Supplementary Materials

Data collection and pre-processing

Normalized microarray datasets and their array annotation files were downloaded from GEO (Table S1). The transcript-level data along with gene annotation for all the public datasets were generated for downstream meta-analysis. A further 2 datasets belonged to our research group as part of the Genomics of Chronic Allograft Dysfunction (GoCAR) study, one of which is published and available via GEO. Datasets were randomly divided into discovery and validation cohorts. Samples were dichotomized to AR (which consisted of TCMR including borderline TCMR, ABMR and mixed cases) or non-AR, as identified by their original studies. The majority of patients in each of these datasets were under CNI-based immunosuppression, as described in their relevant publications. **Discovery Set**(1-6)**:** In the meta-analysis, 2 datasets were from the GoCAR study-GSE57387 (published) which consists of 3 month post-transplant protocol biopsies and GSE138043 which consists of 12 month post-transplant protocol biopsies. Biopsies were scored by the revised Banff 2009 classification of renal allograft pathology, rejection cases here are TCMR including borderline cases. The other 5 publicly available datasets were downloaded from the GEO database: 17 transplant biopsy cases from GSE1563 (7 with acute rejection, 10 from stable allografts without) were graded by the Banff 1995 classification (rejection subtypes not defined at that time) as referenced in their original study. GSE9493 consisted of biopsies from 42 patients graded by Banff 1997 version (rejection subtypes not defined at that time) (7), by two independent pathologists. GSE34437 contained 33 samples from both indication and protocol biopsies of pediatric and young adult patients, with Banff 2007 classification acute TCMR grades IA, IB and borderline cases included in the rejection group. All 403 indication biopsies in GSE36059 were examined by two pathologists (3/5 of samples were read by a third pathologist additionally). They used a modified Banff classification (2012 classification system) which included C4d negative ABMR and probable ABMR and divided 122 acute rejection cases into ABMR, TCMR and mixed. GSE50084 had 28 samples with ABMR, and 20 normal biopsies. **Validation Set** (8-18)**:** Validation set consisted of 5 publicly available kidney allograft tissue microarray datasets. GSE21374 (282 samples) included TCMR, borderline TCMR and ABMR (Banff 2007), while GSE25902 (120 protocol samples) only included TCMR cases (Banff 2007) (none with ABMR) as the rejection cases for analysis. GSE48581 had 300 biopsies from TCMR versus non-rejection patients (Banff 2007). GSE50058 had 101 samples and acute rejection subtype was not available, and biopsies from GSE14328 (36 samples) were from pediatric recipients and classified according to Banff 2005 classification (rejection cases were TCMR with Banff grades IA, IIA, IIB)(19). Moreover, GSE21374 also contained graft failure/censoring information with post-biopsy follow-up durations ranging from 4 months to 37 years. All heart transplant data sets- GSE2596 (50 samples), GSE4470 (25 samples) and GSE9377 (26 samples) used the International Society of Heart and Lung Transplant (ISHLT) grading system to classify samples. Both GSE6095 (66 samples) and GSE2018 (34 samples) were scored separately on A (vascular) and B (airway) scales according to ISHLT and acute rejection was determined as A + B greater or equal to 2.

Meta-Analysis and Meta-Network

Meta-analysis was performed across the seven microarray datasets using two approaches to identify differential meta-gene signatures between AR and non-AR sample groups: 1) combined effect size and 2) combined p-values. The overlap genes from these two approaches made up the final 982-gene meta-signature for further downstream network construction.

Combining Effect Size

Effect size refers to the magnitude of effect observed in a study/dataset, independent of sample size. In our bioinformatic analyses, we calculated two measures of effect size : Firstly in the meta-analysis to derive a differential meta-gene signature of AR versus non-AR samples, *Hedges' g* was calculated, which estimates the standardized mean difference of gene expression between groups (20). Secondly in meta-network and module construction, effect size calculation using Fisher z-transformation score was employed (21). Both measures of effect sizes were combined across the datasets later to provide meta effect size.

To estimate the standardized mean difference, unbiased *Hedges' g* was firstly calculated for each probe set as (Eq. 1) (20, 22)

$$g = \left(1 - \frac{3}{4(n_1+n_2)-9}\right)\frac{\overline{x_1}-\overline{x_2}}{s^*} \quad \text{where} \quad s^* = \sqrt{\frac{(n_1-1)s_1^2+(n_2-1)s_2^2}{n_1+n_2-2}} \qquad \text{(Eq.1)}$$

Secondly, we combined ES of probes to gene level for each dataset by applying Fixed-Effects Model (Eq.2), where the ES of each gene was weighted by inverse of variance within each dataset. Then the ES of each gene in each dataset was further combined into one meta-ES across all datasets, using the Random Effects Model in which the amount of heterogeneity (τ_2) was added to denote the between-dataset variance and was estimated via DerSimonian-Laird method. (Eq.3) (23) Finally, a Z-score test was performed to identify significant meta-differentially-expressed genes, and corresponding p values were corrected by Benjamini-Hochberg method.

$$\overline{ES} = \frac{\sum w_i es_i}{\sum w_i} \quad \text{where} \quad w_i = \frac{1}{v_i} \qquad \text{(Eq.2)}$$

$$\text{or} \quad w_i = \frac{1}{(v_i+\hat{\tau}^2)} \qquad \text{(Eq.3)}$$

When correlation coefficients are used as the metric of the effect size, one can also weigh and combine them into meta-correlation coefficients in a similar way. We first constructed the co-expression network for each data set for AR and non-AR groups separately and let $r_{a,b}$ denote the Pearson correlation coefficient between gene a and gene b. $r_{a,b}$ was then converted to a normal Z score (Fisher z-transformation) as (Eq.4)

$$z_{a,b} = \frac{1}{2}\ln\left(\frac{1+r_{a,b}}{1-r_{a,b}}\right) \qquad \text{(Eq.4)}$$

Thereafter the meta effect size $\bar{z}_{a,b}$ was computed as Eq.2 and Eq.3 whereas $v_i = \frac{1}{n_i-3}$, and n_i was the sample size of *i*th data set. At the final step we reconverted the meta $\bar{z}_{a,b}$ to a meta-correlation coefficient r.

Combining P-values

We calculated p values from limma test(24) for each data set separately and summarize p values into an overall p for each gene using weighted inverse normal method by Marot and Mayer (Eq. 5). Here $\tilde{p}_g(s)$ denotes individual p value for gene g in study s and $n(s)$ be the sample size of study s. (25, 26)

$$S_g = \sum_{s=1}^{k} w_s\, \Phi^{-1}\left(1-\tilde{p}_g(s)\right) \quad \text{Where } w_s = \sqrt{\frac{n(s)}{\sum_{i=1}^{k} n(i)}} \qquad \text{(Eq.5)}$$

Since S_g follows a standard normal distribution, overall significance is obtained by Eq.6. Additionally, the Benjamini-Hochberg method was applied to adjust for multiple testing at $\alpha = 0.05$.

$$P_g = 2(1-\Phi(|S_g|)) \qquad \text{(Eq.6)}$$

Meta-gene and Meta-network definition

Significant meta-genes were selected if the following conditions were fulfilled: 1) FDR of the combined ES < 0.05; 2) individual ES was in the same direction, either up or down, in at least 6 out of 7 data sets; 3) FDR of combined P-values < 0.05. Meta-co-Expression-Network was identified by picking up gene-gene connections with meta $|r| >= 0.6$ and FDR < 0.05.

Functional Analysis of meta-genes

Gene expression profiles of 214 mouse samples across 15 immune cell types on Affymetrix microarray were downloaded from the ImmGene database (https://www.immgen.org/). In order to build an immune cell type database containing gene-immune cell type linkage information based on expression levels, we first ranked expression values across samples for each gene to construct an original rank matrix. 100000 random rank matrices were then calculated from 100000 times sample permutations. To obtain significance of each cell type, a permutation test was performed by comparing original matrix to random matrices. The database was constructed by assigning genes to different cell types according to the expression in the cell type compared with random chance. Lastly we input the upregulated meta-genes to the database and performed a Fisher's exact test to identify enriched cell types. Similarly, the Gene Ontology enrichment analysis was performed on the same set of upregulated meta-genes by Fisher’s exact test, the database was download directly from https://david.ncifcrf.gov.

Module Searching and Differential Network

Markov Cluster Algorithm is a scalable unsupervised cluster algorithm for networks. It is based on random walks which turns a network to a transition probability matrix, thus it tends to discover flows that are more likely to gather together in graphs. An input parameter Inflation I is needed when learning Markov Cluster structure(27). It is responsible for strengthening dense regions and weakening sparse boundaries by repeatedly raising a single column in transition metric to a non-negative power, and then re-normalizing till convergence (Eq. 7). In our analysis, we used MCL-edge software downloaded from http://micans.org/mcl/. We input our Meta-co-expression-Network for AR patients as the initial graph and chose $I = 5$ to obtain fine-grained clusters(27). Thus Meta-co-expression Network was divided into 31 modules with size larger than 5.

$$(\Gamma_{\mathrm{r}} M)_{pq} = \frac{(M_{pq})^r}{\sum_{i=1}^{k}(M_{iq})^r} \qquad \text{(Eq.7)}$$

The Differential Network was done resting on modules identified by MCL. The aim was to see whether connectivity of gene clusters which highly correlated in AR group differentiates from that of the non-AR group. To bring in definition of DN, we first introduced distance between two networks. Because we constructed the Meta-co-expression Network for AR and non-AR patients separately, the distance between AR and non-AR modules can be given by Euclidean distance, adjusted for the size of the gene set considered. (Eq. 8) Here r_c^{ACR}, r_c^{CTRL} are co-expression coefficients in two groups for the same gene pair(28).

$$D(\boldsymbol{r_c^{ACR}}, \boldsymbol{r_c^{CTRL}}) = \sqrt{\frac{1}{P_c}\sum_{p=1}^{P_c}(r_p^{ACR} - r_p^{CTRL})^2} \quad \text{where} \quad P_c = \binom{n_c}{2} \qquad \text{(Eq. 8)}$$

Likewise, we rebuilt the null Meta-co-expression-Network by randomly shuffling samples into two groups and calculated D_{null} in 1000 times permutation. P-value was computed as times of D_{null} larger than $D_{original}$ divided by 1000. Therefore, Differential Network was defined as modules with significant ($p < 0.05$) larger distance between AR and non-AR samples than random conditions.

Bayesian Network Construction and Key Drivers Identification

Differentially connected modules were then used to build directed regulatory networks to identify key drivers which may play a causal role in acute rejection and be evaluated as drug targets in AR prophylaxis. SNP information was incorporated as a prior to aid the construction of a directed network.

By examining the association between the expression of meta-genes and genome-wide SNP data, it is possible to identify Expression Quantitative Trait Loci (eQTL) that may inform on the regulation of gene expression in acute rejection pathways to improve the construction of a directed network. Gender- adjusted microarray data of all meta-genes were included for the Pearson correlation test with ~ 10 million SNP dosage data from 122 donors in the GOCAR project. Considering only SNPs that are on the same chromosome with the corresponding gene, SNPs located within 500kb flanking region of such gene were defined as cis-SNPs otherwise they were regarded as trans-SNPs. We first tested the correlation between meta-genes and their cis-SNPs and adjusted p values using the Bonferroni correction method cutting off at 0.05. Genes which were selected with significant cis-SNPs were then used to search for correlated trans-SNPs in the same manner.

Firstly, we performed normalization per sample for each original data set by transforming expression values to a standard Z-score and integrated all 7 datasets into one data set. This new set contained 241 AR samples which was later used to construct the Bayesian Network in module scale. As mentioned before eQTLs were incorporated as a prior following one rule: assuming SNP *s* is in the cis-location to gene *a* and in the trans-location to gene *b*, meanwhile *s* is significantly correlated with expression of both *a* and *b*, then *b* cannot be the parent of *a* ($\mathrm{P}(\mathrm{b} \rightarrow \mathrm{a}) = 0$)(29).

A Bayesian Network is a directed graph model for reasoning uncertain domains, where nodes represent variables (genes in our analysis) and arrows represent probabilistic dependencies between them. Given a set of variables $\boldsymbol{X} = \{X_1, \ldots, X_n\}$, a Bayesian Network is a graph $\boldsymbol{G}$ that defines a joint probability distribution where every X_i only depends on its parents Π_{X_i} (Eq. 9)(30)

$$P(X_1, \ldots, X_n) = \prod_{i=1}^{n} P(X_i | \Pi_{X_i}) \qquad \text{(Eq. 9)}$$

To learn the structure of the graph, a log-likelihood function was first defined (Eq. 10). Assuming a training set $\boldsymbol{\mathcal{D}} = \{\boldsymbol{X}_1, \ldots, \boldsymbol{X}_m\}$ where $\boldsymbol{X}_m$ is the m*th* instance of $\boldsymbol{X}$, the strategy of learning Bayesian Network is to find a structure $\boldsymbol{G}$ and parameter $\boldsymbol{\Theta}$ that maximizes the likelihood of $\boldsymbol{\mathcal{D}}$. Bayesian Information Criterion is one of the commonly used methods that takes into account not only likelihood function but also model complexity (Eq. 11). Therefore, the attempt of learning the structure becomes a heuristic search procedure that optimizes its solution by maximizing the BIC score. Here M is the number of instances in $\boldsymbol{\mathcal{D}}$ and $Dim[\boldsymbol{G}]$ is the number of parameters in $\boldsymbol{G}$ (31).

$$L(\boldsymbol{\mathcal{D}}: \boldsymbol{G}, \boldsymbol{\Theta}) = logP(\boldsymbol{\mathcal{D}}: \boldsymbol{G}, \boldsymbol{\Theta}) = \sum_m logP(\boldsymbol{X_m}: \boldsymbol{G}, \boldsymbol{\Theta}) \qquad \text{(Eq. 10)}$$

$$BIC(\boldsymbol{\mathcal{D}}, \boldsymbol{G}) = \max_{\theta} L(\boldsymbol{\mathcal{D}}: \boldsymbol{G}, \boldsymbol{\Theta}) - \frac{logM}{2} Dim[\boldsymbol{G}] \qquad \text{(Eq. 11)}$$

In this study, a modified hill climbing greedy search algorithm Tabu Search was used (32). It starts with an initial network $\boldsymbol{G_0}$ created by eQTL information. In each iteration, it calculates a BIC score for a new structure $\boldsymbol{G'}$ by ADDING, DELETING, REVERSING or REPLACING an edge from the previous structure $\boldsymbol{G}$. Finally, the optimum structure $\boldsymbol{G_{best}}$ is reached when no BIC score of $\boldsymbol{G'}$ is larger than that of $\boldsymbol{G_{best}}$.

We overlapped the Bayesian Network with the Meta-co-expression-Network for identified modules to obtain final directed networks. Gene b is said to be downstream of Gene a if it can be reached following paths of origin from a. In addition, the number of arrows that directly point outward from a is called an out-degree of Gene a. For a module of genes, Key Drivers were then selected as genes that had downstream numbers above $\overline{DS} + \sigma(DS)$ and had out-degrees above $\overline{OD} + 2\sigma(OD)$. (29) Furthermore, we defined that if a Key Driver is not in the downstream of any other KDs in the same module it becomes a global driver, otherwise it is a local driver(33).

Validation in additional kidney and other solid organ transplant datasets

The validation of the up-regulation of key driver genes in additional AR datasets was also sought, and evaluated in 5 external kidney datasets along with 3 heart, 2 lung and 2 liver allograft datasets to determine their expression in other solid organ types. The expression of the key driver genes in these datasets between AR and non-AR samples were calculated using the limma test(24). The number of key drivers that were significantly differentially expressed in each dataset for each organ type was counted and expressed as an average percentage per dataset per organ type. A receiver-operating characteristic (ROC) curve analysis of the 14- key driver signature was performed on each of these independent solid organ datasets for validation, and their discriminatory ability for AR versus non-AR samples were compared using area under the curve (AUC) in a pairwise manner. The ROC curve was generated by calculating the geometric means of the identified KDGs, since all were up-regulated. The geometric mean of the KDGs was aligned with AR to produce true positive rates and false positive rates at different cut-offs, and then plotted these to generate an ROC curve.

Survival Analysis

Expressions of 14 KDGs were fitted into a Cox regression model using “survival” package in R. The median cut-off of the predicted values was used as the cut-off for a ‘low’ versus ‘high’ risk, which was then applied to the GoCAR 3month cohort comprising protocol biopsy samples and the independent dataset GSE21374 which provided graft loss data from biopsy samples (GOCAR which contains 11 graft losses (total 159 patients) and GSE21374 which contains 51 graft losses (total 282 recipients)). Log rank p-value was presented to show significance. Time-dependent ROC curves were estimated using “timeROC” package in R at one and two years post-transplant in the GoCAR dataset, and one and two years post-biopsy in the independent dataset.

Computational identification of novel therapeutics for drug repurposing

The key driver-based signature of AR was used to query Connectivity Map (CMAP), based on the hypothesis that drugs which induce opposing effects on gene expression of this input AR signature would potentially have therapeutic impact on AR. This strategy has been similarly employed by our group previously (34). The 6,100 individual experiments were merged into a single representative signature for each of the 1,309 compounds in the CMAP library, according to the prototype-ranked list method (35). A modified Kolmogorov-Smirnov (KS) algorithm is provided by the CMAP website and used to calculate a connectivity score for each compound which assumes a value from -1 to +1, representing the degree of concordance between each compound’s transcriptional profile and the AR signature. Ranking of all 1,309 compounds is generated based on the connectivity score. Significance of individual scores was estimated by generating an empirical KS score distribution from the AR input gene set to 1,000 permuted compound signatures.

DrugBank (36) version 5.1.2 ‘Targets’ search tab was also used to input the individual key driver genes, to identify compounds with inhibitory activity against these. Filtering by ‘approved’ and ‘U.S.’ as provided by the database was applied to identify drugs with U.S. market availability. The drug targets from CMAP and DrugBank were compared to choose the candidate drug for experimental validation in the mouse heart transplant model.

Image analysis

For IHC image analysis, 10 high powered fields within each CD3 and galectin-3 stained image and 5 high powered fields within each troponin I stained image were randomly selected by an independent observer blinded to the experimental groups, using Aperio Image scope (Version 12.4.0; Leica Biosystem USA). Fields were restricted to within a cross-section of the left ventricle, and the spread of the fields within the cross section was conserved between all analyzed images to prevent grouping of certain areas. Selected fields for CD3 stained images were conserved to ventricular lumen adjacent (3 fields selected), mid-portion of myocardium (5 fields selected) and outer epicardial surface (2 fields selected). Selected fields for troponin stained images were conserved to mid-portion of myocardium (5 fields selected). The staining was quantified by the Positive Pixel Count algorithm (Version 9; Leica Biosystems) as per the manufacturer’s instructions, and as per previous studies(37, 38). The ratio of positive pixels over total pixel number was analyzed per field, and an average of total positive pixels per mm^2 was calculated for each image. For the analysis of the CD3 staining across all experimental groups, the total number of strong, positive pixels was standardized against the total number of pixels. This pixel intensity was chosen to exclude false-positive, weak-intensity pixel count within the cardiac muscle as seen in all experimental group images.

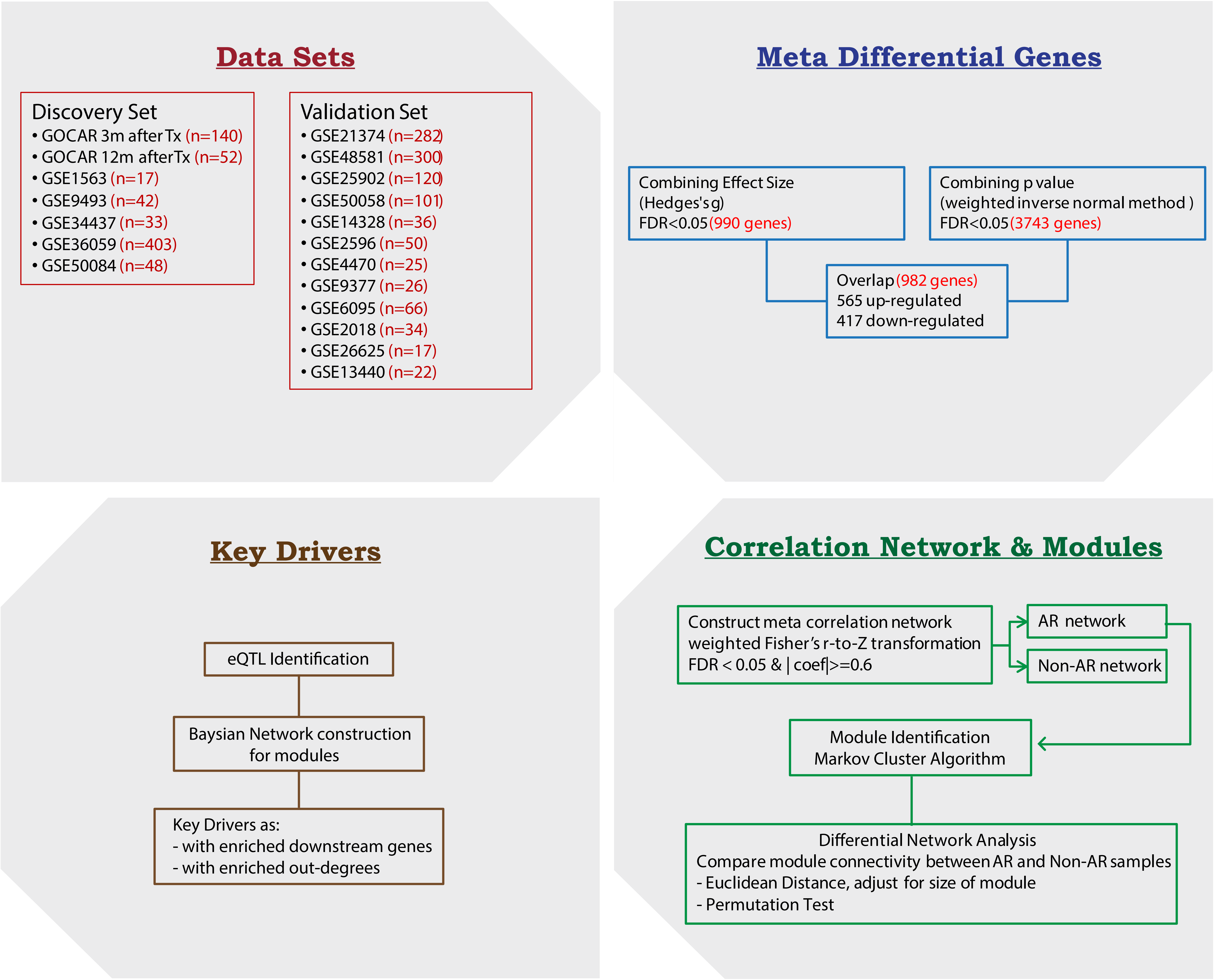


Figure S1. Detailed work flow of the meta-analysis. The discovery set consisted of 7 microarray datasets; 12 independent publicly available datasets of 5 kidney, 3 heart, 2 lung and 2 liver transplant biopsy samples were validation sets. 982 meta-genes were identified by overlapping results from combing effect size and combing p-value approaches. Meta-correlation networks were constructed amongst AR samples and non-AR samples separately. We performed Markov Cluster Algorithm in the AR network to obtain sub-modules. Those modules were later compared with the same set of genes in the non-AR network by connectivity using permutation test. Modules which had significantly different connectivity between AR and non-AR samples were used to build directional Bayesian Network. Key drivers in each module were finally identified as the gene with both enriched downstream counts and out-degrees.

