Supplementary Text Manuscript Appendix "AS03-Adjuvanted H5N1 Avian Influenza Vaccine Modulates Early Innate Immune Signatures In Human PBMC"

Version 1.0

August 9, 2018

Table of Contents

List of Figures

List of Tables

1 Introduction

This appendix provides supporting information for the manuscript entitled "'AS03-Adjuvanted H5N1 Avian Influenza Vaccine Modulates Early Innate Immune Signatures In Human PBMC"'. The study for which this data was collected, was a single center randomized, double-blinded, controlled, Phase I small targeted prospective study in healthy male and non-pregnant female subjects, 19 to 39 years old, inclusive, designed to assess the safety, reactogenicity, immunogenicity, and molecular immune responses of an intramuscular (IM) inactivated monovalent influenza A/H5N1 (Hemagglutinin [HA] of A/Indonesia/05/2005) split-virus (SV) vaccine manufactured by Sanofi Pasteur administered at 3.75 mcg given with the AS03 adjuvant (SV-AS03) manufactured by GlaxoSmithKline (GSK) or Phosphate Buffered Saline (PBS) diluent (SV-PBS). Subjects who met the entry criteria for the study and provided informed consent were randomized 1:1 to SV-AS03 and SV-PBS vaccine and each subject received two doses of the respective vaccine approximately 28 days apart (**Figure A1**).

2 Supplemental methods

2.1 Analysis population

The analysis population included all subjects who met all inclusion and exclusion criteria, who contributed at least one pre-vaccination blood sample (at Day -28, -14, or 0) and at least one post-vaccination blood sample (at Day 1, 3, 7, or 28) for which valid results were reported. The analyses included subjects by study product actually received. This population included 20 subjects (10 for each vaccine group randomly labeled) including subject B in the SV-AS03 group, who received the second vaccination (Day 28) out-of-window.

2.2 RNA-Seq experiment

Whole blood samples (90 mL) underwent Ficoll separation to yield PBMC and polymorphonuclear cell (PMN) populations. Bulk PBMC were frozen in homogenization buffer (Maxwell 16 LEV simply RNA kit, Promega) and stored at -80℃. Total RNA was extracted from each PBMC sample using the Maxwell 16 LEV simply RNA kit (Promega Corp.). RNA was quantified by Quant-iT RiboGreen RNA Assay, and samples were evaluated on the Caliper LabChip GX to assess RNA integrity. 100ng total RNA and RNA integrity numbers greater than 7 were required for proceeding to downstream RNA-Seq applications. Poly(A) mRNAs were isolated using NEBNext magnetic oligo d(T)25 beads. NEBNext mRNA Library Prep Reagent Set for Illumina (New England BioLabs Inc.) was used to prepare individually bar-coded next generation sequencing expression libraries. Overall, 136 RNA sequence libraries were constructed, one for each subject and study visit combination. Construction of four libraries failed due to insufficient amounts of RNA. Libraries were pooled (10mM each sample). Approximately 50-bp, paired-end read sequencing with a sequencing coverage of 50 million reads / 25 million fragments (paired-end reads) was performed for each library utilizing a 200 cycle TruSeq SBS HS v3 kit on an Illumina HiSeq2000 sequencer (Illumina, Inc.).

2.3 RNA-Seq data preprocessing

Reference Consortium Human Build 37 (GRCh37) genomic assembly was used as reference sequence. Human gene models and annotations were obtained from the Ensembl database (Version 63, June 2011). Paired-end reads were mapped against the human reference genome using the *TopHat* splice-aware read aligner (Version 2.0.0). Ensembl gene models were used to guide the alignment process. Alignment QC statistics were obtained using the *RSeQC* software (Version 2.3.7). Gene expression quantification was carried out using the *featureCounts* function as implemented in the *Subread* software (Version 1.4.6). *featureCounts* options were set to count fragments, i.e. paired-end reads that reconstitute a fragment for which both ends were successfully mapped to a gene. Reads/fragments that overlapped with multiple genes or had multiple mapping locations on the reference genome were excluded. Systematic sample differences in sequencing depth (number of fragments) were corrected for by calculating RNA composition-robust scaling factors for each sample using the trimmed mean of M-values (TMM) method (Liao et al., 2013; Robinson and Oshlack, 2010) as implemented in the *edgeR* software (Version 3.2.4). TMM normalization was executed across all 136 samples. Post normalization, 4,185 genes that were known ribosomal and mitochondrial RNA genes or genes located on the X or Y chromosomes were excluded to avoid gender-specific effects leaving a total of 46,870 genes to be analyzed (**Table A1**). For data visualization and multivariate analyses, TMM normalized moderated $\log_2$ fragment counts per million were computed using *edgeR*. To avoid taking the log of zero values, a TMM-scaled fragment count of 0.5 was added to each gene (the imputed value was different for each sample based on its TMM scaling factor). Genes with less than 1 count per million in 60% of the samples at any post-baseline study visit (Days 1, 3, 7, 28) were deemed lowly expressed and were excluded (at a minimum, 8 samples were required to pass the cut-off). For time-trend analyses, filtering was carried out for all samples keeping genes that met the cut-off at any post-baseline day. For differential analysis, filtering was carried out for each post-baseline study visit sample. **Table A2** lists the number of genes that were retained for each study visit day. Subject specific $\log_2$ fold changes from baseline were calculated for each subject and post-baseline day (Day 1, 3, 7, 28) by subtracting the mean of the $\log_2$ baseline values from each of the subject's post-baseline days.

2.4 RNA-Seq statistical analysis

2.4.1 Statistical model for identifying differentially expressed genes

For each post-vaccination day, negative binomial generalized linear models with a dispersion estimation component that leverages information across genes as implemented in *edgeR* were fitted. In particular, trended dispersion estimates based on the mean-variance trend across all genes were obtained, and gene-wise negative binomial dispersion parameters were shrunk towards the trended dispersion estimates using empirical Bayes as implemented in *edgeR*. The design matrix included fixed effects for subject, study day (baseline or post-baseline day), and a day*treatment interaction term. The study visit day and treatment group effects had two fixed levels (0: for baseline days -28, -14 or 0, and 1: for the respective post-vaccination day), and (0:SV-PBS and 1:SV-AS03), respectively. The subject effect for estimating subject-specific mean baseline levels was added to account for correlations between samples from the same subject. Maximum likelihood estimates of the coefficients including baseline levels were estimated using the parallelized line search algorithm described by McCarthy et al. (2012). The interaction term represents the $\log_2$ fold change difference (LFCD) between SV-AS03 and SV-PBS treatment group responses. The statistical significance of the interaction term was evaluated for each gene using a likelihood ratio test to identify genes that significantly differed in their response from baseline between treatment groups. To control for testing multiple genes, the false-discovery rate (FDR) based on the Benjamini-Hochberg procedure as implemented in the *p.adjust* R function was applied. Genes with a FDR-adjusted p-value ≤ 0.05 and a fold change of ≥ 1.5-fold (up or down regulation based on LFCD) were deemed to be significantly differentially expressed between treatment groups.

2.4.2 Determination of robustly co-expressed gene clusters

Pairwise distances between genes based on their baseline $\log_2$ change profiles were calculated for each post-vaccination day individually (Day 1, 3, 7, 28) as well as across all post-vaccination days (Day 1-28). Uncentered Pearson correlation distance was used as distance measure as $\log_2$ fold changes are, by definition, centered around zero. The input list of genes for this clustering analysis included DE genes that were identified for any of the four post-vaccination days. Clusters were obtained using the hierarchical complete linkage clustering algorithm. To evaluate robustness of gene clusters, multiscale bootstrapping (Suzuki and Shimodaira, 2006) was carried out separately for each post-vaccination day using varying dataset sizes (0.4*N, 0.5*N, 0.6*N, 0.7*N, 0.8*N, 0.9*N, 1*N, 1.1*N, 1.2*N, 1.3*N; where N stands for the respective dataset size). For each dataset size bin, 1,000 bootstrap samples were obtained, and bootstrap probabilities and p-values were calculated. A p-value cut-off of 0.05 was applied to determine significant clusters. The maximum distance to form a significant cluster was set to 0.5 (equivalent to minimum uncentered Pearson correlation of 0.5). Clusters that were formed at larger distance were excluded.

2.4.3 Pathway enrichment analysis

Pathway enrichment analysis was carried out separately for each post-vaccination day. Genes were grouped and analyzed based on 8,101 known pathways/modules/gene sets obtained from the KEGG database (Version 70.0 (06/09/2014), Kanehisa et al., 2012) and MSigDB (Version 4.0 (05/31/2013), Liberzon et al., 2011). The KEGG subset included KEGG pathways and KEGG modules. The MSigDB gene set collection comprised GO Biological Processes, GO Cellular Components, GO Molecular Functions, Reactome Pathway, BioCarta Pathway, Chemical/Genetic Perturbations, and Immunologic Signature pathways/gene sets. **Table A11** summarizes the gene set collection used in this report. For each of these gene sets, enrichment was evaluated using the *goseq* R package (Version 1.12.0). The GOseq algorithm adjusts for gene length bias when modeling the null distribution (Young et al.,2010). Gene length was specified as the length of the longest cDNA of a gene. Gene length information was obtained from the *tweeDEseqCountData* R package (Version 1.0.9). GOseq probability weighting functions were estimated for each post-vaccination day based on DE genes. Null distributions were generated using GOseq's random sampling option (100,000 randomizations were applied). Lists of enriched gene sets were obtained separately for each of the nine category types (KEGG pathways, KEGG modules, GO Biological Processes, etc.). To control for testing multiple gene sets, the false-discovery rate (FDR) based on the Benjamini-Hochberg procedure as implemented in the *p.adjust* R function was applied. Gene sets with a FDR $\leq$ 0.01 were considered to be significantly enriched. Enrichment trends across post-vaccination days were visualized using heatmaps and binary Jaccard-distance based complete-linkage hierarchical clustering. For significantly enriched KEGG pathways, color-coded KEGG pathway maps were generated (KEGG KGML pathway layout information Version 82.0, 06/06/2017). Pathways were color-coded by mean $\log_2$ fold change difference between treatments. If nodes in the pathway referred to multiple genes, the median $\log_2$ fold change was used to set the background color of a node (red: up-regulated in the adjuvant group compared to the unadjuvanted group, blue: down-regulated in the adjuvanted group compared to the unadjuvanted group). If one of the genes of a multi-gene node was significantly enriched, the node label and border was color-coded (red: up-regulated, blue: down-regulated, yellow: conflict if one gene was up but another was down regulated).

2.4.4 Regularized linear regression

For each post-vaccination day, a regularized linear regression model was fit to identify gene responses that were correlated with $\log_2$ peak hemagglutination inhibition (HAI) antibody titer using the *glmnet* R package (Version 2.0-2). The predictor variable set was based on $\log_2$ baseline fold changes and included genes with an average absolute fold change from baseline $\geq$ 1.5 in at least one of the two seroprotection response groups (group 1: HAI $\geq$ 1:40, group 2: HAI $<$ 1:40). To avoid overfitting ($n << p$ and collinearity among gene responses) and facilitate variable selection, an elastic net regularization step (combination of L1 Lasso and L2 ridge penalization, α = 0.5) was included as part of the fitting procedure. Leave-one-out cross validation was used to determine the optimum regularization parameter λ that minimizes the model mean squared error.

2.5 Software

Data was analyzed using the *R statistical programming language* and *R Bioconductor* packages. A complete listing of R and package versions are given in **Table A21**. This report was generated using the *knitr* R package (Version 1.5) and *LaTeX* typesetting software (Version TeX Live 2012/Debian). The operating system used was *Ubuntu* (Version 13.04).

3 Supplemental results

3.1 Data QC and normalization

3.1.1 RNA-Seq reference alignment and other experimental statistics

Tables A3 and A4 summarize key technical variables and alignment statistics. On average, 48.3 million individual reads were mapped for each sample against the reference, of which, 94% uniquely mapped to a location on the human reference assembly. There were no cases in which one of the paired-end reads mapped to different chromosomes. When reads were mapped against known gene models, on average, 17.4 million fragments (combined paired reads that mapped to the same gene) were uniquely counted in the expression quantification step. Sample mean %GC content of mapped sequences ranged from 50% to 53%. The number of Illumina flow cells per sample ranged from 2 to 3. The range for Illumina lanes was 3 to 4 lanes per sample.

The vast majority (on average 86.6%) of tags (spliced reads) mapped to known[1] exon regions followed by intronic (12%), and intergenic regions (1.4%). Coverage for coding DNA sequence regions was, on average, 529 tags per Kb of sequence, compared to 4.8 tags per Kb for introns, and a maximum of 4.2 tags per Kb for intragenic regions (10Kb up/downstream). Novel splice junctions were not analyzed in this sub study. Boxplots of subsets of these statistics are given in **Figures A2 and A3**. Starplots that visualize alignment statistics across time points and treatments are shown in **Figure A4**. Subject-specific patterns were not observed, and no strong effects related to treatment or study visit day were evident. The Day 7 sample for Subject G had the lowest number of total and mapped reads when compared to the rest of the samples **Figure A4**.

3.1.2 Impact of TMM normalization

The impact of between-sample normalization using the trimmed mean of M-values (TMM) method is visualized in **Figures A5 to A7**. The plots summarize $\log_2$ counts per million (LCPM) distributions for each sample before and after normalization. The medians and interquartile ranges of LCPM distributions were very similar for most of the 136 samples before and after normalization. For some samples

---

[1] Ensembl gene models (Version 63, June 2011)

(e.g. the Day 7 sample for Subject G), alignment of LCPM distributions was slightly improved following TMM normalization. Subsequent results are based on TMM-normalized data.

3.1.3 Global gene expression patterns, confounding effects, outlying samples

Principal component analysis (PCA), non-metric multidimensional scaling, and hierarchical clustering results based on LCPM gene variables are shown in **Figures A8 to A11**. The Day 7 sample for Subject G showed an outlying profile in the MDS plot based on its Spearman correlation distance compared to all other samples (**Figure A10**) as well as based on Euclidean distance when using hierarchical clustering analysis **Figure A11**. For the same sample, outlying reference alignment statistics compared to all other samples were observed (**Figure A4**). Thus this sample was flagged as a global outlier and removed from downstream analyses.

3.1.4 GC content bias correction

To evaluate the impact of sample %GC content on $\log_2$ fold change between treatments, negative binomial models were fit with and without sample-specific %GC content added as a covariate. Under the assumption that %GC content does not have an influence on model outcome, GC content rich/poor genes would exhibit a random pattern with respect to their fold change with an overall center of fold changes at zero. Any deviation from this pattern would indicate a systematic bias. **Figure A12** shows the estimated $\log_2$ fold changes (SV-AS03 adjuvant group vs. unadjuvanted group) plotted against gene-specific %GC content before and after correcting for % sample GC content (left two panel columns). Panels to the right show MA plots with $\log_2$ fold change plotted against average LCPM with genes colored according to their GC content (in red: >%60) and (in blue: <%40). Generally, none or slight effects were observed (e.g. for PBMC at Day 3). Inclusion of sample %GC content as a covariate corrected the $\log_2$ fold change bias, reestablishing a center at zero fold change and random pattern for high/low GC genes (**Figure A12**).

3.2 Differentially expressed genes

Venn diagrams that summarize DE gene overlap across post-baseline days before and after GC adjustment are summarized in **Figures A14 and A15**. Negative binomial dispersion trends of GC-adjusted models and MA plots that contrast average gene expression (LCPM) versus treatment fold change difference (LFCD) are provided in **Figure A13**.

3.3 Unsupervised gene clustering results

Tables A9 and A10 list clusters of genes that were found to be robustly co-expressed based on their $\log_2$ fold change profile as determined by multiscale bootstrap resampling. Dendrograms with bootstrap probabilities and gene cluster assignments are summarized in **Figures A16 and A17**. Mean gene cluster $\log_2$ fold changes from baseline were plotted for each vaccine group across post-vaccination days (**Figures A18 to A22**). A subset of clusters are discussed:

Immunoglobulin gamma binding receptor gene cluster PBMC cluster *CPMCP1-008* (n=2: *FCGR1A*, *FCGR1B* showed strongly increased gene expression levels (>4-fold on average) for the adjuvant group at Day 1 while levels remained close to baseline for the unadjuvanted group (**Figure A18**). For both genes, levels in the adjuvant group returned to baseline levels by Day 3. This cluster contained genes that encode for Immunoglobulin gamma (IgG) Fc receptor I binding proteins which are known to bind to the Fc region of IgG and play a role in innate as well as adaptive immune responses (see also related pathway maps **Figures A28 and A35**).

Interferon-responsive gene cluster The Day 1 PBMC cluster *CPMCD1-021* (n=7: *GBP1*, *GBP2*, *GBP3*, *STAT1*, *PARP9*, *WARS*, *LAP3*, showed an increase of >2.5-fold on average for the adjuvant group at Day 1 while levels remained close to baseline for the unadjuvanted group (**Figure A19**). For all genes, levels in the adjuvant group returned to baseline levels by Day 3. This cluster contained several interferon-responsive genes or genes that induce the expression of interferon-responsive genes including 3 genes that encode for guanylate-binding protein (GBP) family proteins and *STAT1*, and *PARP9*, all of which are known to protect against viral infection.

IP-10 cytokine cluster The Day 1-Day28 PBMC cluster *CPMCD1D28-012* (n=15: *APOBEC3A*, *CXCL10*, *EPSTI1*, *IFI35*, *JAK2*, *MYOF*, *ODF3B*, *PARP14*, *PARP9*, *SAMD4A*, *SAMD9L*, *SCO2*, *SERPING1*, *STAT2*, *TYMP*, had an increase of >2-fold on average for the adjuvant group at Day 1 while levels remained close to baseline for the unadjuvanted group (**Figure A22**). Levels in the adjuvant group reached baseline levels by Day 3. This cluster contained Jak-STAT signaling pathway genes, genes that induce the expression of interferon-responsive genes (*PARP9*, *PARP14*), an interferon-responsive gene (*IFI35*, and the gene that encodes for IP-10 cytokine (*CXCL10*) (see also related pathway maps **Figures A23 and A35**).

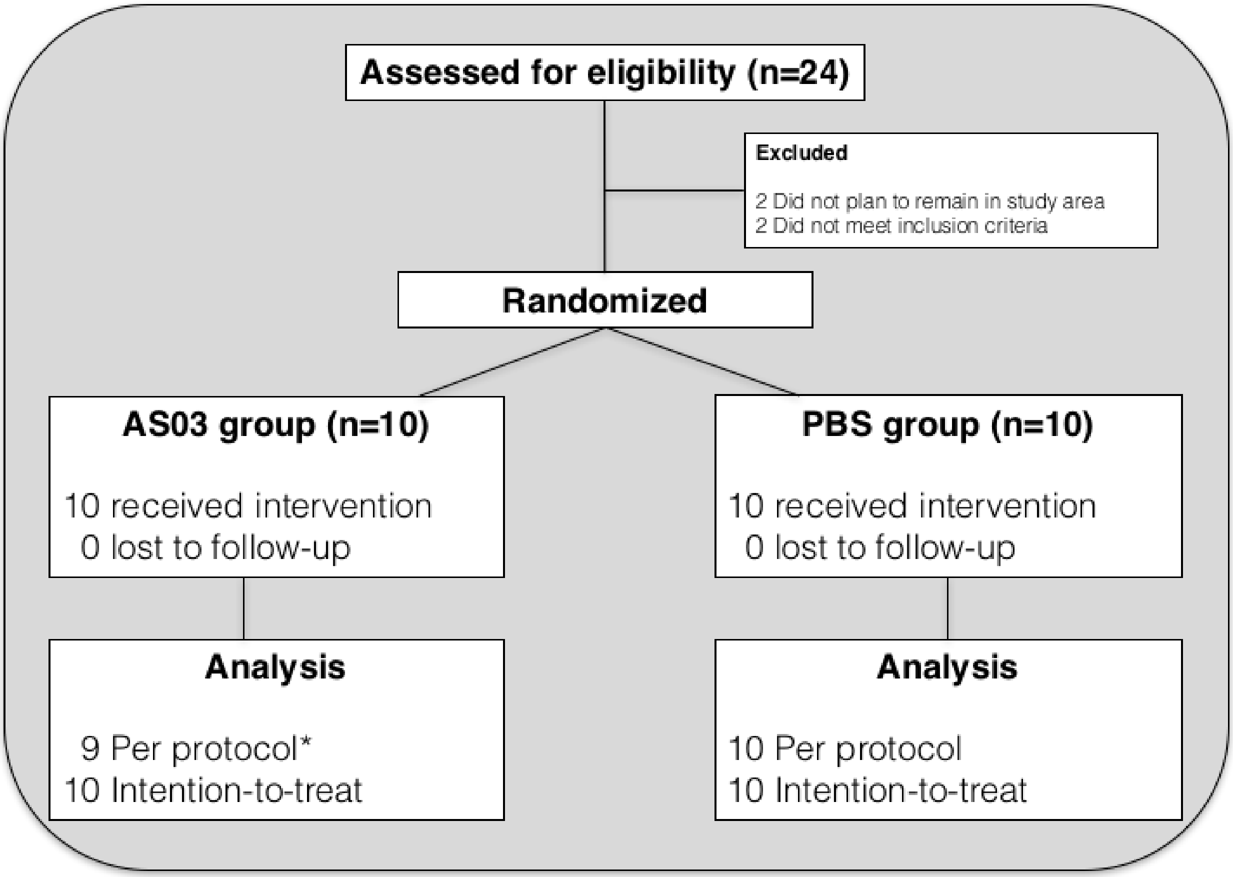
3.4 Pathway enrichment results

Gene set enrichment analysis was carried out by post-vaccination day using published gene sets outlined in **Table A11** (**Table A12**). Significantly enriched pathways/gene sets for each of the nine pathway categories are provided in **Tables A13 to A19**. Enriched KEGG pathway maps color-coded by expression fold change and fold change significance are shown in **Figures A23 to A54**.

3.5 Gene responses that best correlate with peak HAI titer response

A regularized linear regression model was fit for each post-vaccination day to identify combinations of gene responses that best correlate with $\log_2$ peak HAI titer. **Table A20** summarizes regularized linear regression model statistics including the minimum cross-validated mean square error (MSE) for each model. Scatterplots that summarize the correlation between peak $\log_2$ HAI titer and $\log_2$ fold change response for each gene that was selected by the best model are shown in **Figures A55 to A58**.

Figures



** One subject received Vaccine Dose 2 on Study Day 39 (9 days outside of window)*

Figure A1: Consort diagram outlining study group enrollment and randomization.

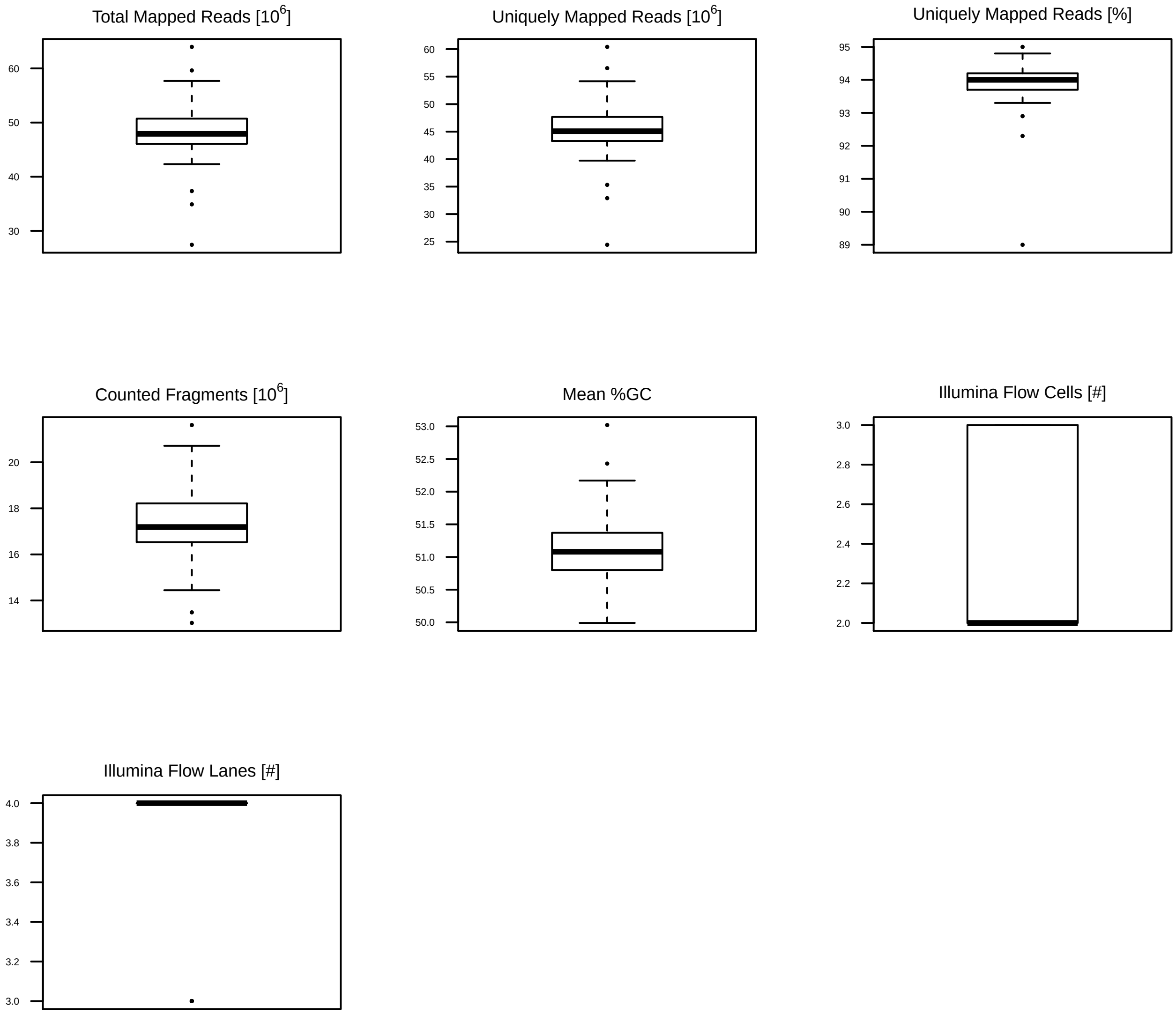


Figure A2: Boxplots of technical variables (RNA-Seq, PBMC).

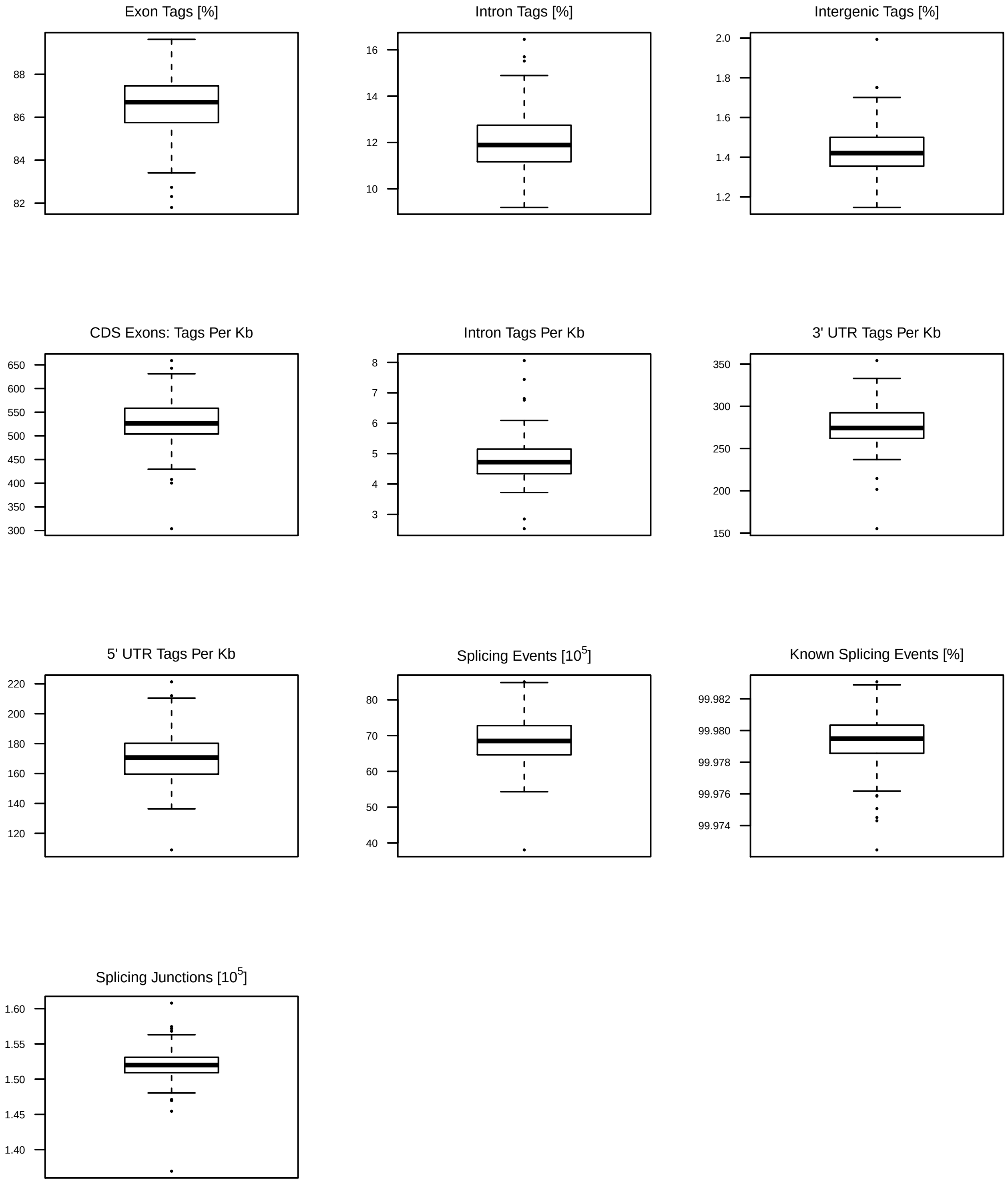


Figure A3: Boxplots of gene model variables (RNA-Seq, PBMC).

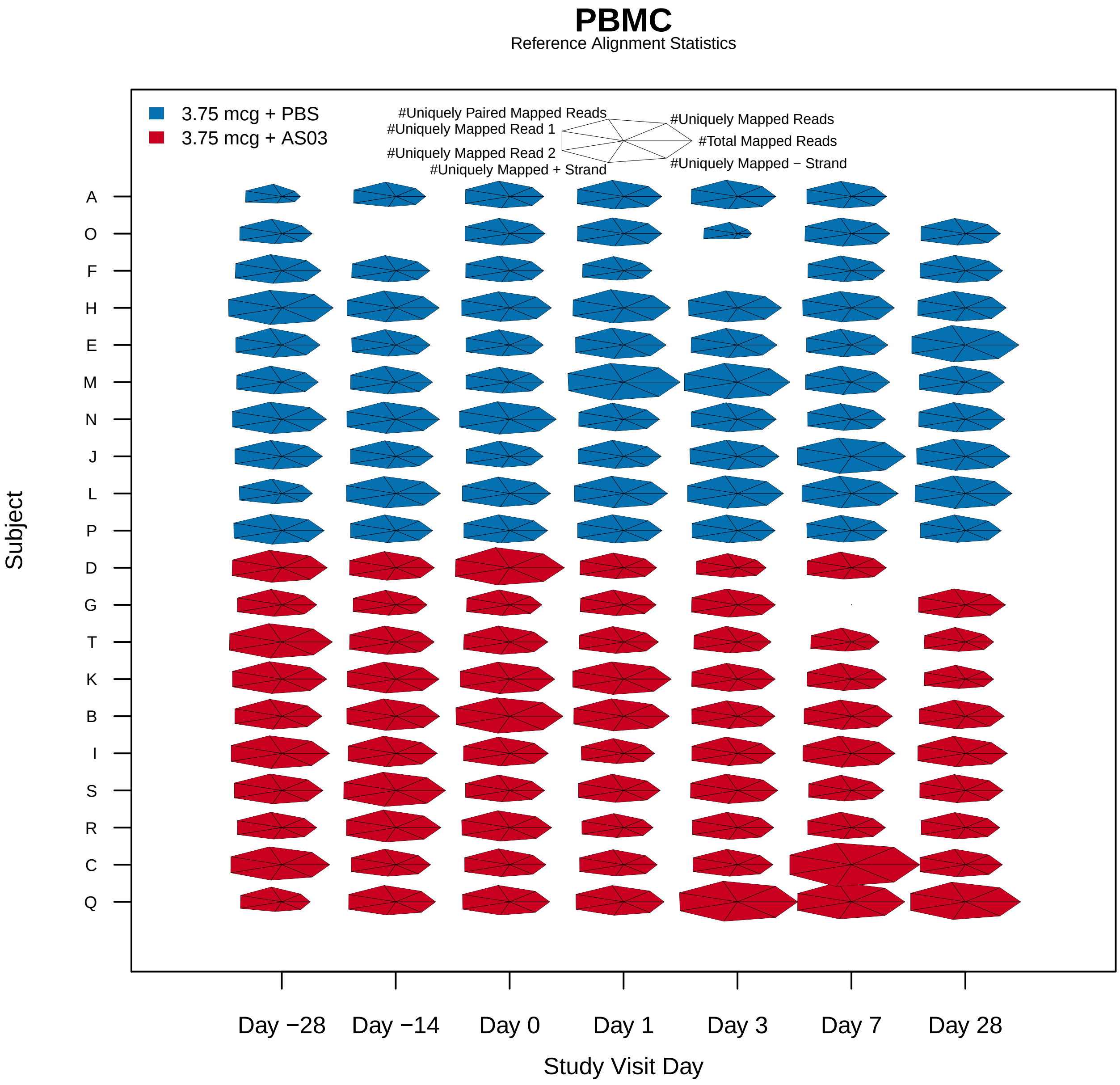


Figure A4: Starplots of human genome reference alignment statistics (RNA-Seq, PBMC).

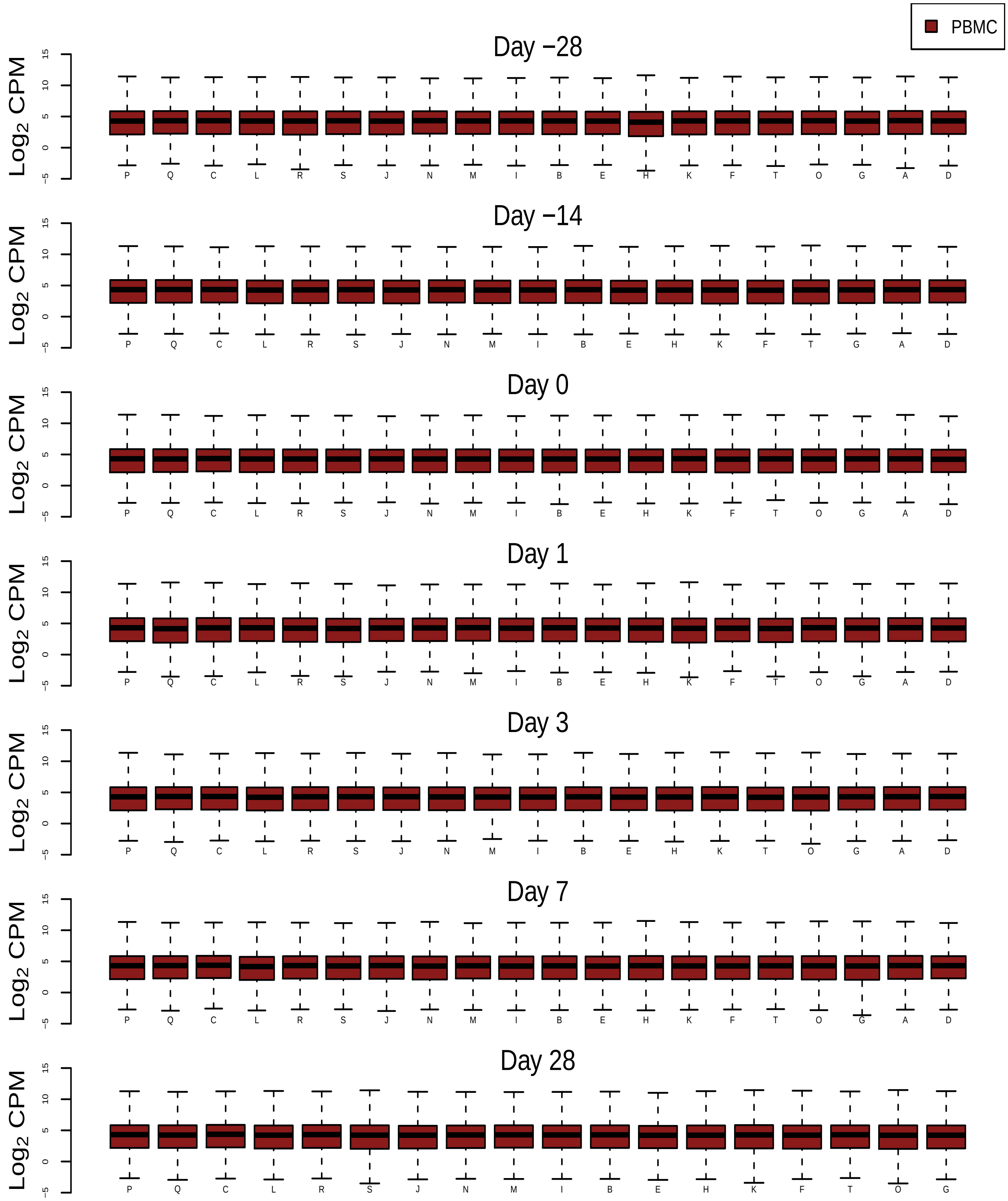


Figure A5: Boxplots of log_2 counts per million before TMM normalization. Boxplot outliers are omitted for clarity. Ordering by day was chosen to optimize visual representation (RNA-Seq, PBMC).

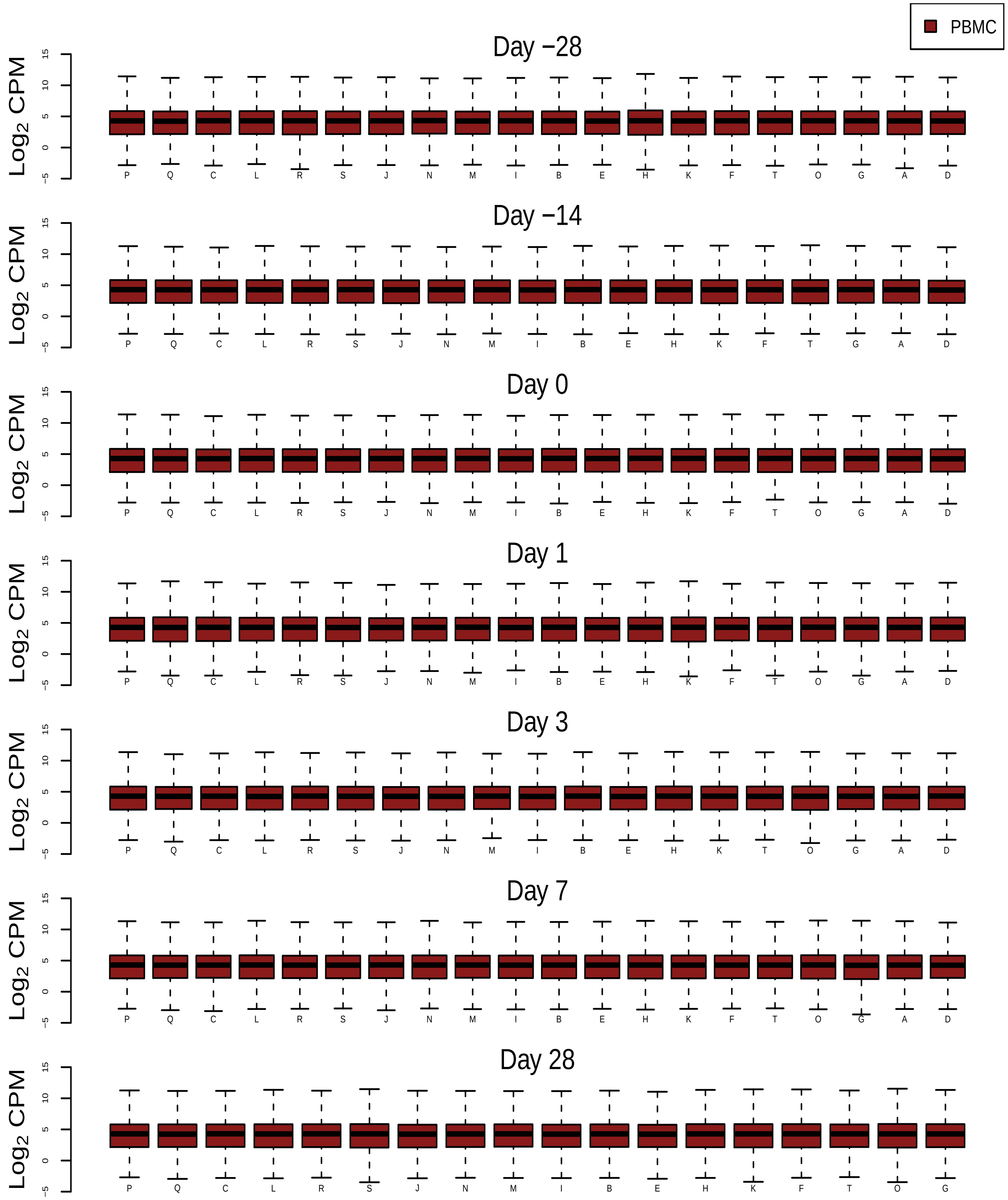


Figure A6: Boxplots of log_2 counts per million after TMM normalization. Boxplot outliers are omitted for clarity. Ordering by day was chosen to optimize visual representation (RNA-Seq, PBMC).

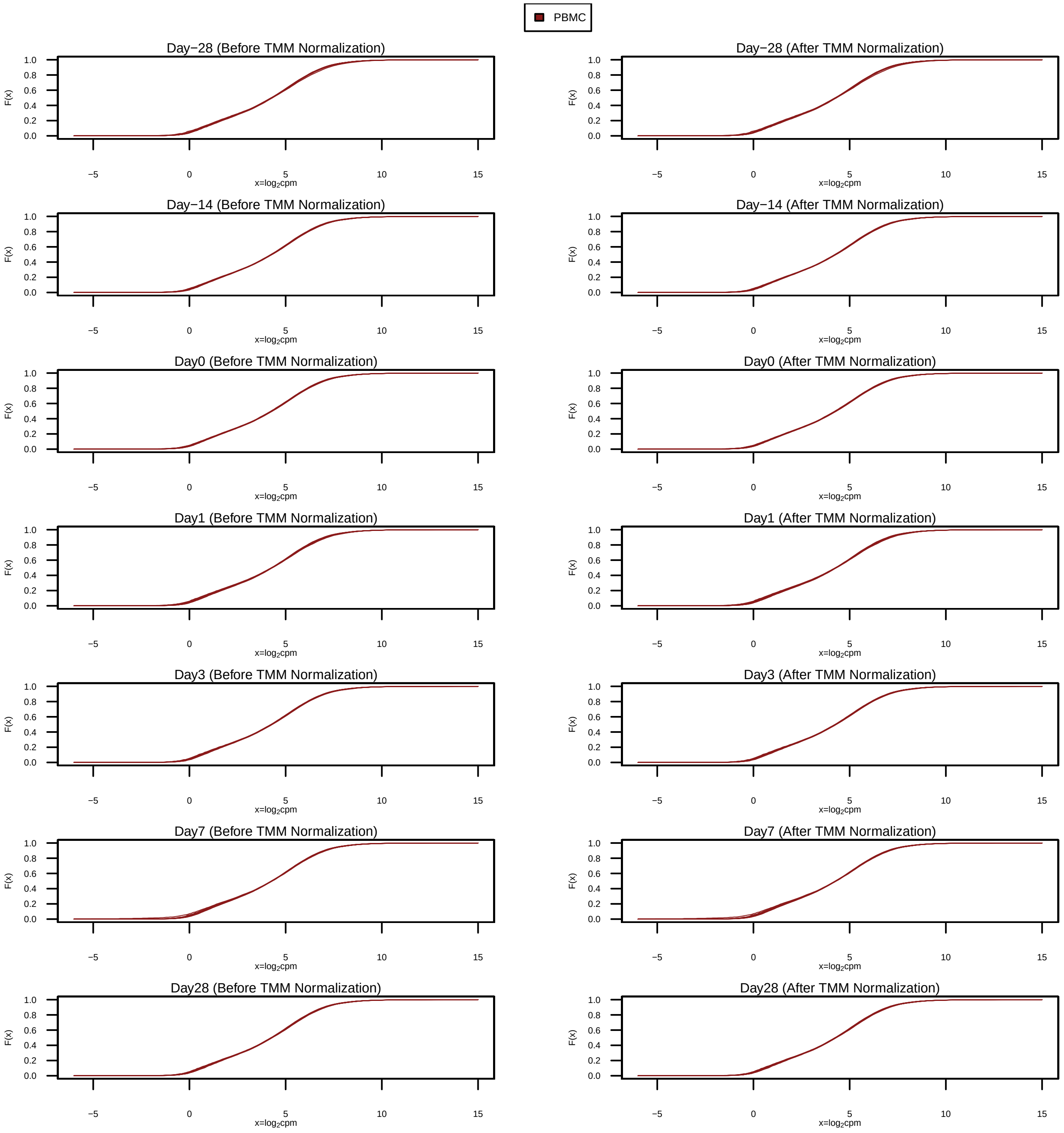


Figure A7: Empirical cumulative distribution function plots of log_2 counts per million before and after TMM normalization (RNA-Seq, PBMC).

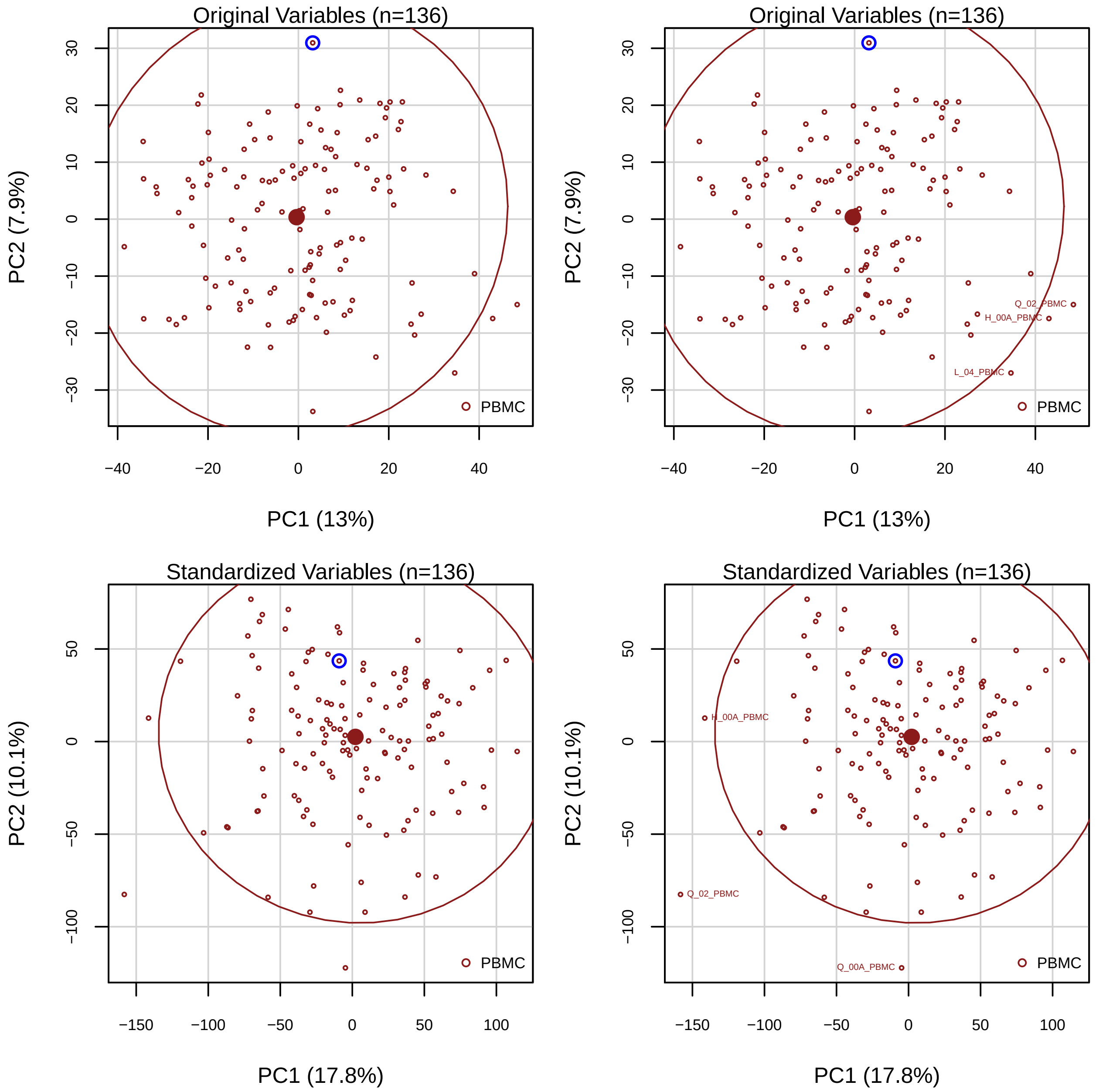


Figure A8: PCA biplots (RNA-Seq, PBMC, n=136). The 99% confidence ellipse for the bivariate mean is shown. Identified outliers are highlighted in blue. The right panels are identical to the left panels except that they show dataset labels for the three most distinct samples based on maximum Mahalanobis distance.

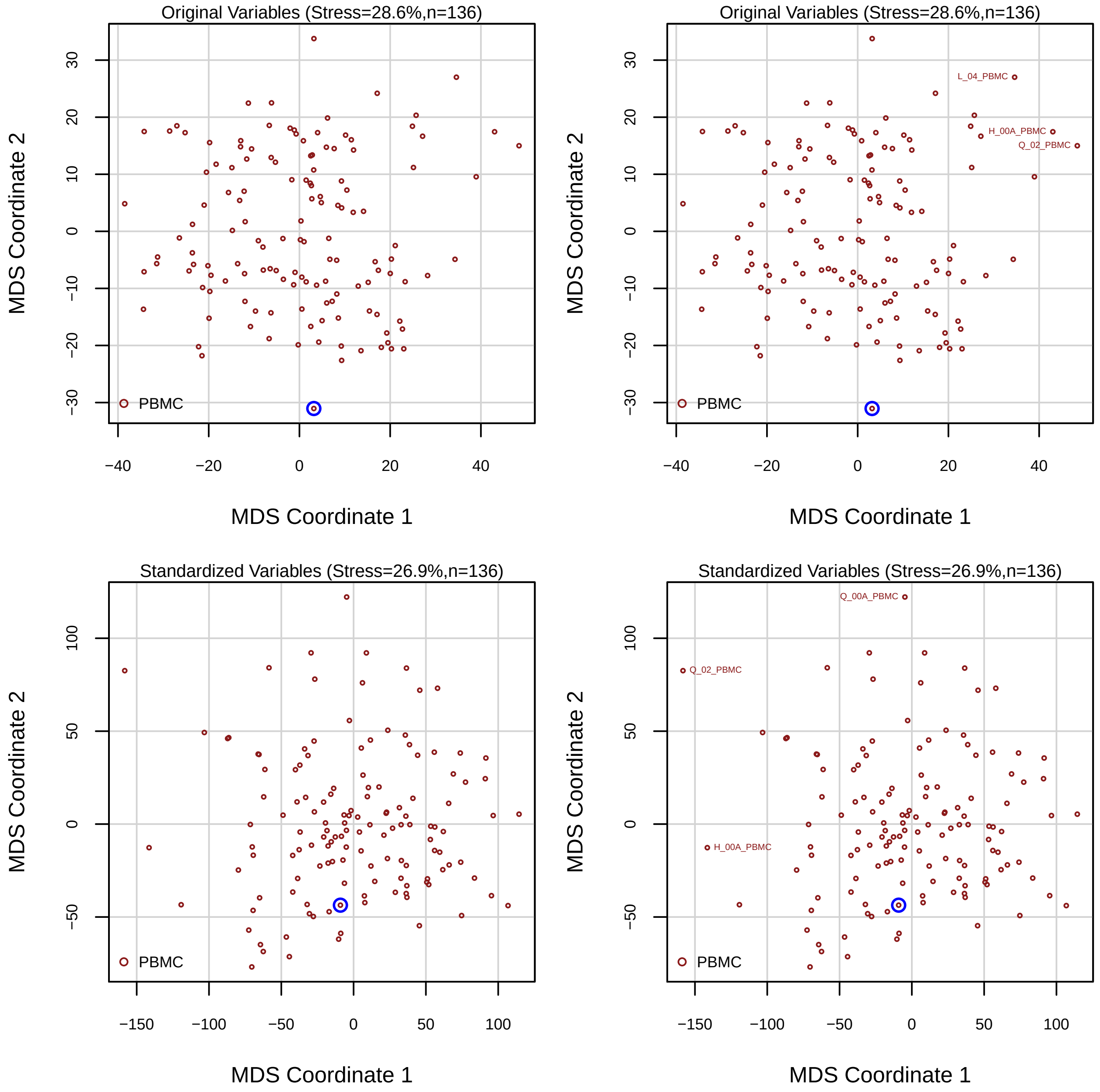


Figure A9: Non-metric multidimensional scaling biplots based on Euclidean distance (RNA-Seq, PBMC, n=136). Euclidean distance was used to determine pairwise differences. Identified outliers are highlighted in blue. The right panels are identical to the left panels except that they show dataset labels for the three most distinct samples based on maximum Mahalanobis distance.

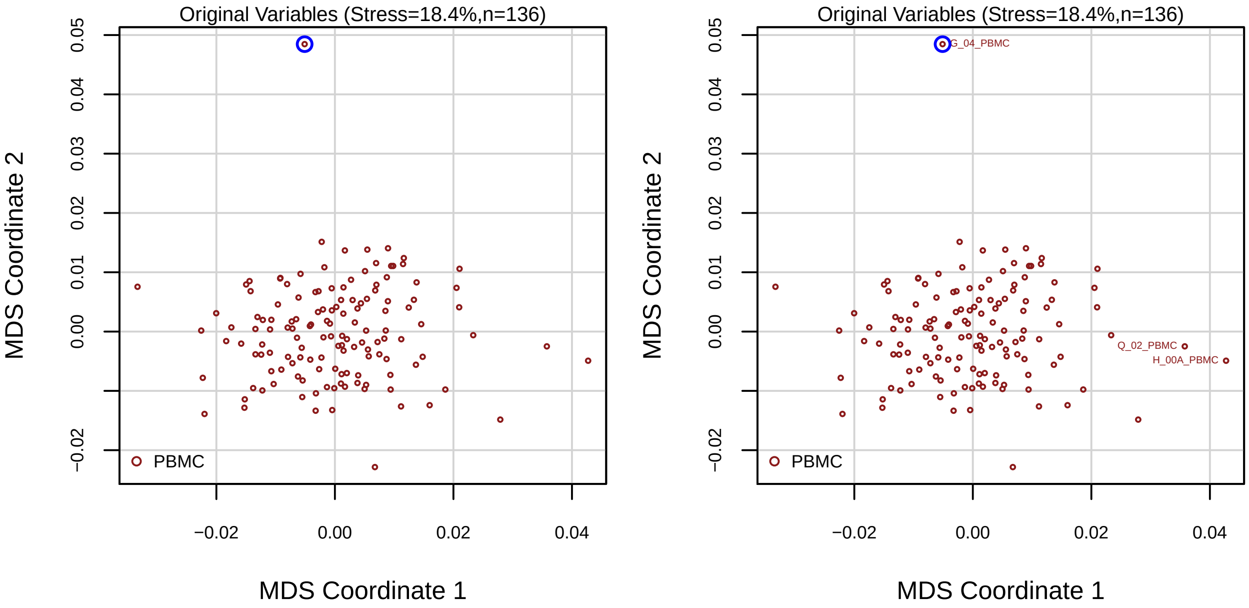
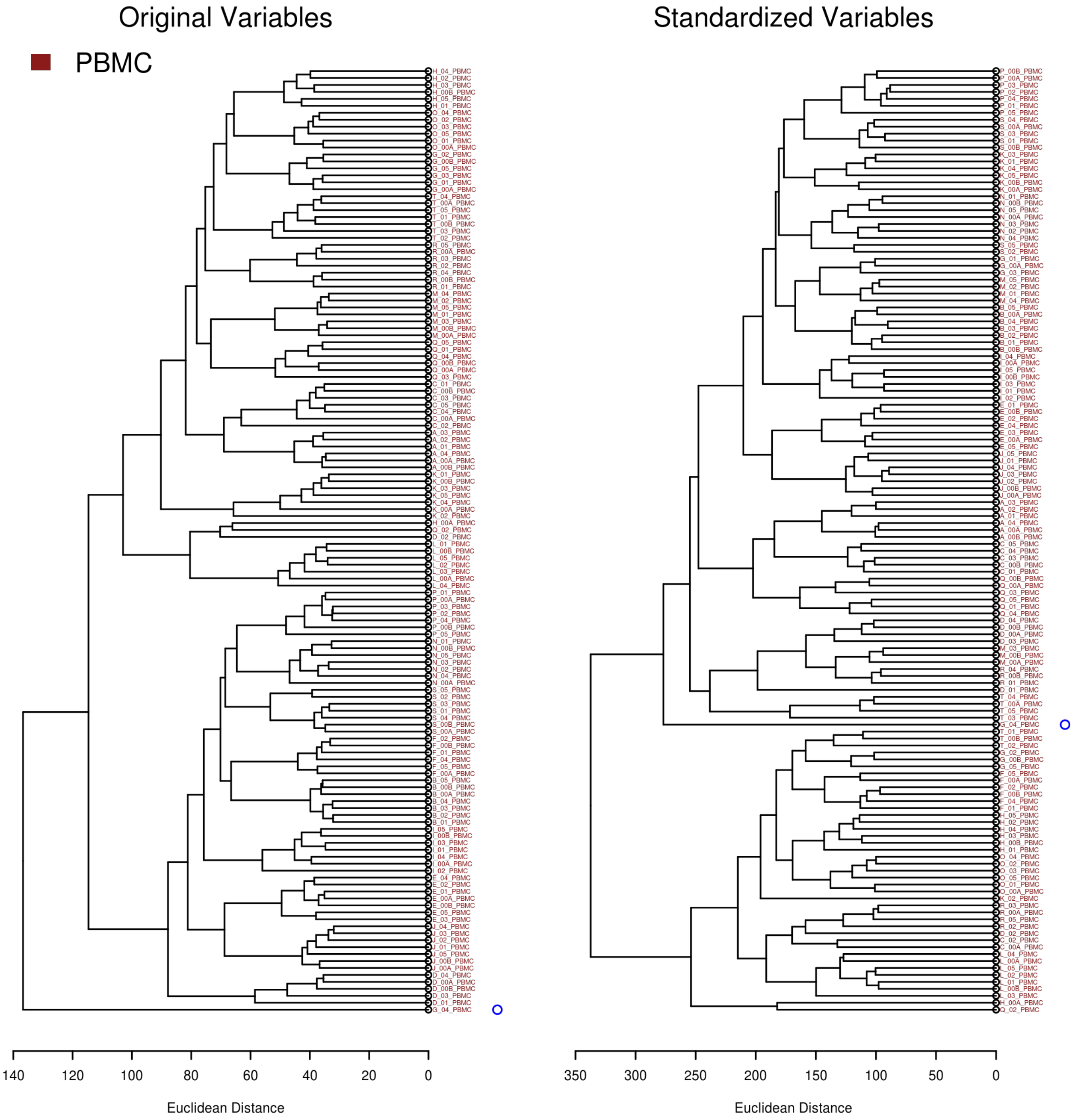


Figure A10: Non-metric multidimensional scaling biplots based on Spearman correlation distance (RNA-Seq, PBMC, n=136). Spearman correlation distance was used to determine pairwise differences. Identified outliers are highlighted in blue. The right panels are identical to the left panels except that they show dataset labels for the three most distinct samples based on maximum Mahalanobis distance.



Original Variables

Standardized Variables

Figure A11: Hierarchical Clustering Plots (RNA-Seq, PBMC, n=136). Euclidean distances hierarchically clustered using the complete linkage clustering algorithm. Identified outliers are highlighted in blue.

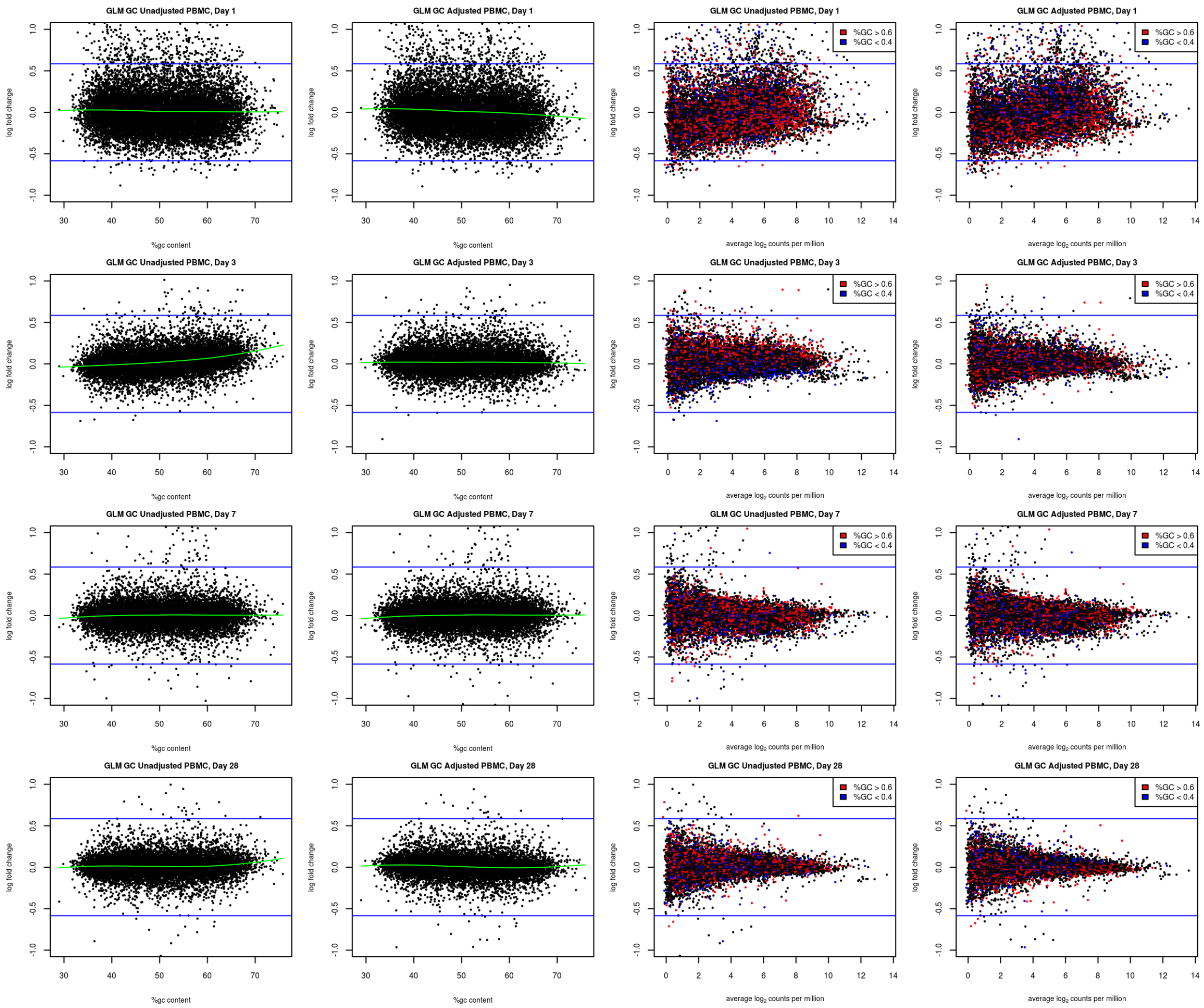


Figure A12: Impact of GC on fold change (RNA-Seq, PBMC).

[Panels to the left show the estimated log_2 fold changes (SV-AS03 adjuvant group vs. unadjuvanted SV-PBS group) plotted against gene-specific %GC content before and after correcting for % sample GC content, respectively. Panels to the right show MA plots with log_2 fold change plotted against average LCPM with genes colored according to their GC content (in red: >%60) and (in blue: <%40).]

