at	KIAA1576 protein	KIAA1576	16q22.1	AA156723	Hs.22975	77.3	Above	40
6	222409_at	coronin, actin binding protein, 1C	CORO1C	12q24.1	AL162070.1	Hs.17377	71.1	Above	5
7	242172_at	ESTs			N50406	Hs.191349	71.1	Above	33
8	235879_at	ESTs			AI697540	Hs.310286	70.0	Above	4
9	231899_at	KIAA1726 protein	KIAA1726	11q23.1	AB051513.1	Hs.164719	65.6	Above	33
10	212386_at	Homo sapiens cDNA FLJ11918 fis, clone HEMBB1000272			AK021980.1	Hs.289068	64.5	Below	3
11	201153_s_at	muscleblind-like (Drosophila)	MBNL	3q25	NM_021038.1	Hs.28578	63.4	Above	2
12	218217_at	likely homolog of rat and mouse retinoid-inducible serine carboxypeptidase	RISC	17q23.2	NM_021626.1	Hs.106747	63.4	Above	3
13	201875_s_at	hypothetical protein FLJ21047	FLJ21047	1q23.2	NM_024569.1	Hs.14891	63.0	Above	2
14	205717_x_at	protocadherin gamma subfamily C, 3	PCDHGC3	5q31	NM_002588.1	Hs.284180	63.0	Above	5
15	205821_at	DNA segment on chromosome 12 (unique) 2489 expressed sequence	D12S2489E	12p13.2-p12.3	NM_007360.1	Hs.74085	63.0	Above	9
16	205899_at	cyclin A1	CCNA1	13q12.3-q13	NM_003914.1	Hs.79378	63.0	Above	104
17	209079_x_at	protocadherin gamma subfamily A, 1	PCDHGA1	5q31	AF152318.1	Hs.333404	63.0	Above	5
18	210660_at	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1	LILRA1	19q13.4	AF025529.1	Hs.166156	63.0	Above	532
19	211066_x_at	protocadherin gamma subfamily C, 3	PCDHGC3	5q31	BC006439.1	Hs.284180	63.0	Above	5

20	215836_s_at	protocadherin gamma subfamily B, 7	PCDHGB7	5q31	AK026188.1	Hs.256783	63.0	Above	4
21	212135_s_at	calcium transporting ATPase plasma membrane protein.	ATP2B4		AW517686	Hs.356388	62.6	Below	2
22	226668_at	hypothetical protein FLJ36175	FLJ36175		W80623	Hs.20848	62.4	Above	2
23	201152_s_at	muscleblind-like (Drosophila)	MBNL	3q25	NM_021038.1	Hs.28578	60.7	Above	2
24	218847_at	IGF-II mRNA-binding protein 2	IMP-2	3q28	NM_006548.1	Hs.30299	60.7	Above	23
25	238712_at	ESTs			BF801735	Hs.181574	60.7	Above	3
26	234032_at				AF119847.1		60.1	Above	4
27	218764_at	hypothetical protein MGC5363	MGC5363	14q22.1-q22.3	NM_024064.1	Hs.1880	59.3	Below	8
28	203345_s_at	likely ortholog of mouse metal response element binding transcription factor 2	M96	1p22.1	AI566096	Hs.31016	58.5	Below	2
29	203836_s_at	mitogen-activated protein kinase kinase kinase 5	MAP3K5	6q22.33	D84476.1	Hs.151988	58.5	Above	14
30	227999_at	hypothetical protein BC011630	LOC170394	10q26.3	AI290476	Hs.157728	58.5	Above	17
31	235479_at	ESTs, Moderately similar to KIAA0940 protein [Homo sapiens] [H.sapiens]			AI948598	Hs.156469	58.5	Above	4
32	220643_s_at	Fas apoptotic inhibitory molecule	FAIM	3q23	NM_018147.1	Hs.173438	58.2	Above	3
33	201151_s_at	muscleblind-like (Drosophila)	MBNL	3q25	NM_021038.1	Hs.28578	56.8	Above	3
34	205668_at	lymphocyte antigen 75	LY75	2q24	NM_002349.1	Hs.153563	56.8	Above	2
35	52164_at	chromosome 11 open reading frame 24	C11orf24	11q13	AA065185	Hs.303025	56.4	Above	2
36	56256_at	CGI-40 protein	LOC51092	11q23.3	AA150165	Hs.33724	56.4	Above	2
37	228855_at	nudix (nucleoside diphosphate linked moiety X)-type motif 7	NUDT7		AI927964	Hs.115920	56.4	Above	6
38	235173_at	muscleblind-like (Drosophila)	MBNL	3q25	AA093668	Hs.28578	56.0	Above	41
39	241391_at	ESTs, Moderately similar to hypothetical protein FLJ20378 [Homo sapiens] [H.sapiens]			AA654772	Hs.186564	56.0	Above	3
40	201105_at	lectin, galactoside-binding, soluble, 1 (galectin 1)	LGALS1	22q13.1	NM_002305.2	Hs.227751	55.9	Above	15
41	202975_s_at	Rho-related BTB domain containing 3	RHOBTB3	5q21.2	N21138	Hs.10432	55.9	Above	6
42	236558_at	ESTs			AA699809	Hs.189900	55.9	Above	18
43	225563_at	Homo sapiens cDNA FLJ33988 fis, clone DFNES2006346, weakly similar to PAB-DEPENDENT POLY(A)-SPECIFIC RIBONUCLEASE SUBUNIT PAN3 (EC 3.1.13.4)			AI970788	Hs.190153	55.7	Above	3
44	221286_s_at	proapoptotic caspase adaptor protein	FLJ32987	5q23-5q31	NM_016459.1	Hs.122492	54.1	Below	4
45	203375_s_at	tripeptidyl peptidase II	TPP2	13q32-q33	NM_003291.1	Hs.1117	52.9	Above	2
46	215000_s_at	fasciculation and elongation protein zeta 2 (zygin II)	FEZ2	2p21	AL117593.1	Hs.103419	52.9	Above	2
47	209191_at	tubulin beta-5	TUBB-5		BC002654.1	Hs.274398	52.9	Above	6
48	225202_at	Rho-related BTB domain containing 3	RHOBTB3	5q21.2	BE620739	Hs.10432	52.5	Above	6
49	225232_at	phosphatidylinositol-3 phosphate 3-phosphatase	3PAP	5p13.2	AA524700	Hs.93872	51.6	Above	2

