SUPPLEMENTARY MATERIALS

Signatures of $CD8^+$ T-cell dysfunction in AML patients and their reversibility with response to chemotherapy

Hanna A. Knaus, Sofia Berglund, Hubert Hackl, Amanda L. Blackford, Joshua F. Zeidner, Raúl Montiel-Esparza, Rupkatha Mukhopadhyay, Katrina Vanura, Bruce R. Blazar, Judith E. Karp, Leo Luznik*, Ivana Gojo*

*Corresponding authors. E-mail: luznile@jhmi.edu, igojo1@jhmi.edu

The file includes:

Table S5. Ingenuity Pathway Analysis of differentially expressed genes in pre-treatment AML patients relative to healthy controls.

Table S6. Ingenuity Pathway Analysis of differentially expressed genes in CR relative to NR AML patients post induction chemotherapy.

Table S7. Characteristics of AML patients-summary.

Table S8. Detailed clinical information on AML patients.

Table S9. Statistical comparison of $CD8^+$ T-cell differentiation subsets in PB and BM, before and after treatment.

Table S10. Antibodies used for flow cytometric analyses.

SUPPLEMENTARY METHODS

Quantitative real-time polymerase chain reaction

RNA was isolated and purified from sorted PB CD3$^+$CD8$^+$ T-cells and total RNA was amplified using the NuGEN™ Ovation Pico WTA system. cDNA was pre-amplified with the TaqMan PreAmp Master Mix Kit (Thermo Fisher Scientific) using manufacturer's protocol. Relative target gene expression was determined by multiplexed qPCR using an Applied Biosystems (ABI) StepOnePlus System. Samples were run in duplicate using primer/probe sets for the FAM-labeled target genes and GAPDH as endogenous control. The TaqMan primer/probe sets [Hs01007422_m1, (CD28), Hs01013469_m1 (CCR7), Hs00163934_m1 (CD40LG), Hs00172872_m1 (EOMES), Hs00195153_m1 (KLRG1), Hs00894392_m1 (TBX21), Hs00188051_m1(GZMB), and Hs02786624_g1 (GAPDH)] and other ABI reagents were from Thermo Fisher Scientific. Expression relative to the housekeeping gene GADPH was determined and log2 fold changes of patients relative to the mean of HC samples were calculated.

viSNE and CITRUS bioinformatics tools

viSNE analysis was performed as previously published by Amir et al. (1). Samples included in the analysis were gated and exported as separate .fcs files including only CD8$^+$ T-cells using flowjo v10, and imported into the CYT tool. The measured fluorescence intensity data of the samples were transformed using the arcsin function with a co-factor of 150. Randomly generated subsamples were extracted from each sample to adjust all groups of samples to include the same number of events, and thus make the groups comparable (the number of cells extracted for analysis from each sample varied between analyses, depending on the size of the included samples, from 600-2500 cells/sample).

The CITRUS tool was used as previously described (2). The CITRUS tool associates clusters of phenotypically similar cells with group-related parameters. Hierarchical clustering is performed using Ward's linkage and Euclidean distance. Cells were clustered based on the fluorescence intensity of the markers. The fluorescence intensity data were transformed using the arcsin function with a co-factor of 150, as instructed for flow cytometry in the software instruction. Repeated re-analysis with identical parameters confirmed that the results were reproducible. One thousand events were sampled from each patient sample for clustering. Minimum cluster size was 5% of all cells. Associations between groups and cluster properties were then identified using the SAM quantitative method (3).

Statistical and data analysis

For *in vitro* studies, log-scale mean percentages of CD8$^+$ T-cells expressing each marker were calculated using standard- and mixed-effects linear regression models, and interaction for the effect of IL-2 and blasts between the AML patients and HC group was assessed. For T-cell expansion analysis, differences in log-scale fold-changes were calculated using the MLME framework. Specifically, log-scale fold-changes were included as dependent terms in linear regression models that included fixed effects for the difference of interest (cell type, agent, time point or sample) with random intercept for the subject to account for clustering. Ninetyfive percent confidence intervals for fold changes on the natural scale were obtained by exponentiating confidence intervals obtained from regression models on the logarithmic scale. For specific comparisons of interest between time points, cell types and/or agents, appropriate contrasts of the regression parameter estimates were derived. The mixed effects modelling and standard linear regression modelling were completed using R version 3.3.2. The IRs' co-expression was analyzed with SPICE software version 5.3 (4). Heatmaps were created with Morpheus (https://software.broadinstitute.org/morpheus/) or CIMminer (https://discover.nci.nih.gov/cimminer/), using Pearson correlation and average linkage cluster algorithm.

For simple comparisons, data were analyzed with the Mann–Whitney *U* test or an unpaired *t* test when comparing measurements between different groups or with the Wilcoxon sum-rank test or a paired *t* test when comparing measurements between different interventions or time points in the same group. Mann-Whitney *U* test, Wilcoxon sum-rank test or *t* test results are reported in the text, and are shown in the figures as indicated. GraphPad Prism 6 (GraphPad Software) was used for data presentation. These analyses were exploratory, and no adjustment was made for multiple comparisons. All *P* values are presented for descriptive purpose only.

Gene expression analyses

Data were preprocessed and normalized by the Robust Multiarray Average (RMA) method and log2 transformed. Significant DEGs were detected using the R/Bioconductor package *limma*. *P* values were adjusted for multiple testing based on the FDR according to the Benjamini-Hochberg approach. The significant DEGs were selected based on a log2 fold change (Log2FC)

>1 between patient and HC and FDR < 0.1 (or $P < 0.01$, $P < 0.05$ where stated). Annotation was directly assessed from Affymetrix and only probe sets with RefSeq annotation (NM_) and with interquartile range IQR > 0.8 across all samples were considered. For probe sets with identical gene annotations the one with the smallest P value was selected. Based on these criteria, data were further analyzed using ClueGO (5) and genes were queried for gene ontology biological and immune system process terms (http://www.geneontology.org/). For gene ontology network analysis, the option GO Term fusion was used, at least 3% of genes have to be included for the respective GO term with FDR < 0.05, and GO terms (nodes in the network) were connected if they shared genes with kappa score > 0.4. Differentially regulated genes (log2FC > 1) were also analyzed for specific cellular pathways using IPA (QIAGEN) using a fold change filter of |2| and $P < 0.05$. Briefly, the software calculates both an overlap P value (based on Fisher's exact test) and an activation z score, which is based on the expression state of activating and inhibiting genes, and takes the directional effect of one molecule on another molecule into account. GSEA (http://software.broadinstitute.org/gsea/index.jsp) (6) was used on pre-ranked lists (based on log2FC) to assess whether an *a priori* defined gene set was significantly enriched at the top or the bottom of the list. Enrichment was considered significant if it had a |NES| > 2, and FDR (q-value) < 0.1. Heatmap visualization and hierarchical clustering were performed using Genesis (7), and all other gene expression analyses were performed using R.

Supplementary Figure 1

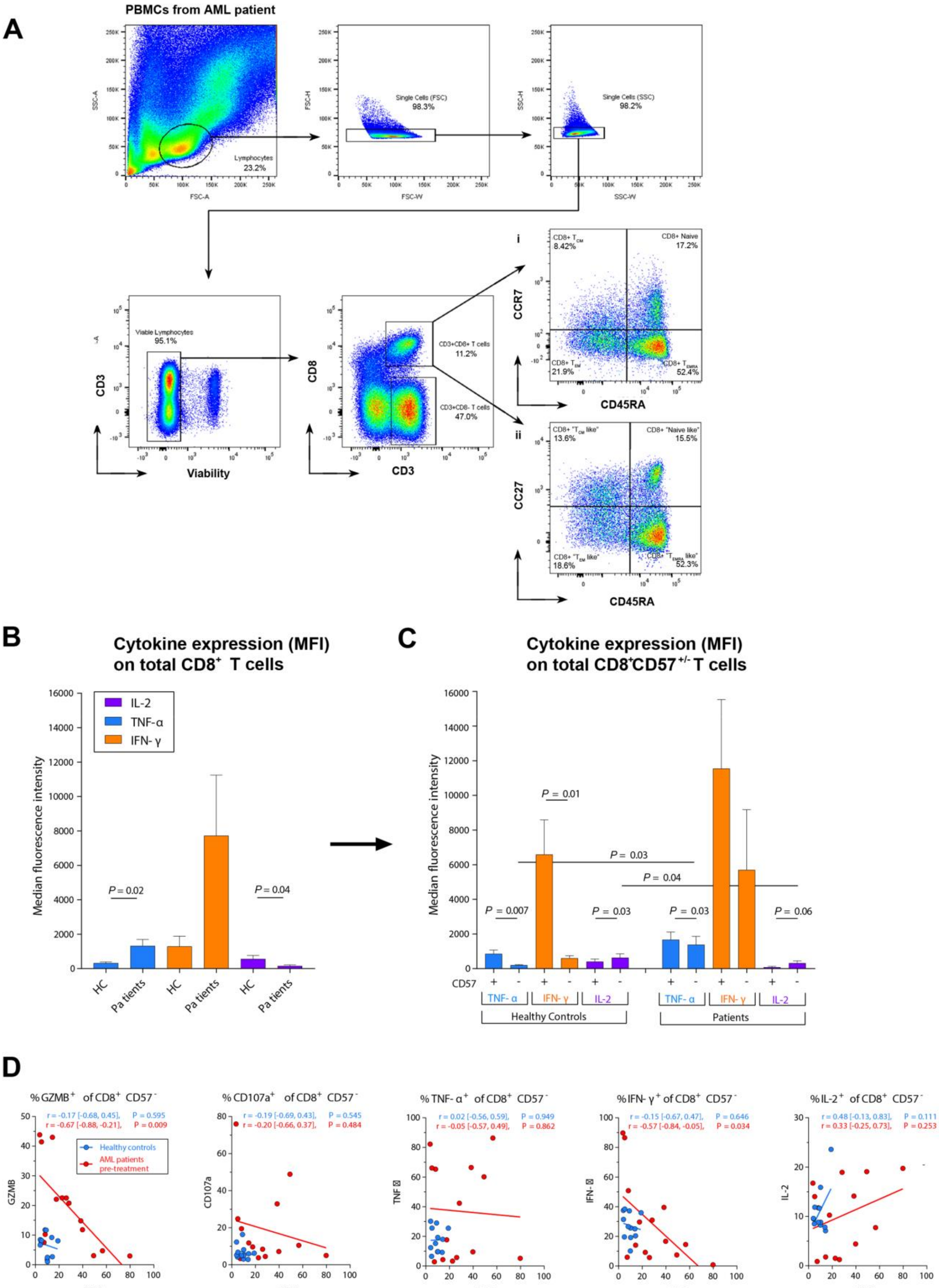


Fig. S1. Gating strategy and cytokine production by AML CD8$^+$ T-cells. (**A**) Gating of AML CD8$^+$ T-cell subsets (i) based on the expression of CD45RA and CCR7: naïve (CCR7$^+$CD45RA$^+$), central memory (T$_{CM}$, CCR7$^+$CD45RA$^-$), effector memory (T$_{EM}$, CCR7$^-$CD45RA$^-$), and terminally differentiated effector cells (T$_{EMRA}$, CCR7$^-$CD45RA$^+$); and (ii) based on the expression of CD45RA and CD27: "naive-like" (CD27$^+$CD45RA$^+$), "T$_{CM}$-like" (CD27$^+$CD45RA$^-$), "T$_{EM}$-like" (CD27$^-$CD45RA$^-$), and "T$_{EMRA}$-like" (CD27$^-$CD45RA$^+$). (**B**) MFI of cytokines expression (TNF-α, IFN-γ, and IL-2) on CD8$^+$ T-cells after 4 hours of *in vitro* stimulation with PMA/ionomycin; HC (n = 12) and newly diagnosed AML patients (n = 14). P values were calculated by unpaired t-test. Bar graphs show means ± SEM. (**C**) CD8$^+$ T-cells from (B) were divided into two populations according to CD57 expression and the MFI of cytokine expression was assessed separately for HC and AML patients. P values were calculated using paired- or unpaired t-test. Bar graphs show means ± SEM. (**D**) Nonlinear regression (curve fit) of PD-1 expression was correlated with the expression of effector molecules (GZMB, CD107a) and cytokines (TNF-α, IFN-γ, IL-2) on CD8$^+$CD57$^-$ T-cells.

Supplementary Figure 2

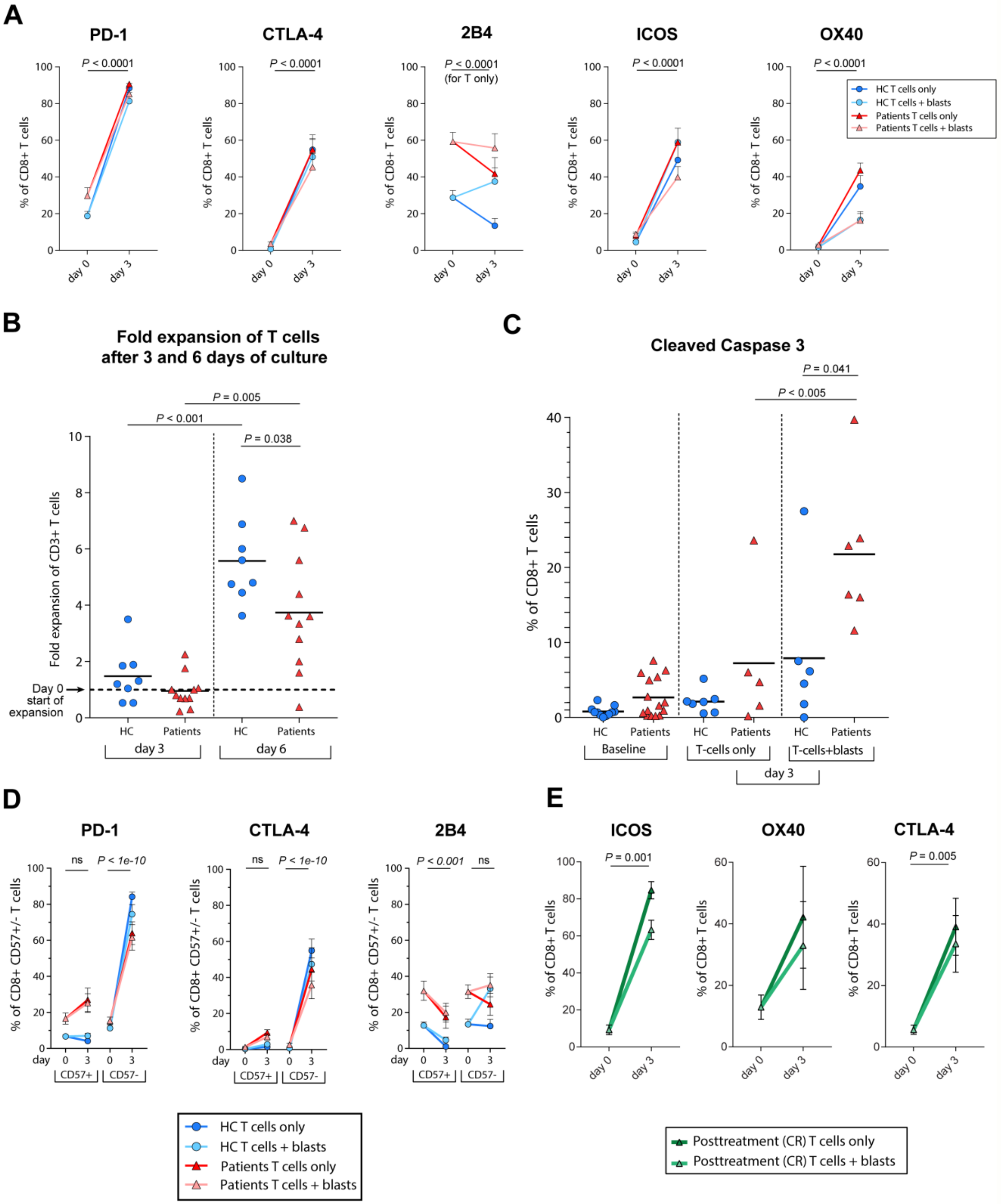


Fig. S2. AML blasts affect co-signaling molecules expression, expansion, and apoptosis of CD8$^+$ T-cells. (**A**) Change in the percentages of PB CD8$^+$ T-cells expressing co-signaling receptors (PD-1, CTLA-4, 2B4, ICOS, OX40) from day 0 to day +3 after *in vitro* stimulation with anti-CD3/CD28 beads in the presence or absence of AML blasts, for HC (n = 15) and AML patients (n = 20). P values were calculated using linear mixed effects regression models. (**B**) Fold expansion of HC and AML patients CD3$^+$ T-cells on days 3 and 6 after stimulation. Dashed line represents cell count on day 0. P values were calculated using Mann–Whitney U test (HC versus AML) and Wilcoxon signed-rank test (day 3 versus day 6). (**C**) Percentage of HC and AML patients PB CD8$^+$ T-cells expressing cleaved caspases 3 at baseline, and after 3 days of stimulation and culture with or without blasts. P values were calculated using Mann–Whitney U test (HC versus AML comparisons) and otherwise by Wilcoxon signed-rank test. (**D**) CD8$^+$ T-cells from (A) were divided into two populations according to CD57 expression and the changes of IRs expression were assessed. P values were calculated using linear mixed effects regression models. (**E**) CD8$^+$ T-cells collected from same patients (n = 3) at diagnosis and at the time of confirmed CR were stimulated with anti-CD3/CD28 beads in the presence or absence of autologous AML blasts. Change in the percentages of CD8$^+$ T-cells expressing co-signaling receptors (CTLA-4, ICOS, OX40) from day 0 to day +3 are presented.

Supplementary Figure 3

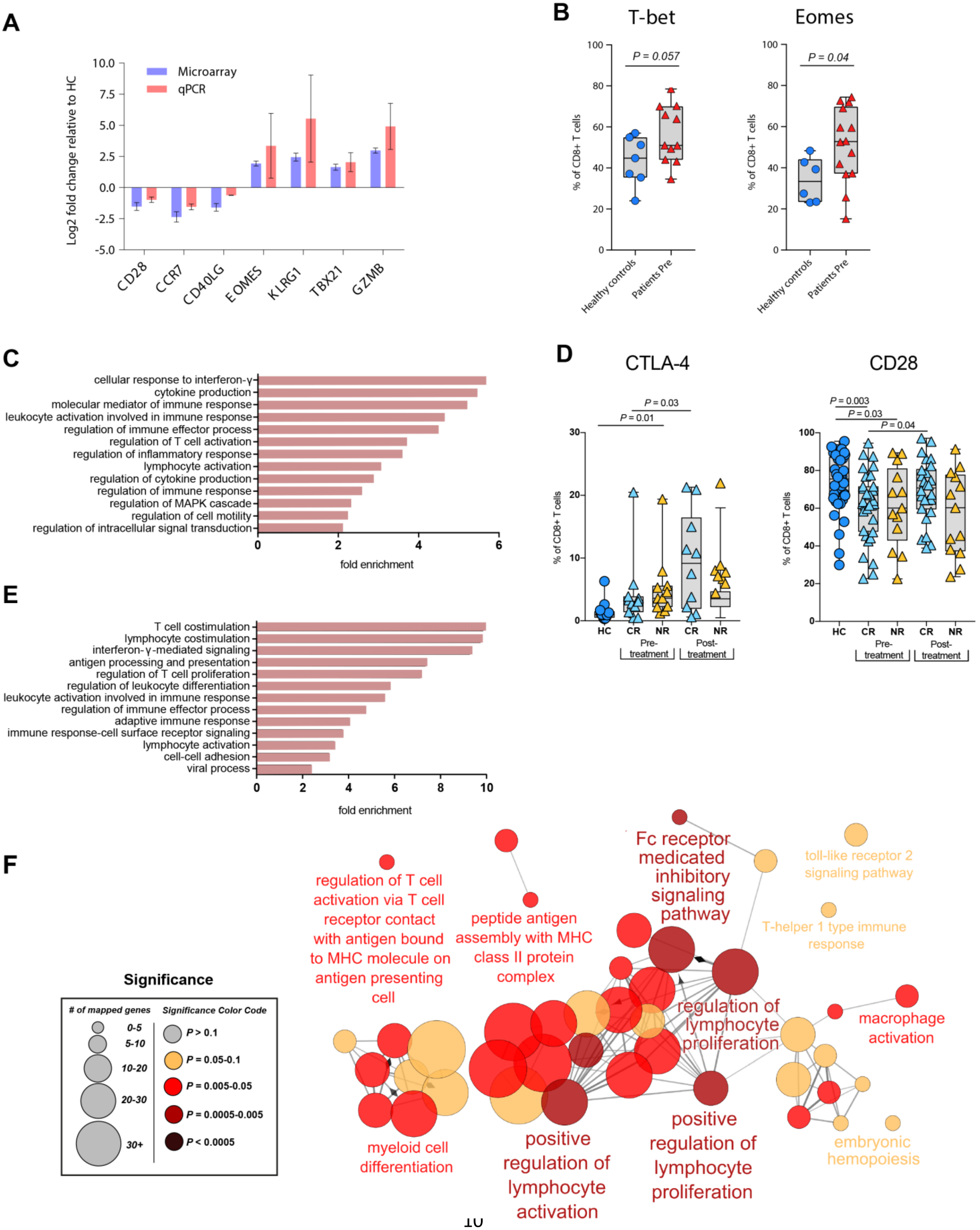


Fig. S3. **Validation of gene expression differences identified by microarray analysis, and gene ontology analysis for pre-treatment AML versus HC and post-treatment AML CR versus NR CD8$^+$ T-cell comparisons.** (**A**) Bar graph of qPCR validation of 7 select genes in PB (*n* = 7, pink bars) and corresponding microarray gene expression values (*n* = 9, blue) from AML patients pre-treatment. Log2FC relative to HC (*n* = 4) and data are represented as mean ± SEM. (**B**) PB samples of AML patients at pre-treatment and HC were stained for T-bet and EOMES and examined by flow cytometry. (**C**) Relative enrichment for GO biological processes (*Log2FC* >1; $P < 0.05$; and >10 genes per process) associated with the top differentially regulated genes ($P < 0.01$) in pre-treatment AML versus HC comparison. (**D**) PB samples of CR and NR AML patients were stained for CTLA-4 and CD28 expression at pre- and post-treatment. Data are presented as median percentages and interquartile ranges. *P* values were calculated using paired or unpaired *t* test. (**E**) Relative enrichment for GO biological processes (*Log2FC* >1; $P < 0.05$; and >10 genes per process) associated with the top differentially regulated genes ($P < 0.01$) in post-treatment AML CR versus NR comparison. (**F**) GO terms and KEGG/BioCarta pathways ($P < 0.01$) were functionally grouped into a network and interconnected based on the number of shared genes (kappa score > 0.4) using ClueGO. The size of the nodes correlates with the number of mapped genes per term and color correlates with *P* values.

