Supplementary Appendix

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Supplementary Appendix

Gene Expression Unmasks Two Clinical Phenotypes in Polycythemia Vera

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Supplementary Appendix

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CD34+ cell isolation and analysis

Peripheral blood CD34+ cells from PV patients were isolated from Ficoll Paque (G5 Healthcare, St. Louis, MO)-processed buffy coats with a purity of greater than 95% and a viability of 98% using immunomagnetic beads (Miltenyi, Auburn, CA) according to the manufacturer's instructions, and frozen at -80^0 C in 10% DMSO and 90% fetal bovine serum until studied. As controls, G-CSF mobilized peripheral blood CD34+ cells from three normal men and three normal women were obtained from commercial sources (AllCell Technologies LLC, Chicago, IL and StemCell Technologies Inc, Vancouver, BC).

The CD34+ cells were analyzed for CD34, CD38, CD33, CD41 and glycophorin expression using commercially available fluorescent-labeled antibodies (Becton Dickinson, San Jose CA). Fluorescence of at least 10,000 cells was measured on a FACS Caliber and analyzed with Cellquest and Paint-a-gate software (BD Biosciences, San Jose, CA). Similar to published reports of the peripheral blood CD34+ cell immunophenotype in normal individuals and MPD patients [1, 2], CD34+ cells from both sources were greater than 98% CD38-positive and 85% CD33-positive; CD41 was expressed on less than 3% of CD34+ cells from both sources, while glycophorin was not expressed by either

CD34+ cell population. Cell cycle analysis by flow cytometry using propidium iodide revealed that 91% of the PV and 90% of the mobilized normal CD34+ cells were in Go/G_1 (data not shown).

Total CD34+ cell RNA was isolated by the RNeasy technique (Qiagen, Valencia, CA) with an added DNAse step according to the manufacturer's instructions. To confirm sample quality, we employed duplex RT-PCR to assess RNA integrity [3], and the Agilent Bioanalyzer Lab on a Chip (Agilent Technologies, Inc., Santa Clara, CA) was used to confirm that all samples had an optimal rRNA ratio (1:2, for 18S and 28S, respectively), and clean run patterns before microarray analysis.

Oligonucleotide microarray analysis

Total RNA samples were processed using the Affymetrix two-round RNA amplification protocol (Affymetrix, Santa Clara, CA). Briefly, 100ng of starting total RNA were used to synthesize first strand cDNA using oligonucleotide probes with 24 oligo-dT plus T7 promoter as primer (Proligo LLC, Boulder, CO), and the SuperScript Choice System (Invitrogen, Carlsbad, CA). Following the double stranded cDNA synthesis, the product was purified by Affymetrix sample clean up columns, and unlabeled ribonucleotides were used in a first round of in vitro transcription cRNA amplification (MegaScript, Ambion, Austin, TX). The following cycle of cDNA synthesis was started with random primers, and the oligo-dT with T7 promoter was again used as primer at the second strand cDNA synthesis step.

The ds cDNA product was again column purified. Subsequently, biotinylated anti-sense cRNA was generated through in vitro transcription using the BioArray RNA High Yield Transcript Labelling kit (ENZO Life Sciences Inc, Plymouth Meeting,PA). 15ug of the biotinylated labeled cRNA was fragmented at 94^0C for 35 min (100mM Tris-acetate, pH 8.2, 500mM KOAc, 150mM MgOAC), and 10ug of total fragmented cRNA was hybridized to the Affymetrix human genome GeneChip array U133A for 16hr at 45^0C with constant rotation (60 rpm).The Affymetrix Fluidics Station 450 was then used to wash and stain the chips, remove the non-hybridized target and incubate with a streptavidin-phycoerythrin conjugate to stain the biotinylated cRNA. The staining was amplified using goat IgG as blocking reagent and biotinylated goat streptavidin antibody, followed by a second staining step with a streptavidin-phycoerythrin conjugate.

Fluorescence was detected using the Affymetrix GS3000 GeneArray Scanner and image analysis of each GeneChip was done with the GeneChip Operating System software from Affymetrix (GCOS1.1.1), using the standard default settings. For comparison between different chips, global scaling was used, scaling all probe sets to a user-defined target intensity of 150. To assess the QC of the hybridization, chip image, and comparison between chips, the following parameters were studied: the scaling factor, related to the overall intensity of the chip, to confirm the similar signal intensity and staining throughout the samples; background estimation of nonspecific or cross-hybridization; percentage of transcripts that were considered significantly hybridized to the chip (present) by the algorithm; RNA integrity by measurement of the ratio of 3’ to 5’ regions for the housekeeping gene GAPDH, since its presence in the chip and a ratio close to 1 indicates good integrity of the target sample; spikes (BioB/BioC), to confirm the detection level and sensitivity after hybridization.

The quality of the microarray experiments was assessed using the R/Bioconductor packages, affyPLM and affy. The graphics of Residual Images, NUSE, RLE and histograms were checked for image artifacts and outliers. Using the default algorithms for image analysis provided by Affymetrix, approximately 30%-45% of genes represented in the chips were recorded as present in the RNA samples, indicating good quality data. For quality control, we also analyzed differential calls (up or down regulated) and correlation analyses from the different replicates to demonstrate reproducibility amongst the experiments. Consistently, the Pearson’s correlation coefficients obtained in these studies were between 0.97 and 0.99 for all replicated samples.

To achieve gene expression signal intensity estimates with a higher precision and a lower false discovery rate (FDR) in differential gene expression analysis, we used RMA (Robust Multiarray Analysis www.bioconductor.org) to obtain the gene level (probe set) expression signals. RMA also performs quantile normalization to reduce the obscuring variation between microarrays, which might be introduced during the processes of sample preparation, manufacture, fluorescence labeling, hybridization and scanning. With the expression signals estimated as above, a parametric empirical Bayes statistical modeling method, which uses a hierarchical mixture model to account for differences amongst genes in their average expression levels and measurement fluctuations, was employed for differential gene expression analysis between the PV samples and the normal controls. Based on this method, posterior probabilities were obtained, from which inferences regarding differential expression patterns could be made. Specifically, a posterior probability of > 0.5 was taken to assert significance in differential gene expression and minimize the false discovery rate. The microarray data were deposited as Series GSE47018 in the Gene Expression Omnibus MIAME compliant database at http://www.ncbi.nlm.nih.gov/geo.

Q-RT-PCR validation of the microarray results

To validate the microarray results, we analyzed additional CD34+ cell samples from a subset of the patients by real-time PCR (Q-RT-PCR) without prior RNA amplification. For the mRNA transcripts, first-strand cDNA synthesis was carried out on RNA extracted from the cells with the TaqMan Reverse Transcription Reagents kit (Applied Biosystems, Carlsbad CA.) using the oligo d $(T)_{16}$ RT primer following the manufacturer’s suggested protocol. For miR-21 expression, CD34+ cell RNA was isolated using the mirVana miRNA Isolation Kit (Applied Biosystems) following the manufacturer’s procedure for total RNA isolation. The TaqMan MicroRNA Reverse Transcription Kit (Applied Biosystems) was used as directed to generate cDNA.

Relative quantitation by Q-RT-PCR was carried out using the gene expression GEX or microRNA assays (Applied Biosystems) listed in **Table S3**. Duplicate 20 µl reactions were set up using the TaqMan® Universal PCR Master Mix, No AmpErase® UNG (2X), and performed on an Applied Biosystems 7500 sequence detection system using the default "standard 7500" PCR conditions (95^{o}C for 10 minutes followed by 40 cycles of 95^{o}C for 15 seconds and 60^{o}C for 1 minute). For each GEX primer/probe set, a standard curve with known relative concentrations of RNA from either a patient or normal control sample was used to calculate reaction efficiency and quantitate the reaction products. GAPDH reactions were run in parallel samples on the same assay plate. All the GEX Q-RT-PCR results were calculated using the "Standard Curve Assay" program of the 7500 SDS system (Applied Biosystems) and normalized to the GAPDH (glyceraldehyde-3-phosphate dehydrogenase) and the data are shown in Figure S3. For the miR-21 primer/probe set, relative quantitation using the $\Delta\Delta C_T$ calculation method was utilized rather than a standard curve. U6 RNA was the reference RNA. In each case, the direction of gene expression (up or down) was the same for the Q-RT-PCR assay as for the microarray.

Supervised analysis of the 19 patient cohort by top scoring pairs

EBarrays analysis was performed for male and female patients separately. The 549 probes that showed a posterior probability greater than 0.5 of differential expression between aggressive and indolent phenotypes in both male and female patients were retained for further analysis, with both genders included. Top-scoring pair analysis [4] was run on the 549 probes and we retained the top 30 top-scoring pairs (TSPs). As some genes had duplicate probes, using the R limma package we applied an empirical Bayes test to this data (now both genders) and retained the highest scoring probe for each gene.[5] The dendrogram and heat map for the supervised analysis of the 19 PV patient cohort using the 30 top scoring pairs are shown in **Figure S5** and discussed in the Results section of the manuscript.

External validation of the unsupervised hierarchical clustering by top scoring pairs

For external validation with a test group of PV patients, instead of the 30 genes used for the supervised analysis of the original 19 patients (**Figure S5**), the number of TSP was narrowed to 6 to permit gene expression analysis by Q-RT-PCR rather than by microarray. Ten genes (PCNA, IFI30, TSN, CTSA, SMC4, CDKN1A, CTTN, SON, TIA1 and MYL9) were identified for the following pairwise comparisons: PCNA > IFI30; TSN > CTSA; SMC4 > CDKN1A; PCNA > CTTN; SON > CTTN and TIA1> MYL9, scoring 1 for true and 0 for false with the prediction that a score of 5-6/6 indicated aggressive disease (**Figure S6**).

Methods

Since the 6 gene pair Q-RT-PCR assay compares 10 different genes in a single patient sample, absolute quantitation of RNA expression was employed, as opposed to comparing relative RNA expression levels, which can only compare the same gene in different samples. Therefore, with the exception of CTTN, which was obtained commercially (OriGene Technologies, Inc., Rockville, MD Catologue No. SC124848), either a full length or partial cDNA of the targeted region for each gene was cloned into the plasmid pCR®2.1-TOPO® from patient CD34+ cell RNA using a TopoTA® cloning kit (Cat. No. K4520-01, Life Technologies, Grand Island, NY) according to the manufacturer's instructions (**Table S7**). These plasmids were then used to generate standard curves (**Figure S7**). Once optimized, three standard dilutions were chosen for use in the Q-RT-PCR assay based on the observed expression range of each gene. The Q-RT-PCR assays were performed using Applied Biosystems TaqMan® Gene Expression Assay kits for each of the 10 genes (**Table S8**). Copy numbers were calculated based on the known size and concentration of each plasmid.

Before assay, Beta-actin levels for each RNA sample were measured to determine if the RNA concentration and quality were acceptable for analysis (Applied Biosystems cat. # 4333762F; ACTB endogenous control).

Intra-assay precision was assessed by running all samples in duplicate. Replicate Ct values with standard deviations of greater than 0.5 were rejected. Inter-assay precision was assessed by performing replicate assays on different days with fresh template cDNA from the same RNA sample from eight patients (**Table S9a**). In each case, the Q-RT-PCR assay generated the same calls, either 5-6/6 or < 5/6 (**Figure S6**).

In addition, extended inter-assay assessment was made by assaying the CD34+ cell RNA of 3 clinically stable patients from two separate blood draws within a 6 month period. Again, in all instances, there was no difference in the clinical phenotype stratification of these patients using the Q-RT-PCR assay (**Table S9b**).

Results

Training set

We used the available RNA samples from 7 of the original 19 patients (**Table S1**) as the training set to verify the validity of the Q-RT-PCR assay. One patient is included twice because her 10 gene assay score increased from 3 to 6 six months before overt transformation to acute leukemia occurred. As indicated in the scoring algorithm (**Figure S6**), a score of 5-6/6 was taken as an indication of aggressive disease.

Table S10 shows the clinical features of these 7 patients according to gender, which conformed to the clinical features observed in the 19 patient cohort at study entry (**Table1**) except that no difference in the platelet count was observed in the smaller group. **Table S11** correlates the patients' clinical features with their 10 gene assay scores, which again segregated the patients into the same phenotypes assigned by both the unsupervised hierarchical clustering. (**Figure 1 and Table 2**), and the supervised analysis using top scoring pairs (**Figure S5**). Patient numbers in this training set were too small to perform meaningful comparisons of most of their clinical features, but as shown in **Table S12,** they did differ significantly as expected with respect to disease duration, transformation to acute leukemia and survival.

Test set

For external validation of the unsupervised hierarchical clustering results (**Figure 1 and Table 2**), a test set of 30 PV patients was selected and assayed in a blinded fashion. The selection criterion was the same as for the original 19 patients, sufficient CD34+ cell RNA for analysis. The clinical features of the 30 patients according to gender are shown in **Table S13** and as with the original 19 patient cohort (**Table 1**), with the exception of the platelet count, were no differences between the men and women patients. Their individual clinical features and 10 gene assay scores are shown in **Table S14.**

As shown in **Table S15,** patient clinical phenotypes segregated according to the 10 gene assay score. Congruent with both the results of the unsupervised hierarchical clustering (**Table 2**) and top scoring pairs analysis using 30 genes (**Figure S5**), a clinical score of 5 or 6/6 correlated with an aggressive phenotype, with a significantly higher incidence of thrombosis, splenomegaly, greater spleen size and more exposure to chemotherapy. Disease duration was also greater in this group. In contrast to the original 19 patients, however, there was no difference in hemoglobin level but platelet counts were lower in the patients scoring 5-6/6. The allele burden was also higher in the aggressive group, consistent with their longer disease duration and the absence of JAK2 V617F heterozygous patients in this group; however, this is a distinction without a difference since clonal dominance was the rule in both groups as in the original 19 patients (**Table 1**).

As shown in **Figure S8**, the AUC of the ROC curve for these results was 0.925 and, as predicted, setting the call of an aggressive phenotype at 5-6/6, had a sensitivity of 0.875 and specificity of 1.0. The positive predictive value (PPV) at this threshold was 1.0 and the negative predictive value (NPV) was 0.95.

No patient in the test group transformed to acute leukemia and only one died, which may reflect the shorter prospective observation period for this group (mean 1 year) in contrast to initial 19 patient cohort (mean of 4 years for the aggressive patients and 7 years for the indolent patients); the low incidence of splenectomy reflects our current practice to avoid this procedure if at all possible. Taking everything together, the results of the 10 gene Q-RT-PCR assay in the 30 patient test group recapitulated the segregation of the original 19 PV patient cohort into aggressive and indolent phenotypes by unsupervised hierarchical clustering (**Figure 1 and Table 2**).

Additional pathway analyses

To determine if accounting for gender was critical, we performed analysis on the entire set of deregulated genes (i.e., the union of the male and female sets rather than the intersection). Using empirical Bayes analysis, only one gene in this set, XIST, was significantly differentially regulated between PV patients and normal controls after Benjamini-Hochberg (B-H) multiple testing correction. This X-linked gene may likely be a false-positive as well, arising from the mixing of male and female patients and normals in unequal proportions. Gene set analysis of the ranked gene list identified no significant pathways after B-H correction (data not shown).

We also interrogated male and female gene expression separately by IPA (Ingenuity Systems) as well as KEGG. With IPA, there was significant pathway overlap between the men and women patients (data not shown), while with KEGG analysis (**Figures S2a and b**), as discussed in the main body of the text, there was differential regulation of 12 pathways in the women patients that were not upregulated in the men.

Figure S1a. KEGG Pathways – Males.

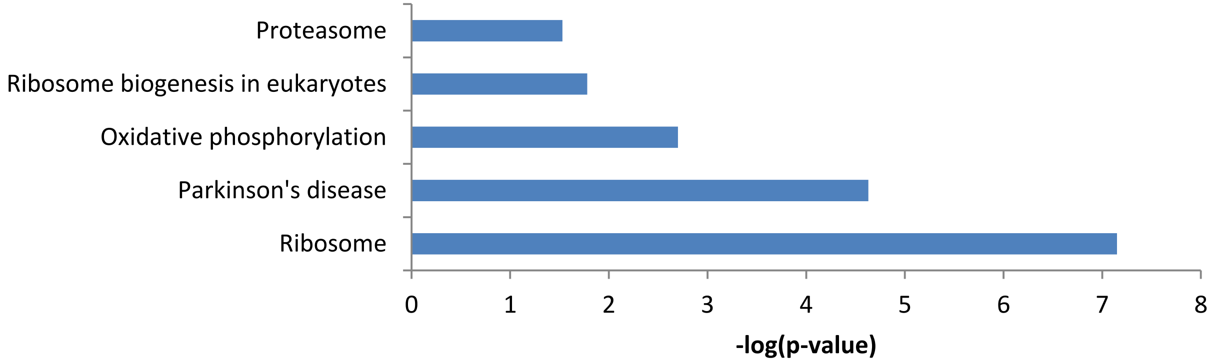


Figure S1b. KEGG Pathways – Females.

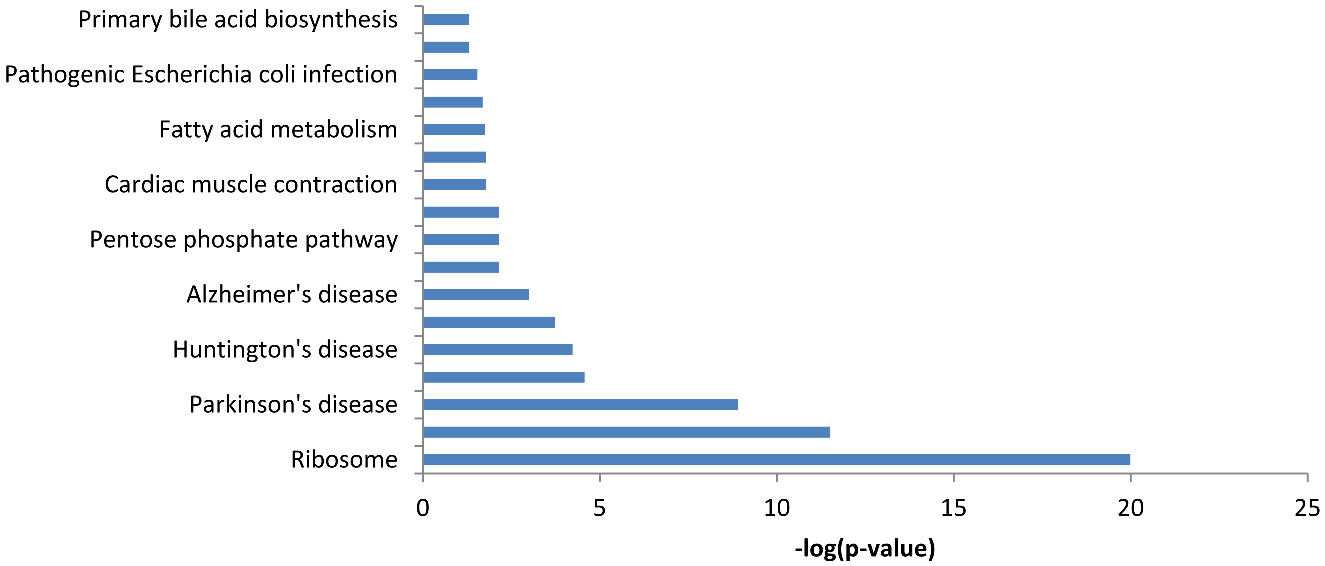


Figure S2. Venn diagram illustrating the differential and concordant deregulation of gene expression by the male and female PV patients.

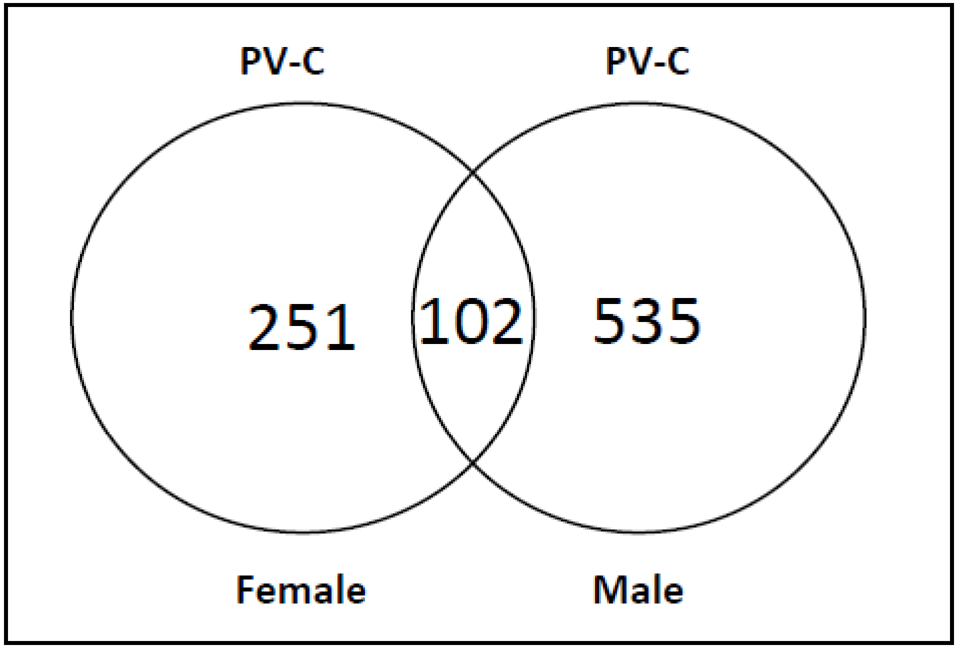


Figure S3. Q-RT-PCR confirmation of gene expression in PV CD34+ cells using the primer/probe sets listed in Table S3.

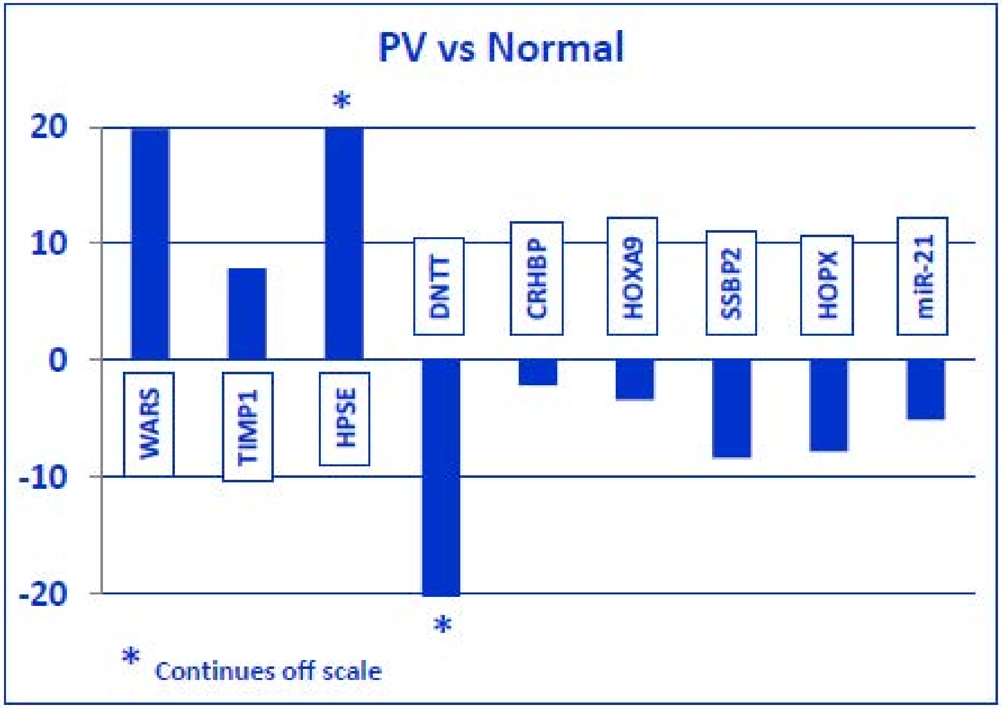


Figure S4a. KEGG Pathways- Indolent Group.

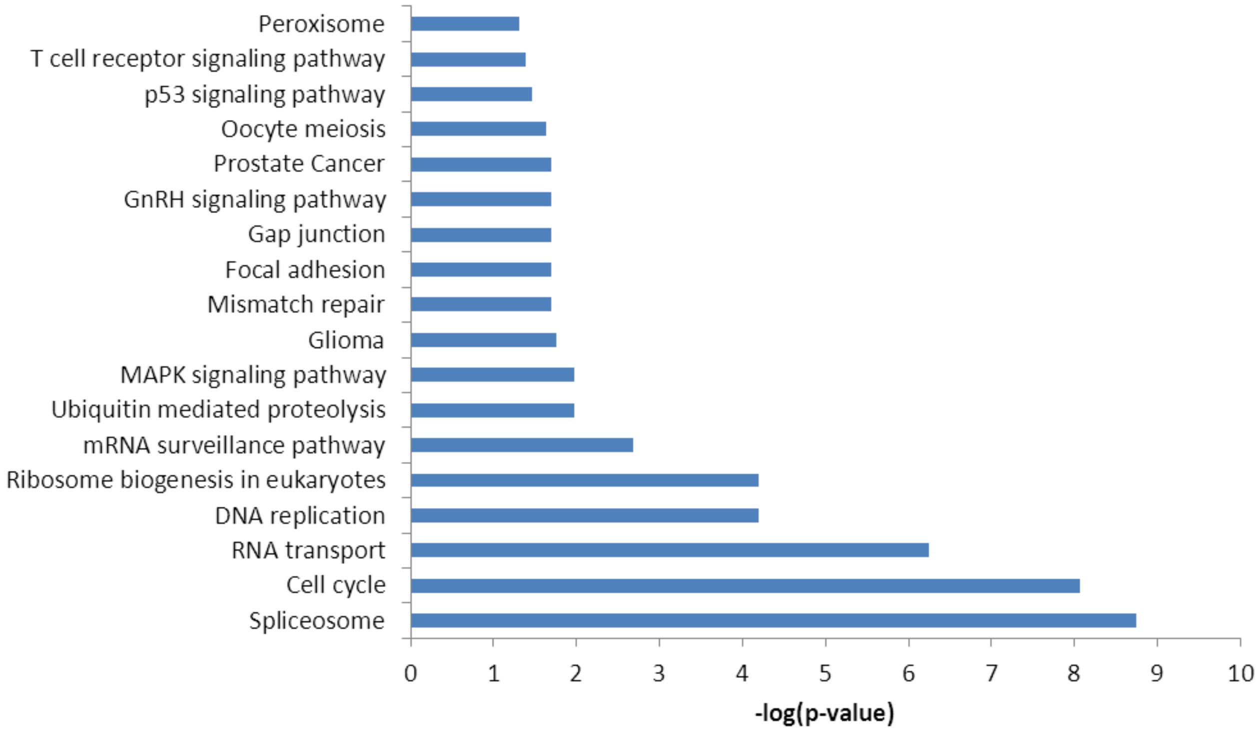


Figure S4b. KEGG Pathways -Aggressive Group.

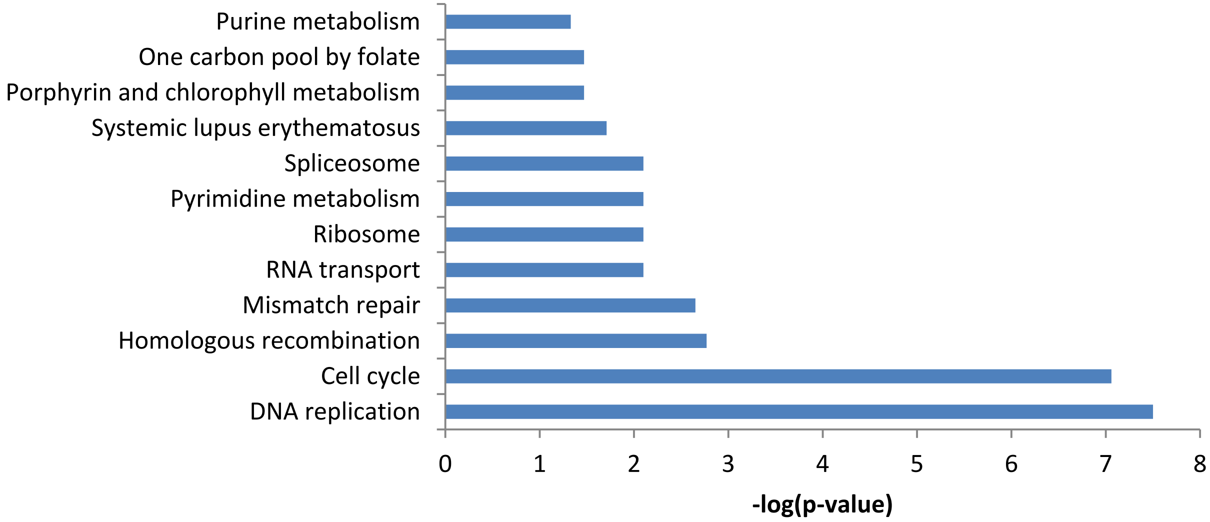


Figure S5. Heat map of the supervised clustering of the 19 PV patients using the 30 genes identified by top scoring pairs analysis. For the heat map, red indicates decreased gene expression and green increased gene expression. Each column represents one patient and each row a single gene.

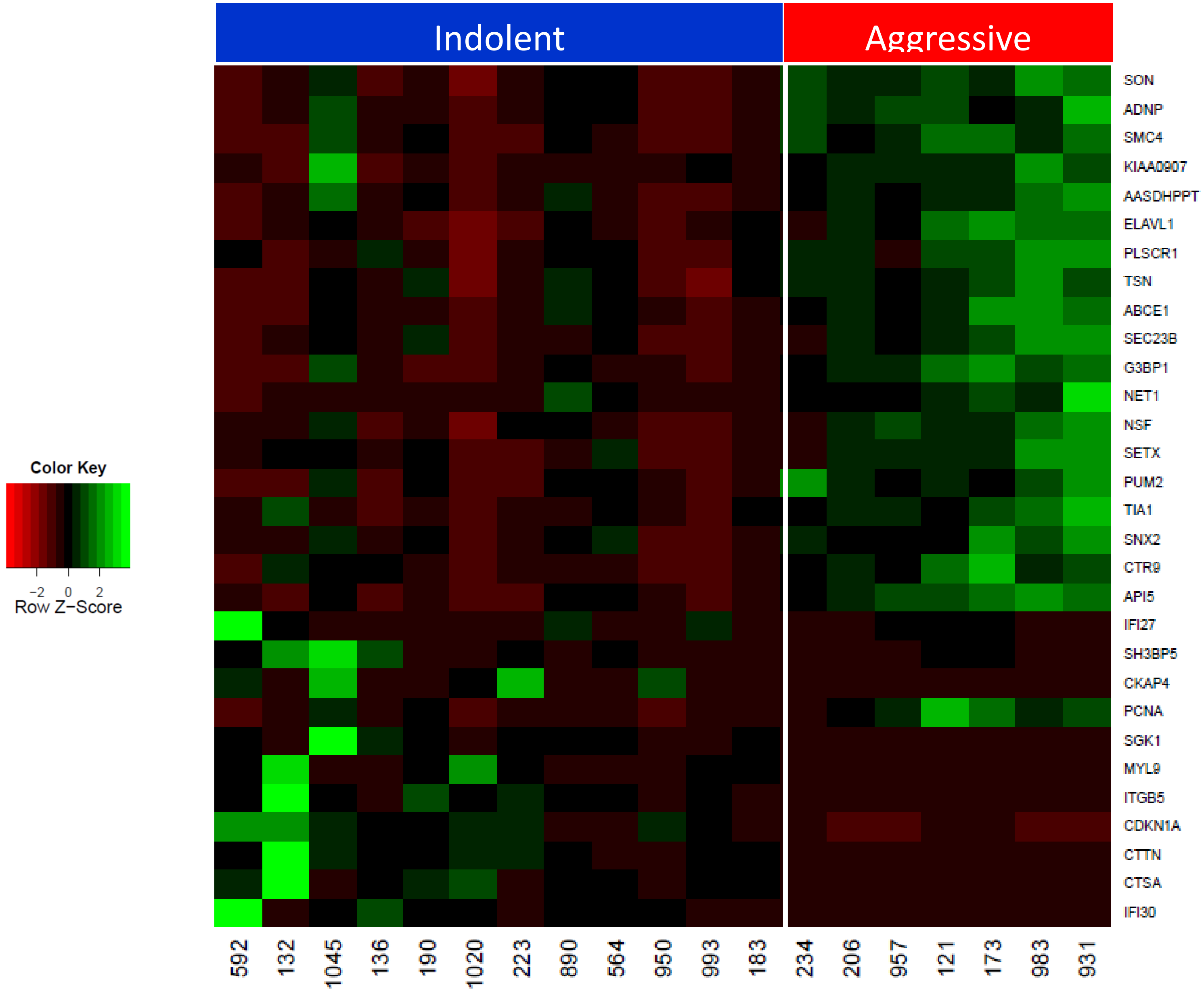


Figure S6. Algorithm for clinical stratification of PV patients by the ten gene assay.

Ten Gene Assay Panel

Measure the transcript levels for the following 10 genes:

PCNA, IFI30, TSN, CTSA, SMC4, CTTN, CDKN1A, SON, TIA1, MYL9

Make the following gene transcript level comparisons:

PCNA > IFI30

TSN > CTSA

SMC4 > CDKN1A

PCNA > CTTN

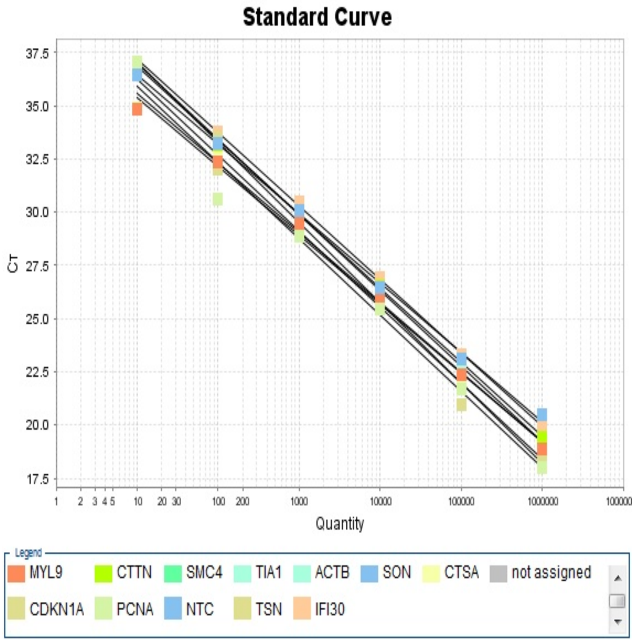
SON > CTTN

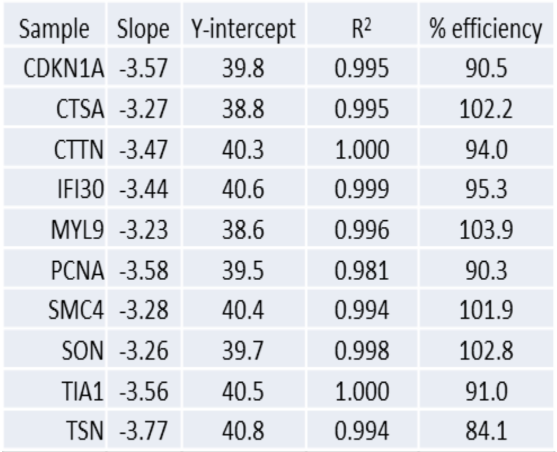
TIA1 > MYL9

- If **TRUE score 1**
- If **FALSE score 0**

Probability for Aggressive Disease = Score of 5-6/6

Figure S7**.** Standard curves for quantitation of transcript copy numbers for each of the genes used in the ten gene assay.





Sample	Slope	Y-intercept	R^2	% efficiency
CDKN1A	-3.57	39.8	0.995	90.5
CTSA	-3.27	38.8	0.995	102.2
CTTN	-3.47	40.3	1.000	94.0
IFI30	-3.44	40.6	0.999	95.3
MYL9	-3.23	38.6	0.996	103.9
PCNA	-3.58	39.5	0.981	90.3
SMC4	-3.28	40.4	0.994	101.9
SON	-3.26	39.7	0.998	102.8
TIA1	-3.56	40.5	1.000	91.0
TSN	-3.77	40.8	0.994	84.1

Figure S8. Receiver Operating Characteristic (ROC) Curve for the ten gene assay using the 30 PV patient test group.