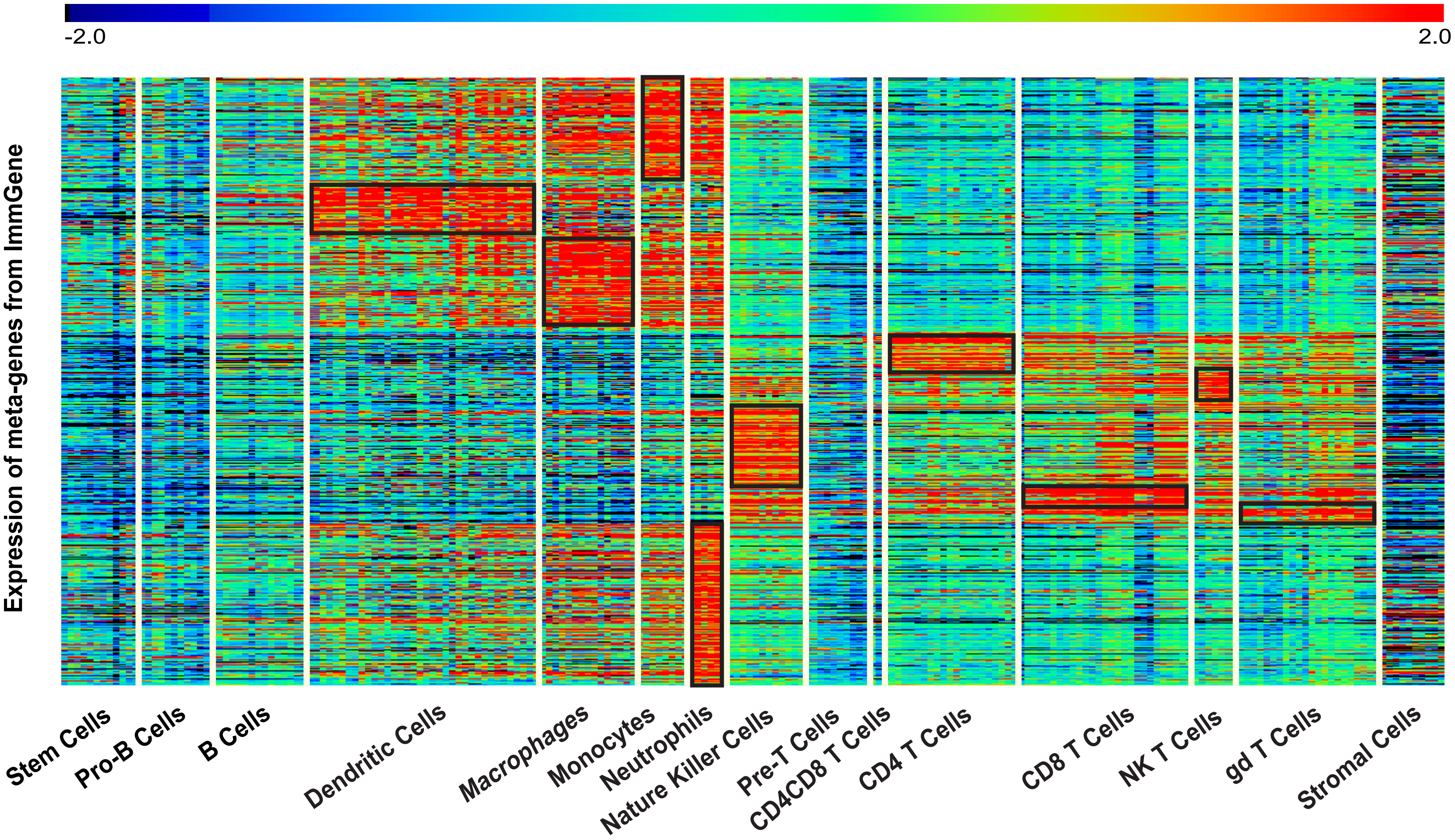


Figure S2. Heatmap representation of innate immune cell enrichment analysis. Strong representation of innate immune cell populations was identified amongst the upregulated DEGs by cell enrichment analysis based on ImmGene database. The database contains varying numbers of samples for any given cell type, which is reflected by the segmented width along the x-axis. Color of the heatmap image denotes gene-level normalized (zero-centered) expression value. Significantly enriched cell types with higher expression comparing across other cell populations are highlighted in black boxes.

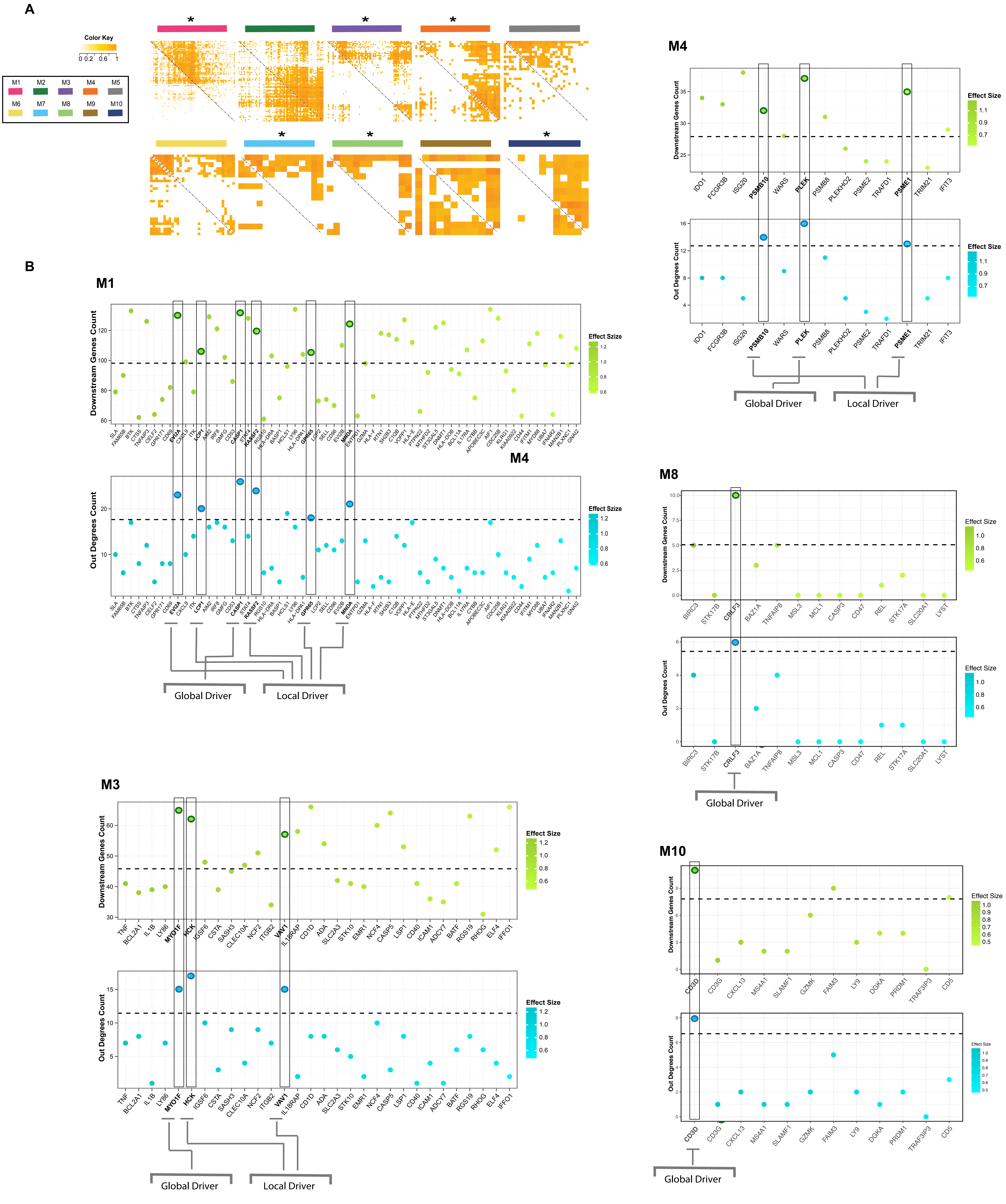


Figure S3 Identification of differential AR modules and KDGs. A) Heatmaps of network connectivity for the top 10 co-expression-modules. Each heatmap consists of upper triangle part (co-expression connectivity in AR patients) and lower triangle part (co-expression connectivity in no AR patients). Color of heatmap represents correlation coefficient of gene pairs in each module. Differential modules are marked with asterisk. **B)**. Key Drivers identification in Module 1, 3, 4, 8, 10. The scatter plots of downstream gene count (upper panel) and out-degree of genes (lower panel) in each module demonstrates the process of Key Driver identification. Genes are ordered by effect size (high to low) and darkness of the either blue or green color indicates level of effect size. M1, M3, M4 only show genes with top downstream count whereas M8 and M10 show all genes in the module due to size limit. Key Drivers are highlighted in black boxes. We selected Key Drivers as genes which had downstream numbers above mean(DS) + σ(DS) and had out-degrees above mean(OD) + 2σ(OD). If a Key Driver was not in the downstream of any other KDs in the same module, it became a global driver otherwise it was a local driver.

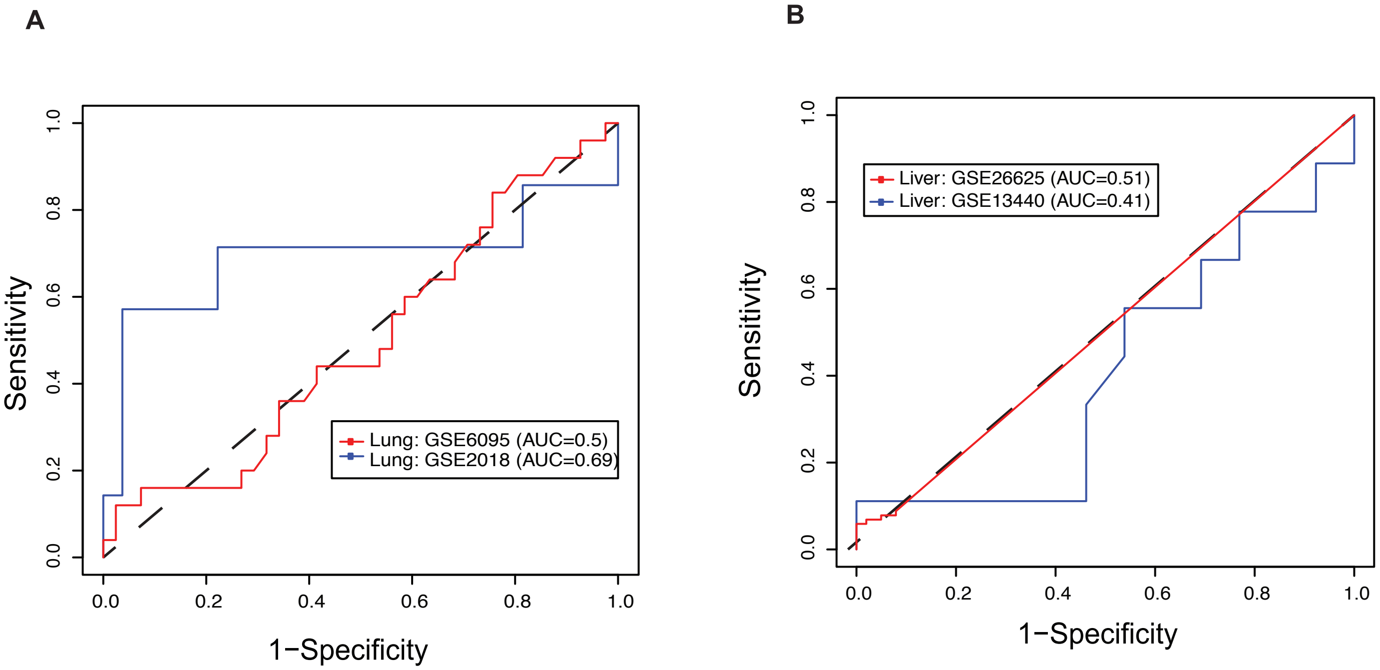


Figure S4. Discriminatory ability of KDGs to differentiate biopsy samples with AR from non-AR in lung and liver transplant data sets. ROC curves were generated using the geometric mean of the expression of all 14 KDGs in independent lung **(A)** and liver **(B)** data sets.

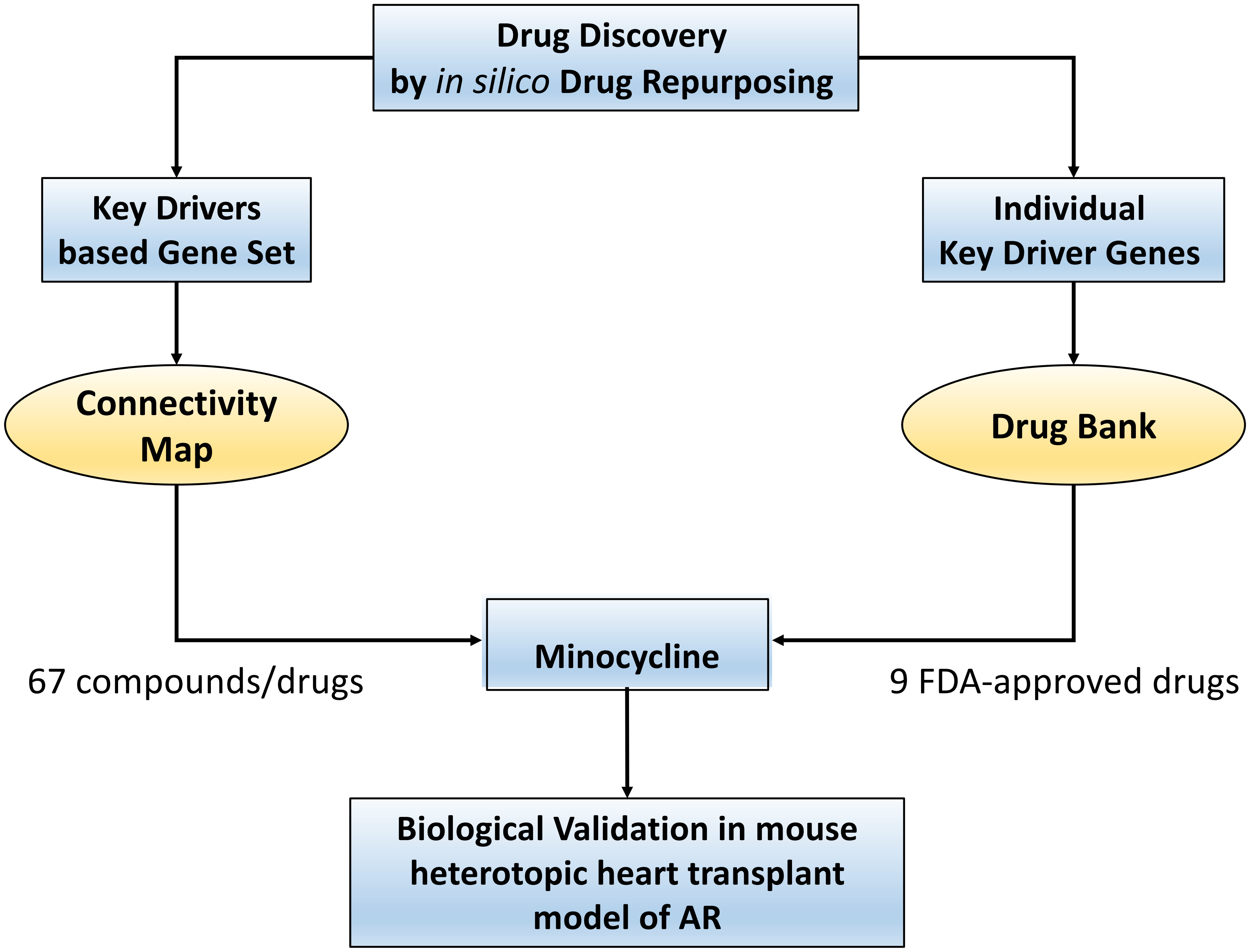


Figure S5. Workflow. Minocycline was the only therapeutic agent discovered in both the DrugBank and CMAP interrogation. Individual KDGs were the input target in DrugBank, whilst a key drivers- based gene set was used to query CMAP, the genes in this set were derived from the largest three differential modules of AR, and consisted of 12 KDGs and 30 secondary genes with large out-degrees.
FDA, U.S. Food and Drug Administration

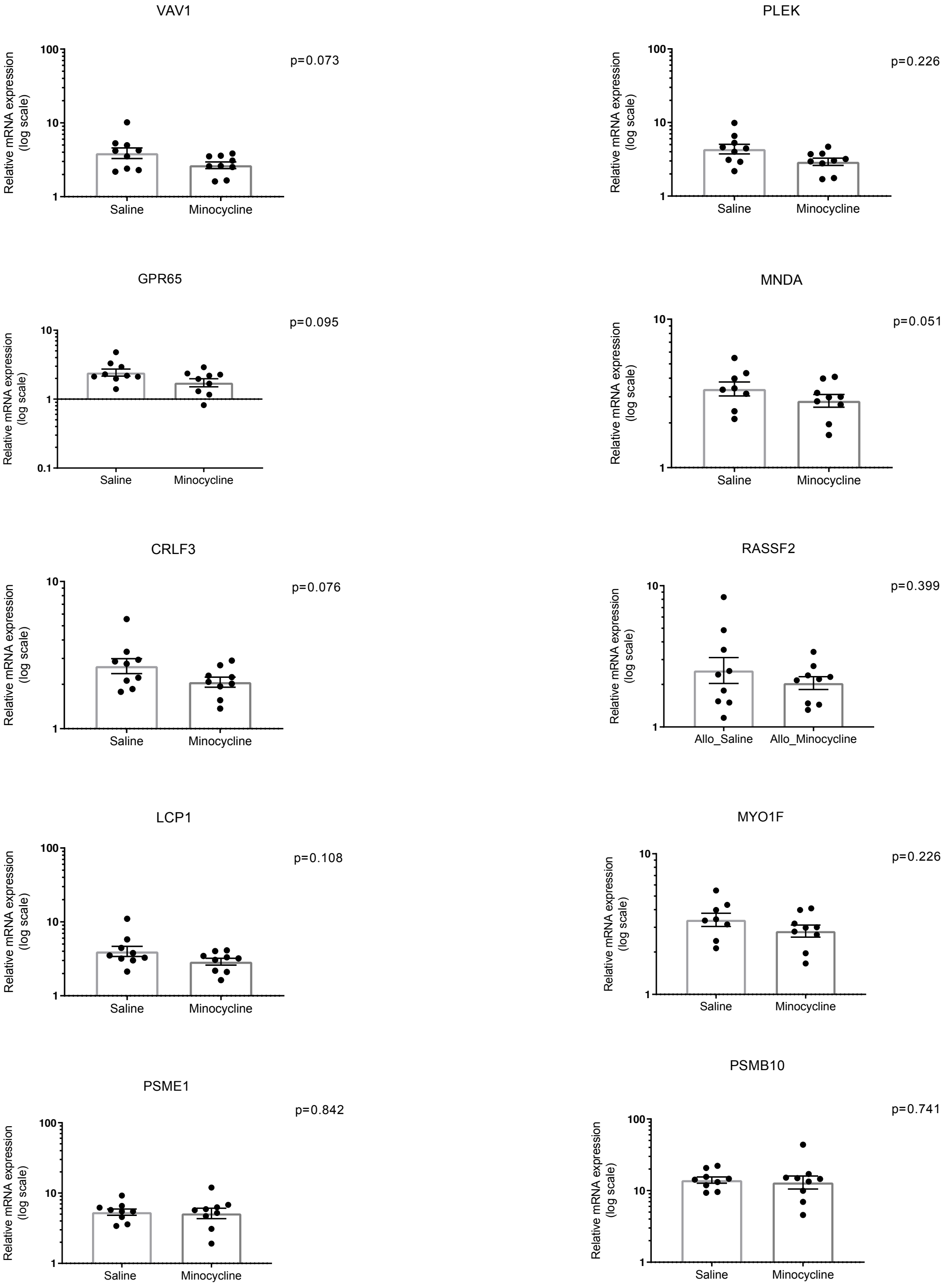


Figure S6(A). The expression of the remaining key driver genes in murine cardiac allografts harvested at post-operative day 4.

mRNA transcrip-tion expression (presented on a log scale) measured by RT-PCR of 10 of the 14 key driver genes. Relative expression of mRNA transcripts was calculated by the ΔΔCT method normalized to expression in a syngeneic transplant group with GAPDH as the house keeper gene. Student's t-test was used for comparing normally distributed data, Mann-Whitney U-Test was used for non-normally distributed data. Data was presented as mean ± SEM (*$p<0.05$).

