Supplementary Materials for: Transcriptional profile of platelets and iPSC-derived megakaryocytes from whole genome and RNA sequencing

Kai Kammers[1,*], Margaret A Taub[2,*], Benjamin Rodriguez[3], Lisa R Yanek[4], Ingo Ruczinski[2], Joshua Martin[4], Kanika Kanchan[5], Alexis Battle[6], Linzhao Cheng[7], Zack Z. Wang[7], Andrew D. Johnson[3], Jeffrey T Leek[2], Nauder Faraday[4], Lewis C Becker[4], Rasika A Mathias[4,5].

** equal contribution from both authors.*

[1] Division of Biostatistics and Bioinformatics, Department of Oncology, Sidney Kimmel Comprehensive Cancer Center, Johns Hopkins University School of Medicine, Baltimore, MD, USA

[2] Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, USA

[3] NHLBI Population Sciences Branch, The Framingham Heart Study, Framingham, MA, USA

[4] The GeneSTAR Research Program, Johns Hopkins University School of Medicine, Baltimore, MD, USA

[5] Division of Allergy and Clinical Immunology, Johns Hopkins University School of Medicine, Baltimore, MD, USA

[6] Department of Biomedical Engineering, Johns Hopkins University, Baltimore, MD, USA

[7] Division of Hematology and Institute for Cell Engineering, Johns Hopkins University School of Medicine, Baltimore, MD, USA

Corresponding author E-mail: rmathias@jhmi.edu

Supplementary Methods

Study Participants

The GeneSTAR study population is constituted of apparently healthy siblings identified from probands with coronary artery disease prior to age 60, spouses of the siblings, and their adult offspring (>21 years of age), with a total n > 4000 participants[1-3]. The study was approved by the Institutional Review Board of the Johns Hopkins Medical Institutions. Written informed consent was obtained from all participants.

iPSC-derived MK sample: Subjects (n=251) were included if they were members of the original GeneSTAR Study population and were over 21 years of age. Subjects were excluded if they had developed diabetes, cardiovascular disease, or any bleeding disorder, AIDS, advanced cancer, cancer under treatment or autoimmune diseases under treatment since study entry.

Platelet sample: Subjects (n=307) were included if they had participated in the prior GeneSTAR study of platelet aggregation[3], were healthy and not pregnant, were over 21 years of age, and were able to participate along with a full sibling. Subjects were excluded if they had cardiovascular disease, any bleeding disorder, AIDS, advanced cancer, cancer under treatment, or autoimmune diseases under treatment.

Samples underwent quality control as described in Methods and Results to determine the final set for analysis, and clinical characteristics are shown by race and tissue type for each of the final included samples in **Supplementary Table S1** (MKs, n=185: 84 AAs, 101 EAs; Platelets, n=290: 110 AAs, 180 EAs).

Generation of iPSC and derived MKs

The protocols used to generate the iPSCs and derive MKs are described in detail by Liu et al[4]. Briefly, iPSC lines were reprogrammed from peripheral blood mononuclear cells using non-integrating episomal vectors. After establishment, they were all expanded in Essential 8 medium on either Matrigel (1:30; BD Biosciences, San Diego, CA, http://www.bdbiosciences.com) or vitronectin (5 μg/cm^2, Life Technologies). Human iPSCs were differentiated into definitive CD34+CD45+ hematopoietic progenitor cells (HPCs), using the "spin-embryoid body" (spin-EB) method in feeder- and serum-free conditions. Single iPSCs were suspended in serum-free medium (SFM). We used Food and Drug Administration (FDA)-approved pharmacological agents to replace thrombopoietin (TPO) and bovine serum albumin (BSA) in the culture medium, an important factor for future clinical applications[4]. On day 14, the suspended cells were harvested and seeded for MK culture, generating a cell population enriched for CD41+CD42a+ MKs. Flow cytometry was performed as described previously[4]. Briefly, single cells from EB culture were harvested, and labeled with anti-human CD34-PE (Miltenyi Biotec), CD45-Alexa Fluor 700 (eBioscience), CD41-APC (BD Biosciences), CD42a-efluor 450 (eBioscience), and CD42b-FITC (eBioscience). All samples were analyzed with LSRII flow cytometer (BD Biosciences). Ig isotype controls were used as the control for flow cytometry in each experiment. There is variability in the percent CD41$^+$CD42a$^+$ MKs in MK pellets of our iPSCs (see **Supplementary Table S1**) which is accounted for in the transcriptomic analysis using percent CD41$^+$CD42a$^+$ MKs as a covariate in the model, as described below.

Genotyping protocol, genotype calling, and data quality

To perform this eQTL analysis, we leveraged the whole genome sequence (WGS) data available through the NHLBI's Trans Omics for Precision Medicine (TOPMed) [5] program. WGS was performed to an average depth of 38X using DNA isolated from blood, PCR-free library construction, and Illumina HiSeq X technology. Details for variant calling and quality control are described in Taliun et al. [5] For this analysis, only the GeneSTAR samples in Freeze 6a (August 2018) were included (n=1755). For the eQTL analysis, we retained all SNPs that are located on autosomes with at least 2 samples for each genotype and a call rate greater than 80%.

RNA isolation, library preparation, and sequencing

After thawing the MK pellets, Quick-RNA™ MicroPrep (Zymo Research, Cat# R1050) was used for total RNA isolation following the manufacturer's protocols. Platelet samples were prepared from whole blood specimens that were centrifuged and treated with leukocyte-depletion beads, with platelets separated from whole blood cells over a column and washed (Miltenyi Biotec). EDTA was then added and samples were spun again to pellets. After adding 1ml Qiazol (Trizol), samples were frozen at -80. Phenol chloroform was added to frozen samples, which were then spun. The top layer was then pulled off and treated with the RNAeasy clean-up kit by Qiagen, with modifications. An Agilent BioAnalyzer was used for quality control prior to library creation, with RIN (RNA Integrity Number) over 8.0.

TruSeq RNA Library Preparation Kit v2 (Illumina, Cat# RS-122-2001 and RS-122-2002) was used to generate libraries following the manufacturer's procedures. Specifically, Poly-A RNA was first purified from 10-200 ng RNA, fragmented to about 150-200 nucleotides in length, and then converted to cDNA. End repair was performed to remove 3’ end overhangs and fill in 5’ overhangs; next an “A” base was added to the 3’ end for adaptor ligation and PCR amplification was performed. The resulting library was quantified and quality checked on an Agilent BioAnalyzer using DNA 1000 chips. High sensitivity chips were used for further quality control to ensure adequate concentration and optimal fragment size. Libraries were uniquely barcoded and pooled for sequencing.

DNA sequencing was performed on an Illumina® HiSeq 2500 instrument using standard protocols for paired end 100bp sequencing. Samples were multiplexed in groups of four samples per sequencing lane. Average yield was ~15 Gb of raw sequencing data per lane, or ~300 million reads per lane. As per Illumina’s recommendation, 3% PhiX was added to each lane as a control, and to assist the analysis software with any library diversity issues.

RNA-seq data preprocessing

A detailed overview of the data processing is presented in **Figure 1**. RNA-sequencing reads were aligned to the human genome (USCS, hg19) using the spliced-read mapper *HISAT2*[6] in default mode (version 2.0.1). We used *StringTie*[7] (version 1.3.1c) to assemble and quantify RNA-seq alignments into full-length transcripts representing multiple splice variants for each gene loci including the *de novo* assembly option and the UCSC reference annotation genes.gtf (version archive-2014-06-02-13-47-56). Transcript abundances were quantified in terms of FPKM (fragments per kilobase of transcript per million reads sequenced). For statistical downstream analyses, we integrated the results from *StringTie* into the software environment R (version 3.5.1) [8] and then used the software package *Ballgown* [9] (version 2.12.0), a statistical backend for *HISAT-StringTie* suite[10], for efficient data storage, processing, and analysis. We ran the program *gffcompare*[11] to obtain gene symbols for de-novo transcripts that map to known genes stored in the reference annotation, and all subsequent analyses were carried out on a gene level. To aggregate transcript abundances that belong the same gene, given by the gene symbol, we used the built-in function *gexpr* of the Ballgown package. De-novo transcripts that were not associated with a known gene were dropped from further analysis. Genes with median FPKM across all samples less than or equal to 1 (for MKs) or 0.3 (for platelets) were excluded (the lower cutoff for platelets is similar to prior studies, e.g., Eicher et al. [12] and Londin et al. [13]). Next, we performed a variance stabilizing transformation of the filtered FPKM measurements. If Y_{ij} is the FPKM expression level of gene i in sample j, we used expression levels $E_{ij} = log_2(Y_{ij}+1)$ for all downstream analyses.

Quality control of RNA-seq and WGS data

iPSC-derived MKs: The RNA-sequencing data set was collected in 10 batches totaling 233 MK samples. We removed (i) 14 samples that were technical duplicates used to assess the integrity of the MK generation as previously described [14], (ii) 25 samples that showed low data quality scores in term of overall expression, and (iii) 9 samples due to missing WGS data. The remaining N=185 MK samples had an average of 41.1 million reads per sample with an average alignment rate of 90.79%.

Platelets: RNA-sequencing data was collected in 4 batches totaling 307 platelet samples. We removed (i) 4 samples that were low-expression outliers, (ii) 6 samples that were excluded due to poor quality or unexpected familial relationships, and (iii) 7 samples due to missing WGS data. The remaining N=290 platelet samples had an average of 38.8 million reads per samples with an average alignment rate of 93.18%.

WGS of MK samples: After filtering the genotype data to autosomal SNPs with at least two samples per genotype and a call rate of at least 80%, we retained 5,004,400 SNPs in the AA cohort and 4,433,801 in the EA cohort.

WGS of platelet samples: After filtering genotype data to only autosomal SNPs with at least two samples per genotype and a call rate of at least 80%, we retained 5,500,942 SNPs in the AA cohort and 5,064,974 in the EA cohort.

Cis-eQTL analysis

A detailed overview of the full analysis pipeline is presented in **Figure 1**. eQTL analyses were carried out within a tissue (MKs and platelets) and stratified by ancestry (AAs and EAs) with analysis performed for each gene within a 1Mb window of each SNP using the R package MatrixEQTL[15] (version 2.2). Sex, age, percent $CD41^{+}CD42a^{+}$ in MK pellets (not included in platelet analysis), RNA-sequencing batch, 15 principal components (PCs) of the filtered and log-transformed gene expression matrix, and ancestry PCs (3 PCs for EAs and 1 PC for AAs) were included as covariates in each linear model fit. To adjust for family relationships among samples, we used a kinship matrix based on known pedigree information to integrate the correlation structure among samples using the *errorCovariance* option within the *Matrix_eQTL_main* function. Results from eQTL analyses of AAs and EAs were combined within MKs and platelets, respectively, by meta-analyses using fixed effects models. The meta analyses were carried out with the R package meta[16] (version 4.9-5). We used these meta-analysis results to identify the most significant eQTL SNP for each gene using eigenMT[17], yielding a single SNP-gene pair for each gene.

These eQTL results were summarized and reported at two levels, similar to the 'Single-Tissue cis-eQTL Data' provided by the GTEx Consortium (gtexportal.org): (i) the level of *all* SNP-gene pairs (referred to below as the MatrixEQTL results); and (ii) the level of the *peak* SNP-gene pair (referred to below as the eigenMT results). We used (i) as the input to eigenMT and provide these full results to the community for completeness. The eigenMT results (ii) are the basis for our downstream enrichment analyses as well as comparisons to results from the GTEx portal. For the eigenMT results (*peak* SNP-gene pair), the peak SNP per gene was identified while accounting for linkage disequilibrium between nearby variants, and adjustments were then made for multiple testing using the eigenMT method for each gene separately. Given the set of all peak SNPs per gene and their corresponding eigenMT-adjusted p-values, we calculated false discovery rate (FDR) adjusted q-values[18] from the set of eigenMT-adjusted p-values to perform multiple testing correction across genes. We called a SNP-gene pair an eQTL if the calculated q-value was below 0.05. The genes associated with the significant SNP-gene pairs from the eigenMT analysis are referred to below as eGenes.

