Cystic Fibrosis Plasma Blunts the Immune Response to Bacterial Infection

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ONLINE DATA SUPPLEMENT

DETAILED METHODS

Subject recruitment

A discovery cohort of 12 randomly selected CF probands was recruited (Fig. 1). Gene expression profiling and the following analyses were validated in validation cohort of 103 CF probands as previously profiled using the Human Genome U133 Plus 2.0 Array (GSE71799) (1). Cell composition analysis was performed on an additional cohort of 6 CF probands and 6 mothers, profiled using the transcriptome-level proofing tool Clariom D assay (ThermoFisher). Study subjects in all cohorts were diagnosed with cystic fibrosis (CF) based on pilocarpine iontophoresis (CF Foundation guidelines) (2), symptoms, pancreatic status, cystic fibrosis transmembrane conductance regulator (*CFTR*) mutation class, family history of CF, and information about the phenotypes of *CFTR* mutations (3-6). The detailed inclusion criteria included: 1) a confirmed CF diagnosis (sweat chloride value ≥60 mmol/L and/or *CFTR* genotype documenting 2 CF-causing mutations); 2) follow-up at least once per year; and 3) *CFTR* genotyping performed at the time of diagnosis or, in older subjects, after genetic testing became available. Patients diagnosed via newborn screening were evaluated by the Wisconsin Newborn Screening Laboratory for the recommended American College of Medical Genetics panel of 23 *CFTR* mutations (7). Additional genetic testing was carried out for patients with 1 identified mutation, including expanded mutation panel testing (Genzyme Genetics, Cambridge, MA), modified temporal temperature gradient electrophoresis of *CFTR* (Ambry Genetics, Aliso Viejo, CA), and multiplex ligation-dependent probe amplification for deletions and duplications (Ambry Genetics).

Data collection and sampling

General demographics information (age, sex, and genotype) was collected by standardized questionnaire. Pancreatic insufficient (PI) status was defined as fecal pancreatic elastase <200 μg/g. Documented pancreatic function status was included indicating disease severity (5). *P. aeruginosa* infection data was collected in standard screening for microbiological flora, in which *P. aeruginosa* infection was reported as 1 positive microbiological growth from nasopharyngeal, sputum, and/or bronchoalveolar lavage specimens within 6 consecutive months of study enrollment. As the Children's Hospital of Wisconsin is an accredited CF Care Center, patients received standard CF care as outlined by the CF Consortium guidelines for recording of infection (8, 9). Forced expiratory volume in 1 second (FEV1) data was collected during clinical lung function measurements performed at baseline according to ATS-ERS Task Force guidelines (10). Sweat chloride value was collected by sweat tests performed closest to the date of serum sample collection. Healthy controls (HC) subjects were free of known infection at the time of sample collection. Plasma and/or serum from CF patients and age-matched, unrelated HCs were aseptically collected in acid citrate dextrose solution A or K+ EDTA anti-coagulant for the peripheral blood mononuclear cell (PBMC)-based bioassay. The demographics information for the discovery cohort and validation cohort are shown in Table 1. An additional CF cohort included a group (n=6) of young CF probands (3 [50%] female, median age 7.5 [range 6-16] years, 1 [16.7%] *P. aeruginosa*-positive, median sweat chloride 102.7 [range 89.5-121.5] mEq/l, and median FEV1% 94.5 [range 74.0-96.0]) and their mothers (n=6, median age 43.5 [range 35-48] years). Two CF probands had 2 copies of the F508del mutation and the other four probands harbored at least one copy of the F508del mutation and one copy of another *CFTR* mutation (G542X, c.2184_2185insA, W128X, and G551D).

PBMC stimulation and RNA processing

Plasma was collected from each CF and HC subject in the discovery cohort. Healthy human PBMCs (UPN727, Cleveland, OH) were co-cultured with the plasma for 9 hours and then total RNA was isolated using Trizol (Invitrogen, Waltham, MA) (11) or the Direct-zol RNA kit (Zymo Research, Irvine, CA). In this approach, healthy human PBMCs are used as reporters that sensitively respond to soluble disease-associated factors present in the periphery; this approach was previously used to study type 1 diabetes (12-14), cancer (15), CF (1, 11, 16) and other disease (17). Autologous plasma was initially incubated with PBMCs, but we found that the gene expression response was minor compared to the plasma-induced cell response. Thus, we stopped use of autologous plasma as a baseline control in these studies.

Expression profiling

For gene expression profiling in the discovery cohort, 24 total RNA samples (12 CF and 6 HC) were isolated using Trizol (Invitrogen, Waltham, MA) and submitted to analysis with the nCounter Gene Expression Assay – Human Immunology v2 Panel (NanoString Technologies, Seattle, WA). Gene expression data from the validation cohort was generated using the GeneChip Human Genome U133 Plus 2.0 (Affymetrix, Santa Clara, CA), as reported previously (1). The original microarray data are accessible from the NCBI Gene Expression Omnibus repository (GSE71799). For miRNA expression profiling, 18 total RNA samples (12 CF and 6 HC) isolated using the Direct-zol RNA kit (Zymo Research, Irvine, CA) were submitted to analysis with the nCounter Human v3 miRNA Assay. At least 100 ng total RNA was processed for each sample. Raw mRNA or miRNA counts for each assay were collected and processed using the NanoString data analysis application nSolver 3.0. Normalization of the data was based on the geometric mean of housekeeping genes (gene expression analysis) or top-100 expressed miRNAs (miRNA analysis) that accounted for cell number variations. Gene expression profiling in other cohorts was performed following the manufacturer's instructions and as described in prior study (1).

Immune cell subset composition analysis

Cell composition analysis in the discovery cohort was performed using the Immune Cell Type Profiling Module in nSolver 3.0 (NanoString), which quantifies cell subsets based on a set of pre-defined marker genes. A modified version of Pearson’s correlation metric measurement (18) was employed to obtain the pairwise similarity (Advanced Analysis User Manual MAN-C0030, NanoString), with a low p value ($p \leq 0.01$), indicating that the expression of each gene pair is highly correlated, with slopes near 1. Various immune cell subsets were quantified using cell type-specific marker genes. The underlying assumptions were that the marker genes are expressed only in their nominal cell type and are expressed at the same level in each cell subset. To examine these assumptions, pairwise relationships of each marker gene were visualized in scatter plots. Pairwise similarity was measured to test the null hypothesis that the given gene set exhibits no greater cell type-specific-like behavior than a randomly selected gene set of similar size. A slightly modified version of Pearson’s correlation metric measurement was employed to obtain the pairwise similarity (Advanced Analysis User Manual MAN-C0030, NanoString). A low p-value ($p \leq 0.01$) indicated the data are highly consistent with the assumptions of consistent expression within each cell subset. Cell subset compositions were measured by taking the average log2 expression of its characteristic genes.

Cell composition analysis in the validation cohort and the additional CF cohort was performed using a novel signature matrix optimized for human PBMC deconvolution. First, more than 20 candidate marker genes for each cell subset were selected from a previously described matrix based on their expression patterns across the immune cell subsets (19). Next, the pairwise similarity statistic was computed between all pairs of the candidate marker genes within the microarray data from the validation cohort. Using the criteria (average Pearson correlation factor > 0.48, $p < 0.01$) and this similarity matrix, we identified a number of selected marker genes that share marker-like co-expression in each cell subset, and we defined these subsets as our final marker genes. Cell composition was evaluated following a recently reported method (18), which allows comparison of cell composition across various subject groups. The raw cell composition score was calculated as simple averages of the marker genes' log2 expression. Additionally, a relative measurement was calculated to compare composition scores of each cell subset and the total T cells. The T cell normalized score measurement was reported to be cleaner, easier to interpret, and concordant with flow cytometry measurements (18).

CD14+CD16- monocytes isolation and analysis

Human PBMCs were seeded (7.5×10^5 per well) and cultured with serum for 9 hours. The serum samples were collected from 6 HC and 24 CF subjects randomly selected from the validation cohort. The surviving PBMCs were counted (n of PBMCs) and CD14+CD16- monocytes were isolated using the EasySep Human Monocyte Isolation Kit (Stemcell) according to the manufacturer's instructions. Briefly, PBMCs were resuspended in PBS buffer containing 0.5% FBS and DNase I solution (100 µg/ml) for 15 min, and incubated with monocyte isolation cocktail containing monoclonal antibodies for 5 min, and then incubated with magnetic particles for 5 min. The cell suspension was loaded into a new tube placed in the magnetic field of an EasySep Magnet (Stemcell) for 5 min. Non-monocytes, CD16+ monocytes, and platelets were eluted while CD14+ cells were retained. The tube was then removed from the magnetic field, followed by elution of the CD14+ fraction. The isolated monocytes were counted to obtain the n of monocytes, which was used to calculate monocyte frequency (monocyte % = n of monocytes/n of PBMCs × 100%). All cells were counted using a hemocytometer following staining with trypan blue.

Bioinformatics analysis

Gene expression data of nCounter profiling (discovery cohort) was analyzed using nSolver 3.0. Gene expression data from microarray profiling (validation cohort) was analyzed using Expression Console and Transcriptome Analysis Console (Affymetrix). Raw microarray data files are accessible from the NCBI Gene Expression Omnibus repository (GEO# GSE71799). The complete differentially expressed gene lists from each cohort were linked by gene symbols to evaluate the correlation between 2 cohorts/platforms. Heatmaps and hierarchical clustering were plotted using nSolver 3.0. or Morpheus (Broad Institute, Cambridge, MA) (https://software.broadinstitute.org/morpheus/). All dendrograms were developed based on an average linkage and were clustered using 1 minus Pearson's correlation values as a distance metric. Raw count data of each mRNA or miRNA signature were normalized in each row and shown in a relative color scheme to indicate the minimum and maximum values and to highlight expression differences among different samples.

Biological functions, signaling pathways, and miRNA filter analyses were performed through Ingenuity Pathway Analysis/IPA (Hilden, Germany). All significantly differently expressed genes validated in the 2 cohorts (n = 34) and miRNAs (n = 44) were submitted to IPA analysis, and only predicted targets with miRNA-target interactions classified as medium and high were retained. Furthermore, these miRNA-target interactions were validated through databases miRTarBase and miRNet (20, 21). Reporter gene assays were considered as direct evidence; all other validation methods (e.g., microarray and sequencing) were considered as indirect evidence.

Statistical analysis

Demographic and clinical characteristics were summarized as median and range or n (%). Associations between categorical variables were examined by Chi-square test or Fisher's exact test. A non-parametric-Mann-Whitney-Wilcoxon test, Kruskal-Wallis test, and Wilcoxon matched-pairs test were used to compare continuous variables between groups. In addition, Pearson and Spearman correlation coefficients were calculated to examine the associations between continuous variables. Statistical analyses were performed and illustrated using SAS 9.4 (SAS, Cary, NC), SPSS 24 (SPSS, Chicago, IL), Prism 7 (GraphPad, La Jolla, CA), and Morpheus (Broad Institute, Cambridge, MA) (https://software.broadinstitute.org/morpheus/). A p value less than 0.05, without multiple testing adjustment, was considered statistically significant.

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SUPPLEMENTARY FIGURES

Figure E1. Heatmap showing hierarchical clustering of PBMC samples based on alterations of all immune-related genes measured with the nCounter immunology panel. Orange indicates high expression; blue indicates low expression.

Figure E2. Scatter plots matrix of pairwise marker genes in 6 cell subsets. Gene expression across all 12 subjects in the discovery cohort is shown. *Mostly CD8 T cells. $^\#$Cell subsets with limited marker genes.

Figure E3. Pairwise similarity (upper right) of 15 candidate marker genes and scatter plots matrix (lower left) of 5 selected marker genes in monocytes. Gene expression across all 143 subjects in the validation cohort is shown.

Figure E4. T cell-normalized cell composition scores of all cell subsets. T: T cells; B: B cells; NK: natural killer cells; Mφ: macrophages. Cell subset score was evaluated across all 143 subjects in the validation cohort.

SUPPLEMENTARY TABLES

Table E1. Differentially expressed genes identified by nCounter.

Table E2. Differentially expressed gene sets identified by nCounter.

Table E3. Pathway signatures identified by nCounter.

Table E4. Shared gene signatures identified by nCounter and microarray.

Table E5. Significant biological functions identified by IPA.

Table E6. Significant canonical pathways identified by IPA.

Table E7. Marker gene matrix used in immune cell subset composition analysis.

Table E8. Details of immune cell subsets analyzed in the validation cohort.

Table E9. Differentially expressed miRNAs identified by nCounter.

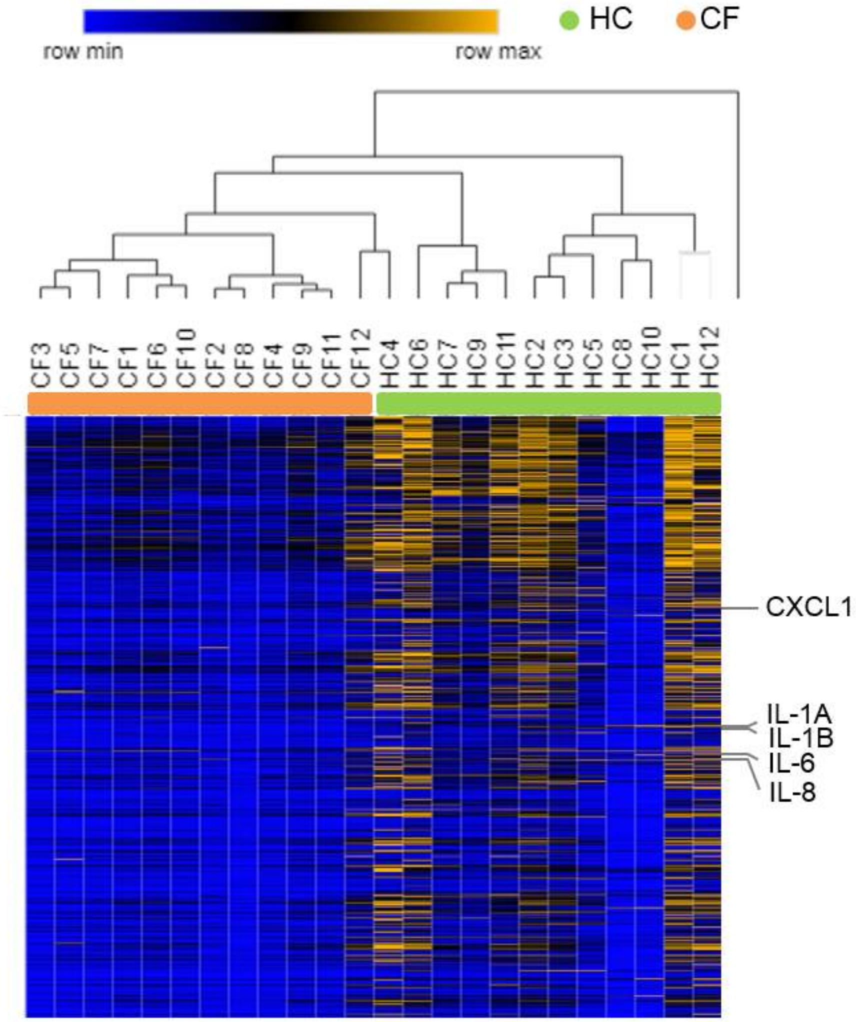

Fig. E1

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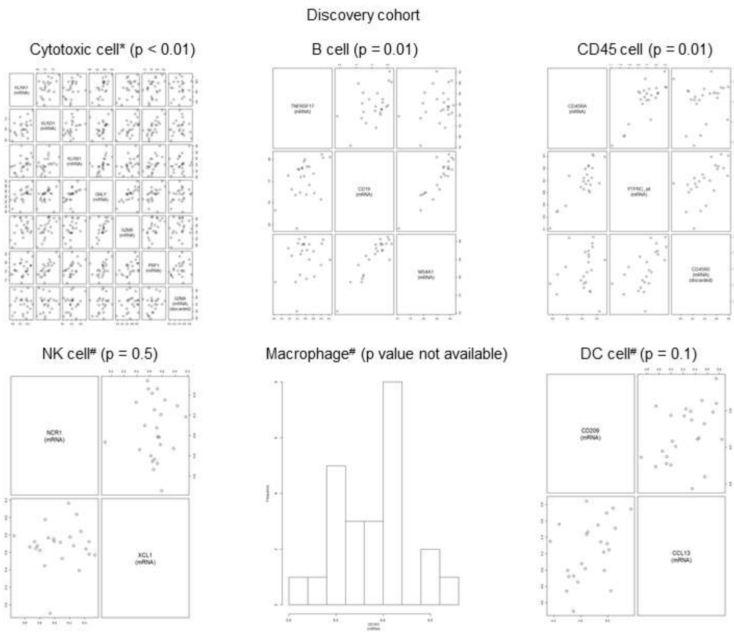

Fig. E2

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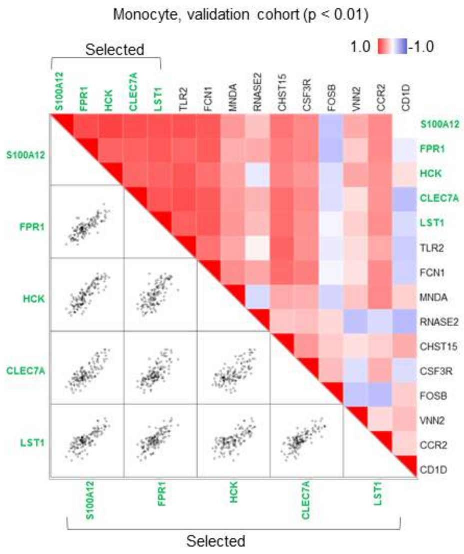

Fig. E3

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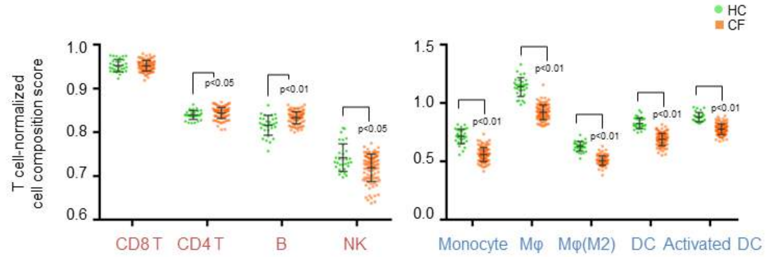

Fig. E4

254x190mm (96 x 96 DPI)

Table E1

mRNA name	probe.ID	Log2 fold change	std error	Lower confidence limit	Upper confidence limit	P-value	BH. adj. p-value	Gene.sets
CXCL1	NM_001511.1:742	-2.71	0.429	-3.55	-1.87	2.35E-06	6.10E-05	Behavior, Cell Surface Receptor Linked Signal Transduction Go 0007166, Defense Response, Extracellular Region,
CXCL2	NM_002089.3:854	-2.65	0.445	-3.52	-1.77	5.52E-06	8.98E-05	Behavior, Cell Fraction, Chemokine Activity, Defense Response, Extracellular Region, Extracellular Region Part,
IL6	NM_000600.1:220	-2.46	0.628	-3.69	-1.23	0.000735	0.0042	Cell Development, Extracellular Region, Extracellular Region Part, Extracellular Space, Negative Regulation Of Apoptosis,
IL1B	NM_000576.2:840	-2.25	0.282	-2.8	-1.69	6.31E-08	3.76E-06	Apoptosis Go, Cell Cell Signaling, Cell Development, Cell Proliferation Go 0008283, Extracellular Region, Extracellular
IL8 (CXCL8)	NM_000584.2:25	-2.16	0.266	-2.68	-1.64	4.61E-08	3.09E-06	Cell Activation, Cell Surface Receptor Linked Signal Transduction Go 0007166, Extracellular Region,
IL1A	NM_000575.3:1085	-2.09	0.31	-2.69	-1.48	9.00E-07	3.08E-05	Cell Development, Defense Response, Extracellular Region, Extracellular Region Part, Extracellular Space, Inflammatory
CCL7	NM_006273.2:120	-1.89	0.703	-3.27	-0.512	0.0134	0.0455	Behavior, Cell Cell Signaling, Cellular Cation Homeostasis, Cellular Homeostasis, Chemical Homeostasis, Extracellular
PLAUR(MO3)	NM_001005376.1:4	-1.86	0.227	-2.31	-1.42	3.89E-08	2.99E-06	Behavior, Cell Surface, Locomotory Behavior, Membrane, Membrane Part, Plasma Membrane, Response To Chemical
PTGS2(C	NM_0009	-1.78	0.352	-2.47	-1.09	4.61E-05	0.00042	Cytoplasm, Nucleus, Regulation Of Biological Quality
CCL3(MIP-1A)	NM_002983.2:159	-1.73	0.355	-2.43	-1.04	7.07E-05	0.000602	Cell Fraction, Cell Surface Receptor Linked Signal Transduction Go 0007166, Establishment Of Localization,
CCL20	NM_004591.1:35	-1.72	0.298	-2.3	-1.14	8.29E-06	0.000124	Behavior, Cell Cell Signaling, Defense Response, Extracellular Region, Extracellular Region Part, Extracellular
TLR2	NM_003264.3:180	-1.72	0.305	-2.32	-1.12	1.14E-05	0.000157	Cell Development, Cell Surface, Integral To Membrane, Integral To Plasma Membrane, Intrinsic To Membrane,
PPBP(CX	NM_0027	-1.6	0.139	-1.87	-1.33	9.18E-11	4.93E-08	Establishment Of Localization, Transport
ITGAX(CD11c)	NM_000887.3:700	-1.51	0.17	-1.84	-1.17	1.06E-08	1.24E-06	Anatomical Structure Morphogenesis, Integral To Membrane, Integral To Plasma Membrane, Intrinsic To
TNF	NM_000594.2:1010	-1.44	0.368	-2.16	-0.72	0.000742	0.0042	Cell Development, Cell Fraction, Establishment Of Protein Localization, Multi Organism Process, Negative Regulation