Supplementary Figure 4

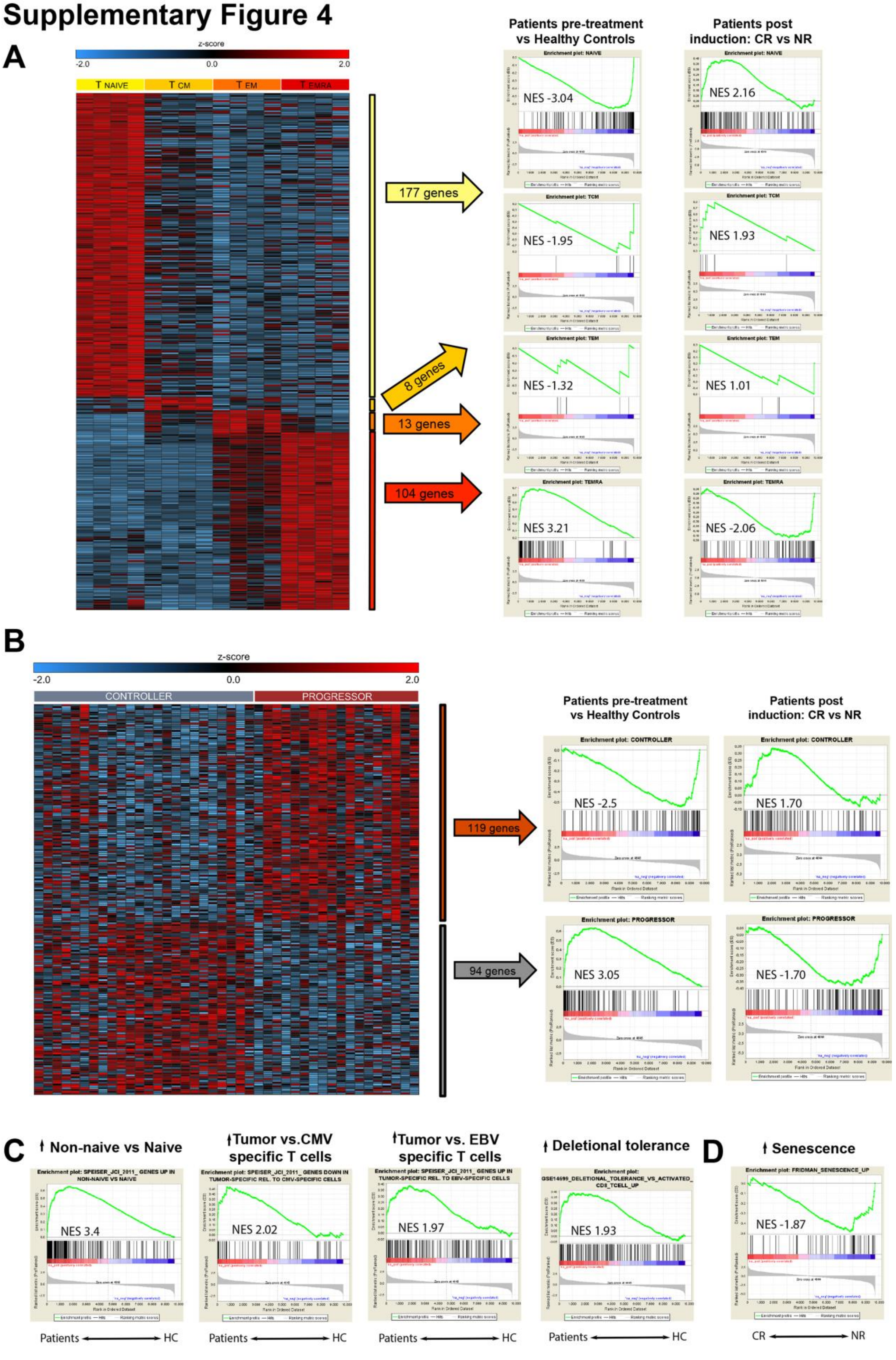
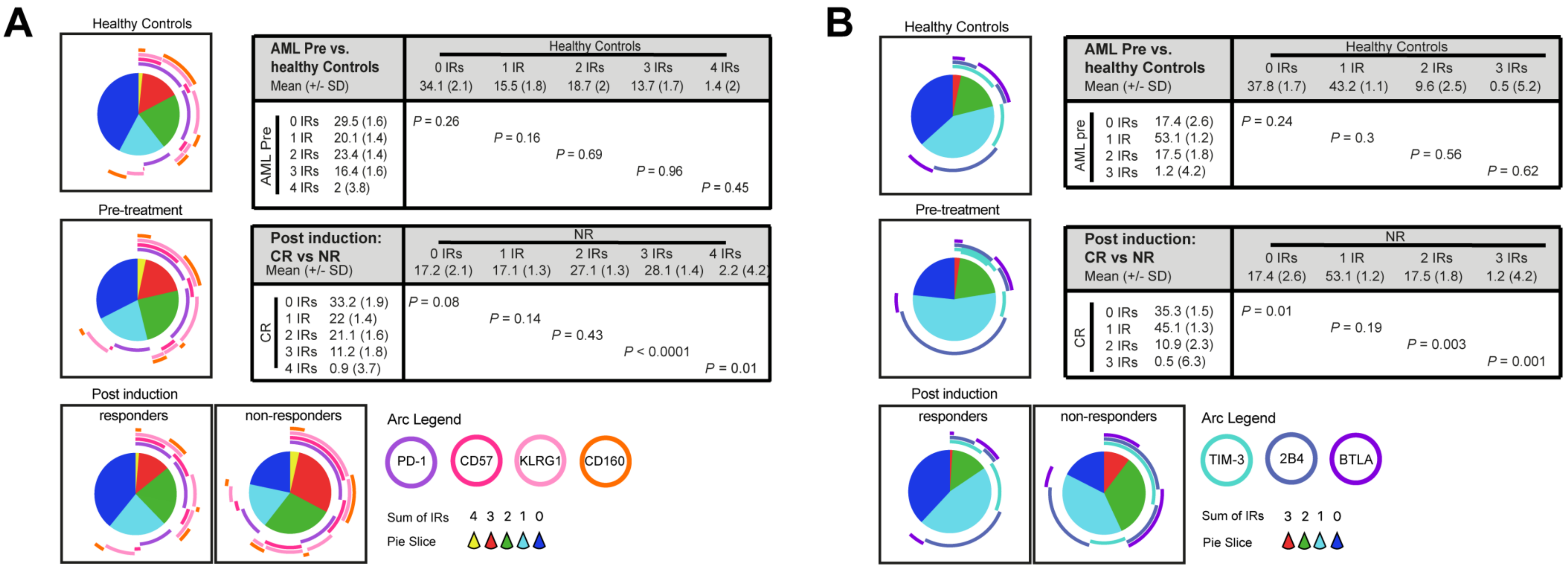


Fig. S4. Derived gene sets and representative GSEA enrichment plots. (**A** and **B**) Custom gene sets from array data by (A) Willinger et al (8) (ArrayExpress E-TABM-40) based on genes with IQR > 0.6 across all samples and upregulated in the respective group with FC > 1 and FDR < 0.05 compared to each of the other groups, and (B) Quigley et al (9) (GEO GSE24081) based on genes with IQR > 0.5 and $P < 0.01$.The identified unique gene sets were applied to AML array data presented here. (**C** and **D**) Representative GSEA enrichment plots of select immune-related gene sets overrepresented in (C) pre-treatment and (D) post-treatment analyses from gene sets derived from the MSigDB (Broad Institute).

Supplementary Figure 5



AML Pre vs. healthy Controls Mean (+/- SD)			Healthy Controls				
			0 IRs	1 IR	2 IRs	3 IRs	4 IRs
			34.1 (2.1)	15.5 (1.8)	18.7 (2)	13.7 (1.7)	1.4 (2)
AML Pre	0 IRs	29.5 (1.6)	$P = 0.26$				
	1 IR	20.1 (1.4)		$P = 0.16$			
	2 IRs	23.4 (1.4)			$P = 0.69$		
	3 IRs	16.4 (1.6)				$P = 0.96$	
	4 IRs	2 (3.8)					$P = 0.45$

Post induction: CR vs NR Mean (+/- SD)			NR				
			0 IRs	1 IR	2 IRs	3 IRs	4 IRs
			17.2 (2.1)	17.1 (1.3)	27.1 (1.3)	28.1 (1.4)	2.2 (4.2)
CR	0 IRs	33.2 (1.9)	$P = 0.08$				
	1 IR	22 (1.4)		$P = 0.14$			
	2 IRs	21.1 (1.6)			$P = 0.43$		
	3 IRs	11.2 (1.8)				$P < 0.0001$	
	4 IRs	0.9 (3.7)					$P = 0.01$

AML Pre vs. healthy Controls Mean (+/- SD)			Healthy Controls			
			0 IRs	1 IR	2 IRs	3 IRs
			37.8 (1.7)	43.2 (1.1)	9.6 (2.5)	0.5 (5.2)
AML pre	0 IRs	17.4 (2.6)	$P = 0.24$			
	1 IR	53.1 (1.2)		$P = 0.3$		
	2 IRs	17.5 (1.8)			$P = 0.56$	
	3 IRs	1.2 (4.2)				$P = 0.62$

Post induction: CR vs NR Mean (+/- SD)			NR			
			0 IRs	1 IR	2 IRs	3 IRs
			17.4 (2.6)	53.1 (1.2)	17.5 (1.8)	1.2 (4.2)
CR	0 IRs	35.3 (1.5)	$P = 0.01$			
	1 IR	45.1 (1.3)		$P = 0.19$		
	2 IRs	10.9 (2.3)			$P = 0.003$	
	3 IRs	0.5 (6.3)				$P = 0.001$

Fig. S5. Co-expression of IRs in the marrow CD8$^+$ T-cells from AML patients. (**A** and **B**) Boolean gating analysis of the simultaneous expression of multiple IRs on paired pre- and post-treatment BM CD8$^+$CD56$^-$ T-cells from AML patients (*n* = 29) and HC (*n* = 11). (A) Co-expression of PD-1, CD57, KLRG1, and CD160 (panel 1). (B) Co-expression of Tim3, 2B4, and BTLA (panel 2). Colors of the pie slices depict the number of co-expressed IRs (0-3/4 IRs), while the arcs depict the expression of individual IR. Co-expression was analyzed with SPICE software version 5.3. Mean percentages (± SD) distribution of IR co-expression was compared, and corresponding *P* values for the differences in mean co-expression between HC and AML patients pre-treatment and CR versus NR patients post-treatment within categories of the number of co-expressed IRs were calculated using Mann-Whitney *U* test and shown in tables.

Supplementary Figure 6

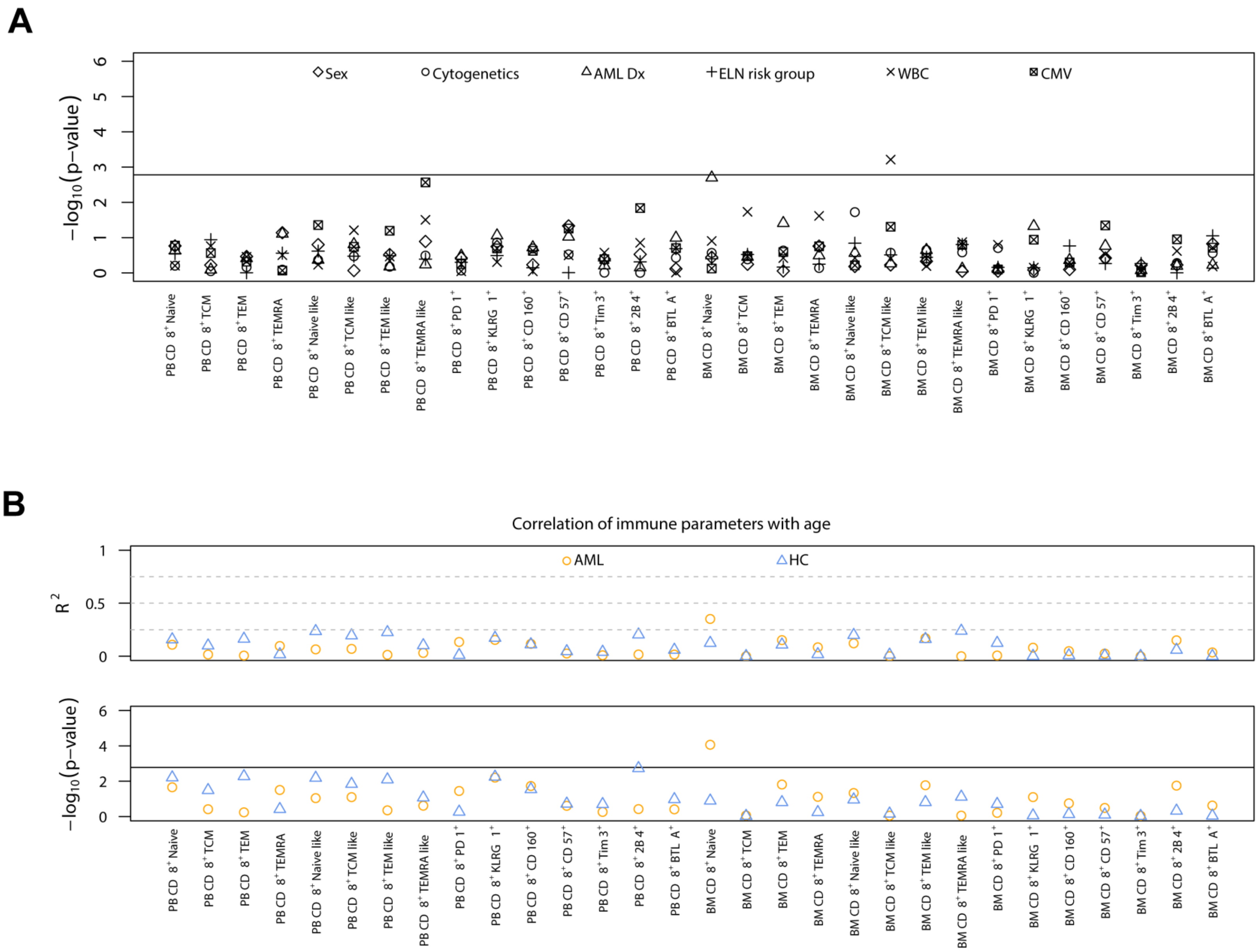


Fig. S6. Correlation of immune subsets with disease and patient variables. (**A** and **B**) Immune phenotypes of pre-treatment AML patients (*n* = 55 for PB; *n* = 45 for BM) and HC (*n* = 55 for PB; *n* = 21 for BM) were analyzed by flow cytometry. (**A**) The influence of pre-treatment disease (cytogenetic risk group: favorable/interemediate versus adverse; pathogenesis: de novo versus secondary AML; European LeukemiaNet category: adverse/intermediate-2 versus favorable/intermediate-1; WBC count ≥ versus < 30,000/µl; percent blast in the PB; percent blast in the BM; absolute PB blast count) and patient variables (CMV status, sex) on T-cell subsets expressing different differentiation, co-IRs and senescence markers. (**B**) The influence of age on T-cell subsets expressing different differentiation, co-IRs and senescence markers, in AML patients and HC. (A and B) Linear regression models with corresponding R^2 values (top) and $-\log_{10}$ of Bonferroni-adjusted P values (significance threshold of $P < 0.0167$) (bottom) for each $CD8^+$ T-cell subset.

Supplementary Figure 7

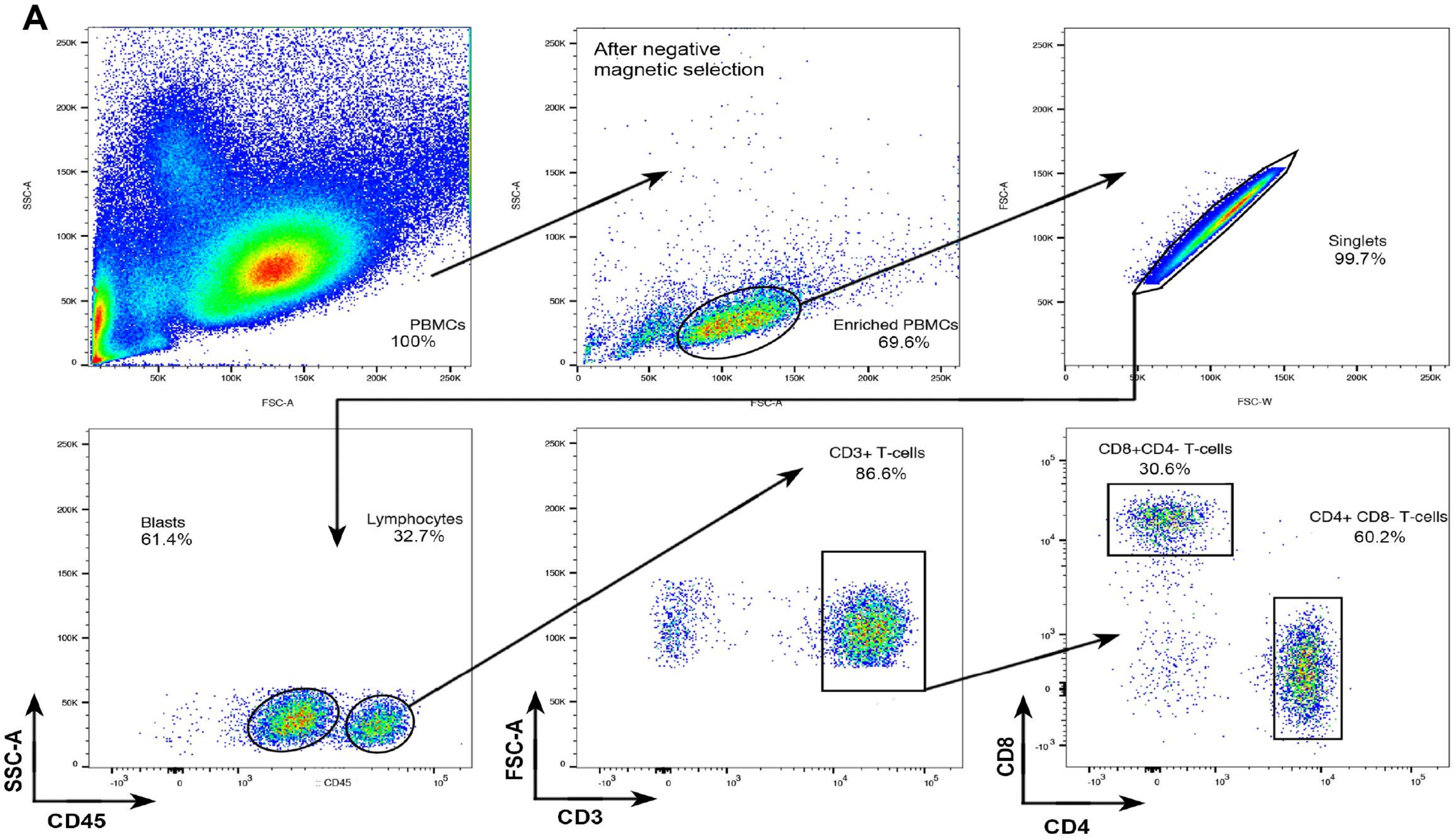


Fig. S7. Fluorescence activated cell sorting gating strategy for isolation of highly purified CD8$^+$ T-cells. T-cells were first separated from PB mononuclear cells by T-cell negative magnetic selection with a custom made kit (Stem Cell Technology) containing Abs against CD33, CD34, CD123, CD11c, and CD36, followed by sorting for CD45^{hi} SSClo CD3$^+$ CD4$^-$ CD8$^+$ T-cells.

TABLES

Supplementary Table S1. *Differentially expressed genes in pre-treatment AML patients relative to healthy controls.*

ID	NAME	GENE	A	PRE	HC	LOG2FC	PVAL	FDR
11735551_a_at	Fc receptor-like 6	FCRL6	7.93	9.20	5.07	4.12	5.3E-05	0.072
11728480_a_at	janus kinase and microtubule interacting protein 1	JAKMIP1	5.96	7.20	3.18	4.02	2.1E-06	0.020
11756847_a_at	chemokine (C-X3-C motif) receptor 1	CX3CR1	8.67	9.85	6.00	3.85	8.5E-04	0.093
11745699_a_at	killer cell lectin-like receptor subfamily F, member 1	KLRF1	8.04	9.08	5.69	3.39	1.8E-05	0.058
11757368_x_at	annexin A4	ANXA4	7.50	8.52	5.20	3.32	2.8E-04	0.079
11733004_s_at	Fc fragment of IgG, low affinity IIIa, receptor (CD16a)	FCGR3A	9.50	10.51	7.20	3.31	3.8E-04	0.079
11722856_a_at	platelet derived growth factor D	PDGFD	7.11	8.06	4.96	3.10	8.1E-05	0.075
11731848_s_at	killer cell lectin-like receptor subfamily C, member 1	KLRC1	8.04	8.98	5.95	3.03	4.9E-04	0.081
11724900_a_at	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	GZMB	10.05	10.96	7.98	2.98	4.3E-05	0.072
11740478_a_at	Fc receptor-like 3	FCRL3	8.25	9.17	6.19	2.98	1.4E-03	0.113
11753190_x_at	killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 1	KIR2DS1	6.66	7.57	4.62	2.96	2.9E-03	0.146
11731197_a_at	proline rich 5 like	PRR5L	6.35	7.25	4.32	2.93	1.4E-04	0.076
11737746_a_at	G protein-coupled receptor 56	GPR56	9.09	9.99	7.08	2.91	1.3E-04	0.076
11724256_s_at	2'-5'-oligoadenylate synthetase 1, 40/46kDa	OAS1	5.64	6.49	3.74	2.75	7.3E-03	0.190
11732266_x_at	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1	LILRB1	6.76	7.59	4.88	2.71	5.0E-04	0.082
11754678_a_at	solute carrier family 25, member 43	SLC25A43	5.50	6.33	3.65	2.69	1.8E-03	0.120
11748899_a_at	CD244 molecule, natural killer cell receptor 2B4	CD244	7.06	7.88	5.22	2.66	2.3E-03	0.138
11717467_a_at	tetratricopeptide repeat domain 38	TTC38	6.69	7.51	4.85	2.65	4.5E-04	0.080
11732480_s_at	integrin, alpha M (complement component 3 receptor 3 subunit)	ITGAM	8.68	9.50	6.86	2.64	2.9E-04	0.079
11736113_at	Rho GTPase activating protein 18	ARHGAP18	5.45	6.25	3.63	2.62	7.7E-04	0.092
11719671_a_at	regulator of calcineurin 2	RCAN2	5.61	6.42	3.80	2.62	9.5E-03	0.212
11732809_a_at	prokineticin 2	PROK2	6.72	7.52	4.92	2.60	4.4E-03	0.162
11758673_s_at	sorbitol dehydrogenase	SORD	6.72	7.52	4.94	2.58	5.2E-04	0.082
11738094_a_at	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 6	ST8SIA6	5.45	6.24	3.67	2.57	3.9E-03	0.155
11730723_a_at	neural cell adhesion molecule 1	NCAM1	6.17	6.95	4.40	2.56	2.0E-03	0.129
11761050_at	Homo sapiens Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog (FGR), transcript variant 3, mRNA.	FGR	6.40	7.18	4.66	2.52	9.5E-06	0.046
11718766_at	protease, serine, 23	PRSS23	6.09	6.86	4.35	2.51	1.3E-03	0.113

11755998_x_at	major histocompatibility complex, class II, DR beta 4	HLA-DRB4	6.13	6.90	4.40	2.50	5.3E-03	0.169
11735224_a_at	killer cell lectin-like receptor subfamily G, member 1	KLRG1	9.05	9.80	7.36	2.45	3.9E-04	0.079
11750925_a_at	thymocyte selection-associated high mobility group box	TOX	6.51	7.24	4.87	2.37	1.2E-04	0.076
11739822_a_at	copine VIII	CPNE8	6.78	7.51	5.14	2.37	1.4E-04	0.076
11739489_a_at	ATPase, class V, type 10D	ATP10D	4.62	5.35	2.99	2.36	1.2E-03	0.109
11720830_at	chromosome 1 open reading frame 21	C1orf21	6.28	7.00	4.66	2.33	7.1E-04	0.090
11736122_a_at	golgi integral membrane protein 4	GOLIM4	6.57	7.29	4.96	2.33	3.8E-04	0.079
11757990_s_at	complement factor H	CFH	6.88	7.60	5.27	2.33	3.9E-04	0.079
11751899_a_at	discs, large homolog 5 (Drosophila)	DLG5	6.49	7.19	4.90	2.29	3.0E-05	0.072
11740452_x_at	killer cell lectin-like receptor subfamily D, member 1	KLRD1	10.36	11.06	8.78	2.28	5.9E-04	0.083
11755997_a_at	sterile alpha motif domain containing 9-like	SAMD9L	8.50	9.20	6.93	2.27	4.5E-03	0.163
11736761_at	caspase recruitment domain family, member 16	CARD16	8.12	8.82	6.55	2.26	8.5E-03	0.204
11736632_at	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3H	APOBEC3H	7.64	8.34	6.08	2.26	8.9E-04	0.094
11748062_s_at	chemokine (C-C motif) receptor 5 (gene/pseudogene)	CCR5	6.00	6.69	4.44	2.25	7.2E-04	0.090
11736225_a_at	spermatogenesis associated, serine-rich 2	SPATS2	6.60	7.29	5.05	2.24	3.1E-03	0.146
11727969_a_at	solute carrier family 14 (urea transporter), member 1 (Kidd blood group)	SLC14A1	6.50	7.19	4.95	2.24	3.4E-04	0.079
11719254_at	cyclin-dependent kinase 19	CDK19	5.25	5.94	3.71	2.22	9.0E-04	0.094
11748500_a_at	ectonucleotide pyrophosphatase/phosphodiesterase 5 (putative)	ENPP5	6.03	6.71	4.50	2.22	6.2E-03	0.180
11754474_a_at	pleckstrin	PLEK	9.59	10.27	8.07	2.21	2.5E-03	0.141
11732781_a_at	NME/NM23 family member 8	NME8	4.82	5.50	3.31	2.19	2.7E-03	0.145
11752500_a_at	mannosidase, alpha, class 1A, member 1	MAN1A1	8.24	8.91	6.74	2.18	1.1E-04	0.075
11757954_s_at	ArfGAP with GTPase domain, ankyrin repeat and PH domain 1	AGAP1	6.75	7.42	5.25	2.17	7.0E-03	0.187
11752490_x_at	neuromedin U receptor 1	NMUR1	6.72	7.39	5.22	2.17	3.8E-03	0.153
11744374_x_at	major histocompatibility complex, class II, DR beta 1	HLA-DRB1	8.88	9.54	7.39	2.16	1.3E-03	0.113
11728858_at	centrosomal protein 19kDa	CEP19	4.60	5.26	3.11	2.15	6.3E-03	0.180
11756106_a_at	SET binding protein 1	SETBP1	5.72	6.37	4.24	2.14	9.5E-05	0.075
11717563_a_at	deltex 3 like, E3 ubiquitin ligase	DTX3L	7.28	7.93	5.81	2.13	3.7E-03	0.153
11745004_x_at	HOP homeobox	HOPX	8.69	9.34	7.22	2.12	1.4E-03	0.114
11748798_a_at	phosphoinositide-3-kinase adaptor protein 1	PIK3AP1	6.63	7.28	5.18	2.10	1.7E-03	0.120
11756818_a_at	protein associated with topoisomerase II homolog 2 (yeast)	PATL2	8.00	8.65	6.55	2.10	7.1E-04	0.090
11749753_a_at	KIAA1328	KIAA1328	6.42	7.07	4.97	2.09	1.7E-03	0.120
11750960_a_at	aminoadipate-semialdehyde synthase	AASS	4.85	5.49	3.40	2.09	4.6E-04	0.080
11746537_x_at	eukaryotic translation initiation factor 4 gamma, 3	EIF4G3	7.53	8.18	6.09	2.09	1.3E-03	0.113
11750456_s_at	Rh blood group, CcEe antigens	RHCE	4.48	5.12	3.04	2.08	4.6E-03	0.163
11739989_a_at	calcineurin-like phosphoesterase domain containing 1	CPPED1	5.70	6.34	4.26	2.07	3.5E-03	0.148
11739553_a_at	growth arrest-specific 7	GAS7	6.62	7.25	5.21	2.04	2.4E-03	0.139