There was a small number of eQTLs in each tissue (84 of 946 and 151 out of 1,830 in MKs and platelets, respectively) where the homozygous minor allele was only noted in two individuals. Of these, a few are of note because the two individuals with the rare homozygous variant are in the same family (4 and 41 in MKs and platelets, respectively). Although our methods are robust to relatedness, we do include a flag in our results files available for download on our website to indicate these special cases.

Cross-tissue comparison of eQTL results

To compare results across tissues, in addition to examining significant SNP-gene pairs that were exactly shared between the tissues, we allowed for flexibility in the specific SNP showing association with a gene across tissues, to encompass similar but not identical regulatory features or to allow for variation in allele frequencies across the samples included in each tissue-specific analysis. We did this by taking each eQTL in one tissue and seeing whether a significant eQTL targeting the same gene was present in the other tissue, within a genomic window of a certain size. We examined window sizes ranging from 5kb to 1Mb in either direction of the SNP of interest with the restriction that the set of potential SNPs in the other tissue was within the range of 1Mb on either side of the gene. We note that we did not use an LD-based approach here due to the complexities of our analysis design: with a meta-analysis across two population groups, followed by selection of only the top eQTL per eGene, we were unable to determine a reasonable way to assess correlation of genotype across the two tissues.

Overlap of eQTLs with functional annotation tracks

To characterize the location of our eigenMT-identified peak SNPs relative to relevant functional annotations, we obtained bed-file tracks of regulatory signatures specific to MKs from the EU Blueprint project (http://www.blueprint-epigenome.eu) including DNAse hotspot regions, H3K27 acetylation loci (including those which do or do not overlap with promoter elements), h3k4me3 loci, enhancer elements derived by chromatin segmentation, and MK super-enhancer elements, as defined in Petersen et al.[19]. As controls, we also included two additional tracks: HMEC (Human Mammary Epithelial Cell) super-enhancers and a version of the MK super-enhancer track with the coordinates shuffled. Enrichment of overlap of significant eigenMT results (FDR-corrected p-value < 0.05) compared to all eigenMT results was assessed using Fisher's exact test.

Gene-set enrichment and pathway analysis

Gene-set enrichment analysis was performed to assess for enrichment of biologically relevant gene categories among highly expressed genes in MKs, relative to all known genes, using Fisher's exact test as implemented in the topGO package[20] (v2.37.0). topGO takes the hierarchical structure of the ontology into account in assessing significance of enrichment. To increase power, we limited gene sets considered for testing to those with at least three genes in our dataset included in the node of the gene ontology graph, and used the top 10% of expressed genes to define our set of true hits for the Fisher's exact test. The same enrichment analysis was repeated for platelet gene expression.

We also investigated gene-set enrichment analysis in the set of significant eigenMT eQTL hits (eGenes, q-value < 0.05)) to address two questions: (1) are the eGenes in MKs and platelets enriched for biologically meaningful pathways; and (2) are the eGenes in MKs and platelets mapping to a relevant annotation track enriched for biologically meaningful pathways. For (1) we considered eGenes from eigenMT in the MKs/platelets relative to all expressed genes in the MKs/platelets, respectively. Enrichment of gene ontology categories was evaluated with both Fisher's exact test (binary classification of eQTLs) and the Kolmogorov-Smirnov test (to allow for weighting based on strength of eQTL association) using topGO, and enrichment of canonical pathways and immunologic gene sets from the Molecular Signatures Database (MSigDB[21]) was evaluated with Fisher's exact test. In all cases we required at least 10 genes in our dataset to be included among those comprising the ontology node or pathway being tested, to provide adequate power for significance assessment. For (2) we considered significant eGenes from eigenMT in the MKs/platelets that overlapped one of our functional annotation tracks, relative to all significant eGenes from eigenMT in the MKs/platelets, respectively. Here, we evaluated enrichment of gene ontology categories with topGO and pathways from MSigDB[21] using Fisher's exact test, again requiring at least 10 genes in our dataset to be included among those comprising the ontology node or pathway being tested.

GWAS catalog overlap

To assess whether our eQTLs had previously been reported in GWAS of platelet-related traits, we downloaded the full NHGRI-EBI GWAS catalog (v1.0.2) from https://www.ebi.ac.uk/gwas/docs/file-downloads and selected any entries where the word "platelet" was included in either the trait or the manuscript title, and which had reported GWAS p-values < 5×10^{-8}. We compared these reported SNPs with our eQTLs and report all exact matches.

The GWAS catalog was examined for the following phenotypes: Cardiometabolic and hematological traits[22], Mean platelet volume [23-28], Platelet count [24-26,29-34] , Platelet distribution width [24] , Platelet-derived growth factor BB levels [35] , Plateletcrit [24]. SNPs within the catalog were limited to those with $p<5x10^{-8}$, and all eGenes for this full set of curated variants are listed in this table. Note: 1065 variants were looked up, and 24 variants had a significant eGene in one or both tissues.

Data sharing resources

WGS variant calls are available for all samples through the Database of Genotypes and Phenotypes (dbGaP) under accession number phs001218.v2.p1.

RNA-seq data (raw reads) are available through application and approval from the GeneSTAR Study Steering Committee:

https://www.hopkinsmedicine.org/gim/research/GeneSTAR/for_researchers

eQTL analysis results are hosted on a website at:

http://www.biostat.jhsph.edu/~kkammers/GeneSTAR/.

Code for analyses is available from the authors upon request.

Supplementary Results

Comparison of MK expression to published data

Given that we are working with iPSC-derived rather than primary MK cells, we sought to confirm whether our results corresponded to previously published data on MK gene expression. The Bloodomics Consortium described gene expression using microarrays in CD34+ derived MKs from 4 cord blood samples as part of the HaemAtlas project of human differentiated blood cells [36]. The numbers of genes expressed in derived MKs was similar between our study (N=9,808) and the Bloodomics study (10,444 probe sets mapping to 9,089 unique genes, their Table S3), but of these, there were only 6,867 genes with matching annotated gene names. 6,017 of these 6,867 genes (87.7%) were expressed in common in the two studies. Given the extremely small number of samples in the Bloodomics study, we consider this to be good concordance.

Comparison of platelet expression to published data

We also compared the expressed genes and their expression levels in platelets with previously published data sets [13,37]. Londin et al. [13] presented an RNA-seq analysis of platelets from 10 individuals. Their Supplementary file 4 contains the gene expression matrix of 5,591 unique genes observed in all 10 samples. 3,674 of the 5,034 genes expressed in our study (73.0%) were expressed their study as well. Across these shared genes, the Spearman's correlation between the mean of the normalized RPKM values from Londin et al. [13] and the mean of the log-transformed FPKM values from our study is 71.6%.

Bray et al. [37] described the gene expression of platelets from four healthy individuals using RNA-Seq. Their Supplementary Table S2A consists of a list of protein-coding transcripts and their normalized expression levels for each of the four total RNA samples. Similar to Bray et al., we selected the most abundant isoform for each gene to represent the gene. The number of expressed genes for the four samples varied between 5,511 and 10,860. Comparing the 5,034 expressed genes in our study to each of the four individual expression profiles in Bray's study, we found that between 3,105 and 4,305 genes (61.7% and 85.5%) were in common. For these shared genes, the Spearman correlation between the expression in each of the four samples and the average expression for each gene in our study ranged from 55.8% to 66.2% (all p-values $< 2.2 \times 10^{-16}$). Considering the small sample sizes of these studies, we consider this to be good overlap.

Finally, comparing the 5,034 expressed genes in our study to the starting set of 5,695 expressed genes in Simon et al. 2016 eQTL study [38] we found that 3,292 (65.5%) genes were in common. For these genes expressed in common, the Spearman correlation between the average gene expression in Simon's study and our study (data obtained from Simon et al. 2014, Table S2A, [39]) is 62% (p-value $< 2.2 \times 10^{-16}$), similar to what we see above.

Supplementary Tables

Supplementary Table S1: Sample demographics

Supplementary Tables S2A and S2B: Significant gene ontology categories for expressed genes in MKs (S2A) and platelets (S2B)

Supplementary Table S3: eQTLs significant in both Platelets and MKs

Supplementary Table S4: Full results from GWAS catalog lookup of significant eQTL results

Web-based results tables: Searchable interactive tables and downloadable .csv files for four sets of eQTL results are available at http://www.biostat.jhsph.edu/~kkammers/GeneSTAR/ including full MatrixEQTL and eigenMT results for MKs and platelets.

Supplementary Table S1: Sample demographics

	MKs		Platelets	
	AA	**EA**	**AA**	**EA**
Sample size	84	101	110	180
Female sex: N (%)	52 (61.90)	47 (46.53)	74 (67.27)	95 (52.78)
Age in years: Mean (SD)	50.2 (12.7)	54.41 (13.6)	53.88 (11.9)	51.97 (11)
CD 41/42 %: Mean (SD)	62.81 (15.8)	60.54 (15.7)	--	--

Supplementary Table S2A: Significant gene ontology categories for expressed genes in MKs