ICAM1 (CD54)	NM_000201.2:2253	-1.32	0.134	-1.58	-1.06	1.70E-09	4.58E-07	Integral To Membrane, Integral To Plasma Membrane, Intrinsic To Membrane, Intrinsic To Plasma Membrane,
NLRP3	NM_001079821.2:4	-1.31	0.2	-1.71	-0.923	1.27E-06	3.89E-05	Cell Development, Cytoplasm, Establishment Of Localization, Establishment Of Protein Localization,
S100A9	NM_0029	-1.22	0.29	-1.79	-0.654	0.000359	0.00227	Cell Cell Signaling, Defense Response, Inflammatory
CSF3R	NM_1560	-1.19	0.215	-1.61	-0.768	1.49E-05	0.000188	Defense Response, Integral To Membrane, Integral To
IL1R1	NM_000877.2:4295	-1.18	0.255	-1.68	-0.677	0.000135	0.000994	Integral To Membrane, Integral To Plasma Membrane, Interleukin Binding, Intrinsic To Membrane, Intrinsic To
FCER1G	NM_0041	-1.16	0.213	-1.58	-0.745	1.75E-05	0.000195	Integral To Membrane, Integral To Plasma Membrane,
IRAK2	NM_001570.3:1285	-1.14	0.139	-1.41	-0.869	3.64E-08	2.99E-06	Biopolymer Metabolic Process, Biopolymer Modification, Cell Surface, Cellular Protein Metabolic Process, Defense
TNFSF15	NM_001204344.1:2	-1.14	0.318	-1.76	-0.517	0.00166	0.0084	Cell Development, Integral To Membrane, Integral To Plasma Membrane, Intrinsic To Membrane, Intrinsic To
IL1RN	NM_0005	-1.05	0.288	-1.61	-0.484	0.00145	0.00754	Cytokine Activity, Extracellular Region, Extracellular Region
SRC	NM_005417.3:1410	-1.01	0.168	-1.34	-0.685	4.52E-06	8.10E-05	Cell Surface Receptor Linked Signal Transduction Go 0007166, Cellular Component Assembly, Cellular Protein
CD9	NM_0017	-1	0.298	-1.59	-0.421	0.00272	0.013	Anatomical Structure Morphogenesis, Macromolecular
FCGR2A	NM_0216	-0.945	0.107	-1.15	-0.734	1.16E-08	1.24E-06	
NT5E	NM_0025	-0.908	0.237	-1.37	-0.444	0.000907	0.00502	Biopolymer Metabolic Process, Cell Fraction, Dna Metabolic
CRADD	NM_003805.3:675	-0.865	0.149	-1.16	-0.573	7.47E-06	0.000115	Apoptosis Go, Cell Development, Positive Regulation Of Biological Process, Positive Regulation Of Cellular Process,
PTAFR	NM_000952.3:1035	-0.864	0.322	-1.49	-0.234	0.0135	0.0455	Behavior, Cell Surface Receptor Linked Signal Transduction Go 0007166, Defense Response, Inflammatory Response,
HAVCR2	NM_0327	-0.835	0.138	-1.11	-0.564	4.45E-06	8.10E-05	
LGALS3	NM_001177388.1:4	-0.821	0.149	-1.11	-0.528	1.61E-05	0.000191	Carbohydrate Binding, Cytoplasm, Membrane, Nucleus, Plasma Membrane
SLAMF7	NM_0211	-0.807	0.143	-1.09	-0.527	1.12E-05	0.000157	
CDKN1A	NM_0003	-0.778	0.125	-1.02	-0.534	2.72E-06	6.30E-05	Cell Development, Negative Regulation Of Cellular
CCL4	NM_002984.2:35	-0.77	0.252	-1.26	-0.276	0.00583	0.0237	Anatomical Structure Morphogenesis, Cell Cell Signaling, Defense Response, Extracellular Region, Extracellular Region
CEBPB	NM_005194.2:1420	-0.767	0.182	-1.12	-0.411	0.000354	0.00226	Biopolymer Metabolic Process, Defense Response, Immune Response, Immune System Process, Inflammatory
CLEC7A	NM_197954.2:55	-0.748	0.111	-0.965	-0.532	8.38E-07	3.08E-05	Cell Activation, Establishment Of Localization, Integral To Membrane, Intrinsic To Membrane, Leukocyte Activation,

CASP1	NM_001223.3:971	-0.733	0.151	-1.03	-0.436	7.79E-05	0.000634	Cellular Protein Metabolic Process, I Kappab Kinase Nf Kappab Cascade, Positive Regulation Of Biological Process,
CCRL2	NM_003965.4:1110	-0.728	0.129	-0.982	-0.475	1.17E-05	0.000157	Behavior, Cell Surface Receptor Linked Signal Transduction Go 0007166, Integral To Membrane, Integral To Plasma
GP1BB	NM_0004	-0.718	0.107	-0.927	-0.509	9.18E-07	3.08E-05	
ADA	NM_0000	-0.704	0.0954	-0.891	-0.517	2.20E-07	1.06E-05	
NFKB1	NM_003998.2:1675	-0.682	0.11	-0.897	-0.466	3.05E-06	6.30E-05	Biopolymer Metabolic Process, Cell Development, Cytoplasm, Defense Response, Negative Regulation Of
NFKBIA	NM_0205	-0.675	0.142	-0.954	-0.397	9.63E-05	0.000738	Apoptosis Go, Cell Development, Cytoplasm, Identical
PRKCD	NM_006254.3:2165	-0.631	0.0865	-0.8	-0.461	2.67E-07	1.10E-05	Biopolymer Metabolic Process, Biopolymer Modification, Cellular Macromolecule Metabolic Process, Cellular Protein
FCGR2A	NM_2015	-0.628	0.148	-0.918	-0.337	0.000344	0.00225	
PRDM1	NM_001198.3:798	-0.619	0.11	-0.833	-0.404	1.12E-05	0.000157	Biopolymer Metabolic Process, Negative Regulation Of Cellular Metabolic Process, Negative Regulation Of
TLR4	NM_138554.2:2570	-0.606	0.153	-0.906	-0.307	0.000649	0.00385	Biosynthetic Process, Cell Activation, Cytoplasm, Cytoplasmic Part, Integral To Membrane, Integral To Plasma
NFKBIZ	NM_001005474.1:2	-0.585	0.135	-0.851	-0.32	0.000274	0.00184	
EGR2	NM_0003	-0.583	0.181	-0.938	-0.229	0.00389	0.017	Anatomical Structure Development, Dna Binding,
LTBR	NM_002342.1:1435	-0.582	0.176	-0.926	-0.238	0.00315	0.0146	I Kappab Kinase Nf Kappab Cascade, Intracellular Signaling Cascade, Positive Regulation Of Biological Process, Positive
DUSP4	NM_057158.2:3115	-0.57	0.11	-0.786	-0.355	3.34E-05	0.000315	Biopolymer Metabolic Process, Biopolymer Modification, Cellular Macromolecule Metabolic Process, Cellular Protein
TRAF4	NM_0042	-0.563	0.129	-0.817	-0.31	0.000252	0.00171	Dna Binding, Nucleus, Signal Transduction
TNFAIP6	NM_0071	-0.563	0.195	-0.946	-0.18	0.00868	0.0326	Carbohydrate Binding, Cell Cell Signaling, Defense Response,
ITGA2B	NM_0004	-0.557	0.103	-0.759	-0.355	2.02E-05	0.000213	Identical Protein Binding
TNFRSF	NM_0010	-0.556	0.0929	-0.739	-0.374	5.02E-06	8.48E-05	Receptor Activity, Transmembrane Receptor Activity
AHR	NM_001621.3:1900	-0.533	0.12	-0.768	-0.298	0.000204	0.00144	Biopolymer Metabolic Process, Cell Development, Nucleobasenucleosidenucleotide And Nucleic Acid
CD48	NM_0017	0.508	0.0669	0.377	0.64	1.38E-07	7.40E-06	Defense Response, Integral To Membrane, Integral To
TRAF5	NM_004619.3:400	0.527	0.0899	0.351	0.703	6.72E-06	0.000106	I Kappab Kinase Nf Kappab Cascade, Intracellular Signaling Cascade, Positive Regulation Of Biological Process, Positive
MX1	NM_002462.2:1485	0.534	0.183	0.175	0.894	0.00805	0.0311	Apoptosis Go, Cell Development, Cytoplasm, Defense Response, Positive Regulation Of Biological Process, Positive

IFITM1	NM_0036 41.3:482	0.567	0.0863	0.398	0.736	1.30E-06	3.89E-05	Cell Proliferation Go 0008283, Cell Surface Receptor Linked Signal Transduction Go 0007166, Membrane, Negative
ATM	NM_0000	0.572	0.0917	0.392	0.752	2.82E-06	6.30E-05	Biopolymer Metabolic Process, Dna Metabolic Process,
MS4A1	NM_1528	0.609	0.168	0.28	0.938	0.00149	0.00764	Immune Response, Immune System Process, Integral To

Table E2

Gene Sets	**Undirected Type: differential expression in CF vs. baseline of HC**	**Directed Type: differential expression in CF vs. baseline of HC**
Protein Amino Acid Phosphorylation	5.784	-5.064
Phosphorylation	5.224	-4.414
Negative Regulation Of Biological Process	4.651	-1.865
Viral Genome Replication	4.633	-4.633
Transport	4.619	-4.497
Biopolymer Modification	4.58	-4.009
Protein Oligomerization	4.508	-4.484
Post Translational Protein Modification	4.476	-3.983
Protein Kinase Cascade	4.442	-3.807
Protein Modification Process	4.301	-3.79
Negative Regulation Of Cellular Process	4.202	-2.17
Cytoskeleton	4.189	2.687
Cell Surface	4.054	-3.208
Organelle Organization And Biogenesis	4.051	-3.053
Reproductive Process	4.028	-4.028
Positive Regulation Of I Kappab Kinase Nf Kappab Cascade	4.008	-2.411
Cellular Protein Metabolic Process	3.979	-3.518
Leukocyte Activation	3.971	-1.519
Establishment Of Localization	3.863	-3.709
Protein Metabolic Process	3.862	-3.545
Lipid Raft	3.848	3.758
Nuclear Import	3.835	-3.835
I Kappab Kinase Nf Kappab Cascade	3.792	-2.64
Cellular Macromolecule Metabolic Process	3.753	-3.212
Lymphocyte Differentiation	3.752	3.752
Extracellular Region Part	3.716	-2.79
Extracellular Space	3.716	-2.79

Positive Regulation Of Cellular Process	3.712	-1.714
Regulation Of Programmed Cell Death	3.708	-0.892
Regulation Of Transferase Activity	3.677	1.403
Cellular Component Assembly	3.596	-3.251
Regulation Of Cell Proliferation	3.562	3.145
Positive Regulation Of Signal Transduction	3.555	-1.715
Apoptosis Go	3.553	-2.427
Regulation Of Apoptosis	3.549	-1.22
Regulation Of Dna Binding	3.53	-2.404
Regulation Of Signal Transduction	3.529	-0.6
Identical Protein Binding	3.504	-3.005
Cell Activation	3.493	-0.514
Macromolecular Complex Assembly	3.488	-2.791
Nucleus	3.487	-3.166
Receptor Complex	3.451	-2.742
Nervous System Development	3.44	-3.423
Positive Regulation Of Biological Process	3.44	-1.89
Enzyme Linked Receptor Protein Signaling Pathway	3.412	-1.667
Immune System Development	3.405	3.102
Anatomical Structure Morphogenesis	3.402	-3.255
Extracellular Region	3.398	-2.431
Humoral Immune Response	3.382	2.446
Cell Proliferation Go 0008283	3.37	-1.778
Response To External Stimulus	3.369	-3.128
Positive Regulation Of Catalytic Activity	3.365	1.302
Regulation Of Kinase Activity	3.344	-1.645
Regulation Of Protein Kinase Activity	3.344	-1.645
Positive Regulation Of Developmental Process	3.294	-0.552
Regulation Of Developmental Process	3.263	-1.54
Response To Stress	3.259	-2.834

Negative Regulation Of Cellular Metabolic Process	3.257	-2.721
Dna Metabolic Process	3.217	0.864
System Development	3.192	-1.786
Carbohydrate Binding	3.19	-3.19
Negative Regulation Of Apoptosis	3.18	-1.814
Receptor Signaling Protein Activity	3.175	2.01
Programmed Cell Death	3.164	-2.045
Transmembrane Receptor Activity	3.158	-2.87
Positive Regulation Of Response To Stimulus	3.147	-2.78
Hemopoiesis	3.143	2.781
Cell Development	3.127	-2.304
Intracellular Non Membrane Bound Organelle	3.12	2.103
Non Membrane Bound Organelle	3.12	2.103
Inflammatory Response	3.119	-2.739
Regulation Of Secretion	3.114	-3.012
Membrane Organization And Biogenesis	3.109	-3.044
Response To Wounding	3.072	-2.893
Intracellular Signaling Cascade	3.049	-1.606
Establishment Of Protein Localization	3.046	-2.744
Biopolymer Metabolic Process	3.045	-2.284
Nucleobasenucleosidenucleotide And Nucleic Acid Metabolic Process	2.92	-1.621
Cytoplasm	2.918	-1.947
Transcription From Rna Polymerase Ii Promoter	2.909	-2.782
Positive Regulation Of Cell Differentiation	2.891	2.458
Response To Chemical Stimulus	2.86	-2.469
Membrane	2.842	-1.53
Defense Response	2.84	-2.079
Rna Metabolic Process	2.84	-2.328

Multicellular Organismal Development	2.838	-1.311
Signal Transduction	2.83	-1.813
Soluble Fraction	2.828	-2.103
Plasma Membrane	2.819	-1.542
Receptor Activity	2.813	-2.335
Lysosome	2.797	-2.442
Lytic Vacuole	2.797	-2.442
Transcription Dna Dependent	2.795	-2.158
Immune System Process	2.79	0.51
Membrane Part	2.763	-1.606
Plasma Membrane Part	2.754	-1.448
Cell Cell Signaling	2.747	-1.957
Regulation Of Biological Quality	2.747	-1.832
Positive Regulation Of Immune System Process	2.735	1.304
Macromolecular Complex	2.721	-2.159
Protein Complex	2.721	-2.159
Hemostasis	2.718	-1.665
Mitochondrion	2.709	1.068
Integral To Plasma Membrane	2.704	-1.634
Intrinsic To Plasma Membrane	2.688	-1.61
Interleukin Binding	2.673	-2.602
Cytoplasmic Part	2.671	-0.761
Integral To Membrane	2.669	-1.638
Response To Other Organism	2.669	-2.263
Immune Response	2.662	0.412
Intrinsic To Membrane	2.656	-1.617
Negative Regulation Of Nucleobasenucleosidenucleotide And Nucleic Acid Metabolic Process	2.655	-2.519
Immunological Synapse	2.647	-0.628
Behavior	2.625	-2.266
T Cell Proliferation	2.618	2.003
Positive Regulation Of Cell Proliferation	2.616	-1.08

Cell Surface Receptor Linked Signal Transduction Go 0007166	2.612	-1.831
Rna Biosynthetic Process	2.602	-1.596
Regulation Of Molecular Function	2.586	1.151
Chemokine Activity	2.563	-2.563
G Protein Coupled Receptor Binding	2.563	-2.563
Vacuole	2.555	-2.227
Dna Binding	2.551	-1.613
Receptor Binding	2.541	1.063
Transcription	2.539	-2.214
Locomotory Behavior	2.523	-2.114
External Side Of Plasma Membrane	2.505	2.267
Regulation Of Transcription From Rna Polymerase Ii Promoter	2.486	2.378
Anatomical Structure Development	2.474	1.946
Endoplasmic Reticulum	2.472	0.48
Cell Fraction	2.46	-1.569
Organelle Part	2.434	1.279
Intracellular Organelle Part	2.424	1.435
Organelle Membrane	2.357	-0.992
Cell Cell Adhesion	2.248	-2.079
Response To Biotic Stimulus	2.226	-1.791
Response To Virus	2.219	-1.496
Regulation Of Cellular Metabolic Process	2.185	-0.612
Multi Organism Process	2.18	-1.086
Proteolysis	2.172	-1.879
Regulation Of Gene Expression	2.08	0.819
Positive Regulation Of Translation	2.068	-1.751
Positive Regulation Of Multicellular Organismal Process	2.056	-0.719
Nucleolus	2.039	2.011
Membrane Fraction	2.028	-1.553
Nucleoplasm	2.026	1.73
Chemical Homeostasis	1.987	-1.261

Ion Homeostasis	1.987	-1.261
Membrane Enclosed Lumen	1.92	1.651
Nuclear Lumen	1.92	1.619
Organelle Lumen	1.92	1.651
Transcription Factor Activity	1.909	-1.8
P	1.894	1.893
Biosynthetic Process	1.879	-0.871
Endosome	1.872	-1.094
Cytosol	1.845	-1.397
Cellular Defense Response	1.84	-0.912
Nuclear Part	1.805	1.38
Regulation Of Translation	1.77	-1.586
Antigen Binding	1.756	-0.18
Phosphotransferase Activity Alcohol Group As Acceptor	1.747	1.474
Cytokine Activity	1.708	-1.708
Jak Stat Cascade	1.706	-1.366
Nucleoplasm Part	1.7	1.186
Peptidase Activity	1.666	1.164
Cellular Cation Homeostasis	1.657	0.104
Cellular Homeostasis	1.648	-0.863
Homeostatic Process	1.648	-0.863
Cytokine Metabolic Process	1.566	-1.364
Serine Hydrolase Activity	1.566	1.383
Positive Regulation Of Cytokine Biosynthetic Process	1.528	-1.196
Regulation Of Protein Metabolic Process	1.467	-1.388
Serine Type Peptidase Activity	1.464	1.294
Endopeptidase Activity	1.1	-0.625
Regulation Of Protein Modification Process	1.032	-0.919
Chemokine Receptor Binding	0.995	-0.993
Positive Regulation Of Phosphate Metabolic Process	0.942	0.897

Serine Type Endopeptidase Activity	0.928	0.482
Regulation Of Defense Response	0.448	0.297
Regulation Of Protein Amino Acid Phosphorylation	0.435	0.267
Positive Regulation Of Phosphorylation	0.416	0.234

TabLe E3

Gene set name	**Samples**																								**Average difference**
	HC-1	HC-2	HC-3	HC-4	HC-5	HC-6	HC-7	HC-8	HC-9	HC-10	HC-11	HC-12	CF-1	CF-2	CF-3	CF-4	CF-5	CF-6	CF-7	CF-8	CF-9	CF-10	CF-11	CF-12	
Signal Transduction	3.97	3.77	3.98	-0.81	6.09	2.72	-1.40	5.54	0.58	4.05	-0.60	0.95	-2.13	-1.85	-1.50	-1.97	-2.39	-1.89	-2.20	-2.94	-2.99	-3.33	-2.71	-2.93	-4.8079
Membrane	3.18	3.14	3.84	-0.49	6.36	2.87	-0.45	4.51	-0.09	2.75	-0.56	0.10	-2.06	-1.20	-1.07	-1.28	-1.99	-1.50	-1.76	-2.14	-2.91	-3.14	-2.87	-3.25	-4.1956
Plasma Membrane	3.09	3.02	3.74	-0.63	6.20	2.80	-0.51	4.43	-0.05	2.67	-0.62	0.09	-2.07	-1.16	-0.91	-1.29	-1.90	-1.44	-1.64	-2.06	-2.85	-3.07	-2.72	-3.13	-4.0411
Membrane Part	2.68	2.74	3.46	0.05	5.71	2.47	-0.48	4.32	-0.03	3.16	-0.47	0.25	-1.85	-1.28	-1.17	-1.39	-1.98	-1.51	-1.72	-2.10	-2.70	-2.73	-2.59	-2.83	-3.9764
Extracellular Region	2.65	2.52	2.19	0.69	3.24	1.32	-1.11	4.56	0.66	5.09	-0.38	2.31	-0.88	-2.65	-2.22	-2.58	-2.59	-1.91	-2.68	-2.93	-1.65	-2.04	-1.31	-0.31	-3.9571
Extracellular Region Part	2.75	2.54	2.09	0.28	2.97	1.44	-0.90	4.59	0.96	4.46	-0.22	2.21	-0.71	-2.55	-2.11	-2.59	-2.63	-1.79	-2.66	-2.70	-1.42	-2.13	-1.39	-0.49	-3.8636
Extracellular Space	2.75	2.54	2.09	0.28	2.97	1.44	-0.90	4.59	0.96	4.46	-0.22	2.21	-0.71	-2.55	-2.11	-2.59	-2.63	-1.79	-2.66	-2.70	-1.42	-2.13	-1.39	-0.49	-3.8636
Cell Development	2.21	1.89	1.72	1.04	3.16	1.14	-0.35	4.56	0.19	5.48	-0.08	1.66	-1.03	-2.27	-1.93	-2.24	-2.73	-1.62	-2.48	-2.44	-1.66	-2.19	-1.27	-0.78	-3.772
Defense Response	3.02	2.60	2.61	0.66	3.78	2.16	-1.15	3.95	0.25	3.57	-0.59	1.35	-1.49	-1.35	-1.30	-1.58	-1.92	-1.38	-1.85	-2.15	-2.41	-2.58	-2.12	-2.08	-3.703
Intrinsic To Membrane	2.41	2.61	3.34	-0.25	5.46	2.28	-0.36	3.93	0.08	2.74	-0.43	0.03	-1.66	-1.09	-0.92	-1.34	-1.80	-1.38	-1.38	-1.78	-2.46	-2.57	-2.59	-2.87	-3.6403
Plasma Membrane Part	2.47	2.54	3.31	-0.25	5.51	2.39	-0.50	4.04	-0.03	2.79	-0.57	0.10	-1.83	-1.15	-0.98	-1.28	-1.72	-1.43	-1.38	-1.87	-2.48	-2.52	-2.41	-2.75	-3.6334
Integral To Membrane	2.42	2.63	3.36	-0.32	5.45	2.27	-0.34	3.92	0.11	2.69	-0.41	0.01	-1.66	-1.09	-0.90	-1.34	-1.80	-1.37	-1.38	-1.73	-2.45	-2.58	-2.61	-2.89	-3.6323
Intrinsic To Plasma Membrane	2.38	2.49	3.21	-0.22	5.31	2.27	-0.49	3.92	0.01	2.75	-0.58	0.11	-1.77	-1.08	-0.89	-1.28	-1.67	-1.36	-1.30	-1.79	-2.41	-2.48	-2.41	-2.71	-3.5232
Integral To Plasma Membrane	2.40	2.52	3.23	-0.29	5.29	2.26	-0.47	3.91	0.03	2.71	-0.56	0.08	-1.77	-1.08	-0.87	-1.28	-1.66	-1.35	-1.30	-1.74	-2.40	-2.48	-2.42	-2.74	-3.5153
Cell Surface Receptor Linked Signal Transduction Go 0007166	2.55	2.66	2.59	-0.54	3.86	1.91	-0.94	3.59	0.39	2.31	-0.31	0.48	-1.44	-1.44	-0.68	-1.50	-1.27	-1.13	-1.53	-1.88	-1.78	-1.90	-1.94	-2.07	-3.0929
Inflammatory Response	2.17	1.85	1.35	0.46	2.33	1.31	-0.25	3.49	0.72	3.35	0.17	1.45	-0.68	-1.30	-1.46	-1.82	-1.85	-1.43	-1.80	-2.03	-1.42	-1.96	-1.55	-1.09	-3.0651
Response To Stress	2.31	1.77	1.32	0.83	2.43	1.39	-0.29	3.37	0.53	3.34	0.11	1.25	-0.83	-1.27	-1.30	-1.76	-1.73	-1.40	-1.65	-2.15	-1.61	-1.91	-1.56	-1.19	-3.0623
Response To External Stimulus	2.91	2.44	2.46	0.25	3.44	2.02	-1.24	2.89	0.04	2.55	-0.55	0.91	-1.48	-1.17	-1.01	-1.06	-1.22	-1.12	-1.30	-2.09	-1.96	-2.31	-1.64	-1.73	-3.0169
Behavior	2.31	2.35	2.18	0.02	3.20	1.43	-1.27	3.30	0.57	2.98	-0.41	1.34	-1.00	-1.54	-1.33	-1.84	-1.42	-1.29	-1.48	-2.21	-1.41	-1.72	-1.50	-1.27	-3.0025
Programmed Cell Death	2.09	1.64	1.79	0.62	3.02	1.08	-0.42	3.41	-0.16	4.08	-0.22	0.94	-1.21	-1.47	-1.23	-1.48	-2.14	-1.02	-1.82	-1.73	-1.60	-1.97	-1.16	-1.05	-2.9787
System Development	1.93	2.01	2.50	0.02	4.35	1.64	-1.27	3.15	-0.18	3.12	-0.67	0.92	-1.39	-1.56	-0.97	-1.06	-1.41	-1.32	-1.29	-1.81	-1.99	-1.86	-1.48	-1.35	-2.9179
Regulation Of Biological Quality	1.98	1.88	2.00	0.51	3.46	1.23	-1.47	3.30	0.00	3.53	-0.86	1.25	-1.21	-1.86	-1.14	-1.38	-1.29	-1.31	-1.33	-2.23	-1.57	-1.48	-1.17	-0.83	-2.8003
Negative Regulation Of Cellular Process	2.11	1.66	1.59	0.23	2.36	0.98	-0.39	3.17	0.49	3.12	0.14	1.14	-1.04	-1.42	-1.14	-1.55	-1.89	-0.76	-2.00	-1.34	-1.15	-1.90	-1.28	-1.12	-2.7633
Response To Chemical Stimulus	2.15	2.06	2.02	0.63	2.83	1.21	-1.11	2.69	0.15	2.75	-0.26	1.12	-0.91	-1.48	-1.45	-1.35	-1.28	-1.12	-1.37	-2.13	-1.36	-1.49	-1.34	-0.94	-2.7053
Locomotory Behavior	2.10	2.06	1.86	0.35	2.78	1.22	-1.03	2.69	0.46	2.57	-0.24	1.20	-0.86	-1.45	-1.31	-1.61	-1.16	-1.23	-1.23	-2.07	-1.26	-1.50	-1.35	-0.99	-2.6698
Cytoplasm	1.56	1.32	1.14	1.83	2.30	0.97	-0.27	3.25	-0.15	3.10	-0.19	0.68	-1.11	-1.46	-1.35	-1.28	-1.68	-1.26	-1.85	-1.55	-1.16	-1.39	-0.71	-0.75	-2.59
Cell Cell Signaling	2.25	2.14	2.21	0.07	2.96	1.60	-1.41	2.74	0.19	2.15	-0.62	1.00	-1.32	-1.19	-1.06	-1.18	-0.97	-0.80	-0.79	-1.74	-1.57	-1.76	-1.53	-1.37	-2.5467
Biopolymer Metabolic Process	2.35	1.87	1.84	0.80	3.24	1.18	-0.67	2.95	0.16	1.86	-0.55	0.23	-1.52	-0.69	-0.90	-0.85	-1.19	-0.92	-1.20	-1.55	-1.88	-1.54	-1.44	-1.57	-2.5436
Nucleus	1.78	1.15	0.83	1.99	2.06	0.96	0.01	2.87	-0.27	2.79	-0.24	0.42	-0.96	-1.58	-1.17	-0.95	-1.54	-0.93	-1.75	-1.58	-1.02	-1.49	-0.61	-0.77	-2.3926
Cell Fraction	0.89	0.99	0.70	0.50	1.49	0.04	0.38	2.63	0.30	3.29	0.70	1.76	0.24	-1.84	-1.80	-2.15	-2.10	-1.47	-1.81	-1.71	-0.12	-0.78	-0.66	0.53	-2.2776
Response To Wounding	1.92	1.47	1.39	0.21	2.12	1.16	-0.42	2.40	0.17	2.12	-0.02	0.92	-0.71	-0.94	-0.77	-1.03	-1.15	-0.87	-1.10	-1.52	-1.20	-1.71	-1.31	-1.16	-2.2436