11729338_x_at	proline-serine-threonine phosphatase interacting protein 2	PSTPIP2	6.23	6.85	4.83	2.03	4.4E-03	0.162
11751857_a_at	granulysin	GNLY	11.97	12.59	10.58	2.02	2.1E-03	0.132
11736229_a_at	cysteine rich transmembrane BMP regulator 1 (chordin-like)	CRIM1	6.15	6.77	4.76	2.01	3.6E-03	0.151
11755251_x_at	fatty acid desaturase 1	FADS1	5.91	6.53	4.53	2.00	1.1E-03	0.107
11720597_s_at	cysteine-serine-rich nuclear protein 2	CSRNP2	6.00	6.62	4.62	1.99	8.8E-05	0.075
11754601_s_at	spondin 2, extracellular matrix protein	SPON2	8.75	9.36	7.38	1.98	1.1E-03	0.107
11723698_a_at	2'-5'-oligoadenylate synthetase 3, 100kDa	OAS3	6.35	6.95	5.00	1.95	9.6E-03	0.212
11750731_a_at	eomesodermin	EOMES	7.11	7.71	5.77	1.93	3.9E-03	0.155
11757914_a_at	lysine-rich nucleolar protein 1	KNOP1	5.60	6.20	4.26	1.93	3.4E-03	0.148
11753685_a_at	angiotensin II receptor-associated protein	AGTRAP	6.01	6.60	4.67	1.93	5.0E-03	0.167
11728125_a_at	granzyme H (cathepsin G-like 2, protein h-CCPX)	GZMH	11.34	11.94	10.01	1.93	5.6E-04	0.082
11761683_x_at	pyrin and HIN domain family, member 1	PYHIN1	5.95	6.54	4.62	1.92	2.6E-03	0.143
11754627_s_at	RAB37, member RAS oncogene family	RAB37	8.72	9.31	7.39	1.92	7.7E-04	0.092
11739972_at	NUAK family, SNF1-like kinase, 1	NUAK1	4.12	4.71	2.79	1.92	3.1E-03	0.146
11747113_a_at	CD160 molecule	CD160	7.46	8.04	6.14	1.91	4.3E-03	0.161
11715258_s_at	parathymosin	PTMS	8.85	9.44	7.53	1.91	5.4E-04	0.082
11717863_a_at	dual specificity phosphatase 5	DUSP5	7.83	8.41	6.52	1.90	2.1E-03	0.133
11735204_a_at	methylmalonic aciduria (cobalamin deficiency) cblA type	MMAA	6.99	7.57	5.68	1.89	8.7E-03	0.204
11731425_at	chemokine (C-X-C motif) receptor 2	CXCR2	5.49	6.07	4.19	1.88	6.8E-03	0.185
11718084_a_at	LYN proto-oncogene, Src family tyrosine kinase	LYN	6.51	7.08	5.23	1.86	3.4E-03	0.148
11730296_a_at	toll-like receptor 3	TLR3	5.28	5.85	3.99	1.85	2.6E-04	0.079
11729139_x_at	SLAM family member 7	SLAMF7	8.65	9.22	7.37	1.85	1.9E-03	0.128
11718081_a_at	ATPase, Ca++ transporting, plasma membrane 4	ATP2B4	8.24	8.80	6.97	1.83	1.6E-03	0.120
11753788_x_at	cyclin-dependent kinase inhibitor 3	CDKN3	4.47	5.03	3.20	1.83	6.3E-04	0.086
11725506_s_at	growth differentiation factor 11	GDF11	7.09	7.65	5.83	1.82	2.0E-04	0.079
11747295_a_at	perforin 1 (pore forming protein)	PRF1	10.08	10.64	8.81	1.82	7.4E-04	0.091
11743398_s_at	STARD3 N-terminal like	STARD3NL	6.85	7.41	5.61	1.80	1.5E-03	0.116
11734902_a_at	cytochrome P450, family 4, subfamily V, polypeptide 2	CYP4V2	7.90	8.45	6.66	1.79	5.0E-03	0.167
11717935_a_at	endoplasmic reticulum metallopeptidase 1	ERMP1	8.06	8.61	6.82	1.79	2.8E-03	0.145
11731629_a_at	missing oocyte, meiosis regulator, homolog (Drosophila)	MIOS	7.40	7.95	6.16	1.78	8.6E-04	0.093
11717844_x_at	ethanolamine kinase 1	ETNK1	7.87	8.41	6.63	1.78	3.3E-03	0.148
11742639_a_at	RAD52 motif containing 1	RDM1	4.54	5.08	3.31	1.78	5.5E-03	0.172
11720496_at	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)	GZMA	11.19	11.73	9.96	1.78	4.1E-03	0.159
11735270_a_at	glucosaminyl (N-acetyl) transferase 1, core 2	GCNT1	5.77	6.32	4.55	1.77	2.0E-03	0.129
11762067_at	FCF1 rRNA-processing protein	FCF1	6.71	7.25	5.48	1.77	7.4E-03	0.192
11728389_at	tetraspanin 2	TSPAN2	4.66	5.20	3.44	1.76	7.9E-03	0.199

11734395_x_at	killer cell lectin-like receptor subfamily C, member 3	KLRC3	8.17	8.71	6.95	1.76	3.7E-03	0.152
11740297_a_at	chromosome 10 open reading frame 128	C10orf128	7.79	8.33	6.57	1.76	8.9E-03	0.206
11717820_a_at	solute carrier family 4 (sodium bicarbonate cotransporter), member 4	SLC4A4	4.01	4.55	2.80	1.76	6.6E-04	0.087
11717035_s_at	KIAA0141	KIAA0141	7.04	7.58	5.84	1.74	4.5E-03	0.163
11732379_a_at	decapping exoribonuclease	DXO	7.86	8.39	6.66	1.73	4.3E-04	0.079
11728712_x_at	ZFP64 zinc finger protein	ZFP64	5.97	6.50	4.78	1.73	9.7E-03	0.212
11747018_x_at	multiple C2 domains, transmembrane 2	MCTP2	7.11	7.64	5.91	1.73	5.8E-03	0.177
11726329_x_at	guanylate binding protein 1, interferon-inducible	GBP1	7.30	7.83	6.11	1.72	2.3E-03	0.138
11756287_a_at	acyloxyacyl hydrolase (neutrophil)	AOAH	8.87	9.40	7.68	1.72	7.4E-04	0.091
11751136_a_at	coiled-coil domain containing 30	CCDC30	5.03	5.56	3.84	1.72	9.1E-04	0.094
11726916_at	solute carrier organic anion transporter family, member 4C1	SLCO4C1	5.94	6.47	4.75	1.72	6.2E-03	0.180
11744799_a_at	X-ray repair complementing defective repair in Chinese hamster cells 4	XRCC4	4.63	5.16	3.44	1.72	9.7E-03	0.212
11758050_s_at	regulator of G-protein signaling 3	RGS3	7.46	7.99	6.27	1.71	3.6E-03	0.151
11720994_x_at	chemokine (C-C motif) ligand 3	CCL3	9.01	9.54	7.83	1.71	3.2E-03	0.148
11759141_at	huntingtin interacting protein 1	HIP1	5.00	5.52	3.81	1.71	7.9E-04	0.093
11724042_a_at	PDZ domain containing 4	PDZD4	9.01	9.53	7.82	1.71	4.3E-03	0.161
11743458_a_at	family with sequence similarity 49, member A	FAM49A	7.01	7.52	5.84	1.68	2.9E-04	0.079
11720510_a_at	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3G	APOBEC3G	9.85	10.37	8.68	1.68	5.2E-03	0.168
11719313_a_at	family with sequence similarity 111, member A	FAM111A	7.67	8.18	6.50	1.68	4.1E-03	0.159
11752664_a_at	sphingosine-1-phosphate receptor 5	S1PR5	10.25	10.77	9.09	1.68	5.2E-03	0.168
11725641_at	EF-hand domain family, member D2	EFHD2	9.58	10.09	8.42	1.67	1.9E-03	0.127
11723194_x_at	major histocompatibility complex, class II, DQ beta 1	HLA-DQB1	9.12	9.63	7.97	1.67	2.1E-03	0.133
11722782_at	fibroblast growth factor binding protein 2	FGFBP2	11.32	11.84	10.17	1.66	2.8E-03	0.145
11762018_at	DNA cross-link repair 1C	DCLRE1C	4.63	5.14	3.49	1.66	4.4E-03	0.162
11721421_s_at	RAP1 GTPase activating protein 2	RAP1GAP2	8.77	9.28	7.63	1.65	6.7E-03	0.184
11751714_a_at	testis-specific kinase 2	TESK2	5.99	6.49	4.84	1.65	2.6E-03	0.143
11736843_a_at	killer cell lectin-like receptor subfamily A pseudogene 1	KLRAP1	5.44	5.95	4.31	1.64	1.4E-03	0.113
11724683_a_at	CD300a molecule	CD300A	9.23	9.73	8.09	1.64	6.3E-03	0.180
11739979_a_at	A kinase (PRKA) anchor protein 2	AKAP2	9.35	9.86	8.22	1.64	9.2E-04	0.094
11732538_at	T-box 21	TBX21	9.13	9.63	8.00	1.64	3.7E-03	0.152
11736718_a_at	neurocalcin delta	NCALD	7.15	7.66	6.03	1.63	9.7E-03	0.212
11757926_s_at	solute carrier family 9, subfamily A (NHE9, cation proton antiporter 9), member 9	SLC9A9	6.29	6.79	5.16	1.63	3.8E-03	0.153
11732555_at	Fas ligand (TNF superfamily, member 6)	FASLG	5.38	5.88	4.26	1.62	1.7E-03	0.120
11745775_a_at	lipase A, lysosomal acid, cholesterol esterase	LIPA	6.79	7.29	5.67	1.62	8.0E-03	0.200
11761636_at	SLAM family member 6	SLAMF6	7.38	7.87	6.26	1.61	9.2E-03	0.210

11752690_a_at	RanBP-type and C3HC4-type zinc finger containing 1	RBCK1	5.98	6.47	4.86	1.61	8.0E-03	0.200
11750138_a_at	pogo transposable element with KRAB domain	POGK	6.88	7.38	5.77	1.61	9.5E-04	0.096
11728817_x_at	ubiquitin specific peptidase 28	USP28	5.76	6.26	4.65	1.61	1.4E-03	0.113
11755389_s_at	netrin G2	NTNG2	7.20	7.70	6.10	1.60	4.7E-03	0.163
11720064_a_at	GLI pathogenesis-related 2	GLIPR2	8.70	9.19	7.59	1.60	7.5E-03	0.192
11756458_a_at	MSH5-SAPCD1 readthrough (NMD candidate)	MSH5-SAPCD1	7.22	7.71	6.12	1.59	6.9E-03	0.187
11759125_at	F-box and leucine-rich repeat protein 17	FBXL17	4.35	4.84	3.25	1.59	5.9E-03	0.178
11750732_x_at	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 interacting protein	NFATC2IP	6.51	7.00	5.41	1.59	6.1E-03	0.180
11758417_s_at	major histocompatibility complex, class II, DP alpha 1	HLA-DPA1	8.90	9.39	7.81	1.57	2.7E-03	0.145
11732037_a_at	protein tyrosine phosphatase, non-receptor type 12	PTPN12	8.89	9.37	7.80	1.57	1.6E-03	0.120
11757769_s_at	vinculin	VCL	8.68	9.16	7.60	1.56	1.9E-03	0.128
11754437_a_at	microtubule-actin crosslinking factor 1	MACF1	9.25	9.73	8.17	1.56	6.9E-03	0.187
11719911_at	tumor necrosis factor (ligand) superfamily, member 12	TNFSF12	7.85	8.33	6.77	1.56	7.4E-03	0.192
11756090_s_at	zinc fingers and homeoboxes 1	ZHX1	6.16	6.64	5.09	1.55	3.3E-03	0.148
11754854_a_at	activating transcription factor 7 interacting protein 2	ATF7IP2	6.91	7.38	5.84	1.54	8.3E-03	0.202
11727784_x_at	tropomyosin 4	TPM4	7.91	8.39	6.84	1.54	3.6E-03	0.151
11733593_a_at	pregnancy-zone protein	PZP	7.94	8.41	6.88	1.53	5.9E-03	0.178
11715638_s_at	lysophosphatidylcholine acyltransferase 1	LPCAT1	9.50	9.97	8.44	1.53	2.6E-03	0.142
11728348_a_at	ribosomal protein L39-like	RPL39L	6.83	7.30	5.78	1.52	5.2E-03	0.168
11716728_s_at	tropomyosin 1 (alpha)	TPM1	5.21	5.68	4.16	1.52	2.2E-03	0.136
11716928_a_at	TBC1 domain family, member 5	TBC1D5	8.25	8.72	7.20	1.52	7.0E-03	0.187
11741809_at	histone cluster 1, H3j	HIST1H3J	7.76	8.22	6.71	1.51	4.2E-03	0.161
11725474_a_at	mitogen-activated protein kinase kinase kinase 5	MAP3K5	7.97	8.43	6.93	1.50	2.6E-03	0.142
11750484_a_at	MRE11 meiotic recombination 11 homolog A (S. cerevisiae)	MRE11A	5.75	6.21	4.71	1.49	8.1E-03	0.201
11731693_at	histone cluster 1, H2ae	HIST1H2AE	9.65	10.11	8.62	1.49	3.5E-03	0.148
11718944_a_at	pyroglutamyl-peptidase I	PGPEP1	6.85	7.31	5.82	1.49	7.5E-03	0.192
11736217_at	mitogen-activated protein kinase kinase kinase 8	MAP3K8	5.56	6.02	4.53	1.49	6.5E-03	0.181
11746954_s_at	chemokine (C-C motif) ligand 4	CCL4	11.01	11.47	9.99	1.48	4.8E-04	0.081
11716833_a_at	transmembrane 7 superfamily member 3	TM7SF3	6.88	7.33	5.87	1.47	8.6E-03	0.204
11716766_a_at	IQ motif containing GTPase activating protein 1	IQGAP1	9.47	9.92	8.45	1.47	4.0E-03	0.157
11743881_s_at	melanoregulin	MREG	7.05	7.50	6.04	1.46	4.7E-03	0.163
11735394_s_at	chemokine (C motif) ligand 1	XCL1	10.39	10.84	9.37	1.46	4.5E-03	0.163
11739754_at	SLAM family member 8	SLAMF8	6.16	6.61	5.16	1.46	1.4E-03	0.114
11733794_at	syntaxin 7	STX7	5.96	6.41	4.96	1.45	6.3E-03	0.180
11727533_a_at	fasciculation and elongation protein zeta 2 (zygin II)	FEZ2	5.46	5.91	4.46	1.45	9.0E-03	0.206

11730947_at	interferon, gamma	IFNG	9.21	9.66	8.21	1.45	3.0E-03	0.146
11727389_a_at	transient receptor potential cation channel, subfamily V, member 2	TRPV2	8.12	8.56	7.12	1.44	4.2E-04	0.079
11719059_a_at	attractin	ATRN	5.99	6.43	4.99	1.44	3.4E-03	0.148
11724646_at	VANGL planar cell polarity protein 1	VANGL1	6.58	7.02	5.59	1.43	6.4E-03	0.181
11742386_a_at	caspase 1, apoptosis-related cysteine peptidase	CASP1	8.23	8.67	7.24	1.43	5.9E-03	0.178
11723351_a_at	ATP-binding cassette, sub-family A (ABC1), member 3	ABCA3	5.86	6.30	4.87	1.43	1.1E-03	0.107
11743530_a_at	centromere protein K	CENPK	3.53	3.97	2.54	1.43	5.4E-03	0.172
11747942_a_at	zinc finger E-box binding homeobox 2	ZEB2	8.82	9.25	7.85	1.40	3.9E-03	0.156
11723178_s_at	solute carrier family 15 (oligopeptide transporter), member 4	SLC15A4	8.66	9.09	7.70	1.39	7.0E-03	0.187
11747369_x_at	chromosome 1 open reading frame 112	C1orf112	3.88	4.31	2.92	1.39	8.4E-03	0.204
11719016_at	PQ loop repeat containing 3	PQLC3	8.28	8.71	7.32	1.39	6.5E-03	0.181
11715910_a_at	myosin VI	MYO6	7.56	7.98	6.60	1.39	4.5E-03	0.163
11715363_a_at	alpha-2-macroglobulin	A2M	7.80	8.23	6.85	1.39	5.0E-03	0.167
11725347_a_at	transcription factor Dp-1	TFDP1	6.03	6.46	5.07	1.39	8.2E-03	0.201
11743021_a_at	zinc finger protein 195	ZNF195	5.28	5.70	4.33	1.37	6.0E-03	0.178
11744768_a_at	Z-DNA binding protein 1	ZBP1	8.15	8.57	7.21	1.37	1.3E-03	0.113
11722522_a_at	sushi domain containing 1	SUSD1	7.92	8.34	6.98	1.36	9.1E-03	0.208
11722217_x_at	G protein-coupled receptor 108	GPR108	7.85	8.27	6.91	1.36	9.7E-03	0.212
11727375_a_at	3-hydroxy-3-methylglutaryl-CoA reductase	HMGCR	7.05	7.47	6.12	1.35	4.7E-03	0.163
11751616_a_at	lactamase, beta 2	LACTB2	7.01	7.43	6.08	1.35	4.4E-03	0.162
11757779_s_at	protein phosphatase 4, regulatory subunit 1	PPP4R1	6.70	7.12	5.77	1.35	5.0E-03	0.167
11720244_at	phospholipase C, gamma 2 (phosphatidylinositol-specific)	PLCG2	7.29	7.70	6.36	1.34	2.8E-03	0.145
11726431_a_at	oxysterol binding protein-like 3	OSBPL3	7.37	7.79	6.45	1.34	5.2E-03	0.168
11754404_a_at	poly (ADP-ribose) polymerase family, member 14	PARP14	8.37	8.78	7.45	1.33	3.5E-03	0.148
11754036_s_at	chromosome 20 open reading frame 194	C20orf194	6.12	6.53	5.21	1.33	8.0E-03	0.200
11759157_at	histone cluster 1, H2bf	HIST1H2BF	9.27	9.67	8.35	1.32	3.0E-03	0.146
11717718_at	fibronectin type III domain containing 3B	FNDC3B	7.06	7.46	6.17	1.29	7.6E-03	0.192
11727868_a_at	galactokinase 2	GALK2	4.82	5.22	3.93	1.29	4.8E-03	0.164
11750561_a_at	lysosomal trafficking regulator	LYST	8.29	8.69	7.41	1.28	6.7E-03	0.184
11725716_a_at	kinesin family member 21A	KIF21A	8.63	9.02	7.74	1.27	4.9E-03	0.166
11716430_a_at	solute carrier family 39 (zinc transporter), member 13	SLC39A13	7.37	7.77	6.49	1.27	5.1E-03	0.168
11756310_a_at	nuclear transport factor 2-like export factor 2	NXT2	5.86	6.25	4.98	1.27	5.9E-03	0.178
11736238_a_at	ATP-binding cassette, sub-family A (ABC1), member 5	ABCA5	4.67	5.06	3.79	1.27	6.0E-03	0.179
11736573_a_at	protein kinase C, delta	PRKCD	5.03	5.41	4.16	1.25	6.3E-03	0.180
11751127_a_at	shisa family member 5	SHISA5	8.68	9.06	7.82	1.25	7.2E-03	0.189
11730147_a_at	G protein-coupled receptor 114	GPR114	5.10	5.48	4.23	1.25	9.4E-03	0.212

11739563_a_at	inositol 1,4,5-trisphosphate receptor, type 1	ITPR1	7.65	8.03	6.79	1.24	7.5E-03	0.192
11736144_at	ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative)	ENPP4	8.06	8.44	7.20	1.24	3.7E-03	0.152
11745366_x_at	protein O-linked mannose N-acetylglucosaminyltransferase 1 (beta 1,2-)	POMGNT1	7.43	7.81	6.58	1.23	9.8E-03	0.212
11759648_at	cAMP responsive element binding protein 3-like 2	CREB3L2	5.67	6.04	4.81	1.23	7.4E-03	0.192
11762400_s_at	peptidylprolyl isomerase (cyclophilin)-like 2	PPIL2	10.46	10.83	9.61	1.22	7.4E-03	0.192
11726009_a_at	carbonyl reductase 4	CBR4	7.13	7.50	6.30	1.21	7.6E-03	0.192
11730865_a_at	vitamin K epoxide reductase complex, subunit 1-like 1	VKORC1L1	7.30	7.67	6.46	1.21	6.5E-03	0.181
11750103_a_at	hydroxyacyl-CoA dehydrogenase	HADH	7.23	7.60	6.39	1.21	6.8E-03	0.185
11743046_a_at	flotillin 1	FLOT1	8.71	9.08	7.87	1.21	8.3E-03	0.202
11735942_at	histone cluster 1, H4d	HIST1H4D	7.13	7.50	6.29	1.21	9.8E-03	0.212
11717727_s_at	hematological and neurological expressed 1	HN1	8.01	8.38	7.19	1.19	7.1E-03	0.188
11732376_a_at	TBC1 domain family, member 19	TBC1D19	6.45	6.81	5.63	1.18	3.4E-03	0.148
11751304_a_at	integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide)	ITGAL	9.53	9.89	8.72	1.18	7.2E-03	0.188
11740879_s_at	annexin A2	ANXA2	10.43	10.79	9.61	1.18	6.3E-03	0.180
11742740_at	gem (nuclear organelle) associated protein 5	GEMIN5	7.56	7.91	6.75	1.17	9.6E-03	0.212
11751748_a_at	chimerin 2	CHN2	9.99	10.34	9.21	1.14	5.2E-03	0.168
11742718_a_at	SAFB-like, transcription modulator	SLTM	6.34	6.69	5.55	1.13	8.2E-03	0.201
11715371_a_at	ubiquitin-like modifier activating enzyme 1	UBA1	10.33	10.68	9.54	1.13	9.8E-03	0.212
11752885_x_at	tripeptidyl peptidase I	TPP1	8.70	9.05	7.93	1.12	9.9E-03	0.212
11759961_at	ArfGAP with FG repeats 2	AGFG2	5.55	5.89	4.78	1.11	5.2E-03	0.168
11744083_at	ankyrin repeat and IBR domain containing 1	ANKIB1	6.21	6.55	5.44	1.11	5.5E-03	0.173
11725124_at	cystatin F (leukocystatin)	CST7	11.76	12.10	11.00	1.11	8.2E-03	0.201
11717956_s_at	serine threonine kinase 39	STK39	9.34	9.68	8.57	1.10	9.6E-03	0.212
11733439_a_at	guanylate binding protein 5	GBP5	8.41	8.75	7.65	1.10	4.8E-03	0.164
11743615_s_at	ubiquitin specific peptidase 47	USP47	5.86	6.19	5.10	1.09	9.0E-03	0.206
11756255_x_at	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta	YWHAH	8.76	9.10	8.01	1.08	8.5E-03	0.204
11750408_a_at	CD97 molecule	CD97	10.33	10.66	9.58	1.08	3.1E-03	0.148
11748654_a_at	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	PTPN22	9.36	9.68	8.63	1.05	6.4E-03	0.181
11717526_a_at	radixin	RDX	6.24	6.55	5.52	1.03	9.7E-03	0.212
11725416_at	natural killer cell granule protein 7	NKG7	12.05	12.37	11.34	1.03	9.5E-03	0.212
11747253_a_at	uracil-DNA glycosylase	UNG	6.08	6.39	5.37	1.02	9.8E-03	0.212
11716987_a_at	3-hydroxy-3-methylglutaryl-CoA synthase 1 (soluble)	HMGCS1	7.67	7.98	6.96	1.02	9.2E-03	0.208
11723958_s_at	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae)	LSM5	8.93	8.62	9.64	-1.02	5.7E-03	0.176
11728647_at	nuclear casein kinase and cyclin-dependent kinase substrate 1	NUCKS1	8.82	8.51	9.53	-1.02	7.6E-03	0.192
11755413_a_at	DENN/MADD domain containing 6B	DENND6B	4.88	4.57	5.59	-1.02	9.4E-03	0.212