GO.ID	Term	Annotated	Significant	Expected	pval	qval
GO:0045047	protein targeting to ER	97	80	5.52	1.00E-30	1.69E-28
GO:0006413	translational initiation	170	102	9.68	1.00E-30	1.69E-28
GO:0006614	SRP-dependent cotranslational protein targeting to membrane	92	77	5.24	1.00E-30	1.69E-28
GO:0006613	cotranslational protein targeting to membrane	95	78	5.41	1.00E-30	1.69E-28
GO:0072599	establishment of protein localization to endoplasmic reticulum	101	80	5.75	1.00E-30	1.69E-28
GO:0070972	protein localization to endoplasmic reticulum	117	84	6.66	1.00E-30	1.69E-28
GO:0044403	symbiont process	831	204	47.31	1.00E-30	1.69E-28
GO:0016032	viral process	772	195	43.95	1.00E-30	1.69E-28
GO:0044419	interspecies interaction between organisms	873	207	49.7	1.00E-30	1.69E-28
GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	110	77	6.26	1.00E-30	1.69E-28
GO:0019080	viral gene expression	182	94	10.36	1.00E-30	1.69E-28
GO:0072594	establishment of protein localization to organelle	423	132	24.08	1.00E-30	1.69E-28
GO:0006612	protein targeting to membrane	151	82	8.6	1.00E-30	1.69E-28
GO:0006402	mRNA catabolic process	318	114	18.1	1.00E-30	1.69E-28
GO:0019083	viral transcription	169	85	9.62	1.00E-30	1.69E-28
GO:0006401	RNA catabolic process	346	115	19.7	1.00E-30	1.69E-28
GO:0006605	protein targeting	337	111	19.19	1.00E-30	1.69E-28
GO:0006810	transport	4395	465	250.21	1.00E-30	1.69E-28
GO:0051234	establishment of localization	4501	471	256.25	1.00E-30	1.69E-28
GO:0000956	nuclear-transcribed mRNA catabolic process	181	82	10.3	1.00E-30	1.69E-28
GO:0090150	establishment of protein localization to membrane	262	97	14.92	1.00E-30	1.69E-28
GO:0033365	protein localization to organelle	742	162	42.24	1.00E-30	1.69E-28
GO:0016071	mRNA metabolic process	732	160	41.67	1.00E-30	1.69E-28
GO:0046907	intracellular transport	1421	229	80.9	1.00E-30	1.69E-28
GO:0006886	intracellular protein transport	778	162	44.29	1.00E-30	1.69E-28
GO:0006518	peptide metabolic process	755	159	42.98	1.00E-30	1.69E-28
GO:0006412	translation	624	142	35.53	1.00E-30	1.69E-28
GO:0070727	cellular macromolecule localization	1449	226	82.49	1.00E-30	1.69E-28
GO:0034613	cellular protein localization	1442	225	82.1	1.00E-30	1.69E-28
GO:0043043	peptide biosynthetic process	647	143	36.83	1.00E-30	1.69E-28
GO:0051641	cellular localization	2356	300	134.13	1.00E-30	1.69E-28
GO:0034655	nucleobase-containing compound catabolic process	562	131	32	1.00E-30	1.69E-28
GO:0051649	establishment of localization in cell	1773	249	100.94	1.00E-30	1.69E-28
GO:0051179	localization	5680	525	323.37	1.00E-30	1.69E-28
GO:0044270	cellular nitrogen compound catabolic process	604	134	34.39	1.00E-30	1.69E-28
GO:0045055	regulated exocytosis	724	146	41.22	1.00E-30	1.69E-28
GO:0044265	cellular macromolecule catabolic process	931	168	53	1.00E-30	1.69E-28
GO:0046700	heterocycle catabolic process	603	132	34.33	1.00E-30	1.69E-28
GO:0019439	aromatic compound catabolic process	615	133	35.01	1.00E-30	1.69E-28
GO:0043604	amide biosynthetic process	767	150	43.67	1.00E-30	1.69E-28
GO:1901361	organic cyclic compound catabolic process	644	135	36.66	1.00E-30	1.69E-28
GO:0043603	cellular amide metabolic process	975	170	55.51	1.00E-30	1.69E-28
GO:0072657	protein localization to membrane	511	119	29.09	1.00E-30	1.69E-28
GO:0045184	establishment of protein localization	1691	235	96.27	1.00E-30	1.69E-28
GO:0009057	macromolecule catabolic process	1136	184	64.67	1.00E-30	1.69E-28
GO:0006887	exocytosis	809	150	46.06	1.00E-30	1.69E-28
GO:0008104	protein localization	2265	279	128.95	1.00E-30	1.69E-28
GO:0033036	macromolecule localization	2563	299	145.92	1.00E-30	1.69E-28
GO:0015031	protein transport	1589	219	90.46	1.00E-30	1.69E-28
GO:0015833	peptide transport	1620	221	92.23	1.00E-30	1.69E-28
GO:0051704	multi-organism process	2290	275	130.37	1.00E-30	1.69E-28
GO:0042886	amide transport	1649	223	93.88	1.00E-30	1.69E-28
GO:0043312	neutrophil degranulation	461	106	26.25	1.00E-30	1.69E-28
GO:0044248	cellular catabolic process	1926	245	109.65	1.00E-30	1.69E-28
GO:0002283	neutrophil activation involved in immune response	464	106	26.42	1.00E-30	1.69E-28
GO:0002446	neutrophil mediated immunity	475	107	27.04	1.00E-30	1.69E-28
GO:0042119	neutrophil activation	475	107	27.04	1.00E-30	1.69E-28
GO:0036230	granulocyte activation	482	107	27.44	1.00E-30	1.69E-28
GO:0043299	leukocyte degranulation	505	109	28.75	1.00E-30	1.69E-28
GO:0071705	nitrogen compound transport	1907	240	108.57	1.00E-30	1.69E-28
GO:0016192	vesicle-mediated transport	1728	225	98.38	1.00E-30	1.69E-28
GO:0002444	myeloid leukocyte mediated immunity	522	109	29.72	1.00E-30	1.69E-28
GO:0009056	catabolic process	2172	258	123.66	1.00E-30	1.69E-28
GO:0002275	myeloid cell activation involved in immune response	515	108	29.32	1.00E-30	1.69E-28
GO:0002274	myeloid leukocyte activation	618	116	35.18	1.00E-30	1.69E-28
GO:0001775	cell activation	1268	177	72.19	1.20E-30	1.99E-28
GO:0071702	organic substance transport	2270	258	129.23	1.80E-30	2.94E-28
GO:0002263	cell activation involved in immune response	651	116	37.06	3.70E-29	5.96E-27
GO:1901575	organic substance catabolic process	1800	218	102.48	4.70E-29	7.46E-27
GO:0002366	leukocyte activation involved in immune response	648	115	36.89	9.50E-29	1.49E-26
GO:1901566	organonitrogen compound biosynthetic process	1668	204	94.96	1.40E-27	2.16E-25
GO:0002443	leukocyte mediated immunity	713	119	40.59	3.10E-27	4.72E-25
GO:0043933	protein-containing complex subunit organization	1858	214	105.78	1.80E-25	2.70E-23
GO:1901564	organonitrogen compound metabolic process	5942	488	338.29	2.00E-25	2.96E-23
GO:0044267	cellular protein metabolic process	4512	396	256.87	2.30E-24	3.36E-22
GO:0002181	cytoplasmic translation	65	33	3.7	3.00E-24	4.33E-22
GO:0032940	secretion by cell	1368	171	77.88	6.30E-24	8.97E-22
GO:0071840	cellular component organization or biogenesis	5415	449	308.28	2.80E-23	3.93E-21
GO:0002252	immune effector process	1076	144	61.26	6.70E-23	9.29E-21
GO:0065003	protein-containing complex assembly	1579	184	89.89	3.10E-22	4.25E-20

Supplementary Table S2A: Significant gene ontology categories for expressed genes in MKs

GO.ID	Term	Annotated	Significant	Expected	pval	qval
GO:0002376	immune system process	2684	266	152.8	4.50E-22	6.09E-20
GO:0046903	secretion	1493	176	85	8.90E-22	1.19E-19
GO:0045321	leukocyte activation	1122	145	63.88	1.40E-21	1.85E-19
GO:0044085	cellular component biogenesis	2682	264	152.69	1.90E-21	2.48E-19
GO:0065008	regulation of biological quality	3417	314	194.53	3.20E-21	4.13E-19
GO:0019538	protein metabolic process	5028	417	286.25	6.60E-21	8.41E-19
GO:0034622	cellular protein-containing complex assembly	826	115	47.03	1.20E-19	1.49E-17
GO:0006955	immune response	1823	196	103.79	1.20E-19	1.49E-17
GO:0070887	cellular response to chemical stimulus	2925	275	166.52	1.60E-19	1.97E-17
GO:0010033	response to organic substance	2960	277	168.52	2.10E-19	2.56E-17
GO:0016043	cellular component organization	5288	427	301.05	3.20E-19	3.85E-17
GO:0009892	negative regulation of metabolic process	3025	278	172.22	2.40E-18	2.86E-16
GO:0010605	negative regulation of macromolecule metabolic process	2811	263	160.03	2.90E-18	3.42E-16
GO:0009058	biosynthetic process	5480	435	311.98	3.20E-18	3.73E-16
GO:0019884	antigen processing and presentation of exogenous antigen	169	44	9.62	5.80E-18	6.69E-16
GO:0006119	oxidative phosphorylation	90	32	5.12	8.80E-18	1.00E-15
GO:1901576	organic substance biosynthetic process	5409	428	307.94	1.60E-17	1.81E-15
GO:0048519	negative regulation of biological process	5075	407	288.93	2.20E-17	2.44E-15
GO:0002478	antigen processing and presentation of exogenous peptide antigen	167	43	9.51	2.20E-17	2.44E-15
GO:0002576	platelet degranulation	118	36	6.72	2.40E-17	2.63E-15
GO:0034641	cellular nitrogen compound metabolic process	6042	464	343.98	5.40E-17	5.86E-15
GO:0044237	cellular metabolic process	9600	663	546.54	5.80E-17	6.23E-15
GO:0022607	cellular component assembly	2516	238	143.24	6.60E-17	7.02E-15
GO:0006996	organelle organization	3069	276	174.72	6.70E-17	7.06E-15
GO:0044271	cellular nitrogen compound biosynthetic process	4361	360	248.28	8.90E-17	9.29E-15
GO:0006457	protein folding	167	42	9.51	1.30E-16	1.34E-14
GO:0042590	antigen processing and presentation of exogenous peptide antigen via MHC class I	75	28	4.27	2.30E-16	2.36E-14
GO:0019882	antigen processing and presentation	210	47	11.96	2.80E-16	2.84E-14
GO:0042775	mitochondrial ATP synthesis coupled electron transport	70	27	3.99	3.00E-16	3.02E-14
GO:0022613	ribonucleoprotein complex biogenesis	316	59	17.99	3.50E-16	3.49E-14
GO:0042221	response to chemical	4227	349	240.65	3.90E-16	3.85E-14
GO:0048002	antigen processing and presentation of peptide antigen	180	43	10.25	4.30E-16	4.21E-14
GO:0042773	ATP synthesis coupled electron transport	71	27	4.04	4.50E-16	4.36E-14
GO:0002479	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent	72	27	4.1	6.80E-16	6.54E-14
GO:0007599	hemostasis	321	59	18.28	7.40E-16	7.05E-14
GO:0031145	anaphase-promoting complex-dependent catabolic process	79	28	4.5	1.10E-15	1.04E-13
GO:0007596	blood coagulation	317	58	18.05	1.60E-15	1.50E-13
GO:0044249	cellular biosynthetic process	5342	415	304.13	2.60E-15	2.41E-13
GO:0009611	response to wounding	630	88	35.87	2.80E-15	2.58E-13
GO:0050817	coagulation	322	58	18.33	3.40E-15	3.11E-13
GO:0006950	response to stress	3494	298	198.92	3.50E-15	3.17E-13
GO:0071310	cellular response to organic substance	2428	226	138.23	3.60E-15	3.23E-13
GO:0002474	antigen processing and presentation of peptide antigen via MHC class I	91	29	5.18	8.50E-15	7.57E-13
GO:1903311	regulation of mRNA metabolic process	265	51	15.09	1.10E-14	9.72E-13
GO:0038093	Fc receptor signaling pathway	173	40	9.85	1.50E-14	1.32E-12
GO:0010389	regulation of G2/M transition of mitotic cell cycle	174	40	9.91	1.80E-14	1.57E-12
GO:0043488	regulation of mRNA stability	151	37	8.6	2.10E-14	1.81E-12
GO:0030168	platelet activation	145	36	8.26	3.00E-14	2.57E-12
GO:0009059	macromolecule biosynthetic process	4449	355	253.29	3.80E-14	3.23E-12
GO:0043487	regulation of RNA stability	154	37	8.77	4.10E-14	3.46E-12
GO:1902749	regulation of cell cycle G2/M phase transition	188	41	10.7	5.80E-14	4.85E-12
GO:0033554	cellular response to stress	1774	175	101	7.40E-14	6.14E-12
GO:0042060	wound healing	522	75	29.72	8.40E-14	6.92E-12
GO:0034645	cellular macromolecule biosynthetic process	4298	344	244.69	8.60E-14	7.03E-12
GO:0010629	negative regulation of gene expression	2070	196	117.85	8.90E-14	7.22E-12
GO:0022904	respiratory electron transport chain	86	27	4.9	1.10E-13	8.86E-12
GO:0061418	regulation of transcription from RNA polymerase II promoter in response to hypoxia	74	25	4.21	1.30E-13	1.04E-11
GO:0031647	regulation of protein stability	250	47	14.23	3.00E-13	2.38E-11
GO:0048522	positive regulation of cellular process	4675	365	266.15	3.40E-13	2.68E-11
GO:0019222	regulation of metabolic process	6186	456	352.18	4.00E-13	3.13E-11
GO:0006521	regulation of cellular amino acid metabolic process	60	22	3.42	5.80E-13	4.51E-11
GO:2001233	regulation of apoptotic signaling pathway	373	59	21.24	7.10E-13	5.48E-11
GO:0051246	regulation of protein metabolic process	2465	220	140.34	8.30E-13	6.36E-11
GO:0009894	regulation of catabolic process	853	101	48.56	1.10E-12	8.37E-11
GO:0061013	regulation of mRNA catabolic process	171	37	9.74	1.30E-12	9.83E-11
GO:0031329	regulation of cellular catabolic process	760	93	43.27	1.40E-12	1.05E-10
GO:0098869	cellular oxidant detoxification	88	26	5.01	1.50E-12	1.12E-10
GO:0009141	nucleoside triphosphate metabolic process	282	49	16.05	2.00E-12	1.46E-10
GO:0000086	G2/M transition of mitotic cell cycle	226	43	12.87	2.00E-12	1.46E-10
GO:0043618	regulation of transcription from RNA polymerase II promoter in response to stress	103	28	5.86	2.00E-12	1.46E-10
GO:1990748	cellular detoxification	96	27	5.47	2.10E-12	1.52E-10
GO:0034097	response to cytokine	1104	120	62.85	2.50E-12	1.79E-10
GO:0006807	nitrogen compound metabolic process	9077	616	516.77	2.50E-12	1.79E-10
GO:0010941	regulation of cell death	1558	154	88.7	2.90E-12	2.06E-10
GO:0009144	purine nucleoside triphosphate metabolic process	267	47	15.2	3.50E-12	2.47E-10
GO:0030163	protein catabolic process	739	90	42.07	4.30E-12	3.02E-10
GO:0051130	positive regulation of cellular component organization	1102	119	62.74	4.80E-12	3.35E-10
GO:0009205	purine ribonucleoside triphosphate metabolic process	260	46	14.8	5.00E-12	3.47E-10
GO:0008219	cell death	2061	189	117.34	5.50E-12	3.77E-10
GO:0010498	proteasomal protein catabolic process	360	56	20.5	5.50E-12	3.77E-10

