Supplementary Online Content

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This supplementary material has been provided by the authors to give readers additional information about their work.
Data collection. We carried out a comprehensive search for publicly available microarray data at NCBI GEO (Gene Expression Omnibus) database \(^1\) (http://www.ncbi.nlm.nih.gov/geo/). We used the keywords “kidney”, “renal”, “transplant”, and “biopsy”, among organisms “Homo Sapiens” and study type “Expression profiling by array”. We identified and collected publicly available microarray data from 38 datasets with a total of 4,845 human kidney biopsy samples (eTable 1). For each dataset, we carefully collected the platform information, annotations, and expression data. The gene expression measurements were made on 18 different platforms (eTable 1). The commercial chips were designed by the manufacturers Affymetrix, Agilent and Illumina, and the custom chips were by Functional Genomics Facility at Stanford University and Bioinformatics and Gene Network Research Group at Zhejiang University. The number of probes varied widely from 1,347 to 54,675. In order to preserve as many genes as possible for further analysis we filtered out two datasets GSE26578 and GSE1563 with the lowest number of probes. We also filtered out 5 more datasets: GSE1743, GSE21785, GSE98320, GSE83486, and GSE109346, due to multiple absent or poor annotations such that it was impossible to confidently identify phenotypes associated with the individual samples. The dataset GSE343 was removed since the data of only log2 ratios of intensities in Cy5 and Cy3 channels were available. We found two datasets, GSE14700 and GSE82337, and one sample from GSE36059 with very sparse expression data and significant percentage of missing values, hence we filtered out these datasets as well. In the last step, we examined all datasets for any duplicate samples since many studies recycle previously published data. We were able to identify and remove 179 duplicate samples from GSE11166, GSE14328, GSE34437, GSE50058, and GSE72925 based on available metadata. We then used an R package DoppelgangR \(^2\) that is based on calculations of correlations between samples and manually curated its results for any false positives and identified 257 samples as highly possible duplicates that were then also removed. Using the PCA plots, boxplots, and density plots, we analyzed the datasets for any presence of outliers. After stringent data quality control procedures, we composed the final dataset consisted of 28 studies with 2,273 samples. Their diagnostic annotations included 510 Acute rejection (AR) (including Antibody mediated rejection (ABMR), T cell mediated rejection (TCMR), AR, AR with Chronic allograft nephropathy (AR+CAN), Borderline rejection (BL), BL+CAN, Mixed rejection), 1,154 Stable (STA), and 609 Normal (i.e., biopsy taken prior to transplantation). The summary for the collected studies is represented in eTable 1.

Data processing and normalization. Several pre-processing steps were applied prior to the main analysis. Raw fluorescence intensity data stored in .CEL or .txt files were downloaded and pre-processed depending on the platform. The data processing included background correction, log2 transformation, quantile normalization and probe to gene mapping using R language version 3.5.1 \(^3\). For the Affymetrix platform, we used the R package SCAN.UPC \(^4\) available at Bioconductor \(^5\) (http://ww.bioconductor.org). In contrast to some other popular multi-array normalization algorithms like RMA \(^6\) that estimate probe-level effects and standardize variances across arrays based on the information from a whole dataset, SCAN.UPC is a single-array method that normalizes every sample independently from other samples. This is considered as an advantage \(^4\) since this approach is robust to any influence from possible outliers in the data. The database for the mapping between probes and Entrez gene IDs were taken from the BrainArray resource \(^7\) version 22 (http://brainarray.mbni.med.umich.edu/Brainarray/Database/CustomCDF/22.0.0/entrezg.asp). For the Agilent and Illumina platforms, we downloaded non-normalized raw data and performed data processing using negc() function within limma package \(^8\) from Bioconductor. This algorithm \(^9\) estimates parameters based on normal-exponential (normexp) convolutional model with joint likelihood estimation and with the help of negative control probes. The offset 16 was added to the intensities after the background adjustment by default, as it was shown as the most optimal value to improve FDR of the normexp algorithm \(^8\). However, some data from the Agilent and Stanford platforms did not contain any negative control probes. Therefore, we used similar processing steps manually to reproduce the methodology by applying backgroundCorrect() function from limma package by the mle normexp
method with offset $16$. Log$_2$ transformation and quantile normalization was performed after this. The probe-gene mapping was implemented using the information from biomaRt database $^{10}$ or GPL files.

To gain additional statistical power from the large dataset we were able to collect, we chose to merge all the studies to perform a meta-analysis. In order to merge data from different studies and different platforms we had to first correct for potential batch effects. There are a number of papers that address this issue $^{11-15}$ but unfortunately, a one-fits-all solution doesn’t exist. Different normalization methods have their advantages and disadvantages in removing batch effects, however, they can also become a critical problem in correcting the imbalanced data $^{11,15}$. We examined the performance of several approaches that included ComBat $^{19}$ as a part of sva package $^{20}$, Quantile Normalization (QN) $^{21}$, Remove Unwanted Variation (RUV) $^{22}$ and Harman $^{23}$. We identified superior batch effect minimization with ComBat in comparison to other methods and used it to normalize the data. The process of data aggregation, normalization and merging is schematically described in eFigure 1a.

Cross-study normalization in data merging. We have examined several batch correction methods: ComBat $^{19}$ as a part of sva package $^{20}$, Quantile Normalization (QN) $^{21}$, Remove Unwanted Variation (RUV) $^{22}$ and Harman $^{23}$. Currently, the most common technique to remove the systematic batch effects from biological data is ComBat $^{19}$ which based on empirical Bayes method to estimate batch effects and to adjust data across genes. However, often a major limitation of its use is missed: the studies merged have to be more or less balanced with respect to the case-control breakdown of samples. If it is not the case, some biological heterogeneity can vanish $^{15}$. The breakdown by phenotype for each study we use in our work is represented in the eTable 1 and shows presence of some imbalance in outcomes. Therefore, we wanted to additionally examine some other normalization methods comprehensively.

The Quantile Normalization technique is the same method used for normalization at the probe level, but as it was shown before $^{21}$ it can be applied for batch effect elimination as well.

The RUV method $^{22}$ is based on adjustment on so-called negative control genes, that are expected not to be differentially expressed across phenotypes. There is still an open question which set of genes would be most suitable for this role. Basically, so far there are two possible ways to obtain a list of control genes: housekeeping genes and empirically found ones. The housekeeping genes are defined to be expressed on the similar level across all tissues and involved in basic cell processes $^{24}$. However, besides the fact that there is no fully established list of housekeeping genes $^{25}$, it was shown that they might not be the best to represent negative controls in adjustments $^{22}$ since they can be differentially expressed in some tissues $^{12}$ or related to diseases $^{26}$. Another method is to empirically find genes that are expressed steadily across merging studies. However, there is some freedom in setting a number of such genes. Too small number can be not enough for proper adjustment, too large – can include some genes important for a current study. Some dependence on studies involved is presented in the search for negative control genes. For some discussion of advantages and disadvantages of both methods see reference $^{27}$. Another challenging factor in applying the RUV method is the parameters adjustment. Depending on implementation of the algorithm, there are two main parameters to adjust: the dimension of the unwanted systematic noise and the ridge smoothing parameter. To find an optimal set of parameters is actually a tricky problem. In our study, we examined three different implementations of RUV method in R packages RUVcorr $^{27}$, RUVnormalize $^{28}$, and RUVSeq $^{29}$ (RUVg function). The first two packages implement naïve RUV-random method which is a variation of the RUV-2 method originally described in $^{22}$. The third method RUVg within RUVseq package is originally designed as a discrete version of RUV-2 methods for RNA-seq counts data. We used this method for performance comparison with other approaches. We compared the performance of these RUV implementations with the housekeeping and empirical negative control genes. We also varied the parameter of the noise dimension $k$ but set the smoothing ridge parameter to 0.001 for RUVnormalize and 0 for RUVcorr.

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Another promising normalization method we examined is *Harman* [23]. This method is a Principal Component Analysis based optimization technique that maximizes batch removal but keeps some probability of the overcorrection as a parameter. We compared the method performance with the overcorrection parameter set to 0.95.

We considered three types of benchmarks to perform the comparison for normalization methods. We computed the percentage of variability in first ten principal components that can be explained by batch (i.e. by dataset study) and kept the maximum value among those ten as one of three benchmarks. For the other two we used the R package gPCA [30] to compute guided principal components (i.e. the principal components of batch modified data) and obtained a p-value (i.e. the probability of having batch effect in data) and delta statistic (i.e. the ratio of guided and unguided first principal component; the lower the better). Since all three metrics are in the range from 0 to 1, we summed them and normalized to one and used as a final metric to justify the normalization method performance. The results are represented in the eFigure 7.

We found the Harman normalization to outperform all methods followed by ComBat and RUV implementations in RUVcorr and RUVseq with housekeeping genes at the noise dimension parameter $k = 15$-$17$. Further comparison analysis showed that while the data seems batch free, RUV and Harman adjusted a bit too much leaving minimum of biological variability, resulting in much fewer differentially expressed genes in comparison to ComBat. Therefore, we decided to use ComBat for cross-study normalization to keep as much heterogeneity as possible while successfully adjusting for batch effects. We observed that the results of the normalization performance vary depending on datasets: their number, platform, processing methods. There is no one-fit-all technique that should be used blindly to correct for batch effects when merging data. Therefore, it should be advised to perform such comparisons of normalization methods each time performing meta-analysis to choose best among available methods [14].

Statistics. To identify differentially expressed genes in the first analysis AR vs Normal we used the Significance Analysis of Microarrays (SAM) [31] method that was implemented in the R package siggenes [32]. We utilized the false discovery rate (FDR) [33] with Benjamini-Hochberg procedure [34] for multiple testing correction and use the adjusted cutoff of 0.05. For the second level of significance, we selected only those genes that have the fold change greater than 1.5.

Pathway Analysis. We leveraged the Gene Ontology database using the gene set enrichment analysis implemented in the R package clusterProfiler [35] to perform functional annotations for the significantly up- and down-regulated genes. We used FDR multiple correction method with the enrichment significance cut-off at level 0.05. For the gene network analysis, we utilized the STRING protein–protein association networks database [36] (https://string-db.org).

Cell type enrichment analysis. In order to estimate the presence of certain cell types in biopsy samples, we leveraged a recently published cell type enrichment tool xCell [37]. xCell leverages gene expression data from microarray and RNA-seq experiments and is used to perform enrichment analysis for up to 64 immune and stromal cell types. We focused on 34 immune related and 11 non-immune cell types (eTable 3) that we selected manually as relevant to the transplant injury process. In our analysis, we used a dedicated R package that is available on the author’s GitHub account for this purpose. This analytical method is a gene signatures-based method and converts the gene expression into cell type enrichment scores. The authors especially emphasize that this is not a deconvolution method that provides percentage of cell types containing in a tissue but rather the enrichment tool allowing to compare samples.
for each cell type but not otherwise. The enrichment scores for each cell type were used to compare AR and Normal samples and to identify cell types that are significantly different in individuals with AR as opposed to normal controls by performing the non-parametric two-sample Mann-Whitney-Wilcoxon statistical test. We utilized the multiple testing correction by using the Benjamini-Hochberg method. Adjusted p-value < 0.05 was used as the threshold.

Feature selection procedure. In our efforts to select the most important features in distinguishing AR vs Normal samples, we performed the following steps. First, we split the whole data into training and testing sets in the ratio 80:20 and performed all feature selection procedures on the training set with benchmarking on the testing set. After identifying the significant features from a statistical test described above on the training set, we searched for features that correlate with the outcome no less than 2/3 of a maximum correlation value. In the final step, we applied Recursive Feature Elimination (RFE) technique with Random Forest (RF) model from the R package caret 38. We used 5-fold cross validation (CV) technique with 100 repeats. To benchmark the model, we used the area under the ROC curve that is more suitable for data with some disbalance in outcome - in our case the ratio AR:Normal is 0.84. To decrease the bias of random split as well as to avoid the model overfitting, we also introduced the tolerance of 1% to the feature selection mechanism, i.e. the algorithm was choosing the simplest model with the smallest number of features that performs within range 99-100% of the best model.

To perform the steps described above, we adopted the R package feseR 39 and modified it to implement the parallel computations, the AUROC metric for model benchmarking, and the tolerance parameter of model performance. After the feature selection steps, we benchmarked the features with RF model on the testing set.

Instability Score and hSTA sub-phenotyping. The method of sub-phenotyping hSTA samples is formed on creating a scoring system based on selected features and scoring the hSTA samples. Based on the score values, histologically STA samples are identified as molecularly AR or molecularly STA. We denoted this split as hSTA/mAR and hSTA/mSTA, respectively.

For our current analysis, two types of data were available: gene expression data and cell type enrichment scores (obtained computationally using xCell). Based on these two data types, we performed the feature selection procedure described above to find sets of genes and cell types that highly associated with AR. Next, we z-scaled each feature, a gene or a cell type, and built a logistic regression model with all features to identify feature importance as model coefficients. Using these coefficients, we created a linear formula to compute a score, that we called the Instability Score (or InstaScore):

\[
\text{InstaScore} = 0.596 + 2.096 \times \text{KLF4} + 2.534 \times \text{CENPJ} + 0.311 \times \text{KLF2} + 1.447 \times \text{PPP1R15A} \\
- 1.633 \times \text{FOSB} + 0.268 \times \text{TNFAIP3} + 2.249 \times \text{NK cells} + 0.542 \times \text{CD4+ T}_{\text{em}} \text{ cells} \\
+ 0.833 \times \text{CD4+ T}_{\text{em}} \text{ cells} + 0.709 \times \text{CD8+ T}_{\text{em}} \text{ cells} + 0.146 \times \text{Th1 cells}.
\]

The positive InstaScore values separate AR from Normal samples which obtain negative values. By following the same steps, we then computed the InstaScore for the histologically STA samples and applied the zeroth threshold to obtain the split into mAR and mSTA subtypes. This whole approach is schematically represented in the form of the flow chart in the eFigures 1b and 1c.

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eFigure 1. Flow Chart

(a) Data pre-processing and Normalization. (b) Feature selection and creating the Instability Score (InstaScore). (c) Applying InstaScore to hSTA for sub-phenotyping and validating results.

(a) Kidney transplant biopsies
   - Quality Control
     - Poor annotations
     - Mixed signal
     - Low probe platform
     - Sparse expression matrix
     - Search for duplicates
   - Pre-processing
     - Background correction
     - Quantile normalization
     - Probe-gene mapping
     - Clean data
     - 28 datasets
   - Datasets merging, Normalization across studies
   - 37 datasets, 4,201 samples
     - remove 4 datasets and 12 samples
     - remove 1 dataset
     - remove 2 datasets
     - remove 2 datasets and 1 sample
     - remove 257 samples

(b) Discovery data, 1,119 AR and Normal samples
   - Gene expression data
   - xCell: Cell type enrichment scores
   - Feature selection procedure
   - Train logistic regression model with combined selected features
   - InstaScore as linear combination of selected features and model coefficients

(c) Prediction data, 1,154 hSTA samples
   - Computing InstaScore for each sample
   - hSTA subtyping into mAR & mSTA based on InstaScore
   - Validation on independent clinical data

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eFigure 2. Scatterplots of Gene Expression Data After Data Sets Merging

PCA and UMAP plots (a) before normalization colored by study, (b) after normalization with ComBat colored by study, (c) after normalization colored by phenotypes.
eFigure 3. PCA Clustering Plot for Differentially Expressed Genes From Analysis of AR vs Normals
eFigure 4. Pathway Enrichment Analysis of DE Genes

The top 20 GO terms enriched among (a) up- and (c) down-regulated genes in AR vs Normal analysis. Functional networking with STRING for the differentially expressed (b) up- and (d) down-regulated genes. We used the minimum required interaction score equal to 0.9. The edges mean a type of interaction evidence. The colors mean as follows. The known interactions are cyan for curated databases and magenta for experimentally determined interactions. The predicted interactions are represented in green for gene neighborhood, red for gene fusions, and blue for gene co-occurrence. The other types of interactions are in lime based on text mining, black on co-expression, and indigo on protein homology.