Regulation Of Developmental Process	1.58	1.21	1.25	-0.03	2.03	0.81	0.00	2.66	0.33	2.62	0.06	0.74	-0.90	-0.85	-0.85	-1.17	-1.67	-0.64	-1.30	-1.17	-1.04	-1.44	-1.26	-0.97	-2.2131
Reproductive Process	1.48	1.60	1.70	-0.47	2.55	0.81	-0.51	2.78	0.48	1.88	-0.17	0.97	-0.73	-1.40	-0.82	-1.04	-1.13	-1.12	-1.16	-1.45	-1.11	-1.10	-1.29	-0.73	-2.181
Negative Regulation Of Apoptosis	1.10	0.76	0.53	0.98	1.27	0.43	-0.36	2.65	0.02	4.22	-0.12	1.46	-0.65	-1.53	-1.30	-1.23	-1.68	-0.97	-1.52	-1.65	-0.82	-1.03	-0.45	-0.09	-2.1539
Establishment Of Localization	0.89	0.93	1.29	0.30	2.15	0.69	0.18	2.73	0.33	2.13	0.38	0.85	-0.93	-0.93	-1.06	-0.96	-1.20	-0.80	-1.21	-1.21	-1.27	-1.15	-1.17	-0.99	-2.1442
Cell Surface	1.38	1.38	1.51	0.10	2.28	1.23	-0.08	2.20	0.06	2.01	0.07	0.46	-0.96	-0.41	-0.88	-0.68	-1.20	-0.87	-1.30	-1.37	-1.38	-1.45	-0.99	-1.12	-2.0997
Soluble Fraction	0.65	0.82	0.39	0.54	0.81	0.02	0.52	2.27	0.50	3.23	0.88	1.78	0.38	-1.80	-1.76	-2.07	-1.86	-1.48	-1.73	-1.63	0.12	-0.69	-0.58	0.70	-2.0677
Viral Genome Replication	1.16	1.39	1.11	-0.21	1.68	0.60	-0.33	2.64	0.51	2.36	0.00	1.17	-0.20	-1.48	-1.16	-1.37	-1.38	-1.21	-1.36	-1.41	-0.52	-0.89	-0.88	-0.21	-2.0135
Protein Kinase Cascade	1.65	1.36	1.11	0.35	2.06	1.00	-0.08	2.09	0.10	1.88	-0.08	0.40	-0.96	-0.67	-0.71	-0.69	-0.97	-0.62	-1.00	-1.39	-1.45	-1.57	-0.89	-0.93	-1.9747
Rna Metabolic Process	1.04	0.98	0.45	2.26	1.49	0.37	-0.09	2.69	-0.50	2.48	-0.06	0.67	-0.66	-1.22	-0.96	-0.99	-1.31	-1.12	-1.13	-1.42	-0.72	-1.00	-0.82	-0.42	-1.962
Receptor Activity	1.84	1.56	2.16	-0.33	2.85	1.54	-0.26	2.41	0.46	0.49	-0.39	-0.64	-1.44	-0.42	0.34	-0.55	-0.70	0.13	-0.66	-0.54	-1.64	-1.59	-2.19	-2.44	-1.9476
Apoptosis Go	1.56	1.40	1.48	-0.21	2.02	0.85	-0.09	2.13	0.19	1.63	-0.17	0.60	-0.68	-0.99	-0.49	-0.90	-1.45	-0.65	-1.13	-1.03	-1.10	-1.31	-0.90	-0.76	-1.8987
Nucleobasenucleosidenucleotide And Nucleic Acid Metabolic Process	1.61	1.27	1.15	1.09	2.28	0.39	-0.18	2.58	0.02	1.26	-0.17	0.09	-1.03	-0.36	-0.76	-0.78	-1.28	-0.85	-0.91	-0.91	-1.21	-1.03	-1.06	-1.20	-1.8975
Cellular Protein Metabolic Process	1.50	1.18	1.02	0.34	2.29	1.03	0.13	1.85	0.01	1.46	-0.04	0.24	-0.73	-1.19	-0.71	-0.43	-0.80	-0.63	-1.03	-1.28	-1.32	-1.38	-0.66	-0.85	-1.8326
Protein Metabolic Process	1.47	1.14	1.01	0.28	2.27	1.03	0.14	2.00	-0.12	1.54	-0.11	0.24	-0.75	-1.26	-0.68	-0.46	-0.75	-0.58	-0.99	-1.31	-1.29	-1.31	-0.70	-0.78	-1.8126
Negative Regulation Of Cellular Metabolic Process	0.49	0.46	-0.34	0.90	0.41	0.16	0.65	2.53	0.48	3.05	0.65	1.42	0.22	-1.53	-1.32	-1.76	-1.94	-1.04	-1.55	-1.35	0.18	-0.61	-0.54	0.38	-1.8102
Cell Proliferation Go 0008283	1.70	1.35	1.67	-0.45	2.09	0.98	-0.09	1.62	0.29	1.04	0.22	0.35	-0.71	-0.87	-0.39	-0.53	-1.19	-0.58	-1.21	-0.53	-0.77	-1.40	-1.35	-1.24	-1.7942
Organelle Organization And Biogenesis	0.94	1.25	1.08	-0.31	1.41	0.50	-0.46	2.25	0.48	2.12	0.04	1.15	-0.33	-1.07	-0.93	-1.36	-1.18	-0.91	-1.31	-1.08	-0.51	-0.84	-0.67	-0.28	-1.744
Macromolecular Complex Assembly	1.24	1.00	1.22	-0.06	2.42	0.85	-0.20	2.05	-0.10	1.42	0.11	0.36	-1.23	-0.41	-0.36	-0.45	-0.76	-0.51	-0.67	-0.90	-1.65	-1.31	-0.75	-1.30	-1.716
Macromolecular Complex	0.94	1.05	1.28	1.46	2.36	1.20	-0.45	1.47	-0.47	1.38	-0.40	0.19	-0.71	-1.57	-0.79	-0.58	-0.65	-0.93	-0.82	-1.23	-1.15	-0.87	-0.44	-0.27	-1.6678
Protein Complex	0.94	1.05	1.28	1.46	2.36	1.20	-0.45	1.47	-0.47	1.38	-0.40	0.19	-0.71	-1.57	-0.79	-0.58	-0.65	-0.93	-0.82	-1.23	-1.15	-0.87	-0.44	-0.27	-1.6678
Multicellular Organismal Development	0.77	1.24	1.76	-0.89	3.40	1.27	-0.10	1.54	0.06	0.69	0.08	0.14	-0.99	-0.92	-0.27	-0.27	-0.81	-0.71	-0.49	-0.43	-1.14	-1.36	-1.36	-1.23	-1.6612
Nervous System Development	1.14	1.37	1.62	-0.45	2.53	0.84	-0.70	1.91	0.09	1.20	-0.31	0.65	-0.98	-0.72	-0.32	-0.55	-0.60	-0.56	-0.73	-0.87	-1.36	-1.21	-0.98	-1.01	-1.6504
I Kappab Kinase Nf Kappab Cascade	1.16	1.09	1.01	0.08	1.73	0.66	0.02	1.77	0.25	1.67	0.11	0.19	-0.65	-0.39	-0.77	-0.61	-0.93	-0.57	-0.65	-1.07	-1.28	-1.27	-0.83	-0.71	-1.621
Negative Regulation Of Biological Process	1.61	1.17	1.51	0.06	1.75	0.80	-0.48	1.72	-0.08	1.31	-0.22	0.56	-0.74	-0.86	-0.45	-0.66	-1.12	-0.45	-1.03	-0.70	-0.74	-1.21	-0.96	-0.78	-1.6203
Transcription Dna Dependent	1.24	1.09	0.75	1.68	1.59	0.58	-0.26	2.16	-0.17	1.21	-0.24	-0.02	-0.94	-0.14	-0.63	-0.54	-1.05	-0.86	-0.75	-0.90	-0.99	-0.91	-0.86	-1.04	-1.6008
Positive Regulation Of Developmental Process	1.18	1.08	1.36	-0.40	2.12	0.75	-0.08	1.54	0.09	1.53	0.08	0.32	-0.67	-0.28	-0.58	-0.70	-1.38	-0.55	-0.73	-0.80	-0.95	-1.08	-0.87	-0.96	-1.593
Transmembrane Receptor Activity	1.43	1.01	1.08	0.52	1.85	0.67	-0.38	2.10	0.12	1.72	-0.41	-0.21	-0.89	-0.90	-0.19	-0.77	-0.91	-0.37	-0.61	-0.38	-1.18	-0.92	-1.31	-1.08	-1.5832
Positive Regulation Of Biological Process	1.30	1.20	1.53	-0.47	2.04	0.64	0.14	1.48	0.43	0.95	0.06	0.15	-0.45	-0.46	-0.31	-0.57	-1.27	-0.55	-0.66	-0.70	-1.22	-1.07	-1.25	-0.99	-1.5804
Anatomical Structure Morphogenesis	0.73	0.93	1.04	-0.34	2.13	0.70	0.00	1.81	0.08	1.21	0.24	0.82	-0.85	-0.80	-0.58	-0.31	-0.86	-0.87	-0.68	-0.65	-1.21	-1.14	-0.96	-0.43	-1.5557
Receptor Complex	0.76	1.10	1.24	-0.17	2.09	1.08	0.15	1.39	0.08	0.95	0.31	0.19	-0.89	-0.72	-0.56	-0.51	-0.66	-0.71	-0.71	-0.72	-1.15	-1.12	-0.77	-0.65	-1.5263
Post Translational Protein Modification	1.01	0.65	0.35	0.42	1.20	0.69	0.51	1.63	0.34	1.60	0.32	0.29	-0.71	-0.54	-0.71	-0.56	-0.99	-0.42	-1.03	-0.95	-0.90	-1.14	-0.49	-0.56	-1.4991

Biopolymer Modification	1.01	0.64	0.33	0.77	1.30	0.64	0.43	1.22	0.48	1.44	0.37	0.27	-0.50	-0.63	-0.89	-0.46	-0.91	-0.62	-1.24	-0.85	-0.78	-1.28	-0.30	-0.45	-1.483
Nuclear Import	0.48	0.65	0.30	0.87	0.55	0.11	0.12	1.98	0.06	2.44	0.30	0.86	-0.19	-1.03	-0.76	-1.37	-1.10	-0.65	-1.06	-0.84	-0.34	-0.73	-0.65	-0.03	-1.456
Positive Regulation Of Response To Stimulus	0.73	0.74	0.84	0.44	1.37	0.95	-0.14	1.62	0.00	1.44	0.18	0.47	-0.22	-0.95	-0.74	-0.81	-0.99	-0.83	-1.08	-0.94	-0.59	-0.94	-0.22	-0.33	-1.4408
Chemokine Activity	0.73	0.85	0.86	-0.26	1.13	0.53	0.05	1.52	0.35	1.51	0.26	1.05	0.16	-1.07	-0.93	-1.20	-1.08	-0.73	-1.20	-1.10	-0.15	-0.68	-0.53	-0.10	-1.4322
G Protein Coupled Receptor Binding	0.73	0.85	0.86	-0.26	1.13	0.53	0.05	1.52	0.35	1.51	0.26	1.05	0.16	-1.07	-0.93	-1.20	-1.08	-0.73	-1.20	-1.10	-0.15	-0.68	-0.53	-0.10	-1.4322
Establishment Of Protein Localization	0.41	0.62	0.25	0.77	0.51	0.12	0.16	1.81	0.21	2.47	0.40	0.86	-0.14	-0.96	-0.86	-1.35	-1.12	-0.75	-1.03	-0.87	-0.28	-0.70	-0.58	0.04	-1.432
Positive Regulation Of Cellular Process	1.18	1.01	1.30	-0.26	1.67	0.38	0.13	1.26	0.49	0.99	0.23	0.18	-0.39	-0.38	-0.32	-0.58	-1.41	-0.58	-0.51	-0.43	-1.16	-1.04	-0.88	-0.88	-1.4257
Regulation Of Dna Binding	0.36	0.57	0.20	0.59	0.45	0.03	0.35	1.81	0.22	2.42	0.52	0.94	-0.09	-0.91	-0.95	-1.36	-1.11	-0.76	-1.02	-0.84	-0.23	-0.67	-0.57	0.05	-1.4106
Positive Regulation Of Signal Transduction	1.12	0.89	1.07	0.07	1.83	0.70	-0.24	1.43	0.18	1.40	-0.02	0.03	-0.65	-0.43	-0.58	-0.49	-0.66	-0.46	-0.41	-0.88	-1.21	-1.15	-0.83	-0.72	-1.4082
Transport	0.79	0.67	1.50	-0.28	2.16	0.63	0.37	1.65	0.02	0.59	0.06	0.13	-1.09	-0.32	-0.38	0.12	-0.37	-0.27	-0.40	-0.61	-1.20	-0.97	-1.35	-1.44	-1.3796
Response To Virus	0.06	0.70	0.14	1.41	0.50	-0.25	0.00	1.39	0.07	2.43	0.06	1.49	0.04	-1.47	-1.45	-1.42	-1.07	-1.17	-0.98	-1.22	-0.23	0.17	-0.23	1.02	-1.336
Rna Biosynthetic Process	1.05	1.10	0.80	0.97	1.38	0.45	-0.26	1.89	-0.10	0.71	-0.32	0.04	-0.60	-0.05	-0.45	-0.31	-0.99	-0.78	-0.49	-0.66	-0.90	-0.86	-0.59	-1.02	-1.2846
Negative Regulation Of Nucleobasenucleosidenucleotide And Nucleic Acid Metabolic Process	0.35	0.44	-0.01	1.33	0.42	-0.07	0.23	1.70	-0.02	2.15	0.35	0.81	-0.01	-1.15	-0.82	-1.15	-1.00	-0.77	-0.95	-0.93	-0.04	-0.53	-0.61	0.27	-1.2815
Regulation Of Signal Transduction	0.99	0.92	1.18	-0.06	1.66	0.60	-0.29	1.29	0.22	1.15	-0.13	0.09	-0.61	-0.31	-0.52	-0.51	-0.62	-0.36	-0.24	-0.78	-1.10	-0.90	-0.95	-0.74	-1.2726
Protein Oligomerization	0.72	0.73	0.66	0.41	0.92	0.55	-0.23	1.62	0.09	1.32	0.01	0.17	-0.66	-0.20	-0.34	-0.71	-0.65	-0.34	-0.78	-0.54	-0.92	-0.87	-0.31	-0.65	-1.1618
Regulation Of Molecular Function	0.57	0.44	0.20	-0.25	1.14	-0.14	0.33	1.80	0.52	1.73	0.27	0.23	0.66	-0.77	-0.97	-0.93	-1.04	-1.02	-0.94	-0.87	-0.24	-0.74	-0.15	0.16	-1.1428
Positive Regulation Of I Kappab Kinase Nf Kappab Cascade	0.85	0.91	1.13	-0.26	1.50	0.50	-0.18	1.22	0.30	0.84	-0.09	0.01	-0.52	-0.27	-0.25	-0.34	-0.42	-0.23	-0.17	-0.68	-1.06	-0.91	-1.11	-0.76	-1.1212
Regulation Of Kinase Activity	0.42	0.45	0.17	-0.09	1.06	-0.07	0.30	1.61	0.46	1.87	0.12	0.28	0.47	-0.73	-0.99	-0.85	-1.01	-0.87	-1.01	-0.80	-0.29	-0.57	-0.07	0.14	-1.0954
Regulation Of Protein Kinase Activity	0.42	0.45	0.17	-0.09	1.06	-0.07	0.30	1.61	0.46	1.87	0.12	0.28	0.47	-0.73	-0.99	-0.85	-1.01	-0.87	-1.01	-0.80	-0.29	-0.57	-0.07	0.14	-1.0954
Protein Modification Process	0.69	0.39	0.32	0.64	1.13	0.46	0.35	1.03	0.17	0.89	0.11	0.15	-0.53	-0.57	-0.44	-0.36	-0.48	-0.42	-0.92	-0.53	-0.59	-0.86	-0.32	-0.30	-1.0532
Dna Binding	0.73	0.46	0.73	1.82	1.29	0.04	-0.34	1.73	-0.57	1.28	-0.56	-0.35	-0.57	-0.86	-0.70	-0.30	-0.49	-0.28	-0.84	-0.47	-0.35	-0.45	-0.49	-0.47	-1.0436
Cellular Component Assembly	0.99	0.64	0.59	0.13	1.40	0.63	0.00	0.86	-0.38	1.04	0.18	0.17	-0.55	-0.37	-0.42	-0.37	-0.64	-0.18	-0.52	-0.78	-0.66	-0.84	-0.24	-0.70	-1.0429
Regulation Of Secretion	0.64	0.59	0.55	0.23	0.76	0.49	-0.16	1.45	0.25	1.29	0.04	0.14	-0.49	-0.17	-0.36	-0.74	-0.65	-0.18	-0.67	-0.36	-0.86	-0.79	-0.37	-0.61	-1.0425
Regulation Of Apoptosis	0.94	0.69	0.87	-0.01	1.17	0.51	-0.24	1.18	0.01	1.04	-0.37	0.37	-0.33	-0.49	-0.26	-0.51	-1.28	-0.37	-0.58	-0.35	-0.61	-0.64	-0.45	-0.30	-1.0279
Cellular Macromolecule Metabolic Process	1.02	0.58	0.60	0.52	1.55	0.38	-0.02	1.19	-0.21	0.67	-0.27	0.11	-0.41	-1.46	-0.31	-0.28	-0.42	-0.33	-0.60	-0.79	-0.71	-0.53	-0.27	-0.01	-1.0191
Enzyme Linked Receptor Protein Signaling Pathway	0.97	0.71	0.53	0.15	1.17	0.63	0.03	0.85	-0.11	0.81	0.14	0.22	-0.53	-0.39	-0.20	-0.17	-0.34	-0.34	-0.41	-0.81	-1.02	-0.73	-0.25	-0.91	-1.0169
Transcription	0.84	0.97	0.59	0.60	0.93	0.16	-0.04	1.64	0.24	0.21	-0.26	0.06	-0.58	0.39	-0.20	-0.13	-0.78	-0.81	-0.17	-0.45	-0.72	-0.79	-0.47	-1.23	-0.9911
Identical Protein Binding	0.83	0.69	0.41	0.56	0.95	0.36	0.07	0.72	0.03	0.85	0.02	0.38	-0.31	-0.31	-0.71	-0.26	-0.75	-0.47	-0.44	-0.50	-0.52	-0.77	-0.38	-0.45	-0.9796
Cellular Homeostasis	1.43	1.44	1.62	-0.07	1.71	1.02	-1.77	0.67	0.02	0.61	-1.08	0.23	-0.94	-0.34	-0.33	-0.38	0.09	-0.24	0.17	-0.88	-0.86	-0.67	-0.77	-0.68	-0.9715
Homeostatic Process	1.43	1.44	1.62	-0.07	1.71	1.02	-1.77	0.67	0.02	0.61	-1.08	0.23	-0.94	-0.34	-0.33	-0.38	0.09	-0.24	0.17	-0.88	-0.86	-0.67	-0.77	-0.68	-0.9715
Interleukin Binding	0.89	0.81	0.99	-0.41	1.57	0.40	-0.20	1.13	-0.03	0.67	0.08	-0.07	-0.56	-0.57	-0.15	-0.65	-0.51	-0.03	-0.35	-0.40	-0.80	-0.59	-0.56	-0.64	-0.9692