Supplementary Table S2A: Significant gene ontology categories for expressed genes in MKs

GO.ID	Term	Annotated	Significant	Expected	pval	qval
GO:0044839	cell cycle G2/M phase transition	242	44	13.78	5.60E-12	3.79E-10
GO:0043620	regulation of DNA-templated transcription in response to stress	107	28	6.09	5.60E-12	3.79E-10
GO:0009123	nucleoside monophosphate metabolic process	291	49	16.57	6.50E-12	4.37E-10
GO:0006915	apoptotic process	1797	170	102.31	6.80E-12	4.54E-10
GO:0048518	positive regulation of biological process	5298	397	301.62	7.40E-12	4.91E-10
GO:0046034	ATP metabolic process	235	43	13.38	7.90E-12	5.22E-10
GO:0032268	regulation of cellular protein metabolic process	2287	204	130.2	8.20E-12	5.38E-10
GO:0009199	ribonucleoside triphosphate metabolic process	264	46	15.03	8.60E-12	5.61E-10
GO:1901360	organic cyclic compound metabolic process	5787	426	329.46	8.90E-12	5.77E-10
GO:0043067	regulation of programmed cell death	1445	144	82.27	9.30E-12	6.00E-10
GO:0044772	mitotic cell cycle phase transition	539	72	30.69	9.70E-12	6.22E-10
GO:0098754	detoxification	102	27	5.81	1.00E-11	6.37E-10
GO:0050896	response to stimulus	7976	552	454.09	1.20E-11	7.51E-10
GO:0019058	viral life cycle	306	50	17.42	1.20E-11	7.51E-10
GO:0051128	regulation of cellular component organization	2181	196	124.17	1.20E-11	7.51E-10
GO:0050878	regulation of body fluid levels	475	66	27.04	1.30E-11	8.05E-10
GO:0060071	Wnt signaling pathway, planar cell polarity pathway	103	27	5.86	1.30E-11	8.05E-10
GO:0044238	primary metabolic process	9494	635	540.51	1.40E-11	8.62E-10
GO:0044260	cellular macromolecule metabolic process	7140	504	406.49	1.50E-11	9.18E-10
GO:0045333	cellular respiration	151	33	8.6	1.60E-11	9.74E-10
GO:0033238	regulation of cellular amine metabolic process	76	23	4.33	1.70E-11	1.03E-09
GO:0070498	interleukin-1-mediated signaling pathway	97	26	5.52	1.80E-11	1.07E-09
GO:0097190	apoptotic signaling pathway	546	72	31.08	1.80E-11	1.07E-09
GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process	309	50	17.59	1.80E-11	1.07E-09
GO:0042981	regulation of apoptotic process	1419	141	80.79	2.00E-11	1.18E-09
GO:0090175	regulation of establishment of planar polarity	105	27	5.98	2.10E-11	1.24E-09
GO:0071345	cellular response to cytokine stimulus	1027	111	58.47	2.60E-11	1.52E-09
GO:0010638	positive regulation of organelle organization	553	72	31.48	3.30E-11	1.92E-09
GO:0008380	RNA splicing	378	56	21.52	4.00E-11	2.32E-09
GO:0010972	negative regulation of G2/M transition of mitotic cell cycle	79	23	4.5	4.10E-11	2.36E-09
GO:0000375	RNA splicing, via transesterification reactions	296	48	16.85	4.20E-11	2.41E-09
GO:0012501	programmed cell death	1938	177	110.33	4.50E-11	2.56E-09
GO:0006446	regulation of translational initiation	66	21	3.76	4.50E-11	2.56E-09
GO:0009987	cellular process	14228	864	810.02	4.70E-11	2.66E-09
GO:0055114	oxidation-reduction process	860	97	48.96	5.10E-11	2.87E-09
GO:0001736	establishment of planar polarity	117	28	6.66	5.70E-11	3.17E-09
GO:0007164	establishment of tissue polarity	117	28	6.66	5.70E-11	3.17E-09
GO:2001242	regulation of intrinsic apoptotic signaling pathway	150	32	8.54	6.30E-11	3.49E-09
GO:0006139	nucleobase-containing compound metabolic process	5394	398	307.09	7.10E-11	3.91E-09
GO:0022900	electron transport chain	151	32	8.6	7.60E-11	4.16E-09
GO:0044770	cell cycle phase transition	576	73	32.79	8.40E-11	4.58E-09
GO:0031146	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process	68	21	3.87	8.50E-11	4.61E-09
GO:0009167	purine ribonucleoside monophosphate metabolic process	262	44	14.92	8.60E-11	4.64E-09
GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	292	47	16.62	8.80E-11	4.70E-09
GO:0000398	mRNA splicing, via spliceosome	292	47	16.62	8.80E-11	4.70E-09
GO:0009126	purine nucleoside monophosphate metabolic process	263	44	14.97	9.80E-11	5.21E-09
GO:0009161	ribonucleoside monophosphate metabolic process	273	45	15.54	1.00E-10	5.27E-09
GO:1901990	regulation of mitotic cell cycle phase transition	409	58	23.28	1.00E-10	5.27E-09
GO:1904869	regulation of protein localization to Cajal body	8	8	0.46	1.10E-10	5.74E-09
GO:1904871	positive regulation of protein localization to Cajal body	8	8	0.46	1.10E-10	5.74E-09
GO:0035722	interleukin-12-mediated signaling pathway	45	17	2.56	1.50E-10	7.79E-09
GO:0033043	regulation of organelle organization	1071	112	60.97	1.60E-10	8.19E-09
GO:0046483	heterocycle metabolic process	5541	405	315.46	1.60E-10	8.19E-09
GO:0022618	ribonucleoprotein complex assembly	164	33	9.34	1.60E-10	8.19E-09
GO:0006897	endocytosis	586	73	33.36	1.90E-10	9.60E-09
GO:0009636	response to toxic substance	471	63	26.81	1.90E-10	9.60E-09
GO:0038095	Fc-epsilon receptor signaling pathway	107	26	6.09	1.90E-10	9.60E-09
GO:0001738	morphogenesis of a polarized epithelium	131	29	7.46	2.00E-10	1.00E-08
GO:0044257	cellular protein catabolic process	599	74	34.1	2.00E-10	1.00E-08
GO:0006120	mitochondrial electron transport, NADH to ubiquinone	46	17	2.62	2.20E-10	1.09E-08
GO:0050821	protein stabilization	157	32	8.94	2.20E-10	1.09E-08
GO:0098657	import into cell	660	79	37.57	2.20E-10	1.09E-08
GO:1903047	mitotic cell cycle process	771	88	43.89	2.40E-10	1.18E-08
GO:0071826	ribonucleoprotein complex subunit organization	176	34	10.02	2.70E-10	1.32E-08
GO:0001732	formation of cytoplasmic translation initiation complex	14	10	0.8	2.80E-10	1.36E-08
GO:1904874	positive regulation of telomerase RNA localization to Cajal body	14	10	0.8	2.80E-10	1.36E-08
GO:0006725	cellular aromatic compound metabolic process	5583	406	317.85	3.20E-10	1.54E-08
GO:0071349	cellular response to interleukin-12	47	17	2.68	3.20E-10	1.54E-08
GO:0080134	regulation of response to stress	1425	137	81.13	3.90E-10	1.87E-08
GO:0008152	metabolic process	10627	688	605.01	4.40E-10	2.10E-08
GO:1902750	negative regulation of cell cycle G2/M phase transition	88	23	5.01	4.50E-10	2.13E-08
GO:0070671	response to interleukin-12	48	17	2.73	4.80E-10	2.26E-08
GO:0048523	negative regulation of cellular process	4237	323	241.22	4.80E-10	2.26E-08
GO:0034109	homotypic cell-cell adhesion	74	21	4.21	4.90E-10	2.29E-08
GO:1901987	regulation of cell cycle phase transition	438	59	24.94	5.60E-10	2.61E-08
GO:0060255	regulation of macromolecule metabolic process	5723	413	325.82	5.70E-10	2.65E-08
GO:0015980	energy derivation by oxidation of organic compounds	228	39	12.98	5.90E-10	2.73E-08
GO:0050790	regulation of catalytic activity	1987	176	113.12	6.10E-10	2.81E-08
GO:0007049	cell cycle	1604	149	91.32	6.80E-10	3.12E-08
GO:1902600	proton transmembrane transport	113	26	6.43	6.90E-10	3.15E-08