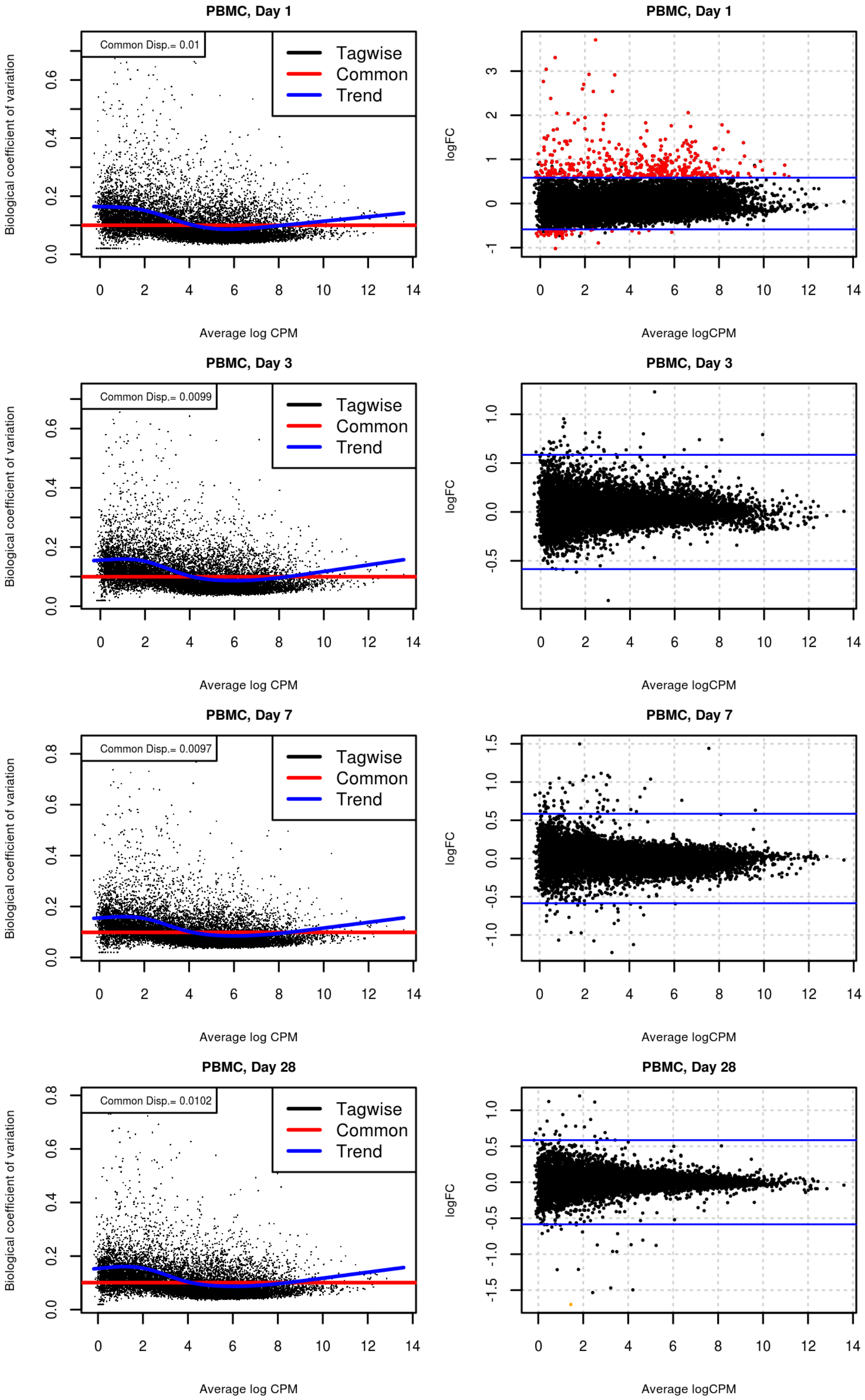


Figure A13: Model QC summary plots (RNA-Seq, PBMC).

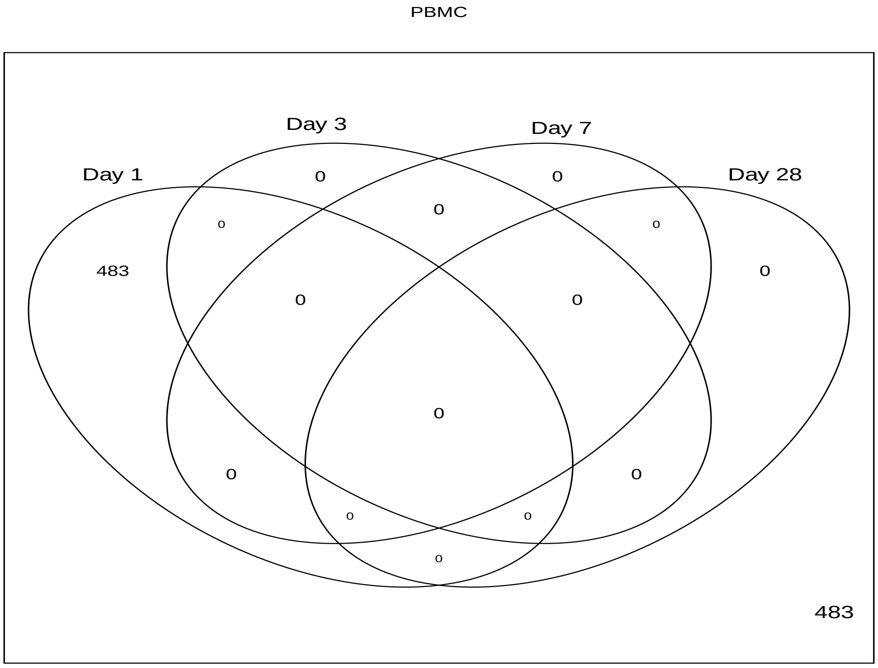


Figure A14: Venn diagrams of DE genes by post-vaccination day (RNA-Seq, PBMC, before GC adjustment).

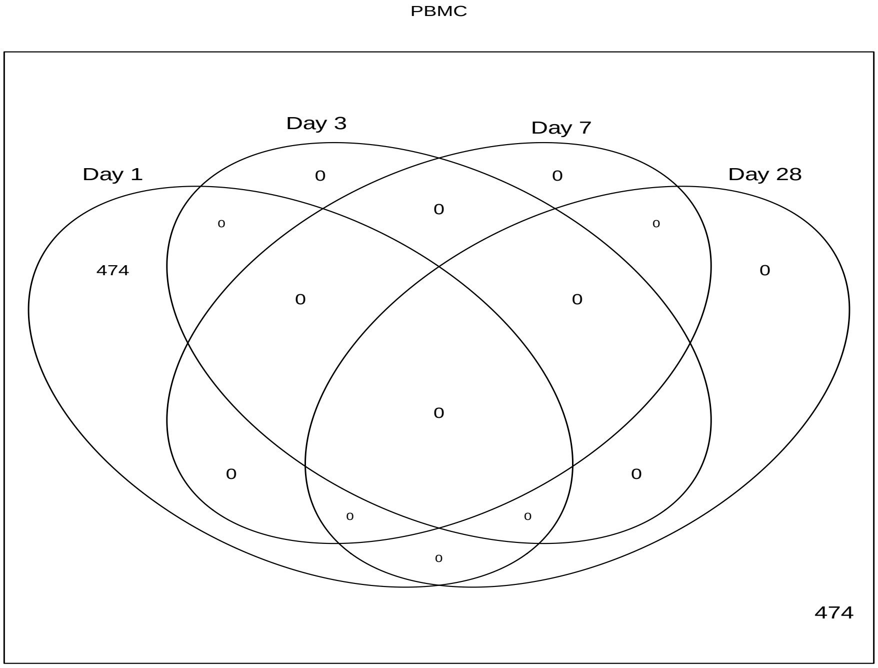


Figure A15: Venn diagrams of DE genes by post-vaccination day (RNA-Seq, PBMC, after GC adjustment).

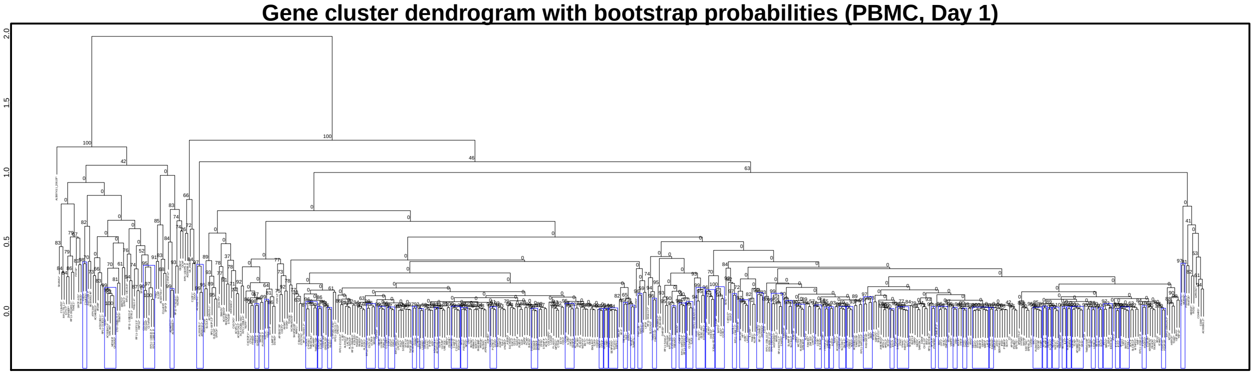


Figure A16: Gene cluster dendrogram with bootstrap probabilities (RNA-Seq, PBMC, Day 1). The y axis shows the distance at which clusters were formed by the complete linkage clustering algorithm based on uncentered Pearson correlation distance between log_2 fold changes. Multiscale bootstrap probabilities are shown at each branch intersection. Significant clusters are highlighted in blue. Asterisks indicate genes that were significantly expressed at a certain day.

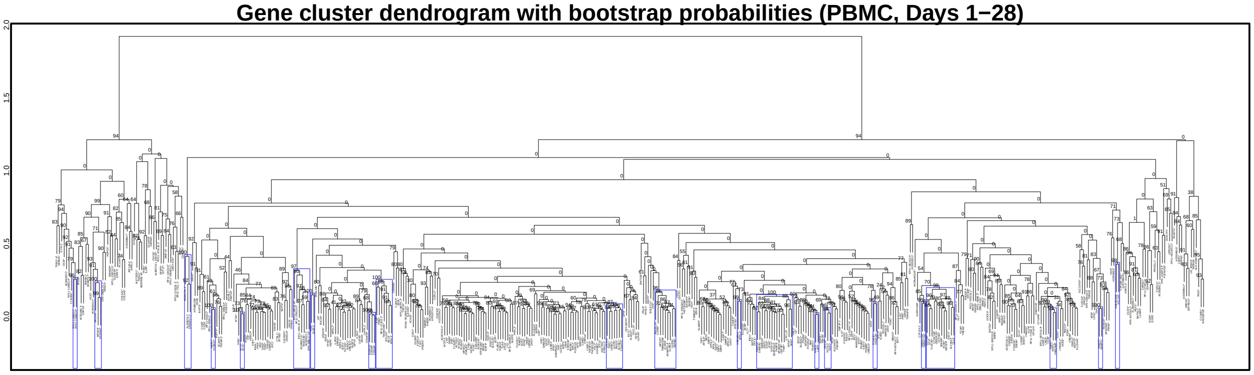


Figure A17: Gene cluster dendrogram with bootstrap probabilities (RNA-Seq, PBMC, Day 1-28). The y axis shows the distance at which clusters were formed by the complete linkage clustering algorithm based on uncentered Pearson correlation distance between log_2 fold changes. Multiscale bootstrap probabilities are shown at each branch intersection. Significant clusters are highlighted in blue. Asterisks indicate genes that were significantly expressed at a certain day.

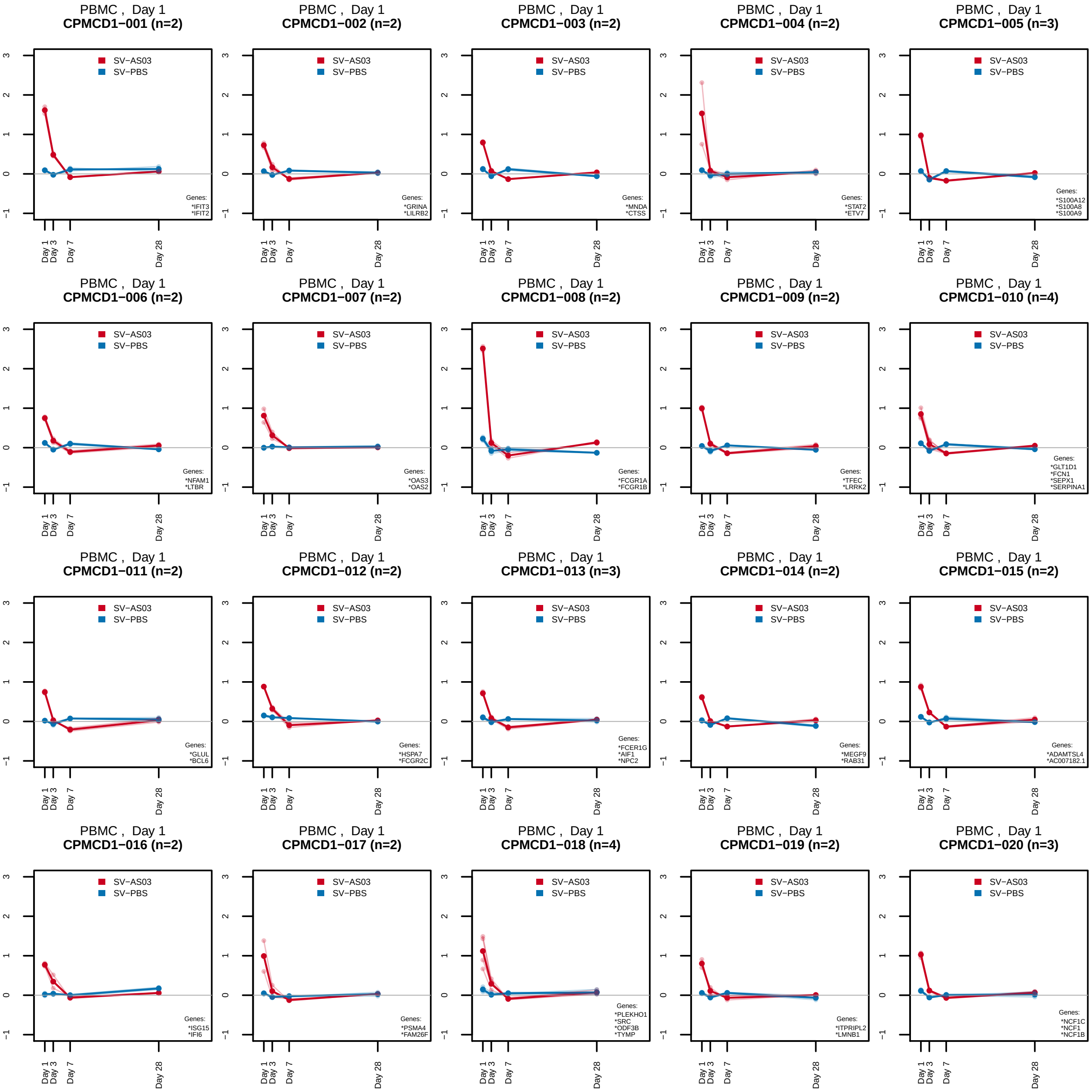


Figure A18: Gene cluster time trends of baseline log_2 fold change by treatment (RNA-Seq, PBMC). Header indicates cluster ID. Mean log_2 fold change across cluster genes is drawn in bold. Individual mean gene log_2 fold changes are plotted in lighter colors. Asterisks indicate significantly differentially expressed genes for a given day.

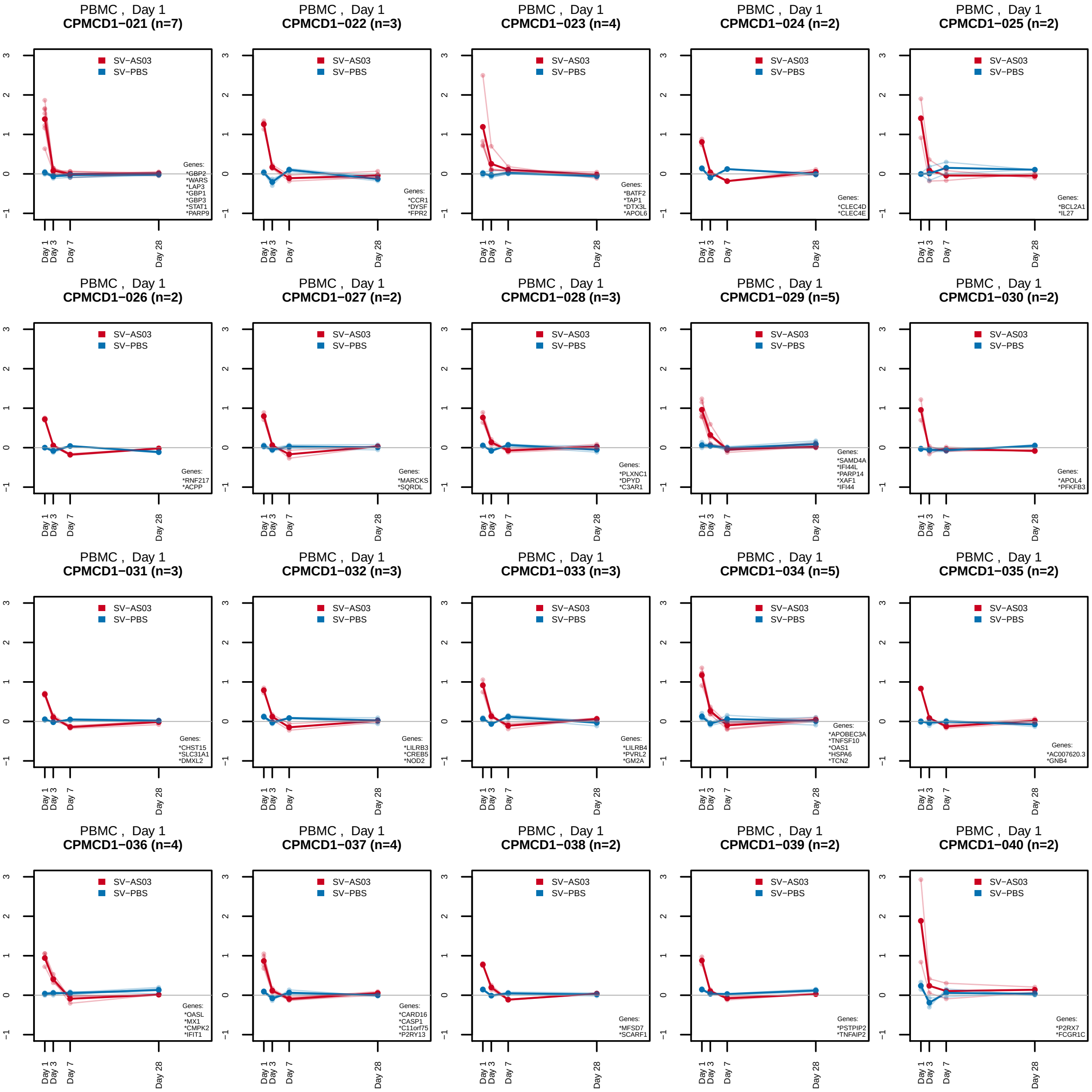


Figure A19: Gene cluster time trends of baseline log_2 fold change by treatment (RNA-Seq, PBMC). Header indicates cluster ID. Mean log_2 fold change across cluster genes is drawn in bold. Individual mean gene log_2 fold changes are plotted in lighter colors. Asterisks indicate significantly differentially expressed genes for a given day.

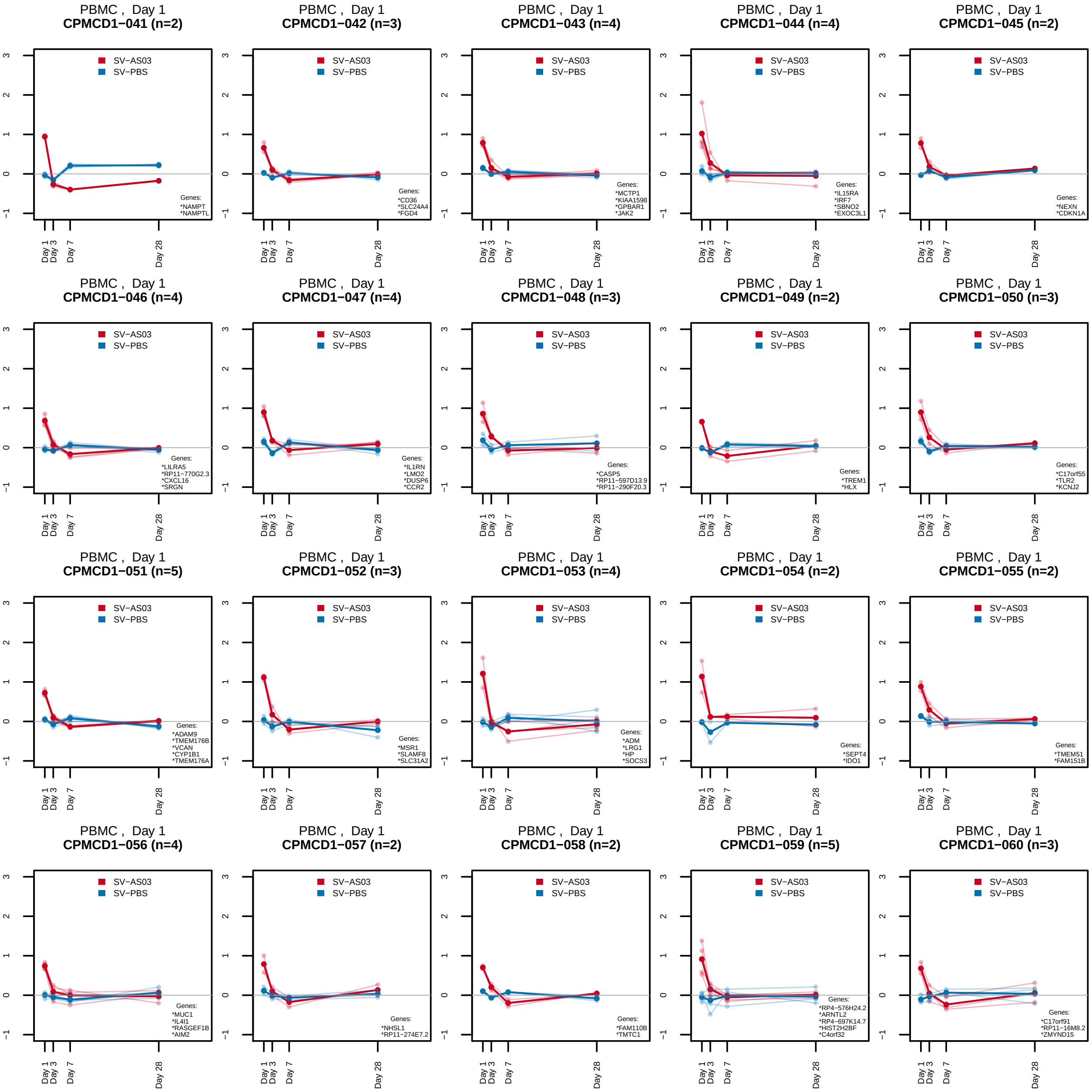
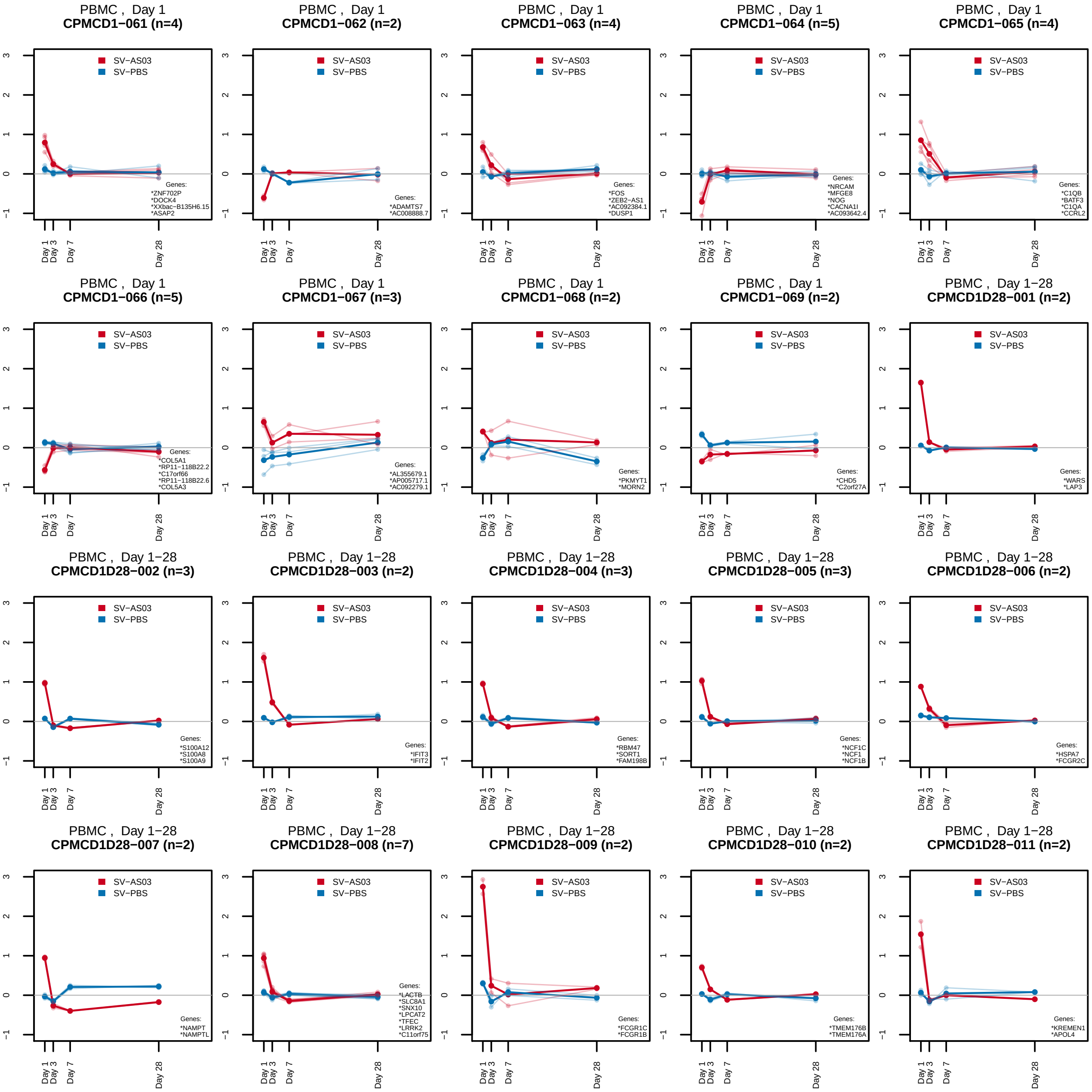


Figure A20: Gene cluster time trends of baseline log_2 fold change by treatment (RNA-Seq, PBMC). Header indicates cluster ID. Mean log_2 fold change across cluster genes is drawn in bold. Individual mean gene log_2 fold changes are plotted in lighter colors. Asterisks indicate significantly differentially expressed genes for a given day.



PBMC , Day 1 **CPMCD1−061 (n=4)**

PBMC , Day 1 **CPMCD1−062 (n=2)**

PBMC , Day 1 **CPMCD1−063 (n=4)**

PBMC , Day 1 **CPMCD1−064 (n=5)**

PBMC , Day 1 **CPMCD1−065 (n=4)**

PBMC , Day 1 **CPMCD1−066 (n=5)**

PBMC , Day 1 **CPMCD1−067 (n=3)**

PBMC , Day 1 **CPMCD1−068 (n=2)**

PBMC , Day 1 **CPMCD1−069 (n=2)**

PBMC , Day 1−28 **CPMCD1D28−001 (n=2)**

PBMC , Day 1−28 **CPMCD1D28−002 (n=3)**

PBMC , Day 1−28 **CPMCD1D28−003 (n=2)**

PBMC , Day 1−28 **CPMCD1D28−004 (n=3)**

PBMC , Day 1−28 **CPMCD1D28−005 (n=3)**

PBMC , Day 1−28 **CPMCD1D28−006 (n=2)**

PBMC , Day 1−28 **CPMCD1D28−007 (n=2)**

PBMC , Day 1−28 **CPMCD1D28−008 (n=7)**

PBMC , Day 1−28 **CPMCD1D28−009 (n=2)**

PBMC , Day 1−28 **CPMCD1D28−010 (n=2)**

PBMC , Day 1−28 **CPMCD1D28−011 (n=2)**

Figure A21: Gene cluster time trends of baseline log_2 fold change by treatment (RNA-Seq, PBMC). Header indicates cluster ID. Mean log_2 fold change across cluster genes is drawn in bold. Individual mean gene log_2 fold changes are plotted in lighter colors. Asterisks indicate significantly differentially expressed genes for a given day.

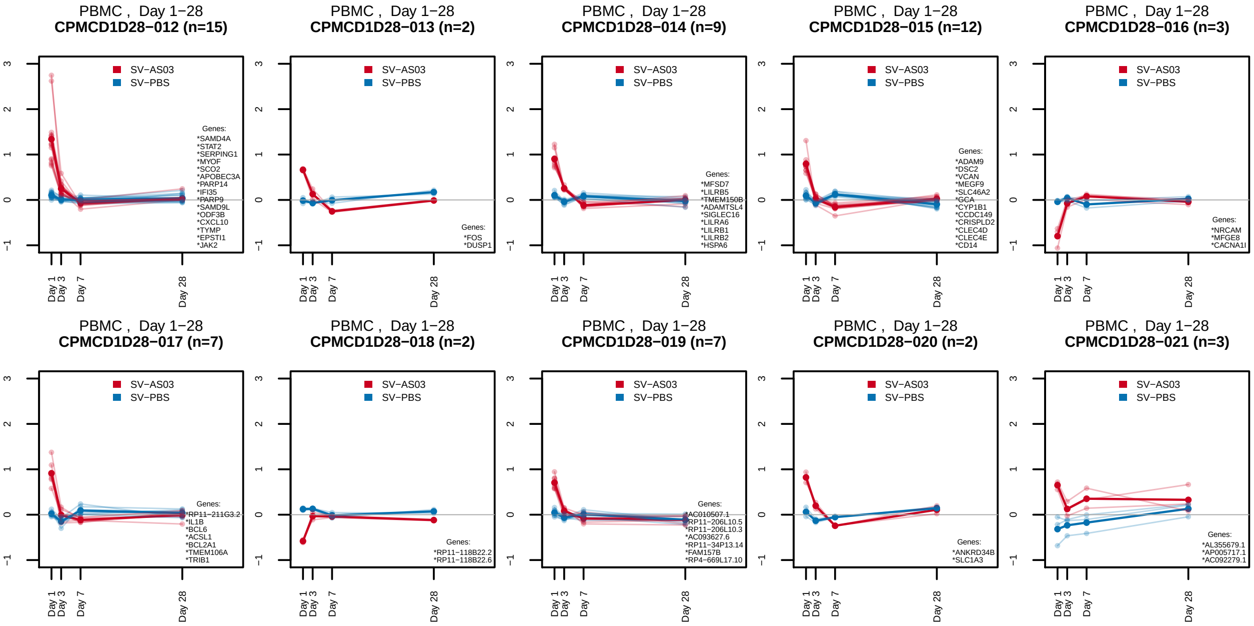


Figure A22: Gene cluster time trends of baseline log_2 fold change by treatment (RNA-Seq, PBMC). Header indicates cluster ID. Mean log_2 fold change across cluster genes is drawn in bold. Individual mean gene log_2 fold changes are plotted in lighter colors. Asterisks indicate significantly differentially expressed genes for a given day.

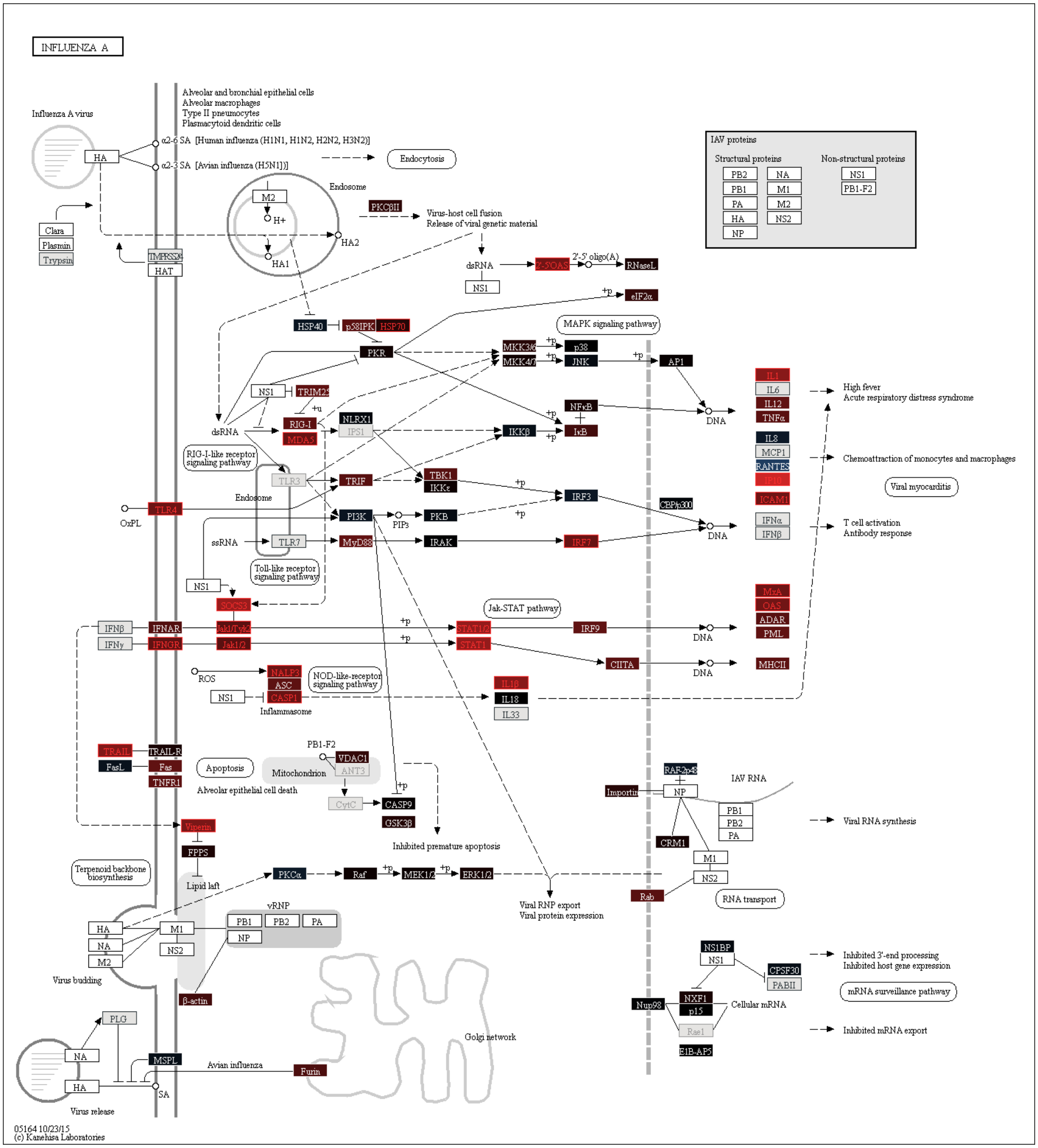


Figure A23: KEGG Pathway Map - Influenza A (RNA-Seq, PBMC, Day 1). Node color gradient encodes mean log_2 fold change difference between treatment groups (for multi-gene nodes the median fold change is used). In red: up-regulated for the SV-AS03 group compared to the SV-PBS group, in blue: down-regulated for the SV-AS03 group compared to the SV-PBS group, in black: fold change close to 1, in dark grey: genes filtered out due to low overall expression, light grey: gene missing database mapping, white: non-human gene. DE genes are highlighted using red (significantly up-regulated in the SV-AS03 group compared to the SV-PBS group) and blue (significantly down-regulated in the SV-AS03 group compared to the SV-PBS group) node label and border colors.

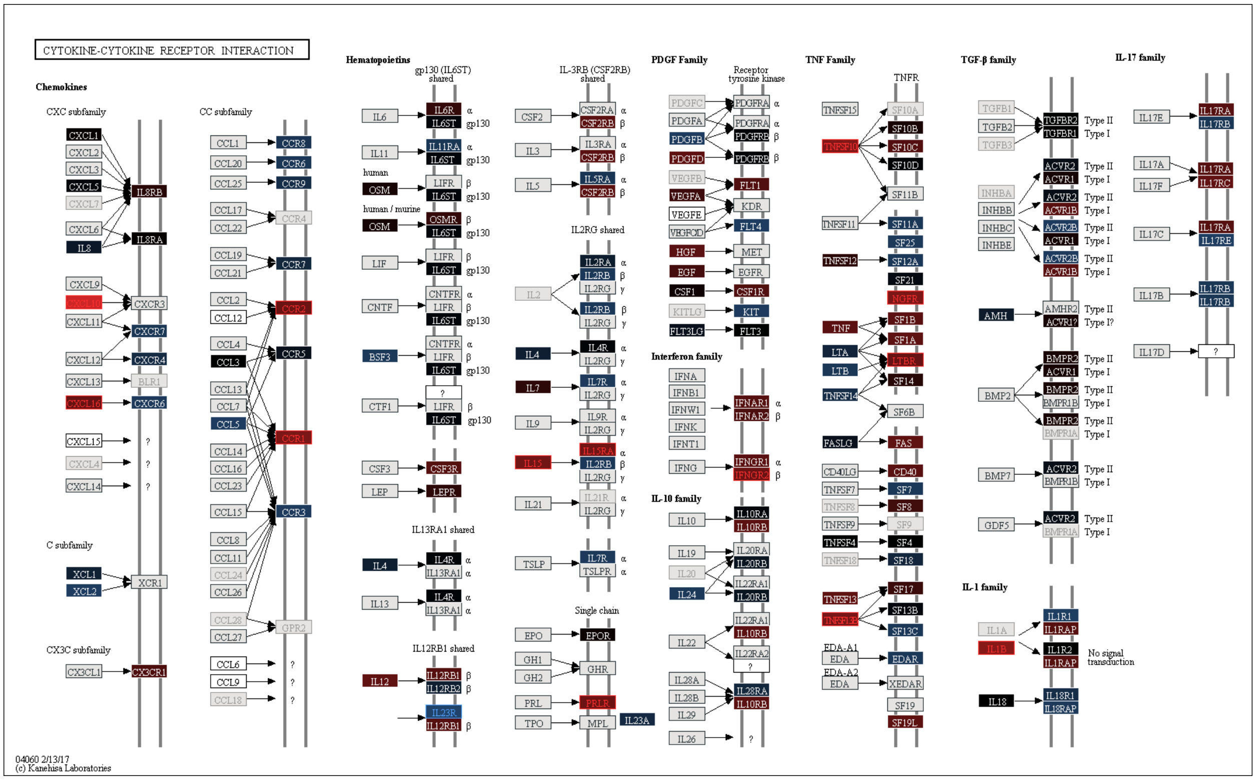


Figure A24: KEGG Pathway Map - Cytokine-cytokine receptor interaction (RNA-Seq, PBMC, Day 1). Node color gradient encodes mean log_2 fold change difference between treatment groups (for multi-gene nodes the median fold change is used). In red: up-regulated for the SV-AS03 group compared to the SV-PBS group, in blue: down-regulated for the SV-AS03 group compared to the SV-PBS group, in black: fold change close to 1, in dark grey: genes filtered out due to low overall expression, light grey: gene missing database mapping, white: non-human gene. DE genes are highlighted using red (significantly up-regulated in the SV-AS03 group compared to the SV-PBS group) and blue (significantly down-regulated in the SV-AS03 group compared to the SV-PBS group) node label and border colors.

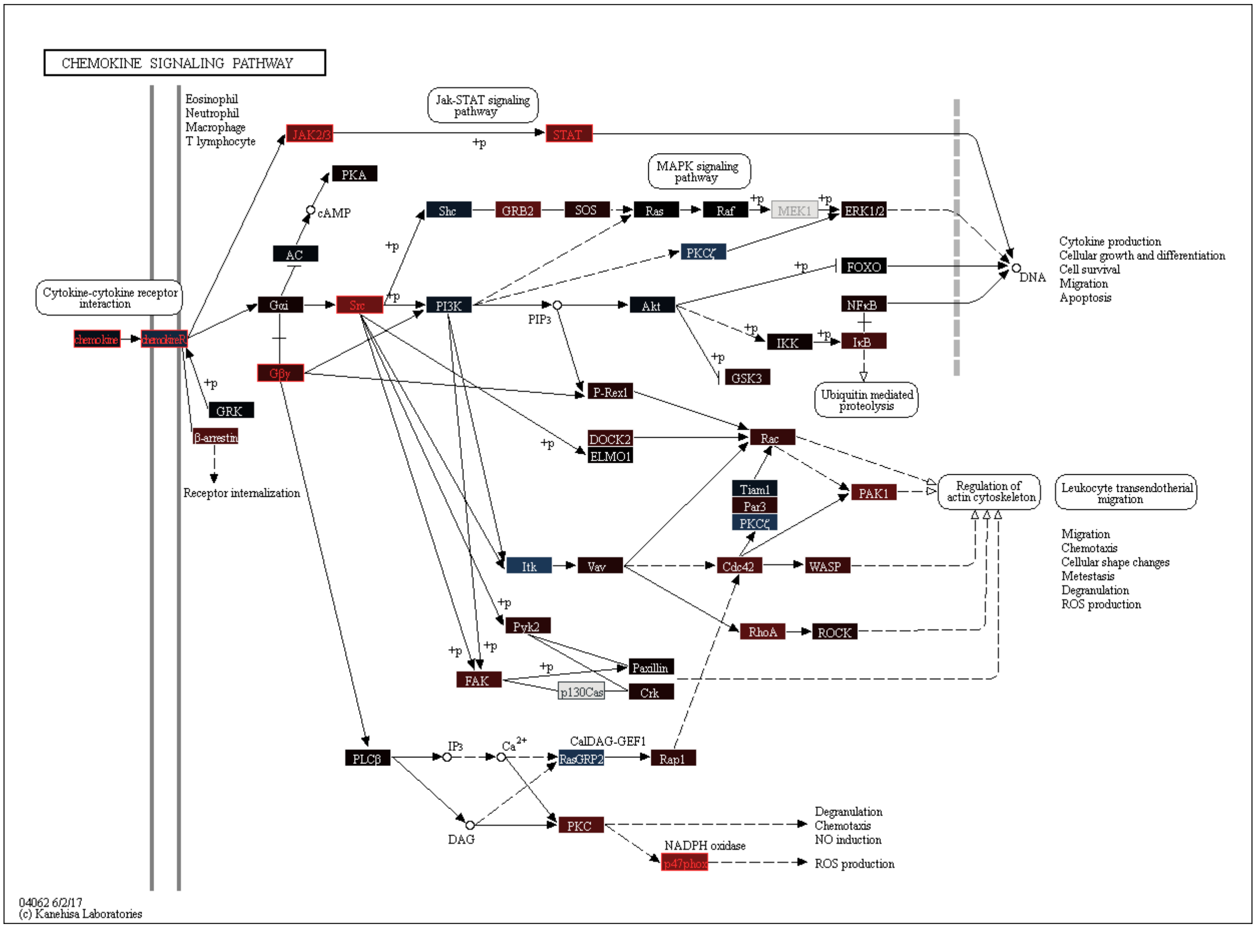


Figure A25: KEGG Pathway Map - Chemokine signaling pathway (RNA-Seq, PBMC, Day 1). Node color gradient encodes mean log_2 fold change difference between treatment groups (for multi-gene nodes the median fold change is used). In red: up-regulated for the SV-AS03 group compared to the SV-PBS group, in blue: down-regulated for the SV-AS03 group compared to the SV-PBS group, in black: fold change close to 1, in dark grey: genes filtered out due to low overall expression, light grey: gene missing database mapping, white: non-human gene. DE genes are highlighted using red (significantly up-regulated in the SV-AS03 group compared to the SV-PBS group) and blue (significantly down-regulated in the SV-AS03 group compared to the SV-PBS group) node label and border colors.

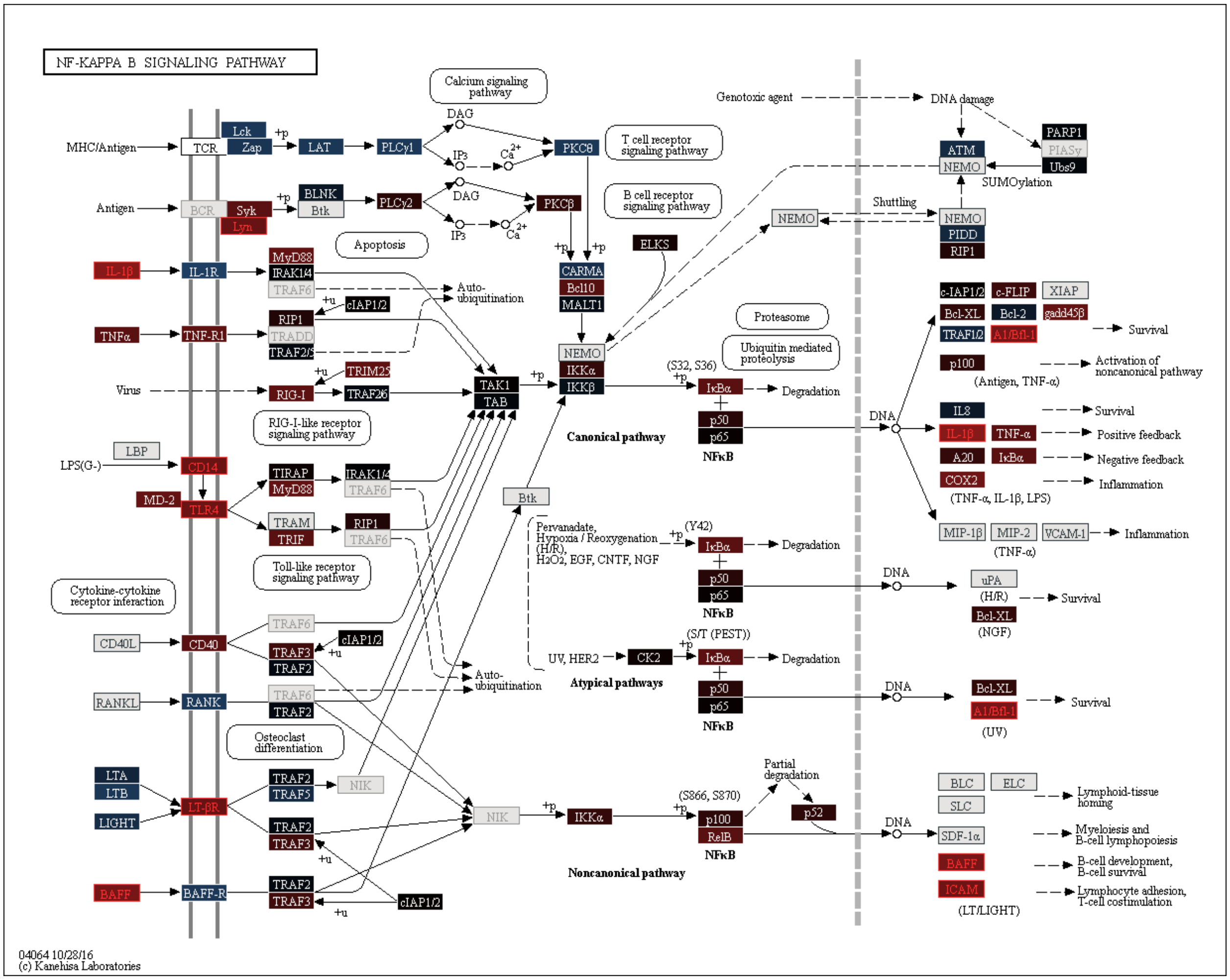


Figure A26: KEGG Pathway Map - NF-kappa B signaling pathway (RNA-Seq, PBMC, Day 1). Node color gradient encodes mean log_2 fold change difference between treatment groups (for multi-gene nodes the median fold change is used). In red: up-regulated for the SV-AS03 group compared to the SV-PBS group, in blue: down-regulated for the SV-AS03 group compared to the SV-PBS group, in black: fold change close to 1, in dark grey: genes filtered out due to low overall expression, light grey: gene missing database mapping, white: non-human gene. DE genes are highlighted using red (significantly up-regulated in the SV-AS03 group compared to the SV-PBS group) and blue (significantly down-regulated in the SV-AS03 group compared to the SV-PBS group) node label and border colors.

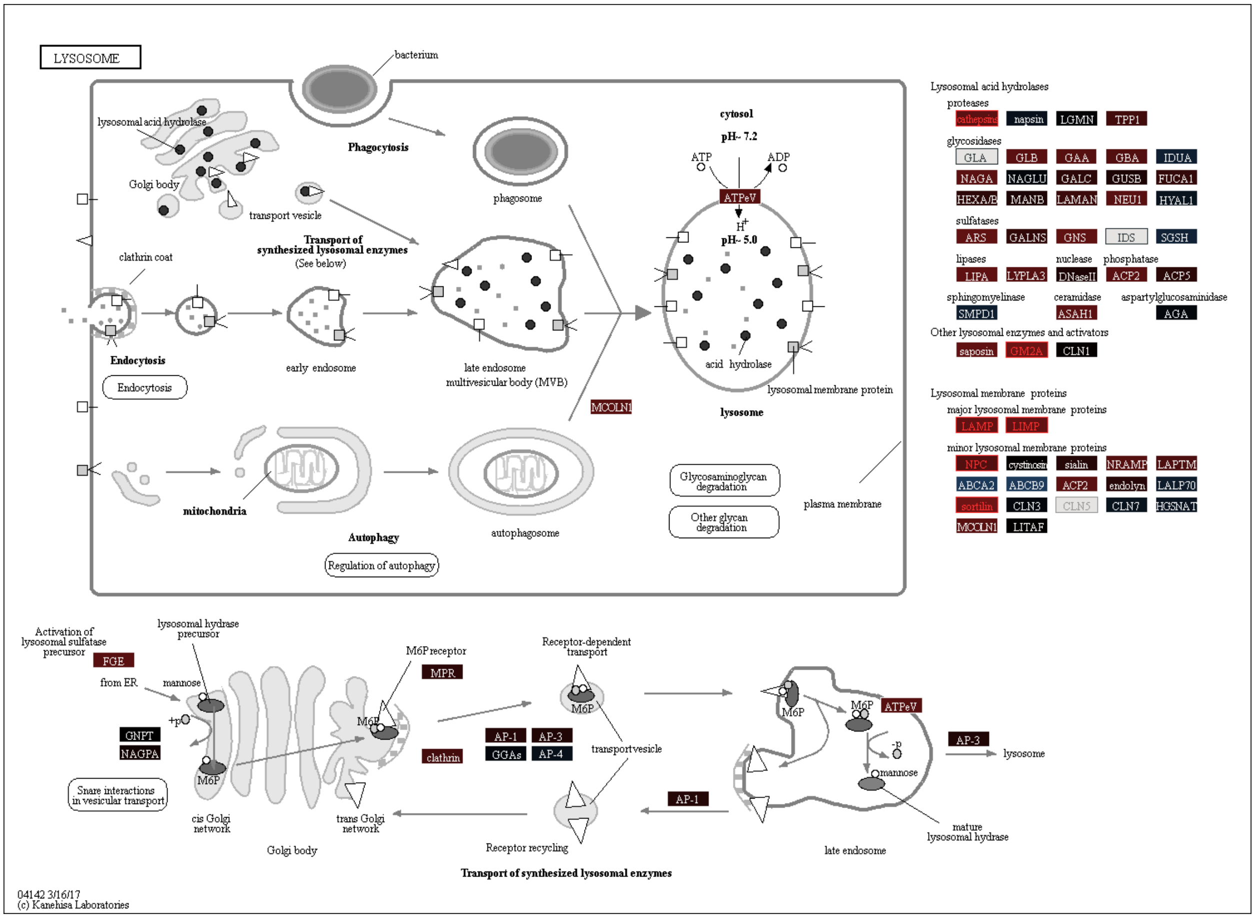


Figure A27: KEGG Pathway Map - Lysosome (RNA-Seq, PBMC, Day 1). Node color gradient encodes mean log_2 fold change difference between treatment groups (for multi-gene nodes the median fold change is used). In red: up-regulated for the SV-AS03 group compared to the SV-PBS group, in blue: down-regulated for the SV-AS03 group compared to the SV-PBS group, in black: fold change close to 1, in dark grey: genes filtered out due to low overall expression, light grey: gene missing database mapping, white: non-human gene. DE genes are highlighted using red (significantly up-regulated in the SV-AS03 group compared to the SV-PBS group) and blue (significantly down-regulated in the SV-AS03 group compared to the SV-PBS group) node label and border colors.

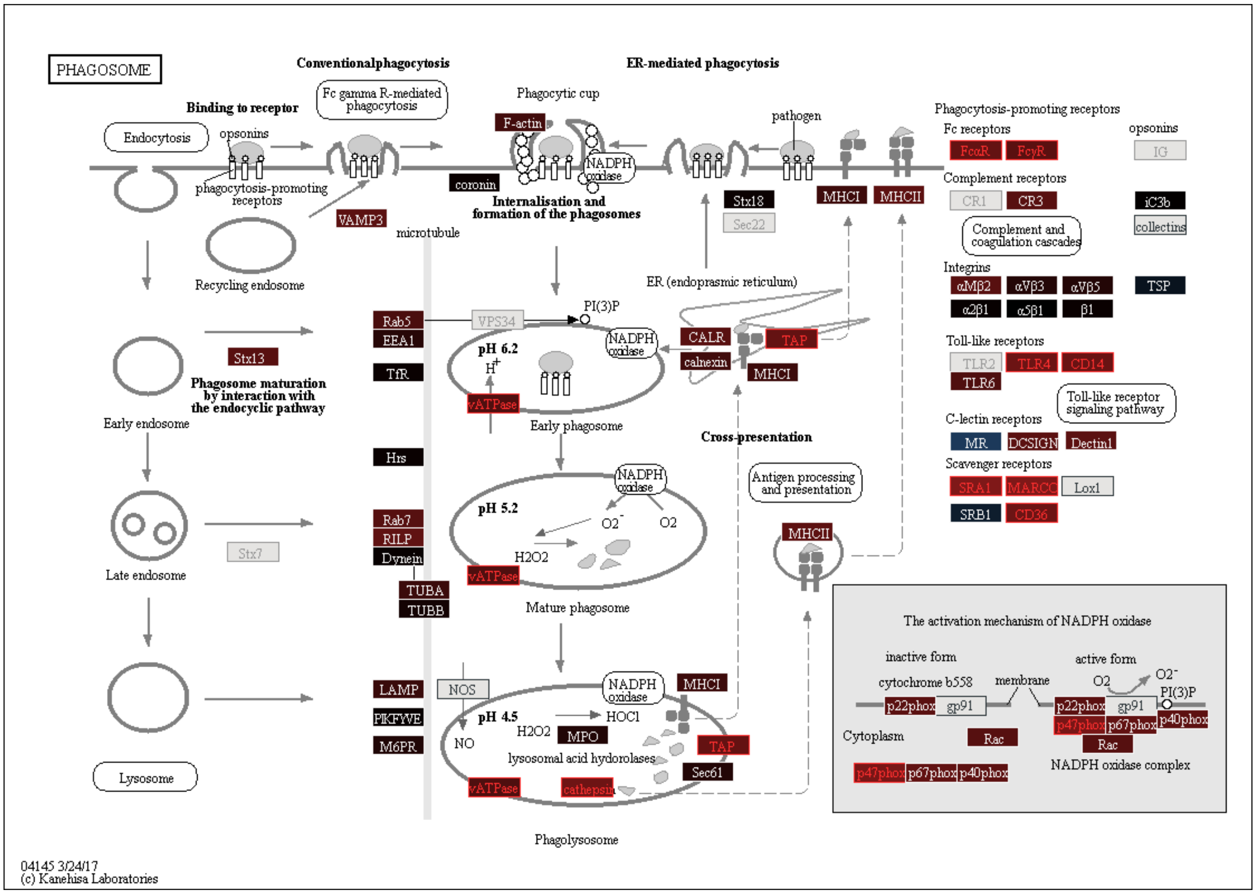


Figure A28: KEGG Pathway Map - Phagosome (RNA-Seq, PBMC, Day 1). Node color gradient encodes mean log_2 fold change difference between treatment groups (for multi-gene nodes the median fold change is used). In red: up-regulated for the SV-AS03 group compared to the SV-PBS group, in blue: down-regulated for the SV-AS03 group compared to the SV-PBS group, in black: fold change close to 1, in dark grey: genes filtered out due to low overall expression, light grey: gene missing database mapping, white: non-human gene. DE genes are highlighted using red (significantly up-regulated in the SV-AS03 group compared to the SV-PBS group) and blue (significantly down-regulated in the SV-AS03 group compared to the SV-PBS group) node label and border colors.

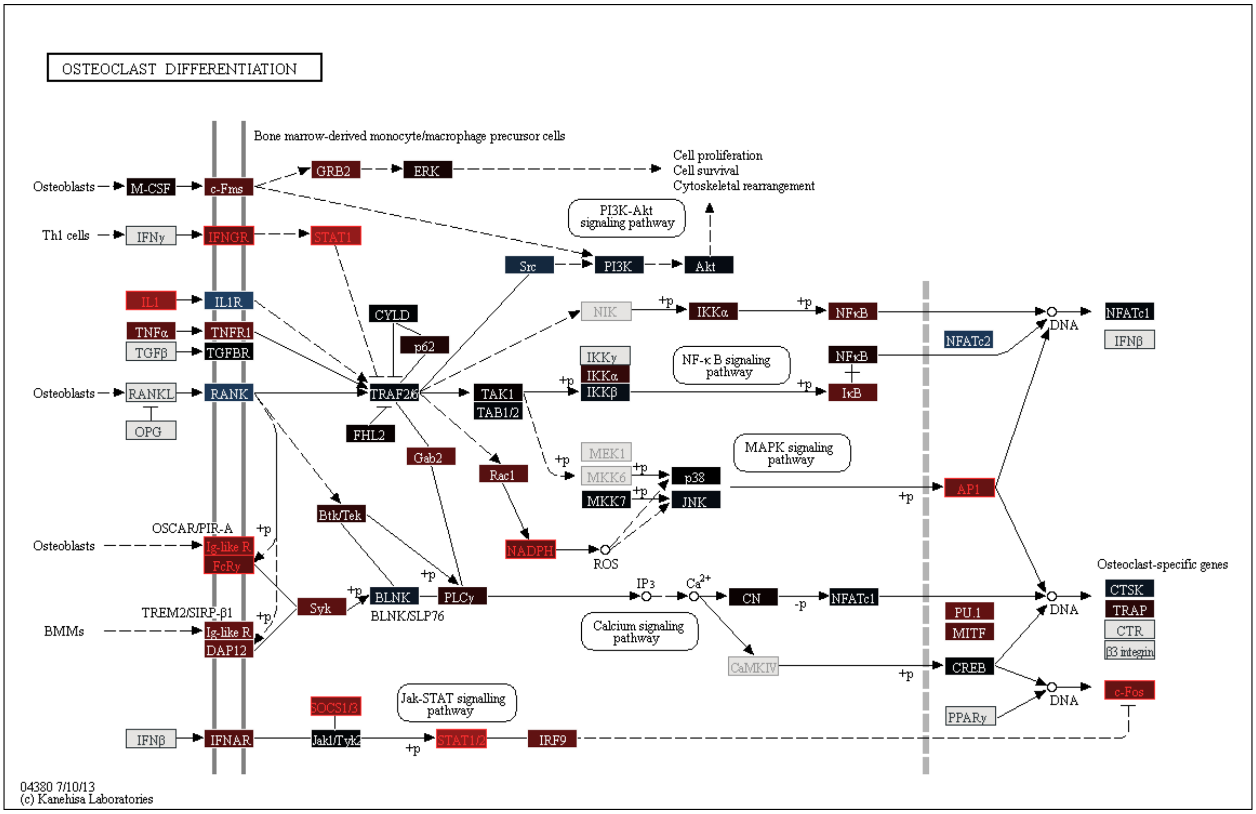


Figure A29: KEGG Pathway Map - Osteoclast differentiation (RNA-Seq, PBMC, Day 1). Node color gradient encodes mean log_2 fold change difference between treatment groups (for multi-gene nodes the median fold change is used). In red: up-regulated for the SV-AS03 group compared to the SV-PBS group, in blue: down-regulated for the SV-AS03 group compared to the SV-PBS group, in black: fold change close to 1, in dark grey: genes filtered out due to low overall expression, light grey: gene missing database mapping, white: non-human gene. DE genes are highlighted using red (significantly up-regulated in the SV-AS03 group compared to the SV-PBS group) and blue (significantly down-regulated in the SV-AS03 group compared to the SV-PBS group) node label and border colors.

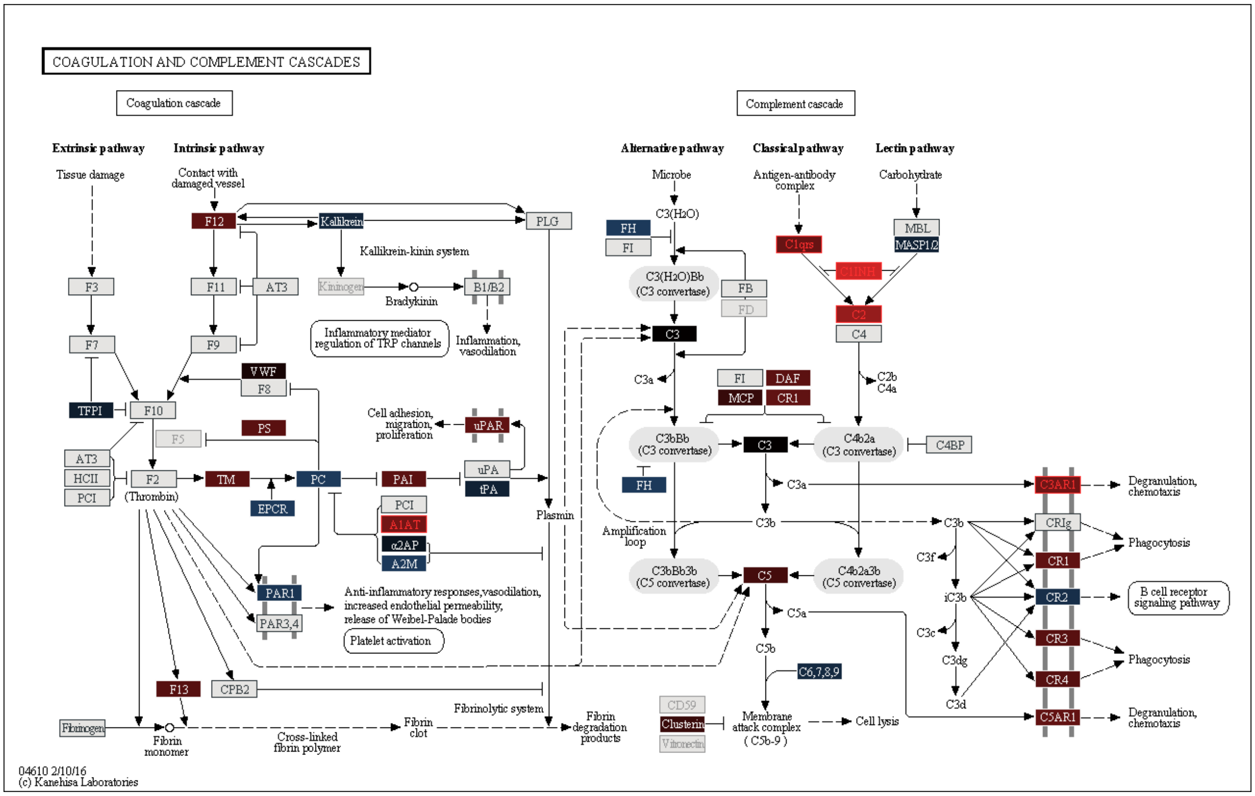


Figure A30: KEGG Pathway Map - Complement and coagulation cascades (RNA-Seq, PBMC, Day 1). Node color gradient encodes mean log_2 fold change difference between treatment groups (for multi-gene nodes the median fold change is used). In red: up-regulated for the SV-AS03 group compared to the SV-PBS group, in blue: down-regulated for the SV-AS03 group compared to the SV-PBS group, in black: fold change close to 1, in dark grey: genes filtered out due to low overall expression, light grey: gene missing database mapping, white: non-human gene. DE genes are highlighted using red (significantly up-regulated in the SV-AS03 group compared to the SV-PBS group) and blue (significantly down-regulated in the SV-AS03 group compared to the SV-PBS group) node label and border colors.