Regulation Of Programmed Cell Death	0.71	0.58	0.80	-0.25	1.13	0.31	0.15	0.84	0.30	0.84	0.03	0.31	-0.14	-0.35	-0.15	-0.41	-1.44	-0.42	-0.43	-0.30	-0.72	-0.56	-0.45	-0.37	-0.9571
Chemical Homeostasis	1.38	1.52	1.63	-0.27	1.64	0.97	-1.64	0.75	0.14	0.51	-1.02	0.13	-0.91	-0.35	-0.19	-0.45	0.14	-0.22	0.16	-0.85	-0.79	-0.70	-0.77	-0.81	-0.9567
Ion Homeostasis	1.38	1.52	1.63	-0.27	1.64	0.97	-1.64	0.75	0.14	0.51	-1.02	0.13	-0.91	-0.35	-0.19	-0.45	0.14	-0.22	0.16	-0.85	-0.79	-0.70	-0.77	-0.81	-0.9567
Dna Metabolic Process	0.95	0.62	0.90	-0.31	1.59	0.00	-0.23	1.33	-0.04	0.64	-0.17	0.46	-0.46	-0.67	-0.30	-0.53	-0.67	-0.28	-0.45	-0.30	-0.72	-0.45	-0.39	-0.50	-0.9533
Jak Stat Cascade	1.48	1.31	1.86	-0.26	1.73	0.97	-1.65	0.91	0.14	0.21	-1.22	0.21	-1.18	-0.43	-0.28	-0.17	0.45	-0.26	0.04	-0.77	-1.35	-0.20	-0.67	-0.88	-0.9484
Membrane Fraction	0.84	0.89	1.10	-1.05	1.96	0.16	-0.05	1.51	-0.11	0.39	-0.07	-0.05	-0.27	-0.46	-0.01	-0.38	-0.88	-0.35	-0.35	-0.10	-0.50	-0.51	-0.67	-1.03	-0.9208
Intracellular Signaling Cascade	0.80	0.85	0.89	0.07	1.18	0.05	-0.30	0.79	0.23	0.69	0.06	-0.02	-0.39	-0.16	-0.18	-0.50	-0.44	-0.40	0.28	-0.45	-1.12	-0.78	-0.62	-0.54	-0.8828
Protein Amino Acid Phosphorylation	0.53	0.34	0.29	0.53	0.81	0.15	0.45	0.89	0.32	0.73	0.23	-0.02	-0.29	-0.36	-0.37	-0.42	-0.46	-0.54	-0.63	-0.34	-0.63	-0.56	-0.26	-0.38	-0.873
Regulation Of I	0.68	0.73	0.83	-0.01	1.01	0.16	-0.24	0.80	0.33	0.71	0.09	0.02	-0.41	-0.13	-0.19	-0.41	-0.39	-0.22	0.17	-0.33	-1.07	-0.93	-0.59	-0.63	-0.8517
Leukocyte Activation	0.28	0.47	0.53	1.16	0.88	0.21	-0.02	0.55	0.05	0.65	0.16	0.09	-0.23	-0.29	-0.39	-0.11	-0.36	-0.29	-0.19	-0.69	-0.65	-0.36	-0.75	-0.69	-0.8344
Phosphorylation	0.52	0.40	0.33	0.37	0.72	0.20	0.52	0.80	0.16	0.70	0.21	-0.09	-0.27	-0.30	-0.33	-0.37	-0.44	-0.44	-0.52	-0.29	-0.63	-0.54	-0.28	-0.40	-0.8056
Cellular Defense Response	1.25	1.03	1.47	-0.30	2.23	1.16	-1.34	1.04	-0.58	0.34	-1.33	-0.16	-0.64	0.33	-0.04	0.39	0.05	-0.30	0.02	-0.46	-1.66	-0.87	-0.61	-1.02	-0.8017
Membrane Organization And Biogenesis	0.73	0.63	1.40	-0.81	1.93	0.76	-0.01	1.24	-0.52	0.18	-0.66	-0.19	-0.96	0.08	-0.02	0.41	0.03	0.14	0.03	-0.33	-0.76	-0.66	-1.35	-1.28	-0.7792
Carbohydrate Binding	0.16	-0.15	0.46	-0.70	1.27	0.31	0.62	1.84	-0.60	1.44	-0.46	0.46	-0.95	0.00	-0.43	0.13	-0.06	-0.17	0.15	-0.56	-0.71	-0.36	-0.89	-0.76	-0.7708
Transcription Factor Activity	0.58	0.43	0.55	1.69	1.03	0.07	-0.68	1.38	-0.79	1.34	-0.78	-0.26	-0.50	-0.62	-0.50	-0.12	-0.20	-0.22	-0.68	-0.56	-0.39	-0.26	-0.23	-0.31	-0.764
Regulation Of Cellular Metabolic Process	0.65	0.42	0.53	0.77	1.16	-0.04	-0.41	1.34	-0.45	1.03	-0.38	-0.26	-0.27	-0.63	-0.30	-0.38	-0.50	-0.21	-0.49	-0.23	-0.32	-0.38	-0.38	-0.29	-0.7286
Proteolysis	0.62	0.67	0.91	-0.66	1.45	0.61	-0.29	0.93	-0.08	0.08	-0.29	-0.17	-0.16	-0.62	-0.12	0.16	0.11	-0.34	0.05	-0.19	-0.48	-0.81	-0.77	-0.61	-0.629
Chemokine Receptor Binding	0.77	0.75	1.27	-1.31	1.77	0.88	-0.43	0.46	-0.23	-0.36	-0.30	0.02	-0.65	-0.50	0.53	-0.16	0.29	0.27	0.22	-0.01	-0.48	-0.87	-0.53	-1.40	-0.547
Antigen Binding	0.28	0.59	0.95	-1.10	0.70	1.04	0.42	0.24	0.49	-0.65	0.36	-0.67	-0.51	0.44	0.55	0.23	-0.13	0.56	-0.28	-0.10	-0.10	-1.07	-0.79	-1.44	-0.4394
Mitochondrion	0.43	0.28	0.28	-0.27	0.62	-0.64	-0.31	0.98	0.21	0.28	0.42	-0.17	-0.26	-0.34	0.32	0.14	-0.53	-0.03	0.29	0.44	-0.57	-0.25	-0.46	-0.85	-0.3526
Organelle Membrane	0.63	0.42	0.22	-0.33	0.20	0.82	-0.15	0.35	-0.07	-0.02	-0.17	0.14	-0.47	-0.07	-0.03	0.49	0.22	-0.08	-0.31	-0.12	-0.15	-0.72	-0.35	-0.47	-0.3404
Lysosome	0.58	0.48	0.23	-0.53	0.23	0.74	-0.11	0.21	0.08	-0.14	0.04	0.18	-0.51	-0.09	0.09	0.47	0.17	-0.06	-0.28	-0.08	-0.21	-0.76	-0.27	-0.45	-0.3284
Lytic Vacuole	0.58	0.48	0.23	-0.53	0.23	0.74	-0.11	0.21	0.08	-0.14	0.04	0.18	-0.51	-0.09	0.09	0.47	0.17	-0.06	-0.28	-0.08	-0.21	-0.76	-0.27	-0.45	-0.3284
Vacuole	0.57	0.48	0.23	-0.55	0.22	0.75	-0.10	0.20	0.08	-0.14	0.03	0.19	-0.51	-0.10	0.09	0.47	0.17	-0.05	-0.29	-0.06	-0.20	-0.76	-0.27	-0.45	-0.3266
Cytoplasmic Part	1.21	0.20	0.69	-2.80	1.19	0.72	0.22	0.39	0.51	-0.56	-0.05	-0.40	0.09	0.13	0.90	0.37	-0.36	0.45	0.14	0.54	-0.76	-1.01	-0.56	-1.23	-0.2159
Regulation Of Gene Expression	-0.10	0.35	-0.07	0.12	0.01	0.81	0.16	-0.19	0.27	-1.63	0.32	0.34	0.06	-0.39	0.08	-0.31	-0.54	0.22	0.50	-0.75	0.15	0.30	-0.39	0.67	-0.0647
Serine Hydrolase Activity	-0.18	-0.18	0.13	-0.86	0.21	0.08	0.78	0.30	1.15	-0.48	0.34	-1.28	0.43	-0.45	0.89	0.31	0.31	0.34	0.05	0.88	0.22	-1.06	-0.59	-1.35	-0.0014
Serine Type Peptidase Activity	-0.17	-0.17	0.13	-0.86	0.22	0.08	0.77	0.30	1.15	-0.49	0.34	-1.29	0.43	-0.46	0.89	0.31	0.31	0.34	0.06	0.87	0.22	-1.05	-0.59	-1.35	-0.0014
Nucleolus	0.35	0.17	0.27	-0.28	0.39	-0.35	0.39	-0.40	0.38	-0.76	0.11	-0.38	-0.03	-0.17	0.31	-0.42	-0.44	0.26	-0.09	0.15	0.48	-0.13	0.17	0.01	0.01819
Regulation Of Defense Response	-0.40	-0.42	0.04	-1.36	-0.16	-0.63	1.13	0.86	0.80	0.25	0.27	-0.51	0.52	0.20	0.61	-0.22	-0.13	-0.19	0.01	0.28	0.62	0.02	-1.15	-0.45	0.02198
Endopeptidase Activity	-0.17	-0.22	0.09	-0.86	0.21	0.05	0.77	0.31	1.10	-0.50	0.29	-1.28	0.47	-0.44	0.91	0.30	0.37	0.36	0.13	0.86	0.23	-1.03	-0.60	-1.35	0.03511
Serine Type Endopeptidase Activity	-0.18	-0.24	0.08	-0.86	0.19	0.06	0.78	0.31	1.10	-0.49	0.30	-1.27	0.47	-0.43	0.91	0.30	0.36	0.36	0.13	0.86	0.24	-1.03	-0.59	-1.35	0.03734
Positive Regulation Of Phosphorylation	-0.16	0.29	-0.05	-1.15	-0.45	-0.16	0.86	0.33	0.95	-1.00	0.72	-0.52	0.35	0.21	0.17	0.11	-0.31	0.13	-0.16	0.58	0.46	0.03	-0.20	-1.05	0.05471
Positive Regulation Of Multicellular Organismal Process	-0.54	-0.04	-0.18	-0.59	-0.27	-0.63	0.41	0.42	0.04	0.91	0.07	-0.18	-0.45	0.54	-0.04	0.67	0.27	0.22	0.37	-0.41	0.22	0.38	-1.17	-0.02	0.09708

P	-0.07	-0.47	-0.11	0.64	-0.38	0.61	-0.59	0.41	-0.46	0.28	-0.67	0.18	-0.07	0.08	0.05	0.31	0.27	0.15	-0.12	-0.25	-0.16	-0.03	0.26	0.14	0.10405
Regulation Of Protein Modification Process	-0.31	-0.15	-1.24	-0.20	0.07	-0.06	0.64	1.29	-0.44	-0.03	0.34	-0.53	0.78	0.34	1.17	0.50	-0.23	-0.13	-0.77	0.23	0.75	-1.53	-0.41	-0.08	0.10411
Cytosol	0.43	-0.33	-0.12	-1.45	-0.02	0.30	0.29	0.81	0.26	-0.69	0.28	-0.45	0.13	0.22	1.06	-0.15	0.06	0.05	0.34	0.78	-0.11	-0.32	-0.57	-0.82	0.11387
Regulation Of Protein Amino Acid Phosphorylation	-0.29	-0.11	-1.25	-0.28	-0.03	-0.14	0.79	1.28	-0.30	-0.13	0.40	-0.66	0.92	0.34	1.14	0.49	-0.31	-0.20	-0.73	0.33	0.83	-1.51	-0.42	-0.19	0.11662
Peptidase Activity	-0.14	-0.19	0.05	-1.01	-0.18	0.06	0.98	0.06	1.23	-0.60	0.38	-1.34	0.46	-0.20	0.95	0.26	0.33	0.41	0.00	1.09	0.31	-0.99	-0.53	-1.38	0.11788
Cell Cell Adhesion	0.27	0.27	0.19	-1.13	-0.61	-0.29	0.22	0.20	0.22	-0.11	0.74	-0.83	-0.08	0.51	0.24	0.48	0.55	0.28	0.00	0.93	0.23	-0.22	-1.05	-1.02	0.141
Regulation Of Protein Metabolic Process	-0.37	-0.01	-1.32	-0.73	0.32	-0.30	0.48	2.01	-0.39	0.52	-0.39	-0.66	0.36	0.75	1.31	0.52	-0.11	0.04	-0.57	0.26	0.83	-1.66	-0.57	-0.32	0.14167
Positive Regulation Of Phosphate Metabolic Process	-0.18	-0.39	-0.67	-1.34	-0.42	-0.40	0.67	0.53	0.96	-0.43	0.72	-0.54	0.61	0.66	0.68	0.27	-0.47	0.42	0.03	0.93	1.05	-0.09	-1.24	-1.37	0.24837
T Cell Proliferation	0.06	-0.04	0.53	-2.21	0.25	0.00	0.65	-0.52	0.26	-0.06	0.10	-0.55	0.28	0.67	0.63	0.27	-0.45	0.14	-0.22	0.49	-0.05	0.15	-0.14	-0.25	0.25257
Phosphotransferase Activity Alcohol Group As Acceptor	-0.03	-0.17	-0.02	-0.86	-0.24	0.25	0.41	0.00	0.56	-1.00	0.39	-0.98	0.34	0.63	0.22	0.56	0.21	0.63	-0.67	0.41	0.30	0.02	0.09	-1.04	0.2823
Cytokine Metabolic Process	-0.27	0.25	0.10	-1.78	-0.04	-0.53	0.44	0.72	0.40	0.00	-0.26	-0.73	0.14	0.55	0.74	0.68	0.09	0.27	-0.03	0.15	0.52	-0.88	-0.40	-0.12	0.28348
Response To Other Organism	0.53	0.08	-0.06	-1.20	-0.57	0.63	0.17	-0.61	0.00	-0.61	-0.16	-0.10	-0.09	-0.17	0.95	0.54	0.49	0.75	-0.14	0.78	0.03	-0.56	0.01	-0.71	0.31243
Nuclear Lumen	-0.77	-0.43	-0.47	-0.32	-0.97	0.18	0.12	-0.30	0.34	0.08	0.26	0.40	-0.41	1.02	-0.01	-0.01	0.65	0.26	0.16	0.21	-0.25	-0.16	0.29	0.14	0.31645
Nucleoplasm Part	-0.69	-0.31	-0.34	-0.46	-0.76	0.10	0.05	-0.37	0.35	-0.10	0.22	0.35	-0.40	1.12	0.07	-0.05	0.39	0.25	0.19	0.39	-0.19	-0.18	0.26	0.11	0.32793
Response To Biotic Stimulus	0.39	0.07	-0.04	-1.40	-0.74	0.24	0.84	-0.80	0.66	-0.90	0.37	-0.66	0.08	-0.04	1.04	0.12	0.39	0.58	-0.02	0.72	0.57	-0.68	0.02	-0.81	0.32826
Regulation Of Translation	-0.23	0.23	0.11	-1.62	-0.04	-0.58	0.39	0.59	0.29	-0.03	-0.31	-0.79	0.15	0.56	0.77	0.71	0.25	0.28	-0.02	0.10	0.49	-0.94	-0.33	-0.03	0.33275
Nucleoplasm	-0.75	-0.40	-0.41	-0.37	-0.96	0.13	0.11	-0.34	0.35	-0.01	0.25	0.37	-0.37	1.08	0.00	-0.03	0.61	0.25	0.18	0.24	-0.24	-0.13	0.29	0.13	0.33583
Nuclear Part	-0.87	-0.40	-0.52	-0.15	-1.05	-0.01	0.08	-0.36	0.28	0.16	0.32	0.49	-0.34	1.02	-0.08	-0.08	0.58	0.24	0.13	0.20	-0.13	0.00	0.31	0.18	0.33743
Membrane Enclosed Lumen	-0.79	-0.43	-0.45	-0.34	-0.97	0.14	0.17	-0.35	0.35	0.00	0.26	0.38	-0.44	1.03	0.03	-0.05	0.68	0.28	0.16	0.27	-0.21	-0.15	0.32	0.11	0.3393
Organelle Lumen	-0.79	-0.43	-0.45	-0.34	-0.97	0.14	0.17	-0.35	0.35	0.00	0.26	0.38	-0.44	1.03	0.03	-0.05	0.68	0.28	0.16	0.27	-0.21	-0.15	0.32	0.11	0.3393
Regulation Of Transcription From Rna Polymerase Ii Promoter	-0.24	-0.35	-0.42	0.28	-0.75	0.24	0.10	-0.54	0.05	-0.19	-0.16	-0.10	-0.11	-0.30	0.32	0.14	0.75	0.15	0.35	-0.22	0.22	0.28	0.16	0.34	0.34668
Endoplasmic Reticulum	0.17	-0.49	-0.22	-1.02	-0.96	-0.07	0.91	0.16	0.25	-0.20	0.27	-0.94	0.28	-0.24	0.73	0.02	0.01	0.45	0.72	0.84	0.46	-0.16	-0.04	-0.93	0.35629
Hemostasis	-0.47	-0.33	-0.21	-0.71	-0.81	-0.32	0.37	-0.77	0.38	-0.51	0.65	0.31	-0.01	0.50	-0.17	0.47	0.42	0.39	0.22	0.38	-0.06	0.09	-0.14	0.32	0.40191
Positive Regulation Of Cytokine Biosynthetic Process	-0.15	0.04	0.44	-2.41	-0.14	-0.30	0.69	0.33	0.22	-0.08	-0.18	-1.01	0.31	0.79	1.16	0.64	0.06	0.35	-0.07	0.35	0.32	-0.72	-0.49	-0.15	0.42684
Biosynthetic Process	-0.32	0.08	0.45	-2.98	-0.27	-0.47	1.08	0.78	0.56	-0.40	-0.10	-1.17	0.04	0.87	1.26	0.51	0.02	0.49	0.25	0.59	0.32	-0.30	-0.83	-0.44	0.46179
Endosome	0.11	-0.10	-0.60	-0.43	-0.56	-1.20	0.31	-0.80	0.47	-0.41	0.29	0.09	0.19	0.07	0.10	0.07	0.04	0.37	0.49	0.38	0.25	0.04	0.19	0.63	0.47103
External Side Of Plasma Membrane	0.14	-0.17	-0.55	-0.85	-0.76	-1.01	0.41	-0.59	0.60	-0.72	0.40	-0.23	0.29	0.08	0.44	-0.04	0.09	0.51	0.49	0.86	0.41	0.15	-0.03	0.10	0.55669
Humoral Immune Response	0.26	-0.16	0.06	-1.20	-0.60	0.01	0.08	-0.66	0.38	-1.32	0.22	-0.45	0.57	0.63	0.65	0.46	0.29	0.04	0.23	0.88	0.28	0.04	0.00	-0.66	0.56709
Cytoskeleton	-0.78	-0.55	-0.48	0.14	-0.81	-0.19	-0.05	-0.52	0.06	-0.43	0.15	-0.04	0.20	0.24	0.29	0.26	0.43	0.22	0.37	0.30	0.24	0.36	0.33	0.27	0.58333
Immunological Synapse	-0.19	-0.33	-0.80	-0.20	-0.92	-1.14	0.30	-0.80	0.38	-0.24	0.19	0.14	0.34	0.20	0.29	-0.01	0.15	0.36	0.41	0.38	0.34	0.22	0.30	0.62	0.6005

Positive Regulation Of Catalytic Activity	-0.51	-0.31	-0.09	-1.19	-0.58	-0.06	0.21	-0.55	0.15	-0.52	0.12	-0.30	0.17	-0.10	0.57	0.48	0.49	0.44	0.21	0.58	0.51	0.28	0.12	-0.12	0.60481
Lipid Raft	-0.13	0.07	-0.50	-0.71	-0.92	-1.19	0.39	-0.73	0.42	-0.81	0.21	-0.17	0.49	0.06	0.36	0.19	0.11	0.42	0.54	0.73	0.48	0.14	0.24	0.30	0.6789
Transcription From Rna Polymerase Ii Promoter	-0.29	-0.65	-0.36	-0.41	-0.16	0.01	-0.34	-1.62	-0.58	0.43	-0.02	-0.11	0.29	-0.51	0.15	0.23	0.76	0.81	-0.14	0.17	0.35	0.33	0.46	1.19	0.68306
Regulation Of Transferase Activity	-0.58	-0.40	-0.25	-0.37	-0.76	-0.02	-0.21	-0.65	-0.12	-0.70	-0.04	-0.11	0.05	-0.07	0.44	0.41	0.53	0.51	0.48	0.47	0.54	0.44	0.10	0.29	0.69927
Anatomical Structure Development	-0.43	-0.53	-0.96	-0.25	-1.57	-1.17	0.44	-0.25	0.63	-0.47	0.51	-0.27	0.32	0.53	0.53	0.04	0.33	0.54	0.42	0.29	0.32	0.47	0.00	0.52	0.71939
Intracellular Organelle Part	-0.91	-0.60	-0.52	-1.08	-1.17	-0.02	0.37	-0.89	0.66	-0.90	0.51	0.01	-0.14	0.96	0.55	0.05	0.60	0.30	0.45	0.66	0.17	0.22	0.56	0.16	0.75524
Intracellular Non Membrane Bound Organelle	-0.73	-0.60	-0.56	-0.64	-1.15	-0.10	0.26	-0.77	0.42	-0.88	0.41	-0.21	0.17	0.40	0.46	0.30	0.72	0.21	0.48	0.46	0.31	0.38	0.53	0.14	0.75925
Non Membrane Bound Organelle	-0.73	-0.60	-0.56	-0.64	-1.15	-0.10	0.26	-0.77	0.42	-0.88	0.41	-0.21	0.17	0.40	0.46	0.30	0.72	0.21	0.48	0.46	0.31	0.38	0.53	0.14	0.75925
Organelle Part	-0.87	-0.57	-0.50	-1.13	-1.16	0.00	0.34	-0.90	0.65	-0.97	0.46	-0.01	-0.13	0.95	0.56	0.10	0.59	0.35	0.47	0.66	0.16	0.21	0.56	0.17	0.7769
Positive Regulation Of Cell Differentiation	-0.37	-0.18	-0.67	-0.59	-1.21	0.18	0.53	-0.76	0.75	-2.72	0.42	-0.24	0.41	0.47	0.38	0.36	0.46	0.54	0.29	0.79	0.67	0.29	0.11	0.09	0.81013
Lymphocyte Differentiation	-0.11	0.07	-0.26	-1.18	-1.05	0.16	0.64	-0.59	0.77	-3.31	0.28	-0.34	0.34	0.45	0.62	0.20	0.67	0.61	0.32	0.90	0.71	0.21	0.02	-0.13	0.81863
Regulation Of Cell Proliferation	-0.95	-0.61	-0.85	-0.04	-0.99	0.03	-0.26	-0.38	0.20	-0.25	-0.73	-0.13	0.04	0.06	0.42	0.51	0.92	0.54	0.82	0.05	0.23	0.30	0.60	0.48	0.82664
Cytokine Activity	-0.19	-0.31	-0.19	-0.92	-0.99	-0.33	0.38	-1.63	0.83	-1.43	0.61	-1.00	-0.25	0.94	0.96	0.84	0.64	0.80	0.87	1.12	0.25	-0.19	0.06	-0.88	0.85942
Immune System Development	-0.44	-0.22	-0.16	-0.95	-1.72	-0.80	0.61	-0.94	0.49	-1.90	0.60	-0.12	0.14	0.52	0.79	0.43	0.86	0.51	0.36	0.73	0.35	0.17	0.44	0.26	0.92638
Positive Regulation Of Immune System Process	-0.22	-0.27	-0.53	-1.31	-1.25	0.18	0.79	-0.84	0.81	-2.84	0.38	-0.61	0.63	0.63	0.58	0.25	0.60	0.59	0.35	0.87	0.74	0.44	0.01	0.03	0.95338
Cellular Cation Homeostasis	-1.32	-1.37	-1.60	-0.28	-1.83	-1.15	2.03	-0.64	0.26	-0.77	1.27	-0.47	0.94	0.58	0.40	0.39	-0.24	0.33	-0.27	1.07	1.03	0.60	0.63	0.41	0.9793
Receptor Signaling Protein Activity	-1.02	-0.70	-0.74	-0.49	-1.59	-0.74	0.51	-1.10	0.71	-1.10	0.77	-0.42	0.14	1.09	0.76	0.72	0.71	0.57	0.37	0.88	0.42	0.40	0.13	-0.28	0.98398
Receptor Binding	-0.50	-0.65	-0.35	-0.57	-1.25	-0.56	0.32	-1.52	0.66	-1.76	0.45	-0.85	-0.15	0.93	1.00	1.12	0.97	0.87	1.05	1.05	0.08	0.22	0.20	-0.74	1.10002
Hemopoiesis	-0.46	-0.20	-0.48	-1.19	-1.94	-0.41	0.89	-1.11	0.92	-3.33	0.73	-0.32	0.39	0.67	0.80	0.50	0.94	0.75	0.40	1.00	0.70	0.27	0.30	0.19	1.15044
Positive Regulation Of Translation	-0.30	-0.44	0.29	-1.79	-0.10	-0.16	-0.06	-1.32	-0.11	-1.88	-0.27	-1.69	0.12	1.83	1.41	1.27	1.29	0.91	1.04	1.22	0.07	-0.05	-0.44	-0.83	1.30493
Multi Organism Process	-0.04	-0.41	0.09	-1.85	-1.19	0.06	0.81	-1.92	0.54	-2.99	0.50	-1.59	-0.10	1.07	1.36	1.36	1.24	1.03	0.87	1.47	0.22	-0.16	0.53	-0.91	1.33227
Positive Regulation Of Cell Proliferation	-0.38	-0.16	-0.11	-1.82	-1.14	0.12	0.29	-1.86	0.34	-3.88	-0.06	-1.18	0.19	1.52	1.34	1.04	1.63	1.03	0.99	1.41	0.57	0.43	0.06	-0.38	1.64253
Cell Activation	-0.67	-0.70	-1.00	-1.32	-2.17	-0.43	0.47	-2.02	0.47	-3.38	0.08	-0.73	0.51	1.17	1.07	0.72	1.33	1.16	1.04	1.37	1.05	0.94	0.58	0.45	1.90093
Immune Response	-1.55	-0.97	-0.79	-3.10	-2.34	-1.40	1.43	-2.03	1.30	-2.46	1.41	-1.00	1.00	1.12	1.63	0.94	0.77	1.11	1.16	1.94	1.49	0.46	0.16	-0.28	1.91589
Immune System Process	-1.71	-1.13	-0.85	-2.59	-2.60	-1.78	1.15	-1.93	1.06	-2.26	1.39	-1.00	1.22	1.36	1.39	0.97	0.91	0.97	1.11	1.95	1.55	0.70	0.21	-0.10	2.03978