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GO.ID	Term	Annotated	Significant	Expected	pval	qval
GO:0009628	response to abiotic stimulus	1114	113	63.42	8.10E-10	3.68E-08
GO:0071453	cellular response to oxygen levels	221	38	12.58	8.40E-10	3.80E-08
GO:0070527	platelet aggregation	56	18	3.19	9.10E-10	4.10E-08
GO:1903405	protein localization to nuclear body	9	8	0.51	9.20E-10	4.10E-08
GO:1904851	positive regulation of establishment of protein localization to telomere	9	8	0.51	9.20E-10	4.10E-08
GO:1904867	protein localization to Cajal body	9	8	0.51	9.20E-10	4.10E-08
GO:0007005	mitochondrion organization	399	55	22.72	9.30E-10	4.13E-08
GO:0035567	non-canonical Wnt signaling pathway	141	29	8.03	1.20E-09	5.30E-08
GO:0038061	NIK/NF-kappaB signaling	168	32	9.56	1.30E-09	5.72E-08
GO:0034504	protein localization to nucleus	215	37	12.24	1.40E-09	6.14E-08
GO:0036294	cellular response to decreased oxygen levels	206	36	11.73	1.50E-09	6.55E-08
GO:0060548	negative regulation of cell death	942	99	53.63	1.60E-09	6.93E-08
GO:0071456	cellular response to hypoxia	197	35	11.22	1.60E-09	6.93E-08
GO:0050789	regulation of biological process	10213	663	581.44	1.90E-09	8.17E-08
GO:0044106	cellular amine metabolic process	110	25	6.26	1.90E-09	8.17E-08
GO:0070482	response to oxygen levels	363	51	20.67	2.00E-09	8.56E-08
GO:0097435	supramolecular fiber organization	512	64	29.15	2.30E-09	9.81E-08
GO:0006091	generation of precursor metabolites and energy	432	57	24.59	2.40E-09	1.02E-07
GO:0022402	cell cycle process	1190	117	67.75	2.50E-09	1.05E-07
GO:0006695	cholesterol biosynthetic process	66	19	3.76	2.50E-09	1.05E-07
GO:1902653	secondary alcohol biosynthetic process	66	19	3.76	2.50E-09	1.05E-07
GO:0070555	response to interleukin-1	173	32	9.85	2.90E-09	1.21E-07
GO:0050792	regulation of viral process	192	34	10.93	3.00E-09	1.25E-07
GO:0016579	protein deubiquitination	232	38	13.21	3.50E-09	1.45E-07
GO:0051716	cellular response to stimulus	6378	447	363.11	4.10E-09	1.69E-07
GO:0010564	regulation of cell cycle process	715	80	40.71	4.10E-09	1.69E-07
GO:0070203	regulation of establishment of protein localization to telomere	10	8	0.57	4.40E-09	1.79E-07
GO:1904816	positive regulation of protein localization to chromosome, telomeric region	10	8	0.57	4.40E-09	1.79E-07
GO:1990173	protein localization to nucleoplasm	10	8	0.57	4.40E-09	1.79E-07
GO:1904872	regulation of telomerase RNA localization to Cajal body	17	10	0.97	4.60E-09	1.87E-07
GO:0070646	protein modification by small protein removal	245	39	13.95	4.90E-09	1.98E-07
GO:0002183	cytoplasmic translational initiation	26	12	1.48	5.00E-09	2.01E-07
GO:0042254	ribosome biogenesis	177	32	10.08	5.10E-09	2.05E-07
GO:0006753	nucleoside phosphate metabolic process	583	69	33.19	5.30E-09	2.12E-07
GO:0048524	positive regulation of viral process	99	23	5.64	5.50E-09	2.19E-07
GO:0016126	sterol biosynthetic process	69	19	3.93	5.70E-09	2.26E-07
GO:0009967	positive regulation of signal transduction	1500	138	85.4	6.20E-09	2.44E-07
GO:0051603	proteolysis involved in cellular protein catabolic process	549	66	31.26	6.20E-09	2.44E-07
GO:0009117	nucleotide metabolic process	575	68	32.74	7.10E-09	2.79E-07
GO:1902036	regulation of hematopoietic stem cell differentiation	70	19	3.99	7.50E-09	2.93E-07
GO:0009308	amine metabolic process	117	25	6.66	7.50E-09	2.93E-07
GO:0097193	intrinsic apoptotic signaling pathway	259	40	14.75	7.60E-09	2.95E-07
GO:0034248	regulation of cellular amide metabolic process	424	55	24.14	8.50E-09	3.29E-07
GO:0061024	membrane organization	664	75	37.8	8.70E-09	3.36E-07
GO:0019693	ribose phosphate metabolic process	459	58	26.13	8.80E-09	3.38E-07
GO:0043903	regulation of symbiosis, encompassing mutualism through parasitism	220	36	12.52	9.20E-09	3.53E-07
GO:0090670	RNA localization to Cajal body	18	10	1.02	9.80E-09	3.70E-07
GO:0090671	telomerase RNA localization to Cajal body	18	10	1.02	9.80E-09	3.70E-07
GO:0090672	telomerase RNA localization	18	10	1.02	9.80E-09	3.70E-07
GO:0090685	RNA localization to nucleus	18	10	1.02	9.80E-09	3.70E-07
GO:0007346	regulation of mitotic cell cycle	593	69	33.76	1.10E-08	4.11E-07
GO:0000278	mitotic cell cycle	885	92	50.38	1.10E-08	4.11E-07
GO:0048584	positive regulation of response to stimulus	2108	179	120.01	1.10E-08	4.11E-07
GO:0097237	cellular response to toxic substance	222	36	12.64	1.20E-08	4.47E-07
GO:0071897	DNA biosynthetic process	174	31	9.91	1.30E-08	4.81E-07
GO:0042592	homeostatic process	1632	146	92.91	1.30E-08	4.81E-07
GO:0022411	cellular component disassembly	465	58	26.47	1.40E-08	5.15E-07
GO:0006364	rRNA processing	138	27	7.86	1.40E-08	5.15E-07
GO:0007229	integrin-mediated signaling pathway	88	21	5.01	1.50E-08	5.48E-07
GO:0070202	regulation of establishment of protein localization to chromosome	11	8	0.63	1.50E-08	5.48E-07
GO:0030162	regulation of proteolysis	650	73	37.01	1.80E-08	6.55E-07
GO:0002757	immune response-activating signal transduction	469	58	26.7	1.90E-08	6.89E-07
GO:0002682	regulation of immune system process	1416	130	80.61	2.10E-08	7.60E-07
GO:1901565	organonitrogen compound catabolic process	1045	103	59.49	2.20E-08	7.93E-07
GO:0006163	purine nucleotide metabolic process	460	57	26.19	2.40E-08	8.57E-07
GO:0043069	negative regulation of programmed cell death	860	89	48.96	2.40E-08	8.57E-07
GO:0010647	positive regulation of cell communication	1633	145	92.97	2.40E-08	8.57E-07
GO:0010942	positive regulation of cell death	668	74	38.03	2.50E-08	8.90E-07
GO:0002223	stimulatory C-type lectin receptor signaling pathway	107	23	6.09	2.60E-08	9.22E-07
GO:0002684	positive regulation of immune system process	955	96	54.37	2.70E-08	9.54E-07
GO:0006796	phosphate-containing compound metabolic process	2879	228	163.91	2.80E-08	9.87E-07
GO:0051726	regulation of cell cycle	1078	105	61.37	3.00E-08	1.05E-06
GO:0023056	positive regulation of signaling	1639	145	93.31	3.00E-08	1.05E-06
GO:0002429	immune response-activating cell surface receptor signaling pathway	315	44	17.93	3.10E-08	1.08E-06
GO:0043066	negative regulation of apoptotic process	839	87	47.77	3.20E-08	1.11E-06
GO:0051248	negative regulation of protein metabolic process	1039	102	59.15	3.20E-08	1.11E-06
GO:0065007	biological regulation	10751	685	612.07	3.30E-08	1.14E-06
GO:0006417	regulation of translation	372	49	21.18	3.40E-08	1.17E-06
GO:0016072	rRNA metabolic process	172	30	9.79	3.60E-08	1.23E-06
GO:0090263	positive regulation of canonical Wnt signaling pathway	126	25	7.17	3.60E-08	1.23E-06

Supplementary Table S2A: Significant gene ontology categories for expressed genes in MKs

GO.ID	Term	Annotated	Significant	Expected	pval	qval
GO:0035966	response to topologically incorrect protein	163	29	9.28	3.90E-08	1.33E-06
GO:0009719	response to endogenous stimulus	1488	134	84.71	3.90E-08	1.33E-06
GO:0019941	modification-dependent protein catabolic process	479	58	27.27	4.10E-08	1.39E-06
GO:0042493	response to drug	910	92	51.81	4.20E-08	1.42E-06
GO:0062012	regulation of small molecule metabolic process	409	52	23.28	4.30E-08	1.44E-06
GO:0006123	mitochondrial electron transport, cytochrome c to oxygen	12	8	0.68	4.30E-08	1.44E-06
GO:0019646	aerobic electron transport chain	12	8	0.68	4.30E-08	1.44E-06
GO:1904814	regulation of protein localization to chromosome, telomeric region	12	8	0.68	4.30E-08	1.44E-06
GO:0010948	negative regulation of cell cycle process	319	44	18.16	4.50E-08	1.49E-06
GO:0009150	purine ribonucleotide metabolic process	433	54	24.65	4.50E-08	1.49E-06
GO:0002220	innate immune response activating cell surface receptor signaling pathway	110	23	6.26	4.60E-08	1.52E-06
GO:0009259	ribonucleotide metabolic process	445	55	25.33	4.60E-08	1.52E-06
GO:0036293	response to decreased oxygen levels	342	46	19.47	4.80E-08	1.57E-06
GO:0044093	positive regulation of molecular function	1536	137	87.45	4.80E-08	1.57E-06
GO:0044281	small molecule metabolic process	1855	159	105.61	4.90E-08	1.59E-06
GO:0043281	regulation of cysteine-type endopeptidase activity involved in apoptotic process	184	31	10.48	4.90E-08	1.59E-06
GO:0002253	activation of immune response	542	63	30.86	4.90E-08	1.59E-06
GO:0006793	phosphorus metabolic process	2901	228	165.16	5.40E-08	1.75E-06
GO:0043632	modification-dependent macromolecule catabolic process	483	58	27.5	5.50E-08	1.78E-06
GO:0001666	response to hypoxia	333	45	18.96	5.80E-08	1.87E-06
GO:0006909	phagocytosis	236	36	13.44	5.90E-08	1.90E-06
GO:2001243	negative regulation of intrinsic apoptotic signaling pathway	87	20	4.95	6.50E-08	2.08E-06
GO:0043068	positive regulation of programmed cell death	621	69	35.35	6.70E-08	2.14E-06
GO:0006511	ubiquitin-dependent protein catabolic process	474	57	26.99	6.80E-08	2.17E-06
GO:0071704	organic substance metabolic process	10184	653	579.79	7.10E-08	2.26E-06
GO:0071347	cellular response to interleukin-1	149	27	8.48	7.60E-08	2.41E-06
GO:2001235	positive regulation of apoptotic signaling pathway	168	29	9.56	7.70E-08	2.43E-06
GO:0019221	cytokine-mediated signaling pathway	726	77	41.33	8.10E-08	2.55E-06
GO:2001234	negative regulation of apoptotic signaling pathway	209	33	11.9	9.10E-08	2.86E-06
GO:1901700	response to oxygen-containing compound	1481	132	84.32	9.30E-08	2.91E-06
GO:0043065	positive regulation of apoptotic process	614	68	34.96	9.50E-08	2.97E-06
GO:0002764	immune response-regulating signaling pathway	503	59	28.64	9.70E-08	3.02E-06
GO:0060218	hematopoietic stem cell differentiation	81	19	4.61	9.80E-08	3.04E-06
GO:0043484	regulation of RNA splicing	106	22	6.03	1.00E-07	3.10E-06
GO:0006508	proteolysis	1470	131	83.69	1.10E-07	3.38E-06
GO:0019081	viral translation	13	8	0.74	1.10E-07	3.38E-06
GO:0080135	regulation of cellular response to stress	655	71	37.29	1.10E-07	3.38E-06
GO:0006986	response to unfolded protein	152	27	8.65	1.20E-07	3.63E-06
GO:0010257	NADH dehydrogenase complex assembly	52	15	2.96	1.20E-07	3.63E-06
GO:0032981	mitochondrial respiratory chain complex I assembly	52	15	2.96	1.20E-07	3.63E-06
GO:0017144	drug metabolic process	707	75	40.25	1.20E-07	3.63E-06
GO:0016310	phosphorylation	2075	172	118.13	1.20E-07	3.63E-06
GO:1902905	positive regulation of supramolecular fiber organization	172	29	9.79	1.30E-07	3.91E-06
GO:1905330	regulation of morphogenesis of an epithelium	172	29	9.79	1.30E-07	3.91E-06
GO:0006259	DNA metabolic process	880	88	50.1	1.40E-07	4.19E-06
GO:0051338	regulation of transferase activity	854	86	48.62	1.40E-07	4.19E-06
GO:1901532	regulation of hematopoietic progenitor cell differentiation	83	19	4.73	1.50E-07	4.47E-06
GO:0007015	actin filament organization	299	41	17.02	1.50E-07	4.47E-06
GO:0043902	positive regulation of multi-organism process	174	29	9.91	1.70E-07	5.02E-06
GO:0008203	cholesterol metabolic process	136	25	7.74	1.70E-07	5.02E-06
GO:1901991	negative regulation of mitotic cell cycle phase transition	225	34	12.81	1.70E-07	5.02E-06
GO:0042176	regulation of protein catabolic process	323	43	18.39	1.80E-07	5.29E-06
GO:0051702	interaction with symbiont	76	18	4.33	1.80E-07	5.29E-06
GO:0060341	regulation of cellular localization	807	82	45.94	1.90E-07	5.57E-06
GO:0042274	ribosomal small subunit biogenesis	23	10	1.31	2.00E-07	5.83E-06
GO:0030036	actin cytoskeleton organization	526	60	29.95	2.00E-07	5.83E-06
GO:0072521	purine-containing compound metabolic process	490	57	27.9	2.10E-07	6.09E-06
GO:0002768	immune response-regulating cell surface receptor signaling pathway	348	45	19.81	2.10E-07	6.09E-06
GO:0031334	positive regulation of protein complex assembly	217	33	12.35	2.30E-07	6.65E-06
GO:0030029	actin filament-based process	629	68	35.81	2.40E-07	6.90E-06
GO:0042743	hydrogen peroxide metabolic process	41	13	2.33	2.40E-07	6.90E-06
GO:0045786	negative regulation of cell cycle	579	64	32.96	2.50E-07	7.17E-06
GO:0002218	activation of innate immune response	294	40	16.74	2.70E-07	7.69E-06
GO:0045930	negative regulation of mitotic cell cycle	294	40	16.74	2.70E-07	7.69E-06
GO:0055086	nucleobase-containing small molecule metabolic process	657	70	37.4	2.70E-07	7.69E-06
GO:0032269	negative regulation of cellular protein metabolic process	976	94	55.57	2.90E-07	8.23E-06
GO:0050776	regulation of immune response	909	89	51.75	3.00E-07	8.47E-06
GO:0051701	interaction with host	199	31	11.33	3.00E-07	8.47E-06
GO:1902652	secondary alcohol metabolic process	140	25	7.97	3.10E-07	8.71E-06
GO:0010565	regulation of cellular ketone metabolic process	169	28	9.62	3.10E-07	8.71E-06
GO:0051172	negative regulation of nitrogen compound metabolic process	2105	172	119.84	3.30E-07	9.25E-06
GO:0051235	maintenance of location	275	38	15.66	3.50E-07	9.78E-06
GO:0006979	response to oxidative stress	413	50	23.51	3.60E-07	1.00E-05
GO:0006278	RNA-dependent DNA biosynthetic process	64	16	3.64	3.90E-07	1.08E-05
GO:0019725	cellular homeostasis	768	78	43.72	4.00E-07	1.10E-05
GO:0030097	hemopoiesis	808	81	46	4.00E-07	1.10E-05
GO:0090304	nucleic acid metabolic process	4846	344	275.89	4.00E-07	1.10E-05
GO:0050852	T cell receptor signaling pathway	162	27	9.22	4.50E-07	1.24E-05
GO:0051169	nuclear transport	289	39	16.45	4.60E-07	1.26E-05
GO:0043085	positive regulation of catalytic activity	1223	111	69.63	4.60E-07	1.26E-05