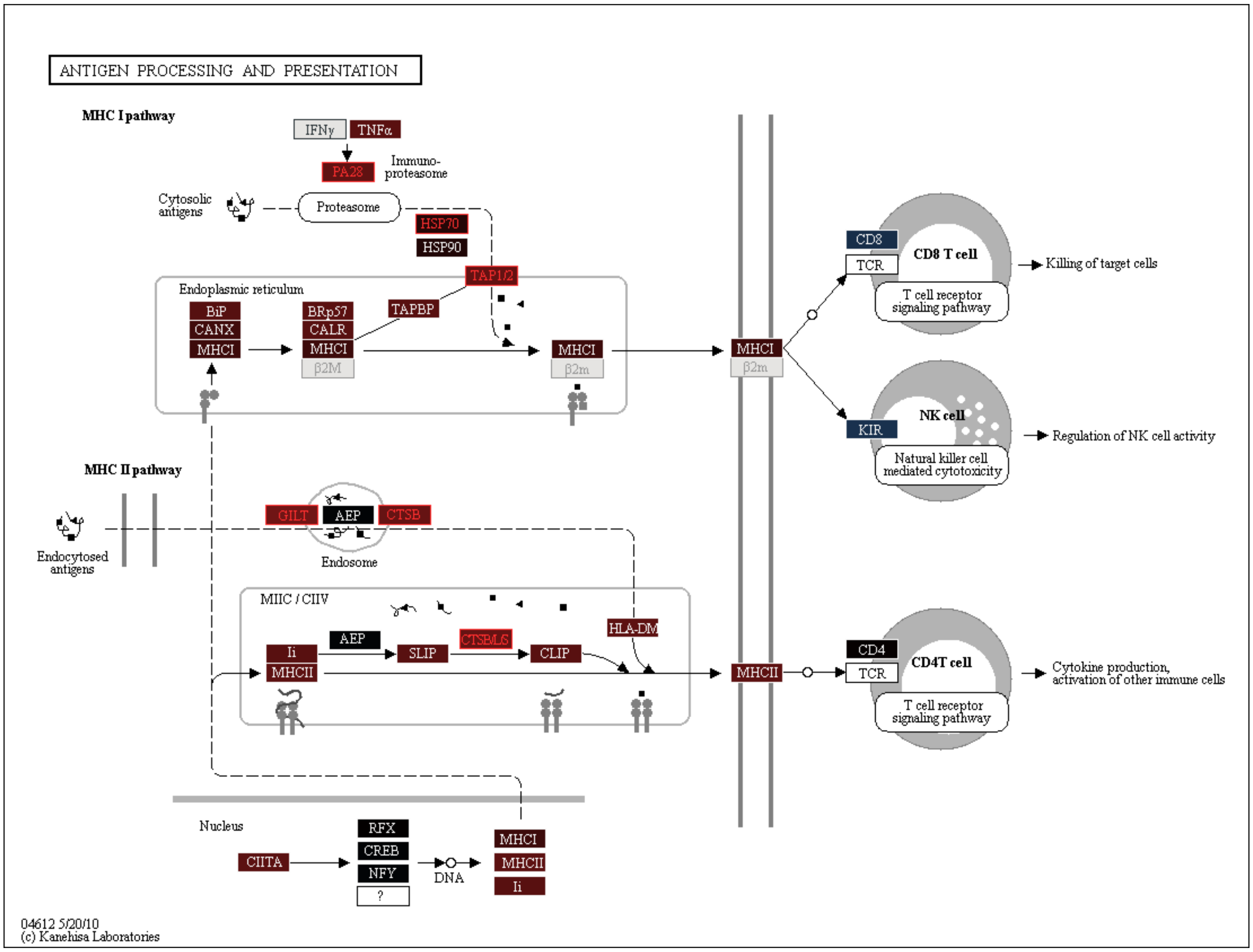


Figure A31: KEGG Pathway Map - Antigen processing and presentation (RNA-Seq, PBMC, Day 1). Node color gradient encodes mean log_2 fold change difference between treatment groups (for multi-gene nodes the median fold change is used). In red: up-regulated for the SV-AS03 group compared to the SV-PBS group, in blue: down-regulated for the SV-AS03 group compared to the SV-PBS group, in black: fold change close to 1, in dark grey: genes filtered out due to low overall expression, light grey: gene missing database mapping, white: non-human gene. DE genes are highlighted using red (significantly up-regulated in the SV-AS03 group compared to the SV-PBS group) and blue (significantly down-regulated in the SV-AS03 group compared to the SV-PBS group) node label and border colors.

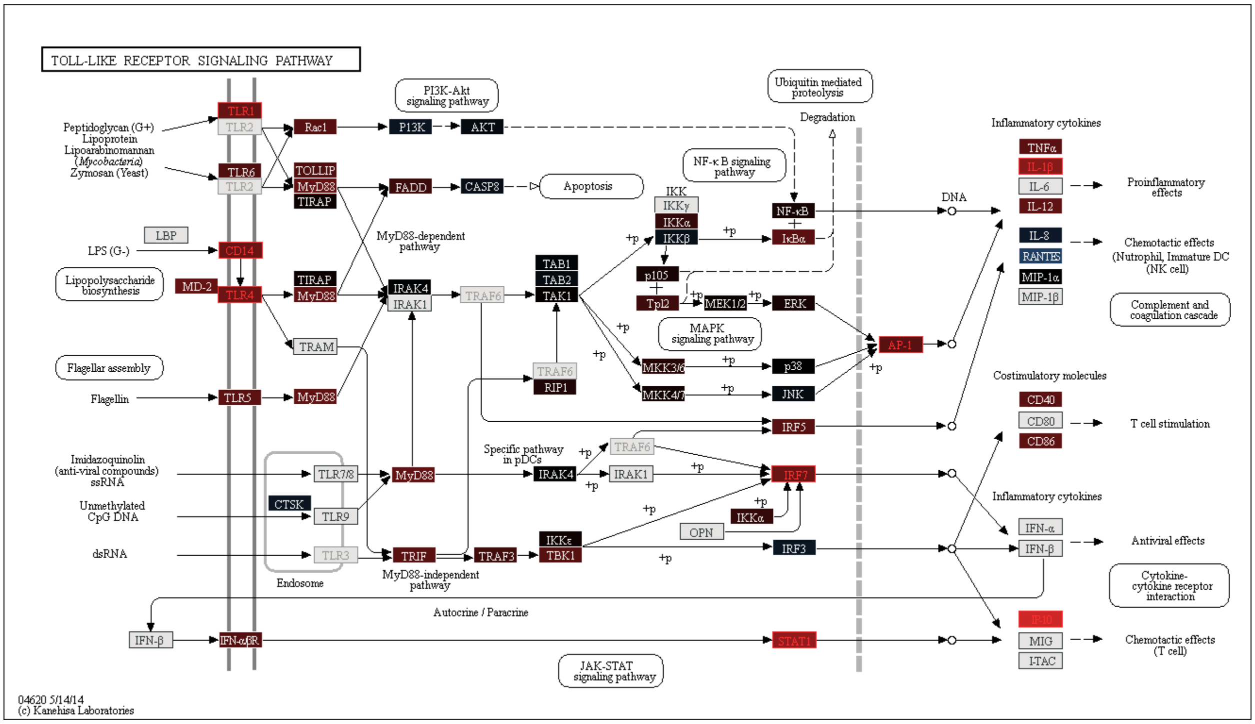


Figure A32: KEGG Pathway Map - Toll-like receptor signaling pathway (RNA-Seq, PBMC, Day 1). Node color gradient encodes mean log_2 fold change difference between treatment groups (for multi-gene nodes the median fold change is used). In red: up-regulated for the SV-AS03 group compared to the SV-PBS group, in blue: down-regulated for the SV-AS03 group compared to the SV-PBS group, in black: fold change close to 1, in dark grey: genes filtered out due to low overall expression, light grey: gene missing database mapping, white: non-human gene. DE genes are highlighted using red (significantly up-regulated in the SV-AS03 group compared to the SV-PBS group) and blue (significantly down-regulated in the SV-AS03 group compared to the SV-PBS group) node label and border colors.

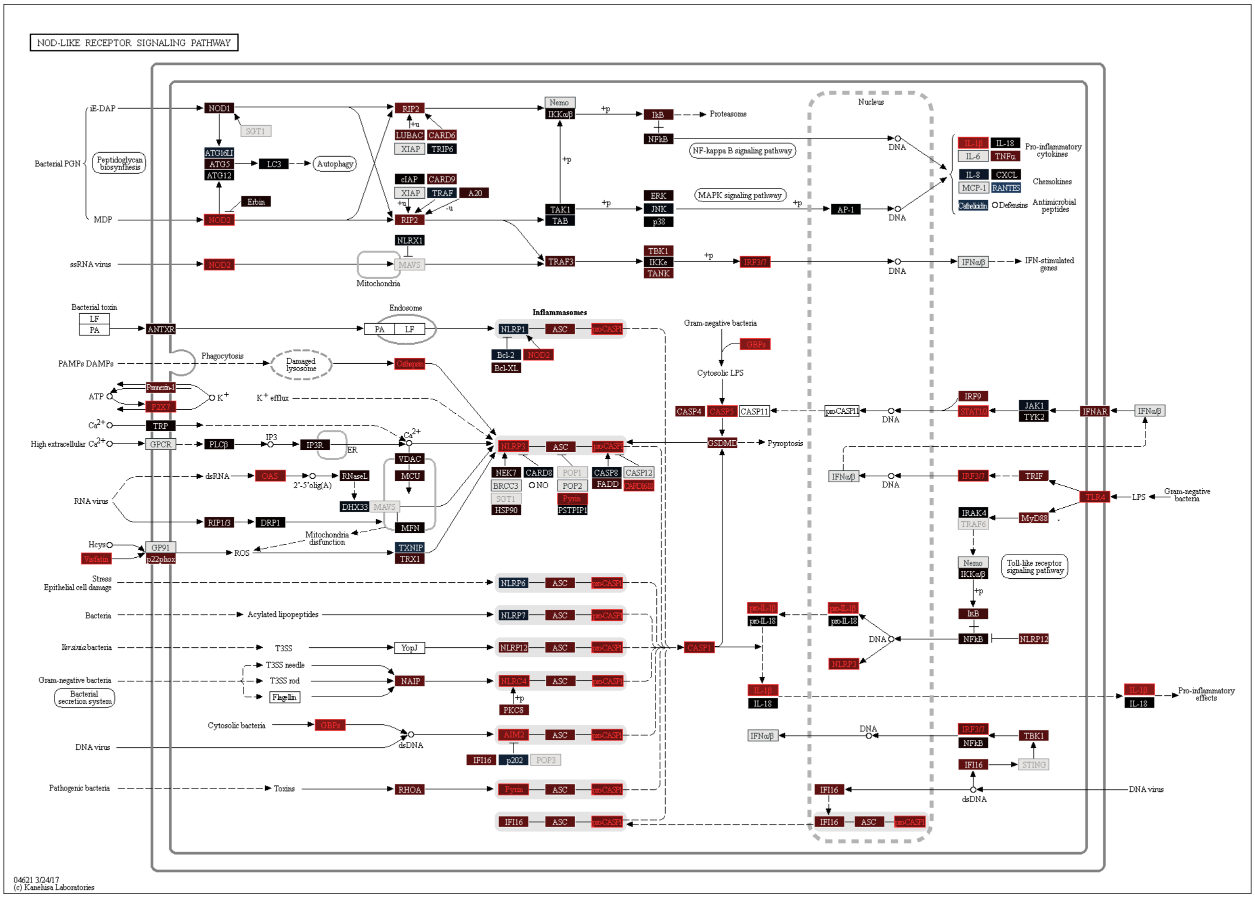


Figure A33: KEGG Pathway Map - NOD-like receptor signaling pathway (RNA-Seq, PBMC, Day 1). Node color gradient encodes mean log_2 fold change difference between treatment groups (for multi-gene nodes the median fold change is used). In red: up-regulated for the SV-AS03 group compared to the SV-PBS group, in blue: down-regulated for the SV-AS03 group compared to the SV-PBS group, in black: fold change close to 1, in dark grey: genes filtered out due to low overall expression, light grey: gene missing database mapping, white: non-human gene. DE genes are highlighted using red (significantly up-regulated in the SV-AS03 group compared to the SV-PBS group) and blue (significantly down-regulated in the SV-AS03 group compared to the SV-PBS group) node label and border colors.

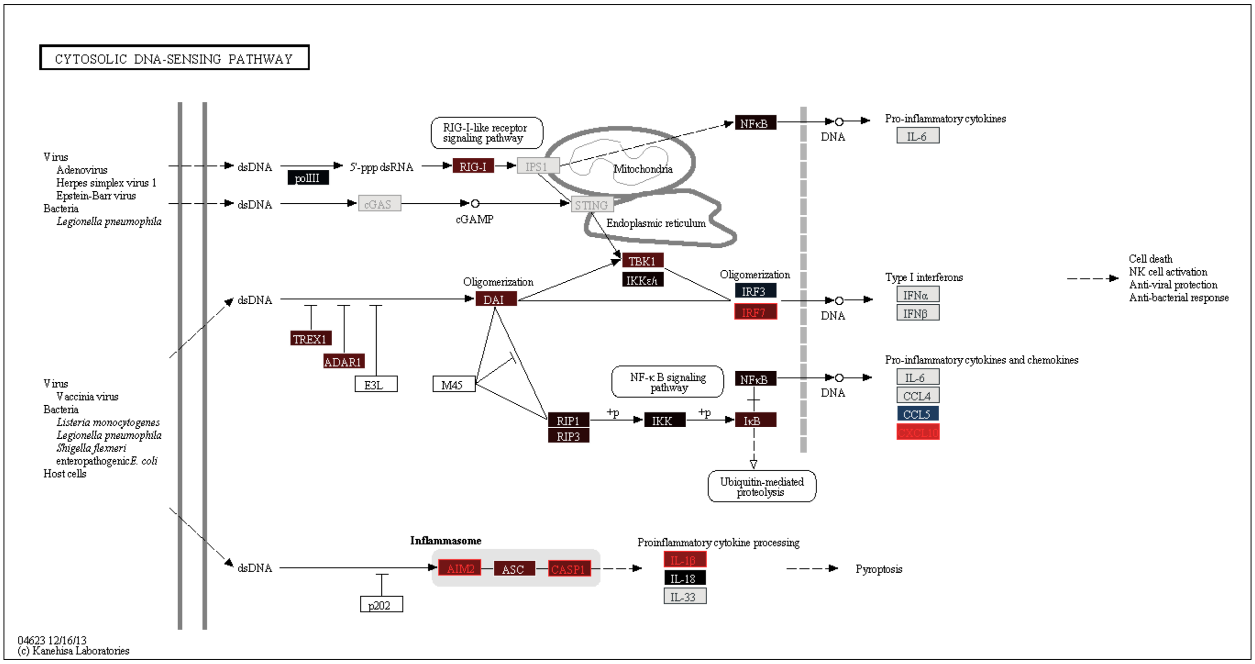


Figure A34: KEGG Pathway Map - Cytosolic DNA-sensing pathway (RNA-Seq, PBMC, Day 1). Node color gradient encodes mean log_2 fold change difference between treatment groups (for multi-gene nodes the median fold change is used). In red: up-regulated for the SV-AS03 group compared to the SV-PBS group, in blue: down-regulated for the SV-AS03 group compared to the SV-PBS group, in black: fold change close to 1, in dark grey: genes filtered out due to low overall expression, light grey: gene missing database mapping, white: non-human gene. DE genes are highlighted using red (significantly up-regulated in the SV-AS03 group compared to the SV-PBS group) and blue (significantly down-regulated in the SV-AS03 group compared to the SV-PBS group) node label and border colors.

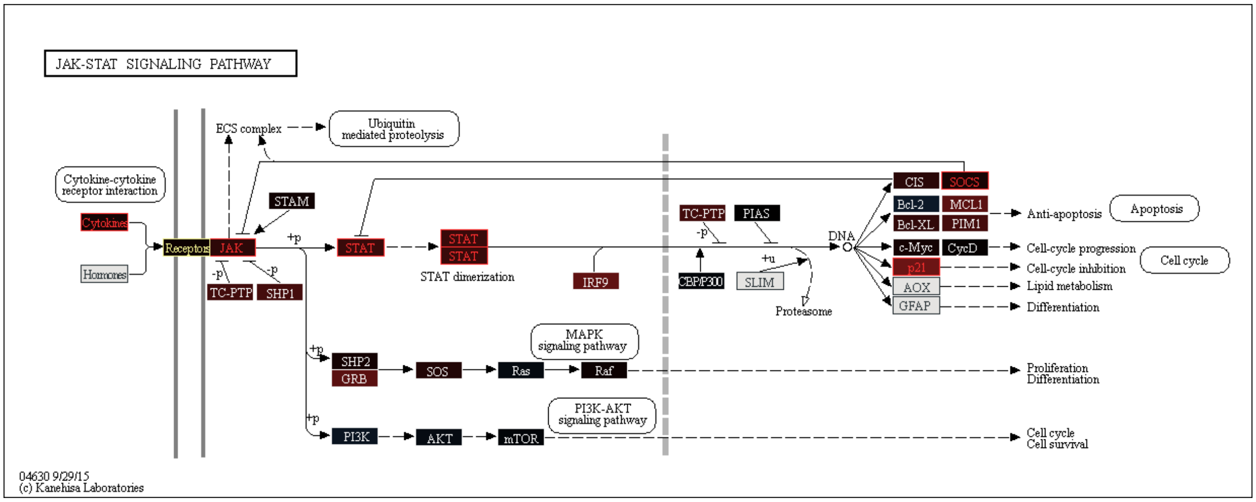


Figure A35: KEGG Pathway Map - Jak-STAT signaling pathway (RNA-Seq, PBMC, Day 1). Node color gradient encodes mean log_2 fold change difference between treatment groups (for multi-gene nodes the median fold change is used). In red: up-regulated for the SV-AS03 group compared to the SV-PBS group, in blue: down-regulated for the SV-AS03 group compared to the SV-PBS group, in black: fold change close to 1, in dark grey: genes filtered out due to low overall expression, light grey: gene missing database mapping, white: non-human gene. DE genes are highlighted using red (significantly up-regulated in the SV-AS03 group compared to the SV-PBS group) and blue (significantly down-regulated in the SV-AS03 group compared to the SV-PBS group) node label and border colors.

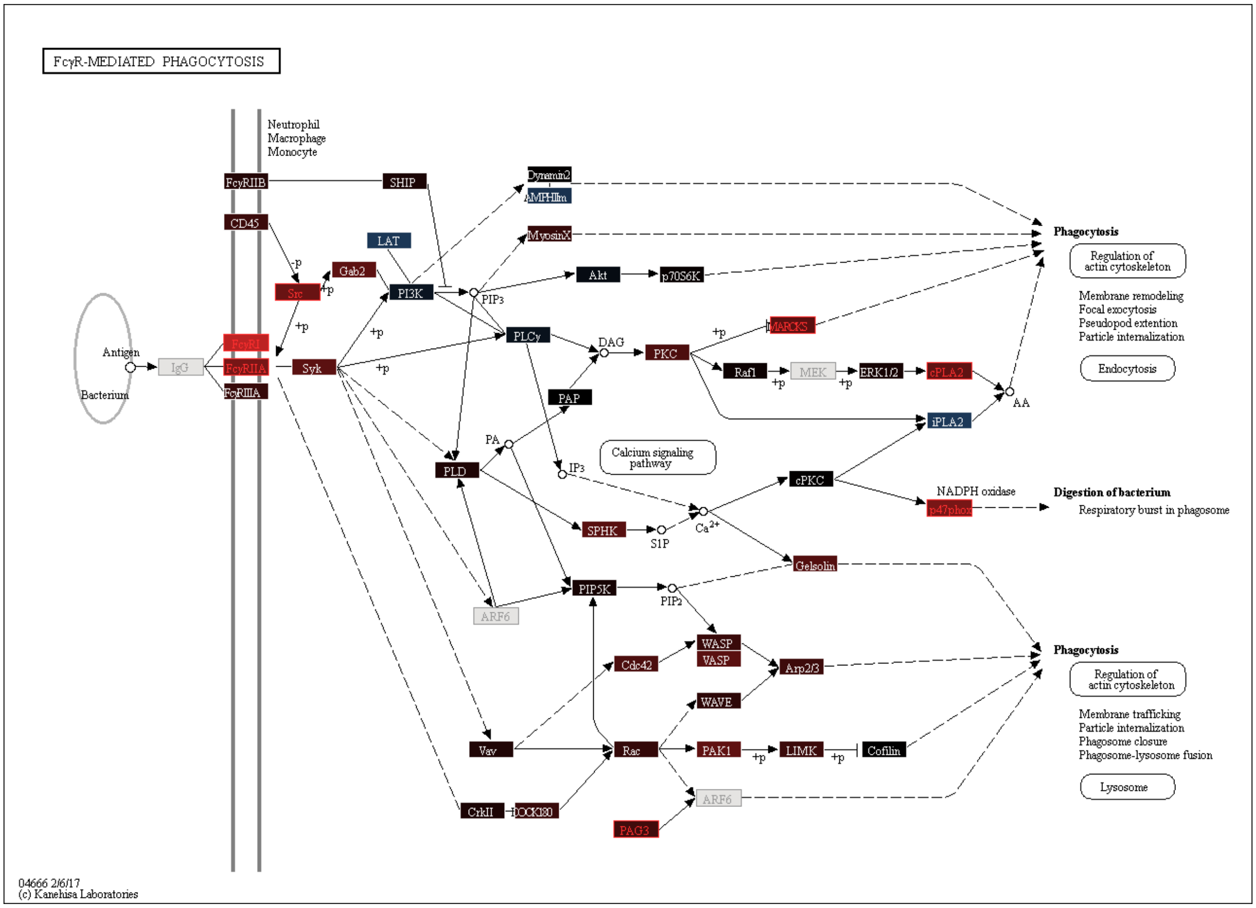


Figure A36: KEGG Pathway Map - Fc gamma R-mediated phagocytosis (RNA-Seq, PBMC, Day 1). Node color gradient encodes mean log_2 fold change difference between treatment groups (for multi-gene nodes the median fold change is used). In red: up-regulated for the SV-AS03 group compared to the SV-PBS group, in blue: down-regulated for the SV-AS03 group compared to the SV-PBS group, in black: fold change close to 1, in dark grey: genes filtered out due to low overall expression, light grey: gene missing database mapping, white: non-human gene. DE genes are highlighted using red (significantly up-regulated in the SV-AS03 group compared to the SV-PBS group) and blue (significantly down-regulated in the SV-AS03 group compared to the SV-PBS group) node label and border colors.

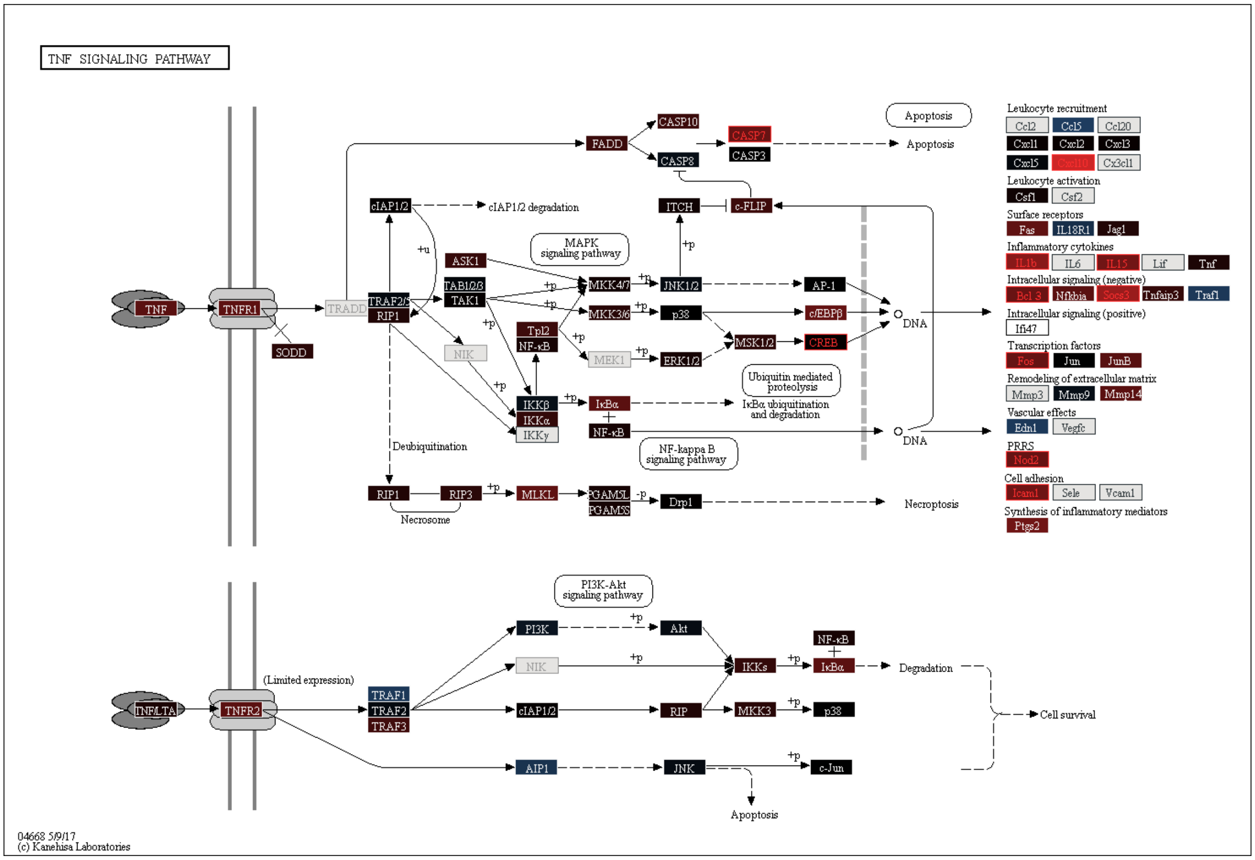


Figure A37: KEGG Pathway Map - TNF signaling pathway (RNA-Seq, PBMC, Day 1). Node color gradient encodes mean log_2 fold change difference between treatment groups (for multi-gene nodes the median fold change is used). In red: up-regulated for the SV-AS03 group compared to the SV-PBS group, in blue: down-regulated for the SV-AS03 group compared to the SV-PBS group, in black: fold change close to 1, in dark grey: genes filtered out due to low overall expression, light grey: gene missing database mapping, white: non-human gene. DE genes are highlighted using red (significantly up-regulated in the SV-AS03 group compared to the SV-PBS group) and blue (significantly down-regulated in the SV-AS03 group compared to the SV-PBS group) node label and border colors.

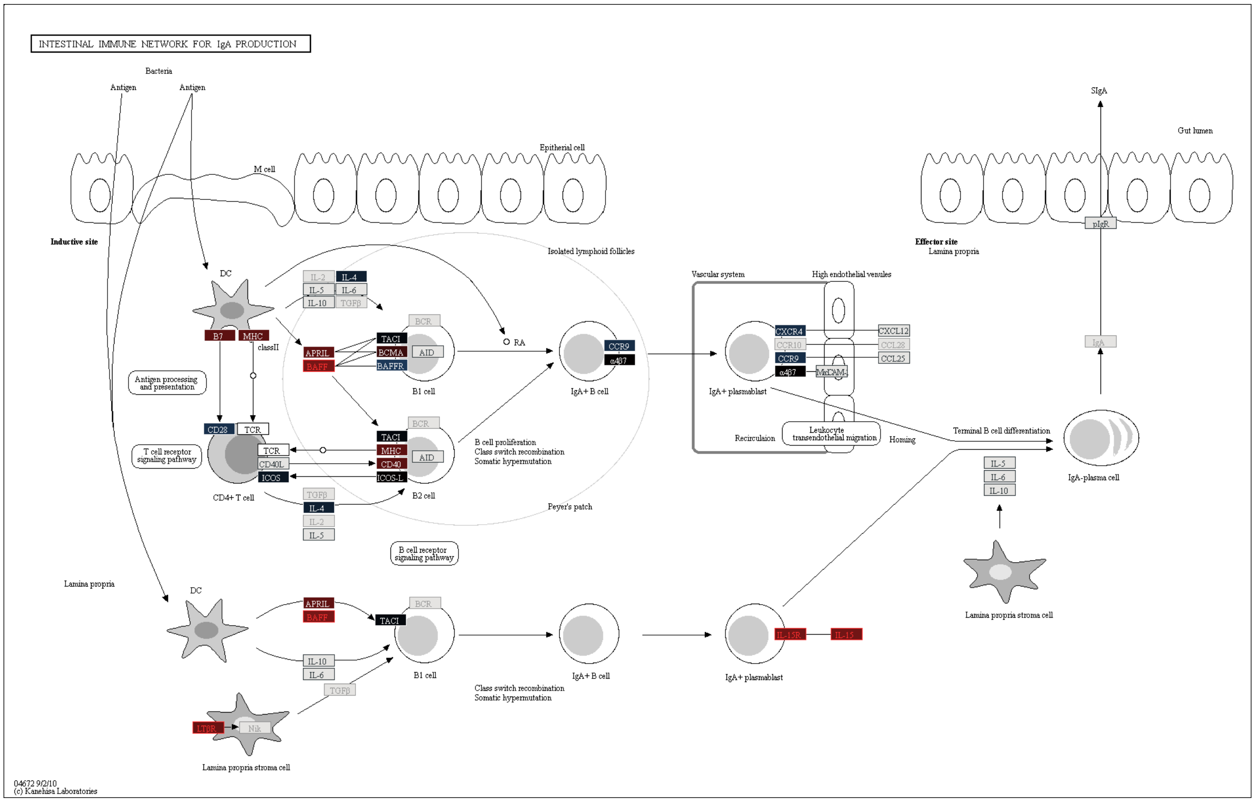


Figure A38: KEGG Pathway Map - Intestinal immune network for IgA production (RNA-Seq, PBMC, Day 1). Node color gradient encodes mean log_2 fold change difference between treatment groups (for multi-gene nodes the median fold change is used). In red: up-regulated for the SV-AS03 group compared to the SV-PBS group, in blue: down-regulated for the SV-AS03 group compared to the SV-PBS group, in black: fold change close to 1, in dark grey: genes filtered out due to low overall expression, light grey: gene missing database mapping, white: non-human gene. DE genes are highlighted using red (significantly up-regulated in the SV-AS03 group compared to the SV-PBS group) and blue (significantly down-regulated in the SV-AS03 group compared to the SV-PBS group) node label and border colors.

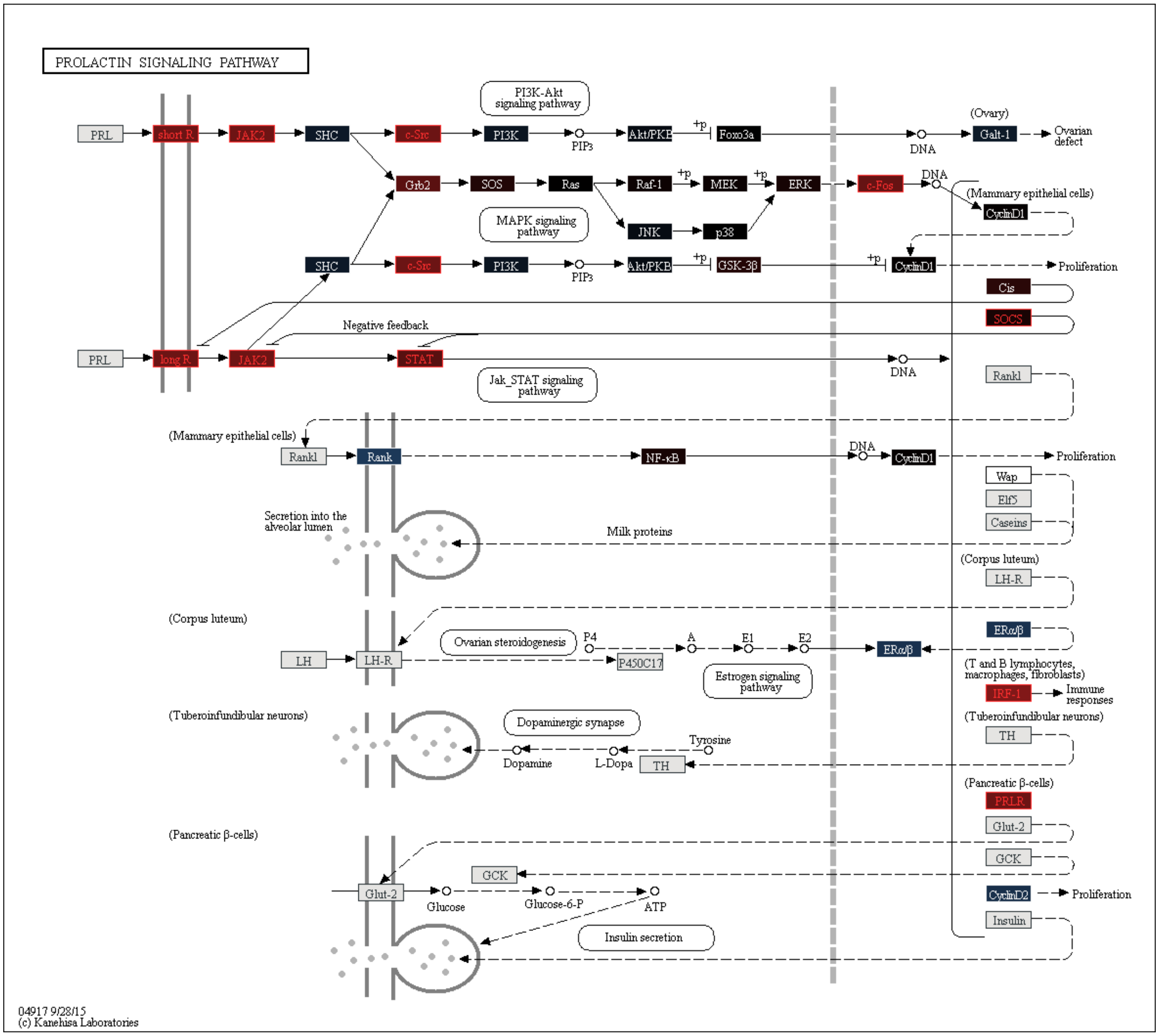


Figure A39: KEGG Pathway Map - Prolactin signaling pathway (RNA-Seq, PBMC, Day 1). Node color gradient encodes mean log_2 fold change difference between treatment groups (for multi-gene nodes the median fold change is used). In red: up-regulated for the SV-AS03 group compared to the SV-PBS group, in blue: down-regulated for the SV-AS03 group compared to the SV-PBS group, in black: fold change close to 1, in dark grey: genes filtered out due to low overall expression, light grey: gene missing database mapping, white: non-human gene. DE genes are highlighted using red (significantly up-regulated in the SV-AS03 group compared to the SV-PBS group) and blue (significantly down-regulated in the SV-AS03 group compared to the SV-PBS group) node label and border colors.

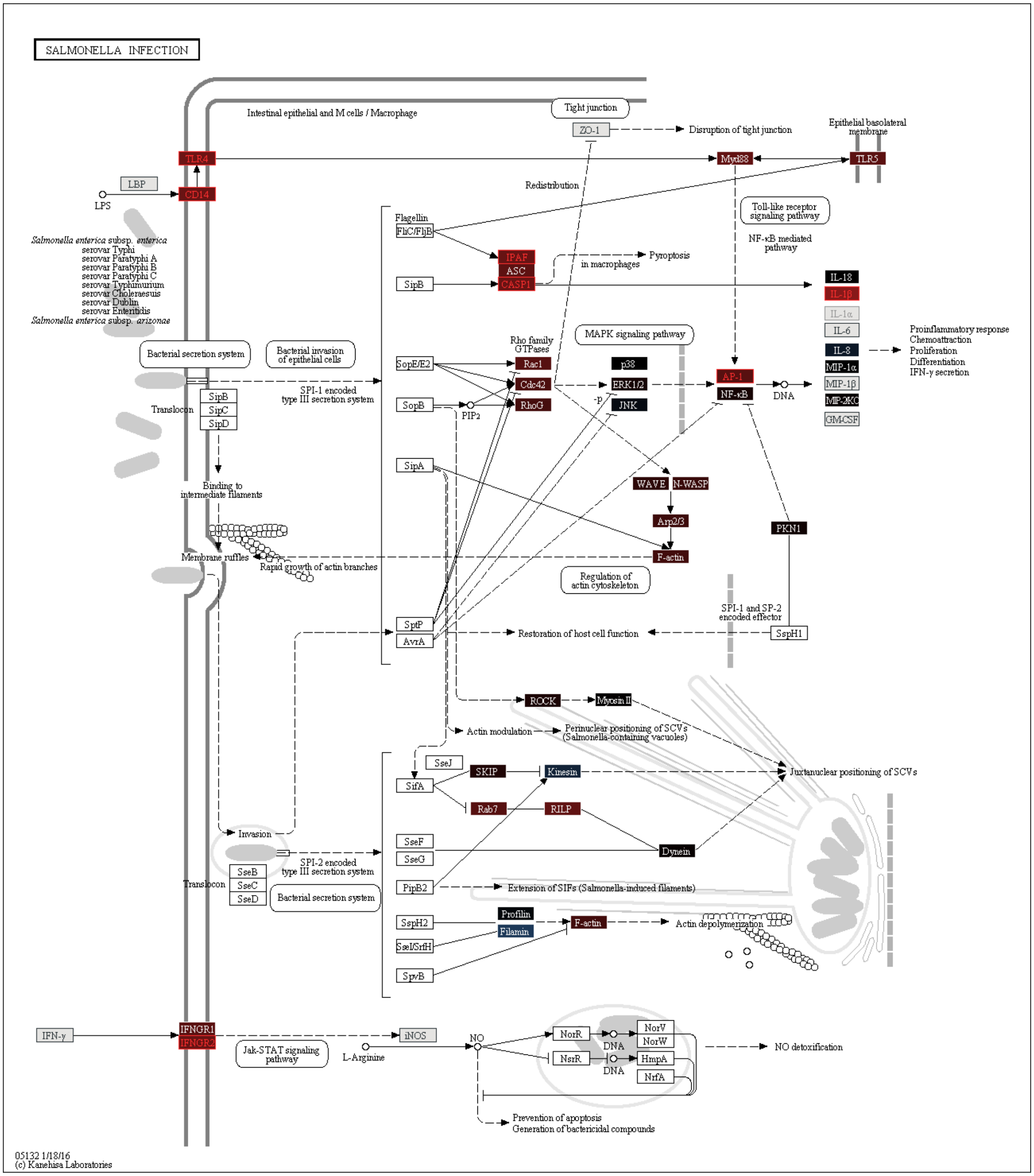


Figure A40: KEGG Pathway Map - Salmonella infection (RNA-Seq, PBMC, Day 1). Node color gradient encodes mean log_2 fold change difference between treatment groups (for multi-gene nodes the median fold change is used). In red: up-regulated for the SV-AS03 group compared to the SV-PBS group, in blue: down-regulated for the SV-AS03 group compared to the SV-PBS group, in black: fold change close to 1, in dark grey: genes filtered out due to low overall expression, light grey: gene missing database mapping, white: non-human gene. DE genes are highlighted using red (significantly up-regulated in the SV-AS03 group compared to the SV-PBS group) and blue (significantly down-regulated in the SV-AS03 group compared to the SV-PBS group) node label and border colors.

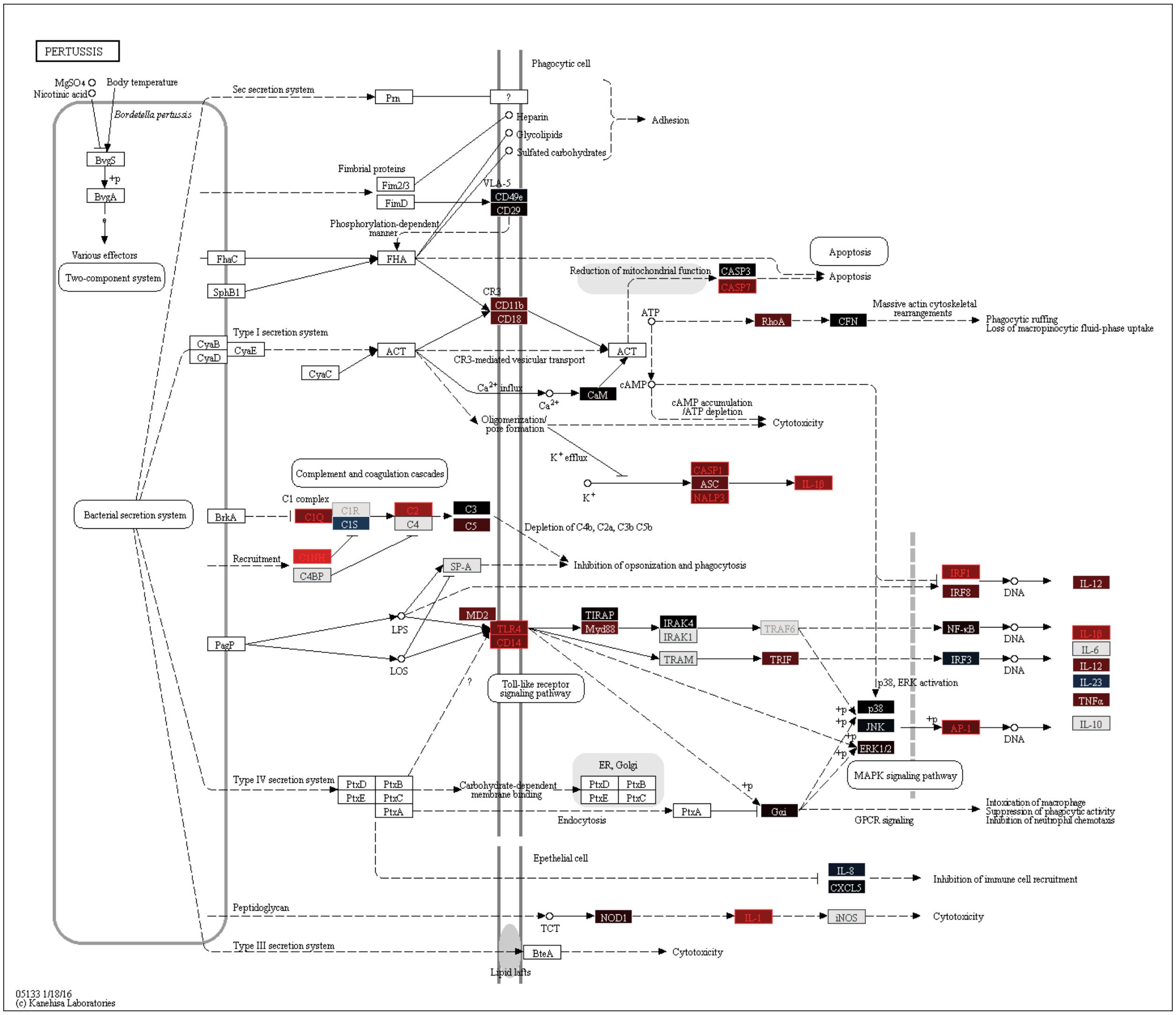


Figure A41: KEGG Pathway Map - Pertussis (RNA-Seq, PBMC, Day 1). Node color gradient encodes mean log_2 fold change difference between treatment groups (for multi-gene nodes the median fold change is used). In red: up-regulated for the SV-AS03 group compared to the SV-PBS group, in blue: down-regulated for the SV-AS03 group compared to the SV-PBS group, in black: fold change close to 1, in dark grey: genes filtered out due to low overall expression, light grey: gene missing database mapping, white: non-human gene. DE genes are highlighted using red (significantly up-regulated in the SV-AS03 group compared to the SV-PBS group) and blue (significantly down-regulated in the SV-AS03 group compared to the SV-PBS group) node label and border colors.

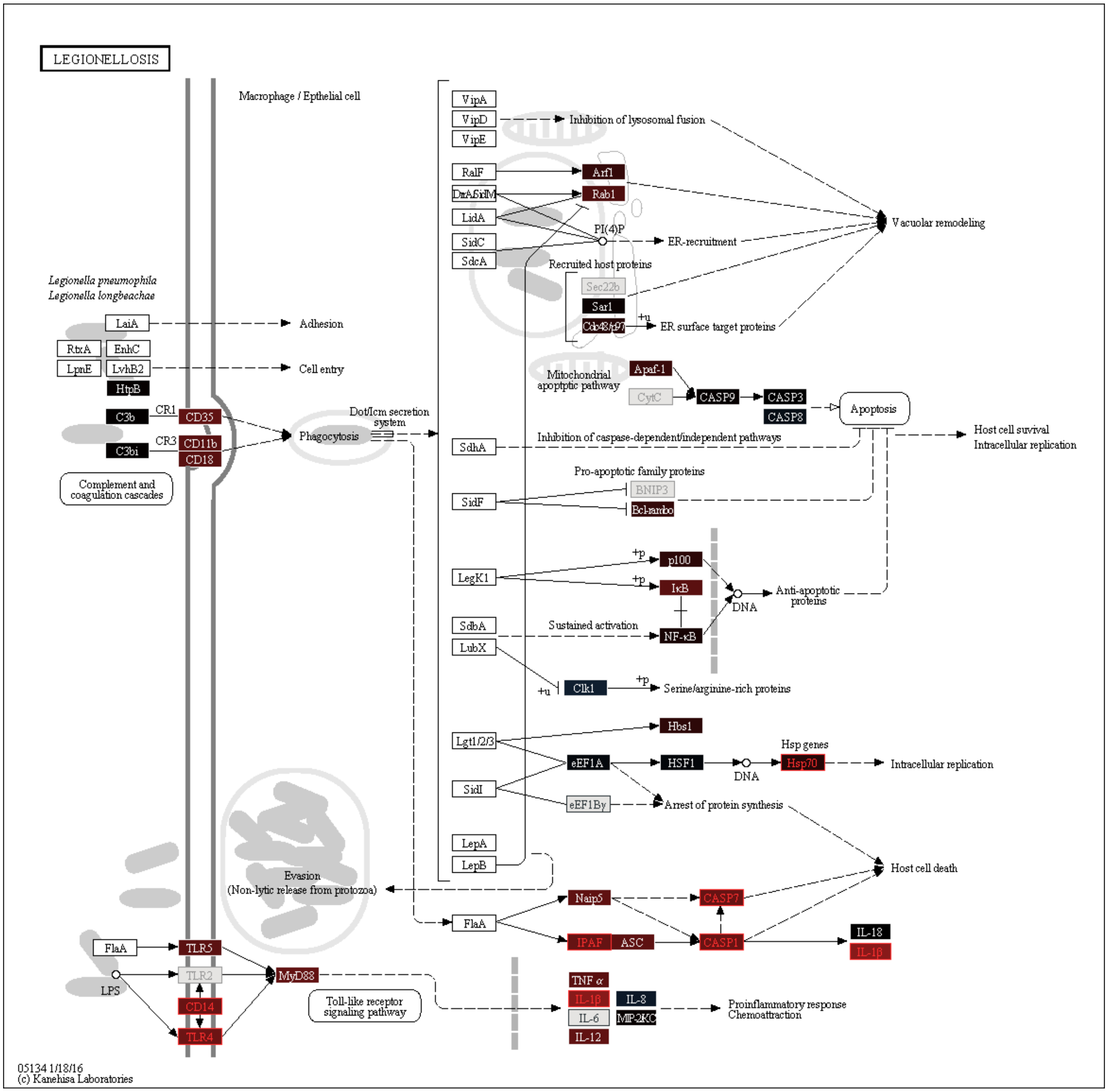


Figure A42: KEGG Pathway Map - Legionellosis (RNA-Seq, PBMC, Day 1). Node color gradient encodes mean log_2 fold change difference between treatment groups (for multi-gene nodes the median fold change is used). In red: up-regulated for the SV-AS03 group compared to the SV-PBS group, in blue: down-regulated for the SV-AS03 group compared to the SV-PBS group, in black: fold change close to 1, in dark grey: genes filtered out due to low overall expression, light grey: gene missing database mapping, white: non-human gene. DE genes are highlighted using red (significantly up-regulated in the SV-AS03 group compared to the SV-PBS group) and blue (significantly down-regulated in the SV-AS03 group compared to the SV-PBS group) node label and border colors.

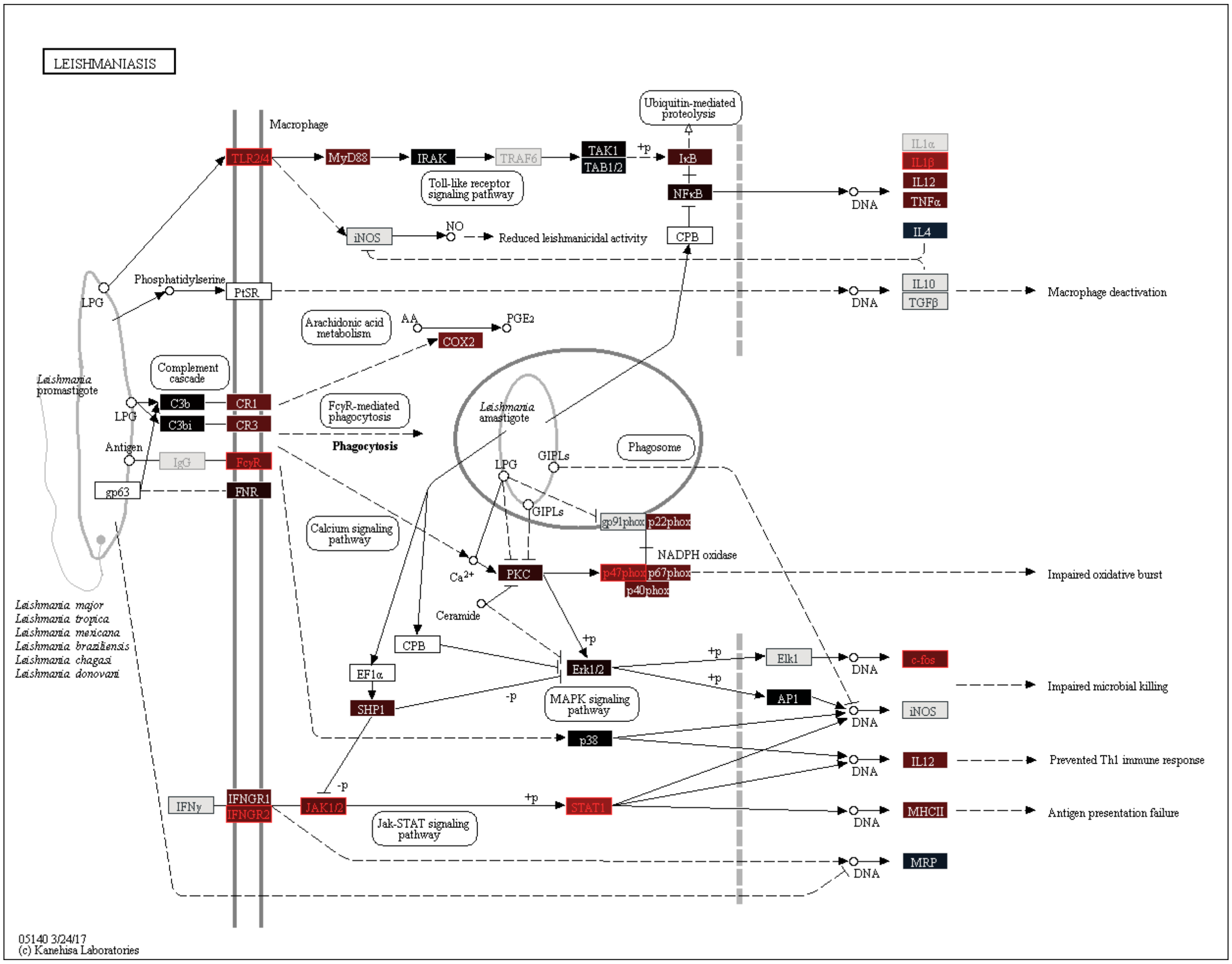


Figure A43: KEGG Pathway Map - Leishmaniasis (RNA-Seq, PBMC, Day 1). Node color gradient encodes mean log_2 fold change difference between treatment groups (for multi-gene nodes the median fold change is used). In red: up-regulated for the SV-AS03 group compared to the SV-PBS group, in blue: down-regulated for the SV-AS03 group compared to the SV-PBS group, in black: fold change close to 1, in dark grey: genes filtered out due to low overall expression, light grey: gene missing database mapping, white: non-human gene. DE genes are highlighted using red (significantly up-regulated in the SV-AS03 group compared to the SV-PBS group) and blue (significantly down-regulated in the SV-AS03 group compared to the SV-PBS group) node label and border colors.

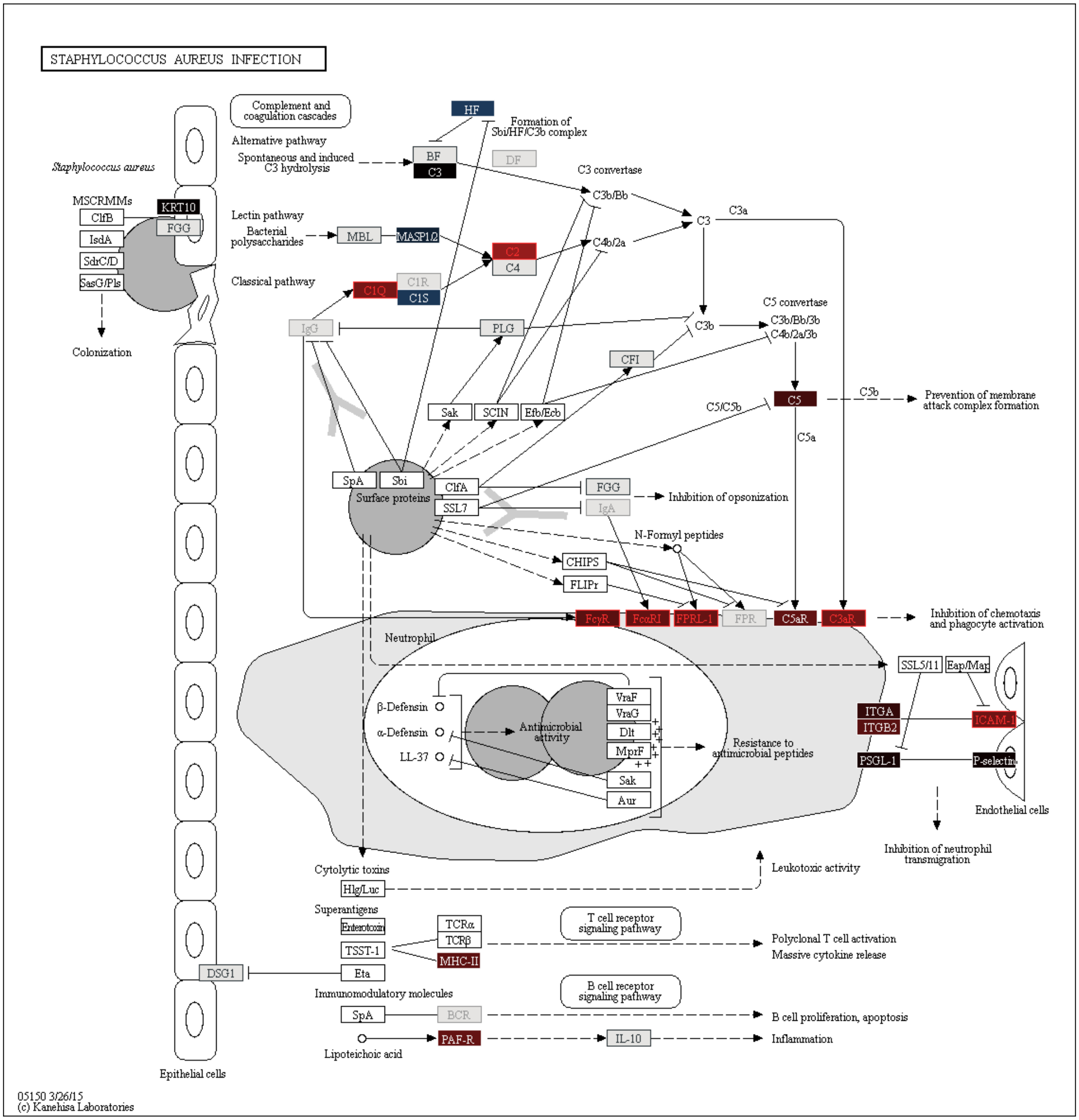


Figure A44: KEGG Pathway Map - Staphylococcus aureus infection (RNA-Seq, PBMC, Day 1). Node color gradient encodes mean log_2 fold change difference between treatment groups (for multi-gene nodes the median fold change is used). In red: up-regulated for the SV-AS03 group compared to the SV-PBS group, in blue: down-regulated for the SV-AS03 group compared to the SV-PBS group, in black: fold change close to 1, in dark grey: genes filtered out due to low overall expression, light grey: gene missing database mapping, white: non-human gene. DE genes are highlighted using red (significantly up-regulated in the SV-AS03 group compared to the SV-PBS group) and blue (significantly down-regulated in the SV-AS03 group compared to the SV-PBS group) node label and border colors.

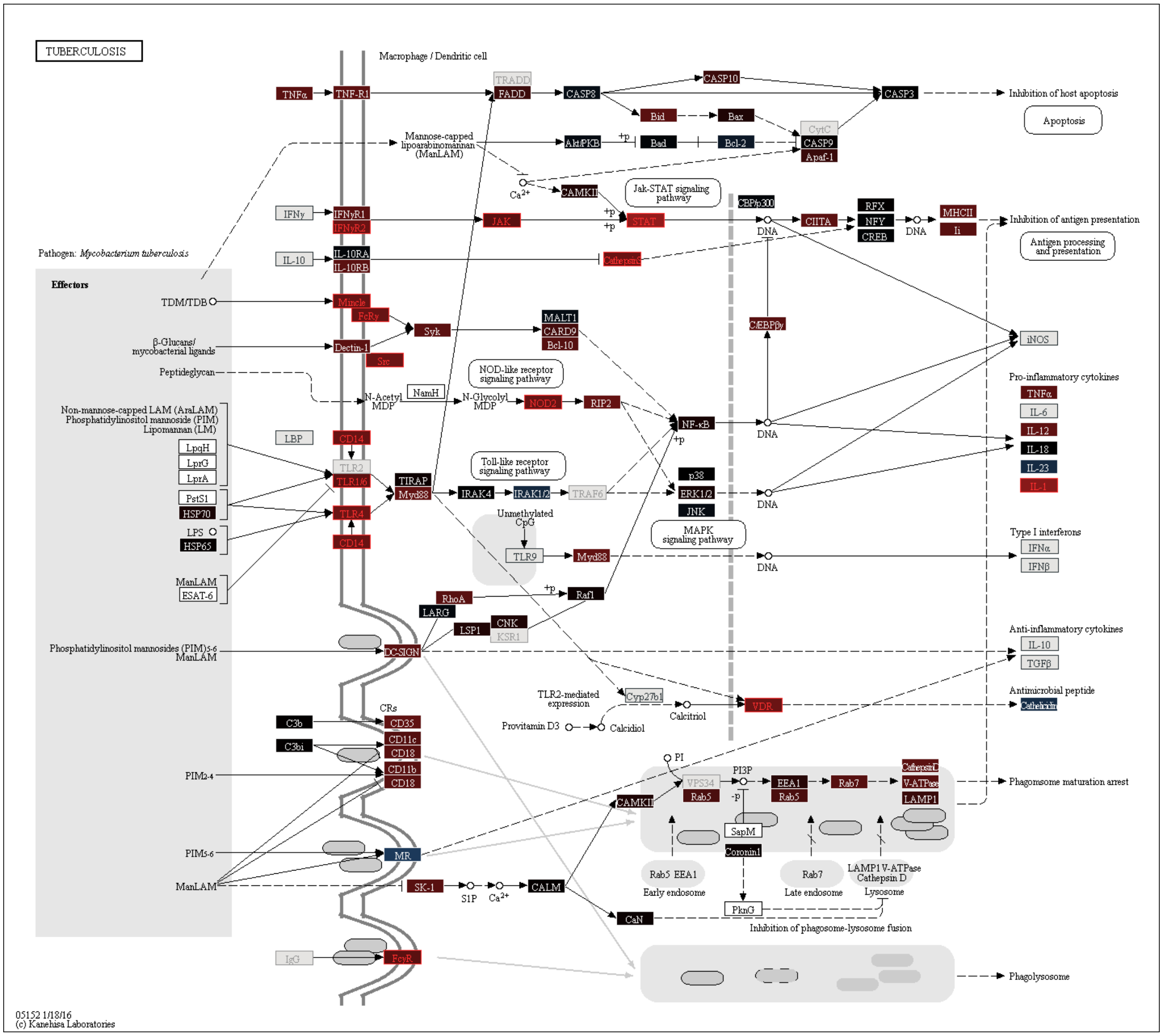


Figure A45: KEGG Pathway Map - Tuberculosis (RNA-Seq, PBMC, Day 1). Node color gradient encodes mean log_2 fold change difference between treatment groups (for multi-gene nodes the median fold change is used). In red: up-regulated for the SV-AS03 group compared to the SV-PBS group, in blue: down-regulated for the SV-AS03 group compared to the SV-PBS group, in black: fold change close to 1, in dark grey: genes filtered out due to low overall expression, light grey: gene missing database mapping, white: non-human gene. DE genes are highlighted using red (significantly up-regulated in the SV-AS03 group compared to the SV-PBS group) and blue (significantly down-regulated in the SV-AS03 group compared to the SV-PBS group) node label and border colors.

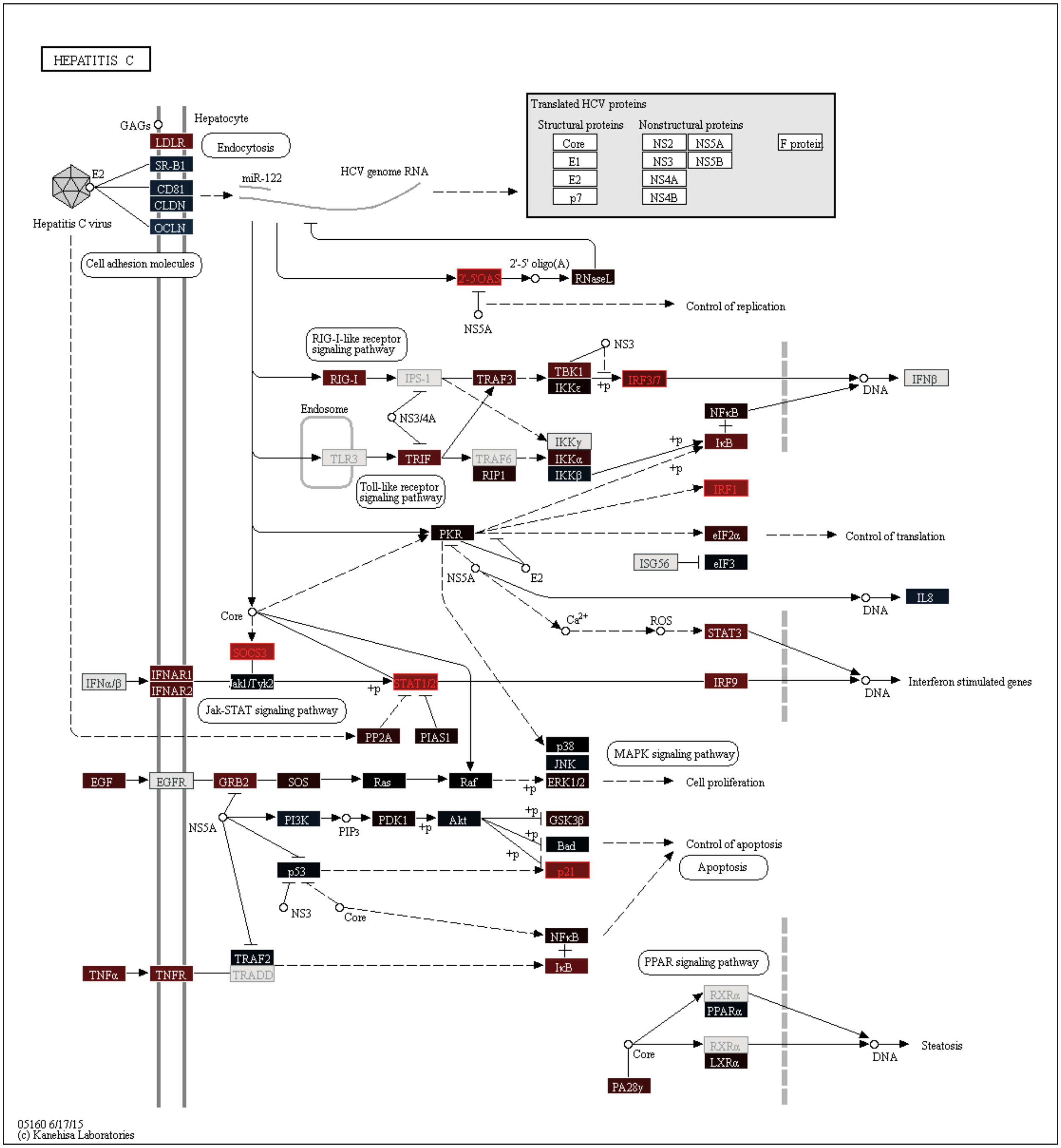


Figure A46: KEGG Pathway Map - Hepatitis C (RNA-Seq, PBMC, Day 1). Node color gradient encodes mean log_2 fold change difference between treatment groups (for multi-gene nodes the median fold change is used). In red: up-regulated for the SV-AS03 group compared to the SV-PBS group, in blue: down-regulated for the SV-AS03 group compared to the SV-PBS group, in black: fold change close to 1, in dark grey: genes filtered out due to low overall expression, light grey: gene missing database mapping, white: non-human gene. DE genes are highlighted using red (significantly up-regulated in the SV-AS03 group compared to the SV-PBS group) and blue (significantly down-regulated in the SV-AS03 group compared to the SV-PBS group) node label and border colors.