11733100_at	ubiquitin specific peptidase 12	USP12	7.69	7.37	8.40	-1.03	9.5E-03	0.212
11748277_a_at	activating signal cointegrator 1 complex subunit 1	ASCC1	6.38	6.05	7.11	-1.06	8.7E-03	0.204
11721121_a_at	spinster homolog 1 (Drosophila)	SPNS1	6.71	6.38	7.44	-1.07	8.9E-03	0.206
11736803_at	fibroblast growth factor 9	FGF9	3.96	3.62	4.72	-1.10	8.6E-03	0.204
11728093_a_at	mitogen-activated protein kinase kinase kinase 1, E3 ubiquitin protein ligase	MAP3K1	9.58	9.23	10.36	-1.13	5.7E-03	0.176
11729536_a_at	synaptonemal complex central element protein 2	SYCE2	5.22	4.87	6.00	-1.13	8.3E-03	0.202
11717559_a_at	actin binding LIM protein 1	ABLIM1	9.79	9.44	10.58	-1.14	3.2E-03	0.148
11751644_a_at	pre-B-cell leukemia homeobox interacting protein 1	PBXIP1	6.96	6.61	7.75	-1.14	6.6E-03	0.182
11755616_a_at	solute carrier family 8 (sodium/lithium/calcium exchanger), member B1	SLC8B1	7.61	7.26	8.41	-1.16	8.1E-03	0.201
11732764_x_at	coiled-coil domain containing 120	CCDC120	5.82	5.47	6.62	-1.16	8.8E-03	0.205
11743906_a_at	UDP-glucuronate decarboxylase 1	UXS1	8.49	8.14	9.30	-1.16	9.1E-03	0.208
11715823_x_at	synaptophysin-like 1	SYPL1	7.47	7.11	8.28	-1.17	2.0E-03	0.129
11748850_a_at	fms-related tyrosine kinase 3 ligand	FLT3LG	8.85	8.49	9.66	-1.17	7.2E-03	0.188
11732338_a_at	K(lysine) acetyltransferase 8	KAT8	7.62	7.26	8.43	-1.17	1.0E-02	0.213
11726018_a_at	family with sequence similarity 222, member B	FAM222B	7.11	6.74	7.92	-1.18	5.1E-03	0.168
11729926_at	zinc finger protein 510	ZNF510	6.03	5.67	6.86	-1.19	3.2E-03	0.148
11728454_s_at	dedicator of cytokinesis 9	DOCK9	6.23	5.86	7.06	-1.20	4.2E-03	0.161
11747889_x_at	SH3 and SYLF domain containing 1	SH3YL1	6.63	6.26	7.46	-1.20	5.8E-03	0.176
11718540_at	transmembrane protein 243, mitochondrial	TMEM243	6.98	6.60	7.81	-1.21	9.9E-03	0.212
11736473_a_at	transcription factor 7 (T-cell specific, HMG-box)	TCF7	9.99	9.61	10.83	-1.22	5.7E-03	0.176
11757404_x_at	inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	ID3	5.85	5.47	6.69	-1.22	5.1E-03	0.168
11727090_a_at	zinc finger and BTB domain containing 18	ZBTB18	7.18	6.80	8.04	-1.24	5.8E-03	0.176
11716483_x_at	glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1 (glutamate binding)	GRINA	6.27	5.89	7.13	-1.25	4.5E-03	0.163
11732278_at	forkhead box P1	FOXP1	9.56	9.18	10.42	-1.25	1.6E-03	0.120
11753051_x_at	zinc finger protein 483	ZNF483	5.87	5.49	6.74	-1.25	6.7E-03	0.184
11721186_a_at	Rab geranylgeranyltransferase, alpha subunit	RABGGTA	7.17	6.79	8.04	-1.25	4.3E-03	0.161
11758239_s_at	chromosome 9 open reading frame 72	C9orf72	3.33	2.94	4.20	-1.26	5.9E-03	0.178
11718674_a_at	transmembrane protein 245	TMEM245	5.30	4.91	6.17	-1.26	1.6E-03	0.120
11759532_at	factor interacting with PAPOLA and CPSF1	FIP1L1	4.68	4.29	5.56	-1.27	3.9E-03	0.155
11725301_x_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19A	DDX19A	6.64	6.25	7.52	-1.27	4.9E-03	0.167
11728004_s_at	Ral GEF with PH domain and SH3 binding motif 2	RALGPS2	3.19	2.80	4.07	-1.27	5.2E-03	0.168
11742747_a_at	signal peptide peptidase like 3	SPPL3	7.01	6.62	7.89	-1.27	4.1E-03	0.159
11755772_a_at	forkhead box O1	FOXO1	9.18	8.79	10.07	-1.28	8.7E-03	0.204
11718618_a_at	DnaJ (Hsp40) homolog, subfamily A, member 4	DNAJA4	5.27	4.88	6.16	-1.28	7.0E-03	0.187
11725441_a_at	forkhead box M1	FOXM1	5.15	4.76	6.04	-1.28	8.7E-03	0.204

11724377_at	phosphoprotein membrane anchor with glycosphingolipid microdomains 1	PAG1	6.84	6.44	7.73	-1.29	2.4E-03	0.138
11752636_a_at	transient receptor potential cation channel, subfamily C, member 4 associated protein	TRPC4AP	6.19	5.79	7.08	-1.30	6.3E-03	0.180
11721295_a_at	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1	STAM	5.93	5.53	6.83	-1.30	4.8E-03	0.165
11744600_a_at	thymocyte expressed, positive selection associated 1	TESPA1	8.53	8.13	9.43	-1.30	4.0E-03	0.159
11762132_a_at	adhesion molecule, interacts with CXADR antigen 1	AMICA1	5.19	4.79	6.10	-1.30	6.2E-03	0.180
11734292_x_at	zinc finger protein 417	ZNF417	4.77	4.36	5.67	-1.31	8.9E-03	0.206
11758571_s_at	neural precursor cell expressed, developmentally down-regulated 4-like, E3 ubiquitin protein ligase	NEDD4L	5.33	4.92	6.24	-1.32	3.4E-03	0.148
11716124_a_at	N-acetyltransferase 10 (GCN5-related)	NAT10	6.68	6.27	7.59	-1.32	1.7E-03	0.120
11762238_a_at	transmembrane protein 128	TMEM128	4.77	4.36	5.70	-1.33	4.6E-03	0.163
11727633_at	solute carrier family 16 (aromatic amino acid transporter), member 10	SLC16A10	3.47	3.06	4.40	-1.33	5.4E-03	0.171
11721900_at	ficolin (collagen/fibrinogen domain containing) 1	FCN1	4.55	4.13	5.47	-1.34	1.1E-03	0.107
11756268_a_at	F-box protein 4	FBXO4	5.52	5.11	6.45	-1.34	7.9E-03	0.198
11743962_at	consortin, connexin sorting protein	CNST	5.53	5.12	6.46	-1.35	2.1E-03	0.133
11731828_at	glypican 2	GPC2	5.31	4.89	6.24	-1.35	6.4E-03	0.181
11721958_at	yippee-like 2 (Drosophila)	YPEL2	6.65	6.23	7.58	-1.35	1.7E-03	0.120
11731513_at	exportin 4	XPO4	7.10	6.68	8.04	-1.35	4.3E-03	0.161
11755826_a_at	selectin P (granule membrane protein 140kDa, antigen CD62)	SELP	3.84	3.42	4.77	-1.35	1.5E-03	0.116
11738261_at	zinc finger protein 493	ZNF493	4.00	3.59	4.94	-1.35	6.1E-03	0.180
11718453_a_at	axin 2	AXIN2	6.16	5.75	7.11	-1.36	5.3E-03	0.169
11722541_a_at	human immunodeficiency virus type I enhancer binding protein 2	HIVEP2	6.08	5.66	7.03	-1.36	2.8E-03	0.145
11727470_x_at	zinc finger protein 544	ZNF544	7.32	6.89	8.28	-1.38	7.7E-03	0.195
11719463_a_at	lipolysis stimulated lipoprotein receptor	LSR	8.20	7.78	9.16	-1.38	3.3E-03	0.148
11763504_at	neurofibromin 1	NF1	4.00	3.57	4.96	-1.38	4.7E-03	0.163
11734742_a_at	LIM domain kinase 2	LIMK2	8.20	7.77	9.16	-1.39	3.4E-03	0.148
11763283_at	phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit alpha	PIK3CA	6.57	6.14	7.53	-1.39	6.3E-03	0.180
11757737_s_at	recombination signal binding protein for immunoglobulin kappa J region	RBPJ	8.77	8.34	9.74	-1.39	1.8E-03	0.123
11725181_a_at	Rho guanine nucleotide exchange factor (GEF) 4	ARHGEF4	5.56	5.13	6.53	-1.40	4.0E-04	0.079
11756230_a_at	filamin B, beta	FLNB	5.17	4.74	6.13	-1.40	5.6E-03	0.173
11743991_at	MRG/MORF4L binding protein	MRGBP	6.59	6.16	7.56	-1.40	1.8E-03	0.120
11763594_a_at	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	HS3ST3B1	5.94	5.51	6.91	-1.40	9.1E-03	0.208
11756585_a_at	aquaporin 3 (Gill blood group)	AQP3	9.30	8.87	10.27	-1.40	1.7E-03	0.120
11739738_at	DCN1, defective in cullin neddylation 1, domain containing 2	DCUN1D2	7.76	7.33	8.73	-1.40	3.5E-03	0.148
11717073_a_at	AE binding protein 1	AEBP1	7.24	6.80	8.22	-1.41	2.2E-03	0.134
11752398_a_at	chromosome 1 open reading frame 228	C1orf228	8.44	8.01	9.42	-1.42	9.3E-03	0.210

11755726_a_at	transmembrane protein 30B	TMEM30B	5.70	5.26	6.68	-1.43	3.3E-03	0.148
11725252_at	family with sequence similarity 120C	FAM120C	3.77	3.33	4.76	-1.43	7.2E-03	0.188
11732301_at	interleukin 23, alpha subunit p19	IL23A	5.31	4.87	6.31	-1.44	1.4E-03	0.113
11717710_a_at	mitochondrial fission process 1	MTFP1	8.93	8.49	9.93	-1.44	7.4E-03	0.192
11728375_x_at	actinin, alpha 1	ACTN1	7.54	7.10	8.54	-1.44	9.7E-03	0.212
11743718_a_at	zinc finger protein interacting with K protein 1	ZIK1	2.98	2.53	3.98	-1.45	2.4E-03	0.138
11734084_a_at	sushi domain containing 3	SUSD3	7.71	7.26	8.72	-1.46	4.1E-03	0.159
11743384_at	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)	PRPF40A	5.15	4.70	6.16	-1.46	4.6E-03	0.163
11747669_x_at	integral membrane protein 2C	ITM2C	6.83	6.38	7.84	-1.46	8.6E-03	0.204
11751822_a_at	minichromosome maintenance complex component 6	MCM6	5.86	5.41	6.88	-1.46	4.7E-03	0.163
11728161_at	wingless-type MMTV integration site family, member 7A	WNT7A	5.59	5.14	6.61	-1.47	1.4E-03	0.113
11742872_s_at	phosphoinositide-3-kinase interacting protein 1	PIK3IP1	7.26	6.80	8.28	-1.48	2.5E-03	0.141
11722850_a_at	baculoviral IAP repeat containing 3	BIRC3	8.36	7.91	9.38	-1.48	8.6E-04	0.093
11731967_a_at	calcium channel, voltage-dependent, T type, alpha 1I subunit	CACNA1I	6.43	5.98	7.46	-1.49	5.5E-03	0.172
11733355_x_at	complement component 5a receptor 1	C5AR1	3.38	2.92	4.42	-1.49	9.0E-04	0.094
11759784_at	supervillin	SVIL	5.00	4.54	6.03	-1.50	9.8E-03	0.212
11732752_at	RNA binding motif protein 44	RBM44	3.29	2.83	4.33	-1.50	6.0E-03	0.178
11717949_a_at	sterol-C5-desaturase	SC5D	4.83	4.37	5.87	-1.50	1.2E-03	0.109
11723960_at	sec1 family domain containing 2	SCFD2	4.13	3.67	5.17	-1.51	9.0E-03	0.207
11717017_a_at	OCIA domain containing 2	OCIAD2	8.95	8.48	9.99	-1.51	3.0E-03	0.146
11732763_at	glutamate receptor, ionotropic, N-methyl-D-aspartate 3A	GRIN3A	4.10	3.64	5.15	-1.51	3.2E-03	0.148
11746747_a_at	coenzyme Q2 4-hydroxybenzoate polyprenyltransferase	COQ2	5.16	4.70	6.21	-1.51	2.3E-03	0.138
11720144_s_at	centriole, cilia and spindle-associated protein	CCSAP	6.21	5.74	7.26	-1.52	8.6E-03	0.204
11747157_a_at	cerebral dopamine neurotrophic factor	CDNF	3.42	2.95	4.47	-1.52	1.6E-03	0.120
11737790_a_at	peptidyl-tRNA hydrolase 2	PTRH2	7.88	7.41	8.93	-1.52	7.0E-03	0.187
11753854_a_at	CD28 molecule	CD28	8.93	8.46	9.98	-1.52	5.1E-03	0.168
11739641_a_at	actin filament associated protein 1	AFAP1	5.54	5.07	6.59	-1.52	5.6E-03	0.175
11716553_a_at	rhomboid domain containing 2	RHBDD2	7.69	7.22	8.74	-1.52	8.3E-03	0.202
11720845_a_at	CD248 molecule, endosialin	CD248	6.08	5.61	7.14	-1.53	5.8E-03	0.177
11716812_x_at	SIN3 transcription regulator family member B	SIN3B	5.85	5.38	6.91	-1.53	2.9E-03	0.146
11716263_s_at	leptin receptor overlapping transcript-like 1	LEPROTL1	9.40	8.93	10.45	-1.53	5.4E-04	0.082
11737745_a_at	oviductal glycoprotein 1, 120kDa	OVGP1	4.98	4.51	6.04	-1.53	8.8E-03	0.204
11741089_x_at	CD79a molecule, immunoglobulin-associated alpha	CD79A	4.78	4.31	5.84	-1.53	4.3E-04	0.079
11745217_a_at	MKL/myocardin-like 2	MKL2	5.45	4.98	6.51	-1.53	4.4E-03	0.162
11747357_a_at	cytokine induced apoptosis inhibitor 1	CIAPIN1	4.63	4.15	5.70	-1.55	8.2E-03	0.201
11730474_at	phosphodiesterase 3B, cGMP-inhibited	PDE3B	9.23	8.76	10.31	-1.55	3.8E-03	0.153

11727378_at	TBC1 domain family, member 15	TBC1D15	5.14	4.66	6.22	-1.55	4.9E-03	0.167
11750148_a_at	sushi, nidogen and EGF-like domains 1	SNED1	5.48	5.00	6.56	-1.56	3.0E-03	0.146
11725445_x_at	B-cell CLL/lymphoma 3	BCL3	7.28	6.80	8.36	-1.56	3.0E-03	0.146
11722997_s_at	nucleolar protein 11	NOL11	7.44	6.96	8.52	-1.56	4.6E-03	0.163
11756224_s_at	zinc finger, DHHC-type containing 9	ZDHHC9	4.52	4.04	5.61	-1.56	1.3E-03	0.113
11745703_a_at	RCAN family member 3	RCAN3	9.54	9.06	10.63	-1.58	2.4E-03	0.138
11726961_at	small glutamine-rich tetratricopeptide repeat (TPR)-containing, beta	SGTB	8.74	8.26	9.84	-1.58	6.5E-03	0.181
11746331_a_at	adenosine kinase	ADK	6.68	6.20	7.78	-1.59	2.6E-03	0.143
11735105_a_at	CD40 ligand	CD40LG	5.73	5.24	6.83	-1.59	5.0E-03	0.167
11719737_a_at	family with sequence similarity 134, member B	FAM134B	6.37	5.88	7.47	-1.59	3.7E-03	0.152
11742215_s_at	amyloid beta (A4) precursor protein	APP	3.72	3.23	4.82	-1.59	3.3E-03	0.148
11737845_x_at	family with sequence similarity 102, member A	FAM102A	9.44	8.95	10.55	-1.60	8.3E-04	0.093
11763378_a_at	zinc finger protein 302	ZNF302	3.95	3.46	5.06	-1.60	4.1E-03	0.159
11759658_a_at	reversion-inducing-cysteine-rich protein with kazal motifs	RECK	5.03	4.54	6.14	-1.60	3.0E-03	0.146
11758312_x_at	TBC1 domain family, member 3	TBC1D3	6.01	5.52	7.12	-1.60	2.5E-03	0.141
11749344_a_at	dehydrogenase/reductase (SDR family) member 3	DHRS3	6.31	5.81	7.43	-1.62	3.5E-04	0.079
11734216_a_at	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	MPP7	6.40	5.90	7.52	-1.62	3.3E-04	0.079
11764149_s_at	dual specificity phosphatase 16	DUSP16	8.19	7.69	9.31	-1.62	2.7E-04	0.079
11721889_a_at	heat shock factor binding protein 1-like 1	HSBP1L1	6.05	5.55	7.17	-1.62	3.0E-03	0.146
11722853_a_at	hyaluronan binding protein 4	HABP4	7.11	6.61	8.24	-1.63	3.5E-03	0.148
11727757_at	oncostatin M	OSM	5.91	5.41	7.04	-1.64	4.2E-04	0.079
11729955_x_at	fragile histidine triad	FHIT	6.39	5.88	7.52	-1.64	2.3E-03	0.138
11716147_s_at	charged multivesicular body protein 7	CHMP7	7.96	7.45	9.09	-1.64	2.4E-03	0.140
11759805_at	Williams-Beuren syndrome chromosome region 16	WBSCR16	4.33	3.82	5.47	-1.65	3.1E-04	0.079
11759059_at	zinc finger protein 134	ZNF134	5.74	5.23	6.88	-1.65	3.9E-03	0.155
11759232_at	chromosome 6 open reading frame 25	C6orf25	4.08	3.57	5.22	-1.65	2.3E-03	0.138
11736352_at	transmembrane protein 220	TMEM220	4.56	4.05	5.70	-1.65	2.5E-03	0.141
11715490_s_at	actin, gamma 1 pseudogene 4	ACTG1P4	5.96	5.45	7.11	-1.66	5.4E-03	0.172
11759346_a_at	mastermind-like 2 (Drosophila)	MAML2	6.10	5.59	7.25	-1.66	2.4E-03	0.138
11725799_a_at	ubiquitin specific peptidase 46	USP46	4.43	3.92	5.58	-1.66	2.1E-03	0.133
11745071_a_at	transcription elongation factor A (SII)-like 4	TCEAL4	8.13	7.62	9.29	-1.67	1.1E-04	0.075
11753716_a_at	adaptor-related protein complex 4, sigma 1 subunit	AP4S1	4.22	3.70	5.38	-1.67	1.9E-04	0.079
11719406_a_at	homeodomain interacting protein kinase 2	HIPK2	5.48	4.96	6.66	-1.69	4.3E-03	0.161
11718705_at	insulin-like growth factor 1 receptor	IGF1R	4.25	3.73	5.42	-1.69	8.1E-03	0.201
11752282_a_at	PTPRF interacting protein, binding protein 2 (liprin beta 2)	PPFIBP2	5.05	4.52	6.22	-1.70	2.9E-03	0.146
11762418_x_at	SCAN domain containing 2 pseudogene	SCAND2P	5.44	4.91	6.63	-1.72	1.1E-03	0.108

11725411_at	neuron navigator 1	NAV1	3.85	3.32	5.05	-1.72	8.8E-03	0.204
11759527_at	solute carrier family 11 (proton-coupled divalent metal ion transporter), member 2	SLC11A2	5.40	4.87	6.59	-1.72	3.3E-04	0.079
11716148_a_at	TRAF3 interacting protein 2	TRAF3IP2	6.21	5.67	7.41	-1.74	8.7E-03	0.204
11739658_a_at	lymphotoxin beta (TNF superfamily, member 3)	LTB	8.11	7.57	9.33	-1.75	8.8E-04	0.094
11756641_a_at	zinc finger protein 256	ZNF256	6.45	5.91	7.67	-1.76	7.1E-04	0.090
11751420_a_at	zinc finger, CW type with PWWP domain 1	ZCWPW1	5.49	4.95	6.71	-1.76	2.0E-04	0.079
11717435_a_at	cell division cycle associated 7-like	CDCA7L	5.23	4.69	6.45	-1.76	9.9E-03	0.212
11729409_at	zinc finger protein 764	ZNF764	7.25	6.70	8.47	-1.77	3.1E-03	0.146
11758485_s_at	ankyrin repeat domain 13C	ANKRD13C	4.51	3.96	5.74	-1.77	2.3E-03	0.138
11748351_a_at	thrombospondin 3	THBS3	6.20	5.65	7.43	-1.78	6.1E-03	0.180
11746678_a_at	RNA binding motif protein 11	RBM11	5.12	4.57	6.35	-1.78	1.5E-03	0.119
11756191_a_at	mannosidase, alpha, class 1C, member 1	MAN1C1	5.54	4.99	6.79	-1.79	2.8E-03	0.145
11731237_at	zinc finger, DBF-type containing 2	ZDBF2	4.03	3.48	5.28	-1.80	4.1E-03	0.159
11737749_a_at	serum/glucocorticoid regulated kinase 1	SGK1	6.62	6.06	7.86	-1.80	9.9E-03	0.212
11749407_a_at	ZNF667 antisense RNA 1 (head to head)	ZNF667-AS1	4.51	3.94	5.78	-1.84	5.2E-04	0.082
11731703_x_at	zinc finger protein 551	ZNF551	4.21	3.64	5.49	-1.85	3.3E-04	0.079
11719155_a_at	DNA-damage regulated autophagy modulator 1	DRAM1	2.89	2.32	4.17	-1.86	3.0E-03	0.146
11723209_s_at	kelch repeat and BTB (POZ) domain containing 6	KBTBD6	3.64	3.06	4.93	-1.86	3.5E-03	0.148
11744162_a_at	dual specificity phosphatase 4	DUSP4	5.63	5.05	6.93	-1.87	9.3E-03	0.211
11715949_s_at	potassium channel tetramerization domain containing 12	KCTD12	4.92	4.34	6.22	-1.89	1.3E-03	0.113
11763531_a_at	methyltransferase like 15	METTL15	5.01	4.43	6.32	-1.89	3.5E-03	0.148
11758027_s_at	hook microtubule-tethering protein 1	HOOK1	3.35	2.77	4.66	-1.89	2.0E-04	0.079
11756787_a_at	hyaluronan and proteoglycan link protein 3	HAPLN3	6.81	6.23	8.13	-1.89	2.6E-03	0.143
11760058_at	solute carrier family 3 (amino acid transporter heavy chain), member 1	SLC3A1	4.36	3.78	5.67	-1.90	3.0E-03	0.146
11734854_a_at	V-set and immunoglobulin domain containing 1	VSIG1	7.45	6.86	8.79	-1.93	6.2E-03	0.180
11754557_s_at	protein kinase C, alpha	PRKCA	5.80	5.21	7.14	-1.93	4.2E-04	0.079
11725517_x_at	ATP-binding cassette, sub-family G (WHITE), member 1	ABCG1	7.38	6.78	8.72	-1.94	8.5E-03	0.204
11715270_s_at	Kruppel-like factor 7 (ubiquitous)	KLF7	8.27	7.67	9.61	-1.94	8.0E-04	0.093
11758432_s_at	cytoplasmic polyadenylation element binding protein 1	CPEB1	4.51	3.91	5.85	-1.94	7.0E-03	0.187
11730192_x_at	SEC14-like 2 (S. cerevisiae)	SEC14L2	5.88	5.28	7.24	-1.96	6.0E-04	0.083
11752084_a_at	kelch-like family member 6	KLHL6	6.02	5.41	7.38	-1.97	6.6E-03	0.183
11727300_a_at	fibroblast growth factor receptor 1	FGFR1	4.57	3.96	5.94	-1.98	1.4E-03	0.113
11754769_a_at	BEN domain containing 5	BEND5	4.06	3.45	5.44	-1.99	1.6E-04	0.079
11720910_a_at	NEL-like 2 (chicken)	NELL2	8.57	7.95	9.97	-2.02	4.0E-04	0.079
11729655_a_at	SMAD family member 2	SMAD2	5.74	5.12	7.14	-2.02	8.2E-04	0.093