		adaptor subunit								
50	227611_at	hypothetical protein FLJ25005	FLJ25005	15q26.3	AA442856	Hs.181426	51.6	Above	3	
51	212136_at	calcium transporting ATPase plasma membrane protein.	ATP2B4		AW517686	Hs.356388	50.2	Below	2	
52	215925_s_at	CD72 antigen	CD72	9p11.2	AF283777.2	Hs.116481	50.2	Above	3	
53	221676_s_at	coronin, actin binding protein, 1C	CORO1C	12q24.1	BC002342.1	Hs.17377	50.2	Above	4	
54	212660_at	KIAA0239 protein	KIAA0239	5q31.1	AI735639	Hs.9729	49.6	Below	2	
55	234987_at	SAM domain and HD domain 1	SAMHD1	20pter-q12	AV715309	Hs.23889	49.4	Above	4	
56	205550_s_at	brain and reproductive organ-expressed (TNFRSF1A modulator)	BRE	2p23.3	NM_004899.1	Hs.80426	49.3	Above	2	
57	210993_s_at	MAD, mothers against decapentaplegic homolog 1 (Drosophila)	MADH1	4q28	U54826.1	Hs.79067	49.3	Below	96	
58	205078_at	phosphatidylinositol glycan, class F	PIGF	2p21-p16	NM_002643.1	Hs.348397	49.3	Above	2	
59	212174_at	adenylate kinase 2	AK2	1p34	AK023758.1	Hs.171811	49.3	Above	2	
60	241681_at	ESTs			AW296451	Hs.24605	49.3	Above	2	
61	203820_s_at	IGF-II mRNA-binding protein 3	KOC1	7p11	NM_006547.1	Hs.79440	49.0	Above	3	
62	209168_at	Homo sapiens cDNA FLJ38338 fis, clone FCBBF3027104, highly similar to Mus musculus proteolipid M6B isoform alpha-beta-TMD-omega (M6B) mRNA			AF016004.1	Hs.379090	49.0	Above	4	
63	213566_at	ribonuclease, RNase A family, k6	RNASE6	14q11.1	NM_005615.1	Hs.23262	49.0	Above	6	
64	224622_at	KIAA1322 protein	KIAA1322	4p16.2	AB037743.1	Hs.72242	49.0	Above	2	
65	236921_at	ESTs			BE504716	Hs.372166	49.0	Above	3	
66	239278_at	ESTs, Weakly similar to JC5238 galactosylceramide-like protein, GCP - human [H.sapiens]			AI471969	Hs.182606	49.0	Above	3	
67	226459_at	Homo sapiens gastric cancer-related protein GCYS-20 (gcys-20) mRNA, complete cds			AW575754	Hs.86437	47.7	Above	2	
68	239369_at	Homo sapiens cDNA FLJ33328 fis, clone BRACE1000051, weakly similar to KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN			AW966156	Hs.323991	47.3	Above	5	
69	218581_at	hypothetical protein FLJ12816	FLJ12816	14q11.1	NM_022060.1	Hs.9175	47.1	Above	23	
70	214651_s_at	homeo box A9	HOX A9	7p15-p14	U41813.1	Hs.380229	47.1	Above	28	
71	224933_s_at	hypothetical protein DKFZp761F0118	DKFZp761F0118	10q22.1	AB037801.1	Hs.6685	47.1	Above	2	
72	239393_at	ESTs			AW510927	Hs.371883	46.5	Above	6	
73	209112_at	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	CDKN1B	12p13.1-p12	BC001971.1	Hs.238990	46.0	Above	2	
74	217707_x_at	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SMARCA2	9p22.3	AI535683	Hs.198296	46.0	Above	2	

75	221830_at	Homo sapiens cDNA FLJ37267 fis, clone BRAMY2011297			AI302106	Hs.301746	46.0	Above	2
76	202761_s_at	synaptic nuclei expressed gene 2	SYNE-2	14q23.1-q23.2	NM_015180.1	Hs.57749	45.9	Below	4
77	202976_s_at	Rho-related BTB domain containing 3	RHOBTB3	5q21.2	NM_014899.1	Hs.10432	45.9	Above	12
78	213241_at	plexin C1	PLXNC1		AF035307.1	Hs.184697	45.9	Above	3
79	230332_at	ESTs			AA872187	Hs.33665	45.4	Above	3
80	209905_at	hypothetical protein MGC1934	MGC1934	7p21.1	AI246769	Hs.127428	44.9	Above	31
81	226789_at	ESTs, Weakly similar to A46506 leukocyte activation antigen M6 - human [H.sapiens]			W84421	Hs.356113	44.9	Above	2
82	204019_s_at	likely ortholog of mouse Sh3 domain YSC-like 1	SH3YL1	2p25.2	NM_015677.1	Hs.25213	44.0	Above	2
83	201874_at	hypothetical protein FLJ21047	FLJ21047	1q23.2	BF978611	Hs.14891	43.9	Above	2
84	238558_at	ESTs			AI445833	Hs.282887	43.9	Above	4
85	235964_x_at	SAM domain and HD domain 1	SAMHD1	20pter-q12	AA603344	Hs.23889	43.6	Above	3
86	219099_at	chromosome 12 open reading frame 5	C12orf5	12p13.3	NM_020375.1	Hs.24792	43.3	Above	3
87	201064_s_at	poly(A) binding protein, cytoplasmic 4 (inducible form)	PABPC4	1p32-p36	NM_003819.2	Hs.169900	43.3	Above	2
88	206471_s_at	plexin C1	PLXNC1	12q23.3	NM_005761.1	Hs.286229	43.3	Above	9
89	208717_at	oxidase (cytochrome c) assembly 1-like	OXA1L	14q11.2	BC001669.1	Hs.151134	43.3	Above	2
90	210594_x_at	myelin protein zero-like 1	MPZL1	1q23.2	AF239756.1	Hs.287832	43.3	Above	5
91	221675_s_at	choline phosphotransferase 1	CHPT1	12q	AF195624.1	Hs.171889	43.3	Above	2
92	225810_at	hypothetical protein FLJ20313	FLJ20313	15q12	AL572015	Hs.126721	43.3	Above	2
93	242260_at	ESTs, Moderately similar to cytokine receptor-like factor 2; cytokine receptor CRL2 precursor [Homo sapiens] [H.sapiens]			BG283790	Hs.214238	43.3	Above	10
94	224763_at	ESTs			AL137450.1	Hs.374308	43.3	Above	2
95	227534_at	ESTs, Highly similar to RIKEN cDNA 1110018J18 [Mus musculus] [M.musculus]			AL535879	Hs.42311	43.3	Above	35
96	235529_x_at	SAM domain and HD domain 1	SAMHD1	20pter-q12	BF437747	Hs.23889	43.3	Above	4
97	212588_at	protein tyrosine phosphatase, receptor type, C	PTPRC	1q31-q32	AI809341	Hs.170121	43.2	Above	2
98	233931_at	Homo sapiens cDNA FLJ11919 fis, clone HEMBB1000274			AK021981.1	Hs.193525	43.2	Above	22
99	240666_at	ESTs			AI732568	Hs.191453	43.2	Above	4
100	209167_at	glycoprotein M6B	GPM6B	Xp22.2	AF016004.1	Hs.5422	43.0	Above	10