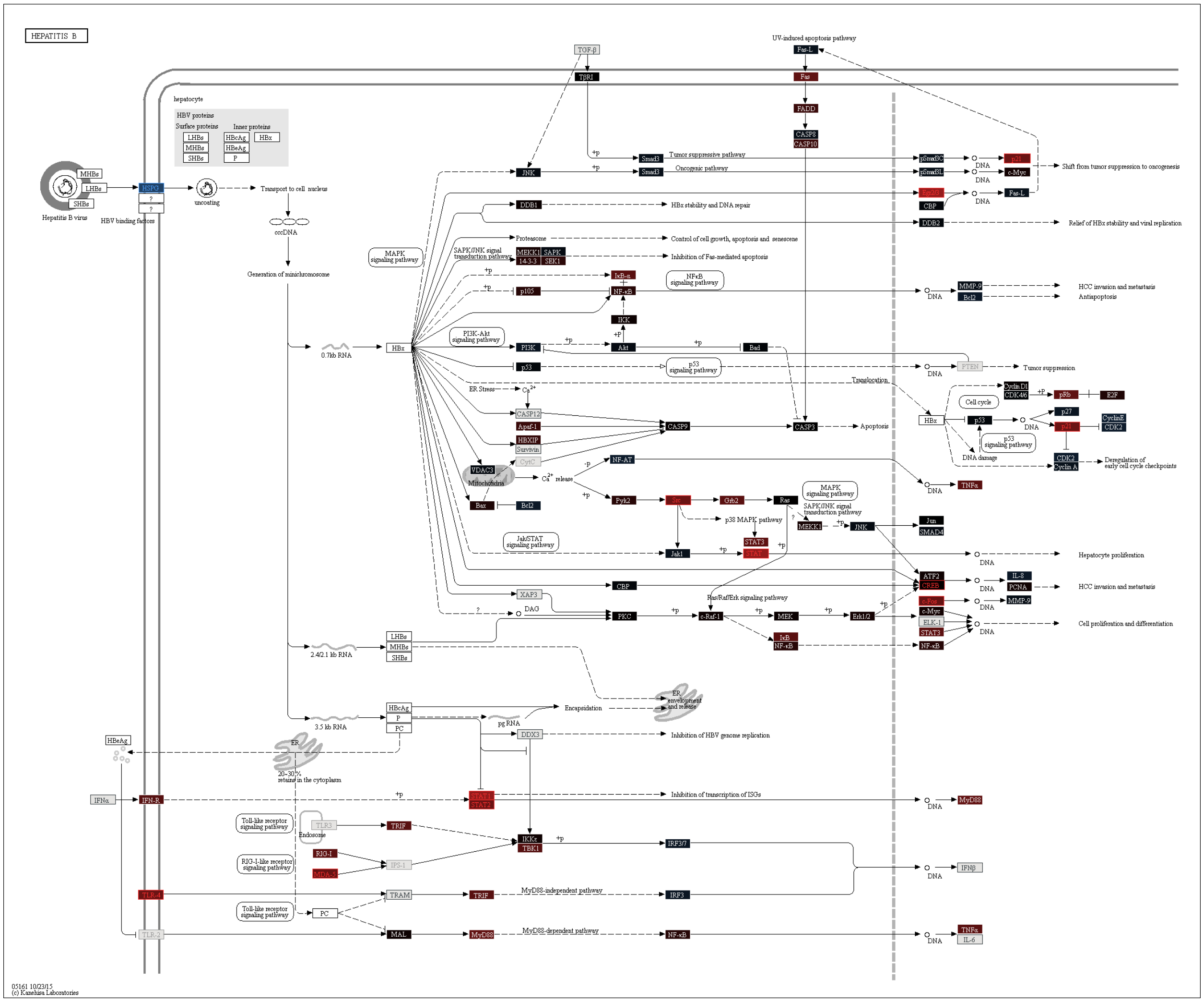


Figure A47: KEGG Pathway Map - Hepatitis B (RNA-Seq, PBMC, Day 1). Node color gradient encodes mean log_2 fold change difference between treatment groups (for multi-gene nodes the median fold change is used). In red: up-regulated for the SV-AS03 group compared to the SV-PBS group, in blue: down-regulated for the SV-AS03 group compared to the SV-PBS group, in black: fold change close to 1, in dark grey: genes filtered out due to low overall expression, light grey: gene missing database mapping, white: non-human gene. DE genes are highlighted using red (significantly up-regulated in the SV-AS03 group compared to the SV-PBS group) and blue (significantly down-regulated in the SV-AS03 group compared to the SV-PBS group) node label and border colors.

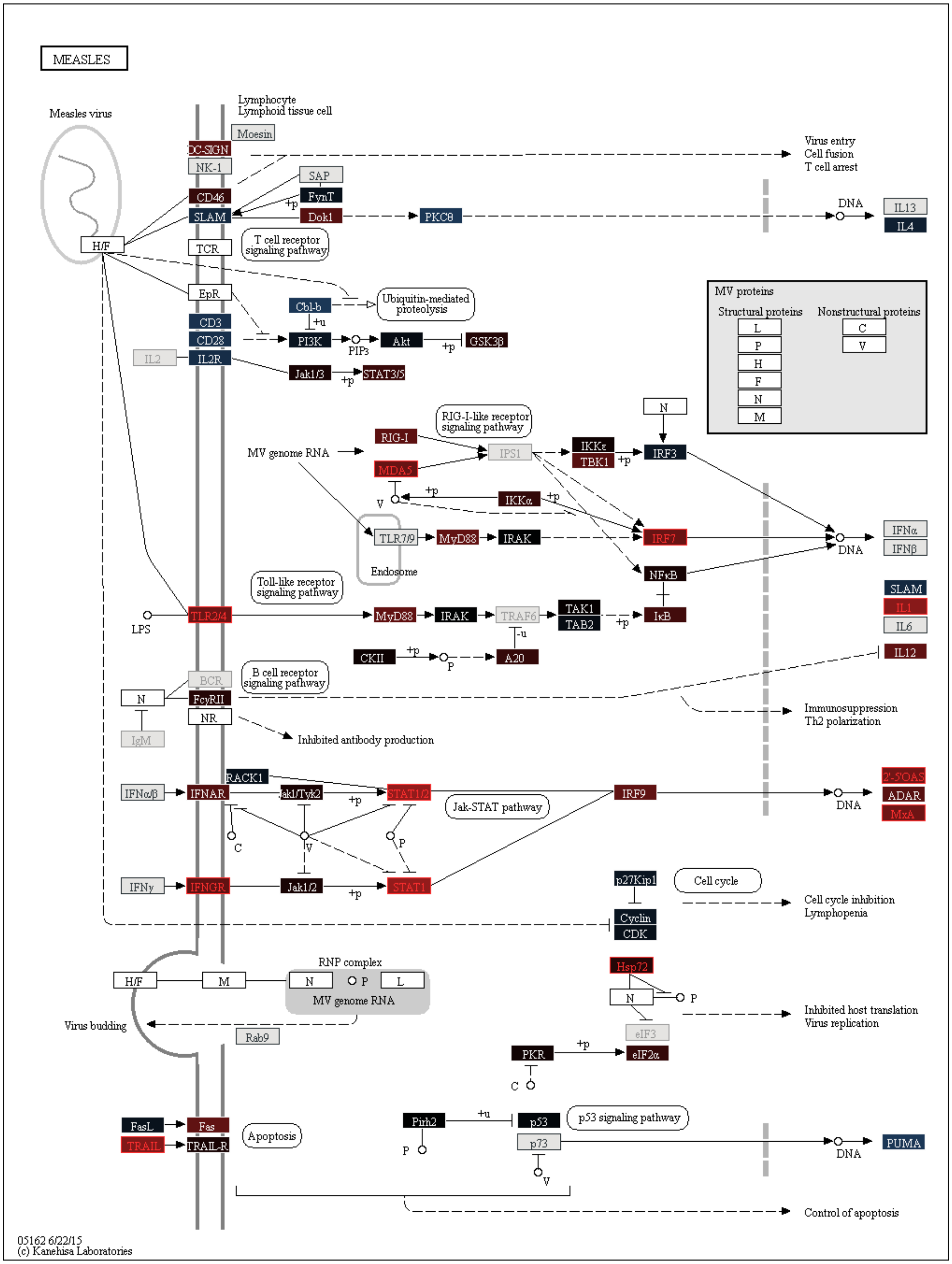


Figure A48: KEGG Pathway Map - Measles (RNA-Seq, PBMC, Day 1). Node color gradient encodes mean log_2 fold change difference between treatment groups (for multi-gene nodes the median fold change is used). In red: up-regulated for the SV-AS03 group compared to the SV-PBS group, in blue: down-regulated for the SV-AS03 group compared to the SV-PBS group, in black: fold change close to 1, in dark grey: genes filtered out due to low overall expression, light grey: gene missing database mapping, white: non-human gene. DE genes are highlighted using red (significantly up-regulated in the SV-AS03 group compared to the SV-PBS group) and blue (significantly down-regulated in the SV-AS03 group compared to the SV-PBS group) node label and border colors.

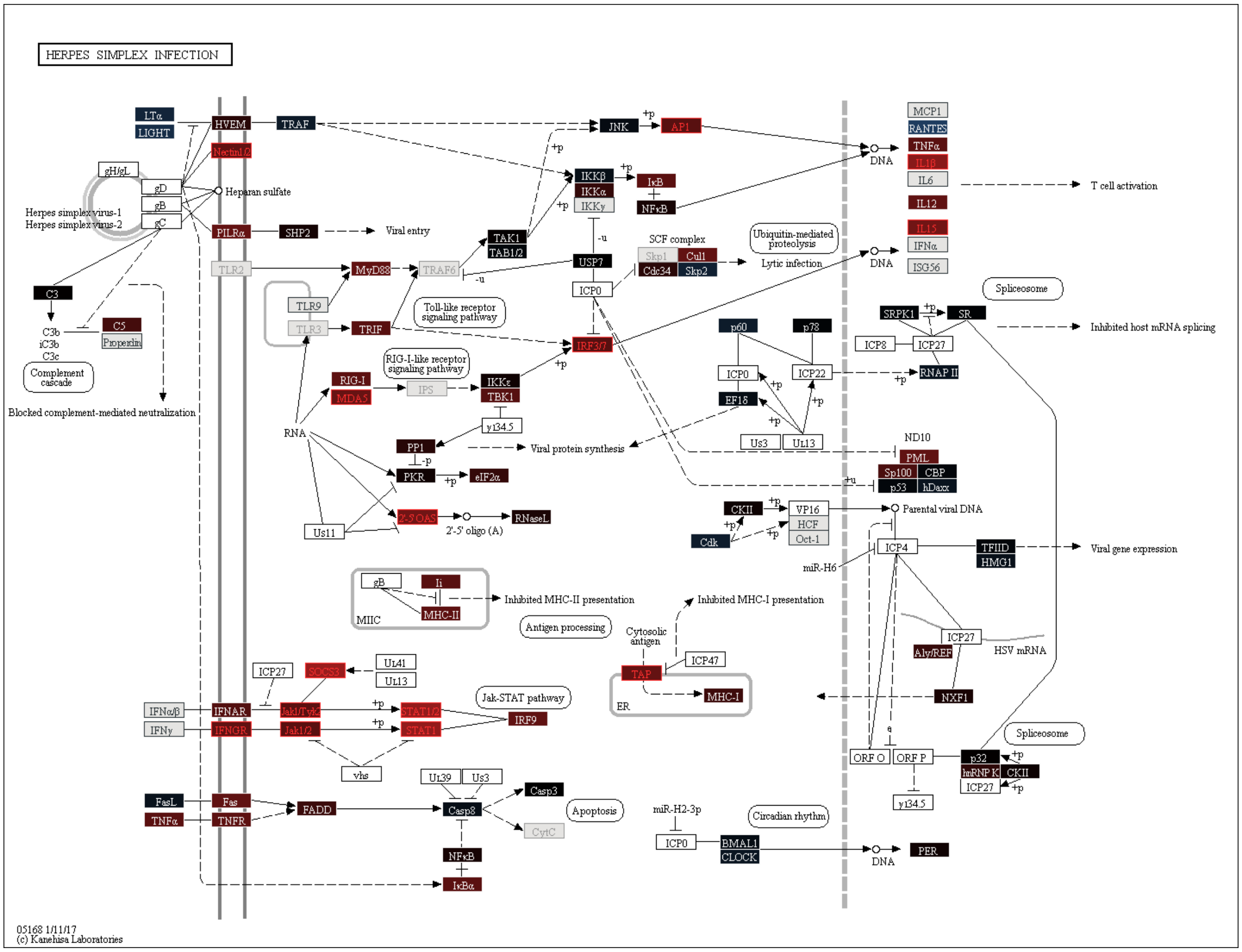


Figure A49: KEGG Pathway Map - Herpes simplex infection (RNA-Seq, PBMC, Day 1). Node color gradient encodes mean log_2 fold change difference between treatment groups (for multi-gene nodes the median fold change is used). In red: up-regulated for the SV-AS03 group compared to the SV-PBS group, in blue: down-regulated for the SV-AS03 group compared to the SV-PBS group, in black: fold change close to 1, in dark grey: genes filtered out due to low overall expression, light grey: gene missing database mapping, white: non-human gene. DE genes are highlighted using red (significantly up-regulated in the SV-AS03 group compared to the SV-PBS group) and blue (significantly down-regulated in the SV-AS03 group compared to the SV-PBS group) node label and border colors.

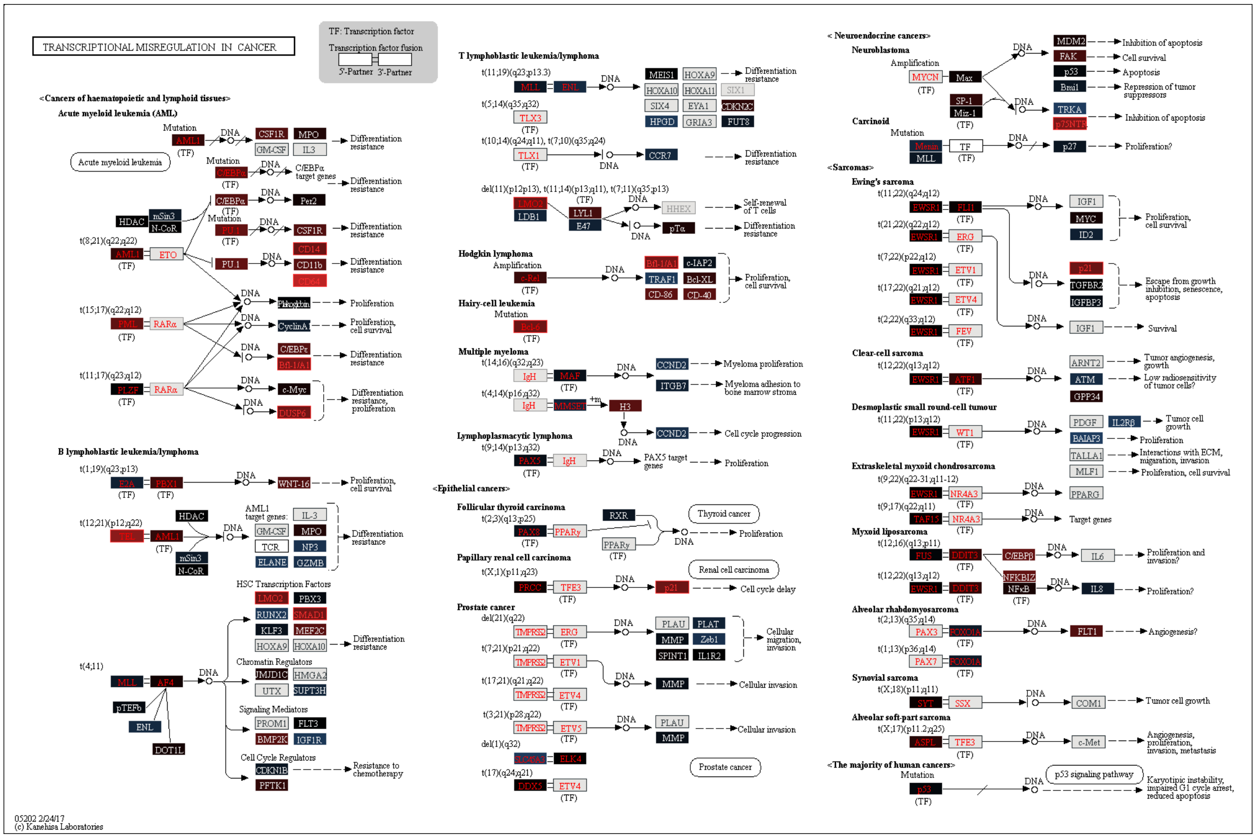


Figure A50: KEGG Pathway Map - Transcriptional misregulation in cancer (RNA-Seq, PBMC, Day 1). Node color gradient encodes mean log_2 fold change difference between treatment groups (for multi-gene nodes the median fold change is used). In red: up-regulated for the SV-AS03 group compared to the SV-PBS group, in blue: down-regulated for the SV-AS03 group compared to the SV-PBS group, in black: fold change close to 1, in dark grey: genes filtered out due to low overall expression, light grey: gene missing database mapping, white: non-human gene. DE genes are highlighted using red (significantly up-regulated in the SV-AS03 group compared to the SV-PBS group) and blue (significantly down-regulated in the SV-AS03 group compared to the SV-PBS group) node label and border colors.

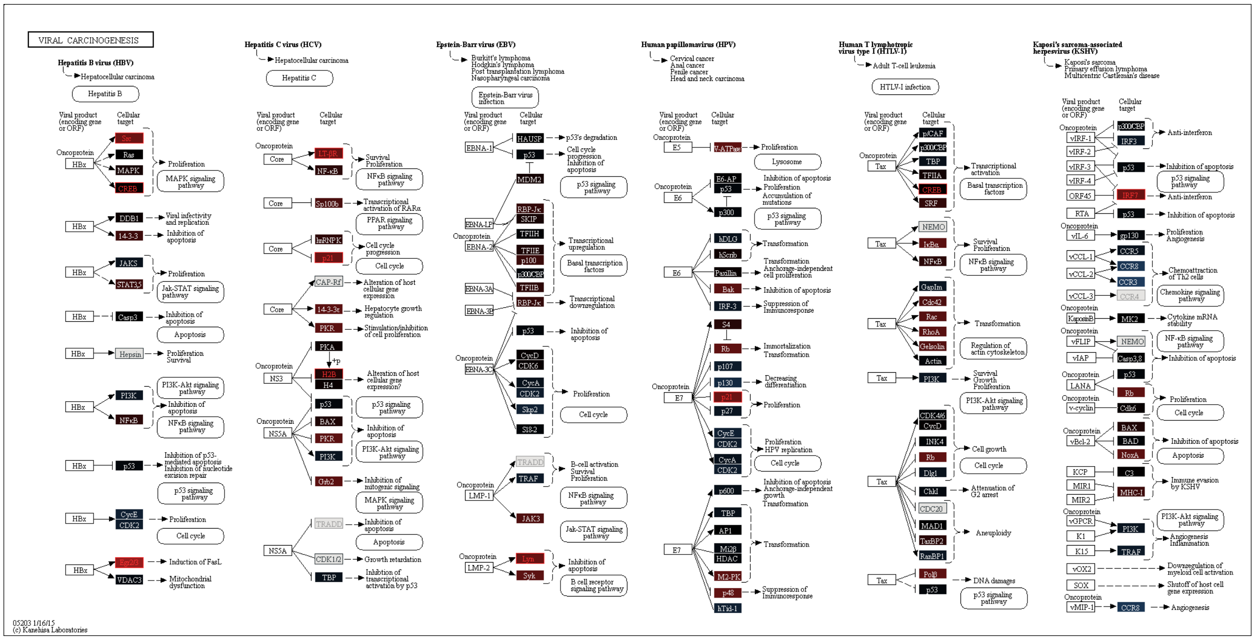


Figure A51: KEGG Pathway Map - Viral carcinogenesis (RNA-Seq, PBMC, Day 1). Node color gradient encodes mean log_2 fold change difference between treatment groups (for multi-gene nodes the median fold change is used). In red: up-regulated for the SV-AS03 group compared to the SV-PBS group, in blue: down-regulated for the SV-AS03 group compared to the SV-PBS group, in black: fold change close to 1, in dark grey: genes filtered out due to low overall expression, light grey: gene missing database mapping, white: non-human gene. DE genes are highlighted using red (significantly up-regulated in the SV-AS03 group compared to the SV-PBS group) and blue (significantly down-regulated in the SV-AS03 group compared to the SV-PBS group) node label and border colors.

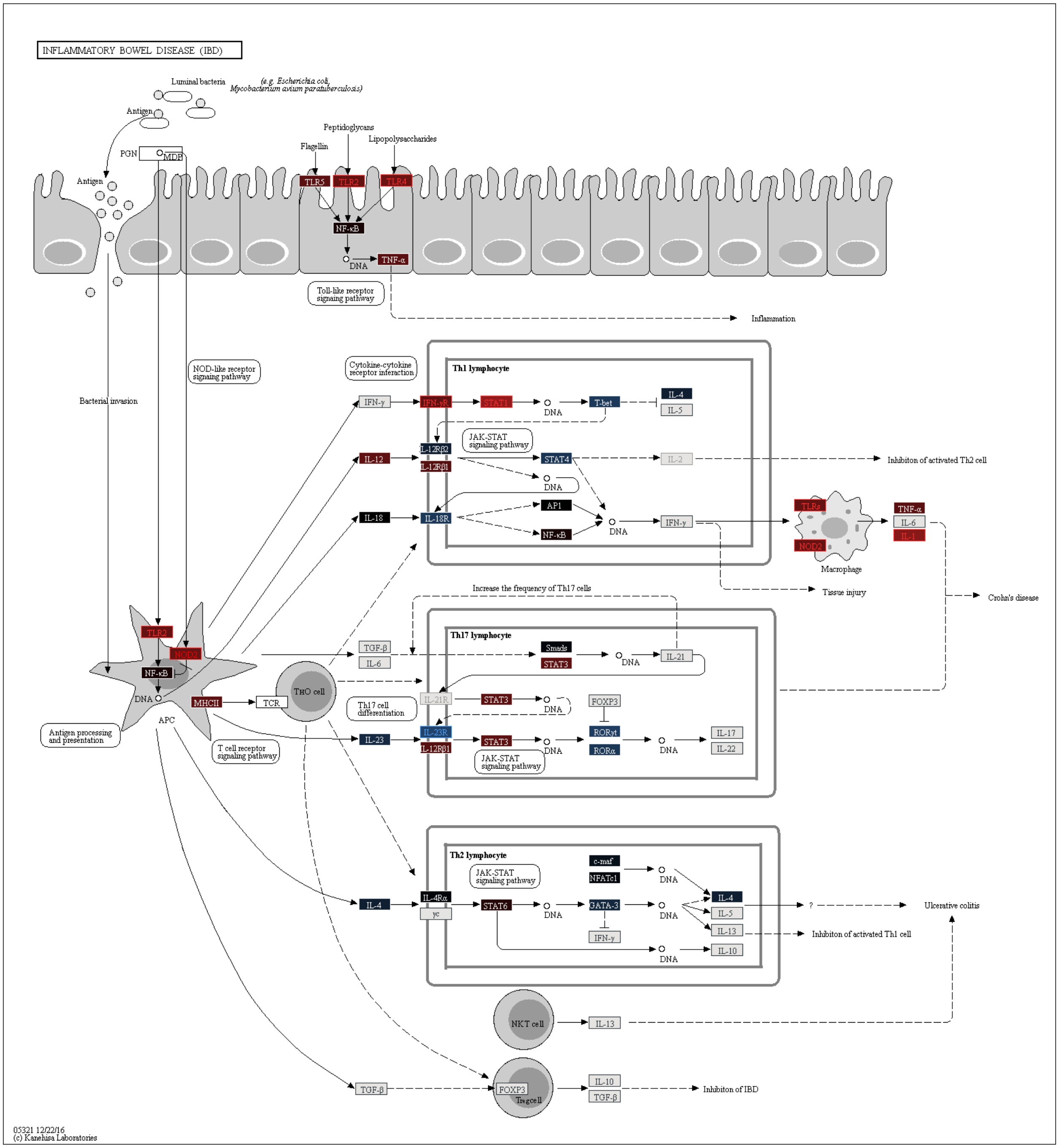


Figure A52: KEGG Pathway Map - Inflammatory bowel disease (IBD) (RNA-Seq, PBMC, Day 1). Node color gradient encodes mean log_2 fold change difference between treatment groups (for multi-gene nodes the median fold change is used). In red: up-regulated for the SV-AS03 group compared to the SV-PBS group, in blue: down-regulated for the SV-AS03 group compared to the SV-PBS group, in black: fold change close to 1, in dark grey: genes filtered out due to low overall expression, light grey: gene missing database mapping, white: non-human gene. DE genes are highlighted using red (significantly up-regulated in the SV-AS03 group compared to the SV-PBS group) and blue (significantly down-regulated in the SV-AS03 group compared to the SV-PBS group) node label and border colors.

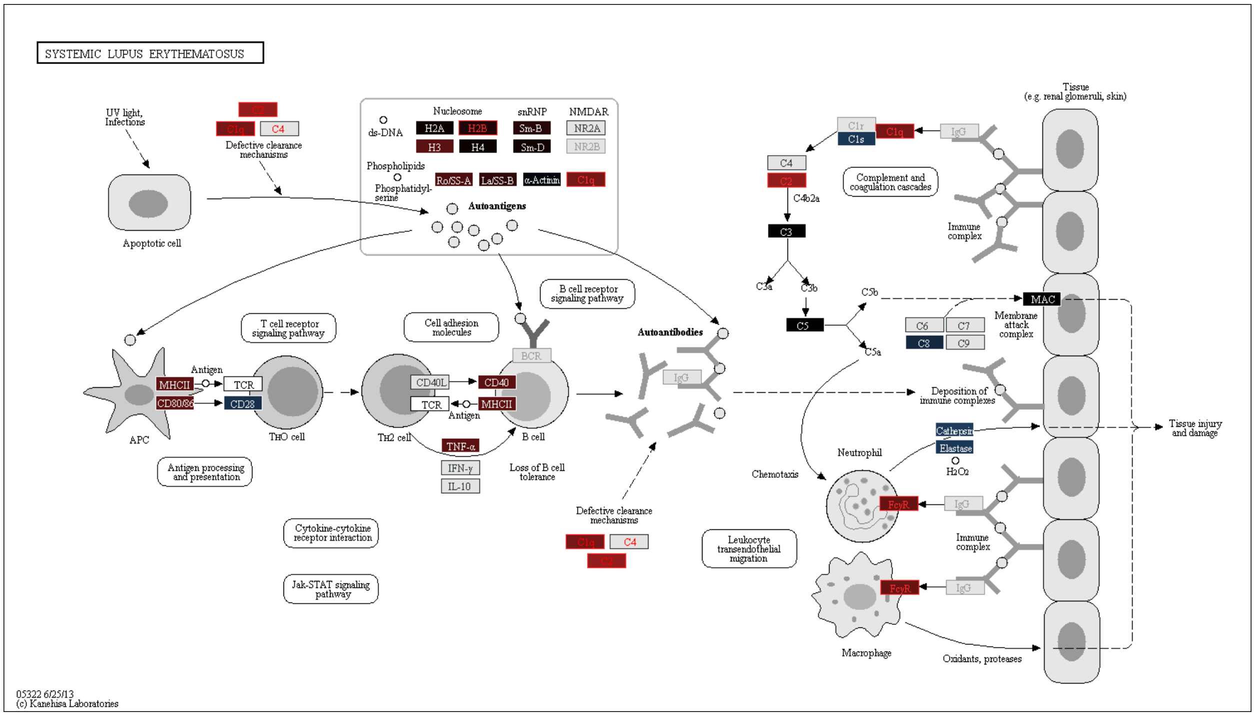


Figure A53: KEGG Pathway Map - Systemic lupus erythematosus (RNA-Seq, PBMC, Day 1). Node color gradient encodes mean log_2 fold change difference between treatment groups (for multi-gene nodes the median fold change is used). In red: up-regulated for the SV-AS03 group compared to the SV-PBS group, in blue: down-regulated for the SV-AS03 group compared to the SV-PBS group, in black: fold change close to 1, in dark grey: genes filtered out due to low overall expression, light grey: gene missing database mapping, white: non-human gene. DE genes are highlighted using red (significantly up-regulated in the SV-AS03 group compared to the SV-PBS group) and blue (significantly down-regulated in the SV-AS03 group compared to the SV-PBS group) node label and border colors.

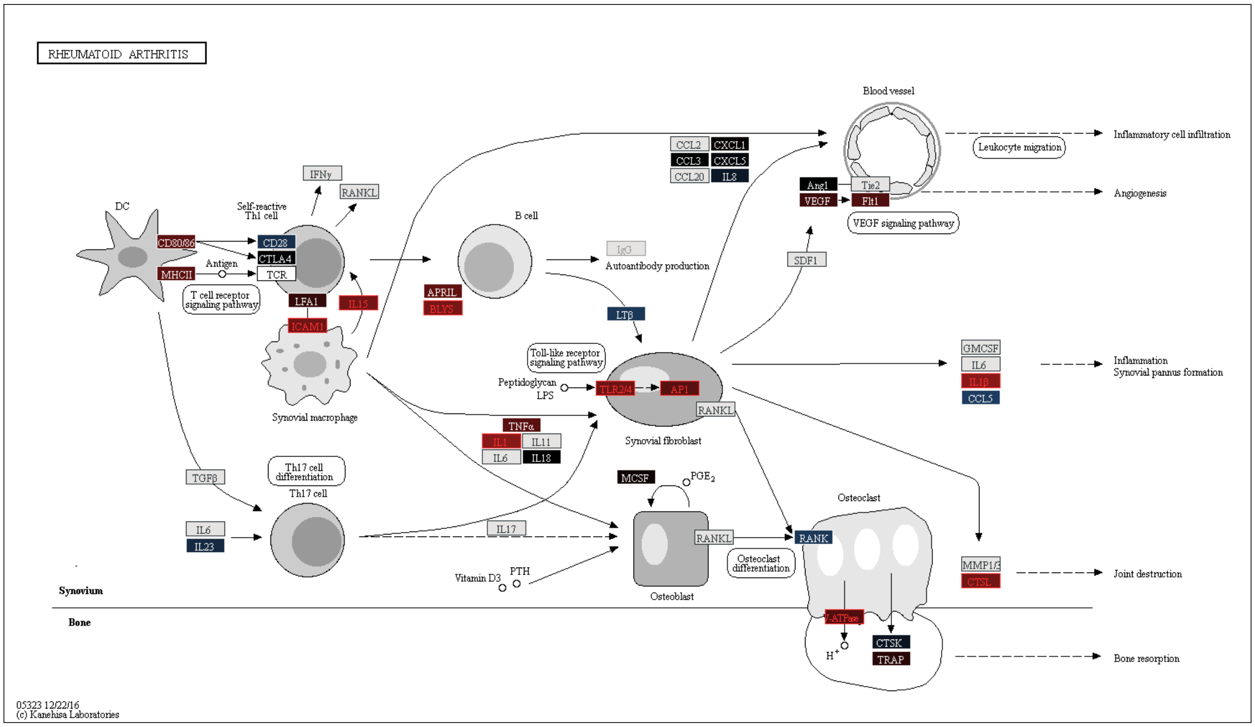


Figure A54: KEGG Pathway Map - Rheumatoid arthritis (RNA-Seq, PBMC, Day 1). Node color gradient encodes mean log_2 fold change difference between treatment groups (for multi-gene nodes the median fold change is used). In red: up-regulated for the SV-AS03 group compared to the SV-PBS group, in blue: down-regulated for the SV-AS03 group compared to the SV-PBS group, in black: fold change close to 1, in dark grey: genes filtered out due to low overall expression, light grey: gene missing database mapping, white: non-human gene. DE genes are highlighted using red (significantly up-regulated in the SV-AS03 group compared to the SV-PBS group) and blue (significantly down-regulated in the SV-AS03 group compared to the SV-PBS group) node label and border colors.

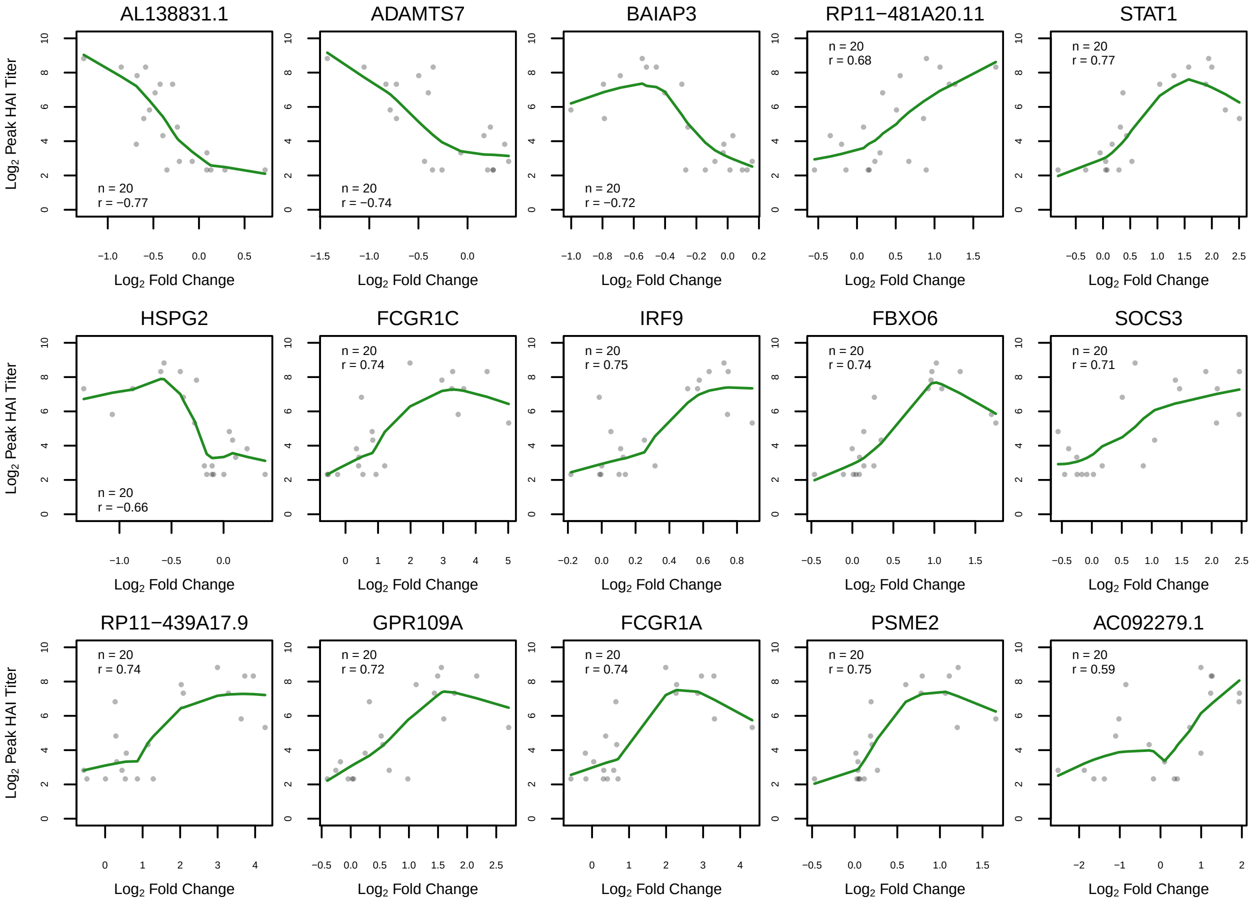


Figure A55: Scatterplots that summarize the correlation between peak log_2 HAI titer and log_2 fold change response for genes identified using regularized linear regression (RNA-Seq, PBMC, Day 1). Sorted by absolute descending regularized linear regression coefficient. The green solid trend line represents a locally weighted regression fit.

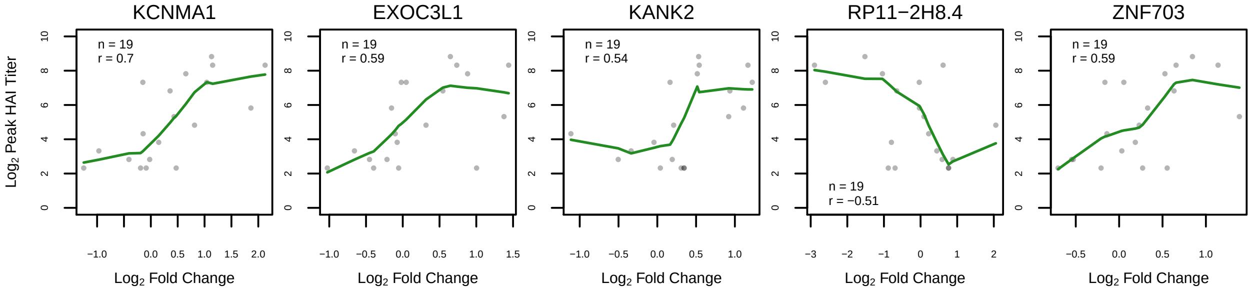


Figure A56: Scatterplots that summarize the correlation between peak log_2 HAI titer and log_2 fold change response for genes identified using regularized linear regression (RNA-Seq, PBMC, Day 3). Sorted by absolute descending regularized linear regression coefficient. The green solid trend line represents a locally weighted regression fit.

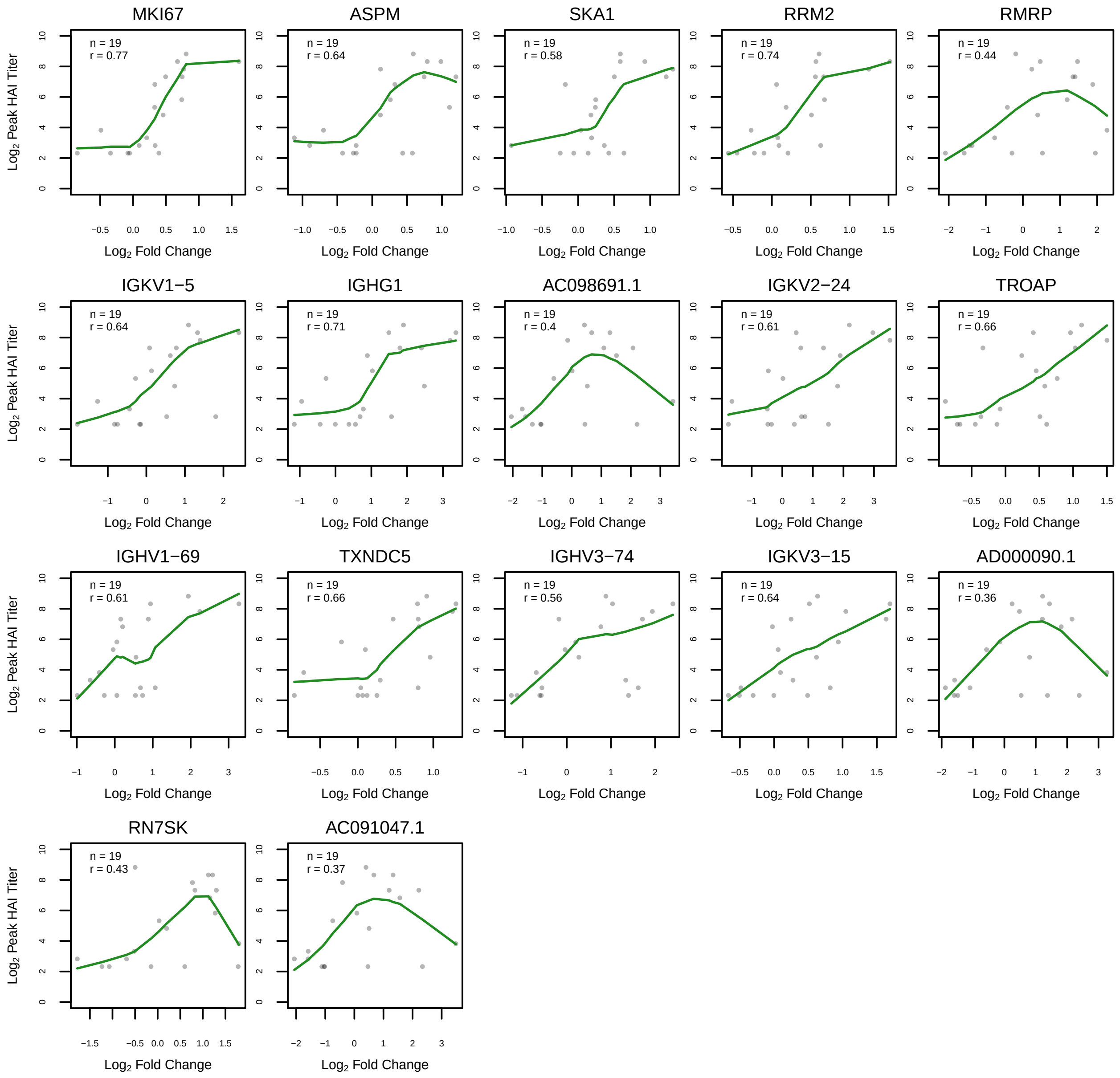


Figure A57: Scatterplots that summarize the correlation between peak log_2 HAI titer and log_2 fold change response for genes identified using regularized linear regression (RNA-Seq, PBMC, Day 7). Sorted by absolute descending regularized linear regression coefficient. The green solid trend line represents a locally weighted regression fit.

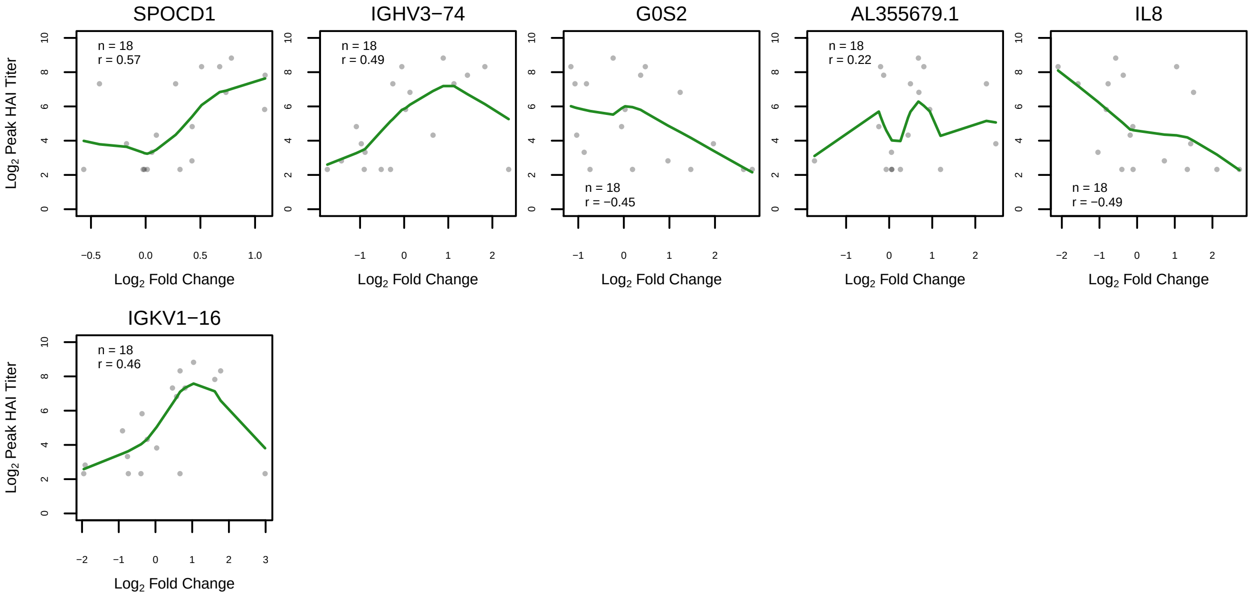


Figure A58: Scatterplots that summarize the correlation between peak log_2 HAI titer and log_2 fold change response for genes identified using regularized linear regression (RNA-Seq, PBMC, Day 28). Sorted by absolute descending regularized linear regression coefficient. The green solid trend line represents a locally weighted regression fit.

Tables

Category/Chromosome	#Genes
Mt_rRNA	2
Mt_tRNA	22
Mt_tRNA_pseudogene	580
rRNA	530
rRNA_pseudogene	179
tRNA_pseudogene	128
X	2326
Y	509
Total	4185

Table A1: Number of excluded genes by category/chromosome (RNA-Seq, PBMC).

	Day 1	Day 3	Day 7	Day 28	Day 1-28
PBMC	14513	14547	14525	14491	14793

Table A2: Number of genes that passed the low expression cut off (RNA-Seq, PBMC).

	Min	Q1	Median	Mean	Q3	Max	SD	MAD
Total Mapped Reads [10^6]	27.43	46.09	47.91	48.34	50.71	63.98	4.39	3.24
Uniquely Mapped Reads [10^6]	24.42	43.30	45.08	45.43	47.66	60.41	4.16	2.85
Uniquely Mapped Reads [%]	89.00	93.70	94.00	93.97	94.20	95.00	0.58	0.37
Paired Reads (Mapped to Different Chromosomes)	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Counted Fragments [10^6]	13.02	16.54	17.19	17.38	18.21	21.62	1.40	1.26
Median GC [%]	50.00	52.00	52.00	51.65	52.00	54.00	0.80	0.00
Mean GC [%]	49.99	50.80	51.08	51.11	51.37	53.02	0.47	0.43
Illumina Flow Cells	2.00	2.00	2.00	2.38	3.00	3.00	0.49	0.00
Illumina Flow Lanes	3.00	4.00	4.00	3.89	4.00	4.00	0.31	0.00

Table A3: Summary statistics (RNA-Seq, PBMC, technical variables)

	Min	Q1	Median	Mean	Q3	Max	SD	MAD
Exon Tags [%]	81.80	85.77	86.71	86.55	87.45	89.63	1.44	1.25
Intron Tags [%]	9.20	11.19	11.89	12.02	12.74	16.45	1.32	1.18
Intergenic Tags [%]	1.15	1.35	1.42	1.43	1.50	1.99	0.13	0.11
CDS Exons Tags Per Kb	303.85	503.98	526.64	529.11	558.25	659.01	47.88	38.68
Intron Tags Per Kb	2.53	4.34	4.72	4.78	5.14	8.06	0.72	0.61
3' UTR Tags Per Kb	155.12	262.07	274.36	276.68	292.00	354.06	26.24	22.15
5' UTR Tags Per Kb	108.89	159.68	170.63	170.99	180.16	221.31	15.89	14.57
TSS upstream 10Kb Tags Per Kb	0.47	0.76	0.82	0.83	0.88	1.70	0.13	0.09
TES downstream 10Kb Tags Per Kb	1.39	2.41	2.58	2.60	2.78	4.18	0.36	0.26
Splicing Events [10^5]	38.03	64.64	68.50	68.68	72.78	85.03	6.59	5.86
Splicing Junctions [10^5]	1.37	1.51	1.52	1.52	1.53	1.61	0.02	0.01

Table A4: Summary statistics (RNA-Seq, PBMC, gene model variables)

	1st PC (12.9%) Before TMM Normalization.	2nd PC (7.9%) Before TMM Normalization.	1st PC (13%) After TMM Normalization.	2nd PC (7.9%) After TMM Normalization.
Total Mapped Reads [10^6]	-0.13	-0.30	-0.13	-0.29
Uniquely Mapped Reads [10^6]	-0.10	-0.28	-0.10	-0.28
Uniquely Mapped Reads [%]	0.59	0.26	0.61	0.23
Median GC [%]	0.31	0.16	0.31	0.15
Mean GC [%]	0.44	0.32	0.43	0.31
Illumina Flow Cells [#]	0.06	0.21	0.06	0.21
Illumina Flow Lanes [#]	-0.07	-0.28	-0.07	-0.28

Table A5: Spearman correlation with technical variables (RNA-Seq, PBMC, original variables).

	1st PC (18.7%) Before TMM Normalization.	2nd PC (9.6%) Before TMM Normalization.	1st PC (17.8%) After TMM Normalization.	2nd PC (10.1%) After TMM Normalization.
Total Mapped Reads [10^6]	0.15	0.13	0.14	-0.15
Uniquely Mapped Reads [10^6]	0.12	0.16	0.12	-0.17
Uniquely Mapped Reads [%]	-0.51	0.43	-0.54	-0.39
Median GC [%]	-0.33	-0.11	-0.35	0.15
Mean GC [%]	-0.47	-0.32	-0.50	0.37
Illumina Flow Cells [#]	-0.05	-0.13	-0.06	0.16
Illumina Flow Lanes [#]	0.09	0.26	0.10	-0.26

Table A6: Spearman correlation with technical variables (RNA-Seq, PBMC, standardized variables).

	1st PC (12.9%) Before TMM Normalization.	2nd PC (7.9%) Before TMM Normalization.	1st PC (13%) After TMM Normalization.	2nd PC (7.9%) After TMM Normalization.
Exon Tags [%]	0.26	0.25	0.24	0.28
Intron Tags [%]	-0.24	-0.25	-0.23	-0.28
Intergenic Tags [%]	-0.47	-0.24	-0.45	-0.26
CDS Exons Tags Per Kb	-0.08	-0.20	-0.08	-0.19
Intron Tags Per Kb	-0.27	-0.36	-0.26	-0.38
3’ UTR Tags Per Kb	0.02	-0.21	0.02	-0.21
5’ UTR Tags Per Kb	0.09	-0.05	0.09	-0.05
TSS upstream 10Kb Tags Per Kb	-0.43	-0.44	-0.42	-0.45
TES downstream 10Kb Tags Per Kb	-0.43	-0.34	-0.42	-0.35
Splicing Events [10^5]	-0.01	-0.09	-0.01	-0.08

Table A7: Spearman correlation with gene model variables (RNA-Seq, PBMC, original variables).

	1st PC (18.7%) Before TMM Normalization.	2nd PC (9.6%) Before TMM Normalization.	1st PC (17.8%) After TMM Normalization.	2nd PC (10.1%) After TMM Normalization.
Exon Tags [%]	-0.37	-0.82	-0.37	0.83
Intron Tags [%]	0.35	0.82	0.36	-0.83
Intergenic Tags [%]	0.57	0.70	0.57	-0.71
CDS Exons Tags Per Kb	0.06	-0.13	0.06	0.11
Intron Tags Per Kb	0.37	0.72	0.37	-0.74
3’ UTR Tags Per Kb	0.00	0.13	-0.01	-0.14
5’ UTR Tags Per Kb	-0.11	-0.11	-0.12	0.11
TSS upstream 10Kb Tags Per Kb	0.49	0.55	0.51	-0.58
TES downstream 10Kb Tags Per Kb	0.51	0.57	0.51	-0.59
Splicing Events [10^5]	-0.03	-0.22	-0.04	0.21

Table A8: Spearman correlation with gene model variables (RNA-Seq, PBMC, standardized variables).

Cluster ID	Cluster Size	Gene ID	Gene Name	Gene Description	Log_2 Fold Change
CPMCD1-001	2	ENSG00000119922	IFIT2	interferon-induced protein with tetratricopeptide repeats 2 [Source:HGNC Symbol;Acc:5409]	1.65
CPMCD1-001	2	ENSG00000119917	IFIT3	interferon-induced protein with tetratricopeptide repeats 3 [Source:HGNC Symbol;Acc:5411]	1.83
CPMCD1-002	2	ENSG00000178719	GRINA	glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1 (glutamate binding) [Source:HGNC Symbol;Acc:4589]	0.64
CPMCD1-002	2	ENSG00000131042	LILRB2	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2 [Source:HGNC Symbol;Acc:6606]	0.71
CPMCD1-003	2	ENSG00000163131	CTSS	cathepsin S [Source:HGNC Symbol;Acc:2545]	0.68
CPMCD1-003	2	ENSG00000163563	MNDA	myeloid cell nuclear differentiation antigen [Source:HGNC Symbol;Acc:7183]	0.68

Cluster ID	Cluster Size	Gene ID	Gene Name	Gene Description	Log_2 Fold Change
CPMCD1-004	2	ENSG00000010030	ETV7	ets variant 7 [Source:HGNC Symbol;Acc:18160]	2.54
CPMCD1-004	2	ENSG00000170581	STAT2	signal transducer and activator of transcription 2, 113kDa [Source:HGNC Symbol;Acc:11363]	0.73
CPMCD1-005	3	ENSG00000163221	S100A12	S100 calcium binding protein A12 [Source:HGNC Symbol;Acc:10489]	0.99
CPMCD1-005	3	ENSG00000143546	S100A8	S100 calcium binding protein A8 [Source:HGNC Symbol;Acc:10498]	0.96
CPMCD1-005	3	ENSG00000163220	S100A9	S100 calcium binding protein A9 [Source:HGNC Symbol;Acc:10499]	0.87
CPMCD1-006	2	ENSG00000111321	LTBR	lymphotoxin beta receptor (TNFR superfamily, member 3) [Source:HGNC Symbol;Acc:6718]	0.65
CPMCD1-006	2	ENSG00000235568	NFAM1	NFAT activating protein with ITAM motif 1 [Source:HGNC Symbol;Acc:29872]	0.60
CPMCD1-007	2	ENSG00000111335	OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa [Source:HGNC Symbol;Acc:8087]	0.72
CPMCD1-007	2	ENSG00000111331	OAS3	2'-5'-oligoadenylate synthetase 3, 100kDa [Source:HGNC Symbol;Acc:8088]	1.07
CPMCD1-008	2	ENSG00000150337	FCGR1A	Fc fragment of IgG, high affinity Ia, receptor (CD64) [Source:HGNC Symbol;Acc:3613]	2.54
CPMCD1-008	2	ENSG00000198019	FCGR1B	Fc fragment of IgG, high affinity Ib, receptor (CD64) [Source:HGNC Symbol;Acc:3614]	2.60
CPMCD1-009	2	ENSG00000188906	LRRK2	leucine-rich repeat kinase 2 [Source:HGNC Symbol;Acc:18618]	1.09
CPMCD1-009	2	ENSG00000105967	TFEC	transcription factor EC [Source:HGNC Symbol;Acc:11754]	0.99
CPMCD1-010	4	ENSG00000085265	FCN1	ficolin (collagen/fibrinogen domain containing) 1 [Source:HGNC Symbol;Acc:3623]	0.65
CPMCD1-010	4	ENSG00000151948	GLT1D1	glycosyltransferase 1 domain containing 1 [Source:HGNC Symbol;Acc:26483]	0.74
CPMCD1-010	4	ENSG00000198736	SEPX1	selenoprotein X, 1 [Source:HGNC Symbol;Acc:14133]	0.67
CPMCD1-010	4	ENSG00000197249	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 [Source:HGNC Symbol;Acc:8941]	0.92
CPMCD1-011	2	ENSG00000113916	BCL6	B-cell CLL/lymphoma 6 [Source:HGNC Symbol;Acc:1001]	0.78
CPMCD1-011	2	ENSG00000135821	GLUL	glutamate-ammonia ligase [Source:HGNC Symbol;Acc:4341]	0.72
CPMCD1-012	2	ENSG00000244682	FCGR2C	Fc fragment of IgG, low affinity IIc, receptor for (CD32) (gene/pseudogene) [Source:HGNC Symbol;Acc:15626]	0.83
CPMCD1-012	2	ENSG00000225217	HSPA7	heat shock 70kDa protein 7 (HSP70B) [Source:HGNC Symbol;Acc:5240]	0.76
CPMCD1-013	3	ENSG00000204472	AIF1	allograft inflammatory factor 1 [Source:HGNC Symbol;Acc:352]	0.60
CPMCD1-013	3	ENSG00000158869	FCER1G	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide [Source:HGNC Symbol;Acc:3611]	0.64
CPMCD1-013	3	ENSG00000119655	NPC2	Niemann-Pick disease, type C2 [Source:HGNC Symbol;Acc:14537]	0.69
CPMCD1-014	2	ENSG00000106780	MEGF9	multiple EGF-like-domains 9 [Source:HGNC Symbol;Acc:3234]	0.59
CPMCD1-014	2	ENSG00000168461	RAB31	RAB31, member RAS oncogene family [Source:HGNC Symbol;Acc:9771]	0.61
CPMCD1-015	2	ENSG00000119686	AC007182.1	Feline leukemia virus subgroup C receptor-related protein 2 [Source:UniProtKB/Swiss-Prot;Acc:Q9UPI3]	0.86
CPMCD1-015	2	ENSG00000143382	ADAMTSL4	ADAMTS-like 4 [Source:HGNC Symbol;Acc:19706]	0.72

Cluster ID	Cluster Size	Gene ID	Gene Name	Gene Description	Log_2 Fold Change
CPMCD1-016	2	ENSG00000126709	IFI6	interferon, alpha-inducible protein 6 [Source:HGNC Symbol;Acc:4054]	0.85
CPMCD1-016	2	ENSG00000187608	ISG15	ISG15 ubiquitin-like modifier [Source:HGNC Symbol;Acc:4053]	0.82
CPMCD1-017	2	ENSG00000188820	FAM26F	family with sequence similarity 26, member F [Source:HGNC Symbol;Acc:33391]	1.49
CPMCD1-017	2	ENSG00000041357	PSMA4	proteasome (prosome, macropain) subunit, alpha type, 4 [Source:HGNC Symbol;Acc:9533]	0.62
CPMCD1-018	4	ENSG00000177989	ODF3B	outer dense fiber of sperm tails 3B [Source:HGNC Symbol;Acc:34388]	1.39
CPMCD1-018	4	ENSG00000023902	PLEKHO1	pleckstrin homology domain containing, family O member 1 [Source:HGNC Symbol;Acc:24310]	0.62
CPMCD1-018	4	ENSG00000197122	SRC	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian) [Source:HGNC Symbol;Acc:11283]	0.77
CPMCD1-018	4	ENSG00000025708	TYMP	thymidine phosphorylase [Source:HGNC Symbol;Acc:3148]	1.38
CPMCD1-019	2	ENSG00000205730	ITPRIPL2	inositol 1,4,5-trisphosphate receptor interacting protein-like 2 [Source:HGNC Symbol;Acc:27257]	0.65
CPMCD1-019	2	ENSG00000113368	LMNB1	lamin B1 [Source:HGNC Symbol;Acc:6637]	0.93
CPMCD1-020	3	ENSG00000158517	NCF1	neutrophil cytosolic factor 1 [Source:HGNC Symbol;Acc:7660]	1.04
CPMCD1-020	3	ENSG00000182487	NCF1B	neutrophil cytosolic factor 1B pseudogene [Source:HGNC Symbol;Acc:32522]	0.88
CPMCD1-020	3	ENSG00000165178	NCF1C	neutrophil cytosolic factor 1C pseudogene [Source:HGNC Symbol;Acc:32523]	1.03
CPMCD1-021	7	ENSG00000117228	GBP1	guanylate binding protein 1, interferon-inducible [Source:HGNC Symbol;Acc:4182]	2.06
CPMCD1-021	7	ENSG00000162645	GBP2	guanylate binding protein 2, interferon-inducible [Source:HGNC Symbol;Acc:4183]	1.25
CPMCD1-021	7	ENSG00000117226	GBP3	guanylate binding protein 3 [Source:HGNC Symbol;Acc:4184]	0.71
CPMCD1-021	7	ENSG00000002549	LAP3	leucine aminopeptidase 3 [Source:HGNC Symbol;Acc:18449]	1.74
CPMCD1-021	7	ENSG00000138496	PARP9	poly (ADP-ribose) polymerase family, member 9 [Source:HGNC Symbol;Acc:24118]	1.29
CPMCD1-021	7	ENSG00000115415	STAT1	signal transducer and activator of transcription 1, 91kDa [Source:HGNC Symbol;Acc:11362]	1.63
CPMCD1-021	7	ENSG00000140105	WARS	tryptophanyl-tRNA synthetase [Source:HGNC Symbol;Acc:12729]	1.78
CPMCD1-022	3	ENSG00000163823	CCR1	chemokine (C-C motif) receptor 1 [Source:HGNC Symbol;Acc:1602]	1.11
CPMCD1-022	3	ENSG00000135636	DYSF	dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive) [Source:HGNC Symbol;Acc:3097]	1.43
CPMCD1-022	3	ENSG00000171049	FPR2	formyl peptide receptor 2 [Source:HGNC Symbol;Acc:3827]	1.34
CPMCD1-023	4	ENSG00000221963	APOL6	apolipoprotein L, 6 [Source:HGNC Symbol;Acc:14870]	0.92
CPMCD1-023	4	ENSG00000168062	BATF2	basic leucine zipper transcription factor, ATF-like 2 [Source:HGNC Symbol;Acc:25163]	2.70
CPMCD1-023	4	ENSG00000163840	DTX3L	deltex 3-like (Drosophila) [Source:HGNC Symbol;Acc:30323]	0.76

Cluster ID	Cluster Size	Gene ID	Gene Name	Gene Description	Log_2 Fold Change
CPMCD1-023	4	ENSG00000168394	TAP1	transporter 1, ATP-binding cassette, sub-family B (MDR/-TAP) [Source:HGNC Symbol;Acc:43]	0.73
CPMCD1-024	2	ENSG00000166527	CLEC4D	C-type lectin domain family 4, member D [Source:HGNC Symbol;Acc:14554]	0.76
CPMCD1-024	2	ENSG00000166523	CLEC4E	C-type lectin domain family 4, member E [Source:HGNC Symbol;Acc:14555]	0.63
CPMCD1-025	2	ENSG00000140379	BCL2A1	BCL2-related protein A1 [Source:HGNC Symbol;Acc:991]	1.00
CPMCD1-025	2	ENSG00000197272	IL27	interleukin 27 [Source:HGNC Symbol;Acc:19157]	2.05
CPMCD1-026	2	ENSG00000014257	ACPP	acid phosphatase, prostate [Source:HGNC Symbol;Acc:125]	0.70
CPMCD1-026	2	ENSG00000146373	RNF217	ring finger protein 217 [Source:HGNC Symbol;Acc:21487]	0.76
CPMCD1-027	2	ENSG00000155130	MARCKS	myristoylated alanine-rich protein kinase C substrate [Source:HGNC Symbol;Acc:6759]	0.86
CPMCD1-027	2	ENSG00000137767	SQRDL	sulfide quinone reductase-like (yeast) [Source:HGNC Symbol;Acc:20390]	0.73
CPMCD1-028	3	ENSG00000171860	C3AR1	complement component 3a receptor 1 [Source:HGNC Symbol;Acc:1319]	0.84
CPMCD1-028	3	ENSG00000188641	DPYD	dihydropyrimidine dehydrogenase [Source:HGNC Symbol;Acc:3012]	0.75
CPMCD1-028	3	ENSG00000136040	PLXNC1	plexin C1 [Source:HGNC Symbol;Acc:9106]	0.60
CPMCD1-029	5	ENSG00000137965	IFI44	interferon-induced protein 44 [Source:HGNC Symbol;Acc:16938]	1.01
CPMCD1-029	5	ENSG00000137959	IFI44L	interferon-induced protein 44-like [Source:HGNC Symbol;Acc:17817]	1.30
CPMCD1-029	5	ENSG00000173193	PARP14	poly (ADP-ribose) polymerase family, member 14 [Source:HGNC Symbol;Acc:29232]	0.85
CPMCD1-029	5	ENSG00000020577	SAMD4A	sterile alpha motif domain containing 4A [Source:HGNC Symbol;Acc:23023]	1.25
CPMCD1-029	5	ENSG00000132530	XAF1	XIAP associated factor 1 [Source:HGNC Symbol;Acc:30932]	0.81
CPMCD1-030	2	ENSG00000100336	APOL4	apolipoprotein L, 4 [Source:HGNC Symbol;Acc:14867]	1.41
CPMCD1-030	2	ENSG00000170525	PFKFB3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 [Source:HGNC Symbol;Acc:8874]	0.79
CPMCD1-031	3	ENSG00000182022	CHST15	carbohydrate (N-acetylgalactosamine 4-sulfate 6-O) sulfotransferase 15 [Source:HGNC Symbol;Acc:18137]	0.65
CPMCD1-031	3	ENSG00000104093	DMXL2	Dmx-like 2 [Source:HGNC Symbol;Acc:2938]	0.71
CPMCD1-031	3	ENSG00000136868	SLC31A1	solute carrier family 31 (copper transporters), member 1 [Source:HGNC Symbol;Acc:11016]	0.66
CPMCD1-032	3	ENSG00000146592	CREB5	cAMP responsive element binding protein 5 [Source:HGNC Symbol;Acc:16844]	0.79
CPMCD1-032	3	ENSG00000204577	LILRB3	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 [Source:HGNC Symbol;Acc:6607]	0.73
CPMCD1-032	3	ENSG00000167207	NOD2	nucleotide-binding oligomerization domain containing 2 [Source:HGNC Symbol;Acc:5331]	0.61
CPMCD1-033	3	ENSG00000196743	GM2A	GM2 ganglioside activator [Source:HGNC Symbol;Acc:4367]	0.76
CPMCD1-033	3	ENSG00000186818	LILRB4	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4 [Source:HGNC Symbol;Acc:6608]	0.87