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**eFigure 5.** Heatmap of Enrichment Scores of Significant Cell Types From the AR vs Normal Comparison

The colored vertical bars represent results from AR vs Normal analysis. The plot combines all AR, hSTA, and Normal samples and shows clustering of some hSTA samples together with AR hinting to possible hidden inflammation processes going in those grafts.
**eFigure 6.** Plots of Feature Selected Genes and Cell Types for all AR and Normal Samples

Heatmap and UMAP plot of (a) feature selected gene expression and (b) feature selected cell types.
eFigure 7. AUROC and AUCPR Plots of Feature Selected Genes, Cell Types and InstaScore
**eFigure 8.** Combined Benchmark Based on $P$-Value, Delta Statistic and the Percentage of Variability for Batch Correction Methods Tested

HK – Housekeeping genes, ENC – Empirical Negative Control genes
**eTable 1. Datasets Collected From Gene Expression Omnibus (GEO)**

| Study       | PMID     | Platform                                  | Probes   | Total | AR | STA | Normal | Year | Country |
|-------------|----------|-------------------------------------------|----------|-------|----|-----|--------|------|---------|
| GSE343      | 128535   | GPL271 LC-17 & GPL272 LC-20               | 28032 & 37632 | 41    | 2  | 6   | 15     | 2003 | USA     |
| GSE1563     | 153078   | GPL8300 [HG_U95Av2] Affymetrix Human Genome U95 Version 2 | 12625   | 31    | 7  | 10  | 9      | 2004 | USA     |
| GSE1743     | 154764   | GPL96 [HG-U133A] Affymetrix Human Genome U133A | 22283   | 41    | 0  | 41  | 0      | 2004 | USA     |
| GSE7392     | 173975   | GPL570 [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 | 54675   | 22    | 0  | 7   | 15     | 2007 | USA     |
| GSE9493     | 190173   | GPL570 [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 | 54675   | 56    | 2  | 21  | 14     | 2007 | Switzerland |
| GSE10419    | 205254   | GPL887 Agilent-012097 Human 1A Microarray (V2) G4110B | 22153   | 29    | 0  | 29  | 0      | 2008 | Japan   |
| GSE11166    | 194436   | GPL570 [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 | 54675   | 49    | 1  | 27  | 21     | 2008 | USA     |
| GSE14328    | 201505   | GPL570 [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 | 54675   | 36    | 1  | 18  | 0      | 2009 | USA     |
| GSE14700    | 207137   | GPL8150 Stanford Microarray Functional Genomics Homo sapiens 34.6K | 34599   | 40    | 0  | 0   | 40     | 2009 | Austria |
| GSE21374    | 205019   | GPL570 [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 | 54675   | 28    | 2  | 6   | 20     | 2010 | Canada  |
| GSE22459    | 208138   | GPL570 [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 | 54675   | 25    | 0  | 25  | 0      | 2010 | USA     |
| GSE25902    | 218815   | GPL570 [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 | 54675   | 88    | 2  | 7   | 37     | 2010 | USA     |
| Study   | PMID   | Platform                                      | Probes | Total | A   | R   | ST  | A Normal | Year | Country     |
|---------|--------|----------------------------------------------|--------|-------|-----|-----|-----|---------|------|-------------|
| GSE26578* | -     | GPL9301 Zhejiang university human 449 oligonucleotide array | 1347   | 85    | 3   | 4   | 51  | 0       | 201  | China       |
| GSE30718 | 223431 | GPL570 [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 | 54675  | 19    | 0   | 11  | 8   | 201    | Canada |
| GSE34437 | 234372 | GPL570 [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 | 54675  | 36    | 1   | 7   | 12  | 201    | USA   |
| GSE34748 | 223354 | GPL570 [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 | 54675  | 36    | 0   | 36  | 0   | 201    | USA   |
| GSE36059 | 233569 | GPL570 [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 | 54675  | 41    | 0   | 12  | 28  | 8      | 201   | Canada      |
| GSE43974 | 254271 | GPL10558 Illumina HumanHT-12 V4.0 expression beadchip | 47323  | 46    | 0   | 11  | 2   | 351    | 201   | Netherland s |
| GSE44131 | 240307 | GPL6244 [HuGene-1_0-st] Affymetrix Human Gene 1.0 ST Array | 29096  | 12    | 0   | 12  | 0   | 201    | USA   |
| GSE47097 | 237634 | GPL6883 Illumina HumanRef-8 v3.0 expression beadchip | 47323  | 40    | 3   | 2   | 6   | 6      | 201   | Netherland s |
| GSE48581 | 239154 | GPL570 [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 | 54675  | 30    | 6   | 7   | 22  | 5      | 201   | Canada      |
| GSE50058 | 241274 | GPL570 [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 | 54675  | 30    | 6   | 7   | 22  | 5      | 201   | USA         |
| GSE50084 | 264841 | GPL6244 [HuGene-1_0-st] Affymetrix Human Gene 1.0 ST Array | 29096  | 48    | 2   | 8   | 20  | 0      | 201   | USA         |
| GSE52694 | 261768 | GPL10558 Illumina HumanHT-12 V4.0 expression beadchip | 23719  | 14    | 0   | 14  | 0   | 201    | Czech Republic |
| GSE53605 | 246985 | GPL571 [HG-U133A_2] Affymetrix Human Genome U133A 2.0 | 22277  | 31    | 1   | 3   | 18  | 0      | 201   | USA         |
| GSE53769 | 208191 | GPL16686 [HuGene-2_0-st] Affymetrix Human Gene 2.0 ST Array | 53617  | 28    | 0   | 10  | 18  | 0      | 201   | Austria     |
| GSE54888 | -      | GPL6244 [HuGene-1_0-st] Affymetrix Human Gene 1.0 ST | 33252  | 54    | 0   | 54  | 0   | 201    | Brazil    |

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| Dataset ID   | Accession | Study Type | Platform | Array | Samples | Study Name | GEO ID | GEO ID | Study ID | Country |
|-------------|-----------|------------|----------|-------|----------|------------|--------|--------|----------|---------|
| GSE57387    | 27452608  | GPL5175    | Human Exon 1.0 ST | Affymetrix | 17881 | 10 | 0 | 10 | 0 | 2014 | USA |
| GSE60807    | 26908771  | GPL6480    | Whole Human Genome Microarray 4x44K G4112F | Affymetrix | 41093 | 37 | 0 | 37 | 0 | 2014 | Austria |
| GSE65326    | 25307039  | GPL10558   | Illumina HumanHT-12 V4.0 expression beadchip | Affymetrix | 47323 | 6 | 0 | 6 | 0 | 2015 | Australia |
| GSE69677    | 27369853  | GPL14951   | Illumina HumanHT-12 WG-DASL V4.0 R2 expression beadchip | Affymetrix | 29360 | 76 | 2 | 4 | 0 | 52 | 2015 | Italy |
| GSE72925    | 27140517  | GPL570     | [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 | Affymetrix | 54675 | 46 | 1 | 0 | 36 | 0 | 2015 | USA |
| GSE76882    | 26990570  | GPL13158   | [HT_HG-U133_Plus_PM] Affymetrix HT HG-U133+ PM | Affymetrix | 17564 | 18 | 2 | 3 | 99 | 0 | 2016 | USA |
| GSE82337a   | 27225518  | GPL10558   | Illumina HumanHT-12 V4.0 expression beadchip | Affymetrix | 47323 | 78 | 0 | 78 | 0 | 2016 | USA |
| GSE83486a   | 28436117  | GPL10558   | Illumina HumanHT-12 V4.0 expression beadchip | Affymetrix | 47323 | 60 | ? | ? | 0 | 2016 | Norway |
| GSE98320a   | 28614805  | GPL15207   | [PrimeView] Affymetrix Human Gene Expression Array | Affymetrix | 49395 | 12 | 08 | ? | ? | 0 | 2017 | Canada |
| GSE109346a  | -         | GPL10558   | Illumina HumanHT-12 V4.0 expression beadchip | Affymetrix | 47323 | 26 | 0 | 26 | 0 | 2018 | Czech Republic |

*Datasets not included into this study*
**eTable 2a. Upregulated Differentially Expressed Genes From SAM Analysis of Comparison of Acute Rejection to Normal Kidney Tissues**

| gene     | raw p.value | q.value | Bonferroni adj. p-value | fold change |
|----------|-------------|---------|-------------------------|-------------|
| KLF4     | 0           | 0       | 0                       | 2.98997063  |
| TNFAIP3  | 0           | 0       | 0                       | 2.8158084   |
| CENPJ    | 0           | 0       | 0                       | 2.7977016   |
| KLF2     | 0           | 0       | 0                       | 2.7489507   |
| PPP1R15A | 0           | 0       | 0                       | 2.73240129  |
| CD69     | 0           | 0       | 0                       | 2.72655781  |
| IER5     | 0           | 0       | 0                       | 2.64068239  |
| IRF1     | 0           | 0       | 0                       | 2.62101798  |
| CXCL9    | 0           | 0       | 0                       | 2.57674401  |
| PMAIP1   | 0           | 0       | 0                       | 2.49996879  |
| CXCL10   | 0           | 0       | 0                       | 2.49878491  |
| GBP1     | 0           | 0       | 0                       | 2.45983835  |
| CXCL11   | 0           | 0       | 0                       | 2.43386819  |
| PRF1     | 0           | 0       | 0                       | 2.43312954  |
| EVI2A    | 0           | 0       | 0                       | 2.42265645  |
| RGS1     | 0           | 0       | 0                       | 2.41594949  |
| ZC3H12A  | 0           | 0       | 0                       | 2.4151211   |
| IL10RA   | 0           | 0       | 0                       | 2.40736767  |
| PLAC8    | 0           | 0       | 0                       | 2.40119639  |
| MAP3K8   | 0           | 0       | 0                       | 2.40089927  |
| CTSS     | 0           | 0       | 0                       | 2.39761543  |
| HCP5     | 0           | 0       | 0                       | 2.38530964  |
| PTPRC    | 0           | 0       | 0                       | 2.38466318  |
| KLRD1    | 0           | 0       | 0                       | 2.38176354  |
| TNF      | 0           | 0       | 0                       | 2.37953081  |

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| Gene        | Value1 | Value2 | Value3 | Value4 | Value5 |
|-------------|--------|--------|--------|--------|--------|
| TRIM22      | 0      | 0      | 0      | 0      | 2.37940218 |
| IRF8        | 0      | 0      | 0      | 0      | 2.37358637 |
| CD48        | 0      | 0      | 0      | 0      | 2.37304314 |
| BTG2        | 0      | 0      | 0      | 0      | 2.37162986 |
| CD3D        | 0      | 0      | 0      | 0      | 2.36786309 |
| NKG7        | 0      | 0      | 0      | 0      | 2.36695982 |
| CREB5       | 0      | 0      | 0      | 0      | 2.36661777 |
| HLA-DQB2    | 0      | 0      | 0      | 0      | 2.36364457 |
| TAP1        | 0      | 0      | 0      | 0      | 2.36149907 |
| RUNX3       | 0      | 0      | 0      | 0      | 2.35113981 |
| LST1        | 0      | 0      | 0      | 0      | 2.34840646 |
| B2M         | 0      | 0      | 0      | 0      | 2.34566138 |
| HLA-DPA1    | 0      | 0      | 0      | 0      | 2.33798069 |
| ITGAL       | 0      | 0      | 0      | 0      | 2.33385739 |
| CSF2RB      | 0      | 0      | 0      | 0      | 2.32885078 |
| P2RX7       | 0      | 0      | 0      | 0      | 2.32479792 |
| IL7R        | 0      | 0      | 0      | 0      | 2.32355007 |
| ARHGAP25    | 0      | 0      | 0      | 0      | 2.32177361 |
| CCL5        | 0      | 0      | 0      | 0      | 2.32053852 |
| MCL1        | 0      | 0      | 0      | 0      | 2.31631316 |
| CST7        | 0      | 0      | 0      | 0      | 2.31616257 |
| CD52        | 0      | 0      | 0      | 0      | 2.31387121 |
| IKZF1       | 0      | 0      | 0      | 0      | 2.30961855 |
| IDO1        | 0      | 0      | 0      | 0      | 2.30943484 |
| AIM2        | 0      | 0      | 0      | 0      | 2.30837824 |
| UBD         | 0      | 0      | 0      | 0      | 2.30495914 |
| LCP2        | 0      | 0      | 0      | 0      | 2.30422715 |
| KLRB1       | 0      | 0      | 0      | 0      | 2.30390509 |
| EVI2B       | 0      | 0      | 0      | 0      | 2.29552135 |

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| Gene     | Score |
|----------|-------|
| PSMB9    | 2.29262263 |
| CD86     | 2.29258553 |
| BTN3A1   | 2.28967261 |
| BTN3A2   | 2.28821269 |
| CD247    | 2.28565063 |
| CD8A     | 2.2850551 |
| DEPP1    | 2.28276845 |
| STK17B   | 2.28200493 |
| HLA-DOB  | 2.28074243 |
| ANXA1    | 2.27219254 |
| APOBEC3G | 2.27113781 |
| HLA-DPB1 | 2.2665779 |
| MYO1F    | 2.26465237 |
| GZMK     | 2.26222309 |
| GPR18    | 2.26205506 |
| BCL11B   | 2.2616775 |
| CXCR4    | 2.25937535 |
| CD2      | 2.25318882 |
| RGS10    | 2.25285452 |
| P2RY13   | 2.2491914 |
| GPR65    | 2.24744526 |
| SP140    | 2.2454099 |
| AOAH     | 2.24370008 |
| ADRB2    | 2.24320158 |
| LY9      | 2.24133679 |
| FOSB     | 2.24000744 |
| ISG20    | 2.23911862 |
| MXD1     | 2.23635215 |
| RIPOR2   | 2.23627031 |
| Gene     | Fold Change |
|----------|-------------|
| ITK      | 2.23363861  |
| KLF6     | 2.23235675  |
| DNAJB1   | 2.23096799  |
| LILRB1   | 2.23086453  |
| CD96     | 2.23032482  |
| HLA-E    | 2.22476943  |
| STAT4    | 2.22381082  |
| CLIC2    | 2.2235431   |
| GZMB     | 2.22202816  |
| MNDA     | 2.2167427   |
| GPR171   | 2.21539441  |
| SLAMF8   | 2.2142648   |
| IL2RB    | 2.20896132  |
| MICB     | 2.20499951  |
| WEE1     | 2.20455374  |
| MARCH1   | 2.20291497  |
| LYZ      | 2.18920863  |
| CLEC10A  | 2.1802396   |
| CXCL2    | 2.17895268  |
| P2RY10   | 2.1683341   |
| CASP1    | 2.16819752  |
| GIMAP6   | 2.16746414  |
| HLA-DMA  | 2.16708189  |
| DUSP5    | 2.16613359  |
| ST8SIA4  | 2.15984574  |
| PTPN22   | 2.15949268  |
| BIRC3    | 2.15651003  |
| GPR183   | 2.15341854  |
| LCK      | 2.15216208  |