11759827_at	zinc finger protein 154	ZNF154	4.24	3.62	5.64	-2.02	7.1E-03	0.188
11756313_x_at	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1	SERPINF1	5.04	4.42	6.45	-2.03	1.3E-03	0.113
11763472_x_at	zinc finger CCCH-type containing 12D	ZC3H12D	7.83	7.20	9.24	-2.04	5.6E-04	0.082
11753266_a_at	transcription elongation factor A (SII), 3	TCEA3	6.36	5.72	7.78	-2.05	3.3E-03	0.148
11733867_a_at	major histocompatibility complex, class II, DO alpha	HLA-DOA	6.13	5.50	7.56	-2.06	1.2E-03	0.109
11725692_a_at	von Willebrand factor A domain containing 5A	VWA5A	3.85	3.22	5.29	-2.07	5.6E-04	0.082
11733811_a_at	FAST kinase domains 2	FASTKD2	4.25	3.61	5.68	-2.07	2.5E-03	0.141
11728910_a_at	zinc finger protein 615	ZNF615	5.28	4.64	6.71	-2.07	6.4E-04	0.087
11717854_a_at	zinc finger and SCAN domain containing 18	ZSCAN18	5.70	5.06	7.13	-2.07	6.5E-03	0.181
11744855_at	serpin peptidase inhibitor, clade B (ovalbumin), member 9, pseudogene 1	SERPINB9P1	6.46	5.81	7.92	-2.11	1.0E-03	0.102
11744219_at	G0/G1 switch 2	G0S2	5.54	4.89	7.02	-2.14	1.6E-03	0.120
11741079_x_at	cAMP responsive element modulator	CREM	8.01	7.33	9.52	-2.18	8.1E-03	0.201
11724886_a_at	leucine rich repeat neuronal 3	LRRN3	5.18	4.50	6.71	-2.21	1.7E-03	0.120
11752913_a_at	sestrin 3	SESN3	8.11	7.42	9.67	-2.25	3.8E-04	0.079
11725492_at	RAB20, member RAS oncogene family	RAB20	3.67	2.98	5.23	-2.25	3.5E-04	0.079
11745722_x_at	four and a half LIM domains 1	FHL1	4.38	3.69	5.94	-2.26	4.5E-04	0.080
11734368_s_at	DMRT-like family C1	DMRTC1	4.90	4.19	6.52	-2.33	2.8E-03	0.145
11731019_x_at	allograft inflammatory factor 1	AIF1	7.65	6.92	9.27	-2.35	1.8E-03	0.120
11746543_a_at	sorting nexin 9	SNX9	6.12	5.39	7.75	-2.36	3.0E-03	0.146
11725981_at	chemokine (C-C motif) receptor 7	CCR7	9.71	8.98	11.34	-2.36	5.4E-04	0.082
11757812_s_at	inositol polyphosphate-5-phosphatase, 40kDa	INPP5A	8.06	7.32	9.72	-2.40	1.4E-03	0.114
11727336_at	sterile alpha motif domain containing 12	SAMD12	5.89	5.14	7.57	-2.43	5.8E-04	0.083
11726145_at	carbonic anhydrase VI	CA6	4.97	4.22	6.66	-2.45	6.8E-03	0.185
11747110_a_at	PAS domain containing serine/threonine kinase	PASK	7.97	7.20	9.71	-2.51	9.1E-05	0.075
11726583_s_at	cytoskeleton-associated protein 4	CKAP4	6.59	5.82	8.33	-2.52	3.6E-04	0.079
11734200_at	zinc finger protein 844	ZNF844	5.78	5.01	7.53	-2.53	1.3E-03	0.113
11739942_s_at	Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA synthase	SEPSECS	4.37	3.60	6.12	-2.53	2.0E-04	0.079
11753823_a_at	S100 calcium binding protein A8	S100A8	5.86	5.07	7.63	-2.55	4.5E-03	0.163
11740488_x_at	desmocollin 1	DSC1	5.98	5.17	7.80	-2.63	8.4E-04	0.093
11749644_s_at	zinc finger E-box binding homeobox 1	ZEB1	7.10	6.28	8.94	-2.66	4.6E-05	0.072
11719372_s_at	nerve growth factor receptor (TNFRSF16) associated protein 1	NGFRAP1	7.48	6.65	9.36	-2.70	2.7E-03	0.145
11718419_at	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide	FCER1G	5.91	5.02	7.93	-2.91	3.5E-04	0.079
11728239_at	Ras-related GTP binding D	RRAGD	3.90	3.00	5.93	-2.93	1.6E-03	0.120
11741379_a_at	BTB and CNC homology 1, basic leucine zipper transcription factor 2	BACH2	6.17	5.26	8.22	-2.95	1.7E-04	0.079
11745496_a_at	serine peptidase inhibitor, Kunitz type, 2	SPINT2	7.05	6.08	9.21	-3.13	3.8E-04	0.079

11718841_s_at	chemokine (C-X-C motif) ligand 8	CXCL8	5.15	4.16	7.39	-3.23	3.0E-04	0.079
11736801_a_at	pleiomorphic adenoma gene 1	PLAG1	4.43	3.40	6.75	-3.34	5.9E-05	0.072
11728469_a_at	BTB (POZ) domain containing 11	BTBD11	5.46	4.43	7.78	-3.35	1.7E-03	0.120

Supplementary Table S2. *Characterization of CD8$^+$ T-cell transcriptional signatures from AML patients at diagnosis according to their subsequent response to chemotherapy*. Gene expression analysis of PB CD8$^+$ T-cells from AML patients at diagnosis (pre-treatment) (*n* = 6) according to their subsequent response; complete remission (CR) (*n* = 3) and nonresponders (NR) (*n* = 3). Venn diagram of differentially expressed gene sets by CD8$^+$ T-cells for pre-treatment AML CR versus NR patient comparison (red circle) and post-treatment AML CR versus NR patient comparison (yellow, downregulated; and blue; upregulated). Only 7 overlapping genes were identified between the data sets and presented in accompanying tables. The remaining differentially expressed genes (195) for pre-treatment comparison are also listed to the right.

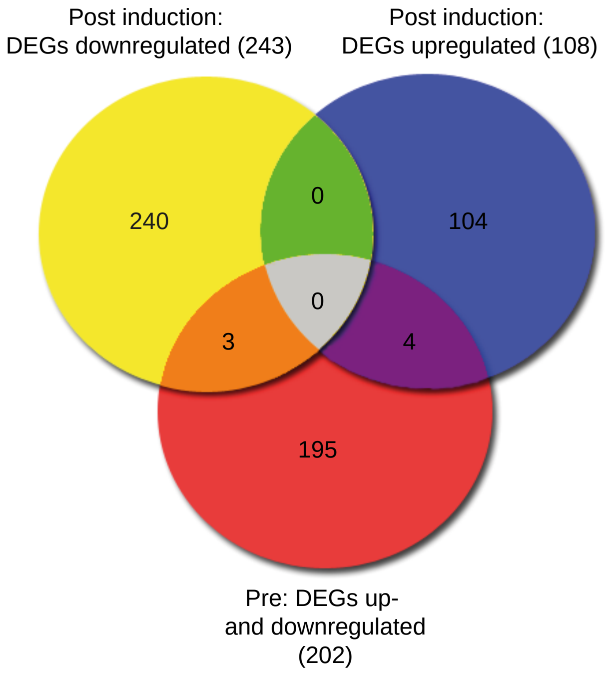
Supplementary Table 2.

240	0	104	0
Table S3		Table S3	

3	
GENE	logFC
FCGR2A	2.40
JAK2	1.51
PHF20L1	-1.78

4	
GENE	logFC
REV1	2.48
IL11RA	1.59
ELL2	-2.17
FAM169A	-1.77

195							
GENE UP	logFC	GENE UP (continued)	logFC	GENE Down	logFC	GENE Down (continued)	logFC
HLA-C	3.23	WDR52	1.74	CHN1	-3.00	SGTB	-1.81
GTF2H1	3.10	MIR6845	1.74	BTBD11	-2.71	GABPB1	-1.80
DDX26B	2.90	ZNF883	1.74	MSRA	-2.61	GAB2	-1.79
ZNF208	2.89	CARF	1.73	TMEM2	-2.52	NLE1	-1.78
PIAS2	2.86	FANCD2	1.73	MVB12B	-2.45	CCNE1	-1.77
HDAC8	2.69	OPA3	1.72	ACSL1	-2.45	UBXN2A	-1.75
CEP63	2.67	CDRT4	1.72	ABCG1	-2.40	ANAPC10	-1.75
ZNF232	2.65	MCM8	1.70	TUBGCP3	-2.39	TLE3	-1.73
ZNF559	2.61	CCDC88A	1.70	LSM5	-2.38	METTL9	-1.73
SLC16A4	2.60	ANKRD32	1.70	MEST	-2.37	ABL2	-1.72
LINC00612	2.59	EXOG	1.70	FBXO42	-2.36	NSF	-1.71
SOCS2	2.46	DBNL	1.68	APH1B	-2.35	MTHFD1L	-1.70
RNF214	2.40	MRPS36	1.66	STS	-2.32	EXD2	-1.70
APTX	2.38	TRIOBP	1.66	ZNF77	-2.30	FAF2	-1.69
ZNF41	2.36	CACYBP	1.63	RIBC1	-2.25	TRMT61B	-1.67
CHST2	2.35	ZC3H6	1.61	GNL1	-2.24	GORAB	-1.66
AK5	2.32	KIF1B	1.61	SKI	-2.19	ACOT9	-1.66
KLRC4	2.29	DOCK7	1.61	ABCF2	-2.19	PIK3R1	-1.65
ZNF514	2.25	CLCC1	1.60	TNKS2	-2.18	TMEM184B	-1.64
UCHL5	2.18	FAM178A	1.60	MBD5	-2.18	PDCD2	-1.64
NANP	2.14	SLC12A6	1.58	SSH1	-2.18	NOL10	-1.64
AMY1A	2.12	ATF7	1.58	SPEG	-2.18	HLA-DMA	-1.63
CFLAR	2.09	RCCD1	1.57	ZSCAN29	-2.16	ZDHHC3	-1.63



CAPRIN2	2.08
NIT1	2.08
ITGB1	2.06
C11orf65	2.05
VPS45	2.04
MYO6	2.03
CELF4	2.01
RGS3	2.00
SEPT8	1.97
ATP10D	1.97
TRAC	1.95
GINS1	1.95
ATP8B1	1.95
WDR92	1.94
ZNF83	1.89
SSBP2	1.88
SLC38A9	1.88
SLC17A5	1.87
PDE4DIP	1.87
DGKH	1.87
CDKN3	1.83
CASP10	1.81
SNX11	1.81
COX15	1.79
SPICE1	1.74

SLFN13	1.57
BPNT1	1.53
PRH1-PRR4	1.52
GCFC2	1.52
ATG2B	1.52
LRRC8D	1.50
HIST1H2BJ	1.50
RAB11FIP1	1.49
PLEKHB1	1.48
FRY	1.46
TBC1D2B	1.46
INTS3	1.46
WSB1	1.43
VANGL1	1.43
PACRGL	1.40
XYLT1	1.40
SPON2	1.39
UVSSA	1.35
C15orf39	1.35
C14orf93	1.34
FARSB	1.33
MSH5	1.33
DLEC1	1.32
STMN3	1.32
ELAC1	1.26

ZNF805	-2.15
UBR5	-2.12
ZNF367	-2.10
POLR1B	-2.10
PDE4D	-2.10
SH3TC1	-2.07
BTBD10	-2.07
HIPK2	-2.06
CREM	-2.04
USP30	-2.03
ZC3H7B	-2.03
RRM2B	-2.01
NCOA7	-1.99
TMEM242	-1.97
PRKCE	-1.97
CEP76	-1.97
RANBP2	-1.96
PAPSS2	-1.95
TYW1	-1.94
TGFB3	-1.94
FANCM	-1.93
RPS28	-1.91
DDA1	-1.82
USP37	-1.82
WDR44	-1.81
ZNF778	-1.81

SLA2	-1.60
RCAN1	-1.59
HDAC6	-1.59
TRAPPC11	-1.58
SEPHS1	-1.58
RRP15	-1.57
ARL1	-1.56
FAM177A1	-1.56
TMEM241	-1.56
MCOLN2	-1.52
CCDC174	-1.51
SLC19A2	-1.50
MTFR2	-1.50
NBPF1	-1.50
PRMT5	-1.49
PSMD12	-1.45
PHF12	-1.44
ZER1	-1.44
NUPL1	-1.40
HUS1	-1.40
REXO4	-1.38
HMGXB4	-1.37
HERPUD1	-1.35
ZRANB1	-1.35
ZBED4	-1.34
TIMM8A	-1.33
ARID5B	-1.32

Supplementary Table S3. *Differentially expressed genes in CR relative to NR AML patients post induction chemotherapy*.

ID	NAME	GENE	A	CR	NR	LOG2FC	PVAL	FDR
11729555_a_at	sushi domain containing 4	SUSD4	4.91	6.98	2.83	4.14	6.3E-05	0.057
11723236_at	interferon-induced protein 44-like	IFI44L	5.49	7.39	3.60	3.79	3.4E-03	0.203
11761557_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47	DDX47	5.87	7.63	4.11	3.52	1.9E-03	0.172
11763326_s_at	fer (fps/fes related) tyrosine kinase	FER	5.53	7.27	3.78	3.48	8.7E-04	0.145
11723952_at	keratin 1	KRT1	5.20	6.92	3.48	3.44	6.3E-03	0.246
11736977_x_at	zinc finger protein 431	ZNF431	5.52	7.21	3.82	3.39	7.2E-05	0.058
11725797_a_at	ubiquitin specific peptidase 46	USP46	6.53	8.13	4.92	3.21	3.0E-03	0.201
11738262_a_at	autism susceptibility candidate 2	AUTS2	6.55	8.13	4.96	3.17	3.0E-03	0.201
11762445_a_at	chromosome 14 open reading frame 182	C14orf182	5.50	7.06	3.94	3.12	1.1E-03	0.157
11731360_a_at	inducible T-cell co-stimulator	ICOS	7.70	9.25	6.14	3.11	8.5E-04	0.145
11739685_a_at	exocyst complex component 6B	EXOC6B	5.66	7.20	4.11	3.09	1.8E-03	0.169
11762083_at	casein kinase 2, alpha 1 polypeptide	CSNK2A1	4.90	6.44	3.35	3.09	1.1E-03	0.157
11753580_s_at	small EDRK-rich factor 1A (telomeric)	SERF1A	6.24	7.75	4.73	3.02	1.5E-03	0.158
11756058_a_at	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	CEACAM1	5.78	7.28	4.28	3.01	2.3E-03	0.187
11725928_s_at	neurofilament, light polypeptide	NEFL	4.67	6.17	3.16	3.00	3.0E-03	0.201
11720597_s_at	cysteine-serine-rich nuclear protein 2	CSRNP2	5.31	6.79	3.83	2.96	1.3E-03	0.158
11734985_at	ELK4, ETS-domain protein (SRF accessory protein 1)	ELK4	3.67	5.13	2.21	2.92	2.4E-03	0.189
11759281_at	serine incorporator 5	SERINC5	7.77	9.22	6.31	2.91	5.2E-03	0.228
11728067_at	prostaglandin D2 receptor 2	PTGDR2	6.83	8.28	5.38	2.90	6.0E-03	0.238
11760468_at	REV1, polymerase (DNA directed)	REV1	4.32	5.76	2.89	2.87	9.8E-04	0.151
11729907_a_at	methyltransferase like 15	METTL15	5.52	6.93	4.12	2.81	7.6E-03	0.262
11736720_at	chemokine (C-C motif) receptor 4	CCR4	6.91	8.30	5.52	2.78	3.6E-03	0.208
11755239_a_at	elongation factor, RNA polymerase II, 2	ELL2	4.89	6.28	3.50	2.77	2.1E-03	0.180
11730307_a_at	RIC3 acetylcholine receptor chaperone	RIC3	5.83	7.21	4.45	2.76	1.3E-03	0.158
11740345_at	sorting nexin 29	SNX29	6.12	7.50	4.74	2.76	1.7E-03	0.168
11730666_at	forkhead box P1	FOXP1	5.96	7.33	4.58	2.75	8.1E-03	0.262
11727341_a_at	autophagy related 9B	ATG9B	5.67	7.04	4.29	2.75	1.6E-03	0.167
11753266_a_at	transcription elongation factor A (SII), 3	TCEA3	7.49	8.83	6.15	2.68	7.0E-03	0.258
11752420_x_at	nuclear pore complex interacting protein family, member B6	NPIPB6	6.29	7.63	4.96	2.67	5.3E-04	0.125
11730637_a_at	cytotoxic T-lymphocyte-associated protein 4	CTLA4	6.26	7.56	4.96	2.60	6.9E-03	0.258
11758629_s_at	spectrin, beta, non-erythrocytic 1	SPTBN1	6.27	7.57	4.97	2.60	2.6E-03	0.190
11728763_x_at	galactose-3-O-sulfotransferase 4	GAL3ST4	5.86	7.16	4.56	2.60	8.3E-03	0.262

11729766_x_at	zinc finger protein 331	ZNF331	7.84	9.12	6.55	2.57	2.4E-03	0.189
11759932_at	CDC-like kinase 4	CLK4	5.37	6.64	4.11	2.52	2.0E-03	0.175
11757973_x_at	N-myristoyltransferase 2	NMT2	6.42	7.67	5.17	2.51	2.6E-03	0.190
11759586_s_at	RAB18, member RAS oncogene family	RAB18	6.56	7.80	5.32	2.49	3.7E-03	0.210
11726964_at	synaptic Ras GTPase activating protein 1	SYNGAP1	6.53	7.77	5.29	2.49	4.1E-03	0.214
11737677_at	BTB (POZ) domain containing 18	BTBD18	5.28	6.52	4.04	2.48	5.4E-03	0.231
11762601_x_at	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa	NDUFB8	5.49	6.73	4.26	2.47	8.1E-03	0.262
11750468_a_at	nucleoporin 35kDa	NUP35	5.92	7.14	4.69	2.45	3.0E-03	0.201
11760630_at	ring finger protein 43	RNF43	4.99	6.19	3.78	2.41	1.4E-03	0.158
11745063_x_at	leucine rich repeat containing 8 family, member B	LRRC8B	5.55	6.74	4.36	2.38	4.7E-03	0.219
11763025_a_at	mucin 1, cell surface associated	MUC1	6.54	7.73	5.35	2.38	9.1E-03	0.266
11756458_a_at	MSH5-SAPCD1 readthrough (NMD candidate)	MSH5-SAPCD1	6.74	7.93	5.55	2.38	8.4E-03	0.262
11749137_a_at	family with sequence similarity 169, member A	FAM169A	6.78	7.96	5.61	2.34	9.6E-03	0.273
11747527_a_at	zinc finger protein 275	ZNF275	6.26	7.43	5.09	2.34	2.5E-03	0.189
11721024_a_at	interleukin 11 receptor, alpha	IL11RA	7.07	8.23	5.90	2.33	1.7E-03	0.168
11728988_at	fumarylacetoacetate hydrolase domain containing 2B	FAHD2B	4.76	5.93	3.60	2.33	1.7E-03	0.168
11763366_s_at	ankyrin repeat domain 36B	ANKRD36B	5.71	6.87	4.55	2.32	3.5E-03	0.204
11719527_a_at	F-box and leucine-rich repeat protein 16	FBXL16	6.14	7.29	4.98	2.31	6.5E-03	0.252
11759966_at	inositol-trisphosphate 3-kinase B	ITPKB	6.81	7.96	5.66	2.30	8.9E-03	0.262
11736300_a_at	ORMDL sphingolipid biosynthesis regulator 1	ORMDL1	5.74	6.89	4.60	2.29	4.1E-03	0.214
11740146_a_at	tRNA methyltransferase 10 homolog A (S. cerevisiae)	TRMT10A	5.28	6.42	4.14	2.28	7.8E-03	0.262
11720028_x_at	low density lipoprotein receptor	LDLR	5.84	6.98	4.71	2.27	9.0E-03	0.264
11761077_at	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2	SPOCK2	6.42	7.56	5.29	2.27	7.1E-03	0.258
11759991_at	craniofacial development protein 1	CFDP1	4.66	5.79	3.53	2.26	8.5E-03	0.262
11717471_at	protein kinase C, alpha	PRKCA	8.81	9.94	7.69	2.25	8.9E-03	0.262
11735380_s_at	olfactory receptor, family 2, subfamily A, member 4	OR2A4	5.30	6.43	4.17	2.25	5.2E-03	0.228
11724218_s_at	G patch domain containing 2	GPATCH2	6.11	7.24	4.98	2.25	9.9E-03	0.276
11724472_at	squamous cell carcinoma antigen recognized by T cells	SART1	5.38	6.50	4.26	2.24	3.1E-03	0.203
11748184_a_at	neuroligin 3	NLGN3	6.79	7.91	5.68	2.23	2.0E-03	0.175
11753579_a_at	interleukin 6 signal transducer	IL6ST	9.30	10.41	8.19	2.22	3.7E-03	0.210
11744408_x_at	golgin A8 family, member A	GOLGA8A	7.68	8.79	6.58	2.21	4.0E-03	0.214
11746635_a_at	lymphoid enhancer-binding factor 1	LEF1	9.49	10.59	8.39	2.20	5.8E-03	0.235
11763763_a_at	diacylglycerol kinase, alpha 80kDa	DGKA	6.86	7.95	5.76	2.19	4.4E-03	0.218
11736352_at	transmembrane protein 220	TMEM220	4.69	5.78	3.60	2.18	3.2E-03	0.203
11745624_s_at	InaD-like (Drosophila)	INADL	6.10	7.19	5.02	2.18	5.6E-03	0.233
11760126_at	THO complex 3	THOC3	5.61	6.69	4.53	2.15	4.1E-03	0.214

11731881_a_at	protein phosphatase 2, regulatory subunit A, beta	PPP2R1B	5.48	6.56	4.41	2.15	3.2E-03	0.203
11735627_x_at	zinc finger protein 841	ZNF841	6.41	7.48	5.33	2.15	7.1E-03	0.258
11723584_x_at	Rac GTPase activating protein 1	RACGAP1	5.80	6.87	4.73	2.14	5.3E-03	0.228
11747127_a_at	regulation of nuclear pre-mRNA domain containing 1B	RPRD1B	5.47	6.54	4.40	2.14	7.3E-03	0.258
11719948_at	GRIP and coiled-coil domain containing 1	GCC1	5.83	6.90	4.76	2.13	8.5E-03	0.262
11752492_a_at	activin A receptor, type IIA	ACVR2A	6.41	7.46	5.36	2.10	6.8E-03	0.258
11749723_a_at	fucosyltransferase 8 (alpha (1,6) fucosyltransferase)	FUT8	7.66	8.71	6.61	2.10	5.1E-03	0.227
11724285_at	FERM domain containing 4A	FRMD4A	5.36	6.41	4.32	2.09	6.7E-03	0.257
11749825_a_at	septin 6	Sep.06	8.80	9.84	7.75	2.09	6.9E-03	0.258
11761134_at	K(lysine) acetyltransferase 6A	KAT6A	4.79	5.83	3.75	2.08	5.7E-03	0.234
11719575_x_at	RAD50 interactor 1	RINT1	5.80	6.84	4.76	2.08	4.9E-03	0.225
11747427_a_at	SEC14-like 2 (S. cerevisiae)	SEC14L2	5.05	6.08	4.01	2.07	9.7E-03	0.273
11756814_a_at	ATP-binding cassette, sub-family B (MDR/TAP), member 8	ABCB8	5.90	6.93	4.87	2.06	4.6E-03	0.219
11736628_s_at	Rho guanine nucleotide exchange factor (GEF) 34, pseudogene	ARHGEF34P	4.91	5.94	3.88	2.06	3.5E-03	0.206
11751687_a_at	ER degradation enhancer, mannosidase alpha-like 1	EDEM1	6.26	7.28	5.24	2.04	9.1E-03	0.266
11724107_s_at	mitochondrial ribosomal protein S31 pseudogene 5	MRPS31P5	6.62	7.64	5.60	2.04	8.3E-03	0.262
11722997_s_at	nucleolar protein 11	NOL11	7.10	8.11	6.08	2.03	8.0E-03	0.262
11741895_a_at	OTU deubiquitinase 4	OTUD4	5.73	6.74	4.73	2.01	8.1E-03	0.262
11747964_a_at	solute carrier family 4, sodium bicarbonate cotransporter, member 7	SLC4A7	6.94	7.94	5.93	2.01	5.3E-03	0.229
11739953_at	zinc finger protein 14	ZNF14	5.18	6.18	4.17	2.01	8.6E-03	0.262
11761177_at	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	DLST	6.04	7.04	5.04	2.00	6.0E-03	0.238
11747110_a_at	PAS domain containing serine/threonine kinase	PASK	8.20	9.20	7.21	2.00	8.8E-03	0.262
11749380_a_at	WD repeat domain 74	WDR74	6.24	7.23	5.25	1.98	3.8E-03	0.212
11739690_a_at	DDB1 and CUL4 associated factor 11	DCAF11	6.72	7.71	5.74	1.97	8.8E-03	0.262
11745853_a_at	ring finger protein 145	RNF145	5.49	6.47	4.51	1.96	8.4E-03	0.262
11751388_a_at	flap structure-specific endonuclease 1	FEN1	3.99	4.96	3.02	1.94	4.7E-03	0.219
11756787_a_at	hyaluronan and proteoglycan link protein 3	HAPLN3	7.35	8.32	6.38	1.94	5.7E-03	0.234
11761001_at	Rh blood group, D antigen	RHD	5.59	6.55	4.62	1.94	6.3E-03	0.246
11763686_x_at	formin-like 1	FMNL1	5.33	6.28	4.37	1.91	5.6E-03	0.233
11721089_a_at	YLP motif containing 1	YLPM1	7.91	8.86	6.95	1.90	7.4E-03	0.261
11761834_at	embryonic ectoderm development	EED	4.21	5.15	3.26	1.89	7.4E-03	0.261
11717960_a_at	potassium channel tetramerization domain containing 2	KCTD2	6.43	7.37	5.49	1.88	1.0E-02	0.276
11734955_a_at	sex comb on midleg-like 1 (Drosophila)	SCML1	3.84	4.77	2.91	1.86	5.6E-03	0.233
11761431_at	phosphoglycerate mutase family member 5	PGAM5	4.69	5.61	3.77	1.85	6.0E-03	0.238
11751206_s_at	aurora kinase A	AURKA	4.55	5.47	3.63	1.84	7.3E-03	0.258