Cluster ID	Cluster Size	Gene ID	Gene Name	Gene Description	Log_2 Fold Change
CPMCD1-033	3	ENSG00000130202	PVRL2	poliovirus receptor-related 2 (herpesvirus entry mediator B) [Source:HGNC Symbol;Acc:9707]	0.97
CPMCD1-034	5	ENSG00000128383	APOBEC3A	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3A [Source:HGNC Symbol;Acc:17343]	1.20
CPMCD1-034	5	ENSG00000173110	HSPA6	heat shock 70kDa protein 6 (HSP70B‘) [Source:HGNC Symbol;Acc:5239]	1.08
CPMCD1-034	5	ENSG00000089127	OAS1	2‘,5‘-oligoadenylate synthetase 1, 40/46kDa [Source:HGNC Symbol;Acc:8086]	0.88
CPMCD1-034	5	ENSG00000185339	TCN2	transcobalamin II [Source:HGNC Symbol;Acc:11653]	1.34
CPMCD1-034	5	ENSG00000121858	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10 [Source:HGNC Symbol;Acc:11925]	1.23
CPMCD1-035	2	ENSG00000242539	AC007620.3		0.93
CPMCD1-035	2	ENSG00000114450	GNB4	guanine nucleotide binding protein (G protein), beta polypeptide 4 [Source:HGNC Symbol;Acc:20731]	0.82
CPMCD1-036	4	ENSG00000134326	CMPK2	cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial [Source:HGNC Symbol;Acc:27015]	1.12
CPMCD1-036	4	ENSG00000185745	IFIT1	interferon-induced protein with tetratricopeptide repeats 1 [Source:HGNC Symbol;Acc:5407]	1.21
CPMCD1-036	4	ENSG00000157601	MX1	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse) [Source:HGNC Symbol;Acc:7532]	0.83
CPMCD1-036	4	ENSG00000135114	OASL	2‘-5‘-oligoadenylate synthetase-like [Source:HGNC Symbol;Acc:8090]	0.99
CPMCD1-037	4	ENSG00000166002	C11orf75	chromosome 11 open reading frame 75 [Source:HGNC Symbol;Acc:24810]	1.01
CPMCD1-037	4	ENSG00000204397	CARD16	caspase recruitment domain family, member 16 [Source:HGNC Symbol;Acc:33701]	0.65
CPMCD1-037	4	ENSG00000137752	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase) [Source:HGNC Symbol;Acc:1499]	0.69
CPMCD1-037	4	ENSG00000181631	P2RY13	purinergic receptor P2Y, G-protein coupled, 13 [Source:HGNC Symbol;Acc:4537]	0.94
CPMCD1-038	2	ENSG00000169026	MFSD7	major facilitator superfamily domain containing 7 [Source:HGNC Symbol;Acc:26177]	0.61
CPMCD1-038	2	ENSG00000074660	SCARF1	scavenger receptor class F, member 1 [Source:HGNC Symbol;Acc:16820]	0.67
CPMCD1-039	2	ENSG00000152229	PSTPIP2	proline-serine-threonine phosphatase interacting protein 2 [Source:HGNC Symbol;Acc:9581]	0.97
CPMCD1-039	2	ENSG00000185215	TNFAIP2	tumor necrosis factor, alpha-induced protein 2 [Source:HGNC Symbol;Acc:11895]	0.68
CPMCD1-040	2	ENSG00000253193	FCGR1C	Fc fragment of IgG, high affinity Ic, receptor (CD64) [Source:HGNC Symbol;Acc:3615]	3.04
CPMCD1-040	2	ENSG00000089041	P2RX7	purinergic receptor P2X, ligand-gated ion channel, 7 [Source:HGNC Symbol;Acc:8537]	0.76
CPMCD1-041	2	ENSG00000105835	NAMPT	nicotinamide phosphoribosyltransferase [Source:HGNC Symbol;Acc:30092]	1.06
CPMCD1-041	2	ENSG00000229644	NAMPTL	nicotinamide phosphoribosyltransferase-like [Source:HGNC Symbol;Acc:17633]	0.91
CPMCD1-042	3	ENSG00000135218	CD36	CD36 molecule (thrombospondin receptor) [Source:HGNC Symbol;Acc:1663]	0.78

Cluster ID	Cluster Size	Gene ID	Gene Name	Gene Description	Log_2 Fold Change
CPMCD1-042	3	ENSG00000139132	FGD4	FYVE, RhoGEF and PH domain containing 4 [Source:HGNC Symbol;Acc:19125]	0.60
CPMCD1-042	3	ENSG00000140090	SLC24A4	solute carrier family 24 (sodium/potassium/calcium exchanger), member 4 [Source:HGNC Symbol;Acc:10978]	0.61
CPMCD1-043	4	ENSG00000179921	GPBAR1	G protein-coupled bile acid receptor 1 [Source:HGNC Symbol;Acc:19680]	0.62
CPMCD1-043	4	ENSG00000096968	JAK2	Janus kinase 2 [Source:HGNC Symbol;Acc:6192]	0.82
CPMCD1-043	4	ENSG00000187164	KIAA1598	KIAA1598 [Source:HGNC Symbol;Acc:29319]	0.59
CPMCD1-043	4	ENSG00000175471	MCTP1	multiple C2 domains, transmembrane 1 [Source:HGNC Symbol;Acc:26183]	0.63
CPMCD1-044	4	ENSG00000179044	EXOC3L1	exocyst complex component 3-like 1 [Source:HGNC Symbol;Acc:27540]	1.69
CPMCD1-044	4	ENSG00000134470	IL15RA	interleukin 15 receptor, alpha [Source:HGNC Symbol;Acc:5978]	0.88
CPMCD1-044	4	ENSG00000185507	IRF7	interferon regulatory factor 7 [Source:HGNC Symbol;Acc:6122]	0.70
CPMCD1-044	4	ENSG00000064932	SBNO2	strawberry notch homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:29158]	0.64
CPMCD1-045	2	ENSG00000124762	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1) [Source:HGNC Symbol;Acc:1784]	0.72
CPMCD1-045	2	ENSG00000162614	NEXN	nexilin (F actin binding protein) [Source:HGNC Symbol;Acc:29557]	1.07
CPMCD1-046	4	ENSG00000161921	CXCL16	chemokine (C-X-C motif) ligand 16 [Source:HGNC Symbol;Acc:16642]	0.65
CPMCD1-046	4	ENSG00000187116	LILRA5	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 5 [Source:HGNC Symbol;Acc:16309]	0.98
CPMCD1-046	4	ENSG00000254470	RP11-770G2.3		0.64
CPMCD1-046	4	ENSG00000122862	SRGN	serglycin [Source:HGNC Symbol;Acc:9361]	0.64
CPMCD1-047	4	ENSG00000121807	CCR2	chemokine (C-C motif) receptor 2 [Source:HGNC Symbol;Acc:1603]	0.70
CPMCD1-047	4	ENSG00000139318	DUSP6	dual specificity phosphatase 6 [Source:HGNC Symbol;Acc:3072]	0.84
CPMCD1-047	4	ENSG00000136689	IL1RN	interleukin 1 receptor antagonist [Source:HGNC Symbol;Acc:6000]	0.81
CPMCD1-047	4	ENSG00000135363	LMO2	LIM domain only 2 (rhombotin-like 1) [Source:HGNC Symbol;Acc:6642]	0.72
CPMCD1-048	3	ENSG00000137757	CASP5	caspase 5, apoptosis-related cysteine peptidase [Source:HGNC Symbol;Acc:1506]	0.88
CPMCD1-048	3	ENSG00000224397	RP11-290F20.3		0.63
CPMCD1-048	3	ENSG00000248429	RP11-597D13.9		0.65
CPMCD1-049	2	ENSG00000136630	HLX	H2.0-like homeobox [Source:HGNC Symbol;Acc:4978]	0.61
CPMCD1-049	2	ENSG00000124731	TREM1	triggering receptor expressed on myeloid cells 1 [Source:HGNC Symbol;Acc:17760]	0.66
CPMCD1-050	3	ENSG00000185168	C17orf55	chromosome 17 open reading frame 55 [Source:HGNC Symbol;Acc:26816]	0.66
CPMCD1-050	3	ENSG00000123700	KCNJ2	potassium inwardly-rectifying channel, subfamily J, member 2 [Source:HGNC Symbol;Acc:6263]	1.00

Cluster ID	Cluster Size	Gene ID	Gene Name	Gene Description	Log_2 Fold Change
CPMCD1-050	3	ENSG00000137462	TLR2	toll-like receptor 2 [Source:HGNC Symbol;Acc:11848]	0.66
CPMCD1-051	5	ENSG00000168615	ADAM9	ADAM metallopeptidase domain 9 [Source:HGNC Symbol;Acc:216]	0.65
CPMCD1-051	5	ENSG00000138061	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1 [Source:HGNC Symbol;Acc:2597]	0.64
CPMCD1-051	5	ENSG00000002933	TMEM176A	transmembrane protein 176A [Source:HGNC Symbol;Acc:24930]	0.65
CPMCD1-051	5	ENSG00000106565	TMEM176B	transmembrane protein 176B [Source:HGNC Symbol;Acc:29596]	0.69
CPMCD1-051	5	ENSG00000038427	VCAN	versican [Source:HGNC Symbol;Acc:2464]	0.76
CPMCD1-052	3	ENSG00000038945	MSR1	macrophage scavenger receptor 1 [Source:HGNC Symbol;Acc:7376]	1.18
CPMCD1-052	3	ENSG00000158714	SLAMF8	SLAM family member 8 [Source:HGNC Symbol;Acc:21391]	1.25
CPMCD1-052	3	ENSG00000136867	SLC31A2	solute carrier family 31 (copper transporters), member 2 [Source:HGNC Symbol;Acc:11017]	1.14
CPMCD1-053	4	ENSG00000148926	ADM	adrenomedullin [Source:HGNC Symbol;Acc:259]	1.23
CPMCD1-053	4	ENSG00000257017	HP	haptoglobin [Source:HGNC Symbol;Acc:5141]	1.15
CPMCD1-053	4	ENSG00000171236	LRG1	leucine-rich alpha-2-glycoprotein 1 [Source:HGNC Symbol;Acc:29480]	0.85
CPMCD1-053	4	ENSG00000184557	SOCS3	suppressor of cytokine signaling 3 [Source:HGNC Symbol;Acc:19391]	1.76
CPMCD1-054	2	ENSG00000131203	IDO1	indoleamine 2,3-dioxygenase 1 [Source:HGNC Symbol;Acc:6059]	2.04
CPMCD1-054	2	ENSG00000108387	SEPT4	septin 4 [Source:HGNC Symbol;Acc:9165]	0.89
CPMCD1-055	2	ENSG00000152380	FAM151B	family with sequence similarity 151, member B [Source:HGNC Symbol;Acc:33716]	0.66
CPMCD1-055	2	ENSG00000171729	TMEM51	transmembrane protein 51 [Source:HGNC Symbol;Acc:25488]	0.86
CPMCD1-056	4	ENSG00000163568	AIM2	absent in melanoma 2 [Source:HGNC Symbol;Acc:357]	0.92
CPMCD1-056	4	ENSG00000104951	IL4I1	interleukin 4 induced 1 [Source:HGNC Symbol;Acc:19094]	0.62
CPMCD1-056	4	ENSG00000185499	MUC1	mucin 1, cell surface associated [Source:HGNC Symbol;Acc:7508]	0.90
CPMCD1-056	4	ENSG00000138670	RASGEF1B	RasGEF domain family, member 1B [Source:HGNC Symbol;Acc:24881]	0.83
CPMCD1-057	2	ENSG00000135540	NHSL1	NHS-like 1 [Source:HGNC Symbol;Acc:21021]	0.62
CPMCD1-057	2	ENSG00000238000	RP11-274E7.2		0.93
CPMCD1-058	2	ENSG00000169122	FAM110B	family with sequence similarity 110, member B [Source:HGNC Symbol;Acc:28587]	0.68
CPMCD1-058	2	ENSG00000133687	TMTC1	transmembrane and tetratricopeptide repeat containing 1 [Source:HGNC Symbol;Acc:24099]	0.64
CPMCD1-059	5	ENSG00000029153	ARNTL2	aryl hydrocarbon receptor nuclear translocator-like 2 [Source:HGNC Symbol;Acc:18984]	1.49
CPMCD1-059	5	ENSG00000174749	C4orf32	chromosome 4 open reading frame 32 [Source:HGNC Symbol;Acc:26813]	0.67
CPMCD1-059	5	ENSG00000203814	HIST2H2BF	histone cluster 2, H2bf [Source:HGNC Symbol;Acc:24700]	1.46
CPMCD1-059	5	ENSG00000242324	RP4-576H24.2		0.96

Cluster ID	Cluster Size	Gene ID	Gene Name	Gene Description	Log_2 Fold Change
CPMCD1-059	5	ENSG00000130589	RP4-697K14.7	Peroxisomal proliferator-activated receptor A-interacting complex 285 kDa protein [Source:UniProtKB/Swiss-Prot;Acc:Q9BYK8]	0.66
CPMCD1-060	3	ENSG00000186594	C17orf91	chromosome 17 open reading frame 91 [Source:HGNC Symbol;Acc:28219]	0.76
CPMCD1-060	3	ENSG00000246430	RP11-16M8.2		0.95
CPMCD1-060	3	ENSG00000141497	ZMYND15	zinc finger, MYND-type containing 15 [Source:HGNC Symbol;Acc:20997]	0.65
CPMCD1-061	4	ENSG00000151693	ASAP2	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2 [Source:HGNC Symbol;Acc:2721]	0.88
CPMCD1-061	4	ENSG00000128512	DOCK4	dedicator of cytokinesis 4 [Source:HGNC Symbol;Acc:19192]	0.80
CPMCD1-061	4	ENSG00000237476	XXbac-B135H6.15		0.59
CPMCD1-061	4	ENSG00000242779	ZNF702P	zinc finger protein 702, pseudogene [Source:HGNC Symbol;Acc:25775]	0.60
CPMCD1-062	2	ENSG00000232871	AC008888.7	secretory blood group 1 (SEC1), non-coding RNA [Source:RefSeq DNA;Acc:NR$_0 04401]$	-0.65
CPMCD1-062	2	ENSG00000136378	ADAMTS7	ADAM metallopeptidase with thrombospondin type 1 motif, 7 [Source:HGNC Symbol;Acc:223]	-0.71
CPMCD1-063	4	ENSG00000205018	AC092384.1	cDNA FLJ26728 fis, clone PNC06635 [Source:UniProtKB/TrEMBL;Acc:Q6ZP14]	0.69
CPMCD1-063	4	ENSG00000120129	DUSP1	dual specificity phosphatase 1 [Source:HGNC Symbol;Acc:3064]	0.71
CPMCD1-063	4	ENSG00000170345	FOS	FBJ murine osteosarcoma viral oncogene homolog [Source:HGNC Symbol;Acc:3796]	0.61
CPMCD1-063	4	ENSG00000238057	ZEB2-AS1	ZEB2 antisense RNA 1 (non-protein coding) [Source:HGNC Symbol;Acc:37149]	0.59
CPMCD1-064	5	ENSG00000226423	AC093642.4		-0.61
CPMCD1-064	5	ENSG00000100346	CACNA1I	calcium channel, voltage-dependent, T type, alpha 1I subunit [Source:HGNC Symbol;Acc:1396]	-0.65
CPMCD1-064	5	ENSG00000140545	MFGE8	milk fat globule-EGF factor 8 protein [Source:HGNC Symbol;Acc:7036]	-0.61
CPMCD1-064	5	ENSG00000183691	NOG	noggin [Source:HGNC Symbol;Acc:7866]	-0.62
CPMCD1-064	5	ENSG00000091129	NRCAM	neuronal cell adhesion molecule [Source:HGNC Symbol;Acc:7994]	-0.89
CPMCD1-065	4	ENSG00000123685	BATF3	basic leucine zipper transcription factor, ATF-like 3 [Source:HGNC Symbol;Acc:28915]	0.61
CPMCD1-065	4	ENSG00000173372	C1QA	complement component 1, q subcomponent, A chain [Source:HGNC Symbol;Acc:1241]	0.66
CPMCD1-065	4	ENSG00000173369	C1QB	complement component 1, q subcomponent, B chain [Source:HGNC Symbol;Acc:1242]	1.35
CPMCD1-065	4	ENSG00000121797	CCRL2	chemokine (C-C motif) receptor-like 2 [Source:HGNC Symbol;Acc:1612]	0.65
CPMCD1-066	5	ENSG00000172653	C17orf66	chromosome 17 open reading frame 66 [Source:HGNC Symbol;Acc:26548]	-0.70
CPMCD1-066	5	ENSG00000130635	COL5A1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]	-0.61
CPMCD1-066	5	ENSG00000080573	COL5A3	collagen, type V, alpha 3 [Source:HGNC Symbol;Acc:14864]	-0.67

Cluster ID	Cluster Size	Gene ID	Gene Name	Gene Description	Log_2 Fold Change
CPMCD1-066	5	ENSG00000237248	RP11-118B22.2		-0.59
CPMCD1-066	5	ENSG00000256069	RP11-118B22.6		-0.67
CPMCD1-067	3	ENSG00000251948	AC092279.1		1.45
CPMCD1-067	3	ENSG00000244230	AL355679.1		0.87
CPMCD1-067	3	ENSG00000244642	AP005717.1		0.66
CPMCD1-068	2	ENSG00000188010	MORN2	MORN repeat containing 2 [Source:HGNC Symbol;Acc:30166]	0.60
CPMCD1-068	2	ENSG00000127564	PKMYT1	protein kinase, membrane associated tyrosine/threonine 1 [Source:HGNC Symbol;Acc:29650]	0.68
CPMCD1-069	2	ENSG00000197927	C2orf27A	chromosome 2 open reading frame 27A [Source:HGNC Symbol;Acc:25077]	-0.62
CPMCD1-069	2	ENSG00000116254	CHD5	chromodomain helicase DNA binding protein 5 [Source:HGNC Symbol;Acc:16816]	-0.62

Table A9: Significant gene clusters (RNA-Seq, PBMC, Day 1)

Cluster ID	Cluster Size	Gene ID	Gene Name	Gene Description
CPMCD1D28-001	2	ENSG00000002549	LAP3	leucine aminopeptidase 3 [Source:HGNC Symbol;Acc:18449]
CPMCD1D28-001	2	ENSG00000140105	WARS	tryptophanyl-tRNA synthetase [Source:HGNC Symbol;Acc:12729]
CPMCD1D28-002	3	ENSG00000163221	S100A12	S100 calcium binding protein A12 [Source:HGNC Symbol;Acc:10489]
CPMCD1D28-002	3	ENSG00000143546	S100A8	S100 calcium binding protein A8 [Source:HGNC Symbol;Acc:10498]
CPMCD1D28-002	3	ENSG00000163220	S100A9	S100 calcium binding protein A9 [Source:HGNC Symbol;Acc:10499]
CPMCD1D28-003	2	ENSG00000119922	IFIT2	interferon-induced protein with tetratricopeptide repeats 2 [Source:HGNC Symbol;Acc:5409]
CPMCD1D28-003	2	ENSG00000119917	IFIT3	interferon-induced protein with tetratricopeptide repeats 3 [Source:HGNC Symbol;Acc:5411]
CPMCD1D28-004	3	ENSG00000164125	FAM198B	family with sequence similarity 198, member B [Source:HGNC Symbol;Acc:25312]
CPMCD1D28-004	3	ENSG00000163694	RBM47	RNA binding motif protein 47 [Source:HGNC Symbol;Acc:30358]
CPMCD1D28-004	3	ENSG00000134243	SORT1	sortilin 1 [Source:HGNC Symbol;Acc:11186]
CPMCD1D28-005	3	ENSG00000158517	NCF1	neutrophil cytosolic factor 1 [Source:HGNC Symbol;Acc:7660]
CPMCD1D28-005	3	ENSG00000182487	NCF1B	neutrophil cytosolic factor 1B pseudogene [Source:HGNC Symbol;Acc:32522]
CPMCD1D28-005	3	ENSG00000165178	NCF1C	neutrophil cytosolic factor 1C pseudogene [Source:HGNC Symbol;Acc:32523]
CPMCD1D28-006	2	ENSG00000244682	FCGR2C	Fc fragment of IgG, low affinity IIc, receptor for (CD32) (gene/pseudogene) [Source:HGNC Symbol;Acc:15626]
CPMCD1D28-006	2	ENSG00000225217	HSPA7	heat shock 70kDa protein 7 (HSP70B) [Source:HGNC Symbol;Acc:5240]
CPMCD1D28-007	2	ENSG00000105835	NAMPT	nicotinamide phosphoribosyltransferase [Source:HGNC Symbol;Acc:30092]

Cluster ID	Cluster Size	Gene ID	Gene Name	Gene Description
CPMCD1D28-007	2	ENSG00000229644	NAMPTL	nicotinamide phosphoribosyltransferase-like [Source:HGNC Symbol;Acc:17633]
CPMCD1D28-008	7	ENSG00000166002	C11orf75	chromosome 11 open reading frame 75 [Source:HGNC Symbol;Acc:24810]
CPMCD1D28-008	7	ENSG00000103642	LACTB	lactamase, beta [Source:HGNC Symbol;Acc:16468]
CPMCD1D28-008	7	ENSG00000087253	LPCAT2	lysophosphatidylcholine acyltransferase 2 [Source:HGNC Symbol;Acc:26032]
CPMCD1D28-008	7	ENSG00000188906	LRRK2	leucine-rich repeat kinase 2 [Source:HGNC Symbol;Acc:18618]
CPMCD1D28-008	7	ENSG00000183023	SLC8A1	solute carrier family 8 (sodium/calcium exchanger), member 1 [Source:HGNC Symbol;Acc:11068]
CPMCD1D28-008	7	ENSG00000086300	SNX10	sorting nexin 10 [Source:HGNC Symbol;Acc:14974]
CPMCD1D28-008	7	ENSG00000105967	TFEC	transcription factor EC [Source:HGNC Symbol;Acc:11754]
CPMCD1D28-009	2	ENSG00000198019	FCGR1B	Fc fragment of IgG, high affinity Ib, receptor (CD64) [Source:HGNC Symbol;Acc:3614]
CPMCD1D28-009	2	ENSG00000253193	FCGR1C	Fc fragment of IgG, high affinity Ic, receptor (CD64) [Source:HGNC Symbol;Acc:3615]
CPMCD1D28-010	2	ENSG00000002933	TMEM176A	transmembrane protein 176A [Source:HGNC Symbol;Acc:24930]
CPMCD1D28-010	2	ENSG00000106565	TMEM176B	transmembrane protein 176B [Source:HGNC Symbol;Acc:29596]
CPMCD1D28-011	2	ENSG00000100336	APOL4	apolipoprotein L, 4 [Source:HGNC Symbol;Acc:14867]
CPMCD1D28-011	2	ENSG00000183762	KREMEN1	kringle containing transmembrane protein 1 [Source:HGNC Symbol;Acc:17550]
CPMCD1D28-012	15	ENSG00000128383	APOBEC3A	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3A [Source:HGNC Symbol;Acc:17343]
CPMCD1D28-012	15	ENSG00000169245	CXCL10	chemokine (C-X-C motif) ligand 10 [Source:HGNC Symbol;Acc:10637]
CPMCD1D28-012	15	ENSG00000133106	EPSTI1	epithelial stromal interaction 1 (breast) [Source:HGNC Symbol;Acc:16465]
CPMCD1D28-012	15	ENSG00000068079	IFI35	interferon-induced protein 35 [Source:HGNC Symbol;Acc:5399]
CPMCD1D28-012	15	ENSG00000096968	JAK2	Janus kinase 2 [Source:HGNC Symbol;Acc:6192]
CPMCD1D28-012	15	ENSG00000138119	MYOF	myoferlin [Source:HGNC Symbol;Acc:3656]
CPMCD1D28-012	15	ENSG00000177989	ODF3B	outer dense fiber of sperm tails 3B [Source:HGNC Symbol;Acc:34388]
CPMCD1D28-012	15	ENSG00000173193	PARP14	poly (ADP-ribose) polymerase family, member 14 [Source:HGNC Symbol;Acc:29232]
CPMCD1D28-012	15	ENSG00000138496	PARP9	poly (ADP-ribose) polymerase family, member 9 [Source:HGNC Symbol;Acc:24118]
CPMCD1D28-012	15	ENSG00000020577	SAMD4A	sterile alpha motif domain containing 4A [Source:HGNC Symbol;Acc:23023]
CPMCD1D28-012	15	ENSG00000177409	SAMD9L	sterile alpha motif domain containing 9-like [Source:HGNC Symbol;Acc:1349]
CPMCD1D28-012	15	ENSG00000130489	SCO2	SCO cytochrome oxidase deficient homolog 2 (yeast) [Source:HGNC Symbol;Acc:10604]
CPMCD1D28-012	15	ENSG00000149131	SERPING1	serpin peptidase inhibitor, clade G (C1 inhibitor), member 1 [Source:HGNC Symbol;Acc:1228]
CPMCD1D28-012	15	ENSG00000170581	STAT2	signal transducer and activator of transcription 2, 113kDa [Source:HGNC Symbol;Acc:11363]
CPMCD1D28-012	15	ENSG00000025708	TYMP	thymidine phosphorylase [Source:HGNC Symbol;Acc:3148]

Cluster ID	Cluster Size	Gene ID	Gene Name	Gene Description
CPMCD1D28-013	2	ENSG00000120129	DUSP1	dual specificity phosphatase 1 [Source:HGNC Symbol;Acc:3064]
CPMCD1D28-013	2	ENSG00000170345	FOS	FBJ murine osteosarcoma viral oncogene homolog [Source:HGNC Symbol;Acc:3796]
CPMCD1D28-014	9	ENSG00000143382	ADAMTSL4	ADAMTS-like 4 [Source:HGNC Symbol;Acc:19706]
CPMCD1D28-014	9	ENSG00000173110	HSPA6	heat shock 70kDa protein 6 (HSP70B') [Source:HGNC Symbol;Acc:5239]
CPMCD1D28-014	9	ENSG00000244482	LILRA6	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 6 [Source:HGNC Symbol;Acc:15495]
CPMCD1D28-014	9	ENSG00000104972	LILRB1	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1 [Source:HGNC Symbol;Acc:6605]
CPMCD1D28-014	9	ENSG00000131042	LILRB2	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2 [Source:HGNC Symbol;Acc:6606]
CPMCD1D28-014	9	ENSG00000105609	LILRB5	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5 [Source:HGNC Symbol;Acc:6609]
CPMCD1D28-014	9	ENSG00000169026	MFSD7	major facilitator superfamily domain containing 7 [Source:HGNC Symbol;Acc:26177]
CPMCD1D28-014	9	ENSG00000161643	SIGLEC16	sialic acid binding Ig-like lectin 16 (gene/pseudogene) [Source:HGNC Symbol;Acc:24851]
CPMCD1D28-014	9	ENSG00000180061	TMEM150B	transmembrane protein 150B [Source:HGNC Symbol;Acc:34415]
CPMCD1D28-015	12	ENSG00000168615	ADAM9	ADAM metallopeptidase domain 9 [Source:HGNC Symbol;Acc:216]
CPMCD1D28-015	12	ENSG00000181982	CCDC149	coiled-coil domain containing 149 [Source:HGNC Symbol;Acc:25405]
CPMCD1D28-015	12	ENSG00000170458	CD14	CD14 molecule [Source:HGNC Symbol;Acc:1628]
CPMCD1D28-015	12	ENSG00000166527	CLEC4D	C-type lectin domain family 4, member D [Source:HGNC Symbol;Acc:14554]
CPMCD1D28-015	12	ENSG00000166523	CLEC4E	C-type lectin domain family 4, member E [Source:HGNC Symbol;Acc:14555]
CPMCD1D28-015	12	ENSG00000103196	CRISPLD2	cysteine-rich secretory protein LCCL domain containing 2 [Source:HGNC Symbol;Acc:25248]
CPMCD1D28-015	12	ENSG00000138061	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1 [Source:HGNC Symbol;Acc:2597]
CPMCD1D28-015	12	ENSG00000134755	DSC2	desmocollin 2 [Source:HGNC Symbol;Acc:3036]
CPMCD1D28-015	12	ENSG00000115271	GCA	grancalcin, EF-hand calcium binding protein [Source:HGNC Symbol;Acc:15990]
CPMCD1D28-015	12	ENSG00000106780	MEGF9	multiple EGF-like-domains 9 [Source:HGNC Symbol;Acc:3234]
CPMCD1D28-015	12	ENSG00000119457	SLC46A2	solute carrier family 46, member 2 [Source:HGNC Symbol;Acc:16055]
CPMCD1D28-015	12	ENSG00000038427	VCAN	versican [Source:HGNC Symbol;Acc:2464]
CPMCD1D28-016	3	ENSG00000100346	CACNA1I	calcium channel, voltage-dependent, T type, alpha 1I subunit [Source:HGNC Symbol;Acc:1396]
CPMCD1D28-016	3	ENSG00000140545	MFGE8	milk fat globule-EGF factor 8 protein [Source:HGNC Symbol;Acc:7036]
CPMCD1D28-016	3	ENSG00000091129	NRCAM	neuronal cell adhesion molecule [Source:HGNC Symbol;Acc:7994]

Cluster ID	Cluster Size	Gene ID	Gene Name	Gene Description
CPMCD1D28-017	7	ENSG00000151726	ACSL1	acyl-CoA synthetase long-chain family member 1 [Source:HGNC Symbol;Acc:3569]
CPMCD1D28-017	7	ENSG00000140379	BCL2A1	BCL2-related protein A1 [Source:HGNC Symbol;Acc:991]
CPMCD1D28-017	7	ENSG00000113916	BCL6	B-cell CLL/lymphoma 6 [Source:HGNC Symbol;Acc:1001]
CPMCD1D28-017	7	ENSG00000125538	IL1B	interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
CPMCD1D28-017	7	ENSG00000223401	RP11-211G3.2	
CPMCD1D28-017	7	ENSG00000184988	TMEM106A	transmembrane protein 106A [Source:HGNC Symbol;Acc:28288]
CPMCD1D28-017	7	ENSG00000173334	TRIB1	tribbles homolog 1 (Drosophila) [Source:HGNC Symbol;Acc:16891]
CPMCD1D28-018	2	ENSG00000237248	RP11-118B22.2	
CPMCD1D28-018	2	ENSG00000256069	RP11-118B22.6	
CPMCD1D28-019	7	ENSG00000206082	AC010507.1	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:E7EMX1]
CPMCD1D28-019	7	ENSG00000244758	AC093627.6	
CPMCD1D28-019	7	ENSG00000233013	FAM157B	family with sequence similarity 157, member B [Source:HGNC Symbol;Acc:34080]
CPMCD1D28-019	7	ENSG00000235373	RP11-206L10.3	
CPMCD1D28-019	7	ENSG00000240618	RP11-206L10.5	
CPMCD1D28-019	7	ENSG00000239906	RP11-34P13.14	
CPMCD1D28-019	7	ENSG00000237094	RP4-669L17.10	
CPMCD1D28-020	2	ENSG00000189127	ANKRD34B	ankyrin repeat domain 34B [Source:HGNC Symbol;Acc:33736]
CPMCD1D28-020	2	ENSG00000079215	SLC1A3	solute carrier family 1 (glial high affinity glutamate transporter), member 3 [Source:HGNC Symbol;Acc:10941]
CPMCD1D28-021	3	ENSG00000251948	AC092279.1	
CPMCD1D28-021	3	ENSG00000244230	AL355679.1	
CPMCD1D28-021	3	ENSG00000244642	AP005717.1	

Table A10: Significant gene clusters (RNA-Seq, PBMC, Day 1-28)

Category Type	Categories	Distinct #Genes In Sets	Median #Genes Per Set
MSigDB BioCarta Pathways	217	1228	18
MSigDB Chemical/Genetic Perturbations	3398	18288	44
MSigDB GO Biological Processes	825	5914	26
MSigDB GO Cellular Components	233	5065	27
MSigDB GO Molecular Functions	396	5108	26
MSigDB Immunologic Signatures	1910	17782	193
KEGG Modules	162	1075	6
KEGG Pathways	286	6107	58
MSigDB Reactome Pathways	674	5595	26

Category Type	Categories	Distinct #Genes In Sets	Median #Genes Per Set

Table A11: Overview of gene sets used for the enrichment analysis (RNA-Seq).

Cell Type (Study Visit Day)	KEGGP n/N(%)	KEGGM n/N(%)	GOBP n/N(%)	GOCC n/N(%)	GOMF n/N(%)	REACP n/N(%)	BIOCP n/N(%)	CHEMG n/N(%)	IMMO n/N(%)
PBMC (Day 1)	179/474(38)	15/474(3)	192/474(41)	144/474(30)	158/474(33)	170/474(36)	50/474(11)	401/474(85)	392/474(83)

Table A12: Overview of differential genes that mapped to any gene set by category (RNA-Seq). KEGGP: KEGG Pathways, KEGGM: KEGG Modules, GOBP: GO Biological Processes, GOCC: GO Cellular Components, GOMF: GO Molecular Functions, REACP: Reactome Pathways, BIOCP: BioCarta Pathways, CHEMG: Chemical/Genetic Perturbations, IMMO: Immunologic Signatures. n=#mapped DE genes, N=#DE genes.

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Ad-justed P-Value	Jaccard Index	Cell Type Over-lap
Influenza A	149	20 (13.4)	20 (13.4)	0 (0)	<0.0001	0.0002	0.0649	neu, mnc, tcl
Osteoclast differentiation	113	17 (15)	17 (15)	0 (0)	<0.0001	0.0002	0.0618	mnc
Pertussis	70	12 (17.1)	12 (17.1)	0 (0)	<0.0001	0.0002	0.0506	neu, dnc
Measles	115	14 (12.2)	14 (12.2)	0 (0)	<0.0001	0.0002	0.0500	neu, mnc
Herpes simplex infection	154	15 (9.7)	15 (9.7)	0 (0)	<0.0001	0.0002	0.0472	neu, mnc, dnc
Tuberculosis	159	15 (9.4)	15 (9.4)	0 (0)	<0.0001	0.0002	0.0464	neu
Phagosome	131	13 (9.9)	13 (9.9)	0 (0)	<0.0001	0.0002	0.0438	neu, mnc
Staphylococcus aureus infection	47	9 (19.1)	9 (19.1)	0 (0)	<0.0001	0.0002	0.0415	neu, mnc, dnc
Hepatitis B	131	12 (9.2)	11 (8.4)	1 (0.8)	<0.0001	0.0002	0.0403	
Leishmaniasis	60	9 (15)	9 (15)	0 (0)	<0.0001	0.0002	0.0391	neu
Chemokine signaling pathway	162	12 (7.4)	12 (7.4)	0 (0)	<0.0001	0.0002	0.0365	
Cytokine-cytokine receptor interaction	225	14 (6.2)	13 (5.8)	1 (0.4)	<0.0001	0.0002	0.0359	
Rheumatoid arthritis	77	8 (10.4)	8 (10.4)	0 (0)	<0.0001	0.0002	0.0323	neu, tcl
Legionellosis	51	7 (13.7)	7 (13.7)	0 (0)	<0.0001	0.0002	0.0314	
Antigen processing and presentation	64	7 (10.9)	7 (10.9)	0 (0)	<0.0001	0.0002	0.0297	neu, mnc
TNF signaling pathway	102	10 (9.8)	10 (9.8)	0 (0)	<0.0001	0.0003	0.0369	tcl
Jak-STAT signaling pathway	139	11 (7.9)	8 (5.8)	3 (2.2)	<0.0001	0.0003	0.0358	
NF-kappa B signaling pathway	78	8 (10.3)	8 (10.3)	0 (0)	<0.0001	0.0004	0.0321	
NOD-like receptor signaling pathway	52	7 (13.5)	7 (13.5)	0 (0)	<0.0001	0.0004	0.0312	neu
Toll-like receptor signaling pathway	92	8 (8.7)	8 (8.7)	0 (0)	<0.0001	0.0004	0.0304	
Fc gamma R-mediated phagocytosis	86	8 (9.3)	8 (9.3)	0 (0)	<0.0001	0.001	0.0311	
Hepatitis C	117	9 (7.7)	9 (7.7)	0 (0)	<0.0001	0.0011	0.0314	neu, mnc, dnc, tcl
Inflammatory bowel disease (IBD)	53	6 (11.3)	5 (9.4)	1 (1.9)	<0.0001	0.0011	0.0265	neu
Prolactin signaling pathway	67	7 (10.4)	7 (10.4)	0 (0)	<0.0001	0.0012	0.0293	tcl
Transcriptional misregulation in cancer	163	10 (6.1)	10 (6.1)	0 (0)	0.0001	0.0013	0.0301	dnc
Salmonella infection	78	7 (9)	7 (9)	0 (0)	0.0001	0.0013	0.0280	
Lysosome	108	8 (7.4)	8 (7.4)	0 (0)	0.0002	0.0019	0.0287	
Complement and coagulation cascades	61	6 (9.8)	6 (9.8)	0 (0)	0.0003	0.0029	0.0256	dnc
Cytosolic DNA-sensing pathway	54	5 (9.3)	5 (9.3)	0 (0)	0.0005	0.0047	0.0219	
Systemic lupus erythematosus	106	6 (5.7)	6 (5.7)	0 (0)	0.0006	0.0062	0.0215	neu, dnc
Viral carcinogenesis	182	9 (4.9)	9 (4.9)	0 (0)	0.0008	0.0077	0.0256	
Intestinal immune network for IgA production	37	4 (10.8)	4 (10.8)	0 (0)	0.001	0.0093	0.0189	neu

Table A13: Significantly enriched KEGG Pathways (RNA-Seq, PBMC, Day 1). Results sorted by FDR and Jaccard index. The last column indicates overlap with cell type-specific results: dnc: dendritic cells, mnc: monocytes, neu: neutrophils, tcl: T-cells, nkc: NK-cells, bcl: B-cells.

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
DEFENSE RESPONSE	262	30 (11.5)	30 (11.5)	0 (0)	<0.0001	0.0003	0.0708	neu, mnc
IMMUNE RESPONSE	231	24 (10.4)	24 (10.4)	0 (0)	<0.0001	0.0003	0.0602	neu, mnc, dnc
INFLAMMATORY RESPONSE	129	18 (14)	18 (14)	0 (0)	<0.0001	0.0003	0.0594	neu, mnc
RESPONSE TO WOUNDING	185	21 (11.4)	21 (11.4)	0 (0)	<0.0001	0.0003	0.0590	neu, mnc
RESPONSE TO EXTERNAL STIMULUS	304	27 (8.9)	27 (8.9)	0 (0)	<0.0001	0.0003	0.0576	neu
IMMUNE SYSTEM PROCESS	324	28 (8.6)	28 (8.6)	0 (0)	<0.0001	0.0003	0.0574	neu, mnc
RESPONSE TO STRESS	494	28 (5.7)	28 (5.7)	0 (0)	<0.0001	0.0003	0.0426	
SIGNAL TRANSDUCTION	1580	68 (4.3)	67 (4.2)	1 (0.1)	<0.0001	0.0003	0.0399	neu, mnc
PROTEIN KINASE CASCADE	285	18 (6.3)	18 (6.3)	0 (0)	<0.0001	0.0003	0.0392	neu
POSITIVE REGULATION OF BIOLOGICAL PROCESS	690	32 (4.6)	32 (4.6)	0 (0)	<0.0001	0.0003	0.0376	neu, mnc
POSITIVE REGULATION OF CELLULAR PROCESS	652	30 (4.6)	30 (4.6)	0 (0)	<0.0001	0.0003	0.0369	neu, mnc
RESPONSE TO BIOTIC STIMULUS	117	11 (9.4)	11 (9.4)	0 (0)	<0.0001	0.0003	0.0369	neu, mnc
MULTI ORGANISM PROCESS	157	12 (7.6)	12 (7.6)	0 (0)	<0.0001	0.0003	0.0356	neu, mnc
POSITIVE REGULATION OF CELLULAR PROTEIN METABOLIC PROCESS	70	9 (12.9)	9 (12.9)	0 (0)	<0.0001	0.0003	0.0356	
POSITIVE REGULATION OF PROTEIN METABOLIC PROCESS	71	9 (12.7)	9 (12.7)	0 (0)	<0.0001	0.0003	0.0354	
RESPONSE TO OTHER ORGANISM	79	9 (11.4)	9 (11.4)	0 (0)	<0.0001	0.0003	0.0344	neu, mnc
CELL SURFACE RECEPTOR LINKED SIGNAL TRANSDUCTION GO 0007166	622	27 (4.3)	27 (4.3)	0 (0)	<0.0001	0.0003	0.0343	
INTRACELLULAR SIGNALING CASCADE	647	27 (4.2)	27 (4.2)	0 (0)	<0.0001	0.0003	0.0333	neu
REGULATION OF DEVELOPMENTAL PROCESS	434	20 (4.6)	20 (4.6)	0 (0)	<0.0001	0.0003	0.0330	mnc
JAK STAT CASCADE	31	7 (22.6)	7 (22.6)	0 (0)	<0.0001	0.0003	0.0324	mnc
CYTOKINE PRODUCTION	67	8 (11.9)	8 (11.9)	0 (0)	<0.0001	0.0003	0.0319	
CELLULAR PROTEIN METABOLIC PROCESS	1077	35 (3.2)	34 (3.2)	1 (0.1)	<0.0001	0.0003	0.0284	
CELLULAR MACROMOLECULE METABOLIC PROCESS	1089	35 (3.2)	34 (3.1)	1 (0.1)	<0.0001	0.0003	0.0281	
PROTEIN METABOLIC PROCESS	1185	37 (3.1)	36 (3)	1 (0.1)	<0.0001	0.0003	0.0276	neu, mnc
RESPONSE TO VIRUS	47	6 (12.8)	6 (12.8)	0 (0)	<0.0001	0.0003	0.0258	neu, mnc
APOPTOSIS GO	428	19 (4.4)	19 (4.4)	0 (0)	<0.0001	0.0006	0.0316	
PROGRAMMED CELL DEATH	429	19 (4.4)	19 (4.4)	0 (0)	<0.0001	0.0006	0.0316	mnc
ORGAN DEVELOPMENT	544	22 (4)	20 (3.7)	2 (0.4)	<0.0001	0.0011	0.0308	
MULTICELLULAR ORGANISMAL DEVELOPMENT	987	31 (3.1)	27 (2.7)	4 (0.4)	<0.0001	0.0011	0.0270	
MEMBRANE ORGANIZATION AND BIOGENESIS	135	10 (7.4)	9 (6.7)	1 (0.7)	<0.0001	0.0013	0.0315	neu, mnc
REGULATION OF MOLECULAR FUNCTION	312	15 (4.8)	15 (4.8)	0 (0)	<0.0001	0.0013	0.0307	
CYTOKINE SECRETION	17	4 (23.5)	4 (23.5)	0 (0)	<0.0001	0.0013	0.0195	
POSITIVE REGULATION OF TRANSLATION	32	5 (15.6)	5 (15.6)	0 (0)	<0.0001	0.0015	0.0228	
PHAGOCYTOSIS	18	4 (22.2)	4 (22.2)	0 (0)	<0.0001	0.0015	0.0194	mnc
REGULATION OF BIOLOGICAL QUALITY	395	17 (4.3)	17 (4.3)	0 (0)	<0.0001	0.0021	0.0298	

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
REGULATION OF APOPTOSIS	338	15 (4.4)	15 (4.4)	0 (0)	0.0001	0.0025	0.0291	mnc
REGULATION OF PROGRAMMED CELL DEATH	339	15 (4.4)	15 (4.4)	0 (0)	0.0001	0.0025	0.0291	mnc
POSITIVE REGULATION OF SIGNAL TRANSDUCTION	127	9 (7.1)	9 (7.1)	0 (0)	0.0001	0.0026	0.0290	neu
RESPONSE TO CHEMICAL STIMULUS	313	14 (4.5)	14 (4.5)	0 (0)	0.0002	0.0034	0.0285	
MESODERM DEVELOPMENT	20	4 (20)	4 (20)	0 (0)	0.0002	0.0039	0.0192	
ANATOMICAL STRUCTURE DEVELOPMENT	965	29 (3)	25 (2.6)	4 (0.4)	0.0002	0.0042	0.0257	
CELL DEVELOPMENT	571	20 (3.5)	19 (3.3)	1 (0.2)	0.0002	0.0045	0.0269	mnc
I KAPPAB KINASE NF KAPPAB CASCADE	113	8 (7.1)	8 (7.1)	0 (0)	0.0002	0.0046	0.0269	neu
INTERLEUKIN 1 SECRETION	10	3 (30)	3 (30)	0 (0)	0.0003	0.0051	0.0151	
REGULATION OF CELLULAR PROTEIN METABOLIC PROCESS	156	9 (5.8)	9 (5.8)	0 (0)	0.0003	0.0051	0.0265	
PROTEOLYSIS	185	10 (5.4)	10 (5.4)	0 (0)	0.0003	0.0061	0.0272	
REGULATION OF CELLULAR METABOLIC PROCESS	751	24 (3.2)	24 (3.2)	0 (0)	0.0003	0.0061	0.0261	
REGULATION OF CELL PROLIFERATION	300	13 (4.3)	13 (4.3)	0 (0)	0.0004	0.0065	0.0271	
REGULATION OF METABOLIC PROCESS	761	24 (3.2)	24 (3.2)	0 (0)	0.0004	0.0069	0.0258	
POSITIVE REGULATION OF CELLULAR METABOLIC PROCESS	220	11 (5)	11 (5)	0 (0)	0.0004	0.0069	0.0274	
REGULATION OF CATALYTIC ACTIVITY	265	12 (4.5)	12 (4.5)	0 (0)	0.0004	0.007	0.0270	
REGULATION OF PROTEIN METABOLIC PROCESS	164	9 (5.5)	9 (5.5)	0 (0)	0.0004	0.007	0.0259	
DETECTION OF BIOTIC STIMULUS	10	3 (30)	3 (30)	0 (0)	0.0005	0.0075	0.0151	
POSITIVE REGULATION OF METABOLIC PROCESS	225	11 (4.9)	11 (4.9)	0 (0)	0.0005	0.0081	0.0271	
TYROSINE PHOSPHORYLATION OF STAT PROTEIN	13	3 (23.1)	3 (23.1)	0 (0)	0.0006	0.0087	0.0149	
CELL PROLIFERATION GO 0008283	493	17 (3.4)	17 (3.4)	0 (0)	0.0006	0.0091	0.0254	neu, mnc
PROTEIN SECRETION	31	4 (12.9)	4 (12.9)	0 (0)	0.0007	0.0096	0.0183	

Table A14: Significantly enriched MSigDB GO Biological Processes (RNA-Seq, PBMC, Day 1). Results sorted by FDR and Jaccard index. The last column indicates overlap with cell type-specific results: dnc: dendritic cells, mnc: monocytes, neu: neutrophils, tcl: T-cells, nkc: NK-cells, bcl: B-cells.

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
EXTRACELLULAR SPACE	234	18 (7.7)	17 (7.3)	1 (0.4)	<0.0001	0.0002	0.0500	
EXTRACELLULAR REGION PART	324	21 (6.5)	18 (5.6)	3 (0.9)	<0.0001	0.0002	0.0470	
EXTRACELLULAR REGION	430	24 (5.6)	21 (4.9)	3 (0.7)	<0.0001	0.0002	0.0436	
PLASMA MEMBRANE	1358	61 (4.5)	58 (4.3)	3 (0.2)	<0.0001	0.0002	0.0423	dnc
MEMBRANE	1902	74 (3.9)	71 (3.7)	3 (0.2)	<0.0001	0.0002	0.0375	mnc, dnc
CELL FRACTION	480	22 (4.6)	21 (4.4)	1 (0.2)	<0.0001	0.0002	0.0365	neu

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
INTEGRAL TO PLASMA MEMBRANE	930	37 (4)	35 (3.8)	2 (0.2)	<0.0001	0.0002	0.0357	
INTRINSIC TO PLASMA MEMBRANE	943	37 (3.9)	35 (3.7)	2 (0.2)	<0.0001	0.0002	0.0352	
INTEGRAL TO MEMBRANE	1272	48 (3.8)	46 (3.6)	2 (0.2)	<0.0001	0.0002	0.0351	
INTRINSIC TO MEMBRANE	1289	48 (3.7)	46 (3.6)	2 (0.2)	<0.0001	0.0002	0.0347	
PLASMA MEMBRANE PART	1101	41 (3.7)	39 (3.5)	2 (0.2)	<0.0001	0.0002	0.0341	
MEMBRANE PART	1597	55 (3.4)	53 (3.3)	2 (0.1)	<0.0001	0.0002	0.0326	dnc
MEMBRANE FRACTION	330	14 (4.2)	13 (3.9)	1 (0.3)	0.0004	0.0081	0.0304	
CYTOPLASM	2054	48 (2.3)	47 (2.3)	1 (0)	0.0006	0.0098	0.0223	neu

Table A15: Significantly enriched MSigDB GO Cellular Components (RNA-Seq, PBMC, Day 1). Results sorted by FDR and Jaccard index. The last column indicates overlap with cell type-specific results: dnc: dendritic cells, mnc: monocytes, neu: neutrophils, tcl: T-cells, nkc: NK-cells, bcl: B-cells.

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
RECEPTOR ACTIVITY	554	28 (5.1)	28 (5.1)	0 (0)	<0.0001	0.002	0.0409	mnc
PATTERN BINDING	44	7 (15.9)	7 (15.9)	0 (0)	<0.0001	0.002	0.0359	
CYSTEINE TYPE PEPTIDASE ACTIVITY	48	6 (12.5)	6 (12.5)	0 (0)	<0.0001	0.0066	0.0300	

Table A16: Significantly enriched MSigDB GO Molecular Functions (RNA-Seq, PBMC, Day 1). Results sorted by FDR and Jaccard index. The last column indicates overlap with cell type-specific results: dnc: dendritic cells, mnc: monocytes, neu: neutrophils, tcl: T-cells, nkc: NK-cells, bcl: B-cells.

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
INTERFERON SIGNALING	153	30 (19.6)	30 (19.6)	0 (0)	<0.0001	0.0006	0.1024	neu, mnc, dnc, tcl, nkc, bcl
CYTOKINE SIGNALING IN IMMUNE SYSTEM	258	37 (14.3)	37 (14.3)	0 (0)	<0.0001	0.0006	0.0946	neu, mnc, dnc, tcl, nkc, bcl
INTERFERON ALPHA BETA SIGNALING	62	19 (30.6)	19 (30.6)	0 (0)	<0.0001	0.0006	0.0892	neu, mnc, dnc, tcl, nkc, bcl
INTERFERON GAMMA SIGNALING	59	18 (30.5)	18 (30.5)	0 (0)	<0.0001	0.0006	0.0853	neu, mnc, dnc, tcl, nkc, bcl

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
IMMUNE SYSTEM	871	76 (8.7)	76 (8.7)	0 (0)	<0.0001	0.0006	0.0788	neu, mnc, dnc, tcl, bcl
INNATE IMMUNE SYSTEM	263	29 (11)	29 (11)	0 (0)	<0.0001	0.0006	0.0718	neu, mnc, dnc
TOLL RECEPTOR CASCADES	108	13 (12)	13 (12)	0 (0)	<0.0001	0.0006	0.0491	
ADAPTIVE IMMUNE SYSTEM	495	27 (5.5)	27 (5.5)	0 (0)	<0.0001	0.0006	0.0423	neu, mnc, dnc
ACTIVATED TLR4 SIGNALLING	87	10 (11.5)	10 (11.5)	0 (0)	<0.0001	0.0006	0.0405	
ANTIGEN PROCESSING CROSS PRESENTATION	72	8 (11.1)	8 (11.1)	0 (0)	<0.0001	0.0006	0.0342	neu, mnc, dnc
NUCLEOTIDE BINDING DOMAIN LEUCINE RICH REPEAT CONTAINING RECEPTOR NLR SIGNALING PATHWAYS	43	7 (16.3)	7 (16.3)	0 (0)	<0.0001	0.0006	0.0340	neu
INFLAMMASOMES	16	6 (37.5)	6 (37.5)	0 (0)	<0.0001	0.0006	0.0333	
G ALPHA I SIGNALLING EVENTS	185	13 (7)	13 (7)	0 (0)	<0.0001	0.0008	0.0380	
IMMUNOREGULATORY INTERACTIONS BETWEEN A LYMPHOID AND A NON LYMPHOID CELL	62	8 (12.9)	8 (12.9)	0 (0)	<0.0001	0.0008	0.0357	mnc
RIG I MDA5 MEDIATED INDUCTION OF IFN ALPHA BETA PATHWAYS	70	8 (11.4)	8 (11.4)	0 (0)	<0.0001	0.0008	0.0345	neu, dnc
THE NLRP3 INFLAMMASOME	11	4 (36.4)	4 (36.4)	0 (0)	<0.0001	0.0008	0.0226	
CLASS I MHC MEDIATED ANTIGEN PROCESSING PRESENTATION	228	13 (5.7)	13 (5.7)	0 (0)	<0.0001	0.001	0.0338	neu, mnc, dnc
MYD88 MAL CASCADE INITIATED ON PLASMA MEMBRANE	76	8 (10.5)	8 (10.5)	0 (0)	<0.0001	0.001	0.0336	
GPCR LIGAND BINDING	383	16 (4.2)	16 (4.2)	0 (0)	<0.0001	0.001	0.0298	
GROWTH HORMONE RECEPTOR SIGNALING	24	5 (20.8)	5 (20.8)	0 (0)	<0.0001	0.001	0.0265	
NFKB AND MAP KINASES ACTIVATION MEDIATED BY TLR4 SIGNALING REPERTOIRE	66	7 (10.6)	7 (10.6)	0 (0)	<0.0001	0.0013	0.0306	
REGULATION OF IFNG SIGNALING	13	4 (30.8)	4 (30.8)	0 (0)	<0.0001	0.0015	0.0223	
SIGNALING BY ILS	101	9 (8.9)	9 (8.9)	0 (0)	<0.0001	0.0018	0.0344	dnc
HEMOSTASIS	440	18 (4.1)	18 (4.1)	0 (0)	<0.0001	0.002	0.0304	
NEGATIVE REGULATORS OF RIG I MDA5 SIGNALING	29	5 (17.2)	5 (17.2)	0 (0)	<0.0001	0.0022	0.0258	neu, dnc
SIGNAL AMPLIFICATION	31	5 (16.1)	5 (16.1)	0 (0)	<0.0001	0.0026	0.0255	
PLATELET ACTIVATION SIGNALING AND AGGREGATION	191	11 (5.8)	11 (5.8)	0 (0)	0.0001	0.0032	0.0314	
CLASS A1 RHODOPSIN LIKE RECEPTORS	282	12 (4.3)	12 (4.3)	0 (0)	0.0002	0.0046	0.0273	
TRAFFICKING AND PROCESSING OF ENDOSOMAL TLR	10	3 (30)	3 (30)	0 (0)	0.0003	0.006	0.0169	
CROSS PRESENTATION OF SOLUBLE EXOGENOUS ANTIGENS ENDOSOMES	48	5 (10.4)	5 (10.4)	0 (0)	0.0003	0.0061	0.0235	neu, dnc
ADP SIGNALLING THROUGH P2RY1	25	4 (16)	4 (16)	0 (0)	0.0003	0.0076	0.0209	
CHONDROITIN SULFATE DERMATAN SULFATE METABOLISM	42	5 (11.9)	4 (9.5)	1 (2.4)	0.0004	0.0078	0.0242	
IL 6 SIGNALING	10	3 (30)	3 (30)	0 (0)	0.0004	0.0078	0.0169	tcl
ANTIVIRAL MECHANISM BY IFN STIMULATED GENES	65	6 (9.2)	6 (9.2)	0 (0)	0.0005	0.0093	0.0262	neu, dnc

Table A17: Significantly enriched MSigDB Reactome Pathways (RNA-Seq, PBMC, Day 1). Results sorted by FDR and Jaccard index. The last column indicates overlap with cell type-specific results: dnc: dendritic cells, mnc: monocytes, neu: neutrophils, tcl: T-cells, nkc: NK-cells, bcl: B-cells.

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
VERHAAK AML WITH NPM1 MUTATED UP	190	58 (30.5)	58 (30.5)	0 (0)	<0.0001	0.0001	0.1088	neu, mnc, dnc
FULCHER INFLAMMATORY RESPONSE LECTIN VS LPS DN	462	81 (17.5)	80 (17.3)	1 (0.2)	<0.0001	0.0001	0.1036	neu, mnc, dnc, tcl, nkc, bcl
HECKER IFNB1 TARGETS	92	45 (48.9)	45 (48.9)	0 (0)	<0.0001	0.0001	0.1004	neu, mnc, dnc, tcl, nkc, bcl
ALTEMEIER RESPONSE TO LPS WITH MECHANICAL VENTILATION	126	48 (38.1)	48 (38.1)	0 (0)	<0.0001	0.0001	0.1002	neu, mnc, dnc, tcl, nkc, bcl
RUTELLA RESPONSE TO HGF VS CSF2RB AND IL4 UP	391	61 (15.6)	61 (15.6)	0 (0)	<0.0001	0.0001	0.0834	neu, mnc, dnc
MCLACHLAN DENTAL CARIES UP	227	48 (21.1)	48 (21.1)	0 (0)	<0.0001	0.0001	0.0828	neu, mnc, dnc, tcl
JISON SICKLE CELL DISEASE UP	174	42 (24.1)	42 (24.1)	0 (0)	<0.0001	0.0001	0.0788	neu, mnc, dnc, tcl, nkc, bcl
BROWNE INTERFERON RESPONSIVE GENES	68	34 (50)	34 (50)	0 (0)	<0.0001	0.0001	0.0782	neu, mnc, dnc, tcl, nkc, bcl
RUTELLA RESPONSE TO CSF2RB AND IL4 DN	303	51 (16.8)	51 (16.8)	0 (0)	<0.0001	0.0001	0.0781	neu, mnc, dnc
MARKEY RB1 ACUTE LOF UP	214	43 (20.1)	43 (20.1)	0 (0)	<0.0001	0.0001	0.0752	neu, mnc, dnc, tcl, nkc, bcl
SANA RESPONSE TO IFNG UP	74	32 (43.2)	32 (43.2)	0 (0)	<0.0001	0.0001	0.0722	neu, mnc, dnc, tcl, nkc, bcl
BOSCO INTERFERON INDUCED ANTIVIRAL MODULE	76	32 (42.1)	32 (42.1)	0 (0)	<0.0001	0.0001	0.0719	neu, mnc, dnc, tcl, nkc, bcl
TAKEDA TARGETS OF NUP98 HOXA9 FUSION 3D UP	178	38 (21.3)	38 (21.3)	0 (0)	<0.0001	0.0001	0.0702	neu, mnc, dnc, tcl, nkc, bcl
GAL LEUKEMIC STEM CELL DN	244	42 (17.2)	42 (17.2)	0 (0)	<0.0001	0.0001	0.0697	neu, mnc, dnc
TAKEDA TARGETS OF NUP98 HOXA9 FUSION 10D UP	186	37 (19.9)	37 (19.9)	0 (0)	<0.0001	0.0001	0.0673	neu, mnc, dnc, tcl, nkc, bcl
MCLACHLAN DENTAL CARIES DN	219	39 (17.8)	39 (17.8)	0 (0)	<0.0001	0.0001	0.0671	neu, mnc, dnc, tcl
NUYTTEN EZH2 TARGETS UP	1002	87 (8.7)	83 (8.3)	4 (0.4)	<0.0001	0.0001	0.0661	neu, mnc, dnc, tcl, nkc, bcl
ZHANG RESPONSE TO IKK INHIBITOR AND TNF UP	221	38 (17.2)	37 (16.7)	1 (0.5)	<0.0001	0.0001	0.0651	neu, mnc, dnc, tcl
CHEN METABOLIC SYNDROM NETWORK	1172	90 (7.7)	86 (7.3)	4 (0.3)	<0.0001	0.0001	0.0607	neu, mnc, dnc, tcl
RUTELLA RESPONSE TO HGF UP	398	45 (11.3)	45 (11.3)	0 (0)	<0.0001	0.0001	0.0597	neu, mnc, dnc
WALLACE PROSTATE CANCER RACE UP	275	38 (13.8)	38 (13.8)	0 (0)	<0.0001	0.0001	0.0596	neu, mnc, dnc, tcl, nkc, bcl

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
BERTUCCI MEDULLARY VS DUCTAL BREAST CANCER UP	200	33 (16.5)	32 (16)	1 (0.5)	<0.0001	0.0001	0.0581	neu, mnc, dnc, tcl, nkc, bcl
JAATINEN HEMATOPOIETIC STEM CELL DN	221	34 (15.4)	34 (15.4)	0 (0)	<0.0001	0.0001	0.0578	dnc
WIELAND UP BY HBV INFECTION	100	27 (27)	27 (27)	0 (0)	<0.0001	0.0001	0.0570	neu, mnc, dnc, tcl, bcl
ICHIBA GRAFT VERSUS HOST DISEASE D7 UP	105	27 (25.7)	27 (25.7)	0 (0)	<0.0001	0.0001	0.0564	neu, mnc, dnc, tcl, nkc, bcl
RODWELL AGING KIDNEY UP	465	46 (9.9)	43 (9.2)	3 (0.6)	<0.0001	0.0001	0.0561	neu, mnc, dnc, tcl
DELYS THYROID CANCER UP	435	44 (10.1)	42 (9.7)	2 (0.5)	<0.0001	0.0001	0.0556	neu, mnc, dnc, tcl
TONKS TARGETS OF RUNX1 RUNX1T1 FUSION ERYTHROCYTE UP	151	29 (19.2)	28 (18.5)	1 (0.7)	<0.0001	0.0001	0.0554	neu, mnc, dnc, tcl
SMIRNOV CIRCULATING ENDOTHELIOCYTES IN CANCER UP	152	29 (19.1)	29 (19.1)	0 (0)	<0.0001	0.0001	0.0553	neu, mnc
MOSERLE IFNA RESPONSE	31	22 (71)	22 (71)	0 (0)	<0.0001	0.0001	0.0537	neu, mnc, dnc, tcl, nkc, bcl
SCHUETZ BREAST CANCER DUCTAL INVASIVE UP	338	37 (10.9)	36 (10.7)	1 (0.3)	<0.0001	0.0001	0.0527	neu, mnc, dnc, tcl
THUM SYSTOLIC HEART FAILURE UP	404	40 (9.9)	39 (9.7)	1 (0.2)	<0.0001	0.0001	0.0523	neu, mnc, dnc
ICHIBA GRAFT VERSUS HOST DISEASE 35D UP	126	26 (20.6)	26 (20.6)	0 (0)	<0.0001	0.0001	0.0519	neu, mnc, dnc, bcl
TAKEDA TARGETS OF NUP98 HOXA9 FUSION 16D UP	169	28 (16.6)	28 (16.6)	0 (0)	<0.0001	0.0001	0.0517	neu, mnc, dnc, tcl, nkc
HELLER SILENCED BY METHYLATION UP	273	33 (12.1)	32 (11.7)	1 (0.4)	<0.0001	0.0001	0.0515	neu, mnc, dnc, tcl, nkc
FOSTER TOLERANT MACROPHAGE DN	405	39 (9.6)	38 (9.4)	1 (0.2)	<0.0001	0.0001	0.0508	neu, mnc, dnc, tcl
BROWN MYELOID CELL DEVELOPMENT UP	159	27 (17)	27 (17)	0 (0)	<0.0001	0.0001	0.0507	neu, mnc, dnc
TAKEDA TARGETS OF NUP98 HOXA9 FUSION 8D UP	155	26 (16.8)	25 (16.1)	1 (0.6)	<0.0001	0.0001	0.0491	neu, mnc, dnc, tcl, nkc, bcl
LENAOUR DENDRITIC CELL MATURATION DN	139	25 (18)	25 (18)	0 (0)	<0.0001	0.0001	0.0485	dnc
DEBIASI APOPTOSIS BY REOVIRUS INFECTION UP	317	33 (10.4)	32 (10.1)	1 (0.3)	<0.0001	0.0001	0.0482	neu, mnc, dnc, tcl, nkc, bcl
LIAN LIPA TARGETS 3M	56	21 (37.5)	21 (37.5)	0 (0)	<0.0001	0.0001	0.0482	dnc
SANA TNF SIGNALING UP	81	22 (27.2)	22 (27.2)	0 (0)	<0.0001	0.0001	0.0478	neu, mnc, dnc, tcl, nkc

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
GRAESSMANN RESPONSE TO MC AND SERUM DEPRIVATION UP	203	27 (13.3)	26 (12.8)	1 (0.5)	<0.0001	0.0001	0.0468	neu, mnc, dnc, tcl, nkc, bcl
POOLA INVASIVE BREAST CANCER UP	272	30 (11)	29 (10.7)	1 (0.4)	<0.0001	0.0001	0.0467	neu, mnc, dnc, tcl
LIAN LIPA TARGETS 6M	70	21 (30)	21 (30)	0 (0)	<0.0001	0.0001	0.0467	dnc
BOQUEST STEM CELL CULTURED VS FRESH UP	409	36 (8.8)	34 (8.3)	2 (0.5)	<0.0001	0.0001	0.0465	neu, mnc, dnc
SEKI INFLAMMATORY RESPONSE LPS UP	77	21 (27.3)	20 (26)	1 (1.3)	<0.0001	0.0001	0.0460	neu, mnc, dnc, tcl, bcl
BENNETT SYSTEMIC LUPUS ERYTHEMATOSUS	32	19 (59.4)	19 (59.4)	0 (0)	<0.0001	0.0001	0.0459	neu, mnc, dnc, tcl, nkc
FEVR CTNNB1 TARGETS UP	672	47 (7)	46 (6.8)	1 (0.1)	<0.0001	0.0001	0.0458	neu, mnc, dnc, tcl, nkc
ZHOU INFLAMMATORY RESPONSE LPS UP	401	35 (8.7)	35 (8.7)	0 (0)	<0.0001	0.0001	0.0456	neu, mnc, dnc, tcl
GRAESSMANN APOPTOSIS BY DOXORUBICIN UP	1132	65 (5.7)	60 (5.3)	5 (0.4)	<0.0001	0.0001	0.0443	neu, mnc, dnc, tcl
GRAESSMANN APOPTOSIS BY SERUM DEPRIVATION UP	541	40 (7.4)	37 (6.8)	3 (0.6)	<0.0001	0.0001	0.0443	neu, mnc, dnc, tcl, nkc
DAUER STAT3 TARGETS DN	51	19 (37.3)	19 (37.3)	0 (0)	<0.0001	0.0001	0.0439	neu, mnc, dnc, tcl, nkc
RADAEVA RESPONSE TO IFNA1 UP	52	19 (36.5)	19 (36.5)	0 (0)	<0.0001	0.0001	0.0438	neu, mnc, dnc, tcl, nkc, bcl
FOSTER TOLERANT MACROPHAGE UP	155	23 (14.8)	23 (14.8)	0 (0)	<0.0001	0.0001	0.0432	neu, mnc, dnc, tcl
PICCALUGA ANGIOIMMUNOBLASTIC LYMPHOMA UP	205	25 (12.2)	24 (11.7)	1 (0.5)	<0.0001	0.0001	0.0430	mnc, dnc
ONDER CDH1 TARGETS 2 DN	454	35 (7.7)	34 (7.5)	1 (0.2)	<0.0001	0.0001	0.0427	neu, mnc, dnc
DIAZ CHRONIC MEYLOGENOUS LEUKEMIA DN	112	21 (18.8)	21 (18.8)	0 (0)	<0.0001	0.0001	0.0427	neu, mnc, dnc
NUYTTEN NIPP1 TARGETS UP	748	47 (6.3)	47 (6.3)	0 (0)	<0.0001	0.0001	0.0426	neu, mnc, dnc, tcl, bcl
PHONG TNF RESPONSE NOT VIA P38	333	30 (9)	30 (9)	0 (0)	<0.0001	0.0001	0.0426	mnc, dnc, tcl
NAKAYAMA SOFT TISSUE TUMORS PCA1 UP	69	19 (27.5)	19 (27.5)	0 (0)	<0.0001	0.0001	0.0421	neu, mnc, dnc
SEITZ NEOPLASTIC TRANSFORMATION BY 8P DELETION UP	69	19 (27.5)	19 (27.5)	0 (0)	<0.0001	0.0001	0.0421	neu, mnc, dnc, tcl, nkc
RUTELLA RESPONSE TO HGF DN	224	25 (11.2)	25 (11.2)	0 (0)	<0.0001	0.0001	0.0417	mnc, dnc
YANG BCL3 TARGETS UP	351	30 (8.5)	30 (8.5)	0 (0)	<0.0001	0.0001	0.0416	neu, mnc, dnc, tcl