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| Gene   | Fold Change |
|--------|-------------|
| HLA-DMB | 2.15053615  |
| IKZF3  | 2.14858732  |
| CBX4   | 2.14598088  |
| SP110  | 2.14380387  |
| ACSL5  | 2.14223594  |
| APOL3  | 2.13987992  |
| SELL   | 2.13968371  |
| CELF2  | 2.13866275  |
| SP140L | 2.13763051  |
| CSTA   | 2.13088689  |
| GNLY   | 2.13065208  |
| JUNB   | 2.13053963  |
| RIPK2  | 2.1286435   |
| PSMB8  | 2.12774922  |
| JUN    | 2.12526537  |
| TNFAIP8| 2.12453999  |
| RAC2   | 2.11800249  |
| MAP4K1 | 2.11599607  |
| NFKBIE | 2.1131527   |
| NOD2   | 2.1119409   |
| CLEC4A | 2.11130621  |
| TYROBP | 2.11073863  |
| PLK2   | 2.10985017  |
| CD1C   | 2.10894258  |
| ARHGAP15| 2.10693429 |
| CORO1A | 2.10679548  |
| MS4A6A | 2.10658045  |
| SLA    | 2.10636427  |
| NCF2   | 2.10529116  |
| Gene    | Log2FoldChange |
|---------|---------------|
| FOXJ1   | 2.10425914    |
| IFI16   | 2.10310793    |
| HSPA1A  | 2.10295144    |
| PELI1   | 2.10186002    |
| TLR2    | 2.10115727    |
| SH2D1A  | 2.09767889    |
| MYC     | 2.09732699    |
| FCN1    | 2.09723406    |
| LAX1    | 2.09504128    |
| PTPRCAP | 2.09413584    |
| RHOB    | 2.09263867    |
| SIRPG   | 2.0911939     |
| IFNG    | 2.08976079    |
| HCK     | 2.08955668    |
| MAFB    | 2.08872583    |
| CLEC2D  | 2.08446512    |
| TRAF3IP3| 2.08387276    |
| ZFP36L2 | 2.08310434    |
| PRKCB   | 2.07722812    |
| SASH3   | 2.07441304    |
| CD38    | 2.07378644    |
| CD160   | 2.07176452    |
| DPEP2   | 2.07159006    |
| ADGRE5  | 2.07126431    |
| PYCARD  | 2.07070006    |
| ADCY7   | 2.06925373    |
| HLA-DRA | 2.06894425    |
| UBE2L6  | 2.06593758    |
| CRLF3   | 2.06126017    |
| Gene   | log2FoldChange |
|--------|---------------|
| DOK2   | 2.06030902    |
| VMP1   | 2.06020704    |
| TENT5A | 2.05872026    |
| LYN    | 2.05847505    |
| EZH2   | 2.05703329    |
| CCNL1  | 2.05521972    |
| ITGAX  | 2.05505202    |
| INPP5D | 2.05274694    |
| RNF125 | 2.05195938    |
| DYRK2  | 2.04307727    |
| FAM53C | 2.04258896    |
| IRF7   | 2.04170872    |
| HLA-B  | 2.04143156    |
| LAT2   | 2.04058043    |
| APOL1  | 2.0403936     |
| LAPT5M | 2.04032522    |
| FYB1   | 2.0400202     |
| CLEC7A | 2.03907773    |
| TRAT1  | 2.03828489    |
| IL16   | 2.0380657     |
| RRAD   | 2.03760206    |
| FAM49A | 2.03460842    |
| RUBCNL | 2.03453033    |
| SAM5N1 | 2.03442298    |
| PLEKHO2| 2.03227139    |
| RTN1   | 2.02967175    |
| MCUB   | 2.0294391     |
| CD300A | 2.02925183    |
| UBASH3A| 2.02613114    |

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| Gene       | Log2FC  |
|------------|---------|
| PIK3CG     | 2.02611959 |
| KIAA1551   | 2.0260504  |
| PRDM1      | 2.02375524 |
| RASSF2     | 2.02326564 |
| TCIRG1     | 2.02210548 |
| ADAMDEC1   | 2.01991221 |
| MYLIP      | 2.0186271  |
| ITGAM      | 2.01630828 |
| PVRIG      | 2.01473335 |
| STAT1      | 2.01429309 |
| TLR8       | 2.01404994 |
| PTGDR      | 2.01108627 |
| CFP        | 2.01085542 |
| BTN2A2     | 2.01038137 |
| SOCS3      | 2.00865113 |
| C1QA       | 2.00796476 |
| SAMHD1     | 2.00746237 |
| FGR        | 2.0054924  |
| CASP3      | 2.00509585 |
| IL21R      | 2.0043075  |
| ITGB2      | 2.00417258 |
| POU2AF1    | 2.00377665 |
| PTPN6      | 2.0020436  |
| CD27       | 2.00177412 |
| RGS19      | 1.99981528 |
| GBP2       | 1.99785514 |
| ELF4       | 1.99639093 |
| DDIT3      | 1.99400543 |
| LILRB2     | 1.99287834 |

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| Gene     | C1  | C2  | C3  | FDR |
|----------|-----|-----|-----|-----|
| GIMAP4   | 0   | 0   | 0   | 1.9920831 |
| ZAP70    | 0   | 0   | 0   | 1.99182192 |
| HLA-DOA | 0   | 0   | 0   | 1.99131317 |
| CD8B     | 0   | 0   | 0   | 1.98886458 |
| IGSF6    | 0   | 0   | 0   | 1.98812839 |
| DNAJA1   | 0   | 0   | 0   | 1.98733308 |
| GCNT1    | 0   | 0   | 0   | 1.98698841 |
| FCMR     | 0   | 0   | 0   | 1.98692169 |
| DNAJB4   | 0   | 0   | 0   | 1.98534535 |
| OAS2     | 0   | 0   | 0   | 1.98424631 |
| PTPRE    | 0   | 0   | 0   | 1.98342392 |
| ST3GAL5  | 0   | 0   | 0   | 1.98159439 |
| P2RY14   | 0   | 0   | 0   | 1.97909875 |
| REL      | 0   | 0   | 0   | 1.97905329 |
| SRF      | 0   | 0   | 0   | 1.97313036 |
| CX3CR1   | 0   | 0   | 0   | 1.97167246 |
| LAIR1    | 0   | 0   | 0   | 1.97127262 |
| IL2RG    | 0   | 0   | 0   | 1.97107721 |
| CD180    | 0   | 0   | 0   | 1.9709026  |
| ELOVL1   | 0   | 0   | 0   | 1.96958038 |
| HSPA8    | 0   | 0   | 0   | 1.96898397 |
| CXCL1    | 0   | 0   | 0   | 1.96815369 |
| DUSP1    | 0   | 0   | 0   | 1.96663177 |
| TRIB1    | 0   | 0   | 0   | 1.96518202 |
| NMI      | 0   | 0   | 0   | 1.96096383 |
| KLRC3    | 0   | 0   | 0   | 1.96068833 |
| FGL2     | 0   | 0   | 0   | 1.96065735 |
| HBEGF    | 0   | 0   | 0   | 1.96027009 |
| HLA-DRB1 | 0   | 0   | 0   | 1.9599303  |

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| gene   | fold change |
|--------|-------------|
| DOCK10 | 1.9593274   |
| TLR7   | 1.95783505  |
| LY86   | 1.95747111  |
| LCP1   | 1.95485984  |
| BCL2A1 | 1.95022069  |
| DUSP6  | 1.9482675   |
| NCF4   | 1.94488048  |
| ALOX5  | 1.94476151  |
| CX3CL1 | 1.94438257  |
| WIPF1  | 1.94412603  |
| C3AR1  | 1.94320305  |
| CD3G   | 1.94275676  |
| ARPC2  | 1.94275454  |
| APOBEC3A | 1.94216227 |
| ADA    | 1.94184678  |
| DUSP2  | 1.94061147  |
| XAF1   | 1.94040151  |
| CD37   | 1.93799495  |
| CTSW   | 1.93610919  |
| NLRP1  | 1.93558212  |
| ZFP36L1 | 1.93447777  |
| PSTPIP2 | 1.93439906 |
| HLA-C  | 1.93078022  |
| IL12RB1 | 1.92876709  |
| SRGN   | 1.92844358  |
| MAN2B1 | 1.92774418  |
| TNFRSF1B | 1.92743362 |
| TMSB10 | 1.92659658  |
| CD84   | 1.92429219  |

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| Gene   | Fold Change |
|--------|-------------|
| PLEKHO1 | 1.92315891  |
| LAMP3  | 1.92306466  |
| LAT    | 1.92271261  |
| CCR7   | 1.92056913  |
| CNTRL  | 1.91987418  |
| TAP2   | 1.91852928  |
| VAMP1  | 1.91840413  |
| CAMK1D | 1.91706925  |
| THEMIS2| 1.91592596  |
| CXCL8  | 1.91498407  |
| PARP12 | 1.91288996  |
| PIK3R5 | 1.91143136  |
| CASP4  | 1.91028827  |
| MCTP1  | 1.9091806   |
| CEBPB  | 1.90915733  |
| ARL4C  | 1.90817935  |
| ACKR1  | 1.9068612   |
| PSTPIP1| 1.90549377  |
| EVL    | 1.90530416  |
| SP100  | 1.90249529  |
| ERN1   | 1.90238376  |
| RTP4   | 1.90175352  |
| IFIT3  | 1.90155478  |
| HSPH1  | 1.90127208  |
| C1QB   | 1.89829302  |
| NCKAP1L| 1.8982184   |
| AHR    | 1.89633779  |
| SLC20A1| 1.89576799  |
| DHR59  | 1.89386659  |
| Gene      | FDR 1   | FDR 2   | FDR 3   | FDR 4   |
|-----------|---------|---------|---------|---------|
| CHIC2     | 0.00    | 0.00    | 0.00    | 1.89354804 |
| MS4A4A    | 0.00    | 0.00    | 0.00    | 1.89331474 |
| SLFN12    | 0.00    | 0.00    | 0.00    | 1.89263102 |
| ADGRE2    | 0.00    | 0.00    | 0.00    | 1.89047958 |
| RNASET2   | 0.00    | 0.00    | 0.00    | 1.88729402 |
| FCGR2B    | 0.00    | 0.00    | 0.00    | 1.88665576 |
| HOPX      | 0.00    | 0.00    | 0.00    | 1.88659649 |
| IFI44L    | 0.00    | 0.00    | 0.00    | 1.88521157 |
| AP1S2     | 0.00    | 0.00    | 0.00    | 1.88454226 |
| WAS       | 0.00    | 0.00    | 0.00    | 1.88348658 |
| AIF1      | 0.00    | 0.00    | 0.00    | 1.88286408 |
| GLI1PR1   | 0.00    | 0.00    | 0.00    | 1.88249235 |
| SERTAD2   | 0.00    | 0.00    | 0.00    | 1.8823785 |
| DAP1      | 0.00    | 0.00    | 0.00    | 1.88159526 |
| FAM129A   | 0.00    | 0.00    | 0.00    | 1.88137884 |
| SDC3      | 0.00    | 0.00    | 0.00    | 1.87967227 |
| SIGLEC1   | 0.00    | 0.00    | 0.00    | 1.87925645 |
| DCK       | 0.00    | 0.00    | 0.00    | 1.87737708 |
| RGS16     | 0.00    | 0.00    | 0.00    | 1.87641639 |
| ELMO1     | 0.00    | 0.00    | 0.00    | 1.87600998 |
| BAZ1A     | 0.00    | 0.00    | 0.00    | 1.87593474 |
| IGL1      | 0.00    | 0.00    | 0.00    | 1.87570879 |
| TARP      | 0.00    | 0.00    | 0.00    | 1.87544739 |
| CTLA4     | 0.00    | 0.00    | 0.00    | 1.87449183 |
| BID       | 0.00    | 0.00    | 0.00    | 1.87368882 |
| ARHGEF6   | 0.00    | 0.00    | 0.00    | 1.87049913 |
| BTK       | 0.00    | 0.00    | 0.00    | 1.86868858 |
| RND3      | 0.00    | 0.00    | 0.00    | 1.86855943 |
| WARS      | 0.00    | 0.00    | 0.00    | 1.86585704 |

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| Gene     | 0 | 0 | 0 | Value     |
|----------|---|---|---|-----------|
| RHOH     | 0 | 0 | 0 | 1.86556438 |
| FOS      | 0 | 0 | 0 | 1.86544956 |
| IL18RAP  | 0 | 0 | 0 | 1.86529522 |
| MX2      | 0 | 0 | 0 | 1.8647553  |
| CD1D     | 0 | 0 | 0 | 1.86404656 |
| CXCR6    | 0 | 0 | 0 | 1.86353797 |
| KLRF1    | 0 | 0 | 0 | 1.8628973  |
| OGFRL1   | 0 | 0 | 0 | 1.86063546 |
| PLA2G7   | 0 | 0 | 0 | 1.86001606 |
| H2AFY    | 0 | 0 | 0 | 1.85773294 |
| PSMB10   | 0 | 0 | 0 | 1.85673482 |
| SRSF7    | 0 | 0 | 0 | 1.8554265  |
| ARHGDI8  | 0 | 0 | 0 | 1.85440944 |
| DUSP4    | 0 | 0 | 0 | 1.85437137 |
| CD40     | 0 | 0 | 0 | 1.85384103 |
| CD33     | 0 | 0 | 0 | 1.85306627 |
| IFIT2    | 0 | 0 | 0 | 1.85287826 |
| SERPINH1 | 0 | 0 | 0 | 1.85195787 |
| DDB2     | 0 | 0 | 0 | 1.85154538 |
| TRAF5    | 0 | 0 | 0 | 1.85064829 |
| IFFO1    | 0 | 0 | 0 | 1.84865504 |
| PKRCH    | 0 | 0 | 0 | 1.84639427 |
| BTG1     | 0 | 0 | 0 | 1.84552933 |
| PTPN7    | 0 | 0 | 0 | 1.84410823 |
| TLR4     | 0 | 0 | 0 | 1.84382548 |
| KIF21B   | 0 | 0 | 0 | 1.84370578 |
| CXCL13   | 0 | 0 | 0 | 1.84273866 |
| JCHAIN   | 0 | 0 | 0 | 1.84083479 |
| SLAMF7   | 0 | 0 | 0 | 1.84047916 |

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| Gene   | Fold Change |
|--------|-------------|
| CLK1   | 1.83892865  |
| TMEM131L | 1.83535327 |
| MARCKSL1 | 1.83431175 |
| VAV1   | 1.83420174  |
| SECTM1 | 1.83406348  |
| CD44   | 1.83359946  |
| FN1    | 1.83323341  |
| DUSP10 | 1.83313566  |
| HLA-DQA1 | 1.83310857 |
| MARCKS | 1.83110396  |
| ZFP36  | 1.83106185  |
| DGKA   | 1.83052584  |
| SLAMF1 | 1.8294436   |
| OASL   | 1.82666909  |
| HMGB2  | 1.82484549  |
| BASP1  | 1.82397046  |
| CTSC   | 1.8233423   |
| EFHD2  | 1.82321991  |
| ZC3HAV1 | 1.82068014 |
| PIK3CD | 1.82056002  |
| SIT1   | 1.8195582   |
| CSK    | 1.81866637  |
| LTB    | 1.81845229  |
| APOC1  | 1.81671309  |
| TCF7   | 1.81630922  |
| CXorf21 | 1.81411418 |
| BATF   | 1.81388217  |
| RASSF1 | 1.81345543  |
| TSC22D1 | 1.81320778  |