**Table S13. Top 100 chi-square probe sets selected for T-ALL in parallel format**

	<b>U133 probe set</b>	<b>Gene description</b>	<b>Symbol</b>	<b>Location</b>	<b>GenBank Reference</b>	<b>Unigene Reference</b>	<b>Chi-square value</b>	<b>T-ALL Above/below mean</b>	<b>Fold change</b>
1	201137_s_at	major histocompatibility complex, class II, DP beta 1	HLA-DPB1	6p21.3	NM_002121.1	Hs.814	100.0	Below	24.2
2	202113_s_at	sorting nexin 2	SNX2	5q23	AF043453.1	Hs.11183	100.0	Below	4.2
3	202114_at	sorting nexin 2	SNX2	5q23	NM_003100.1	Hs.11183	100.0	Below	4.7
4	203675_at	nucleobindin 2	NUCB2	11p15.1-p14	NM_005013.1	Hs.3164	100.0	Above	3.7
5	204670_x_at	major histocompatibility complex, class II, DR beta 3	HLA-DRB3	6p21.3	NM_002125.1	Hs.308026	100.0	Below	15.3
6	205297_s_at	CD79B antigen (immunoglobulin-associated beta)	CD79B	17q23	NM_000626.1	Hs.89575	100.0	Below	21.8
7	205456_at	CD3E antigen, epsilon polypeptide (TiT3 complex)	CD3E	11q23	NM_000733.1	Hs.3003	100.0	Above	20.8
8	206398_s_at	CD19 antigen	CD19	16p11.2	NM_001770.1	Hs.96023	100.0	Below	5693.6
9	208306_x_at	major histocompatibility complex, class II, DR beta 4	HLA-DRB4	6p21.3	NM_021983.2	Hs.318720	100.0	Below	9.8
10	208894_at	major histocompatibility complex, class II, DR alpha	HLA-DRA	6p21.3	M60334.1	Hs.76807	100.0	Below	27.5
11	209312_x_at	major histocompatibility complex, class II, DR beta 1	HLA-DRB1	6p21.3	U65585.1	Hs.375570	100.0	Below	14.6
12	209619_at	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)	CD74	5q32	K01144.1	Hs.84298	100.0	Below	18.9
13	210116_at	SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome)	SH2D1A	Xq25-q26	AF072930.1	Hs.151544	100.0	Above	159.0
14	210982_s_at	major histocompatibility complex, class II, DR alpha	HLA-DRA	6p21.3	M60333.1	Hs.76807	100.0	Below	32.5
15	211990_at	major histocompatibility complex, class II, DP alpha 1	HLA-DPA1	6p21.3	M27487.1	Hs.914	100.0	Below	29.4
16	211991_s_at	major histocompatibility complex, class II, DP alpha 1	HLA-DPA1	6p21.3	M27487.1	Hs.914	100.0	Below	35.9
17	213539_at	CD3D antigen, delta polypeptide (TiT3 complex)	CD3D	11q23	NM_000732.1	Hs.95327	100.0	Above	37.0
18	214049_x_at	CD7 antigen (p41)	CD7	17q25.2-q25.3	A1829961	Hs.36972	100.0	Above	327.3
19	214551_s_at	CD7 antigen (p41)	CD7	17q25.2-q25.3	NM_006137.2	Hs.36972	100.0	Above	241.8
20	217147_s_at	T-cell receptor interacting molecule	TRIM	3q13	AJ240085.1	Hs.138701	100.0	Above	43.6
21	217478_s_at	MHC, class IIa, HLA-DMA	HLA-DMA		X76775		100.0	Below	14.1
22	221969_at	paired box gene 5 (B-cell lineage specific activator protein)	PAX5	9p13	BF510692	Hs.22030	100.0	Below	3922.0

23	227646_at	early B-cell factor	EBF	5q34	BG435302	Hs.32425	100.0	Below	79.2
24	229487_at	Homo sapiens cDNA FLJ39389			W73890	Hs.120785	100.0	Below	7685.7
25	229838_at	Homo sapiens cDNA FLJ39156			AI377271	Hs.376140	100.0	Above	13.4
26	232204_at	early B-cell factor	EBF	5q34	AF208502.1	Hs.32425	100.0	Below	7112.4
27	266_s_at	CD24 antigen (small cell lung carcinoma cluster 4 antigen)	CD24	6q21	L33930	Hs.286124	91.3	Below	135.5
28	39318_at	T-cell leukemia/lymphoma 1A	TCL1A	14q32.1	X82240	Hs.2484	91.3	Below	18114.7
29	203965_at	ubiquitin specific protease 20	USP20	9q34.12-q34.13	NM_006676.1	Hs.5452	91.3	Above	9.6
30	204891_s_at	lymphocyte-specific protein tyrosine kinase	LCK	1p34.3	NM_005356.1	Hs.1765	91.3	Above	14.3
31	205255_x_at	transcription factor 7 (T-cell specific, HMG-box)	TCF7	5q31.1	NM_003202.1	Hs.169294	91.3	Above	8.5
32	207655_s_at	B-cell linker	BLNK	10q23.2-q23.33	NM_013314.1	Hs.167746	91.3	Below	133.1
33	209771_x_at	CD24 antigen (small cell lung carcinoma cluster 4 antigen)	CD24	6q21	AA761181	Hs.286124	91.3	Below	51.5
34	211796_s_at	T cell receptor beta locus	TRB	7q34	AF043179.1	Hs.303157	91.3	Above	21.5
35	213792_s_at	insulin receptor	INSR	19p13.3-p13.2	AA485908	Hs.89695	91.3	Below	8.6
36	215193_x_at	major histocompatibility complex, class II, DR beta 3	HLA-DRB3	6p21.3	AJ297586.1	Hs.308026	91.3	Below	16.7
37	216379_x_at	KIAA1919 protein	KIAA1919	6q22.1	AK000168.1	Hs.381004	91.3	Below	56.0
38	219191_s_at	bridging integrator 2	BIN2	12q13	NM_016293.1	Hs.14770	91.3	Above	264.1
39	219563_at	hypothetical protein FLJ21276	FLJ21276	14q32.2	NM_024633.1	Hs.41502	91.3	Below	5.8
40	219724_s_at	KIAA0748 gene product	KIAA0748	12q12	NM_014796.1	Hs.33187	91.3	Above	11.4
41	221750_at	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	HMGCS1	5p14-p13	BG035985	Hs.77910	91.3	Above	3.5
42	226157_at	Homo sapiens cDNA FLJ39131			AI569747	Hs.379018	91.3	Above	4.6
43	226496_at	hypothetical protein FLJ22611	FLJ22611	9p11.1	BG291039	Hs.27774	91.3	Below	7.7
44	204214_s_at	RAB32, member RAS oncogene family	RAB32	6q24.3	NM_006834.1	Hs.32217	90.6	Above	137.0
45	204777_s_at	mal, T-cell differentiation protein	MAL	2cen-q13	NM_002371.2	Hs.80395	90.6	Above	95.2
46	204890_s_at	lymphocyte-specific protein tyrosine kinase	LCK	1p34.3	U07236.1	Hs.1765	90.6	Above	19.4
47	205049_s_at	CD79A antigen (immunoglobulin-associated alpha)	CD79A	19q13.2	NM_001783.1	Hs.79630	90.6	Below	11.6
48	205254_x_at	transcription factor 7 (T-cell specific, HMG-box)	TCF7	5q31.1	AW027359	Hs.169294	90.6	Above	377.1
49	205504_at	Bruton agammaglobulinemia tyrosine kinase	BTK	Xq21.33-q22	NM_000061.1	Hs.159494	90.6	Below	7.3
50	210915_x_at	T cell receptor beta locus	TRB	7q34	M15564.1	Hs.303157	90.6	Above	16.2
51	211211_x_at	SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome)	SH2D1A	Xq25-q26	AF100542.1	Hs.151544	90.6	Above	2103.7
52	213830_at	T cell receptor delta locus	TRD	14q11.2	AW007751	Hs.2014	90.6	Above	7379.7
53	216191_s_at	T cell receptor delta locus	TRD	14q11.2	X72501.1	Hs.2014	90.6	Above	253.1
54	217143_s_at	T cell receptor delta locus	TRD	14q11.2	X06557.1	Hs.2014	90.6	Above	150.1
55	219528_s_at	B-cell CLL/lymphoma 11B (zinc finger protein)	BCL11B	14q32.31-q32.32	NM_022898.1	Hs.57987	90.6	Above	11.9