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
QI PLASMACYTOMA UP	251	26 (10.4)	26 (10.4)	0 (0)	<0.0001	0.0001	0.0415	neu, mnc, dnc, tcl
OSWALD HEMATOPOIETIC STEM CELL IN COLLAGEN GEL UP	227	25 (11)	24 (10.6)	1 (0.4)	<0.0001	0.0001	0.0415	mnc, dnc
DER IFN BETA RESPONSE UP	101	20 (19.8)	20 (19.8)	0 (0)	<0.0001	0.0001	0.0415	neu, mnc, dnc, tcl, nkc, bcl
HESS TARGETS OF HOXA9 AND MEIS1 DN	76	19 (25)	19 (25)	0 (0)	<0.0001	0.0001	0.0415	neu, mnc, dnc
VERHAAK GLIOBLASTOMA NEURAL	205	24 (11.7)	23 (11.2)	1 (0.5)	<0.0001	0.0001	0.0412	neu, mnc, dnc
HIRSCH CELLULAR TRANSFORMATION SIGNATURE UP	239	25 (10.5)	25 (10.5)	0 (0)	<0.0001	0.0001	0.0407	neu, mnc, dnc
RIGGINS TAMOXIFEN RESISTANCE DN	215	24 (11.2)	23 (10.7)	1 (0.5)	<0.0001	0.0001	0.0405	neu, mnc, dnc, tcl, bcl
HAHTOLA MYCOSIS FUNGOIDES CD4 UP	61	18 (29.5)	18 (29.5)	0 (0)	<0.0001	0.0001	0.0405	neu
MISSIAGLIA REGULATED BY METHYLATION UP	120	20 (16.7)	18 (15)	2 (1.7)	<0.0001	0.0001	0.0399	neu, mnc, dnc, tcl
DER IFN ALPHA RESPONSE UP	74	18 (24.3)	18 (24.3)	0 (0)	<0.0001	0.0001	0.0394	neu, mnc, dnc, tcl, nkc, bcl
LEE BMP2 TARGETS UP	723	42 (5.8)	40 (5.5)	2 (0.3)	<0.0001	0.0001	0.0388	neu, mnc, dnc, tcl
BOYLAN MULTIPLE MYELOMA C D DN	244	24 (9.8)	24 (9.8)	0 (0)	<0.0001	0.0001	0.0386	neu, mnc, dnc
TAKEDA TARGETS OF NUP98 HOXA9 FUSION 8D DN	193	22 (11.4)	22 (11.4)	0 (0)	<0.0001	0.0001	0.0385	mnc, dnc
LIU VAV3 PROSTATE CARCINOGENESIS UP	85	18 (21.2)	18 (21.2)	0 (0)	<0.0001	0.0001	0.0385	neu, mnc, dnc, tcl, nkc, bcl
BROCKE APOPTOSIS REVERSED BY IL6	144	20 (13.9)	20 (13.9)	0 (0)	<0.0001	0.0001	0.0381	neu, mnc, dnc, tcl
WONG ADULT TISSUE STEM MODULE	697	40 (5.7)	38 (5.5)	2 (0.3)	<0.0001	0.0001	0.0378	neu, mnc, dnc
VANTVEER BREAST CANCER ESR1 DN	232	23 (9.9)	22 (9.5)	1 (0.4)	<0.0001	0.0001	0.0377	neu, mnc, dnc
FARMER BREAST CANCER CLUSTER 1	39	16 (41)	16 (41)	0 (0)	<0.0001	0.0001	0.0377	neu, mnc, dnc, tcl, nkc
ONKEN UVEAL MELANOMA UP	763	42 (5.5)	41 (5.4)	1 (0.1)	<0.0001	0.0001	0.0374	neu, mnc, dnc
WANG RESPONSE TO GSK3 INHIBITOR SB216763 UP	378	28 (7.4)	28 (7.4)	0 (0)	<0.0001	0.0001	0.0373	neu, tcl
HORIUCHI WTAP TARGETS UP	295	25 (8.5)	23 (7.8)	2 (0.7)	<0.0001	0.0001	0.0373	neu, mnc, dnc, tcl
GOZGIT ESR1 TARGETS DN	741	41 (5.5)	40 (5.4)	1 (0.1)	<0.0001	0.0001	0.0372	neu, mnc, dnc, tcl
DANG REGULATED BY MYC DN	247	23 (9.3)	22 (8.9)	1 (0.4)	<0.0001	0.0001	0.0368	neu, mnc, dnc, tcl
HOSHIDA LIVER CANCER SUBCLASS S1	225	22 (9.8)	22 (9.8)	0 (0)	<0.0001	0.0001	0.0364	neu

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
LIANG SILENCED BY METHYLATION 2	55	16 (29.1)	16 (29.1)	0 (0)	<0.0001	0.0001	0.0364	neu, mnc, dnc, tcl, nkc
BOSCO TH1 CYTOTOXIC MODULE	114	18 (15.8)	18 (15.8)	0 (0)	<0.0001	0.0001	0.0362	neu, mnc, dnc
FLECHNER BIOPSY KIDNEY TRANSPLANT REJECTED VS OK UP	85	17 (20)	17 (20)	0 (0)	<0.0001	0.0001	0.0362	neu, mnc, dnc, tcl, bcl
SENGUPTA NASOPHARYNGEAL CARCINOMA UP	287	24 (8.4)	23 (8)	1 (0.3)	<0.0001	0.0001	0.0361	neu, mnc, dnc
CHARAFE BREAST CANCER LUMINAL VS BASAL DN	440	29 (6.6)	27 (6.1)	2 (0.5)	<0.0001	0.0001	0.0357	neu, mnc, dnc, tcl
LINDSTEDT DENDRITIC CELL MATURATION A	67	16 (23.9)	16 (23.9)	0 (0)	<0.0001	0.0001	0.0354	neu, mnc, dnc, tcl
MITSIADES RESPONSE TO APLIDIN UP	450	29 (6.4)	28 (6.2)	1 (0.2)	<0.0001	0.0001	0.0353	neu, mnc
MARTENS TRETINOIN RESPONSE UP	816	41 (5)	37 (4.5)	4 (0.5)	<0.0001	0.0001	0.0349	dnc
SMID BREAST CANCER BASAL UP	607	34 (5.6)	33 (5.4)	1 (0.2)	<0.0001	0.0001	0.0349	neu, mnc, dnc, tcl
DODD NASOPHARYNGEAL CARCINOMA DN	1330	58 (4.4)	57 (4.3)	1 (0.1)	<0.0001	0.0001	0.0347	neu, mnc, dnc, tcl
GRUETZMANN PANCREATIC CANCER UP	351	25 (7.1)	25 (7.1)	0 (0)	<0.0001	0.0001	0.0344	neu, mnc, dnc, tcl, bcl
UROSEVIC RESPONSE TO IMIQUIMOD	23	14 (60.9)	14 (60.9)	0 (0)	<0.0001	0.0001	0.0341	neu, mnc, dnc, tcl
ZHU CMV ALL UP	121	17 (14)	17 (14)	0 (0)	<0.0001	0.0001	0.0337	neu, mnc, dnc
CHICAS RB1 TARGETS SENESCENT	552	31 (5.6)	31 (5.6)	0 (0)	<0.0001	0.0001	0.0336	neu, mnc, dnc
VALK AML CLUSTER 5	30	14 (46.7)	14 (46.7)	0 (0)	<0.0001	0.0001	0.0336	
KRIGE RESPONSE TO TOSEDOSTAT 24HR UP	740	37 (5)	37 (5)	0 (0)	<0.0001	0.0001	0.0335	neu, mnc, dnc
KRIGE RESPONSE TO TOSEDOSTAT 6HR UP	915	42 (4.6)	41 (4.5)	1 (0.1)	<0.0001	0.0001	0.0330	neu, mnc, dnc
SMID BREAST CANCER LUMINAL B DN	513	29 (5.7)	28 (5.5)	1 (0.2)	<0.0001	0.0001	0.0328	neu, mnc, dnc
JOHNSTONE PARVB TARGETS 3 UP	425	26 (6.1)	26 (6.1)	0 (0)	<0.0001	0.0001	0.0325	neu, mnc, dnc, tcl
SWEET LUNG CANCER KRAS DN	425	26 (6.1)	25 (5.9)	1 (0.2)	<0.0001	0.0001	0.0325	neu, mnc, dnc
ZHU CMV 8 HR UP	48	14 (29.2)	14 (29.2)	0 (0)	<0.0001	0.0001	0.0322	neu, mnc, dnc
HELLER HDAC TARGETS SILENCED BY METHYLATION UP	439	26 (5.9)	25 (5.7)	1 (0.2)	<0.0001	0.0001	0.0319	mnc
NEMETH INFLAMMATORY RESPONSE LPS UP	85	15 (17.6)	15 (17.6)	0 (0)	<0.0001	0.0001	0.0318	neu, mnc, dnc
ZHOU INFLAMMATORY RESPONSE LIVE UP	448	26 (5.8)	25 (5.6)	1 (0.2)	<0.0001	0.0001	0.0316	mnc
ZHANG INTERFERON RESPONSE	23	13 (56.5)	13 (56.5)	0 (0)	<0.0001	0.0001	0.0316	neu, mnc, dnc, tcl, nkc, bcl
CHICAS RB1 TARGETS CONFLUENT	550	29 (5.3)	26 (4.7)	3 (0.5)	<0.0001	0.0001	0.0315	neu, mnc, dnc, tcl, bcl

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
EINAV INTERFERON SIGNATURE IN CANCER	27	13 (48.1)	13 (48.1)	0 (0)	<0.0001	0.0001	0.0313	neu, mnc, dnc, tcl, nkc, bcl
BAELDE DIABETIC NEPHROPATHY DN	425	25 (5.9)	25 (5.9)	0 (0)	<0.0001	0.0001	0.0312	neu, mnc, dnc, tcl
WUNDER INFLAMMATORY RESPONSE AND CHOLESTEROL UP	61	14 (23)	14 (23)	0 (0)	<0.0001	0.0001	0.0312	neu, mnc, dnc, tcl, nkc
KATSANOU ELAVL1 TARGETS UP	163	17 (10.4)	16 (9.8)	1 (0.6)	<0.0001	0.0001	0.0311	neu, mnc, dnc
IVANOVA HEMATOPOIESIS LATE PROGENITOR	534	28 (5.2)	27 (5.1)	1 (0.2)	<0.0001	0.0001	0.0309	neu
VECCHI GASTRIC CANCER ADVANCED VS EARLY UP	168	17 (10.1)	17 (10.1)	0 (0)	<0.0001	0.0001	0.0308	mnc
JECHLINGER EPITHELIAL TO MESENCHYMAL TRANSITION UP	71	14 (19.7)	13 (18.3)	1 (1.4)	<0.0001	0.0001	0.0306	neu, mnc, dnc, tcl
DER IFN GAMMA RESPONSE UP	72	14 (19.4)	14 (19.4)	0 (0)	<0.0001	0.0001	0.0305	neu, mnc, dnc, tcl, nkc, bcl
NAKAMURA TUMOR ZONE PERIPHERAL VS CENTRAL DN	615	30 (4.9)	28 (4.6)	2 (0.3)	<0.0001	0.0001	0.0304	
MULLIGHAN MLL SIGNATURE 2 UP	413	24 (5.8)	24 (5.8)	0 (0)	<0.0001	0.0001	0.0304	neu
SWEET LUNG CANCER KRAS UP	482	26 (5.4)	26 (5.4)	0 (0)	<0.0001	0.0001	0.0303	neu
ACEVEDO FGFR1 TARGETS IN PROSTATE CANCER MODEL UP	278	20 (7.2)	18 (6.5)	2 (0.7)	<0.0001	0.0001	0.0303	neu, mnc, dnc, tcl
SENGUPTA NASOPHARYNGEAL CARCINOMA WITH LMP1 UP	387	23 (5.9)	22 (5.7)	1 (0.3)	<0.0001	0.0001	0.0301	neu, mnc, dnc, tcl
MASSARWEH TAMOXIFEN RESISTANCE UP	561	28 (5)	28 (5)	0 (0)	<0.0001	0.0001	0.0300	neu, mnc, dnc
BRUINS UVC RESPONSE VIA TP53 GROUP A	872	37 (4.2)	33 (3.8)	4 (0.5)	<0.0001	0.0001	0.0299	mnc
RICKMAN METASTASIS DN	258	19 (7.4)	19 (7.4)	0 (0)	<0.0001	0.0001	0.0297	neu, mnc, dnc, tcl
KIM GLIS2 TARGETS UP	84	14 (16.7)	14 (16.7)	0 (0)	<0.0001	0.0001	0.0297	neu, mnc, dnc, tcl
PEDRIOLI MIR31 TARGETS DN	398	23 (5.8)	22 (5.5)	1 (0.3)	<0.0001	0.0001	0.0296	neu, mnc
PAPASPYRIDONOS UNSTABLE ATEROSCLEROTIC PLAQUE UP	51	13 (25.5)	13 (25.5)	0 (0)	<0.0001	0.0001	0.0296	tcl
BOWIE RESPONSE TO EXTRACELLULAR MATRIX	17	12 (70.6)	12 (70.6)	0 (0)	<0.0001	0.0001	0.0296	neu, mnc, dnc, tcl, nkc, bcl
ENK UV RESPONSE EPIDERMIS UP	298	20 (6.7)	20 (6.7)	0 (0)	<0.0001	0.0001	0.0295	neu
BOWIE RESPONSE TO TAMOXIFEN	18	12 (66.7)	12 (66.7)	0 (0)	<0.0001	0.0001	0.0295	neu, mnc, dnc, tcl, nkc, bcl
TONKS TARGETS OF RUNX1 RUNX1T1 FUSION MONOCYTE UP	201	17 (8.5)	17 (8.5)	0 (0)	<0.0001	0.0001	0.0291	neu, mnc, dnc, tcl
FULCHER INFLAMMATORY RESPONSE LECTIN VS LPS UP	564	27 (4.8)	26 (4.6)	1 (0.2)	<0.0001	0.0001	0.0288	neu, dnc

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
CHANG IMMORTALIZED BY HPV31 DN	63	13 (20.6)	13 (20.6)	0 (0)	<0.0001	0.0001	0.0288	neu, mnc, dnc, tcl
KUMAR TARGETS OF MLL AF9 FUSION	389	22 (5.7)	22 (5.7)	0 (0)	<0.0001	0.0001	0.0286	neu, mnc, dnc
LEE RECENT THYMIC EMIGRANT	217	17 (7.8)	16 (7.4)	1 (0.5)	<0.0001	0.0001	0.0283	neu, mnc, dnc, tcl
GAUSSMANN MLL AF4 FUSION TARGETS F UP	182	16 (8.8)	14 (7.7)	2 (1.1)	<0.0001	0.0001	0.0282	mnc
KRASNOSELSKAYA ILF3 TARGETS UP	37	12 (32.4)	12 (32.4)	0 (0)	<0.0001	0.0001	0.0282	neu, mnc, dnc, tcl
ZWANG CLASS 3 TRANSIENTLY INDUCED BY EGF	220	17 (7.7)	17 (7.7)	0 (0)	<0.0001	0.0001	0.0281	mnc
ZHAN MULTIPLE MYELOMA LB DN	39	12 (30.8)	12 (30.8)	0 (0)	<0.0001	0.0001	0.0280	neu, mnc, dnc, tcl, bcl
ODONNELL TFRC TARGETS UP	409	22 (5.4)	19 (4.6)	3 (0.7)	<0.0001	0.0001	0.0279	neu, mnc, dnc
SATO SILENCED BY METHYLATION IN PANCREATIC CANCER 1	412	22 (5.3)	21 (5.1)	1 (0.2)	<0.0001	0.0001	0.0278	neu, mnc
LI INDUCED T TO NATURAL KILLER UP	302	19 (6.3)	19 (6.3)	0 (0)	<0.0001	0.0001	0.0278	neu, mnc, dnc
MCBRYAN PUBERTAL BREAST 4 5WK UP	264	18 (6.8)	15 (5.7)	3 (1.1)	<0.0001	0.0001	0.0278	neu, dnc
WANG SMARCE1 TARGETS DN	340	20 (5.9)	20 (5.9)	0 (0)	<0.0001	0.0001	0.0277	neu, mnc, dnc
PEREZ TP53 TARGETS	1124	41 (3.6)	38 (3.4)	3 (0.3)	<0.0001	0.0001	0.0276	neu, mnc, dnc
LIM MAMMARY STEM CELL DN	422	22 (5.2)	22 (5.2)	0 (0)	<0.0001	0.0001	0.0275	neu, dnc, tcl
MEISSNER BRAIN HCP WITH H3K4ME3 AND H3K27ME3	1060	39 (3.7)	35 (3.3)	4 (0.4)	<0.0001	0.0001	0.0274	neu, mnc, dnc
TARTE PLASMA CELL VS PLASMABLAST UP	388	21 (5.4)	21 (5.4)	0 (0)	<0.0001	0.0001	0.0273	mnc
DAUER STAT3 TARGETS UP	50	12 (24)	12 (24)	0 (0)	<0.0001	0.0001	0.0273	mnc, dnc, tcl
STAMBOLSKY TARGETS OF MUTATED TP53 DN	51	12 (23.5)	12 (23.5)	0 (0)	<0.0001	0.0001	0.0273	neu, mnc, dnc, tcl
MARTINEZ RB1 AND TP53 TARGETS UP	582	26 (4.5)	26 (4.5)	0 (0)	<0.0001	0.0001	0.0272	mnc, dnc
MARTINEZ TP53 TARGETS UP	584	26 (4.5)	25 (4.3)	1 (0.2)	<0.0001	0.0001	0.0271	
RUTELLA RESPONSE TO CSF2RB AND IL4 UP	319	19 (6)	19 (6)	0 (0)	<0.0001	0.0001	0.0271	neu, mnc, dnc
HINATA NFKB TARGETS KERATINOCYTE UP	91	13 (14.3)	13 (14.3)	0 (0)	<0.0001	0.0001	0.0271	neu, mnc, dnc, tcl
LIM MAMMARY STEM CELL UP	474	23 (4.9)	20 (4.2)	3 (0.6)	<0.0001	0.0001	0.0270	
WIERENGA STAT5A TARGETS UP	210	16 (7.6)	16 (7.6)	0 (0)	<0.0001	0.0001	0.0269	neu, mnc, dnc, tcl
BOYLAN MULTIPLE MYELOMA PCA1 UP	96	13 (13.5)	13 (13.5)	0 (0)	<0.0001	0.0001	0.0269	neu, mnc, dnc
BOQUEST STEM CELL DN	213	16 (7.5)	16 (7.5)	0 (0)	<0.0001	0.0001	0.0268	neu
ZWANG TRANSIENTLY UP BY 2ND EGF PULSE ONLY	1568	51 (3.3)	44 (2.8)	7 (0.4)	<0.0001	0.0001	0.0266	mnc, dnc
HUTTMANN B CLL POOR SURVIVAL UP	258	17 (6.6)	17 (6.6)	0 (0)	<0.0001	0.0001	0.0265	neu, mnc
LINDGREN BLADDER CANCER CLUSTER 2B	376	20 (5.3)	19 (5.1)	1 (0.3)	<0.0001	0.0001	0.0264	neu, mnc

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
CHIARADONNA NEOPLASTIC TRANSFORMATION KRAS DN	143	14 (9.8)	12 (8.4)	2 (1.4)	<0.0001	0.0001	0.0264	neu, mnc, dnc
GRAESSMANN RESPONSE TO MC AND DOXORUBICIN UP	615	26 (4.2)	23 (3.7)	3 (0.5)	<0.0001	0.0001	0.0263	neu
HAN SATB1 TARGETS DN	421	21 (5)	21 (5)	0 (0)	<0.0001	0.0001	0.0262	neu, mnc, dnc
ZHOU INFLAMMATORY RESPONSE FIMA UP	504	23 (4.6)	22 (4.4)	1 (0.2)	<0.0001	0.0001	0.0261	mnc
KRIEG KDM3A TARGETS NOT HYPOXIA	189	15 (7.9)	15 (7.9)	0 (0)	<0.0001	0.0001	0.0261	neu, mnc, dnc, tcl, nkc, bcl
FARMER BREAST CANCER APOCRINE VS LUMINAL	312	18 (5.8)	17 (5.4)	1 (0.3)	<0.0001	0.0001	0.0259	
PLASARI TGFB1 TARGETS 10HR DN	233	16 (6.9)	16 (6.9)	0 (0)	<0.0001	0.0001	0.0259	neu, mnc, dnc, tcl, nkc, bcl
MIKKELSEN MCV6 LCP WITH H3K4ME3	153	14 (9.2)	14 (9.2)	0 (0)	<0.0001	0.0001	0.0259	neu, mnc, dnc, tcl
BUYTAERT PHOTODYNAMIC THERAPY STRESS UP	795	30 (3.8)	29 (3.6)	1 (0.1)	<0.0001	0.0001	0.0257	
SENESE HDAC3 TARGETS UP	477	22 (4.6)	21 (4.4)	1 (0.2)	<0.0001	0.0001	0.0257	mnc
PETROVA ENDOTHELIUM LYMPHATIC VS BLOOD DN	157	14 (8.9)	13 (8.3)	1 (0.6)	<0.0001	0.0001	0.0257	neu, mnc
MARKEY RB1 CHRONIC LOF DN	118	13 (11)	12 (10.2)	1 (0.8)	<0.0001	0.0001	0.0257	
SCHLOSSER SERUM RESPONSE DN	680	27 (4)	27 (4)	0 (0)	<0.0001	0.0001	0.0256	neu
MAHAJAN RESPONSE TO IL1A UP	79	12 (15.2)	11 (13.9)	1 (1.3)	<0.0001	0.0001	0.0256	neu, mnc
CREIGHTON ENDOCRINE THERAPY RESISTANCE 3	696	27 (3.9)	25 (3.6)	2 (0.3)	<0.0001	0.0001	0.0252	neu, mnc
TAVOR CEBPA TARGETS UP	47	11 (23.4)	11 (23.4)	0 (0)	<0.0001	0.0001	0.0252	neu, mnc
ENK UV RESPONSE EPIDERMIS DN	496	22 (4.4)	19 (3.8)	3 (0.6)	<0.0001	0.0001	0.0251	mnc
YAMAZAKI TCEB3 TARGETS UP	172	14 (8.1)	12 (7)	2 (1.2)	<0.0001	0.0001	0.0250	mnc
COLINA TARGETS OF 4EBP1 AND 4EBP2	339	18 (5.3)	18 (5.3)	0 (0)	<0.0001	0.0001	0.0249	neu, mnc, dnc, tcl, bcl
ZHU CMV 24 HR UP	93	12 (12.9)	12 (12.9)	0 (0)	<0.0001	0.0001	0.0249	neu, mnc, dnc, tcl
HAHTOLA SEZARY SYNDROM UP	94	12 (12.8)	12 (12.8)	0 (0)	<0.0001	0.0001	0.0248	
BASSO CD40 SIGNALING UP	99	12 (12.1)	12 (12.1)	0 (0)	<0.0001	0.0001	0.0246	neu, dnc, tcl
NADLER OBESITY UP	59	11 (18.6)	10 (16.9)	1 (1.7)	<0.0001	0.0001	0.0245	
SMID BREAST CANCER NORMAL LIKE UP	443	20 (4.5)	19 (4.3)	1 (0.2)	<0.0001	0.0001	0.0243	neu, mnc, dnc
FLECHNER BIOPSY KIDNEY TRANSPLANT OK VS DONOR UP	529	22 (4.2)	22 (4.2)	0 (0)	<0.0001	0.0001	0.0242	neu, mnc
KEEN RESPONSE TO ROSIGLITAZONE DN	106	12 (11.3)	12 (11.3)	0 (0)	<0.0001	0.0001	0.0242	neu, dnc
WANG MLL TARGETS	280	16 (5.7)	16 (5.7)	0 (0)	<0.0001	0.0001	0.0241	mnc, dnc
GROSS HYPOXIA VIA ELK3 DN	151	13 (8.6)	12 (7.9)	1 (0.7)	<0.0001	0.0001	0.0241	
GRAHAM NORMAL QUIESCENT VS NORMAL DIVIDING UP	66	11 (16.7)	10 (15.2)	1 (1.5)	<0.0001	0.0001	0.0241	dnc
XU AKT1 TARGETS 6HR	27	10 (37)	10 (37)	0 (0)	<0.0001	0.0001	0.0239	neu, mnc, dnc
CHYLA CBFA2T3 TARGETS UP	372	18 (4.8)	18 (4.8)	0 (0)	<0.0001	0.0001	0.0238	

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
YOSHIMURA MAPK8 TARGETS UP	1281	39 (3)	35 (2.7)	4 (0.3)	<0.0001	0.0001	0.0237	mnc, dnc
BILD HRAS ONCOGENIC SIGNATURE	250	15 (6)	15 (6)	0 (0)	<0.0001	0.0001	0.0236	
GHANDHI BYSTANDER IRRADIATION UP	78	11 (14.1)	11 (14.1)	0 (0)	<0.0001	0.0001	0.0235	neu, mnc
GEISS RESPONSE TO DSRNA UP	35	10 (28.6)	10 (28.6)	0 (0)	<0.0001	0.0001	0.0235	neu, mnc, dnc, bcl
LEE AGING CEREBELLUM UP	81	11 (13.6)	11 (13.6)	0 (0)	<0.0001	0.0001	0.0234	mnc, dnc
IZADPANAH STEM CELL ADIPOSE VS BONE UP	125	12 (9.6)	12 (9.6)	0 (0)	<0.0001	0.0001	0.0233	neu, mnc
GALINDO IMMUNE RESPONSE TO ENTEROTOXIN	85	11 (12.9)	11 (12.9)	0 (0)	<0.0001	0.0001	0.0232	tcl
CAIRO LIVER DEVELOPMENT DN	219	14 (6.4)	14 (6.4)	0 (0)	<0.0001	0.0001	0.0231	
KHETCHOUMIAN TRIM24 TARGETS UP	45	10 (22.2)	10 (22.2)	0 (0)	<0.0001	0.0001	0.0229	dnc, tcl
DOANE RESPONSE TO ANDROGEN DN	232	14 (6)	14 (6)	0 (0)	<0.0001	0.0001	0.0226	neu, mnc
ZHENG IL22 SIGNALING UP	56	10 (17.9)	10 (17.9)	0 (0)	<0.0001	0.0001	0.0224	mnc, dnc
SARRIO EPITHELIAL MESENCHYMAL TRANSITION DN	149	12 (8.1)	12 (8.1)	0 (0)	<0.0001	0.0001	0.0223	neu, mnc, dnc
GHANDHI DIRECT IRRADIATION UP	106	11 (10.4)	11 (10.4)	0 (0)	<0.0001	0.0001	0.0222	mnc
ROETH TERT TARGETS UP	14	9 (64.3)	9 (64.3)	0 (0)	<0.0001	0.0001	0.0222	neu, mnc, dnc, tcl, nkc
CASTELLANO NRAS TARGETS UP	68	10 (14.7)	10 (14.7)	0 (0)	<0.0001	0.0001	0.0218	neu, mnc, dnc, tcl
AFFAR YY1 TARGETS UP	212	13 (6.1)	11 (5.2)	2 (0.9)	<0.0001	0.0001	0.0217	
MIKKELSEN MEF LCP WITH H3K4ME3	121	11 (9.1)	11 (9.1)	0 (0)	<0.0001	0.0001	0.0215	neu, mnc, dnc
JACKSON DNMT1 TARGETS UP	76	10 (13.2)	10 (13.2)	0 (0)	<0.0001	0.0001	0.0214	neu, mnc, dnc, tcl
MCBRYAN PUBERTAL BREAST 6 7WK DN	77	10 (13)	10 (13)	0 (0)	<0.0001	0.0001	0.0214	
HUANG DASATINIB RESISTANCE UP	79	10 (12.7)	9 (11.4)	1 (1.3)	<0.0001	0.0001	0.0213	neu, dnc
KIM LRRC3B TARGETS	30	9 (30)	9 (30)	0 (0)	<0.0001	0.0001	0.0213	neu, mnc, dnc
GERY CEBP TARGETS	137	11 (8)	11 (8)	0 (0)	<0.0001	0.0001	0.0209	neu, mnc
ROSS AML WITH CBFB MYH11 FUSION	48	9 (18.8)	9 (18.8)	0 (0)	<0.0001	0.0001	0.0205	
BROWNE HCMV INFECTION 8HR UP	102	10 (9.8)	10 (9.8)	0 (0)	<0.0001	0.0001	0.0203	neu, mnc
LINDSTEDT DENDRITIC CELL MATURATION B	51	9 (17.6)	9 (17.6)	0 (0)	<0.0001	0.0001	0.0203	neu, mnc
DEMAGALHAES AGING UP	56	9 (16.1)	9 (16.1)	0 (0)	<0.0001	0.0001	0.0201	neu, mnc, dnc
WANG ESOPHAGUS CANCER VS NORMAL UP	118	10 (8.5)	10 (8.5)	0 (0)	<0.0001	0.0001	0.0196	neu, mnc, dnc
GRANDVAUX IRF3 TARGETS UP	15	8 (53.3)	8 (53.3)	0 (0)	<0.0001	0.0001	0.0196	neu, mnc, dnc, tcl, nkc
BOYLAN MULTIPLE MYELOMA D DN	71	9 (12.7)	9 (12.7)	0 (0)	<0.0001	0.0001	0.0194	neu
THEILGAARD NEUTROPHIL AT SKIN WOUND UP	76	9 (11.8)	9 (11.8)	0 (0)	<0.0001	0.0001	0.0192	
HELLEBREKERS SILENCED DURING TUMOR ANGIOGENESIS	78	9 (11.5)	8 (10.3)	1 (1.3)	<0.0001	0.0001	0.0191	

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
AMIT SERUM RESPONSE 40 MCF10A	31	8 (25.8)	8 (25.8)	0 (0)	<0.0001	0.0001	0.0189	
GRAHAM CML DIVIDING VS NORMAL QUIESCENT DN	88	9 (10.2)	8 (9.1)	1 (1.1)	<0.0001	0.0001	0.0188	neu
UZONYI RESPONSE TO LEUKOTRIENE AND THROMBIN	37	8 (21.6)	8 (21.6)	0 (0)	<0.0001	0.0001	0.0186	neu
KAAB FAILED HEART VENTRICLE DN	41	8 (19.5)	8 (19.5)	0 (0)	<0.0001	0.0001	0.0184	neu, mnc, dnc
MCDOWELL ACUTE LUNG INJURY UP	43	8 (18.6)	8 (18.6)	0 (0)	<0.0001	0.0001	0.0183	
ABBUD LIF SIGNALING 1 UP	46	8 (17.4)	8 (17.4)	0 (0)	<0.0001	0.0001	0.0182	tcl
BROWNE HCMV INFECTION 4HR UP	53	8 (15.1)	8 (15.1)	0 (0)	<0.0001	0.0001	0.0179	neu, mnc, dnc
GRAHAM CML QUIESCENT VS NORMAL DIVIDING UP	55	8 (14.5)	8 (14.5)	0 (0)	<0.0001	0.0001	0.0179	mnc, tcl
WORSCHECH TUMOR REJECTION UP	53	8 (15.1)	7 (13.2)	1 (1.9)	<0.0001	0.0001	0.0179	
LEE LIVER CANCER E2F1 UP	62	8 (12.9)	7 (11.3)	1 (1.6)	<0.0001	0.0001	0.0176	mnc, dnc
PHONG TNF TARGETS UP	62	8 (12.9)	8 (12.9)	0 (0)	<0.0001	0.0001	0.0176	
MCBRYAN PUBERTAL TGFB1 TARGETS DN	65	8 (12.3)	8 (12.3)	0 (0)	<0.0001	0.0001	0.0175	neu, mnc
PETROVA PROX1 TARGETS DN	64	8 (12.5)	7 (10.9)	1 (1.6)	<0.0001	0.0001	0.0175	
BROWNE HCMV INFECTION 6HR UP	69	8 (11.6)	8 (11.6)	0 (0)	<0.0001	0.0001	0.0173	neu
FURUKAWA DUSP6 TARGETS PCI35 UP	73	8 (11)	7 (9.6)	1 (1.4)	<0.0001	0.0001	0.0172	neu, mnc, dnc, tcl
GRANDVAUX IFN RESPONSE NOT VIA IRF3	14	7 (50)	7 (50)	0 (0)	<0.0001	0.0001	0.0172	neu, mnc, dnc, tcl, nkc, bcl
ROSS AML WITH MLL FUSIONS	76	8 (10.5)	7 (9.2)	1 (1.3)	<0.0001	0.0001	0.0171	mnc
XU HGF TARGETS INDUCED BY AKT1 6HR	18	7 (38.9)	7 (38.9)	0 (0)	<0.0001	0.0001	0.0170	neu, mnc, dnc
MAHADEVAN RESPONSE TO MP470 UP	19	7 (36.8)	7 (36.8)	0 (0)	<0.0001	0.0001	0.0169	neu, mnc, dnc, tcl
NIELSEN SYNOVIAL SARCOMA DN	19	7 (36.8)	7 (36.8)	0 (0)	<0.0001	0.0001	0.0169	neu, mnc, dnc
DAVIES MULTIPLE MYELOMA VS MGUS DN	26	7 (26.9)	7 (26.9)	0 (0)	<0.0001	0.0001	0.0167	
YAN ESCAPE FROM ANOIKIS	24	7 (29.2)	7 (29.2)	0 (0)	<0.0001	0.0001	0.0167	neu, mnc, dnc, tcl, nkc, bcl
LU TUMOR VASCULATURE UP	27	7 (25.9)	6 (22.2)	1 (3.7)	<0.0001	0.0001	0.0166	mnc
WILENSKY RESPONSE TO DARAPLADIB	27	7 (25.9)	7 (25.9)	0 (0)	<0.0001	0.0001	0.0166	
ZHANG ANTIVIRAL RESPONSE TO RIBAVIRIN UP	29	7 (24.1)	7 (24.1)	0 (0)	<0.0001	0.0001	0.0165	neu, mnc, dnc
ZHAN MULTIPLE MYELOMA DN	39	7 (17.9)	7 (17.9)	0 (0)	<0.0001	0.0001	0.0162	
PARK APL PATHOGENESIS DN	47	7 (14.9)	7 (14.9)	0 (0)	<0.0001	0.0001	0.0159	
BECKER TAMOXIFEN RESISTANCE UP	49	7 (14.3)	7 (14.3)	0 (0)	<0.0001	0.0001	0.0158	neu, mnc, dnc
TSAI DNAJB4 TARGETS UP	13	6 (46.2)	6 (46.2)	0 (0)	<0.0001	0.0001	0.0147	neu, mnc, dnc, tcl, nkc
MURATA VIRULENCE OF H PILORI	23	6 (26.1)	6 (26.1)	0 (0)	<0.0001	0.0001	0.0144	mnc, dnc
LIAN NEUTROPHIL GRANULE CONSTITUENTS	24	6 (25)	6 (25)	0 (0)	<0.0001	0.0001	0.0143	

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
BOYAULT LIVER CANCER SUBCLASS G5 DN	27	6 (22.2)	6 (22.2)	0 (0)	<0.0001	0.0001	0.0142	neu, dnc, tcl
APPEL IMATINIB RESPONSE	32	6 (18.8)	6 (18.8)	0 (0)	<0.0001	0.0001	0.0141	
TAKEDA TARGETS OF NUP98 HOXA9 FUSION 3D DN	30	6 (20)	6 (20)	0 (0)	<0.0001	0.0001	0.0141	
BOHN PRIMARY IMMUNODEFICIENCY SYNDROM DN	39	6 (15.4)	6 (15.4)	0 (0)	<0.0001	0.0001	0.0138	
LU TUMOR ENDOTHELIAL MARKERS UP	20	5 (25)	4 (20)	1 (5)	<0.0001	0.0001	0.0120	
HAHTOLA CTCL CUTANEOUS	25	5 (20)	5 (20)	0 (0)	<0.0001	0.0001	0.0119	
RUAN RESPONSE TO TNF UP	12	4 (33.3)	4 (33.3)	0 (0)	<0.0001	0.0001	0.0098	mnc, dnc, tcl, nkc, bcl
DURAND STROMA MAX UP	270	17 (6.3)	16 (5.9)	1 (0.4)	<0.0001	0.0002	0.0260	neu, mnc, dnc, bcl
CHARAFE BREAST CANCER LUMINAL VS MESENCHYMAL DN	447	21 (4.7)	18 (4)	3 (0.7)	<0.0001	0.0002	0.0254	mnc
FORTSCHEGGER PHF8 TARGETS DN	749	28 (3.7)	24 (3.2)	4 (0.5)	<0.0001	0.0002	0.0250	neu, mnc
DUTERTRE ESTRADIOL RESPONSE 24HR DN	502	22 (4.4)	22 (4.4)	0 (0)	<0.0001	0.0002	0.0250	neu, mnc
MIYAGAWA TARGETS OF EWSR1 ETS FUSIONS UP	247	15 (6.1)	15 (6.1)	0 (0)	<0.0001	0.0002	0.0237	neu, tcl, bcl
CHIANG LIVER CANCER SUBCLASS CTNNB1 DN	161	13 (8.1)	12 (7.5)	1 (0.6)	<0.0001	0.0002	0.0237	
SERVITJA ISLET HNF1A TARGETS UP	160	13 (8.1)	13 (8.1)	0 (0)	<0.0001	0.0002	0.0237	mnc, dnc
ZWANG TRANSIENTLY UP BY 1ST EGF PULSE ONLY	1723	48 (2.8)	45 (2.6)	3 (0.2)	<0.0001	0.0002	0.0231	neu, mnc, dnc, tcl, bcl
RODWELL AGING KIDNEY NO BLOOD UP	213	13 (6.1)	10 (4.7)	3 (1.4)	<0.0001	0.0002	0.0216	dnc
RASHI RESPONSE TO IONIZING RADIATION 2	126	11 (8.7)	11 (8.7)	0 (0)	<0.0001	0.0002	0.0213	neu
CONCANNON APOPTOSIS BY EPOXOMICIN UP	227	13 (5.7)	13 (5.7)	0 (0)	<0.0001	0.0002	0.0211	neu
TONKS TARGETS OF RUNX1 RUNX1T1 FUSION HSC UP	180	12 (6.7)	11 (6.1)	1 (0.6)	<0.0001	0.0002	0.0211	neu
JOHNSTONE PARVB TARGETS 2 UP	136	11 (8.1)	11 (8.1)	0 (0)	<0.0001	0.0002	0.0209	neu, mnc, dnc
HUANG GATA2 TARGETS UP	146	11 (7.5)	11 (7.5)	0 (0)	<0.0001	0.0002	0.0205	neu, dnc
TSAI RESPONSE TO IONIZING RADIATION	146	11 (7.5)	11 (7.5)	0 (0)	<0.0001	0.0002	0.0205	dnc
DARWICHE SQUAMOUS CELL CARCINOMA UP	143	10 (7)	10 (7)	0 (0)	<0.0001	0.0002	0.0187	neu
WINZEN DEGRADED VIA KHSRP	101	9 (8.9)	7 (6.9)	2 (2)	<0.0001	0.0002	0.0183	
GROSS HYPOXIA VIA HIF1A DN	107	9 (8.4)	8 (7.5)	1 (0.9)	<0.0001	0.0002	0.0180	
NAGASHIMA EGF SIGNALING UP	59	8 (13.6)	8 (13.6)	0 (0)	<0.0001	0.0002	0.0177	
COATES MACROPHAGE M1 VS M2 UP	81	8 (9.9)	7 (8.6)	1 (1.2)	<0.0001	0.0002	0.0169	
HAN JNK SINGALING UP	34	7 (20.6)	7 (20.6)	0 (0)	<0.0001	0.0002	0.0164	neu, mnc, dnc, tcl, bcl
TONKS TARGETS OF RUNX1 RUNX1T1 FUSION SUSTAINDED IN ERYTHROCYTE UP	42	7 (16.7)	6 (14.3)	1 (2.4)	<0.0001	0.0002	0.0161	
FAELT B CLL WITH VH REARRANGEMENTS UP	46	7 (15.2)	7 (15.2)	0 (0)	<0.0001	0.0002	0.0159	neu
BROWNE HCMV INFECTION 30MIN UP	51	7 (13.7)	7 (13.7)	0 (0)	<0.0001	0.0002	0.0157	dnc
LEE LIVER CANCER CIPROFIBRATE UP	58	7 (12.1)	6 (10.3)	1 (1.7)	<0.0001	0.0002	0.0155	

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
LIM MAMMARY LUMINAL PROGENITOR UP	59	7 (11.9)	7 (11.9)	0 (0)	<0.0001	0.0002	0.0155	
SHIN B CELL LYMPHOMA CLUSTER 8	36	6 (16.7)	6 (16.7)	0 (0)	<0.0001	0.0002	0.0139	tcl
SHIPP DLBCL VS FOLLICULAR LYMPHOMA UP	44	6 (13.6)	6 (13.6)	0 (0)	<0.0001	0.0002	0.0137	
LEE SP4 THYMOCYTE	14	5 (35.7)	4 (28.6)	1 (7.1)	<0.0001	0.0002	0.0122	mnc, tcl
RIGGI EWING SARCOMA PROGENITOR UP	429	19 (4.4)	18 (4.2)	1 (0.2)	<0.0001	0.0003	0.0234	neu
BASAKI YBX1 TARGETS DN	361	17 (4.7)	15 (4.2)	2 (0.6)	<0.0001	0.0003	0.0228	neu, mnc
WEST ADRENOCORTICAL TUMOR DN	508	20 (3.9)	20 (3.9)	0 (0)	<0.0001	0.0003	0.0225	
ZHENG GLIOBLASTOMA PLASTICITY UP	252	14 (5.6)	10 (4)	4 (1.6)	<0.0001	0.0003	0.0219	dnc
WANG CISPLATIN RESPONSE AND XPC DN	223	13 (5.8)	13 (5.8)	0 (0)	<0.0001	0.0003	0.0213	
VERHAAK AML WITH NPM1 MUTATED DN	238	13 (5.5)	11 (4.6)	2 (0.8)	<0.0001	0.0003	0.0208	neu, mnc, dnc, tcl
FOSTER KDM1A TARGETS UP	250	13 (5.2)	12 (4.8)	1 (0.4)	<0.0001	0.0003	0.0204	neu, mnc, dnc
KOKKINAKIS METHIONINE DEPRIVATION 48HR UP	126	10 (7.9)	10 (7.9)	0 (0)	<0.0001	0.0003	0.0193	
TAKEDA TARGETS OF NUP98 HOXA9 FUSION 10D DN	135	10 (7.4)	10 (7.4)	0 (0)	<0.0001	0.0003	0.0190	neu, mnc, dnc
KOBAYASHI EGFR SIGNALING 24HR UP	110	9 (8.2)	9 (8.2)	0 (0)	<0.0001	0.0003	0.0179	neu
HUMMERICH SKIN CANCER PROGRESSION UP	87	8 (9.2)	8 (9.2)	0 (0)	<0.0001	0.0003	0.0167	neu
LEE LIVER CANCER MYC E2F1 UP	56	7 (12.5)	7 (12.5)	0 (0)	<0.0001	0.0003	0.0156	neu, mnc, dnc
ZHAN MULTIPLE MYELOMA CD1 VS CD2 UP	64	7 (10.9)	6 (9.4)	1 (1.6)	<0.0001	0.0003	0.0153	neu
PEPPER CHRONIC LYMPHOCYTIC LEUKEMIA UP	45	6 (13.3)	6 (13.3)	0 (0)	<0.0001	0.0003	0.0136	
CUI TCF21 TARGETS 2 DN	813	29 (3.6)	28 (3.4)	1 (0.1)	<0.0001	0.0004	0.0245	neu
KRIEG HYPOXIA NOT VIA KDM3A	718	26 (3.6)	25 (3.5)	1 (0.1)	<0.0001	0.0004	0.0238	neu, mnc, dnc
RICKMAN TUMOR DIFFERENTIATED WELL VS POORLY DN	380	18 (4.7)	17 (4.5)	1 (0.3)	<0.0001	0.0004	0.0236	
LEI MYB TARGETS	307	16 (5.2)	15 (4.9)	1 (0.3)	<0.0001	0.0004	0.0231	neu, mnc, dnc
GOLDRATH ANTIGEN RESPONSE	333	16 (4.8)	16 (4.8)	0 (0)	<0.0001	0.0004	0.0223	neu
MARTINEZ RB1 TARGETS DN	525	20 (3.8)	18 (3.4)	2 (0.4)	<0.0001	0.0004	0.0221	
WANG SMARCE1 TARGETS UP	265	14 (5.3)	12 (4.5)	2 (0.8)	<0.0001	0.0004	0.0215	neu, mnc, dnc
ENK UV RESPONSE KERATINOCYTE UP	529	19 (3.6)	17 (3.2)	2 (0.4)	<0.0001	0.0004	0.0209	neu
HOSHIDA LIVER CANCER SUBCLASS S3	259	13 (5)	13 (5)	0 (0)	<0.0001	0.0004	0.0201	mnc
IWANAGA CARCINOGENESIS BY KRAS PTEN UP	167	11 (6.6)	10 (6)	1 (0.6)	<0.0001	0.0004	0.0197	
WU CELL MIGRATION	174	11 (6.3)	11 (6.3)	0 (0)	<0.0001	0.0004	0.0195	
YAGI AML SURVIVAL	124	10 (8.1)	10 (8.1)	0 (0)	<0.0001	0.0004	0.0194	
LIEN BREAST CARCINOMA METAPLASTIC VS DUCTAL UP	78	8 (10.3)	8 (10.3)	0 (0)	<0.0001	0.0004	0.0170	mnc
CHEN LVAD SUPPORT OF FAILING HEART DN	42	6 (14.3)	6 (14.3)	0 (0)	<0.0001	0.0004	0.0137	
TRACEY RESISTANCE TO IFNA2 DN	30	5 (16.7)	5 (16.7)	0 (0)	<0.0001	0.0004	0.0117	
IIZUKA LIVER CANCER PROGRESSION G1 G2 UP	12	4 (33.3)	4 (33.3)	0 (0)	<0.0001	0.0004	0.0098	neu, mnc, tcl, bcl

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
BENPORATH SUZ12 TARGETS	953	31 (3.3)	29 (3)	2 (0.2)	<0.0001	0.0005	0.0234	
MOOTHA PGC	407	17 (4.2)	16 (3.9)	1 (0.2)	<0.0001	0.0005	0.0215	
ROZANOV MMP14 TARGETS UP	270	14 (5.2)	12 (4.4)	2 (0.7)	<0.0001	0.0005	0.0213	neu, mnc, dnc
CASORELLI ACUTE PROMYELOCYTIC LEUKEMIA UP	162	11 (6.8)	9 (5.6)	2 (1.2)	<0.0001	0.0005	0.0199	
CADWELL ATG16L1 TARGETS UP	94	8 (8.5)	8 (8.5)	0 (0)	<0.0001	0.0005	0.0164	mnc
KUROZUMI RESPONSE TO ONCOCYTIC VIRUS	40	6 (15)	6 (15)	0 (0)	<0.0001	0.0005	0.0138	
ABE VEGFA TARGETS 30MIN	28	5 (17.9)	5 (17.9)	0 (0)	<0.0001	0.0005	0.0118	
WATANABE ULCERATIVE COLITIS WITH CANCER DN	13	4 (30.8)	4 (30.8)	0 (0)	<0.0001	0.0005	0.0098	neu, mnc, dnc, tcl, bcl
MASSARWEH TAMOXIFEN RESISTANCE DN	235	13 (5.5)	10 (4.3)	3 (1.3)	<0.0001	0.0006	0.0209	
KAN RESPONSE TO ARSENIC TRIOXIDE	114	9 (7.9)	9 (7.9)	0 (0)	<0.0001	0.0006	0.0178	mnc
BASSO HAIRY CELL LEUKEMIA DN	79	8 (10.1)	7 (8.9)	1 (1.3)	<0.0001	0.0006	0.0169	dnc
LABBE TGFB1 TARGETS DN	100	8 (8)	8 (8)	0 (0)	<0.0001	0.0006	0.0162	
NATSUME RESPONSE TO INTERFERON BETA UP	71	7 (9.9)	7 (9.9)	0 (0)	<0.0001	0.0006	0.0151	mnc, tcl
SESTO RESPONSE TO UV C1	71	7 (9.9)	7 (9.9)	0 (0)	<0.0001	0.0006	0.0151	
BILBAN B CLL LPL DN	45	6 (13.3)	6 (13.3)	0 (0)	<0.0001	0.0006	0.0136	
SAGIV CD24 TARGETS DN	46	6 (13)	6 (13)	0 (0)	<0.0001	0.0006	0.0136	neu
CROONQUIST STROMAL STIMULATION UP	55	6 (10.9)	6 (10.9)	0 (0)	<0.0001	0.0006	0.0133	
SESTO RESPONSE TO UV C3	20	4 (20)	4 (20)	0 (0)	<0.0001	0.0006	0.0096	
BOCHKIS FOXA2 TARGETS	425	18 (4.2)	17 (4)	1 (0.2)	<0.0001	0.0007	0.0223	neu
MONNIER POSTRADIATION TUMOR ESCAPE DN	357	16 (4.5)	15 (4.2)	1 (0.3)	<0.0001	0.0007	0.0216	neu, mnc, dnc, tcl, bcl
ZHANG TLX TARGETS 60HR UP	289	14 (4.8)	11 (3.8)	3 (1)	<0.0001	0.0007	0.0207	
PEREZ TP63 TARGETS	343	16 (4.7)	16 (4.7)	0 (0)	<0.0001	0.0008	0.0220	mnc
SANSOM APC TARGETS DN	359	16 (4.5)	16 (4.5)	0 (0)	<0.0001	0.0008	0.0215	neu, mnc, dnc
YAO TEMPORAL RESPONSE TO PROGESTERONE CLUSTER 9	72	7 (9.7)	7 (9.7)	0 (0)	<0.0001	0.0008	0.0150	neu
MEISSNER NPC HCP WITH H3 UNMETHYLATED	523	20 (3.8)	19 (3.6)	1 (0.2)	<0.0001	0.0009	0.0221	
OKUMURA INFLAMMATORY RESPONSE LPS	174	11 (6.3)	11 (6.3)	0 (0)	<0.0001	0.0009	0.0195	
HSIAO LIVER SPECIFIC GENES	234	12 (5.1)	12 (5.1)	0 (0)	<0.0001	0.0009	0.0193	mnc
DURAND STROMA MAX DN	152	10 (6.6)	10 (6.6)	0 (0)	<0.0001	0.0009	0.0184	
CHUNG BLISTER CYTOTOXICITY UP	130	9 (6.9)	9 (6.9)	0 (0)	<0.0001	0.0009	0.0172	neu
TURASHVILI BREAST LOBULAR CARCINOMA VS DUCTAL NORMAL UP	65	7 (10.8)	6 (9.2)	1 (1.5)	<0.0001	0.0009	0.0153	
ROY WOUND BLOOD VESSEL UP	46	6 (13)	5 (10.9)	1 (2.2)	<0.0001	0.0009	0.0136	
MAHADEVAN RESPONSE TO MP470 DN	20	4 (20)	4 (20)	0 (0)	<0.0001	0.0009	0.0096	neu
WU SILENCED BY METHYLATION IN BLADDER CANCER	53	6 (11.3)	6 (11.3)	0 (0)	<0.0001	0.0009	0.0134	
STEARMAN TUMOR FIELD EFFECT UP	35	5 (14.3)	5 (14.3)	0 (0)	<0.0001	0.0009	0.0116	

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
RUAN RESPONSE TO TNF TROGLITAZONE UP	17	4 (23.5)	4 (23.5)	0 (0)	<0.0001	0.0009	0.0097	mnc, dnc, tcl, nkc, bcl
SHIN B CELL LYMPHOMA CLUSTER 6	10	3 (30)	3 (30)	0 (0)	<0.0001	0.0009	0.0074	
LEE LIVER CANCER SURVIVAL UP	167	10 (6)	10 (6)	0 (0)	0.0001	0.001	0.0179	mnc
LABBE TARGETS OF TGFB1 AND WNT3A DN	106	8 (7.5)	8 (7.5)	0 (0)	0.0001	0.001	0.0160	mnc, dnc
FRIDMAN SENESCENCE UP	78	7 (9)	7 (9)	0 (0)	0.0001	0.001	0.0148	dnc
ROZANOV MMP14 TARGETS DN	32	5 (15.6)	5 (15.6)	0 (0)	0.0001	0.001	0.0117	
CROONQUIST NRAS SIGNALING UP	35	5 (14.3)	5 (14.3)	0 (0)	0.0001	0.001	0.0116	neu
BLALOCK ALZHEIMERS DISEASE UP	1628	44 (2.7)	44 (2.7)	0 (0)	0.0001	0.0011	0.0222	neu, mnc, dnc
VANHARANTA UTERINE FIBROID DN	66	7 (10.6)	7 (10.6)	0 (0)	0.0001	0.0012	0.0152	neu, mnc
SARTIPY BLUNTED BY INSULIN RESISTANCE UP	19	4 (21.1)	4 (21.1)	0 (0)	0.0001	0.0012	0.0096	mnc, dnc, tcl
GUTIERREZ WALDENSTROEMS MACROGLOBULINEMIA 1 DN	9	3 (33.3)	3 (33.3)	0 (0)	0.0001	0.0012	0.0074	
LEE LIVER CANCER MYC TGFA UP	62	6 (9.7)	5 (8.1)	1 (1.6)	0.0001	0.0013	0.0131	dnc
FARMER BREAST CANCER CLUSTER 4	16	4 (25)	4 (25)	0 (0)	0.0001	0.0013	0.0097	
NIELSEN GIST VS SYNOVIAL SARCOMA DN	20	4 (20)	4 (20)	0 (0)	0.0001	0.0013	0.0096	
MARTENS BOUND BY PML RARA FUSION	446	18 (4)	18 (4)	0 (0)	0.0001	0.0013	0.0217	neu, mnc, tcl
WINTER HYPOXIA METAGENE	226	12 (5.3)	9 (4)	3 (1.3)	0.0001	0.0013	0.0195	neu
TONKS TARGETS OF RUNX1 RUNX1T1 FUSION HSC DN	179	10 (5.6)	10 (5.6)	0 (0)	0.0001	0.0013	0.0175	
RASHI RESPONSE TO IONIZING RADIATION 6	79	7 (8.9)	7 (8.9)	0 (0)	0.0001	0.0013	0.0148	dnc
SCHLINGEMANN SKIN CARCINOGENESIS TPA UP	42	5 (11.9)	5 (11.9)	0 (0)	0.0001	0.0013	0.0114	
EBAUER TARGETS OF PAX3 FOXO1 FUSION UP	199	11 (5.5)	10 (5)	1 (0.5)	0.0002	0.0014	0.0187	
LINDGREN BLADDER CANCER CLUSTER 2A DN	131	9 (6.9)	9 (6.9)	0 (0)	0.0002	0.0014	0.0172	
SPIRA SMOKERS LUNG CANCER UP	35	5 (14.3)	5 (14.3)	0 (0)	0.0002	0.0014	0.0116	
ELVIDGE HYPOXIA UP	166	10 (6)	9 (5.4)	1 (0.6)	0.0002	0.0015	0.0180	neu, mnc, dnc
BROWNE HCMV INFECTION 12HR UP	105	8 (7.6)	8 (7.6)	0 (0)	0.0002	0.0015	0.0161	neu, mnc, dnc
GESERICK TERT TARGETS DN	21	4 (19)	4 (19)	0 (0)	0.0002	0.0015	0.0096	neu
MATTIOLI MULTIPLE MYELOMA WITH 14Q32 TRANSLOCATIONS	33	5 (15.2)	5 (15.2)	0 (0)	0.0002	0.0016	0.0117	neu
GARGALOVIC RESPONSE TO OXIDIZED PHOSPHOLIPIDS BLACK UP	35	5 (14.3)	5 (14.3)	0 (0)	0.0002	0.0016	0.0116	
BROWNE HCMV INFECTION 2HR UP	38	5 (13.2)	5 (13.2)	0 (0)	0.0002	0.0016	0.0115	neu
BRUINS UVC RESPONSE LATE	1111	32 (2.9)	30 (2.7)	2 (0.2)	0.0002	0.0016	0.0216	neu, mnc
HELLER HDAC TARGETS SILENCED BY METHYLATION DN	269	13 (4.8)	13 (4.8)	0 (0)	0.0002	0.0016	0.0198	neu, tcl
GAVIN FOXP3 TARGETS CLUSTER P2	77	7 (9.1)	7 (9.1)	0 (0)	0.0002	0.0016	0.0149	mnc
SMITH TERT TARGETS DN	83	7 (8.4)	7 (8.4)	0 (0)	0.0002	0.0016	0.0147	
NAGASHIMA NRG1 SIGNALING UP	175	10 (5.7)	10 (5.7)	0 (0)	0.0002	0.0018	0.0177	
SAKAI CHRONIC HEPATITIS VS LIVER CANCER UP	82	7 (8.5)	7 (8.5)	0 (0)	0.0002	0.0018	0.0147	
WEINMANN ADAPTATION TO HYPOXIA DN	41	5 (12.2)	3 (7.3)	2 (4.9)	0.0002	0.0018	0.0114	

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
JIANG HYPOXIA NORMAL	300	14 (4.7)	13 (4.3)	1 (0.3)	0.0002	0.0019	0.0204	dnc
SMIRNOV RESPONSE TO IR 6HR DN	113	8 (7.1)	8 (7.1)	0 (0)	0.0002	0.0019	0.0158	neu, dnc
WANG HCP PROSTATE CANCER	112	8 (7.1)	7 (6.2)	1 (0.9)	0.0002	0.0019	0.0158	neu
SAFFORD T LYMPHOCYTE ANERGY	85	7 (8.2)	7 (8.2)	0 (0)	0.0002	0.0019	0.0146	
SMID BREAST CANCER RELAPSE IN BONE DN	279	13 (4.7)	12 (4.3)	1 (0.4)	0.0002	0.002	0.0195	
STEGER ADIPOGENESIS UP	21	4 (19)	4 (19)	0 (0)	0.0002	0.002	0.0096	mnc, dnc
DELACROIX RAR BOUND ES	449	17 (3.8)	16 (3.6)	1 (0.2)	0.0002	0.0021	0.0204	
SHETH LIVER CANCER VS TXNIP LOSS PAM4	250	12 (4.8)	11 (4.4)	1 (0.4)	0.0002	0.0021	0.0188	
WIERENGA STAT5A TARGETS DN	219	11 (5)	11 (5)	0 (0)	0.0002	0.0021	0.0181	neu, dnc
CHIANG LIVER CANCER SUBCLASS INTERFERON UP	24	4 (16.7)	4 (16.7)	0 (0)	0.0002	0.0021	0.0095	neu, dnc
DAZARD RESPONSE TO UV NHEK UP	243	11 (4.5)	10 (4.1)	1 (0.4)	0.0003	0.0022	0.0174	neu
TAKEDA TARGETS OF NUP98 HOXA9 FUSION 6HR UP	85	7 (8.2)	7 (8.2)	0 (0)	0.0003	0.0022	0.0146	
CHASSOT SKIN WOUND	10	3 (30)	3 (30)	0 (0)	0.0003	0.0022	0.0074	
VERHAAK GLIOBLASTOMA CLASSICAL	195	11 (5.6)	10 (5.1)	1 (0.5)	0.0003	0.0022	0.0188	
LU EZH2 TARGETS UP	289	12 (4.2)	11 (3.8)	1 (0.3)	0.0003	0.0022	0.0177	neu, mnc, dnc
MOHANKUMAR TLX1 TARGETS DN	181	10 (5.5)	9 (5)	1 (0.6)	0.0003	0.0022	0.0175	
AZARE NEOPLASTIC TRANSFORMATION BY STAT3 DN	115	8 (7)	7 (6.1)	1 (0.9)	0.0003	0.0023	0.0157	neu
BACOLOD RESISTANCE TO ALKYLATING AGENTS UP	24	4 (16.7)	4 (16.7)	0 (0)	0.0003	0.0023	0.0095	
LOPEZ MBD TARGETS	925	27 (2.9)	24 (2.6)	3 (0.3)	0.0003	0.0024	0.0208	neu
FONTAINE FOLLICULAR THYROID ADENOMA DN	63	6 (9.5)	6 (9.5)	0 (0)	0.0003	0.0024	0.0131	
ALCALAY AML BY NPM1 LOCALIZATION UP	136	9 (6.6)	9 (6.6)	0 (0)	0.0003	0.0025	0.0170	
CHANG CORE SERUM RESPONSE DN	205	11 (5.4)	10 (4.9)	1 (0.5)	0.0003	0.0026	0.0185	neu, mnc, dnc
RIZKI TUMOR INVASIVENESS 3D DN	262	12 (4.6)	12 (4.6)	0 (0)	0.0003	0.0027	0.0184	
DELPUECH FOXO3 TARGETS UP	66	6 (9.1)	6 (9.1)	0 (0)	0.0003	0.0027	0.0130	
GAJATE RESPONSE TO TRABECTEDIN UP	68	6 (8.8)	6 (8.8)	0 (0)	0.0003	0.0027	0.0130	neu, mnc
KAMIKUBO MYELOID CEBPA NETWORK	26	4 (15.4)	4 (15.4)	0 (0)	0.0003	0.0027	0.0095	
YAGI AML WITH 11Q23 REARRANGED	332	14 (4.2)	12 (3.6)	2 (0.6)	0.0003	0.0027	0.0195	mnc
DACOSTA UV RESPONSE VIA ERCC3 UP	301	13 (4.3)	12 (4)	1 (0.3)	0.0003	0.0027	0.0189	neu, dnc
FRASOR RESPONSE TO ESTRADIOL UP	38	5 (13.2)	5 (13.2)	0 (0)	0.0003	0.0027	0.0115	
CHIBA RESPONSE TO TSA	48	5 (10.4)	5 (10.4)	0 (0)	0.0004	0.003	0.0113	mnc
HELLER HDAC TARGETS UP	318	13 (4.1)	13 (4.1)	0 (0)	0.0004	0.003	0.0184	neu
LEIN ASTROCYTE MARKERS	42	5 (11.9)	4 (9.5)	1 (2.4)	0.0004	0.003	0.0114	
ZHAN MULTIPLE MYELOMA MF UP	44	5 (11.4)	5 (11.4)	0 (0)	0.0004	0.0031	0.0114	neu
DOANE BREAST CANCER ESR1 DN	45	5 (11.1)	5 (11.1)	0 (0)	0.0004	0.0032	0.0113	
OSADA ASCL1 TARGETS DN	23	4 (17.4)	4 (17.4)	0 (0)	0.0004	0.0032	0.0095	
NEWMAN ERCC6 TARGETS UP	26	4 (15.4)	4 (15.4)	0 (0)	0.0004	0.0033	0.0095	neu