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| Gene   | Value 1 | Value 2 | Value 3 | Value 4 | Score  |
|--------|---------|---------|---------|---------|--------|
| VNN2   | 0       | 0       | 0       | 0       | 1.81227913 |
| LAG3   | 0       | 0       | 0       | 0       | 1.8122329 |
| PLA1A  | 0       | 0       | 0       | 0       | 1.81015378 |
| TNFAIP2| 0       | 0       | 0       | 0       | 1.80815742 |
| TNFRSF17| 0     | 0       | 0       | 0       | 1.80546766 |
| VIM    | 0       | 0       | 0       | 0       | 1.80541718 |
| IFI44  | 0       | 0       | 0       | 0       | 1.80271739 |
| FCHSD2 | 0       | 0       | 0       | 0       | 1.80231917 |
| TNFRSF9| 0       | 0       | 0       | 0       | 1.80129713 |
| GIT2   | 0       | 0       | 0       | 0       | 1.80113696 |
| RAB27A | 0       | 0       | 0       | 0       | 1.79455542 |
| IFITM1 | 0       | 0       | 0       | 0       | 1.79287394 |
| CPA3   | 0       | 0       | 0       | 0       | 1.79108156 |
| FCER1G | 0       | 0       | 0       | 0       | 1.78901746 |
| SOCS1  | 0       | 0       | 0       | 0       | 1.78458929 |
| CSF3R  | 0       | 0       | 0       | 0       | 1.78449721 |
| MZB1   | 0       | 0       | 0       | 0       | 1.78433334 |
| MKNK2  | 0       | 0       | 0       | 0       | 1.78210981 |
| TLR1   | 0       | 0       | 0       | 0       | 1.7820085 |
| B2M    | 0       | 0       | 0       | 0       | 1.78142226 |
| EBI3   | 0       | 0       | 0       | 0       | 1.78005656 |
| GMIP   | 0       | 0       | 0       | 0       | 1.78000393 |
| PTAFR  | 0       | 0       | 0       | 0       | 1.77706039 |
| ATP8B2 | 0       | 0       | 0       | 0       | 1.77703527 |
| CBFA2T3| 0       | 0       | 0       | 0       | 1.77658697 |
| FASLG  | 0       | 0       | 0       | 0       | 1.77630409 |
| CD74   | 0       | 0       | 0       | 0       | 1.77562647 |
| IFNAR2 | 0       | 0       | 0       | 0       | 1.7732499 |
| CCL19  | 0       | 0       | 0       | 0       | 1.77252545 |

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| Gene     | Rank | VAF | Alpha | p-value |
|----------|------|-----|-------|---------|
| NELL2    | 0    | 0   | 0     | 1.77202311 |
| FXYD5    | 0    | 0   | 0     | 1.77185315 |
| BRD2     | 0    | 0   | 0     | 1.76772958 |
| JAK3     | 0    | 0   | 0     | 1.76724512 |
| LAIR2    | 0    | 0   | 0     | 1.76502577 |
| DDX60    | 0    | 0   | 0     | 1.76476678 |
| CD7      | 0    | 0   | 0     | 1.76360243 |
| NDC80    | 0    | 0   | 0     | 1.76311006 |
| PRPF38B  | 0    | 0   | 0     | 1.76224003 |
| FAR2     | 0    | 0   | 0     | 1.75902018 |
| ARPC1B   | 0    | 0   | 0     | 1.75835304 |
| MAP3K3   | 0    | 0   | 0     | 1.75834941 |
| CKLF     | 0    | 0   | 0     | 1.75797445 |
| MS4A1    | 0    | 0   | 0     | 1.75783386 |
| ARNTL2   | 0    | 0   | 0     | 1.75621308 |
| TNFSF8   | 0    | 0   | 0     | 1.75446324 |
| RRM2     | 0    | 0   | 0     | 1.75373194 |
| EGR1     | 0    | 0   | 0     | 1.75190521 |
| GRK3     | 0    | 0   | 0     | 1.75167088 |
| SIDT1    | 0    | 0   | 0     | 1.75084914 |
| APBB1IP  | 0    | 0   | 0     | 1.74973631 |
| APOBEC3C | 0    | 0   | 0     | 1.74959712 |
| CD40LG   | 0    | 0   | 0     | 1.74823959 |
| BTN2A1   | 0    | 0   | 0     | 1.74794306 |
| MICAL2   | 0    | 0   | 0     | 1.74741849 |
| PSME1    | 0    | 0   | 0     | 1.74648474 |
| TES      | 0    | 0   | 0     | 1.74638962 |
| ZBP1     | 0    | 0   | 0     | 1.74588639 |
| SDCBP    | 0    | 0   | 0     | 1.7454835 |
| Gene     | Value1 | Value2 | Value3 | Value4 | Value5 |
|----------|--------|--------|--------|--------|--------|
| CD72     | 0      | 0      | 0      | 1.7454823 |
| TGFBI    | 0      | 0      | 0      | 1.74422384 |
| MTMR14   | 0      | 0      | 0      | 1.74329528 |
| CARD8    | 0      | 0      | 0      | 1.74304429 |
| DENND1C  | 0      | 0      | 0      | 1.74239717 |
| TSPAN32  | 0      | 0      | 0      | 1.73972072 |
| RASA2    | 0      | 0      | 0      | 1.73971197 |
| ST8SIA1  | 0      | 0      | 0      | 1.73814596 |
| CCL8     | 0      | 0      | 0      | 1.73702165 |
| SERPINB1 | 0      | 0      | 0      | 1.73620964 |
| DUSP8    | 0      | 0      | 0      | 1.73578473 |
| IRF4     | 0      | 0      | 0      | 1.73526639 |
| FPR3     | 0      | 0      | 0      | 1.73512889 |
| TCIM     | 0      | 0      | 0      | 1.73505704 |
| BLM      | 0      | 0      | 0      | 1.73263421 |
| CD79B    | 0      | 0      | 0      | 1.73097172 |
| GNA13    | 0      | 0      | 0      | 1.72706217 |
| BCL11A   | 0      | 0      | 0      | 1.72641206 |
| WFDC2    | 0      | 0      | 0      | 1.72593419 |
| ELF1     | 0      | 0      | 0      | 1.72581194 |
| C2CD2    | 0      | 0      | 0      | 1.72404254 |
| RAB31    | 0      | 0      | 0      | 1.72298895 |
| LIMD2    | 0      | 0      | 0      | 1.72189114 |
| CCNA2    | 0      | 0      | 0      | 1.71960077 |
| ELF3     | 0      | 0      | 0      | 1.7195446 |
| FOLR2    | 0      | 0      | 0      | 1.71948655 |
| CYTH4    | 0      | 0      | 0      | 1.71866983 |
| MYB      | 0      | 0      | 0      | 1.71823476 |
| NXF1     | 0      | 0      | 0      | 1.71791097 |

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| Gene     | FPKM   | FPKM   | FPKM   | Log2 Fold Change |
|----------|--------|--------|--------|-----------------|
| LDLR     | 0      | 0      | 0      | 1.71763236      |
| SEPT6    | 0      | 0      | 0      | 1.71577512      |
| TTC13    | 0      | 0      | 0      | 1.71560699      |
| CHST11   | 0      | 0      | 0      | 1.71542874      |
| CAV1     | 0      | 0      | 0      | 1.71540046      |
| CCDC69   | 0      | 0      | 0      | 1.71531691      |
| DNMT1    | 0      | 0      | 0      | 1.71501879      |
| JAK2     | 0      | 0      | 0      | 1.71054734      |
| LPAR6    | 0      | 0      | 0      | 1.71008926      |
| MYD88    | 0      | 0      | 0      | 1.70690211      |
| VAMP5    | 0      | 0      | 0      | 1.70675365      |
| FSCN1    | 0      | 0      | 0      | 1.70633955      |
| MIS12    | 0      | 0      | 0      | 1.70426291      |
| TRAFD1   | 0      | 0      | 0      | 1.70177249      |
| BMP2     | 0      | 0      | 0      | 1.7014756       |
| STX11    | 0      | 0      | 0      | 1.70103888      |
| EED      | 0      | 0      | 0      | 1.70083381      |
| RASGRP1  | 0      | 0      | 0      | 1.70070945      |
| LUM      | 0      | 0      | 0      | 1.70058634      |
| SERPING1 | 0      | 0      | 0      | 1.70050886      |
| RFX5     | 0      | 0      | 0      | 1.69983355      |
| RBM15    | 0      | 0      | 0      | 1.69935909      |
| PILRA    | 0      | 0      | 0      | 1.69865201      |
| VPS13C   | 0      | 0      | 0      | 1.69859385      |
| LPAR1    | 0      | 0      | 0      | 1.69726336      |
| IRF9     | 0      | 0      | 0      | 1.69660496      |
| NCAPG    | 0      | 0      | 0      | 1.69583141      |
| TRAF1    | 0      | 0      | 0      | 1.69482668      |
| CH25H    | 0      | 0      | 0      | 1.69392185      |

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| Gene   | Epi1 | Epi2 | Epi3 | Z-score |
|--------|------|------|------|---------|
| SPN    | 0    | 0    | 0    | 1.6934013 |
| HERC5  | 0    | 0    | 0    | 1.69202797 |
| LOXL1  | 0    | 0    | 0    | 1.69136803 |
| MSX1   | 0    | 0    | 0    | 1.69052508 |
| TNFRSF25 | 0   | 0   | 0   | 1.6902624 |
| CD3E   | 0    | 0    | 0    | 1.69017111 |
| CYLD   | 0    | 0    | 0    | 1.68968309 |
| RAP2B  | 0    | 0    | 0    | 1.68963492 |
| TUT7   | 0    | 0    | 0    | 1.68912208 |
| MTHFD2 | 0    | 0    | 0    | 1.6880102 |
| CD80   | 0    | 0    | 0    | 1.68663534 |
| VSIG4  | 0    | 0    | 0    | 1.6863206 |
| S100A6 | 0    | 0    | 0    | 1.68574209 |
| UBA7   | 0    | 0    | 0    | 1.68222646 |
| ANXA2  | 0    | 0    | 0    | 1.68172598 |
| CSF1R  | 0    | 0    | 0    | 1.68013518 |
| CAMK4  | 0    | 0    | 0    | 1.67681373 |
| KCNJ2  | 0    | 0    | 0    | 1.67648154 |
| N4BP2L1| 0    | 0    | 0    | 1.67633222 |
| S100PBP| 0    | 0    | 0    | 1.67347362 |
| REEP4  | 0    | 0    | 0    | 1.67344001 |
| APOL6  | 0    | 0    | 0    | 1.67022575 |
| DLGAP5 | 0    | 0    | 0    | 1.66820897 |
| RSRP1  | 0    | 0    | 0    | 1.66807055 |
| SOX4   | 0    | 0    | 0    | 1.66792417 |
| ATAD2  | 0    | 0    | 0    | 1.66751303 |
| CENPU  | 0    | 0    | 0    | 1.66747276 |
| CD19   | 0    | 0    | 0    | 1.66687771 |
| IRAK3  | 0    | 0    | 0    | 1.66672951 |

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| Gene   | Value1 | Value2 | Value3 | Value4 | Value5 |
|--------|--------|--------|--------|--------|--------|
| CCND3  | 0      | 0      | 0      | 0      | 1.6665844 |
| FILIP1L| 0      | 0      | 0      | 0      | 1.66653097 |
| UCP2   | 0      | 0      | 0      | 0      | 1.66458912 |
| PLXNC1 | 0      | 0      | 0      | 0      | 1.66453026 |
| NUSAP1 | 0      | 0      | 0      | 0      | 1.66404752 |
| STK26  | 0      | 0      | 0      | 0      | 1.66303644 |
| FLI1   | 0      | 0      | 0      | 0      | 1.6619662 |
| ERAP2  | 0      | 0      | 0      | 0      | 1.66131371 |
| CXCR3  | 0      | 0      | 0      | 0      | 1.66070592 |
| RSAD2  | 0      | 0      | 0      | 0      | 1.65988436 |
| PABPC4 | 0      | 0      | 0      | 0      | 1.65970338 |
| LMNB1  | 0      | 0      | 0      | 0      | 1.65930683 |
| C1R    | 0      | 0      | 0      | 0      | 1.65830752 |
| HELLS  | 0      | 0      | 0      | 0      | 1.65749816 |
| FKB11  | 0      | 0      | 0      | 0      | 1.65567463 |
| CD4    | 0      | 0      | 0      | 0      | 1.6553146 |
| ARAP2  | 0      | 0      | 0      | 0      | 1.65520485 |
| CCL18  | 0      | 0      | 0      | 0      | 1.6550502 |
| PCLAF  | 0      | 0      | 0      | 0      | 1.65472466 |
| ITM2A  | 0      | 0      | 0      | 0      | 1.65344785 |
| ZNF266 | 0      | 0      | 0      | 0      | 1.65257028 |
| MCM7   | 0      | 0      | 0      | 0      | 1.65173926 |
| CLIC3  | 0      | 0      | 0      | 0      | 1.65166733 |
| ARHGAP22| 0    | 0      | 0      | 0      | 1.64985989 |
| TENT5C | 0      | 0      | 0      | 0      | 1.64978873 |
| KLRG1  | 0      | 0      | 0      | 0      | 1.64773556 |
| HECA   | 0      | 0      | 0      | 0      | 1.64736233 |
| DOK3   | 0      | 0      | 0      | 0      | 1.64595579 |
| GNPTAB | 0      | 0      | 0      | 0      | 1.64497669 |

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| Gene    | Value 1 | Value 2 | Value 3 | Value 4 | Value 5 |
|---------|---------|---------|---------|---------|---------|
| ASAP1   | 0       | 0       | 0       | 1.64409113 |
| CD47    | 0       | 0       | 0       | 1.6426827  |
| HIST1H3D| 0       | 0       | 0       | 1.64205208 |
| PTGER4  | 0       | 0       | 0       | 1.64113961 |
| SLC15A3 | 0       | 0       | 0       | 1.64061527 |
| TRA2A   | 0       | 0       | 0       | 1.6405512  |
| DTL     | 0       | 0       | 0       | 1.63962487 |
| DCLRE1C | 0       | 0       | 0       | 1.63884978 |
| ZNF165  | 0       | 0       | 0       | 1.63803652 |
| ACAP1   | 0       | 0       | 0       | 1.63735384 |
| RASGRP2 | 0       | 0       | 0       | 1.63733558 |
| KIF20A  | 0       | 0       | 0       | 1.63641669 |
| TOP2A   | 0       | 0       | 0       | 1.63571679 |
| ELK3    | 0       | 0       | 0       | 1.63562165 |
| VPS37B  | 0       | 0       | 0       | 1.63549297 |
| GSDMB   | 0       | 0       | 0       | 1.63544187 |
| TCF4    | 0       | 0       | 0       | 1.63518521 |
| MFGN    | 0       | 0       | 0       | 1.63486088 |
| CBLB    | 0       | 0       | 0       | 1.63474222 |
| TRIM56  | 0       | 0       | 0       | 1.63348557 |
| VCAN    | 0       | 0       | 0       | 1.6302336  |
| LTF     | 0       | 0       | 0       | 1.62950828 |
| MDK     | 0       | 0       | 0       | 1.629157   |
| IFNGR2  | 0       | 0       | 0       | 1.62915645 |
| CEBPA   | 0       | 0       | 0       | 1.62831425 |
| IFI27   | 0       | 0       | 0       | 1.62819676 |
| BUB1    | 0       | 0       | 0       | 1.6280698  |
| TNC     | 0       | 0       | 0       | 1.62644798 |
| NNMT    | 0       | 0       | 0       | 1.62527629 |