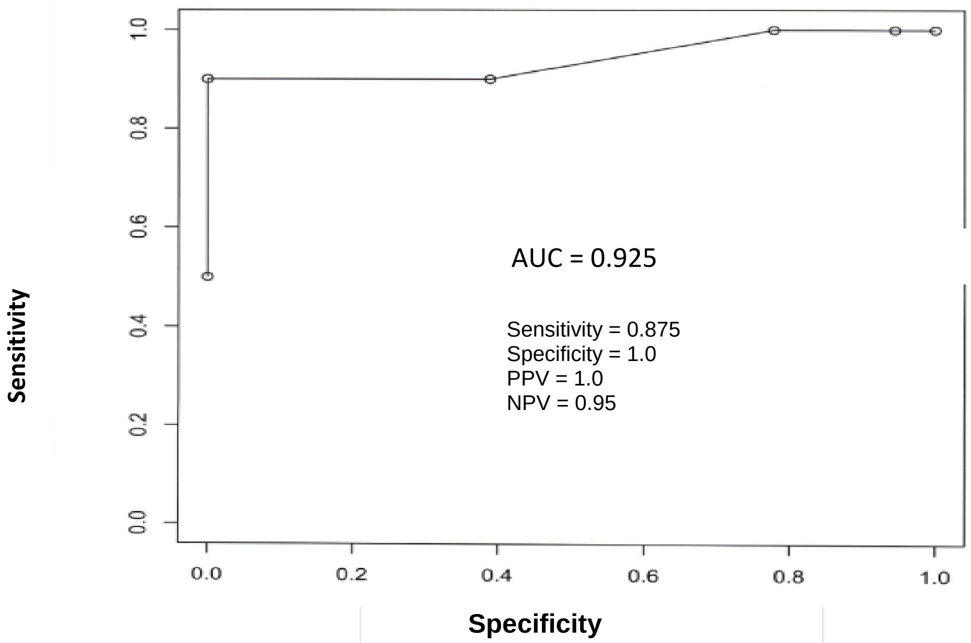


Table S1. Clinical Features of the 19 Polycythemia Vera Patients at Study Entry.

Gender	**Age (years)**	**Disease Duration (years)**	**Hemoglobin (g/dL) (g/L)**	**Leukocyte count $(10^3/\mu L)$ $(10^9/L)$**	**Platelet count $(10^3/\mu L)$ $(10^9/L)$**	**Spleen size (cm below the left costal margin)**	**Splenectomy**	***JAK2* V617F neutro-phil allele burden (%)**	**Thrombosis**	**Therapy**
Male	74	7	12.9 (129)	17.620	388.000	32	No	100	No	Phlebotomy, Anagrelide, Hydroxyurea, Busulfan
Male	66	20	8.3 (83)	177.190	454.000	25	Yes	100	Arterial	Phlebotomy, Thalidomide, Cytoxan
Female	55	13	11.1 (111)	33.110	802.000	20	Yes	100	Portal and hepatic veins	Phlebotomy, Hydroxyurea, Cytoxan, Anagrelide
Female	74	8	11.7 (117)	10.720	366.000	8	No	68	Hepatic vein	Anagrelide, Hydroxyurea
Male	63	16	9.3 (93)	10.020	171.000	8	Yes	86	No	Phlebotomy, Hydroxyurea
Female*	48	18	10.4 (104)	50.070	1,017.000	5	Yes	100	Arterial and venous	Phlebotomy, Hydroxyurea, Busulfan, Imatinib
Male*	72	25	12.5 (125)	16.770	491.000	20	Yes	100	No	Phlebotomy, Hydroxyurea, Cytoxan
Male*	72	1	13.7 (137)	16.490	712.000	0	No	68	No	Phlebotomy
Female	68	11	13.0 (130)	11.980	865.000	5	No	67	No	Phlebotomy
Male	73	4	14.3 (143)	16.610	151.000	12.5	No	95	No	Phlebotomy
Male	82	25	15.9 (159)	4.430	197.000	0	No	50	Arterial	Phlebotomy, Hydroxyurea
Female**	76	10	11.5 (115)	5.080	948.000	0	No	52	No	Phlebotomy, Hydroxyurea
Male	57	4	13.6	19.970	810.000	0	No	88	No	Phlebotomy

			(136)							
Female	57	12	13.0 (130)	19.530	1,119.000	8	No	60	No	Phlebotomy, Hydroxyurea
Female	51	5	10.7 (107)	19.130	1,052.000	5	No	100	No	Phlebotomy
Female*	46	4	11.1 (111)	20.520	1,480.000	0	No	82	No	Phlebotomy
Female	67	7	14.5 (145)	27.270	191.000	14	No	100	No	Phlebotomy
Female*	60	9	12.5 (125)	13.870	1,176.000	4	No	60	No	Phlebotomy
Female*	71	1	14.7 (147)	22.790	332.000	0	No	100	No	Phlebotomy,

*****Denotes patients subsequently used as the training set for the 10 gene assay (see the Supplementary Appendix). ******Denotes a training set patient evaluated with the 10 gene assay both before and after transformation to aggressive phase disease (see the Supplementary Appendix).

Table S2a. Genes differentially regulated by female PV patients compared to normal female controls.

ProbesetID	***Symbol (Na32 consesus Mar13)***	***Gene Title (Na32 consensus Mar13)***	***Entrez GeneID (concensus Mar-13)***	***Log2(FC)***	***P-Value***	***Adjusted P-Value***
204805_s_at	H1FX	H1 histone family, member X	8971	1.91935	0.00114	0.1019
202888_s_at	ANPEP	alanyl (membrane) aminopeptidase	290	1.43197	0.001209	0.1019
213326_at	VAMP1	vesicle-associated membrane protein 1 (synaptobrevin 1)	6843	1.380311	0.001564	0.1019
212543_at	AIM1	absent in melanoma 1	202	1.689059	0.002053	0.1019
201427_s_at	SEPP1	selenoprotein P, plasma, 1	6414	1.427475	0.003366	0.125981
206674_at	FLT3	fms-related tyrosine kinase 3	2322	1.701119	0.003846	0.125981
206385_s_at	ANK3	ankyrin 3, node of Ranvier (ankyrin G)	288	1.257882	0.004488	0.125981
209487_at	RBPMS	RNA binding protein with multiple splicing	11030	1.23478	0.00567	0.125981
219871_at	FLJ13197	uncharacterized FLJ13197	79667	1.301817	0.005704	0.125981
209488_s_at	RBPMS	RNA binding protein with multiple splicing	11030	1.275396	0.006845	0.125981
221645_s_at	ZNF83	zinc finger protein 83	55769	1.200283	0.007674	0.125981
213005_s_at	KANK1	KN motif and ankyrin repeat domains 1	23189	1.707475	0.008166	0.125981
213817_at	IRAK3	interleukin-1 receptor-associated kinase 3	11213	1.218239	0.010346	0.125981
202039_at	MYO18A	myosin XVIIIA	399687	1.175294	0.011058	0.125981
210644_s_at	LAIR1	leukocyte-associated immunoglobulin-like receptor 1	3903	1.348313	0.011154	0.125981
204352_at	TRAF5	TNF receptor-associated factor 5	7188	1.125428	0.012268	0.125981
214290_s_at	HIST2H2AA4	histone cluster 2, H2aa4	723790	1.879605	0.013116	0.125981
222146_s_at	TCF4	transcription factor 4	6925	1.385756	0.013155	0.125981
59375_at	MYO15B	myosin XVB pseudogene	80022	1.108123	0.013372	0.125981
206486_at	LAG3	lymphocyte-activation gene 3	3902	0.994363	0.014533	0.125981
212794_s_at	KIAA1033	KIAA1033	23325	1.287389	0.014972	0.125981
218086_at	NPDC1	neural proliferation, differentiation and control, 1	56654	1.013593	0.015204	0.125981
218280_x_at	HIST2H2AA4	histone cluster 2, H2aa4	723790	1.830191	0.01535	0.125981
213655_at	YWHAE	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	7531	-1.40323	0.015549	0.125981

219173_at	MYO15B	myosin XVB pseudogene	80022	1.147267	0.016111	0.127919
212587_s_at	PTPRC	protein tyrosine phosphatase, receptor type, C	5788	1.942028	0.016627	0.128539
218312_s_at	ZSCAN18	zinc finger and SCAN domain containing 18	65982	1.539329	0.017836	0.128539
207836_s_at	RBPMS	RNA binding protein with multiple splicing	11030	1.091491	0.018254	0.128539
207426_s_at	TNFSF4	tumor necrosis factor (ligand) superfamily, member 4	7292	1.381424	0.019204	0.129221
212762_s_at	TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)	6934	1.046634	0.019813	0.129892
209398_at	HIST1H1C	histone cluster 1, H1c	3006	1.60555	0.020228	0.129892
211675_s_at	MDFIC	MyoD family inhibitor domain containing	29969	1.155886	0.020685	0.129892
206133_at	XAF1	XIAP associated factor 1	54739	1.158372	0.020857	0.129892
218966_at	MYO5C	myosin VC	55930	1.536923	0.02094	0.129892
214455_at	HIST1H2BC	histone cluster 1, H2bc	8347	1.482403	0.023205	0.131273
205471_s_at	DACH1	dachshund homolog 1 (Drosophila)	1602	0.95962	0.023854	0.131273
218346_s_at	SESN1	sestrin 1	27244	1.057229	0.024057	0.131273
209993_at	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP), member 1	5243	1.012543	0.024783	0.131273
206710_s_at	EPB41L3	erythrocyte membrane protein band 4.1-like 3	23136	0.977202	0.024885	0.131273
202708_s_at	HIST2H2BE	histone cluster 2, H2be	8349	1.769114	0.02667	0.131273
200986_at	SERPING1	serpin peptidase inhibitor, clade G (C1 inhibitor), member 1	710	1.048714	0.026758	0.131273
207111_at	EMR1	egf-like module containing, mucin-like, hormone receptor-like 1	2015	1.04867	0.026977	0.131273
219355_at	CXorf57	chromosome X open reading frame 57	55086	0.956366	0.027482	0.131273
201196_s_at	AMD1	adenosylmethionine decarboxylase 1	262	1.127364	0.02763	0.131273
207564_x_at	OGT	O-linked N-acetylglucosamine (GlcNAc) transferase	8473	1.180955	0.027642	0.131273
202686_s_at	AXL	AXL receptor tyrosine kinase	558	-1.17476	0.027808	0.131273
208268_at	ADAM28	ADAM metallopeptidase domain 28	10863	1.222576	0.028106	0.131273
215307_at	ZNF529	zinc finger protein 529	57711	1.029099	0.028782	0.132865
219571_s_at	ZNF12	zinc finger protein 12	7559	1.033403	0.030225	0.136525
209994_s_at	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP), member 1	5243	0.988532	0.030956	0.136933
212560_at	SORL1	sortilin-related receptor, L(DLR class) A repeats containing	6653	1.232375	0.031193	0.136933
205767_at	EREG	epiregulin	2069	1.576209	0.032309	0.137923
221718_s_at	AKAP13	A kinase (PRKA) anchor protein 13	11214	0.990575	0.033371	0.139481
214472_at	HIST1H2AD	histone cluster 1, H2ad	3013	1.221696	0.034306	0.139481
209447_at	SYNE1	spectrin repeat containing, nuclear envelope 1	23345	1.026492	0.034672	0.139481
207571_x_at	THEMIS2	thymocyte selection associated family member 2	9473	1.23688	0.035236	0.139481

210785_s_at	THEMIS2	thymocyte selection associated family member 2	9473	1.258674	0.035631	0.139481
209543_s_at	CD34	CD34 molecule	947	1.31764	0.037479	0.144458
220952_s_at	PLEKHA5	pleckstrin homology domain containing, family A member 5	54477	1.059186	0.039091	0.147854
201448_at	TIA1	TIA1 cytotoxic granule-associated RNA binding protein	7072	1.289342	0.039105	0.147854
221543_s_at	ERLIN2	ER lipid raft associated 2	11160	1.019463	0.040859	0.150196
206715_at	TFEC	transcription factor EC	22797	1.291151	0.042627	0.153844
220122_at	MCTP1	multiple C2 domains, transmembrane 1	79772	1.025269	0.043486	0.155532
209318_x_at	PLAGL1	pleiomorphic adenoma gene-like 1	5325	1.315505	0.046285	0.160061
208056_s_at	CBFA2T3	core-binding factor, runt domain, alpha subunit 2; translocated to, 3	863	1.116738	0.04637	0.160061
204972_at	OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa	4939	1.090829	0.046707	0.160061
201236_s_at	BTG2	BTG family, member 2	7832	1.091134	0.046768	0.160061
214218_s_at	XIST	X inactive specific transcript (non-protein coding)	7503	1.3244	0.04853	0.163276
220940_at	ANKRD36B	ankyrin repeat domain 36B	57730	1.168735	0.049352	0.163699
209930_s_at	NFE2	nuclear factor (erythroid-derived 2), 45kDa	4778	1.331755	0.050315	0.163699
205239_at	AREG	amphiregulin	374	1.205571	0.051692	0.163838
217593_at	ZSCAN18	zinc finger and SCAN domain containing 18	65982	0.840704	0.054078	0.167551
222067_x_at	HIST1H2BD	histone cluster 1, H2bd	3017	1.198697	0.063984	0.189566
213094_at	GPR126	G protein-coupled receptor 126	57211	1.17747	0.06522	0.191029
212775_at	OBSL1	obscurin-like 1	23363	1.331391	0.065586	0.191029
221249_s_at	FAM117A	family with sequence similarity 117, member A	81558	1.637593	0.066403	0.191029
210172_at	SF1	splicing factor 1	7536	0.997588	0.067011	0.191391
207496_at	MS4A2	membrane-spanning 4-domains, subfamily A, member 2	2206	0.772601	0.069284	0.193702
218589_at	LPAR6	lysophosphatidic acid receptor 6	10161	1.080018	0.071983	0.199841
204749_at	NAP1L3	nucleosome assembly protein 1-like 3	4675	1.296406	0.073554	0.202786
211302_s_at	PDE4B	phosphodiesterase 4B, cAMP-specific	5142	0.858839	0.076239	0.207306
215779_s_at	HIST1H2BG	histone cluster 1, H2bg	8339	0.902184	0.076987	0.207917
213293_s_at	TRIM22	tripartite motif containing 22	10346	1.468514	0.077535	0.207984
218352_at	RCBTB1	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 1	55213	1.08448	0.082823	0.214891
220918_at	RUNX1-IT1	RUNX1 intronic transcript 1 (non-protein coding)	80215	1.110688	0.083008	0.214891
204116_at	IL2RG	interleukin 2 receptor, gamma	3561	0.892953	0.085322	0.217134
210254_at	MS4A3	membrane-spanning 4-domains, subfamily A, member 3 (hematopoietic cell-specific)	932	1.032003	0.088393	0.223517

213998_s_at	DDX17	DEAD (Asp-Glu-Ala-Asp) box helicase 17	10521	1.29709	0.090384	0.225675
206631_at	PTGER2	prostaglandin E receptor 2 (subtype EP2), 53kDa	5732	0.863461	0.094568	0.233189
219737_s_at	PCDH9	protocadherin 9	5101	1.423384	0.095952	0.235143
206067_s_at	WT1	Wilms tumor 1	7490	-0.97509	0.097098	0.235189
212813_at	JAM3	junctional adhesion molecule 3	83700	0.851683	0.097156	0.235189
203708_at	PDE4B	phosphodiesterase 4B, cAMP-specific	5142	1.258787	0.098941	0.236778
213734_at	WSB2	WD repeat and SOCS box containing 2	55884	-1.03595	0.103178	0.243147
212382_at	TCF4	transcription factor 4	6925	1.222721	0.103506	0.243147
212044_s_at	RPL27A	ribosomal protein L27a	6157	-1.30359	0.11014	0.255203
209774_x_at	CXCL2	chemokine (C-X-C motif) ligand 2	2920	-1.35733	0.111447	0.255748
204420_at	FOSL1	FOS-like antigen 1	8061	0.777712	0.125065	0.28372
219352_at	HERC6	HECT and RLD domain containing E3 ubiquitin protein ligase family member 6	55008	0.731325	0.126978	0.286421
219371_s_at	KLF2	Kruppel-like factor 2 (lung)	10365	0.952494	0.133808	0.29512
208436_s_at	IRF7	interferon regulatory factor 7	3665	0.817301	0.142117	0.308309
208490_x_at	HIST1H2BF	histone cluster 1, H2bf	8343	0.823714	0.153384	0.325493
217168_s_at	HERPUD1	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	9709	-1.02032	0.153554	0.325493
218723_s_at	RGCC	regulator of cell cycle	28984	1.178353	0.16831	0.347202
221943_x_at	RPL38	ribosomal protein L38	6169	-0.87537	0.169666	0.347202
202912_at	ADM	adrenomedullin	133	-0.90139	0.175228	0.356746
202086_at	MX1	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	4599	1.082812	0.179388	0.362009
204794_at	DUSP2	dual specificity phosphatase 2	1844	-1.05607	0.185851	0.370769
200878_at	EPAS1	endothelial PAS domain protein 1	2034	-0.94127	0.187138	0.371469
214395_x_at	EEF1D	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	1936	-0.75421	0.221404	0.418581
39248_at	AQP3	aquaporin 3 (Gill blood group)	360	-1.0387	0.221416	0.418581
201590_x_at	ANXA2	annexin A2	302	-0.83364	0.224539	0.422475
202087_s_at	CTSL1	cathepsin L1	1514	-0.72277	0.227535	0.426091
201897_s_at	CKS1B	CDC28 protein kinase regulatory subunit 1B	1163	-0.75777	0.23559	0.436077
202869_at	OAS1	2'-5'-oligoadenylate synthetase 1, 40/46kDa	4938	0.645604	0.239395	0.44
204351_at	S100P	S100 calcium binding protein P	6286	-1.19041	0.248298	0.447645
205220_at	HCAR3	hydroxycarboxylic acid receptor 3	8843	-0.75269	0.248929	0.447645
201289_at	CYR61	cysteine-rich, angiogenic inducer, 61	3491	-0.94996	0.249241	0.447645

213943_at	TWIST1	twist basic helix-loop-helix transcription factor 1	7291	-0.76051	0.251394	0.447645
201566_x_at	ID2	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	3398	0.738645	0.252916	0.448249
204286_s_at	PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	5366	0.658217	0.254968	0.449876
203038_at	PTPRK	protein tyrosine phosphatase, receptor type, K	5796	-0.89732	0.259282	0.450102
212097_at	CAV1	caveolin 1, caveolae protein, 22kDa	857	-0.8953	0.259704	0.450102
202733_at	P4HA2	prolyl 4-hydroxylase, alpha polypeptide II	8974	-0.88547	0.260765	0.450102
203917_at	CXADR	coxsackie virus and adenovirus receptor	1525	-0.70323	0.261975	0.450233
204103_at	CCL4	chemokine (C-C motif) ligand 4	6351	-0.93799	0.264919	0.453331
202458_at	PRSS23	protease, serine, 23	11098	-0.75062	0.266945	0.454838
213539_at	CD3D	CD3d molecule, delta (CD3-TCR complex)	915	-0.74368	0.268679	0.455836
210321_at	GZMH	granzyme H (cathepsin G-like 2, protein h-CCPX)	2999	-0.6763	0.279967	0.472525
214453_s_at	IFI44	interferon-induced protein 44	10561	0.80743	0.280897	0.472525
211560_s_at	ALAS2	aminolevulinate, delta-, synthase 2	212	-0.96058	0.293731	0.486931
201744_s_at	LUM	lumican	4060	-0.72481	0.298238	0.491288
211340_s_at	MCAM	melanoma cell adhesion molecule	4162	-0.77567	0.306814	0.499201
204959_at	MNDA	myeloid cell nuclear differentiation antigen	4332	-0.90022	0.316701	0.504456
202587_s_at	AK1	adenylate kinase 1	203	-0.63641	0.317949	0.504456
218959_at	HOXC10	homeobox C10	3226	-0.61573	0.319085	0.504456
205495_s_at	GNLY	granulysin	10578	-0.68517	0.320209	0.504456
221958_s_at	WLS	wntless homolog (Drosophila)	79971	-0.70884	0.324929	0.50696
202688_at	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10	8743	0.618043	0.325629	0.50696
209087_x_at	MCAM	melanoma cell adhesion molecule	4162	-0.81432	0.326954	0.507034
209210_s_at	FERMT2	fermitin family member 2	10979	-1.11824	0.329723	0.50854
205488_at	GZMA	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)	3001	-0.59006	0.330487	0.50854
201739_at	SGK1	serum/glucocorticoid regulated kinase 1	6446	-1.0293	0.335357	0.508988
211506_s_at	IL8	interleukin 8	3576	-0.69682	0.336251	0.508988
204962_s_at	CENPA	centromere protein A	1058	-0.67424	0.336317	0.508988
212698_s_at	10-Sep	septin 10	151011	-0.74724	0.337188	0.508988
33322_i_at	SFN	stratifin	2810	-0.75401	0.341463	0.509458
218705_s_at	SNX24	sorting nexin 24	28966	-0.57987	0.342374	0.509458
205552_s_at	OAS1	2'-5'-oligoadenylate synthetase 1, 40/46kDa	4938	0.50836	0.344124	0.509458
201506_at	TGFBI	transforming growth factor, beta-induced, 68kDa	7045	-0.66233	0.345804	0.509458

202011_at	TJP1	tight junction protein 1	7082	-0.64431	0.347774	0.509458
204517_at	PPIC	peptidylprolyl isomerase C (cyclophilin C)	5480	-0.59936	0.349374	0.509458
209230_s_at	NUPR1	nuclear protein, transcriptional regulator, 1	26471	-0.65323	0.350449	0.509458
219073_s_at	OSBPL10	oxysterol binding protein-like 10	114884	-0.59261	0.351262	0.509458
205476_at	CCL20	chemokine (C-C motif) ligand 20	6364	-0.6399	0.357651	0.512993
221577_x_at	GDF15	growth differentiation factor 15	9518	-0.65491	0.364519	0.516042
202718_at	IGFBP2	insulin-like growth factor binding protein 2, 36kDa	3485	-0.57195	0.365259	0.516042
207039_at	CDKN2A	cyclin-dependent kinase inhibitor 2A	1029	-0.71306	0.36807	0.517873
204920_at	CPS1	carbamoyl-phosphate synthase 1, mitochondrial	1373	-0.81774	0.369164	0.517873
200771_at	LAMC1	laminin, gamma 1 (formerly LAMB2)	3915	-0.65676	0.37062	0.518085
219454_at	EGFL6	EGF-like-domain, multiple 6	25975	-0.56974	0.374512	0.518966
212328_at	LIMCH1	LIM and calponin homology domains 1	22998	-0.72538	0.37555	0.518966
207076_s_at	ASS1	argininosuccinate synthase 1	445	-0.96506	0.376479	0.518966
201983_s_at	EGFR	epidermal growth factor receptor	1956	-0.56631	0.379717	0.519326
203438_at	STC2	stanniocalcin 2	8614	-0.54868	0.385726	0.520981
212012_at	PXDN	peroxidasin homolog (Drosophila)	7837	-0.69905	0.3859	0.520981
203153_at	IFIT1	interferon-induced protein with tetratricopeptide repeats 1	3434	0.55537	0.389138	0.520981
206785_s_at	KLRC1	killer cell lectin-like receptor subfamily C, member 1	3821	-0.5784	0.393476	0.520981
217564_s_at	CPS1	carbamoyl-phosphate synthase 1, mitochondrial	1373	-0.79731	0.394672	0.520981
202052_s_at	RAI14	retinoic acid induced 14	26064	-0.5724	0.3967	0.520981
204992_s_at	PFN2	profilin 2	5217	-0.772	0.396957	0.520981
204007_at	FCGR3B	Fc fragment of IgG, low affinity IIIb, receptor (CD16b)	2215	-0.64158	0.397187	0.520981
210095_s_at	IGFBP3	insulin-like growth factor binding protein 3	3486	-0.60033	0.397625	0.520981
200798_x_at	MCL1	myeloid cell leukemia sequence 1 (BCL2-related)	4170	0.540947	0.39956	0.521124
212364_at	MYO1B	myosin IB	4430	-0.55526	0.401476	0.521124
212765_at	CAMSAP2	calmodulin regulated spectrin-associated protein family, member 2	23271	-0.56269	0.401672	0.521124
204284_at	PPP1R3C	protein phosphatase 1, regulatory subunit 3C	5507	-0.54464	0.406184	0.523753
201976_s_at	MYO10	myosin X	4651	-0.55951	0.406337	0.523753
208079_s_at	AURKA	aurora kinase A	6790	-0.65513	0.408025	0.524226
219959_at	MOCOS	molybdenum cofactor sulfurase	55034	-0.85667	0.410521	0.525731
213139_at	SNAI2	snail homolog 2 (Drosophila)	6591	-0.55315	0.414603	0.526676
201292_at	TOP2A	topoisomerase (DNA) II alpha 170kDa	7153	-0.61773	0.41473	0.526676
209101_at	CTGF	connective tissue growth factor	1490	-0.63969	0.416358	0.526676

210587_at	INHBE	inhibin, beta E	83729	-0.61908	0.419791	0.526676
202768_at	FOSB	FBJ murine osteosarcoma viral oncogene homolog B	2354	0.785327	0.421407	0.526676
219148_at	PBK	PDZ binding kinase	55872	-0.62389	0.422616	0.526676
201505_at	LAMB1	laminin, beta 1	3912	-0.59203	0.422812	0.526676
204439_at	IFI44L	interferon-induced protein 44-like	10964	0.779572	0.423198	0.526676
204688_at	SGCE	sarcoglycan, epsilon	8910	-0.53807	0.427632	0.530004
210274_at	MAGEA8	melanoma antigen family A, 8	4107	-0.55437	0.440077	0.53411
218400_at	OAS3	2'-5'-oligoadenylate synthetase 3, 100kDa	4940	0.401878	0.441825	0.53411
204033_at	TRIP13	thyroid hormone receptor interactor 13	9319	-0.53242	0.443536	0.53411
205033_s_at	DEFA1	defensin, alpha 1	1667	-0.68446	0.443688	0.53411
209921_at	SLC7A11	solute carrier family 7 (anionic amino acid transporter light chain, xc- system), member 11	23657	-0.67363	0.443971	0.53411
204415_at	IFI6	interferon, alpha-inducible protein 6	2537	0.448113	0.446822	0.53412
203510_at	MET	met proto-oncogene (hepatocyte growth factor receptor)	4233	-0.59266	0.449267	0.53412
33323_r_at	SFN	stratifin	2810	-0.63466	0.450623	0.53412
212671_s_at	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1	3117	-0.73617	0.45086	0.53412
205047_s_at	ASNS	asparagine synthetase (glutamine-hydrolyzing)	440	-0.62208	0.454871	0.534967
200606_at	DSP	desmoplakin	1832	-0.6615	0.455463	0.534967
205573_s_at	SNX7	sorting nexin 7	51375	-0.50744	0.460196	0.538931
204684_at	NPTX1	neuronal pentraxin I	4884	-0.48978	0.463571	0.540181
204483_at	ENO3	enolase 3 (beta, muscle)	2027	-0.57582	0.463984	0.540181
221008_s_at	AGXT2L1	alanine-glyoxylate aminotransferase 2-like 1	64850	-0.59789	0.471814	0.545637
200795_at	SPARCL1	SPARC-like 1 (hevin)	8404	-0.50481	0.475562	0.546517
211618_s_at	ALPI	alkaline phosphatase, intestinal	248	-0.48827	0.477352	0.546517
207140_at	ALPI	alkaline phosphatase, intestinal	248	-0.90959	0.477868	0.546517
204288_s_at	SORBS2	sorbin and SH3 domain containing 2	8470	-0.52462	0.481567	0.546517
201681_s_at	DLG5	discs, large homolog 5 (Drosophila)	9231	-0.47202	0.48294	0.546517
203881_s_at	DMD	dystrophin	1756	-0.49504	0.483193	0.546517
219599_at	EIF4B	eukaryotic translation initiation factor 4B	1975	-0.53684	0.487369	0.548489
203636_at	MID1	midline 1 (Opitz/BBB syndrome)	4281	-0.45754	0.488315	0.548489
214240_at	GAL	galanin/GMAP prepropeptide	51083	-0.50116	0.489081	0.548489
209094_at	DDAH1	dimethylarginine dimethylaminohydrolase 1	23576	-0.51772	0.495452	0.554068
218631_at	AVPI1	arginine vasopressin-induced 1	60370	-0.49809	0.500208	0.556142
204540_at	EEF1A2	eukaryotic translation elongation factor 1 alpha 2	1917	-0.42637	0.500471	0.556142

210016_at	MYT1L	myelin transcription factor 1-like	23040	-0.55739	0.502376	0.556142
205289_at	BMP2	bone morphogenetic protein 2	650	-0.51385	0.50342	0.556142
205751_at	SH3GL2	SH3-domain GRB2-like 2	6456	-0.43617	0.50431	0.556142
218541_s_at	C8orf4	chromosome 8 open reading frame 4	56892	-0.52893	0.509174	0.559951
214247_s_at	DKK3	dickkopf 3 homolog (Xenopus laevis)	27122	-0.51465	0.511216	0.560643
214212_x_at	FERMT2	fermitin family member 2	10979	-0.44903	0.514141	0.562297
208209_s_at	C4BPB	complement component 4 binding protein, beta	725	-0.49739	0.518251	0.565235
208396_s_at	PDE1A	phosphodiesterase 1A, calmodulin-dependent	5136	-0.46854	0.526142	0.571827
209942_x_at	MAGEA3	melanoma antigen family A, 3	4102	-0.58148	0.5289	0.572135
214612_x_at	MAGEA6	melanoma antigen family A, 6	4105	-0.60458	0.532798	0.57304
201660_at	ACSL3	acyl-CoA synthetase long-chain family member 3	2181	-0.42544	0.533497	0.57304
204975_at	EMP2	epithelial membrane protein 2	2013	-0.47324	0.536232	0.57304
201667_at	GJA1	gap junction protein, alpha 1, 43kDa	2697	-0.55978	0.536604	0.57304
201291_s_at	TOP2A	topoisomerase (DNA) II alpha 170kDa	7153	-0.51625	0.536954	0.57304
204653_at	TFAP2A	transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)	7020	-0.43406	0.544838	0.579895
205132_at	ACTC1	actin, alpha, cardiac muscle 1	70	-0.38632	0.55232	0.584901
217127_at	CTH	cystathionase (cystathionine gamma-lyase)	1491	-0.44229	0.552489	0.584901
205381_at	LRRC17	leucine rich repeat containing 17	10234	-0.39955	0.554073	0.585019
209967_s_at	CREM	cAMP responsive element modulator	1390	-0.45103	0.557616	0.587198
202672_s_at	ATF3	activating transcription factor 3	467	0.490404	0.560082	0.587586
209631_s_at	GPR37	G protein-coupled receptor 37 (endothelin receptor type B-like)	2861	-0.44217	0.560945	0.587586
221730_at	COL5A2	collagen, type V, alpha 2	1290	-0.40443	0.562469	0.587632
210467_x_at	MAGEA12	melanoma antigen family A, 12	4111	-0.46503	0.566943	0.590752
203083_at	THBS2	thrombospondin 2	7058	-0.37936	0.569007	0.59135
215034_s_at	TM4SF1	transmembrane 4 L six family member 1	4071	-0.4484	0.571318	0.592202
206377_at	FOXF2	forkhead box F2	2295	-0.36443	0.585328	0.605143
213131_at	OLFM1	olfactomedin 1	10439	-0.35953	0.610643	0.629676
202976_s_at	RHOBTB3	Rho-related BTB domain containing 3	22836	-0.3467	0.614674	0.63219
202887_s_at	DDIT4	DNA-damage-inducible transcript 4	54541	-0.45548	0.618537	0.63452
203984_s_at	CASP9	caspase 9, apoptosis-related cysteine peptidase	842	-0.35376	0.632586	0.647259
205290_s_at	BMP2	bone morphogenetic protein 2	650	-0.47882	0.640799	0.653977
204337_at	RGS4	regulator of G-protein signaling 4	5999	-0.26477	0.708833	0.717874

217867_x_at	BACE2	beta-site APP-cleaving enzyme 2	25825	-0.2906	0.71423	0.721499
212327_at	LIMCH1	LIM and calponin homology domains 1	22998	-0.28139	0.723086	0.728591
202391_at	BASP1	brain abundant, membrane attached signal protein 1	10409	0.338672	0.73503	0.738752

Table S2b. Genes differentially regulated by male PV patients compared to normal male controls.