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
WORSCHECH TUMOR EVASION AND TOLEROGENICITY UP	29	4 (13.8)	3 (10.3)	1 (3.4)	0.0004	0.0033	0.0094	
GRAHAM CML QUIESCENT VS NORMAL QUIESCENT DN	45	5 (11.1)	5 (11.1)	0 (0)	0.0004	0.0034	0.0113	
DELYS THYROID CANCER DN	219	11 (5)	10 (4.6)	1 (0.5)	0.0004	0.0035	0.0181	
JECHLINGER EPITHELIAL TO MESENCHYMAL TRANSITION DN	65	6 (9.2)	6 (9.2)	0 (0)	0.0004	0.0035	0.0130	
PROVENZANI METASTASIS DN	133	8 (6)	8 (6)	0 (0)	0.0005	0.0036	0.0152	mnc, dnc
DARWICHE SKIN TUMOR PROMOTER UP	139	8 (5.8)	8 (5.8)	0 (0)	0.0005	0.0036	0.0150	neu
FONTAINE THYROID TUMOR UNCERTAIN MALIGNANCY DN	25	4 (16)	4 (16)	0 (0)	0.0005	0.0036	0.0095	
GENTILE UV LOW DOSE UP	27	4 (14.8)	4 (14.8)	0 (0)	0.0005	0.0036	0.0094	neu
MIKKELSEN IPS LCP WITH H3K4ME3	170	9 (5.3)	9 (5.3)	0 (0)	0.0005	0.0039	0.0160	mnc, dnc
GILDEA METASTASIS	30	4 (13.3)	4 (13.3)	0 (0)	0.0005	0.0039	0.0094	mnc
MIYAGAWA TARGETS OF EWSR1 ETS FUSIONS DN	219	11 (5)	10 (4.6)	1 (0.5)	0.0005	0.0039	0.0181	dnc
CHANDRAN METASTASIS DN	301	13 (4.3)	13 (4.3)	0 (0)	0.0005	0.0041	0.0189	
KOKKINAKIS METHIONINE DEPRIVATION 96HR DN	73	6 (8.2)	5 (6.8)	1 (1.4)	0.0005	0.0041	0.0128	
KRIGE AMINO ACID DEPRIVATION	29	4 (13.8)	4 (13.8)	0 (0)	0.0005	0.0041	0.0094	
TARTE PLASMA CELL VS B LYMPHOCYTE UP	73	6 (8.2)	6 (8.2)	0 (0)	0.0005	0.0042	0.0128	
HATADA METHYLATED IN LUNG CANCER UP	382	15 (3.9)	13 (3.4)	2 (0.5)	0.0006	0.0042	0.0195	
RODRIGUES NTN1 TARGETS DN	154	9 (5.8)	5 (3.2)	4 (2.6)	0.0006	0.0042	0.0165	
WIERENGA STAT5A TARGETS GROUP1	130	8 (6.2)	8 (6.2)	0 (0)	0.0006	0.0042	0.0153	neu, mnc, dnc
ELVIDGE HYPOXIA BY DMOG UP	126	8 (6.3)	7 (5.6)	1 (0.8)	0.0006	0.0044	0.0154	neu, mnc, dnc
RUIZ TNC TARGETS UP	149	9 (6)	9 (6)	0 (0)	0.0006	0.0044	0.0166	mnc, dnc
MARTINEZ RB1 TARGETS UP	654	21 (3.2)	21 (3.2)	0 (0)	0.0006	0.0045	0.0203	
GARGALOVIC RESPONSE TO OXIDIZED PHOSPHOLIPIDS GREY DN	73	6 (8.2)	6 (8.2)	0 (0)	0.0006	0.0045	0.0128	neu, mnc, dnc, tcl, nkc
BURTON ADIPOGENESIS PEAK AT 2HR	50	5 (10)	5 (10)	0 (0)	0.0006	0.0045	0.0112	
TAVOR CEBPA TARGETS DN	30	4 (13.3)	4 (13.3)	0 (0)	0.0006	0.0045	0.0094	
COATES MACROPHAGE M1 VS M2 DN	74	6 (8.1)	5 (6.8)	1 (1.4)	0.0006	0.0045	0.0128	
DARWICHE PAPILLOMA RISK HIGH UP	145	8 (5.5)	8 (5.5)	0 (0)	0.0006	0.0047	0.0149	neu
ZHAN MULTIPLE MYELOMA HP UP	50	5 (10)	5 (10)	0 (0)	0.0006	0.0047	0.0112	mnc
DORN ADENOVIRUS INFECTION 12HR UP	28	4 (14.3)	3 (10.7)	1 (3.6)	0.0006	0.0047	0.0094	
CAVARD LIVER CANCER MALIGNANT VS BENIGN	32	4 (12.5)	4 (12.5)	0 (0)	0.0006	0.0047	0.0093	
SMID BREAST CANCER ERBB2 UP	132	8 (6.1)	7 (5.3)	1 (0.8)	0.0006	0.0047	0.0152	
BAUS TFF2 TARGETS UP	32	4 (12.5)	4 (12.5)	0 (0)	0.0007	0.0049	0.0093	neu, mnc, dnc
ZHANG GATA6 TARGETS UP	13	3 (23.1)	3 (23.1)	0 (0)	0.0007	0.0051	0.0073	
HAN SATB1 TARGETS UP	380	15 (3.9)	15 (3.9)	0 (0)	0.0007	0.0051	0.0196	mnc
PEDERSEN METASTASIS BY ERBB2 ISOFORM 7	401	15 (3.7)	15 (3.7)	0 (0)	0.0007	0.0051	0.0191	mnc
PEDERSEN METASTASIS BY ERBB2 ISOFORM 1	47	5 (10.6)	5 (10.6)	0 (0)	0.0007	0.0052	0.0113	

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
VANASSE BCL2 TARGETS DN	72	6 (8.3)	5 (6.9)	1 (1.4)	0.0007	0.0052	0.0128	
CREIGHTON ENDOCRINE THERAPY RESISTANCE 5	460	17 (3.7)	17 (3.7)	0 (0)	0.0007	0.0053	0.0201	
FARMER BREAST CANCER APOCRINE VS BASAL	314	13 (4.1)	13 (4.1)	0 (0)	0.0008	0.0055	0.0185	
ONDER CDH1 TARGETS 2 UP	235	11 (4.7)	10 (4.3)	1 (0.4)	0.0008	0.0055	0.0176	mnc
BOYAULT LIVER CANCER SUBCLASS G3 DN	52	5 (9.6)	5 (9.6)	0 (0)	0.0008	0.0055	0.0112	
YAO TEMPORAL RESPONSE TO PROGESTERONE CLUSTER 5	29	4 (13.8)	4 (13.8)	0 (0)	0.0008	0.0055	0.0094	neu
KONDO EZH2 TARGETS	241	11 (4.6)	11 (4.6)	0 (0)	0.0008	0.0055	0.0174	
ADDYA ERYTHROID DIFFERENTIATION BY HEMIN	76	6 (7.9)	6 (7.9)	0 (0)	0.0008	0.0055	0.0127	
PETROVA ENDOTHELIUM LYMPHATIC VS BLOOD UP	143	8 (5.6)	7 (4.9)	1 (0.7)	0.0008	0.0056	0.0149	
URS ADIPOCYTE DIFFERENTIATION UP	73	6 (8.2)	6 (8.2)	0 (0)	0.0008	0.0056	0.0128	
CHIARADONNA NEOPLASTIC TRANSFORMATION KRAS CDC25 DN	48	5 (10.4)	5 (10.4)	0 (0)	0.0008	0.0056	0.0113	
BRUECKNER TARGETS OF MIRLET7A3 DN	74	6 (8.1)	4 (5.4)	2 (2.7)	0.0008	0.0058	0.0128	mnc
HERNANDEZ ABERRANT MITOSIS BY DOCETACEL 2NM UP	76	6 (7.9)	5 (6.6)	1 (1.3)	0.0008	0.0058	0.0127	
GUILLAUMOND KLF10 TARGETS DN	28	4 (14.3)	4 (14.3)	0 (0)	0.0008	0.0059	0.0094	
MCBRYAN PUBERTAL TGFB1 TARGETS UP	163	9 (5.5)	7 (4.3)	2 (1.2)	0.0008	0.006	0.0162	
ZHONG RESPONSE TO AZACITIDINE AND TSA UP	180	9 (5)	8 (4.4)	1 (0.6)	0.0009	0.0061	0.0157	neu, mnc
PRAMOONJAGO SOX4 TARGETS UP	51	5 (9.8)	4 (7.8)	1 (2)	0.0009	0.0061	0.0112	
PHONG TNF RESPONSE VIA P38 PARTIAL	160	9 (5.6)	9 (5.6)	0 (0)	0.0009	0.0062	0.0163	
GROSS ELK3 TARGETS DN	32	4 (12.5)	4 (12.5)	0 (0)	0.0009	0.0062	0.0093	mnc, tcl
KIM RESPONSE TO TSA AND DECITABINE UP	120	7 (5.8)	7 (5.8)	0 (0)	0.0009	0.0062	0.0136	mnc, dnc
HU GENOTOXIC DAMAGE 24HR	35	4 (11.4)	4 (11.4)	0 (0)	0.0009	0.0062	0.0093	neu
TSAI RESPONSE TO RADIATION THERAPY	32	4 (12.5)	4 (12.5)	0 (0)	0.0009	0.0063	0.0093	neu, mnc, dnc
MORI IMMATURE B LYMPHOCYTE UP	52	5 (9.6)	5 (9.6)	0 (0)	0.0009	0.0064	0.0112	neu
ZHAN V1 LATE DIFFERENTIATION GENES UP	32	4 (12.5)	4 (12.5)	0 (0)	0.0009	0.0064	0.0093	
GREGORY SYNTHETIC LETHAL WITH IMATINIB	144	8 (5.6)	8 (5.6)	0 (0)	0.0009	0.0065	0.0149	neu
DAZARD RESPONSE TO UV SCC UP	111	7 (6.3)	7 (6.3)	0 (0)	0.0009	0.0065	0.0139	
LEE LIVER CANCER DENA UP	56	5 (8.9)	4 (7.1)	1 (1.8)	0.0009	0.0065	0.0111	
WANG IMMORTALIZED BY HOXA9 AND MEIS1 UP	29	4 (13.8)	4 (13.8)	0 (0)	0.0009	0.0065	0.0094	
HOUSTIS ROS	35	4 (11.4)	4 (11.4)	0 (0)	0.0009	0.0065	0.0093	
DUTTA APOPTOSIS VIA NFKB	32	4 (12.5)	4 (12.5)	0 (0)	0.001	0.0066	0.0093	mnc
KANG GIST WITH PDGFRA UP	50	5 (10)	5 (10)	0 (0)	0.001	0.0066	0.0112	mnc, dnc
FARMER BREAST CANCER BASAL VS LULMINAL	316	13 (4.1)	12 (3.8)	1 (0.3)	0.001	0.0068	0.0185	
CREIGHTON ENDOCRINE THERAPY RESISTANCE 4	286	12 (4.2)	10 (3.5)	2 (0.7)	0.001	0.0068	0.0178	
KIM WT1 TARGETS 8HR UP	166	9 (5.4)	7 (4.2)	2 (1.2)	0.001	0.0068	0.0161	
LANDIS ERBB2 BREAST TUMORS 324 DN	145	8 (5.5)	7 (4.8)	1 (0.7)	0.001	0.0068	0.0149	
FRASOR RESPONSE TO ESTRADIOL DN	79	6 (7.6)	6 (7.6)	0 (0)	0.001	0.0069	0.0127	neu

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
LIU CDX2 TARGETS UP	34	4 (11.8)	4 (11.8)	0 (0)	0.001	0.0069	0.0093	
BOYLAN MULTIPLE MYELOMA PCA3 UP	76	6 (7.9)	6 (7.9)	0 (0)	0.001	0.0069	0.0127	neu, mnc
LEE TARGETS OF PTCH1 AND SUFU UP	55	5 (9.1)	5 (9.1)	0 (0)	0.001	0.0071	0.0111	dnc
HINATA NFKB TARGETS FIBROBLAST UP	83	6 (7.2)	6 (7.2)	0 (0)	0.0011	0.0072	0.0126	neu, mnc
HADDAD T LYMPHOCYTE AND NK PROGENITOR DN	62	5 (8.1)	5 (8.1)	0 (0)	0.0011	0.0072	0.0109	
KUMAR PATHOGEN LOAD BY MACROPHAGES	261	11 (4.2)	11 (4.2)	0 (0)	0.0011	0.0072	0.0169	
CHIARADONNA NEOPLASTIC TRANSFORMATION CDC25 UP	108	7 (6.5)	7 (6.5)	0 (0)	0.0011	0.0075	0.0139	
ZWANG EGF PERSISTENTLY UP	30	4 (13.3)	4 (13.3)	0 (0)	0.0011	0.0075	0.0094	
CAIRO HEPATOBLASTOMA DN	259	11 (4.2)	10 (3.9)	1 (0.4)	0.0011	0.0076	0.0169	mnc
SPIELMAN LYMPHOBLAST EUROPEAN VS ASIAN DN	570	19 (3.3)	19 (3.3)	0 (0)	0.0011	0.0076	0.0200	neu, mnc, dnc
ODONNELL TARGETS OF MYC AND TFRC UP	78	6 (7.7)	4 (5.1)	2 (2.6)	0.0012	0.0077	0.0127	neu
ZHANG TLX TARGETS 36HR UP	219	10 (4.6)	10 (4.6)	0 (0)	0.0012	0.0078	0.0164	neu
ACEVEDO METHYLATED IN LIVER CANCER DN	813	23 (2.8)	22 (2.7)	1 (0.1)	0.0012	0.0079	0.0193	
SCHOEN NFKB SIGNALING	34	4 (11.8)	4 (11.8)	0 (0)	0.0012	0.0081	0.0093	
LEE NEURAL CREST STEM CELL DN	107	7 (6.5)	5 (4.7)	2 (1.9)	0.0012	0.0082	0.0140	
MARIADASON REGULATED BY HISTONE ACETYLATION UP	82	6 (7.3)	5 (6.1)	1 (1.2)	0.0012	0.0082	0.0126	
MUELLER COMMON TARGETS OF AML FUSIONS DN	42	4 (9.5)	4 (9.5)	0 (0)	0.0012	0.0082	0.0091	neu, mnc
IVANOVA HEMATOPOIESIS MATURE CELL	281	12 (4.3)	12 (4.3)	0 (0)	0.0013	0.0084	0.0179	
YAGI AML RELAPSE PROGNOSIS	34	4 (11.8)	4 (11.8)	0 (0)	0.0013	0.0086	0.0093	
BOQUEST STEM CELL UP	247	11 (4.5)	10 (4)	1 (0.4)	0.0013	0.0087	0.0173	
SCHAVOLT TARGETS OF TP53 AND TP63	16	3 (18.8)	3 (18.8)	0 (0)	0.0013	0.0087	0.0072	
XU RESPONSE TO TRETINOIN AND NSC682994 UP	16	3 (18.8)	3 (18.8)	0 (0)	0.0013	0.0087	0.0072	mnc, dnc
PLASARI TGFB1 SIGNALING VIA NFIC 10HR UP	54	5 (9.3)	5 (9.3)	0 (0)	0.0014	0.0088	0.0111	neu, mnc, tcl
WIERENGA STAT5A TARGETS GROUP2	59	5 (8.5)	5 (8.5)	0 (0)	0.0014	0.0088	0.0110	neu
DAVICIONI TARGETS OF PAX FOXO1 FUSIONS UP	245	11 (4.5)	8 (3.3)	3 (1.2)	0.0014	0.009	0.0173	
GAURNIER PSMD4 TARGETS	68	5 (7.4)	5 (7.4)	0 (0)	0.0014	0.0091	0.0108	neu, dnc
STEARMAN LUNG CANCER EARLY VS LATE DN	59	5 (8.5)	5 (8.5)	0 (0)	0.0014	0.0092	0.0110	
KRIGE RESPONSE TO TOSEDOSTAT 24HR DN	993	26 (2.6)	25 (2.5)	1 (0.1)	0.0014	0.0092	0.0190	neu
MARTINEZ RESPONSE TO TRABECTEDIN UP	66	5 (7.6)	5 (7.6)	0 (0)	0.0014	0.0092	0.0108	neu
SMID BREAST CANCER RELAPSE IN LIVER UP	6	2 (33.3)	2 (33.3)	0 (0)	0.0014	0.0092	0.0049	
KOINUMA COLON CANCER MSI DN	16	3 (18.8)	2 (12.5)	1 (6.2)	0.0015	0.0094	0.0072	mnc
SWEET KRAS ONCOGENIC SIGNATURE	88	6 (6.8)	6 (6.8)	0 (0)	0.0015	0.0095	0.0124	
MATSUDA NATURAL KILLER DIFFERENTIATION	463	16 (3.5)	16 (3.5)	0 (0)	0.0015	0.0096	0.0189	
KYNG DNA DAMAGE UP	214	10 (4.7)	8 (3.7)	2 (0.9)	0.0015	0.0096	0.0165	
MARCHINI TRABECTEDIN RESISTANCE UP	18	3 (16.7)	3 (16.7)	0 (0)	0.0015	0.0098	0.0072	
CERVERA SDHB TARGETS 1 UP	114	7 (6.1)	7 (6.1)	0 (0)	0.0016	0.0099	0.0138	

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
WIEDERSCHAIN TARGETS OF BMI1 AND PCGF2	56	5 (8.9)	4 (7.1)	1 (1.8)	0.0016	0.0099	0.0111	

Table A18: Significantly enriched MSigDB Chemical/Genetic Perturbation Sets (RNA-Seq, PBMC, Day 1). Results sorted by FDR and Jaccard index. The last column indicates overlap with cell type-specific results: dnc: dendritic cells, mnc: monocytes, neu: neutrophils, tcl: T-cells, nkc: NK-cells, bcl: B-cells.

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
GSE13485 CTRL VS DAY7 YF17D VACCINE PBMC DN	195	87 (44.6)	87 (44.6)	0 (0)	<0.0001	<0.0001	0.1740	neu, mnc, dnc, tcl, nkc, bcl
GSE13485 CTRL VS DAY3 YF17D VACCINE PBMC DN	193	71 (36.8)	71 (36.8)	0 (0)	<0.0001	<0.0001	0.1381	neu, mnc, dnc, tcl, nkc, bcl
GSE13485 DAY1 VS DAY7 YF17D VACCINE PBMC DN	193	71 (36.8)	71 (36.8)	0 (0)	<0.0001	<0.0001	0.1381	neu, mnc, dnc, tcl, nkc, bcl
GSE1432 CTRL VS IFNG 24H MICROGLIA DN	200	65 (32.5)	65 (32.5)	0 (0)	<0.0001	<0.0001	0.1233	neu, mnc, dnc, tcl, nkc, bcl
GSE13485 PRE VS POST YF17D VACCINATION PBMC DN	192	64 (33.3)	64 (33.3)	0 (0)	<0.0001	<0.0001	0.1231	neu, mnc, dnc, tcl, nkc, bcl
GSE10325 LUPUS CD4 TCELL VS LUPUS MYELOID DN	191	61 (31.9)	61 (31.9)	0 (0)	<0.0001	<0.0001	0.1169	neu, mnc, dnc
GSE13485 DAY3 VS DAY7 YF17D VACCINE PBMC DN	205	60 (29.3)	60 (29.3)	0 (0)	<0.0001	<0.0001	0.1117	neu, mnc, dnc, tcl, nkc, bcl
GSE13484 UNSTIM VS YF17D VACCINE STIM PBMC DN	198	59 (29.8)	59 (29.8)	0 (0)	<0.0001	<0.0001	0.1111	neu, mnc, dnc, tcl, nkc, bcl
GSE1432 CTRL VS IFNG 6H MICROGLIA DN	198	59 (29.8)	59 (29.8)	0 (0)	<0.0001	<0.0001	0.1111	neu, mnc, dnc, tcl, nkc, bcl
GSE14000 UNSTIM VS 4H LPS DC DN	199	59 (29.6)	59 (29.6)	0 (0)	<0.0001	<0.0001	0.1109	neu, mnc, dnc, tcl, nkc, bcl
GSE29618 MONOCYTE VS MDC UP	196	58 (29.6)	58 (29.6)	0 (0)	<0.0001	<0.0001	0.1094	mnc
GSE14000 UNSTIM VS 4H LPS DC TRANSLATED RNA DN	194	56 (28.9)	56 (28.9)	0 (0)	<0.0001	<0.0001	0.1057	neu, mnc, dnc, tcl, nkc, bcl
GSE22886 NAIVE CD8 TCELL VS MONOCYTE DN	196	56 (28.6)	56 (28.6)	0 (0)	<0.0001	<0.0001	0.1053	
GSE18791 CTRL VS NEWCASTLE VIRUS DC 8H DN	189	55 (29.1)	55 (29.1)	0 (0)	<0.0001	<0.0001	0.1046	neu, mnc, dnc, tcl, nkc, bcl
GSE22886 NAIVE CD4 TCELL VS MONOCYTE DN	197	55 (27.9)	55 (27.9)	0 (0)	<0.0001	<0.0001	0.1030	neu
GSE29618 MONOCYTE VS PDC UP	197	55 (27.9)	55 (27.9)	0 (0)	<0.0001	<0.0001	0.1030	mnc

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
GSE11057 PBMC VS MEM CD4 TCELL UP	191	54 (28.3)	54 (28.3)	0 (0)	<0.0001	<0.0001	0.1021	mnc, dnc
GSE10325 MYELOID VS LUPUS MYELOID DN	197	54 (27.4)	54 (27.4)	0 (0)	<0.0001	<0.0001	0.1009	neu, mnc, dnc, tcl, nkc, bcl
GSE18791 UNSTIM VS NEWCATSLE VIRUS DC 10H DN	190	53 (27.9)	53 (27.9)	0 (0)	<0.0001	<0.0001	0.1002	neu, mnc, dnc, tcl, nkc, bcl
GSE29618 MONOCYTE VS PDC DAY7 FLU VACCINE UP	194	53 (27.3)	53 (27.3)	0 (0)	<0.0001	<0.0001	0.0994	neu, mnc, dnc
GSE13485 DAY7 VS DAY21 YF17D VACCINE PBMC UP	192	52 (27.1)	52 (27.1)	0 (0)	<0.0001	<0.0001	0.0977	neu, mnc, dnc, tcl, nkc, bcl
GSE18791 UNSTIM VS NEWCATSLE VIRUS DC 6H DN	192	52 (27.1)	51 (26.6)	1 (0.5)	<0.0001	<0.0001	0.0977	neu, mnc, dnc, tcl, nkc, bcl
GSE22886 NAIVE TCELL VS MONOCYTE DN	197	51 (25.9)	51 (25.9)	0 (0)	<0.0001	<0.0001	0.0948	
GSE29618 MONOCYTE VS MDC DAY7 FLU VACCINE UP	194	50 (25.8)	50 (25.8)	0 (0)	<0.0001	<0.0001	0.0933	neu, mnc
GSE10325 BCELL VS MYELOID DN	196	50 (25.5)	50 (25.5)	0 (0)	<0.0001	<0.0001	0.0929	neu, mnc, dnc
GSE10325 LUPUS BCELL VS LUPUS MYELOID DN	194	49 (25.3)	49 (25.3)	0 (0)	<0.0001	<0.0001	0.0912	neu, mnc
GSE22886 NAIVE BCELL VS NEUTROPHIL DN	196	49 (25)	49 (25)	0 (0)	<0.0001	<0.0001	0.0909	mnc, dnc
GSE6269 HEALTHY VS STREP AUREUS INF PBMC DN	162	46 (28.4)	46 (28.4)	0 (0)	<0.0001	<0.0001	0.0906	neu, mnc, dnc, tcl
GSE18791 CTRL VS NEWCASTLE VIRUS DC 6H DN	192	48 (25)	48 (25)	0 (0)	<0.0001	<0.0001	0.0896	neu, mnc, dnc, tcl, nkc, bcl
GSE24634 TEFF VS TCONV DAY3 IN CULTURE DN	188	47 (25)	46 (24.5)	1 (0.5)	<0.0001	<0.0001	0.0882	neu, mnc, dnc
GSE24634 IL4 VS CTRL TREATED NAIVE CD4 TCELL DAY3 DN	189	46 (24.3)	46 (24.3)	0 (0)	<0.0001	<0.0001	0.0860	neu, mnc, dnc, tcl, nkc, bcl
GSE22886 CTRL VS LPS 24H DC DN	216	48 (22.2)	48 (22.2)	0 (0)	<0.0001	<0.0001	0.0857	neu, mnc, dnc, tcl, nkc, bcl
GSE1432 1H VS 6H IFNG MICROGLIA DN	198	45 (22.7)	45 (22.7)	0 (0)	<0.0001	<0.0001	0.0826	neu, mnc, dnc, tcl, nkc, bcl
GSE18791 CTRL VS NEWCASTLE VIRUS DC 10H DN	193	44 (22.8)	44 (22.8)	0 (0)	<0.0001	<0.0001	0.0813	neu, mnc, dnc, tcl, nkc, bcl
GSE18791 CTRL VS NEWCASTLE VIRUS DC 4H DN	184	43 (23.4)	43 (23.4)	0 (0)	<0.0001	<0.0001	0.0807	neu, mnc, dnc, tcl, nkc, bcl
GSE10325 CD4 TCELL VS LUPUS CD4 TCELL DN	193	43 (22.3)	43 (22.3)	0 (0)	<0.0001	<0.0001	0.0793	neu, mnc, dnc, tcl, nkc, bcl
GSE10325 BCELL VS LUPUS BCELL DN	196	43 (21.9)	43 (21.9)	0 (0)	<0.0001	<0.0001	0.0789	neu, mnc, dnc, tcl, nkc, bcl
GSE18791 CTRL VS NEWCASTLE VIRUS DC 12H DN	203	43 (21.2)	43 (21.2)	0 (0)	<0.0001	<0.0001	0.0779	neu, mnc, dnc, tcl, nkc, bcl

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
GSE24634 IL4 VS CTRL TREATED NAIVE CD4 TCELL DAY10 DN	193	42 (21.8)	41 (21.2)	1 (0.5)	<0.0001	<0.0001	0.0773	neu, mnc, dnc, tcl, nkc, bcl
GSE1432 1H VS 24H IFNG MICROGLIA DN	200	42 (21)	42 (21)	0 (0)	<0.0001	<0.0001	0.0764	neu, mnc, dnc, tcl, nkc, bcl
GSE24634 TREG VS TCONV POST DAY10 IL4 CONVERSION DN	196	41 (20.9)	41 (20.9)	0 (0)	<0.0001	<0.0001	0.0750	neu, mnc, dnc
GSE18791 CTRL VS NEWCASTLE VIRUS DC 16H DN	188	40 (21.3)	40 (21.3)	0 (0)	<0.0001	<0.0001	0.0741	neu, mnc, dnc, tcl, nkc, bcl
GSE10325 CD4 TCELL VS MYELOID DN	190	40 (21.1)	40 (21.1)	0 (0)	<0.0001	<0.0001	0.0738	neu, mnc, dnc
GSE29618 PDC VS MDC DN	193	40 (20.7)	40 (20.7)	0 (0)	<0.0001	<0.0001	0.0734	neu, mnc, dnc, tcl
GSE29618 BCELL VS MONOCYTE DN	194	40 (20.6)	40 (20.6)	0 (0)	<0.0001	<0.0001	0.0733	neu
GSE360 CTRL VS M TUBERCULOSIS DC DN	199	40 (20.1)	40 (20.1)	0 (0)	<0.0001	<0.0001	0.0726	neu, mnc, dnc, tcl
GSE2706 UNSTIM VS 8H R848 DC DN	186	39 (21)	39 (21)	0 (0)	<0.0001	<0.0001	0.0724	neu, mnc, dnc, tcl, nkc, bcl
GSE34205 HEALTHY VS FLU INF INFANT PBMC DN	201	40 (19.9)	40 (19.9)	0 (0)	<0.0001	<0.0001	0.0723	neu, mnc, dnc, tcl, nkc
GSE13485 DAY1 VS DAY3 YF17D VACCINE PBMC DN	190	39 (20.5)	39 (20.5)	0 (0)	<0.0001	<0.0001	0.0718	neu, mnc, dnc, tcl, nkc, bcl
GSE360 HIGH DOSE B MALAYI VS M TUBERCULOSIS DC DN	191	39 (20.4)	39 (20.4)	0 (0)	<0.0001	<0.0001	0.0717	neu, mnc, dnc, tcl, nkc, bcl
GSE16755 CTRL VS IFNA TREATED MAC DN	193	38 (19.7)	38 (19.7)	0 (0)	<0.0001	<0.0001	0.0695	neu, mnc, dnc, tcl, nkc, bcl
GSE2706 UNSTIM VS 2H LPS AND R848 DC DN	188	37 (19.7)	37 (19.7)	0 (0)	<0.0001	<0.0001	0.0681	neu, mnc, dnc, tcl, nkc
GSE18791 UNSTIM VS NEWCATSLE VIRUS DC 18H DN	191	37 (19.4)	37 (19.4)	0 (0)	<0.0001	<0.0001	0.0678	neu, mnc, dnc, tcl, nkc, bcl
GSE24634 TEFF VS TCONV DAY7 IN CULTURE DN	193	37 (19.2)	36 (18.7)	1 (0.5)	<0.0001	<0.0001	0.0675	neu, mnc, dnc
GSE22886 DC VS MONOCYTE DN	194	37 (19.1)	37 (19.1)	0 (0)	<0.0001	<0.0001	0.0674	neu, mnc, dnc
GSE360 T GONDII VS M TUBERCULOSIS DC DN	194	37 (19.1)	37 (19.1)	0 (0)	<0.0001	<0.0001	0.0674	neu, mnc, dnc, tcl
GSE2706 2H VS 8H R848 STIM DC DN	186	36 (19.4)	36 (19.4)	0 (0)	<0.0001	<0.0001	0.0664	neu, mnc, dnc, tcl, nkc, bcl
GSE6269 HEALTHY VS FLU INF PBMC DN	155	34 (21.9)	34 (21.9)	0 (0)	<0.0001	<0.0001	0.0663	neu, mnc, dnc, tcl, nkc
GSE2706 UNSTIM VS 8H LPS AND R848 DC DN	188	36 (19.1)	35 (18.6)	1 (0.5)	<0.0001	<0.0001	0.0662	neu, mnc, dnc, tcl

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
GSE360 LOW DOSE B MALAYI VS M TUBERCULOSIS DC DN	190	36 (18.9)	36 (18.9)	0 (0)	<0.0001	<0.0001	0.0659	neu, mnc, dnc, tcl
GSE22886 NAIVE TCELL VS NEUTROPHIL DN	199	36 (18.1)	35 (17.6)	1 (0.5)	<0.0001	<0.0001	0.0649	mnc
GSE14000 UNSTIM VS 16H LPS DC TRANSLATED RNA DN	192	35 (18.2)	35 (18.2)	0 (0)	<0.0001	<0.0001	0.0638	neu, mnc, dnc, tcl, nkc, bcl
GSE360 L DONOVANI VS M TUBERCULOSIS DC DN	194	35 (18)	35 (18)	0 (0)	<0.0001	<0.0001	0.0635	neu, mnc, dnc, tcl
GSE29618 BCELL VS MONOCYTE DAY7 FLU VACCINE DN	197	35 (17.8)	35 (17.8)	0 (0)	<0.0001	<0.0001	0.0632	
GSE22886 NAIVE BCELL VS MONOCYTE DN	199	35 (17.6)	35 (17.6)	0 (0)	<0.0001	<0.0001	0.0629	
GSE24634 TREG VS TCONV POST DAY7 IL4 CONVERSION DN	193	34 (17.6)	34 (17.6)	0 (0)	<0.0001	<0.0001	0.0617	neu, mnc
GSE6269 HEALTHY VS STREP PNEUMO INF PBMC DN	163	32 (19.6)	32 (19.6)	0 (0)	<0.0001	<0.0001	0.0612	neu, mnc, dnc
GSE2706 2H VS 8H LPS STIM DC DN	189	33 (17.5)	33 (17.5)	0 (0)	<0.0001	<0.0001	0.0602	neu, mnc, dnc, tcl, nkc, bcl
GSE2706 UNSTIM VS 2H LPS DC DN	189	32 (16.9)	32 (16.9)	0 (0)	<0.0001	<0.0001	0.0583	neu, mnc, dnc, tcl, nkc
GSE3982 EOSINOPHIL VS NEUTROPHIL DN	189	32 (16.9)	32 (16.9)	0 (0)	<0.0001	<0.0001	0.0583	neu, mnc, dnc, tcl
GSE29618 PDC VS MDC DAY7 FLU VACCINE DN	190	32 (16.8)	32 (16.8)	0 (0)	<0.0001	<0.0001	0.0582	neu, mnc
GSE9988 ANTI TREM1 VS LPS MONOCYTE DN	191	32 (16.8)	32 (16.8)	0 (0)	<0.0001	<0.0001	0.0581	neu, mnc, dnc
GSE13484 3H UNSTIM VS YF17D VACCINE STIM PBMC DN	193	32 (16.6)	32 (16.6)	0 (0)	<0.0001	<0.0001	0.0579	neu, mnc, dnc, tcl
GSE2706 UNSTIM VS 8H LPS DC DN	193	32 (16.6)	32 (16.6)	0 (0)	<0.0001	<0.0001	0.0579	neu, mnc, dnc, tcl
GSE11057 CD4 EFF MEM VS PBMC DN	194	32 (16.5)	31 (16)	1 (0.5)	<0.0001	<0.0001	0.0578	neu, mnc
GSE2706 R848 VS R848 AND LPS 2H STIM DC DN	181	31 (17.1)	31 (17.1)	0 (0)	<0.0001	<0.0001	0.0572	neu, mnc, dnc, tcl, nkc, bcl
GSE6269 FLU VS STREP PNEUMO INF PBMC UP	165	30 (18.2)	30 (18.2)	0 (0)	<0.0001	<0.0001	0.0569	neu, mnc, dnc, tcl, nkc, bcl
GSE9988 ANTI TREM1 VS LOW LPS MONOCYTE DN	187	31 (16.6)	31 (16.6)	0 (0)	<0.0001	<0.0001	0.0566	neu, mnc, dnc
GSE3982 NEUTROPHIL VS NKCELL UP	210	32 (15.2)	32 (15.2)	0 (0)	<0.0001	<0.0001	0.0561	neu, mnc, dnc
GSE24634 IL4 VS CTRL TREATED NAIVE CD4 TCELL DAY7 DN	192	31 (16.1)	31 (16.1)	0 (0)	<0.0001	<0.0001	0.0561	neu, mnc, dnc
GSE14769 UNSTIM VS 80MIN LPS BMDM DN	196	31 (15.8)	31 (15.8)	0 (0)	<0.0001	<0.0001	0.0557	neu, mnc, dnc, tcl
GSE3982 CTRL VS LPS 48H DC DN	198	31 (15.7)	31 (15.7)	0 (0)	<0.0001	<0.0001	0.0555	neu, mnc, dnc, tcl, nkc
GSE15767 MED VS SCS MAC LN UP	194	30 (15.5)	29 (14.9)	1 (0.5)	<0.0001	<0.0001	0.0540	mnc, dnc

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
GSE2706 2H VS 8H R848 AND LPS STIM DC DN	197	30 (15.2)	30 (15.2)	0 (0)	<0.0001	<0.0001	0.0537	neu, mnc, dnc, tcl, bcl
GSE18791 CTRL VS NEWCASTLE VIRUS DC 14H DN	186	29 (15.6)	29 (15.6)	0 (0)	<0.0001	<0.0001	0.0528	neu, mnc, dnc, tcl, nkc, bcl
GSE2706 UNSTIM VS 2H R848 DC DN	187	29 (15.5)	29 (15.5)	0 (0)	<0.0001	<0.0001	0.0527	neu, mnc, dnc, tcl, nkc
GSE24634 TEFF VS TCONV DAY10 IN CULTURE DN	189	29 (15.3)	29 (15.3)	0 (0)	<0.0001	<0.0001	0.0525	neu, mnc
GSE22886 NAIVE CD4 TCELL VS NEUTROPHIL DN	212	30 (14.2)	29 (13.7)	1 (0.5)	<0.0001	<0.0001	0.0523	neu, mnc
GSE360 L DONOVANI VS M TUBERCULOSIS MAC DN	193	29 (15)	29 (15)	0 (0)	<0.0001	<0.0001	0.0522	neu, mnc, dnc, tcl, bcl
GSE22886 NAIVE CD8 TCELL VS NEUTROPHIL DN	197	29 (14.7)	28 (14.2)	1 (0.5)	<0.0001	<0.0001	0.0518	mnc
GSE14769 UNSTIM VS 120MIN LPS BMDM DN	200	29 (14.5)	28 (14)	1 (0.5)	<0.0001	<0.0001	0.0515	neu, mnc, dnc, tcl
GSE11057 CD4 CENT MEM VS PBMC DN	185	28 (15.1)	27 (14.6)	1 (0.5)	<0.0001	<0.0001	0.0510	neu, mnc, dnc
GSE24634 TREG VS TCONV POST DAY3 IL4 CONVERSION DN	193	28 (14.5)	28 (14.5)	0 (0)	<0.0001	<0.0001	0.0503	dnc
GSE360 L DONOVANI VS B MALAYI HIGH DOSE DC UP	186	27 (14.5)	27 (14.5)	0 (0)	<0.0001	<0.0001	0.0490	neu, mnc, dnc
GSE17974 IL4 AND ANTI IL12 VS UNTREATED 24H ACT CD4 TCELL DN	192	27 (14.1)	27 (14.1)	0 (0)	<0.0001	<0.0001	0.0485	neu, mnc, dnc, tcl, nkc
GSE24081 CONTROLLER VS PROGRESSOR HIV SPECIFIC CD8 TCELL DN	184	26 (14.1)	25 (13.6)	1 (0.5)	<0.0001	<0.0001	0.0473	neu, mnc, dnc, tcl, nkc, bcl
GSE9988 LPS VS CTRL TREATED MONOCYTE UP	185	26 (14.1)	26 (14.1)	0 (0)	<0.0001	<0.0001	0.0472	neu, mnc, tcl
GSE11864 CSF1 PAM3CYS VS CSF1 IFNG PAM3CYS IN MAC DN	189	26 (13.8)	26 (13.8)	0 (0)	<0.0001	<0.0001	0.0468	neu, mnc, dnc, tcl
GSE17974 IL4 AND ANTI IL12 VS UNTREATED 72H ACT CD4 TCELL DN	190	26 (13.7)	26 (13.7)	0 (0)	<0.0001	<0.0001	0.0468	neu, mnc, dnc, tcl, nkc, bcl
GSE24634 TREG VS TCONV POST DAY5 IL4 CONVERSION DN	189	26 (13.8)	26 (13.8)	0 (0)	<0.0001	<0.0001	0.0468	neu, dnc
GSE24634 IL4 VS CTRL TREATED NAIVE CD4 TCELL DAY5 DN	191	26 (13.6)	26 (13.6)	0 (0)	<0.0001	<0.0001	0.0467	neu, mnc, dnc, tcl, nkc, bcl
GSE360 HIGH DOSE B MALAYI VS M TUBERCULOSIS MAC DN	205	26 (12.7)	26 (12.7)	0 (0)	<0.0001	<0.0001	0.0455	neu, mnc, dnc, tcl, bcl
GSE360 CTRL VS L MAJOR DC DN	191	25 (13.1)	25 (13.1)	0 (0)	<0.0001	<0.0001	0.0448	neu, mnc, dnc, tcl
GSE9006 TYPE 1 DIABETES AT DX VS 4MONTH POST DX PBMC UP	192	25 (13)	25 (13)	0 (0)	<0.0001	<0.0001	0.0447	mnc, dnc
GSE14769 UNSTIM VS 60MIN LPS BMDM DN	200	25 (12.5)	24 (12)	1 (0.5)	<0.0001	<0.0001	0.0441	neu, mnc
GSE15930 STIM VS STIM AND IFNAB 48H CD8 T CELL DN	200	25 (12.5)	25 (12.5)	0 (0)	<0.0001	<0.0001	0.0441	neu, mnc, dnc, tcl, nkc

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
GSE17974 IL4 AND ANTI IL12 VS UNTREATED 48H ACT CD4 TCELL DN	188	24 (12.8)	24 (12.8)	0 (0)	<0.0001	<0.0001	0.0432	neu, mnc, dnc, tcl, nkc, bcl
GSE9988 LOW LPS VS ANTI TREM1 AND LPS MONOCYTE UP	190	24 (12.6)	24 (12.6)	0 (0)	<0.0001	<0.0001	0.0430	neu, mnc
GSE22886 NAIVE CD8 TCELL VS DC DN	197	24 (12.2)	24 (12.2)	0 (0)	<0.0001	<0.0001	0.0425	neu
GSE34205 HEALTHY VS RSV INF INFANT PBMC DN	199	24 (12.1)	24 (12.1)	0 (0)	<0.0001	<0.0001	0.0423	mnc, dnc
GSE14000 UNSTIM VS 16H LPS DC DN	206	24 (11.7)	24 (11.7)	0 (0)	<0.0001	<0.0001	0.0418	neu, mnc, dnc, tcl
GSE18791 CTRL VS NEWCASTLE VIRUS DC 18H DN	183	23 (12.6)	23 (12.6)	0 (0)	<0.0001	<0.0001	0.0417	neu, mnc, dnc, tcl, nkc, bcl
GSE9988 ANTI TREM1 VS ANTI TREM1 AND LPS MONOCYTE DN	183	23 (12.6)	23 (12.6)	0 (0)	<0.0001	<0.0001	0.0417	neu, mnc
GSE9988 LOW LPS VS VEHICLE TREATED MONOCYTE UP	182	23 (12.6)	23 (12.6)	0 (0)	<0.0001	<0.0001	0.0417	neu, mnc
GSE9006 HEALTHY VS TYPE 1 DIABETES PBMC AT DX DN	184	23 (12.5)	23 (12.5)	0 (0)	<0.0001	<0.0001	0.0416	mnc, dnc
GSE9988 LOW LPS VS CTRL TREATED MONOCYTE UP	184	23 (12.5)	23 (12.5)	0 (0)	<0.0001	<0.0001	0.0416	neu, mnc, tcl
GSE3982 DC VS MAC LPS STIM DN	186	23 (12.4)	22 (11.8)	1 (0.5)	<0.0001	<0.0001	0.0414	neu, mnc, dnc
GSE9988 LPS VS LPS AND ANTI TREM1 MONOCYTE UP	188	23 (12.2)	23 (12.2)	0 (0)	<0.0001	<0.0001	0.0413	neu, mnc, dnc
GSE22886 DAY0 VS DAY7 MONOCYTE IN CULTURE UP	192	23 (12)	23 (12)	0 (0)	<0.0001	<0.0001	0.0410	neu
GSE11057 NAIVE CD4 VS PBMC CD4 TCELL DN	193	23 (11.9)	22 (11.4)	1 (0.5)	<0.0001	<0.0001	0.0409	neu, mnc, dnc
GSE13485 DAY3 VS DAY21 YF17D VACCINE PBMC UP	194	23 (11.9)	23 (11.9)	0 (0)	<0.0001	<0.0001	0.0409	neu, mnc, dnc, tcl, nkc
GSE3982 CTRL VS LPS 4H MAC DN	194	23 (11.9)	23 (11.9)	0 (0)	<0.0001	<0.0001	0.0409	neu, mnc, dnc, tcl, nkc
GSE3982 NEUTROPHIL VS CENT MEMORY CD4 TCELL UP	206	23 (11.2)	23 (11.2)	0 (0)	<0.0001	<0.0001	0.0400	neu, mnc, dnc
GSE29617 DAY3 VS DAY7 TIV FLU VACCINE PBMC 2008 UP	181	22 (12.2)	22 (12.2)	0 (0)	<0.0001	<0.0001	0.0399	neu, mnc, dnc, tcl
GSE9988 LPS VS VEHICLE TREATED MONOCYTE UP	184	22 (12)	22 (12)	0 (0)	<0.0001	<0.0001	0.0397	neu, mnc
GSE360 CTRL VS T GONDII DC DN	187	22 (11.8)	22 (11.8)	0 (0)	<0.0001	<0.0001	0.0395	neu, mnc, dnc, tcl
GSE9006 1MONTH VS 4MONTH POST TYPE 1 DIABETES DX PBMC UP	189	22 (11.6)	22 (11.6)	0 (0)	<0.0001	<0.0001	0.0394	neu, mnc, dnc
GSE17721 PAM3CSK4 VS CPG 4H BMDM DN	190	22 (11.6)	21 (11.1)	1 (0.5)	<0.0001	<0.0001	0.0393	neu, mnc, dnc, tcl, bcl
GSE360 T GONDII VS B MALAYI HIGH DOSE DC UP	190	22 (11.6)	22 (11.6)	0 (0)	<0.0001	<0.0001	0.0393	neu, mnc, dnc, tcl
GSE360 T GONDII VS M TUBERCULOSIS MAC DN	194	22 (11.3)	22 (11.3)	0 (0)	<0.0001	<0.0001	0.0390	neu, mnc, dnc, bcl
GSE3982 NEUTROPHIL VS EFF MEMORY CD4 TCELL UP	197	22 (11.2)	22 (11.2)	0 (0)	<0.0001	<0.0001	0.0388	neu, mnc, dnc
GSE22886 DAY1 VS DAY7 MONOCYTE IN CULTURE UP	191	21 (11)	21 (11)	0 (0)	<0.0001	<0.0001	0.0374	neu, mnc

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
GSE1432 CTRL VS IFNG 1H MICROGLIA DN	192	21 (10.9)	21 (10.9)	0 (0)	<0.0001	<0.0001	0.0373	neu, mnc, dnc, tcl, nkc, bcl
GSE22886 NAIVE TCELL VS DC DN	195	21 (10.8)	21 (10.8)	0 (0)	<0.0001	<0.0001	0.0371	neu
GSE2706 R848 VS LPS 2H STIM DC DN	176	20 (11.4)	20 (11.4)	0 (0)	<0.0001	<0.0001	0.0365	neu, mnc, dnc, tcl, bcl
GSE29617 CTRL VS DAY7 TIV FLU VACCINE PBMC 2008 UP	184	20 (10.9)	20 (10.9)	0 (0)	<0.0001	<0.0001	0.0360	neu, mnc, dnc
GSE6269 FLU VS E COLI INF PBMC UP	159	19 (11.9)	19 (11.9)	0 (0)	<0.0001	<0.0001	0.0357	neu, mnc, dnc, tcl
GSE22886 DAY0 VS DAY1 MONOCYTE IN CULTURE DN	191	20 (10.5)	20 (10.5)	0 (0)	<0.0001	<0.0001	0.0355	neu, mnc
GSE360 L MAJOR VS B MALAYI HIGH DOSE DC UP	191	20 (10.5)	20 (10.5)	0 (0)	<0.0001	<0.0001	0.0355	neu, mnc, dnc
GSE6269 FLU VS STREP AUREUS INF PBMC UP	162	19 (11.7)	19 (11.7)	0 (0)	<0.0001	<0.0001	0.0355	neu, mnc, dnc, tcl, nkc
GSE24026 PD1 LIGATION VS CTRL IN ACT TCELL LINE UP	193	20 (10.4)	20 (10.4)	0 (0)	<0.0001	<0.0001	0.0354	neu, mnc, dnc, tcl, nkc, bcl
GSE29618 BCELL VS MDC DAY7 FLU VACCINE DN	196	20 (10.2)	20 (10.2)	0 (0)	<0.0001	<0.0001	0.0352	
GSE14769 UNSTIM VS 40MIN LPS BMDM DN	197	20 (10.2)	20 (10.2)	0 (0)	<0.0001	<0.0001	0.0351	neu, mnc, dnc
GSE30083 SP2 VS SP4 THYMOCYTE DN	198	20 (10.1)	20 (10.1)	0 (0)	<0.0001	<0.0001	0.0351	neu, mnc, dnc, tcl
GSE3982 DC VS BASOPHIL UP	202	20 (9.9)	19 (9.4)	1 (0.5)	<0.0001	<0.0001	0.0348	
GSE360 T GONDII VS B MALAYI LOW DOSE DC UP	182	19 (10.4)	19 (10.4)	0 (0)	<0.0001	<0.0001	0.0342	neu, mnc, dnc, tcl, nkc
GSE360 DC VS MAC M TUBERCULOSIS UP	186	19 (10.2)	19 (10.2)	0 (0)	<0.0001	<0.0001	0.0340	neu, mnc, dnc, tcl, nkc
GSE360 L DONOVANI VS B MALAYI HIGH DOSE MAC UP	189	19 (10.1)	18 (9.5)	1 (0.5)	<0.0001	<0.0001	0.0338	mnc
GSE2197 CPG DNA VS UNTREATED IN DC UP	193	19 (9.8)	18 (9.3)	1 (0.5)	<0.0001	<0.0001	0.0336	neu, mnc
GSE24634 IL4 VS CTRL TREATED NAIVE CD4 TCELL DAY5 UP	192	19 (9.9)	18 (9.4)	1 (0.5)	<0.0001	<0.0001	0.0336	neu, mnc
GSE3982 DC VS CENT MEMORY CD4 TCELL UP	192	19 (9.9)	17 (8.9)	2 (1)	<0.0001	<0.0001	0.0336	mnc, dnc
GSE24142 EARLY THYMIC PROGENITOR VS DN2 THYMOCYTE FETAL UP	195	19 (9.7)	19 (9.7)	0 (0)	<0.0001	<0.0001	0.0335	neu, mnc, dnc
GSE3337 CTRL VS 4H IFNG IN CD8POS DC DN	195	19 (9.7)	19 (9.7)	0 (0)	<0.0001	<0.0001	0.0335	neu, mnc, dnc, tcl, nkc, bcl
GSE3982 DC VS NKCELL UP	195	19 (9.7)	19 (9.7)	0 (0)	<0.0001	<0.0001	0.0335	neu, dnc
GSE3982 DC VS TH2 UP	194	19 (9.8)	19 (9.8)	0 (0)	<0.0001	<0.0001	0.0335	
GSE17721 CTRL VS POLYIC 4H BMDM DN	196	19 (9.7)	19 (9.7)	0 (0)	<0.0001	<0.0001	0.0334	neu, mnc, dnc, tcl
GSE17721 LPS VS PAM3CSK4 2H BMDM UP	196	19 (9.7)	18 (9.2)	1 (0.5)	<0.0001	<0.0001	0.0334	neu, mnc, dnc
GSE360 DC VS MAC B MALAYI HIGH DOSE DN	196	19 (9.7)	19 (9.7)	0 (0)	<0.0001	<0.0001	0.0334	neu, mnc, dnc

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
GSE24142 EARLY THYMIC PROGENITOR VS DN3 THYMOCYTE UP	197	19 (9.6)	19 (9.6)	0 (0)	<0.0001	<0.0001	0.0333	
GSE3982 MAST CELL VS DC DN	198	19 (9.6)	19 (9.6)	0 (0)	<0.0001	<0.0001	0.0333	neu
GSE15930 STIM VS STIM AND TRICHOSTATINA 48H CD8 T CELL DN	199	19 (9.5)	19 (9.5)	0 (0)	<0.0001	<0.0001	0.0332	neu, mnc, dnc, tcl, nkc
GSE3982 DC VS TH1 UP	203	19 (9.4)	18 (8.9)	1 (0.5)	<0.0001	<0.0001	0.0330	
GSE12845 PRE GC VS DARKZONE GC TONSIL BCELL UP	185	18 (9.7)	18 (9.7)	0 (0)	<0.0001	<0.0001	0.0322	neu, mnc, dnc
GSE3982 DC VS EFF MEMORY CD4 TCELL UP	190	18 (9.5)	18 (9.5)	0 (0)	<0.0001	<0.0001	0.0319	neu
GSE3982 NEUTROPHIL VS BCELL UP	192	18 (9.4)	18 (9.4)	0 (0)	<0.0001	<0.0001	0.0318	neu, mnc
GSE13484 12H UNSTIM VS YF17D VACCINE STIM PBMC DN	193	18 (9.3)	18 (9.3)	0 (0)	<0.0001	<0.0001	0.0317	neu, mnc, dnc, tcl
GSE17721 PAM3CSK4 VS GADIQUIMOD 4H BMDM DN	194	18 (9.3)	18 (9.3)	0 (0)	<0.0001	<0.0001	0.0317	neu, mnc, dnc, tcl, nkc
GSE22886 DAY0 VS DAY1 MONOCYTE IN CULTURE UP	198	18 (9.1)	18 (9.1)	0 (0)	<0.0001	<0.0001	0.0315	neu
GSE3982 DC VS BCELL UP	207	18 (8.7)	17 (8.2)	1 (0.5)	<0.0001	<0.0001	0.0310	
GSE2706 R848 VS LPS 8H STIM DC DN	176	17 (9.7)	17 (9.7)	0 (0)	<0.0001	<0.0001	0.0309	neu, mnc, dnc
GSE3982 EOSINOPHIL VS EFF MEMORY CD4 TCELL UP	182	17 (9.3)	16 (8.8)	1 (0.5)	<0.0001	<0.0001	0.0305	neu, mnc
GSE2706 LPS VS R848 AND LPS 8H STIM DC UP	184	17 (9.2)	17 (9.2)	0 (0)	<0.0001	<0.0001	0.0304	neu, mnc, dnc, tcl, bcl
GSE360 CTRL VS M TUBERCULOSIS MAC DN	185	17 (9.2)	17 (9.2)	0 (0)	<0.0001	<0.0001	0.0304	neu, mnc
GSE15733 BM VS SPLEEN MEMORY CD4 TCELL UP	190	17 (8.9)	17 (8.9)	0 (0)	<0.0001	<0.0001	0.0301	
GSE34205 RSV VS FLU INF INFANT PBMC DN	189	17 (9)	17 (9)	0 (0)	<0.0001	<0.0001	0.0301	neu, mnc, dnc, tcl, nkc
GSE3982 MAC VS BCELL UP	190	17 (8.9)	16 (8.4)	1 (0.5)	<0.0001	<0.0001	0.0301	
GSE13484 UNSTIM VS 3H YF17D VACCINE STIM PBMC DN	192	17 (8.9)	17 (8.9)	0 (0)	<0.0001	<0.0001	0.0300	neu, mnc, dnc
GSE17721 LPS VS GARDIQUIMOD 2H BMDM UP	192	17 (8.9)	16 (8.3)	1 (0.5)	<0.0001	<0.0001	0.0300	neu, mnc
GSE360 LOW DOSE B MALAYI VS M TUBERCULOSIS MAC DN	191	17 (8.9)	17 (8.9)	0 (0)	<0.0001	<0.0001	0.0300	neu, mnc, dnc, tcl, bcl
GSE3982 EFF MEMORY CD4 TCELL VS NKCELL DN	192	17 (8.9)	17 (8.9)	0 (0)	<0.0001	<0.0001	0.0300	
GSE7460 CD8 TCELL VS CD4 TCELL ACT UP	192	17 (8.9)	17 (8.9)	0 (0)	<0.0001	<0.0001	0.0300	neu, mnc, dnc, tcl, bcl
GSE22886 NAIVE BCELL VS DC DN	196	17 (8.7)	17 (8.7)	0 (0)	<0.0001	<0.0001	0.0298	neu
GSE24142 EARLY THYMIC PROGENITOR VS DN2 THYMOCYTE ADULT UP	195	17 (8.7)	17 (8.7)	0 (0)	<0.0001	<0.0001	0.0298	dnc
GSE1460 DP VS CD4 THYMOCYTE DN	197	17 (8.6)	17 (8.6)	0 (0)	<0.0001	<0.0001	0.0297	neu, mnc, dnc, tcl, nkc, bcl
GSE29618 BCELL VS MDC DN	197	17 (8.6)	17 (8.6)	0 (0)	<0.0001	<0.0001	0.0297	
GSE14769 UNSTIM VS 240MIN LPS BMDM DN	199	17 (8.5)	17 (8.5)	0 (0)	<0.0001	<0.0001	0.0296	neu, mnc, dnc

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
GSE17721 12H VS 24H CPG BMDM UP	199	17 (8.5)	16 (8)	1 (0.5)	<0.0001	<0.0001	0.0296	neu, dnc
GSE22886 NAIVE CD4 TCELL VS DC DN	199	17 (8.5)	17 (8.5)	0 (0)	<0.0001	<0.0001	0.0296	neu
GSE6269 HEALTHY VS E COLI INF PBMC DN	164	16 (9.8)	16 (9.8)	0 (0)	<0.0001	<0.0001	0.0296	mnc
GSE360 L MAJOR VS M TUBERCULOSIS DC DN	180	16 (8.9)	16 (8.9)	0 (0)	<0.0001	<0.0001	0.0288	neu, mnc, dnc
GSE17974 IL4 AND ANTI IL12 VS UNTREATED 6H ACT CD4 TCELL DN	185	16 (8.6)	15 (8.1)	1 (0.5)	<0.0001	<0.0001	0.0285	neu, mnc, dnc, tcl, bcl
GSE9988 ANTI TREM1 VS CTRL TREATED MONOCYTES UP	187	16 (8.6)	15 (8)	1 (0.5)	<0.0001	<0.0001	0.0284	
GSE3982 EOSINOPHIL VS CENT MEMORY CD4 TCELL UP	189	16 (8.5)	16 (8.5)	0 (0)	<0.0001	<0.0001	0.0283	neu
GSE17721 PAM3CSK4 VS GADIQUIMOD 16H BMDM DN	191	16 (8.4)	16 (8.4)	0 (0)	<0.0001	<0.0001	0.0282	neu, mnc, dnc
GSE9988 ANTI TREM1 VS VEHICLE TREATED MONOCYTES DN	192	16 (8.3)	16 (8.3)	0 (0)	<0.0001	<0.0001	0.0282	
GSE36476 CTRL VS TSST ACT 16H MEMORY CD4 TCELL YOUNG DN	194	16 (8.2)	16 (8.2)	0 (0)	<0.0001	<0.0001	0.0281	neu, dnc
GSE17721 0.5H VS 24H CPG BMDM UP	195	16 (8.2)	16 (8.2)	0 (0)	<0.0001	<0.0001	0.0280	neu
GSE17721 0.5H VS 8H CPG BMDM DN	195	16 (8.2)	16 (8.2)	0 (0)	<0.0001	<0.0001	0.0280	neu, mnc, dnc
GSE17721 LPS VS POLYIC 8H BMDM DN	195	16 (8.2)	16 (8.2)	0 (0)	<0.0001	<0.0001	0.0280	neu, mnc, dnc
GSE24142 EARLY THYMIC PROGENITOR VS DN2 THYMOCYTE UP	196	16 (8.2)	16 (8.2)	0 (0)	<0.0001	<0.0001	0.0280	dnc
GSE360 L DONOVANI VS B MALAYI HIGH DOSE MAC DN	195	16 (8.2)	16 (8.2)	0 (0)	<0.0001	<0.0001	0.0280	neu, mnc, dnc, tcl
GSE22886 NEUTROPHIL VS DC UP	198	16 (8.1)	15 (7.6)	1 (0.5)	<0.0001	<0.0001	0.0279	neu, mnc
GSE16522 MEMORY VS NAIVE ANTI CD3CD28 STIM CD8 TCELL DN	200	16 (8)	16 (8)	0 (0)	<0.0001	<0.0001	0.0278	neu, mnc, dnc, tcl, bcl
GSE17721 0.5H VS 24H CPG BMDM DN	199	16 (8)	15 (7.5)	1 (0.5)	<0.0001	<0.0001	0.0278	neu, dnc
GSE3982 DC VS NEUTROPHIL DN	207	16 (7.7)	15 (7.2)	1 (0.5)	<0.0001	<0.0001	0.0274	neu, mnc, dnc
GSE11864 CSF1 VS CSF1 IFNG IN MAC DN	184	15 (8.2)	15 (8.2)	0 (0)	<0.0001	<0.0001	0.0267	neu, mnc, dnc
GSE3982 EOSINOPHIL VS BASOPHIL UP	184	15 (8.2)	15 (8.2)	0 (0)	<0.0001	<0.0001	0.0267	
GSE360 L DONOVANI VS B MALAYI LOW DOSE DC UP	187	15 (8)	15 (8)	0 (0)	<0.0001	<0.0001	0.0266	neu, mnc, dnc
GSE17721 POLYIC VS PAM3CSK4 1H BMDM DN	190	15 (7.9)	13 (6.8)	2 (1.1)	<0.0001	<0.0001	0.0265	
GSE36392 TYPE 2 MYELOID VS EOSINOPHIL IL25 TREATED LUNG DN	191	15 (7.9)	15 (7.9)	0 (0)	<0.0001	<0.0001	0.0264	neu, mnc, dnc
GSE17721 12H VS 24H GARDIQUIMOD BMDM UP	193	15 (7.8)	15 (7.8)	0 (0)	<0.0001	<0.0001	0.0263	neu, mnc, dnc
GSE20366 EX VIVO VS DEC205 CONVERSION NAIVE CD4 TCELL UP	194	15 (7.7)	15 (7.7)	0 (0)	<0.0001	<0.0001	0.0263	neu, mnc, dnc, bcl
GSE3337 CTRL VS 16H IFNG IN CD8POS DC DN	193	15 (7.8)	15 (7.8)	0 (0)	<0.0001	<0.0001	0.0263	neu, mnc, dnc, tcl, bcl
GSE3982 MAST CELL VS CENT MEMORY CD4 TCELL UP	194	15 (7.7)	14 (7.2)	1 (0.5)	<0.0001	<0.0001	0.0263	mnc
GSE7460 TREG VS TCONV ACT UP	194	15 (7.7)	15 (7.7)	0 (0)	<0.0001	<0.0001	0.0263	neu, mnc, dnc, tcl, bcl
GSE7852 TREG VS TCONV THYMUS UP	193	15 (7.8)	14 (7.3)	1 (0.5)	<0.0001	<0.0001	0.0263	neu, mnc, tcl

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
GSE2197 IMMUNOSUPPRESSIVE DNA VS UNTREATED IN DC UP	195	15 (7.7)	15 (7.7)	0 (0)	<0.0001	<0.0001	0.0262	neu, mnc, dnc, tcl
GSE360 DC VS MAC T GONDII DN	195	15 (7.7)	14 (7.2)	1 (0.5)	<0.0001	<0.0001	0.0262	mnc
GSE11864 CSF1 IFNG VS CSF1 PAM3CYS IN MAC UP	197	15 (7.6)	15 (7.6)	0 (0)	<0.0001	<0.0001	0.0261	neu, mnc, dnc, tcl, bcl
GSE17721 CTRL VS CPG 12H BMDM DN	198	15 (7.6)	15 (7.6)	0 (0)	<0.0001	<0.0001	0.0261	neu, mnc
GSE17721 LPS VS PAM3CSK4 8H BMDM UP	198	15 (7.6)	15 (7.6)	0 (0)	<0.0001	<0.0001	0.0261	dnc
GSE17721 PAM3CSK4 VS CPG 12H BMDM DN	197	15 (7.6)	15 (7.6)	0 (0)	<0.0001	<0.0001	0.0261	neu, mnc, dnc, bcl
GSE3982 MAC VS CENT MEMORY CD4 TCELL UP	198	15 (7.6)	15 (7.6)	0 (0)	<0.0001	<0.0001	0.0261	
GSE17721 0.5H VS 4H CPG BMDM DN	200	15 (7.5)	15 (7.5)	0 (0)	<0.0001	<0.0001	0.0260	neu, mnc, dnc
GSE17721 PAM3CSK4 VS GADIQUIMOD 12H BMDM DN	200	15 (7.5)	15 (7.5)	0 (0)	<0.0001	<0.0001	0.0260	neu, mnc, dnc, tcl
GSE7852 THYMUS VS FAT TREG DN	203	15 (7.4)	14 (6.9)	1 (0.5)	<0.0001	<0.0001	0.0259	neu, mnc
GSE10325 LUPUS CD4 TCELL VS LUPUS BCELL DN	181	14 (7.7)	14 (7.7)	0 (0)	<0.0001	<0.0001	0.0250	neu
GSE37416 12H VS 24H F TULARENSIS LVS NEUTROPHIL UP	187	14 (7.5)	14 (7.5)	0 (0)	<0.0001	<0.0001	0.0248	neu
GSE37416 CTRL VS 48H F TULARENSIS LVS NEUTROPHIL UP	189	14 (7.4)	14 (7.4)	0 (0)	<0.0001	<0.0001	0.0247	neu, mnc, dnc, tcl
GSE17580 UNINFECTED VS S MANSONI INF TEFF DN	190	14 (7.4)	14 (7.4)	0 (0)	<0.0001	<0.0001	0.0246	neu, mnc, tcl
GSE17721 0.5H VS 4H POLYIC BMDM DN	192	14 (7.3)	14 (7.3)	0 (0)	<0.0001	<0.0001	0.0246	neu, mnc, tcl
GSE17721 CTRL VS LPS 1H BMDM DN	191	14 (7.3)	14 (7.3)	0 (0)	<0.0001	<0.0001	0.0246	neu
GSE30962 ACUTE VS CHRONIC LCMV PRIMARY INF CD8 TCELL DN	190	14 (7.4)	14 (7.4)	0 (0)	<0.0001	<0.0001	0.0246	neu, mnc
GSE360 CTRL VS L DONOVANI DC DN	190	14 (7.4)	14 (7.4)	0 (0)	<0.0001	<0.0001	0.0246	neu, mnc
GSE37416 0H VS 48H F TULARENSIS LVS NEUTROPHIL UP	190	14 (7.4)	14 (7.4)	0 (0)	<0.0001	<0.0001	0.0246	neu, mnc
GSE9006 HEALTHY VS TYPE 2 DIABETES PBMC AT DX DN	190	14 (7.4)	13 (6.8)	1 (0.5)	<0.0001	<0.0001	0.0246	
GSE17721 CTRL VS PAM3CSK4 1H BMDM DN	193	14 (7.3)	13 (6.7)	1 (0.5)	<0.0001	<0.0001	0.0245	
GSE17721 CTRL VS POLYIC 6H BMDM DN	194	14 (7.2)	14 (7.2)	0 (0)	<0.0001	<0.0001	0.0245	neu, mnc, tcl, bcl
GSE17721 LPS VS POLYIC 1H BMDM UP	193	14 (7.3)	14 (7.3)	0 (0)	<0.0001	<0.0001	0.0245	neu, dnc
GSE30083 SP1 VS SP3 THYMOCYTE UP	194	14 (7.2)	14 (7.2)	0 (0)	<0.0001	<0.0001	0.0245	neu
GSE30083 SP3 VS SP4 THYMOCYTE DN	194	14 (7.2)	13 (6.7)	1 (0.5)	<0.0001	<0.0001	0.0245	neu, tcl
GSE30962 PRIMARY VS SECONDARY CHRONIC LCMV INF CD8 TCELL DN	193	14 (7.3)	12 (6.2)	2 (1)	<0.0001	<0.0001	0.0245	
GSE9988 ANTI TREM1 VS LPS MONOCYTE UP	193	14 (7.3)	13 (6.7)	1 (0.5)	<0.0001	<0.0001	0.0245	neu
GSE20366 TREG VS NAIVE CD4 TCELL DEC205 CONVERSION UP	196	14 (7.1)	14 (7.1)	0 (0)	<0.0001	<0.0001	0.0244	neu, mnc, dnc
GSE3982 MAST CELL VS BCELL UP	195	14 (7.2)	12 (6.2)	2 (1)	<0.0001	<0.0001	0.0244	mnc
GSE13484 UNSTIM VS 12H YF17D VACCINE STIM PBMC DN	199	14 (7)	14 (7)	0 (0)	<0.0001	<0.0001	0.0243	neu, mnc, dnc