56	220418_at	ubiquitin associated and SH3 domain containing, A	UBASH3A	21q22.3	NM_018961.1	Hs.183924	90.6	Above	766.4
57	222895_s_at	B-cell CLL/lymphoma 11B (zinc finger protein)	BCL11B	14q32.31-q32.32	AA918317	Hs.57987	90.6	Above	12.1
58	223553_s_at	hypothetical protein FLJ22570	FLJ22570	5q35.3	BC004564.1	Hs.122559	90.6	Below	7.0
59	225090_at	HRD1 protein	HRD1	11q12	AA844682	Hs.334819	90.6	Below	3.8
60	226459_at	Homo sapiens gastric cancer-related protein GCYS-20 (gcys-20) mRNA, complete cds			AW575754	Hs.86437	90.6	Below	11.9
61	228314_at	Homo sapiens cDNA FLJ37485			BE877357	Hs.24181	90.6	Below	5.1
62	201384_s_at	membrane component, chromosome 17, surface marker 2 (ovarian carcinoma antigen CA125)	M17S2	17q21.1	NM_005899.1	Hs.277721	83.8	Above	3.3
63	202540_s_at	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	HMGCR	5q13.3-q14	NM_000859.1	Hs.11899	83.8	Above	4.6
64	203198_at	cyclin-dependent kinase 9 (CDC2-related kinase)	CDK9	9q34.1	NM_001261.1	Hs.150423	83.8	Below	5.2
65	203932_at	major histocompatibility complex, class II, DM beta	HLA-DMB	6p21.3	NM_002118.1	Hs.1162	83.8	Below	8.2
66	204613_at	phospholipase C, gamma 2 (phosphatidylinositol-specific)	PLCG2	16q24.1	NM_002661.1	Hs.75648	83.8	Below	4.0
67	205267_at	POU domain, class 2, associating factor 1	POU2AF1	11q23.1	NM_006235.1	Hs.2407	83.8	Below	11.7
68	208650_s_at	CD24 antigen (small cell lung carcinoma cluster 4 antigen)	CD24	6q21	BG327863	Hs.286124	83.8	Below	110.8
69	208651_x_at	CD24 antigen (small cell lung carcinoma cluster 4 antigen)	CD24	6q21	M58664.1	Hs.286124	83.8	Below	49.3
70	209995_s_at	T-cell leukemia/lymphoma 1A	TCL1A	14q32.1	BC003574.1	Hs.2484	83.8	Below	20166.2
71	210038_at	protein kinase C, theta	PRKCQ	10p15	AL137145	Hs.211593	83.8	Above	12.7
72	211126_s_at	cysteine and glycine-rich protein 2	CSRP2	12q21.1	U46006.1	Hs.10526	83.8	Below	16.8
73	220068_at	pre-B lymphocyte gene 3	VPREB3	22q11.23	NM_013378.1	Hs.136713	83.8	Below	6559.8
74	226245_at	Homo sapiens mRNA; cDNA DKFZp451C132			U55984	Hs.356531	83.8	Above	9.1
75	202615_at	Homo sapiens mRNA; cDNA DKFZp686D0521			BF222895	Hs.356786	82.2	Above	3.1
76	224861_at	Homo sapiens cDNA FLJ31057			BF477658	Hs.296261	82.2	Above	3.5
77	201194_at	selenoprotein W, 1	SEPW1	19q13.3	NM_003009.1	Hs.14231	82.0	Above	4.0
78	201349_at	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 1	SLC9A3R1	17q25.2	NM_004252.1	Hs.184276	82.0	Above	2.7
79	202539_s_at	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	HMGCR	5q13.3-q14	AL518627	Hs.11899	82.0	Above	3.5
80	203588_s_at	transcription factor Dp-2 (E2F dimerization partner 2)	TFDP2	3q23	BG034328	Hs.19131	82.0	Above	18.5
81	204852_s_at	protein tyrosine phosphatase, non-receptor type 7	PTPN7	1q32.1	NM_002832.1	Hs.35	82.0	Above	9.3
82	207434_s_at	FXVD domain containing ion transport regulator 2	FXVD2	11q23	NM_021603.1	Hs.19520	82.0	Above	15.7

83	208872_s_at	DNA segment, single copy probe LNS-CAI/LNS-CAII (deleted in polyposis)	D5S346	5q22-q23	AA814140	Hs.178112	82.0	Below	2.7
84	209200_at	MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C)	MEF2C	5q14	N22468	Hs.78995	82.0	Below	9.1
85	212795_at	KIAA1033 protein	KIAA1033	12q24.11	AL137753.1	Hs.12144	82.0	Below	2.5
86	212827_at	immunoglobulin heavy constant mu	IGHM	14q32.33	X17115.1	Hs.153261	82.0	Below	16.1
87	213193_x_at	T cell receptor beta locus	TRB	7q34	AL559122	Hs.303157	82.0	Above	11.1
88	221002_s_at	tetraspanin similar to TM4SF9	DC-TM4F2	10q23.2	NM_030927.1	Hs.101395	82.0	Below	2.1
89	225314_at	hypothetical protein MGC45416	MGC45416	4p12	BG291649	Hs.95835	82.0	Above	5.7
90	227432_s_at	insulin receptor	INSR	19p13.3-p13.2	AI215106	Hs.89695	82.0	Below	6.9
91	203332_s_at	inositol polyphosphate-5-phosphatase, 145kDa	INPP5D	2q36-q37	NM_005541.1	Hs.155939	81.5	Below	2.4
92	203589_s_at	transcription factor Dp-2 (E2F dimerization partner 2)	TFDP2	3q23	NM_006286.1	Hs.19131	81.5	Above	37.6
93	205674_x_at	FXVD domain containing ion transport regulator 2	FXVD2	11q23	NM_001680.2	Hs.19520	81.5	Above	13.0
94	209881_s_at	linker for activation of T cells	LAT	16q13	AF036905.1	Hs.83496	81.5	Above	1953.6
95	211005_at	linker for activation of T cells	LAT	16q13	AF036906.1	Hs.83496	81.5	Above	70.4
96	211075_s_at	CD47			Z25521.1		81.5	Above	2.1
97	211210_x_at	SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome)	SH2D1A	Xq25-q26	AF100539.1	Hs.151544	81.5	Above	315.1
98	213601_at	slit homolog 1 (Drosophila)	SLIT1	10q23.3-q24	AB011537.2	Hs.133466	81.5	Above	1877.2
99	213857_s_at	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	CD47	3q13.1-q13.2	BG230614	Hs.82685	81.5	Above	2.2
100	214924_s_at	KIAA1042 protein	KIAA1042	3p25.3-p24.1	AK000754.1	Hs.6705	81.5	Below	2.4

**Table S14. Top 100 chi-square probe sets selected for *TEL-AML1* in parallel format**

	U133 probe set	Gene description	Symbol	Location	GenBank Reference	Unigene Reference	Chi-square value	Above/below	Fold change
1	224722_at	KIAA1323	KIAA1323	18q11.1	W80418	Hs.34892	100.0	Above	7.7
2	227377_at	FLJ12722	FLJ12722		AK022784.1	Hs.24739	100.0	Above	2446.3
3	237206_at	Homo sapiens cDNA FLJ39434	FLJ39434		AI452798	Hs.42128	100.0	Above	23.5
4	241505_at	ESTs			BF513468	Hs.196779	100.0	Above	13.2
5	205109_s_at	Rho guanine nucleotide exchange factor (GEF) 4	ARHGEF4	2q22	NM_015320.1	Hs.6066	92.6	Above	147.0
6	210650_s_at	piccolo (presynaptic cytomatrix protein)	PCLO	7q11.23-q21.3	BC001304.1	Hs.12376	92.6	Above	100.4
7	213558_at	piccolo (presynaptic cytomatrix protein)	PCLO	7q11.23-q21.3	AB011131.1	Hs.12376	92.6	Above	76.8
8	224720_at	KIAA1323 protein	KIAA1323	18q11.1	W80418	Hs.34892	92.6	Above	4.3