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| Gene  | Log2 Fold Change |
|-------|-----------------|
| CD244 | 1.62509357      |
| CEP55 | 1.62488989      |
| COL3A1| 1.62386121      |
| ADAP2 | 1.62285782      |
| RHOG  | 1.62264651      |
| PLXND1| 1.62261016      |
| IRF2  | 1.6224868       |
| ISG15 | 1.62224174      |
| IMPDH1| 1.62109375      |
| SNW1  | 1.62073662      |
| MMP7  | 1.620502        |
| CARD9 | 1.61909898      |
| GNAI2 | 1.61904287      |
| IL12B | 1.61862507      |
| CD79A | 1.61840524      |
| CHFR  | 1.61663011      |
| AKAP13| 1.61471276      |
| OAS3  | 1.61390275      |
| MEOX1 | 1.61332761      |
| TDO2  | 1.61326664      |
| OLFM12B| 1.61166499     |
| UBE2C | 1.61067853      |
| KPNB1 | 1.61053089      |
| CP    | 1.61036798      |
| PDCD4 | 1.60856048      |
| TYMP  | 1.60849228      |
| CBR3  | 1.60826161      |
| TSC22D2| 1.60811616     |
| FAM111A| 1.6066557     |

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| Gene      | Value1 | Value2 | Value3 | Value4 | Value5 |
|-----------|--------|--------|--------|--------|--------|
| NECAP2    | 0      | 0      | 0      | 1.60571054 |
| PIK3IP1   | 0      | 0      | 0      | 1.60430458 |
| GFOD1     | 0      | 0      | 0      | 1.6036544  |
| GZMM      | 0      | 0      | 0      | 1.60351277 |
| CYTH1     | 0      | 0      | 0      | 1.60332448 |
| ATM       | 0      | 0      | 0      | 1.6030466  |
| INPP4B    | 0      | 0      | 0      | 1.60263985 |
| DENND2D   | 0      | 0      | 0      | 1.60204307 |
| STK4      | 0      | 0      | 0      | 1.60157483 |
| LAP3      | 0      | 0      | 0      | 1.60133438 |
| TNFRSF4   | 0      | 0      | 0      | 1.60087427 |
| EMP3      | 0      | 0      | 0      | 1.60021588 |
| ADRA2A    | 0      | 0      | 0      | 1.60007262 |
| PIM1      | 0      | 0      | 0      | 1.59987341 |
| C21orf91  | 0      | 0      | 0      | 1.59971125 |
| LY96      | 0      | 0      | 0      | 1.59950292 |
| MSL3      | 0      | 0      | 0      | 1.59927518 |
| PTGER2    | 0      | 0      | 0      | 1.59901072 |
| RPS11     | 0      | 0      | 0      | 1.59898459 |
| CLEC4E    | 0      | 0      | 0      | 1.5985495  |
| TPX2      | 0      | 0      | 0      | 1.59793469 |
| C1S       | 0      | 0      | 0      | 1.59736586 |
| FES       | 0      | 0      | 0      | 1.59660446 |
| XBP1      | 0      | 0      | 0      | 1.59485273 |
| MCAM      | 0      | 0      | 0      | 1.5946111  |
| LBH       | 0      | 0      | 0      | 1.59378322 |
| CENPA     | 0      | 0      | 0      | 1.59349213 |
| BCL10     | 0      | 0      | 0      | 1.59321777 |
| SH3BGL3   | 0      | 0      | 0      | 1.59272262 |

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| Gene   | Value | Value | Value | 1.59217166 |
|-------|-------|-------|-------|-------------|
| NDEL1 | 0     | 0     | 0     | 1.59217166  |
| IER2  | 0     | 0     | 0     | 1.59190133  |
| CD1E  | 0     | 0     | 0     | 1.5916335   |
| TRIM21| 0     | 0     | 0     | 1.59113097  |
| CMKLR1| 0     | 0     | 0     | 1.59051555  |
| GNA15 | 0     | 0     | 0     | 1.59005716  |
| ERAP1 | 0     | 0     | 0     | 1.58978212  |
| SAMD9 | 0     | 0     | 0     | 1.58959091  |
| ETS1  | 0     | 0     | 0     | 1.58930415  |
| GPSM3 | 0     | 0     | 0     | 1.58870132  |
| ARPC5 | 0     | 0     | 0     | 1.58710684  |
| PLSCR1| 0     | 0     | 0     | 1.58670584  |
| KIF14 | 0     | 0     | 0     | 1.58649839  |
| PMP22 | 0     | 0     | 0     | 1.58647722  |
| ZBED2 | 0     | 0     | 0     | 1.58630476  |
| TUBA1A| 0     | 0     | 0     | 1.58581074  |
| PRR5L | 0     | 0     | 0     | 1.58571366  |
| CD226 | 0     | 0     | 0     | 1.5855409   |
| TMEM156| 0    | 0     | 0     | 1.58506789  |
| PMCH  | 0     | 0     | 0     | 1.58481651  |
| RNF19A| 0     | 0     | 0     | 1.58461757  |
| CCNE2 | 0     | 0     | 0     | 1.5844883   |
| RBMS1 | 0     | 0     | 0     | 1.58444775  |
| TAPBPL| 0     | 0     | 0     | 1.58417677  |
| PDLIM1| 0     | 0     | 0     | 1.58382954  |
| CDKN1B| 0     | 0     | 0     | 1.58365374  |
| BCL6  | 0     | 0     | 0     | 1.5832491   |
| CD6   | 0     | 0     | 0     | 1.58174635  |
| LFNG  | 0     | 0     | 0     | 1.58157241  |

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| Gene     | Log2 Fold Change | p-value   |
|----------|-----------------|-----------|
| NAGK     | 0.000000        | 1.58039514|
| RIPK4    | 0.000000        | 1.57852986|
| NABP1    | 0.000000        | 1.57736644|
| HIST1H2BG| 0.000000        | 1.57670043|
| NTM      | 0.000000        | 1.5763966 |
| SAT1     | 0.000000        | 1.57598707|
| TIPARP   | 0.000000        | 1.57538386|
| FNTA     | 0.000000        | 1.57536563|
| HSP90AA1 | 0.000000        | 1.57456349|
| NR3C1    | 0.000000        | 1.57382185|
| ZNF217   | 0.000000        | 1.57327555|
| CCND2    | 0.000000        | 1.57271228|
| TSC22D3  | 0.000000        | 1.57224168|
| TNIP3    | 0.000000        | 1.57191221|
| KIF4A    | 0.000000        | 1.5712038 |
| TAPBP    | 0.000000        | 1.5691961 |
| PRC1     | 0.000000        | 1.56853573|
| PRKD2    | 0.000000        | 1.56819464|
| CDKN2AIP | 0.000000        | 1.56647593|
| BACH2    | 0.000000        | 1.56642363|
| BATF3    | 0.000000        | 1.56609817|
| PABPC3   | 0.000000        | 1.56603305|
| H2AFX    | 0.000000        | 1.56234496|
| SELE     | 0.000000        | 1.56216495|
| UBE2E1   | 0.000000        | 1.56174541|
| CST3     | 0.000000        | 1.56169459|
| HHEX     | 0.000000        | 1.56125914|
| FCRL2    | 0.000000        | 1.56038949|
| TIMP2    | 0.000000        | 1.55960415|

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| Gene | Log2 Fold Change |
|------|-----------------|
| HDC  | 1.55941959      |
| SLC16A6 | 1.55881788   |
| C3   | 1.55828046      |
| KIF11| 1.55739121      |
| IL7  | 1.55707654      |
| KLF11| 1.55682229      |
| NINJ2| 1.55679518      |
| NPDC1| 1.55666889      |
| TMC6 | 1.55608342      |
| MMP9 | 1.55601107      |
| IL1B | 1.55480441      |
| IL27RA| 1.5547195      |
| SSR2 | 1.55462966      |
| PNOC | 1.55384537      |
| GAS7 | 1.55366868      |
| MYO9B| 1.55296802      |
| CCL11| 1.55293404      |
| AGBL2| 1.55212726      |
| GEM  | 1.55160141      |
| GTF2B| 1.55096697      |
| SETX | 1.55092221      |
| NFkB1| 1.55058188      |
| PBK  | 1.54964689      |
| SELP | 1.54915175      |
| ZEB2 | 1.54855891      |
| ORC6 | 1.54799812      |
| TIMP1| 1.54778926      |
| BLK  | 1.54745075      |
| GLA  | 1.54694853      |

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| Gene     | Log2 Fold Change |
|----------|-----------------|
| DUSP22  | 1.54549389      |
| KBTBD2  | 1.54525509      |
| IL2RA   | 1.54518642      |
| FBXO5   | 1.5451359       |
| KIF15   | 1.54475812      |
| MGAT1   | 1.54469839      |
| TOB2    | 1.54406523      |
| ASPM    | 1.54363838      |
| ADAMTS1 | 1.5431586       |
| CITED2  | 1.54298474      |
| CENPM   | 1.54256655      |
| CDH5    | 1.54253433      |
| CDC25B  | 1.5407365       |
| ASTE1   | 1.54072184      |
| FANCL   | 1.54059533      |
| GLUL    | 1.54057029      |
| NFATC1  | 1.54002935      |
| HLX     | 1.53990829      |
| MAD2L1  | 1.53983885      |
| CCL13   | 1.53979585      |
| WASF2   | 1.53892004      |
| ATG12   | 1.5387196       |
| GALNT6  | 1.5381675       |
| MELK    | 1.53744022      |
| CHORDC1 | 1.53732117      |
| KIF2C   | 1.53660845      |
| SPRY1   | 1.53635951      |
| NPAT    | 1.53602363      |
| LIPA    | 1.53550836      |
| Gene   | Fold Change |
|--------|-------------|
| APBA2  | 1.53504876  |
| FHL2   | 1.53438862  |
| QPCT   | 1.53300864  |
| CXCL6  | 1.53275773  |
| EDN1   | 1.53248591  |
| LHFPL2 | 1.53166749  |
| NXPE3  | 1.53084475  |
| IL6    | 1.52863482  |
| SMC4   | 1.52786386  |
| CNOT2  | 1.52785618  |
| MX1    | 1.52736379  |
| COL4A1 | 1.52675306  |
| INPP4A | 1.52644134  |
| INHBA  | 1.52618051  |
| MYOF   | 1.52614095  |
| FAS    | 1.52599056  |
| H1FX   | 1.52530175  |
| VRK2   | 1.5252127   |
| ARGLU1 | 1.52478537  |
| FRAT2  | 1.5245678   |
| NFE2L3 | 1.5244434   |
| IL12A  | 1.52442253  |
| CYBC1  | 1.52402704  |
| ARID5A | 1.5234248   |
| FBN2   | 1.5221886   |
| CALHM2 | 1.52215745  |
| CCNB2  | 1.52193922  |
| SPHK1  | 1.52151297  |
| MAP7D1 | 1.52136532  |

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| Gene   | Fold Change |
|--------|-------------|
| ABCA7  | 1.52071519  |
| FBXW7  | 1.52029374  |
| TOPBP1 | 1.51999377  |
| EFEMP1 | 1.51988885  |
| LBR    | 1.51849527  |
| FNBP4  | 1.51786188  |
| CHI3L2 | 1.5177083   |
| CDK1   | 1.5176316   |
| RARRES3| 1.51611087  |
| KCNMA1 | 1.51594839  |
| TICAM1 | 1.51481621  |
| GRB2   | 1.51462834  |
| MYCNP2 | 1.51459376  |
| TM6SF1 | 1.51401445  |
| CENPE  | 1.51383525  |
| TSPAN13| 1.51264487  |
| BCAT1  | 1.51257381  |
| STAT5A | 1.51250663  |
| CCNB1  | 1.5118339   |
| MCM5   | 1.51143735  |
| DENND5A| 1.51094099  |
| ZNF211 | 1.51070651  |
| BMP2K  | 1.50972453  |
| ARHGAP17| 1.5085973  |
| NEDD9  | 1.50832738  |
| DEGS1  | 1.50804227  |
| OSER1  | 1.5078846   |
| APOBEC3F| 1.50788158  |
| CPVL   | 1.50718093  |

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| Gene  | 0 | 0 | 0 | 1.50618707 |
|-------|---|---|---|------------|
| ITPKC | 0 | 0 | 0 | 1.50449833 |
| LHFPL6| 0 | 0 | 0 | 1.50424811 |
| NAP1L1| 0 | 0 | 0 | 1.50413413 |
| IL4R  | 0 | 0 | 0 | 1.50355445 |
| C5AR1 | 0 | 0 | 0 | 1.50271748 |
| PAK3  | 0 | 0 | 0 | 1.50206433 |
| BUB1B | 0 | 0 | 0 | 1.50116617 |
| HIVEP3| 0 | 0 | 0 | 1.50105813 |
| CD14  | 0 | 0 | 0 | 1.50040446 |
| WDR82 | 0 | 0 | 0 | 1.50023789 |
**eTable 2b.** Downregulated Differentially Expressed Genes From SAM Analysis of Comparison of Acute Rejection to Normal Kidney Tissues

| gene    | raw p.value | q.value | Bonferroni adj. p-value | fold change |
|---------|-------------|---------|-------------------------|-------------|
| KLK1    | 0           | 0       | 0                       | 0.48693773  |
| GOT1    | 0           | 0       | 0                       | 0.49355899  |
| PTGER3  | 0           | 0       | 0                       | 0.4943702   |
| PVALB   | 0           | 0       | 0                       | 0.49798708  |
| HYAL1   | 0           | 0       | 0                       | 0.50742891  |
| EPB41L5 | 0           | 0       | 0                       | 0.51470652  |
| DAR52   | 0           | 0       | 0                       | 0.51750457  |
| NNT     | 0           | 0       | 0                       | 0.51877222  |
| FGF1    | 0           | 0       | 0                       | 0.52043111  |
| MAGI2   | 0           | 0       | 0                       | 0.52166555  |
| CERS2   | 0           | 0       | 0                       | 0.52282638  |
| PTPN3   | 0           | 0       | 0                       | 0.52743075  |
| MOCS1   | 0           | 0       | 0                       | 0.52829329  |
| NEDD4L  | 0           | 0       | 0                       | 0.52829374  |
| GAD1    | 0           | 0       | 0                       | 0.52831202  |
| RHCG    | 0           | 0       | 0                       | 0.53137225  |
| KBTBD11 | 0           | 0       | 0                       | 0.53250661  |
| HADH    | 0           | 0       | 0                       | 0.53293268  |
| SGK2    | 0           | 0       | 0                       | 0.53511649  |
| FCN3    | 0           | 0       | 0                       | 0.53743944  |
| DLAT    | 0           | 0       | 0                       | 0.53832852  |
| KLK7    | 0           | 0       | 0                       | 0.53880302  |
| DNAJA3  | 0           | 0       | 0                       | 0.54192505  |
| LRPPRC  | 0           | 0       | 0                       | 0.54362972  |
| EPHX1   | 0           | 0       | 0                       | 0.54501674  |
| Gene      | Value1 | Value2 | Value3 | Value4 | Score  |
|-----------|--------|--------|--------|--------|--------|
| GRB10     | 0      | 0      | 0      | 0      | 0.54524437 |
| DMTN      | 0      | 0      | 0      | 0      | 0.54590412 |
| FOX1      | 0      | 0      | 0      | 0      | 0.5459359  |
| SMPD1     | 0      | 0      | 0      | 0      | 0.54642479 |
| HSPA9     | 0      | 0      | 0      | 0      | 0.54762147 |
| PHB       | 0      | 0      | 0      | 0      | 0.54820387 |
| TMEM177   | 0      | 0      | 0      | 0      | 0.54909008 |
| GPD1L     | 0      | 0      | 0      | 0      | 0.54963689 |
| DHDDS     | 0      | 0      | 0      | 0      | 0.54968704 |
| ATP6V1H   | 0      | 0      | 0      | 0      | 0.5501728  |
| SPOCK1    | 0      | 0      | 0      | 0      | 0.5509999  |
| SLC4A1    | 0      | 0      | 0      | 0      | 0.55186191 |
| GHR       | 0      | 0      | 0      | 0      | 0.5528509  |
| BCL2L13   | 0      | 0      | 0      | 0      | 0.55294053 |
| TMEM59    | 0      | 0      | 0      | 0      | 0.55513674 |
| DPP6      | 0      | 0      | 0      | 0      | 0.55538654 |
| B4GAT1    | 0      | 0      | 0      | 0      | 0.55817151 |
| CRISP2    | 0      | 0      | 0      | 0      | 0.55921448 |
| CRHBP     | 0      | 0      | 0      | 0      | 0.55942343 |
| HMGCS2    | 0      | 0      | 0      | 0      | 0.56031121 |
| ADTRP     | 0      | 0      | 0      | 0      | 0.56037491 |
| SLC25A16  | 0      | 0      | 0      | 0      | 0.5603992  |
| AGAP1     | 0      | 0      | 0      | 0      | 0.56158299 |
| NECAB3    | 0      | 0      | 0      | 0      | 0.56204669 |
| SPR       | 0      | 0      | 0      | 0      | 0.56226431 |
| SYT13     | 0      | 0      | 0      | 0      | 0.56245316 |
| RPUSD2    | 0      | 0      | 0      | 0      | 0.56256769 |
| BCL2L2    | 0      | 0      | 0      | 0      | 0.5625695  |
| AQP6      | 0      | 0      | 0      | 0      | 0.5632812  |
| Gene    | Expression | Fold Change | Log2 Fold Change |
|---------|------------|-------------|-----------------|
| GRPEL1  | 0          | 0           | 0.56398692      |
| SELENBP1| 0          | 0           | 0.56420905      |
| AMFR    | 0          | 0           | 0.56512681      |
| ST7     | 0          | 0           | 0.56621966      |
| BMP7    | 0          | 0           | 0.56669982      |
| PLA2R1  | 0          | 0           | 0.56698494      |
| AK2     | 0          | 0           | 0.56707115      |
| METTL1  | 0          | 0           | 0.56770595      |
| SEMA4G  | 0          | 0           | 0.56804585      |
| MPP5    | 0          | 0           | 0.5681029       |
| MDH2    | 0          | 0           | 0.56865825      |
| TSFM    | 0          | 0           | 0.56886242      |
| COQ3    | 0          | 0           | 0.57009015      |
| TEX2    | 0          | 0           | 0.57081985      |
| CYP2B6  | 0          | 0           | 0.57109868      |
| RHBG    | 0          | 0           | 0.57141713      |
| PATJ    | 0          | 0           | 0.57151787      |
| DERA    | 0          | 0           | 0.57168891      |
| EEF1AKMT3| 0        | 0           | 0.57185939      |
| UNC13B  | 0          | 0           | 0.57238605      |
| ETFDH   | 0          | 0           | 0.57250322      |
| ALKBH4  | 0          | 0           | 0.572826        |
| SUCLG1  | 0          | 0           | 0.57333157      |
| SDC1    | 0          | 0           | 0.57336569      |
| MAOA    | 0          | 0           | 0.57338253      |
| USP46   | 0          | 0           | 0.57369374      |
| ADGRF5  | 0          | 0           | 0.57378664      |
| CA2     | 0          | 0           | 0.57380655      |
| TNNT2   | 0          | 0           | 0.5739987       |