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
GSE17721 12H VS 24H PAM3CSK4 BMDM UP	197	14 (7.1)	14 (7.1)	0 (0)	<0.0001	<0.0001	0.0243	tcl
GSE17721 CPG VS GARDIQUIMOD 12H BMDM DN	199	14 (7)	13 (6.5)	1 (0.5)	<0.0001	<0.0001	0.0243	
GSE17721 POLYIC VS GARDIQUIMOD 16H BMDM UP	198	14 (7.1)	14 (7.1)	0 (0)	<0.0001	<0.0001	0.0243	mnc
GSE9988 ANTI TREM1 AND LPS VS VEHICLE TREATED MONOCYTES DN	199	14 (7)	14 (7)	0 (0)	<0.0001	<0.0001	0.0243	
GSE17721 POLYIC VS CPG 1H BMDM DN	200	14 (7)	14 (7)	0 (0)	<0.0001	<0.0001	0.0242	
GSE30083 SP1 VS SP4 THYMOCYTE DN	201	14 (7)	14 (7)	0 (0)	<0.0001	<0.0001	0.0242	neu, mnc, dnc, tcl
GSE9037 CTRL VS LPS 4H STIM IRAK4 KO BMDM DN	200	14 (7)	14 (7)	0 (0)	<0.0001	<0.0001	0.0242	neu, mnc, dnc
GSE3982 MAST CELL VS MAC DN	204	14 (6.9)	14 (6.9)	0 (0)	<0.0001	<0.0001	0.0241	
GSE9988 ANTI TREM1 AND LPS VS CTRL TREATED MONOCYTES UP	181	13 (7.2)	12 (6.6)	1 (0.6)	<0.0001	<0.0001	0.0232	
GSE17721 CPG VS GARDIQUIMOD 2H BMDM DN	191	13 (6.8)	13 (6.8)	0 (0)	<0.0001	<0.0001	0.0228	
GSE30083 SP1 VS SP2 THYMOCYTE UP	192	13 (6.8)	13 (6.8)	0 (0)	<0.0001	<0.0001	0.0228	
GSE37416 0H VS 6H F TULARENSIS LVS NEUTROPHIL UP	191	13 (6.8)	12 (6.3)	1 (0.5)	<0.0001	<0.0001	0.0228	
GSE3982 BCELL VS NKCELL DN	190	13 (6.8)	12 (6.3)	1 (0.5)	<0.0001	<0.0001	0.0228	mnc
GSE3982 NEUTROPHIL VS BASOPHIL UP	191	13 (6.8)	13 (6.8)	0 (0)	<0.0001	<0.0001	0.0228	neu, mnc
GSE9988 LOW LPS VS ANTI TREM1 AND LPS MONOCYTE DN	190	13 (6.8)	12 (6.3)	1 (0.5)	<0.0001	<0.0001	0.0228	
GSE1448 CTRL VS ANTI VBETA5 DP THYMOCYTE DN	194	13 (6.7)	13 (6.7)	0 (0)	<0.0001	<0.0001	0.0227	neu, mnc, dnc, tcl, bcl
GSE17721 LPS VS GARDIQUIMOD 24H BMDM DN	194	13 (6.7)	12 (6.2)	1 (0.5)	<0.0001	<0.0001	0.0227	
GSE17721 PAM3CSK4 VS CPG 2H BMDM DN	193	13 (6.7)	13 (6.7)	0 (0)	<0.0001	<0.0001	0.0227	neu
GSE3982 MAST CELL VS TH1 UP	193	13 (6.7)	12 (6.2)	1 (0.5)	<0.0001	<0.0001	0.0227	
GSE9988 ANTI TREM1 VS LOW LPS MONOCYTE UP	194	13 (6.7)	13 (6.7)	0 (0)	<0.0001	<0.0001	0.0227	
GSE17721 CPG VS GARDIQUIMOD 4H BMDM UP	197	13 (6.6)	12 (6.1)	1 (0.5)	<0.0001	<0.0001	0.0226	neu, dnc
GSE17721 CTRL VS GARDIQUIMOD 4H BMDM DN	197	13 (6.6)	13 (6.6)	0 (0)	<0.0001	<0.0001	0.0226	mnc, dnc
GSE2826 XID VS BTK KO BCELL DN	195	13 (6.7)	13 (6.7)	0 (0)	<0.0001	<0.0001	0.0226	neu, mnc, dnc
GSE39820 IL1B IL6 VS IL1B IL6 IL23A TREATED CD4 TCELL UP	196	13 (6.6)	13 (6.6)	0 (0)	<0.0001	<0.0001	0.0226	neu, mnc, tcl, nkc
GSE3982 MAST CELL VS NEUTROPHIL DN	197	13 (6.6)	13 (6.6)	0 (0)	<0.0001	<0.0001	0.0226	neu, mnc, dnc
GSE7764 IL15 TREATED VS CTRL NK CELL 24H DN	196	13 (6.6)	12 (6.1)	1 (0.5)	<0.0001	<0.0001	0.0226	neu
GSE17721 0.5H VS 12H CPG BMDM DN	199	13 (6.5)	12 (6)	1 (0.5)	<0.0001	<0.0001	0.0225	neu
GSE17721 POLYIC VS GARDIQUIMOD 2H BMDM DN	198	13 (6.6)	12 (6.1)	1 (0.5)	<0.0001	<0.0001	0.0225	
GSE26669 CTRL VS COSTIM BLOCK MLR CD8 TCELL UP	199	13 (6.5)	13 (6.5)	0 (0)	<0.0001	<0.0001	0.0225	neu, mnc, tcl
GSE17974 CTRL VS ACT IL4 AND ANTI IL12 0.5H CD4 TCELL UP	171	12 (7)	12 (7)	0 (0)	<0.0001	<0.0001	0.0218	
GSE360 DC VS MAC DN	184	12 (6.5)	12 (6.5)	0 (0)	<0.0001	<0.0001	0.0213	neu
GSE3982 BCELL VS CENT MEMORY CD4 TCELL UP	188	12 (6.4)	11 (5.9)	1 (0.5)	<0.0001	<0.0001	0.0211	neu, mnc
GOLDRATH NAIVE VS EFF CD8 TCELL DN	192	12 (6.2)	12 (6.2)	0 (0)	<0.0001	<0.0001	0.0210	neu

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
GSE27786 LIN NEG VS ERYTHROBLAST UP	195	12 (6.2)	12 (6.2)	0 (0)	<0.0001	<0.0001	0.0209	mnc, dnc, nkc
GSE36392 EOSINOPHIL VS NEUTROPHIL IL25 TREATED LUNG UP	193	14 (7.3)	13 (6.7)	1 (0.5)	<0.0001	0.0001	0.0245	mnc
GSE3982 DC VS NEUTROPHIL LPS STIM DN	188	13 (6.9)	13 (6.9)	0 (0)	<0.0001	0.0001	0.0229	
GSE20715 0H VS 6H OZONE LUNG DN	192	13 (6.8)	12 (6.2)	1 (0.5)	<0.0001	0.0001	0.0228	neu
GSE25087 FETAL VS ADULT TREG UP	190	13 (6.8)	13 (6.8)	0 (0)	<0.0001	0.0001	0.0228	neu, mnc, nkc
GSE37416 12H VS 48H F TULARENSIS LVS NEUTROPHIL UP	192	13 (6.8)	13 (6.8)	0 (0)	<0.0001	0.0001	0.0228	
GSE7460 FOXP3 MUT VS WT ACT TCONV UP	191	13 (6.8)	13 (6.8)	0 (0)	<0.0001	0.0001	0.0228	neu, mnc
GSE8868 SPLEEN VS INTESTINE CD11B POS CD11C NEG DC DN	191	13 (6.8)	13 (6.8)	0 (0)	<0.0001	0.0001	0.0228	neu
GSE13306 RA VS UNTREATED MEM CD4 TCELL UP	194	13 (6.7)	13 (6.7)	0 (0)	<0.0001	0.0001	0.0227	neu, mnc, dnc
GSE17721 LPS VS CPG 16H BMDM UP	194	13 (6.7)	13 (6.7)	0 (0)	<0.0001	0.0001	0.0227	neu, mnc, dnc
GSE17721 LPS VS POLYIC 24H BMDM DN	194	13 (6.7)	12 (6.2)	1 (0.5)	<0.0001	0.0001	0.0227	neu
GSE360 L MAJOR VS B MALAYI HIGH DOSE MAC UP	193	13 (6.7)	13 (6.7)	0 (0)	<0.0001	0.0001	0.0227	
GSE17721 CTRL VS POLYIC 2H BMDM DN	200	13 (6.5)	11 (5.5)	2 (1)	<0.0001	0.0001	0.0225	
GSE17721 LPS VS POLYIC 12H BMDM DN	199	13 (6.5)	11 (5.5)	2 (1)	<0.0001	0.0001	0.0225	neu, mnc, dnc
GSE20715 0H VS 24H OZONE LUNG DN	199	13 (6.5)	13 (6.5)	0 (0)	<0.0001	0.0001	0.0225	neu
GSE37416 0H VS 12H F TULARENSIS LVS NEUTROPHIL UP	205	13 (6.3)	13 (6.3)	0 (0)	<0.0001	0.0001	0.0223	neu
GSE18791 CTRL VS NEWCASTLE VIRUS DC 2H DN	178	12 (6.7)	12 (6.7)	0 (0)	<0.0001	0.0001	0.0215	neu, mnc, dnc
GSE2706 R848 VS R848 AND LPS 8H STIM DC DN	183	12 (6.6)	10 (5.5)	2 (1.1)	<0.0001	0.0001	0.0213	dnc
GSE7460 WT VS FOXP3 HET ACT WITH TGFB TCONV DN	184	12 (6.5)	12 (6.5)	0 (0)	<0.0001	0.0001	0.0213	mnc
GSE11864 CSF1 VS CSF1 PAM3CYS IN MAC DN	187	12 (6.4)	12 (6.4)	0 (0)	<0.0001	0.0001	0.0212	neu
GSE24634 TEFF VS TCONV DAY5 IN CULTURE DN	185	12 (6.5)	12 (6.5)	0 (0)	<0.0001	0.0001	0.0212	neu, mnc, dnc, tcl, nkc
GSE360 DC VS MAC L DONOVANI DN	188	12 (6.4)	12 (6.4)	0 (0)	<0.0001	0.0001	0.0211	neu
GSE3982 BCELL VS TH1 DN	188	12 (6.4)	10 (5.3)	2 (1.1)	<0.0001	0.0001	0.0211	neu, mnc
GOLDRATH EFF VS MEMORY CD8 TCELL UP	192	12 (6.2)	12 (6.2)	0 (0)	<0.0001	0.0001	0.0210	
KAECH DAY15 EFF VS MEMORY CD8 TCELL UP	195	12 (6.2)	12 (6.2)	0 (0)	<0.0001	0.0001	0.0209	neu, mnc
GSE17721 LPS VS PAM3CSK4 16H BMDM UP	198	12 (6.1)	12 (6.1)	0 (0)	<0.0001	0.0001	0.0208	mnc, dnc
GSE17721 LPS VS CPG 24H BMDM UP	200	12 (6)	12 (6)	0 (0)	<0.0001	0.0001	0.0207	neu, mnc, dnc, tcl, bcl
GSE17721 PAM3CSK4 VS GADIQUIMOD 24H BMDM DN	199	12 (6)	12 (6)	0 (0)	<0.0001	0.0001	0.0207	neu, mnc, dnc
GSE6566 STRONG VS WEAK DC STIMULATED CD4 TCELL UP	177	11 (6.2)	11 (6.2)	0 (0)	<0.0001	0.0001	0.0197	neu, mnc, dnc
GSE9988 ANTI TREM1 AND LPS VS VEHICLE TREATED MONOCYTES UP	181	11 (6.1)	10 (5.5)	1 (0.6)	<0.0001	0.0001	0.0196	
GSE17721 PAM3CSK4 VS GADIQUIMOD 1H BMDM UP	190	13 (6.8)	11 (5.8)	2 (1.1)	<0.0001	0.0002	0.0228	
GSE3982 MAC VS TH1 UP	193	13 (6.7)	12 (6.2)	1 (0.5)	<0.0001	0.0002	0.0227	
GSE17721 0.5H VS 12H POLYIC BMDM DN	196	13 (6.6)	13 (6.6)	0 (0)	<0.0001	0.0002	0.0226	tcl, bcl
GSE17721 LPS VS CPG 12H BMDM UP	197	13 (6.6)	13 (6.6)	0 (0)	<0.0001	0.0002	0.0226	neu, mnc, dnc

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
GSE17721 LPS VS CPG 4H BMDM UP	197	13 (6.6)	13 (6.6)	0 (0)	<0.0001	0.0002	0.0226	neu, tcl, bcl
GSE17721 CTRL VS GARDIQUIMOD 12H BMDM DN	199	13 (6.5)	12 (6)	1 (0.5)	<0.0001	0.0002	0.0225	neu
GSE3982 MAC VS NEUTROPHIL DN	186	12 (6.5)	12 (6.5)	0 (0)	<0.0001	0.0002	0.0212	mnc
GSE11864 CSF1 VS CSF1 IFNG PAM3CYS IN MAC DN	188	12 (6.4)	11 (5.9)	1 (0.5)	<0.0001	0.0002	0.0211	neu, nkc
GSE17974 0H VS 0.5H IN VITRO ACT CD4 TCELL UP	189	12 (6.3)	12 (6.3)	0 (0)	<0.0001	0.0002	0.0211	neu, mnc
GSE360 L DONOVANI VS L MAJOR DC DN	191	12 (6.3)	11 (5.8)	1 (0.5)	<0.0001	0.0002	0.0210	neu
GSE3982 CENT MEMORY CD4 TCELL VS NKCELL DN	191	12 (6.3)	12 (6.3)	0 (0)	<0.0001	0.0002	0.0210	
GOLDRATH NAIVE VS MEMORY CD8 TCELL DN	193	12 (6.2)	12 (6.2)	0 (0)	<0.0001	0.0002	0.0209	
GSE17721 LPS VS POLYIC 2H BMDM UP	194	12 (6.2)	12 (6.2)	0 (0)	<0.0001	0.0002	0.0209	mnc
GSE360 T GONDII VS B MALAYI HIGH DOSE MAC DN	194	12 (6.2)	12 (6.2)	0 (0)	<0.0001	0.0002	0.0209	neu, mnc, dnc
GSE36476 CTRL VS TSST ACT 16H MEMORY CD4 TCELL OLD DN	196	12 (6.1)	12 (6.1)	0 (0)	<0.0001	0.0002	0.0208	neu, dnc
GSE7460 CTRL VS TGFB TREATED ACT TCONV DN	197	12 (6.1)	12 (6.1)	0 (0)	<0.0001	0.0002	0.0208	neu, mnc
GSE9988 LPS VS LPS AND ANTI TREM1 MONOCYTE DN	184	12 (6.5)	11 (6)	1 (0.5)	<0.0001	0.0002	0.0213	
GSE12366 GC BCELL VS PLASMA CELL DN	185	12 (6.5)	10 (5.4)	2 (1.1)	<0.0001	0.0002	0.0212	
GSE12366 GC VS NAIVE BCELL DN	190	12 (6.3)	11 (5.8)	1 (0.5)	<0.0001	0.0002	0.0211	neu, mnc, dnc, tcl
GSE24142 ADULT VS FETAL DN3 THYMOCYTE UP	189	12 (6.3)	12 (6.3)	0 (0)	<0.0001	0.0002	0.0211	neu, mnc, tcl
GSE17721 POLYIC VS PAM3CSK4 4H BMDM UP	193	12 (6.2)	12 (6.2)	0 (0)	<0.0001	0.0002	0.0209	neu
GSE20715 0H VS 48H OZONE LUNG UP	193	12 (6.2)	12 (6.2)	0 (0)	<0.0001	0.0002	0.0209	
GSE24142 ADULT VS FETAL EARLY THYMIC PROGENITOR UP	193	12 (6.2)	10 (5.2)	2 (1)	<0.0001	0.0002	0.0209	
GSE24142 DN2 VS DN3 THYMOCYTE FETAL UP	195	12 (6.2)	12 (6.2)	0 (0)	<0.0001	0.0002	0.0209	
GSE29618 BCELL VS PDC DAY7 FLU VACCINE DN	194	12 (6.2)	12 (6.2)	0 (0)	<0.0001	0.0002	0.0209	neu, mnc
GSE3982 MAST CELL VS TH2 UP	193	12 (6.2)	11 (5.7)	1 (0.5)	<0.0001	0.0002	0.0209	
GSE7460 TCONV VS TREG THYMUS DN	195	12 (6.2)	12 (6.2)	0 (0)	<0.0001	0.0002	0.0209	neu, mnc, dnc, tcl
GSE17721 LPS VS CPG 24H BMDM DN	197	12 (6.1)	11 (5.6)	1 (0.5)	<0.0001	0.0002	0.0208	
GSE24102 GRANULOCYSTIC MDSC VS NEUTROPHIL DN	196	12 (6.1)	11 (5.6)	1 (0.5)	<0.0001	0.0002	0.0208	
GSE24142 DN2 VS DN3 THYMOCYTE UP	197	12 (6.1)	12 (6.1)	0 (0)	<0.0001	0.0002	0.0208	neu
GSE24142 EARLY THYMIC PROGENITOR VS DN3 THYMOCYTE ADULT UP	197	12 (6.1)	11 (5.6)	1 (0.5)	<0.0001	0.0002	0.0208	
GSE17721 CTRL VS GARDIQUIMOD 8H BMDM DN	199	12 (6)	11 (5.5)	1 (0.5)	<0.0001	0.0002	0.0207	neu
GSE17721 CTRL VS PAM3CSK4 12H BMDM DN	201	12 (6)	12 (6)	0 (0)	<0.0001	0.0002	0.0207	neu
GSE7852 LN VS FAT TREG DN	201	12 (6)	12 (6)	0 (0)	<0.0001	0.0002	0.0207	neu
GSE15930 STIM VS STIM AND TRICHOSTATINA 72H CD8 T CELL DN	202	12 (5.9)	10 (5)	2 (1)	<0.0001	0.0002	0.0206	neu, mnc
GSE17721 POLYIC VS CPG 2H BMDM DN	202	12 (5.9)	11 (5.4)	1 (0.5)	<0.0001	0.0002	0.0206	
GSE17721 CTRL VS CPG 2H BMDM DN	196	12 (6.1)	10 (5.1)	2 (1)	<0.0001	0.0003	0.0208	
GSE17721 LPS VS PAM3CSK4 12H BMDM UP	196	12 (6.1)	12 (6.1)	0 (0)	<0.0001	0.0003	0.0208	neu, mnc, dnc

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
GSE1460 CD4 THYMOCYTE VS NAIVE CD4 TCELL ADULT BLOOD UP	200	12 (6)	11 (5.5)	1 (0.5)	<0.0001	0.0003	0.0207	tcl
GSE24142 DN2 VS DN3 THYMOCYTE ADULT UP	199	12 (6)	12 (6)	0 (0)	<0.0001	0.0003	0.0207	neu, mnc, tcl
GSE9006 TYPE 1 DIABETES AT DX VS 1MONTH POST DX PBMC UP	191	11 (5.8)	11 (5.8)	0 (0)	<0.0001	0.0003	0.0192	
GSE36392 TYPE 2 MYELOID VS NEUTROPHIL IL25 TREATED LUNG UP	194	12 (6.2)	12 (6.2)	0 (0)	<0.0001	0.0003	0.0209	mnc
GSE17721 CTRL VS CPG 4H BMDM DN	197	12 (6.1)	11 (5.6)	1 (0.5)	<0.0001	0.0003	0.0208	neu, mnc
GSE7460 CD8 TCELL VS TREG ACT UP	197	12 (6.1)	11 (5.6)	1 (0.5)	<0.0001	0.0003	0.0208	
GSE17721 0.5H VS 12H LPS BMDM DN	194	11 (5.7)	11 (5.7)	0 (0)	<0.0001	0.0003	0.0191	neu, mnc
GSE27786 NKCELL VS NKTCELL UP	198	12 (6.1)	11 (5.6)	1 (0.5)	<0.0001	0.0004	0.0208	neu
GSE13484 12H VS 3H YF17D VACCINE STIM PBMC UP	196	11 (5.6)	11 (5.6)	0 (0)	<0.0001	0.0004	0.0191	
GSE3337 CTRL VS 16H IFNG IN CD8POS DC UP	198	12 (6.1)	11 (5.6)	1 (0.5)	<0.0001	0.0004	0.0208	
GSE2706 2H VS 8H R848 STIM DC UP	189	11 (5.8)	11 (5.8)	0 (0)	<0.0001	0.0004	0.0193	neu
GSE17721 LPS VS CPG 2H BMDM UP	191	11 (5.8)	9 (4.7)	2 (1)	<0.0001	0.0004	0.0192	neu
GSE9037 WT VS IRAK4 KO BMDM DN	196	11 (5.6)	10 (5.1)	1 (0.5)	<0.0001	0.0004	0.0191	dnc
GSE17721 0.5H VS 24H LPS BMDM DN	197	11 (5.6)	8 (4.1)	3 (1.5)	<0.0001	0.0004	0.0190	
GSE3982 MAC VS TH2 UP	187	11 (5.9)	10 (5.3)	1 (0.5)	<0.0001	0.0005	0.0194	
GSE8515 CTRL VS IL1 4H STIM MAC DN	185	11 (5.9)	11 (5.9)	0 (0)	<0.0001	0.0005	0.0194	
GSE8384 CTRL VS B ABORTUS 4H MAC CELL LINE DN	190	11 (5.8)	10 (5.3)	1 (0.5)	<0.0001	0.0005	0.0193	
GSE37416 0H VS 24H F TULARENSIS LVS NEUTROPHIL UP	191	11 (5.8)	11 (5.8)	0 (0)	<0.0001	0.0005	0.0192	
GSE9988 ANTI TREM1 VS VEHICLE TREATED MONOCYTES UP	180	11 (6.1)	11 (6.1)	0 (0)	<0.0001	0.0005	0.0196	
GSE17721 LPS VS CPG 8H BMDM DN	187	11 (5.9)	11 (5.9)	0 (0)	<0.0001	0.0005	0.0194	
GSE360 L DONOVANI VS B MALAYI HIGH DOSE DC DN	187	11 (5.9)	10 (5.3)	1 (0.5)	<0.0001	0.0005	0.0194	
GSE20366 CD103 POS VS CD103 KLRG1 DP TREG DN	190	11 (5.8)	10 (5.3)	1 (0.5)	<0.0001	0.0005	0.0193	
GSE22886 NAIVE VS IGM MEMORY BCELL DN	193	11 (5.7)	11 (5.7)	0 (0)	<0.0001	0.0005	0.0192	neu, mnc, dnc
GSE27786 CD4 TCELL VS NKCELL DN	192	11 (5.7)	10 (5.2)	1 (0.5)	<0.0001	0.0005	0.0192	neu
KAECH NAIVE VS MEMORY CD8 TCELL DN	195	11 (5.6)	11 (5.6)	0 (0)	<0.0001	0.0005	0.0191	dnc
GSE3982 MEMORY CD4 TCELL VS TH1 DN	199	11 (5.5)	10 (5)	1 (0.5)	<0.0001	0.0005	0.0190	neu, mnc
GSE36392 EOSINOPHIL VS MAC IL25 TREATED LUNG UP	190	11 (5.8)	11 (5.8)	0 (0)	0.0001	0.0006	0.0193	
GSE9037 CTRL VS LPS 1H STIM IRAK4 KO BMDM DN	189	11 (5.8)	11 (5.8)	0 (0)	0.0001	0.0006	0.0193	neu, mnc, dnc, nkc
GSE17721 PAM3CSK4 VS CPG 16H BMDM DN	191	11 (5.8)	11 (5.8)	0 (0)	0.0001	0.0006	0.0192	neu, tcl, bcl
GSE17721 LPS VS PAM3CSK4 4H BMDM UP	194	11 (5.7)	11 (5.7)	0 (0)	0.0001	0.0006	0.0191	neu
GSE27786 CD4 VS CD8 TCELL UP	194	11 (5.7)	11 (5.7)	0 (0)	0.0001	0.0006	0.0191	neu
GSE3982 MAC VS BASOPHIL UP	194	11 (5.7)	11 (5.7)	0 (0)	0.0001	0.0006	0.0191	
GSE17721 CTRL VS CPG 6H BMDM DN	197	11 (5.6)	10 (5.1)	1 (0.5)	0.0001	0.0006	0.0190	neu
GSE17974 CTRL VS ACT IL4 AND ANTI IL12 1H CD4 TCELL UP	185	11 (5.9)	11 (5.9)	0 (0)	0.0001	0.0006	0.0194	tcl
GSE360 L MAJOR VS B MALAYI LOW DOSE DC UP	190	11 (5.8)	11 (5.8)	0 (0)	0.0001	0.0006	0.0193	neu, mnc, dnc

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
GSE15930 NAIVE VS 24H IN VITRO STIM CD8 TCELL UP	192	11 (5.7)	10 (5.2)	1 (0.5)	0.0001	0.0006	0.0192	
GSE24142 EARLY THYMIC PROGENITOR VS DN3 THYMOCYTE FETAL UP	192	11 (5.7)	11 (5.7)	0 (0)	0.0001	0.0006	0.0192	neu
GSE17721 POLYIC VS CPG 24H BMDM UP	196	11 (5.6)	10 (5.1)	1 (0.5)	0.0001	0.0006	0.0191	neu, dnc
GSE32423 CTRL VS IL4 MEMORY CD8 TCELL DN	194	11 (5.7)	11 (5.7)	0 (0)	0.0001	0.0006	0.0191	neu, dnc, tcl
GSE17974 CTRL VS ACT IL4 AND ANTI IL12 2H CD4 TCELL DN	190	11 (5.8)	10 (5.3)	1 (0.5)	0.0001	0.0006	0.0193	neu
GSE17721 12H VS 24H POLYIC BMDM UP	193	11 (5.7)	11 (5.7)	0 (0)	0.0001	0.0006	0.0192	neu
GSE17721 CTRL VS POLYIC 1H BMDM UP	193	11 (5.7)	10 (5.2)	1 (0.5)	0.0001	0.0006	0.0192	
GSE8515 IL1 VS IL6 4H STIM)MAC UP	187	11 (5.9)	11 (5.9)	0 (0)	0.0001	0.0007	0.0194	neu
GSE20715 0H VS 24H OZONE LUNG UP	193	11 (5.7)	11 (5.7)	0 (0)	0.0001	0.0007	0.0192	
GSE24142 ADULT VS FETAL DN2 THYMOCYTE UP	192	11 (5.7)	11 (5.7)	0 (0)	0.0001	0.0007	0.0192	neu, mnc, dnc, tcl
GSE17721 CTRL VS LPS 2H BMDM DN	195	11 (5.6)	11 (5.6)	0 (0)	0.0001	0.0007	0.0191	neu, mnc
GSE36476 YOUNG VS OLD DONOR MEMORY CD4 TCELL 72H TSST ACT DN	196	11 (5.6)	11 (5.6)	0 (0)	0.0001	0.0007	0.0191	neu
GSE9650 NAIVE VS MEMORY CD8 TCELL DN	194	11 (5.7)	11 (5.7)	0 (0)	0.0001	0.0007	0.0191	dnc
GSE30083 SP2 VS SP3 THYMOCYTE DN	197	11 (5.6)	11 (5.6)	0 (0)	0.0001	0.0007	0.0190	neu
GSE1432 6H VS 24H IFNG MICROGLIA UP	192	11 (5.7)	11 (5.7)	0 (0)	0.0001	0.0007	0.0192	
GSE20715 0H VS 24H OZONE TLR4 KO LUNG UP	195	11 (5.6)	11 (5.6)	0 (0)	0.0001	0.0007	0.0191	neu
GSE17721 LPS VS POLYIC 16H BMDM DN	197	11 (5.6)	10 (5.1)	1 (0.5)	0.0001	0.0007	0.0190	neu, mnc
GSE26669 CTRL VS COSTIM BLOCK MLR CD4 TCELL UP	199	11 (5.5)	11 (5.5)	0 (0)	0.0001	0.0007	0.0190	neu, mnc, dnc
GSE3982 BCELL VS BASOPHIL DN	202	11 (5.4)	11 (5.4)	0 (0)	0.0001	0.0007	0.0189	
GSE3982 EOSINOPHIL VS BCELL UP	210	11 (5.2)	10 (4.8)	1 (0.5)	0.0001	0.0007	0.0186	
GSE17721 LPS VS GARDIQUIMOD 4H BMDM UP	190	11 (5.8)	11 (5.8)	0 (0)	0.0002	0.0008	0.0193	neu
GSE3982 EOSINOPHIL VS DC DN	204	11 (5.4)	11 (5.4)	0 (0)	0.0002	0.0008	0.0188	
GSE17721 CTRL VS LPS 12H BMDM DN	204	11 (5.4)	11 (5.4)	0 (0)	0.0002	0.0008	0.0188	neu, mnc
GSE17974 IL4 AND ANTI IL12 VS UNTREATED 12H ACT CD4 TCELL DN	176	10 (5.7)	10 (5.7)	0 (0)	0.0002	0.0008	0.0179	neu, mnc, tcl, bcl
GSE13411 IGM VS SWITCHED MEMORY BCELL DN	193	11 (5.7)	11 (5.7)	0 (0)	0.0002	0.0009	0.0192	
GSE36392 MAC VS NEUTROPHIL IL25 TREATED LUNG DN	194	11 (5.7)	11 (5.7)	0 (0)	0.0002	0.0009	0.0191	neu, dnc
GSE7460 CTRL VS TGFB TREATED ACT FOXP3 MUT TCONV DN	198	11 (5.6)	11 (5.6)	0 (0)	0.0002	0.0009	0.0190	mnc
GSE3982 BASOPHIL VS TH1 UP	215	11 (5.1)	11 (5.1)	0 (0)	0.0002	0.0009	0.0185	
GSE12845 IGD NEG BLOOD VS DARKZONE GC TONSIL BCELL UP	175	10 (5.7)	10 (5.7)	0 (0)	0.0002	0.001	0.0180	mnc
GSE20366 TREG VS NAIVE CD4 TCELL HOMEOSTATIC CONVERSION DN	194	11 (5.7)	11 (5.7)	0 (0)	0.0002	0.0011	0.0191	neu
GSE7460 TCONV VS TREG THYMUS UP	191	11 (5.8)	11 (5.8)	0 (0)	0.0002	0.0011	0.0192	
GSE17721 12H VS 24H LPS BMDM UP	196	11 (5.6)	11 (5.6)	0 (0)	0.0002	0.0012	0.0191	neu, mnc

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Ad-justed P-Value	Jaccard Index	Cell Type Over-lap
GSE9988 ANTI TREM1 VS CTRL TREATED MONOCYTES DN	194	11 (5.7)	11 (5.7)	0 (0)	0.0003	0.0012	0.0191	
GSE17974 0H VS 0.5H IN VITRO ACT CD4 TCELL DN	182	10 (5.5)	9 (4.9)	1 (0.5)	0.0003	0.0013	0.0177	
GSE3982 MEMORY CD4 TCELL VS BCELL DN	184	10 (5.4)	10 (5.4)	0 (0)	0.0003	0.0013	0.0177	neu, dnc, tcl
GSE9037 CTRL VS LPS 1H STIM BMDM DN	190	10 (5.3)	10 (5.3)	0 (0)	0.0003	0.0013	0.0175	neu
GSE360 L MAJOR VS T GONDII MAC UP	190	10 (5.3)	10 (5.3)	0 (0)	0.0003	0.0014	0.0175	
GSE1448 CTRL VS ANTI VALPHA2 DP THYMOCYTE DN	191	10 (5.2)	9 (4.7)	1 (0.5)	0.0003	0.0015	0.0175	neu, mnc, dnc
GSE10325 CD4 TCELL VS BCELL DN	179	10 (5.6)	10 (5.6)	0 (0)	0.0003	0.0016	0.0178	neu, mnc, dnc
GSE22886 NAIVE BCELL VS BM PLASMA CELL DN	193	10 (5.2)	10 (5.2)	0 (0)	0.0004	0.0016	0.0174	mnc
GSE36392 TYPE 2 MYELOID VS NEUTROPHIL IL25 TREATED LUNG DN	195	10 (5.1)	10 (5.1)	0 (0)	0.0004	0.0017	0.0173	
GSE20151 CTRL VS FUSOBACT NUCLEATUM NEUTROPHIL UP	190	10 (5.3)	9 (4.7)	1 (0.5)	0.0004	0.0018	0.0175	neu, mnc, nkc
GSE22886 NAIVE VS IGG IGA MEMORY BCELL DN	193	10 (5.2)	10 (5.2)	0 (0)	0.0004	0.0018	0.0174	neu, dnc
GSE20715 0H VS 48H OZONE TLR4 KO LUNG DN	197	10 (5.1)	9 (4.6)	1 (0.5)	0.0004	0.0018	0.0173	
GSE3982 DC VS MAC DN	187	10 (5.3)	10 (5.3)	0 (0)	0.0004	0.0019	0.0176	neu
GSE7764 NKCELL VS SPLENOCYTE DN	195	10 (5.1)	10 (5.1)	0 (0)	0.0004	0.0019	0.0173	neu, mnc
GSE360 L DONOVANI VS B MALAYI LOW DOSE DC DN	191	10 (5.2)	10 (5.2)	0 (0)	0.0004	0.0019	0.0175	neu
GSE29617 CTRL VS TIV FLU VACCINE PBMC 2008 UP	179	10 (5.6)	10 (5.6)	0 (0)	0.0004	0.0019	0.0178	
GSE17974 0H VS 2H IN VITRO ACT CD4 TCELL DN	194	10 (5.2)	8 (4.1)	2 (1)	0.0004	0.0019	0.0174	
GSE17721 0.5H VS 4H PAM3CSK4 BMDM UP	196	10 (5.1)	10 (5.1)	0 (0)	0.0004	0.002	0.0173	
GSE11057 NAIVE VS EFF MEMORY CD4 TCELL DN	194	10 (5.2)	10 (5.2)	0 (0)	0.0005	0.002	0.0174	neu
GSE13738 TCR VS BYSTANDER ACTIVATED CD4 TCELL DN	186	10 (5.4)	9 (4.8)	1 (0.5)	0.0005	0.0021	0.0176	neu
GSE7460 FOXP3 MUT VS HET ACT TCONV UP	195	10 (5.1)	9 (4.6)	1 (0.5)	0.0005	0.0021	0.0173	neu
KAECH NAIVE VS DAY15 EFF CD8 TCELL DN	195	10 (5.1)	10 (5.1)	0 (0)	0.0005	0.0021	0.0173	neu
GSE25087 FETAL VS ADULT TCONV UP	199	10 (5)	10 (5)	0 (0)	0.0005	0.0021	0.0172	neu, tcl
GSE22886 NAIVE CD4 TCELL VS 48H ACT TH2 UP	191	10 (5.2)	9 (4.7)	1 (0.5)	0.0005	0.0022	0.0175	
GSE17974 CTRL VS ACT IL4 AND ANTI IL12 72H CD4 TCELL UP	187	10 (5.3)	10 (5.3)	0 (0)	0.0005	0.0022	0.0176	mnc, dnc
GSE17721 LPS VS GARDIQUIMOD 24H BMDM UP	198	10 (5.1)	10 (5.1)	0 (0)	0.0005	0.0022	0.0172	neu, dnc
GSE17721 LPS VS CPG 6H BMDM UP	189	10 (5.3)	10 (5.3)	0 (0)	0.0005	0.0023	0.0175	neu, dnc
GSE17721 POLYIC VS GARDIQUIMOD 2H BMDM UP	192	10 (5.2)	9 (4.7)	1 (0.5)	0.0005	0.0023	0.0174	neu
GSE13484 12H VS 3H YF17D VACCINE STIM PBMC DN	196	10 (5.1)	10 (5.1)	0 (0)	0.0005	0.0023	0.0173	neu, tcl, nkc
GSE17721 0.5H VS 8H POLYIC BMDM UP	197	10 (5.1)	9 (4.6)	1 (0.5)	0.0005	0.0023	0.0173	
GSE17721 PAM3CSK4 VS GADIQUIMOD 8H BMDM DN	191	10 (5.2)	10 (5.2)	0 (0)	0.0005	0.0024	0.0175	neu
GSE3982 MAC VS NKCELL UP	191	10 (5.2)	10 (5.2)	0 (0)	0.0005	0.0024	0.0175	
GSE7852 LN VS THYMUS TCONV UP	190	10 (5.3)	10 (5.3)	0 (0)	0.0006	0.0024	0.0175	neu, mnc, tcl
GSE17974 0H VS 72H IN VITRO ACT CD4 TCELL UP	193	10 (5.2)	10 (5.2)	0 (0)	0.0006	0.0024	0.0174	
GSE17721 POLYIC VS CPG 12H BMDM UP	195	10 (5.1)	9 (4.6)	1 (0.5)	0.0006	0.0024	0.0173	
GSE7460 TREG VS TCONV ACT WITH TGFB UP	187	10 (5.3)	9 (4.8)	1 (0.5)	0.0006	0.0024	0.0176	

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
GSE2826 WT VS XID BCELL UP	195	10 (5.1)	10 (5.1)	0 (0)	0.0006	0.0024	0.0173	
GSE9988 LPS VS VEHICLE TREATED MONOCYTE DN	196	10 (5.1)	10 (5.1)	0 (0)	0.0006	0.0024	0.0173	
GSE13485 CTRL VS DAY3 YF17D VACCINE PBMC UP	178	9 (5.1)	9 (5.1)	0 (0)	0.0006	0.0024	0.0160	
GSE17721 PAM3CSK4 VS GADIQUIMOD 6H BMDM DN	191	10 (5.2)	10 (5.2)	0 (0)	0.0006	0.0024	0.0175	neu
KAECH DAY8 EFF VS MEMORY CD8 TCELL DN	194	10 (5.2)	10 (5.2)	0 (0)	0.0006	0.0024	0.0174	neu, mnc
GSE17721 CTRL VS POLYIC 12H BMDM DN	197	10 (5.1)	10 (5.1)	0 (0)	0.0006	0.0024	0.0173	neu, mnc, dnc, bcl
GSE13306 RA VS UNTREATED MEM CD4 TCELL DN	204	10 (4.9)	10 (4.9)	0 (0)	0.0006	0.0024	0.0171	neu
GSE17721 CPG VS GARDIQUIMOD 6H BMDM UP	196	10 (5.1)	10 (5.1)	0 (0)	0.0006	0.0025	0.0173	neu, tcl
GSE17721 CTRL VS LPS 0.5H BMDM UP	194	10 (5.2)	10 (5.2)	0 (0)	0.0006	0.0025	0.0174	neu, mnc
GSE30083 SP1 VS SP3 THYMOCYTE DN	196	10 (5.1)	10 (5.1)	0 (0)	0.0006	0.0026	0.0173	neu, mnc
GSE9650 EFFECTOR VS MEMORY CD8 TCELL DN	195	10 (5.1)	10 (5.1)	0 (0)	0.0006	0.0026	0.0173	
GSE37416 0H VS 6H F TULARENSIS LVS NEUTROPHIL DN	190	10 (5.3)	10 (5.3)	0 (0)	0.0006	0.0026	0.0175	neu
GSE9037 WT VS IRAK4 KO LPS 4H STIM BMDM UP	194	10 (5.2)	10 (5.2)	0 (0)	0.0006	0.0026	0.0174	
GSE27786 NEUTROPHIL VS MONO MAC UP	199	10 (5)	9 (4.5)	1 (0.5)	0.0006	0.0027	0.0172	
GSE31082 DP VS CD4 SP THYMOCYTE DN	193	10 (5.2)	10 (5.2)	0 (0)	0.0007	0.0027	0.0174	neu, mnc, dnc, tcl
GSE17721 POLYIC VS GARDIQUIMOD 4H BMDM UP	196	10 (5.1)	9 (4.6)	1 (0.5)	0.0007	0.0027	0.0173	neu
GSE20366 CD103 KLRG1 DP VS DN TREG DN	194	10 (5.2)	10 (5.2)	0 (0)	0.0007	0.0028	0.0174	
GSE17721 CTRL VS GARDIQUIMOD 1H BMDM DN	198	10 (5.1)	10 (5.1)	0 (0)	0.0007	0.0029	0.0172	neu
GSE17721 CTRL VS LPS 6H BMDM DN	202	10 (5)	10 (5)	0 (0)	0.0007	0.0029	0.0171	neu
GSE9988 LOW LPS VS VEHICLE TREATED MONOCYTE DN	195	10 (5.1)	10 (5.1)	0 (0)	0.0007	0.0029	0.0173	
GSE20715 0H VS 24H OZONE TLR4 KO LUNG DN	201	10 (5)	10 (5)	0 (0)	0.0007	0.0029	0.0172	mnc
GSE6269 E COLI VS STREP AUREUS INF PBMC DN	166	9 (5.4)	9 (5.4)	0 (0)	0.0007	0.0029	0.0164	
GSE7852 TREG VS TCONV FAT UP	193	10 (5.2)	10 (5.2)	0 (0)	0.0007	0.0029	0.0174	neu
GSE17721 LPS VS PAM3CSK4 1H BMDM DN	196	10 (5.1)	8 (4.1)	2 (1)	0.0007	0.0029	0.0173	neu
GSE17721 PAM3CSK4 VS CPG 24H BMDM DN	199	10 (5)	10 (5)	0 (0)	0.0007	0.0029	0.0172	neu, mnc, tcl
GSE17721 POLYIC VS GARDIQUIMOD 6H BMDM UP	198	10 (5.1)	10 (5.1)	0 (0)	0.0007	0.0029	0.0172	tcl
GSE14769 UNSTIM VS 20MIN LPS BMDM DN	197	10 (5.1)	10 (5.1)	0 (0)	0.0007	0.003	0.0173	dnc, tcl
GSE17721 POLYIC VS GARDIQUIMOD 12H BMDM UP	196	10 (5.1)	10 (5.1)	0 (0)	0.0008	0.003	0.0173	neu, mnc, dnc
GSE13306 RA VS UNTREATED TREG DN	202	10 (5)	9 (4.5)	1 (0.5)	0.0008	0.003	0.0171	
GSE17721 CTRL VS CPG 8H BMDM DN	198	10 (5.1)	9 (4.5)	1 (0.5)	0.0008	0.0031	0.0172	neu, dnc
GSE7852 TREG VS TCONV LN UP	191	10 (5.2)	9 (4.7)	1 (0.5)	0.0008	0.0032	0.0175	tcl
GSE17721 0.5H VS 8H POLYIC BMDM DN	194	10 (5.2)	9 (4.6)	1 (0.5)	0.0008	0.0032	0.0174	mnc
GSE22886 TH1 VS TH2 48H ACT DN	200	10 (5)	10 (5)	0 (0)	0.0008	0.0032	0.0172	neu
GSE7460 TCONV VS TREG LN DN	194	10 (5.2)	10 (5.2)	0 (0)	0.0008	0.0033	0.0174	dnc, tcl

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
GSE27786 CD8 TCELL VS NKCELL DN	197	10 (5.1)	10 (5.1)	0 (0)	0.0009	0.0036	0.0173	neu, mnc
GSE17974 0H VS 1H IN VITRO ACT CD4 TCELL UP	180	9 (5)	9 (5)	0 (0)	0.001	0.0041	0.0160	neu, mnc
GSE14000 4H VS 16H LPS DC UP	184	9 (4.9)	9 (4.9)	0 (0)	0.0011	0.0042	0.0159	neu
GSE360 DC VS MAC B MALAYI LOW DOSE DN	186	9 (4.8)	9 (4.8)	0 (0)	0.0011	0.0044	0.0158	neu, mnc
GSE29615 CTRL VS LAIV FLU VACCINE PBMC UP	184	9 (4.9)	8 (4.3)	1 (0.5)	0.0012	0.0045	0.0159	neu, mnc
GSE11864 UNTREATED VS CSF1 IN MAC UP	185	9 (4.9)	9 (4.9)	0 (0)	0.0012	0.0046	0.0158	dnc
GSE13411 SWITCHED MEMORY BCELL VS PLASMA CELL DN	199	9 (4.5)	8 (4)	1 (0.5)	0.0012	0.0049	0.0155	neu, mnc
GSE9037 WT VS IRAK4 KO LPS 1H STIM BMDM DN	189	9 (4.8)	8 (4.2)	1 (0.5)	0.0013	0.0049	0.0157	
GSE17721 0.5H VS 12H CPG BMDM UP	191	9 (4.7)	8 (4.2)	1 (0.5)	0.0013	0.0051	0.0157	
GSE7400 CTRL VS CSF3 IN VIVO TREATED PBMC DN	193	9 (4.7)	9 (4.7)	0 (0)	0.0013	0.0051	0.0156	neu
GSE17974 IL4 AND ANTI IL12 VS UNTREATED 2H ACT CD4 TCELL UP	187	9 (4.8)	8 (4.3)	1 (0.5)	0.0013	0.0051	0.0158	neu, mnc
GSE17721 LPS VS CPG 12H BMDM DN	187	9 (4.8)	8 (4.3)	1 (0.5)	0.0013	0.0052	0.0158	
GSE11864 UNTREATED VS CSF1 IFNG PAM3CYS IN MAC DN	186	9 (4.8)	9 (4.8)	0 (0)	0.0014	0.0053	0.0158	
GSE15930 STIM VS STIM AND IL-12 24H CD8 T CELL DN	198	9 (4.5)	7 (3.5)	2 (1)	0.0014	0.0053	0.0155	
GSE3337 4H VS 16H IFNG IN CD8POS DC UP	200	9 (4.5)	9 (4.5)	0 (0)	0.0014	0.0055	0.0154	
KAECH DAY8 EFF VS MEMORY CD8 TCELL UP	198	9 (4.5)	9 (4.5)	0 (0)	0.0014	0.0055	0.0155	neu
GSE36476 CTRL VS TSST ACT 40H MEMORY CD4 TCELL YOUNG DN	193	9 (4.7)	9 (4.7)	0 (0)	0.0015	0.0058	0.0156	neu, dnc
GSE3982 MAC VS NEUTROPHIL LPS STIM UP	194	9 (4.6)	9 (4.6)	0 (0)	0.0015	0.0058	0.0156	
GSE17721 CTRL VS CPG 24H BMDM UP	192	9 (4.7)	9 (4.7)	0 (0)	0.0015	0.0059	0.0157	
GSE17974 CTRL VS ACT IL4 AND ANTI IL12 0.5H CD4 TCELL DN	193	9 (4.7)	8 (4.1)	1 (0.5)	0.0016	0.0059	0.0156	
GSE22886 NAIVE BCELL VS BLOOD PLASMA CELL DN	185	9 (4.9)	9 (4.9)	0 (0)	0.0016	0.0059	0.0158	mnc, tcl
GSE22886 NAIVE CD4 TCELL VS MEMORY TCELL UP	189	9 (4.8)	7 (3.7)	2 (1.1)	0.0016	0.0059	0.0157	
GSE36476 CTRL VS TSST ACT 72H MEMORY CD4 TCELL YOUNG DN	192	9 (4.7)	9 (4.7)	0 (0)	0.0016	0.0059	0.0157	neu
GSE17721 LPS VS GARDIQUIMOD 0.5H BMDM UP	195	9 (4.6)	9 (4.6)	0 (0)	0.0016	0.0059	0.0156	
GSE10094 LCMV VS LISTERIA IND EFF CD4 TCELL DN	193	9 (4.7)	9 (4.7)	0 (0)	0.0016	0.0059	0.0156	
GSE9650 NAIVE VS EFF CD8 TCELL DN	200	9 (4.5)	9 (4.5)	0 (0)	0.0016	0.0059	0.0154	neu
GSE15930 NAIVE VS 72H IN VITRO STIM IFNAB CD8 TCELL DN	196	9 (4.6)	9 (4.6)	0 (0)	0.0016	0.0059	0.0155	neu, tcl
GSE17721 CTRL VS LPS 4H BMDM DN	199	9 (4.5)	8 (4)	1 (0.5)	0.0016	0.006	0.0155	neu
GSE2706 UNSTIM VS 8H R848 DC UP	196	9 (4.6)	7 (3.6)	2 (1)	0.0016	0.0061	0.0155	mnc
GSE3982 MAST CELL VS TH1 DN	185	9 (4.9)	8 (4.3)	1 (0.5)	0.0017	0.0062	0.0158	neu, mnc
GSE3337 4H VS 16H IFNG IN CD8POS DC DN	197	9 (4.6)	9 (4.6)	0 (0)	0.0017	0.0062	0.0155	neu, mnc
GSE26928 NAIVE VS CENT MEMORY CD4 TCELL DN	188	9 (4.8)	9 (4.8)	0 (0)	0.0017	0.0062	0.0158	neu
GSE39820 CTRL VS IL1B IL6 CD4 TCELL DN	190	9 (4.7)	7 (3.7)	2 (1.1)	0.0017	0.0062	0.0157	
GSE32423 MEMORY VS NAIVE CD8 TCELL UP	194	9 (4.6)	7 (3.6)	2 (1)	0.0017	0.0063	0.0156	
GSE22886 CD8 TCELL VS BCELL NAIVE DN	186	9 (4.8)	9 (4.8)	0 (0)	0.0017	0.0064	0.0158	
GSE13306 RA VS UNTREATED TCONV DN	196	9 (4.6)	9 (4.6)	0 (0)	0.0017	0.0064	0.0155	

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
GSE10856 CTRL VS TNFRSF6B IN MACROPHAGE UP	184	9 (4.9)	9 (4.9)	0 (0)	0.0018	0.0065	0.0159	neu, mnc
GSE17721 4 VS 24H CPG BMDM UP	190	9 (4.7)	7 (3.7)	2 (1.1)	0.0018	0.0065	0.0157	neu
GSE17721 CTRL VS PAM3CSK4 2H BMDM DN	192	9 (4.7)	8 (4.2)	1 (0.5)	0.0018	0.0065	0.0157	
GSE2706 R848 VS R848 AND LPS 8H STIM DC UP	190	9 (4.7)	9 (4.7)	0 (0)	0.0018	0.0065	0.0157	
GSE17721 CPG VS GARDIQUIMOD 2H BMDM UP	197	9 (4.6)	9 (4.6)	0 (0)	0.0018	0.0065	0.0155	mnc
GSE6269 E COLI VS STREP PNEUMO INF PBMC DN	156	8 (5.1)	7 (4.5)	1 (0.6)	0.0018	0.0065	0.0148	
GSE11864 UNTREATED VS CSF1 IFNG IN MAC DN	187	9 (4.8)	9 (4.8)	0 (0)	0.0018	0.0066	0.0158	neu, mnc, nkc
GSE7852 LN VS FAT TCONV DN	185	9 (4.9)	9 (4.9)	0 (0)	0.0018	0.0066	0.0158	
GSE36392 TYPE 2 MYELOID VS MAC IL25 TREATED LUNG UP	192	9 (4.7)	9 (4.7)	0 (0)	0.0019	0.0068	0.0157	
GSE17721 LPS VS GARDIQUIMOD 12H BMDM DN	195	9 (4.6)	9 (4.6)	0 (0)	0.0019	0.0068	0.0156	
GSE15930 STIM VS STIM AND IL-12 48H CD8 T CELL UP	196	9 (4.6)	9 (4.6)	0 (0)	0.0019	0.0068	0.0155	neu, mnc
GSE339 CD8POS VS CD4CD8DN DC IN CULTURE UP	201	9 (4.5)	9 (4.5)	0 (0)	0.0019	0.0068	0.0154	neu
KAECH DAY15 EFF VS MEMORY CD8 TCELL DN	193	9 (4.7)	8 (4.1)	1 (0.5)	0.0019	0.007	0.0156	neu
GSE17721 4 VS 24H CPG BMDM DN	194	9 (4.6)	9 (4.6)	0 (0)	0.0019	0.007	0.0156	
GSE17974 2H VS 72H UNTREATED IN VITRO CD4 TCELL UP	188	9 (4.8)	9 (4.8)	0 (0)	0.002	0.007	0.0158	
GSE17721 POLYIC VS PAM3CSK4 6H BMDM UP	192	9 (4.7)	7 (3.6)	2 (1)	0.002	0.007	0.0157	
GSE17721 LPS VS GARDIQUIMOD 8H BMDM UP	194	9 (4.6)	8 (4.1)	1 (0.5)	0.002	0.007	0.0156	neu
GSE15930 STIM VS STIM AND IL-12 48H CD8 T CELL DN	197	9 (4.6)	9 (4.6)	0 (0)	0.002	0.007	0.0155	neu, mnc, dnc
GSE7764 IL15 NK CELL 24H VS SPLENOCYTE DN	193	9 (4.7)	9 (4.7)	0 (0)	0.002	0.007	0.0156	neu
GSE27786 BCELL VS NKCELL DN	194	9 (4.6)	8 (4.1)	1 (0.5)	0.002	0.0071	0.0156	
GSE17721 POLYIC VS PAM3CSK4 2H BMDM DN	194	9 (4.6)	9 (4.6)	0 (0)	0.002	0.0071	0.0156	
GSE2826 WT VS BTK KO BCELL DN	197	9 (4.6)	9 (4.6)	0 (0)	0.002	0.0071	0.0155	mnc
GSE15930 NAIVE VS 48H IN VITRO STIM CD8 TCELL UP	190	9 (4.7)	8 (4.2)	1 (0.5)	0.002	0.0071	0.0157	neu
GSE360 CTRL VS L DONOVANI DC UP	193	9 (4.7)	9 (4.7)	0 (0)	0.002	0.0071	0.0156	
GSE24634 NAIVE CD4 TCELL VS DAY3 IL4 CONV TREG DN	199	9 (4.5)	9 (4.5)	0 (0)	0.002	0.0071	0.0155	neu
GSE17721 LPS VS GARDIQUIMOD 8H BMDM DN	192	9 (4.7)	9 (4.7)	0 (0)	0.002	0.0072	0.0157	
GSE17721 PAM3CSK4 VS CPG 8H BMDM DN	194	9 (4.6)	8 (4.1)	1 (0.5)	0.0021	0.0072	0.0156	
GSE14769 20MIN VS 360MIN LPS BMDM DN	188	9 (4.8)	8 (4.3)	1 (0.5)	0.0021	0.0072	0.0158	
GSE27786 LSK VS NKTCELL UP	190	9 (4.7)	9 (4.7)	0 (0)	0.0021	0.0072	0.0157	
GSE3982 MAST CELL VS EFF MEMORY CD4 TCELL UP	192	9 (4.7)	9 (4.7)	0 (0)	0.0021	0.0072	0.0157	
GSE16522 MEMORY VS NAIVE CD8 TCELL DN	194	9 (4.6)	9 (4.6)	0 (0)	0.0021	0.0073	0.0156	
GSE30083 SP1 VS SP2 THYMOCYTE DN	194	9 (4.6)	9 (4.6)	0 (0)	0.0021	0.0074	0.0156	neu, mnc, dnc, tcl
GSE17721 CTRL VS POLYIC 24H BMDM DN	200	9 (4.5)	8 (4)	1 (0.5)	0.0021	0.0074	0.0154	mnc
GSE17721 POLYIC VS CPG 16H BMDM UP	194	9 (4.6)	9 (4.6)	0 (0)	0.0022	0.0075	0.0156	
GSE13306 TREG VS TCONV UP	196	9 (4.6)	8 (4.1)	1 (0.5)	0.0022	0.0075	0.0155	neu, tcl

Category Name	Category Genes #	Any-reg. DE Genes #(%)	Up-reg. DE Genes #(%)	Down-reg. DE Genes #(%)	P-Value	FDR Adjusted P-Value	Jaccard Index	Cell Type Overlap
GSE17721 CTRL VS PAM3CSK4 24H BMDM UP	198	9 (4.5)	9 (4.5)	0 (0)	0.0022	0.0075	0.0155	
GSE15930 NAIVE VS 24H IN VITRO STIM INFAB CD8 TCELL UP	194	9 (4.6)	8 (4.1)	1 (0.5)	0.0022	0.0075	0.0156	
GSE17721 0.5H VS 24H GARDIQUIMOD BMDM DN	194	9 (4.6)	9 (4.6)	0 (0)	0.0022	0.0076	0.0156	neu
GSE20715 WT VS TLR4 KO 24H OZONE LUNG UP	196	9 (4.6)	9 (4.6)	0 (0)	0.0022	0.0076	0.0155	
GSE17721 LPS VS GARDIQUIMOD 6H BMDM UP	195	9 (4.6)	9 (4.6)	0 (0)	0.0022	0.0077	0.0156	neu
GSE27786 CD4 TCELL VS MONO MAC DN	199	9 (4.5)	8 (4)	1 (0.5)	0.0022	0.0077	0.0155	
GSE14308 TH1 VS TH17 UP	197	9 (4.6)	7 (3.6)	2 (1)	0.0023	0.0077	0.0155	neu
GSE14769 40MIN VS 360MIN LPS BMDM DN	194	9 (4.6)	8 (4.1)	1 (0.5)	0.0023	0.0078	0.0156	
GSE17721 POLYIC VS GARDIQUIMOD 24H BMDM UP	194	9 (4.6)	8 (4.1)	1 (0.5)	0.0023	0.0078	0.0156	
GSE20715 0H VS 48H OZONE TLR4 KO LUNG UP	195	9 (4.6)	9 (4.6)	0 (0)	0.0023	0.0078	0.0156	neu, dnc
GSE17721 POLYIC VS GARDIQUIMOD 8H BMDM UP	195	9 (4.6)	9 (4.6)	0 (0)	0.0023	0.0078	0.0156	neu
KAECH DAY8 EFF VS DAY15 EFF CD8 TCELL DN	194	9 (4.6)	9 (4.6)	0 (0)	0.0023	0.0078	0.0156	neu, mnc
GSE360 T GONDII VS B MALAYI HIGH DOSE MAC UP	208	9 (4.3)	9 (4.3)	0 (0)	0.0023	0.0078	0.0152	neu, dnc
GSE17721 4H VS 24H POLYIC BMDM DN	198	9 (4.5)	8 (4)	1 (0.5)	0.0024	0.008	0.0155	
GSE15930 STIM VS STIM AND IL-12 72H CD8 T CELL UP	205	9 (4.4)	9 (4.4)	0 (0)	0.0024	0.0081	0.0153	neu, mnc
GSE17721 0.5H VS 8H LPS BMDM DN	192	9 (4.7)	9 (4.7)	0 (0)	0.0024	0.0081	0.0157	neu, mnc
GSE37416 CTRL VS 12H F TULARENSIS LVS NEUTROPHIL DN	197	9 (4.6)	9 (4.6)	0 (0)	0.0024	0.0081	0.0155	
GSE3982 NEUTROPHIL VS TH1 UP	190	9 (4.7)	9 (4.7)	0 (0)	0.0025	0.0083	0.0157	
GSE12366 GC VS MEMORY BCELL DN	193	9 (4.7)	9 (4.7)	0 (0)	0.0025	0.0083	0.0156	neu
GSE9006 HEALTHY VS TYPE 1 DIABETES PBMC 4MONTH POST DX UP	193	9 (4.7)	9 (4.7)	0 (0)	0.0025	0.0083	0.0156	neu, dnc
GSE14350 IL2RB KO VS WT TREG UP	196	9 (4.6)	8 (4.1)	1 (0.5)	0.0025	0.0084	0.0155	tcl
GSE27786 NKTCELL VS ERYTHROBLAST UP	198	9 (4.5)	9 (4.5)	0 (0)	0.0025	0.0084	0.0155	neu
GSE17721 LPS VS CPG 8H BMDM UP	197	9 (4.6)	8 (4.1)	1 (0.5)	0.0025	0.0084	0.0155	neu, mnc, dnc
GSE20366 EX VIVO VS DEC205 CONVERSION UP	194	9 (4.6)	9 (4.6)	0 (0)	0.0026	0.0085	0.0156	
GSE30962 ACUTE VS CHRONIC LCMV SECONDARY INF CD8 TCELL DN	194	9 (4.6)	9 (4.6)	0 (0)	0.0026	0.0087	0.0156	neu, mnc
GSE7852 THYMUS VS FAT TCONV DN	192	9 (4.7)	9 (4.7)	0 (0)	0.0026	0.0087	0.0157	neu, mnc
GSE27786 LSK VS LIN NEG CELL UP	194	9 (4.6)	8 (4.1)	1 (0.5)	0.0026	0.0087	0.0156	neu
GSE14308 TH17 VS NATURAL TREG DN	194	9 (4.6)	8 (4.1)	1 (0.5)	0.0028	0.0092	0.0156	
GSE26669 CD4 VS CD8 TCELL IN MLR COSTIM BLOCK UP	196	9 (4.6)	9 (4.6)	0 (0)	0.0029	0.0095	0.0155	
GSE17721 0.5H VS 4H GARDIQUIMOD BMDM DN	197	9 (4.6)	9 (4.6)	0 (0)	0.0029	0.0096	0.0155	
GSE9037 CTRL VS LPS 4H STIM BMDM DN	201	9 (4.5)	9 (4.5)	0 (0)	0.003	0.0099	0.0154	dnc

Table A19: Significantly enriched MSigDB Immunologic Signature Sets (RNA-Seq, PBMC, Day 1). Results sorted by FDR and Jaccard index. The last column indicates overlap with cell type-specific results: dnc: dendritic cells, mnc: monocytes, neu: neutrophils, tcl: T-cells, nkc: NK-cells, bcl: B-cells.

Study Visit	Input Gene Variables	Selected Gene Variables	Mean Squared Error	SDEG [%]	Opt. λ	Intercept
Day 1	738	15	4.67	80	1.8872	4.1763
Day 3	46	5	5.43	0	1.3319	4.6850
Day 7	61	17	3.32	0	0.8291	3.9268
Day 28	29	6	5.79	0	0.5915	4.5415

Table A20: Regularized linear logistic regression model summary statistics (RNA-Seq, PBMC). Log_2 transformed peak HAI titer was used as the response variable. The predictor variables included standardized gene variables with $\geq$1.5 absolute fold change for the respective post-vaccination day in either treatment group. SDEG [%]: percent overlap between selected genes (HAI pos. vs. neg.) and differentially expressed genes (AS03 vs. PBS).

Package Name	Version	Package Name	Version	Package Name	Version
bitops	1.0-6	RGCCA	2.0	foreach	1.4.1
caTools	1.16	rgl	0.93.996	Matrix	1.1-2
chron	2.3-45	R.methodsS3	1.6.1	plyr	1.8.1
codetools	0.2-8	R.oo	1.18.0	mixOmics	5.0-3
digest	0.6.4	R.utils	1.29.8	gtools	3.3.0
evaluate	0.5.1	stats4	3.0.1	vegan	2.0-10
formatR	0.10	stringr	0.6.2	lattice	0.20-27
gdata	2.13.2	tools	3.0.1	permute	0.8-3
grid	3.0.1	coin	1.0-23	gplots	2.12.1
igraph	0.7.1	survival	2.37-7	MASS	7.3-29
iterators	1.0.6	impute	1.34.0	car	2.0-19
KernSmooth	2.23-10	sqldf	0.4-7	png	0.1-7
modeltools	0.2-21	RSQLite.extfuns	0.0.1	edgeR	3.2.4
mvtnorm	0.9-9997	RSQLite	0.11.4	limma	3.16.8
nnet	7.3-7	DBI	0.2-7	xtable	1.7-1
pheatmap	0.7.7	gsubfn	0.6-5	knitr	1.5
RColorBrewer	1.0-5	proto	0.3-10		
Rcpp	0.11.0	glmnet	2.0-2		

Table A21: List of R packages and versions used for the analyses presented in this report. R version 3.0.1 (2013-05-16) 'Good Sport' run on Ubuntu (release 13.04, x86-64-pc-linux-gnu (64-bit) platform).

References

Robinson, Mark D., and Alicia Oshlack. "A scaling normalization method for differential expression analysis of RNA-seq data." Genome Biol 11.3 (2010): R25.

McCarthy, Davis J., Yunshun Chen, and Gordon K. Smyth. "Differential expression analysis of multifactor RNA-Seq experiments with respect to biological variation." Nucleic acids research (2012): gks042.

Young, Matthew D., et al. "Method Gene ontology analysis for RNA-seq: accounting for selection bias." Genome Biol 11 (2010): R14