11717532_at	mannosidase, alpha, class 2A, member 2	MAN2A2	7.03	7.95	6.11	1.84	9.9E-03	0.276
11721794_a_at	complement component (3d/Epstein Barr virus) receptor 2	CR2	4.38	5.30	3.47	1.82	9.5E-03	0.269
11728686_a_at	sideroflexin 1	SFXN1	7.02	7.91	6.13	1.78	7.3E-03	0.258
11750362_a_at	cyclin N-terminal domain containing 1	CNTD1	4.45	5.34	3.56	1.77	7.0E-03	0.258
11734982_a_at	G protein-coupled receptor associated sorting protein 1	GPRASP1	5.97	6.85	5.08	1.77	9.2E-03	0.267
11754505_a_at	solute carrier family 39 (zinc transporter), member 4	SLC39A4	6.77	5.92	7.63	-1.71	9.6E-03	0.273
11723111_a_at	elastin microfibril interfacer 2	EMILIN2	7.09	6.22	7.96	-1.74	7.7E-03	0.262
11722064_at	receptor accessory protein 3	REEP3	6.41	5.53	7.28	-1.75	9.7E-03	0.274
11752622_a_at	PX domain containing serine/threonine kinase	PXK	7.33	6.43	8.22	-1.80	8.9E-03	0.262
11742191_a_at	runt-related transcription factor 1	RUNX1	7.08	6.18	7.98	-1.80	8.1E-03	0.262
11716104_a_at	myelin protein zero-like 1	MPZL1	6.28	5.36	7.20	-1.84	8.6E-03	0.262
11717338_a_at	cut-like homeobox 1	CUX1	6.20	5.28	7.12	-1.84	9.4E-03	0.269
11748175_x_at	chromosome 19 open reading frame 54	C19orf54	7.60	6.68	8.53	-1.85	7.8E-03	0.262
11720624_a_at	myeloid differentiation primary response 88	MYD88	8.61	7.69	9.54	-1.85	9.4E-03	0.269
11721151_s_at	RAB40C, member RAS oncogene family	RAB40C	6.71	5.79	7.64	-1.86	8.3E-03	0.262
11759424_at	annexin A5	ANXA5	4.88	3.94	5.81	-1.87	8.3E-03	0.262
11730128_a_at	SET domain containing 9	SETD9	3.99	3.04	4.94	-1.90	1.0E-02	0.276
11736156_a_at	family with sequence similarity 168, member A	FAM168A	6.99	6.04	7.94	-1.91	6.7E-03	0.257
11725980_at	complement factor D (adipsin)	CFD	7.26	6.30	8.21	-1.91	8.8E-03	0.262
11751578_a_at	tetratricopeptide repeat domain 31	TTC31	6.32	5.37	7.27	-1.91	8.4E-03	0.262
11756347_x_at	proline rich 11	PRR11	6.02	5.06	6.98	-1.92	4.8E-03	0.224
11716718_at	galactosidase, alpha	GLA	7.15	6.19	8.12	-1.93	5.9E-03	0.237
11732797_x_at	KIAA1841	KIAA1841	4.01	3.04	4.97	-1.93	5.1E-03	0.227
11725351_x_at	KIAA0930	KIAA0930	6.31	5.34	7.27	-1.94	7.8E-03	0.262
11725316_x_at	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa	VAPA	4.71	3.74	5.68	-1.95	8.6E-03	0.262
11745928_a_at	transmembrane protein 68	TMEM68	5.04	4.06	6.02	-1.96	8.8E-03	0.262
11755915_a_at	Hermansky-Pudlak syndrome 3	HPS3	6.71	5.73	7.69	-1.96	8.3E-03	0.262
11716870_a_at	polyhomeotic homolog 2 (Drosophila)	PHC2	7.37	6.39	8.36	-1.97	4.5E-03	0.219
11742824_a_at	microRNA 4723	MIR4723	7.54	6.55	8.53	-1.98	8.9E-03	0.262
11755464_a_at	TBC1 domain family, member 31	TBC1D31	6.12	5.13	7.12	-1.99	8.1E-03	0.262
11716323_at	isoprenylcysteine carboxyl methyltransferase	ICMT	6.12	5.12	7.11	-1.99	8.0E-03	0.262
11716580_s_at	cysteine-rich transmembrane module containing 1	CYSTM1	7.00	6.00	8.00	-2.00	7.2E-03	0.258
11716595_s_at	solute carrier family 44 (choline transporter), member 1	SLC44A1	6.21	5.21	7.21	-2.00	3.8E-03	0.212
11753600_x_at	H1 histone family, member 0	H1F0	7.38	6.37	8.38	-2.01	7.2E-03	0.258
11726258_at	ring finger protein 141	RNF141	6.58	5.57	7.58	-2.01	3.9E-03	0.213
11723409_s_at	McKusick-Kaufman syndrome	MKKS	5.95	4.94	6.96	-2.02	3.4E-03	0.203

11723221_a_at	exocyst complex component 6	EXOC6	6.07	5.05	7.09	-2.04	5.4E-03	0.231
11725995_x_at	xyloside xylosyltransferase 1	XXYLT1	4.90	3.88	5.93	-2.04	7.5E-03	0.261
11756028_a_at	glycerophosphodiester phosphodiesterase domain containing 1	GDPD1	4.76	3.74	5.79	-2.05	6.6E-03	0.254
11730720_a_at	neural cell adhesion molecule 1	NCAM1	6.07	5.04	7.10	-2.06	6.5E-03	0.250
11747801_a_at	histone deacetylase 9	HDAC9	4.08	3.05	5.11	-2.06	4.3E-03	0.216
11758037_s_at	myotubularin related protein 12	MTMR12	6.71	5.68	7.74	-2.07	7.8E-03	0.262
11755889_at	zinc finger protein 407	ZNF407	4.37	3.34	5.41	-2.07	8.3E-03	0.262
11763382_a_at	numb homolog (Drosophila)	NUMB	6.30	5.26	7.34	-2.08	6.8E-03	0.258
11745916_x_at	zinc finger protein 549	ZNF549	4.51	3.47	5.56	-2.09	6.0E-03	0.239
11757367_s_at	heat shock 70kDa protein 6 (HSP70B')	HSPA6	6.14	5.09	7.19	-2.09	9.3E-03	0.268
11740581_s_at	N-acylsphingosine amidohydrolase (acid ceramidase) 1	ASAH1	7.88	6.83	8.93	-2.10	3.1E-03	0.203
11734777_a_at	phosphatidylcholine transfer protein	PCTP	6.00	4.94	7.05	-2.11	4.1E-03	0.214
11723106_a_at	neutrophil cytosolic factor 4, 40kDa	NCF4	8.15	7.09	9.21	-2.11	5.9E-03	0.238
11759642_x_at	major histocompatibility complex, class II, DR beta 1	HLA-DRB1	10.18	9.12	11.23	-2.11	9.2E-03	0.267
11744939_x_at	chromosome 11 open reading frame 74	C11orf74	5.40	4.33	6.46	-2.12	3.1E-03	0.203
11717937_at	small integral membrane protein 3	SMIM3	5.67	4.61	6.74	-2.12	2.7E-03	0.190
11758417_s_at	major histocompatibility complex, class II, DP alpha 1	HLA-DPA1	9.82	8.75	10.90	-2.15	7.2E-03	0.258
11723194_x_at	major histocompatibility complex, class II, DQ beta 1	HLA-DQB1	10.20	9.12	11.28	-2.16	8.6E-03	0.262
11721897_a_at	DEXH (Asp-Glu-X-His) box polypeptide 58	DHX58	6.93	5.83	8.02	-2.19	4.4E-03	0.218
11721735_at	dehydrogenase E1 and transketolase domain containing 1	DHTKD1	5.33	4.24	6.43	-2.19	2.9E-03	0.198
11727754_a_at	phospholipase A2, group IVA (cytosolic, calcium-dependent)	PLA2G4A	3.90	2.80	5.01	-2.21	5.2E-03	0.227
11745804_s_at	LIM and senescent cell antigen-like domains 1	LIMS1	6.68	5.57	7.79	-2.22	4.3E-03	0.217
11728228_at	hepatitis A virus cellular receptor 2	HAVCR2	5.32	4.21	6.43	-2.22	6.8E-03	0.258
11719523_s_at	torsin family 1, member B (torsin B)	TOR1B	6.81	5.70	7.92	-2.22	5.1E-03	0.227
11718447_s_at	SH3 domain binding glutamate-rich protein like 2	SH3BGRL2	4.85	3.73	5.96	-2.23	3.0E-03	0.201
11756527_a_at	sorting nexin 10	SNX10	4.63	3.51	5.75	-2.23	2.6E-03	0.190
11723696_at	Fli-1 proto-oncogene, ETS transcription factor	FLI1	5.56	4.44	6.68	-2.24	8.4E-03	0.262
11756138_a_at	hexokinase 2	HK2	5.94	4.81	7.07	-2.26	8.7E-03	0.262
11718121_x_at	ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A	ATP6V1A	4.35	3.22	5.49	-2.28	2.7E-03	0.190
11758881_x_at	ribosomal protein S15a	RPS15A	6.46	5.32	7.60	-2.28	5.0E-03	0.226
11763266_at	family with sequence similarity 120B	FAM120B	5.77	4.62	6.92	-2.29	9.8E-03	0.274
11756947_a_at	cathepsin B	CTSB	9.03	7.88	10.18	-2.30	8.7E-03	0.262
11726272_a_at	ATPase, Na+/K+ transporting, beta 1 polypeptide	ATP1B1	7.69	6.54	8.84	-2.31	5.6E-03	0.233
11719308_a_at	Ras association (RalGDS/AF-6) domain family member 4	RASSF4	6.19	5.03	7.34	-2.31	5.6E-03	0.233
11758370_s_at	v-ets avian erythroblastosis virus E26 oncogene homolog 2	ETS2	5.32	4.17	6.48	-2.31	3.4E-03	0.203
11727307_x_at	zinc finger protein 320	ZNF320	3.59	2.42	4.76	-2.34	2.2E-03	0.183

11759513_at	leucine zipper and CTNNBIP1 domain containing	LZIC	7.57	6.40	8.75	-2.35	3.8E-03	0.212
11719922_a_at	GM2 ganglioside activator	GM2A	7.47	6.30	8.65	-2.36	5.6E-03	0.233
11719367_a_at	pleckstrin homology domain containing, family O member 2	PLEKHO2	6.75	5.57	7.93	-2.36	5.2E-03	0.228
11734760_at	huntingtin interacting protein 1	HIP1	4.84	3.65	6.02	-2.38	2.1E-03	0.180
11725549_a_at	phosphodiesterase 4A, cAMP-specific	PDE4A	5.61	4.42	6.80	-2.38	2.9E-03	0.200
11733373_at	Janus kinase 2	JAK2	5.81	4.61	7.01	-2.39	8.7E-03	0.262
11746805_a_at	excision repair cross-complementation group 8	ERCC8	4.11	2.92	5.31	-2.39	2.6E-03	0.190
11738995_a_at	dihydropyrimidinase-like 2	DPYSL2	8.26	7.07	9.46	-2.39	4.6E-03	0.219
11755028_a_at	DENN/MADD domain containing 1A	DENND1A	5.97	4.76	7.17	-2.41	6.9E-03	0.258
11733779_a_at	dual specificity phosphatase 3	DUSP3	6.29	5.08	7.49	-2.41	7.1E-03	0.258
11716678_a_at	solute carrier family 39, member 9	SLC39A9	4.07	2.87	5.28	-2.41	3.3E-03	0.203
11729953_a_at	StAR-related lipid transfer (START) domain containing 5	STARD5	6.44	5.23	7.64	-2.42	7.5E-03	0.262
11722359_x_at	erythrocyte membrane protein band 4.1-like 2	EPB41L2	6.67	5.46	7.89	-2.43	7.0E-03	0.258
11732433_s_at	glycerol kinase	GK	5.23	4.01	6.44	-2.43	1.4E-03	0.158
11755251_x_at	fatty acid desaturase 1	FADS1	6.30	5.09	7.52	-2.43	1.8E-03	0.169
11750769_s_at	chemokine (C-C motif) receptor 2	CCR2	5.29	4.08	6.51	-2.44	1.4E-03	0.158
11723072_x_at	NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa	NDUFV3	5.63	4.41	6.85	-2.44	1.8E-03	0.169
11716186_s_at	activated leukocyte cell adhesion molecule	ALCAM	5.39	4.15	6.62	-2.47	2.1E-03	0.180
11756561_a_at	mediator complex subunit 20	MED20	6.56	5.32	7.81	-2.50	3.7E-03	0.211
11736842_x_at	killer cell lectin-like receptor subfamily A pseudogene 1	KLRAP1	6.13	4.88	7.38	-2.51	7.7E-03	0.262
11729368_at	glucosidase, alpha; neutral C	GANC	6.06	4.80	7.32	-2.51	3.2E-03	0.203
11759499_at	family with sequence similarity 49, member A	FAM49A	4.88	3.61	6.15	-2.55	9.1E-03	0.266
11741060_a_at	hydrogen voltage-gated channel 1	HVCN1	5.93	4.66	7.21	-2.55	2.2E-03	0.182
11728617_at	caspase recruitment domain family, member 6	CARD6	5.21	3.93	6.50	-2.57	4.7E-03	0.219
11736122_a_at	golgi integral membrane protein 4	GOLIM4	7.92	6.63	9.20	-2.57	2.7E-03	0.190
11758114_x_at	src kinase associated phosphoprotein 2	SKAP2	7.82	6.54	9.11	-2.57	2.3E-03	0.185
11728839_s_at	transmembrane and coiled-coil domain family 3	TMCC3	5.74	4.44	7.04	-2.60	7.7E-03	0.262
11739404_at	suppressor of variegation 4-20 homolog 1 (Drosophila)	SUV420H1	4.12	2.81	5.43	-2.62	7.1E-03	0.258
11729035_at	inositol 1,4,5-trisphosphate receptor interacting protein-like 2	ITPRIPL2	6.68	5.35	8.00	-2.65	6.0E-04	0.130
11730090_a_at	TNFSF12-TNFSF13 readthrough	TNFSF12-TNFSF13	7.08	5.75	8.40	-2.66	1.7E-03	0.168
11745504_a_at	membrane protein, palmitoylated 1, 55kDa	MPP1	5.91	4.58	7.24	-2.66	4.2E-03	0.214
11732266_x_at	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1	LILRB1	6.72	5.39	8.05	-2.67	8.9E-03	0.262
11726660_a_at	GPN-loop GTPase 3	GPN3	5.32	3.98	6.65	-2.67	2.3E-03	0.187
11759205_a_at	dedicator of cytokinesis 5	DOCK5	6.08	4.75	7.42	-2.67	1.5E-03	0.160

11755181_a_at	transcription factor 7-like 2 (T-cell specific, HMG-box)	TCF7L2	5.98	4.64	7.33	-2.69	1.2E-03	0.158
11739553_a_at	growth arrest-specific 7	GAS7	7.97	6.63	9.31	-2.69	8.0E-04	0.141
11726628_a_at	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A	SEMA4A	6.54	5.19	7.89	-2.70	3.6E-03	0.208
11742735_a_at	nucleolar and spindle associated protein 1	NUSAP1	5.86	4.50	7.21	-2.71	4.2E-03	0.214
11754678_a_at	solute carrier family 25, member 43	SLC25A43	5.12	3.76	6.47	-2.71	8.0E-04	0.141
11729120_x_at	heat shock 70kDa protein 1A	HSPA1A	7.84	6.48	9.20	-2.73	4.6E-03	0.219
11727531_at	PHD finger protein 20-like 1	PHF20L1	4.87	3.51	6.23	-2.73	1.7E-03	0.168
11723706_at	abhydrolase domain containing 5	ABHD5	6.11	4.75	7.48	-2.73	1.5E-03	0.160
11726594_at	cathepsin Z	CTSZ	6.15	4.79	7.52	-2.73	3.9E-03	0.214
11732307_a_at	cAMP responsive element binding protein 1	CREB1	5.90	4.53	7.27	-2.74	3.4E-03	0.203
11725418_a_at	lysophosphatidylcholine acyltransferase 2	LPCAT2	8.44	7.07	9.82	-2.75	7.6E-03	0.262
11761050_at	Homo sapiens Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog (FGR), transcript variant 3, mRNA.	FGR	7.05	5.67	8.43	-2.76	1.5E-03	0.159
11725927_a_at	chloride intracellular channel 4	CLIC4	5.58	4.19	6.97	-2.78	4.0E-03	0.214
11759373_a_at	cysteine and glycine-rich protein 1	CSRP1	6.23	4.84	7.62	-2.78	8.6E-03	0.262
11747792_a_at	solute carrier family 31 (copper transporter), member 1	SLC31A1	7.74	6.35	9.13	-2.78	3.4E-03	0.203
11726294_s_at	CCAAT/enhancer binding protein (C/EBP), alpha	CEBPA	6.33	4.93	7.73	-2.80	6.7E-04	0.132
11731775_a_at	egf-like module containing, mucin-like, hormone receptor-like 1	EMR1	5.90	4.50	7.30	-2.80	9.3E-03	0.267
11747086_a_at	grancalcin, EF-hand calcium binding protein	GCA	6.18	4.78	7.59	-2.81	4.5E-03	0.219
11721236_a_at	lipoma HMGIC fusion partner-like 2	LHFPL2	4.51	3.11	5.92	-2.81	5.2E-04	0.125
11732542_at	tripartite motif containing 7	TRIM7	6.98	5.57	8.40	-2.83	1.3E-03	0.158
11731595_x_at	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	STAM2	6.48	5.06	7.90	-2.84	1.2E-03	0.158
11759775_a_at	solute carrier family 9, subfamily B (NHA2, cation proton antiporter 2), member 2	SLC9B2	5.81	4.39	7.23	-2.84	1.4E-03	0.158
11752341_a_at	coagulation factor VIII, procoagulant component	F8	4.40	2.98	5.82	-2.84	2.5E-03	0.190
11755858_a_at	membrane-spanning 4-domains, subfamily A, member 1	MS4A1	5.19	3.76	6.61	-2.85	2.1E-03	0.180
11737052_x_at	pleiomorphic adenoma gene-like 1	PLAGL1	4.06	2.64	5.48	-2.85	8.0E-03	0.262
11754681_s_at	major histocompatibility complex, class II, DM beta	HLA-DMB	7.36	5.92	8.79	-2.87	2.7E-03	0.190
11754989_a_at	Dmx-like 2	DMXL2	5.04	3.58	6.51	-2.92	2.6E-03	0.190
11720103_a_at	p21 protein (Cdc42/Rac)-activated kinase 1	PAK1	6.47	4.99	7.96	-2.97	2.7E-03	0.190
11743316_x_at	C-terminal binding protein 2	CTBP2	6.23	4.74	7.72	-2.97	1.1E-03	0.157
11723104_at	guanine nucleotide binding protein (G protein), beta polypeptide 4	GNB4	4.51	3.02	5.99	-2.98	8.7E-03	0.262
11718085_s_at	LYN proto-oncogene, Src family tyrosine kinase	LYN	7.70	6.21	9.20	-3.00	4.0E-03	0.214
11735751_a_at	solute carrier family 43, member 3	SLC43A3	8.66	7.16	10.16	-3.00	1.8E-03	0.169
11723691_at	CD302 molecule	CD302	7.10	5.60	8.60	-3.00	4.2E-03	0.214

11741153_a_at	neutrophil cytosolic factor 2	NCF2	6.55	5.05	8.05	-3.01	3.2E-03	0.203
11743900_at	class II, major histocompatibility complex, transactivator	CIITA	5.38	3.88	6.89	-3.01	2.9E-04	0.110
11719029_at	phosphoinositide-3-kinase adaptor protein 1	PIK3AP1	8.51	7.01	10.02	-3.02	2.4E-03	0.189
11717625_a_at	transducin (beta)-like 2	TBL2	5.23	3.71	6.75	-3.04	4.7E-04	0.125
11715973_a_at	mitochondrial fission regulator 1-like	MTFR1L	5.58	4.06	7.10	-3.04	3.3E-03	0.203
11759029_at	BRI3 binding protein	BRI3BP	4.84	3.31	6.36	-3.06	2.0E-03	0.175
11730942_s_at	osteoclast associated, immunoglobulin-like receptor	OSCAR	6.27	4.72	7.81	-3.09	8.9E-03	0.262
11737134_x_at	zinc finger protein 385A	ZNF385A	7.09	5.55	8.64	-3.09	9.5E-04	0.149
11717056_a_at	coronin, actin binding protein, 1C	CORO1C	6.63	5.08	8.17	-3.09	5.8E-04	0.130
11723215_s_at	myocyte enhancer factor 2C	MEF2C	5.62	4.08	7.17	-3.09	4.8E-04	0.125
11742911_at	immunoglobulin superfamily, member 6	IGSF6	7.43	5.88	8.97	-3.09	2.3E-03	0.187
11754998_a_at	multiple C2 domains, transmembrane 1	MCTP1	4.71	3.17	6.26	-3.09	6.1E-04	0.130
11722321_at	hematopoietically expressed homeobox	HHEX	4.66	3.11	6.22	-3.10	1.1E-03	0.157
11720989_a_at	solute carrier family 7 (amino acid transporter light chain, y+L system), member 7	SLC7A7	5.75	4.19	7.30	-3.11	7.9E-03	0.262
11758838_at	serine palmitoyltransferase, long chain base subunit 2	SPTLC2	6.21	4.64	7.78	-3.14	8.3E-04	0.144
11744484_s_at	major histocompatibility complex, class II, DR alpha	HLA-DRA	9.45	7.88	11.02	-3.15	6.2E-03	0.245
11733955_at	solute carrier family 22, member 15	SLC22A15	4.25	2.68	5.83	-3.15	4.0E-04	0.119
11750359_x_at	CD68 molecule	CD68	8.11	6.53	9.68	-3.15	1.2E-03	0.158
11743475_a_at	integrin, alpha X (complement component 3 receptor 4 subunit)	ITGAX	7.07	5.48	8.67	-3.19	4.1E-03	0.214
11753823_a_at	S100 calcium binding protein A8	S100A8	10.33	8.73	11.94	-3.21	8.7E-03	0.262
11730121_a_at	ATPase, class I, type 8B, member 4	ATP8B4	4.33	2.71	5.95	-3.24	1.6E-03	0.166
11720836_a_at	Ras and Rab interactor 2	RIN2	5.16	3.53	6.79	-3.26	8.7E-03	0.262
11715461_at	lysozyme	LYZ	11.13	9.49	12.76	-3.27	3.4E-03	0.203
11725827_s_at	CD1d molecule	CD1D	5.52	3.89	7.16	-3.27	4.5E-03	0.219
11715947_a_at	potassium channel tetramerization domain containing 12	KCTD12	7.85	6.22	9.49	-3.27	1.4E-03	0.158
11723287_at	TYRO protein tyrosine kinase binding protein	TYROBP	9.49	7.85	11.13	-3.28	1.1E-03	0.157
11722970_a_at	cAMP responsive element binding protein 5	CREB5	5.37	3.73	7.01	-3.29	9.4E-04	0.149
11716742_a_at	tight junction protein 2	TJP2	5.05	3.40	6.70	-3.30	2.0E-04	0.104
11716523_at	S100 calcium binding protein A9	S100A9	9.90	8.24	11.57	-3.34	5.1E-03	0.227
11739257_a_at	family with sequence similarity 63, member A	FAM63A	4.71	3.04	6.38	-3.34	3.8E-04	0.118
11763447_x_at	SubName: Full=cDNA FLJ52034;	TCRDV2	8.03	6.35	9.70	-3.35	9.4E-04	0.149
11715681_s_at	cellular repressor of E1A-stimulated genes 1	CREG1	7.71	6.03	9.39	-3.36	4.9E-03	0.225
11720146_a_at	death-associated protein kinase 1	DAPK1	4.32	2.63	6.01	-3.38	4.4E-03	0.218
11732719_at	epiregulin	EREG	4.02	2.33	5.72	-3.39	5.3E-03	0.228
11718321_at	CD93 molecule	CD93	7.22	5.53	8.92	-3.40	1.7E-03	0.168