Table E4

mRNA name	**probe.ID**
CXCL2	M57731
IL6	NM_000600
IL1B	NM_000576
IL8	NM_000584
CCL7	NM_006273
PLAUR	U08839
PTGS2	NM_000963
CCL3	NM_002983
CCL20	NM_004591
TLR2	NM_003264
PPBP	R64130
ITGAX	M81695
TNFAIP6	NM_007115
ICAM1	NM_000201
NLRP3	NM_004895
S100A9	NM_002965
IL1R1	NM_000877
FCER1G	NM_004106
FCGR2A	NM_021642
NT5E	NM_002526
CRADD	U79115
HAVCR2	AW025572
LGALS3	BC001120
CCL4	NM_002984
CEBPB	AL564683
CLEC7A	AF313468
CCRL2	AF015524
GP1BB	NM_000407
ADA	NM_000022
FCGR2A	NM_021642
TLR4	U93091
TNFAIP6	NM_007115
ITGA2B	NM_000419
TNFRSF1B	NM_001066

Table E5

Diseases or Functions Annotation	-log p-Value	Predicted Activation State	Activation z-score	# Molecules	Molecules	Categories
Binding of blood cells	24.63827216	Decreased	-4.148	18	CCL20,CCL3,CCL4,CXCL2,CXCL8,FCGR2A,ICAM1,IL1B,IL6,ITGA2B,ITGAX,LGALS3,NT5E,PLAUR,PPBP,S100A9,TLR2,TLR4	Cell-To-Cell Signaling and Interaction
Binding of leukocytes	24.15366289	Decreased	-4.033	17	CCL20,CCL3,CCL4,CXCL2,CXCL8,FCGR2A,ICAM1,IL1B,IL6,ITGAX,LGALS3,NT5E,PLAUR,PPBP,S100A9,TLR2,TLR4	Cell-To-Cell Signaling and Interaction, Hematological System Development and Function
Adhesion of blood cells	23.93181414	Decreased	-3.884	17	CCL20,CCL4,CXCL2,CXCL8,FCGR2A,ICAM1,IL1B,IL6,ITGA2B,ITGAX,LGALS3,NT5E,PLAUR,PPBP,S100A9,TLR2,TLR4	Cell-To-Cell Signaling and Interaction
Inflammatory response	23.7721133	Decreased	-2.75	19	CCL20,CCL3,CCL4,CCL7,CEBPB,CXCL2,CXCL8,IL1B,IL1R1,IL6,LGALS3,NLRP3,PLAUR,PPBP,PTGS2,S100A9,TLR2,TLR4,TNFAIP6	Inflammatory Response
Adhesion of immune cells	23.08460016	Decreased	-3.766	16	CCL20,CCL4,CXCL2,CXCL8,FCGR2A,ICAM1,IL1B,IL6,ITGAX,LGALS3,NT5E,PLAUR,PPBP,S100A9,TLR2,TLR4	Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Immune Cell Trafficking
Cell movement of blood cells	21.46852108	Decreased	-3.411	18	CCL20,CCL3,CCL4,CCL7,CXCL2,CXCL8,FCGR2A,ICAM1,IL1B,IL6,ITGAX,LGALS3,PLAUR,PPBP,S100A9,TLR2,TLR4,TNFRSF1B	Cellular Movement

Activation of cells	20.83268267	Decreased	-3.352	18	ADA,CCL3,CCL7,CEBPB,CLEC7A,CXCL8,FCER1G,FCGR2A,HAVCR2,ICAM1,IL1B,IL1R1,IL6,LGALS3,NT5E,TLR2,TLR4,TNFRSF1B	Cell-To-Cell Signaling and Interaction
Cell movement of leukocytes	20.42945706	Decreased	-3.232	17	CCL20,CCL3,CCL4,CCL7,CXCL2,CXCL8,ICAM1,IL1B,IL6,ITGAX,LGALS3,PLAUR,PPBP,S100A9,TLR2,TLR4,TNFRSF1B	Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking
Activation of leukocytes	18.95860731	Decreased	-2.682	15	ADA,CCL3,CCL7,CLEC7A,CXCL8,FCER1G,FCGR2A,HAVCR2,IL1B,IL6,LGALS3,NT5E,TLR2,TLR4,TNFRSF1B	Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response
Chemotaxis of leukocytes	18.30891851	Decreased	-2.372	14	CCL20,CCL3,CCL4,CCL7,CXCL2,CXCL8,IL1B,IL6,LGALS3,PLAUR,PPBP,S100A9,TLR2,TLR4	Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response
Binding of myeloid cells	18.07007044	Decreased	-3.382	12	CCL3,CXCL2,CXCL8,FCGR2A,ICAM1,IL1B,ITGAX,LGALS3,PLAUR,PPBP,S100A9,TLR2	Cell-To-Cell Signaling and Interaction
Cell movement of myeloid cells	17.86327943	Decreased	-3.162	14	CCL20,CCL3,CCL4,CCL7,CXCL2,CXCL8,ICAM1,IL1B,ITGAX,LGALS3,PLAUR,PPBP,S100A9,TLR4	Cellular Movement
Cell movement of phagocytes	17.86327943	Decreased	-2.947	14	CCL20,CCL3,CCL4,CCL7,CXCL2,CXCL8,ICAM1,IL1B,ITGAX,LGALS3,PLAUR,PPBP,S100A9,TLR4	Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response

Cell movement of granulocytes	16.84771166	Decreased	-2.972	12	CCL3,CCL4,CCL7,CXCL2,CXCL8,ICAM1,IL1B,LGALS3,PLAUR,PPBP,S100A9,TLR4	Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking
Binding of professional phagocytic cells	16.66554625	Decreased	-3.248	11	CCL3,CXCL2,CXCL8,FCGR2A,ICAM1,IL1B,ITGAX,PLAUR,PPBP,S100A9,TLR2	Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Inflammatory Response
Chemotaxis	16.43415218	Decreased	-2.893	15	CCL20,CCL3,CCL4,CCL7,CXCL2,CXCL8,IL1B,IL6,LGALS3,PLAUR,PPBP,PTGS2,S100A9,TLR2,TLR4	Cellular Movement
Cell movement of neutrophils	16.4134127	Decreased	-2.634	11	CCL3,CCL4,CCL7,CXCL2,CXCL8,ICAM1,IL1B,LGALS3,PPBP,S100A9,TLR4	Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response
Chemotaxis of phagocytes	16.37778598	Decreased	-2.509	12	CCL20,CCL3,CCL4,CCL7,CXCL2,CXCL8,IL1B,LGALS3,PLAUR,PPBP,S100A9,TLR4	Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response
Binding of granulocytes	16.28316228	Decreased	-3.092	10	CXCL2,CXCL8,FCGR2A,ICAM1,IL1B,LGALS3,PLAUR,PPBP,S100A9,TLR2	Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Immune Cell Trafficking

Binding of neutrophils	16.05207638	Decreased	-2.931	9	CXCL2,CXCL8,FCGR2A,ICAM1,IL1B,PLAUR,PPBP,S100A9,TLR2	Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response
Adhesion of myeloid cells	15.80410035	Decreased	-3.086	10	CXCL2,CXCL8,ICAM1,IL1B,ITGAX,LGALS3,PLAUR,PPBP,S100A9,TLR2	Cell-To-Cell Signaling and Interaction
Cell movement of mononuclear leukocytes	15.80134291	Decreased	-2.735	13	CCL20,CCL3,CCL4,CCL7,CXCL8,ICAM1,IL1B,ITGAX,LGALS3,PLAUR,TLR2,TLR4,TNFRSF1B	Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking
Adhesion of granulocytes	15.11918641	Decreased	-2.939	9	CXCL2,CXCL8,ICAM1,IL1B,LGALS3,PLAUR,PPBP,S100A9,TLR2	Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Immune Cell Trafficking
Cell movement	14.92445304	Decreased	-4.331	22	CCL20,CCL3,CCL4,CCL7,CCRL2,CEBPB,CXCL2,CXCL8,FCGR2A,HAVCR2,ICAM1,IL1B,IL6,ITGAX,LGALS3,PLAUR,PPBP,PTGS2,S100A9,TLR2,TLR4,TNFRSF1B	Cellular Movement
Migration of cells	14.77728353	Decreased	-4.159	21	CCL20,CCL3,CCL4,CCL7,CCRL2,CEBPB,CXCL2,CXCL8,HAVCR2,ICAM1,IL1B,IL6,ITGAX,LGALS3,PLAUR,PPBP,PTGS2,S100A9,TLR2,TLR4,TNFRSF1B	Cellular Movement

Adhesion of phagocytes	14.58502665	Decreased	-2.94	9	CXCL2,CXCL8,ICAM1,IL1B,ITGAX,PLAUR,PPBP,S100A9,TLR2	Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response
Adhesion of neutrophils	14.54363397	Decreased	-2.772	8	CXCL2,CXCL8,ICAM1,IL1B,PLAUR,PPBP,S100A9,TLR2	Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response
Chemotaxis of myeloid cells	14.50031292	Decreased	-2.489	11	CCL3,CCL4,CCL7,CXCL2,CXCL8,IL1B,LGALS3,PLAUR,PPBP,S100A9,TLR4	Cellular Movement
Binding of tumor cell lines	14.34294415	Decreased	-3.058	14	CCL3,CCL4,CXCL2,CXCL8,FCGR2A,GP1BB,ICAM1,IL1B,IL6,ITGAX,LGALS3,PLAUR,TLR2,TLR4	Cell-To-Cell Signaling and Interaction
Interaction of mononuclear leukocytes	13.95467702	Decreased	-3.122	10	CCL20,CCL3,CCL4,ICAM1,IL6,ITGAX,NT5E,PLAUR,TLR2,TLR4	Cell-To-Cell Signaling and Interaction, Hematological System Development and Function
Cell movement of peripheral blood leukocytes	13.42945706	Decreased	-2.016	8	CCL20,CCL3,CCL4,CCL7,CXCL8,ICAM1,PLAUR,TLR2	Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking
Chemotaxis of granulocytes	12.90657831	Decreased	-2.263	9	CCL3,CCL7,CXCL2,CXCL8,LGALS3,PLAUR,PPBP,S100A9,TLR4	Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response

Binding of endothelial cells	12.74472749	Decreased	-3.037	10	CCL3,CCL4,CXCL2,CXCL8,ICAM1,IL1B,LGALS3,NT5E,PLAUR,PPBP	Cardiovascular System Development and Function, Cell-To-Cell Signaling and Interaction
Activation of phagocytes	12.69680394	Decreased	-2.448	9	CCL3,CCL7,CXCL8,HAVCR2,IL1B,IL6,TLR2,TLR4,TNFRSF1B	Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response
Cell movement of monocytes	12.59687948	Decreased	-2.586	9	CCL20,CCL3,CCL4,CCL7,CXCL8,IL1B,ITGAX,LGALS3,PLAUR	Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response
Migration of phagocytes	12.3419886	Decreased	-2.484	9	CCL20,CCL3,CCL4,CCL7,CXCL8,ICAM1,IL1B,ITGAX,LGALS3	Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response
Binding of mononuclear leukocytes	12.28066871	Decreased	-2.958	9	CCL20,CCL3,CCL4,ICAM1,IL6,ITGAX,NT5E,PLAUR,TLR4	Cell-To-Cell Signaling and Interaction, Hematological System Development and Function
Adhesion of endothelial cells	12.25026368	Decreased	-2.931	9	CCL3,CCL4,CXCL2,CXCL8,ICAM1,IL1B,LGALS3,PLAUR,PPBP	Cardiovascular System Development and Function, Cell-To-Cell Signaling and Interaction

Migration of mononuclear leukocytes	12.21609642	Decreased	-2.955	10	CCL20,CCL3,CCL4,CCL7,CXCL8,ICAM1,ITGAX,LGALS3,TLR4,TNFRSF1B	Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking
Quantity of ca2+	11.4867824	Decreased	-2.915	10	CCL3,CCL4,CCL7,CXCL8,FCGR2A,IL1B,IL6,PLAUR,PPBP,S100A9	Cell Signaling, Molecular Transport, Vitamin and Mineral Metabolism
Adhesion of tumor cell lines	11.27736608	Decreased	-2.679	11	CCL3,CCL4,CXCL2,CXCL8,GP1BB,ICAM1,IL6,ITGAX,LGALS3,PLAUR,TLR2	Cell-To-Cell Signaling and Interaction
Cell movement of tumor cell lines	10.838632	Decreased	-3.721	16	CCL20,CCL3,CCL4,CCL7,CEBPB,CXCL2,CXCL8,HAVCR2,IL1B,IL6,LGALS3,PLAUR,PTGS2,S100A9,TLR2,TLR4	Cellular Movement
Synthesis of reactive oxygen species	10.56703071	Decreased	-3.057	10	CLEC7A,CXCL8,FCGR2A,IL1B,IL6,ITGAX,PLAUR,PTGS2,TLR2,TLR4	Free Radical Scavenging
Chemotaxis of monocytes	10.33068312	Decreased	-2.195	7	CCL3,CCL4,CCL7,CXCL8,IL1B,LGALS3,PLAUR	Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response
Activation of antigen presenting cells	10.2541448	Decreased	-2.007	7	CCL3,HAVCR2,IL1B,IL6,TLR2,TLR4,TNFRSF1B	Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response

Cell movement of eosinophils	10.09258864	Decreased	-2.207	6	CCL3,CCL7,CXCL8,IL1B,LGALS3,PLAUR	Cellular Movement, Hematological System Development and Function, Hypersensitivity Response, Immune Cell Trafficking
Immune response of cells	10.03952922	Decreased	-2.751	10	CLEC7A,CXCL8,FCER1G,FCGR2A,IL1B,IL6,LGALS3,S100A9,TLR2,TLR4	Inflammatory Response
Adhesion of mononuclear leukocytes	9.863279433	Decreased	-2.608	7	CCL20,CCL4,ICAM1,IL6,ITGAX,PLAUR,TLR4	Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Immune Cell Trafficking
Activation of myeloid cells	9.795880017	Decreased	-2.381	7	CCL3,CCL7,CXCL8,FCGR2A,IL1B,TLR2,TLR4	Cell-To-Cell Signaling and Interaction, Hematological System Development and Function
Mobilization of ca2+	9.752026734	Decreased	-2.518	9	CCL3,CCL4,CCL7,CXCL8,FCER1G,FCGR2A,LGALS3,PLAUR,TLR2	Cell Signaling, Molecular Transport, Vitamin and Mineral Metabolism
Migration of tumor cell lines	9.588380294	Decreased	-3.507	14	CCL20,CCL7,CEBPB,CXCL2,CXCL8,HAVCR2,IL1B,IL6,LGALS3,PLAUR,PTGS2,S100A9,TLR2,TLR4	Cellular Movement
Interaction of lymphocytes	9.458420756	Decreased	-2.607	7	CCL20,CCL4,ICAM1,IL6,NT5E,TLR2,TLR4	Cell-To-Cell Signaling and Interaction, Hematological System Development and Function

Recruitment of leukocytes	9.446116973	Decreased	-2.19	5	CCL3,CCL7,CXCL8,IL1B,TNFRSF1B	Cell-To-Cell Signaling and Interaction, Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking
Cell movement of carcinoma cell lines	9.412289035	Decreased	-2.933	9	CCL3,CCL4,CCL7,CEBPB,CXCL8,IL1B,IL6,PTGS2,TLR2	Cellular Movement
Migration of antigen presenting cells	9.388276692	Decreased	-2.028	6	CCL20,CCL3,CCL4,CCL7,IL1B,LGALS3	Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking
Migration of lymphatic system cells	9.364516253	Decreased	-2.765	8	CCL20,CCL3,CCL4,CXCL8,ICAM1,IL6,TLR4,TNFRSF1B	Cellular Movement, Immune Cell Trafficking
Cell viability of blood cells	9.289036881	Decreased	-2.595	7	CCL3,CXCL8,ICAM1,IL1B,IL6,PPBP,TLR4	Cell Death and Survival
Migration of peripheral blood leukocytes	9.083546051	Decreased	-2.219	5	CCL3,CCL4,CCL7,CXCL8,ICAM1	Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking
Proliferation of smooth muscle cells	9.027334408	Decreased	-2.586	7	CCL3,CXCL8,IL1B,IL6,PLAUR,TLR2,TLR4	Cellular Development, Cellular Growth and Proliferation, Organ Development, Skeletal and Muscular System Development and Function, Tissue Development
Production of reactive oxygen species	8.88941029	Decreased	-2.736	8	CLEC7A,CXCL8,FCGR2A,IL1B,ITGAX,PTGS2,TLR2,TLR4	Free Radical Scavenging
Binding of leukemia cell lines	8.628932138	Decreased	-2.087	7	CCL3,CCL4,GP1BB,ICAM1,IL6,PLAUR,TLR2	Cell-To-Cell Signaling and Interaction

Cell movement of smooth muscle cells	8.448550002	Decreased	-2.383	6	CCL3,CXCL2,IL1B,IL6,PLAUR,PTGS2	Cellular Movement, Skeletal and Muscular System Development and Function
Migration of myeloid cells	8.415668776	Decreased	-2.193	6	CCL3,CXCL8,ICAM1,IL1B,ITGAX,PLAUR	Cellular Movement
Lymphocyte migration	8.074172425	Decreased	-2.604	7	CCL20,CCL3,CCL4,CXCL8,ICAM1,TLR4,TNFRSF1B	Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking
Cell viability of leukocytes	7.920818754	Decreased	-2.425	6	CXCL8,ICAM1,IL1B,IL6,PPBP,TLR4	Cell Death and Survival
Cell viability of myeloid cells	7.853871964	Decreased	-2.224	5	CXCL8,ICAM1,IL1B,PPBP,TLR4	Cell Death and Survival, Hematological System Development and Function
Migration of PBMCs	7.850780887	Decreased	-2	4	CCL3,CCL4,CCL7,CXCL8	Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking
Adhesion of leukemia cell lines	7.841637508	Decreased	-2.418	6	CCL3,CCL4,GP1BB,ICAM1,PLAUR,TLR2	Cell-To-Cell Signaling and Interaction
Binding of lymphocytes	7.841637508	Decreased	-2.408	6	CCL20,CCL4,ICAM1,IL6,NT5E,TLR4	Cell-To-Cell Signaling and Interaction, Hematological System Development and Function
Flux of ca2+	7.815308569	Decreased	-2.57	7	CCL20,CCL3,CCL4,CCL7,CXCL8,PPBP,TLR2	Cell Signaling, Cellular Function and Maintenance, Molecular Transport, Vitamin and Mineral Metabolism
Cell movement of vascular smooth muscle cells	7.630784143	Decreased	-2.236	5	CCL3,IL1B,IL6,PLAUR,PTGS2	Cellular Movement, Skeletal and Muscular System Development and Function

Proliferation of vascular smooth muscle cells	7.508638306	Decreased	-2.236	5	CXCL8,IL1B,PLAUR,TLR2,TLR4	Cardiovascular System Development and Function, Cellular Development, Cellular Growth and Proliferation, Organ Development, Skeletal and Muscular System Development and Function, Tissue Development
Cellular homeostasis	7.390405591	Decreased	-3.041	12	CCL20,CCL3,CCL4,CCL7,CXCL8,ICAM1,IL1B,IL6,NT5E,PPBP,S100A9,TLR2	Cellular Function and Maintenance
Binding of vascular endothelial cells	7.331614083	Decreased	-2.411	6	CXCL8,ICAM1,LGALS3,NT5E,PLAUR,PPBP	Cardiovascular System Development and Function, Cell-To-Cell Signaling and Interaction
Chemotaxis of tumor cell lines	7.331614083	Decreased	-2.221	6	CCL20,CCL3,CCL4,CCL7,CXCL8,PLAUR	Cellular Movement
Migration of granulocytes	7.211831629	Decreased	-2.193	5	CCL3,CXCL8,ICAM1,IL1B,PLAUR	Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking
Migration of carcinoma cell lines	7.142667504	Decreased	-2.6	7	CCL7,CEBPB,CXCL8,IL1B,IL6,PTGS2,TLR2	Cellular Movement
Cell movement of epithelial cell lines	7.130181792	Decreased	-2.2	6	CCL20,CCRL2,ICAM1,PLAUR,PTGS2,TLR2	Cellular Movement, Hair and Skin Development and Function
Cell viability	7.106238238	Decreased	-2.628	13	CCL3,CEBPB,CXCL8,ICAM1,IL1B,IL6,LGALS3,PLAUR,PPBP,PTGS2,S100A9,TLR2,TLR4	Cell Death and Survival
Migration of smooth muscle cells	7.045757491	Decreased	-2.169	5	CXCL2,IL1B,IL6,PLAUR,PTGS2	Cellular Movement, Skeletal and Muscular System Development and Function