Probeset ID	*Symbol (Na32 consesus Mar13)*	*Gene Title (Na32 consensus Mar13)*	*Entrez GeneID (concensus Mar-13)*	*Log2(FC)*	*P-Value*	*Adjusted p-Value*
208730_x_at	RAB2A	RAB2A, member RAS oncogene family	5862	-2.23913	0.00173	0.22461
201242_s_at	ATP1B1	ATPase, Na+/K+ transporting, beta 1 polypeptide	481	-2.30995	0.001936	0.22461
206857_s_at	FKBP1B	FK506 binding protein 1B, 12.6 kDa	2281	-2.18904	0.003742	0.22461
208636_at	ACTN1	actinin, alpha 1	87	-1.91968	0.005679	0.22461
206493_at	ITGA2B	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41)	3674	-2.94275	0.006689	0.22461
211986_at	AHNAK	AHNAK nucleoprotein	79026	1.54422	0.00875	0.22461
203509_at	SORL1	sortilin-related receptor, L(DLR class) A repeats containing	6653	1.561462	0.009157	0.22461
206494_s_at	ITGA2B	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41)	3674	-3.20741	0.009481	0.22461
201846_s_at	RYBP	RING1 and YY1 binding protein	23429	-1.62523	0.009701	0.22461
213229_at	DICER1	dicer 1, ribonuclease type III	23405	-1.70923	0.010255	0.22461
202620_s_at	PLOD2	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2	5352	-1.86792	0.010535	0.22461
202760_s_at	AKAP2	A kinase (PRKA) anchor protein 2	11217	-1.66558	0.010984	0.22461
215813_s_at	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	5742	-2.12304	0.011371	0.22461
219054_at	NPR3	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)	4883	1.815762	0.012117	0.22461
37462_i_at	SF3A2	splicing factor 3a, subunit 2, 66kDa	8175	-1.73475	0.01271	0.22461
212266_s_at	SRSF5	serine/arginine-rich splicing factor 5	6430	1.814328	0.012914	0.22461
201489_at	PPIF	peptidylprolyl isomerase F	10105	-1.57807	0.013197	0.22461
203096_s_at	RAPGEF2	Rap guanine nucleotide exchange factor (GEF) 2	9693	-1.90184	0.013308	0.22461
205128_x_at	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	5742	-1.98263	0.013941	0.22461
221059_s_at	COTL1	coactosin-like 1 (Dictyostelium)	23406	-2.38475	0.014419	0.22461
212268_at	SERPINB1	serpin peptidase inhibitor, clade B (ovalbumin), member 1	1992	1.576065	0.015209	0.22461
201012_at	ANXA1	annexin A1	301	1.431866	0.015821	0.22461

207808_s_at	PROS1	protein S (alpha)	5627	-2.54684	0.01834	0.22461
206302_s_at	NUDT4	nudix (nucleoside diphosphate linked moiety X)-type motif 4	11163	-1.35819	0.01853	0.22461
203320_at	SH2B3	SH2B adaptor protein 3	10019	-1.48125	0.019452	0.22461
205647_at	RAD52	RAD52 homolog (S. cerevisiae)	5893	1.244884	0.019524	0.22461
210105_s_at	FYN	FYN oncogene related to SRC, FGR, YES	2534	-1.57809	0.020057	0.22461
200598_s_at	HSP90B1	heat shock protein 90kDa beta (Grp94), member 1	7184	-1.77815	0.020317	0.22461
200964_at	UBA1	ubiquitin-like modifier activating enzyme 1	7317	-1.39778	0.020397	0.22461
221493_at	TSPYL1	TSPY-like 1	7259	1.744517	0.021178	0.22461
206174_s_at	PPP6C	protein phosphatase 6, catalytic subunit	5537	-1.35248	0.021364	0.22461
202284_s_at	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	1026	-2.00033	0.023319	0.22461
206207_at	CLC	Charcot-Leyden crystal protein	1178	-1.88811	0.023511	0.22461
206655_s_at	GP1BB	glycoprotein Ib (platelet), beta polypeptide	2812	-2.92989	0.023514	0.22461
206571_s_at	MAP4K4	mitogen-activated protein kinase kinase kinase kinase 4	9448	-1.25865	0.02388	0.22461
209651_at	TGFB1I1	transforming growth factor beta 1 induced transcript 1	7041	-2.18243	0.024567	0.22461
204689_at	HHEX	hematopoietically expressed homeobox	3087	1.462027	0.024863	0.22461
205067_at	IL1B	interleukin 1, beta	3553	1.255404	0.025653	0.22461
203380_x_at	SRSF5	serine/arginine-rich splicing factor 5	6430	1.503237	0.025756	0.22461
200923_at	LGALS3BP	lectin, galactoside-binding, soluble, 3 binding protein	3959	-1.56076	0.025836	0.22461
202949_s_at	FHL2	four and a half LIM domains 2	2274	-1.37209	0.026399	0.22461
201695_s_at	PNP	purine nucleoside phosphorylase	4860	-1.41068	0.026458	0.22461
220748_s_at	ZNF580	zinc finger protein 580	51157	-1.34215	0.028123	0.22461
217901_at	DSG2	desmoglein 2	1829	1.320976	0.028803	0.22461
219798_s_at	MEPCE	methylphosphate capping enzyme	56257	-1.33001	0.029245	0.22461
209381_x_at	SF3A2	splicing factor 3a, subunit 2, 66kDa	8175	-1.41034	0.029259	0.22461
204222_s_at	GLIPR1	GLI pathogenesis-related 1	11010	1.439903	0.030437	0.22461
221004_s_at	ITM2C	integral membrane protein 2C	81618	1.219859	0.030753	0.22461
206049_at	SELP	selectin P (granule membrane protein 140kDa, antigen CD62)	6403	-2.17111	0.031111	0.22461
37966_at	PARVB	parvin, beta	29780	-2.06542	0.031383	0.22461
219681_s_at	RAB11FIP1	RAB11 family interacting protein 1 (class I)	80223	-1.35248	0.031529	0.22461
212242_at	TUBA4A	tubulin, alpha 4a	7277	-2.39641	0.03153	0.22461
218237_s_at	SLC38A1	solute carrier family 38, member 1	81539	1.547237	0.032294	0.22461
213726_x_at	TUBB4B	tubulin, beta 4B class IVb	10383	-1.30164	0.032486	0.22461
39402_at	IL1B	interleukin 1, beta	3553	1.235287	0.032639	0.22461
209820_s_at	TBL3	transducin (beta)-like 3	10607	-1.20712	0.032649	0.22461

212312_at	BCL2L1	BCL2-like 1	598	-1.39562	0.033632	0.22461
211600_at	PTPRO	protein tyrosine phosphatase, receptor type, O	5800	-1.45225	0.03416	0.22461
214783_s_at	ANXA11	annexin A11	311	-1.22688	0.034175	0.22461
200616_s_at	MLEC	malectin	9761	-1.20495	0.034386	0.22461
211926_s_at	MYH9	myosin, heavy chain 9, non-muscle	4627	-1.2641	0.034926	0.22461
202059_s_at	KPNA1	karyopherin alpha 1 (importin alpha 5)	3836	-1.12248	0.034962	0.22461
221899_at	N4BP2L2	NEDD4 binding protein 2-like 2	10443	1.316587	0.035008	0.22461
210347_s_at	BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	53335	1.273905	0.035019	0.22461
221748_s_at	TNS1	tensin 1	7145	-1.4894	0.035747	0.22461
203940_s_at	VASH1	vasohibin 1	22846	-1.35628	0.037032	0.22461
204610_s_at	CCDC85B	coiled-coil domain containing 85B	11007	-1.5951	0.037663	0.22461
222231_s_at	LRRC59	leucine rich repeat containing 59	55379	-1.11855	0.038092	0.22461
212177_at	PNISR	PNN-interacting serine/arginine-rich protein	25957	1.175547	0.038211	0.22461
201692_at	SIGMAR1	sigma non-opioid intracellular receptor 1	10280	-1.06876	0.038307	0.22461
202112_at	VWF	von Willebrand factor	7450	-1.36382	0.039327	0.22461
206310_at	SPINK2	serine peptidase inhibitor, Kazal type 2 (acrosin-trypsin inhibitor)	6691	1.568851	0.039466	0.22461
218899_s_at	BAALC	brain and acute leukemia, cytoplasmic	79870	1.51143	0.039771	0.22461
208308_s_at	GPI	glucose-6-phosphate isomerase	2821	-1.24247	0.040139	0.22461
221834_at	LONP2	lon peptidase 2, peroxisomal	83752	1.261036	0.040303	0.22461
210719_s_at	HMG20B	high mobility group 20B	10362	-1.39762	0.040525	0.22461
200808_s_at	ZYX	zyxin	7791	-1.54764	0.041293	0.22461
209945_s_at	GSK3B	glycogen synthase kinase 3 beta	2932	-1.28118	0.041713	0.22461
208637_x_at	ACTN1	actinin, alpha 1	87	-1.74284	0.041994	0.22461
209088_s_at	UBN1	ubinuclein 1	29855	-1.14187	0.042143	0.22461
211005_at	LAT	linker for activation of T cells	27040	-1.83145	0.042364	0.22461
218131_s_at	GATAD2A	GATA zinc finger domain containing 2A	54815	-1.22531	0.042653	0.22461
202729_s_at	LTBP1	latent transforming growth factor beta binding protein 1	4052	-1.87245	0.042694	0.22461
219357_at	GTPBP1	GTP binding protein 1	9567	-1.11964	0.042776	0.22461
201980_s_at	RSU1	Ras suppressor protein 1	6251	-1.33636	0.043967	0.22461
211671_s_at	NR3C1	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	2908	1.257541	0.044183	0.22461
203007_x_at	LYPLA1	lysophospholipase I	10434	-1.24485	0.04487	0.22461
210299_s_at	FHL1	four and a half LIM domains 1	2273	1.459962	0.045279	0.22461

210783_x_at	CLEC11A	C-type lectin domain family 11, member A	6320	-1.14617	0.045531	0.22461
209154_at	TAX1BP3	Tax1 (human T-cell leukemia virus type I) binding protein 3	30851	-1.80171	0.045558	0.22461
212279_at	TMEM97	transmembrane protein 97	27346	-1.20825	0.046373	0.22461
202102_s_at	BRD4	bromodomain containing 4	23476	-1.31832	0.046377	0.22461
200719_at	SKP1	S-phase kinase-associated protein 1	6500	-1.18511	0.046416	0.22461
213416_at	ITGA4	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)	3676	1.500306	0.046971	0.22461
201251_at	PKM	pyruvate kinase, muscle	5315	-1.61415	0.04732	0.22461
220094_s_at	CCDC90A	coiled-coil domain containing 90A	63933	-1.33066	0.048464	0.22461
202275_at	G6PD	glucose-6-phosphate dehydrogenase	2539	-1.46785	0.04883	0.22461
214146_s_at	PPBP	pro-platelet basic protein (chemokine (C-X-C motif) ligand 7)	5473	-2.44242	0.049566	0.22461
204081_at	NRGN	neurogranin (protein kinase C substrate, RC3)	4900	-2.56374	0.049579	0.22461
209868_s_at	RBMS1	RNA binding motif, single stranded interacting protein 1	5937	1.165728	0.050155	0.22461
211922_s_at	CAT	catalase	847	1.232958	0.051088	0.22461
222310_at	SCAF4	SR-related CTD-associated factor 4	57466	1.077534	0.05119	0.22461
200697_at	HK1	hexokinase 1	3098	-1.1627	0.051949	0.22461
200706_s_at	LITAF	lipopolysaccharide-induced TNF factor	9516	1.091394	0.052104	0.22461
220964_s_at	RAB1B	RAB1B, member RAS oncogene family	81876	-1.24067	0.052429	0.22461
210215_at	TFR2	transferrin receptor 2	7036	-1.65926	0.052589	0.22461
201260_s_at	SYPL1	synaptophysin-like 1	6856	1.519931	0.052716	0.22461
221771_s_at	MPHOSPH8	M-phase phosphoprotein 8	54737	1.277564	0.053033	0.22461
210986_s_at	TPM1	tropomyosin 1 (alpha)	7168	-1.54226	0.053308	0.22461
203674_at	HELZ	helicase with zinc finger	9931	1.115528	0.053318	0.22461
207238_s_at	PTPRC	protein tyrosine phosphatase, receptor type, C	5788	1.189131	0.053365	0.22461
201864_at	GDI1	GDP dissociation inhibitor 1	2664	-1.17328	0.053513	0.22461
212036_s_at	PNN	pinin, desmosome associated protein	5411	1.514285	0.053837	0.22461
213521_at	PTPN18	protein tyrosine phosphatase, non-receptor type 18 (brain-derived)	26469	-1.32436	0.05412	0.22461
202644_s_at	TNFAIP3	tumor necrosis factor, alpha-induced protein 3	7128	-1.72075	0.054213	0.22461
219090_at	SLC24A3	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	57419	-1.33752	0.054392	0.22461
209117_at	WBP2	WW domain binding protein 2	23558	-1.30969	0.054585	0.22461
209160_at	AKR1C3	aldo-keto reductase family 1, member C3	8644	1.332339	0.054731	0.22461
203085_s_at	TGFB1	transforming growth factor, beta 1	7040	-1.75422	0.055437	0.22461

200613_at	AP2M1	adaptor-related protein complex 2, mu 1 subunit	1173	-1.26768	0.05634	0.22461
212406_s_at	PCMTD2	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2	55251	1.40919	0.057779	0.22461
212281_s_at	TMEM97	transmembrane protein 97	27346	-1.25212	0.058007	0.22461
222113_s_at	EPS15L1	epidermal growth factor receptor pathway substrate 15-like 1	58513	-1.22321	0.058228	0.22461
41047_at	C9orf16	chromosome 9 open reading frame 16	79095	-1.3784	0.058369	0.22461
202083_s_at	SEC14L1	SEC14-like 1 (S. cerevisiae)	6397	-1.60251	0.058462	0.22461
43544_at	MED16	mediator complex subunit 16	10025	-1.37264	0.059358	0.22461
208398_s_at	TBPL1	TBP-like 1	9519	-1.09285	0.060353	0.22461
200001_at	CAPNS1	calpain, small subunit 1	826	-1.38469	0.060708	0.22461
203321_s_at	ADNP2	ADNP homeobox 2	22850	-1.14224	0.060952	0.22461
214752_x_at	FLNA	filamin A, alpha	2316	-1.51816	0.061564	0.22461
221539_at	EIF4EBP1	eukaryotic translation initiation factor 4E binding protein 1	1978	-1.09846	0.062496	0.22461
208860_s_at	ATRX	alpha thalassemia/mental retardation syndrome X-linked	546	1.305128	0.06313	0.22461
215933_s_at	HHEX	hematopoietically expressed homeobox	3087	1.399528	0.063251	0.22461
214753_at	N4BP2L2	NEDD4 binding protein 2-like 2	10443	1.043575	0.063268	0.22461
208284_x_at	GGT1	gamma-glutamyltransferase 1	2678	-1.13931	0.063281	0.22461
203163_at	KATNB1	katanin p80 (WD repeat containing) subunit B 1	10300	-1.04468	0.06434	0.22461
209301_at	CA2	carbonic anhydrase II	760	-1.80993	0.064349	0.22461
204480_s_at	C9orf16	chromosome 9 open reading frame 16	79095	-1.50337	0.064729	0.22461
205668_at	LY75	lymphocyte antigen 75	4065	1.143917	0.064806	0.22461
211047_x_at	AP2S1	adaptor-related protein complex 2, sigma 1 subunit	1175	-1.1541	0.065359	0.22461
201563_at	SORD	sorbitol dehydrogenase	6652	-1.02865	0.066229	0.225836
214246_x_at	MINK1	misshapen-like kinase 1	50488	-1.37631	0.066383	0.225836
212563_at	BOP1	block of proliferation 1	23246	-1.07647	0.067055	0.226454
215706_x_at	ZYX	zyxin	7791	-1.14429	0.067478	0.226454
215116_s_at	DNM1	dynamin 1	1759	-1.02496	0.067568	0.226454
209044_x_at	SF3B4	splicing factor 3b, subunit 4, 49kDa	10262	-1.14403	0.069176	0.227703
208977_x_at	TUBB4B	tubulin, beta 4B class IVb	10383	-1.06783	0.069385	0.227703
203175_at	RHOG	ras homolog family member G	391	-1.12466	0.07026	0.227703
212739_s_at	NME4	NME/NM23 nucleoside diphosphate kinase 4	4833	-1.18	0.070482	0.227703
200734_s_at	ARF3	ADP-ribosylation factor 3	377	-1.10487	0.070887	0.227703
213036_x_at	ATP2A3	ATPase, Ca++ transporting, ubiquitous	489	-1.21253	0.07161	0.227703
210428_s_at	HGS	hepatocyte growth factor-regulated tyrosine kinase substrate	9146	-1.08114	0.071709	0.227703

206272_at	SPHAR	S-phase response (cyclin related)	10638	-1.37986	0.071711	0.227703
200742_s_at	TPP1	tripeptidyl peptidase I	1200	-1.44492	0.071977	0.227703
202944_at	NAGA	N-acetylgalactosaminidase, alpha-	4668	-1.0861	0.073258	0.229457
216841_s_at	SOD2	superoxide dismutase 2, mitochondrial	6648	-1.07023	0.073344	0.229457
203414_at	MMD	monocyte to macrophage differentiation-associated	23531	-1.57415	0.073626	0.229457
215438_x_at	GSPT1	G1 to S phase transition 1	2935	-1.03476	0.074204	0.229457
217918_at	DYNLRB1	dynein, light chain, roadblock-type 1	83658	-1.21177	0.07474	0.229995
204628_s_at	ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	3690	-1.70942	0.076434	0.233122
214450_at	CTSW	cathepsin W	1521	-1.09904	0.076703	0.233122
203262_s_at	FAM50A	family with sequence similarity 50, member A	9130	-1.05318	0.077683	0.233565
216956_s_at	ITGA2B	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41)	3674	-2.02417	0.07797	0.233565
201639_s_at	CPSF1	cleavage and polyadenylation specific factor 1, 160kDa	29894	-1.05345	0.079365	0.234598
36711_at	MAFF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	23764	-2.66779	0.079702	0.234598
210910_s_at	POMZP3	POM121 and ZP3 fusion	22932	-0.98043	0.080921	0.234598
206390_x_at	PF4	platelet factor 4	5196	-2.17632	0.081141	0.234598
218443_s_at	DAZAP1	DAZ associated protein 1	26528	-0.99013	0.081405	0.234598
201052_s_at	PSMF1	proteasome (prosome, macropain) inhibitor subunit 1 (PI31)	9491	-1.17083	0.081493	0.234598
211716_x_at	ARHGDIA	Rho GDP dissociation inhibitor (GDI) alpha	396	-1.05994	0.081516	0.234598
200839_s_at	CTSB	cathepsin B	1508	-1.23855	0.081791	0.234598
203561_at	FCGR2A	Fc fragment of IgG, low affinity IIa, receptor (CD32)	2212	-1.50392	0.082039	0.234598
218611_at	IER5	immediate early response 5	51278	-1.41626	0.082127	0.234598
202619_s_at	PLOD2	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2	5352	-1.06567	0.082911	0.234625
204627_s_at	ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	3690	-2.11954	0.083412	0.234625
201224_s_at	SRRM1	serine/arginine repetitive matrix 1	10250	-1.23842	0.08352	0.234625
217736_s_at	EIF2AK1	eukaryotic translation initiation factor 2-alpha kinase 1	27102	-1.07432	0.083557	0.234625
200649_at	NUCB1	nucleobindin 1	4924	-1.0434	0.085339	0.23596
209555_s_at	CD36	CD36 molecule (thrombospondin receptor)	948	-1.82889	0.086873	0.23596
212520_s_at	SMARCA4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	6597	-1.12786	0.086976	0.23596
209367_at	STXBP2	syntaxin binding protein 2	6813	-1.12693	0.087289	0.23596
53071_s_at	OGFOD3	2-oxoglutarate and iron-dependent oxygenase domain containing 3	79701	-1.02384	0.087372	0.23596
221953_s_at	MMP24	matrix metallopeptidase 24 (membrane-inserted)	10893	-1.14292	0.087422	0.23596

212640_at	PTPLB	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b	201562	1.184144	0.087703	0.23596
201797_s_at	VARS	valyl-tRNA synthetase	7407	-0.95792	0.087831	0.23596
204232_at	FCER1G	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide	2207	-1.72735	0.088324	0.236346
202201_at	BLVRB	biliverdin reductase B (flavin reductase (NADPH))	645	-1.03625	0.088981	0.236552
203192_at	ABCB6	ATP-binding cassette, sub-family B (MDR/TAP), member 6	10058	-1.03424	0.090022	0.237141
221829_s_at	TNPO1	transportin 1	3842	-1.16481	0.090459	0.237366
213016_at	BBX	bobby sox homolog (Drosophila)	56987	-1.01796	0.091007	0.237691
207574_s_at	GADD45B	growth arrest and DNA-damage-inducible, beta	4616	-1.53642	0.091507	0.237691
207134_x_at	TPSB2	tryptase beta 2 (gene/pseudogene)	64499	-1.2023	0.092025	0.237791
211962_s_at	ZFP36L1	ZFP36 ring finger protein-like 1	677	-1.08806	0.094727	0.239603
201412_at	LRP10	low density lipoprotein receptor-related protein 10	26020	-1.16907	0.095687	0.239603
200859_x_at	FLNA	filamin A, alpha	2316	-1.28906	0.09598	0.239603
201760_s_at	WSB2	WD repeat and SOCS box containing 2	55884	-0.9579	0.097393	0.239603
212256_at	GALNT10	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (GalNAc-T10)	55568	-0.9355	0.097486	0.239603
202411_at	IFI27	interferon, alpha-inducible protein 27	3429	-1.2038	0.097807	0.239603
209190_s_at	DIAPH1	diaphanous homolog 1 (Drosophila)	1729	-1.03246	0.097812	0.239603
212886_at	CCDC69	coiled-coil domain containing 69	26112	-1.0779	0.098162	0.239603
215087_at	C15orf39	chromosome 15 open reading frame 39	56905	-1.19136	0.09937	0.239603
211417_x_at	GGT1	gamma-glutamyltransferase 1	2678	-0.97792	0.09942	0.239603
218039_at	NUSAP1	nucleolar and spindle associated protein 1	51203	-1.16811	0.100201	0.239603
215535_s_at	AGPAT1	1-acylglycerol-3-phosphate O-acyltransferase 1	10554	-1.14266	0.10071	0.239603
219938_s_at	PSTPIP2	proline-serine-threonine phosphatase interacting protein 2	9050	-1.02201	0.100884	0.239603
213746_s_at	FLNA	filamin A, alpha	2316	-1.37828	0.100915	0.239603
200611_s_at	WDR1	WD repeat domain 1	9948	-1.08654	0.101143	0.239603
208615_s_at	PTP4A2	protein tyrosine phosphatase type IVA, member 2	8073	-1.16457	0.101287	0.239603
208002_s_at	ACOT7	acyl-CoA thioesterase 7	11332	-0.98943	0.101855	0.239603
201280_s_at	DAB2	Dab, mitogen-responsive phosphoprotein, homolog 2 (Drosophila)	1601	-1.47352	0.10199	0.239603
217529_at	ORAI2	ORAI calcium release-activated calcium modulator 2	80228	-0.94855	0.102013	0.239603
214054_at	DOK2	docking protein 2, 56kDa	9046	-1.44148	0.102476	0.239603
222043_at	CLU	clusterin	1191	-1.34754	0.102489	0.239603
201059_at	CTTN	cortactin	2017	-1.75221	0.102546	0.239603

220239_at	KLHL7	kelch-like family member 7	55975	-1.04556	0.102824	0.239603
201950_x_at	CAPZB	capping protein (actin filament) muscle Z-line, beta	832	-0.9793	0.10316	0.239603
207196_s_at	TNIP1	TNFAIP3 interacting protein 1	10318	-1.00708	0.103374	0.239603
211160_x_at	ACTN1	actinin, alpha 1	87	-1.26927	0.103783	0.239603
209350_s_at	GPS2	G protein pathway suppressor 2	2874	-1.10209	0.103921	0.239603
219667_s_at	BANK1	B-cell scaffold protein with ankyrin repeats 1	55024	-1.00308	0.104821	0.239603
210075_at	MARCH2	membrane-associated ring finger (C3HC4) 2, E3 ubiquitin protein ligase	51257	-1.43742	0.104896	0.239603
201170_s_at	BHLHE40	basic helix-loop-helix family, member e40	8553	-1.52602	0.105204	0.239603
204254_s_at	VDR	vitamin D (1,25- dihydroxyvitamin D3) receptor	7421	-1.04354	0.10546	0.239603
210128_s_at	LTB4R	leukotriene B4 receptor	1241	-0.92553	0.105789	0.239603
221210_s_at	NPL	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)	80896	-1.20989	0.105822	0.239603
210512_s_at	VEGFA	vascular endothelial growth factor A	7422	-1.15461	0.10674	0.240343
202499_s_at	SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	6515	-1.58321	0.106858	0.240343
201125_s_at	ITGB5	integrin, beta 5	3693	-1.33107	0.107555	0.24035
206414_s_at	ASAP2	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2	8853	-1.34473	0.107572	0.24035
201360_at	CST3	cystatin C	1471	-1.68937	0.108964	0.242661
215047_at	TRIM58	tripartite motif containing 58	25893	-0.99092	0.11023	0.243627
204493_at	BID	BH3 interacting domain death agonist	637	-0.9825	0.110478	0.243627
202728_s_at	LTBP1	latent transforming growth factor beta binding protein 1	4052	-1.27115	0.113678	0.246714
209969_s_at	STAT1	signal transducer and activator of transcription 1, 91kDa	6772	-1.15673	0.113691	0.246714
205241_at	SCO2	SCO2 cytochrome c oxidase assembly protein	9997	-1.4845	0.114175	0.246714
203017_s_at	SSX2IP	synovial sarcoma, X breakpoint 2 interacting protein	117178	-0.94238	0.114827	0.246714
203833_s_at	TGOLN2	trans-golgi network protein 2	10618	-0.93445	0.115059	0.246714
205269_at	LCP2	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)	3937	-0.97027	0.115226	0.246714
209522_s_at	CRAT	carnitine O-acetyltransferase	1384	-1.01234	0.116038	0.246714
204629_at	PARVB	parvin, beta	29780	-1.33625	0.116976	0.246714
200609_s_at	WDR1	WD repeat domain 1	9948	-0.99605	0.11718	0.246714
203680_at	PRKAR2B	protein kinase, cAMP-dependent, regulatory, type II, beta	5577	-1.23212	0.117344	0.246714
208918_s_at	NADK	NAD kinase	65220	-1.16887	0.119342	0.248598
213716_s_at	SECTM1	secreted and transmembrane 1	6398	-1.08088	0.119767	0.248718
221269_s_at	SH3BGRL3	SH3 domain binding glutamic acid-rich protein like 3	83442	-1.35229	0.120323	0.24911

212492_s_at	KDM4B	lysine (K)-specific demethylase 4B	23030	-0.91067	0.121784	0.251366
209729_at	GAS2L1	growth arrest-specific 2 like 1	10634	-1.27348	0.12433	0.255074
204928_s_at	SLC10A3	solute carrier family 10 (sodium/bile acid cotransporter family), member 3	8273	-1.17192	0.124419	0.255074
205390_s_at	ANK1	ankyrin 1, erythrocytic	286	-0.88253	0.124711	0.255074
211795_s_at	FYB	FYN binding protein	2533	-1.18122	0.125242	0.255154
31845_at	ELF4	E74-like factor 4 (ets domain transcription factor)	2000	-0.94729	0.125919	0.255154
212573_at	ENDOD1	endonuclease domain containing 1	23052	-1.40577	0.126395	0.255154
209560_s_at	DLK1	delta-like 1 homolog (Drosophila)	8788	-1.19672	0.126533	0.255154
201095_at	DAP	death-associated protein	1611	-1.11419	0.126929	0.255154
212840_at	UBXN7	UBX domain protein 7	26043	-1.01058	0.127011	0.255154
221267_s_at	FAM108A1	family with sequence similarity 108, member A1	81926	-1.01634	0.128163	0.256705
208074_s_at	AP2S1	adaptor-related protein complex 2, sigma 1 subunit	1175	-0.99964	0.128569	0.256758
200990_at	TRIM28	tripartite motif containing 28	10155	-1.00558	0.129664	0.257321
209839_at	DNM3	dynamin 3	26052	-1.34338	0.130264	0.257321
201714_at	TUBG1	tubulin, gamma 1	7283	-0.88297	0.130361	0.257321
200752_s_at	CAPN1	calpain 1, (mu/I) large subunit	823	-0.92096	0.131139	0.258085
220751_s_at	FAXDC2	fatty acid hydroxylase domain containing 2	10826	-1.32403	0.132172	0.258731
210357_s_at	SMOX	spermine oxidase	54498	-1.03467	0.132612	0.258731
218175_at	CCDC92	coiled-coil domain containing 92	80212	-1.09884	0.132796	0.258731
204000_at	GNB5	guanine nucleotide binding protein (G protein), beta 5	10681	-1.19778	0.133164	0.258731
217748_at	ADIPOR1	adiponectin receptor 1	51094	-0.93144	0.13362	0.258731
207389_at	GP1BA	glycoprotein Ib (platelet), alpha polypeptide	2811	-1.24025	0.134051	0.258731
217992_s_at	EFHD2	EF-hand domain family, member D2	79180	-1.0245	0.134143	0.258731
200884_at	CKB	creatine kinase, brain	1152	-0.88314	0.13483	0.259317
206145_at	RHAG	Rh-associated glycoprotein	6005	-1.17935	0.13531	0.259504
220757_s_at	UBXN6	UBX domain protein 6	80700	-0.88851	0.136128	0.259746
213274_s_at	CTSB	cathepsin B	1508	-0.90565	0.136204	0.259746
202464_s_at	PFKFB3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	5209	-1.06242	0.137167	0.26039
202665_s_at	WIPF1	WAS/WASL interacting protein family, member 1	7456	-1.08477	0.13731	0.26039
206488_s_at	CD36	CD36 molecule (thrombospondin receptor)	948	-1.53958	0.138985	0.260645
212089_at	LMNA	lamin A/C	4000	-0.92285	0.140733	0.261597
205436_s_at	H2AFX	H2A histone family, member X	3014	-1.00358	0.140821	0.261597
206834_at	HBD	hemoglobin, delta	3045	-1.42844	0.141235	0.261597

209919_x_at	GGT1	gamma-glutamyltransferase 1	2678	-0.89741	0.141427	0.261597
207741_x_at	TPSAB1	tryptase alpha/beta 1	7177	-1.06406	0.142116	0.261597
31874_at	GAS2L1	growth arrest-specific 2 like 1	10634	-1.54272	0.142456	0.261597
201700_at	CCND3	cyclin D3	896	-0.99741	0.142709	0.261597
205683_x_at	TPSAB1	tryptase alpha/beta 1	7177	-1.01525	0.142713	0.261597
201061_s_at	STOM	stomatin	2040	-1.01078	0.14297	0.261597
203016_s_at	SSX2IP	synovial sarcoma, X breakpoint 2 interacting protein	117178	-0.95396	0.143425	0.261722
220496_at	CLEC1B	C-type lectin domain family 1, member B	51266	-1.54811	0.14406	0.262175
209929_s_at	IKBKG	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma	8517	-0.89402	0.145589	0.262942
37028_at	PPP1R15A	protein phosphatase 1, regulatory subunit 15A	23645	-1.05228	0.14582	0.262942
212769_at	TLE3	transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)	7090	-0.90676	0.14604	0.262942
203581_at	RAB4A	RAB4A, member RAS oncogene family	5867	-1.01651	0.146743	0.262942
213956_at	CEP350	centrosomal protein 350kDa	9857	-0.85883	0.146813	0.262942
215382_x_at	TPSB2	tryptase beta 2 (gene/pseudogene)	64499	-0.977	0.148064	0.263547
201830_s_at	NET1	neuroepithelial cell transforming 1	10276	-0.9677	0.148301	0.263547
201693_s_at	EGR1	early growth response 1	1958	-1.15545	0.148318	0.263547
215498_s_at	MAP2K3	mitogen-activated protein kinase kinase 3	5606	-1.08177	0.149281	0.264012
204026_s_at	ZWINT	ZW10 interactor, kinetochore protein	11130	-1.12549	0.149413	0.264012
209170_s_at	GPM6B	glycoprotein M6B	2824	0.976338	0.14975	0.264012
221211_s_at	MAP3K7CL	MAP3K7 C-terminal like	56911	-1.30326	0.150281	0.264261
203045_at	NINJ1	ninjurin 1	4814	-1.13628	0.15069	0.264293
210084_x_at	TPSAB1	tryptase alpha/beta 1	7177	-0.99706	0.151879	0.264649
207945_s_at	CSNK1D	casein kinase 1, delta	1453	-0.90784	0.152234	0.264649
204158_s_at	TCIRG1	T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 subunit A3	10312	-1.17593	0.152276	0.264649
200766_at	CTSD	cathepsin D	1509	-0.93104	0.153066	0.265027
215819_s_at	RHCE	Rh blood group, CcEe antigens	6006	-0.9917	0.154157	0.266177
203485_at	RTN1	reticulon 1	6252	-1.21235	0.154517	0.266177
215240_at	ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	3690	-1.44118	0.156	0.267603
201761_at	MTHFD2	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase	10797	-0.98494	0.156692	0.267603
201904_s_at	CTDSPL	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like	10217	-0.91323	0.156796	0.267603

201906_s_at	CTDSPL	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like	10217	-0.94383	0.156925	0.267603
203854_at	CFI	complement factor I	3426	0.869863	0.158526	0.268092
204925_at	CTNS	cystinosin, lysosomal cystine transporter	1497	-0.97532	0.158632	0.268092
204306_s_at	CD151	CD151 molecule (Raph blood group)	977	-0.94181	0.158669	0.268092
206380_s_at	CFP	complement factor properdin	5199	-1.1026	0.158939	0.268092
204961_s_at	NCF1	neutrophil cytosolic factor 1	653361	-1.43048	0.159385	0.268092
201810_s_at	SH3BP5	SH3-domain binding protein 5 (BTK-associated)	9467	-1.02141	0.159588	0.268092
204192_at	CD37	CD37 molecule	951	-1.01901	0.162409	0.270814
202082_s_at	SEC14L1	SEC14-like 1 (S. cerevisiae)	6397	-0.89139	0.163106	0.271309
218009_s_at	PRC1	protein regulator of cytokinesis 1	9055	-1.11022	0.16572	0.274981
218522_s_at	MAP1S	microtubule-associated protein 1S	55201	-0.95913	0.166988	0.275781
214369_s_at	RASGRP2	RAS guanyl releasing protein 2 (calcium and DAG-regulated)	10235	-0.91512	0.167017	0.275781
218243_at	RUFY1	RUN and FYVE domain containing 1	80230	-1.00705	0.168966	0.278235
214965_at	SPATA2L	spermatogenesis associated 2-like	124044	-0.97367	0.169324	0.278235
212027_at	RBM25	RNA binding motif protein 25	58517	-1.0829	0.17147	0.279943
218148_at	CENPT	centromere protein T	80152	-0.88627	0.171898	0.279943
203234_at	UPP1	uridine phosphorylase 1	7378	-1.02931	0.172377	0.279943
200661_at	CTSA	cathepsin A	5476	-1.40173	0.172629	0.279943
210793_s_at	NUP98	nucleoporin 98kDa	4928	-1.01125	0.173817	0.279943
215464_s_at	TAX1BP3	Tax1 (human T-cell leukemia virus type I) binding protein 3	30851	-1.07322	0.174266	0.279943
204482_at	CLDN5	claudin 5	7122	-1.19654	0.174447	0.279943
204198_s_at	RUNX3	runt-related transcription factor 3	864	-0.98615	0.174457	0.279943
212195_at	IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)	3572	-0.93935	0.174626	0.279943
209304_x_at	GADD45B	growth arrest and DNA-damage-inducible, beta	4616	-0.99482	0.174913	0.279943
204079_at	TPST2	tyrosylprotein sulfotransferase 2	8459	-1.11621	0.177613	0.283594
206167_s_at	ARHGAP6	Rho GTPase activating protein 6	395	-1.27531	0.178208	0.283875
220336_s_at	GP6	glycoprotein VI (platelet)	51206	-1.06098	0.183391	0.290763
214464_at	CDC42BPA	CDC42 binding protein kinase alpha (DMPK-like)	8476	-0.96701	0.186028	0.292695
213887_s_at	POLR2E	polymerase (RNA) II (DNA directed) polypeptide E, 25kDa	5434	-0.91232	0.186513	0.292695
216261_at	ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	3690	-1.19784	0.187072	0.292695
213836_s_at	WIPI1	WD repeat domain, phosphoinositide interacting 1	55062	-1.00273	0.187347	0.292695
218032_at	SNN	stannin	8303	-1.21538	0.189158	0.293378
200931_s_at	VCL	vinculin	7414	-0.92232	0.190234	0.294037

220110_s_at	NXF3	nuclear RNA export factor 3	56000	-0.84883	0.194112	0.298064
219998_at	LGALSL	lectin, galactoside-binding-like	29094	-0.88669	0.19416	0.298064
200648_s_at	GLUL	glutamate-ammonia ligase	2752	-0.885	0.196266	0.300615
207075_at	NLRP3	NLR family, pyrin domain containing 3	114548	-1.04141	0.196978	0.300727
202814_s_at	HEXIM1	hexamethylene bis-acetamide inducible 1	10614	-0.86963	0.197227	0.300727
211582_x_at	LST1	leukocyte specific transcript 1	7940	-0.89977	0.198407	0.301846
57588_at	SLC24A3	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	57419	-0.8268	0.199252	0.301985
209881_s_at	LAT	linker for activation of T cells	27040	-0.84958	0.199391	0.301985
213537_at	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	3113	-1.00128	0.200355	0.302768
214084_x_at	NCF1C	neutrophil cytosolic factor 1C pseudogene	654817	-1.32671	0.201691	0.303721
202555_s_at	MYLK	myosin light chain kinase	4638	-1.35821	0.201883	0.303721
222024_s_at	AKAP13	A kinase (PRKA) anchor protein 13	11214	-0.9453	0.20348	0.305445
207522_s_at	ATP2A3	ATPase, Ca++ transporting, ubiquitous	489	-0.86192	0.204597	0.305832
202228_s_at	NPTN	neuroplastin	27020	-0.94477	0.204641	0.305832
204396_s_at	GRK5	G protein-coupled receptor kinase 5	2869	-1.18973	0.205515	0.306089
214073_at	CTTN	cortactin	2017	-1.42385	0.205717	0.306089
217764_s_at	RAB31	RAB31, member RAS oncogene family	11031	-1.28868	0.206889	0.306253
208792_s_at	CLU	clusterin	1191	-1.32868	0.207424	0.306253
218945_at	METTL22	methyltransferase like 22	79091	-0.81822	0.207478	0.306253
209166_s_at	MAN2B1	mannosidase, alpha, class 2B, member 1	4125	-0.87235	0.207908	0.306253
221856_s_at	FAM63A	family with sequence similarity 63, member A	55793	-0.90737	0.208242	0.306253
200622_x_at	CALM3	calmodulin 3 (phosphorylase kinase, delta)	808	-1.05371	0.208541	0.306253
216834_at	RGS1	regulator of G-protein signaling 1	5996	-1.58039	0.209603	0.307146
201234_at	ILK	integrin-linked kinase	3611	-0.893	0.210231	0.307401
212016_s_at	PTBP1	polypyrimidine tract binding protein 1	5725	-0.82271	0.214043	0.311628
203196_at	ABCC4	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	10257	-0.94809	0.215339	0.312842
204838_s_at	MLH3	mutL homolog 3 (E. coli)	27030	-1.17819	0.217494	0.314178
210314_x_at	TNFSF13	tumor necrosis factor (ligand) superfamily, member 13	8741	-0.85424	0.217651	0.314178
221027_s_at	PLA2G12A	phospholipase A2, group XIIA	81579	-1.0047	0.219833	0.31622
207206_s_at	ALOX12	arachidonate 12-lipoxygenase	239	-1.20411	0.221481	0.316376
336_at	TBXA2R	thromboxane A2 receptor	6915	-0.9854	0.221852	0.316376
208924_at	RNF11	ring finger protein 11	26994	-0.85227	0.222362	0.316376
204440_at	CD83	CD83 molecule	9308	-0.86406	0.222738	0.316376