11721153_a_at	serine/threonine kinase 3	STK3	5.25	3.54	6.96	-3.42	3.9E-04	0.118
11742301_x_at	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 3	KIR2DL3	5.42	3.71	7.13	-3.42	2.2E-03	0.185
11735429_x_at	ring finger protein 135	RNF135	6.92	5.20	8.63	-3.42	5.8E-04	0.130
11727219_a_at	dermatan sulfate epimerase	DSE	5.91	4.19	7.62	-3.42	2.7E-03	0.190
11729721_s_at	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	LILRB3	8.07	6.35	9.79	-3.44	2.7E-03	0.190
11727118_a_at	complement factor properdin	CFP	7.55	5.83	9.28	-3.46	1.4E-03	0.158
11719718_a_at	spleen tyrosine kinase	SYK	5.39	3.66	7.12	-3.46	3.3E-03	0.203
11725439_at	hemoglobin, delta	HBD	4.28	2.54	6.01	-3.47	2.7E-03	0.190
11734549_s_at	transforming growth factor, beta-induced, 68kDa	TGFBI	5.11	3.37	6.85	-3.48	4.9E-03	0.225
11746995_a_at	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)	NPL	4.79	3.04	6.54	-3.49	1.3E-03	0.158
11723025_at	family with sequence similarity 26, member F	FAM26F	7.15	5.40	8.90	-3.50	1.2E-03	0.158
11741594_a_at	leukocyte specific transcript 1	LST1	8.99	7.24	10.74	-3.50	3.6E-04	0.118
11732435_at	SLP adaptor and CSK interacting membrane protein	SCIMP	6.25	4.49	8.02	-3.52	4.8E-03	0.223
11745725_a_at	granulin	GRN	6.99	5.23	8.75	-3.52	3.4E-04	0.118
11752837_x_at	egf-like module containing, mucin-like, hormone receptor-like 2	EMR2	5.91	4.15	7.68	-3.54	6.2E-04	0.130
11724771_x_at	Fc fragment of IgG, low affinity IIa, receptor (CD32)	FCGR2A	7.79	6.01	9.57	-3.56	3.9E-03	0.213
11740218_a_at	signal-regulatory protein beta 1	SIRPB1	7.38	5.59	9.16	-3.57	3.4E-03	0.203
11715358_x_at	cystatin C	CST3	8.66	6.87	10.45	-3.58	1.4E-03	0.158
11755606_x_at	interferon, gamma-inducible protein 30	IFI30	10.63	8.84	12.43	-3.59	4.5E-03	0.219
11750527_s_at	major histocompatibility complex, class II, DQ alpha 1	HLA-DQA1	7.71	5.91	9.50	-3.59	1.4E-03	0.158
11737425_x_at	RAS guanyl releasing protein 4	RASGRP4	6.00	4.20	7.80	-3.60	4.8E-04	0.125
11757815_s_at	methyltransferase like 7A	METTL7A	8.87	7.06	10.68	-3.62	5.0E-03	0.225
11756867_a_at	tumor necrosis factor (ligand) superfamily, member 13b	TNFSF13B	7.19	5.33	9.05	-3.72	3.8E-04	0.118
11717873_x_at	interferon regulatory factor 8	IRF8	6.61	4.73	8.49	-3.76	7.1E-04	0.132
11720616_a_at	dynamin 1	DNM1	5.27	3.39	7.16	-3.77	9.8E-03	0.274
11736375_a_at	CD86 molecule	CD86	5.87	3.98	7.76	-3.78	7.1E-04	0.132
11722728_a_at	early growth response 2	EGR2	5.36	3.47	7.25	-3.78	3.4E-03	0.203
11745090_a_at	plexin domain containing 2	PLXDC2	6.46	4.56	8.36	-3.80	1.2E-03	0.158
11724836_at	neutral cholesterol ester hydrolase 1	NCEH1	5.20	3.26	7.14	-3.88	4.1E-05	0.050
11737388_s_at	myotubularin related protein 11	MTMR11	4.57	2.63	6.52	-3.89	1.3E-03	0.158
11718419_at	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide	FCER1G	9.14	7.19	11.09	-3.89	1.2E-03	0.158
11736141_a_at	intersectin 1 (SH3 domain protein)	ITSN1	6.34	4.38	8.30	-3.91	5.2E-05	0.056
11738980_a_at	CD4 molecule	CD4	6.44	4.48	8.41	-3.93	9.0E-03	0.264
11726473_a_at	docking protein 3	DOK3	6.64	4.67	8.61	-3.94	1.8E-04	0.098
11722615_s_at	hydroxycarboxylic acid receptor 2	HCAR2	6.26	4.29	8.24	-3.95	5.7E-03	0.234

11724470_s_at	microsomal glutathione S-transferase 1	MGST1	4.44	2.47	6.42	-3.95	2.2E-03	0.182
11743135_s_at	CCAAT/enhancer binding protein (C/EBP), delta	CEBPD	7.30	5.30	9.30	-4.00	5.6E-03	0.233
11738053_x_at	plasminogen activator, urokinase receptor	PLAUR	7.57	5.56	9.58	-4.02	1.8E-03	0.169
11716309_a_at	cytochrome b reductase 1	CYBRD1	4.89	2.85	6.92	-4.07	1.2E-04	0.073
11733802_a_at	calcineurin-like phosphoesterase domain containing 1	CPPED1	6.21	4.17	8.26	-4.09	2.6E-04	0.110
11758608_s_at	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)	CSF2RB	5.14	3.04	7.24	-4.21	4.9E-04	0.125
11729479_a_at	C-type lectin domain family 12, member A	CLEC12A	5.97	3.85	8.08	-4.23	6.9E-04	0.132
11744435_a_at	dual specificity phosphatase 6	DUSP6	6.49	4.35	8.62	-4.27	2.5E-04	0.110
11716049_a_at	tribbles pseudokinase 1	TRIB1	8.14	5.99	10.29	-4.30	2.4E-04	0.110
11729251_at	myeloid cell nuclear differentiation antigen	MNDA	7.84	5.68	10.00	-4.33	5.2E-04	0.125
11723044_at	SMAD family member 1	SMAD1	4.74	2.57	6.90	-4.33	2.5E-04	0.110
11741223_s_at	family with sequence similarity 198, member B	FAM198B	4.74	2.56	6.92	-4.35	4.2E-03	0.214
11758525_s_at	SRY (sex determining region Y)-box 4	SOX4	5.35	3.16	7.54	-4.38	1.0E-05	0.019
11721456_x_at	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	SERPINA1	7.02	4.83	9.22	-4.39	7.3E-03	0.258
11715347_s_at	hemoglobin, beta	HBB	8.94	6.71	11.17	-4.46	5.9E-03	0.237
11728489_a_at	C-type lectin domain family 4, member A	CLEC4A	6.07	3.82	8.31	-4.49	6.5E-05	0.057
11758263_s_at	cytochrome b-245, beta polypeptide	CYBB	7.98	5.72	10.24	-4.52	4.4E-04	0.124
11722426_a_at	fibrinogen-like 2	FGL2	7.32	5.01	9.62	-4.61	2.3E-05	0.032
11755743_a_at	ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) pseudogene	ECRP	6.51	4.20	8.82	-4.61	7.8E-04	0.141
11717823_s_at	tumor necrosis factor, alpha-induced protein 2	TNFAIP2	7.76	5.43	10.10	-4.66	4.9E-03	0.225
11743197_at	toll-like receptor 4	TLR4	6.54	4.17	8.90	-4.72	8.9E-05	0.066
11731798_a_at	lectin, galactoside-binding, soluble, 2	LGALS2	7.52	5.15	9.89	-4.74	2.8E-04	0.110
11737147_a_at	C-type lectin domain family 7, member A	CLEC7A	6.46	4.08	8.84	-4.75	4.4E-03	0.219
11719634_a_at	Kruppel-like factor 4 (gut)	KLF4	7.64	5.26	10.02	-4.75	3.5E-04	0.118
11746972_a_at	membrane-associated ring finger (C3HC4) 1, E3 ubiquitin protein ligase	MARCH1	5.79	3.41	8.18	-4.77	7.8E-06	0.019
11757817_s_at	brain abundant, membrane attached signal protein 1	BASP1	6.35	3.93	8.78	-4.85	9.3E-04	0.149
11755688_a_at	ADAMTS-like 4	ADAMTSL4	5.61	3.18	8.04	-4.86	1.7E-04	0.097
11729758_at	regulator of G-protein signaling 18	RGS18	6.25	3.81	8.70	-4.88	5.1E-06	0.018
11728266_a_at	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2	LILRB2	6.51	4.04	8.97	-4.93	4.0E-03	0.214
11729772_at	ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin)	RNASE2	7.27	4.78	9.76	-4.98	2.9E-04	0.110
11759403_x_at	versican	VCAN	6.00	3.45	8.55	-5.10	6.3E-04	0.130
11750299_a_at	interleukin 13 receptor, alpha 1	IL13RA1	5.04	2.47	7.60	-5.13	4.2E-06	0.018
11730469_s_at	LIM domain only 2 (rhombotin-like 1)	LMO2	6.92	4.29	9.56	-5.27	1.1E-03	0.157

11717762_a_at	carboxypeptidase, vitellogenic-like	CPVL	7.58	4.86	10.30	-5.44	7.0E-04	0.132
11749817_a_at	colony stimulating factor 1 receptor	CSF1R	6.51	3.78	9.24	-5.46	5.5E-06	0.018
11755523_a_at	RNA binding motif protein 47	RBM47	5.94	3.21	8.68	-5.47	1.4E-05	0.023
11719480_a_at	cystatin A (stefin A)	CSTA	8.38	5.60	11.15	-5.55	1.8E-03	0.169
11716846_a_at	membrane-spanning 4-domains, subfamily A, member 6A	MS4A6A	6.89	4.06	9.72	-5.66	1.1E-04	0.073
11721347_a_at	macrophage expressed 1	MPEG1	6.84	3.86	9.83	-5.97	1.2E-04	0.073

Supplementary Table S4. *Gene signatures specific for naive, T_{CM}, T_{EM}, T_{EMRA} cells and $CD8^+$ T-cells of HIV progressors*. Custom gene sets were obtained using publically available gene expression data from (**A**) Willinger et al. (8) (ArrayExpress E-TABM-40) and include genes with IQR > 0.6 across all samples and which were upregulated in the respective group with FC > 1 and FDR < 0.05 compared to each of the other groups (**B**) Quigley et al. (9) (GEO GSE24081) and include genes with IQR > 0.5 and P < 0.01 between progressors and controllers.

A. Willinger et al.							**B. Quigley et al.**			
NAIVE			**TCM**	**TEM**	**TEMRA**		**HIV Progressor**		**HIV Controller**	
N=177	continued	continued	N=8	N=13	N=104	continued	N=119	continued	N=94	continued
ACTN1	GSTM2	RGMB	ACVR2A	CA2	ANKDD1A	MDM1	IFI44L	WDR70	ADCK3	TNFAIP3
ADD3	GTF3A	RGS10	AP3M2	CCL20	ARHGEF3	METTL3	IFI44	SP110	BTG1	LONP2
ADPRM	HABP4	RIN3	CDH1	CCR6	BAG2	MINPP1	METTL7A	VRK2	CLK1	TGFB1
AGPAT5	HIP1R	RNF138	CHN1	CEBPD	CASZ1	MYL12A	RSAD2	STAT1	KDM2A	IFRD1
AIF1	HIST1H4A	RPL31	F2RL1	CXCR6	CCDC117	NBN	DDX60	TRIM5	PRDM2	CD28
AK6	HIST1H4E	RSL1D1	GPR15	ELOVL4	CD244	NFYB	XAF1	SLC16A7	LEPROTL1	CXCR3
AKIP1	HIVEP1	SAMHD1	SESN3	GRAMD1B	CEP78	OSGEPL1	OAS2	CD38	NENF	ETV3
AMIGO1	HOOK1	SATB1	TIAM1	KIT	CTBP2	P2RX7	CX3CR1	UNG	TAPT1	HLA-DQB1
APBA2	HOOK2	SCML1		MCAM	CUL4A	PALLD	CTBP1	STOM	TMOD1	LRIG1
ARHGEF7	HPCAL4	SELL		ME1	CX3CR1	PCID2	SLAMF7	KIDINS220	RPLP0	GADD45A
ARRDC2	HSF2	SERINC5		SIPA1L2	DGKD	PKD2	MNDA	ASUN	TSN	SYNJ2
ATHL1	IGF1R	SF1		SPRY1	DOCK5	PROK2	M6PR	MFSD9	ILKAP	RASA1
ATM	IL23A	SGK223		ZBTB16	DPYSL2	PRSS23	KLRAP1	RBL1	SPSB3	PRKCI
ATP5L	IL6ST	SGTB			EMC2	PSTPIP2	TARP	TNFRSF9	ZNF136	NR4A2
ATP8A2	ITGA6	SHISA2			EXOC4	PTCH1	AKAP2	TAF1B	IP6K1	KLHL11
BACH2	JAK3	SLC18B1			FAM122B	PTGDS	ATP2B4	METTL2A	APBA2	MVB12B
BEX2	KCTD12	SLC36A4			FAM126A	PTPN12	AIM2	MPHOSPH9	C16orf72	ZBTB10
BNIP3	KIAA1147	SLC44A2			FAM204A	PTPN4	GBP1	XPO7	SESN1	JMJD6
BTBD11	KIAA1958	SNN			FAM49A	RAB29	PRSS23	VPS8	MED14	PIK3IP1
C12orf65	KIF2A	SPG20			FAM63B	RHEBL1	IFI35	CHM	CCNH	ELL2
C1orf228	KLF7	SPINT2			FAM69A	RNF135	OAS1	PRPS2	DNAJC2	IL7R
C4orf32	LEF1	SPPL2B			FCGR3A	SAMD3	JAK2	FDFT1	CEBPG	SLC39A8

CBX5
CCDC57
CCND3
CCS
CD248
CDK5R1
CEP68
CEP85L
CHKA
CHMP3
CLMP
CLN5
CLNS1A
DCHS1
DEAF1
DENND5A
DGKA
DHRS3
DPEP2
DPH5
DSC1
EFNA1
ERCC6L2
FAM134B
FAM229B
FAM65B
FCMR
FHIT
FIS1
FKBP5
FYB
LGALS3BP
LIAS
LMF1
LMO7
LRRN3
LTB
LY96
LYRM4
LZTS3
MAL
MAN1C1
MAST4
MATR3
MICU3
MRPS33
MTUS1
MYC
NDFIP1
NDUFB5
NELL2
NGFRAP1
NUCB2
OMA1
OXNAD1
PCSK5
PDK1
PECAM1
PIGP
PIK3CD
PLAC8
PRKCA
TATDN1
TBC1D4
TCEA3
TCP11L2
TECPR1
TESPA1
TIMP2
TMC8
TMEM123
TMEM204
TMEM256
TMEM63A
TMSB15B
TNFRSF10D
TPP2
TRABD2A
TSPAN3
TSPAN32
TTN
TXK
VIPR1
VPS13B
VPS8
VSIG1
YPEL2
ZBTB20
ZBTB4
ZEB1
ZFP90
ZNF10
ZNF141
FGL2
FNIP2
GBP3
GNPTAB
GOLIM4
GSAP
HDAC8
HENMT1
HMGN3
HSPB11
IDH1
IGF2R
ITGAM
JAZF1
KIR2DL1
KIR2DL2
KIR2DL3
KIR2DL4
KIR2DL5A
KIR2DS1
KIR2DS2
KIR2DS3
KIR2DS4
KIR2DS5
KIR3DL1
KIR3DL2
KIR3DL3
KIR3DS1
KLRC3
KLRD1
KLRF1
SEC23IP
SLC15A4
SLFN13
SPIN4
SRPK2
SSBP3
STK39
STX8
TBK1
TEP1
TGFBR1
TMEM14A
TMEM64
TTC38
TTC39B
TYROBP
UBE2F
USP28
VRK2
YME1L1
ZBP1
ZEB2
ZNF600

STX7
SAC3D1
NDC80
PLSCR1
MX1
IFI6
ZNF224
DEDD
FANCL
TPP1
RDH11
TPGS2
GZMH
CHI3L2
EIF2AK2
BST2
DHFR
LYST
USP18
CD244
GPD2
IRF9
RBM8A
PLEK
PRF1
CASP4
TMX1
MAN1A1
HSPA6
PPP2R2B
CASP7
ADAM10
CCNA2
DCAF11
SCP2
SUPT4H1
ITGB7
CCT3
MAB21L2
CENPU
MAVS
TMEM140
MAGEH1
PCMT1
OSGEPL1
ARIH2
CLCN3
RAB11A
KEAP1
RAB27A
KIAA0101
RAB3GAP2
SPIN2A
C6orf47
NCAPG
INTS9
NF1
ACTR3
OAZ3
IFI16
ADGRG1
MSH2
GABARAPL1
ATHL1
CD44
SDHB
PCIF1
CCT6B
ZDHHC7
WWP2
ACVR1B
TOR1AIP2
BIRC3
SYPL1
ISCA1
KLF9
ITGA5
FAM102A
TNF
TGIF1
SMAD7
EMG1
RBPJ
FGF9
PDCD4
FBXO42
ZNF395
PLXND1
CD6
CCR7
SPATA2
ZBTB18
FKBP11
PHLDA1
ABCG1
PTGER4
SPOCK2
PDE4B
LMNA
SLC7A5
NELL2
TNFRSF25
CYP1B1
MAFF
PLXDC1
HLA-DQA1

GIMAP6	PRMT2	ZNF274	LILRB1	ARL6IP5	MANEA	HSPH1
GIMAP8	RAB33A	ZNF302	LUC7L3	DERA	IVD	RGPD5
GNAQ	RALGPS2	ZNF496	LYN	CAPN3	NCKAP1L	ETS2
GOLGA8A	RAPGEF6	ZNF542P	LYPLA1	FEZ2	CAPZB	TAF9B
GPRASP1	RBM11	ZNF677	MAPK1	SCD	HEMK1	RGS1
GSTM1	RCAN3	ZSCAN18	MCTP2	FAS	TTC38	AREG
				TRAF3IP3		

Supplemenatry Table S5. *Ingenuity Pathway Analysis of differentially expressed genes in pre-treatment AML patients relative to healthy controls.* z-score values indicate activation (positive z-score) or inhibition (negative z-score) of the canonical pathways.

Ingenuity Canonical Pathways	-log(p-value)	Ratio	z-score	Molecules
Apoptosis Signaling	1.55E00	1.82E-01	0.500	MAPK8,APAF1,MAP3K5,NFKB1,XIAP,BCL2,IKBKB,PLCG2,DFFB,CAPN2,RPS6KA1,TNF,BIRC3,BCL2L11,FASLG,PRKCA
OX40 Signaling Pathway	4.17E00	3.26E-01	-1.633	TRAF3,HLA-DOA,HLA-DQA1,MAPK8,HLA-DQB1,NFKB1,CD3D,BCL2,HLA-DRB1,HLA-DRB4,HLA-C,FCER1G,HLA-DPB1,HLA-DRB5,HLA-DPA1
PKCθ Signaling in T Lymphocytes	2.9E00	2.13E-01	-0.577	RAC2,HLA-DOA,PIK3CA,MAP3K13,PIK3R1,MAP3K1,HLA-DQA1,MAPK8,MAP3K5,HLA-DQB1,NFKB1,CD3D,NFATC1,PIK3R3,IKBKB,MAP3K12,CD28,HLA-DRB1,VAV3,PLCG2,FCER1G,MAP3K8,HLA-DRB5
Role of NFAT in Regulation of the Immune Response	2.7E00	1.89E-01	-0.426	HLA-DOA,PIK3CA,CAMK4,PIK3R1,HLA-DQA1,HLA-DQB1,NFKB1,FCGR2B,NFATC1,GNG7,IKBKB,CD28,HLA-DRB1,PLCB1,XPO1,FCGR3A/FCGR3B,FCGR2A,GNA12,GNAQ,CD79A,ITPR1,CD3D,PIK3R3,PLCG2,FCER1G,LYN,RCAN3,MEF2C,RCAN2,HLA-DRB5
iCOS-iCOSL Signaling	2.01E00	2.04E-01	-2.236	GAB2,HLA-DOA,PIK3CA,CD40LG,IL2RG,CAMK4,PIK3R1,HLA-DQA1,ITPR1,HLA-DQB1,NFKB1,CD3D,NFATC1,PIK3R3,IKBKB,CD28,HLA-DRB1,ICOS,FCER1G,HLA-DRB5
Calcium-induced T Lymphocyte Apoptosis	1.98E00	2.26E-01	0.816	HLA-DOA,CAMK4,HLA-DRB1,PRKCD,HLA-DQA1,FCER1G,CAPN2,HLA-DQB1,ITPR1,CD3D,HLA-DRB5,PRKCA
CD28 Signaling	1.76E+00	2.13E-01	-1.732	HLA-DOA,PTPN6,PIK3CA,CAMK4,PIK3R1,ARPC5,MAP3K1,HLA-DQA1,MAPK8,ITPR1,HLA-DQB1,NFKB1,CTLA4,CD3D,NFATC1,PIK3R3,IKBKB,CD28,HLA-DRB1,PTPN11,CDC42,FCER1G,HLA-DRB5
Interferon Signaling	1.87E00	2.5E-01	1.414	IFNG,OAS1,IFNGR2,IFI35,IRF9,STAT1,IFITM2,BCL2,ISG15

Supplementary Table S6. *Ingenuity Pathway Analysis of differentially expressed genes in CR relative to NR AML patients post induction chemotherapy.* z-score values indicate activation (positive z-score) or inhibition (negative z-score) of the canonical pathways.

Ingenuity Canonical Pathways	-log(p-value)	Ratio	z-score	Molecules
Chemokine Signaling	1.36E00	1.79E-01	1.732	GNAI3,RAF1,CCR5,CAMK4,CAMK2D,PPP1R12B,CCL2,PLCG2,MRAS,GNAQ,LIMK2,PRKCA
Role of NFAT in Regulation of the Immune Response	5.64E+00	2.33E-01	-2.414	BLNK,RAF1,FCGR2C,PIK3CA,HLA-DOA,CAMK4,CD4,FCER1A,HLA-DQA1,FCGR2B,FCGR1A,NFATC1,CD28,GNB4,HLA-DRB1,GNA15,HLA-DMA,HLA-DMB,HLA-DRA,MRAS,PIK3R2,FCGR1B,FCGR3A/FCGR3B,AKT2,FCGR2A,CHP1,GNAQ,GNG10,BTK,GNAI3,SYK,PLCG2,FCER1G,LYN,CD86,MEF2C,RCAN2
OX40 Signaling Pathway	3.19E00	2.83E-01	0.500	TNFSF4,HLA-DOA,HLA-DRB4,HLA-DRB1,HLA-C,HLA-DMA,CD4,HLA-DRA,HLA-DMB,HLA-DQA1,FCER1G,HLA-DPB1,HLA-DPA1
NF-κB Signaling	3.09E00	1.89E-01	-1.257	RAF1,PIK3CA,CSNK2A1,TLR8,BMPR2,TLR10,TNIP1,TLR1,IGF1R,MRAS,PIK3R2,LTBR,TNFSF13B,AKT2,MYD88,FGFR1,IRAK3,TNFRSF11A,DDR1,TLR2,TLR4,IL18,ARAF,IL1RN,PLCG2,PELI1,TLR6,FCER1G,IL1B,INSR,EIF2AK2
Calcium-induced T Lymphocyte Apoptosis	2.58E00	2.45E-01	-0.816	HLA-DOA,HLA-DRB1,CAMK4,HLA-DMA,PRKCD,CD4,HLA-DMB,HLA-DRA,CHP1,FCER1G,NR4A1,HLA-DQA1,PRKCA
PI3K Signaling	2.38E00	1.87E-01	-2.132	VAV2,BLNK,RAF1,AKT2,PIK3CA,ATF3,CAMK4,CHP1,FCGR2B,NFATC1,BTK,TLR4,CAMK2D,DAPP1,SYK,PLCG2,VAV3,CREB1,MRAS,LYN,PIK3AP1,PIK3R2,CR2
iCOS-iCOSL Signaling	1.9E00	1.84E-01	0.905	PIK3CA,AKT2,HLA-DOA,CAMK4,CD4,CHP1,HLA-DQA1,NFATC1,CD28,HLA-DRB1,CAMK2D,HLA-DMA,ICOS,HLA-DRA,HLA-DMB,FCER1G,IL2RA,PIK3R2
PKCθ Signaling in T Lymphocytes	1.68E00	1.85E-01	-2,828	VAV2,PIK3CA,HLA-DOA,CD4,MAP3K13,CHP1,HLA-DQA1,NFATC1,CD28,HLA-DRB1,CAMK2D,HLA-DMA,VAV3,PLCG2,HLA-DRA,HLA-DMB,MRAS,FCER1G,CD86,PIK3R2

Supplementary Table S7. *Characteristics of AML patients.*

		*N**	(%)*
Patients included		72	100
Age	Years, *Median (range)*	57 *(21-76)*	
	< 60 yrs	34	47.2
	≥ 60 yrs	38	52.8
Sex	Females	38	52.8
	Males	34	47.2
AML	Primary (de novo)	60	83.3
	Secondary (MDS related)	9	12.5
	Secondary (treatment related)	3	4.2
Prognostic Group (ELN)	Favorable	18	25
	Intermediate I	23	32
	Intermediate II	15	20.8
	Adverse	16	22.2
Cytogenetics	Favorable	6	18.1
	Intermediate	53	73.6
	Adverse	13	8.3
Molecular features	NPM1 mutation	20	27.8
	FLT3 mutation	12	16.7
	CEBPA mutation	6	8.3
White Blood Count	< 30 000/mm3	52	72.2
	≥ 30 000/mm3	20	27.8
Induction Regimen*	high intensity	37	51.4
	intermediate intensity	19	40.3
	low intensity	6	8.3
Response to Induction Chemotherapy	Complete Remission (CR)	56	77.8
	Non Responders (NR)	16	22.2
CMV status	Positive	23	32
	Negative	38	52.8
	N/A	11	15.2

AML - acute myeloid leukemia; ELN – European LeukemiaNet (10); N/A – not available.