9	235694_at	Homo sapiens, clone IMAGE:4661943, mRNA, partial cds			N49233	Hs.46914	92.6	Above	9.2
10	202808_at	hypothetical protein FLJ20154	FLJ20154	10q24.32	AK000161.1	Hs.10346	92.2	Above	3.7
11	206032_at	desmocollin 3	DSC3	18q12.1	AI797281	Hs.41690	92.2	Above	53.6
12	206033_s_at	desmocollin 3	DSC3	18q12.1	NM_001941.2	Hs.41690	92.2	Above	354.6
13	224725_at	KIAA1323 protein	KIAA1323	18q11.1	W80418	Hs.34892	92.2	Above	3.6
14	204849_at	transcription factor-like 5 (basic helix-loop-helix)	TCFL5	20q13.3-qter	NM_006602.1	Hs.30696	86.2	Above	8.8
15	206231_at	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 1	KCNN1	19p13.1	NM_002248.2	Hs.158173	86.2	Above	72.1
16	220451_s_at	baculoviral IAP repeat-containing 7 (livin)	BIRC7	20q13.3	NM_022161.1	Hs.256126	86.2	Above	25.2
17	211222_s_at	huntingtin-associated protein 1 (neuroan 1)	HAP1	17q21.2-q21.3	AF040723.1	Hs.158300	84.9	Above	80.2
18	228158_at	ESTs, Highly similar to A43542 lymphocyte-specific protein 1 - human			AI623211	Hs.374584	84.9	Above	8.2
19	203464_s_at	epsin 2	EPN2	17p11.1	NM_014964.1	Hs.7407	84.7	Above	42.9
20	213317_at	chloride intracellular channel 5	CLIC5	6p21.1	AL049313.1	Hs.21103	84.7	Above	98.5
21	226817_at	Desmocollin 2	DSC2	18q12.1	AU154691	Hs.95612	84.7	Above	47.9
22	229339_at	EST			AI093327	Hs.42128	84.7	Above	30.8
23	203184_at	fibryllin 2 (congenital contractural arachnodactyly)	FBN2	5q23-q31	NM_001999.2	Hs.79432	80.4	Above	14.3
24	218627_at	hypothetical protein FLJ11259	FLJ11259	12q23.1	NM_018370.1	Hs.184465	78.5	Above	4.6
25	221748_s_at	Tensin	TNS	2q35	AL046979	Hs.9973	78.5	Above	6.5
26	37986_at	erythropoietin receptor	EPOR	19p13.3-p13.2	M60459	Hs.127826	78.5	Above	16.8
27	204615_x_at	isopentenyl-diphosphate delta isomerase	IDI1	10p15.3	NM_004508.1	Hs.76038	77.3	Above	2.6
28	208881_x_at	isopentenyl-diphosphate delta isomerase	IDI1	10p15.3	BC005247.1	Hs.76038	77.3	Above	2.6
29	221747_at	Tensin	TNS	2q35	AL046979	Hs.9973	77.3	Above	48.7
30	232750_at	Homo sapiens cDNA FLJ13750			AU158570	Hs.298099	77.3	Above	34.7
31	227862_at	ESTs, Weakly similar to hypothetical protein FLJ22184			AA037766	Hs.125073	77.1	Above	14.3
32	203910_at	PTPL1-associated RhoGAP 1	PARG1	1p22.1	NM_004815.1	Hs.70983	75.2	Above	7.1
33	239673_at	ESTs			AW080999	Hs.163924	72.9	Above	8.9
34	240950_s_at	hypothetical protein FLJ32658	FLJ32658	19q13.33	AA400740	Hs.177990	72.9	Above	10.3
35	208056_s_at	core-binding factor, runt domain, alpha subunit 2; translocated to, 3	CBFA2T3	16q24	NM_005187.2	Hs.110099	71.8	Above	2.5
36	206591_at	recombination activating gene 1	RAG1	11p13	NM_000448.1	Hs.73958	71.1	Above	5.4
37	209963_s_at	erythropoietin receptor	EPOR	19p13.3-p13.2	M34986.1	Hs.127826	71.1	Above	8.0
38	219866_at	chloride intracellular channel 5	CLIC5	6p12.1-21.1	NM_016929.1	Hs.283021	71.1	Above	59.8
39	224726_at	KIAA1323 protein	KIAA1323	18q11.1	W80418	Hs.34892	71.1	Above	25.8
40	204297_at	phosphoinositide-3-kinase, class 3	PIK3C3	18q12.3	NM_002647.1	Hs.32971	70.6	Above	4.5
41	217628_at	chloride intracellular channel 5	CLIC5	6p21.1	BF032808	Hs.21103	70.0	Above	86.8

42	218804_at	hypothetical protein FLJ10261	FLJ10261	11q13.3	NM_018043.1	Hs.26176	70.0	Above	41.3
43	211891_s_at	Rho guanine nucleotide exchange factor (GEF) 4	ARHGEF4	2q22	AB042199.1	Hs.6066	70.0	Above	452.6
44	240446_at	KIAA1323	KIAA1323		AI798164	Hs.140903	70.0	Above	101.4
45	244107_at	ESTs			AW189097	Hs.370922	70.0	Above	518.9
46	209228_x_at	Putative prostate cancer tumor suppressor	N33	8p22	U42349.1	Hs.71119	67.9	Above	20.6
47	225129_at	Homo sapiens cDNA FLJ37548 fis, clone BRCAN2027970, moderately similar to Homo sapiens copine I mRNA			AW170571	Hs.376310	67.9	Above	2.9
48	203611_at	telomeric repeat binding factor 2	TERF2	16q22.1	NM_005652.1	Hs.100030	66.4	Above	5.3
49	236430_at	hypothetical protein MGC23911	MGC23911	16q23.1	AA708152	Hs.119840	66.4	Above	16.6
50	200709_at	FK506 binding protein 1A (12kDa)	FKBP1A	20p13	NM_000801.1	Hs.380080	65.6	Above	1.8
51	209035_at	midkine (neurite growth-promoting factor 2)	MDK	11p11.2	M69148.1	Hs.82045	65.6	Above	4.5
52	226038_at	hypothetical protein FLJ23749	FLJ23749	8p23.1	BF680438	Hs.180178	65.6	Above	5.2
53	232227_at	ESTs, Moderately similar to AF161442_1 HSPC324			AV736391	Hs.191591	65.6	Above	14.7
54	205794_s_at	neuro-oncological ventral antigen 1	NOVA1	14q	NM_002515.1	Hs.214	63.8	Above	40.1
55	227111_at	Homo sapiens cDNA FLJ31099 fis, clone IMR321000230			BG179317	Hs.177633	63.8	Above	2.7
56	230698_at	Homo sapiens mRNA; cDNA DKFZp434H205			AW072102	Hs.101375	63.8	Above	8.7
57	203038_at	protein tyrosine phosphatase, receptor type, K	PTPRK	6q22.2-23.1	NM_002844.1	Hs.79005	63.4	Above	9.0
58	202838_at	fucosidase, alpha-L- 1, tissue	FUCA1	1p34	NM_000147.1	Hs.576	63.0	Above	4.8
59	225835_at	Homo sapiens cDNA: FLJ21409 fis, clone COL03924			AK025062.1	Hs.172129	63.0	Above	3.6
60	229790_at	telomeric repeat binding factor 2	TERF2	16q22.1	AW006832	Hs.100030	63.0	Above	7.3
61	235872_at	ESTs			BE408975	Hs.63335	63.0	Above	17.5
62	239300_at	ESTs			AI632214	Hs.193041	63.0	Above	3.0
63	241940_at	ESTs			BF477544	Hs.188270	63.0	Above	2.9
64	203370_s_at	enigma (LIM domain protein)	ENIGMA	5q35.3	NM_005451.2	Hs.102948	62.9	Above	8.1
65	218152_at	high-mobility group 20A	HMG20A	15q24	NM_018200.1	Hs.69594	62.9	Above	1.7
66	218813_s_at	SH3-domain GRB2-like endophilin B2	SH3GLB2	9q34	NM_020145.1	Hs.30002	62.9	Above	6.1
67	210058_at	mitogen-activated protein kinase 13	MAPK13	6p21.1	BC000433.1	Hs.178695	62.6	Above	2.3
68	218856_at	tumor necrosis factor receptor superfamily, member 21	TNFRSF21	6p21.1-12.2	NM_016629.1	Hs.159651	62.6	Above	13.1
69	234983_at	ESTs			BE893995	Hs.31447	62.6	Above	2.4
70	209193_at	pim-1 oncogene	PIM1	6p21.2	M24779.1	Hs.81170	60.7	Above	2.0
71	209962_at	erythropoietin receptor	EPOR	19p13.3-p13.2	M34986.1	Hs.127826	60.7	Above	18.9
72	218625_at	neuritin 1	NRN1	6p24.1	NM_016588.1	Hs.103291	60.7	Above	5.0
73	223468_s_at	hypothetical protein from EUROIMAGE 363668 RGM: likely ortholog of chicken repulsive guidance molecule	RGM	15q26.1	AL136826.1	Hs.271277	60.7	Above	10.5