Binding of lymphoma cell lines	6.863279433	Decreased	-2.194	5	CXCL2,ICAM1,IL1B,IL6,ITGAX	Cell-To-Cell Signaling and Interaction
Adhesion of vascular endothelial cells	6.301899454	Decreased	-2.179	5	CXCL8,ICAM1,LGALS3,PLAUR,PPBP	Cardiovascular System Development and Function, Cell-To-Cell Signaling and Interaction
Cell movement of t lymphocytes	6.109578981	Decreased	-2.222	5	CCL20,CCL3,CCL4,CXCL8,ICAM1	Cell-mediated Immune Response, Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking
Migration of vascular smooth muscle cells	5.991399828	Decreased	-2	4	IL1B,IL6,PLAUR,PTGS2	Cellular Movement, Skeletal and Muscular System Development and Function
Engulfment of cells	5.452225295	Decreased	-2.177	6	CEBPB,CLEC7A,FCGR2A,IL1B,IL6,LGALS3	Cellular Function and Maintenance
Differentiation of mononuclear leukocytes	4.716698771	Decreased	-2.096	5	CXCL8,IL1B,IL6,TLR2,TLR4	Cellular Development, Cellular Growth and Proliferation, Hematological System Development and Function, Hematopoiesis, Lymphoid Tissue Structure and Development, Tissue Development
Invasion of cells	4.581698709	Decreased	-2.897	9	CEBPB,CXCL8,HAVCR2,IL1B,IL6,LGALS3,PLAUR,PTGS2,S100A9	Cellular Movement
Concentration of lipid	4.278189385	Decreased	-2.163	5	CXCL8,FCER1G,IL1B,PPBP,PTGS2	Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry

Invasion of tumor cell lines	4.014573526	Decreased	-2.697	8	CEBPB,CXCL8,HAVCR2,IL6,LGALS3,PLAUR,PTGS2,S100A9	Cellular Movement

Table E6

Ingenuity Canonical Pathways	**-log(p-value)**	**Ratio**	**z-score**	**Downregulated**	**No change**	**Upregulated**	**No overlap with**	**Molecules**
TREM1 Signaling	17	0.143	-3.162	10/70 (14%)	0/70 (0%)	0/70 (0%)	60/70 (86%)	TLR2,CXCL8,TLR4,ICAM1,NLRP3,IL1B,IL6,CCL3,ITGAX,CCL7
Osteoarthritis Pathway	10.5	0.0439	-2.646	9/205 (4%)	0/205 (0%)	0/205 (0%)	196/205 (96%)	TLR2,CXCL8,TLR4,S100A9,IL1B,CEBPB,PTGS2,IL1R1,TNFRSF1B
Dendritic Cell Maturation	9.33	0.0435	-2.646	8/184 (4%)	0/184 (0%)	0/184 (0%)	176/184 (96%)	TLR2,TLR4,ICAM1,FCGR2A,FCER1G,IL1B,IL6,TNFRSF1B
LXR/RXR Activation	9.05	0.0579	2.646	7/121 (6%)	0/121 (0%)	0/121 (0%)	114/121 (94%)	TLR4,IL1B,IL6,PTGS2,IL1R1,TNFRSF1B,CCL7
IL-6 Signaling	8.88	0.0547	-2.646	7/128 (5%)	0/128 (0%)	0/128 (0%)	121/128 (95%)	CXCL8,TNFAIP6,IL1B,IL6,CEBPB,IL1R1,TNFRSF1B
Role of Pattern Recognition Receptors in Recognition of Bacteria and Viruses	8.81	0.0534	-2.236	7/131 (5%)	0/131 (0%)	0/131 (0%)	124/131 (95%)	TLR2,CXCL8,TLR4,CLEC7A,NLRP3,IL1B,IL6
Role of IL-17F in Allergic Inflammatory Airway Diseases	8.21	0.122	-2.236	5/41 (12%)	0/41 (0%)	0/41 (0%)	36/41 (88%)	CXCL8,CCL4,IL1B,IL6,CCL7
Inflammasome pathway	7.45	0.19	-2	4/21 (19%)	0/21 (0%)	0/21 (0%)	17/21 (81%)	CXCL8,TLR4,NLRP3,IL1B
NF-κB Signaling	6.4	0.0337	-2.449	6/178 (3%)	0/178 (0%)	0/178 (0%)	172/178 (97%)	TLR2,TLR4,FCER1G,IL1B,IL1R1,TNFRSF1B
Acute Phase Response Signaling	5.11	0.0296	-2.236	5/169 (3%)	0/169 (0%)	0/169 (0%)	164/169 (97%)	IL1B,IL6,CEBPB,IL1R1,TNFRSF1B
PPAR Signaling	4.82	0.0435	2	4/92 (4%)	0/92 (0%)	0/92 (0%)	88/92 (96%)	IL1B,PTGS2,IL1R1,TNFRSF1B
Type I Diabetes Mellitus Signaling	4.56	0.0374	-2	4/107 (4%)	0/107 (0%)	0/107 (0%)	103/107 (96%)	FCER1G,IL1B,IL1R1,TNFRSF1B
IL-8 Signaling	3.54	0.0204	-2	4/196 (2%)	0/196 (0%)	0/196 (0%)	192/196 (98%)	CXCL8,ICAM1,PTGS2,ITGAX
LPS/IL-1 Mediated Inhibition of RXR Function	3.44	0.0192	-2	4/208 (2%)	0/208 (0%)	0/208 (0%)	204/208 (98%)	TLR4,IL1B,IL1R1,TNFRSF1B
Colorectal Cancer Metastasis Signaling	3.19	0.0165	-2	4/243 (2%)	0/243 (0%)	0/243 (0%)	239/243 (98%)	TLR2,TLR4,IL6,PTGS2

Table E7-1: Candidated marker genes and selected marker genes used in analysis of validation cohort

Cell subset	**Marker gene type**	**n**	**Marker gene name**																					
T cells	Candidate	20	CD3D	LTB	TRBC1	CD2	LCK	ITK	CD247	CD3E	BCL11B	KIR2DS1	CD27	CD69	GZMK	PTPRCAP	ZAP70	CD3G	NKG7	DGKA	CD6	SH2D1A		
	Selected	8	CD3D	TRBC1	CD2	LCK	CD27	PTPRCAP	ZAP70	CD6														
CD8 T cells	Candidate	20	IL7R	CD8A	GZMK	GZMH	CD3E	PIK3IP1	CST7	DUSP2	GNLY	CD8B	TCF7	NCR3	MAP4K1	CD6	CRTAM	LY9	ZGPAT	FLT3LG	CDC14B	KLRF1		
	Selected	4	CD8A	GZMK	CD8B	TCF7																		
CD4 T cells	Candidate	21	LAT	IL9	ASGR2	ZFP36L2	PBXIP1	ETS1	ACAP1	ANGPT4	CD40LG	IL3	GAL3ST4	RPL10L	VILL	EPHA1	RRP9	ORC1	EPB41	ZNF204P	CXorf57	FBXL8	CD28	
	Selected	4	LAT	PBXIP1	ACAP1	CD28																		
Monocytes	Candidate	15	FCN1	MNDA	S100A12	FPR1	HCK	LST1	TLR2	RNASE2	FOSB	CHST15	VNN2	CCR2	CD1D	CSF3R	CLEC7A							
	Selected	5	S100A12	FPR1	HCK	LST1	CLEC7A																	
Macrophages	Candidate	20	MMP9	CXCL9	CD40	CD38	APOL3	CYP27B1	SLAMF1	NPL	CCL23	BHLHE41	CXCL5	PPBP	QPCT	CCL14	DCSTAMP	RENBP	ADAM28	CHI3L1	CXCL3	CCL7		
	Selected	5	MMP9	CXCL5	PPBP	CXCL3	CCL7																	
Macrophages(M2)	Candidate	22	MS4A6A	CCL18	ADRB2	CD4	CLEC4A	CCL13	SLC15A3	CLEC10A	CCL23	ADAM28	NPL	TREM2	SIGLEC1	P2RY13	CCL8	CD68	CD209	CCL14	CLIC2	HRH1	CHI3L1	CFP
	Selected	5	CLEC4A	SLC15A3	NPL	CLIC2	CFP																	
B cells	Candidate	21	IGK	IGHM	MS4A1	CD37	CD79A	SELL	P2RX5	GUSBP11	IRF8	BANK1	IGLL3P	LY86	IGHD	IL4R	TCL1A	CD19	KIAA0226L	HLA-DOB	SIK1	CD79B	FAM65B	
	Selected	7	IGK	IGHM	CD37	CD79A	SELL	CD19	CD79B															
DCs	Candidate	21	CCL22	LAMP3	IDO1	MMP12	CD1B	ACP5	CD1A	HLA-DQA1	CXCL10	BIRC3	PLA2G7	CD1E	FPR3	KYNU	RNASE6	CCL13	TNFAIP6	CCL17	RSAD2	CLIC2	TREM2	
	Selected	5	LAMP3	PLA2G7	KYNU	TNFAIP6	CLIC2																	
DCs(activated)	Candidate	21	LAMP3	IDO1	CXCL10	BIRC3	TNFAIP6	RSAD2	KYNU	CCL17	CD80	CD86	FPR3	IFI44L	CXCL11	MMP12	CHST7	CCL19	AQP9	RASSF4	IL12B	CD1B	NR4A3	

	Selected	5	LAMP3	IDO1	TNFAIP6	KYNU	NR4A3																
NK cells	Candidate	21	CCL4	IL2RB	APOBEC3A	IL18RAP	TBX21	CCND2	KIR2DS1	FASLG	TXK	TTC38	CD244	DEFA4	CD160	PLEKHF1	KIR2DL2	PRR5L	IL12RB2	IL18R1	CAMP	KIR3DL1	CEACAM8
	Selected	4	IL2RB	FASLG	PRR5L	IL18RAP																	

Total number of candidate marker genes: 202

Total number of selected marker gene: 52

Table E7-2: Pairwise similarity across 134 subjects in validation cohort (T cells)

Similarity metrix	**CD3D**	**LTB**	**TRBC1**	**CD2**	**LCK**	**ITK**	**CD247**	**CD3E**	**BCL11B**	**KIR2DS1**	**CD27**	**CD69**	**GZMK**	**PTPRCAP**	**ZAP70**	**CD3G**	**NKG7**	**DGKA**	**CD6**	**SH2D1A**	**Probe #**
CD3D	1.00	0.62	0.78	0.73	0.74	0.51	0.43	0.37	0.46	-0.20	0.64	0.19	0.56	0.69	0.60	0.34	0.31	0.58	0.59	0.35	213539_at
LTB	0.62	1.00	0.70	0.60	0.68	0.36	0.54	0.17	0.52	-0.24	0.65	0.17	0.52	0.63	0.44	0.41	0.41	0.57	0.48	0.49	207339_s_at
TRBC1	0.78	0.70	1.00	0.79	0.84	0.50	0.42	0.43	0.46	-0.19	0.72	0.12	0.56	0.68	0.59	0.31	0.49	0.62	0.71	0.39	213193_x_at
CD2	0.73	0.60	0.79	1.00	0.84	0.70	0.49	0.48	0.58	-0.19	0.66	0.32	0.70	0.72	0.68	0.41	0.60	0.74	0.72	0.53	205831_at
LCK	0.74	0.68	0.84	0.84	1.00	0.58	0.37	0.51	0.57	-0.24	0.72	0.22	0.57	0.75	0.69	0.34	0.54	0.72	0.70	0.46	204891_s_at
ITK	0.51	0.36	0.50	0.70	0.58	1.00	0.48	0.33	0.45	-0.15	0.30	0.63	0.59	0.42	0.43	0.19	0.25	0.49	0.49	0.49	211339_s_at
CD247	0.43	0.54	0.42	0.49	0.37	0.48	1.00	0.01	0.55	-0.07	0.30	0.35	0.50	0.27	0.19	0.21	0.45	0.46	0.38	0.63	210031_at
CD3E	0.37	0.17	0.43	0.48	0.51	0.33	0.01	1.00	0.24	-0.07	0.30	0.02	0.33	0.32	0.32	0.18	0.28	0.36	0.48	0.12	205456_at
BCL11B	0.46	0.52	0.46	0.58	0.57	0.45	0.55	0.24	1.00	-0.09	0.46	0.39	0.56	0.32	0.35	0.11	0.45	0.44	0.49	0.64	219528_s_at
KIR2DS1	-0.20	-0.24	-0.19	-0.19	-0.24	-0.15	-0.07	-0.07	-0.09	1.00	-0.21	0.05	-0.06	-0.18	-0.30	-0.10	-0.16	-0.16	-0.08	-0.17	211532_x_at
CD27	0.64	0.65	0.72	0.66	0.72	0.30	0.30	0.30	0.46	-0.21	1.00	-0.11	0.53	0.73	0.58	0.36	0.52	0.62	0.53	0.39	206150_at

CD69	0.19	0.17	0.12	0.32	0.22	0.63	0.35	0.02	0.39	0.05	-0.11	1.00	0.33	0.06	0.12	0.08	0.03	0.16	0.22	0.36	209795_at
GZMK	0.56	0.52	0.56	0.70	0.57	0.59	0.50	0.33	0.56	-0.06	0.53	0.33	1.00	0.43	0.44	0.26	0.58	0.39	0.55	0.60	206666_at
PTPRCAP	0.69	0.63	0.68	0.72	0.75	0.42	0.27	0.32	0.32	-0.18	0.73	0.06	0.43	1.00	0.60	0.45	0.49	0.80	0.53	0.25	204960_at
ZAP70	0.60	0.44	0.59	0.68	0.69	0.43	0.19	0.32	0.35	-0.30	0.58	0.12	0.44	0.60	1.00	0.32	0.37	0.51	0.57	0.36	214032_at
CD3G	0.34	0.41	0.31	0.41	0.34	0.19	0.21	0.18	0.11	-0.10	0.36	0.08	0.26	0.45	0.32	1.00	0.21	0.39	0.25	0.13	206804_at
NKG7	0.31	0.41	0.49	0.60	0.54	0.25	0.45	0.28	0.45	-0.16	0.52	0.03	0.58	0.49	0.37	0.21	1.00	0.48	0.43	0.54	213915_at
DGKA	0.58	0.57	0.62	0.74	0.72	0.49	0.46	0.36	0.44	-0.16	0.62	0.16	0.39	0.80	0.51	0.39	0.48	1.00	0.57	0.39	203385_at
CD6	0.59	0.48	0.71	0.72	0.70	0.49	0.38	0.48	0.49	-0.08	0.53	0.22	0.55	0.53	0.57	0.25	0.43	0.57	1.00	0.34	213958_at
SH2D1A	0.35	0.49	0.39	0.53	0.46	0.49	0.63	0.12	0.64	-0.17	0.39	0.36	0.60	0.25	0.36	0.13	0.54	0.39	0.34	1.00	210116_at

Table E7-3: Pairwise similarity across 134 subjects in validation cohort (CD8 T cells)

Similarity metrix	**IL7R**	**CD8A**	**GZMK**	**GZMH**	**CD3E**	**PIK3IP1**	**CST7**	**DUSP2**	**GNLY**	**CD8B**	**TCF7**	**NCR3**	**MAP4K1**	**CD6**	**CRTAM**	**LY9**	**ZGPAT**	**FLT3LG**	**CDC14B**	**KLRF1**	**Probe #**
IL7R	1.00	0.02	0.15	0.00	0.12	0.60	-0.13	-0.15	-0.28	0.18	-0.06	-0.06	0.10	0.19	0.08	0.23	-0.07	0.11	-0.14	-0.01	205798_at
CD8A	0.02	1.00	0.55	0.38	0.19	0.28	0.46	0.18	0.53	0.53	0.44	0.19	0.43	0.60	0.29	0.09	0.27	0.29	-0.16	0.32	205758_at
GZMK	0.15	0.55	1.00	0.50	0.33	0.39	0.23	-0.31	0.30	0.63	0.54	0.12	0.44	0.55	0.48	0.01	0.20	0.29	-0.25	0.43	206666_at
GZMH	0.00	0.38	0.50	1.00	0.08	0.22	0.65	0.14	0.51	0.17	0.09	-0.06	0.18	0.26	0.22	0.20	0.32	0.09	-0.01	0.75	210321_at
CD3E	0.12	0.19	0.33	0.08	1.00	0.24	-0.01	-0.26	-0.04	0.31	0.32	0.01	0.39	0.48	0.21	0.04	0.17	0.35	-0.08	0.12	205456_at

PIK3IP1	0.60	0.28	0.39	0.22	0.24	1.00	0.08	-0.23	-0.14	0.38	0.03	-0.02	0.36	0.41	0.03	0.17	0.00	0.19	-0.11	0.09	221756_at
CST7	-0.13	0.46	0.23	0.65	-0.01	0.08	1.00	0.47	0.73	0.01	0.01	0.00	0.22	0.23	-0.01	0.23	0.34	0.05	0.05	0.58	210140_at
DUSP2	-0.15	0.18	-0.31	0.14	-0.26	-0.23	0.47	1.00	0.43	-0.40	-0.35	-0.01	-0.16	-0.09	-0.21	0.18	0.16	-0.21	0.23	0.18	204794_at
GNLY	-0.28	0.53	0.30	0.51	-0.04	-0.14	0.73	0.43	1.00	0.08	0.21	0.11	0.24	0.32	0.16	0.19	0.41	0.05	-0.01	0.55	205495_s_at
CD8B	0.18	0.53	0.63	0.17	0.31	0.38	0.01	-0.40	0.08	1.00	0.58	0.13	0.53	0.55	0.34	0.01	0.20	0.50	-0.41	0.06	207979_s_at
TCF7	-0.06	0.44	0.54	0.09	0.32	0.03	0.01	-0.35	0.21	0.58	1.00	0.26	0.49	0.52	0.36	-0.13	0.11	0.36	-0.20	0.06	205255_x_at
NCR3	-0.06	0.19	0.12	-0.06	0.01	-0.02	0.00	-0.01	0.11	0.13	0.26	1.00	0.07	0.11	-0.13	-0.25	-0.15	-0.13	-0.04	-0.07	210763_x_at
MAP4K1	0.10	0.43	0.44	0.18	0.39	0.36	0.22	-0.16	0.24	0.53	0.49	0.07	1.00	0.61	0.21	0.19	0.41	0.51	-0.23	0.02	214339_s_at
CD6	0.19	0.60	0.55	0.26	0.48	0.41	0.23	-0.09	0.32	0.55	0.52	0.11	0.61	1.00	0.31	0.13	0.35	0.43	-0.16	0.13	213958_at
CRTAM	0.08	0.29	0.48	0.22	0.21	0.03	-0.01	-0.21	0.16	0.34	0.36	-0.13	0.21	0.31	1.00	0.09	0.31	0.43	-0.29	0.24	206914_at
LY9	0.23	0.09	0.01	0.20	0.04	0.17	0.23	0.18	0.19	0.01	-0.13	-0.25	0.19	0.13	0.09	1.00	0.38	0.25	-0.05	0.28	215967_s_at
ZGPAT	-0.07	0.27	0.20	0.32	0.17	0.00	0.34	0.16	0.41	0.20	0.11	-0.15	0.41	0.35	0.31	0.38	1.00	0.46	-0.24	0.38	57539_at
FLT3LG	0.11	0.29	0.29	0.09	0.35	0.19	0.05	-0.21	0.05	0.50	0.36	-0.13	0.51	0.43	0.43	0.25	0.46	1.00	-0.37	0.02	210607_at
CDC14B	-0.14	-0.16	-0.25	-0.01	-0.08	-0.11	0.05	0.23	-0.01	-0.41	-0.20	-0.04	-0.23	-0.16	-0.29	-0.05	-0.24	-0.37	1.00	-0.08	221555_x_at
KLRF1	-0.01	0.32	0.43	0.75	0.12	0.09	0.58	0.18	0.55	0.06	0.06	-0.07	0.02	0.13	0.24	0.28	0.38	0.02	-0.08	1.00	220646_s_at

Table E7-4: Pairwise similarity across 134 subjects in validation cohort (CD4 T cells)

Similarity metrix	LAT	IL9	ASGR2	ZFP36L2	PBXIP1	ETS1	ACAP1	ANGPT4	CD40LG	IL3	GAL3ST4	RPL10L	VILL	EPHA1	RRP9	ORC1	EPB41	ZNF204P	CXorf57	FBXL8	CD28	Probe #	
LAT	1.00	-0.10	0.02	0.06	0.47	0.01	0.65	-0.25	0.00	-0.03	-0.01	0.24	0.39	0.39	0.15	0.12	-0.14	0.26	0.37	0.09	0.53	211005_at	
IL9	-0.10	1.00	0.22	0.03	-0.11	-0.19	-0.05	0.18	0.16	0.15	0.04	0.10	0.01	0.17	0.07	0.01	-0.27	-0.13	-0.25	0.03	-0.21	208193_at	
ASGR2	0.02	0.22	1.00	-0.06	-0.07	-0.06	-0.12	0.20	0.13	0.23	0.04	0.14	0.06	-0.02	-0.12	0.21	-0.22	-0.06	-0.26	0.03	-0.17	206130_s_at	
ZFP36L2	0.06	0.03	-0.06	1.00	0.50	0.30	0.23	-0.35	-0.25	0.10	0.13	0.20	0.32	-0.02	0.04	0.11	0.13	0.35	0.37	0.09	0.40	201368_at	
PBXIP1	0.47	-0.11	-0.07	0.50	1.00	0.18	0.53	-0.31	-0.21	-0.03	0.27	0.21	0.38	0.10	0.13	0.10	-0.02	0.37	0.44	0.16	0.61	214177_s_at	
ETS1	0.01	-0.19	-0.06	0.30	0.18	1.00	0.10	-0.14	-0.09	-0.01	-0.09	-0.08	0.04	-0.12	-0.10	-0.02	0.14	0.10	0.35	0.00	0.25	214447_at	
ACAP1	0.65	-0.05	-0.12	0.23	0.53	0.10	1.00	-0.26	0.03	-0.04	0.08	0.28	0.55	0.48	0.29	0.15	-0.04	0.38	0.35	0.29	0.53	205213_at	
ANGPT4	-0.25	0.18	0.20	-0.35	-0.31	-0.14	-0.26	1.00	0.25	0.03	-0.15	-0.14	-0.06	0.12	-0.04	0.11	-0.09	-0.32	-0.37	-0.03	-0.29	221134_at	
CD40LG	0.00	0.16	0.13	-0.25	-0.21	-0.09	0.03	0.25	1.00	0.08	-0.15	0.03	-0.04	0.20	0.10	-0.05	-0.11	-0.11	-0.16	0.18	-0.26	207892_at	
IL3	-0.03	0.15	0.23	0.10	-0.03	-0.01	-0.04	0.03	0.08	1.00	-0.03	0.11	0.10	-0.14	0.00	0.14	0.02	-0.13	-0.05	0.00	-0.09	207906_at	
GAL3ST4	-0.01	0.04	0.04	0.13	0.27	-0.09	0.08	-0.15	-0.15	-0.03	1.00	-0.03	0.09	0.01	0.13	0.03	-0.14	0.04	-0.07	0.15	-0.06	219815_at	
RPL10L	0.24	0.10	0.14	0.20	0.21	-0.08	0.28	-0.14	0.03	0.11	-0.03	1.00	0.21	0.09	0.14	0.19	-0.24	0.07	-0.02	0.04	0.18	217559_at	
VILL	0.39	0.01	0.06	0.32	0.38	0.04	0.55	-0.06	-0.04	0.10	0.09	0.21	1.00	0.32	0.26	0.26	0.13	0.26	0.27	0.24	0.35	209950_s_at	
EPHA1	0.39	0.17	-0.02	-0.02	0.10	-0.12	0.48	0.12	0.20	-0.14	0.01	0.09	0.32	1.00	0.37	0.15	-0.10	0.08	-0.01	0.25	0.14	205977_s_at	
RRP9	0.15	0.07	-0.12	0.04	0.13	-0.10	0.29	-0.04	0.10	0.00	0.13	0.14	0.26	0.37	1.00	0.16	-0.07	0.01	0.02	0.34	0.04	204133_at	