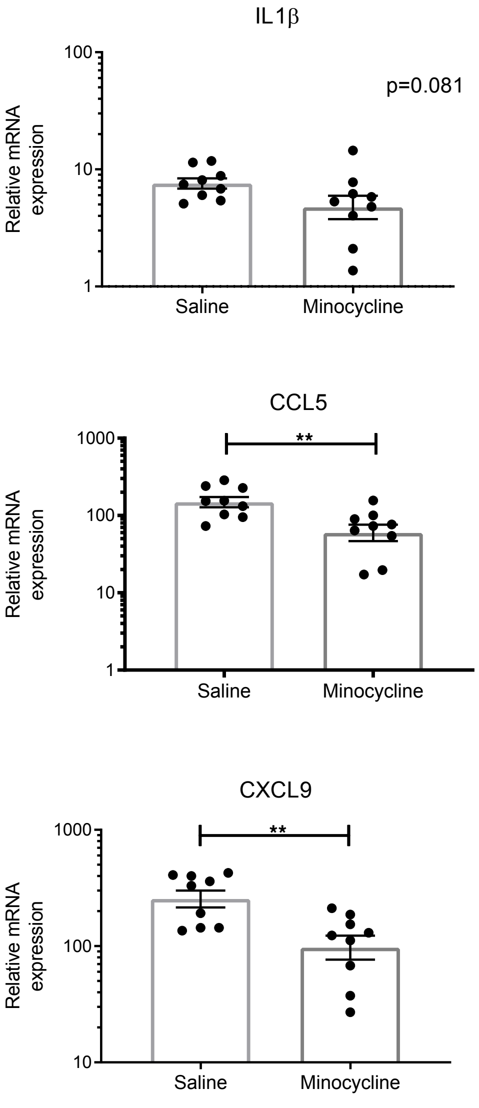
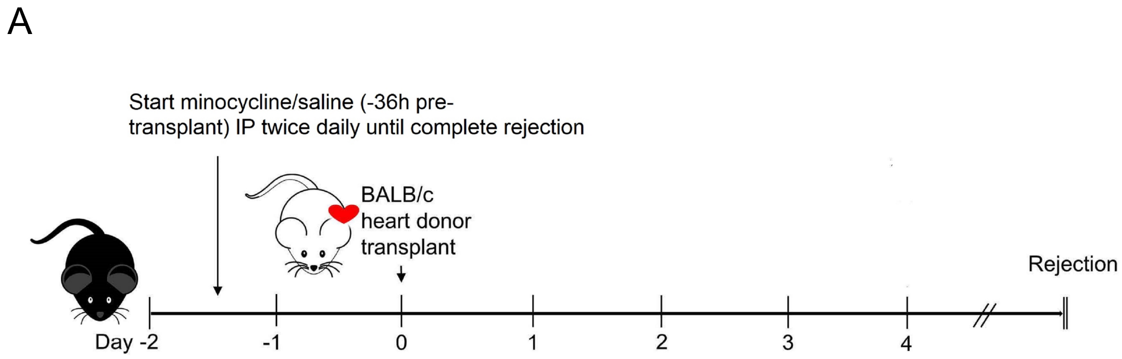


Figure S6(B). The expression of additional pro-inflammatory cytokines in murine cardiac allografts harvested at post-operative day 4. mRNA transcript expression (presented on a log scale) measured by RT-PCR of IL1β, CXCL9 and CCL5. Relative expression of mRNA transcripts was calculated by the ΔΔCT method normalized to expression in a syngeneic transplant group with GAPDH as the house keeper gene. Student's t-test was used for comparing normally distributed data, Mann-Whitney U-Test was used for non-normally distributed data. Data was presented as mean ± SEM (*$p<0.05$).



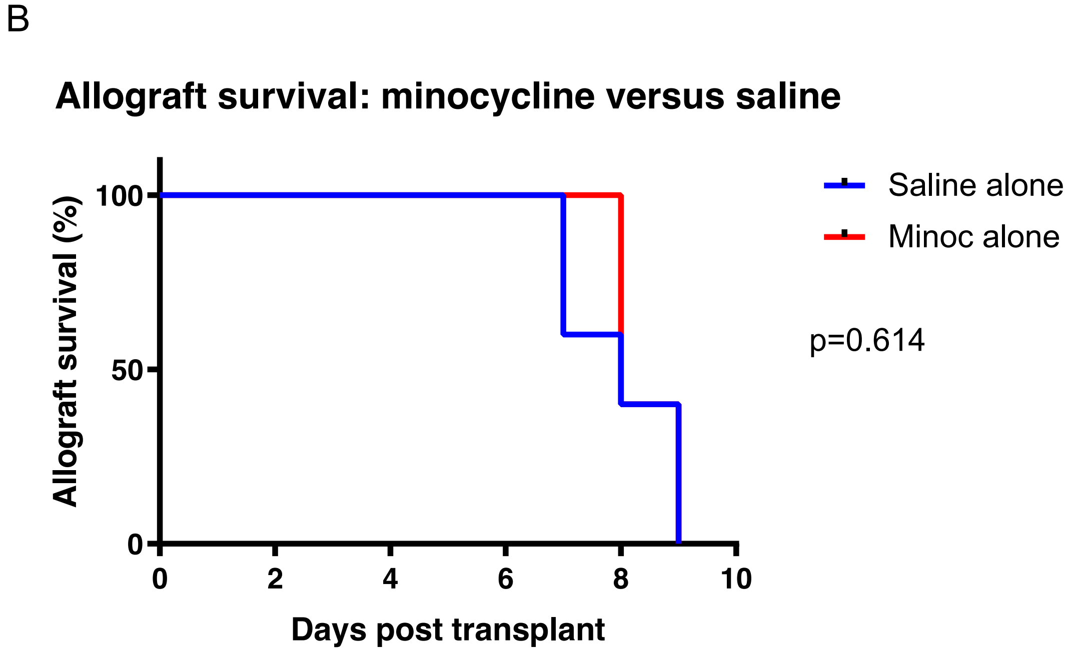


Figure S7. Murine cardiac allograft survival following minocycline monotherapy versus saline. (A) Minocycline or saline monotherapy was administered starting 36 hours prior to transplant twice daily until complete allograft rejection (cessation of allograft beat). **(B)** No significant difference was observed in allograft survival between transplanted animals treated with minocycline versus saline through to allograft loss (n=5 each group). Kaplan-Meier survival was assessed by log-rank analysis, with significance level at $p < 0.05$.

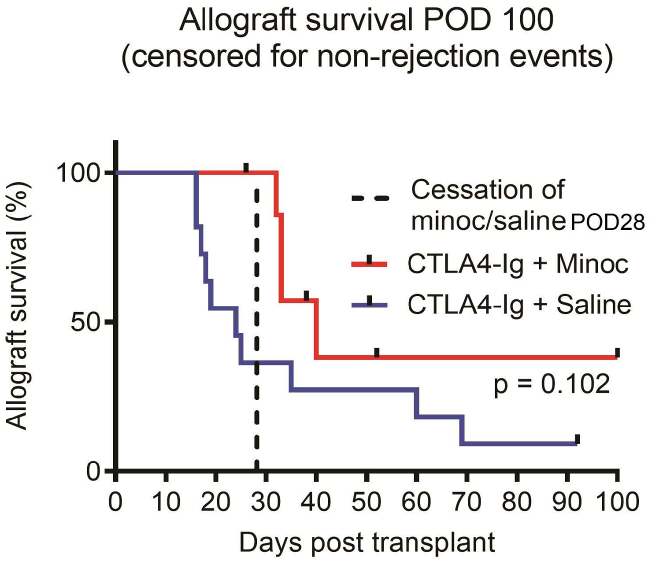


Figure S8. Evaluation of allograft survival at POD 100. When re-evaluated at the end of the experimental period at POD 100, there was no statistically significant difference between the two groups (p=0.102). Kaplan-Meier survival analysis using the log-rank test was applied to compare allograft survival at PODs 100.

Table S1. Summary of discovery and validation microarray data sets of clinical biopsy samples from kidney, heart, lung and liver transplants.

Organ	Dataset	Sample Size	Platform	Number of acute rejection cases and subtype*	Biopsy type (protocol versus indication) of rejection cases	Reference
Discovery Datasets						
Kidney	GSE57387 (GOCAR)	140	GPL5175	31 TCMR	Protocol (3 months post TX)	O'Connell PJ et al. Lancet 2016
	GSE138043 (GOCAR)	52	GPL5175	15 TCMR	Protocol (12 months post TX)	This paper
	GSE1563	17	GPL8300	7	Indication	Flechner SM et al. Am J Transplant 2004
	GSE9493	42	GPL570	21	Indication	Saint-Mezard P et al. Transpl Int 2009
	GSE34437	33	GPL570	17 TCMR	Indication and protocol	Roedder S et al. PLoS ONE 2013
	GSE36059	403	GPL570	35 TCMR, 65 ABMR, 22 Mixed	Indication	Reeve J et al. Am J Transplant 2013
	GSE50084	48	GPL6244	28 ABMR	Indication	Ó Broin P et al. Genom Data 2014
Validation Datasets						
Kidney	GSE21374	282	GPL570	76 TCMR/ABMR/Mixed	Indication	Einecke G et al. J Clin Invest 2010
	GSE48581	300	GPL570	32 TCMR, 40 ABMR, 6 Mixed	Indication	Halloran P et al. Am J Transplant 2013
	GSE25902	120	GPL570	24 TCMR	Protocol	Naesens M et al. Kidney Int 2011
	GSE50058	101	GPL570	43	Not specified	Khatri P et al. J Exp Med 2013
	GSE14328	36	GPL570	17	Not specified	Ling XB et al. J Am Soc Nephrol 2010
Heart	GSE2596	50	GPL1053	16	Indication	Morgun A et al. Circ Res 2006
	GSE4470	25	GPL1053	12	Indication	Morgun A et al. Circ Res 2006
	GSE9377	26	GPL887	12	Indication	Holweg CT et al. Circulation 2011
Lung	GSE6095	66	GPL96	25	Protocol and Indication	Patil J et al. Transplantation 2008

	GSE2018	34	GPL96	7	Protocol and Indication	Gimino VJ et al. Am J Respir Crit Care Med 2003
Liver	GSE26625	17	GPL6947	9	Protocol	Bohne F et al. J Clin Invest 2012
	GSE13440	22	GPL1291	9	Indication	Asaoka T et al. Liver Transpl 2009

GOCAR, Genomics of chronic allograft dysfunction study; GSE, Gene Expression Omnibus Series; TCMR, T-cell mediated rejection; ABMR, antibody mediated rejection; TX, transplant. *Acute rejection subtype (TCMR, ABMR or mixed) specified for kidney biopsy datasets if available from the original studies, TCMR includes borderline cases.

Table S1. Full list of the 982 meta-genes identified from the meta-analysis. Meta-p-values are adjusted by FDR correction method.

Gene Symbol	RefSeq Accession	Full Name	Meta-Effect Size*	Meta-p-value
CD86	NM_176892	CD86 molecule	1.40	1.97E-03
IFNG	NM_000619	interferon, gamma	1.36	1.16E-04
CXCL11	NM_005409	chemokine (C-X-C motif) ligand 11	1.36	4.99E-03
LST1	NM_205837	leukocyte specific transcript 1	1.34	1.40E-06
IL2RB	NM_000878	interleukin 2 receptor, beta	1.33	5.62E-06
AOAH	NM_001637	acyloxyacyl hydrolase (neutrophil)	1.32	1.23E-03
SLA	NM_006748	Src-like-adaptor	1.28	2.09E-06
IL10RA	NR_026691	interleukin 10 receptor, alpha	1.28	1.11E-06
IDO1	NM_002164	indoleamine 2,3-dioxygenase 1	1.27	2.08E-07
PRKCB	NM_212535	protein kinase C, beta	1.27	5.18E-03
TNFRSF9	NM_001561	tumor necrosis factor receptor superfamily, member 9	1.26	8.88E-04
TNF	NM_000594	tumor necrosis factor	1.26	1.73E-03
FAM65B	NM_001286446	family with sequence similarity 65, member B	1.26	9.34E-03
BTK	NM_001287344	Bruton agammaglobulinemia tyrosine kinase	1.24	3.98E-04
CTSS	NM_001199739	cathepsin S	1.23	6.49E-04
TNFAIP3	NM_001270507	tumor necrosis factor, alpha-induced protein 3	1.23	2.98E-04
PMAIP1	NM_021127	phorbol-12-myristate-13-acetate-induced protein 1	1.23	6.30E-03
CSF2RB	NM_000395	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)	1.22	2.08E-07
CELF2	NM_001083591	CUGBP, Elav-like family member 2	1.22	2.47E-03
CD8A	NM_001145873	CD8a molecule	1.20	1.02E-03
GPR171	NM_013308	G protein-coupled receptor 171	1.19	1.60E-04

FGR	NM_005248	feline Gardner-Rasheed sarcoma viral oncogene homolog	1.19	2.56E-04
CD69	NM_001781	CD69 molecule	1.19	8.68E-04
TAP1	NM_001292022	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	1.18	5.00E-06
EVI2A	NM_014210	ecotropic viral integration site 2A	1.18	2.21E-03
CXCL9	NM_002416	chemokine (C-X-C motif) ligand 9	1.18	1.36E-06
BCL2A1	NM_001114735	BCL2-related protein A1	1.17	1.32E-03
IL1B	NM_000576	interleukin 1, beta	1.17	1.48E-04
LY86	NM_004271	lymphocyte antigen 86	1.16	2.08E-03
ICOS	NM_012092	inducible T-cell co-stimulator	1.16	2.02E-04
FCGR3B	NM_000570	Fc fragment of IgG, low affinity IIIb, receptor (CD16b)	1.16	1.40E-06
ITK	NM_005546	IL2-inducible T-cell kinase	1.16	2.85E-03
MYO1F	NM_012335	myosin IF	1.16	1.36E-06
LCP1	NM_002298	lymphocyte cytosolic protein 1 (L-plastin)	1.16	2.16E-04
EGR2	NM_001136179	early growth response 2	1.15	6.02E-04
UBD	NM_006398	ubiquitin D	1.14	1.16E-05
KLRD1	NM_002262	killer cell lectin-like receptor subfamily D, member 1	1.14	3.30E-03
HCK	NM_001172133	hemopoietic cell kinase	1.14	1.36E-06
IGSF6	NM_005849	immunoglobulin superfamily, member 6	1.14	7.55E-04
BIRC3	NM_001165	baculoviral IAP repeat containing 3	1.14	1.52E-02
CXCL10	NM_001565	chemokine (C-X-C motif) ligand 10	1.13	1.85E-06
AIM2	NM_004833	absent in melanoma 2	1.13	1.40E-06
FAM49A	NM_030797	family with sequence similarity 49, member A	1.13	3.46E-05
IRF8	NM_002163	interferon regulatory factor 8	1.12	2.09E-06
IRF1	NM_002198	interferon regulatory factor 1	1.12	2.08E-07
GMFG	NM_004877	glia maturation factor, gamma	1.12	6.72E-04

FCER1G	NM_004106	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide	1.12	2.18E-05
IL2RG	NM_000206	interleukin 2 receptor, gamma	1.12	2.45E-06
CD53	NM_000560	CD53 molecule	1.11	1.82E-03
RGS1	NM_002922	regulator of G-protein signaling 1	1.11	6.05E-03
RHOH	NM_001278366	ras homolog family member H	1.10	2.00E-03
EMR2	NM_013447	egf-like module containing, mucin-like, hormone receptor-like 2	1.09	5.44E-04
CASP1	NM_001223	caspase 1, apoptosis-related cysteine peptidase	1.09	6.82E-05
ISG20	NM_002201	interferon stimulated exonuclease gene 20kDa	1.08	5.48E-07
CSK	NM_001127190	c-src tyrosine kinase	1.08	2.61E-03
STAT4	NM_001243835	signal transducer and activator of transcription 4	1.08	5.54E-06
RASSF2	NM_014737	Ras association (RalGDS/AF-6) domain family member 2	1.08	1.14E-03
SRGN	NM_002727	serglycin	1.08	7.88E-04
NKG7	NM_005601	natural killer cell granule protein 7	1.07	7.91E-06
PIK3CG	NM_001282427	phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit gamma	1.07	1.05E-02
HLA-DPB1	NM_002121	major histocompatibility complex, class II, DP beta 1	1.06	6.45E-04
RGS10	NM_001005339	regulator of G-protein signaling 10	1.06	2.39E-03
CD48	NM_001778	CD48 molecule	1.06	2.51E-04
RAC2	NM_002872	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)	1.06	1.44E-04
CSF1R	NM_005211	colony stimulating factor 1 receptor	1.05	1.02E-05
HLA-DRA	NM_019111	major histocompatibility complex, class II, DR alpha	1.05	9.04E-04
CD3D	NM_001040651	CD3d molecule, delta (CD3-TCR complex)	1.05	1.48E-04
CSTA	NM_005213	cystatin A (stefin A)	1.05	1.10E-03
ADAM19	NM_033274	ADAM metallopeptidase domain 19	1.04	2.96E-03

CCR7	NM_001838	chemokine (C-C motif) receptor 7	1.04	6.16E-03
BASP1	NM_001271606	brain abundant, membrane attached signal protein 1	1.04	1.44E-02
GZMB	NM_004131	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	1.04	1.27E-05
CD52	NM_001803	CD52 molecule	1.04	3.36E-04
FCN1	NM_002003	ficolin (collagen/fibrinogen domain containing) 1	1.04	2.30E-05
HCLS1	NM_005335	hematopoietic cell-specific Lyn substrate 1	1.04	8.02E-05
PRF1	NM_001083116	perforin 1 (pore forming protein)	1.04	1.40E-06
HLA-DMB	NM_002118	major histocompatibility complex, class II, DM beta	1.03	1.28E-05
SP140	NM_001278452	SP140 nuclear body protein	1.03	2.56E-04
SASH3	NM_018990	SAM and SH3 domain containing 3	1.03	1.00E-03
PTPRC	NM_001267798	protein tyrosine phosphatase, receptor type, C	1.03	1.94E-05
LY96	NM_001195797	lymphocyte antigen 96	1.03	4.19E-03
IL10	NM_000572	interleukin 10	1.03	2.10E-02
HLA-DPA1	NM_001242525	major histocompatibility complex, class II, DP alpha 1	1.03	1.07E-04
CD38	NM_001775	CD38 molecule	1.03	7.93E-04
GPR65	NM_003608	G protein-coupled receptor 65	1.02	1.94E-05
TNFRSF1B	NM_001066	tumor necrosis factor receptor superfamily, member 1B	1.02	2.16E-04
CLEC10A	NM_182906	C-type lectin domain family 10, member A	1.02	1.94E-05
S100B	NM_006272	S100 calcium binding protein B	1.02	1.75E-02
IFI16	NM_005531	interferon, gamma-inducible protein 16	1.01	1.33E-02
LCP2	NM_005565	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)	1.01	4.53E-07
CD2	NM_001767	CD2 molecule	1.01	2.30E-05
PSMB10	NM_002801	proteasome (prosome, macropain) subunit, beta type, 10	1.01	2.42E-05

SELL	NR_029467	selectin L	1.00	1.32E-03
LAIR1	NM_001289027	leukocyte-associated immunoglobulin-like receptor 1	1.00	1.87E-03
NCF2	NM_000433	neutrophil cytosolic factor 2	1.00	2.66E-05
ITGB2	NM_001127491	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	1.00	5.27E-04
RNASE6	NM_005615	ribonuclease, RNase A family, k6	1.00	7.55E-04
ARHGAP25	NM_001007231	Rho GTPase activating protein 25	1.00	1.36E-03
PLCB2	NM_001284298	phospholipase C, beta 2	0.99	4.68E-02
UBE2L6	NM_004223	ubiquitin-conjugating enzyme E2L 6	0.99	3.46E-05
CD3G	NM_000073	CD3g molecule, gamma (CD3-TCR complex)	0.99	4.50E-03
CD163	NM_004244	CD163 molecule	0.99	1.34E-03
KLRB1	NM_002258	killer cell lectin-like receptor subfamily B, member 1	0.99	3.53E-05
SIT1	NM_014450	signaling threshold regulating transmembrane adaptor 1	0.99	9.94E-03
CD96	NM_198196	CD96 molecule	0.99	1.51E-03
DOK2	NM_003974	docking protein 2, 56kDa	0.99	1.07E-04
CCL5	NM_002985	chemokine (C-C motif) ligand 5	0.99	6.29E-07
PIM2	NM_006875	pim-2 oncogene	0.98	5.42E-03
WARS	NM_213645	tryptophanyl-tRNA synthetase	0.98	3.78E-03
ITGAL	NM_001114380	integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide)	0.98	4.86E-06
S1PR1	NM_001400	sphingosine-1-phosphate receptor 1	0.98	4.39E-03
CD180	NM_005582	CD180 molecule	0.98	4.25E-05
GPR18	NM_001098200	G protein-coupled receptor 18	0.98	2.47E-03
EVI2B	NM_006495	ecotropic viral integration site 2B	0.98	1.12E-03
GCNT1	NM_001490	glucosaminyl (N-acetyl) transferase 1, core 2	0.97	3.53E-05
CXCR4	NM_001008540	chemokine (C-X-C motif) receptor 4	0.97	1.07E-04