74	229356_x_at	hypothetical protein KIAA1259	KIAA1259	15q13.3	AK002176.1	Hs.40193	60.7	Above	1.7
75	204404_at	solute carrier family 12 (sodium/potassium/chloride transporters), member 2	SLC12A2	5q23.3	NM_001046.1	Hs.110736	59.3	Above	2.0
76	212063_at	CD44 antigen (homing function and Indian blood group system)	CD44	11p13	BE903880	Hs.169610	59.3	Below	7.4
77	221773_at	ELK3, ETS-domain protein (SRF accessory protein 2)	ELK3	12q23	AW575374	Hs.288555	59.1	Above	3.1
78	208886_at	H1 histone family, member 0	H1F0	22q13.1	BC000145.1	Hs.226117	58.5	Above	4.2
79	212399_s_at	KIAA0121 gene product	KIAA0121	3p25.2	D50911.2	Hs.155584	58.5	Above	1.8
80	219954_s_at	cytosolic beta-glucosidase	GLUC	4p15.31	NM_020973.1	Hs.146182	58.5	Above	37.3
81	220692_at	HSPC047 protein	HSPC047	7q11.22	NM_014147.1	Hs.278943	58.5	Above	16.8
82	225357_s_at	hypothetical protein KIAA1259	KIAA1259	15q13.3	AI659419	Hs.40193	58.5	Above	4.9
83	206316_s_at	kinetochore associated 1	KNTC1	12q24.31	NM_014708.1	Hs.115778	58.2	Above	2.7
84	207957_s_at	protein kinase C, beta 1	PRKCB1	16p11.2	NM_002738.1	Hs.77202	56.8	Above	2.1
85	213122_at	KIAA1750 protein	KIAA1750	8q22.1	AI096375	Hs.173094	56.8	Above	8.9
86	226885_at	ESTs			AI743880	Hs.12876	56.8	Above	10.7
87	218742_at	protein related to Narf	HPRN	16p13.3	NM_022493.1	Hs.22158	56.6	Above	4.2
88	206574_s_at	protein tyrosine phosphatase type IVA, member 3	PTP4A3		NM_007079.1	Hs.43666	56.4	Above	6.9
89	209199_s_at	MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C)	MEF2C	5q14	N22468	Hs.78995	56.4	Above	1.8
90	212154_at	syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan)	SDC2	8q22-q23	J04621.1	Hs.1501	56.4	Above	6.6
91	213423_x_at	Putative prostate cancer tumor suppressor	N33	8p22	AI884858	Hs.71119	56.4	Above	15.6
92	228831_s_at	hypothetical protein FLJ00058	FLJ00058	19p13.3	AL039870	Hs.6750	56.4	Above	2.0
93	208910_s_at	complement component 1, q subcomponent binding protein	C1QBP	17p13.3	L04636.1	Hs.78614	56.0	Below	1.9
94	217873_at	MO25 protein	MO25	2q36.1	NM_016289.1	Hs.6406	56.0	Above	1.4
95	201976_s_at	myosin X	MYO10	5p15.1-p14.3	NM_012334.1	Hs.61638	55.9	Above	12.5
96	209685_s_at	protein kinase C, beta 1	PRKCB1	16p11.2	M13975.1	Hs.77202	55.9	Above	1.9
97	213017_at	abhydrolase domain containing 3	ABHD3	18q11.1	AL534702	Hs.13377	55.9	Above	4.0
98	213261_at	KIAA0342 gene product	KIAA0342	3p22.1	AA035414	Hs.16950	55.9	Above	1.6
99	224881_at	Homo sapiens mRNA; cDNA DKFZp434B1620 (from clone DKFZp434B1620)			AV724827	Hs.43112	55.9	Above	1.7
100	225731_at	KIAA1223	KIAA1223	4q26	AB033049.1	Hs.28783	55.9	Above	2.8

#### IV: Diagnostic Accuracy

The class discriminating genes were identified as described above, and then used in an ANN-based supervised learning algorithm. As previously discussed (section II, Supplemental Information), class assignment was based on a differential diagnostic tree format and required that the node value for assignment exceeded a statistically defined confidence level. The results of this analysis are shown in Table 4 of the paper and are included below for the reader's convenience.

**Table 4. ALL subgroup prediction accuracies using top 50 chi-square selected genes from U133A and B and Artificial Neural Network (ANN) in decision tree format.**

Subgroup	Training Set <sup>a</sup>		Test Set <sup>b</sup>	
	Apparent Accuracy <sup>c</sup>	True Accuracy <sup>d</sup>	Sensitivity <sup>e</sup>	Specificity <sup>f</sup>
<i>T-ALL</i>	100%	100%	100%	100%
<i>E2A-PBX1</i>	100%	100%	100%	100%
<i>TEL-AML1</i>	98%	100%	100%	100%
<i>BCR-ABL</i>	100%	95%	75%	100%
<i>MLL</i> rearrangement	100%	100%	100%	100%
Hyperdiploid >50	100%	100%	100%	100%

<sup>a</sup> training set consisted of 100 cases with distribution: [T-ALL 12, *E2A-PBX1* 13, *TEL-AML1* 15, *BCR-ABL* 11, *MLL* 15, HD>50 13, other 21]

<sup>b</sup> blinded test set consisted of 32 cases [T-ALL 2, *E2A-PBX1* 5, *TEL-AML1* 5, *BCR-ABL* 4, *MLL* 5, HD>50 4, other 7]

<sup>c</sup> apparent accuracy determined by 3-fold cross-validation

<sup>d</sup> true accuracy determined by class prediction on the blinded test set.