216033_s_at	FYN	FYN oncogene related to SRC, FGR, YES	2534	-0.86181	0.222912	0.316376
207414_s_at	PCSK6	proprotein convertase subtilisin/kexin type 6	5046	-1.24651	0.224243	0.317072
202014_at	PPP1R15A	protein phosphatase 1, regulatory subunit 15A	23645	-0.9299	0.224339	0.317072
204256_at	ELOVL6	ELOVL fatty acid elongase 6	79071	-0.916	0.225463	0.317997
216474_x_at	TPSB2	tryptase beta 2 (gene/pseudogene)	64499	-0.84525	0.227141	0.319076
200696_s_at	GSN	gelsolin	2934	-0.94992	0.227466	0.319076
206632_s_at	APOBEC3B	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B	9582	-1.04605	0.228843	0.320097
221496_s_at	TOB2	transducer of ERBB2, 2	10766	-0.78204	0.231572	0.323245
219630_at	PDZK1IP1	PDZK1 interacting protein 1	10158	-1.15529	0.234788	0.326336
214696_at	MIR22HG	MIR22 host gene (non-protein coding)	84981	-0.82752	0.235232	0.326336
213275_x_at	CTSB	cathepsin B	1508	-0.98223	0.235914	0.326614
215343_at	CCDC88C	coiled-coil domain containing 88C	440193	-0.83997	0.23881	0.328606
205347_s_at	TMSB15A	thymosin beta 15a	11013	-0.82645	0.241173	0.329982
213093_at	PRKCA	protein kinase C, alpha	5578	-0.92248	0.241407	0.329982
218217_at	SCPEP1	serine carboxypeptidase 1	59342	-0.82069	0.2415	0.329982
201490_s_at	PPIF	peptidylprolyl isomerase F	10105	-0.81917	0.242498	0.329982
204187_at	GMPR	guanosine monophosphate reductase	2766	-0.83239	0.248436	0.336382
217762_s_at	RAB31	RAB31, member RAS oncogene family	11031	-1.02517	0.252078	0.339954
204790_at	SMAD7	SMAD family member 7	4092	-0.76543	0.253693	0.341452
209813_x_at	TARP	TCR gamma alternate reading frame protein	445347	-0.85554	0.256336	0.344324
212636_at	QKI	QKI, KH domain containing, RNA binding	9444	-0.79642	0.257784	0.344583
211429_s_at	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	5265	-1.37823	0.258343	0.344583
205253_at	PBX1	pre-B-cell leukemia homeobox 1	5087	-0.76555	0.258565	0.344583
201735_s_at	CLCN3	chloride channel, voltage-sensitive 3	1182	-0.94043	0.260503	0.346484
205950_s_at	CA1	carbonic anhydrase I	759	-0.96583	0.262137	0.347974
201334_s_at	ARHGEF12	Rho guanine nucleotide exchange factor (GEF) 12	23365	-0.77329	0.264462	0.350312
210987_x_at	TPM1	tropomyosin 1 (alpha)	7168	-0.82871	0.265224	0.350312
209806_at	HIST1H2BK	histone cluster 1, H2bk	85236	-0.86055	0.266486	0.350312
215492_x_at	PTCRA	pre T-cell antigen receptor alpha	171558	-0.904	0.271153	0.355069
205099_s_at	CCR1	chemokine (C-C motif) receptor 1	1230	-0.80241	0.275833	0.359113
202007_at	NID1	nidogen 1	4811	-0.78832	0.278249	0.361563
210845_s_at	PLAUR	plasminogen activator, urokinase receptor	5329	-0.82653	0.280926	0.364343

218662_s_at	NCAPG	non-SMC condensin I complex, subunit G	64151	-0.73805	0.281927	0.364942
209459_s_at	ABAT	4-aminobutyrate aminotransferase	18	-0.83695	0.28286	0.365451
208161_s_at	ABCC3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	8714	-0.87352	0.283451	0.365517
210429_at	RHD	Rh blood group, D antigen	6007	-1.02292	0.285289	0.365856
208791_at	CLU	clusterin	1191	-1.10749	0.285331	0.365856
36566_at	CTNS	cystinosin, lysosomal cystine transporter	1497	-0.72179	0.285335	0.365856
218711_s_at	SDPR	serum deprivation response	8436	-0.86687	0.285908	0.365897
201732_s_at	CLCN3	chloride channel, voltage-sensitive 3	1182	-0.82971	0.287865	0.367365
212570_at	ENDOD1	endonuclease domain containing 1	23052	-0.73257	0.289756	0.368708
203411_s_at	LMNA	lamin A/C	4000	-0.7781	0.290282	0.368708
211252_x_at	PTCRA	pre T-cell antigen receptor alpha	171558	-0.8545	0.291611	0.369032
204908_s_at	BCL3	B-cell CLL/lymphoma 3	602	-0.87358	0.292902	0.369953
218935_at	EHD3	EH-domain containing 3	30845	-0.93363	0.293563	0.370097
219983_at	HRASLS	HRAS-like suppressor	57110	-0.72599	0.298402	0.374935
220091_at	SLC2A6	solute carrier family 2 (facilitated glucose transporter), member 6	11182	-0.7439	0.298508	0.374935
212657_s_at	IL1RN	interleukin 1 receptor antagonist	3557	-0.78633	0.300604	0.376172
210240_s_at	CDKN2D	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)	1032	-0.7304	0.304949	0.380904
213338_at	TMEM158	transmembrane protein 158 (gene/pseudogene)	25907	-0.83724	0.308131	0.382561
218559_s_at	MAFB	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	9935	-1.05359	0.308532	0.382561
221050_s_at	GTPBP2	GTP binding protein 2	54676	-0.69663	0.308832	0.382561
201131_s_at	CDH1	cadherin 1, type 1, E-cadherin (epithelial)	999	-0.70327	0.3091	0.382561
216253_s_at	PARVB	parvin, beta	29780	-0.85494	0.309748	0.382663
202988_s_at	RGS1	regulator of G-protein signaling 1	5996	-1.01339	0.312601	0.385484
205786_s_at	ITGAM	integrin, alpha M (complement component 3 receptor 3 subunit)	3684	-0.83414	0.314385	0.386979
210757_x_at	DAB2	Dab, mitogen-responsive phosphoprotein, homolog 2 (Drosophila)	1601	-0.74514	0.315103	0.387159
212723_at	JMJD6	jumonji domain containing 6	23210	-0.75129	0.319118	0.391333
211743_s_at	PRG2	proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major basic protein)	5553	-0.78462	0.319656	0.391333
222108_at	AMIGO2	adhesion molecule with Ig-like domain 2	347902	-0.67947	0.320818	0.392046
204240_s_at	SMC2	structural maintenance of chromosomes 2	10592	-0.70057	0.322141	0.392954
217763_s_at	RAB31	RAB31, member RAS oncogene family	11031	-0.86003	0.327317	0.397715

204467_s_at	SNCA	synuclein, alpha (non A4 component of amyloid precursor)	6622	-0.70464	0.327807	0.397715
216063_at	HBBP1	hemoglobin, beta pseudogene 1	3044	-0.94717	0.329519	0.399078
202581_at	HSPA1A	heat shock 70kDa protein 1A	3303	-0.98594	0.331291	0.40042
210169_at	SEC14L5	SEC14-like 5 (S. cerevisiae)	9717	-0.74193	0.33181	0.40042
57082_at	LDLRAP1	low density lipoprotein receptor adaptor protein 1	26119	-0.8255	0.333963	0.402301
217022_s_at	IGH	immunoglobulin heavy locus	3492	-0.84526	0.336016	0.404055
210734_x_at	MAX	MYC associated factor X	4149	-0.69037	0.337578	0.405064
204099_at	SMARCD3	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3	6604	-0.66865	0.338052	0.405064
218585_s_at	DTL	denticleless E3 ubiquitin protein ligase homolog (Drosophila)	51514	-0.76574	0.338678	0.405098
220968_s_at	TSPAN9	tetraspanin 9	10867	-0.64905	0.342149	0.408528
204993_at	GNAZ	guanine nucleotide binding protein (G protein), alpha z polypeptide	2781	-0.77214	0.343386	0.409282
210992_x_at	FCGR2C	Fc fragment of IgG, low affinity IIc, receptor for (CD32) (gene/pseudogene)	9103	-0.70674	0.344048	0.409351
219412_at	RAB38	RAB38, member RAS oncogene family	23682	-0.70456	0.345526	0.410051
219892_at	TM6SF1	transmembrane 6 superfamily member 1	53346	-0.67737	0.345848	0.410051
205098_at	CCR1	chemokine (C-C motif) receptor 1	1230	-0.67251	0.348407	0.411654
206883_x_at	GP9	glycoprotein IX (platelet)	2815	-0.93388	0.348416	0.411654
204546_at	KIAA0513	KIAA0513	9764	-0.6776	0.354075	0.416884
211984_at	CALM1	calmodulin 1 (phosphorylase kinase, delta)	801	-0.67903	0.356016	0.418443
212681_at	EPB41L3	erythrocyte membrane protein band 4.1-like 3	23136	-0.74882	0.363256	0.426212
209586_s_at	PRUNE	prune homolog (Drosophila)	58497	-0.71365	0.365133	0.427673
204122_at	TYROBP	TYRO protein tyrosine kinase binding protein	7305	-0.98164	0.368409	0.429921
221698_s_at	CLEC7A	C-type lectin domain family 7, member A	64581	-0.72388	0.368957	0.429921
202269_x_at	GBP1	guanylate binding protein 1, interferon-inducible	2633	-0.72489	0.374443	0.434817
37965_at	PARVB	parvin, beta	29780	-0.73203	0.378544	0.438076
206937_at	SPTA1	spectrin, alpha, erythrocytic 1 (elliptocytosis 2)	6708	-0.63911	0.379343	0.438252
205863_at	S100A12	S100 calcium binding protein A12	6283	-0.76877	0.385662	0.443766
206465_at	ACSBG1	acyl-CoA synthetase bubblegum family member 1	23205	-0.69391	0.386083	0.443766
208601_s_at	TUBB1	tubulin, beta 1 class VI	81027	-0.7751	0.38836	0.445627
208501_at	GFI1B	growth factor independent 1B transcription repressor	8328	-0.69445	0.391518	0.44802
204319_s_at	RGS10	regulator of G-protein signaling 10	6001	-0.66481	0.391769	0.44802
204115_at	GNG11	guanine nucleotide binding protein (G protein), gamma 11	2791	-0.85973	0.396611	0.450473

222204_s_at	RRN3	RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae)	54700	-0.6018	0.396615	0.450473
204446_s_at	ALOX5	arachidonate 5-lipoxygenase	240	-0.88998	0.397241	0.450473
203508_at	TNFRSF1B	tumor necrosis factor receptor superfamily, member 1B	7133	-0.6867	0.398463	0.451103
203305_at	F13A1	coagulation factor XIII, A1 polypeptide	2162	-0.84164	0.401077	0.453304
208438_s_at	FGR	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog	2268	-0.62594	0.406618	0.458801
205463_s_at	PDGFA	platelet-derived growth factor alpha polypeptide	5154	-0.67628	0.408281	0.459911
202917_s_at	S100A8	S100 calcium binding protein A8	6279	-1.20152	0.411847	0.463156
207156_at	HIST1H2AG	histone cluster 1, H2ag	8969	-0.70408	0.413233	0.463944
202833_s_at	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	5265	-0.91706	0.413994	0.46403
207315_at	CD226	CD226 molecule	10666	-0.62666	0.418074	0.466595
204971_at	CSTA	cystatin A (stefin A)	1475	-0.89766	0.418207	0.466595
201954_at	ARPC1B	actin related protein 2/3 complex, subunit 1B, 41kDa	10095	-0.64277	0.41835	0.466595
206254_at	EGF	epidermal growth factor	1950	-0.61118	0.425271	0.472756
204475_at	MMP1	matrix metallopeptidase 1 (interstitial collagenase)	4312	-0.79765	0.427481	0.474434
205229_s_at	COCH	coagulation factor C homolog, cochlin (Limulus polyphemus)	1690	-0.53396	0.432368	0.479072
205127_at	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	5742	-0.54531	0.44234	0.488522
203087_s_at	KIF2A	kinesin heavy chain member 2A	3796	-0.59853	0.443634	0.488965
202953_at	C1QB	complement component 1, q subcomponent, B chain	713	-0.82302	0.444186	0.488965
218656_s_at	LHFP	lipoma HMGIC fusion partner	10186	-0.56539	0.445989	0.489822
214511_x_at	FCGR1B	Fc fragment of IgG, high affinity Ib, receptor (CD64)	2210	-0.69072	0.446411	0.489822
208406_s_at	GRAP2	GRB2-related adaptor protein 2	9402	-0.68765	0.451229	0.492736
56256_at	SIDT2	SID1 transmembrane family, member 2	51092	-0.74229	0.451977	0.492736
209204_at	LMO4	LIM domain only 4	8543	-0.52105	0.454155	0.494314
205612_at	MMRN1	multimerin 1	22915	-0.58072	0.457551	0.496919
206116_s_at	TPM1	tropomyosin 1 (alpha)	7168	-0.61863	0.458017	0.496919
204858_s_at	TYMP	thymidine phosphorylase	1890	-0.62323	0.459985	0.497869
204308_s_at	TECPR2	tectonin beta-propeller repeat containing 2	9895	-0.56607	0.460363	0.497869
204466_s_at	SNCA	synuclein, alpha (non A4 component of amyloid precursor)	6622	-0.60596	0.461512	0.498316
202270_at	GBP1	guanylate binding protein 1, interferon-inducible	2633	-0.55471	0.469505	0.505333
218223_s_at	PLEKHO1	pleckstrin homology domain containing, family O member 1	51177	-0.63829	0.474253	0.509634
206881_s_at	LILRA3	leukocyte immunoglobulin-like receptor, subfamily A (without	11026	-0.61236	0.483816	0.518375

		TM domain), member 3				
222218_s_at	PILRA	paired immunoglobin-like type 2 receptor alpha	29992	-0.60956	0.483919	0.518375
213566_at	RNASE6	ribonuclease, RNase A family, k6	6039	-0.53861	0.485481	0.519227
221160_s_at	CABP5	calcium binding protein 5	56344	-0.52004	0.487926	0.521019
206964_at	NAT8B	N-acetyltransferase 8B (GCN5-related, putative, gene/pseudogene)	51471	-0.52553	0.491589	0.523279
206420_at	IGSF6	immunoglobulin superfamily, member 6	10261	-0.58815	0.495872	0.52701
219386_s_at	SLAMF8	SLAM family member 8	56833	-0.64079	0.500574	0.531173
209949_at	NCF2	neutrophil cytosolic factor 2	4688	-0.64425	0.501391	0.531207
206110_at	HIST1H3H	histone cluster 1, H3h	8357	-0.78197	0.502267	0.531304
210660_at	LILRA1	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1	11024	-0.51819	0.518847	0.547986
203560_at	GGH	gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase)	8836	-0.53164	0.520075	0.548428
214677_x_at	CYAT1	immunoglobulin lambda light chain-like	100290481	-0.49954	0.537027	0.564546
211985_s_at	CALM1	calmodulin 1 (phosphorylase kinase, delta)	801	-0.5249	0.539781	0.566561
200660_at	S100A11	S100 calcium binding protein A11	6282	-0.57564	0.542655	0.568696
201279_s_at	DAB2	Dab, mitogen-responsive phosphoprotein, homolog 2 (Drosophila)	1601	-0.47879	0.546344	0.571676
203585_at	ZNF185	zinc finger protein 185 (LIM domain)	7739	-0.5405	0.548693	0.573249
203140_at	BCL6	B-cell CLL/lymphoma 6	604	-0.48632	0.5566	0.580552
202295_s_at	CTSH	cathepsin H	1512	-0.54025	0.557399	0.580552
210146_x_at	LILRB2	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2	10288	-0.42185	0.572195	0.593923
212188_at	KCTD12	potassium channel tetramerisation domain containing 12	115207	-0.40898	0.572868	0.593923
203973_s_at	CEBPD	CCAAT/enhancer binding protein (C/EBP), delta	1052	-0.50468	0.574596	0.594804
204588_s_at	SLC7A7	solute carrier family 7 (amino acid transporter light chain, y+L system), member 7	9056	-0.52401	0.57568	0.595016
218232_at	C1QA	complement component 1, q subcomponent, A chain	712	-0.45679	0.578484	0.597002
219159_s_at	SLAMF7	SLAM family member 7	57823	-0.41122	0.581677	0.599384
209448_at	HTATIP2	HIV-1 Tat interactive protein 2, 30kDa	10553	-0.4519	0.584526	0.601404
208450_at	LGALS2	lectin, galactoside-binding, soluble, 2	3957	-0.61288	0.591141	0.607288
207857_at	LILRA2	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2	11027	-0.38829	0.612701	0.626584
220088_at	C5AR1	complement component 5a receptor 1	728	-0.41369	0.614585	0.627563

204912_at	IL10RA	interleukin 10 receptor, alpha	3587	-0.36301	0.677582	0.688773
201005_at	CD9	CD9 molecule	928	-0.46299	0.696997	0.707447
205119_s_at	FPR1	formyl peptide receptor 1	2357	-0.34184	0.703731	0.713213
213831_at	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1	3117	-0.41115	0.757666	0.766726
205898_at	CX3CR1	chemokine (C-X3-C motif) receptor 1	1524	-0.2373	0.789441	0.797689
201422_at	IFI30	interferon, gamma-inducible protein 30	10437	-0.26145	0.793548	0.800643
208579_x_at	H2BFS	H2B histone family, member S (pseudogene)	54145	-0.20818	0.82651	0.83266
212192_at	KCTD12	potassium channel tetramerisation domain containing 12	115207	-0.19775	0.828056	0.832977
219505_at	CECR1	cat eye syndrome chromosome region, candidate 1	51816	-0.18017	0.84442	0.848178
215071_s_at	HIST1H2AC	histone cluster 1, H2ac	8334	-0.16128	0.864886	0.867448

Table S3. Primer/probe sets of the genes used for Q-RT-PCR validation of the microarray results.

ABI GEX Assay ID	Gene Symbol	Gene Name	GEX Target Exon Boundaries
Hs00188259_m1	WARS	tryptophanyl-tRNA synthetase	9-10
Hs99999139_m1	TIMP1	TIMP metallopeptidase inhibitor 1	2-3
Hs00180737_m1	HPSE	heparanase	8-9
Hs00172743_m1	DNTT	deoxynucleotidyltransferase, terminal	10-11
Hs00181810_m1	CRHBP	corticotropin releasing hormone binding protein	6-7
Hs00365956_m1	HOXA9	homeobox A9	1-2
Hs00202825_m1	SSBP2	single-stranded DNA binding protein 2	7-8
Hs00261238_m1	HOPX	HOP homeobox	2-3
Hs99999905_m1	GAPDH	glyceraldehyde-3-phosphate dehydrogenase	3-3
000397	miR-21	Human microRNA-21 (hsa-miR-21-5p)	N/A
001093	RNU6B	U6 small nuclear 2, small nuclear RNA	N/A

Table S4. Genes concordantly deregulated by both men and women patients.

Probeset ID	***Symbol (Na32 consesus Mar13)***	***Gene Title (Na32 consensus Mar13)***	***GeneID (concensus1 Mar-13)***	***Log2(FC)***	***P-Value***	***Adjusted p-Value***

202627_s_at	SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	5054	1.668478	0.005	0.45412
201324_at	EMP1	epithelial membrane protein 1	2012	1.16186	0.0077	0.45412
212667_at	SPARC	secreted protein, acidic, cysteine-rich (osteonectin)	6678	1.45459	0.0147	0.45412
201438_at	COL6A3	collagen, type VI, alpha 3	1293	1.278559	0.0258	0.45412
211161_s_at	COL3A1	collagen, type III, alpha 1	1281	1.254327	0.0296	0.45412
215076_s_at	COL3A1	collagen, type III, alpha 1	1281	1.488017	0.03	0.45412
210809_s_at	POSTN	periostin, osteoblast specific factor	10631	1.804584	0.0358	0.45412
212464_s_at	FN1	fibronectin 1	2335	1.813392	0.0368	0.45412
202404_s_at	COL1A2	collagen, type III, alpha 1	1281	1.791759	0.038	0.45412
202403_s_at	COL1A2	collagen, type III, alpha 1	1281	1.442683	0.043	0.45412
211719_x_at	FN1	fibronectin 1	2335	1.960598	0.0434	0.45412
216442_x_at	FN1	fibronectin 1	2335	1.658895	0.0472	0.45412
210495_x_at	FN1	fibronectin 1	2335	1.692178	0.0472	0.45412
211964_at	COL4A2	collagen, type IV, alpha 2	1284	1.078275	0.0537	0.46673
202310_s_at	COL1A1	collagen, type I, alpha 1	1277	1.496322	0.056	0.46673
217388_s_at	KYNU	kynureninase	8942	-1.22118	0.0727	0.47094
217232_x_at	HBB	hemoglobin, beta	3043	-1.35066	0.0734	0.47094
205547_s_at	TAGLN	transgelin	6876	1.275409	0.0758	0.47094
204848_x_at	HBG1 /// HBG2	hemoglobin, gamma A	3047	-1.4219	0.0773	0.47094
211980_at	COL4A1	collagen, type IV, alpha 1	1282	1.083935	0.082	0.47094
209116_x_at	HBB	hemoglobin, beta	3043	-1.47367	0.0876	0.47094
213515_x_at	HBG1 /// HBG2	hemoglobin, gamma A	3047	-1.72304	0.0895	0.47094
201842_s_at	EFEMP1	EGF containing fibulin-like extracellular matrix protein 1	2202	1.153114	0.09	0.47094
204897_at	PTGER4	prostaglandin E receptor 4 (subtype EP4)	5734	0.979697	0.0942	0.47094
209183_s_at	C10orf10	chromosome 10 open reading frame 10	11067	0.631696	0.0942	0.47094
204419_x_at	HBG1 /// HBG2	hemoglobin, gamma A	3047	-1.4151	0.1059	0.50908
211696_x_at	HBB	hemoglobin, beta	3043	-1.18995	0.112	0.51362
204141_at	TUBB2A	tubulin, beta 2A class IIa	7280	1.288228	0.116	0.51362
211699_x_at	HBA1 /// HBA2	hemoglobin, alpha 1	3039	-1.21697	0.1224	0.51362
209458_x_at	HBA1 /// HBA2	hemoglobin, alpha 1	3039	-1.38137	0.1306	0.51362

221760_at	MAN1A1	mannosidase, alpha, class 1A, member 1	4121	0.85605	0.1307	0.51362
204018_x_at	HBA1 /// HBA2	hemoglobin, alpha 1	3039	-1.23966	0.1315	0.51362
213350_at	RPS11	ribosomal protein S11	6205	0.933771	0.1365	0.51563
215772_x_at	SUCLG2	succinate-CoA ligase, GDP-forming, beta subunit	8801	-0.64738	0.1459	0.51563
217414_x_at	HBA1 /// HBA2	hemoglobin, alpha 1	3039	-1.27841	0.1498	0.51563
205382_s_at	CFD	complement factor D (adipsin)	1675	-0.8048	0.1571	0.51563
201890_at	RRM2	ribonucleotide reductase M2	6241	-0.95289	0.1584	0.51563
208960_s_at	KLF6	Kruppel-like factor 6	1316	0.571081	0.1595	0.51563
206157_at	PTX3	pentraxin 3, long	5806	0.825089	0.1609	0.51563
205237_at	FCN1	ficolin (collagen/fibrinogen domain containing) 1	2219	-1.15146	0.1702	0.51686
204834_at	FGL2	fibrinogen-like 2	10875	-0.90858	0.1719	0.51686
211745_x_at	HBA1 /// HBA2	hemoglobin, alpha 1	3039	-1.33507	0.1737	0.51686
209803_s_at	PHLDA2	pleckstrin homology-like domain, family A, member 2	7262	0.879169	0.18	0.52092
200629_at	WARS	tryptophanyl-tRNA synthetase	7453	-0.69785	0.184	0.52092
219602_s_at	PIEZO2	piezo-type mechanosensitive ion channel component 2	63895	-0.56733	0.1875	0.52092
205848_at	GAS2	growth arrest-specific 2	2620	-0.77375	0.1965	0.52799
210487_at	DNTT	deoxynucleotidyltransferase, terminal	1791	0.622562	0.1985	0.52799
214414_x_at	HBA1 /// HBA2	hemoglobin, alpha 1	3039	-1.40997	0.2155	0.56124
209374_s_at	IGHM	immunoglobulin heavy constant mu	3507	0.614952	0.2261	0.57678
201110_s_at	THBS1	thrombospondin 1	7057	0.617073	0.251	0.58604
220377_at	KIAA0125	KIAA0125	9834	0.553273	0.2511	0.58604
213524_s_at	G0S2	G0/G1switch 2	50486	-0.85706	0.2656	0.58604
204304_s_at	PROM1	prominin 1	8842	0.705885	0.27	0.58604
208961_s_at	KLF6	Kruppel-like factor 6	1316	0.50248	0.2729	0.58604
203787_at	SSBP2	single-stranded DNA binding protein 2	23635	0.483855	0.2743	0.58604
212952_at	LOC100507328	hypothetical LOC100507328	1E+08	0.637258	0.2765	0.58604
209763_at	CHRDL1	chordin-like 1	91851	0.393371	0.2787	0.58604
202600_s_at	NRIP1	nuclear receptor interacting protein 1	8204	0.586587	0.2792	0.58604
209290_s_at	NFIB	nuclear factor I/B	4781	-0.55308	0.2809	0.58604
214041_x_at	RPL37A	ribosomal protein L37a	6168	0.490226	0.2835	0.58604
202237_at	NNMT	nicotinamide N-methyltransferase	4837	0.748218	0.286	0.58604
211074_at	FOLR1	folate receptor 1 (adult)	2348	0.905935	0.3061	0.61707
204872_at	TLE4	transducin-like enhancer of split 4 (E(sp1) homolog,	7091	0.422998	0.3313	0.65741

		Drosophila)				
217683_at	HBE1	hemoglobin, epsilon 1	3046	-0.47414	0.3666	0.68713
205933_at	SETBP1	SET binding protein 1	26040	0.325978	0.3682	0.68713
204430_s_at	SLC2A5	solute carrier family 2 (facilitated glucose/fructose transporter), member 5	6518	0.430164	0.3789	0.68713
209894_at	LEPR	leptin receptor	3953	-0.51789	0.379	0.68713
221556_at	CDC14B	cell division cycle 14B	8555	0.488325	0.3791	0.68713
202870_s_at	CDC20	cell division cycle 20	991	-0.50504	0.3793	0.68713
204755_x_at	HLF	hepatic leukemia factor	3131	0.315735	0.4259	0.75009
209576_at	GNAI1	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1	2770	0.312521	0.4427	0.75009
204030_s_at	IQCJ-SCHIP1	IQCJ-SCHIP1 readthrough	1E+08	0.349599	0.4474	0.75009
213979_s_at	---	---	---	0.43757	0.4482	0.75009
203535_at	S100A9	S100 calcium binding protein A9	6280	-0.55271	0.4611	0.75009
216248_s_at	NR4A2	nuclear receptor subfamily 4, group A, member 2	4929	-0.44972	0.465	0.75009
211597_s_at	HOPX	HOP homeobox	84525	0.403732	0.4669	0.75009
204622_x_at	NR4A2	nuclear receptor subfamily 4, group A, member 2	4929	-0.37372	0.4687	0.75009
220990_s_at	MIR21	microRNA 21	406991	0.336172	0.4696	0.75009
213668_s_at	SOX4	SRY (sex determining region Y)-box 4	6659	0.449329	0.4741	0.75009
205984_at	CRHBP	corticotropin releasing hormone binding protein	1393	0.377363	0.5185	0.80784
209773_s_at	RRM2	ribonucleotide reductase M2	6241	-0.42832	0.5282	0.80784
201058_s_at	MYL9	myosin, light chain 9, regulatory	10398	0.492397	0.5381	0.80784
201631_s_at	IER3	immediate early response 3	8870	0.438819	0.5428	0.80784
219777_at	GIMAP6	GTPase, IMAP family member 6	474344	0.266496	0.5488	0.80784
212077_at	CALD1	caldesmon 1	800	0.443992	0.5493	0.80784
210873_x_at	APOBEC3A	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3A	200315	-0.3463	0.5991	0.8526
201669_s_at	MARCKS	myristoylated alanine-rich protein kinase C substrate	4082	-0.26494	0.6005	0.8526
206478_at	KIAA0125	KIAA0125	9834	0.32879	0.6097	0.8526
201666_at	TIMP1	TIMP metallopeptidase inhibitor 1	7076	0.267758	0.6197	0.8526
219304_s_at	PDGFD	platelet derived growth factor D	80310	0.204115	0.624	0.8526
212531_at	LCN2	lipocalin 2	3934	0.323764	0.6246	0.8526
212589_at	RRAS2	related RAS viral (r-ras) oncogene homolog 2	22800	-0.24032	0.63	0.8526
206698_at	XK	X-linked Kx blood group (McLeod syndrome)	7504	-0.27856	0.6343	0.8526

209069_s_at	H3F3B	H3 histone, family 3B (H3.3B)	3021	0.19436	0.6415	0.85308
213593_s_at	TRA2A	transformer 2 alpha homolog (Drosophila)	29896	0.256365	0.6504	0.85581
222044_at	PCIF1	PDX1 C-terminal inhibiting factor 1	63935	0.1951	0.6678	0.86141
201798_s_at	MYOF	myoferlin	26509	0.273459	0.6685	0.86141
201369_s_at	ZFP36L2	ZFP36 ring finger protein-like 2	678	0.230642	0.6846	0.86907
211998_at	H3F3B	H3 histone, family 3B (H3.3B)	3021	0.193469	0.6932	0.86907
214974_x_at	CXCL5	chemokine (C-X-C motif) ligand 5	6374	-0.26165	0.6953	0.86907
200999_s_at	CKAP4	cytoskeleton-associated protein 4	10970	0.213798	0.709	0.87669
208180_s_at	HIST1H4H	histone cluster 1, H4h	8365	0.215184	0.7256	0.87669
214651_s_at	HOXA9	homeobox A9	3205	0.201432	0.7276	0.87669
204563_at	SELL	selectin L	6402	0.218847	0.7294	0.87669
74694_s_at	RABEP2	rabaptin, RAB GTPase binding effector protein 2	79874	0.156251	0.7423	0.8796
209112_at	CDKN1B	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	1027	-0.16341	0.7463	0.8796
220416_at	ATP8B4	ATPase, class I, type 8B, member 4	79895	0.16502	0.7529	0.8796
1405_i_at	CCL5	chemokine (C-C motif) ligand 5	6352	-0.25823	0.7902	0.89548
201195_s_at	SLC7A5	solute carrier family 7 (amino acid transporter light chain, L system), member 5	8140	-0.13019	0.7977	0.89548
205442_at	MFAP3L	microfibrillar-associated protein 3-like	9848	0.165446	0.7982	0.89548
214911_s_at	BRD2	bromodomain containing 2	6046	0.126061	0.8026	0.89548
203395_s_at	HES1	hairy and enhancer of split 1, (Drosophila)	3280	-0.15322	0.8083	0.89548
213757_at	EIF5A	eukaryotic translation initiation factor 5A	1984	0.139559	0.8106	0.89548
204655_at	CCL5	chemokine (C-C motif) ligand 5	6352	-0.23378	0.8167	0.89548
208892_s_at	DUSP6	dual specificity phosphatase 6	1848	0.125339	0.8394	0.91234
214805_at	EIF4A1	eukaryotic translation initiation factor 4A1	1973	0.086848	0.8471	0.91278
208835_s_at	LUC7L3	LUC7-like 3 (S. cerevisiae)	51747	0.092821	0.8544	0.91281
205114_s_at	CCL3 /// CCL3L1 /// CCL3L3	chemokine (C-C motif) ligand 3-like 3	414062	0.116024	0.8826	0.93496
219922_s_at	LTBP3	latent transforming growth factor beta binding protein 3	4054	-0.06412	0.8939	0.93622
207815_at	PF4V1	platelet factor 4 variant 1	5197	-0.10475	0.8988	0.93622
208949_s_at	LGALS3	lectin, galactoside-binding, soluble, 3	3958	-0.06541	0.9175	0.94106
203394_s_at	HES1	hairy and enhancer of split 1, (Drosophila)	3280	-0.06134	0.9229	0.94106
204753_s_at	HLF	hepatic leukemia factor	3131	0.037675	0.933	0.94106

219410_at	TMEM45A	transmembrane protein 45A	55076	0.044462	0.9335	0.94106
219403_s_at	HPSE	heparanase	10855	-0.01752	0.9787	0.97868

Table S5a. Genes differentially regulated by the 12 PV patients with an indolent phenotype.