VAV1	NM_005428	vav 1 guanine nucleotide exchange factor	0.97	3.56E-05
CD84	NM_003874	CD84 molecule	0.96	1.51E-03
MNDA	NM_002432	myeloid cell nuclear differentiation antigen	0.96	6.08E-05
PLEK	NM_002664	pleckstrin	0.96	8.11E-06
NCKAP1L	NM_005337	NCK-associated protein 1-like	0.96	7.06E-05
CHI3L2	NM_001025197	chitinase 3-like 2	0.95	2.38E-02
ENTPD1	NM_001164178	ectonucleoside triphosphate diphosphohydrolase 1	0.95	1.75E-02
CLIC2	NM_001289	chloride intracellular channel 2	0.95	1.21E-04
GZMA	NM_006144	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)	0.94	8.72E-05
MAP3K8	NM_001244134	mitogen-activated protein kinase kinase kinase 8	0.94	4.36E-05
LAPTM5	NM_006762	lysosomal protein transmembrane 5	0.94	2.26E-05
CD3E	NM_000733	CD3e molecule, epsilon (CD3-TCR complex)	0.94	8.89E-05
PTPN6	NM_080549	protein tyrosine phosphatase, non-receptor type 6	0.94	3.20E-02
TARP	NM_001003799	TCR gamma alternate reading frame protein	0.94	1.94E-04
CXCL13	NM_006419	chemokine (C-X-C motif) ligand 13	0.94	6.05E-03
APOL1	NM_001136541	apolipoprotein L, 1	0.93	1.79E-04
DOCK2	NM_004946	dedicator of cytokinesis 2	0.93	1.21E-02
PNOC	NM_001284244	prepronociceptin	0.93	3.71E-02
C3AR1	NM_004054	complement component 3a receptor 1	0.93	1.07E-04
HLA-F	NM_001098478	major histocompatibility complex, class I, F	0.93	4.25E-06
MSR1	NM_138715	macrophage scavenger receptor 1	0.93	1.82E-03
FASLG	NM_000639	Fas ligand (TNF superfamily, member 6)	0.93	1.23E-04
IL18RAP	NM_003853	interleukin 18 receptor accessory protein	0.93	1.16E-04
PSMB8	NM_148919	proteasome (prosome, macropain) subunit, beta type, 8	0.93	1.02E-02
CST7	NM_003650	cystatin F (leukocystatin)	0.92	1.21E-04

CD1D	NM_001766	CD1d molecule	0.92	6.72E-04
LILRB2	NM_005874	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2	0.92	2.59E-03
PTPN7	NM_002832	protein tyrosine phosphatase, non-receptor type 7	0.92	5.45E-03
RTN1	NM_206852	reticulon 1	0.92	2.07E-05
VSIG4	NM_007268	V-set and immunoglobulin domain containing 4	0.92	1.40E-04
STK17B	NM_004226	serine/threonine kinase 17b	0.91	3.24E-03
IL15RA	NM_002189	interleukin 15 receptor, alpha	0.91	1.30E-04
ADA	NM_000022	adenosine deaminase	0.91	5.45E-03
SLC1A3	NM_001289939	solute carrier family 1 (glial high affinity glutamate transporter), member 3	0.91	2.02E-02
CHN1	NM_001025201	chimerin 1	0.91	4.88E-02
STAT1	NM_139266	signal transducer and activator of transcription 1, 91kDa	0.91	2.08E-07
NLRP3	NM_004895	NLR family, pyrin domain containing 3	0.91	2.53E-02
TRAF1	NM_005658	TNF receptor-associated factor 1	0.91	1.82E-02
SH2B3	NM_001291424	SH2B adaptor protein 3	0.91	1.50E-04
C1QB	NM_000491	complement component 1, q subcomponent, B chain	0.91	2.91E-04
SH2D2A	NM_001161442	SH2 domain containing 2A	0.91	1.10E-03
EMP3	NM_001425	epithelial membrane protein 3	0.91	1.60E-04
VOPP1	NM_001284284	vesicular, overexpressed in cancer, prosurvival protein 1	0.91	1.93E-03
SLC2A3	NM_006931	solute carrier family 2 (facilitated glucose transporter), member 3	0.90	7.96E-04
P2RY10	NM_198333	purinergic receptor P2Y, G-protein coupled, 10	0.90	9.57E-05
PZP	NM_002864	pregnancy-zone protein	0.90	1.58E-02

PTPRE	NM_006504	protein tyrosine phosphatase, receptor type, E	0.90	6.59E-04
PTPRCAP	NM_005608	protein tyrosine phosphatase, receptor type, C-associated protein	0.90	7.96E-04
SECTM1	NM_003004	secreted and transmembrane 1	0.90	1.73E-04
STK10	NM_005990	serine/threonine kinase 10	0.90	4.41E-04
CRLF3	NM_015986	cytokine receptor-like factor 3	0.90	4.54E-03
CD37	NM_001774	CD37 molecule	0.90	1.91E-04
ADAMDEC1	NM_014479	ADAM-like, decysin 1	0.89	6.34E-03
CD14	NM_001174104	CD14 molecule	0.89	4.50E-03
RAB27A	NM_183235	RAB27A, member RAS oncogene family	0.89	1.22E-04
APOBEC3F	NM_001006666	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3F	0.89	1.27E-02
BTN3A1	NM_001145008	butyrophilin, subfamily 3, member A1	0.89	3.78E-05
MFNG	NM_001166343	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	0.89	1.74E-02
PLEKHO2	NM_025201	pleckstrin homology domain containing, family O member 2	0.88	6.08E-03
LYN	NM_001111097	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	0.88	7.09E-06
MYB	NM_001161658	v-myb avian myeloblastosis viral oncogene homolog	0.88	5.80E-03
POU2AF1	NM_006235	POU class 2 associating factor 1	0.88	4.07E-03
VNN2	NR_034173	vanin 2	0.88	2.15E-02
CD27	NM_001242	CD27 molecule	0.88	2.52E-04
HLA-E	NM_005516	major histocompatibility complex, class I, E	0.88	1.27E-03
IFI30	NM_006332	interferon, gamma-inducible protein 30	0.88	1.91E-03
CFP	NM_001145252	complement factor properdin	0.88	2.80E-03
LILRA1	NR_103503	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1	0.88	1.69E-03
LYZ	NM_000239	lysozyme	0.88	5.16E-05

MAP4K1	NM_007181	mitogen-activated protein kinase kinase kinase kinase 1	0.87	2.27E-03
FYB	NM_001465	FYN binding protein	0.87	3.05E-04
APOBEC3G	NM_021822	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3G	0.87	3.81E-03
TRIM22	NM_001199573	tripartite motif containing 22	0.87	1.91E-04
CXCR6	NM_006564	chemokine (C-X-C motif) receptor 6	0.87	8.26E-05
FCGR2A	NM_021642	Fc fragment of IgG, low affinity IIa, receptor (CD32)	0.87	1.73E-03
GAS7	NM_201433	growth arrest-specific 7	0.87	2.93E-03
TLR2	NM_003264	toll-like receptor 2	0.87	2.98E-04
STX11	NM_003764	syntaxin 11	0.87	3.60E-03
PTPN22	NM_001193431	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	0.87	1.45E-05
MS4A1	NM_021950	membrane-spanning 4-domains, subfamily A, member 1	0.86	8.79E-03
SLAMF1	NR_104399	signaling lymphocytic activation molecule family member 1	0.86	3.42E-03
HAS2	NM_005328	hyaluronan synthase 2	0.86	1.00E-02
DUSP2	NM_004418	dual specificity phosphatase 2	0.86	1.66E-02
FPR2	NM_001462	formyl peptide receptor 2	0.86	8.97E-03
SELPLG	NM_001206609	selectin P ligand	0.86	1.32E-03
DUSP4	NM_057158	dual specificity phosphatase 4	0.86	1.10E-03
PMP22	NR_104017	peripheral myelin protein 22	0.86	4.16E-04
HMHA1	NM_001282334	histocompatibility (minor) HA-1	0.86	3.92E-04
JAK3	NM_000215	Janus kinase 3	0.86	1.58E-02
CLEC2B	NM_005127	C-type lectin domain family 2, member B	0.86	8.26E-05
EMR1	NM_001256253	egf-like module containing, mucin-like, hormone receptor-like 1	0.85	3.06E-02
FPR1	NM_001193306	formyl peptide receptor 1	0.85	4.83E-04

LAMP3	NM_014398	lysosomal-associated membrane protein 3	0.85	4.37E-04
BTN3A2	NM_007047	butyrophilin, subfamily 3, member A2	0.85	1.27E-05
LAIR2	NM_021270	leukocyte-associated immunoglobulin-like receptor 2	0.85	4.41E-04
MICB	NM_005931	MHC class I polypeptide-related sequence B	0.85	3.98E-04
LMNB1	NM_001198557	lamin B1	0.85	1.26E-03
GNA15	NM_002068	guanine nucleotide binding protein (G protein), alpha 15 (Gq class)	0.84	4.91E-04
CTSW	NM_001335	cathepsin W	0.84	4.83E-04
GZMK	NM_002104	granzyme K (granzyme 3; tryptase II)	0.84	7.87E-04
FPR3	NM_002030	formyl peptide receptor 3	0.84	7.93E-04
KIAA0101	NR_109934	KIAA0101	0.84	3.14E-02
PRKCH	NM_006255	protein kinase C, eta	0.84	7.74E-04
NCF4	NM_000631	neutrophil cytosolic factor 4, 40kDa	0.83	8.26E-05
IL7R	NR_120485	interleukin 7 receptor	0.83	1.01E-04
KCNJ2	NM_000891	potassium inwardly-rectifying channel, subfamily J, member 2	0.83	3.81E-03
ALOX5	NM_001256153	arachidonate 5-lipoxygenase	0.83	7.17E-03
NELL2	NM_001145110	NEL-like 2 (chicken)	0.83	2.80E-03
CAMK4	NM_001744	calcium/calmodulin-dependent protein kinase IV	0.83	1.43E-02
TAP2	NM_000544	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	0.83	2.48E-05
DLGAP5	NM_014750	discs, large (Drosophila) homolog-associated protein 5	0.83	1.54E-02
MTHFD2	NM_006636	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase	0.83	1.50E-02
TGFBI	NM_000358	transforming growth factor, beta-induced, 68kDa	0.83	6.72E-04
GPR183	NM_004951	G protein-coupled receptor 183	0.82	6.72E-04

MKI67	NM_002417	marker of proliferation Ki-67	0.82	5.45E-03
P2RY14	NM_001081455	purinergic receptor P2Y, G-protein coupled, 14	0.82	9.47E-03
ETS1	NM_001143820	v-ets avian erythroblastosis virus E26 oncogene homolog 1	0.82	2.26E-02
HHEX	NM_002729	hematopoietically expressed homeobox	0.81	1.79E-04
CD40LG	NM_000074	CD40 ligand	0.81	2.32E-02
TXK	NM_003328	TXK tyrosine kinase	0.81	2.76E-03
IL12RB1	NM_005535	interleukin 12 receptor, beta 1	0.81	8.99E-03
BTN3A3	NM_197974	butyrophilin, subfamily 3, member A3	0.81	1.79E-04
HSPA6	NM_002155	heat shock 70kDa protein 6 (HSP70B')	0.81	1.51E-04
TNFSF8	NM_001252290	tumor necrosis factor (ligand) superfamily, member 8	0.81	2.52E-04
MX2	NM_002463	myxovirus (influenza virus) resistance 2 (mouse)	0.80	9.37E-04
CD4	NM_000616	CD4 molecule	0.80	5.81E-04
CCL13	NM_005408	chemokine (C-C motif) ligand 13	0.80	3.81E-03
BCAT1	NM_001178093	branched chain amino-acid transaminase 1, cytosolic	0.80	6.70E-03
FAIM3	NM_001193338	Fas apoptotic inhibitory molecule 3	0.80	1.79E-04
CASP5	NM_001136109	caspase 5, apoptosis-related cysteine peptidase	0.80	1.00E-03
LY9	NM_001261456	lymphocyte antigen 9	0.80	8.26E-05
IL10RB	NM_000628	interleukin 10 receptor, beta	0.80	7.55E-04
CD97	NM_001784	CD97 molecule	0.80	1.02E-03
WAS	NM_000377	Wiskott-Aldrich syndrome	0.80	2.59E-03
CCR2	NM_001123041	chemokine (C-C motif) receptor 2	0.80	1.48E-04
MOXD1	NM_015529	monooxygenase, DBH-like 1	0.79	2.53E-02
PTAFR	NM_000952	platelet-activating factor receptor	0.79	3.28E-03
PSTPIP1	NM_003978	proline-serine-threonine phosphatase interacting protein 1	0.79	2.78E-02

ST3GAL5	NM_001042437	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	0.79	2.85E-03
INPP5D	NM_005541	inositol polyphosphate-5-phosphatase, 145kDa	0.79	1.73E-03
CAV1	NM_001172896	caveolin 1, caveolae protein, 22kDa	0.79	7.84E-04
SH2D1A	NM_002351	SH2 domain containing 1A	0.79	6.14E-03
CD300A	NM_007261	CD300a molecule	0.79	5.95E-03
TCIRG1	NM_006019	T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 subunit A3	0.79	1.26E-03
HCP5	NR_040662	HLA complex P5 (non-protein coding)	0.79	1.26E-03
DNMT1	NM_001130823	DNA (cytosine-5-)-methyltransferase 1	0.78	1.31E-03
LPXN	NM_001143995	leupaxin	0.78	3.07E-04
NDC80	NM_006101	NDC80 kinetochore complex component	0.78	2.18E-03
CDH13	NM_001220491	cadherin 13	0.78	2.93E-03
ARHGDIB	NM_001175	Rho GDP dissociation inhibitor (GDI) beta	0.78	5.83E-04
BAZ1A	NM_182648	bromodomain adjacent to zinc finger domain, 1A	0.78	1.03E-02
OLFML2B	NM_015441	olfactomedin-like 2B	0.78	1.22E-02
CFD	NM_001928	complement factor D (adipsin)	0.78	1.82E-02
CD101	NM_001256111	CD101 molecule	0.77	4.68E-03
HLA-DOA	NM_002119	major histocompatibility complex, class II, DO alpha	0.77	3.28E-03
LCK	NM_005356	lymphocyte-specific protein tyrosine kinase	0.77	3.26E-03
CLC	NM_001828	Charcot-Leyden crystal galectin	0.77	1.64E-03
ADRB2	NM_000024	adrenoceptor beta 2, surface	0.77	1.20E-02
TMSB10	NM_021103	thymosin beta 10	0.77	3.21E-03
IL4R	NM_001257407	interleukin 4 receptor	0.77	1.08E-02
HLA-DOB	NM_002120	major histocompatibility complex, class II, DO beta	0.77	1.28E-03
CD33	NM_001772	CD33 molecule	0.77	1.71E-03

CCR1	NM_001295	chemokine (C-C motif) receptor 1	0.77	2.26E-02
IRF4	NM_001195286	interferon regulatory factor 4	0.76	6.05E-03
RUNX3	NM_001031680	runt-related transcription factor 3	0.76	9.34E-03
CD247	NM_198053	CD247 molecule	0.76	9.86E-04
BCL11A	NM_022893	B-cell CLL/lymphoma 11A (zinc finger protein)	0.76	4.02E-02
SIRPB1	NM_001135844	signal-regulatory protein beta 1	0.75	1.91E-02
ALOX5AP	NM_001629	arachidonate 5-lipoxygenase-activating protein	0.75	2.11E-03
CCND3	NM_001287434	cyclin D3	0.75	5.17E-04
IL17RA	NM_014339	interleukin 17 receptor A	0.75	4.37E-02
CYBB	NM_000397	cytochrome b-245, beta polypeptide	0.75	1.73E-04
IKZF1	NM_001291838	IKAROS family zinc finger 1 (Ikaros)	0.75	4.91E-04
KLF4	NM_004235	Kruppel-like factor 4 (gut)	0.75	6.72E-04
LSP1	NM_001242932	lymphocyte-specific protein 1	0.75	1.79E-03
CD19	NM_001770	CD19 molecule	0.74	2.28E-02
CD40	NM_152854	CD40 molecule, TNF receptor superfamily member 5	0.74	1.07E-04
KIF21B	NM_001252102	kinesin family member 21B	0.74	6.34E-03
NR4A2	NM_006186	nuclear receptor subfamily 4, group A, member 2	0.74	2.32E-04
LHFPL2	NM_005779	lipoma HMGIC fusion partner-like 2	0.74	1.20E-02
ITGAM	NM_001145808	integrin, alpha M (complement component 3 receptor 3 subunit)	0.74	2.22E-03
OAS2	NM_016817	2'-5'-oligoadenylate synthetase 2, 69/71kDa	0.74	2.48E-04
B2M	NM_004048	beta-2-microglobulin	0.74	2.43E-04
RARRES3	NM_004585	retinoic acid receptor responder (tazarotene induced) 3	0.73	2.76E-03
RNASE2	NM_002934	ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin)	0.73	3.20E-03

APOBEC3C	NM_014508	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3C	0.73	2.45E-03
AIF1	NM_032955	allograft inflammatory factor 1	0.73	7.96E-05
CMKLR1	NM_001142344	chemokine-like receptor 1	0.73	1.32E-03
ARHGAP4	NM_001666	Rho GTPase activating protein 4	0.73	2.93E-03
DOCK10	NM_001290263	dedicator of cytokinesis 10	0.73	2.18E-03
TRAF5	NM_001033910	TNF receptor-associated factor 5	0.72	2.72E-03
IKBKE	NM_014002	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon	0.72	2.32E-02
CDC25B	NM_001287516	cell division cycle 25B	0.72	3.36E-03
GZMH	NM_001270781	granzyme H (cathepsin G-like 2, protein h-CCPX)	0.72	3.31E-03
NR4A3	NM_173200	nuclear receptor subfamily 4, group A, member 3	0.72	1.77E-02
KLRG1	NM_005810	killer cell lectin-like receptor subfamily G, member 1	0.72	4.61E-03
PSME2	NM_002818	proteasome (prosome, macropain) activator subunit 2 (PA28 beta)	0.72	3.02E-03
FLI1	NM_001167681	Fli-1 proto-oncogene, ETS transcription factor	0.71	1.32E-03
CYTH1	NM_001292018	cytohesin 1	0.71	2.73E-02
TBXAS1	NM_001130966	thromboxane A synthase 1 (platelet)	0.71	5.72E-03
ARL4C	NM_005737	ADP-ribosylation factor-like 4C	0.71	2.04E-02
C1R	NM_001733	complement component 1, r subcomponent	0.71	4.09E-03
KIAA0922	NM_001131007	KIAA0922	0.70	1.36E-03
DOK1	NM_001197260	docking protein 1, 62kDa (downstream of tyrosine kinase 1)	0.70	2.24E-02
CD44	NM_001202555	CD44 molecule (Indian blood group)	0.70	4.41E-04
IFITM1	NM_003641	interferon induced transmembrane protein 1	0.70	3.28E-03
SERPINB9	NM_004155	serpin peptidase inhibitor, clade B (ovalbumin), member 9	0.70	7.84E-04
DUSP5	NM_004419	dual specificity phosphatase 5	0.69	5.15E-03

ICAM1	NM_000201	intercellular adhesion molecule 1	0.69	7.55E-04
IGJ	NM_144646	immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides	0.69	1.55E-02
TGM2	NM_004613	transglutaminase 2	0.69	3.97E-03
FMNL1	NM_005892	formin-like 1	0.69	3.76E-02
BID	NM_001244569	BH3 interacting domain death agonist	0.69	6.72E-04
TNFAIP8	NM_001286815	tumor necrosis factor, alpha-induced protein 8	0.69	5.56E-03
RAB31	NM_006868	RAB31, member RAS oncogene family	0.69	7.74E-04
ADCY7	NM_001286057	adenylate cyclase 7	0.69	1.96E-03
CASP4	NM_001225	caspase 4, apoptosis-related cysteine peptidase	0.69	1.89E-03
PECAM1	NM_000442	platelet/endothelial cell adhesion molecule 1	0.68	2.98E-04
TDO2	NM_005651	tryptophan 2,3-dioxygenase	0.68	2.68E-02
CD79A	NM_021601	CD79a molecule, immunoglobulin-associated alpha	0.68	2.01E-03
FCGR2B	NM_004001	Fc fragment of IgG, low affinity IIb, receptor (CD32)	0.68	5.21E-03
PIK3CD	NM_005026	phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit delta	0.68	6.85E-03
VCAN	NM_001164097	versican	0.68	5.27E-04
ABCC1	NM_004996	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	0.68	1.71E-03
CD226	NM_006566	CD226 molecule	0.68	6.24E-03
SERPINB8	NM_001031848	serpin peptidase inhibitor, clade B (ovalbumin), member 8	0.68	3.38E-02
C2	NM_000063	complement component 2	0.67	1.49E-03
BATF	NM_006399	basic leucine zipper transcription factor, ATF-like	0.67	1.00E-02
SACS	NM_014363	sacsin molecular chaperone	0.67	2.94E-02
DGKA	NM_201445	diacylglycerol kinase, alpha 80kDa	0.67	2.28E-03