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| Gene   | Count | Count | Count | Score  |
|--------|-------|-------|-------|--------|
| ERAL1  | 0     | 0     | 0     | 0.57514697 |
| CLDN8  | 0     | 0     | 0     | 0.57563316  |
| TMEM53 | 0     | 0     | 0     | 0.57578417  |
| RORC   | 0     | 0     | 0     | 0.57584417  |
| NDUFS1 | 0     | 0     | 0     | 0.57585491  |
| GOT2   | 0     | 0     | 0     | 0.5759408   |
| RAB17  | 0     | 0     | 0     | 0.57597645  |
| CYB5R1 | 0     | 0     | 0     | 0.57603037  |
| AHCYL2 | 0     | 0     | 0     | 0.57637154  |
| MACROD1| 0     | 0     | 0     | 0.5767688   |
| NCS1   | 0     | 0     | 0     | 0.57732837  |
| POMGNT1| 0     | 0     | 0     | 0.57739651  |
| KCNJ3  | 0     | 0     | 0     | 0.577664    |
| EGF    | 0     | 0     | 0     | 0.577745    |
| TACO1  | 0     | 0     | 0     | 0.57782508  |
| CTDSPL | 0     | 0     | 0     | 0.57785348  |
| PLCE1  | 0     | 0     | 0     | 0.57810271  |
| TLN2   | 0     | 0     | 0     | 0.5782955   |
| GATB   | 0     | 0     | 0     | 0.57945595  |
| PCP4   | 0     | 0     | 0     | 0.57954602  |
| INSR   | 0     | 0     | 0     | 0.57960972  |
| ESRRG  | 0     | 0     | 0     | 0.57976357  |
| ACADL  | 0     | 0     | 0     | 0.57985369  |
| CNNM2  | 0     | 0     | 0     | 0.58047182  |
| EBP    | 0     | 0     | 0     | 0.58060167  |
| CHUK   | 0     | 0     | 0     | 0.58073876  |
| SERPINA5| 0   | 0     | 0     | 0.58101498  |
| COASY  | 0     | 0     | 0     | 0.58149283  |
| KCNK10 | 0     | 0     | 0     | 0.58167768  |

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| Gene       | Value1 | Value2 | Value3 | Value4 |
|------------|--------|--------|--------|--------|
| SLC17A5    | 0      | 0      | 0      | 0.582197 |
| PRRG2      | 0      | 0      | 0      | 0.58247622 |
| ACADSB     | 0      | 0      | 0      | 0.58303886 |
| TCTA       | 0      | 0      | 0      | 0.58311468 |
| ATRN       | 0      | 0      | 0      | 0.58319989 |
| NDNF       | 0      | 0      | 0      | 0.58338802 |
| ALAD       | 0      | 0      | 0      | 0.58369689 |
| SLC28A1    | 0      | 0      | 0      | 0.58384042 |
| SPAC9      | 0      | 0      | 0      | 0.58413017 |
| SLC25A11   | 0      | 0      | 0      | 0.58434323 |
| ATG4A      | 0      | 0      | 0      | 0.58486939 |
| SAMM50     | 0      | 0      | 0      | 0.58530405 |
| RMDN3      | 0      | 0      | 0      | 0.585969  |
| PNPO       | 0      | 0      | 0      | 0.58609304 |
| HADHA      | 0      | 0      | 0      | 0.58627052 |
| C11orf71   | 0      | 0      | 0      | 0.58647431 |
| SLC39A7    | 0      | 0      | 0      | 0.58674849 |
| ALB        | 0      | 0      | 0      | 0.58676306 |
| SLC16A1    | 0      | 0      | 0      | 0.5868951  |
| PEX5       | 0      | 0      | 0      | 0.58709234 |
| SPAG5      | 0      | 0      | 0      | 0.58711065 |
| SLC35A2    | 0      | 0      | 0      | 0.58726177 |
| ARHGAP28   | 0      | 0      | 0      | 0.58783024 |
| GHITM      | 0      | 0      | 0      | 0.58802154 |
| DIP2C      | 0      | 0      | 0      | 0.5881149  |
| VEGFA      | 0      | 0      | 0      | 0.5882683  |
| AGBL5      | 0      | 0      | 0      | 0.58917221 |
| PLEKHA6    | 0      | 0      | 0      | 0.58933098 |
| HAGH       | 0      | 0      | 0      | 0.58997309 |
| Gene   | 0  | 0  | 0  | 0.59001746 |
|--------|----|----|----|------------|
| GPMB   | 0  | 0  | 0  | 0.5903418  |
| RNF123 | 0  | 0  | 0  | 0.59034663 |
| THRA   | 0  | 0  | 0  | 0.59050606 |
| IDH3A  | 0  | 0  | 0  | 0.5905642  |
| YIPF6  | 0  | 0  | 0  | 0.59109059 |
| PDHA1  | 0  | 0  | 0  | 0.5915313  |
| SLC25A4| 0  | 0  | 0  | 0.59177679 |
| MME    | 0  | 0  | 0  | 0.59211399 |
| TRPM6  | 0  | 0  | 0  | 0.59231096 |
| ANXA9  | 0  | 0  | 0  | 0.59245628 |
| FBXO3  | 0  | 0  | 0  | 0.59250347 |
| PREPL  | 0  | 0  | 0  | 0.59276339 |
| SLC13A3| 0  | 0  | 0  | 0.59291266 |
| AP1M2  | 0  | 0  | 0  | 0.59312721 |
| DHCR7  | 0  | 0  | 0  | 0.59317922 |
| KIF16B | 0  | 0  | 0  | 0.59333547 |
| APOO   | 0  | 0  | 0  | 0.59343205 |
| ATP6V1D| 0  | 0  | 0  | 0.59345771 |
| DUS4L  | 0  | 0  | 0  | 0.59360866 |
| THR6   | 0  | 0  | 0  | 0.59372501 |
| IDH3B  | 0  | 0  | 0  | 0.5939076  |
| TBC1D13| 0  | 0  | 0  | 0.59435672 |
| MYH14  | 0  | 0  | 0  | 0.59442735 |
| ATP5MC3| 0  | 0  | 0  | 0.59461173 |
| RGS7   | 0  | 0  | 0  | 0.59548685 |
| TXN2   | 0  | 0  | 0  | 0.59604469 |
| ATP6V0A4| 0  | 0  | 0  | 0.59606826 |
| PFKFB2 | 0  | 0  | 0  | 0.59620238 |

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| Gene       | 1 | 2 | 3 | 4 | 5 |
|------------|---|---|---|---|---|
| ACOT11     | 0 | 0 | 0 | 0 | 0.59633406 |
| PRKCA      | 0 | 0 | 0 | 0 | 0.59653172 |
| LARP4      | 0 | 0 | 0 | 0 | 0.59678552 |
| CFAP410    | 0 | 0 | 0 | 0 | 0.59710483 |
| FABP1      | 0 | 0 | 0 | 0 | 0.59711694 |
| MIEF1      | 0 | 0 | 0 | 0 | 0.59742851 |
| ST6GALNAC2 | 0 | 0 | 0 | 0 | 0.59772809 |
| GABARAPL1  | 0 | 0 | 0 | 0 | 0.5984235  |
| ESRRA      | 0 | 0 | 0 | 0 | 0.59848421 |
| THEM6      | 0 | 0 | 0 | 0 | 0.59851838 |
| HIRIP3     | 0 | 0 | 0 | 0 | 0.59920123 |
| LIN7A      | 0 | 0 | 0 | 0 | 0.59945822 |
| RPRD1A     | 0 | 0 | 0 | 0 | 0.5995077  |
| TMPRSS2    | 0 | 0 | 0 | 0 | 0.60050676 |
| RBBP9      | 0 | 0 | 0 | 0 | 0.60057405 |
| SORT1      | 0 | 0 | 0 | 0 | 0.60084207 |
| PHLDA1     | 0 | 0 | 0 | 0 | 0.60109607 |
| MCC1       | 0 | 0 | 0 | 0 | 0.60122329 |
| ACOX1      | 0 | 0 | 0 | 0 | 0.6022099  |
| TM9SF4     | 0 | 0 | 0 | 0 | 0.60260206 |
| SERPINA4   | 0 | 0 | 0 | 0 | 0.60271118 |
| COA3       | 0 | 0 | 0 | 0 | 0.6027593  |
| MIPEP      | 0 | 0 | 0 | 0 | 0.6030818 |
| PCBP2      | 0 | 0 | 0 | 0 | 0.60314059 |
| TFB2M      | 0 | 0 | 0 | 0 | 0.60318532 |
| NAXE       | 0 | 0 | 0 | 0 | 0.60344618 |
| RRAGD      | 0 | 0 | 0 | 0 | 0.60364212 |
| NDUFS3     | 0 | 0 | 0 | 0 | 0.60421724 |
| ANO10      | 0 | 0 | 0 | 0 | 0.60443645 |

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| Gene       | Value1 | Value2 | Value3 | Value4 |
|------------|--------|--------|--------|--------|
| INPP5J     | 0      | 0      | 0      | 0.60461323 |
| ANKRD46    | 0      | 0      | 0      | 0.60489972 |
| CKMT2      | 0      | 0      | 0      | 0.60504564 |
| SLC12A3    | 0      | 0      | 0      | 0.6052145  |
| SLC19A2    | 0      | 0      | 0      | 0.60525228 |
| MAIP1      | 0      | 0      | 0      | 0.60526195 |
| IPO13      | 0      | 0      | 0      | 0.60551276 |
| NDUFAF4    | 0      | 0      | 0      | 0.60562692 |
| SNTA1      | 0      | 0      | 0      | 0.60630246 |
| COPS6      | 0      | 0      | 0      | 0.60630325 |
| SLC12A2    | 0      | 0      | 0      | 0.60630451 |
| CLPB       | 0      | 0      | 0      | 0.60642462 |
| MAPT       | 0      | 0      | 0      | 0.60673555 |
| CEL        | 0      | 0      | 0      | 0.60677796 |
| F8         | 0      | 0      | 0      | 0.60709187 |
| GAS2       | 0      | 0      | 0      | 0.60744796 |
| ILVBL      | 0      | 0      | 0      | 0.60747335 |
| MRPL48     | 0      | 0      | 0      | 0.60752603 |
| NT5DC2     | 0      | 0      | 0      | 0.60772066 |
| ADIPOR1    | 0      | 0      | 0      | 0.60773454 |
| ABCC2      | 0      | 0      | 0      | 0.60773882 |
| PAFAH2     | 0      | 0      | 0      | 0.60808396 |
| NFS1       | 0      | 0      | 0      | 0.60813229 |
| ZC3H7B     | 0      | 0      | 0      | 0.6088623  |
| NECAB2     | 0      | 0      | 0      | 0.60905156 |
| CRYL1      | 0      | 0      | 0      | 0.60905185 |
| TMEM115    | 0      | 0      | 0      | 0.60961812 |
| PEX26      | 0      | 0      | 0      | 0.61020148 |
| WWOX       | 0      | 0      | 0      | 0.61042824 |
| Gene   | 0 | 0 | 0 | 0.61048453  |
|--------|---|---|---|-------------|
| EXOSC7 | 0 | 0 | 0 | 0.61063273  |
| RSA1D  | 0 | 0 | 0 | 0.61093552  |
| PHKA2  | 0 | 0 | 0 | 0.61094959  |
| ESRP2  | 0 | 0 | 0 | 0.61098197  |
| CDADC1 | 0 | 0 | 0 | 0.6110758   |
| VPS13D | 0 | 0 | 0 | 0.61122808  |
| TEX261 | 0 | 0 | 0 | 0.61139246  |
| PCCB   | 0 | 0 | 0 | 0.6113975   |
| PLOD1  | 0 | 0 | 0 | 0.61145839  |
| DMAC2  | 0 | 0 | 0 | 0.61178904  |
| PGM1   | 0 | 0 | 0 | 0.61207341  |
| FBXO22 | 0 | 0 | 0 | 0.61236188  |
| FAAH   | 0 | 0 | 0 | 0.61250224  |
| ATP6V0A1| 0 | 0 | 0 | 0.61268633  |
| HDAC11 | 0 | 0 | 0 | 0.61270468  |
| C16orf58| 0 | 0 | 0 | 0.61275685  |
| SLIT2  | 0 | 0 | 0 | 0.61288669  |
| SIRT5  | 0 | 0 | 0 | 0.61319815  |
| PLPPR1 | 0 | 0 | 0 | 0.61320403  |
| APOOL  | 0 | 0 | 0 | 0.61328219  |
| EYA2   | 0 | 0 | 0 | 0.61331547  |
| MRPL2  | 0 | 0 | 0 | 0.613372264 |
| PIGV   | 0 | 0 | 0 | 0.61395718  |
| ENTPD5 | 0 | 0 | 0 | 0.6139609   |
| SMO    | 0 | 0 | 0 | 0.61414674  |
| SMO    | 0 | 0 | 0 | 0.61462259  |
| COQ9   | 0 | 0 | 0 | 0.61465797  |
| RBKS   | 0 | 0 | 0 | 0.61509214  |