*Induction regimen - high intensity (containing cytarabine at a daily dose >500 mg/m^2 plus anthracycline); intermediate intensity (containing cytarabine at a daily dose ≤500 mg/m^2 plus antracycline such as standard regimen "7+3"); low intensity (hypomethylating agents or clofarabine) (11). Detailed clinical information for each patient is provided in Supplementary Ttable S8.

Supplementary Table S8. *Detailed clinical characteristics of AML patients.* Diagnosis: *arising from myelodysplastic syndrome, ** therapy related. n.a – not available. Induction regimen - high intensity (containing cytarabine at a daily dose > 500 mg/m^2 plus anthracycline); intermediate intensity (containing cytarabine at a daily dose ≤ 500 mg/m^2 plus antracycline such as standard regimen “7+3”); others including hypomethylating agents or clofarabine (11). CR: complete remission; CRi: complete remission with incomplete hematologic recovery; NR: non responder to induction chemotherapy. FLT3 represents ITD mutation unless otherwise indicated. ELN – European LeukemiaNet (10). MRC - Medical Research Council (12).

Patient ID	Sex	Age	Diagnosis	CMV status	Induction regimen intensity categorized*	Response to induction chemo	MRD at remission	ELN Risk group	Cytogenetics risk group (MRC)	NPM1, FLT3 or CEBPa mutated	Total WBC at diagnosis/µl	In vitro studies	Initial cohort - FC	Microarray studies	Extended, paired pre-/post-treatment-FC
1	F	51	de novo AML	neg	high	CR	no	adverse	intermediate	none	4140	YES	YES		
2	M	63	secondary AML*	neg	high	CRi	no	intermediate 1	intermediate	none	124140	YES	YES		
3	M	65	de novo AML	neg	intermediate	CR	no	favorable	intermediate	NPM1	30970	YES	YES		
4	F	65	de novo AML	pos	intermediate	CR	no	intermediate 1	interemediate	none	5250	YES	YES		
5	M	55	de novo AML	n.a.	high	CR	no	favorable	intermediate	NPM1	43200	YES	YES		
6	M	44	de novo AML	n.a.	high	CR	no	favorable	intermediate	FLT3-TKD	50600	YES	YES		
7	F	76	de novo AML	n.a.	intermediate	CR	no	favorable	favorable	NPM1, CEBPa	230000	YES	YES		
8	M	73	secondary AML *	neg	others	CR	no	adverse	intermediate	none	980	YES	YES		
9	F	45	de novo AML	pos	high	CR	no	intermediate 1	intermediate	NPM1, FLT3	13700	YES	YES		
10	F	52	de novo AML	neg	high	CR	YES	favorable	intermediate	FLT3	24660	YES	YES		
11	F	54	de novo AML	neg	high	CR	no	intermediate 1	intermediate	none	5620	YES	YES		YES
12	F	38	de novo AML	pos	high	CR	YES	adverse	adverse	none	24000	YES	YES		YES
13	M	44	de novo AML	neg	intermediate	CR	no	favorable	favorable	none	3380	YES	YES		YES
14	F	31	de novo AML	pos	high	CR	no	favorable	favorable	none	3810	YES	YES		YES
15	F	57	de novo AML	neg	high	CR	no	adverse	adverse	none	30210	YES	YES		YES
16	M	63	secondary AML*	neg	high	CRi	YES	adverse	adverse	none	3860	YES	YES		YES
17	M	61	de novo AML	neg	high	CR	no	intermediate 1	intermediate	NPM1, FLT3	82220	YES	YES		YES
18	F	29	de novo AML	pos	high	CR	no	intermediate 1	intermediate	none	11317	YES	YES		YES
19	M	63	de novo AML	neg	high	CR	no	intermediate 2	intermediate	CEBPa	204770	YES	YES	YES	YES

20	F	68	secondary AML*	neg	intermediate	CR	no	adverse	adverse	none	40000	YES	YES	YES	YES
21	F	63	de novo AML	neg	high	CR	no	intermediate 2	intermediate	none	1180			YES	
22	M	60	de novo AML	neg	high	CR	YES	intermediate 1	intermediate	CEBPa	3500			YES	
23	F	45	de novo AML	pos	high	CR	no	intermediate 1	intermediate	NPM1, FLT3	13700			YES	
24	F	60	de novo AML	pos	intermediate	NR	no	adverse	intermediate	none	11900			YES	YES
25	M	56	de novo AML	neg	high	CR	no	favorable	intermediate	NPM1	20840			YES	YES
26	M	69	de novo AML	pos	intermediate	NR	no	intermediate 2	intermediate	none	15510			YES	YES
27	M	61	de novo AML	pos	high	NR	no	intermediate 2	intermediate	FLT3	65000			YES	YES
28	F	56	de novo AML	neg	high	CR	no	intermediate 1	intermediate	NPM1, FLT3	13600				YES
29	F	71	secondary AML*	n.a.	intermediate	CRi	YES	intermediate 1	intermediate	NPM1, FLT3	55000				YES
30	F	65	de novo AML	neg	others	CR	YES	favorable	intermediate	FLT3	18550				YES
31	M	60	secondary AML*	pos	intermediate	NR	no	intermediate 1	intermediate	none	1240				YES
32	M	23	de novo AML	pos	intermediate	NR	no	adverse	adverse	none	57780				YES
33	M	35	de novo AML	n.a.	intermediate	CR	no	favorable	favorable	none	3850				YES
34	M	67	de novo AML	neg	others	CR	no	adverse	adverse	none	2520				YES
35	F	49	de novo AML	neg	high	CR	no	favorable	intermediate	NPM1	3760				YES
36	M	38	de novo AML	neg	high	CR	no	intermediate 2	intermediate	none	24000				YES
37	F	53	de novo AML	n.a.	high	NR	no	intermediate 1	intermediate	NPM1, FLT3	54670				YES
38	F	56	secondary AML**	pos	high	NR	no	adverse	adverse	none	3600				YES
39	M	75	de novo AML	n.a.	intermediate	NR	no	intermediate 1	intermediate	CEBPa	34330				YES
40	M	69	secondary AML**	neg	intermediate	CR	no	intermediate 1	intermediate	none	16460				YES
41	M	39	de novo AML	neg	high	CR	no	favorable	intermediate	NPM1	1240				YES
42	M	75	de novo AML	n.a.	intermediate	CR	no	intermediate 2	intermediate	none	15510				YES
43	M	52	de novo AML	neg	high	CR	no	favorable	favorable	none	255950				YES
44	F	66	de novo AML	pos	intermediate	NR	no	intermediate 2	intermediate	none	3120				YES
45	F	36	de novo AML	n.a.	high	CR	no	intermediate 2	intermediate	none	2610				YES
46	M	62	de novo AML	neg	high	CR	no	intermediate 1	intermediate	none	420				YES
47	F	50	de novo AML	neg	high	NR	no	adverse	adverse	none	1450				YES
48	F	65	de novo AML	pos	intermediate	CRi	YES	favorable	intermediate	FLT3	83710				YES
49	F	66	de novo AML	pos	high	CRi	YES	intermediate 2	intermediate	none	27370				YES
50	F	66	de novo AML	neg	others	CR	no	intermediate 2	intermediate	none	1780				YES

51	F	73	secondary AML*	pos	intermediate	CR	no	intermediate 1	intermediate	none	3410		YES
52	M	57	de novo AML	n.a.	intermediate	CR	no	favorable	favorable	none	13600		YES
53	M	52	de novo AML	neg	high	CR	no	intermediate 2	intermediate	CEBPa	1490		YES
54	F	65	secondary AML**	pos	high	CR	no	adverse	adverse	none	830		YES
55	M	29	de novo AML	neg	intermediate	NR	no	intermediate 1	intermediate	none	2930		YES
56	F	65	secondary AML*	neg	intermediate	CR	no	intermediate 2	intermediate	none	3260		YES
57	F	68	de novo AML	pos	intermediate	CR	no	intermediate 1	intermediate	NPM1, FLT3	178400		YES
58	M	76	de novo AML	neg	intermediate	CR	YES	favorable	intermediate	NPM1	1290		YES
59	F	60	de novo AML	pos	high	CR	no	intermediate 1	intermediate	NPM1, FLT3	29690		YES
60	F	57	de novo AML	neg	intermediate	CR	no	intermediate 2	intermediate	FLT3	3370		YES
61	M	60	de novo AML	neg	high	CR	no	adverse	adverse	none	1360		YES
62	M	74	de novo AML	pos	intermediate	NR	no	adverse	adverse	none	57670		YES
63	F	69	de novo AML	pos	others	NR	no	intermediate 1	intermediate	none	7430		YES
64	M	37	de novo AML	neg	high	NR	no	intermediate 1	intermediate	none	1220		YES
65	F	75	de novo AML	neg	others	CR	no	adverse	adverse	none	5530		YES
66	M	21	de novo AML	n.a.	intermediate	CR	no	intermediate 1	intermediate	none	3230		YES
67	M	47	de novo AML	neg	high	CR	no	intermediate 1	intermediate	NPM1, FLT3	6620		YES
68	F	67	de novo AML	neg	intermediate	CR	no	favorable	intermediate	CEBPa	3780		YES
69	F	55	de novo AML	pos	intermediate	CR	no	favorable	intermediate	NPM1	35510		YES
70	F	43	de novo AML	neg	intermediate	CR	YES	intermediate 2	intermediate	none	1580		YES
71	F	48	secondary AML*	neg	high	NR	no	intermediate 2	intermediate	none	28110		YES
72	M	72	de novo AML	pos	intermediate	NR	no	adverse	adverse	none	13530		YES

Supplementary Table S9. *Statistical comparison of CD8$^+$ T-cell differentiation subsets in PB and BM, before and after treatment.* Presented are pre-treatment, post-treatment, and over time analyses according to response to therapy for 59 paired patient samples, and HC samples (PB, *n* = 56; BM, *n* = 24). *P* values for differences between HC and AML patients from linear regression models using logarithmically transformed numbers and adjusted for age. *P* values for differences between patient groups over time from mixed effects linear regression models using logarithmically transformed numbers, adjusted for age and including a random intercept for each patient. For more intuitive comprehension by the reader, values are presented as raw mean percentages (±SD).

		AML pre-treatment					**AML post induction chemotherapy**				**Over time analyses**					
Subset	**Controls**	**Pre (all)**	**Contr. vs. Pre (all)**	**CR**	**NR**	**CR vs. NR**	**Post (all)**	**CR**	**NR**	**CR vs. NR**	**Post (all) vs. Pre (all)**		**CR Post vs. CR Pre**		**NR Post vs. NR Pre**	
Peripheral Blood	Mean (SD)	Mean (SD)	*P* value	Mean (SD)	Mean (SD)	*P* value	Mean (SD)	Mean (SD)	Mean (SD)	*P* value		*P* value		*P* value		*P* value
CD8+ Naive	47 (23.5)	28.8 (21.8)	**0.0007**	28.4 (21.4)	29.9 (23.7)	ns	30.5 (21.8)	33.6 (21.7)	22.5 (20.8)	ns	↔	ns	↔	ns	↔	ns
CD8+ CM	5.7 (5.8)	6.8 (4.7)	**0.03**	7.1 (4.8)	6 (4.5)	ns	7.8 (6.5)	7.7 (6.8)	8.2 (6)	ns	↔	ns	↔	ns	↔	ns
CD8+ EM	25 (15.6)	33.3 (17.3)	**0.03**	34.9 (17.6)	28.9 (16.3)	ns	34.7 (17.8)	36 (18.4)	31.3 (16.5)	ns	↔	ns	↔	ns	↔	ns
CD8+ TEMRA	22.3 (13.8)	31 (17.1)	**0.01**	29.5 (15.9)	35.2 (20.3)	ns	27 (17)	22.7 (13.7)	38 (20.3)	**0.06**	↓	**0.03**	↓	**0.008**	↔	ns
CD8+ Naive like	62.7 (18.6)	39.1 (21.6)	**<0.0001**	39.7 (21.5)	37.5 (22.7)	ns	39.7 (21.6)	41.8 (21.7)	34.9 (21.3)	ns	↔	ns	↔	ns	↔	ns
CD8+ CM like	16 (7.5)	22.1 (12.6)	ns	23.4 (13.2)	18.9 (10.8)	ns	23.3 (15.4)	24.2 (15.5)	21.1 (15.8)	ns	↔	ns	↔	ns	↔	ns
CD8+ EM like	10.4 (9.6)	16.8 (13)	**0.03**	16.7 (12.1)	17.1 (15.7)	ns	18.3 (14.9)	17.8 (14)	19.6 (17.3)	ns	↔	ns	↔	ns	↔	ns
CD8+ TEMRA like	10.9 (7.6)	22 (15.5)	**0.0003**	20.2 (15.2)	26.5 (15.8)	ns	18.7 (12.5)	16.2 (11.8)	24.5 (12.6)	**0.05**	↔	ns	↔	ns	↔	ns
Bone Marrow																
CD8+ Naive	34.1 (23.3)	27 (15.5)	ns	26.8 (14.1)	27.5 (20.6)	ns	26.8 (17.8)	29.2 (18.1)	17.3 (14)	ns	↔	ns	↔	ns	↔	ns
CD8+ CM	6.4 (5.3)	7.5 (5.2)	ns	7.7 (5.3)	6.9 (4.8)	ns	8.6 (4.8)	7.8 (3.9)	11.7 (6.6)	ns	↔	ns	↔	ns	↑	**0.006**
CD8+ EM	35 (20)	36.1 (14.3)	ns	39.2 (14.2)	26.1 (9.2)	**0.02**	41.2 (17.6)	42.2 (18.3)	37.2 (15)	ns	↔	ns	↔	ns	↔	ns
CD8+ TEMRA	24.4 (15.6)	29.5 (14.5)	ns	26.3 (12.3)	39.5 (17.3)	**0.05**	23.4 (13.2)	20.8 (12.2)	33.8 (12.4)	**0.04**	↓	**0.03**	↓	**0.02**	↔	ns
CD8+ Naive like	35.3 (24.7)	30.6 (15.9)	ns	28.4 (14)	40.3 (21.3)	ns	27.4 (15.9)	27.9 (15.8)	25.5 (18.2)	ns	↔	ns	↔	ns	↔	ns
CD8+ CM like	9.4 (5.1)	17.4 (10.6)	**0.007**	18.4 (11.2)	12.6 (6.3)	ns	19 (11.3)	18.7 (10.6)	20.4 (15)	ns	↔	ns	↔	ns	↔	ns
CD8+ EM like	29 (23.4)	26.9 (13.9)	ns	28.5 (13.9)	19.4 (12.4)	ns	31.7 (16.7)	32.4 (17.7)	28.5 (12.5)	ns	↔	ns	↔	ns	↔	ns
CD8+ TEMRA like	26.3 (12.8)	25.2 (13.9)	ns	24.6 (13.9)	27.6 (15)	ns	21.9 (9.3)	21 (8.9)	25.6 (11)	ns	↔	ns	↔	ns	↔	ns

Supplementary Table S10. *Antibodies used for flow cytometric analyses.*

Antigen	Fluorochrome	Clone	Company	Catalog #	Antibody type	Staining	Category
CD3	APC	OKT3	eBioscience	17-0037-42	Mouse IgG2a, κ	surface	T-cells
CD3	AF700	HIT3a	BioLegend	300324	Mouse IgG2a, κ	surface	T-cells
CD3	evolve 605	OKT3	eBioscience	83-0037-42	Mouse IgG2a, κ	surface	T-cells
CD4	BV605	OKT4	BioLegend	317438	Mouse IgG2b, κ	surface	T-cells
CD4	PerCP Cy5.5	OKT4	eBioscience	45-0048-42	Mouse IgG2b, κ	surface	T-cells
CD8	PerCP-Cy5.5	RPA-T8	eBioscience	45-0088-42	Mouse IgG_1, κ	surface	T-cells
CD8	pacorange	3B5	Invitrogen	MHCD0830	Mouse IgG2a	surface	T-cells
CD45RA	APC-Cy7	HI100	BioLegend	304128	Mouse IgG2b, κ	surface	Memory marker
CCR7	BV650	G043H7	BioLegend	353234	Mouse IgG2a, κ	surface	Memory marker
CD56	PE-Cy7	HCD56	BioLegend	318318	Mouse IgG_1, κ	surface	NK / NK-T
CD56	PECF594	B159	BD	562289	Mouse IgG_1, κ	surface	NK / NK-T
2B4 (CD244)	FITC	C1.7	BioLegend	329506	Mouse IgG_1, κ	surface	inhibitory
BTLA (CD272)	AF647	MIH26	BioLegend	344510	Mouse IgG2a, κ	surface	inhibitory
BTLA (CD272)	PE	MIH26	BioLegend	344506	Mouse IgG2a, κ	surface	inhibitory
CD160	AF488	BY55	eBioscience	53-1609-42	Mouse IgM	surface	inhibitory
CD244 (2B4)	FITC	C1.7	BioLegend	329506	Mouse IgG_1, κ	surface	inhibitory
CTLA-4 (CD152)	PE-Cy7	L3D10	BioLegend	349914	Mouse IgG2a, κ	surface	inhibitory
PD-1 (CD279)	PE	EH12.1	BD	560795	Mouse IgG_1, κ	surface	inhibitory

TIM3 (CD366)	PE	344823	R & D	FAB2365P	Rat IgG2A	surface	inhibitory
CD57	Pacific Blue (V450)	HCD57	BioLegend	322316	Mouse IgM, κ	surface	senescence
KLRG1	AF488	13F12F2	Pircher, DE		Mouse IgG2a, κ	surface	senescence
4-1BB (CD137)	PerCP Cy5.5	4B4-1	BioLegend	309813/4	Mouse IgG1, κ	surface	stimulatory
CD127	Pacific Blue (V450)	eBioRDR5	eBioscience	48-1278-42	Mouse IgG$_1$, κ	surface	stimulatory
CD127	APC eFluor 780	eBioRDR5	eBioscience	47-1278-42	Mouse IgG$_1$, κ	surface	stimulatory
CD27	AF700	M-T271	BD	560611	Mouse IgG$_1$, κ	surface	stimulatory
CD27	BV605	O323	BioLegend	302830	Mouse IgG1, κ	surface	stimulatory
CD28	PE-Cy7	CD28.2	eBioscience	25-0289-42	Mouse IgG1, κ	surface	stimulatory
ICOS (CD278)	APC (AF647)	C398.4A	BioLegend	313516	Armenian Hamster IgG	surface	stimulatory
OX40 (CD134)	PE	ACT35	BD	555838	Mouse IgG$_1$, κ	surface	stimulatory
CD45	FITC	HI30	BioLegend	304006	Mouse IgG$_1$, κ	surface	T-cells / Blasts
CD45	PE Texas Red (CF594)	HI30	BD	562279	Mouse IgG$_1$, κ	surface	T-cells / Blasts
CD33	Pacific Blue (V450)	P67.6	eBioscience	48-0337-42	Mouse IgG$_1$	surface	Blasts
CD34	APC eFluor 780	4H11	eBioscience	47-0349-42	Mouse IgG$_1$, κ	surface	Blasts
IFN-γ	PE	4S.B3	eBioscience	12-7319-42	Mouse IgG$_1$, κ	intracellular	Cytokines
IL-2	PE-Cy7	MQ1-17H12	eBioscience	25-7029-42	Rat IgG2a, k	intracellular	Cytokines
TNFα	FITC	MabII	BioLegend	502906	Mouse IgG$_1$, κ	intracellular	Cytokines
Granzyme B	FITC	GB11	BioLegend	515403	Mouse IgG$_1$, κ	intracellular	Effector

Ki67	PerCP Cy5.5	B56	BD	561284	Mouse IgG_1, κ	intracellular	proliferation
Eomes	PE	WD1928	eBioscience	12-4877-42	Mouse IgG_1, κ	intracellular	transcription
FoxP3	Pacific Blue (V450)	PCH101	eBioscience	48-4776-42	Mouse IgG2a, κ	intracellular	transcription
T-bet	PECF594	O4-46	BD	562467	Mouse IgG_1, κ	intracellular	transcription
Cleaved Caspase 3	APC (AF647)	C92-605	BD	560626	Rabbit IgG	intracellular	Apoptosis
LIVE/Dead fixable Aqua Dead stain kit			Life Technologies	L34957			Viability
OX40L	Purified		BioLegend	555704		surface	Blocking mAB
PD-1	Purified		BMS			surface	Blocking mAB

SUPPLEMENTARY REFERENCES

1. Amir el AD, Davis KL, Tadmor MD, Simonds EF, Levine JH, Bendall SC*, et al.* viSNE enables visualization of high dimensional single-cell data and reveals phenotypic heterogeneity of leukemia. Nature biotechnology **2013**;31(6):545-52.
2. Bruggner RV, Bodenmiller B, Dill DL, Tibshirani RJ, Nolan GP. Automated identification of stratifying signatures in cellular subpopulations. Proceedings of the National Academy of Sciences of the United States of America **2014**;111(26):E2770-7.
3. Gaudilliere B, Fragiadakis GK, Bruggner RV, Nicolau M, Finck R, Tingle M*, et al.* Clinical recovery from surgery correlates with single-cell immune signatures. Science translational medicine **2014**;6(255):255ra131.
4. Roederer M, Nozzi JL, Nason MC. SPICE: exploration and analysis of post-cytometric complex multivariate datasets. Cytometry Part A : the journal of the International Society for Analytical Cytology **2011**;79(2):167-74.
5. Bindea G, Mlecnik B, Hackl H, Charoentong P, Tosolini M, Kirilovsky A*, et al.* ClueGO: a Cytoscape plug-in to decipher functionally grouped gene ontology and pathway annotation networks. Bioinformatics **2009**;25(8):1091-3.
6. Subramanian A, Tamayo P, Mootha VK, Mukherjee S, Ebert BL, Gillette MA*, et al.* Gene set enrichment analysis: a knowledge-based approach for interpreting genome-wide expression profiles. Proceedings of the National Academy of Sciences of the United States of America **2005**;102(43):15545-50.
7. Sturn A, Quackenbush J, Trajanoski Z. Genesis: cluster analysis of microarray data. Bioinformatics **2002**;18(1):207-8.
8. Willinger T, Freeman T, Hasegawa H, McMichael AJ, Callan MF. Molecular signatures distinguish human central memory from effector memory CD8 T cell subsets. J Immunol **2005**;175(9):5895-903.
9. Quigley M, Pereyra F, Nilsson B, Porichis F, Fonseca C, Eichbaum Q*, et al.* Transcriptional analysis of HIV-specific CD8+ T cells shows that PD-1 inhibits T cell function by upregulating BATF. Nat Med **2010**;16(10):1147-51.
10. Dohner H, Estey E, Grimwade D, Amadori S, Appelbaum FR, Buchner T*, et al.* Diagnosis and management of AML in adults: 2017 ELN recommendations from an international expert panel. Blood **2017**;129(4):424-47.
11. Estey E. Acute myeloid leukemia: 2016 Update on risk-stratification and management. Am J Hematol **2016**;91(8):824-46.
12. Grimwade D, Walker H, Oliver F, Wheatley K, Harrison C, Harrison G*, et al.* The Importance of Diagnostic Cytogenetics on Outcome in AML: Analysis of 1,612 Patients Entered Into the MRC AML 10 Trial. Blood **1998**;92(7):2322-33.