CCL11	NM_002986	chemokine (C-C motif) ligand 11	0.67	6.44E-03
CCNA2	NM_001237	cyclin A2	0.67	2.11E-03
PRDM1	NM_182907	PR domain containing 1, with ZNF domain	0.67	1.22E-03
RGS19	NM_001039467	regulator of G-protein signaling 19	0.67	7.30E-03
LAG3	NM_002286	lymphocyte-activation gene 3	0.66	3.92E-02
UCP2	NM_003355	uncoupling protein 2 (mitochondrial, proton carrier)	0.66	2.76E-03
FBN1	NM_000138	fibrillin 1	0.66	1.28E-03
TOP2A	NM_001067	topoisomerase (DNA) II alpha 170kDa	0.66	4.61E-03
ARHGEF6	NM_004840	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	0.66	8.10E-03
DENND3	NM_014957	DENN/MADD domain containing 3	0.66	2.45E-03
KIAA0125	NR_026800	KIAA0125	0.66	2.07E-02
ITM2A	NM_001171581	integral membrane protein 2A	0.66	3.20E-03
NMI	NM_004688	N-myc (and STAT) interactor	0.66	8.81E-03
S100A8	NM_002964	S100 calcium binding protein A8	0.66	3.38E-02
ELMO1	NM_001039459	engulfment and cell motility 1	0.66	8.73E-03
MARCKS	NM_002356	myristoylated alanine-rich protein kinase C substrate	0.65	4.76E-04
RHOG	NM_001665	ras homolog family member G	0.65	8.81E-03
RARRES1	NM_206963	retinoic acid receptor responder (tazarotene induced) 1	0.65	7.96E-04
CD160	NM_007053	CD160 molecule	0.65	3.62E-02
CD1C	NM_001765	CD1c molecule	0.65	9.75E-03
SP110	NM_004509	SP110 nuclear body protein	0.65	1.10E-02
MYD88	NM_001172566	myeloid differentiation primary response 88	0.64	1.00E-02
UBA7	NM_003335	ubiquitin-like modifier activating enzyme 7	0.64	3.81E-03
IL15	NR_037840	interleukin 15	0.64	6.34E-03
TNFRSF17	NM_001192	tumor necrosis factor receptor superfamily, member 17	0.64	1.08E-02

TBC1D2B	NM_144572	TBC1 domain family, member 2B	0.64	3.41E-02
EZH2	NM_001203248	enhancer of zeste 2 polycomb repressive complex 2 subunit	0.64	1.04E-02
AQP9	NM_020980	aquaporin 9	0.64	3.04E-02
IRAK3	NM_001142523	interleukin-1 receptor-associated kinase 3	0.64	2.15E-03
GFI1	NM_001127216	growth factor independent 1 transcription repressor	0.64	1.09E-02
CD6	NR_045638	CD6 molecule	0.64	1.69E-02
SERPINE1	NM_000602	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	0.64	1.96E-03
ARHGEF1	NM_198977	Rho guanine nucleotide exchange factor (GEF) 1	0.63	7.22E-03
PTGER2	NM_000956	prostaglandin E receptor 2 (subtype EP2), 53kDa	0.63	1.16E-02
IFNAR2	NM_207585	interferon (alpha, beta and omega) receptor 2	0.63	2.23E-03
MAN2B1	NM_000528	mannosidase, alpha, class 2B, member 1	0.63	1.14E-02
PTHLH	NM_198964	parathyroid hormone-like hormone	0.63	8.27E-03
ZAP70	NM_001079	zeta-chain (TCR) associated protein kinase 70kDa	0.63	4.68E-03
OASL	NM_001261825	2'-5'-oligoadenylate synthetase-like	0.63	4.16E-03
S1PR4	NM_003775	sphingosine-1-phosphate receptor 4	0.63	4.28E-02
PDE4B	NM_001037340	phosphodiesterase 4B, cAMP-specific	0.63	3.59E-03
CCRL2	NM_003965	chemokine (C-C motif) receptor-like 2	0.63	9.99E-03
NFKBIA	NM_020529	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	0.63	1.21E-02
PLAUR	NM_001005376	plasminogen activator, urokinase receptor	0.63	2.23E-03
TRAF3IP3	NR_109871	TRAF3 interacting protein 3	0.62	5.94E-03
ADORA3	NM_000677	adenosine A3 receptor	0.62	5.57E-03
TCF7	NM_201632	transcription factor 7 (T-cell specific, HMG-box)	0.62	5.20E-03

FES	NM_002005	feline sarcoma oncogene	0.62	2.67E-02
EGR1	NM_001964	early growth response 1	0.62	2.26E-02
AP1S2	NM_001272071	adaptor-related protein complex 1, sigma 2 subunit	0.61	1.90E-02
MDK	NM_001270550	midkine (neurite growth-promoting factor 2)	0.61	3.44E-02
CD1E	NM_001042584	CD1e molecule	0.61	3.20E-02
TCF4	NM_001243234	transcription factor 4	0.61	2.21E-03
TNFRSF14	NM_003820	tumor necrosis factor receptor superfamily, member 14	0.61	1.50E-02
CPA3	NM_001870	carboxypeptidase A3 (mast cell)	0.61	1.64E-02
FNBP1	NM_015033	formin binding protein 1	0.61	1.10E-02
NNMT	NM_006169	nicotinamide N-methyltransferase	0.61	6.34E-03
PTGER4	NM_000958	prostaglandin E receptor 4 (subtype EP4)	0.61	5.94E-03
CEBPA	NM_001285829	CCAAT/enhancer binding protein (C/EBP), alpha	0.61	1.60E-02
CEBPB	NM_001285878	CCAAT/enhancer binding protein (C/EBP), beta	0.61	3.95E-02
HLA-DRB5	NM_002125	major histocompatibility complex, class II, DR beta 5	0.61	7.17E-03
GPSM3	NM_022107	G-protein signaling modulator 3	0.61	4.50E-03
CNKSR2	NM_001168648	connector enhancer of kinase suppressor of Ras 2	0.60	4.48E-02
VWF	NM_000552	von Willebrand factor	0.60	1.63E-02
KIAA0930	NM_001009880	KIAA0930	0.60	3.81E-03
DDB2	NM_000107	damage-specific DNA binding protein 2, 48kDa	0.60	2.26E-02
PLXNC1	NM_005761	plexin C1	0.60	4.47E-03
HK3	NM_002115	hexokinase 3 (white cell)	0.60	1.75E-02
CCL18	NM_002988	chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)	0.60	4.19E-02
PDLIM1	NM_020992	PDZ and LIM domain 1	0.60	1.78E-02

CXCL6	NM_002993	chemokine (C-X-C motif) ligand 6	0.60	1.82E-02
CXCR3	NM_001142797	chemokine (C-X-C motif) receptor 3	0.59	3.48E-02
XAF1	NM_199139	XIAP associated factor 1	0.59	4.70E-03
DENND4B	NM_014856	DENN/MADD domain containing 4B	0.59	2.04E-02
ARPC2	NM_152862	actin related protein 2/3 complex, subunit 2, 34kDa	0.59	5.41E-03
JUNB	NM_002229	jun B proto-oncogene	0.58	1.84E-02
GNAI2	NM_001282618	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	0.58	1.76E-02
ELF4	NM_001127197	E74-like factor 4 (ets domain transcription factor)	0.58	9.92E-03
PLXND1	NM_015103	plexin D1	0.58	5.45E-03
CH25H	NM_003956	cholesterol 25-hydroxylase	0.58	2.13E-02
CP	NM_000096	ceruloplasmin (ferroxidase)	0.58	3.28E-03
CCR6	NM_031409	chemokine (C-C motif) receptor 6	0.58	2.19E-02
FN1	NM_212482	fibronectin 1	0.58	1.71E-03
F13A1	NM_000129	coagulation factor XIII, A1 polypeptide	0.58	2.23E-02
CENPF	NM_016343	centromere protein F, 350/400kDa	0.58	1.34E-02
HOPX	NM_001145460	HOP homeobox	0.58	1.55E-02
HSD11B1	NM_181755	hydroxysteroid (11-beta) dehydrogenase 1	0.58	4.50E-02
RASGRP2	NM_001098670	RAS guanyl releasing protein 2 (calcium and DAG-regulated)	0.58	4.42E-02
SELP	NM_003005	selectin P (granule membrane protein 140kDa, antigen CD62)	0.58	2.28E-02
CBFA2T3	NM_175931	core-binding factor, runt domain, alpha subunit 2; translocated to, 3	0.57	2.32E-02
IL16	NM_172217	interleukin 16	0.57	5.76E-03
FCHO1	NM_001161357	FCH domain only 1	0.57	3.59E-02
TCL1A	NM_001098725	T-cell leukemia/lymphoma 1A	0.57	1.15E-02

SLC1A4	NM_003038	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	0.57	2.97E-02
CSF3R	NM_000760	colony stimulating factor 3 receptor (granulocyte)	0.57	1.08E-02
TRAFD1	NM_006700	TRAF-type zinc finger domain containing 1	0.57	4.09E-03
INHBA	NM_002192	inhibin, beta A	0.57	9.12E-03
JAK2	NM_004972	Janus kinase 2	0.57	6.67E-03
P2RX1	NM_002558	purinergic receptor P2X, ligand-gated ion channel, 1	0.57	2.51E-02
CRIP1	NM_001311	cysteine-rich protein 1 (intestinal)	0.57	2.53E-02
ELF1	NM_001145353	E74-like factor 1 (ets domain transcription factor)	0.57	2.53E-02
IL2RA	NM_000417	interleukin 2 receptor, alpha	0.56	1.31E-02
IL27RA	NM_004843	interleukin 27 receptor, alpha	0.56	1.58E-02
MSL3	NM_078629	male-specific lethal 3 homolog (Drosophila)	0.56	8.03E-03
CBLB	NM_170662	Cbl proto-oncogene B, E3 ubiquitin protein ligase	0.56	2.54E-02
VIM	NM_003380	vimentin	0.56	1.43E-02
CARD8	NR_033680	caspase recruitment domain family, member 8	0.56	5.42E-03
FBN2	NM_001999	fibrillin 2	0.56	1.81E-02
COL8A1	NM_001850	collagen, type VIII, alpha 1	0.55	1.21E-02
KCNMB1	NM_004137	potassium large conductance calcium-activated channel, subfamily M, beta member 1	0.55	1.52E-02
PSME1	NM_001281528	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)	0.55	3.34E-02
TRIM21	NM_003141	tripartite motif containing 21	0.55	3.07E-02
ITGAD	NM_005353	integrin, alpha D	0.55	4.82E-02
MCL1	NM_021960	myeloid cell leukemia 1	0.55	2.01E-02
TNC	NM_002160	tenascin C	0.55	8.91E-03

TNFRSF11A	NM_001270949	tumor necrosis factor receptor superfamily, member 11a, NFKB activator	0.55	1.66E-02
IRF7	NM_004031	interferon regulatory factor 7	0.55	3.24E-02
TUBA1A	NM_006009	tubulin, alpha 1a	0.55	3.16E-02
MDFIC	NM_199072	MyoD family inhibitor domain containing	0.55	4.24E-02
SMCHD1	NM_015295	structural maintenance of chromosomes flexible hinge domain containing 1	0.55	1.21E-02
DCK	NM_000788	deoxycytidine kinase	0.55	3.29E-02
P2RY6	NM_001277204	pyrimidinergic receptor P2Y, G-protein coupled, 6	0.54	3.36E-02
MARCO	NM_006770	macrophage receptor with collagenous structure	0.54	3.50E-02
ADRA2A	NM_000681	adrenoceptor alpha 2A	0.54	3.53E-02
CIITA	NR_104444	class II, major histocompatibility complex, transactivator	0.54	3.37E-02
CCL19	NM_006274	chemokine (C-C motif) ligand 19	0.54	3.45E-02
ANXA1	NM_000700	annexin A1	0.54	2.07E-02
DKK3	NM_013253	dickkopf WNT signaling pathway inhibitor 3	0.54	1.35E-02
STAB1	NM_015136	stabilin 1	0.54	7.40E-03
PTGS1	NM_001271165	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	0.54	1.44E-02
MCAM	NM_006500	melanoma cell adhesion molecule	0.53	3.81E-03
SYT11	NM_152280	synaptotagmin XI	0.53	1.91E-02
LGALS1	NM_002305	lectin, galactoside-binding, soluble, 1	0.53	3.79E-02
HLX	NM_021958	H2.0-like homeobox	0.53	3.81E-02
S100A9	NM_002965	S100 calcium binding protein A9	0.53	3.81E-02
CASP3	NM_004346	caspase 3, apoptosis-related cysteine peptidase	0.53	3.07E-02
CD47	NM_001777	CD47 molecule	0.53	2.80E-03
RAD51AP1	NM_001130862	RAD51 associated protein 1	0.53	3.92E-02

REL	NM_001291746	v-rel avian reticuloendotheliosis viral oncogene homolog	0.53	3.00E-02
FOLR2	NM_001113534	folate receptor 2 (fetal)	0.52	2.19E-02
SRPX2	NM_014467	sushi-repeat containing protein, X-linked 2	0.52	3.25E-02
CCL2	NM_002982	chemokine (C-C motif) ligand 2	0.52	3.55E-02
FLT3LG	NM_001278638	fms-related tyrosine kinase 3 ligand	0.52	2.28E-02
STK17A	NM_004760	serine/threonine kinase 17a	0.52	1.33E-02
NCAPH	NM_001281712	non-SMC condensin I complex, subunit H	0.52	4.33E-02
MYO9B	NM_004145	myosin IXB	0.52	1.41E-02
ARNTL	NM_001030272	aryl hydrocarbon receptor nuclear translocator-like	0.52	2.43E-02
ATF3	NM_001206488	activating transcription factor 3	0.52	2.68E-02
DNASE2	NM_001375	deoxyribonuclease II, lysosomal	0.52	4.99E-02
CFH	NM_001014975	complement factor H	0.52	4.46E-02
CD7	NM_006137	CD7 molecule	0.51	2.47E-02
FANCI	NM_001113378	Fanconi anemia, complementation group I	0.51	4.80E-02
MAMLD1	NM_001177465	mastermind-like domain containing 1	0.51	4.51E-02
ASCL2	NM_005170	achaete-scute family bHLH transcription factor 2	0.51	4.50E-02
RGS2	NM_002923	regulator of G-protein signaling 2, 24kDa	0.51	4.62E-02
RRAS	NM_006270	related RAS viral (r-ras) oncogene homolog	0.51	4.37E-02
ITGBL1	NM_004791	integrin, beta-like 1 (with EGF-like repeat domains)	0.51	9.99E-03
MANF	NM_006010	mesencephalic astrocyte-derived neurotrophic factor	0.51	4.71E-02
IFIT3	NM_001289758	interferon-induced protein with tetratricopeptide repeats 3	0.51	2.60E-02
RSAD2	NM_080657	radical S-adenosyl methionine domain containing 2	0.51	2.62E-02
CD55	NM_001114752	CD55 molecule, decay accelerating factor for complement (Cromer blood group)	0.51	1.71E-02

STAT5A	NM_001288719	signal transducer and activator of transcription 5A	0.51	4.52E-02
BTG1	NM_001731	B-cell translocation gene 1, anti-proliferative	0.51	2.39E-02
ZNF101	NM_033204	zinc finger protein 101	0.50	2.66E-02
THBD	NM_000361	thrombomodulin	0.50	1.91E-02
NOTCH2	NM_001200001	notch 2	0.50	1.31E-02
RRM2	NM_001034	ribonucleotide reductase M2	0.50	3.00E-02
SLCO3A1	NM_001145044	solute carrier organic anion transporter family, member 3A1	0.50	1.34E-02
VAMP5	NM_006634	vesicle-associated membrane protein 5	0.50	4.44E-02
CCND2	NM_001759	cyclin D2	0.50	1.94E-02
LTB	NM_002341	lymphotoxin beta (TNF superfamily, member 3)	0.49	2.39E-02
KLF6	NR_027653	Kruppel-like factor 6	0.49	1.09E-02
SLC20A1	NM_005415	solute carrier family 20 (phosphate transporter), member 1	0.49	3.24E-02
ARPC5	NM_001270439	actin related protein 2/3 complex, subunit 5, 16kDa	0.49	2.12E-02
ANGPT2	NM_001118887	angiopoietin 2	0.49	1.41E-02
C1S	NM_001734	complement component 1, s subcomponent	0.49	3.28E-02
PRKY	NR_028062	protein kinase, Y-linked, pseudogene	0.49	3.33E-02
TAPBP	NM_003190	TAP binding protein (tapasin)	0.49	1.80E-02
AREG	NM_001657	amphiregulin	0.49	4.25E-02
SSPN	NM_005086	sarcospan	0.49	4.62E-02
DYRK2	NM_006482	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	0.49	1.46E-02
CCL23	NM_005064	chemokine (C-C motif) ligand 23	0.49	3.29E-02
XPO6	NM_015171	exportin 6	0.48	3.70E-02
RAP2B	NM_002886	RAP2B, member of RAS oncogene family	0.48	1.65E-02
SYK	NM_003177	spleen tyrosine kinase	0.48	1.55E-02

FAM89B	NM_001098785	family with sequence similarity 89, member B	0.48	3.79E-02
CD5	NM_014207	CD5 molecule	0.48	3.80E-02
EMP1	NM_001423	epithelial membrane protein 1	0.48	1.80E-02
TNFSF14	NM_172014	tumor necrosis factor (ligand) superfamily, member 14	0.48	3.86E-02
C15orf39	NM_015492	chromosome 15 open reading frame 39	0.47	2.78E-02
KPNA2	NM_002266	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	0.47	3.76E-02
LYST	NM_000081	lysosomal trafficking regulator	0.47	1.97E-02
TEP1	NM_007110	telomerase-associated protein 1	0.47	4.37E-02
N4BP2L1	NM_001079691	NEDD4 binding protein 2-like 1	0.47	7.30E-03
BTN2A1	NM_001197233	butyrophilin, subfamily 2, member A1	0.47	2.27E-02
CAP1	NM_006367	CAP, adenylate cyclase-associated protein 1 (yeast)	0.47	4.45E-02
LILRA2	NM_001290271	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2	0.47	2.27E-02
TFPI2	NM_001271003	tissue factor pathway inhibitor 2	0.46	3.59E-02
IFFO1	NM_001193457	intermediate filament family orphan 1	0.46	4.65E-02
PIP4K2A	NM_005028	phosphatidylinositol-5-phosphate 4-kinase, type II, alpha	0.46	3.08E-02
TLR6	NM_006068	toll-like receptor 6	0.46	4.75E-02
RGS4	NM_001113380	regulator of G-protein signaling 4	0.44	4.42E-02
GLUL	NM_001033056	glutamate-ammonia ligase	0.44	2.94E-02
LRP8	NM_033300	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor	0.44	4.27E-02
IFNGR1	NM_000416	interferon gamma receptor 1	0.43	4.56E-02
SERPINB1	NR_073111	serpin peptidase inhibitor, clade B (ovalbumin), member 1	0.43	3.80E-02
CR1	NM_000573	complement component (3b/4b) receptor 1 (Knops blood group)	0.42	2.92E-02
CASP8	NM_001080124	caspase 8, apoptosis-related cysteine peptidase	0.42	4.99E-02

ETV6	NM_001987	ets variant 6	0.42	4.14E-02
ANXA2	NM_004039	annexin A2	0.42	4.37E-02
IL1RN	NM_173843	interleukin 1 receptor antagonist	0.41	4.83E-02
ARHGEF2	NM_001162384	Rho/Rac guanine nucleotide exchange factor (GEF) 2	0.41	4.42E-02
INPP4A	NM_001566	inositol polyphosphate-4-phosphatase, type I, 107kDa	0.40	3.06E-02
GRK5	NM_005308	G protein-coupled receptor kinase 5	0.40	3.95E-02
6-Sep	NM_015129	septin 6	0.40	4.33E-02
RUNX1T1	NM_001198627	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	0.40	4.91E-02
PTPN2	NM_002828	protein tyrosine phosphatase, non-receptor type 2	0.39	4.05E-02
NAP1L1	NM_139207	nucleosome assembly protein 1-like 1	0.38	3.74E-02
MBNL1	NM_207294	muscleblind-like splicing regulator 1	0.37	4.44E-02
ACACB	NM_001093	acetyl-CoA carboxylase beta	-0.39	4.10E-02
HNF4A	NM_001287183	hepatocyte nuclear factor 4, alpha	-0.40	4.27E-02
SLC25A16	NM_152707	solute carrier family 25 (mitochondrial carrier; Graves disease autoantigen), member 16	-0.41	4.97E-02
ATXN7L1	NM_138495	ataxin 7-like 1	-0.42	2.64E-02
SUCLG2	NM_003848	succinate-CoA ligase, GDP-forming, beta subunit	-0.42	3.79E-02
ANK3	NM_001204403	ankyrin 3, node of Ranvier (ankyrin G)	-0.43	2.95E-02
YIPF6	NM_173834	Yip1 domain family, member 6	-0.43	3.79E-02
ATP6V1C1	NM_001695	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1	-0.43	3.74E-02
WDFY3	NM_014991	WD repeat and FYVE domain containing 3	-0.44	3.52E-02
SEPHS1	NM_001195602	selenophosphate synthetase 1	-0.44	4.14E-02
CLN5	NM_006493	ceroid-lipofuscinosis, neuronal 5	-0.44	4.48E-02
ALDOB	NM_000035	aldolase B, fructose-bisphosphate	-0.44	1.14E-02