Supplementary Table S2A: Significant gene ontology categories for expressed genes in MKs

GO.ID	Term	Annotated	Significant	Expected	pval	qval
GO:0048534	hematopoietic or lymphoid organ development	851	84	48.45	4.70E-07	1.28E-05
GO:0006397	mRNA processing	429	51	24.42	4.80E-07	1.31E-05
GO:0070200	establishment of protein localization to telomere	15	8	0.85	4.80E-07	1.31E-05
GO:0052547	regulation of peptidase activity	370	46	21.06	5.00E-07	1.35E-05
GO:0002520	immune system development	893	87	50.84	5.00E-07	1.35E-05
GO:0021762	substantia nigra development	37	12	2.11	5.30E-07	1.43E-05
GO:0065009	regulation of molecular function	2860	220	162.82	5.50E-07	1.48E-05
GO:0009060	aerobic respiration	58	15	3.3	5.70E-07	1.53E-05
GO:0051247	positive regulation of protein metabolic process	1443	126	82.15	5.80E-07	1.55E-05
GO:0050778	positive regulation of immune response	697	72	39.68	6.00E-07	1.60E-05
GO:0032984	protein-containing complex disassembly	281	38	16	6.10E-07	1.63E-05
GO:0080090	regulation of primary metabolic process	5269	368	299.97	6.70E-07	1.78E-05
GO:0043687	post-translational protein modification	339	43	19.3	6.80E-07	1.80E-05
GO:0010243	response to organonitrogen compound	886	86	50.44	6.90E-07	1.83E-05
GO:0007166	cell surface receptor signaling pathway	2589	202	147.4	7.10E-07	1.87E-05
GO:0043254	regulation of protein complex assembly	376	46	21.41	7.80E-07	2.05E-05
GO:0016125	sterol metabolic process	147	25	8.37	8.00E-07	2.10E-05
GO:1901988	negative regulation of cell cycle phase transition	240	34	13.66	8.10E-07	2.12E-05
GO:1903827	regulation of cellular protein localization	474	54	26.99	8.60E-07	2.25E-05
GO:0046165	alcohol biosynthetic process	138	24	7.86	8.70E-07	2.27E-05
GO:0072593	reactive oxygen species metabolic process	241	34	13.72	9.00E-07	2.34E-05
GO:0052548	regulation of endopeptidase activity	343	43	19.53	9.30E-07	2.42E-05
GO:0031323	regulation of cellular metabolic process	5389	374	306.8	1.00E-06	2.58E-05
GO:2000116	regulation of cysteine-type endopeptidase activity	210	31	11.96	1.00E-06	2.58E-05
GO:0030177	positive regulation of Wnt signaling pathway	159	26	9.05	1.10E-06	2.82E-05
GO:0031324	negative regulation of cellular metabolic process	2250	179	128.1	1.10E-06	2.82E-05
GO:0032270	positive regulation of cellular protein metabolic process	1359	119	77.37	1.10E-06	2.82E-05
GO:0002758	innate immune response-activating signal transduction	277	37	15.77	1.20E-06	3.06E-05
GO:0045089	positive regulation of innate immune response	346	43	19.7	1.20E-06	3.06E-05
GO:0043900	regulation of multi-organism process	382	46	21.75	1.20E-06	3.06E-05
GO:0019218	regulation of steroid metabolic process	122	22	6.95	1.30E-06	3.31E-05
GO:0007004	telomere maintenance via telomerase	62	15	3.53	1.40E-06	3.55E-05
GO:0016055	Wnt signaling pathway	470	53	26.76	1.50E-06	3.79E-05
GO:0070199	establishment of protein localization to chromosome	22	9	1.25	1.50E-06	3.79E-05
GO:0032273	positive regulation of protein polymerization	105	20	5.98	1.60E-06	4.02E-05
GO:0010592	positive regulation of lamellipodium assembly	17	8	0.97	1.60E-06	4.02E-05
GO:0198738	cell-cell signaling by wnt	472	53	26.87	1.70E-06	4.24E-05
GO:0035821	modification of morphology or physiology of other organism	153	25	8.71	1.70E-06	4.24E-05
GO:0045088	regulation of innate immune response	411	48	23.4	1.70E-06	4.24E-05
GO:1903706	regulation of hemopoiesis	448	51	25.51	1.80E-06	4.45E-05
GO:0071495	cellular response to endogenous stimulus	1243	110	70.77	1.80E-06	4.45E-05
GO:0045540	regulation of cholesterol biosynthetic process	48	13	2.73	1.80E-06	4.45E-05
GO:0106118	regulation of sterol biosynthetic process	48	13	2.73	1.80E-06	4.45E-05
GO:1903902	positive regulation of viral life cycle	56	14	3.19	2.10E-06	5.18E-05
GO:0009893	positive regulation of metabolic process	3086	231	175.69	2.20E-06	5.37E-05
GO:1900182	positive regulation of protein localization to nucleus	72	16	4.1	2.20E-06	5.37E-05
GO:0008154	actin polymerization or depolymerization	155	25	8.82	2.20E-06	5.37E-05
GO:2000573	positive regulation of DNA biosynthetic process	64	15	3.64	2.20E-06	5.37E-05
GO:0051817	modification of morphology or physiology of other organism involved in symbiotic interaction	107	20	6.09	2.20E-06	5.37E-05
GO:1902903	regulation of supramolecular fiber organization	285	37	16.23	2.30E-06	5.60E-05
GO:0075522	IRES-dependent viral translational initiation	9	6	0.51	2.40E-06	5.82E-05
GO:0045185	maintenance of protein location	81	17	4.61	2.40E-06	5.82E-05
GO:0045862	positive regulation of proteolysis	309	39	17.59	2.50E-06	6.03E-05
GO:0006913	nucleocytoplasmic transport	286	37	16.28	2.50E-06	6.03E-05
GO:0033108	mitochondrial respiratory chain complex assembly	73	16	4.16	2.60E-06	6.26E-05
GO:0006914	autophagy	442	50	25.16	2.70E-06	6.47E-05
GO:0061919	process utilizing autophagic mechanism	442	50	25.16	2.70E-06	6.47E-05
GO:0019079	viral genome replication	109	20	6.21	3.00E-06	7.18E-05
GO:0010821	regulation of mitochondrion organization	168	26	9.56	3.10E-06	7.40E-05
GO:0010833	telomere maintenance via telomere lengthening	74	16	4.21	3.20E-06	7.62E-05
GO:0051170	import into nucleus	119	21	6.77	3.30E-06	7.84E-05
GO:0006898	receptor-mediated endocytosis	233	32	13.27	3.40E-06	8.07E-05
GO:1902745	positive regulation of lamellipodium organization	24	9	1.37	3.60E-06	8.52E-05
GO:0014070	response to organic cyclic compound	841	80	47.88	3.70E-06	8.74E-05
GO:0006414	translational elongation	120	21	6.83	3.80E-06	8.96E-05
GO:0050810	regulation of steroid biosynthetic process	93	18	5.29	4.20E-06	9.88E-05
GO:0034976	response to endoplasmic reticulum stress	236	32	13.44	4.40E-06	1.03E-04
GO:0002433	immune response-regulating cell surface receptor signaling pathway involved in phagocytosis	76	16	4.33	4.60E-06	1.07E-04
GO:0038096	Fc-gamma receptor signaling pathway involved in phagocytosis	76	16	4.33	4.60E-06	1.07E-04
GO:0015669	gas transport	19	8	1.08	4.60E-06	1.07E-04
GO:0030099	myeloid cell differentiation	389	45	22.15	4.70E-06	1.09E-04
GO:0019637	organophosphate metabolic process	985	90	56.08	4.80E-06	1.11E-04
GO:0090090	negative regulation of canonical Wnt signaling pathway	162	25	9.22	5.00E-06	1.16E-04
GO:0023014	signal transduction by protein phosphorylation	835	79	47.54	5.30E-06	1.22E-04
GO:0042177	negative regulation of protein catabolic process	113	20	6.43	5.30E-06	1.22E-04
GO:0070198	protein localization to chromosome, telomeric region	25	9	1.42	5.40E-06	1.24E-04
GO:0010468	regulation of gene expression	4358	307	248.11	5.60E-06	1.29E-04
GO:0045861	negative regulation of proteolysis	296	37	16.85	5.70E-06	1.31E-04
GO:0008064	regulation of actin polymerization or depolymerization	133	22	7.57	5.80E-06	1.33E-04
GO:0051129	negative regulation of cellular component organization	622	63	35.41	5.90E-06	1.35E-04

Supplementary Table S2A: Significant gene ontology categories for expressed genes in MKs