ProbesetID	*Symbol (Na32 consesus Mar13)*	*Gene Title (Na32 consensus Mar13)*	*Entrez GeneID (concensus Mar-13)*	*Log2(FC)*	*P-Value*	*Adjusted P-Value*
208949_s_at	LGALS3	lectin, galactoside-binding, soluble, 3	3958	-2.46116	4.71E-07	0.000871
202284_s_at	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	1026	-1.98698	2.11E-06	0.002134
201059_at	CTTN	cortactin	2017	-2.72585	6.06E-06	0.002867
211458_s_at	GABARAPL1	GABA(A) receptor-associated protein like 1	23710	-1.79927	1.03E-05	0.003369
210592_s_at	SAT1	spermidine/spermine N1-acetyltransferase 1	6303	-1.22693	1.17E-05	0.003384
201666_at	TIMP1	TIMP metallopeptidase inhibitor 1	7076	-1.63942	2.35E-05	0.004281
203045_at	NINJ1	ninjurin 1	4814	-1.5136	2.55E-05	0.004462
203455_s_at	SAT1	spermidine/spermine N1-acetyltransferase 1	6303	-1.25184	2.78E-05	0.004519
202912_at	ADM	adrenomedullin	133	-1.55855	3.02E-05	0.004672
201058_s_at	MYL9	myosin, light chain 9, regulatory	10398	-2.74637	3.07E-05	0.004672
207815_at	PF4V1	platelet factor 4 variant 1	5197	-2.82239	5.35E-05	0.005828
1405_i_at	CCL5	chemokine (C-C motif) ligand 5	6352	-3.32637	5.85E-05	0.006036
214211_at	FTH1	ferritin, heavy polypeptide 1	2495	-1.47129	8.74E-05	0.006826
201422_at	IFI30	interferon, gamma-inducible protein 30	10437	-2.1056	0.000104	0.00745
210845_s_at	PLAUR	plasminogen activator, urokinase receptor	5329	-1.48981	0.000116	0.007613
214020_x_at	ITGB5	integrin, beta 5	3693	-1.08903	0.000121	0.007815
204115_at	GNG11	guanine nucleotide binding protein (G protein), gamma 11	2791	-2.43614	0.000123	0.007906
213524_s_at	G0S2	G0/G1switch 2	50486	-2.65615	0.000126	0.007998
201125_s_at	ITGB5	integrin, beta 5	3693	-1.67473	0.000134	0.008224
209154_at	TAX1BP3	Tax1 (human T-cell leukemia virus type I) binding protein 3	30851	-1.71214	0.000155	0.008862
201631_s_at	IER3	immediate early response 3	8870	-2.29781	0.000169	0.009257
213988_s_at	SAT1	spermidine/spermine N1-acetyltransferase 1	6303	-1.26095	0.000171	0.009309
200871_s_at	PSAP	prosaposin	5660	-1.0306	0.000195	0.009761
200661_at	CTSA	cathepsin A	5476	-1.96591	0.000218	0.010227
204440_at	CD83	CD83 molecule	9308	-1.34989	0.000228	0.010503

214073_at	CTTN	cortactin	2017	-2.15431	0.000231	0.010534
204655_at	CCL5	chemokine (C-C motif) ligand 5	6352	-3.23424	0.000234	0.010534
219622_at	RAB20	RAB20, member RAS oncogene family	55647	-1.10241	0.000283	0.011722
204546_at	KIAA0513	KIAA0513	9764	-1.19275	0.000321	0.012541
209304_x_at	GADD45B	growth arrest and DNA-damage-inducible, beta	4616	-1.51931	0.000364	0.013369
203535_at	S100A9	S100 calcium binding protein A9	6280	-2.4352	0.00037	0.013372
210075_at	MARCH2	membrane-associated ring finger (C3HC4) 2, E3 ubiquitin protein ligase	51257	-1.72415	0.00043	0.014432
213716_s_at	SECTM1	secreted and transmembrane 1	6398	-1.05168	0.000482	0.015364
209398_at	HIST1H1C	histone cluster 1, H1c	3006	-1.53845	0.000487	0.015374
214246_x_at	MINK1	misshapen-like kinase 1	50488	-1.16871	0.000487	0.015374
204482_at	CLDN5	claudin 5	7122	-1.62602	0.000494	0.015531
206110_at	HIST1H3H	histone cluster 1, H3h	8357	-2.52014	0.000496	0.015566
200736_s_at	GPX1	glutathione peroxidase 1	2876	-1.14943	0.000508	0.015789
31874_at	GAS2L1	growth arrest-specific 2 like 1	10634	-1.87076	0.00052	0.016031
217764_s_at	RAB31	RAB31, member RAS oncogene family	11031	-2.01066	0.000564	0.016422
AFFX-HUMISGF3A/M97935_MA_at	STAT1	signal transducer and activator of transcription 1, 91kDa	6772	-1.37938	0.000621	0.016996
212501_at	CEBPB	CCAAT/enhancer binding protein (C/EBP), beta	1051	-1.54731	0.000671	0.017573
212077_at	CALD1	caldesmon 1	800	-2.04255	0.000688	0.017825
201108_s_at	THBS1	thrombospondin 1	7057	-2.12731	0.000718	0.018258
212647_at	RRAS	related RAS viral (r-ras) oncogene homolog	6237	-1.08906	0.000785	0.019036
205463_s_at	PDGFA	platelet-derived growth factor alpha polypeptide	5154	-1.5857	0.000872	0.020261
202083_s_at	SEC14L1	SEC14-like 1 (S. cerevisiae)	6397	-1.38339	0.000926	0.020823
221211_s_at	MAP3K7CL	MAP3K7 C-terminal like	56911	-1.90471	0.000937	0.020912
221059_s_at	COTL1	coactosin-like 1 (Dictyostelium)	23406	-1.53392	0.000965	0.021237
201743_at	CD14	CD14 molecule	929	-2.10963	0.00106	0.022456
218999_at	TMEM140	transmembrane protein 140	55281	-1.58682	0.001078	0.022646
218032_at	SNN	stannin	8303	-1.79738	0.001083	0.022694
201739_at	SGK1	serum/glucocorticoid regulated kinase 1	6446	-2.23217	0.001109	0.02284
203234_at	UPP1	uridine phosphorylase 1	7378	-1.24029	0.001155	0.023122
215071_s_at	HIST1H2AC	histone cluster 1, H2ac	8334	-2.0219	0.001169	0.02321
202497_x_at	SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	6515	-1.11253	0.001169	0.02321

207574_s_at	GADD45B	growth arrest and DNA-damage-inducible, beta	4616	-1.91282	0.001288	0.024289
AFFX-HUMISGF3A/M97935_MB_at	STAT1	signal transducer and activator of transcription 1, 91kDa	6772	-1.22837	0.001313	0.024575
203414_at	MMD	monocyte to macrophage differentiation-associated	23531	-1.96502	0.001341	0.024732
204081_at	NRGN	neurogranin (protein kinase C substrate, RC3)	4900	-2.55869	0.001354	0.024788
212242_at	TUBA4A	tubulin, alpha 4a	7277	-1.98963	0.001384	0.025003
211600_at	PTPRO	protein tyrosine phosphatase, receptor type, O	5800	-1.25519	0.001385	0.025003
211252_x_at	PTCRA	pre T-cell antigen receptor alpha	171558	-1.20925	0.001454	0.025618
210357_s_at	SMOX	spermine oxidase	54498	-1.0824	0.00148	0.025958
214696_at	MIR22HG	MIR22 host gene (non-protein coding)	84981	-1.24889	0.001532	0.026408
201506_at	TGFBI	transforming growth factor, beta-induced, 68kDa	7045	-1.47238	0.001571	0.026812
215464_s_at	TAX1BP3	Tax1 (human T-cell leukemia virus type I) binding protein 3	30851	-1.19481	0.001588	0.026937
203585_at	ZNF185	zinc finger protein 185 (LIM domain)	7739	-1.63846	0.001619	0.027302
214752_x_at	FLNA	filamin A, alpha	2316	-1.19726	0.001669	0.027658
216261_at	ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	3690	-1.42557	0.001715	0.028036
209729_at	GAS2L1	growth arrest-specific 2 like 1	10634	-1.29217	0.001761	0.02833
217763_s_at	RAB31	RAB31, member RAS oncogene family	11031	-1.57464	0.001927	0.029492
201565_s_at	ID2	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	3398	-2.05847	0.001931	0.029494
202499_s_at	SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	6515	-1.76034	0.001995	0.030069
200859_x_at	FLNA	filamin A, alpha	2316	-1.14829	0.001998	0.030073
214054_at	DOK2	docking protein 2, 56kDa	9046	-1.44762	0.002111	0.030716
209959_at	NR4A3	nuclear receptor subfamily 4, group A, member 3	8013	-1.06248	0.002113	0.030716
222043_at	CLU	clusterin	1191	-1.24582	0.002133	0.030796
204057_at	IRF8	interferon regulatory factor 8	3394	-1.20508	0.002179	0.031039
210873_x_at	APOBEC3A	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3A	200315	-1.7692	0.002336	0.032102
204794_at	DUSP2	dual specificity phosphatase 2	1844	-1.69252	0.002377	0.032376
204232_at	FCER1G	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide	2207	-1.80094	0.002409	0.032561
208792_s_at	CLU	clusterin	1191	-1.89367	0.002436	0.032794
207414_s_at	PCSK6	proprotein convertase subtilisin/kexin type 6	5046	-1.66589	0.00258	0.034033
202295_s_at	CTSH	cathepsin H	1512	-1.47757	0.002604	0.034228
208078_s_at	SIK1	salt-inducible kinase 1	150094	-1.38923	0.002612	0.034234

204446_s_at	ALOX5	arachidonate 5-lipoxygenase	240	-1.78576	0.002664	0.034597
205863_at	S100A12	S100 calcium binding protein A12	6283	-1.44064	0.002691	0.034786
212531_at	LCN2	lipocalin 2	3934	-1.74945	0.002916	0.036334
204698_at	ISG20	interferon stimulated exonuclease gene 20kDa	3669	-1.01523	0.003089	0.037574
213338_at	TMEM158	transmembrane protein 158 (gene/pseudogene)	25907	-1.19059	0.00326	0.038684
215492_x_at	PTCRA	pre T-cell antigen receptor alpha	171558	-1.15689	0.003318	0.038883
204838_s_at	MLH3	mutL homolog 3 (E. coli)	27030	-1.4825	0.00334	0.039
336_at	TBXA2R	thromboxane A2 receptor	6915	-1.13899	0.003359	0.039168
203140_at	BCL6	B-cell CLL/lymphoma 6	604	-1.30948	0.003569	0.040549
220751_s_at	FAXDC2	fatty acid hydroxylase domain containing 2	10826	-1.36	0.003658	0.041081
205495_s_at	GNLY	granulysin	10578	-1.10567	0.003705	0.041271
200660_at	S100A11	S100 calcium binding protein A11	6282	-1.62087	0.003733	0.041423
211429_s_at	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	5265	-1.9862	0.003781	0.041543
202917_s_at	S100A8	S100 calcium binding protein A8	6279	-2.98812	0.003874	0.041998
205114_s_at	CCL3L3	chemokine (C-C motif) ligand 3-like 3	414062	-2.11268	0.003894	0.041998
212509_s_at	MXRA7	matrix-remodelling associated 7	439921	-1.13262	0.003902	0.042016
204627_s_at	ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	3690	-2.30401	0.003953	0.042268
203922_s_at	CYBB	cytochrome b-245, beta polypeptide	1536	-1.0925	0.004058	0.043079
208180_s_at	HIST1H4H	histone cluster 1, H4h	8365	-1.58615	0.004083	0.043185
205237_at	FCN1	ficolin (collagen/fibrinogen domain containing) 1	2219	-2.31794	0.004143	0.043449
204628_s_at	ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	3690	-1.63546	0.004208	0.043687
201810_s_at	SH3BP5	SH3-domain binding protein 5 (BTK-associated)	9467	-1.35593	0.004294	0.044285
204621_s_at	NR4A2	nuclear receptor subfamily 4, group A, member 2	4929	-1.13205	0.004407	0.044874
214414_x_at	HBA1	hemoglobin, alpha 1	3039	-2.92562	0.004429	0.044949
203305_at	F13A1	coagulation factor XIII, A1 polypeptide	2162	-2.17585	0.004493	0.045292
209803_s_at	PHLDA2	pleckstrin homology-like domain, family A, member 2	7262	-1.71861	0.00466	0.046283
208161_s_at	ABCC3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	8714	-1.21045	0.004758	0.046709
208406_s_at	GRAP2	GRB2-related adaptor protein 2	9402	-1.26529	0.004845	0.047046
209806_at	HIST1H2BK	histone cluster 1, H2bk	85236	-1.21587	0.004905	0.047465
217028_at	CXCR4	chemokine (C-X-C motif) receptor 4	7852	-1.25222	0.005221	0.04911
218454_at	PLBD1	phospholipase B domain containing 1	79887	-1.3316	0.005298	0.049397
202833_s_at	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	5265	-1.72053	0.005347	0.049661

205220_at	HCAR3	hydroxycarboxylic acid receptor 3	8843	-1.11127	0.005534	0.050489
201438_at	COL6A3	collagen, type VI, alpha 3	1293	-1.45596	0.005536	0.050489
221731_x_at	VCAN	versican	1462	-2.02316	0.005573	0.050668
201360_at	CST3	cystatin C	1471	-1.47347	0.005761	0.051649
AFFX-HUMISGF3A/M97935_5_at	STAT1	signal transducer and activator of transcription 1, 91kDa	6772	-1.22821	0.005786	0.051736
204858_s_at	TYMP	thymidine phosphorylase	1890	-1.19053	0.005857	0.052078
205547_s_at	TAGLN	transgelin	6876	-1.89687	0.006205	0.053812
208791_at	CLU	clusterin	1191	-1.6535	0.006231	0.053824
209383_at	DDIT3	DNA-damage-inducible transcript 3	1649	-1.19919	0.00626	0.053842
217022_s_at	IGH	immunoglobulin heavy locus	3492	-1.26043	0.006498	0.054967
201280_s_at	DAB2	Dab, mitogen-responsive phosphoprotein, homolog 2 (Drosophila)	1601	-1.35685	0.006817	0.056659
AFFX-DapX-M_at	---	---		-1.10207	0.007018	0.057621
211074_at	FOLR1	folate receptor 1 (adult)	2348	-2.335	0.007106	0.057921
221556_at	CDC14B	cell division cycle 14B	8555	-1.35463	0.007226	0.058222
212723_at	JMJD6	jumonji domain containing 6	23210	-1.10344	0.007325	0.058511
211745_x_at	HBA1	hemoglobin, alpha 1	3039	-2.39195	0.007372	0.058683
204141_at	TUBB2A	tubulin, beta 2A class IIa	7280	-2.1393	0.007748	0.060237
208579_x_at	H2BFS	H2B histone family, member S (pseudogene)	54145	-1.4314	0.008655	0.063919
203973_s_at	CEBPD	CCAAT/enhancer binding protein (C/EBP), delta	1052	-1.24524	0.008766	0.064315
201170_s_at	BHLHE40	basic helix-loop-helix family, member e40	8553	-1.48301	0.008896	0.064843
205119_s_at	FPR1	formyl peptide receptor 1	2357	-1.27582	0.009081	0.065557
204961_s_at	NCF1	neutrophil cytosolic factor 1	653361	-1.3618	0.009093	0.06559
201616_s_at	CALD1	caldesmon 1	800	-1.10576	0.009118	0.065687
204018_x_at	HBA1	hemoglobin, alpha 1	3039	-1.98013	0.009214	0.066107
213539_at	CD3D	CD3d molecule, delta (CD3-TCR complex)	915	-1.04108	0.009761	0.067714
202388_at	RGS2	regulator of G-protein signaling 2, 24kDa	5997	-1.46404	0.009794	0.06779
201798_s_at	MYOF	myoferlin	26509	-1.51466	0.009894	0.068217
203708_at	PDE4B	phosphodiesterase 4B, cAMP-specific	5142	-1.38481	0.01	0.068731
214084_x_at	NCF1C	neutrophil cytosolic factor 1C pseudogene	654817	-1.39567	0.010409	0.070394
209458_x_at	HBA1	hemoglobin, alpha 1	3039	-2.13257	0.010802	0.071832
217762_s_at	RAB31	RAB31, member RAS oncogene family	11031	-1.34439	0.010983	0.072433
208022_s_at	CDC14B	cell division cycle 14B	8555	-1.06029	0.011035	0.072627

204790_at	SMAD7	SMAD family member 7	4092	-1.18892	0.011176	0.072876
217414_x_at	HBA1	hemoglobin, alpha 1	3039	-2.04967	0.011779	0.075213
204480_s_at	C9orf16	chromosome 9 open reading frame 16	79095	-1.0583	0.01178	0.075213
204908_s_at	BCL3	B-cell CLL/lymphoma 3	602	-1.12158	0.011802	0.075244
206883_x_at	GP9	glycoprotein IX (platelet)	2815	-1.39492	0.012283	0.076763
211964_at	COL4A2	collagen, type IV, alpha 2	1284	-1.30407	0.012296	0.076763
AFFX-HUMGAPDH/M33197_5_at	GAPDH	glyceraldehyde-3-phosphate dehydrogenase	2597	-1.07979	0.012327	0.076822
202887_s_at	DDIT4	DNA-damage-inducible transcript 4	54541	-1.42927	0.012333	0.076822
AFFX-HUMGAPDH/M33197_M_at	GAPDH	glyceraldehyde-3-phosphate dehydrogenase	2597	-1.25641	0.012335	0.076822
204588_s_at	SLC7A7	solute carrier family 7 (amino acid transporter light chain, y+L system), member 7	9056	-1.19903	0.012402	0.077024
206655_s_at	GP1BB	glycoprotein Ib (platelet), beta polypeptide	2812	-2.09441	0.0128	0.078521
221841_s_at	KLF4	Kruppel-like factor 4 (gut)	9314	-1.65198	0.012861	0.078835
212657_s_at	IL1RN	interleukin 1 receptor antagonist	3557	-1.14627	0.013221	0.080181
204620_s_at	VCAN	versican	1462	-1.51568	0.013307	0.080358
205442_at	MFAP3L	microfibrillar-associated protein 3-like	9848	-1.52051	0.013437	0.080854
200665_s_at	SPARC	secreted protein, acidic, cysteine-rich (osteonectin)	6678	-1.75861	0.01347	0.080865
204396_s_at	GRK5	G protein-coupled receptor kinase 5	2869	-1.28375	0.013822	0.082085
202207_at	ARL4C	ADP-ribosylation factor-like 4C	10123	-1.06368	0.014043	0.082963
AFFX-HSAC07/X00351_3_at	ACTB	actin, beta	60	-1.37822	0.014382	0.0839
214974_x_at	CXCL5	chemokine (C-X-C motif) ligand 5	6374	-1.55942	0.014408	0.083963
213275_x_at	CTSB	cathepsin B	1508	-1.09109	0.014496	0.084285
214677_x_at	CYAT1	immunoglobulin lambda light chain-like	100290481	-1.19702	0.014517	0.084316
218559_s_at	MAFB	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	9935	-1.60023	0.014906	0.085665
208527_x_at	HIST1H2BE	histone cluster 1, H2be	8344	-1.0534	0.015738	0.08838
202310_s_at	COL1A1	collagen, type I, alpha 1	1277	-1.87619	0.016831	0.091891
208601_s_at	TUBB1	tubulin, beta 1 class VI	81027	-1.17222	0.017934	0.095324
219403_s_at	HPSE	heparanase	10855	-1.31934	0.018497	0.096806
200622_x_at	CALM3	calmodulin 3 (phosphorylase kinase, delta)	808	-1.04785	0.018549	0.096942
212667_at	SPARC	secreted protein, acidic, cysteine-rich (osteonectin)	6678	-1.34731	0.018812	0.097654
209949_at	NCF2	neutrophil cytosolic factor 2	4688	-1.34905	0.01953	0.099726
204122_at	TYROBP	TYRO protein tyrosine kinase binding protein	7305	-1.58727	0.019681	0.100052

201811_x_at	SH3BP5	SH3-domain binding protein 5 (BTK-associated)	9467	-1.02097	0.020101	0.101165
214469_at	HIST1H2AE	histone cluster 1, H2ae	3012	-1.04742	0.020232	0.101492
200999_s_at	CKAP4	cytoskeleton-associated protein 4	10970	-1.1494	0.020405	0.101743
204319_s_at	RGS10	regulator of G-protein signaling 10	6001	-1.05791	0.020642	0.102328
37966_at	PARVB	parvin, beta	29780	-1.18316	0.020871	0.102995
AFFX-HUMISGF3A/M97935_3_at	STAT1	signal transducer and activator of transcription 1, 91kDa	6772	-1.13562	0.022192	0.106109
208546_x_at	HIST1H2BH	histone cluster 1, H2bh	8345	-1.03067	0.022452	0.106776
204834_at	FGL2	fibrinogen-like 2	10875	-1.4682	0.022775	0.107256
216442_x_at	FN1	fibronectin 1	2335	-1.90726	0.023141	0.108166
204103_at	CCL4	chemokine (C-C motif) ligand 4	6351	-1.0683	0.02465	0.111906
221269_s_at	SH3BGRL3	SH3 domain binding glutamic acid-rich protein like 3	83442	-1.17357	0.024677	0.111906
201842_s_at	EFEMP1	EGF containing fibulin-like extracellular matrix protein 1	2202	-1.50062	0.024795	0.112138
208450_at	LGALS2	lectin, galactoside-binding, soluble, 2	3957	-1.55709	0.025744	0.114214
212464_s_at	FN1	fibronectin 1	2335	-1.96353	0.025831	0.114387
204971_at	CSTA	cystatin A (stefin A)	1475	-1.4559	0.026275	0.115382
211719_x_at	FN1	fibronectin 1	2335	-2.20582	0.026796	0.116477
210495_x_at	FN1	fibronectin 1	2335	-1.90768	0.026965	0.116845
216248_s_at	NR4A2	nuclear receptor subfamily 4, group A, member 2	4929	-1.17499	0.028238	0.119726
204912_at	IL10RA	interleukin 10 receptor, alpha	3587	-1.05258	0.02903	0.121428
211699_x_at	HBA1	hemoglobin, alpha 1	3039	-1.60002	0.029162	0.121623
AFFX-HSAC07/X00351_5_at	ACTB	actin, beta	60	-1.04373	0.029941	0.123368
218280_x_at	HIST2H2AA4	histone cluster 2, H2aa4	723790	-1.035	0.029948	0.123368
215240_at	ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	3690	-1.18589	0.030708	0.124841
219630_at	PDZK1IP1	PDZK1 interacting protein 1	10158	-1.16143	0.031505	0.126922
56256_at	SIDT2	SID1 transmembrane family, member 2	51092	-1.06356	0.03192	0.127917
214146_s_at	PPBP	pro-platelet basic protein (chemokine (C-X-C motif) ligand 7)	5473	-2.2804	0.032189	0.128506
217683_at	HBE1	hemoglobin, epsilon 1	3046	-1.01632	0.03275	0.12959
202627_s_at	SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	5054	-1.24155	0.035257	0.134957
218223_s_at	PLEKHO1	pleckstrin homology domain containing, family O member 1	51177	-1.02949	0.035417	0.13521
203394_s_at	HES1	hairy and enhancer of split 1, (Drosophila)	3280	-1.19137	0.036252	0.137146
214511_x_at	FCGR1B	Fc fragment of IgG, high affinity Ib, receptor (CD64)	2210	-1.00332	0.036916	0.1385

211980_at	COL4A1	collagen, type IV, alpha 1	1282	-1.2568	0.037235	0.139094
215076_s_at	COL3A1	collagen, type III, alpha 1	1281	-1.43307	0.038584	0.141774
218723_s_at	RGCC	regulator of cell cycle	28984	-1.35285	0.038884	0.142295
201465_s_at	JUN	jun proto-oncogene	3725	-1.23554	0.039397	0.143388
206493_at	ITGA2B	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41)	3674	-1.40259	0.040966	0.146453
209651_at	TGFB1I1	transforming growth factor beta 1 induced transcript 1	7041	-1.18925	0.043241	0.150602
202403_s_at	COL1A2	collagen, type I, alpha 2	1278	-1.44055	0.046503	0.156448
213975_s_at	LYZ	lysozyme	4069	-1.35445	0.046533	0.156457
202391_at	BASP1	brain abundant, membrane attached signal protein 1	10409	-1.21789	0.050925	0.164058
200897_s_at	PALLD	palladin, cytoskeletal associated protein	23022	-1.19733	0.054484	0.169794
207206_s_at	ALOX12	arachidonate 12-lipoxygenase	239	-1.13633	0.054626	0.170045
202404_s_at	COL1A2	collagen, type I, alpha 2	1278	-1.71166	0.056539	0.173313
210809_s_at	POSTN	periostin, osteoblast specific factor	10631	-1.70047	0.059219	0.177986
217572_at	---	---		-1.0617	0.061496	0.181515
204351_at	S100P	S100 calcium binding protein P	6286	-1.10416	0.061934	0.182039
202953_at	C1QB	complement component 1, q subcomponent, B chain	713	-1.04337	0.061996	0.182121
36711_at	MAFF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	23764	-2.07111	0.062874	0.183657
214290_s_at	HIST2H2AA4	histone cluster 2, H2aa4	723790	-1.00017	0.063196	0.184141
220496_at	CLEC1B	C-type lectin domain family 1, member B	51266	-1.26133	0.068125	0.192398
202628_s_at	SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	5054	-1.0038	0.068895	0.193543
201852_x_at	COL3A1	collagen, type III, alpha 1	1281	-1.06074	0.069846	0.19499
209210_s_at	FERMT2	fermitin family member 2	10979	-1.18848	0.071118	0.197
208937_s_at	ID1	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	3397	-1.06464	0.076912	0.204982
202644_s_at	TNFAIP3	tumor necrosis factor, alpha-induced protein 3	7128	-1.11193	0.077731	0.206126
202555_s_at	MYLK	myosin light chain kinase	4638	-1.20646	0.078352	0.206861
207808_s_at	PROS1	protein S (alpha)	5627	-1.05757	0.080762	0.210082
202237_at	NNMT	nicotinamide N-methyltransferase	4837	-1.16906	0.084988	0.216541
204959_at	MNDA	myeloid cell nuclear differentiation antigen	4332	-1.11553	0.099265	0.237052
206390_x_at	PF4	platelet factor 4	5196	-1.56272	0.105914	0.246063
207076_s_at	ASS1	argininosuccinate synthase 1	445	-1.01934	0.110808	0.252682
206494_s_at	ITGA2B	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa	3674	-1.21162	0.118492	0.262217

		complex, antigen CD41)				
207140_at	ALPI	alkaline phosphatase, intestinal	248	-1.14253	0.12301	0.267727
216834_at	RGS1	regulator of G-protein signaling 1	5996	-1.34806	0.15206	0.303847
202988_s_at	RGS1	regulator of G-protein signaling 1	5996	-1.08916	0.188906	0.346892
213515_x_at	HBG1	hemoglobin, gamma A	3047	-1.06377	0.246664	0.407885
212671_s_at	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1	3117	1.097239	0.126891	0.272796
211734_s_at	FCER1A	Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide	2205	1.009251	0.078698	0.207233
210982_s_at	HLA-DRA	major histocompatibility complex, class II, DR alpha	3122	1.194665	0.07091	0.196595
202016_at	MEST	mesoderm specific transcript	4232	1.10616	0.05007	0.162642
209773_s_at	RRM2	ribonucleotide reductase M2	6241	1.272153	0.049561	0.161602
202946_s_at	BTBD3	BTB (POZ) domain containing 3	22903	1.045621	0.04313	0.150497
208894_at	HLA-DRA	major histocompatibility complex, class II, DR alpha	3122	1.34853	0.028179	0.119545
213376_at	ZBTB1	zinc finger and BTB domain containing 1	22890	1.088786	0.026552	0.116003
206310_at	SPINK2	serine peptidase inhibitor, Kazal type 2 (acrosin-trypsin inhibitor)	6691	1.055612	0.024944	0.112515
203817_at	GUCY1B3	guanylate cyclase 1, soluble, beta 3	2983	1.163996	0.024688	0.111906
209392_at	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2	5168	1.030545	0.023369	0.108718
216640_s_at	PDIA6	protein disulfide isomerase family A, member 6	10130	1.19128	0.020388	0.10174
212588_at	PTPRC	protein tyrosine phosphatase, receptor type, C	5788	1.226601	0.019819	0.100488
209894_at	LEPR	leptin receptor	3953	1.184929	0.018148	0.09595
218039_at	NUSAP1	nucleolar and spindle associated protein 1	51203	1.157405	0.017634	0.094469
213129_s_at	GCSHP5	glycine cleavage system protein H pseudogene 5	100329108	1.10714	0.01585	0.088615
201577_at	NME1	NME/NM23 nucleoside diphosphate kinase 1	4830	1.034901	0.015518	0.087753
214741_at	ZNF131	zinc finger protein 131	7690	1.072298	0.015265	0.086843
212498_at	---	---		1.007129	0.014477	0.084233
200953_s_at	CCND2	cyclin D2	894	1.083456	0.014299	0.083701
207668_x_at	PDIA6	protein disulfide isomerase family A, member 6	10130	1.075588	0.014187	0.083288
208639_x_at	PDIA6	protein disulfide isomerase family A, member 6	10130	1.148925	0.013925	0.082576
212749_s_at	RCHY1	ring finger and CHY zinc finger domain containing 1, E3 ubiquitin protein ligase	25898	1.154346	0.013753	0.081884
213599_at	OIP5	Opa interacting protein 5	11339	1.034915	0.013279	0.080287
218477_at	TMEM14A	transmembrane protein 14A	28978	1.038055	0.01243	0.077084
209160_at	AKR1C3	aldo-keto reductase family 1, member C3	8644	1.050868	0.012306	0.076764

207165_at	HMMR	hyaluronan-mediated motility receptor (RHAMM)	3161	1.12524	0.012278	0.076763
200750_s_at	RAN	RAN, member RAS oncogene family	5901	1.196145	0.012173	0.076447
200853_at	H2AFZ	H2A histone family, member Z	3015	1.133212	0.012107	0.076162
211762_s_at	KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	3838	1.122517	0.011697	0.074903
202591_s_at	SSBP1	single-stranded DNA binding protein 1, mitochondrial	6742	1.079587	0.011546	0.074317
212224_at	ALDH1A1	aldehyde dehydrogenase 1 family, member A1	216	1.532805	0.011256	0.073081
202157_s_at	CELF2	CUGBP, Elav-like family member 2	10659	1.345852	0.011153	0.072851
201018_at	EIF1AX	eukaryotic translation initiation factor 1A, X-linked	1964	1.07069	0.011072	0.072653
214359_s_at	HSP90AB1	heat shock protein 90kDa alpha (cytosolic), class B member 1	3326	1.611725	0.010493	0.070756
202266_at	TDP2	tyrosyl-DNA phosphodiesterase 2	51567	1.168396	0.009941	0.068453
204023_at	RFC4	replication factor C (activator 1) 4, 37kDa	5984	1.161476	0.009896	0.068217
208852_s_at	CANX	calnexin	821	1.147782	0.009836	0.067995
208990_s_at	HNRNPH3	heterogeneous nuclear ribonucleoprotein H3 (2H9)	3189	1.022691	0.009773	0.067735
201193_at	IDH1	isocitrate dehydrogenase 1 (NADP+), soluble	3417	1.109705	0.009675	0.067345
204444_at	KIF11	kinesin family member 11	3832	1.052307	0.009568	0.06712
202899_s_at	SRSF3	serine/arginine-rich splicing factor 3	6428	1.121111	0.009554	0.067103
206834_at	HBD	hemoglobin, delta	3045	1.603183	0.009504	0.066927
213241_at	PLXNC1	plexin C1	10154	1.098497	0.009355	0.066441
208783_s_at	CD46	CD46 molecule, complement regulatory protein	4179	1.009037	0.009253	0.066184
204905_s_at	EEF1E1	eukaryotic translation elongation factor 1 epsilon 1	9521	1.018486	0.009203	0.06606
203755_at	BUB1B	BUB1 mitotic checkpoint serine/threonine kinase B	701	1.106693	0.009061	0.065504
201462_at	SCRN1	secernin 1	9805	1.089176	0.008825	0.064512
207238_s_at	PTPRC	protein tyrosine phosphatase, receptor type, C	5788	1.002292	0.00794	0.060948
202469_s_at	CPSF6	cleavage and polyadenylation specific factor 6, 68kDa	11052	1.017757	0.007655	0.05992
218350_s_at	GMNN	geminin, DNA replication inhibitor	51053	1.289682	0.007592	0.059577
201653_at	CNIH	cornichon homolog (Drosophila)	10175	1.024747	0.007566	0.059412
210759_s_at	PSMA1	proteasome (prosome, macropain) subunit, alpha type, 1	5682	1.025107	0.007534	0.05925
218984_at	PUS7	pseudouridylate synthase 7 homolog (S. cerevisiae)	54517	1.092719	0.007372	0.058683
213541_s_at	ERG	v-ets erythroblastosis virus E26 oncogene homolog (avian)	2078	1.268671	0.007213	0.058222
214214_s_at	C1QBP	complement component 1, q subcomponent binding protein	708	1.081512	0.006939	0.057298
218883_s_at	MLF1IP	MLF1 interacting protein	79682	1.002951	0.006546	0.05522
204798_at	MYB	v-myb myeloblastosis viral oncogene homolog (avian)	4602	1.33907	0.006372	0.054414

214710_s_at	CCNB1	cyclin B1	891	1.30622	0.006365	0.05438
200892_s_at	TRA2B	transformer 2 beta homolog (Drosophila)	6434	1.059953	0.006225	0.053824
201084_s_at	BCLAF1	BCL2-associated transcription factor 1	9774	1.042614	0.006038	0.053075
219306_at	KIF15	kinesin family member 15	56992	1.005174	0.005933	0.052485
209180_at	RABGGTB	Rab geranylgeranyltransferase, beta subunit	5876	1.030791	0.00587	0.05217
201829_at	NET1	neuroepithelial cell transforming 1	10276	1.16411	0.005759	0.051649
213047_x_at	SET	SET nuclear oncogene	6418	1.072575	0.005512	0.05039
201241_at	DDX1	DEAD (Asp-Glu-Ala-Asp) box helicase 1	1653	1.20415	0.005509	0.05039
209728_at	HLA-DRB4	major histocompatibility complex, class II, DR beta 4	3126	2.396871	0.005479	0.050353
201890_at	RRM2	ribonucleotide reductase M2	6241	1.743456	0.005295	0.049397
201477_s_at	RRM1	ribonucleotide reductase M1	6240	1.259059	0.005293	0.049397
200728_at	ACTR2	ARP2 actin-related protein 2 homolog (yeast)	10097	1.079756	0.005255	0.049248
212250_at	MTDH	metadherin	92140	1.112188	0.005254	0.049248
200996_at	ACTR3	ARP3 actin-related protein 3 homolog (yeast)	10096	1.167525	0.005078	0.048328
203405_at	PSMG1	proteasome (prosome, macropain) assembly chaperone 1	8624	1.002781	0.005039	0.048111
200877_at	CCT4	chaperonin containing TCP1, subunit 4 (delta)	10575	1.134112	0.004843	0.047046
210438_x_at	TROVE2	TROVE domain family, member 2	6738	1.075252	0.004643	0.046201
201417_at	SOX4	SRY (sex determining region Y)-box 4	6659	1.240673	0.004546	0.045582
201014_s_at	PAICS	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	10606	1.325476	0.004523	0.045413
200064_at	HSP90AB1	heat shock protein 90kDa alpha (cytosolic), class B member 1	3326	1.128671	0.004413	0.044877
202268_s_at	NAE1	NEDD8 activating enzyme E1 subunit 1	8883	1.117633	0.004311	0.044378
211137_s_at	ATP2C1	ATPase, Ca++ transporting, type 2C, member 1	27032	1.024207	0.004133	0.04339
218694_at	ARMCX1	armadillo repeat containing, X-linked 1	51309	1.240431	0.004091	0.043202
201676_x_at	PSMA1	proteasome (prosome, macropain) subunit, alpha type, 1	5682	1.034639	0.00406	0.043079
217987_at	ASNSD1	asparagine synthetase domain containing 1	54529	1.242982	0.004059	0.043079
219563_at	LINC00341	long intergenic non-protein coding RNA 341	79686	1.115324	0.004051	0.043037
201240_s_at	LOC653566	signal peptidase complex subunit 2 homolog (S. cerevisiae) pseudogene	653566	1.053758	0.004022	0.042778
204146_at	RAD51AP1	RAD51 associated protein 1	10635	1.156331	0.004016	0.042729
209757_s_at	MYCN	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	4613	1.210293	0.003996	0.042614
209095_at	DLD	dihydrolipoamide dehydrogenase	1738	1.319642	0.003935	0.042191

211971_s_at	LRPPRC	leucine-rich pentatricopeptide repeat containing	10128	1.113512	0.003889	0.041998
211746_x_at	PSMA1	proteasome (prosome, macropain) subunit, alpha type, 1	5682	1.018568	0.003854	0.041914
200052_s_at	ILF2	interleukin enhancer binding factor 2	3608	1.0667	0.003851	0.041914
212640_at	PTPLB	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b	201562	1.131425	0.003826	0.041838
200774_at	FAM120A	family with sequence similarity 120A	23196	1.114974	0.003738	0.04145
209318_x_at	PLAGL1	pleiomorphic adenoma gene-like 1	5325	1.23893	0.003682	0.04125
201180_s_at	GNAI3	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3	2773	1.037392	0.003621	0.040838
215933_s_at	HHEX	hematopoietically expressed homeobox	3087	1.279779	0.003597	0.040702
200807_s_at	HSPD1	heat shock 60kDa protein 1 (chaperonin)	3329	1.015247	0.00358	0.040641
202539_s_at	HMGCR	3-hydroxy-3-methylglutaryl-CoA reductase	3156	1.103166	0.003517	0.040158
200072_s_at	HNRNPM	heterogeneous nuclear ribonucleoprotein M	4670	1.402849	0.00349	0.040028
204373_s_at	CEP350	centrosomal protein 350kDa	9857	1.185706	0.003481	0.040028
203209_at	RFC5	replication factor C (activator 1) 5, 36.5kDa	5985	1.113492	0.00338	0.039333
211935_at	ARL6IP1	ADP-ribosylation factor-like 6 interacting protein 1	23204	1.159268	0.003341	0.039
203566_s_at	AGL	amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase	178	1.046125	0.003305	0.038871
201549_x_at	KDM5B	lysine (K)-specific demethylase 5B	10765	1.065448	0.003285	0.038786
208029_s_at	LAPTM4B	lysosomal protein transmembrane 4 beta	55353	1.253963	0.003231	0.038501
218585_s_at	DTL	denticleless E3 ubiquitin protein ligase homolog (Drosophila)	51514	1.350603	0.003194	0.03822
212893_at	ZZZ3	zinc finger, ZZ-type containing 3	26009	1.08034	0.003179	0.038151
215440_s_at	BEX4	brain expressed, X-linked 4	56271	1.274266	0.00308	0.037537
200020_at	TARDBP	TAR DNA binding protein	23435	1.100346	0.002966	0.036705
213293_s_at	TRIM22	tripartite motif containing 22	10346	1.403817	0.00295	0.036579
205612_at	MMRN1	multimerin 1	22915	1.21464	0.002937	0.036484
201930_at	MCM6	minichromosome maintenance complex component 6	4175	1.051838	0.002935	0.036484
208910_s_at	C1QBP	complement component 1, q subcomponent binding protein	708	1.40182	0.00291	0.036295
218870_at	ARHGAP15	Rho GTPase activating protein 15	55843	1.442188	0.002874	0.036047
204236_at	FLI1	Friend leukemia virus integration 1	2313	1.290793	0.002863	0.036016
211784_s_at	SRSF1	serine/arginine-rich splicing factor 1	6426	1.027483	0.002853	0.035922
212215_at	PREPL	prolyl endopeptidase-like	9581	1.016567	0.002832	0.03582
201713_s_at	RANBP2	RAN binding protein 2	5903	1.15906	0.002829	0.035812
201589_at	SMC1A	structural maintenance of chromosomes 1A	8243	1.429532	0.002826	0.035794