ORC1	0.12	0.01	0.21	0.11	0.10	-0.02	0.15	0.11	-0.05	0.14	0.03	0.19	0.26	0.15	0.16	1.00	-0.07	0.07	0.02	0.09	0.09	205085_at	
EPB41	-0.14	-0.27	-0.22	0.13	-0.02	0.14	-0.04	-0.09	-0.11	0.02	-0.14	-0.24	0.13	-0.10	-0.07	-0.07	1.00	0.31	0.24	0.09	0.19	207793_s_at	
ZNF204P	0.26	-0.13	-0.06	0.35	0.37	0.10	0.38	-0.32	-0.11	-0.13	0.04	0.07	0.26	0.08	0.01	0.07	0.31	1.00	0.43	0.17	0.47	214823_at	
CXorf57	0.37	-0.25	-0.26	0.37	0.44	0.35	0.35	-0.37	-0.16	-0.05	-0.07	-0.02	0.27	-0.01	0.02	0.02	0.24	0.43	1.00	0.14	0.52	219355_at	
FBXL8	0.09	0.03	0.03	0.09	0.16	0.00	0.29	-0.03	0.18	0.00	0.15	0.04	0.24	0.25	0.34	0.09	0.09	0.17	0.14	1.00	0.05	220080_at	
CD28	0.53	-0.21	-0.17	0.40	0.61	0.25	0.53	-0.29	-0.26	-0.09	-0.06	0.18	0.35	0.14	0.04	0.09	0.19	0.47	0.52	0.05	1.00	206545_at	

Table E7-5: Pairwise similarity across 134 subjects in validation cohort (Monocytes)

Similarity metrix	**FCN1**	**MNDA**	**S100A12**	**FPR1**	**HCK**	**LST1**	**TLR2**	**RNASE2**	**FOSB**	**CHST15**	**VNN2**	**CCR2**	**CD1D**	**CSF3R**	**CLEC7A**	**Probe #**
FCN1	1.00	0.47	0.55	0.58	0.29	0.59	0.38	0.18	-0.10	0.52	-0.03	0.43	-0.06	0.41	0.59	205237_at
MNDA	0.47	1.00	0.36	0.23	0.18	0.30	0.24	-0.05	-0.12	0.24	0.16	0.42	0.08	0.22	0.29	204959_at
S100A12	0.55	0.36	1.00	0.79	0.80	0.72	0.74	0.10	-0.14	0.50	0.22	0.37	-0.08	0.39	0.74	205863_at
FPR1	0.58	0.23	0.79	1.00	0.64	0.72	0.65	0.16	-0.16	0.46	0.08	0.37	-0.09	0.41	0.69	205119_s_at
HCK	0.29	0.18	0.80	0.64	1.00	0.62	0.76	-0.07	-0.08	0.41	0.24	0.31	-0.02	0.26	0.59	208018_s_at
LST1	0.59	0.30	0.72	0.72	0.62	1.00	0.69	0.10	-0.02	0.59	0.07	0.35	-0.13	0.36	0.73	214574_x_at
TLR2	0.38	0.24	0.74	0.65	0.76	0.69	1.00	-0.01	-0.05	0.65	0.08	0.22	-0.16	0.31	0.75	204924_at
RNASE2	0.18	-0.05	0.10	0.16	-0.07	0.10	-0.01	1.00	0.06	0.09	-0.10	-0.08	-0.19	0.07	0.15	206111_at

FOSB	-0.10	-0.12	-0.14	-0.16	-0.08	-0.02	-0.05	0.06	1.00	0.11	-0.12	-0.13	0.06	0.14	-0.07	202768_at
CHST15	0.52	0.24	0.50	0.46	0.41	0.59	0.65	0.09	0.11	1.00	0.06	0.08	0.13	0.31	0.58	203066_at
VNN2	-0.03	0.16	0.22	0.08	0.24	0.07	0.08	-0.10	-0.12	0.06	1.00	0.05	0.13	-0.05	0.06	205922_at
CCR2	0.43	0.42	0.37	0.37	0.31	0.35	0.22	-0.08	-0.13	0.08	0.05	1.00	0.03	0.21	0.32	206978_at
CD1D	-0.06	0.08	-0.08	-0.09	-0.02	-0.13	-0.16	-0.19	0.06	0.13	0.13	0.03	1.00	-0.08	-0.20	205789_at
CSF3R	0.41	0.22	0.39	0.41	0.26	0.36	0.31	0.07	0.14	0.31	-0.05	0.21	-0.08	1.00	0.39	203591_s_at
CLEC7A	0.59	0.29	0.74	0.69	0.59	0.73	0.75	0.15	-0.07	0.58	0.06	0.32	-0.20	0.39	1.00	221698_s_at

Table E7-6: Pairwise similarity across 134 subjects in validation cohort (Macrophages)

Similarity metrix	**MMP9**	**CXCL9**	**CD40**	**CD38**	**APOL3**	**CYP27B1**	**SLAMF1**	**NPL**	**CCL23**	**BHLHE41**	**CXCL5**	**PPBP**	**QPCT**	**CCL14**	**DCSTAMP**	**RENBP**	**ADAM28**	**CHI3L1**	**CXCL3**	**CCL7**	**Probe #**
MMP9	1.00	-0.43	-0.28	0.11	-0.48	0.00	-0.33	0.66	0.19	-0.18	0.57	0.65	0.12	-0.06	-0.23	0.08	0.07	0.08	0.57	0.71	203936_s_at
CXCL9	-0.43	1.00	0.38	0.07	0.42	0.04	0.21	-0.25	-0.05	-0.01	-0.26	-0.38	-0.14	0.08	0.33	0.03	-0.25	-0.10	-0.32	-0.26	203915_at
CD40	-0.28	0.38	1.00	-0.04	0.02	0.28	-0.11	-0.19	-0.01	0.02	-0.10	-0.18	-0.26	0.17	0.34	0.31	-0.23	0.22	-0.08	-0.20	35150_at
CD38	0.11	0.07	-0.04	1.00	0.26	-0.07	0.11	-0.17	0.01	-0.02	0.15	-0.05	0.12	-0.06	-0.17	-0.07	0.20	0.02	0.00	0.12	205692_s_at
APOL3	-0.48	0.42	0.02	0.26	1.00	-0.20	0.53	-0.37	-0.15	0.11	-0.36	-0.58	0.21	-0.08	0.03	-0.20	0.13	-0.25	-0.53	-0.35	221087_s_at
CYP27B1	0.00	0.04	0.28	-0.07	-0.20	1.00	-0.20	0.01	0.21	0.12	-0.13	-0.12	-0.15	0.03	0.25	0.22	-0.27	0.37	-0.03	0.07	205676_at
SLAMF1	-0.33	0.21	-0.11	0.11	0.53	-0.20	1.00	-0.27	-0.22	0.23	-0.13	-0.45	0.23	-0.20	-0.25	-0.25	0.27	-0.11	-0.36	-0.30	206181_at

NPL	0.66	-0.25	-0.19	-0.17	-0.37	0.01	-0.27	1.00	0.11	-0.13	0.32	0.49	0.07	-0.04	-0.11	0.11	0.04	0.06	0.38	0.58	221210_s_at
CCL23	0.19	-0.05	-0.01	0.01	-0.15	0.21	-0.22	0.11	1.00	-0.15	-0.03	0.15	-0.23	0.11	0.09	0.16	-0.14	0.16	0.25	0.00	210549_s_at
BHLHE41	-0.18	-0.01	0.02	-0.02	0.11	0.12	0.23	-0.13	-0.15	1.00	-0.18	-0.36	0.28	-0.09	-0.16	-0.02	0.22	-0.05	-0.18	-0.18	221530_s_at
CXCL5	0.57	-0.26	-0.10	0.15	-0.36	-0.13	-0.13	0.32	-0.03	-0.18	1.00	0.68	0.19	-0.08	-0.19	-0.10	0.17	-0.02	0.57	0.64	215101_s_at
PPBP	0.65	-0.38	-0.18	-0.05	-0.58	-0.12	-0.45	0.49	0.15	-0.36	0.68	1.00	-0.11	-0.01	-0.11	0.07	0.02	0.06	0.72	0.59	214146_s_at
QPCT	0.12	-0.14	-0.26	0.12	0.21	-0.15	0.23	0.07	-0.23	0.28	0.19	-0.11	1.00	-0.23	-0.27	-0.24	0.33	-0.21	-0.24	0.18	205174_s_at
CCL14	-0.06	0.08	0.17	-0.06	-0.08	0.03	-0.20	-0.04	0.11	-0.09	-0.08	-0.01	-0.23	1.00	0.27	0.18	-0.21	0.14	0.09	-0.02	205392_s_at
DCSTAMP	-0.23	0.33	0.34	-0.17	0.03	0.25	-0.25	-0.11	0.09	-0.16	-0.19	-0.11	-0.27	0.27	1.00	0.21	-0.52	0.03	-0.06	-0.07	221266_s_at
RENBP	0.08	0.03	0.31	-0.07	-0.20	0.22	-0.25	0.11	0.16	-0.02	-0.10	0.07	-0.24	0.18	0.21	1.00	-0.23	0.29	0.08	0.00	206617_s_at
ADAM28	0.07	-0.25	-0.23	0.20	0.13	-0.27	0.27	0.04	-0.14	0.22	0.17	0.02	0.33	-0.21	-0.52	-0.23	1.00	-0.12	0.08	0.01	205997_at
CHI3L1	0.08	-0.10	0.22	0.02	-0.25	0.37	-0.11	0.06	0.16	-0.05	-0.02	0.06	-0.21	0.14	0.03	0.29	-0.12	1.00	0.15	-0.12	209396_s_at
CXCL3	0.57	-0.32	-0.08	0.00	-0.53	-0.03	-0.36	0.38	0.25	-0.18	0.57	0.72	-0.24	0.09	-0.06	0.08	0.08	0.15	1.00	0.44	207850_at
CCL7	0.71	-0.26	-0.20	0.12	-0.35	0.07	-0.30	0.58	0.00	-0.18	0.64	0.59	0.18	-0.02	-0.07	0.00	0.01	-0.12	0.44	1.00	208075_s_at

Table E7-7: Pairwise similarity across 134 subjects in validation cohort (Macrophages-M2)

Similarity metrix	**MS4A6A**	**CCL18**	**ADRB2**	**CD4**	**CLEC4A**	**CCL13**	**SLC15A3**	**CLEC10A**	**CCL23**	**ADAM28**	**NPL**	**TREM2**	**SIGLEC1**	**P2RY13**	**CCL8**	**CD68**	**CD209**	**CCL14**	**CLIC2**	**HRH1**	**CHI3L1**	**CFP**	**Probe #**
MS4A6A	1.00	0.31	-0.16	0.19	-0.12	0.37	0.09	0.18	0.25	-0.28	0.16	0.43	0.41	0.15	0.05	0.10	0.24	0.01	-0.01	0.24	0.18	0.05	219666_at

CCL18	0.31	1.00	-0.15	0.17	-0.21	0.37	0.09	0.12	0.19	-0.26	0.04	0.31	0.28	0.17	-0.07	0.11	0.13	0.27	-0.07	0.14	0.21	-0.04	209924_at
ADRB2	-0.16	-0.15	1.00	-0.09	0.11	-0.04	-0.05	-0.05	-0.12	0.03	-0.04	-0.15	-0.16	0.07	0.04	0.01	-0.02	-0.11	0.06	-0.08	-0.05	-0.10	206170_at
CD4	0.19	0.17	-0.09	1.00	-0.25	0.32	-0.12	0.13	0.20	-0.16	-0.22	0.29	0.18	0.06	0.14	-0.11	0.17	0.23	-0.26	0.04	0.23	-0.12	203547_at
CLEC4A	-0.12	-0.21	0.11	-0.25	1.00	-0.11	0.55	0.04	-0.02	0.13	0.49	-0.17	0.08	-0.08	-0.01	0.42	-0.21	-0.22	0.55	0.12	-0.06	0.69	219947_at
CCL13	0.37	0.37	-0.04	0.32	-0.11	1.00	0.15	0.24	0.20	-0.31	0.01	0.45	0.45	0.09	-0.01	0.13	0.30	0.19	-0.07	0.20	0.43	0.09	206407_s_at
SLC15A3	0.09	0.09	-0.05	-0.12	0.55	0.15	1.00	0.29	0.27	0.05	0.62	0.13	0.38	-0.04	0.11	0.64	-0.08	-0.04	0.51	0.36	0.20	0.70	219593_at
CLEC10A	0.18	0.12	-0.05	0.13	0.04	0.24	0.29	1.00	0.16	-0.08	0.25	0.27	0.35	-0.06	0.07	0.31	0.00	0.16	0.13	0.07	0.27	0.24	206682_at
CCL23	0.25	0.19	-0.12	0.20	-0.02	0.20	0.27	0.16	1.00	-0.14	0.11	0.17	0.25	0.04	-0.03	0.21	0.00	0.11	-0.04	0.07	0.16	0.07	210549_s_at
ADAM28	-0.28	-0.26	0.03	-0.16	0.13	-0.31	0.05	-0.08	-0.14	1.00	0.04	-0.46	-0.27	-0.29	-0.03	-0.03	-0.38	-0.21	0.28	-0.08	-0.12	0.09	205997_at
NPL	0.16	0.04	-0.04	-0.22	0.49	0.01	0.62	0.25	0.11	0.04	1.00	0.04	0.29	0.01	-0.04	0.61	0.04	-0.04	0.36	0.27	0.06	0.52	221210_s_at
TREM2	0.43	0.31	-0.15	0.29	-0.17	0.45	0.13	0.27	0.17	-0.46	0.04	1.00	0.53	0.31	0.01	0.15	0.41	0.26	-0.18	0.14	0.34	0.02	219725_at
SIGLEC1	0.41	0.28	-0.16	0.18	0.08	0.45	0.38	0.35	0.25	-0.27	0.29	0.53	1.00	0.21	0.01	0.41	0.34	0.08	0.10	0.18	0.34	0.29	44673_at
P2RY13	0.15	0.17	0.07	0.06	-0.08	0.09	-0.04	-0.06	0.04	-0.29	0.01	0.31	0.21	1.00	-0.03	0.08	0.19	0.22	-0.09	0.05	0.09	-0.08	220005_at
CCL8	0.05	-0.07	0.04	0.14	-0.01	-0.01	0.11	0.07	-0.03	-0.03	-0.04	0.01	0.01	-0.03	1.00	0.07	-0.09	-0.02	-0.01	0.16	0.02	0.16	214038_at
CD68	0.10	0.11	0.01	-0.11	0.42	0.13	0.64	0.31	0.21	-0.03	0.61	0.15	0.41	0.08	0.07	1.00	0.09	0.01	0.36	0.25	0.12	0.47	203507_at
CD209	0.24	0.13	-0.02	0.17	-0.21	0.30	-0.08	0.00	0.00	-0.38	0.04	0.41	0.34	0.19	-0.09	0.09	1.00	0.08	-0.13	0.03	0.21	-0.21	207277_at

CCL14	0.01	0.27	-0.11	0.23	-0.22	0.19	-0.04	0.16	0.11	-0.21	-0.04	0.26	0.08	0.22	-0.02	0.01	0.08	1.00	-0.16	0.15	0.14	-0.08	205392_s_at
CLIC2	-0.01	-0.07	0.06	-0.26	0.55	-0.07	0.51	0.13	-0.04	0.28	0.36	-0.18	0.10	-0.09	-0.01	0.36	-0.13	-0.16	1.00	0.27	0.02	0.54	213415_at
HRH1	0.24	0.14	-0.08	0.04	0.12	0.20	0.36	0.07	0.07	-0.08	0.27	0.14	0.18	0.05	0.16	0.25	0.03	0.15	0.27	1.00	0.20	0.32	205579_at
CHI3L1	0.18	0.21	-0.05	0.23	-0.06	0.43	0.20	0.27	0.16	-0.12	0.06	0.34	0.34	0.09	0.02	0.12	0.21	0.14	0.02	0.20	1.00	0.09	209396_s_at
CFP	0.05	-0.04	-0.10	-0.12	0.69	0.09	0.70	0.24	0.07	0.09	0.52	0.02	0.29	-0.08	0.16	0.47	-0.21	-0.08	0.54	0.32	0.09	1.00	206380_s_at

Table E7-8: Pairwise similarity across 134 subjects in validation cohort (B cells)

Similarity metrix	**IGK**	**IGHM**	**MS4A1**	**CD37**	**CD79A**	**SELL**	**P2RX5**	**GUSBP11**	**IRF8**	**BANK1**	**IGLL3P**	**LY86**	**IGHD**	**IL4R**	**TCL1A**	**CD19**	**KIAA0226L**	**HLA-DOB**	**SIK1**	**CD79B**	**FAM65B**	**Probe #**
IGK	1.00	0.70	0.31	0.57	0.59	0.30	0.06	0.64	0.38	0.41	0.68	0.10	0.29	-0.08	0.45	0.62	0.15	0.46	-0.16	0.65	0.41	221651_x_at
IGHM	0.70	1.00	0.39	0.63	0.69	0.53	0.26	0.59	0.45	0.51	0.58	0.11	0.13	0.15	0.53	0.72	0.15	0.35	0.05	0.70	0.38	209374_s_at
MS4A1	0.31	0.39	1.00	0.46	0.42	0.33	0.07	0.25	0.29	0.53	0.13	0.16	0.14	0.01	0.16	0.42	0.20	0.07	-0.03	0.45	0.36	210356_x_at
CD37	0.57	0.63	0.46	1.00	0.62	0.50	0.33	0.51	0.26	0.39	0.43	0.17	0.17	0.12	0.27	0.54	0.09	0.30	0.06	0.66	0.46	204192_at
CD79A	0.59	0.69	0.42	0.62	1.00	0.57	0.54	0.55	0.34	0.39	0.46	0.26	0.08	0.20	0.36	0.73	0.03	0.34	0.09	0.69	0.33	205049_s_at
SELL	0.30	0.53	0.33	0.50	0.57	1.00	0.47	0.26	0.38	0.39	0.26	0.16	0.04	0.18	0.33	0.56	-0.11	0.33	0.03	0.46	0.45	204563_at
P2RX5	0.06	0.26	0.07	0.33	0.54	0.47	1.00	0.20	0.34	0.22	0.12	0.22	-0.20	0.37	0.18	0.38	-0.18	0.11	0.34	0.33	0.00	210448_s_at
GUSBP11	0.64	0.59	0.25	0.51	0.55	0.26	0.20	1.00	0.25	0.32	0.70	-0.05	0.07	0.06	0.32	0.43	0.20	0.24	0.02	0.58	0.28	213502_x_at
IRF8	0.38	0.45	0.29	0.26	0.34	0.38	0.34	0.25	1.00	0.58	0.28	0.17	0.02	-0.14	0.30	0.48	-0.05	0.32	0.04	0.34	0.19	204057_at

BANK1	0.41	0.51	0.53	0.39	0.39	0.39	0.22	0.32	0.58	1.00	0.36	0.07	0.10	0.01	0.27	0.53	0.18	0.11	0.16	0.52	0.39	219667_s_at
IGLL3P	0.68	0.58	0.13	0.43	0.46	0.26	0.12	0.70	0.28	0.36	1.00	-0.03	0.05	0.05	0.36	0.51	0.17	0.28	-0.04	0.56	0.32	215946_x_at
LY86	0.10	0.11	0.16	0.17	0.26	0.16	0.22	-0.05	0.17	0.07	-0.03	1.00	0.11	-0.05	0.12	0.26	-0.23	0.14	-0.01	0.09	-0.09	205859_at
IGHD	0.29	0.13	0.14	0.17	0.08	0.04	-0.20	0.07	0.02	0.10	0.05	0.11	1.00	-0.23	-0.09	0.13	-0.02	0.12	-0.05	0.13	0.15	214973_x_at
IL4R	-0.08	0.15	0.01	0.12	0.20	0.18	0.37	0.06	-0.14	0.01	0.05	-0.05	-0.23	1.00	0.20	0.06	0.31	-0.10	0.59	0.13	-0.07	203233_at
TCL1A	0.45	0.53	0.16	0.27	0.36	0.33	0.18	0.32	0.30	0.27	0.36	0.12	-0.09	0.20	1.00	0.41	0.24	0.36	0.01	0.44	0.01	209995_s_at
CD19	0.62	0.72	0.42	0.54	0.73	0.56	0.38	0.43	0.48	0.53	0.51	0.26	0.13	0.06	0.41	1.00	-0.09	0.44	-0.02	0.65	0.40	206398_s_at
KIAA0226L	0.15	0.15	0.20	0.09	0.03	-0.11	-0.18	0.20	-0.05	0.18	0.17	-0.23	-0.02	0.31	0.24	-0.09	1.00	-0.03	0.32	0.25	0.05	219471_at
HLA-DOB	0.46	0.35	0.07	0.30	0.34	0.33	0.11	0.24	0.32	0.11	0.28	0.14	0.12	-0.10	0.36	0.44	-0.03	1.00	-0.12	0.30	0.09	205671_s_at
SIK1	-0.16	0.05	-0.03	0.06	0.09	0.03	0.34	0.02	0.04	0.16	-0.04	-0.01	-0.05	0.59	0.01	-0.02	0.32	-0.12	1.00	0.00	-0.16	208078_s_at
CD79B	0.65	0.70	0.45	0.66	0.69	0.46	0.33	0.58	0.34	0.52	0.56	0.09	0.13	0.13	0.44	0.65	0.25	0.30	0.00	1.00	0.38	205297_s_at
FAM65B	0.41	0.38	0.36	0.46	0.33	0.45	0.00	0.28	0.19	0.39	0.32	-0.09	0.15	-0.07	0.01	0.40	0.05	0.09	-0.16	0.38	1.00	206707_x_at

Table E7-9: Pairwise similarity across 134 subjects in validation cohort (DCs)

Similarity metrix	**CCL22**	**LAMP3**	**IDO1**	**MMP12**	**CD1B**	**ACP5**	**CD1A**	**HLA-DQA1**	**CXCL10**	**BIRC3**	**PLA2G7**	**CD1E**	**FPR3**	**KYNU**	**RNASE6**	**CCL13**	**TNFAIP6**	**CCL17**	**RSAD2**	**CLIC2**	**TREM2**	**Probe #**
CCL22	1.00	0.55	0.35	0.07	-0.12	0.11	0.02	0.12	-0.07	-0.08	0.25	-0.10	-0.23	0.36	-0.03	0.02	0.27	-0.01	-0.19	0.23	-0.06	207861_at
LAMP3	0.55	1.00	0.72	-0.01	-0.21	-0.07	-0.09	0.05	-0.09	-0.05	0.54	-0.23	-0.15	0.68	0.20	-0.08	0.48	-0.27	0.27	0.49	-0.19	205569_at