GO.ID	Term	Annotated	Significant	Expected	pval	qval
GO:2000736	regulation of stem cell differentiation	114	20	6.49	6.10E-06	1.39E-04
GO:1903829	positive regulation of cellular protein localization	297	37	16.91	6.10E-06	1.39E-04
GO:0090181	regulation of cholesterol metabolic process	61	14	3.47	6.20E-06	1.41E-04
GO:0038094	Fc-gamma receptor signaling pathway	78	16	4.44	6.60E-06	1.49E-04
GO:0017038	protein import	134	22	7.63	6.60E-06	1.49E-04
GO:0030832	regulation of actin filament length	134	22	7.63	6.60E-06	1.49E-04
GO:1901698	response to nitrogen compound	951	87	54.14	6.60E-06	1.49E-04
GO:0071356	cellular response to tumor necrosis factor	252	33	14.35	6.70E-06	1.50E-04
GO:0043086	negative regulation of catalytic activity	705	69	40.14	6.90E-06	1.55E-04
GO:0051651	maintenance of location in cell	70	15	3.99	7.20E-06	1.61E-04
GO:0010035	response to inorganic substance	497	53	28.29	7.70E-06	1.72E-04
GO:0002431	Fc receptor mediated stimulatory signaling pathway	79	16	4.5	7.80E-06	1.73E-04
GO:1902930	regulation of alcohol biosynthetic process	79	16	4.5	7.80E-06	1.73E-04
GO:0010591	regulation of lamellipodium assembly	26	9	1.48	7.80E-06	1.73E-04
GO:0045730	respiratory burst	26	9	1.48	7.80E-06	1.73E-04
GO:0000165	MAPK cascade	831	78	47.31	8.10E-06	1.78E-04
GO:0015671	oxygen transport	15	7	0.85	8.10E-06	1.78E-04
GO:0051131	chaperone-mediated protein complex assembly	15	7	0.85	8.10E-06	1.78E-04
GO:0061684	chaperone-mediated autophagy	15	7	0.85	8.10E-06	1.78E-04
GO:0032535	regulation of cellular component size	289	36	16.45	8.20E-06	1.80E-04
GO:1903900	regulation of viral life cycle	136	22	7.74	8.40E-06	1.84E-04
GO:0051258	protein polymerization	211	29	12.01	9.40E-06	2.05E-04
GO:0060627	regulation of vesicle-mediated transport	450	49	25.62	9.70E-06	2.11E-04
GO:0045727	positive regulation of translation	108	19	6.15	9.90E-06	2.15E-04
GO:0033209	tumor necrosis factor-mediated signaling pathway	158	24	9	1.00E-05	2.17E-04
GO:0051851	modification by host of symbiont morphology or physiology	72	15	4.1	1.00E-05	2.17E-04
GO:0045087	innate immune response	824	77	46.91	1.10E-05	2.37E-04
GO:0045454	cell redox homeostasis	64	14	3.64	1.10E-05	2.37E-04
GO:0034975	protein folding in endoplasmic reticulum	7	5	0.4	1.10E-05	2.37E-04
GO:0010608	posttranscriptional regulation of gene expression	994	89	56.59	1.20E-05	2.56E-04
GO:0034250	positive regulation of cellular amide metabolic process	129	21	7.34	1.20E-05	2.56E-04
GO:0043154	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	73	15	4.16	1.20E-05	2.56E-04
GO:0006403	RNA localization	192	27	10.93	1.20E-05	2.56E-04
GO:0044092	negative regulation of molecular function	1010	90	57.5	1.30E-05	2.77E-04
GO:0031325	positive regulation of cellular metabolic process	2814	209	160.21	1.40E-05	2.97E-04
GO:0034329	cell junction assembly	204	28	11.61	1.40E-05	2.97E-04
GO:0060828	regulation of canonical Wnt signaling pathway	250	32	14.23	1.50E-05	3.17E-04
GO:2000027	regulation of animal organ morphogenesis	239	31	13.61	1.50E-05	3.17E-04
GO:0031400	negative regulation of protein modification process	562	57	32	1.60E-05	3.37E-04
GO:0010604	positive regulation of macromolecule metabolic process	2838	210	161.57	1.60E-05	3.37E-04
GO:0032799	low-density lipoprotein receptor particle metabolic process	22	8	1.25	1.70E-05	3.54E-04
GO:0033119	negative regulation of RNA splicing	22	8	1.25	1.70E-05	3.54E-04
GO:0042744	hydrogen peroxide catabolic process	22	8	1.25	1.70E-05	3.54E-04
GO:0048583	regulation of response to stimulus	3919	277	223.11	1.70E-05	3.54E-04
GO:1900180	regulation of protein localization to nucleus	112	19	6.38	1.70E-05	3.54E-04
GO:0006890	retrograde vesicle-mediated transport, Golgi to ER	75	15	4.27	1.70E-05	3.54E-04
GO:0030838	positive regulation of actin filament polymerization	75	15	4.27	1.70E-05	3.54E-04
GO:0045936	negative regulation of phosphate metabolic process	538	55	30.63	1.80E-05	3.73E-04
GO:0010467	gene expression	5488	371	312.44	1.80E-05	3.73E-04
GO:0010563	negative regulation of phosphorus metabolic process	539	55	30.69	1.90E-05	3.93E-04
GO:1903362	regulation of cellular protein catabolic process	208	28	11.84	2.00E-05	4.10E-04
GO:0034599	cellular response to oxidative stress	277	34	15.77	2.00E-05	4.10E-04
GO:2000379	positive regulation of reactive oxygen species metabolic process	94	17	5.35	2.00E-05	4.10E-04
GO:0051186	cofactor metabolic process	501	52	28.52	2.00E-05	4.10E-04
GO:1901701	cellular response to oxygen-containing compound	1022	90	58.18	2.00E-05	4.10E-04
GO:0032271	regulation of protein polymerization	165	24	9.39	2.10E-05	4.29E-04
GO:0051493	regulation of cytoskeleton organization	438	47	24.94	2.10E-05	4.29E-04
GO:0046677	response to antibiotic	314	37	17.88	2.20E-05	4.44E-04
GO:0051276	chromosome organization	996	88	56.7	2.20E-05	4.44E-04
GO:0090201	negative regulation of release of cytochrome c from mitochondria	17	7	0.97	2.20E-05	4.44E-04
GO:1902229	regulation of intrinsic apoptotic signaling pathway in response to DNA damage	36	10	2.05	2.20E-05	4.44E-04
GO:1902743	regulation of lamellipodium organization	36	10	2.05	2.20E-05	4.44E-04
GO:1904358	positive regulation of telomere maintenance via telomere lengthening	36	10	2.05	2.20E-05	4.44E-04
GO:0055076	transition metal ion homeostasis	95	17	5.41	2.30E-05	4.63E-04
GO:1903320	regulation of protein modification by small protein conjugation or removal	199	27	11.33	2.40E-05	4.82E-04
GO:0051171	regulation of nitrogen compound metabolic process	5116	348	291.26	2.40E-05	4.82E-04
GO:0034612	response to tumor necrosis factor	269	33	15.31	2.60E-05	5.21E-04
GO:0070201	regulation of establishment of protein localization	681	65	38.77	2.80E-05	5.60E-04
GO:0051495	positive regulation of cytoskeleton organization	190	26	10.82	2.90E-05	5.78E-04
GO:1905114	cell surface receptor signaling pathway involved in cell-cell signaling	561	56	31.94	2.90E-05	5.78E-04
GO:0034330	cell junction organization	259	32	14.75	3.00E-05	5.96E-04
GO:0002504	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	97	17	5.52	3.00E-05	5.96E-04
GO:1903050	regulation of proteolysis involved in cellular protein catabolic process	180	25	10.25	3.20E-05	6.33E-04
GO:0048872	homeostasis of number of cells	225	29	12.81	3.20E-05	6.33E-04
GO:0032880	regulation of protein localization	921	82	52.43	3.30E-05	6.48E-04
GO:0032970	regulation of actin filament-based process	320	37	18.22	3.30E-05	6.48E-04
GO:0097581	lamellipodium organization	70	14	3.99	3.30E-05	6.48E-04
GO:0016070	RNA metabolic process	4382	303	249.47	3.30E-05	6.48E-04
GO:0030260	entry into host cell	128	20	7.29	3.60E-05	7.02E-04
GO:0044409	entry into host	128	20	7.29	3.60E-05	7.02E-04

Supplementary Table S2A: Significant gene ontology categories for expressed genes in MKs

GO.ID	Term	Annotated	Significant	Expected	pval	qval
GO:0051806	entry into cell of other organism involved in symbiotic interaction	128	20	7.29	3.60E-05	7.02E-04
GO:0051828	entry into other organism involved in symbiotic interaction	128	20	7.29	3.60E-05	7.02E-04
GO:0019068	virion assembly	38	10	2.16	3.70E-05	7.20E-04
GO:0051099	positive regulation of binding	171	24	9.74	3.80E-05	7.38E-04
GO:0006873	cellular ion homeostasis	501	51	28.52	4.00E-05	7.74E-04
GO:0035556	intracellular signal transduction	2450	183	139.48	4.00E-05	7.74E-04
GO:0032802	low-density lipoprotein particle receptor catabolic process	13	6	0.74	4.10E-05	7.90E-04
GO:0050851	antigen receptor-mediated signaling pathway	205	27	11.67	4.10E-05	7.90E-04
GO:0042180	cellular ketone metabolic process	228	29	12.98	4.10E-05	7.90E-04
GO:0030100	regulation of endocytosis	252	31	14.35	4.40E-05	8.46E-04
GO:2000117	negative regulation of cysteine-type endopeptidase activity	81	15	4.61	4.50E-05	8.64E-04
GO:0031396	regulation of protein ubiquitination	173	24	9.85	4.70E-05	8.99E-04
GO:0051098	regulation of binding	350	39	19.93	4.70E-05	8.99E-04
GO:0042273	ribosomal large subunit biogenesis	25	8	1.42	4.90E-05	9.34E-04
GO:0048857	neural nucleus development	55	12	3.13	4.90E-05	9.34E-04
GO:0061136	regulation of proteasomal protein catabolic process	152	22	8.65	5.00E-05	9.48E-04
GO:0075525	viral translational termination-reinitiation	5	4	0.28	5.00E-05	9.48E-04
GO:1902255	positive regulation of intrinsic apoptotic signaling pathway by p53 class mediator	5	4	0.28	5.00E-05	9.48E-04
GO:0007568	aging	302	35	17.19	5.10E-05	9.65E-04
GO:0016999	antibiotic metabolic process	121	19	6.89	5.20E-05	9.79E-04
GO:0010155	regulation of proton transport	19	7	1.08	5.20E-05	9.79E-04
GO:0045859	regulation of protein kinase activity	695	65	39.57	5.20E-05	9.79E-04
GO:0043280	positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	111	18	6.32	5.30E-05	9.95E-04
GO:0031349	positive regulation of defense response	480	49	27.33	5.30E-05	9.95E-04
GO:0030041	actin filament polymerization	132	20	7.51	5.60E-05	1.05E-03
GO:0032507	maintenance of protein location in cell	56	12	3.19	5.90E-05	1.10E-03
GO:2001244	positive regulation of intrinsic apoptotic signaling pathway	56	12	3.19	5.90E-05	1.10E-03
GO:0050794	regulation of cellular process	9281	584	528.38	6.00E-05	1.11E-03
GO:0007010	cytoskeleton organization	1038	89	59.09	6.00E-05	1.11E-03
GO:1903573	negative regulation of response to endoplasmic reticulum stress	40	10	2.28	6.00E-05	1.11E-03
GO:0071407	cellular response to organic cyclic compound	509	51	28.98	6.00E-05	1.11E-03
GO:0055082	cellular chemical homeostasis	630	60	35.87	6.10E-05	1.13E-03
GO:0002244	hematopoietic progenitor cell differentiation	154	22	8.77	6.10E-05	1.13E-03
GO:0044283	small molecule biosynthetic process	685	64	39	6.10E-05	1.13E-03
GO:2000377	regulation of reactive oxygen species metabolic process	176	24	10.02	6.20E-05	1.14E-03
GO:0051881	regulation of mitochondrial membrane potential	65	13	3.7	6.30E-05	1.16E-03
GO:0019886	antigen processing and presentation of exogenous peptide antigen via MHC class II	93	16	5.29	6.50E-05	1.19E-03
GO:0009968	negative regulation of signal transduction	1186	99	67.52	6.50E-05	1.19E-03
GO:0032212	positive regulation of telomere maintenance via telomerase	33	9	1.88	6.70E-05	1.23E-03
GO:0051054	positive regulation of DNA metabolic process	200	26	11.39	7.00E-05	1.28E-03
GO:0030178	negative regulation of Wnt signaling pathway	189	25	10.76	7.20E-05	1.31E-03
GO:0022406	membrane docking	145	21	8.26	7.30E-05	1.33E-03
GO:0051173	positive regulation of nitrogen compound metabolic process	2683	196	152.75	7.40E-05	1.34E-03
GO:0006826	iron ion transport	49	11	2.79	7.60E-05	1.38E-03
GO:0002262	myeloid cell homeostasis	135	20	7.69	7.70E-05	1.39E-03
GO:0007165	signal transduction	5132	345	292.17	7.80E-05	1.41E-03
GO:0051348	negative regulation of transferase activity	260	31	14.8	7.90E-05	1.42E-03
GO:0030111	regulation of Wnt signaling pathway	321	36	18.28	7.90E-05	1.42E-03
GO:0030003	cellular cation homeostasis	488	49	27.78	8.00E-05	1.44E-03
GO:1902533	positive regulation of intracellular signal transduction	960	83	54.65	8.10E-05	1.46E-03
GO:0046718	viral entry into host cell	115	18	6.55	8.50E-05	1.52E-03
GO:0046916	cellular transition metal ion homeostasis	76	14	4.33	8.60E-05	1.54E-03
GO:0006734	NADH metabolic process	34	9	1.94	8.70E-05	1.56E-03
GO:0006694	steroid biosynthetic process	180	24	10.25	8.80E-05	1.57E-03
GO:0051640	organelle localization	584	56	33.25	8.90E-05	1.59E-03
GO:0051050	positive regulation of transport	891	78	50.73	9.00E-05	1.60E-03
GO:0010951	negative regulation of endopeptidase activity	192	25	10.93	9.40E-05	1.67E-03
GO:2000059	negative regulation of ubiquitin-dependent protein catabolic process	42	10	2.39	9.40E-05	1.67E-03
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	640	60	36.44	9.50E-05	1.68E-03
GO:0002495	antigen processing and presentation of peptide antigen via MHC class II	96	16	5.47	9.60E-05	1.70E-03
GO:0010466	negative regulation of peptidase activity	204	26	11.61	9.80E-05	1.73E-03
GO:0043170	macromolecule metabolic process	8778	554	499.74	1.00E-04	1.76E-03
GO:0007167	enzyme linked receptor protein signaling pathway	924	80	52.6	1.00E-04	1.76E-03
GO:0030833	regulation of actin filament polymerization	117	18	6.66	1.10E-04	1.92E-03
GO:1901798	positive regulation of signal transduction by p53 class mediator	21	7	1.2	1.10E-04	1.92E-03
GO:0051347	positive regulation of transferase activity	575	55	32.74	1.10E-04	1.92E-03
GO:1901998	toxin transport	35	9	1.99	1.10E-04	1.92E-03
GO:0071900	regulation of protein serine/threonine kinase activity	455	46	25.9	1.10E-04	1.92E-03
GO:0032956	regulation of actin cytoskeleton organization	277	32	15.77	1.10E-04	1.92E-03
GO:0000302	response to reactive oxygen species	218	27	12.41	1.20E-04	2.07E-03
GO:0042326	negative regulation of phosphorylation	430	44	24.48	1.20E-04	2.07E-03
GO:0010458	exit from mitosis	28	8	1.59	1.20E-04	2.07E-03
GO:0032879	regulation of localization	2500	183	142.33	1.20E-04	2.07E-03
GO:0046890	regulation of lipid biosynthetic process	184	24	10.48	1.20E-04	2.07E-03
GO:0000209	protein polyubiquitination	279	32	15.88	1.30E-04	2.24E-03
GO:0098771	inorganic ion homeostasis	565	54	32.17	1.30E-04	2.24E-03
GO:0043624	cellular protein complex disassembly	185	24	10.53	1.40E-04	2.39E-03
GO:0055080	cation homeostasis	553	53	31.48	1.40E-04	2.39E-03
GO:0060249	anatomical structure homeostasis	381	40	21.69	1.40E-04	2.39E-03
GO:2000278	regulation of DNA biosynthetic process	99	16	5.64	1.40E-04	2.39E-03