<sup>e</sup> Sensitivity = (the number of positive cases predicted)/(the number of true positives).

<sup>f</sup> Specificity = (the number of negative cases predicted)/(the number of true negatives).

To control for over-fitting of the data, we performed 10 additional rounds of analysis. For each round, new training and test sets were developed and discriminating probe sets reselected exclusively using the new training sets. The top 20 and 50 probe sets were then used in an ANN-based supervised learning algorithm, and their true accuracy assessed on the new test sets. This resulted in an average accuracy of class assignment of 97% (range 93.8%-100%) using 20 probes per class. Shown in Tables S15 and S16 are the results from these analyses. The numbers listed under the individual leukemia subtypes represent the number of misclassified cases in the training and test sets. The overall accuracies are listed on the right.

**Table S15. Training and Test Set Permutation Results - Errors per group using 20 probe sets**

	<b>T-ALL</b>		<b>E2A-PBX1</b>		<b>TEL-AML1</b>		<b>BCR-ABL</b>		<b>MLL</b>		<b>Hyperdip&gt;50</b>		<b>Overall Accuracy</b>	
	Training	Test	Training	Test	Training	Test	Training	Test	Training	Test	Training	Test	Training	Test
<b>1</b>	0 <sup>1</sup>	0	0	0	0	1	0	1	0	0	0	0	100	93.8
<b>2</b>	0	0	0	0	0	0	1	1	0	0	0	1	99	93.8
<b>3</b>	0	0	0	0	0	0	2	0	0	0	0	0	98	100
<b>4</b>	0	0	0	0	0	1	2	0	0	0	0	0	98	96.9
<b>5</b>	0	0	0	0	0	0	0	1	0	0	0	0	100	96.9
<b>6</b>	0	0	0	0	1	0	0	0	0	0	0	0	99	100
<b>7</b>	0	0	0	0	0	0	0	0	0	0	0	0	100	100
<b>8</b>	0	0	0	0	0	0	1	1	0	0	0	0	99	96.9
<b>9</b>	0	0	0	0	0	0	0	0	0	0	0	0	100	100
<b>10</b>	0	0	0	0	0	0	0	1	0	0	0	1	99	93.8

<sup>1</sup>The number of misclassified cases obtained when diagnosing the indicated leukemia subtype

**Table S16. Training and test set permutation results – errors per group using 50 probe sets**

	T-ALL		E2A-PBX1		TEL-AML1		BCR-ABL		MLL		Hyperdip>50		Overall Accuracy	
	Training	Test	Training	Test	Training	Test	Training	Test	Training	Test	Training	Test	Training	Test
<b>1</b>	0 <sup>1</sup>	0	0	0	1	0	0	0	0	0	0	0	99	100
<b>2</b>	0	0	0	0	0	1	1	1	0	0	0	1	99	90.6
<b>3</b>	0	0	0	0	1	0	2	1	0	0	0	0	97	96.9
<b>4</b>	0	0	0	0	1	0	2	1	0	0	0	0	97	96.9
<b>5</b>	0	0	0	0	1	0	0	1	0	2	1	0	98	90.6
<b>6</b>	0	0	0	0	2	0	0	0	0	0	0	0	98	100
<b>7</b>	0	0	0	0	1	0	0	0	0	0	0	0	99	100
<b>8</b>	0	0	0	0	1	0	0	0	0	0	0	0	99	100
<b>9</b>	0	0	0	0	0	0	0	1	0	0	0	0	100	96.9
<b>10</b>	0	0	0	0	2	0	1	1	0	0	0	1	97	93.8

<sup>1</sup>The number of misclassified cases obtained when diagnosing the indicated leukemia subtype

### Comparison of supervised learning algorithms

The performance of other supervised learning algorithms was compared to ANN. Using the original training and test sets, chi-squared was used to select the desired number of probes sets, and then the selected probes were used to build a model using ANN, SVM, and *k*-NN. ANN was performed with one hidden layer consisting of 4 nodes and the backpropagation epoch number was 5000. For the other algorithms, the linear SVM kernel was used and the *k*-NN parameter was 3. The comparison of the results is shown in Table S17 below. The comparison was performed using the top 20 and 50 probe sets, as well as the top 20 and 50 genes. The numbers correspond to the number of errors made in either the training or test set by class for each metric. Overall, ANN and SVM performed fairly comparably while *k*-NN gave slightly poorer results.

**Table S17. Comparison of supervised learning algorithms**

	ANN		SVM		<i>k</i> -NN	
	Training	Test	Training	Test	Training	Test
top 20 probes						
T-ALL	0 <sup>1</sup>	0	0	0	0	0
E2A-PBX1	0	0	0	0	0	0
TEL-AML1	0	0	0	0	0	0
BCR-ABL	1	2	1	2	2	1
MLL	0	0	0	0	0	1
Hyperdiploid >50	0	0	0	0	0	0
top 50 probes						
T-ALL	0	0	0	0	0	0
E2A-PBX1	0	0	0	0	0	0
TEL-AML1	1	0	0	0	0	0
BCR-ABL	0	1	1	1	2	1
MLL	0	0	0	0	0	1
Hyperdiploid >50	0	0	0	0	0	0
top 20 genes						
T-ALL	0	0	0	0	0	0
E2A-PBX1	0	0	0	0	0	0
TEL-AML1	1	0	0	0	0	0
BCR-ABL	1	2	1	2	1	1
MLL	0	0	0	0	0	1
Hyperdiploid >50	0	0	0	0	0	0

top 50 genes						
T-ALL	0	0	0	0	0	0
E2A-PBX1	0	0	0	0	0	0
TEL-AML1	1	0	0	0	0	0
BCR-ABL	0	1	1	1	3	1
MLL	0	0	0	0	0	0
Hyperdiploid >50	0	0	0	1	0	0

---

<sup>1</sup> The number of misclassified cases

## V: Comparison of Expression Profiles and Real-time PCR (Taqman)

An evaluation of the discriminating probe sets selected from the U133A and U133B microarrays revealed that 20% of the identified class discriminators correspond to genes that were represented on the U95Av2 microarray, but had not been selected as class discriminators using the latter platform. A possible explanation for this observation is that the improved oligonucleotide design of the U133 microarrays results in an increase in both sensitivity/specificity, and thus allows the identification of class discriminators that had previously on the U95Av2 microarray fallen below statistical significance. To confirm this possibility, real-time RT-PCR (Taqman; Perkin-Elmer/Applied Biosystems, Foster City, CA) assays were developed for eleven genes that met these criteria. The probes selected were against discriminating genes for *BCR-ABL* (Neuropillin1, 212298\_at; and ATP10C, 214255\_at), *E2A-PBX1* (FLJ12280, 213909\_at; and FAM3C, 201889\_at), Hyperdiploid > 50 chromosomes (EST, 212419\_at), T-ALL (RAB32, 204214\_s\_at; and TRIM, 217147\_s\_at), and *TEL-AML1* (Desmocollin 3, 206033\_s\_at; Epsin 2, 203464\_s\_at; NOVA1, 205794\_s\_at; and HAP1, 211222\_s\_at). Taqman primers were developed for each of these genes using the target sequences against which the microarray oligonucleotide probes were designed. Amplified product was quantitated using SYBR green and the resulting values normalized using the commercially available Taqman GAPDH primer and probe sequences.