201327_s_at	CCT6A	chaperonin containing TCP1, subunit 6A (zeta 1)	908	1.110939	0.002792	0.035561
214949_at	---	---		1.096897	0.002708	0.034908
213222_at	PLCB1	phospholipase C, beta 1 (phosphoinositide-specific)	23236	1.045277	0.002634	0.03437
205051_s_at	KIT	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	3815	1.349599	0.002631	0.034353
201652_at	COPS5	COP9 constitutive photomorphogenic homolog subunit 5 (Arabidopsis)	10987	1.133169	0.002622	0.034334
208767_s_at	LAPTM4B	lysosomal protein transmembrane 4 beta	55353	1.125608	0.002597	0.034178
204026_s_at	ZWINT	ZW10 interactor, kinetochore protein	11130	1.36409	0.002574	0.033989
211615_s_at	LRPPRC	leucine-rich pentatricopeptide repeat containing	10128	1.077666	0.002524	0.03353
206332_s_at	IFI16	interferon, gamma-inducible protein 16	3428	1.04713	0.002479	0.033114
213605_s_at	---	---		1.301604	0.002445	0.032816
219054_at	NPR3	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)	4883	1.079574	0.002372	0.032376
212867_at	NCOA2	nuclear receptor coactivator 2	10499	1.169646	0.002371	0.032376
208828_at	POLE3	polymerase (DNA directed), epsilon 3, accessory subunit	54107	1.189315	0.002289	0.031795
204127_at	RFC3	replication factor C (activator 1) 3, 38kDa	5983	1.217624	0.002267	0.031632
202599_s_at	NRIP1	nuclear receptor interacting protein 1	8204	1.485341	0.002258	0.03152
212557_at	ZNF451	zinc finger protein 451	26036	1.087217	0.002254	0.031489
210766_s_at	CSE1L	CSE1 chromosome segregation 1-like (yeast)	1434	1.038634	0.002233	0.031297
211922_s_at	CAT	catalase	847	1.262699	0.002221	0.031297
205345_at	BARD1	BRCA1 associated RING domain 1	580	1.097185	0.002218	0.031297
201197_at	AMD1	adenosylmethionine decarboxylase 1	262	1.147451	0.002213	0.031264
204689_at	HHEX	hematopoietically expressed homeobox	3087	1.069023	0.002165	0.030957
201624_at	DARS	aspartyl-tRNA synthetase	1615	1.026982	0.002159	0.030955
212766_s_at	ISG20L2	interferon stimulated exonuclease gene 20kDa-like 2	81875	1.137911	0.002146	0.030863
201112_s_at	CSE1L	CSE1 chromosome segregation 1-like (yeast)	1434	1.11844	0.002142	0.030838
212038_s_at	VDAC1	voltage-dependent anion channel 1	7416	1.422303	0.002135	0.030796
211953_s_at	IPO5	importin 5	3843	1.242501	0.002132	0.030796
212612_at	RCOR1	REST corepressor 1	23186	1.102759	0.002126	0.030796
218715_at	UTP6	UTP6, small subunit (SSU) processome component, homolog (yeast)	55813	1.287375	0.002119	0.030758
217957_at	C16orf80	chromosome 16 open reading frame 80	29105	1.235392	0.002104	0.030707
208666_s_at	ST13	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)	6767	1.060002	0.00206	0.030421

201054_at	HNRNPA0	heterogeneous nuclear ribonucleoprotein A0	10949	1.042824	0.002053	0.030384
208863_s_at	SRSF1	serine/arginine-rich splicing factor 1	6426	1.155243	0.002024	0.03021
221942_s_at	GUCY1A3	guanylate cyclase 1, soluble, alpha 3	2982	1.274671	0.002022	0.030194
203380_x_at	SRSF5	serine/arginine-rich splicing factor 5	6430	1.094125	0.002013	0.030181
204439_at	IFI44L	interferon-induced protein 44-like	10964	1.917025	0.002005	0.030152
202119_s_at	CPNE3	copine III	8895	1.240924	0.001996	0.030069
202491_s_at	IKBKAP	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein	8518	1.162396	0.001995	0.030069
200816_s_at	PAFAH1B1	platelet-activating factor acetylhydrolase 1b, regulatory subunit 1 (45kDa)	5048	1.041005	0.001981	0.029948
203011_at	IMPA1	inositol(myo)-1(or 4)-monophosphatase 1	3612	1.283329	0.001971	0.029877
202613_at	CTPS1	CTP synthase 1	1503	1.114581	0.001955	0.0297
206937_at	SPTA1	spectrin, alpha, erythrocytic 1 (elliptocytosis 2)	6708	1.151575	0.001936	0.029531
212037_at	PNN	pinin, desmosome associated protein	5411	1.494883	0.001917	0.029474
206052_s_at	SLBP	stem-loop binding protein	7884	1.082828	0.001906	0.029434
201013_s_at	PAICS	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	10606	1.121467	0.00186	0.029062
209642_at	BUB1	BUB1 mitotic checkpoint serine/threonine kinase	699	1.034101	0.001808	0.028585
210425_x_at	GOLGA8B	golgin A8 family, member B	440270	1.211965	0.001808	0.028585
209861_s_at	METAP2	methionyl aminopeptidase 2	10988	1.173435	0.001784	0.0285
221547_at	PRPF18	PRP18 pre-mRNA processing factor 18 homolog (S. cerevisiae)	8559	1.010609	0.001784	0.0285
203138_at	HAT1	histone acetyltransferase 1	8520	1.697742	0.001772	0.028447
209630_s_at	FBXW2	F-box and WD repeat domain containing 2	26190	1.00777	0.001755	0.028286
201330_at	RARS	arginyl-tRNA synthetase	5917	1.048926	0.001753	0.028265
211727_s_at	COX11	cytochrome c oxidase assembly homolog 11 (yeast)	1353	1.104041	0.001747	0.028216
212287_at	SUZ12	suppressor of zeste 12 homolog (Drosophila)	23512	1.060589	0.001742	0.028189
208802_at	SRP72	signal recognition particle 72kDa	6731	1.080033	0.001713	0.028028
200978_at	MDH1	malate dehydrogenase 1, NAD (soluble)	4190	1.102564	0.001677	0.027682
203373_at	SOCS2	suppressor of cytokine signaling 2	8835	1.193044	0.001676	0.027682
218263_s_at	ZBED5	zinc finger, BED-type containing 5	58486	1.068226	0.001674	0.027682
202303_x_at	SMARCA5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	8467	1.013631	0.001653	0.02757
201472_at	VBP1	von Hippel-Lindau binding protein 1	7411	1.093136	0.001639	0.027452

212825_at	PAXIP1	PAX interacting (with transcription-activation domain) protein 1	22976	1.152279	0.001534	0.026427
217993_s_at	MAT2B	methionine adenosyltransferase II, beta	27430	1.083589	0.001528	0.02639
202113_s_at	SNX2	sorting nexin 2	6643	1.270036	0.001506	0.02616
209330_s_at	HNRNPD	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	3184	1.161084	0.001504	0.02616
206958_s_at	UPF3A	UPF3 regulator of nonsense transcripts homolog A (yeast)	65110	1.374126	0.001456	0.025618
201478_s_at	DKC1	dyskeratosis congenita 1, dyskerin	1736	1.420645	0.00145	0.025591
210260_s_at	TNFAIP8	tumor necrosis factor, alpha-induced protein 8	25816	1.079476	0.001424	0.025305
205394_at	CHEK1	checkpoint kinase 1	1111	1.025967	0.001414	0.025236
208966_x_at	IFI16	interferon, gamma-inducible protein 16	3428	1.261519	0.001413	0.025236
202227_s_at	BRD8	bromodomain containing 8	10902	1.211398	0.001397	0.025152
202983_at	HLTF	helicase-like transcription factor	6596	1.292442	0.001395	0.025148
218966_at	MYO5C	myosin VC	55930	1.153543	0.001385	0.025003
208787_at	MRPL3	mitochondrial ribosomal protein L3	11222	1.176304	0.001376	0.02497
203427_at	ASF1A	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	25842	1.059991	0.001373	0.02497
201260_s_at	SYPL1	synaptophysin-like 1	6856	1.204425	0.001372	0.02497
212652_s_at	SNX4	sorting nexin 4	8723	1.052201	0.001368	0.024963
217850_at	GNL3	guanine nucleotide binding protein-like 3 (nucleolar)	26354	1.41406	0.00135	0.024754
212435_at	TRIM33	tripartite motif containing 33	51592	1.036739	0.001348	0.024743
210983_s_at	MCM7	minichromosome maintenance complex component 7	4176	1.380913	0.001341	0.024732
204510_at	CDC7	cell division cycle 7	8317	1.373466	0.001299	0.024412
201970_s_at	NASP	nuclear autoantigenic sperm protein (histone-binding)	4678	1.246396	0.00128	0.024202
214043_at	PTPRD	protein tyrosine phosphatase, receptor type, D	5789	1.253071	0.001271	0.02415
209572_s_at	EED	embryonic ectoderm development	8726	1.058266	0.00127	0.02415
202890_at	MAP7	microtubule-associated protein 7	9053	1.299804	0.001265	0.02408
201129_at	SRSF7	serine/arginine-rich splicing factor 7	6432	1.119633	0.001254	0.023956
201699_at	PSMC6	proteasome (prosome, macropain) 26S subunit, ATPase, 6	5706	1.503145	0.00122	0.023629
212266_s_at	SRSF5	serine/arginine-rich splicing factor 5	6430	1.41576	0.001217	0.023629
206544_x_at	SMARCA2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	6595	1.067396	0.001209	0.023601
209049_s_at	ZMYND8	zinc finger, MYND-type containing 8	23613	1.006778	0.001203	0.023563
213313_at	RABGAP1	RAB GTPase activating protein 1	23637	1.398753	0.001197	0.0235
222204_s_at	RRN3	RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae)	54700	1.07798	0.001196	0.0235

203362_s_at	MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)	4085	1.334952	0.001171	0.02321
221264_s_at	TARDBP	TAR DNA binding protein	23435	1.148261	0.00117	0.02321
204009_s_at	KRAS	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	3845	1.15051	0.001169	0.02321
213416_at	ITGA4	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)	3676	1.585393	0.00116	0.023183
200993_at	IPO7	importin 7	10527	1.052977	0.001144	0.023074
202911_at	MSH6	mutS homolog 6 (E. coli)	2956	1.406267	0.00114	0.023016
201619_at	PRDX3	peroxiredoxin 3	10935	1.166794	0.001136	0.02301
203743_s_at	TDG	thymine-DNA glycosylase	6996	1.30963	0.00113	0.022997
212199_at	MRFAP1L1	Morf4 family associated protein 1-like 1	114932	1.630757	0.001123	0.022952
202164_s_at	CNOT8	CCR4-NOT transcription complex, subunit 8	9337	1.199704	0.001118	0.022906
204809_at	CLPX	ClpX caseinolytic peptidase X homolog (E. coli)	10845	1.04299	0.001099	0.02276
206542_s_at	SMARCA2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	6595	1.42069	0.001047	0.022288
203948_s_at	MPO	myeloperoxidase	4353	1.629289	0.001047	0.022288
200927_s_at	RAB14	RAB14, member RAS oncogene family	51552	1.113603	0.001045	0.022285
205961_s_at	PSIP1	PC4 and SFRS1 interacting protein 1	11168	1.119456	0.001035	0.022115
203139_at	DAPK1	death-associated protein kinase 1	1612	1.135088	0.001004	0.021669
219485_s_at	PSMD10	proteasome (prosome, macropain) 26S subunit, non-ATPase, 10	5716	1.237831	0.000994	0.021584
202169_s_at	AASDHPPT	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	60496	1.491517	0.000983	0.021447
213761_at	MDM1	Mdm1 nuclear protein homolog (mouse)	56890	1.12881	0.000976	0.02135
212544_at	ZNHIT3	zinc finger, HIT-type containing 3	9326	1.294137	0.000971	0.0213
201368_at	ZFP36L2	ZFP36 ring finger protein-like 2	678	1.289879	0.000961	0.021237
218882_s_at	WDR3	WD repeat domain 3	10885	1.059399	0.000955	0.021168
202431_s_at	MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	4609	1.493528	0.000946	0.02101
217828_at	SLTM	SAFB-like, transcription modulator	79811	1.118355	0.000938	0.020912
201111_at	CSE1L	CSE1 chromosome segregation 1-like (yeast)	1434	1.623491	0.000932	0.020833
203474_at	IQGAP2	IQ motif containing GTPase activating protein 2	10788	1.614975	0.000922	0.020814
217906_at	KLHDC2	kelch domain containing 2	23588	1.142864	0.00092	0.020814
203531_at	CUL5	cullin 5	8065	1.096581	0.000891	0.020435
202746_at	ITM2A	integral membrane protein 2A	9452	1.664011	0.000885	0.020363
209421_at	MSH2	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)	4436	1.490121	0.00088	0.020343

213698_at	ZMYM6NB	ZMYM6 neighbor	100506144	1.042591	0.00087	0.020236
218605_at	TFB2M	transcription factor B2, mitochondrial	64216	1.183958	0.000854	0.02007
201947_s_at	CCT2	chaperonin containing TCP1, subunit 2 (beta)	10576	1.143067	0.000853	0.02007
202602_s_at	HTATSF1	HIV-1 Tat specific factor 1	27336	1.187599	0.000849	0.020015
202930_s_at	SUCLA2	succinate-CoA ligase, ADP-forming, beta subunit	8803	1.176902	0.000838	0.019818
201277_s_at	HNRNPAB	heterogeneous nuclear ribonucleoprotein A/B	3182	1.014906	0.000822	0.019567
208798_x_at	GOLGA8A	golgin A8 family, member A	23015	1.082102	0.000821	0.019567
202413_s_at	USP1	ubiquitin specific peptidase 1	7398	1.360578	0.000801	0.01926
201742_x_at	SRSF1	serine/arginine-rich splicing factor 1	6426	1.198562	0.000799	0.01924
218014_at	NUP85	nucleoporin 85kDa	79902	1.180004	0.000796	0.019229
204240_s_at	SMC2	structural maintenance of chromosomes 2	10592	1.406601	0.000787	0.01907
209337_at	PSIP1	PC4 and SFRS1 interacting protein 1	11168	1.241851	0.000784	0.019026
201273_s_at	SRP9	signal recognition particle 9kDa	6726	1.202073	0.000784	0.019026
222303_at	---	---		1.254922	0.000781	0.019002
212330_at	TFDP1	transcription factor Dp-1	7027	1.341814	0.00078	0.019002
203432_at	TMPO	thymopoietin	7112	1.068195	0.000768	0.01881
203493_s_at	CEP57	centrosomal protein 57kDa	9702	1.03691	0.000766	0.018788
202330_s_at	UNG	uracil-DNA glycosylase	7374	1.326002	0.000761	0.018729
209814_at	ZNF330	zinc finger protein 330	27309	1.444996	0.000758	0.018729
203560_at	GGH	gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase)	8836	1.446967	0.00075	0.018617
209112_at	CDKN1B	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	1027	1.181993	0.000749	0.018617
35974_at	LRMP	lymphoid-restricted membrane protein	4033	1.001783	0.000732	0.018537
208643_s_at	XRCC5	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining)	7520	1.057033	0.000731	0.018525
214651_s_at	HOXA9	homeobox A9	3205	1.466349	0.000687	0.017825
204767_s_at	FEN1	flap structure-specific endonuclease 1	2237	1.47296	0.000685	0.017799
202658_at	PEX11B	peroxisomal biogenesis factor 11 beta	8799	1.013624	0.000684	0.017799
218989_x_at	SLC30A5	solute carrier family 30 (zinc transporter), member 5	64924	1.011398	0.000683	0.017799
212740_at	PIK3R4	phosphoinositide-3-kinase, regulatory subunit 4	30849	1.016978	0.000678	0.017687
212378_at	GART	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase	2618	1.210756	0.000671	0.017573
221931_s_at	SEH1L	SEH1-like (S. cerevisiae)	81929	1.151366	0.000671	0.017573

201830_s_at	NET1	neuroepithelial cell transforming 1	10276	1.193353	0.000654	0.017314
202174_s_at	PCM1	pericentriolar material 1	5108	1.195075	0.000641	0.017181
202717_s_at	CDC16	cell division cycle 16	8881	1.000687	0.000632	0.017087
204720_s_at	DNAJC6	DnaJ (Hsp40) homolog, subfamily C, member 6	9829	1.165169	0.00063	0.017071
202503_s_at	KIAA0101	KIAA0101	9768	1.410664	0.000627	0.01707
212513_s_at	USP33	ubiquitin specific peptidase 33	23032	1.349055	0.000623	0.01703
203583_at	UNC50	unc-50 homolog (C. elegans)	25972	1.021413	0.000607	0.016773
209199_s_at	MEF2C	myocyte enhancer factor 2C	4208	1.384786	0.000605	0.016755
203949_at	MPO	myeloperoxidase	4353	2.09466	0.0006	0.016728
213088_s_at	DNAJC9	DnaJ (Hsp40) homolog, subfamily C, member 9	23234	1.165365	0.0006	0.016728
201873_s_at	ABCE1	ATP-binding cassette, sub-family E (OABP), member 1	6059	1.123959	0.000598	0.016728
201518_at	CBX1	chromobox homolog 1	10951	1.118253	0.000591	0.016699
221771_s_at	MPHOSPH8	M-phase phosphoprotein 8	54737	1.003732	0.000588	0.016642
218236_s_at	PRKD3	protein kinase D3	23683	1.039419	0.00058	0.016542
218979_at	RMI1	RMI1, RecQ mediated genome instability 1, homolog (S. cerevisiae)	80010	1.012559	0.000577	0.016542
201532_at	PSMA3	proteasome (prosome, macropain) subunit, alpha type, 3	5684	1.445319	0.000575	0.016531
212653_s_at	EHBP1	EH domain binding protein 1	23301	1.032735	0.000566	0.016422
210338_s_at	HSPA8	heat shock 70kDa protein 8	3312	1.574514	0.000564	0.016422
218642_s_at	CHCHD7	coiled-coil-helix-coiled-coil-helix domain containing 7	79145	1.029917	0.000561	0.016422
221970_s_at	NOL11	nucleolar protein 11	25926	1.054307	0.00056	0.016422
202741_at	PRKACB	protein kinase, cAMP-dependent, catalytic, beta	5567	1.048386	0.000557	0.016422
209905_at	HOXA9	homeobox A9	3205	1.24736	0.000554	0.016422
202589_at	TYMS	thymidylate synthetase	7298	1.65426	0.000548	0.01628
200071_at	SMNDC1	survival motor neuron domain containing 1	10285	1.034914	0.000544	0.016265
201303_at	EIF4A3	eukaryotic translation initiation factor 4A3	9775	1.17097	0.000539	0.016206
205632_s_at	PIP5K1B	phosphatidylinositol-4-phosphate 5-kinase, type I, beta	8395	1.175229	0.000533	0.016113
215380_s_at	GGCT	gamma-glutamylcyclotransferase	79017	1.189841	0.000531	0.016099
203765_at	GCA	grancalcin, EF-hand calcium binding protein	25801	1.046003	0.00053	0.016099
220865_s_at	PDSS1	prenyl (decaprenyl) diphosphate synthase, subunit 1	23590	1.074485	0.000525	0.016054
202446_s_at	PLSCR1	phospholipid scramblase 1	5359	1.327281	0.000524	0.01605
200970_s_at	SERP1	stress-associated endoplasmic reticulum protein 1	27230	1.075633	0.000512	0.015879
216920_s_at	TARP	TCR gamma alternate reading frame protein	445347	1.485156	0.000485	0.015374
212693_at	MDN1	MDN1, midasin homolog (yeast)	23195	1.087501	0.000484	0.015374

213359_at	HNRNPD	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	3184	1.09076	0.000478	0.015321
206102_at	GINS1	GINS complex subunit 1 (Psf1 homolog)	9837	1.575105	0.000474	0.015221
202950_at	CRYZ	crystallin, zeta (quinone reductase)	1429	1.315997	0.000472	0.015221
202395_at	NSF	N-ethylmaleimide-sensitive factor	4905	1.021689	0.000471	0.015221
220615_s_at	FAR2	fatty acyl CoA reductase 2	55711	1.050613	0.000469	0.015212
211700_s_at	TRO	trophinin	7216	1.068948	0.000465	0.015212
206095_s_at	SRSF10	serine/arginine-rich splicing factor 10	10772	1.179453	0.000464	0.015212
208694_at	PRKDC	protein kinase, DNA-activated, catalytic polypeptide	5591	1.097773	0.000458	0.015075
214141_x_at	SRSF7	serine/arginine-rich splicing factor 7	6432	1.331333	0.000439	0.014608
203517_at	MTX2	metaxin 2	10651	1.225852	0.000439	0.014608
205857_at	SLC18A2	solute carrier family 18 (vesicular monoamine), member 2	6571	1.065076	0.000431	0.014432
203856_at	VRK1	vaccinia related kinase 1	7443	1.237886	0.00043	0.014432
203372_s_at	SOCS2	suppressor of cytokine signaling 2	8835	1.09312	0.00042	0.014308
221652_s_at	ASUN	asunder, spermatogenesis regulator	55726	1.363988	0.000412	0.014181
212690_at	DDHD2	DDHD domain containing 2	23259	1.236377	0.000412	0.014181
208808_s_at	HMGB2	high mobility group box 2	3148	1.445021	0.000402	0.014069
212896_at	SKIV2L2	superkiller viralicidic activity 2-like 2 (S. cerevisiae)	23517	1.098253	0.000395	0.013905
221622_s_at	TMEM126B	transmembrane protein 126B	55863	1.103945	0.000394	0.013871
218303_x_at	KRCC1	lysine-rich coiled-coil 1	51315	1.054683	0.000393	0.013857
201479_at	DKC1	dyskeratosis congenita 1, dyskerin	1736	1.261576	0.00039	0.013806
203156_at	AKAP11	A kinase (PRKA) anchor protein 11	11215	1.181561	0.000384	0.013683
201756_at	RPA2	replication protein A2, 32kDa	6118	1.039715	0.000379	0.013533
209903_s_at	ATR	ataxia telangiectasia and Rad3 related	545	1.074716	0.000376	0.013488
206976_s_at	HSPH1	heat shock 105kDa/110kDa protein 1	10808	1.254331	0.000376	0.013488
219454_at	EGFL6	EGF-like-domain, multiple 6	25975	1.30877	0.000367	0.013369
211144_x_at	TARP	TCR gamma alternate reading frame protein	445347	1.365625	0.000366	0.013369
205133_s_at	HSPE1	heat shock 10kDa protein 1 (chaperonin 10)	3336	1.081382	0.000365	0.013369
202429_s_at	PPP3CA	protein phosphatase 3, catalytic subunit, alpha isozyme	5530	1.056462	0.000363	0.013369
210038_at	PRKCQ	protein kinase C, theta	5588	1.046788	0.000358	0.013295
205668_at	LY75	lymphocyte antigen 75	4065	1.075449	0.000357	0.013295
201515_s_at	TSN	translin	7247	1.30897	0.000349	0.01317
221825_at	ANGEL2	angel homolog 2 (Drosophila)	90806	1.010739	0.000347	0.013115
212168_at	RBM12	RNA binding motif protein 12	10137	1.209363	0.000346	0.013115

201555_at	MCM3	minichromosome maintenance complex component 3	4172	1.057831	0.000343	0.013089
208766_s_at	HNRNPR	heterogeneous nuclear ribonucleoprotein R	10236	1.04567	0.000341	0.013032
213294_at	EIF2AK2	eukaryotic translation initiation factor 2-alpha kinase 2	5610	1.224521	0.000339	0.012995
217956_s_at	ENOPH1	enolase-phosphatase 1	58478	1.13057	0.000325	0.012646
212211_at	ANKRD17	ankyrin repeat domain 17	26057	1.06166	0.000321	0.012541
218396_at	VPS13C	vacuolar protein sorting 13 homolog C (S. cerevisiae)	54832	1.169643	0.000315	0.012391
202020_s_at	LANCL1	LanC lantibiotic synthetase component C-like 1 (bacterial)	10314	1.265915	0.000314	0.012374
213304_at	FAM179B	family with sequence similarity 179, member B	23116	1.05681	0.000311	0.01229
214093_s_at	FUBP1	far upstream element (FUSE) binding protein 1	8880	1.19343	0.000311	0.01229
221761_at	ADSS	adenylosuccinate synthase	159	1.010834	0.000308	0.012252
201386_s_at	DHX15	DEAH (Asp-Glu-Ala-His) box polypeptide 15	1665	1.650845	0.000306	0.012244
221505_at	ANP32E	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	81611	1.183054	0.000303	0.012139
218127_at	NFYB	nuclear transcription factor Y, beta	4801	1.104339	0.00029	0.011904
219303_at	RNF219	ring finger protein 219	79596	1.119496	0.000279	0.011636
218133_s_at	NIF3L1	NIF3 NGG1 interacting factor 3-like 1 (S. cerevisiae)	60491	1.192936	0.000269	0.011358
203428_s_at	ASF1A	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	25842	1.128273	0.000268	0.011351
219037_at	RRP15	ribosomal RNA processing 15 homolog (S. cerevisiae)	51018	1.057006	0.000267	0.011351
218889_at	NOC3L	nucleolar complex associated 3 homolog (S. cerevisiae)	64318	1.366019	0.000262	0.011306
201413_at	HSD17B4	hydroxysteroid (17-beta) dehydrogenase 4	3295	1.140766	0.000255	0.011131
212526_at	SPG20	spastic paraplegia 20 (Troyer syndrome)	23111	1.026783	0.000251	0.01101
208021_s_at	RFC1	replication factor C (activator 1) 1, 145kDa	5981	1.039138	0.00025	0.010974
213253_at	SMC2	structural maintenance of chromosomes 2	10592	1.034612	0.000246	0.010839
218713_at	NARG2	NMDA receptor regulated 2	79664	1.010022	0.000244	0.010824
209092_s_at	GLOD4	glyoxalase domain containing 4	51031	1.452265	0.000233	0.010534
208634_s_at	MACF1	microtubule-actin crosslinking factor 1	23499	1.053724	0.000229	0.010503
202854_at	HPRT1	hypoxanthine phosphoribosyltransferase 1	3251	1.377438	0.000227	0.010458
202345_s_at	FABP5	fatty acid binding protein 5 (psoriasis-associated)	2171	1.412774	0.000223	0.010332
217832_at	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	10492	1.449861	0.000222	0.010305
220742_s_at	NGLY1	N-glycanase 1	55768	1.055086	0.00022	0.010287
202318_s_at	SENP6	SUMO1/sentrin specific peptidase 6	26054	1.021802	0.000214	0.010126
202892_at	CDC23	cell division cycle 23	8697	1.142138	0.000212	0.010103
201964_at	SETX	senataxin	23064	1.253372	0.000211	0.010103

209056_s_at	CDC5L	cell division cycle 5-like	988	1.214199	0.000208	0.010028
214047_s_at	MBD4	methyl-CpG binding domain protein 4	8930	1.011612	0.000208	0.010028
201603_at	PPP1R12A	protein phosphatase 1, regulatory subunit 12A	4659	1.089584	0.000204	0.00993
208716_s_at	TMCO1	transmembrane and coiled-coil domains 1	54499	1.113356	0.000202	0.009867
218710_at	TTC27	tetratricopeptide repeat domain 27	55622	1.090229	0.000201	0.009867
216221_s_at	PUM2	pumilio homolog 2 (Drosophila)	23369	1.105518	0.000201	0.009867
202107_s_at	MCM2	minichromosome maintenance complex component 2	4171	1.506995	0.000201	0.009867
214453_s_at	IFI44	interferon-induced protein 44	10561	1.719005	0.0002	0.009867
208775_at	XPO1	exportin 1 (CRM1 homolog, yeast)	7514	1.473631	0.000198	0.009851
211929_at	HNRNPA3	heterogeneous nuclear ribonucleoprotein A3	220988	1.257569	0.000198	0.009839
212406_s_at	PCMTD2	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2	55251	1.452466	0.000196	0.009776
204354_at	POT1	protection of telomeres 1	25913	1.126965	0.000194	0.009746
218323_at	RHOT1	ras homolog family member T1	55288	1.007825	0.000186	0.009582
200994_at	IPO7	importin 7	10527	1.001576	0.000186	0.009582
201773_at	ADNP	activity-dependent neuroprotector homeobox	23394	1.388566	0.000183	0.009532
202060_at	CTR9	Ctr9, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	9646	1.453326	0.00018	0.00945
209218_at	SQLE	squalene epoxidase	6713	1.758399	0.000177	0.009364
209580_s_at	MBD4	methyl-CpG binding domain protein 4	8930	1.160508	0.000174	0.009336
202633_at	TOPBP1	topoisomerase (DNA) II binding protein 1	11073	1.197566	0.000173	0.009336
213106_at	ATP8A1	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	10396	1.20933	0.000168	0.009246
212058_at	U2SURP	U2 snRNP-associated SURP domain containing	23350	1.398897	0.000168	0.009246
212408_at	TOR1AIP1	torsin A interacting protein 1	26092	1.153349	0.000163	0.009063
203067_at	PDHX	pyruvate dehydrogenase complex, component X	8050	1.024437	0.00016	0.009007
202184_s_at	NUP133	nucleoporin 133kDa	55746	1.163427	0.000156	0.008893
204749_at	NAP1L3	nucleosome assembly protein 1-like 3	4675	1.756608	0.000149	0.008702
212621_at	TMEM194A	transmembrane protein 194A	23306	1.117235	0.000148	0.008702
200723_s_at	CAPRIN1	cell cycle associated protein 1	4076	1.360735	0.000145	0.008669
219008_at	C2orf43	chromosome 2 open reading frame 43	60526	1.160627	0.000144	0.008657
202220_at	KIAA0907	KIAA0907	22889	1.542705	0.000144	0.008657
211987_at	TOP2B	topoisomerase (DNA) II beta 180kDa	7155	1.023919	0.000143	0.008633
202441_at	ERLIN1	ER lipid raft associated 1	10613	1.221226	0.000141	0.008533

218171_at	VPS4B	vacuolar protein sorting 4 homolog B (S. cerevisiae)	9525	1.099892	0.000138	0.008402
209974_s_at	BUB3	BUB3 mitotic checkpoint protein	9184	1.177194	0.000136	0.008296
219412_at	RAB38	RAB38, member RAS oncogene family	23682	1.455958	0.000133	0.008144
205474_at	CRLF3	cytokine receptor-like factor 3	51379	1.012784	0.000132	0.008144
222201_s_at	CASP8AP2	caspase 8 associated protein 2	9994	1.164562	0.00013	0.008097
208838_at	CAND1	cullin-associated and neddylation-dissociated 1	55832	1.071114	0.000128	0.007998
204521_at	FAM216A	family with sequence similarity 216, member A	29902	1.272748	0.000124	0.007921
213506_at	F2RL1	coagulation factor II (thrombin) receptor-like 1	2150	1.465639	0.000123	0.007906
214988_s_at	SON	SON DNA binding protein	6651	1.293714	0.00012	0.007803
218005_at	ZNF22	zinc finger protein 22	7570	1.363822	0.000117	0.007673
202798_at	SEC24B	SEC24 family, member B (S. cerevisiae)	10427	1.217371	0.000115	0.007613
203519_s_at	UPF2	UPF2 regulator of nonsense transcripts homolog (yeast)	26019	1.021857	0.000114	0.007613
213227_at	PGRMC2	progesterone receptor membrane component 2	10424	1.088092	0.000114	0.007613
212918_at	RECQL	RecQ protein-like (DNA helicase Q1-like)	5965	1.204724	0.000111	0.007613
218842_at	RPAP3	RNA polymerase II associated protein 3	79657	1.007012	0.000109	0.007613
218370_s_at	S100PBP	S100P binding protein	64766	1.040583	0.000107	0.007601
209043_at	PAPSS1	3'-phosphoadenosine 5'-phosphosulfate synthase 1	9061	1.266585	0.000106	0.007558
213374_x_at	HIBCH	3-hydroxyisobutyryl-CoA hydrolase	26275	1.37257	0.000104	0.00745
201202_at	PCNA	proliferating cell nuclear antigen	5111	1.874541	0.000102	0.00739
208925_at	CLDND1	claudin domain containing 1	56650	1.035219	0.000101	0.007343
208986_at	TCF12	transcription factor 12	6938	1.13518	9.80E-05	0.00719
202706_s_at	UMPS	uridine monophosphate synthetase	7372	1.021819	9.71E-05	0.007147
222209_s_at	TMEM135	transmembrane protein 135	65084	1.139737	9.39E-05	0.007017
202956_at	ARFGEF1	ADP-ribosylation factor guanine nucleotide-exchange factor 1 (brefeldin A-inhibited)	10565	1.048197	9.25E-05	0.006996
208877_at	PAK2	p21 protein (Cdc42/Rac)-activated kinase 2	5062	1.095691	9.02E-05	0.006891
212454_x_at	HNRPDL	heterogeneous nuclear ribonucleoprotein D-like	9987	1.012227	8.99E-05	0.006891
201832_s_at	USO1	USO1 vesicle transport factor	8615	1.196724	8.58E-05	0.006807
218104_at	TEX10	testis expressed 10	54881	1.063963	8.48E-05	0.006794
209585_s_at	MINPP1	multiple inositol-polyphosphate phosphatase 1	9562	1.5483	8.34E-05	0.006749
204160_s_at	ENPP4	ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative)	22875	1.023317	8.15E-05	0.006724
201872_s_at	ABCE1	ATP-binding cassette, sub-family E (OABP), member 1	6059	1.056302	7.77E-05	0.006497
203608_at	ALDH5A1	aldehyde dehydrogenase 5 family, member A1	7915	1.567849	7.76E-05	0.006497

201177_s_at	UBA2	ubiquitin-like modifier activating enzyme 2	10054	1.011771	7.72E-05	0.006497
201663_s_at	SMC4	structural maintenance of chromosomes 4	10051	1.397017	7.58E-05	0.006462
206478_at	KIAA0125	KIAA0125	9834	1.699586	7.39E-05	0.006369
209259_s_at	SMC3	structural maintenance of chromosomes 3	9126	1.536331	7.36E-05	0.006369
201491_at	AHSA1	AHA1, activator of heat shock 90kDa protein ATPase homolog 1 (yeast)	10598	1.017409	7.09E-05	0.006348
200050_at	ZNF146	zinc finger protein 146	7705	1.112747	6.82E-05	0.006137
212798_s_at	ANKMY2	ankyrin repeat and MYND domain containing 2	57037	1.282009	6.82E-05	0.006137
200597_at	EIF3A	eukaryotic translation initiation factor 3, subunit A	8661	1.15333	6.58E-05	0.006137
220416_at	ATP8B4	ATPase, class I, type 8B, member 4	79895	1.319886	6.56E-05	0.006137
218352_at	RCBTB1	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 1	55213	1.401043	6.56E-05	0.006137
208954_s_at	LARP4B	La ribonucleoprotein domain family, member 4B	23185	1.035215	6.55E-05	0.006137
200754_x_at	SRSF2	serine/arginine-rich splicing factor 2	6427	1.189498	6.53E-05	0.006137
213094_at	GPR126	G protein-coupled receptor 126	57211	1.723615	6.36E-05	0.006137
201726_at	ELAVL1	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)	1994	1.210067	6.33E-05	0.006137
202797_at	SACM1L	SAC1 suppressor of actin mutations 1-like (yeast)	22908	1.068996	6.19E-05	0.006092
218932_at	ZNHIT6	zinc finger, HIT-type containing 6	54680	1.533903	6.11E-05	0.006036
205909_at	POLE2	polymerase (DNA directed), epsilon 2, accessory subunit	5427	1.13581	6.10E-05	0.006036
201493_s_at	PUM2	pumilio homolog 2 (Drosophila)	23369	1.045091	6.09E-05	0.006036
203605_at	SRP54	signal recognition particle 54kDa	6729	1.336501	6.08E-05	0.006036
213737_x_at	GOLGA8H	golgin A8 family, member H	728498	1.276782	5.98E-05	0.006036
205848_at	GAS2	growth arrest-specific 2	2620	1.882946	5.69E-05	0.005965
207483_s_at	CAND1	cullin-associated and neddylation-dissociated 1	55832	1.101083	5.60E-05	0.005911
219497_s_at	BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	53335	1.051534	5.48E-05	0.00586
201664_at	SMC4	structural maintenance of chromosomes 4	10051	1.810802	5.39E-05	0.005828
209362_at	MED21	mediator complex subunit 21	9412	1.351739	5.36E-05	0.005828
201458_s_at	BUB3	BUB3 mitotic checkpoint protein	9184	1.194027	5.30E-05	0.005828
203804_s_at	LUC7L3	LUC7-like 3 (S. cerevisiae)	51747	1.117694	5.28E-05	0.005828
206316_s_at	KNTC1	kinetochore associated 1	9735	1.132251	5.10E-05	0.00579
204030_s_at	IQCJ-SCHIP1	IQCJ-SCHIP1 readthrough	100505385	1.123787	5.04E-05	0.005746
218437_s_at	LZTFL1	leucine zipper transcription factor-like 1	54585	1.226372	4.98E-05	0.005732
202502_at	ACADM	acyl-CoA dehydrogenase, C-4 to C-12 straight chain	34	1.024159	4.94E-05	0.005732