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| Gene   | FPKM | FPKM | FPKM | FPKM |
|--------|------|------|------|------|
| SIRT4  | 0    | 0    | 0    | 0.61534091 |
| TGFB3  | 0    | 0    | 0    | 0.6153716 |
| FASTKD5| 0    | 0    | 0    | 0.61554387 |
| FDX1   | 0    | 0    | 0    | 0.61569514 |
| ERLIN2 | 0    | 0    | 0    | 0.61591158 |
| MT3    | 0    | 0    | 0    | 0.61609144 |
| NDUFS2 | 0    | 0    | 0    | 0.61623592 |
| PGRMC2 | 0    | 0    | 0    | 0.61629667 |
| ALDH1L1| 0    | 0    | 0    | 0.61709833 |
| TUBGCP3| 0    | 0    | 0    | 0.61722159 |
| ECHDC3 | 0    | 0    | 0    | 0.61727769 |
| SLC22A4| 0    | 0    | 0    | 0.61755181 |
| ANGPTL3| 0    | 0    | 0    | 0.6176852 |
| DNAJC6 | 0    | 0    | 0    | 0.61782934 |
| GLRX5  | 0    | 0    | 0    | 0.61783796 |
| CREM   | 0    | 0    | 0    | 0.61790933 |
| ASL    | 0    | 0    | 0    | 0.61806758 |
| PC     | 0    | 0    | 0    | 0.61819734 |
| GJA5   | 0    | 0    | 0    | 0.61834751 |
| GJA3   | 0    | 0    | 0    | 0.61894702 |
| TCTN3  | 0    | 0    | 0    | 0.61903001 |
| NPH52  | 0    | 0    | 0    | 0.61920176 |
| SH3GL2 | 0    | 0    | 0    | 0.61934173 |
| DHR511 | 0    | 0    | 0    | 0.6193877 |
| ST3GAL6| 0    | 0    | 0    | 0.61938787 |
| SUOX   | 0    | 0    | 0    | 0.6195785 |
| PEX7   | 0    | 0    | 0    | 0.62008356 |
| ALG8   | 0    | 0    | 0    | 0.62029325 |
| MPDU1  | 0    | 0    | 0    | 0.62039811 |

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| Gene   | Value1 | Value2 | Value3 | Score  |
|--------|--------|--------|--------|--------|
| PDSS2  | 0      | 0      | 0      | 0.62058058 |
| COBL   | 0      | 0      | 0      | 0.62064794 |
| MLYCD  | 0      | 0      | 0      | 0.62068419 |
| FBXO17 | 0      | 0      | 0      | 0.62070449 |
| CALB1  | 0      | 0      | 0      | 0.62084487 |
| CDK18  | 0      | 0      | 0      | 0.62094492 |
| FBXO21 | 0      | 0      | 0      | 0.62100758 |
| NRSN2  | 0      | 0      | 0      | 0.62112565 |
| PLG    | 0      | 0      | 0      | 0.62121514 |
| TPD52  | 0      | 0      | 0      | 0.62137016 |
| MRPS15 | 0      | 0      | 0      | 0.62152315 |
| ATP6AP1| 0      | 0      | 0      | 0.62154654 |
| RITA1  | 0      | 0      | 0      | 0.6216024  |
| C1orf56| 0      | 0      | 0      | 0.62173459 |
| RASSF8 | 0      | 0      | 0      | 0.62179112 |
| SDHB   | 0      | 0      | 0      | 0.62179538 |
| PACRG  | 0      | 0      | 0      | 0.6219101  |
| FH     | 0      | 0      | 0      | 0.62191451 |
| DDX25  | 0      | 0      | 0      | 0.62199322 |
| ALS2CL | 0      | 0      | 0      | 0.62201975 |
| ADCY1  | 0      | 0      | 0      | 0.62314047 |
| ETNK2  | 0      | 0      | 0      | 0.62345784 |
| PCOLCE2| 0      | 0      | 0      | 0.62397057 |
| MTFR1  | 0      | 0      | 0      | 0.62411514 |
| NAGLU  | 0      | 0      | 0      | 0.62426877 |
| NSDHL  | 0      | 0      | 0      | 0.62434014 |
| SEMA3B | 0      | 0      | 0      | 0.62439207 |
| SLC12A6| 0      | 0      | 0      | 0.62439855 |
| FABP3  | 0      | 0      | 0      | 0.62449417 |

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| Gene       | ExpH5  | ATP6V0E2 | LONRF3 | ACAD8  | EPM2A  | AHCYL1 | ATP6V1E1 | CDKL1  | IL1RL1 | RABGGTB | HSD11B2 | KDR     | AMT     | CLCN6   | RDH11  | TBCE   | CALM1  | SIK3    | EMX1   | DNASE1 | MAPKAP1 | TOM1L2 | CAT     | ABHD10  | SNX4    | ABLIM3  | KYAT1   | MFAP3L  | RNF14   |
|------------|--------|----------|--------|--------|--------|--------|---------|--------|--------|---------|---------|---------|--------|---------|---------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|
|            | 0      | 0        | 0      | 0      | 0      | 0      | 0       | 0      | 0      | 0       | 0       | 0       | 0      | 0       | 0       | 0      | 0      | 0      | 0      | 0      | 0      | 0      | 0      | 0      | 0      |
| EXPH5      | 0.62497022 | 0.62499653 | 0.62528715 | 0.62536974 | 0.62545119 | 0.62557471 | 0.62593565 | 0.62600789 | 0.62619322 | 0.62621477 | 0.62629477 | 0.62652338 | 0.62682084 | 0.62695807 | 0.62699175 | 0.62714463 | 0.62717451 | 0.62741656 | 0.62757593 | 0.62770006 | 0.62807001 | 0.6281099 | 0.62821053 | 0.62830921 | 0.62838296 | 0.6284581 | 0.62865012 | 0.62906265 | 0.62910385 |

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| Gene   | 1   | 2   | 3   | Value   |
|--------|-----|-----|-----|---------|
| DEXI   | 0   | 0   | 0   | 0.62916512 |
| TAF7L  | 0   | 0   | 0   | 0.62924244 |
| TM7SF2 | 0   | 0   | 0   | 0.62928578 |
| RPAP1  | 0   | 0   | 0   | 0.62944379 |
| CYC1   | 0   | 0   | 0   | 0.62948498 |
| OSBP2  | 0   | 0   | 0   | 0.62971168 |
| EMCN   | 0   | 0   | 0   | 0.62974627 |
| ABHD6  | 0   | 0   | 0   | 0.62979186 |
| PTPRO  | 0   | 0   | 0   | 0.63010676 |
| ZHX3   | 0   | 0   | 0   | 0.63041814 |
| MAOB   | 0   | 0   | 0   | 0.63047255 |
| LPCAT3 | 0   | 0   | 0   | 0.63076105 |
| CD320  | 0   | 0   | 0   | 0.63077301 |
| UQCRIC1| 0   | 0   | 0   | 0.63081985 |
| ARHGEF12 | 0   | 0   | 0   | 0.63103287 |
| PSME3  | 0   | 0   | 0   | 0.63104238 |
| LDHB   | 0   | 0   | 0   | 0.63120793 |
| ALDH1B1| 0   | 0   | 0   | 0.63133618 |
| HPN    | 0   | 0   | 0   | 0.63137053 |
| AIFM1  | 0   | 0   | 0   | 0.63171872 |
| NDUFS4 | 0   | 0   | 0   | 0.63172519 |
| CORO2B | 0   | 0   | 0   | 0.63181432 |
| ZDHHC3 | 0   | 0   | 0   | 0.63188173 |
| PDK2   | 0   | 0   | 0   | 0.63192757 |
| NDUFB8 | 0   | 0   | 0   | 0.63206378 |
| APEH   | 0   | 0   | 0   | 0.63212384 |
| GLUD2  | 0   | 0   | 0   | 0.63221469 |
| NDUFS8 | 0   | 0   | 0   | 0.6323382 |
| RNF128 | 0   | 0   | 0   | 0.63238062 |

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| Gene    | Value1 | Value2 | Value3 | Value4 | Value5 |
|---------|--------|--------|--------|--------|--------|
| SAP18   | 0      | 0      | 0      | 0      | 0.63256985 |
| EPN3    | 0      | 0      | 0      | 0      | 0.63272262 |
| COX10   | 0      | 0      | 0      | 0      | 0.63278903 |
| PRSS8   | 0      | 0      | 0      | 0      | 0.63298935 |
| SSTR2   | 0      | 0      | 0      | 0      | 0.63329916 |
| PEX19   | 0      | 0      | 0      | 0      | 0.63336093 |
| SULT1C2 | 0      | 0      | 0      | 0      | 0.63336163 |
| AVPR1A  | 0      | 0      | 0      | 0      | 0.63337304 |
| MAP7    | 0      | 0      | 0      | 0      | 0.6336401  |
| COQ6    | 0      | 0      | 0      | 0      | 0.63376709 |
| PLD1    | 0      | 0      | 0      | 0      | 0.63399403 |
| CCDC25  | 0      | 0      | 0      | 0      | 0.63405646 |
| TOM1    | 0      | 0      | 0      | 0      | 0.63408286 |
| OGDH    | 0      | 0      | 0      | 0      | 0.63415406 |
| SC5D    | 0      | 0      | 0      | 0      | 0.63416204 |
| GCNT2   | 0      | 0      | 0      | 0      | 0.6341973  |
| MDH1    | 0      | 0      | 0      | 0      | 0.63435781 |
| ARHGEF28| 0      | 0      | 0      | 0      | 0.63461475 |
| ABCA5   | 0      | 0      | 0      | 0      | 0.63467778 |
| SIGMAR1 | 0      | 0      | 0      | 0      | 0.63475993 |
| ATP5F1B | 0      | 0      | 0      | 0      | 0.63477416 |
| ACAT1   | 0      | 0      | 0      | 0      | 0.63481679 |
| HSDL2   | 0      | 0      | 0      | 0      | 0.63496993 |
| SHANK2  | 0      | 0      | 0      | 0      | 0.6351465  |
| MINDY1  | 0      | 0      | 0      | 0      | 0.63526891 |
| MRP535  | 0      | 0      | 0      | 0      | 0.63528374 |
| STAP1   | 0      | 0      | 0      | 0      | 0.63532722 |
| CDK16   | 0      | 0      | 0      | 0      | 0.63547831 |
| ACO2    | 0      | 0      | 0      | 0      | 0.63572218 |

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| Gene | 0   | 0   | 0   | 0.63585672 |
|------|-----|-----|-----|------------|
| ACAT2 | 0   | 0   | 0   | 0.63595498 |
| ACSS3 | 0   | 0   | 0   | 0.63628514 |
| PXMP4 | 0   | 0   | 0   | 0.63641961 |
| WDR59 | 0   | 0   | 0   | 0.63645301 |
| PANK3 | 0   | 0   | 0   | 0.63646901 |
| STAC  | 0   | 0   | 0   | 0.63649309 |
| SMUG1 | 0   | 0   | 0   | 0.63661915 |
| ACO1  | 0   | 0   | 0   | 0.63680922 |
| ASB9  | 0   | 0   | 0   | 0.63688872 |
| SLC39A4 | 0   | 0   | 0   | 0.63703726 |
| BDH1  | 0   | 0   | 0   | 0.63708972 |
| NDUFA9| 0   | 0   | 0   | 0.63711    |
| MPC2  | 0   | 0   | 0   | 0.63711689 |
| PPARA | 0   | 0   | 0   | 0.637132   |
| IGF1R | 0   | 0   | 0   | 0.63728971 |
| ARL2  | 0   | 0   | 0   | 0.63755803 |
| DOLK  | 0   | 0   | 0   | 0.63758921 |
| EFHD1 | 0   | 0   | 0   | 0.63775323 |
| BNIP3 | 0   | 0   | 0   | 0.63817766 |
| CWH43 | 0   | 0   | 0   | 0.6383168  |
| NARS2 | 0   | 0   | 0   | 0.63832098 |
| ARHGEF17 | 0   | 0   | 0   | 0.63897513 |
| APLP1 | 0   | 0   | 0   | 0.638999   |
| CLICS | 0   | 0   | 0   | 0.63901431 |
| SLC4A2| 0   | 0   | 0   | 0.6390521  |
| SIRT3 | 0   | 0   | 0   | 0.63911534 |
| PRKAG2| 0   | 0   | 0   | 0.63953909 |
| SCN9A | 0   | 0   | 0   | 0.63960949 |

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| Gene     | Score |
|----------|-------|
| CTH      | 0.63992852 |
| NDST1    | 0.640028 |
| ATP1B2   | 0.64031619 |
| ROGD1    | 0.64070625 |
| TOLLIP   | 0.64085755 |
| VT11B    | 0.64101587 |
| LRPAP1   | 0.64115832 |
| NELL1    | 0.64128702 |
| CYFIP2   | 0.64143041 |
| SLC16A10 | 0.64145366 |
| ATP5MC1  | 0.64145609 |
| AIMP2    | 0.6414617 |
| ASB8     | 0.6416399 |
| TXNRD2   | 0.64167039 |
| PRKCE    | 0.64177746 |
| UFSP2    | 0.64186357 |
| NR2F6    | 0.64196695 |
| GRB14    | 0.64211677 |
| EXD2     | 0.64218993 |
| HPGD     | 0.64218996 |
| POLR3B   | 0.64237098 |
| PDE1C    | 0.64249782 |
| ARL15    | 0.64250653 |
| SCNN1B   | 0.6425776 |
| DNAJC11  | 0.64258478 |
| CPT2     | 0.64266474 |
| CYP46A1  | 0.64318176 |
| CKB      | 0.64318991 |
| SSX2IP   | 0.64336309 |

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| Gene       | Value1 | Value2 | Value3 | Value4 | Value5 |
|-----------|--------|--------|--------|--------|--------|
| ARFIP2    | 0      | 0      | 0      | 0      | 0.64341072 |
| SLC22A6   | 0      | 0      | 0      | 0      | 0.64346011 |
| TMBIM6    | 0      | 0      | 0      | 0      | 0.64346594 |
| GALT      | 0      | 0      | 0      | 0      | 0.64376495 |
| PEPD      | 0      | 0      | 0      | 0      | 0.64385641 |
| PKLR      | 0      | 0      | 0      | 0      | 0.64396659 |
| PSEN2     | 0      | 0      | 0      | 0      | 0.64398445 |
| TSG101    | 0      | 0      | 0      | 0      | 0.64407375 |
| UQCR10    | 0      | 0      | 0      | 0      | 0.64409706 |
| DLD       | 0      | 0      | 0      | 0      | 0.64412753 |
| ST8SIA5   | 0      | 0      | 0      | 0      | 0.64413894 |
| SPRYD7    | 0      | 0      | 0      | 0      | 0.64416525 |
| DNAJA2    | 0      | 0      | 0      | 0      | 0.64417773 |
| SPINK1    | 0      | 0      | 0      | 0      | 0.64429495 |
| SFXN1     | 0      | 0      | 0      | 0      | 0.64433592 |
| SLC37A4   | 0      | 0      | 0      | 0      | 0.64433648 |
| ACTR1B    | 0      | 0      | 0      | 0      | 0.64440448 |
| FGFBP1    | 0      | 0      | 0      | 0      | 0.64445276 |
| FAH       | 0      | 0      | 0      | 0      | 0.64451502 |
| NEBL      | 0      | 0      | 0      | 0      | 0.64461942 |
| PAICS     | 0      | 0      | 0      | 0      | 0.64490971 |
| CHI3L1    | 0      | 0      | 0      | 0      | 0.64505794 |
| MOC52     | 0      | 0      | 0      | 0      | 0.64522849 |
| GSS       | 0      | 0      | 0      | 0      | 0.64536848 |
| PDE8A     | 0      | 0      | 0      | 0      | 0.64552791 |
| PEX10     | 0      | 0      | 0      | 0      | 0.64596534 |
| CYP17A1   | 0      | 0      | 0      | 0      | 0.64604305 |
| UQCC1     | 0      | 0      | 0      | 0      | 0.64618577 |
| MINPP1    | 0      | 0      | 0      | 0      | 0.64635729 |