RNA from representative diagnostic bone marrow samples of each class (four per class) were diluted to 35 ng/μl then treated for 15 minutes with 1.0 unit of DNase I (Invitrogen, Carlsbad, California) using the Invitrogen protocol to remove any contaminating DNA. Samples were reverse transcribed following the Taqman RT protocol using 1X RT mix (Perkin-Elmer/Applied Biosystems) and MultiScribe (Applied Biosystems). Samples were incubated at 25°C for 10 minutes, 48°C for 30 minutes, 95°C for 5 minutes, then

placed on ice for 2 minutes. Real-time PCR was performed on a PE Applied Biosystems 7700 prism using oligonucleotide primers designed using Primer Express. The following primers were used: (1) *Desmocollin 3*, 5'- GCA ACC AGT ATC ACT TCC CTG TT - 3' (forward primer), and 5'- GAA TTA CAA ATT CGG GCA TAC ATG -3' (reverse primer); (2) *Epsin 2*, 5'- GGA GGT GCA ATG GGA TGG -3' (forward), and 5'- GCC CTG CAC CGT CTG AAG -3' (reverse); (3) *Nova 1*, 5'- CAT CCC AGC TGC TCC TTT CT -3' (forward), and 5'- AGG CTG GAC GAA ATT CAG ACA -3' (reverse); (4) *HAPI*, 5'- AGC GCC TTC CCA ACA ATG T -3' (forward), and 5'- ACA AGA ACC AGG GTG GCT ACC -3' (reverse); (5) *Neuropilin 1*, 5'- AAA GAC ATT TGT TGG GAG TCA CAT T -3' (forward), and 5'- CAT GGT GAT CAA TAT TTT CCT GGA A -3' (reverse); (6) *ATP10C*, 5'- TTG AGT GCA TCC CAG CAT TC -3' (forward), and 5'- CCA GGG ATG TAA TAC CTA CAA GGC -3' (reverse); (7) *FLJ12280*, 5'- TTG CCT TGC TTA GAG AAT TAC TGC -3' (forward), and 5'- ACC CTG AGG GCC TAG AAA TCT G -3'; (8) *FAM3C*, 5'- TGT GTA TGA AGT ATC TCA AAC TGG AAC AT -3' (forward), and 5'- ATG CAT CTA AAC TTT AGG TTC GAA ATT -3' (reverse); (9) *FAB32*, 5'- CCC TGC TGT CCT CTT GGC T -3' (forward), and 5'- AAT TGG TCC ACC TGG GAA GG -3' (reverse); (10) *TRIM*, 5'- TTA CAA AGT ATT TTT CCC AAA GAT AGC TT -3' (forward), and 5'- TTT CTC CAA GTG ACT ATC TCT GGC TAG -3' (reverse); and (11) 212419: EST, 5'- GAG AAG GCT CCG ACG TCT CC -3', and 5'- CCA GGA ATA AGG CAC ACA ACG -3' (reverse).

The PCR reactions and amplification protocols were set up as previously described.<sup>3</sup> The reverse transcribed cDNA was amplified in 1X SYBR green master mix containing a Taq Polymerase with 100 nM each of a forward and reverse primer. The GAPDH control for each cDNA was set up according to the Applied Biosystems protocol. Amplification proceeded as outlined in the “Quickstart

Guide: ABI Prism™ Dissociation Curve Software” instructions. Data collection was performed by linking a dissociation curve profile on the end of the PCR run. Dilution controls were set up for each gene of interest as well as for GAPDH, and standard curves were generated at the end of the run. The expression levels were quantitated for each gene, and then normalized to the quantitated GAPDH. The normalized real-time result for the four samples of each class were average together and the mean for that class was compared to the mean intensity value for the same four samples from the microchip array. This comparison is shown in Table S18 below.

Although the selected probe sets were from the lower end of the ranked list of discriminating genes for each class, their expression was significantly higher by Taqman measurements in the identical class that was identified to have high expression by microarray analysis. The high degree of correlation between the microarray data and that obtained using Taqman methodology suggests that the U133 microarray platform was correctly identifying these genes as class discriminators.

**Table S18 Comparison of Expression profiles and Real-time PCR (Taqman)**

		<i>TEL- AML1</i>	<i>BCR- ABL</i>	<i>E2A- PBX1</i>	T-ALL	Hyperdip>50	<i>MLL</i>
<b>206033_s_at</b>	Affy	1676.9	1	1	1	1	1
<b>Desmocollin 3</b>	RQ-PCR	474.5	0	50.3	0	0	0
<b>203464_s_at</b>	Affy	320.3	1	1	1	1	1
<b>Epsin 2</b>	RQ-PCR	881.6	6.4	4.2	3.5	29.7	9.5
<b>205794_s_at</b>	Affy	594.5	90.7	1	1	1	1
<b>NOVA1</b>	RQ-PCR	785.9	10.9	0	0.5	0	0

<b>211222_s_at</b>	Affy	1010.3	1	1	1	1	1
<b>HAP1</b>	RQ-PCR	382.4	1.6	4.5	0.06	2.1	0.4
<b>212298_at</b>	Affy	133.6	906.5	1	1	134.1	68.3
<b>Neuropilin1</b>	RQ-PCR	94.1	8784.3	56.8	9.8	435.5	175.1
<b>214255_at</b>	Affy	215	999.6	1	1	94.9	139.1
<b>ATP10C</b>	RQ-PCR	56.3	70406.4	31948.8	30961.9	3387.2	1209.3
<b>213909_at</b>	Affy	1	71.2	1410.1	138.2	116.9	113.9
<b>FLJ12280</b>	RQ-PCR	2.98	0.02	61.4	0.1	0.02	0.02
<b>201889_at</b>	Affy	823.7	1034	3370	435.7	562.5	728.6
<b>FAM3C</b>	RQ-PCR	589.3	2228.4	10631.4	984.6	294.8	1258.9
<b>204214_s_at</b>	Affy	1	1	1	1229.2	1	1
<b>RAB32</b>	RQ-PCR	81.3	6.5	6.3	130.1	1	1.9
<b>217147_s_at</b>	Affy	1	52.6	1	2531.3	1	1
<b>TRIM</b>	RQ-PCR	344.2	5.7	15.4	18.5	8.5	4
<b>212419_at</b>	Affy	220	1	1	1	663.3	1
<b>EST</b>	RQ-PCR	252.5	66.5	83.2	26.2	789.2	179.2

## VI: References

1. Yeoh EJ, Ross ME, Shurtleff SA, et al. Classification, subtype discovery, and prediction of outcome in pediatric acute lymphoblastic leukemia by gene expression profiling. *Cancer Cell*. 2002;1:133-143.
2. Khan J, Wei JS, Ringner M, Saal LH, Ladanyi M, Westermann F, Berthold F, Schwab M, Antonescu CR, Peterson C, Meltzer PS. Classification and diagnostic prediction of cancers using gene expression profiling and artificial neural networks. *Nat Med* 2001;7:673-679.
3. Vandesompele, J, DePaepe A, and Speleman F. Elimination of primer-dimer artifacts and genomic coamplification using a two-step SYBR green 1 real-time RT-PCR. *Analytical Biochemistry* 2002;303: 95-98.