204256_at	ELOVL6	ELOVL fatty acid elongase 6	79071	1.533869	4.93E-05	0.005732
215165_x_at	UMPS	uridine monophosphate synthetase	7372	1.104322	4.89E-05	0.005732
217814_at	CCDC47	coiled-coil domain containing 47	57003	1.430862	4.63E-05	0.005622
212944_at	SLC5A3	solute carrier family 5 (sodium/myo-inositol cotransporter), member 3	6526	1.422266	4.48E-05	0.005619
208861_s_at	ATRX	alpha thalassemia/mental retardation syndrome X-linked	546	1.174112	4.47E-05	0.005619
208848_at	ADH5	alcohol dehydrogenase 5 (class III), chi polypeptide	128	1.350061	4.32E-05	0.005587
209813_x_at	TARP	TCR gamma alternate reading frame protein	445347	1.675539	4.27E-05	0.005556
208860_s_at	ATRX	alpha thalassemia/mental retardation syndrome X-linked	546	1.385939	4.22E-05	0.005556
216199_s_at	MAP3K4	mitogen-activated protein kinase kinase kinase 4	4216	1.101219	4.03E-05	0.005398
218577_at	LRRC40	leucine rich repeat containing 40	55631	1.237191	3.99E-05	0.005382
208955_at	DUT	deoxyuridine triphosphatase	1854	1.439155	3.92E-05	0.005311
203614_at	UTP14C	UTP14, U3 small nucleolar ribonucleoprotein, homolog C (yeast)	9724	1.05731	3.86E-05	0.005287
202540_s_at	HMGCR	3-hydroxy-3-methylglutaryl-CoA reductase	3156	1.149998	3.83E-05	0.005286
209025_s_at	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	10492	1.11864	3.81E-05	0.005286
221884_at	MECOM	MDS1 and EVI1 complex locus	2122	1.313552	3.58E-05	0.005097
213677_s_at	PMS1	PMS1 postmeiotic segregation increased 1 (S. cerevisiae)	5378	1.319836	3.48E-05	0.004995
203482_at	FAM178A	family with sequence similarity 178, member A	55719	1.006684	3.46E-05	0.004994
205395_s_at	MRE11A	MRE11 meiotic recombination 11 homolog A (S. cerevisiae)	4361	1.047297	3.44E-05	0.004994
205541_s_at	GSPT2	G1 to S phase transition 2	23708	1.302983	3.23E-05	0.004813
213111_at	PIKFYVE	phosphoinositide kinase, FYVE finger containing	200576	1.505014	3.21E-05	0.004813
203406_at	MFAP1	microfibrillar-associated protein 1	4236	1.105243	2.95E-05	0.004627
212648_at	DHX29	DEAH (Asp-Glu-Ala-His) box polypeptide 29	54505	1.181102	2.90E-05	0.004616
212905_at	CSTF2T	cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kDa, tau variant	23283	1.012536	2.79E-05	0.004519
203102_s_at	MGAT2	mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	4247	1.02975	2.78E-05	0.004519
212407_at	METTL13	methyltransferase like 13	51603	1.183202	2.73E-05	0.004519
212584_at	AQR	aquarius homolog (mouse)	9716	1.131181	2.71E-05	0.004519
221522_at	ANKRD27	ankyrin repeat domain 27 (VPS9 domain)	84079	1.408053	2.46E-05	0.004336
215143_at	DPY19L2P2	dpy-19-like 2 pseudogene 2 (C. elegans)	349152	1.163809	2.42E-05	0.004298
212402_at	ZC3H13	zinc finger CCCH-type containing 13	23091	1.411241	2.40E-05	0.004298
213005_s_at	KANK1	KN motif and ankyrin repeat domains 1	23189	1.420285	2.37E-05	0.004281

201086_x_at	SON	SON DNA binding protein	6651	1.303827	2.37E-05	0.004281
205885_s_at	ITGA4	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)	3676	1.152728	2.32E-05	0.004281
218957_s_at	PAAF1	proteasomal ATPase-associated factor 1	80227	1.082321	2.32E-05	0.004281
209409_at	GRB10	growth factor receptor-bound protein 10	2887	1.411903	2.31E-05	0.004281
218428_s_at	REV1	REV1, polymerase (DNA directed)	51455	1.014141	2.30E-05	0.004281
212982_at	ZDHHC17	zinc finger, DHHC-type containing 17	23390	1.24448	2.23E-05	0.004281
206854_s_at	MAP3K7	mitogen-activated protein kinase kinase kinase 7	6885	1.362632	2.14E-05	0.004215
213164_at	SLC5A3	solute carrier family 5 (sodium/myo-inositol cotransporter), member 3	6526	1.12656	2.14E-05	0.004215
209662_at	CETN3	centrin, EF-hand protein, 3	1070	1.780447	2.13E-05	0.004215
213092_x_at	DNAJC9	DnaJ (Hsp40) homolog, subfamily C, member 9	23234	1.281922	2.11E-05	0.004215
219130_at	TRMT13	tRNA methyltransferase 13 homolog (S. cerevisiae)	54482	1.054729	2.09E-05	0.004215
218096_at	AGPAT5	1-acylglycerol-3-phosphate O-acyltransferase 5	55326	1.046759	2.05E-05	0.004215
200783_s_at	STMN1	stathmin 1	3925	1.021197	1.99E-05	0.004183
202763_at	CASP3	caspase 3, apoptosis-related cysteine peptidase	836	1.113632	1.97E-05	0.004167
206874_s_at	SLK	STE20-like kinase	9748	1.508576	1.95E-05	0.004162
215806_x_at	TARP	TCR gamma alternate reading frame protein	445347	1.699601	1.94E-05	0.004162
218139_s_at	AP5M1	adaptor-related protein complex 5, mu 1 subunit	55745	1.213838	1.93E-05	0.004162
212731_at	ANKRD46	ankyrin repeat domain 46	157567	1.139853	1.87E-05	0.004117
217317_s_at	HERC2P2	hect domain and RLD 2 pseudogene 2	400322	1.063595	1.62E-05	0.003764
212176_at	PNISR	PNN-interacting serine/arginine-rich protein	25957	1.0103	1.62E-05	0.003764
218313_s_at	GALNT7	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7)	51809	1.507414	1.62E-05	0.003764
219083_at	SHQ1	SHQ1, H/ACA ribonucleoprotein assembly factor	55164	1.675814	1.53E-05	0.003721
203302_at	DCK	deoxycytidine kinase	1633	1.276653	1.43E-05	0.003616
218515_at	PAXBP1	PAX3 and PAX7 binding protein 1	94104	1.243818	1.43E-05	0.003616
213391_at	DPY19L4	dpy-19-like 4 (C. elegans)	286148	1.187053	1.29E-05	0.003444
202907_s_at	NBN	nibrin	4683	1.588244	1.26E-05	0.003444
217886_at	EPS15	epidermal growth factor receptor pathway substrate 15	2060	1.345925	1.23E-05	0.003411
218622_at	NUP37	nucleoporin 37kDa	79023	1.261215	1.22E-05	0.003411
208654_s_at	CD164	CD164 molecule, sialomucin	8763	1.456204	1.21E-05	0.003411
219035_s_at	RNF34	ring finger protein 34, E3 ubiquitin protein ligase	80196	1.187459	1.15E-05	0.003369
220044_x_at	LUC7L3	LUC7-like 3 (S. cerevisiae)	51747	1.199028	1.15E-05	0.003369

218768_at	NUP107	nucleoporin 107kDa	57122	1.457543	1.14E-05	0.003369
208405_s_at	CD164	CD164 molecule, sialomucin	8763	1.103873	1.11E-05	0.003369
212675_s_at	CEP68	centrosomal protein 68kDa	23177	1.33608	1.11E-05	0.003369
209200_at	MEF2C	myocyte enhancer factor 2C	4208	1.964319	1.10E-05	0.003369
209476_at	TMX1	thioredoxin-related transmembrane protein 1	81542	1.209672	1.07E-05	0.003369
212474_at	AVL9	AVL9 homolog (S. cerevisiase)	23080	1.128401	9.17E-06	0.003236
203306_s_at	SLC35A1	solute carrier family 35 (CMP-sialic acid transporter), member A1	10559	1.184632	9.10E-06	0.003236
219405_at	TRIM68	tripartite motif containing 68	55128	1.092848	8.27E-06	0.003067
217954_s_at	PHF3	PHD finger protein 3	23469	1.096771	8.00E-06	0.003017
201448_at	TIA1	TIA1 cytotoxic granule-associated RNA binding protein	7072	1.364827	7.61E-06	0.002919
202918_s_at	MOB4	MOB family member 4, phocein	25843	1.281577	7.60E-06	0.002919
201503_at	G3BP1	GTPase activating protein (SH3 domain) binding protein 1	10146	1.400871	7.40E-06	0.002919
221606_s_at	HMGN5	high mobility group nucleosome binding domain 5	79366	1.041186	7.16E-06	0.002919
212179_at	PNISR	PNN-interacting serine/arginine-rich protein	25957	1.659487	7.06E-06	0.002919
207943_x_at	PLAGL1	pleiomorphic adenoma gene-like 1	5325	1.02225	6.80E-06	0.002919
219002_at	FASTKD1	FAST kinase domains 1	79675	1.139996	6.78E-06	0.002919
219649_at	ALG6	ALG6, alpha-1,3-glucosyltransferase	29929	1.318705	6.36E-06	0.002919
218593_at	RBM28	RNA binding motif protein 28	55131	1.095331	6.00E-06	0.002867
218152_at	HMG20A	high mobility group 20A	10363	1.329726	5.52E-06	0.002834
218108_at	UBR7	ubiquitin protein ligase E3 component n-recognin 7 (putative)	55148	1.468044	4.88E-06	0.002649
212959_s_at	GNPTAB	N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits	79158	1.108946	4.43E-06	0.002528
213653_at	METTL3	methyltransferase like 3	56339	1.135123	4.23E-06	0.002528
201218_at	CTBP2	C-terminal binding protein 2	1488	1.622964	4.00E-06	0.002528
202520_s_at	MLH1	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)	4292	1.112927	3.95E-06	0.002528
209022_at	STAG2	stromal antigen 2	10735	1.149995	3.82E-06	0.002528
218343_s_at	GTF3C3	general transcription factor IIIC, polypeptide 3, 102kDa	9330	1.144191	3.71E-06	0.002528
219960_s_at	UCHL5	ubiquitin carboxyl-terminal hydrolase L5	51377	1.108112	3.64E-06	0.002528
209175_at	SEC23IP	SEC23 interacting protein	11196	1.255797	3.63E-06	0.002528
218170_at	ISOC1	isochorismatase domain containing 1	51015	1.24304	3.49E-06	0.002528
209265_s_at	METTL3	methyltransferase like 3	56339	1.227046	3.29E-06	0.002528
222127_s_at	EXOC1	exocyst complex component 1	55763	1.394408	2.86E-06	0.002528

207002_s_at	PLAGL1	pleiomorphic adenoma gene-like 1	5325	1.171723	2.49E-06	0.002309
204168_at	MGST2	microsomal glutathione S-transferase 2	4258	1.037395	1.79E-06	0.001991
205609_at	ANGPT1	angiopoietin 1	284	1.547029	1.71E-06	0.001991
209537_at	EXTL2	exostosin-like glycosyltransferase 2	2135	1.05732	7.39E-07	0.001096
209748_at	SPAST	spastin	6683	1.096487	6.60E-07	0.001049
218397_at	FANCL	Fanconi anemia, complementation group L	55120	1.889757	4.53E-07	0.000871
210621_s_at	RASA1	RAS p21 protein activator (GTPase activating protein) 1	5921	1.39113	3.67E-07	0.000871
201687_s_at	API5	apoptosis inhibitor 5	8539	1.055434	1.84E-07	0.000682
212828_at	SYNJ2	synaptojanin 2	8871	1.111098	1.84E-07	0.000682
209007_s_at	C1orf63	chromosome 1 open reading frame 63	57035	1.046263	8.11E-08	0.000601
218361_at	GOLPH3L	golgi phosphoprotein 3-like	55204	1.174016	5.59E-08	0.000601
219913_s_at	CRNKL1	crooked neck pre-mRNA splicing factor-like 1 (Drosophila)	51340	1.468407	2.17E-08	0.000482

Table S5b. Genes differentially regulated by the 7 PV patients with an aggressive phenotype.

Probeset ID	***Symbol (Na32 consesus Mar13)***	***Gene Title (Na32 consensus Mar13)***	***Entrez GeneID (concensus Mar-13)***	***Log2(FC)***	***P-Value***	***Adjusted P-Value***
209763_at	CHRDL1	chordin-like 1	91851	-1.17606	5.21E-09	6.67E-05
210487_at	DNTT	deoxynucleotidyltransferase, terminal	1791	-1.91383	6.00E-09	6.67E-05
205933_at	SETBP1	SET binding protein 1	26040	-1.1773	1.51E-08	0.000112
202723_s_at	FOXO1	forkhead box O1	2308	-1.10201	4.34E-06	0.024108
201324_at	EMP1	epithelial membrane protein 1	2012	-1.73635	6.04E-06	0.026802
201325_s_at	EMP1	epithelial membrane protein 1	2012	-1.00997	1.48E-05	0.029925
209398_at	HIST1H1C	histone cluster 1, H1c	3006	-2.26773	3.33E-05	0.061697
212827_at	IGHM	immunoglobulin heavy constant mu	3507	-1.62695	0.000114	0.134692
206385_s_at	ANK3	ankyrin 3, node of Ranvier (ankyrin G)	288	-1.01371	0.000117	0.134692
209183_s_at	C10orf10	chromosome 10 open reading frame 10	11067	-1.07496	0.000131	0.139056
209374_s_at	IGHM	immunoglobulin heavy constant mu	3507	-1.78678	0.000238	0.21202
204430_s_at	SLC2A5	solute carrier family 2 (facilitated glucose/fructose transporter), member 5	6518	-1.13053	0.00026	0.213741
200872_at	S100A10	S100 calcium binding protein A10	6281	-1.47658	0.000279	0.215629
209069_s_at	H3F3B	H3 histone, family 3B (H3.3B)	3021	-1.18661	0.000318	0.221129
210592_s_at	SAT1	spermidine/spermine N1-acetyltransferase 1	6303	-1.08035	0.000376	0.227751
207111_at	EMR1	egf-like module containing, mucin-like, hormone receptor-like 1	2015	-1.08619	0.000401	0.227751

204304_s_at	PROM1	prominin 1	8842	-1.82999	0.00042	0.227751
205984_at	CRHBP	corticotropin releasing hormone binding protein	1393	-1.68559	0.000482	0.239161
218280_x_at	HIST2H2AA4	histone cluster 2, H2aa4	723790	-2.04755	0.000661	0.271413
211997_x_at	H3F3B	H3 histone, family 3B (H3.3B)	3021	-1.22595	0.000753	0.293064
211998_at	H3F3B	H3 histone, family 3B (H3.3B)	3021	-1.37161	0.001101	0.376554
214290_s_at	HIST2H2AA4	histone cluster 2, H2aa4	723790	-2.10063	0.001825	0.399532
202888_s_at	ANPEP	alanyl (membrane) aminopeptidase	290	-1.09433	0.001827	0.399532
210785_s_at	THEMIS2	thymocyte selection associated family member 2	9473	-1.40909	0.001958	0.412534
205402_x_at	PRSS2	protease, serine, 2 (trypsin 2)	5645	-1.05383	0.002001	0.412534
220990_s_at	MIR21	microRNA 21	406991	-1.16662	0.002023	0.412534
201369_s_at	ZFP36L2	ZFP36 ring finger protein-like 2	678	-1.42932	0.002729	0.450281
207571_x_at	THEMIS2	thymocyte selection associated family member 2	9473	-1.3478	0.0028	0.450281
212543_at	AIM1	absent in melanoma 1	202	-1.12719	0.002817	0.450281
204698_at	ISG20	interferon stimulated exonuclease gene 20kDa	3669	-1.19993	0.002841	0.450281
204872_at	TLE4	transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila)	7091	-1.08661	0.004743	0.516178
211597_s_at	HOPX	HOP homeobox	84525	-1.35699	0.004787	0.516178
220377_at	KIAA0125	KIAA0125	9834	-1.15785	0.004957	0.516178
202708_s_at	HIST2H2BE	histone cluster 2, H2be	8349	-1.73994	0.00501	0.516178
222258_s_at	SH3BP4	SH3-domain binding protein 4	23677	-1.25738	0.006817	0.549162
202748_at	GBP2	guanylate binding protein 2, interferon-inducible	2634	-1.47788	0.007224	0.557788
222067_x_at	HIST1H2BD	histone cluster 1, H2bd	3017	-1.3732	0.007682	0.562835
204805_s_at	H1FX	H1 histone family, member X	8971	-1.45025	0.012357	0.587079
214472_at	HIST1H2AD	histone cluster 1, H2ad	3013	-1.33457	0.016968	0.609599
215071_s_at	HIST1H2AC	histone cluster 1, H2ac	8334	-1.59794	0.020339	0.631601
204057_at	IRF8	interferon regulatory factor 8	3394	-1.01328	0.021285	0.631601
221760_at	MAN1A1	mannosidase, alpha, class 1A, member 1	4121	-1.18372	0.02233	0.632753
208490_x_at	HIST1H2BF	histone cluster 1, H2bf	8343	-1.14111	0.027318	0.639545
221556_at	CDC14B	cell division cycle 14B	8555	-1.26289	0.028048	0.64494
210387_at	HIST1H2BG	histone cluster 1, H2bg	8339	-1.14146	0.02951	0.651733
201416_at	SOX4	SRY (sex determining region Y)-box 4	6659	-1.05187	0.032258	0.65293
208579_x_at	H2BFS	H2B histone family, member S (pseudogene)	54145	-1.30549	0.035551	0.658786
208527_x_at	HIST1H2BE	histone cluster 1, H2be	8344	-1.05374	0.035992	0.658786
203708_at	PDE4B	phosphodiesterase 4B, cAMP-specific	5142	-1.26501	0.039076	0.662929

212488_at	COL5A1	collagen, type V, alpha 1	1289	-1.01422	0.041826	0.666611
203140_at	BCL6	B-cell CLL/lymphoma 6	604	-1.00963	0.04395	0.666724
208546_x_at	HIST1H2BH	histone cluster 1, H2bh	8345	-1.02623	0.048771	0.677506
214455_at	HIST1H2BC	histone cluster 1, H2bc	8347	-1.16847	0.051456	0.680853
218999_at	TMEM140	transmembrane protein 140	55281	-1.01862	0.053069	0.682752
208018_s_at	HCK	hemopoietic cell kinase	3055	-1.13981	0.05449	0.684183
204897_at	PTGER4	prostaglandin E receptor 4 (subtype EP4)	5734	-1.13843	0.058834	0.692792
201565_s_at	ID2	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	3398	-1.33513	0.06594	0.694022
212587_s_at	PTPRC	protein tyrosine phosphatase, receptor type, C	5788	-1.10126	0.080672	0.719636
200897_s_at	PALLD	palladin, cytoskeletal associated protein	23022	-1.24085	0.085951	0.722194
208891_at	DUSP6	dual specificity phosphatase 6	1848	-1.07107	0.098612	0.730122
202391_at	BASP1	brain abundant, membrane attached signal protein 1	10409	-1.1892	0.099272	0.730445
201743_at	CD14	CD14 molecule	929	-1.11579	0.106127	0.731069
221841_s_at	KLF4	Kruppel-like factor 4 (gut)	9314	-1.20574	0.106845	0.731355
206110_at	HIST1H3H	histone cluster 1, H3h	8357	-1.19698	0.116318	0.738259
213975_s_at	LYZ	lysozyme	4069	-1.22513	0.117821	0.738667
218723_s_at	RGCC	regulator of cell cycle	28984	-1.01755	0.173123	0.764957
202917_s_at	S100A8	S100 calcium binding protein A8	6279	-1.01114	0.365329	0.843162
209774_x_at	CXCL2	chemokine (C-X-C motif) ligand 2	2920	1.127083	0.184971	0.770504
206488_s_at	CD36	CD36 molecule (thrombospondin receptor)	948	1.062242	0.179158	0.767834
206049_at	SELP	selectin P (granule membrane protein 140kDa, antigen CD62)	6403	1.027039	0.142209	0.749649
202581_at	HSPA1A	heat shock 70kDa protein 1A	3303	1.07338	0.141805	0.749649
212671_s_at	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1	3117	1.256994	0.134567	0.747232
207808_s_at	PROS1	protein S (alpha)	5627	1.076302	0.125868	0.743062
204419_x_at	HBG1	hemoglobin, gamma A	3047	1.666375	0.091429	0.723603
204848_x_at	HBG1	hemoglobin, gamma A	3047	1.565419	0.086123	0.722194
209839_at	DNM3	dynamin 3	26052	1.130837	0.075473	0.711904
217388_s_at	KYNU	kynureninase	8942	1.468314	0.069766	0.703289
214710_s_at	CCNB1	cyclin B1	891	1.019442	0.057837	0.692792
202729_s_at	LTBP1	latent transforming growth factor beta binding protein 1	4052	1.205454	0.056194	0.689409
205950_s_at	CA1	carbonic anhydrase I	759	1.154113	0.05527	0.686498
201014_s_at	PAICS	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide	10606	1.001269	0.054655	0.684183

		synthetase				
215813_s_at	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	5742	1.093699	0.054246	0.684183
216063_at	HBBP1	hemoglobin, beta pseudogene 1	3044	1.237304	0.051626	0.680853
209290_s_at	NFIB	nuclear factor I/B	4781	1.089323	0.047583	0.675495
212224_at	ALDH1A1	aldehyde dehydrogenase 1 family, member A1	216	1.365131	0.047481	0.675495
207165_at	HMMR	hyaluronan-mediated motility receptor (RHAMM)	3161	1.035451	0.04372	0.666724
207668_x_at	PDIA6	protein disulfide isomerase family A, member 6	10130	1.01888	0.042673	0.666611
208639_x_at	PDIA6	protein disulfide isomerase family A, member 6	10130	1.087019	0.04232	0.666611
201202_at	PCNA	proliferating cell nuclear antigen	5111	1.025175	0.040518	0.664974
202705_at	CCNB2	cyclin B2	9133	1.000457	0.037459	0.658786
202870_s_at	CDC20	cell division cycle 20	991	1.339489	0.036577	0.658786
217232_x_at	HBB	hemoglobin, beta	3043	1.819046	0.034587	0.658786
218009_s_at	PRC1	protein regulator of cytokinesis 1	9055	1.316131	0.032297	0.65293
213515_x_at	HBG1	hemoglobin, gamma A	3047	2.417287	0.029879	0.651733
218350_s_at	GMNN	geminin, DNA replication inhibitor	51053	1.197599	0.02966	0.651733
209728_at	HLA-DRB4	major histocompatibility complex, class II, DR beta 4	3126	2.147596	0.028176	0.645955
204023_at	RFC4	replication factor C (activator 1) 4, 37kDa	5984	1.139793	0.027395	0.640611
203755_at	BUB1B	BUB1 mitotic checkpoint serine/threonine kinase B	701	1.078262	0.026537	0.639024
202760_s_at	AKAP2	A kinase (PRKA) anchor protein 2	11217	1.132676	0.023696	0.635738
201477_s_at	RRM1	ribonucleotide reductase M1	6240	1.170464	0.02268	0.635738
218039_at	NUSAP1	nucleolar and spindle associated protein 1	51203	1.296022	0.022485	0.634539
209773_s_at	RRM2	ribonucleotide reductase M2	6241	1.767338	0.021614	0.631601
206632_s_at	APOBEC3B	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B	9582	1.217919	0.021271	0.631601
201563_at	SORD	sorbitol dehydrogenase	6652	1.003384	0.021071	0.631601
211696_x_at	HBB	hemoglobin, beta	3043	1.960803	0.020716	0.631601
201490_s_at	PPIF	peptidylprolyl isomerase F	10105	1.068584	0.02005	0.62633
209969_s_at	STAT1	signal transducer and activator of transcription 1, 91kDa	6772	1.033433	0.018323	0.612297
202112_at	VWF	von Willebrand factor	7450	1.065252	0.017067	0.610194
211005_at	LAT	linker for activation of T cells	27040	1.441264	0.016468	0.605865
206102_at	GINS1	GINS complex subunit 1 (Psf1 homolog)	9837	1.19856	0.014854	0.595174
206698_at	XK	X-linked Kx blood group (McLeod syndrome)	7504	1.473769	0.014747	0.595174
201761_at	MTHFD2	methylenetetrahydrofolate dehydrogenase (NADP+	10797	1.176486	0.01448	0.595174

		dependent) 2, methenyltetrahydrofolate cyclohydrolase				
202589_at	TYMS	thymidylate synthetase	7298	1.284352	0.014339	0.594132
203362_s_at	MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)	4085	1.12377	0.014136	0.591776
204146_at	RAD51AP1	RAD51 associated protein 1	10635	1.138009	0.013242	0.587079
202814_s_at	HEXIM1	hexamethylene bis-acetamide inducible 1	10614	1.018846	0.011855	0.587079
211953_s_at	IPO5	importin 5	3843	1.1663	0.010926	0.587079
212589_at	RRAS2	related RAS viral (r-ras) oncogene homolog 2	22800	1.248922	0.010896	0.587079
201897_s_at	CKS1B	CDC28 protein kinase regulatory subunit 1B	1163	1.237742	0.010699	0.587079
201829_at	NET1	neuroepithelial cell transforming 1	10276	1.249173	0.010403	0.58573
212459_x_at	SUCLG2	succinate-CoA ligase, GDP-forming, beta subunit	8801	1.16554	0.009868	0.58573
201930_at	MCM6	minichromosome maintenance complex component 6	4175	1.046236	0.009628	0.582356
209116_x_at	HBB	hemoglobin, beta	3043	2.529691	0.008816	0.568066
218585_s_at	DTL	denticleless E3 ubiquitin protein ligase homolog (Drosophila)	51514	1.376897	0.008767	0.568066
206937_at	SPTA1	spectrin, alpha, erythrocytic 1 (elliptocytosis 2)	6708	1.114075	0.008321	0.566014
218883_s_at	MLF1IP	MLF1 interacting protein	79682	1.136186	0.008177	0.566014
215772_x_at	SUCLG2	succinate-CoA ligase, GDP-forming, beta subunit	8801	1.175819	0.008054	0.566014
213088_s_at	DNAJC9	DnaJ (Hsp40) homolog, subfamily C, member 9	23234	1.00079	0.007957	0.565327
206145_at	RHAG	Rh-associated glycoprotein	6005	1.393541	0.006392	0.547427
204695_at	CDC25A	cell division cycle 25A	993	1.084134	0.006299	0.547427
204240_s_at	SMC2	structural maintenance of chromosomes 2	10592	1.294656	0.005936	0.540991
202107_s_at	MCM2	minichromosome maintenance complex component 2	4171	1.222252	0.005761	0.536001
222204_s_at	RRN3	RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae)	54700	1.042118	0.005729	0.536001
203560_at	GGH	gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase)	8836	1.340214	0.00547	0.526569
202613_at	CTPS1	CTP synthase 1	1503	1.14984	0.005331	0.526569
208955_at	DUT	deoxyuridine triphosphatase	1854	1.03421	0.005157	0.523702
212282_at	TMEM97	transmembrane protein 97	27346	1.011374	0.004822	0.516178
219412_at	RAB38	RAB38, member RAS oncogene family	23682	1.168702	0.004753	0.516178
202503_s_at	KIAA0101	KIAA0101	9768	1.309228	0.00471	0.516178
204767_s_at	FEN1	flap structure-specific endonuclease 1	2237	1.381621	0.004647	0.516178
205394_at	CHEK1	checkpoint kinase 1	1111	1.045411	0.004442	0.516178
201489_at	PPIF	peptidylprolyl isomerase F	10105	1.118185	0.004062	0.507454
201890_at	RRM2	ribonucleotide reductase M2	6241	2.141038	0.00366	0.47601

219306_at	KIF15	kinesin family member 15	56992	1.266139	0.003389	0.461859
211144_x_at	TARP	TCR gamma alternate reading frame protein	445347	1.260002	0.003285	0.456931
206834_at	HBD	hemoglobin, delta	3045	2.172202	0.003266	0.456931
203476_at	TPBG	trophoblast glycoprotein	7162	1.132385	0.002991	0.450281
212281_s_at	TMEM97	transmembrane protein 97	27346	1.2802	0.002875	0.450281
206067_s_at	WT1	Wilms tumor 1	7490	1.247746	0.002812	0.450281
208694_at	PRKDC	protein kinase, DNA-activated, catalytic polypeptide	5591	1.067872	0.002544	0.438543
206118_at	STAT4	signal transducer and activator of transcription 4	6775	1.012186	0.002506	0.438543
216920_s_at	TARP	TCR gamma alternate reading frame protein	445347	1.474096	0.002252	0.428068
202949_s_at	FHL2	four and a half LIM domains 2	2274	1.107316	0.002224	0.428068
222201_s_at	CASP8AP2	caspase 8 associated protein 2	9994	1.054149	0.001764	0.399532
204026_s_at	ZWINT	ZW10 interactor, kinetochore protein	11130	1.720113	0.001341	0.397293
209894_at	LEPR	leptin receptor	3953	2.015714	0.001141	0.380525
213092_x_at	DNAJC9	DnaJ (Hsp40) homolog, subfamily C, member 9	23234	1.090583	0.000823	0.310206
219454_at	EGFL6	EGF-like-domain, multiple 6	25975	1.45589	0.000616	0.258418
213262_at	SACS	spastic ataxia of Charlevoix-Saguenay (sacsin)	26278	1.042232	0.00059	0.252396
204256_at	ELOVL6	ELOVL fatty acid elongase 6	79071	1.448618	0.000559	0.252191
215806_x_at	TARP	TCR gamma alternate reading frame protein	445347	1.534041	0.000427	0.227751
209813_x_at	TARP	TCR gamma alternate reading frame protein	445347	1.665423	0.000291	0.215629
201830_s_at	NET1	neuroepithelial cell transforming 1	10276	1.530152	0.000251	0.213741
219615_s_at	KCNK5	potassium channel, subfamily K, member 5	8645	1.04543	0.000225	0.21202
219602_s_at	PIEZO2	piezo-type mechanosensitive ion channel component 2	63895	1.504577	7.50E-05	0.117928
219000_s_at	DSCC1	defective in sister chromatid cohesion 1 homolog (S. cerevisiae)	79075	1.081581	4.67E-05	0.079813
205848_at	GAS2	growth arrest-specific 2	2620	2.492596	1.11E-05	0.02744

Table S6a. Differential expression of the 102 core genes in the 7 PV patients with an aggressive phenotype.

Probeset ID	***Symbol (Na32 consesus Mar13)***	***Gene Title (Na32 consensus Mar13)***	***GeneID (NCBI Mar)***	***Log2(FC)***	***P-Value***	***Adjusted p-Value***
209763_at	CHRDL1	chordin-like 1	91851	-1.1760592	5.21E-09	6.67E-05
210487_at	DNTT	deoxynucleotidyltransferase, terminal	1791	-1.91383418	6.00E-09	6.67E-05
205933_at	SETBP1	SET binding protein 1	26040	-1.17729694	1.51E-08	0.0001121
201324_at	EMP1	epithelial membrane protein 1	2012	-1.73634604	6.04E-06	0.0268018
209183_s_at	C10orf10	chromosome 10 open reading frame 10	11067	-1.07496461	0.000131314	0.1390556
209374_s_at	IGHM	immunoglobulin heavy constant mu	3507	-1.78677828	0.000238354	0.2120204
204430_s_at	SLC2A5	solute carrier family 2 (facilitated glucose/fructose transporter), member 5	6518	-1.13053427	0.000259511	0.2137408
209069_s_at	H3F3B	H3 histone, family 3B (H3.3B)	3021	-1.18660722	0.0003182	0.221129
219777_at	GIMAP6	GTPase, IMAP family member 6	474344	-0.96412142	0.000351795	0.2277507

204304_s_at	PROM1	prominin 1	8842	-1.82998841	0.000419599	0.2277507
205984_at	CRHBP	corticotropin releasing hormone binding protein	1393	-1.68558627	0.000481558	0.2391606
211998_at	H3F3B	H3 histone, family 3B (H3.3B)	3021	-1.37160868	0.00110064	0.3765544
220990_s_at	MIR21	microRNA 21	406991	-1.1666179	0.002023122	0.4125343
201369_s_at	ZFP36L2	ZFP36 ring finger protein-like 2	678	-1.42931862	0.002728865	0.4502813
204872_at	TLE4	transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila)	7091	-1.08661045	0.004743456	0.5161776
211597_s_at	HOPX	HOP homeobox	84525	-1.35699251	0.004786898	0.5161776
220377_at	KIAA0125	KIAA0125	9834	-1.15784914	0.004956965	0.5161776
219304_s_at	PDGFD	platelet derived growth factor D	80310	-0.94059913	0.005103212	0.5229734
208960_s_at	KLF6	Kruppel-like factor 6	1316	-0.94664654	0.010221625	0.5857297
203787_at	SSBP2	single-stranded DNA binding protein 2	23635	-0.79229496	0.013428932	0.5870789
204755_x_at	HLF	hepatic leukemia factor	3131	-0.61251884	0.013936253	0.5899467
209576_at	GNAI1	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1	2770	-0.63080373	0.015529376	0.6015332
204753_s_at	HLF	hepatic leukemia factor	3131	-0.70807109	0.021022562	0.6316009
221760_at	MAN1A1	mannosidase, alpha, class 1A, member 1	4121	-1.18371513	0.022329984	0.6327526
206478_at	KIAA0125	KIAA0125	9834	-0.99597623	0.02539777	0.6372958
221556_at	CDC14B	cell division cycle 14B	8555	-1.26288843	0.028047825	0.6449399
214805_at	EIF4A1	eukaryotic translation initiation factor 4A1	1973	-0.67982725	0.028070099	0.6449399
220416_at	ATP8B4	ATPase, class I, type 8B, member 4	79895	-0.73256572	0.031829237	0.6529304
208835_s_at	LUC7L3	LUC7-like 3 (S. cerevisiae)	51747	-0.90441159	0.042521869	0.666611
204030_s_at	IQCJ-SCHIP1	IQCJ-SCHIP1 readthrough	100505385	-0.57342	0.042715691	0.666611
204897_at	PTGER4	prostaglandin E receptor 4 (subtype EP4)	5734	-1.13842542	0.058834073	0.6927923
208949_s_at	LGALS3	lectin, galactoside-binding, soluble, 3	3958	-0.78834036	0.075957894	0.7119044
208961_s_at	KLF6	Kruppel-like factor 6	1316	-0.79400193	0.078101123	0.7129149
209112_at	CDKN1B	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	1027	-0.57998283	0.119332543	0.7386668
204563_at	SELL	selectin L	6402	-0.97868544	0.120606528	0.7393127
214651_s_at	HOXA9	homeobox A9	3205	-0.56640825	0.211940371	0.7838234
208892_s_at	DUSP6	dual specificity phosphatase 6	1848	-0.85096752	0.235607663	0.7928467
213524_s_at	G0S2	G0/G1switch 2	50486	-0.82501945	0.239215682	0.7948695
203535_at	S100A9	S100 calcium binding protein A9	6280	-0.80627992	0.254346668	0.8015736
213668_s_at	SOX4	SRY (sex determining region Y)-box 4	6659	-0.82323589	0.260556623	0.802741
222044_at	PCIF1	PDX1 C-terminal inhibiting factor 1	63935	-0.49806168	0.282560332	0.8109941