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| Gene      | Value1 | Value2 | Value3 | Value4 | Value5 |
|-----------|--------|--------|--------|--------|--------|
| PLEKHB1   | 0      | 0      | 0      | 0      | 0.64648183 |
| SLC35A3   | 0      | 0      | 0      | 0      | 0.64664369 |
| RAB11FIP3 | 0      | 0      | 0      | 0      | 0.6467728 |
| POMT1     | 0      | 0      | 0      | 0      | 0.64682848 |
| GSTM4     | 0      | 0      | 0      | 0      | 0.64691523 |
| ME3       | 0      | 0      | 0      | 0      | 0.64708134 |
| CLN8      | 0      | 0      | 0      | 0      | 0.64738334 |
| MARC1     | 0      | 0      | 0      | 0      | 0.64741742 |
| NR4A1     | 0      | 0      | 0      | 0      | 0.64749709 |
| BTD       | 0      | 0      | 0      | 0      | 0.64801782 |
| SNX27     | 0      | 0      | 0      | 0      | 0.64809249 |
| OSBPL1A   | 0      | 0      | 0      | 0      | 0.64834266 |
| PMVK      | 0      | 0      | 0      | 0      | 0.64837156 |
| AQP3      | 0      | 0      | 0      | 0      | 0.64849579 |
| MFN2      | 0      | 0      | 0      | 0      | 0.64850579 |
| NUDT6     | 0      | 0      | 0      | 0      | 0.64858955 |
| IMPA2     | 0      | 0      | 0      | 0      | 0.6486293 |
| ENDOG     | 0      | 0      | 0      | 0      | 0.64867917 |
| ECSIT     | 0      | 0      | 0      | 0      | 0.64868609 |
| OCEL1     | 0      | 0      | 0      | 0      | 0.64868645 |
| ST18      | 0      | 0      | 0      | 0      | 0.64869864 |
| MRPS2     | 0      | 0      | 0      | 0      | 0.6487683 |
| MPC1      | 0      | 0      | 0      | 0      | 0.6487699 |
| EPB41L4B  | 0      | 0      | 0      | 0      | 0.64881767 |
| PFKM      | 0      | 0      | 0      | 0      | 0.64889656 |
| EHBP1     | 0      | 0      | 0      | 0      | 0.64893805 |
| UPB1      | 0      | 0      | 0      | 0      | 0.64895151 |
| SLC5A6    | 0      | 0      | 0      | 0      | 0.64895577 |
| TUBAL3    | 0      | 0      | 0      | 0      | 0.64907405 |

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| Gene       | Value |
|------------|-------|
| CCNB1IP1   | 0     |
| SLC35D1    | 0     |
| MKKS       | 0     |
| RAP1GAP    | 0     |
| PAK4       | 0     |
| PEX3       | 0     |
| RMND5B     | 0     |
| PDZD8      | 0     |
| C1orf115   | 0     |
| FA2H       | 0     |
| ADGRF1     | 0     |
| ATP6V1C1   | 0     |
| ATP5F1A    | 0     |
| CLMN       | 0     |
| AHCY       | 0     |
| MARC2      | 0     |
| PLEKHA5    | 0     |
| NDRG2      | 0     |
| SDHAF3     | 0     |
| NPHS1      | 0     |
| ADCY9      | 0     |
| CLPTM1     | 0     |
| RALYL      | 0     |
| ANK2       | 0     |
| ACAA1      | 0     |
| GCDH       | 0     |
| ADH5       | 0     |
| CDIP1      | 0     |
| TSPAN7     | 0     |

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| Gene      | Value1 | Value2 | Value3 | Value4 | Score   |
|-----------|--------|--------|--------|--------|---------|
| LMBRD1    | 0      | 0      | 0      | 0      | 0.65279721 |
| TEX264    | 0      | 0      | 0      | 0      | 0.65285213 |
| SHARPIN   | 0      | 0      | 0      | 0      | 0.65351209 |
| CIDEB     | 0      | 0      | 0      | 0      | 0.65354068 |
| HAO1      | 0      | 0      | 0      | 0      | 0.65365529 |
| SETMAR    | 0      | 0      | 0      | 0      | 0.65397413 |
| SLC25A10  | 0      | 0      | 0      | 0      | 0.65399028 |
| RAB3A     | 0      | 0      | 0      | 0      | 0.65401716 |
| SLC7A10   | 0      | 0      | 0      | 0      | 0.65416239 |
| TPMT      | 0      | 0      | 0      | 0      | 0.65418989 |
| HRG       | 0      | 0      | 0      | 0      | 0.65455769 |
| CACNA1D   | 0      | 0      | 0      | 0      | 0.65481452 |
| EMC1      | 0      | 0      | 0      | 0      | 0.65490098 |
| INKA2     | 0      | 0      | 0      | 0      | 0.65491706 |
| CISD1     | 0      | 0      | 0      | 0      | 0.65549494 |
| MRPS7     | 0      | 0      | 0      | 0      | 0.65550108 |
| PHF7      | 0      | 0      | 0      | 0      | 0.65577024 |
| ABCB6     | 0      | 0      | 0      | 0      | 0.65612452 |
| GRTP1     | 0      | 0      | 0      | 0      | 0.65619041 |
| TFAP2A    | 0      | 0      | 0      | 0      | 0.65632531 |
| STUB1     | 0      | 0      | 0      | 0      | 0.65643208 |
| ATP1A1    | 0      | 0      | 0      | 0      | 0.65670569 |
| GRHPR     | 0      | 0      | 0      | 0      | 0.65672816 |
| SUCLG2    | 0      | 0      | 0      | 0      | 0.65675561 |
| FOLR3     | 0      | 0      | 0      | 0      | 0.65689424 |
| GPR137    | 0      | 0      | 0      | 0      | 0.6571419  |
| ATP6V1B1  | 0      | 0      | 0      | 0      | 0.65718845 |
| ETFB      | 0      | 0      | 0      | 0      | 0.65739331 |
| PHYH      | 0      | 0      | 0      | 0      | 0.65748304 |

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| Gene       | Value1 | Value2 | Value3 | Value4 | Score       |
|------------|--------|--------|--------|--------|-------------|
| ATXN7L1    | 0      | 0      | 0      | 0      | 0.65752238  |
| SCAP       | 0      | 0      | 0      | 0      | 0.65765304  |
| DLST       | 0      | 0      | 0      | 0      | 0.65771883  |
| KIAA0232   | 0      | 0      | 0      | 0      | 0.65773484  |
| PCBD1      | 0      | 0      | 0      | 0      | 0.65777665  |
| SLC26A4    | 0      | 0      | 0      | 0      | 0.65794581  |
| WBP2       | 0      | 0      | 0      | 0      | 0.65794832  |
| TACC2      | 0      | 0      | 0      | 0      | 0.65795819  |
| CHCHD3     | 0      | 0      | 0      | 0      | 0.65809824  |
| POLR2C     | 0      | 0      | 0      | 0      | 0.65821282  |
| CRYZ       | 0      | 0      | 0      | 0      | 0.65823033  |
| MAB21L4    | 0      | 0      | 0      | 0      | 0.65825044  |
| PPIF       | 0      | 0      | 0      | 0      | 0.65838071  |
| AKAP1      | 0      | 0      | 0      | 0      | 0.65841778  |
| HTRA1      | 0      | 0      | 0      | 0      | 0.65853041  |
| CYB5A      | 0      | 0      | 0      | 0      | 0.65866192  |
| PEBP1      | 0      | 0      | 0      | 0      | 0.65869036  |
| ZGPAT      | 0      | 0      | 0      | 0      | 0.65873034  |
| ALLC       | 0      | 0      | 0      | 0      | 0.65892579  |
| ITPR1      | 0      | 0      | 0      | 0      | 0.65900321  |
| ATP5F1C    | 0      | 0      | 0      | 0      | 0.6590526   |
| RAB11FIP5  | 0      | 0      | 0      | 0      | 0.65913982  |
| MAGI1      | 0      | 0      | 0      | 0      | 0.65927579  |
| ATP6V1G2   | 0      | 0      | 0      | 0      | 0.65936406  |
| KIAA0391   | 0      | 0      | 0      | 0      | 0.6598485   |
| SHC3       | 0      | 0      | 0      | 0      | 0.66020766  |
| MCOLN3     | 0      | 0      | 0      | 0      | 0.66046096  |
| UAP1       | 0      | 0      | 0      | 0      | 0.66058953  |
| USP5       | 0      | 0      | 0      | 0      | 0.66065441  |

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| Gene   | Value1 | Value2 | Value3 | Value4 | Score   |
|--------|--------|--------|--------|--------|---------|
| PDZRN3 | 0      | 0      | 0      | 0      | 0.66088434 |
| VPS26C | 0      | 0      | 0      | 0      | 0.66091172 |
| CBR1   | 0      | 0      | 0      | 0      | 0.66130666 |
| MARK1  | 0      | 0      | 0      | 0      | 0.66132662 |
| TRPM3  | 0      | 0      | 0      | 0      | 0.6613496  |
| MCAT   | 0      | 0      | 0      | 0      | 0.66143952 |
| MSRA   | 0      | 0      | 0      | 0      | 0.6615252  |
| ZCCHC14| 0      | 0      | 0      | 0      | 0.66159982 |
| VAC14  | 0      | 0      | 0      | 0      | 0.66172644 |
| FASTKD2| 0      | 0      | 0      | 0      | 0.66176906 |
| AP3B1  | 0      | 0      | 0      | 0      | 0.66193913 |
| UBOX5  | 0      | 0      | 0      | 0      | 0.66196981 |
| DUSP3  | 0      | 0      | 0      | 0      | 0.66197201 |
| SLC3A2 | 0      | 0      | 0      | 0      | 0.6619813  |
| ZSCAN5A| 0      | 0      | 0      | 0      | 0.66226148 |
| DCTN1  | 0      | 0      | 0      | 0      | 0.66246816 |
| ADI1   | 0      | 0      | 0      | 0      | 0.66254295 |
| DLEU1  | 0      | 0      | 0      | 0      | 0.66260859 |
| FHIT   | 0      | 0      | 0      | 0      | 0.66266209 |
| ARHGAP24| 0      | 0      | 0      | 0      | 0.66269943 |
| FAM50B | 0      | 0      | 0      | 0      | 0.66289696 |
| THAP9  | 0      | 0      | 0      | 0      | 0.66305098 |
| CES2   | 0      | 0      | 0      | 0      | 0.66324575 |
| GRAMD1C| 0      | 0      | 0      | 0      | 0.66325097 |
| PSM9D  | 0      | 0      | 0      | 0      | 0.6632865  |
| SCNN1A | 0      | 0      | 0      | 0      | 0.66340933 |
| PRLR   | 0      | 0      | 0      | 0      | 0.66341194 |
| ALDH6A1| 0      | 0      | 0      | 0      | 0.66346541 |
| GPS2   | 0      | 0      | 0      | 0      | 0.66350097 |

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| Gene     | 0 | 0 | 0 | 0.66510283  |
|----------|---|---|---|-------------|
| SLC26A6  | 0 | 0 | 0 | 0.66462376  |
| DLGAP2   | 0 | 0 | 0 | 0.664645    |
| ICMT     | 0 | 0 | 0 | 0.66466051  |
| DCXR     | 0 | 0 | 0 | 0.66503721  |
| UROD     | 0 | 0 | 0 | 0.66503874  |
| UQCRC2   | 0 | 0 | 0 | 0.66510283  |
| MRPL42   | 0 | 0 | 0 | 0.66532017  |
| EHD3     | 0 | 0 | 0 | 0.6654402   |
| MICU1    | 0 | 0 | 0 | 0.6656005   |
| MRPS18B  | 0 | 0 | 0 | 0.66579376  |
| LARP6    | 0 | 0 | 0 | 0.66587277  |
| PCTP     | 0 | 0 | 0 | 0.66589734  |
| HMOX2    | 0 | 0 | 0 | 0.66591241  |
| SLC1A1   | 0 | 0 | 0 | 0.66592445  |
| NPAS2    | 0 | 0 | 0 | 0.66605708  |
| ZC2HC1C  | 0 | 0 | 0 | 0.66637196  |
| WDTC1    | 0 | 0 | 0 | 0.66639081  |
| SLC7A8   | 0 | 0 | 0 | 0.66647586  |
| SDHD     | 0 | 0 | 0 | 0.66663406  |
| UBE2D4   | 0 | 0 | 0 | 0.66665164  |

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### eTable 3. Cell Types Considered in Cell Type Enrichment Analysis With xCell

| Cells                              | Family | Type    |
|-----------------------------------|--------|---------|
| Erythrocytes                      | HSC    | HSC     |
| HSC                               | HSC    | HSC     |
| Megakaryocytes                    | HSC    | HSC     |
| Platelets                         | HSC    | HSC     |
| B-cells                           | Immune | Lymphoid|
| CD4+ memory T-cells               | Immune | Lymphoid|
| CD4+ naive T-cells                | Immune | Lymphoid|
| CD4+ T-cells                      | Immune | Lymphoid|
| CD4+ Tem                          | Immune | Lymphoid|
| CD8+ naive T-cells                | Immune | Lymphoid|
| CD8+ T-cells                      | Immune | Lymphoid|
| CD8+ Tem                          | Immune | Lymphoid|
| Class-switched memory B-cells     | Immune | Lymphoid|
| Memory B-cells                    | Immune | Lymphoid|
| naive B-cells                     | Immune | Lymphoid|
| NK cells                          | Immune | Lymphoid|
| NKT                               | Immune | Lymphoid|
| Plasma cells                      | Immune | Lymphoid|
| pro B-cells                       | Immune | Lymphoid|
| Tgd cells                         | Immune | Lymphoid|
| Th1 cells                         | Immune | Lymphoid|
| Th2 cells                         | Immune | Lymphoid|
| Tregs                             | Immune | Lymphoid|
| aDC                               | Immune | Myeloid |
| Basophils                         | Immune | Myeloid |
| Cells                | Immune | Myeloid   | Non-Hematopoietic | Stroma |
|----------------------|--------|-----------|-------------------|--------|
| cDC                  |        |           |                   |        |
| DC                   |        |           |                   |        |
| Eosinophils          |        |           |                   |        |
| iDC                  |        |           |                   |        |
| Macrophages          |        |           |                   |        |
| Macrophages M1       |        |           |                   |        |
| Macrophages M2       |        |           |                   |        |
| Mast cells           |        |           |                   |        |
| Monocytes            |        |           |                   |        |
| Neutrophils          |        |           |                   |        |
| pDC                  |        |           |                   |        |
| Epithelial cells     |        |           |                   |        |
| Endothelial cells    |        |           |                   |        |
| Fibroblasts          |        |           |                   |        |
| Ly Endothelial cells |        |           |                   |        |
| Mesangial cells      |        |           |                   |        |
| MSC                  |        |           |                   |        |
| mv Endothelial cells |        |           |                   |        |

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