WWC1	NM_015238	WW and C2 domain containing 1	-0.45	1.20E-02
MAP3K13	NR_038322	mitogen-activated protein kinase kinase kinase 13	-0.45	4.44E-02
DUSP3	NM_004090	dual specificity phosphatase 3	-0.45	3.48E-02
TSPAN9	NM_006675	tetraspanin 9	-0.45	4.19E-02
GNG12	NM_018841	guanine nucleotide binding protein (G protein), gamma 12	-0.45	3.64E-02
CEL	NM_001807	carboxyl ester lipase	-0.46	4.87E-02
FARP1	NM_001286839	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	-0.46	1.53E-02
BDH1	NM_004051	3-hydroxybutyrate dehydrogenase, type 1	-0.46	4.90E-02
SLC35D1	NM_015139	solute carrier family 35 (UDP-GlcA/UDP-GalNAc transporter), member D1	-0.47	3.12E-02
CHP1	NM_007236	calcineurin-like EF-hand protein 1	-0.47	4.49E-02
TSPYL1	NM_003309	TSPY-like 1	-0.47	3.45E-02
SKP1	NM_006930	S-phase kinase-associated protein 1	-0.47	2.47E-02
ATP5F1	NM_001688	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit B1	-0.47	4.46E-02
NR1I3	NM_001077481	nuclear receptor subfamily 1, group I, member 3	-0.47	4.45E-02
SNX4	NM_003794	sorting nexin 4	-0.47	4.20E-02
LAPTM4B	NM_018407	lysosomal protein transmembrane 4 beta	-0.47	4.25E-02
B3GNT1	NM_006876	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1	-0.47	4.38E-02
B4GALT4	NM_212543	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 4	-0.47	4.25E-02
TFDP2	NM_001178142	transcription factor Dp-2 (E2F dimerization partner 2)	-0.47	1.86E-02
CACNA1D	NM_000720	calcium channel, voltage-dependent, L type, alpha 1D subunit	-0.48	1.80E-02
SIPA1L1	NM_001284247	signal-induced proliferation-associated 1 like	-0.48	4.50E-02

		1		
SERPINC1	NM_000488	serpin peptidase inhibitor, clade C (antithrombin), member 1	-0.48	3.83E-02
NPY6R	NR_002713	neuropeptide Y receptor Y6 (pseudogene)	-0.48	3.71E-02
CALM1	NM_006888	calmodulin 1 (phosphorylase kinase, delta)	-0.48	1.90E-02
COX7B	NM_001866	cytochrome c oxidase subunit VIIb	-0.49	4.03E-02
DNAJC16	NM_001287811	DnaJ (Hsp40) homolog, subfamily C, member 16	-0.49	2.32E-02
STX7	NM_003569	syntaxin 7	-0.49	2.66E-02
ERLIN2	NM_001003791	ER lipid raft associated 2	-0.49	1.89E-02
BRE	NM_199191	brain and reproductive organ-expressed (TNFRSF1A modulator)	-0.49	2.77E-02
PREPL	NM_001042386	prolyl endopeptidase-like	-0.50	3.86E-02
PDZD2	NM_178140	PDZ domain containing 2	-0.50	2.03E-02
PROSC	NM_007198	proline synthetase co-transcribed homolog (bacterial)	-0.50	1.08E-02
APOOL	NM_198450	apolipoprotein O-like	-0.50	1.43E-02
DUS4L	NM_181581	dihydrouridine synthase 4-like (S. cerevisiae)	-0.50	3.01E-02
HSPA4	NM_002154	heat shock 70kDa protein 4	-0.50	3.87E-02
FTH1	NM_002032	ferritin, heavy polypeptide 1	-0.50	1.95E-02
GSTM4	NR_024538	glutathione S-transferase mu 4	-0.50	3.06E-02
OCEL1	NM_024578	occludin/ELL domain containing 1	-0.50	4.92E-02
RNF14	NM_183399	ring finger protein 14	-0.50	3.04E-02
SLC19A2	NM_006996	solute carrier family 19 (thiamine transporter), member 2	-0.51	4.88E-02
HSDL2	NM_001195822	hydroxysteroid dehydrogenase like 2	-0.51	1.20E-02
PRKAA2	NM_006252	protein kinase, AMP-activated, alpha 2 catalytic subunit	-0.51	3.79E-02
PAFAH2	NM_000437	platelet-activating factor acetylhydrolase 2, 40kDa	-0.51	2.67E-02

PEX5	NM_001131023	peroxisomal biogenesis factor 5	-0.51	2.47E-02
ST3GAL1	NM_173344	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	-0.51	1.45E-02
VAPB	NM_001195677	VAMP (vesicle-associated membrane protein)-associated protein B and C	-0.51	3.79E-02
SLC22A13	NM_004256	solute carrier family 22 (organic anion/urate transporter), member 13	-0.51	4.53E-02
MDH2	NR_104165	malate dehydrogenase 2, NAD (mitochondrial)	-0.51	2.52E-02
CDKL1	NM_004196	cyclin-dependent kinase-like 1 (CDC2-related kinase)	-0.52	1.46E-02
FUT6	NM_000150	fucosyltransferase 6 (alpha (1,3) fucosyltransferase)	-0.52	7.40E-03
ACP5	NM_001611	acid phosphatase 5, tartrate resistant	-0.52	4.43E-02
CRADD	NM_003805	CASP2 and RIPK1 domain containing adaptor with death domain	-0.52	4.14E-02
OCRL	NM_001587	oculocerebrorenal syndrome of Lowe	-0.52	2.19E-02
POLR2C	NM_032940	polymerase (RNA) II (DNA directed) polypeptide C, 33kDa	-0.52	4.64E-02
HNF1B	NM_000458	HNF1 homeobox B	-0.52	2.07E-02
PPARA	NM_001001928	peroxisome proliferator-activated receptor alpha	-0.52	3.36E-03
FAM50B	NM_012135	family with sequence similarity 50, member B	-0.52	4.27E-02
EIF4EBP2	NM_004096	eukaryotic translation initiation factor 4E binding protein 2	-0.52	6.47E-03
TBCE	NM_003193	tubulin folding cofactor E	-0.52	2.26E-02
STX3	NM_004177	syntaxin 3	-0.52	1.43E-02
HSPA9	NM_004134	heat shock 70kDa protein 9 (mortalin)	-0.52	1.16E-02
SLC25A20	NM_000387	solute carrier family 25 (carnitine/acylcarnitine translocase), member 20	-0.52	4.11E-02
LAMP2	NM_001122606	lysosomal-associated membrane protein 2	-0.53	2.53E-02

PROC	NM_000312	protein C (inactivator of coagulation factors Va and VIIIa)	-0.53	4.03E-02
AOX1	NM_001159	aldehyde oxidase 1	-0.53	2.07E-02
CCT6B	NM_006584	chaperonin containing TCP1, subunit 6B (zeta 2)	-0.53	3.91E-02
MMACHC	NM_015506	methylmalonic aciduria (cobalamin deficiency) cblC type, with homocystinuria	-0.53	3.86E-02
DFNA5	NM_001127454	deafness, autosomal dominant 5	-0.53	3.83E-02
PTGER3	NR_028293	prostaglandin E receptor 3 (subtype EP3)	-0.53	2.01E-02
MTFR1	NM_001145839	mitochondrial fission regulator 1	-0.53	1.65E-02
PROZ	NM_001256134	protein Z, vitamin K-dependent plasma glycoprotein	-0.53	3.76E-02
ILVBL	NM_006844	ilvB (bacterial acetolactate synthase)-like	-0.53	2.64E-02
FDX1	NM_004109	ferredoxin 1	-0.53	1.17E-02
DNAJA3	NM_001286516	DnaJ (Hsp40) homolog, subfamily A, member 3	-0.54	3.87E-02
LRBA	NM_001199282	LPS-responsive vesicle trafficking, beach and anchor containing	-0.54	1.81E-02
ITM2B	NM_021999	integral membrane protein 2B	-0.54	1.71E-02
PINK1	NM_032409	PTEN induced putative kinase 1	-0.54	2.28E-02
NDUFC1	NM_001184991	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1, 6kDa	-0.54	2.80E-02
NECAB2	NM_019065	N-terminal EF-hand calcium binding protein 2	-0.54	3.30E-02
GK	NM_001205019	glycerol kinase	-0.55	5.09E-03
HPGD	NM_000860	hydroxyprostaglandin dehydrogenase 15-(NAD)	-0.55	5.42E-03
ALPL	NM_000478	alkaline phosphatase, liver/bone/kidney	-0.55	1.53E-02
AMFR	NM_001144	autocrine motility factor receptor, E3 ubiquitin protein ligase	-0.55	2.68E-02
SUPV3L1	NM_003171	suppressor of var1, 3-like 1 (S. cerevisiae)	-0.55	3.36E-02
FCN3	NM_003665	ficolin (collagen/fibrinogen domain	-0.55	3.08E-02

		containing) 3		
PACRG	NM_152410	PARK2 co-regulated	-0.55	1.52E-02
HLF	NM_002126	hepatic leukemia factor	-0.55	7.31E-03
SLC4A1	NM_000342	solute carrier family 4 (anion exchanger), member 1 (Diego blood group)	-0.56	4.42E-02
ISCU	NM_014301	iron-sulfur cluster assembly enzyme	-0.56	2.86E-02
SOSTDC1	NM_015464	sclerostin domain containing 1	-0.56	3.07E-02
FTO	NM_001080432	fat mass and obesity associated	-0.56	2.90E-02
LYRM1	NM_001128302	LYR motif containing 1	-0.56	4.38E-02
SERPINA4	NM_001289032	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 4	-0.56	2.83E-02
ACLY	NM_198830	ATP citrate lyase	-0.56	3.80E-02
COQ9	NM_020312	coenzyme Q9	-0.56	1.40E-02
DSG2	NM_001943	desmoglein 2	-0.56	1.35E-02
EGF	NM_001178131	epidermal growth factor	-0.56	2.67E-02
DDAH1	NM_001134445	dimethylarginine dimethylaminohydrolase 1	-0.56	1.57E-02
MOAP1	NM_022151	modulator of apoptosis 1	-0.57	2.53E-02
BTD	NM_001281726	biotinidase	-0.57	1.80E-02
SLC9A3R1	NM_004252	solute carrier family 9, subfamily A (NHE3, cation proton antiporter 3), member 3 regulator 1	-0.57	2.43E-02
HAAO	NM_012205	3-hydroxyanthranilate 3,4-dioxygenase	-0.57	4.28E-02
ATP6V1D	NM_015994	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	-0.57	6.34E-03
AP3S2	NR_023361	adaptor-related protein complex 3, sigma 2 subunit	-0.57	5.61E-03
ALDH1B1	NM_000692	aldehyde dehydrogenase 1 family, member B1	-0.58	2.26E-02
ZCCHC14	NM_015144	zinc finger, CCHC domain containing 14	-0.58	6.70E-03
SAP18	NM_005870	Sin3A-associated protein, 18kDa	-0.58	2.53E-02
PRLR	NM_000949	prolactin receptor	-0.58	6.69E-03

PKD2	NM_000297	polycystic kidney disease 2 (autosomal dominant)	-0.58	1.97E-02
PDHB	NM_001173468	pyruvate dehydrogenase (lipoamide) beta	-0.58	2.56E-02
SUCLA2	NM_003850	succinate-CoA ligase, ADP-forming, beta subunit	-0.59	2.07E-02
ATP6V1B2	NM_001693	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B2	-0.59	2.05E-02
ATP5C1	NM_005174	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	-0.59	7.17E-03
ALAD	NM_000031	aminolevulinate dehydratase	-0.59	9.21E-03
DSCR3	NM_006052	Down syndrome critical region gene 3	-0.59	1.46E-02
TUBG1	NM_001070	tubulin, gamma 1	-0.59	3.61E-02
CTDSPL	NM_001008392	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like	-0.59	3.30E-02
PRKAG1	NM_001206710	protein kinase, AMP-activated, gamma 1 non-catalytic subunit	-0.59	2.78E-02
RPP14	NR_049757	ribonuclease P/MRP 14kDa subunit	-0.59	8.86E-03
CLDN8	NM_199328	claudin 8	-0.59	1.77E-02
INSR	NM_001079817	insulin receptor	-0.59	1.49E-03
PVALB	NM_002854	parvalbumin	-0.59	1.55E-02
C21orf33	NM_004649	chromosome 21 open reading frame 33	-0.60	7.17E-03
CLIC4	NM_013943	chloride intracellular channel 4	-0.60	3.28E-02
RRAGD	NM_021244	Ras-related GTP binding D	-0.60	7.43E-03
HMGCS2	NM_001166107	3-hydroxy-3-methylglutaryl-CoA synthase 2 (mitochondrial)	-0.60	7.42E-03
ADH6	NM_001102470	alcohol dehydrogenase 6 (class V)	-0.60	7.69E-03
KIF13B	NM_015254	kinesin family member 13B	-0.60	4.53E-02
KIFAP3	NM_001204514	kinesin-associated protein 3	-0.60	4.63E-02
BBOX1	NM_003986	butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine	-0.60	4.01E-02

		hydroxylase) 1		
MOCS1	NR_033233	molybdenum cofactor synthesis 1	-0.60	1.55E-02
FHIT	NM_001166243	fragile histidine triad	-0.61	3.48E-02
MRPL3	NM_007208	mitochondrial ribosomal protein L3	-0.61	1.54E-02
DDB1	NM_001923	damage-specific DNA binding protein 1, 127kDa	-0.61	4.97E-02
GADD45A	NM_001199741	growth arrest and DNA-damage-inducible, alpha	-0.61	1.45E-02
AK2	NM_013411	adenylate kinase 2	-0.61	3.30E-03
USH1C	NM_005709	Usher syndrome 1C (autosomal recessive, severe)	-0.61	9.34E-03
ASAH1	NM_001127505	N-acylsphingosine amidohydrolase (acid ceramidase) 1	-0.61	3.87E-02
LSM3	NM_014463	LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae)	-0.62	2.83E-02
AHCYL2	NM_001130720	adenosylhomocysteinase-like 2	-0.62	3.76E-02
EPCAM	NM_002354	epithelial cell adhesion molecule	-0.62	2.64E-02
ACOX1	NM_007292	acyl-CoA oxidase 1, palmitoyl	-0.62	1.32E-03
ORC4	NM_001190881	origin recognition complex, subunit 4	-0.62	1.48E-02
CDS1	NM_001263	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 1	-0.62	3.19E-02
MT1G	NM_005950	metallothionein 1G	-0.62	3.63E-02
DLST	NR_033814	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	-0.62	1.05E-02
ALDH1A1	NM_000689	aldehyde dehydrogenase 1 family, member A1	-0.62	1.29E-02
NPR3	NM_000908	natriuretic peptide receptor 3	-0.63	2.47E-03
RAB40B	NM_006822	RAB40B, member RAS oncogene family	-0.63	7.40E-03
UBE2G1	NM_003342	ubiquitin-conjugating enzyme E2G 1	-0.63	2.13E-02
GATM	NM_001482	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	-0.63	1.23E-02
ABCB1	NM_000927	ATP-binding cassette, sub-family B	-0.63	8.27E-03

		(MDR/TAP), member 1		
TULP3	NM_003324	tubby like protein 3	-0.63	3.10E-02
SERPINA6	NM_001756	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 6	-0.63	1.16E-02
FH	NM_000143	fumarate hydratase	-0.63	9.68E-03
KLK1	NM_002257	kallikrein 1	-0.64	1.80E-02
USP2	NM_004205	ubiquitin specific peptidase 2	-0.64	1.16E-02
KBTBD11	NM_014867	kelch repeat and BTB (POZ) domain containing 11	-0.64	4.42E-02
GLO1	NM_006708	glyoxalase I	-0.64	1.04E-02
ACADVL	NM_001270448	acyl-CoA dehydrogenase, very long chain	-0.64	1.05E-02
ATP1B1	NM_001677	ATPase, Na+/K+ transporting, beta 1 polypeptide	-0.64	2.30E-03
FBXO21	NM_033624	F-box protein 21	-0.65	1.44E-03
PKP4	NM_001005476	plakophilin 4	-0.65	1.51E-03
CES2	NR_036684	carboxylesterase 2	-0.65	2.95E-03
TLN2	NM_015059	talin 2	-0.65	1.91E-03
SLC25A44	NR_104412	solute carrier family 25, member 44	-0.65	3.30E-03
CKMT2	NM_001099735	creatine kinase, mitochondrial 2 (sarcomeric)	-0.65	1.43E-02
MGAM	NM_004668	maltase-glucoamylase (alpha-glucosidase)	-0.66	8.76E-03
CYP17A1	NM_000102	cytochrome P450, family 17, subfamily A, polypeptide 1	-0.66	2.67E-02
GPR137B	NM_003272	G protein-coupled receptor 137B	-0.66	3.07E-02
SDC1	NM_001006946	syndecan 1	-0.66	2.04E-02
SLIT2	NM_001289135	slit homolog 2 (Drosophila)	-0.66	1.36E-03
GABRB3	NM_001191321	gamma-aminobutyric acid (GABA) A receptor, beta 3	-0.66	1.91E-02
TCP1	NM_001008897	t-complex 1	-0.66	1.77E-02
TRIM15	NM_033229	tripartite motif containing 15	-0.66	8.17E-04
ENPEP	NM_001977	glutamyl aminopeptidase (aminopeptidase A)	-0.66	2.56E-02

TNFRSF21	NM_014452	tumor necrosis factor receptor superfamily, member 21	-0.67	2.53E-03
CCNG1	NM_199246	cyclin G1	-0.67	2.04E-02
FECH	NM_001012515	ferrochelatase	-0.67	4.43E-03
ARSF	NM_001201539	arylsulfatase F	-0.67	3.70E-02
TMPRSS2	NM_001135099	transmembrane protease, serine 2	-0.67	5.67E-04
LRRC6	NR_073525	leucine rich repeat containing 6	-0.67	6.60E-03
NDUFB5	NM_001199957	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16kDa	-0.68	1.55E-02
HRG	NM_000412	histidine-rich glycoprotein	-0.68	2.18E-03
KCNJ1	NM_000220	potassium inwardly-rectifying channel, subfamily J, member 1	-0.68	2.04E-02
UQCRC2	NM_003366	ubiquinol-cytochrome c reductase core protein II	-0.68	3.98E-02
CYFIP2	NM_014376	cytoplasmic FMR1 interacting protein 2	-0.69	9.44E-03
PRDX6	NM_004905	peroxiredoxin 6	-0.69	1.36E-02
TDP2	NM_016614	tyrosyl-DNA phosphodiesterase 2	-0.69	5.57E-03
LRPPRC	NM_133259	leucine-rich pentatricopeptide repeat containing	-0.69	3.57E-02
GSR	NM_001195103	glutathione reductase	-0.69	8.52E-03
CUBN	NM_001081	cubilin (intrinsic factor-cobalamin receptor)	-0.69	2.59E-02
NEDD4L	NM_001144966	neural precursor cell expressed, developmentally down-regulated 4-like, E3 ubiquitin protein ligase	-0.69	1.07E-04
P4HA2	NM_004199	prolyl 4-hydroxylase, alpha polypeptide II	-0.70	3.04E-02
FMO4	NM_002022	flavin containing monooxygenase 4	-0.70	6.34E-03
NDUFAB1	NM_005003	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa	-0.70	1.02E-02
MTHFD1	NM_005956	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenyltetrahydrofolate cyclohydrolase,	-0.70	4.23E-03

		formyltetrahydrofolate synthetase		
CSDC2	NM_014460	cold shock domain containing C2, RNA binding	-0.70	4.96E-02
DLAT	NM_001931	dihydrolipoamide S-acetyltransferase	-0.70	5.96E-04
CYB5A	NM_148923	cytochrome b5 type A (microsomal)	-0.71	6.05E-03
SLC7A8	NM_001267036	solute carrier family 7 (amino acid transporter light chain, L system), member 8	-0.71	4.32E-02
ATP1A1	NM_001160233	ATPase, Na+/K+ transporting, alpha 1 polypeptide	-0.71	4.75E-02
CNPPD1	NM_015680	cyclin Pas1/PHO80 domain containing 1	-0.71	4.42E-02
SOD1	NM_000454	superoxide dismutase 1, soluble	-0.71	9.00E-03
ACADL	NM_001608	acyl-CoA dehydrogenase, long chain	-0.71	1.26E-03
SDHC	NM_001035512	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa	-0.71	2.53E-02
ATP5A1	NM_001257334	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle	-0.71	2.91E-02
SLC22A4	NM_003059	solute carrier family 22 (organic cation/zwitterion transporter), member 4	-0.71	3.71E-03
SLC30A9	NM_006345	solute carrier family 30 (zinc transporter), member 9	-0.72	4.01E-02
NFE2L1	NM_003204	nuclear factor, erythroid 2-like 1	-0.72	2.95E-02
RALYL	NM_001287243	RALY RNA binding protein-like	-0.72	3.66E-03
SORD	NM_003104	sorbitol dehydrogenase	-0.72	3.64E-02
METTL21B	NM_015433	methyltransferase like 21B	-0.72	1.50E-02
ALDH1L1	NM_001270365	aldehyde dehydrogenase 1 family, member L1	-0.72	4.58E-02
SLC16A4	NM_001201548	solute carrier family 16, member 4	-0.72	1.00E-02
MAPK10	NM_138982	mitogen-activated protein kinase 10	-0.72	5.20E-03
CALB1	NM_004929	calbindin 1, 28kDa	-0.72	3.00E-02
ATP5G3	NM_001190329	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit C3 (subunit 9)	-0.73	1.55E-02
NARS	NM_004539	asparaginyl-tRNA synthetase	-0.73	1.86E-02