IDO1	0.35	0.72	1.00	0.03	-0.19	-0.08	-0.08	0.12	-0.10	-0.07	0.39	-0.15	-0.10	0.46	0.16	0.06	0.35	-0.11	0.14	0.37	-0.07	210029_at
MMP12	0.07	-0.01	0.03	1.00	0.18	-0.11	0.31	0.01	0.00	-0.18	0.03	0.15	0.18	-0.04	0.04	0.19	-0.10	0.17	-0.11	0.02	0.28	204580_at
CD1B	-0.12	-0.21	-0.19	0.18	1.00	-0.10	0.35	-0.08	-0.03	-0.04	-0.23	0.10	-0.06	-0.20	-0.21	0.34	-0.15	0.19	-0.17	-0.22	0.32	206749_at
ACP5	0.11	-0.07	-0.08	-0.11	-0.10	1.00	-0.16	0.61	-0.16	0.45	-0.23	0.09	-0.16	-0.35	-0.34	-0.27	-0.28	-0.12	0.16	-0.17	-0.23	204638_at
CD1A	0.02	-0.09	-0.08	0.31	0.35	-0.16	1.00	-0.22	-0.02	-0.20	-0.04	0.17	0.05	-0.04	-0.15	0.27	-0.02	0.37	-0.06	0.00	0.42	210325_at
HLA-DQA1	0.12	0.05	0.12	0.01	-0.08	0.61	-0.22	1.00	-0.08	0.45	0.01	-0.11	0.00	-0.07	-0.13	-0.16	-0.08	-0.16	0.13	0.05	-0.22	212671_s_at
CXCL10	-0.07	-0.09	-0.10	0.00	-0.03	-0.16	-0.02	-0.08	1.00	-0.17	0.26	-0.08	0.09	0.13	0.24	-0.06	0.07	-0.01	-0.20	0.10	-0.05	204533_at
BIRC3	-0.08	-0.05	-0.07	-0.18	-0.04	0.45	-0.20	0.45	-0.17	1.00	-0.32	-0.02	-0.35	-0.28	-0.50	-0.30	-0.11	-0.15	0.20	-0.08	-0.40	210538_s_at
PLA2G7	0.25	0.54	0.39	0.03	-0.23	-0.23	-0.04	0.01	0.26	-0.32	1.00	-0.20	0.34	0.85	0.61	-0.02	0.54	-0.12	0.16	0.59	-0.05	206214_at
CD1E	-0.10	-0.23	-0.15	0.15	0.10	0.09	0.17	-0.11	-0.08	-0.02	-0.20	1.00	0.00	-0.30	-0.18	0.11	-0.23	0.20	-0.05	-0.17	0.29	215784_at
FPR3	-0.23	-0.15	-0.10	0.18	-0.06	-0.16	0.05	0.00	0.09	-0.35	0.34	0.00	1.00	0.20	0.48	0.05	-0.13	0.03	0.01	0.07	0.10	214560_at
KYNU	0.36	0.68	0.46	-0.04	-0.20	-0.35	-0.04	-0.07	0.13	-0.28	0.85	-0.30	0.20	1.00	0.58	0.00	0.68	-0.19	0.13	0.66	-0.13	217388_s_at
RNASE6	-0.03	0.20	0.16	0.04	-0.21	-0.34	-0.15	-0.13	0.24	-0.50	0.61	-0.18	0.48	0.58	1.00	-0.03	0.34	-0.16	-0.01	0.41	-0.05	213566_at
CCL13	0.02	-0.08	0.06	0.19	0.34	-0.27	0.27	-0.16	-0.06	-0.30	-0.02	0.11	0.05	0.00	-0.03	1.00	0.09	0.32	-0.13	-0.07	0.45	206407_s_at
TNFAIP6	0.27	0.48	0.35	-0.10	-0.15	-0.28	-0.02	-0.08	0.07	-0.11	0.54	-0.23	-0.13	0.68	0.34	0.09	1.00	-0.08	0.14	0.48	-0.05	206025_s_at
CCL17	-0.01	-0.27	-0.11	0.17	0.19	-0.12	0.37	-0.16	-0.01	-0.15	-0.12	0.20	0.03	-0.19	-0.16	0.32	-0.08	1.00	-0.15	-0.19	0.34	207900_at

RSAD2	-0.19	0.27	0.14	-0.11	-0.17	0.16	-0.06	0.13	-0.20	0.20	0.16	-0.05	0.01	0.13	-0.01	-0.13	0.14	-0.15	1.00	0.15	-0.10	213797_at
CLIC2	0.23	0.49	0.37	0.02	-0.22	-0.17	0.00	0.05	0.10	-0.08	0.59	-0.17	0.07	0.66	0.41	-0.07	0.48	-0.19	0.15	1.00	-0.18	213415_at
TREM2	-0.06	-0.19	-0.07	0.28	0.32	-0.23	0.42	-0.22	-0.05	-0.40	-0.05	0.29	0.10	-0.13	-0.05	0.45	-0.05	0.34	-0.10	-0.18	1.00	219725_at

Table E7-10: Pairwise similarity across 134 subjects in validation cohort (DCs activated)

Similarity metrix	**LAMP3**	**IDO1**	**CXCL10**	**BIRC3**	**TNFAIP6**	**RSAD2**	**KYNU**	**CCL17**	**CD80**	**CD86**	**FPR3**	**IFI44L**	**CXCL11**	**MMP12**	**CHST7**	**CCL19**	**AQP9**	**RASSF4**	**IL12B**	**CD1B**	**NR4A3**	**Probe #**
LAMP3	1.00	0.72	-0.09	-0.05	0.48	0.27	0.68	-0.27	-0.04	0.46	-0.15	0.24	-0.05	-0.01	0.01	-0.01	-0.16	0.21	-0.08	-0.21	0.52	205569_at
IDO1	0.72	1.00	-0.10	-0.07	0.35	0.14	0.46	-0.11	-0.06	0.42	-0.10	0.08	0.08	0.03	-0.05	0.13	-0.06	0.14	-0.14	-0.19	0.32	210029_at
CXCL10	-0.09	-0.10	1.00	-0.17	0.07	-0.20	0.13	-0.01	-0.20	0.12	0.09	-0.15	0.31	0.00	0.06	-0.01	-0.03	0.15	0.01	-0.03	0.16	204533_at
BIRC3	-0.05	-0.07	-0.17	1.00	-0.11	0.20	-0.28	-0.15	-0.12	-0.22	-0.35	0.17	0.05	-0.18	-0.18	-0.22	-0.16	-0.28	0.00	-0.04	-0.14	210538_s_at
TNFAIP6	0.48	0.35	0.07	-0.11	1.00	0.14	0.68	-0.08	0.12	0.28	-0.13	0.07	-0.05	-0.10	0.45	0.06	-0.04	0.29	0.02	-0.15	0.49	206025_s_at
RSAD2	0.27	0.14	-0.20	0.20	0.14	1.00	0.13	-0.15	-0.01	-0.09	0.01	0.79	-0.06	-0.11	0.05	-0.15	-0.16	0.17	-0.05	-0.17	-0.13	213797_at
KYNU	0.68	0.46	0.13	-0.28	0.68	0.13	1.00	-0.19	0.01	0.69	0.20	-0.05	-0.10	-0.04	0.42	-0.05	-0.09	0.51	-0.04	-0.20	0.63	217388_s_at
CCL17	-0.27	-0.11	-0.01	-0.15	-0.08	-0.15	-0.19	1.00	0.14	-0.25	0.03	-0.07	-0.06	0.17	-0.23	0.20	0.29	-0.03	0.11	0.19	-0.18	207900_at
CD80	-0.04	-0.06	-0.20	-0.12	0.12	-0.01	0.01	0.14	1.00	-0.03	0.04	-0.07	-0.08	0.25	0.23	0.28	0.33	0.02	0.15	0.12	0.04	207176_s_at
CD86	0.46	0.42	0.12	-0.22	0.28	-0.09	0.69	-0.25	-0.03	1.00	0.26	-0.24	-0.07	0.06	0.39	-0.08	-0.02	0.36	-0.11	-0.18	0.52	210895_s_at
FPR3	-0.15	-0.10	0.09	-0.35	-0.13	0.01	0.20	0.03	0.04	0.26	1.00	-0.11	-0.01	0.18	0.17	-0.06	0.00	0.32	-0.06	-0.06	0.01	214560_at

IFI44L	0.24	0.08	-0.15	0.17	0.07	0.79	-0.05	-0.07	-0.07	-0.24	-0.11	1.00	-0.02	-0.05	-0.23	-0.08	-0.13	0.05	0.07	-0.08	-0.20	204439_at
CXCL11	-0.05	0.08	0.31	0.05	-0.05	-0.06	-0.10	-0.06	-0.08	-0.07	-0.01	-0.02	1.00	0.02	-0.05	0.08	-0.01	-0.13	-0.01	0.03	-0.05	211122_s_at
MMP12	-0.01	0.03	0.00	-0.18	-0.10	-0.11	-0.04	0.17	0.25	0.06	0.18	-0.05	0.02	1.00	-0.03	0.21	0.25	0.03	0.13	0.18	-0.06	204580_at
CHST7	0.01	-0.05	0.06	-0.18	0.45	0.05	0.42	-0.23	0.23	0.39	0.17	-0.23	-0.05	-0.03	1.00	-0.14	-0.10	0.21	-0.06	-0.19	0.35	206756_at
CCL19	-0.01	0.13	-0.01	-0.22	0.06	-0.15	-0.05	0.20	0.28	-0.08	-0.06	-0.08	0.08	0.21	-0.14	1.00	0.37	0.05	0.08	0.18	-0.03	210072_at
AQP9	-0.16	-0.06	-0.03	-0.16	-0.04	-0.16	-0.09	0.29	0.33	-0.02	0.00	-0.13	-0.01	0.25	-0.10	0.37	1.00	-0.05	0.19	0.27	-0.09	1556459_at
RASSF4	0.21	0.14	0.15	-0.28	0.29	0.17	0.51	-0.03	0.02	0.36	0.32	0.05	-0.13	0.03	0.21	0.05	-0.05	1.00	-0.05	-0.17	0.30	49306_at
IL12B	-0.08	-0.14	0.01	0.00	0.02	-0.05	-0.04	0.11	0.15	-0.11	-0.06	0.07	-0.01	0.13	-0.06	0.08	0.19	-0.05	1.00	0.18	0.03	207901_at
CD1B	-0.21	-0.19	-0.03	-0.04	-0.15	-0.17	-0.20	0.19	0.12	-0.18	-0.06	-0.08	0.03	0.18	-0.19	0.18	0.27	-0.17	0.18	1.00	-0.18	206749_at
NR4A3	0.52	0.32	0.16	-0.14	0.49	-0.13	0.63	-0.18	0.04	0.52	0.01	-0.20	-0.05	-0.06	0.35	-0.03	-0.09	0.30	0.03	-0.18	1.00	209959_at

Table E7-11: Pairwise similarity across 134 subjects in validation cohort (NK cells)

Similarity metrix	**CCL4**	**IL2RB**	**APOBEC3A**	**IL18RAP**	**TBX21**	**CCND2**	**KIR2DS1**	**FASLG**	**TXK**	**TTC38**	**CD244**	**DEFA4**	**CD160**	**PLEKHF1**	**KIR2DL2**	**PRR5L**	**IL12RB2**	**IL18R1**	**CAMP**	**KIR3DL1**	**CEACAM8**	**Probe #**
CCL4	1.00	-0.16	-0.05	-0.13	-0.19	-0.15	0.01	-0.32	-0.08	0.07	-0.19	-0.09	-0.19	-0.32	0.00	-0.21	0.08	-0.12	-0.07	0.05	0.07	204103_at
IL2RB	-0.16	1.00	-0.09	0.35	0.47	0.61	-0.10	0.54	0.24	0.07	0.44	-0.05	0.16	0.29	-0.42	0.68	0.30	0.27	-0.25	-0.16	-0.25	205291_at
APOBEC3A	-0.05	-0.09	1.00	-0.01	0.01	-0.11	0.10	-0.05	0.01	0.14	-0.03	-0.03	-0.03	-0.07	0.01	-0.02	-0.03	-0.04	-0.01	0.01	-0.04	210873_x_at
IL18RAP	-0.13	0.35	-0.01	1.00	0.57	0.14	0.10	0.51	0.19	0.17	0.32	-0.18	0.05	0.22	-0.01	0.63	-0.12	0.56	-0.35	-0.01	0.04	207072_at

TBX21	-0.19	0.47	0.01	0.57	1.00	0.35	-0.07	0.44	0.08	0.08	0.35	-0.16	0.30	0.33	-0.25	0.53	-0.01	0.40	-0.37	-0.12	-0.13	220684_at
CCND2	-0.15	0.61	-0.11	0.14	0.35	1.00	-0.26	0.35	0.19	-0.08	0.26	-0.04	0.18	0.34	-0.57	0.37	0.23	0.35	-0.20	-0.22	-0.18	200953_s_at
KIR2DS1	0.01	-0.10	0.10	0.10	-0.07	-0.26	1.00	0.07	-0.10	0.08	0.01	0.15	-0.07	-0.04	0.42	-0.06	0.03	-0.14	0.09	0.35	-0.02	211532_x_at
FASLG	-0.32	0.54	-0.05	0.51	0.44	0.35	0.07	1.00	0.17	0.02	0.35	0.17	0.12	0.16	-0.08	0.59	0.13	0.33	-0.03	0.03	-0.17	210865_at
TXK	-0.08	0.24	0.01	0.19	0.08	0.19	-0.10	0.17	1.00	0.04	-0.10	-0.12	0.07	0.01	-0.22	0.33	0.08	0.45	-0.23	-0.21	-0.15	206828_at
TTC38	0.07	0.07	0.14	0.17	0.08	-0.08	0.08	0.02	0.04	1.00	0.08	-0.14	-0.03	0.20	-0.01	0.02	0.06	-0.02	-0.07	-0.12	0.09	218272_at
CD244	-0.19	0.44	-0.03	0.32	0.35	0.26	0.01	0.35	-0.10	0.08	1.00	-0.06	0.07	0.25	-0.22	0.31	0.08	0.10	-0.08	0.13	0.05	220307_at
DEFA4	-0.09	-0.05	-0.03	-0.18	-0.16	-0.04	0.15	0.17	-0.12	-0.14	-0.06	1.00	-0.12	-0.20	0.16	-0.15	-0.10	-0.22	0.30	0.18	0.00	207269_at
CD160	-0.19	0.16	-0.03	0.05	0.30	0.18	-0.07	0.12	0.07	-0.03	0.07	-0.12	1.00	0.36	-0.19	0.13	0.06	-0.01	0.01	-0.13	-0.12	207840_at
PLEKHF1	-0.32	0.29	-0.07	0.22	0.33	0.34	-0.04	0.16	0.01	0.20	0.25	-0.20	0.36	1.00	-0.24	0.26	0.11	0.16	-0.13	-0.06	-0.16	219566_at
KIR2DL2	0.00	-0.42	0.01	-0.01	-0.25	-0.57	0.42	-0.08	-0.22	-0.01	-0.22	0.16	-0.19	-0.24	1.00	-0.20	-0.20	-0.20	0.23	0.35	0.12	208426_x_at
PRR5L	-0.21	0.68	-0.02	0.63	0.53	0.37	-0.06	0.59	0.33	0.02	0.31	-0.15	0.13	0.26	-0.20	1.00	0.13	0.46	-0.34	-0.18	-0.20	219383_at
IL12RB2	0.08	0.30	-0.03	-0.12	-0.01	0.23	0.03	0.13	0.08	0.06	0.08	-0.10	0.06	0.11	-0.20	0.13	1.00	-0.09	-0.06	-0.14	-0.19	206999_at
IL18R1	-0.12	0.27	-0.04	0.56	0.40	0.35	-0.14	0.33	0.45	-0.02	0.10	-0.22	-0.01	0.16	-0.20	0.46	-0.09	1.00	-0.38	-0.14	-0.02	206618_at
CAMP	-0.07	-0.25	-0.01	-0.35	-0.37	-0.20	0.09	-0.03	-0.23	-0.07	-0.08	0.30	0.01	-0.13	0.23	-0.34	-0.06	-0.38	1.00	0.30	0.01	210244_at
KIR3DL1	0.05	-0.16	0.01	-0.01	-0.12	-0.22	0.35	0.03	-0.21	-0.12	0.13	0.18	-0.13	-0.06	0.35	-0.18	-0.14	-0.14	0.30	1.00	0.11	216907_x_at

CEACAM8	0.07	-0.25	-0.04	0.04	-0.13	-0.18	-0.02	-0.17	-0.15	0.09	0.05	0.00	-0.12	-0.16	0.12	-0.20	-0.19	-0.02	0.01	0.11	1.00	206676_at

Table E8

#	Cell subset	Cell types included	Markers used	Cell Separation Method	Original reference (PMID)
1	T cells	CD8 T cells	see below	see below	15789058
		CD4 T cells	see below	see below	16791882 and 15789058
2	CD8 T cells		CD3, CD8, CD45RA	RosetteSep™ CD8+ T-cell enrichment cocktail, CD-8 subset	15789058
3	CD4 T cells	T cells CD4 naive	CD4+	Ficoll, then MACS CD4+ T cell isolation kit	16791882
		T cells CD4 memory resting	CD45ROhigh	Ficoll, then FACS	15789058
		T cells CD4 memory activated	CD45ROhigh; CD69, CD25 for activation	Ficoll, then FACS, then activated by anti-CD3 (plate-bound) + anti-CD28 (soluble)	15789058
4	Monocytes		N/A	MACS® CD14 Microbeads, monocyte subset	15789058
5	Macrophages	Macrophages M0	None known; identified by morphology and phagocytic capability	Differentiated from monocytes	15789058
		Macrophages M1	None known; identified by morphology and phagocytic capability	Histopaque 1.077, then Miltenyi negative selection monocyte isolation kit and LS columns, then differentiated with 1% medium supplement nutridoma-HU + 100 nM M-CSF, then activated with 20 ng/ml IFN-g+ 100 ng/ml LPS	17244792

		Macrophages M2	None known; identified by morphology and phagocytic capability	Histopaque 1.077, then Miltenyi negative selection monocyte isolation kit and LS columns, then differentiated with 1% medium supplement nutridoma-HU + 100 nM M-CSF, then activated with 20 ng/ml IFN-g+ 100 ng/ml LPS and 20 ng/ml IL-4	17244792
6	Macrophages(M2)		None known; identified by morphology and phagocytic capability	Histopaque 1.077, then Miltenyi negative selection monocyte isolation kit and LS columns, then differentiated with 1% medium supplement nutridoma-HU + 100 nM M-CSF, then activated with 20 ng/ml IFN-g+ 100 ng/ml LPS and 20 ng/ml IL-4	17244792
7	B cells	B cells naive	CD19+CD27-IgG/A-	MACS® CD138 microbeads and CD19 microbeads	15789058
		B cells memory	CD19+ CD27+	MACS® CD138 microbeads and CD19 microbeads, then FACS	15789058
8	DCs	Dendritic cells resting	N/A	Monocytes differentiated with 17 ng/ml IL4, and 67 ng/ml GMCSF	15789058
		Dendritic cells activated	N/A	Monocytes differentiated with 17 ng/ml IL4, and 67 ng/ml GMCSF, then stimulated with 1 ug/ml LPS	15789058
9	DCs (activated)		N/A	Monocytes differentiated with 17 ng/ml IL4, and 67 ng/ml GMCSF, then stimulated with 1 ug/ml LPS	15789058
10	NK cells	NK cells resting	CD56	RosetteSep™ NK-cell enrichment cocktail + CD2 Microbeads	15789058
		NK cells activated	CD56 + CD69	RosetteSep™ NK-cell enrichment cocktail + CD2 Microbeads + IL2 or IL15 for activation	15789058

Table E9

Name	**miRNA ID**	**p value**	**Fold change**
hsa-miR-152-3p	MIMAT0000438	0.003	1.772727273
hsa-miR-1260a	MIMAT0005911	0.003	1.567164179
hsa-miR-423-5p	MIMAT0004748	0.005	1.398843931
hsa-miR-30c-5p	MIMAT0000244	0.007	1.464285714
hsa-miR-185-5p	MIMAT0000455	0.007	1.452941176
hsa-miR-499b-3p	MIMAT0019898	0.007	-1.661016949
hsa-miR-133b	MIMAT0000770	0.007	-1.916666667
hsa-miR-34a-5p	MIMAT0000255	0.01	1.5
hsa-miR-194-5p	MIMAT0000460	0.01	-1.419642857
hsa-miR-376c-5p	MIMAT0022861	0.013	1.818181818
hsa-miR-26a-5p	MIMAT0000082	0.013	1.769063181
hsa-miR-454-3p	MIMAT0003885	0.013	1.661016949
hsa-miR-1973	MIMAT0009448	0.013	1.285714286
hsa-miR-612	MIMAT0003280	0.013	-1.396825397
hsa-miR-487b-3p	MIMAT0003180	0.018	1.923076923
hsa-miR-4458	MIMAT0018980	0.018	1.515151515
hsa-miR-423-3p	MIMAT0001340	0.018	1.397790055
hsa-miR-125b-5p	MIMAT0000423	0.018	1.393081761
hsa-miR-16-5p	MIMAT0000069	0.024	2.127266839
hsa-miR-146b-5p	MIMAT0002809	0.024	1.829411765
hsa-miR-92a-3p	MIMAT0000092	0.024	1.646938776
hsa-miR-574-3p	MIMAT0003239	0.024	1.5375
hsa-miR-654-3p	MIMAT0004814	0.024	1.526315789
hsa-miR-155-5p	MIMAT0000646	0.024	1.473523422
hsa-miR-4443	MIMAT0018961	0.024	1.369888476
hsa-miR-140-3p	MIMAT0004597	0.024	1.326666667
hsa-miR-3065-3p	MIMAT0015378	0.024	1.302631579
hsa-miR-331-3p	MIMAT0000760	0.024	1.3
hsa-miR-548c-5p+hsa-miR-548	MIMAT0004806	0.024	-1.362637363
hsa-let-7f-5p	MIMAT0000067	0.032	1.895631068
hsa-miR-31-5p	MIMAT0000089	0.032	1.388888889
hsa-miR-613	MIMAT0003281	0.032	1.373015873
hsa-miR-544a	MIMAT0003164	0.032	-1.173553719
hsa-miR-296-3p	MIMAT0004679	0.032	-1.418803419
hsa-miR-548o-3p+hsa-miR-54	MIMAT0005919	0.032	-1.459459459
hsa-miR-330-5p	MIMAT0004693	0.032	-1.5
hsa-miR-302b-3p	MIMAT0000715	0.032	-1.904761905
hsa-miR-499a-5p	MIMAT0002870	0.041	1.65503876
hsa-miR-29a-3p	MIMAT0000086	0.041	1.571017274
hsa-miR-146a-5p	MIMAT0000449	0.041	1.563071298
hsa-miR-1262	MIMAT0005914	0.041	1.322222222
hsa-miR-509-3-5p	MIMAT0004975	0.041	-1.319148936
hsa-miR-517b-3p	MIMAT0002857	0.041	-1.372093023
hsa-miR-525-3p	MIMAT0002839	0.041	-3.25