213593_s_at	TRA2A	transformer 2 alpha homolog (Drosophila)	29896	-0.60971572	0.344365936	0.8383152
214041_x_at	RPL37A	ribosomal protein L37a	6168	-0.39653673	0.407444152	0.8568069
205442_at	MFAP3L	microfibrillar-associated protein 3-like	9848	-0.51285589	0.449796577	0.8725199
214974_x_at	CXCL5	chemokine (C-X-C motif) ligand 5	6374	-0.41826978	0.551543186	0.9009074
213979_s_at	---	---		-0.35065846	0.599848748	0.9149341
214911_s_at	BRD2	bromodomain containing 2	6046	-0.27608523	0.611740131	0.9174215
211074_at	FOLR1	folate receptor 1 (adult)	2348	-0.45112625	0.632000886	0.9246948
208180_s_at	HIST1H4H	histone cluster 1, H4h	8365	-0.2778544	0.639528185	0.9257406
207815_at	PF4V1	platelet factor 4 variant 1	5197	-0.30911148	0.651979155	0.9286903
205547_s_at	TAGLN	transgelin	6876	-0.28088743	0.708017145	0.9439304
205237_at	FCN1	ficolin (collagen/fibrinogen domain containing) 1	2219	-0.32136788	0.711156716	0.944669
219922_s_at	LTBP3	latent transforming growth factor beta binding protein 3	4054	-0.18060244	0.723881126	0.9484945
204141_at	TUBB2A	tubulin, beta 2A class IIa	7280	-0.29534658	0.735081772	0.9498889
212952_at	LOC100507328	hypothetical LOC100507328	100507328	-0.22415499	0.743954062	0.9528039
209803_s_at	PHLDA2	pleckstrin homology-like domain, family A, member 2	7262	-0.19751659	0.762353226	0.9568355
204834_at	FGL2	fibrinogen-like 2	10875	-0.20803456	0.771018008	0.9582727
213350_at	RPS11	ribosomal protein S11	6205	-0.21555457	0.772923808	0.9589509
211964_at	COL4A2	collagen, type IV, alpha 2	1284	-0.15879898	0.78084214	0.9613311
205114_s_at	CCL3L3	chemokine (C-C motif) ligand 3-like 3	414062	-0.20519345	0.793565216	0.9626063
202310_s_at	COL1A1	collagen, type I, alpha 1	1277	-0.22272495	0.796823974	0.9633788
217683_at	HBE1	hemoglobin, epsilon 1	3046	-0.12978731	0.806948287	0.964919
201842_s_at	EFEMP1	EGF containing fibulin-like extracellular matrix protein 1	2202	-0.17500966	0.813572867	0.9663992
201631_s_at	IER3	immediate early response 3	8870	-0.12662907	0.836432308	0.9684535
201798_s_at	MYOF	myoferlin	26509	-0.12987194	0.839316831	0.9692311
1405_i_at	CCL5	chemokine (C-C motif) ligand 5	6352	-0.16353025	0.840439597	0.9695199
201058_s_at	MYL9	myosin, light chain 9, regulatory	10398	-0.11665284	0.854796069	0.9731863
215076_s_at	COL3A1	collagen, type III, alpha 1	1281	-0.11954993	0.877410108	0.9785103
202403_s_at	COL1A2	collagen, type I, alpha 2	1278	-0.11102553	0.891268391	0.9806744
210809_s_at	POSTN	periostin, osteoblast specific factor	10631	-0.1111146	0.912911705	0.9851423
212531_at	LCN2	lipocalin 2	3934	-0.02914052	0.962852347	0.9923439
210873_x_at	APOBEC3A	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3A	200315	-0.02534114	0.967184016	0.9940037

211980_at	COL4A1	collagen, type IV, alpha 1	1282	-0.01874739	0.977820792	0.9959916
201438_at	COL6A3	collagen, type VI, alpha 3	1293	0.009703779	0.9863171	0.9970689
74694_s_at	RABEP2	rabaptin, RAB GTPase binding effector protein 2	79874	0.011843173	0.981583585	0.9961445
211719_x_at	FN1	fibronectin 1	2335	0.037210894	0.973177363	0.9950096
202404_s_at	COL1A2	collagen, type I, alpha 2	1278	0.034227062	0.972988883	0.9950096
204655_at	CCL5	chemokine (C-C motif) ligand 5	6352	0.038628831	0.965309914	0.9935003
216442_x_at	FN1	fibronectin 1	2335	0.054191701	0.95355946	0.9912349
210495_x_at	FN1	fibronectin 1	2335	0.058226728	0.951550365	0.9910374
212464_s_at	FN1	fibronectin 1	2335	0.081392657	0.933688332	0.988994
211161_s_at	COL3A1	collagen, type III, alpha 1	1281	0.056146834	0.930500411	0.9881951
212667_at	SPARC	secreted protein, acidic, cysteine-rich (osteonectin)	6678	0.058151732	0.926810399	0.9875364
202627_s_at	SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	5054	0.130825837	0.842575178	0.9702264
213757_at	EIF5A	eukaryotic translation initiation factor 5A	1984	0.138314467	0.836269539	0.9684535
202600_s_at	NRIP1	nuclear receptor interacting protein 1	8204	0.146667606	0.81125437	0.9660204
202237_at	NNMT	nicotinamide N-methyltransferase	4837	0.357137196	0.643404225	0.9262055
201666_at	TIMP1	TIMP metallopeptidase inhibitor 1	7076	0.178832267	0.632222051	0.9248966
204018_x_at	HBA1	hemoglobin, alpha 1	3039	0.503353692	0.544752592	0.8986814
200999_s_at	CKAP4	cytoskeleton-associated protein 4	10970	0.335798499	0.541539556	0.8965721
204622_x_at	NR4A2	nuclear receptor subfamily 4, group A, member 2	4929	0.334447219	0.497538974	0.8848345
203394_s_at	HES1	hairy and enhancer of split 1, (Drosophila)	3280	0.443814733	0.487186309	0.8828267
206157_at	PTX3	pentraxin 3, long	5806	0.494269798	0.426649316	0.8638802
205382_s_at	CFD	complement factor D (adipsin)	1675	0.493713983	0.395763648	0.8528093
217414_x_at	HBA1	hemoglobin, alpha 1	3039	0.792680859	0.377115905	0.8469171
211745_x_at	HBA1	hemoglobin, alpha 1	3039	0.872403284	0.371311295	0.8441546
214414_x_at	HBA1	hemoglobin, alpha 1	3039	0.997898457	0.369791698	0.8441546
211699_x_at	HBA1	hemoglobin, alpha 1	3039	0.740693292	0.368184583	0.844099
209458_x_at	HBA1	hemoglobin, alpha 1	3039	0.850433299	0.356237193	0.8404624
212077_at	CALD1	caldesmon 1	800	0.588320285	0.348578502	0.8401911
216248_s_at	NR4A2	nuclear receptor subfamily 4, group A, member 2	4929	0.570789503	0.342393968	0.8375489
219403_s_at	HPSE	heparanase	10855	0.691038194	0.269546864	0.8062958
201110_s_at	THBS1	thrombospondin 1	7057	0.670401219	0.251133297	0.8008466
203395_s_at	HES1	hairy and enhancer of split 1, (Drosophila)	3280	0.85070808	0.193692	0.7743035
200629_at	WARS	tryptophanyl-tRNA synthetase	7453	0.666045516	0.186006457	0.7721508

201669_s_at	MARCKS	myristoylated alanine-rich protein kinase C substrate	4082	0.759568605	0.132720593	0.7472316
201195_s_at	SLC7A5	solute carrier family 7 (amino acid transporter light chain, L system), member 5	8140	0.824741527	0.116329142	0.7382591
204419_x_at	HBG1	hemoglobin, gamma A	3047	1.666375122	0.09142905	0.723603
204848_x_at	HBG1	hemoglobin, gamma A	3047	1.565419124	0.086123226	0.7221941
219410_at	TMEM45A	transmembrane protein 45A	55076	0.991276475	0.082130669	0.7221941
217388_s_at	KYNU	kynureninase	8942	1.468313974	0.069766007	0.7032894
209290_s_at	NFIB	nuclear factor I/B	4781	1.089323355	0.04758335	0.6754948
202870_s_at	CDC20	cell division cycle 20	991	1.339488946	0.036576735	0.658786
217232_x_at	HBB	hemoglobin, beta	3043	1.819045943	0.03458682	0.658786
213515_x_at	HBG1	hemoglobin, gamma A	3047	2.417286959	0.029878597	0.651733
209773_s_at	RRM2	ribonucleotide reductase M2	6241	1.767337745	0.021613828	0.6316009
211696_x_at	HBB	hemoglobin, beta	3043	1.960802898	0.020715624	0.6316009
206698_at	XK	X-linked Kx blood group (McLeod syndrome)	7504	1.473769082	0.01474655	0.5951742
212589_at	RRAS2	related RAS viral (r-ras) oncogene homolog 2	22800	1.248921748	0.010895573	0.5870789
209116_x_at	HBB	hemoglobin, beta	3043	2.529691269	0.008815809	0.5680662
215772_x_at	SUCLG2	succinate-CoA ligase, GDP-forming, beta subunit	8801	1.175819449	0.008054348	0.5660139
201890_at	RRM2	ribonucleotide reductase M2	6241	2.141037934	0.003660296	0.4760098
209894_at	LEPR	leptin receptor	3953	2.015713837	0.00114085	0.3805249
219602_s_at	PIEZO2	piezo-type mechanosensitive ion channel component 2	63895	1.504577032	7.50E-05	0.1179278
205848_at	GAS2	growth arrest-specific 2	2620	2.492595762	1.11E-05	0.0274403

Table S6b. Differential expression of the 102 core genes by the 12 PV patients with an indolent phenotype.

Probeset ID	***Symbol (Na32 consesus Mar13)***	***Gene Title (Na32 consensus Mar13)***	***GeneID (concensus1 Mar-13)***	***Log2(FC)***	***P-Value***	***Adjusted p-Value***
208949_s_at	LGALS3	lectin, galactoside-binding, soluble, 3	3958	-2.46115508	4.71E-07	0.0008705
201666_at	TIMP1	TIMP metallopeptidase inhibitor 1	7076	-1.63941887	2.35E-05	0.0042807
201058_s_at	MYL9	myosin, light chain 9, regulatory	10398	-2.74636917	3.07E-05	0.0046717
207815_at	PF4V1	platelet factor 4 variant 1	5197	-2.82238801	5.35E-05	0.0058277
1405_i_at	CCL5	chemokine (C-C motif) ligand 5	6352	-3.32636522	5.85E-05	0.0060359
213524_s_at	G0S2	G0/G1switch 2	50486	-2.65614662	0.0001262	0.007998
201631_s_at	IER3	immediate early response 3	8870	-2.29780898	0.000169	0.009257
204655_at	CCL5	chemokine (C-C motif) ligand 5	6352	-3.23424391	0.0002336	0.0105336
203535_at	S100A9	S100 calcium binding protein A9	6280	-2.4351969	0.0003703	0.0133722
212077_at	CALD1	caldesmon 1	800	-2.04255108	0.0006877	0.0178246
210873_x_at	APOBEC3A	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3A	200315	-1.76920321	0.0023357	0.032102
212531_at	LCN2	lipocalin 2	3934	-1.74944593	0.0029164	0.0363335
205114_s_at	CCL3L3	chemokine (C-C motif) ligand 3-like 3	414062	-2.11268057	0.0038941	0.0419976
208180_s_at	HIST1H4H	histone cluster 1, H4h	8365	-1.58614736	0.0040832	0.0431848
205237_at	FCN1	ficolin (collagen/fibrinogen domain containing) 1	2219	-2.31794481	0.0041427	0.0434495
214414_x_at	HBA1	hemoglobin, alpha 1	3039	-2.92561932	0.0044286	0.0449487
209803_s_at	PHLDA2	pleckstrin homology-like domain, family A, member 2	7262	-1.71861099	0.0046599	0.0462831
201438_at	COL6A3	collagen, type VI, alpha 3	1293	-1.45596175	0.0055357	0.0504893
205547_s_at	TAGLN	transgelin	6876	-1.89686803	0.0062053	0.0538116
211074_at	FOLR1	folate receptor 1 (adult)	2348	-2.33500441	0.0071061	0.0579213
221556_at	CDC14B	cell division cycle 14B	8555	-1.35462909	0.0072261	0.0582223
211745_x_at	HBA1	hemoglobin, alpha 1	3039	-2.39194906	0.0073721	0.0586827
204141_at	TUBB2A	tubulin, beta 2A class IIa	7280	-2.13929618	0.0077476	0.0602366
204018_x_at	HBA1	hemoglobin, alpha 1	3039	-1.9801303	0.0092138	0.0661068
201798_s_at	MYOF	myoferlin	26509	-1.51465891	0.009894	0.0682173
209458_x_at	HBA1	hemoglobin, alpha 1	3039	-2.13257405	0.0108016	0.071832

217414_x_at	HBA1	hemoglobin, alpha 1	3039	-2.0496731	0.0117787	0.0752125
211964_at	COL4A2	collagen, type IV, alpha 2	1284	-1.30406638	0.0122956	0.0767626
205442_at	MFAP3L	microfibrillar-associated protein 3-like	9848	-1.52050559	0.0134371	0.0808545
214974_x_at	CXCL5	chemokine (C-X-C motif) ligand 5	6374	-1.55942048	0.0144079	0.083963
202310_s_at	COL1A1	collagen, type I, alpha 1	1277	-1.87618778	0.0168309	0.0918907
219403_s_at	HPSE	heparanase	10855	-1.31934206	0.0184966	0.0968056
212667_at	SPARC	secreted protein, acidic, cysteine-rich (osteonectin)	6678	-1.34731184	0.0188123	0.0976538
200999_s_at	CKAP4	cytoskeleton-associated protein 4	10970	-1.14939507	0.0204052	0.1017426
204834_at	FGL2	fibrinogen-like 2	10875	-1.46819648	0.0227746	0.1072555
216442_x_at	FN1	fibronectin 1	2335	-1.90725545	0.023141	0.1081658
201842_s_at	EFEMP1	EGF containing fibulin-like extracellular matrix protein 1	2202	-1.50062086	0.0247947	0.1121383
212464_s_at	FN1	fibronectin 1	2335	-1.96352838	0.0258307	0.1143867
211719_x_at	FN1	fibronectin 1	2335	-2.20581999	0.0267964	0.1164775
210495_x_at	FN1	fibronectin 1	2335	-1.90768224	0.026965	0.1168453
216248_s_at	NR4A2	nuclear receptor subfamily 4, group A, member 2	4929	-1.17498747	0.0282382	0.1197257
211699_x_at	HBA1	hemoglobin, alpha 1	3039	-1.60001534	0.0291616	0.1216234
217683_at	HBE1	hemoglobin, epsilon 1	3046	-1.01631722	0.0327501	0.1295902
202627_s_at	SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	5054	-1.241552	0.0352569	0.1349566
203394_s_at	HES1	hairy and enhancer of split 1, (Drosophila)	3280	-1.1913737	0.0362517	0.1371457
211980_at	COL4A1	collagen, type IV, alpha 1	1282	-1.25680354	0.0372348	0.139094
204622_x_at	NR4A2	nuclear receptor subfamily 4, group A, member 2	4929	-0.91072954	0.037958	0.1405444
215076_s_at	COL3A1	collagen, type III, alpha 1	1281	-1.43307205	0.0385845	0.1417739
202403_s_at	COL1A2	collagen, type I, alpha 2	1278	-1.44054881	0.0465026	0.1564484
202404_s_at	COL1A2	collagen, type I, alpha 2	1278	-1.71166248	0.0565387	0.1733135
210809_s_at	POSTN	periostin, osteoblast specific factor	10631	-1.70047318	0.0592192	0.1779858
200629_at	WARS	tryptophanyl-tRNA synthetase	7453	-0.81407303	0.0632647	0.1842488
205382_s_at	CFD	complement factor D (adipsin)	1675	-0.93430533	0.0674121	0.1911642
211161_s_at	COL3A1	collagen, type III, alpha 1	1281	-0.97790719	0.0849171	0.216434
202237_at	NNMT	nicotinamide N-methyltransferase	4837	-1.16905976	0.0849883	0.216541
206157_at	PTX3	pentraxin 3, long	5806	-0.8886965	0.1017166	0.2401657
222044_at	PCIF1	PDX1 C-terminal inhibiting factor 1	63935	-0.59010446	0.1405898	0.2902372
203395_s_at	HES1	hairy and enhancer of split 1, (Drosophila)	3280	-0.82856755	0.1406431	0.2902934

214041_x_at	RPL37A	ribosomal protein L37a	6168	-0.49636026	0.2288142	0.3892891
213668_s_at	SOX4	SRY (sex determining region Y)-box 4	6659	-0.74126503	0.2366512	0.397241
214911_s_at	BRD2	bromodomain containing 2	6046	-0.55589849	0.237402	0.3980366
213515_x_at	HBG1	hemoglobin, gamma A	3047	-1.06377	0.2466641	0.407885
204419_x_at	HBG1	hemoglobin, gamma A	3047	-0.908371	0.2734668	0.4340414
208892_s_at	DUSP6	dual specificity phosphatase 6	1848	-0.62624686	0.3054404	0.4659019
201669_s_at	MARCKS	myristoylated alanine-rich protein kinase C substrate	4082	-0.4343098	0.308411	0.4689854
201324_at	EMP1	epithelial membrane protein 1	2012	-0.26518451	0.3157697	0.476429
204848_x_at	HBG1	hemoglobin, gamma A	3047	-0.73774161	0.3338994	0.4939304
213350_at	RPS11	ribosomal protein S11	6205	-0.59851213	0.3525386	0.5113994
213593_s_at	TRA2A	transformer 2 alpha homolog (Drosophila)	29896	-0.51180921	0.3529863	0.5117818
209374_s_at	IGHM	immunoglobulin heavy constant mu	3507	-0.31785029	0.3800608	0.5367239
213979_s_at	---	---	---	-0.40184672	0.4828663	0.6262323
201110_s_at	THBS1	thrombospondin 1	7057	-0.32862948	0.50663	0.645676
212952_at	LOC100507328	hypothetical LOC100507328	100507328	-0.3705879	0.5288342	0.6639313
213757_at	EIF5A	eukaryotic translation initiation factor 5A	1984	-0.30685777	0.5926473	0.7155269
201195_s_at	SLC7A5	solute carrier family 7 (amino acid transporter light chain, L system), member 5	8140	-0.21795555	0.6192996	0.7368622
217232_x_at	HBB	hemoglobin, beta	3043	-0.28037802	0.690155	0.7905057
206698_at	XK	X-linked Kx blood group (McLeod syndrome)	7504	-0.15354275	0.7519213	0.8333529
209116_x_at	HBB	hemoglobin, beta	3043	-0.22011194	0.7745612	0.8490507
208960_s_at	KLF6	Kruppel-like factor 6	1316	-0.0669692	0.8198308	0.8804886
211696_x_at	HBB	hemoglobin, beta	3043	-0.11853666	0.8626478	0.9090874
212589_at	RRAS2	related RAS viral (r-ras) oncogene homolog 2	22800	-0.03039679	0.9381282	0.9597619
74694_s_at	RABEP2	rabaptin, RAB GTPase binding effector protein 2	79874	-0.02974959	0.9459227	0.9655037
205933_at	SETBP1	SET binding protein 1	26040	-0.00557713	0.9639004	0.976948
219410_at	TMEM45A	transmembrane protein 45A	55076	-0.01300971	0.9780245	0.9864563
209183_s_at	C10orf10	chromosome 10 open reading frame 10	11067	0.053999237	0.7924264	0.8612892
217388_s_at	KYNU	kynureninase	8942	0.220147884	0.7422951	0.8265151
204872_at	TLE4	transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila)	7091	0.119923227	0.6919854	0.7913794
209290_s_at	NFIB	nuclear factor I/B	4781	0.179441546	0.6912758	0.7909339
209069_s_at	H3F3B	H3 histone, family 3B (H3.3B)	3021	0.099846114	0.6841093	0.7862131
209763_at	CHRDL1	chordin-like 1	91851	0.050254159	0.6660676	0.7731502

208961_s_at	KLF6	Kruppel-like factor 6	1316	0.203610948	0.5862653	0.7103285
219922_s_at	LTBP3	latent transforming growth factor beta binding protein 3	4054	0.265731289	0.5441646	0.676381
210487_at	DNTT	deoxynucleotidyltransferase, terminal	1791	0.159844182	0.4049727	0.5588841
202600_s_at	NRIP1	nuclear receptor interacting protein 1	8204	0.470263901	0.374044	0.5310937
211998_at	H3F3B	H3 histone, family 3B (H3.3B)	3021	0.303014616	0.3488911	0.5083632
219304_s_at	PDGFD	platelet derived growth factor D	80310	0.277596346	0.298783	0.4593071
204897_at	PTGER4	prostaglandin E receptor 4 (subtype EP4)	5734	0.607994686	0.2274529	0.3875045
202870_s_at	CDC20	cell division cycle 20	991	0.762009765	0.1538922	0.3060777
220990_s_at	MIR21	microRNA 21	406991	0.435464726	0.1444477	0.2949163
220377_at	KIAA0125	KIAA0125	9834	0.487203922	0.1414233	0.2913494
215772_x_at	SUCLG2	succinate-CoA ligase, GDP-forming, beta subunit	8801	0.540170913	0.1340248	0.2820253
204563_at	SELL	selectin L	6402	0.910468161	0.0926084	0.2277875
211597_s_at	HOPX	HOP homeobox	84525	0.686080974	0.0787633	0.2073318
205984_at	CRHBP	corticotropin releasing hormone binding protein	1393	0.67956433	0.0697279	0.1948001
208835_s_at	LUC7L3	LUC7-like 3 (S. cerevisiae)	51747	0.690777363	0.0676605	0.1915926
221760_at	MAN1A1	mannosidase, alpha, class 1A, member 1	4121	0.824262339	0.0582629	0.1763029
201369_s_at	ZFP36L2	ZFP36 ring finger protein-like 2	678	0.748937338	0.0520224	0.1657888
209773_s_at	RRM2	ribonucleotide reductase M2	6241	1.272153164	0.0495607	0.1616025
204304_s_at	PROM1	prominin 1	8842	0.925426909	0.0237482	0.1095213
209894_at	LEPR	leptin receptor	3953	1.184929139	0.0181485	0.0959498
203787_at	SSBP2	single-stranded DNA binding protein 2	23635	0.75811153	0.0063777	0.0544303
201890_at	RRM2	ribonucleotide reductase M2	6241	1.743455889	0.0052954	0.0493966
219602_s_at	PIEZO2	piezo-type mechanosensitive ion channel component 2	63895	0.949014365	0.0017907	0.0285001
204755_x_at	HLF	hepatic leukemia factor	3131	0.692860181	0.0017806	0.0285001
204753_s_at	HLF	hepatic leukemia factor	3131	0.867266686	0.0016555	0.0275765
209576_at	GNAI1	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1	2770	0.736228442	0.0015849	0.0269254
214805_at	EIF4A1	eukaryotic translation initiation factor 4A1	1973	0.894052441	0.001431	0.025337
209112_at	CDKN1B	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	1027	1.181992974	0.0007491	0.0186168
214651_s_at	HOXA9	homeobox A9	3205	1.466348689	0.0006873	0.0178246
219777_at	GIMAP6	GTPase, IMAP family member 6	474344	0.787293816	0.000565	0.016422
204430_s_at	SLC2A5	solute carrier family 2 (facilitated glucose/fructose transporter), member 5	6518	0.916940276	0.0004539	0.0149986

206478_at	KIAA0125	KIAA0125	9834	1.699585816	7.39E-05	0.0063689
220416_at	ATP8B4	ATPase, class I, type 8B, member 4	79895	1.319886477	6.56E-05	0.0061373
205848_at	GAS2	growth arrest-specific 2	2620	1.882945739	5.69E-05	0.0059648
204030_s_at	IQCJ-SCHIP1	IQCJ-SCHIP1 readthrough	100505385	1.123786747	5.04E-05	0.0057459

Table S7. Primers used to construct plasmids for standard curve generation in the Q-RT-PCR 10 gene assay.

Gene Symbol:	region of cDNA:	5' primer (5’-3’):	3' primer (5’-3’):	insert size (bp):
CDKN1A	full length	TGCCGAAGTCAGTTCCTTGT	TGCCGAAGTCAGTTCCTTGT	634
CTSA	3’	CCCAAGCTTCAGCTGCTTCCACCTACCTC	CCCAAGCTTGGAGCTGGTTGCTGTGGTC	478
IFI30	full length	CCCAAGCTTGCAGTCGCCACACCTTTG	CCCAAGCTTCACTCGCCTTCCATGAGC	840
MYL9	full length	CACCCACCAGAAGCCAAG	CTGGGAACTGGGACCCTAAC	506
PCNA	full length	CCCAAGCTTGCTCTTCCCTTACGCAAGTCT	CCCAAGCTTGCTGGCATCTTAGAAGCAGTT	1000
SMC4	3’	TGAGGACAAAGCAGCAGAGGTCG	GAGTTCGGCGTCCCCTCCCA	589
SON	3’	GCTCAGGAAAGGATTGATGC	CTGTGGCTTTAGCATGCTTCT	588
TIA1	3’	AGTGGCTTGGTGGAAGACAA	CACTCCCTGTAGCCTCAAGC	536
TSN	full length	CCCAAGCTTGCTACACTGGCTGATTGTTG	CCCAAGCTTGCGCAGTGTTTAGCAACTGA	845
CTTN	full length	n/a	n/a	3000
ACTB	5’	GCACAGAGCCTCGCCTTT	CAGGCAGCTCGTAGCTCTTC	787

Table S8. Primer/probe sets for the Q-RT-PCR 10 gene assay.

ABI GEX Assay ID	Gene Symbol	Gene Name	GEX Target Exon Boundaries
Hs00952870_g1	PCNA	proliferating cell nuclear antigen	4-5
Hs00908857_g1	IFI30	interferon, gamma-inducible protein 30	6-7
Hs00172824_m1	TSN	translin	5-6
Hs01563956_g1	CTSA	cathepsin A	13-14
Hs00909708_g1	SMC4	structural maintenance of chromosomes 4	21-22
Hs00355782_m1	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	2-3
Hs01124227_m1	CTTN	cortactin	17-18
Hs01066142_g1	SON	SON DNA binding protein	11-12
Hs01046922_m1	TIA1	TIA1 cytotoxic granule-associated RNA binding protein	10-11
Hs00382913_m1	MYL9	myosin, light chain 9, regulatory	2-3

Table S9a: Inter-assay comparisons of different cDNA preparations made from the same RNA sample.

A	Patient #	Blood Sample Date	Ten gene score
	1	9/8/2011	5
			5
	2	11/25/2008	2
			2
	3	11/25/2003	5
			5
	4	8/9/2011	3
			3
	5	3/6/2012	3
			4
	6	7/3/2012	5
			6
	7	9/26/2006	5
			5
	8	6/12/2012	4
			4

Table S9b: Inter-assay comparisons of cDNA preparations from two different blood samples from the same patient during a 6 month period during which there was no change in patient clinical phenotype.

B	Patient #	Blood Sample Date	Ten gene score:
	9	6/20/2012	5
		6/22/2012	6
	10	4/17/2012	4
		10/2/2012	4
	11	6/14/2012	3
		10/9/2012	2

Table S10. Clinical features by gender of the 8 patient training set for the 10 gene assay.

	Men (2)	Women (6)*
Median Age (years; range)	72	71[&] (46-84)
Median Disease Duration (years; range)	13 (1-25)	11.5[&] (4-18)
Median JAK2 V617F Neutrophil Allele Burden (%; range)	84 (68-100)	74[&] (52-100)
Median Hemoglobin (g/dL; range) (g/L; range)	13.1(12.5- 13.7) (131) (125-137)	10.7[&] (8.8-15.7) (107)[&] (88-157)
Median Leukocyte Count (10^3/µL; range) (10^9/L; range)	16.550 (16.400-16.700)	12.650[&] (5.000-50.000)
Median Platelet Count (10^3/µL; range) (10^9/µL; range)	601.500 (491.000-712.000)	959.500[&](183.000-1,480.000)
Median Spleen size (cm; range)	10 (0-20)	1[&] (0-5)

* One patient was assayed at 2.5 years and 6 months before clinically apparent transformation to acute leukemia and is represented twice because her 10 gene assay score went from 4 to 6 and subsequently remained above 4. [&] not significantly different

Table S11. Clinical features of the 8 patient training set and their 10 gene assay scores.

Gender	Age (years)	Disease Duration (years)	JAK2 V617F Allele Burden (%)	Hemoglobin (g/dL) (g/L)	Leukocyte Count (10^3/µL) (10^9/L)	Platelet Count (10^3/µL) (10^9/L)	Spleen Size (cm)	Splenectomy	Thrombosis	Therapy	Acute Leukemia	Alive	Gene Expression Phenotype	10 Gene Assay Score
F	48	18	100	10.4 (104)	50.000	1,017.000	5	Yes	Yes	Yes	Yes	No	Aggressive	6
M	72	25	100	12.5 (125)	16.700	491.000	20	Yes	No	Yes	No	No	Aggressive	5
F*	84	13	68	8.8 (88)	9.000	971.000	2	Yes	No	Yes	Yes	No	Aggressive	6
F*	82	10	52	11.5 (115)	5.000	948.000	0	No	No	Yes	No	Yes	Indolent	3
M	72	1	68	13.7 (137)	16.400	712.000	0	No	No	No	No	Yes	Indolent	4
F	46	4	82	11.1 (111)	20.500	1,480.000	0	No	No	Yes	No	Yes	Indolent	4
F	71	1	100	14.7 (147)	22.790	332.000	0	No	No	No	No	Yes	Indolent	3
F	60	9	60	12.5 (125)	13.800	1,117.000	4	No	No	No	No	Yes	Indolent	3

* This patient, who was part of the indolent group in the original 19 patient gene expression profiling cohort, subsequently transformed to acute leukemia four years after gene expression profiling and is represented by two 10 gene assay scores: one 2.5 years before and one 6 months before the leukemia was clinically apparent, which subsequently remained above 4.

Table S12. Clinical phenotype of the 8 patient training set segregated according to their 10 gene assay score.

Phenotype	10 Gene Score		p Value
	>4	<5	
Gender (M/F)	1/2*	1/4*	-
Age (years, median)	72	72	ns&
(range)	(48-84)	(46-82)	
Disease Duration (years, median)	18	5	P = 0.031¶
(range)	(13-25)	(1-15)	
Jak2 V 617F neutrophil allele burden (%)	100	68	ns
(range)	(68-100)	(52-82)	
Hemoglobin (g/dL, median) (g/L; median)	10.4 (104)	11.5 (115)	ns
(range)	(8.8-12.5) (88-125)	(10.4-15.7) (104-157)	
Leukocyte count(10^3/µL, median) (10^9/L; median)	16.700	16.000	ns
(range)	(9.000-50.000)	(5.000-20.500)	
Platelet count ((10^3/µL, median) (10^9/L; median)	971.000	890.000	ns
(range)	(491.000- 1,000.000)	(183.000-1,480.000)	
Thrombosis (n)	1/3	0/5	ns
Palpable splenomegaly (n)	3/3	1/5	ns
Spleen size (cm)	5	0	ns
(range)	(2-20)	(0-4)	
Splenectomy (n)	3/3	0/5	0.017#
Chemotherapy (n)	3/3	3/5	ns
Transformation to AML	2/3	0/5	ns
Survival (n)	0/3	4/5	ns

* One patient was assayed at 2.5 years and 6 months before clinically apparent transformation to acute leukemia and is represented in each group because her 10 gene score went from 4 to 6 and subsequently remained above 4. &not significantly different

¶Student t Test # Fisher Exact Probability Test (two-tailed)

Table S13. Clinical features by gender of the 30 patient test set for the 10 gene assay.

	Men (12)	Women (18)
Median Age (years; range)	69.5 (54-77)	63.5$^{\&}$ (43-79)
Median Disease Duration (years; range)	7 (2-27)	11.5$^{\&}$ (1-39)
Median JAK2 V617F Neutrophil Allele Burden (%; range)	89.5 (48-100)	84.0$^{\&}$ (44-100)
Median Hemoglobin (g/d; range) (g/L; range)	12.9 (10.3-16.0) (129) (103-160)	12.0$^{\&}$ (8.3-15.9) (120) (83-159)
Median Leukocyte Count (10^3/µL; range) (10^9/L; range)	16.800 (7.700-34.100)	11.500$^{\&}$ (5.400-98.500)
Median Platelet Count (10^3/µL; range) (10^9/L; range)	664.000 (110.000-996.000)	492.500$^{\&}$ (38.000-1,556.000)
Median Spleen size (cm; range)	2.0 (0-28)	4.0$^{\&}$ (0-14)

$^{\&}$not significantly different

Table S14. Clinical features of the 30 patient test set with their 10 gene assay scores.

Gender	Age (years)	Disease Duration (years)	Hemoglobin (g/dL) (g/L)	Leukocyte count (10^3/µL) (10^9/L)	Platelet count (10^3/µL) (10^9/L)	Spleen size (cm below the left costal margin)	Splenectomy	JAK2 V617F neutrophil allele burden (%)	Thrombosis	Therapy	10 gene assay score
F	66	12	10.5 (105)	98.500	599.000	Unknown	Yes	100	Yes	Phlebotomy, Hydroxyurea, Anagrelide, Interferon	5
M	54	3	12.1 (121)	15.600	559.000	0	No	90	No	Phlebotomy	2
F	48	3	14.0 (140)	28.200	779.000	0	No	96	No	Phlebotomy	4
F	68	13	13.4 (134)	31.000	422.000	Unknown	Yes	97	Yes	Hydroxyurea	3
M	60	7	12.8 (128)	34.100	959.000	0	No	94	No	Phlebotomy	4
F	64	19	9.8 (98)	39.000	434.000	14	No	90	No	Phlebotomy, Interferon, Anagrelide, TKI*	6
F	66	17	9.3 (93)	5.400	1,556.000	0	No	50	No	Phlebotomy	3
M	77	10	10.7 (107)	24.800	996.000	4	No	97	No	Phlebotomy, Hydroxyurea	2
M	71	6	10.3 (103)	17.200	1,320.000	0	No	52	No	Phlebotomy	2
M	57	3	13.6 (136)	16.400	673.000	0	No	89	No	Phlebotomy	4
F	74	16	15.7 (157)	11.800	811.000	0	No	44	No	Phlebotomy	3
F	64	6	12.0 (120)	22.180	779.000	0	No	64	No	Phlebotomy	3
F	53	24	11.0 (110)	35.200	60.000	14	No	94	Yes	Phlebotomy, hydroxyurea, Interferon, TKI	6
F	63	9	11.8	11.200	177.000	10	No	87	Yes	Phlebotomy	6

			(118)								
M	75	2	13.1 (131)	13.400	936.000	0	No	48	No	Phlebotomy	1
F	79	7	12.0 (120)	26.000	605.000	4	No	81	No	Phlebotomy	4
M	71	2	16.0 (160)	30.600	849.000	2	No	95	No	Phlebotomy	3
F	56	39	8.5 (85)	6,770	38.000	14	No	94	Yes	Phlebotomy, Cytoxan, Splenic irradiation, Thalidomide, TKI	6
F	48	1	13.0 (130)	11.000	551.000	0	No	44	No	Phlebotomy	3
F	46	11	12.3 (123)	46.000	186.000	14	No	94	No	Phlebotomy, Interferon	6
M	68	17	12.6 (126)	10.700	500.000	8	No	100	No	Phlebotomy, Hydroxyurea, Interferon, TKI	5
M	58	8	15.5 (155)	21.000	655.000	3	No	81	No	Phlebotomy	4
F	43	7	10.2 (102)	7.460	695.000	3	No	44	Yes	Phlebotomy	3
F	64	26	13.2 (132)	6.230	169,000	10	No	49	Yes	Phlebotomy, hydroxyurea, irradiation	0
M	76	12	12.7 (127)	26.700	817.000	28	No	98	Yes	Phlebotomy, Anagrelide, Hydroxyurea, Interferon	5
F	61	20	10.8 (108)	10.600	158.000	6	No	52	No	Phlebotomy, Interferon	5
M	64	7	14.0 (140)	7.700	439.000	0	No	49	Yes	Phlebotomy	2
M	75	27	15.8 (158)	13.400	110.000	5	No	87	Yes	Phlebotomy, Hydroxyurea	5
F	71	11	13.7 (137)	6.530	585.000	0	No	51	No	Phlebotomy	4
F	63	10	15.9 (159)	10.000	384.000	0	No	90	No	Phlebotomy Interferon	4

*TKI, tyrosine kinase inhibitor

Table S15. Clinical phenotype of the 30 patient test set segregated according to their 10 gene assay score.

Phenotype	10 Gene Score		p Value
	>4	<5	
Gender (M/F)	3/7	9/11	ns&
Age (years, median)	63.5	64	ns
(range)	(46-76)	(43-79)	
Disease Duration (years, median)	18	7	P< 0.001§
(range)	(9-39)	(1-26)	
Jak2 V 617F neutrophil allele burden (%)	94	72	P < 0.021§
(range)	(52-100)	(44-97)	
Hemoglobin (g/dL; median) (g/L; median)	11.4 (114)	13.1 (131)	ns
(range)	(8.5-15.8) (85-158)	(9.3-16.0) (93-160)	
Leukocyte count (10^3/µL; median) (10^9/L; median)	20.050	16.000	ns
(range)	(6.770-98.500)	(5.400-34.100)	
Platelet count (10^3/µL; median) (10^9/µL;median)	181.500	684.000	P < 0.001¶
(range)	(38.000-817.000)	(169.000-1,556.0000)	
Thrombosis (n)	6/10	4/20	P=0.044#
Palpable splenomegaly (n)	10/10	7/20	P < 0.001#
Spleen size (median, cm)	14	0	P < 0.001§
(range)	(5-28)	(0-10)	
Splenectomy (n)	1/10	0/20	ns
Chemotherapy (n)	6/10	3/20	P < 0.030#
Transformation to AML (n)	0/10	0/20	-
Survival (n)	9/10	20/20	ns

&ns = not significantly different ¶Student t Test #Fisher Exact Probability Test (two-tailed) §Mann-Whitney Rank Sum Test

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