ENOSF1	NM_017512	enolase superfamily member 1	-0.73	7.17E-03
PEX7	NM_000288	peroxisomal biogenesis factor 7	-0.73	3.49E-02
DDX1	NM_004939	DEAD (Asp-Glu-Ala-Asp) box helicase 1	-0.73	2.67E-02
COASY	NM_001042532	CoA synthase	-0.73	2.12E-02
PEX19	NR_036492	peroxisomal biogenesis factor 19	-0.73	1.51E-02
PFN2	NM_053024	profilin 2	-0.74	1.15E-02
HOXD8	NM_001199746	homeobox D8	-0.74	1.26E-02
OAT	NM_001171814	ornithine aminotransferase	-0.74	1.04E-02
AKR1C3	NM_001253908	aldo-keto reductase family 1, member C3	-0.74	3.76E-02
PMPCB	NM_004279	peptidase (mitochondrial processing) beta	-0.74	3.30E-02
CLCN5	NM_001127898	chloride channel, voltage-sensitive 5	-0.74	1.10E-02
FOLR1	NM_000802	folate receptor 1 (adult)	-0.74	4.28E-02
ACAT1	NM_000019	acetyl-CoA acetyltransferase 1	-0.75	2.21E-03
POLD3	NR_046410	polymerase (DNA-directed), delta 3, accessory subunit	-0.75	6.72E-04
AQP1	NM_198098	aquaporin 1 (Colton blood group)	-0.75	3.73E-03
SPAG5	NM_006461	sperm associated antigen 5	-0.75	2.28E-02
HADHA	NM_000182	hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), alpha subunit	-0.75	4.03E-02
ACAA2	NM_006111	acetyl-CoA acyltransferase 2	-0.75	1.91E-02
SLC16A2	NM_006517	solute carrier family 16, member 2 (thyroid hormone transporter)	-0.75	2.76E-03
ACADM	NM_001127328	acyl-CoA dehydrogenase, C-4 to C-12 straight chain	-0.75	1.60E-02
PBX1	NM_001204963	pre-B-cell leukemia homeobox 1	-0.75	3.06E-02
GRHPR	NM_012203	glyoxylate reductase/hydroxypyruvate reductase	-0.75	4.80E-02
DLD	NM_001289750	dihydrolipoamide dehydrogenase	-0.75	1.95E-02
DSP	NM_004415	desmoplakin	-0.75	1.10E-02

RCAN2	NM_005822	regulator of calcineurin 2	-0.76	4.05E-02
SLC27A2	NM_001159629	solute carrier family 27 (fatty acid transporter), member 2	-0.76	1.31E-02
DIO1	NM_001039715	deiodinase, iodothyronine, type I	-0.76	4.37E-02
KNG1	NM_001102416	kininogen 1	-0.76	2.04E-02
ZMPSTE24	NM_005857	zinc metallopeptidase STE24	-0.76	3.92E-02
FMO1	NM_001282694	flavin containing monooxygenase 1	-0.76	2.51E-02
SLC6A13	NM_001243392	solute carrier family 6 (neurotransmitter transporter), member 13	-0.76	2.44E-02
ICMT	NM_012405	isoprenylcysteine carboxyl methyltransferase	-0.77	7.56E-03
PLCL1	NM_006226	phospholipase C-like 1	-0.77	2.25E-02
CCDC28A	NM_015439	coiled-coil domain containing 28A	-0.77	2.02E-02
GHITM	NM_014394	growth hormone inducible transmembrane protein	-0.77	5.51E-03
GABARAPL1	NM_031412	GABA(A) receptor-associated protein like 1	-0.77	1.64E-02
NIT1	NM_001185094	nitrilase 1	-0.77	2.03E-02
DDC	NM_001242886	dopa decarboxylase (aromatic L-amino acid decarboxylase)	-0.77	3.66E-02
PTPN3	NM_001145370	protein tyrosine phosphatase, non-receptor type 3	-0.78	2.23E-02
ACSL1	NM_001286708	acyl-CoA synthetase long-chain family member 1	-0.78	3.28E-04
SH3GL2	NM_003026	SH3-domain GRB2-like 2	-0.78	1.28E-03
GPX3	NM_002084	glutathione peroxidase 3 (plasma)	-0.79	1.10E-02
CS	NM_004077	citrate synthase	-0.79	1.51E-02
PGRMC2	NM_006320	progesterone receptor membrane component 2	-0.79	3.51E-02
VEGFA	NM_001204384	vascular endothelial growth factor A	-0.79	4.50E-03
HRSP12	NM_005836	heat-responsive protein 12	-0.79	1.16E-02
CBR1	NM_001286789	carbonyl reductase 1	-0.80	1.80E-02

PPP2R3A	NM_002718	protein phosphatase 2, regulatory subunit B", alpha	-0.80	3.59E-02
ATP6V1E1	NM_001039367	ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E1	-0.80	7.30E-03
PARM1	NM_015393	prostate androgen-regulated mucin-like protein 1	-0.80	2.02E-02
IPO13	NM_014652	importin 13	-0.80	2.49E-03
BHMT	NM_001713	betaine--homocysteine S-methyltransferase	-0.81	6.59E-03
GLB1L2	NM_138342	galactosidase, beta 1-like 2	-0.81	1.08E-02
IDH1	NM_001282386	isocitrate dehydrogenase 1 (NADP+), soluble	-0.81	2.68E-02
ACOT13	NM_001160094	acyl-CoA thioesterase 13	-0.81	1.03E-02
SLC17A3	NM_001098486	solute carrier family 17 (organic anion transporter), member 3	-0.81	1.80E-02
SLC4A4	NM_001098484	solute carrier family 4 (sodium bicarbonate cotransporter), member 4	-0.81	4.83E-02
PGRMC1	NM_006667	progesterone receptor membrane component 1	-0.82	1.57E-03
LARS2	NM_015340	leucyl-tRNA synthetase 2, mitochondrial	-0.82	2.41E-02
IMPA2	NM_014214	inositol(myo)-1(or 4)-monophosphatase 2	-0.82	4.62E-02
MLEC	NM_014730	malectin	-0.82	4.33E-02
UNC13B	NM_006377	unc-13 homolog B (C. elegans)	-0.82	7.40E-03
AIFM1	NM_004208	apoptosis-inducing factor, mitochondrion-associated, 1	-0.83	8.99E-03
NDUFS2	NM_001166159	NADH dehydrogenase (ubiquinone) Fe-S protein 2, 49kDa (NADH-coenzyme Q reductase)	-0.83	2.53E-02
ALB	NM_000477	albumin	-0.84	1.33E-02
ALDH5A1	NM_001080	aldehyde dehydrogenase 5 family, member A1	-0.84	1.86E-02
MINPP1	NM_001178117	multiple inositol-polyphosphate phosphatase 1	-0.84	2.94E-02
SERPINI1	NM_001122752	serpin peptidase inhibitor, clade I (neuroserpin), member 1	-0.84	1.63E-02
INADL	NM_176877	InaD-like (Drosophila)	-0.84	1.80E-02

STAU1	NM_017454	staufen double-stranded RNA binding protein 1	-0.84	1.73E-03
PLS1	NM_001145319	plastin 1	-0.84	2.25E-02
EHHADH	NM_001966	enoyl-CoA, hydratase/3-hydroxyacyl CoA dehydrogenase	-0.84	2.86E-02
GSTA3	NM_000847	glutathione S-transferase alpha 3	-0.85	3.82E-02
XPO7	NM_015024	exportin 7	-0.85	4.71E-02
APOM	NR_045828	apolipoprotein M	-0.85	2.04E-02
EPS8	NM_004447	epidermal growth factor receptor pathway substrate 8	-0.85	3.88E-02
SEPHS2	NM_012248	selenophosphate synthetase 2	-0.85	2.75E-02
DPP4	NM_001935	dipeptidyl-peptidase 4	-0.86	5.25E-03
CRHBP	NM_001882	corticotropin releasing hormone binding protein	-0.86	1.13E-02
ODC1	NM_002539	ornithine decarboxylase 1	-0.86	1.33E-02
PEBP1	NM_002567	phosphatidylethanolamine binding protein 1	-0.86	3.20E-03
MSMO1	NM_006745	methylsterol monooxygenase 1	-0.86	3.98E-02
SLC22A5	NM_003060	solute carrier family 22 (organic cation/carnitine transporter), member 5	-0.86	2.20E-02
LDHB	NM_002300	lactate dehydrogenase B	-0.86	4.01E-03
CYP4F2	NM_001082	cytochrome P450, family 4, subfamily F, polypeptide 2	-0.86	2.13E-02
TM7SF2	NM_003273	transmembrane 7 superfamily member 2	-0.87	4.55E-02
TMBIM6	NM_003217	transmembrane BAX inhibitor motif containing 6	-0.87	1.80E-02
ECHS1	NM_004092	enoyl CoA hydratase, short chain, 1, mitochondrial	-0.87	2.32E-02
HIBCH	NM_198047	3-hydroxyisobutyryl-CoA hydrolase	-0.87	2.08E-02
CRYZ	NM_001130042	crystallin, zeta (quinone reductase)	-0.87	9.99E-03
GOT2	NM_001286220	glutamic-oxaloacetic transaminase 2, mitochondrial	-0.87	4.37E-02

SCP2	NM_001007099	sterol carrier protein 2	-0.88	1.43E-02
AHCY	NM_001161766	adenosylhomocysteinase	-0.88	4.83E-02
ACOX2	NM_003500	acyl-CoA oxidase 2, branched chain	-0.88	7.43E-03
PEPD	NM_001166056	peptidase D	-0.88	3.40E-02
PLOD1	NM_000302	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1	-0.88	3.20E-02
IVD	NM_001159508	isovaleryl-CoA dehydrogenase	-0.88	4.68E-03
DZIP1	NM_014934	DAZ interacting zinc finger protein 1	-0.88	2.39E-02
NIPSNAP1	NM_001202502	nipsnap homolog 1 (C. elegans)	-0.88	2.50E-02
SLC25A3	NM_213611	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3	-0.89	4.66E-03
HYAL1	NM_153282	hyaluronoglucosaminidase 1	-0.89	3.66E-03
IARS2	NM_018060	isoleucyl-tRNA synthetase 2, mitochondrial	-0.89	1.14E-02
FAH	NM_000137	fumarylacetoacetate hydrolase (fumarylacetoacetase)	-0.89	1.28E-02
PHYH	NM_006214	phytanoyl-CoA 2-hydroxylase	-0.89	2.11E-04
SPR	NM_003124	sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase)	-0.89	3.38E-02
AUH	NM_001698	AU RNA binding protein/enoyl-CoA hydratase	-0.89	1.27E-02
DAO	NM_001917	D-amino-acid oxidase	-0.89	4.08E-02
KCNJ15	NM_001276439	potassium inwardly-rectifying channel, subfamily J, member 15	-0.89	1.26E-02
PKLR	NM_000298	pyruvate kinase, liver and RBC	-0.89	2.26E-02
PLG	NM_001168338	plasminogen	-0.90	2.53E-02
ACO2	NM_001098	aconitase 2, mitochondrial	-0.90	3.59E-02
MAOA	NM_000240	monoamine oxidase A	-0.90	2.10E-02
COX11	NR_027941	cytochrome c oxidase assembly homolog 11 (yeast)	-0.90	4.50E-03
DECR1	NM_001359	2,4-dienoyl CoA reductase 1, mitochondrial	-0.91	1.08E-02

ISCA1	NM_030940	iron-sulfur cluster assembly 1	-0.91	4.09E-02
SLC1A1	NM_004170	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	-0.92	4.26E-02
SLC25A1	NM_005984	solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1	-0.92	4.91E-02
ALDH7A1	NM_001182	aldehyde dehydrogenase 7 family, member A1	-0.92	7.76E-03
SHMT1	NM_001281786	serine hydroxymethyltransferase 1 (soluble)	-0.92	3.87E-02
GRB10	NM_005311	growth factor receptor-bound protein 10	-0.92	1.40E-02
TOM1L1	NM_005486	target of myb1 (chicken)-like 1	-0.92	1.05E-02
GPR116	NM_001098518	G protein-coupled receptor 116	-0.92	2.04E-02
ADD3	NM_016824	adducin 3 (gamma)	-0.92	3.81E-02
SLC22A6	NM_153277	solute carrier family 22 (organic anion transporter), member 6	-0.93	4.62E-02
GLYAT	NM_005838	glycine-N-acyltransferase	-0.93	3.20E-02
MICU1	NM_001195519	mitochondrial calcium uptake 1	-0.93	2.75E-02
GNPDA1	NM_005471	glucosamine-6-phosphate deaminase 1	-0.93	1.03E-02
DMXL1	NM_001290322	Dmx-like 1	-0.94	2.64E-02
XPNPEP2	NM_003399	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound	-0.94	3.87E-02
ESRRG	NM_001243507	estrogen-related receptor gamma	-0.94	1.27E-02
PDE8A	NM_173454	phosphodiesterase 8A	-0.94	4.37E-02
PCBD1	NM_001289797	pterin-4 alpha-carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha	-0.94	3.58E-02
MME	NM_007289	membrane metallo-endopeptidase	-0.95	1.96E-02
PTH1R	NM_000316	parathyroid hormone 1 receptor	-0.95	2.53E-02
ALDH3A2	NM_001031806	aldehyde dehydrogenase 3 family, member A2	-0.95	5.02E-03
GJB1	NM_001097642	gap junction protein, beta 1, 32kDa	-0.95	4.37E-02
ALDH9A1	NM_000696	aldehyde dehydrogenase 9 family, member A1	-0.96	6.04E-03

ANKRD46	NM_198401	ankyrin repeat domain 46	-0.96	3.76E-02
FOXI1	NM_012188	forkhead box I1	-0.96	1.57E-03
DPYS	NM_001385	dihydropyrimidinase	-0.97	2.77E-02
SLC22A2	NM_003058	solute carrier family 22 (organic cation transporter), member 2	-0.97	1.45E-02
GRB14	NM_004490	growth factor receptor-bound protein 14	-0.97	8.79E-03
EPHX2	NM_001256483	epoxide hydrolase 2, cytoplasmic	-0.97	1.46E-02
CLMN	NM_024734	calmin (calponin-like, transmembrane)	-0.98	1.44E-02
ADH5	NM_000671	alcohol dehydrogenase 5 (class III), chi polypeptide	-0.98	1.52E-02
SERPINA5	NM_000624	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 5	-0.99	6.42E-03
AZGP1	NM_001185	alpha-2-glycoprotein 1, zinc-binding	-0.99	2.78E-02
HMGCL	NM_001166059	3-hydroxymethyl-3-methylglutaryl-CoA lyase	-0.99	3.49E-02
HADH	NM_001184705	hydroxyacyl-CoA dehydrogenase	-0.99	1.14E-02
SETD3	NM_032233	SET domain containing 3	-0.99	2.46E-02
FBP1	NM_001127628	fructose-1,6-bisphosphatase 1	-0.99	4.96E-02
PGM1	NM_002633	phosphoglucomutase 1	-0.99	3.97E-02
RAB11FIP5	NM_015470	RAB11 family interacting protein 5 (class I)	-1.00	1.21E-02
SLC17A1	NM_005074	solute carrier family 17 (organic anion transporter), member 1	-1.00	4.25E-02
NQO2	NM_000904	NAD(P)H dehydrogenase, quinone 2	-1.00	4.59E-02
MXI1	NM_005962	MAX interactor 1, dimerization protein	-1.01	1.97E-02
MAP7	NM_001198611	microtubule-associated protein 7	-1.01	1.37E-02
MTX2	NR_027850	metaxin 2	-1.02	3.36E-02
AFG3L2	NM_006796	AFG3-like AAA ATPase 2	-1.02	2.35E-02
COBL	NM_001287436	cordon-bleu WH2 repeat protein	-1.03	3.43E-02
GLDC	NM_000170	glycine dehydrogenase (decarboxylating)	-1.04	3.63E-02
ASPA	NM_001128085	aspartoacylase	-1.04	1.33E-02

EFHD1	NM_025202	EF-hand domain family, member D1	-1.04	1.78E-02
ABCC2	NM_000392	ATP-binding cassette, sub-family C (CFTR/MRP), member 2	-1.05	1.54E-02
MUT	NM_000255	methylmalonyl CoA mutase	-1.07	4.23E-02
ALDH2	NM_001204889	aldehyde dehydrogenase 2 family (mitochondrial)	-1.08	2.53E-02
CA12	NM_206925	carbonic anhydrase XII	-1.08	5.45E-03
CA2	NM_001293675	0	-1.09	1.21E-02
MIPEP	NM_005932	mitochondrial intermediate peptidase	-1.09	7.31E-03
SULT1C2	NM_176825	sulfotransferase family, cytosolic, 1C, member 2	-1.09	3.71E-03
ACADSB	NM_001609	acyl-CoA dehydrogenase, short/branched chain	-1.09	9.90E-03
HADHB	NM_001281512	hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), beta subunit	-1.10	2.56E-03
CTH	NM_153742	cystathionase (cystathionine gamma-lyase)	-1.10	2.19E-02
HSPA4L	NM_014278	heat shock 70kDa protein 4-like	-1.10	2.05E-02
EPHX1	NM_001291163	epoxide hydrolase 1, microsomal (xenobiotic)	-1.11	2.70E-02
GOT1	NM_002079	glutamic-oxaloacetic transaminase 1, soluble	-1.11	1.46E-02
NINL	NM_025176	ninein-like	-1.11	3.38E-02
BCKDHB	NM_000056	branched chain keto acid dehydrogenase E1, beta polypeptide	-1.13	1.98E-02
PNP	NM_000270	purine nucleoside phosphorylase	-1.14	1.59E-02
ETFDH	NM_001281738	electron-transferring-flavoprotein dehydrogenase	-1.16	7.75E-04
HPN	NM_182983	hepsin	-1.17	4.53E-02
AFM	NM_001133	afamin	-1.17	4.33E-02
ENTPD5	NM_001249	ectonucleoside triphosphate diphosphohydrolase 5	-1.18	1.87E-02
GPD1L	NM_015141	glycerol-3-phosphate dehydrogenase 1-like	-1.21	1.05E-02

ACAA1	NM_001607	acetyl-CoA acyltransferase 1	-1.22	1.29E-02
HSD11B2	NM_000196	hydroxysteroid (11-beta) dehydrogenase 2	-1.24	4.28E-02

* Meta-Effect-Size: Hedges' g, which estimates the mean difference between AR and NAR group.

Table S3. Summary of the downstream genes and out/in-degrees of the 14 key driver genes in the differential modules of rejection (M1, M3, M4, M8, M10)

Symbol	Downstream genes	Downstream _count	Out_degrees	In_degrees	Type	Module
CASP1	APOL1;BTN3A3;TLR2;ST3GAL5;SYT11;EVI2A;SP110;CYBB;RASSF2;STAT4;MYD88;P2RY14;CXCL9;VOPP1;CLIC2;KLRB1;GPR183;CTSS;IRF8;RNASE6;UBD;IFNAR2;LCP2;HLA-E;CXCR4;RAB31;BTN3A2;ARHGDIB;CSF1R;BTN3A1;CLEC2B;DOCK10;CD69;AIM2;CD52;ADAMDEC1;CD38;CD53;CD96;GPR18;EVI2B;F13A1;HLA-DPB1;ARPC2;FYB;IKZF1;CD226;CD48;IL7R;ALOX5AP;FPR3;CCR2;FCGR2A;CD4;GMFG;HLA-DPA1;FAM49A;FAM65B;ARL4C;BASP1;CD44;PLXNC1;ITK;GPR65;LHFPL2;HLA-F;KIAA0922;LCP1;MAN2B1;C1QB;LAMP3;GZMA;PTPRC;DDB2;RTN1;EZH2;PIK3CG;NELL2;HLA-DOB;SP140;CD3E;GCNT1;PTPN6;TNFAIP3;DNMT1;IFITM1;TBXAS1;SELL;UCP2;STAT1;FLI1;LYZ;HCLS1;GPR171;FCGR2B;PTPN22;HLA-DRA;MNDA;SLA;LAPTM5;XPO6;NCKAP1L;ICOS;SERPINB9;VNN2;UBA7;SH2B3;TRIM22;6-Sep;APOBEC3C;APOBEC3G;ARHGAP25;CD84;C2;CELF2;ELMO1;CARD8;ADRB2;ENTPD1;LMNB1;P2RY10;PRKCH;SRGN;PIP4K2A;FOLR2;PRKCB;LPXN;RGS1;TNFSF8;MTHFD2;RGS10;KLRG1	132	26	2	global	M1
EVI2A	CD69;DOCK10;CD52;ADAMDEC1;CTSS;AIM2;CLEC2B;PLXNC1;EVI2B;GPR171;PTPN22;MNDA;HLA-F;FAM65B;HCLS1;HLA-DRA;PIK3CG;LCP2;IL7R;GPR65;GZMA;FCGR2B;PTPRC;ARPC2;APOBEC3G;BTN3A1;CSF1R;ARHGDIB;BTN3A3;CYBB;CD53;CELF2;ELMO1;CD96;CARD8;GMFG;BASP1;EZH2;FCGR2A;GPR18;ALOX5AP;ADRB2;FPR3;CD48;CD4;CXCR4;ARL4C;ENTPD1;BTN3A	130	23	2	local	M1

	2;GPR183;CD3E;CCR2;FYB;CD226;CLIC2;F13A1;HLA-E;LAPTM5;LCP1;ITK;P2RY10;ICOS;SP140;RTN1;ST3GAL5;TLR2;SP110;NCKAP1L;C1QB;CXCL9;STAT4;APOL1;CD38;RASSF2;STAT1;LAMP3;LPXN;P2RY14;SERPINB9;RGS1;TRIM22;SRGN;TBXAS1;LHFPL2;PTPN6;MTHFD2;RAB31;SELL;NELL2;IFNAR2;SYT11;KLRG1;UBD;HLA-DPB1;KLRB1;RNASE6;TNFSF8;SLA;LYZ;VNN2;MYD88;RGS10;6-Sep;APOBEC3C;ARHGAP25;CD84;CD44;C2;GCNT1;FLI1;HLA-DPA1;LMNB1;FAM49A;MAN2B1;KIAA0922;FOLR2;DDB2;IKZF1;IRF8;PRKCH;HLA-DOB;PIP4K2A;IFITM1;PRKCB;UCP2;XPO6;SH2B3;UBA7;TNFAIP3;DNMT1					
MNDA	F13A1;ALOX5AP;FYB;CD53;EZH2;CLEC2B;CCR2;LCP1;HLA-E;HLA-F;ARL4C;ITK;HCLS1;LAPTM5;MYD88;P2RY14;SP110;RTN1;RGS10;TLR2;ST3GAL5;CD4;ARPC2;ARHGDIB;ARHGAP25;CD38;C2;DOCK10;CD52;CXCR4;CELF2;ELMO1;BTN3A2;CYBB;ENTPD1;FCGR2B;GPR18;CD96;EVI2B;HLA-DPB1;CD3E;ADAMDEC1;GPR171;CD226;CSF1R;GCNT1;BTN3A3;CARD8;HLA-DPA1;FLI1;CD48;CXCL9;HLA-DRA;CTSS;GMFG;IFNAR2;FAM49A;CLIC2;FOLR2;GZMA;C1QB;DDB2;PIK3CG;IRF8;RASSF2;GPR183;NELL2;SELL;UBD;PRKCB;SLA;TRIM22;SRGN;LMNB1;FPR3;FCGR2A;PTPRC;STAT1;KLRB1;LHFPL2;TNFSF8;KLRG1;SERPINB9;ICOS;RNASE6;IFITM1;RAB31;LAMP3;NCKAP1L;XPO6;P2RY10;UCP2;PRKCH;PLXNC1;MTHFD2;UBA7;SH2B3;PTPN6;BTN3A1;APOBEC3C;APOBEC3G;CD44;CD84;ADRB2;CD69;APOL1;IKZF1;IL7R;6-Sep;BASP1;MAN2B1;KIAA0922;FAM65B;GPR65;LCP2;SP140;TBXAS1;PIP4K2A;SYT11;PTPN22;LYZ;RGS1;LPXN;VNN2	124	21	3	local	M1
RASSF2	CD4;LAMP3;MAN2B1;ARL4C;C1QB;ARPC2;HLA-E;LHFPL2;CD44;KIAA0922;BASP1;GZMA;LCP1;ARHGDIB;GPR65;FAM65B;ITK;PLXNC1;CXCL9;EVI2B;HLA-	120	24	7	local	M1

	F;RTN1;SH2B3;TRIM22;APOBEC3C;BTN3A1;CD3E;CLEC2B;CYBB;BTN3A3;CELF2;CD69;CD53;CTSS;EZH2;CARD8;FCGR2A;GMFG;CD48;GPR171;ADRB2;FPR3;GPR18;ALOX5AP;CD38;HLA-DPB1;F13A1;CD96;CCR2;ARHGAP25;FYB;ADAMDEC1;CD226;CXCR4;DOCK10;ICOS;FLI1;CD52;HLA-DRA;HLA-DPA1;LAPTM5;DDB2;LCP2;HCLS1;APOL1;STAT1;SRGN;CSF1R;KLRB1;GPR183;PIP4K2A;TBXAS1;SELL;SP110;IFITM1;FOLR2;C2;RNASE6;P2RY14;UCP2;UBD;RAB31;MTHFD2;KLRG1;IFNAR2;SP140;SYT11;TLR2;P2RY10;XPO6;SLA;NCKAP1L;PRKCH;LMNB1;PTPRC;RGS10;UBA7;PTPN6;6-Sep;BTN3A2;APOBEC3G;CD84;ELMO1;FCGR2B;ENTPD1;IL7R;GCNT1;CLIC2;FAM49A;NELL2;IKZF1;LYZ;PIK3CG;PRKCB;LPXN;RGS1;SERPINB9;PTPN22;TNFSF8;VNN2					
LCP1	FLI1;CARD8;HLA-DRA;FYB;CYBB;CELF2;CD53;CD52;CD48;CXCL9;CD38;CD4;LAPTM5;HLA-DPA1;PTPRC;PLXNC1;RGS10;MTHFD2;NCKAP1L;PRKCH;CD3E;BTN3A1;ALOX5AP;APOBEC3G;ARPC2;ARHGDIB;ARHGAP25;CLEC2B;CTSS;ELMO1;DOCK10;APOL1;GPR183;GMFG;BTN3A3;C2;CSF1R;GCNT1;CD69;LMNB1;HCLS1;CD96;6-Sep;CLIC2;FOLR2;RNASE6;KLRB1;TLR2;SELL;SLA;ITK;PRKCB;UBD;PIK3CG;P2RY14;HLA-F;UCP2;STAT1;GZMA;LCP2;FCGR2A;RAB31;LYZ;FPR3;SP110;HLA-DPB1;BTN3A2;CD44;CD226;CD84;CCR2;CXCR4;F13A1;GPR18;GPR171;ADRB2;FCGR2B;ENTPD1;ARL4C;ADAMDEC1;IL7R;FAM49A;NELL2;LAMP3;P2RY10;ICOS;DDB2;PTPN6;SYT11;IKZF1;TBXAS1;PIP4K2A;SRGN;RGS1;LPXN;SERPINB9;SP140;PTPN22;EZH2;TNFSF8;TRIM22;LHFPL2;XPO6;KLRG1;VNN2;IFNAR2	106	20	7	local	M1
GPR65	BASP1;CARD8;CTSS;EZH2;FCGR2A;GMFG;UBD;IFNAR2;LCP2;TLR2;SP140;HLA-F;PLXNC1;KLRG1;SP110;P2RY10;SYT11;HLA-DPB1;BTN3A1;CSF1R;ARHGDIB;CLEC2B;CD53;F13A1;CXCL9;C	105	18	5	local	M1

	D52;CD48;GPR18;ARPC2;DOCK10;APOL1;CYBB;CCR2;CD96;BTN3A2;FYB;CD226;CXCR4;CLIC2;ICOS;HCLS1;DDB2;CD38;IKZF1;GCNT1;PTPN6;LAMP3;CD3E;LHFPL2;SELL;TBXAS1;LMNB1;GZMA;RGS10;MTHFD2;KLRB1;XPO6;IL7R;NELL2;RNASE6;VNN2;RAB31;PTPRC;TRIM22;6-Sep;ALOX5AP;APOBEC3G;CD4;ARHGAP25;CD44;CD84;BTN3A3;C2;ELMO1;GPR171;ADRB2;FPR3;CD69;CELF2;ARL4C;FCGR2B;ENTPD1;GPR183;ADAMDEC1;FOLR2;LYZ;SRGN;PIP4K2A;LAPTM5;STAT1;FAM49A;P2RY14;PRKCH;NCKAP1L;PIK3CG;ITK;PRKCB;SLA;TNFSF8;PTPN22;UCP2;FLI1;SERPINB9;LPXN;RGS1					
MYO1F	LILRB2;CLEC10A;CSTA;IGSF6;CSF3R;ADCY7;HCK;ADA;CD97;SELPLG;TRAF1;SECTM1;SLC2A3;RGS19;NCF2;BID;CD180;CD300A;CD40;AOAH;BCL2A1;CD33;BATF;DOCK2;EGR2;GNA15;CMKLR1;CD37;GZMB;FMNL1;LAIR1;CFP;ICAM1;ITGB2;LY86;ITGAM;NCF4;CTSW;IL2RG;IL1B;JUNB;DUSP5;RAC2;LSP1;SASH3;HSPA6;VAV1;HHEX;PLAUR;STK10;RHOG;TCIRG1;TNF;ALOX5;CCR1;CXCR3;ELF4;INPP5D;CXCR6;NLRP3;RHOH;PTAFR;PLCB2;PTPRE;STAT5A	65	15	2	global	M3
HCK	DOCK2;CSF3R;CD180;BID;BATF;ADA;CD33;LILRB2;ITGB2;ICAM1;SECTM1;HHEX;VAV1;NCF4;PLAUR;LSP1;NCF2;AOAH;CD97;GNA15;CD37;CD300A;LAIR1;FMNL1;CFP;GZMB;EGR2;IL2RG;BCL2A1;CXCR3;ELF4;IGSF6;ITGAM;LY86;CD40;CCR1;CTSW;INPP5D;ALOX5;STK10;RHOH;NLRP3;CLEC10A;CSTA;RAC2;HSPA6;RHOG;STAT5A;TCIRG1;SLC2A3;SELPLG;CMKLR1;IL1B;JUNB;DUSP5;PTAFR;TRAF1;PLCB2;SASH3;PTPRE;TNF;CXCR6	62	17	4	local	M3
VAV1	LILRB2;ALOX5;RHOH;DOCK2;LSP1;ITGB2;STK10;CLEC10A;GNA15;NLRP3;INPP5D;ADA;CD97;CD300A;CD37;CD33;CD180;BID;CD40;FMNL1;CFP;GZMB;LAIR1;EGR2;ELF4;CXCR3;IL2RG;BCL2A1;SELPLG;LY86;RHOG;CSTA;IGSF6;RAC2;TRAF1;HHEX;PLCB2;SASH3;PLAUR;STAT5A;NCF2;TCIRG1;AOAH;CTSW;CMKLR1;ICAM1;ITGAM;CXCR6;CCR1;SECTM1;JUNB;SLC2A3;PTPRE;PTAFR;TNF;IL1B;DUSP5	57	15	5	local	M3

PLEK	FCN1;IL15RA;IDO1;CD86;EMP3;FCGR3B;KLRD1;HLA-DMB;IFIT3;IRF1;RARRES3;WARS;UBE2L6;PSME1;PLEKHO2;PSMB8;EMR2;CXCL11;CD14;CSF2RB;HCP5;B2M;CXCL10;IL10RA;IL15;MICB;IL10RB;OAS2;PSMB10;TRAFD1;TAP2;TAP1;IFI30;TRIM21;VAMP5;PSME2;PTGER4	37	16	1	global	M4
PSME1	IL10RB;CXCL10;PSMB10;PLEKHO2;IDO1;FCN1;IFIT3;CD86;PSMB8;HCP5;HLA-DMB;UBE2L6;PSME2;B2M;CSF2RB;CD14;IL15RA;MICB;CXCL11;IL10RA;EMP3;IL15;OAS2;RARRES3;IRF1;TAP1;IFI30;TAP2;KLRD1;WARS;TRIM21;EMR2;TRAFD1;PTGER4;VAMP5	35	13	1	local	M4
PSMB10	EMP3;CD14;PLEKHO2;CXCL11;CD86;IL10RA;CXCL10;HCP5;PSMB8;UBE2L6;TRIM21;PSME2;RARRES3;WARS;B2M;CSF2RB;EMR2;FCN1;MICB;IL15RA;IL15;IFIT3;OAS2;IL10RB;HLA-DMB;TAP2;TRAFD1;TAP1;PTGER4;IFI30;IRF1;VAMP5	32	14	4	local	M4
CRLF3	BIRC3;CASP3;TNFAIP8;SLC20A1;MCL1;STK17B;BAZ1A;REL;CD47;MSL3	10	6	0	global	M8
CD3D	SLAMF1;CXCL13;FAIM3;DGKA;MS4A1;CD3G;GZMK;TRAF3IP3;CD5;LY9;PRDM1	11	8	0	global	M10

Table S4. Key drivers-based gene set used for the Connectivity Map query. Meta-p-values are adjusted by FDR correction method.

Symbol	Meta-Effect Size *	Meta-p-value	Module	Out-degrees
CASP1	1.09	6.82E-05	1	132
RASSF2	1.08	1.14E-03	1	120
EVI2A	1.18	2.21E-03	1	130
MNDA	0.96	6.08E-05	1	124
LCP1	1.16	2.16E-04	1	106
HCLS1	1.04	8.02E-05	1	96
GPR65	1.02	1.94E-05	1	105
AIF1	0.73	7.96E-05	1	134
BTK	1.24	3.98E-04	1	133
IRF8	1.12	2.09E-06	1	121
HLA-E	0.88	1.27E-03	1	112
LY96	1.03	4.19E-03	1	134
AIM2	1.13	1.40E-06	1	129
GMFG	1.12	6.72E-04	1	102
STAT4	1.08	5.54E-06	1	128
C1QB	0.91	2.91E-04	1	114
ITK	1.16	2.85E-03	1	79
MAN2B1	0.63	1.14E-02	1	116
EVI2B	0.98	1.12E-03	1	110
VOPP1	0.91	1.93E-03	1	127
TNFAIP3	1.23	2.98E-04	1	126
MYD88	0.64	1.00E-02	1	118
HCK	1.14	1.36E-06	3	17
MYO1F	1.16	1.36E-06	3	15
VAV1	0.97	3.56E-05	3	15
IGSF6	1.14	7.55E-04	3	10
NCF4	0.83	8.26E-05	3	10
NCF2	1.00	2.66E-05	3	9
SASH3	1.03	1.00E-03	3	9

ADA	0.91	5.45E-03	3	8
CD1D	0.92	6.72E-04	3	8
LSP1	0.75	1.79E-03	3	8
RGS19	0.67	7.30E-03	3	8
PLEK	0.96	8.11E-06	4	16
PSMB10	1.01	2.42E-05	4	14
PSME1	0.55	3.34E-02	4	13
PSMB8	0.93	1.02E-02	4	11
WARS	0.98	3.78E-03	4	9
CXCL10	1.13	1.85E-06	4	8
FCGR3B	1.16	1.40E-06	4	8
IDO1	1.27	2.08E-07	4	8
IFIT3	0.51	2.60E-02	4	8

* Meta-Effect-Size: Hedges' g, which estimates the mean difference between AR and NAR group.

Table S5. A) CMAP predictions with the KDG-based signature of AR. The 67 drugs or compounds with negative connectivity score are listed here, at a p-value of <0.05. Correlation between the drug-induced transcript signature in CMAP with the KDG signature is represented by the connectivity scores, ranging from -1 to +1. A negative correlation emphasizes an inverse similarity between the two profiles, suggesting drug exposure reverses the expression of the AR gene signature.

Compound	Connectivity score	p-value	Drug description
Monastrol	-0.31	0.000	NA
Indoprofen	-0.30	0.001	NA
Mefenamic acid	-0.29	0.001	Analgesic and anti-inflammatory
Naftifine	-0.29	0.001	Anti-fungal
Ticarcillin	-0.29	0.001	Penicillin class anti-bacterial
Memantine	-0.29	0.001	N-methyl-D-aspartate (NMDA) receptor antagonist
PNU-0251126	-0.29	0.002	NA
4-hydroxyphenazone	-0.28	0.003	NA
Carbimazole	-0.28	0.003	Imidazole anti-thyroid agent
Bemegride	-0.28	0.003	NA
Azapropazone	-0.28	0.003	NA
Niflumic acid	-0.27	0.004	NA
Tolnaftate	-0.27	0.004	Anti-fungal
Atracurium besilate	-0.27	0.004	Non-depolarizing neuromuscular blocking agent
Timolol	-0.26	0.008	Non-selective beta adrenergic antagonist
Diprophylline	-0.26	0.008	Theophylline derivative with broncho- and vasodilator properties
Gabexate	-0.26	0.008	NA
Streptozocin	-0.26	0.008	Antibiotic (but used as antineoplastic)
Disopyramide	-0.26	0.009	Class 1 (sodium channel blocker) anti-arrhythmic agent
Sulfaphenazole	-0.26	0.009	Sulphonamide antibacterial
Aciclovir	-0.26	0.009	Antiviral
Levodopa	-0.26	0.010	Amino acid precursor of dopamine
Dacarbazine	-0.26	0.010	Alkylating agent
Fulvestrant	-0.25	0.011	Synthetic estrogen receptor antagonist
Spironolactone	-0.25	0.011	Aldosterone antagonist
Clemastine	-0.25	0.012	Histamine H1 antagonist
Nadolol	-0.25	0.012	Non-selective beta adrenergic antagonist

Cimetidine	-0.25	0.012	Histamine-2 receptor antagonist
Metformin	-0.25	0.013	Biguanide hypoglyaemic agent
Gly-His-Lys	-0.25	0.014	NA
Acetohexamide	-0.25	0.016	Sulfonylurea hypoglycemic agent
Oxybutynin	-0.24	0.016	Antispasmodic and anticholinergic
Propofol	-0.24	0.016	Anaesthetic agent, facilitates inhibitory neurotransmission mediated by gamma-aminobutyric acid (GABA)
5155877	-0.24	0.018	NA
Syrosingopine	-0.24	0.016	NA
Diloxanide	-0.24	0.018	NA
Minocycline	-0.23	0.021	Tetracycline antibiotic
Isoxicam	-0.24	0.018	NA
Sulindac sulfide	-0.24	0.019	Non-steroidal anti-inflammatory agent
Naftopidil	-0.24	0.019	NA
chlormezanone	-0.23	0.025	NA
ursolic acid	-0.23	0.025	Naturally occurring compound
alfaxalone	-0.23	0.026	NA
quipazine	-0.23	0.027	NA
eticlopride	-0.23	0.028	NA
Prestwick-642	-0.23	0.029	NA
piperacetazine	-0.23	0.029	NA
adiphenine	-0.23	0.029	NA
5162773	-0.23	0.030	NA
iocetamic acid	-0.23	0.030	NA
lincomycin	-0.23	0.031	Lincosamide antibiotic
levobunolol	-0.23	0.032	Ophthalmic beta-blocker
benzocaine	-0.23	0.032	Topical anaesthetic
iohexol	-0.23	0.033	Non-ionic contrast agent
BW-B70C	-0.23	0.033	NA
metronidazole	-0.23	0.033	Antibiotic
dizocilpine	-0.23	0.034	NA
decamethonium bromide	-0.22	0.037	Agonist of nicotinic acetycholine receptors

tretinoin	-0.22	0.038	all-*trans*-retinoic acid (ATRA), derivative of vitamin A
colistin	-0.22	0.038	Antibiotic
naproxen	-0.22	0.039	Non-steroidal anti-inflammatory
sulindac	-0.22	0.040	Non-steroid anti-inflammatory
isotretinoin	-0.22	0.041	Retinoid derivative of vitamin A
alprenolol	-0.22	0.045	NA
oxyphenbutazone	-0.22	0.046	NA
meteneprost	-0.22	0.046	NA
vancomycin	-0.22	0.048	Antibiotic

NA: Not applicable, denoting drugs/compounds without USA market availability.

Table S5. B) Drugs in current clinical use which target the individual key driver genes (DrugBank)

Key Driver Gene	**Drugs in Clinical Use**
CASP1	Minocycline, Acetylsalicylic acid
EVI2A	NDI
MNDA	NDI
RASSF2	NDI
LCP1	NDI
GPR65	NDI
MYO1F	NDI
HCK	Bosutinib
VAV1	Pazopanib, Bosutinib, Dasatinib
PLEK	NDI
PSME1	NDI
PSMB10	Carfilzomib
CRLF3	NDI
CD3D	Muromonab, Blinatumomab

Drugs with US market availability only. NDI, no drugs identified.

Table S6. Taqman™ (Thermo Fisher, MA USA) primers for real-time polymerase chain reaction

Gene Symbol	Assay ID	Dye Label
MNDA (Ifi205)	Mm04204354_mH	FAM-MGB
CASP1	Mm00438023_m1	FAM-MGB
CCL5	Mm01302427_m1	FAM-MGB
TNFα	Mm00443258_m1	FAM-MGB
CXCL9	Mm00434946_m1	FAM-MGB
IL2	Mm00434256_m1	FAM-MGB
GPR65	Mm00433695_m1	FAM-MGB
CRLF3	Mm00658175_m1	FAM-MGB
EVI2A	Mm03030107_s1	FAM-MGB
PSMB10	Mm00479052_g1	FAM-MGB
VAV1	Mm01232047_m1	FAM-MGB
PSME1	Mm00650858_g1	FAM-MGB
LCP1	Mm01310735_m1	FAM-MGB
MYO1F	Mm01271176_m1	FAM-MGB
PLEK	Mm00450970_m1	FAM-MGB
HCK	Mm01241463_m1	FAM-MGB
CD3D	Mm00442746_m1	FAM-MGB
RASSF2	Mm00615320_m1	FAM-MGB

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