Supplementary Table S2A: Significant gene ontology categories for expressed genes in MKs

GO.ID	Term	Annotated	Significant	Expected	pval	qval
GO:0099132	ATP hydrolysis coupled cation transmembrane transport	36	9	2.05	1.40E-04	2.39E-03
GO:0051438	regulation of ubiquitin-protein transferase activity	44	10	2.5	1.40E-04	2.39E-03
GO:0110053	regulation of actin filament organization	209	26	11.9	1.50E-04	2.55E-03
GO:0051259	protein complex oligomerization	541	52	30.8	1.50E-04	2.55E-03
GO:1904666	regulation of ubiquitin protein ligase activity	22	7	1.25	1.50E-04	2.55E-03
GO:1902253	regulation of intrinsic apoptotic signaling pathway by p53 class mediator	29	8	1.65	1.60E-04	2.71E-03
GO:0031589	cell-substrate adhesion	307	34	17.48	1.60E-04	2.71E-03
GO:0048024	regulation of mRNA splicing, via spliceosome	71	13	4.04	1.60E-04	2.71E-03
GO:1903051	negative regulation of proteolysis involved in cellular protein catabolic process	62	12	3.53	1.70E-04	2.86E-03
GO:0055085	transmembrane transport	1351	108	76.91	1.70E-04	2.86E-03
GO:0090066	regulation of anatomical structure size	411	42	23.4	1.70E-04	2.86E-03
GO:0034101	erythrocyte homeostasis	111	17	6.32	1.70E-04	2.86E-03
GO:0048585	negative regulation of response to stimulus	1520	119	86.54	1.80E-04	2.98E-03
GO:0051336	regulation of hydrolase activity	1086	90	61.83	1.80E-04	2.98E-03
GO:0019322	pentose biosynthetic process	3	3	0.17	1.80E-04	2.98E-03
GO:0044502	positive regulation of signal transduction in other organism	3	3	0.17	1.80E-04	2.98E-03
GO:0052470	modulation by host of symbiont signal transduction pathway	3	3	0.17	1.80E-04	2.98E-03
GO:0052525	positive regulation by host of symbiont signal transduction pathway	3	3	0.17	1.80E-04	2.98E-03
GO:0052526	positive regulation by organism of signal transduction in other organism involved in symbiotic inter...	3	3	0.17	1.80E-04	2.98E-03
GO:0075205	modulation by host of symbiont cAMP-mediated signal transduction	3	3	0.17	1.80E-04	2.98E-03
GO:0075206	positive regulation by host of symbiont cAMP-mediated signal transduction	3	3	0.17	1.80E-04	2.98E-03
GO:0006283	transcription-coupled nucleotide-excision repair	72	13	4.1	1.90E-04	3.14E-03
GO:0030032	lamellipodium assembly	54	11	3.07	1.90E-04	3.14E-03
GO:0072655	establishment of protein localization to mitochondrion	112	17	6.38	1.90E-04	3.14E-03
GO:0034446	substrate adhesion-dependent cell spreading	82	14	4.67	2.00E-04	3.29E-03
GO:0045116	protein neddylation	11	5	0.63	2.00E-04	3.29E-03
GO:0031399	regulation of protein modification process	1601	124	91.15	2.00E-04	3.29E-03
GO:1902175	regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	23	7	1.31	2.10E-04	3.43E-03
GO:2001252	positive regulation of chromosome organization	156	21	8.88	2.10E-04	3.43E-03
GO:0031667	response to nutrient levels	441	44	25.11	2.10E-04	3.43E-03
GO:0008637	apoptotic mitochondrial changes	113	17	6.43	2.20E-04	3.59E-03
GO:0008631	intrinsic apoptotic signaling pathway in response to oxidative stress	38	9	2.16	2.20E-04	3.59E-03
GO:0034470	ncRNA processing	263	30	14.97	2.30E-04	3.73E-03
GO:0035967	cellular response to topologically incorrect protein	124	18	7.06	2.30E-04	3.73E-03
GO:0001836	release of cytochrome c from mitochondria	55	11	3.13	2.30E-04	3.73E-03
GO:0000723	telomere maintenance	146	20	8.31	2.30E-04	3.73E-03
GO:0032930	positive regulation of superoxide anion generation	17	6	0.97	2.40E-04	3.88E-03
GO:0071800	podosome assembly	17	6	0.97	2.40E-04	3.88E-03
GO:0034660	ncRNA metabolic process	431	43	24.54	2.50E-04	4.02E-03
GO:0009991	response to extracellular stimulus	471	46	26.81	2.50E-04	4.02E-03
GO:1903363	negative regulation of cellular protein catabolic process	74	13	4.21	2.50E-04	4.02E-03
GO:0044089	positive regulation of cellular component biogenesis	458	45	26.07	2.50E-04	4.02E-03
GO:0048013	ephrin receptor signaling pathway	84	14	4.78	2.60E-04	4.17E-03
GO:0048193	Golgi vesicle transport	290	32	16.51	2.60E-04	4.17E-03
GO:0034620	cellular response to unfolded protein	115	17	6.55	2.70E-04	4.30E-03
GO:0043549	regulation of kinase activity	764	67	43.5	2.70E-04	4.30E-03
GO:0032200	telomere organization	159	21	9.05	2.70E-04	4.30E-03
GO:0045010	actin nucleation	39	9	2.22	2.70E-04	4.30E-03
GO:0140056	organelle localization by membrane tethering	137	19	7.8	2.80E-04	4.44E-03
GO:0032386	regulation of intracellular transport	368	38	20.95	2.80E-04	4.44E-03
GO:0030968	endoplasmic reticulum unfolded protein response	105	16	5.98	2.80E-04	4.44E-03
GO:0010952	positive regulation of peptidase activity	171	22	9.74	2.90E-04	4.59E-03
GO:0060070	canonical Wnt signaling pathway	292	32	16.62	2.90E-04	4.59E-03
GO:0001933	negative regulation of protein phosphorylation	395	40	22.49	3.00E-04	4.72E-03
GO:0070585	protein localization to mitochondrion	116	17	6.6	3.00E-04	4.72E-03
GO:0031099	regeneration	183	23	10.42	3.00E-04	4.72E-03
GO:0016236	macroautophagy	255	29	14.52	3.00E-04	4.72E-03
GO:0010648	negative regulation of cell communication	1282	102	72.99	3.10E-04	4.85E-03
GO:0000910	cytokinesis	138	19	7.86	3.10E-04	4.85E-03
GO:0032206	positive regulation of telomere maintenance	48	10	2.73	3.10E-04	4.85E-03
GO:0051187	cofactor catabolic process	48	10	2.73	3.10E-04	4.85E-03
GO:0043388	positive regulation of DNA binding	57	11	3.25	3.20E-04	4.97E-03
GO:1904356	regulation of telomere maintenance via telomere lengthening	57	11	3.25	3.20E-04	4.97E-03
GO:0009157	deoxyribonucleoside monophosphate biosynthetic process	7	4	0.4	3.20E-04	4.97E-03
GO:0051683	establishment of Golgi localization	7	4	0.4	3.20E-04	4.97E-03
GO:0071353	cellular response to interleukin-4	32	8	1.82	3.30E-04	5.11E-03
GO:0045069	regulation of viral genome replication	86	14	4.9	3.30E-04	5.11E-03
GO:0070493	thrombin-activated receptor signaling pathway	12	5	0.68	3.30E-04	5.11E-03
GO:2001056	positive regulation of cysteine-type endopeptidase activity	128	18	7.29	3.40E-04	5.22E-03
GO:0050801	ion homeostasis	629	57	35.81	3.40E-04	5.22E-03
GO:0023057	negative regulation of signaling	1286	102	73.21	3.40E-04	5.22E-03
GO:0010523	negative regulation of calcium ion transport into cytosol	18	6	1.02	3.40E-04	5.22E-03
GO:0042026	protein refolding	18	6	1.02	3.40E-04	5.22E-03
GO:0070987	error-free translesion synthesis	18	6	1.02	3.40E-04	5.22E-03
GO:0019752	carboxylic acid metabolic process	945	79	53.8	3.50E-04	5.36E-03
GO:0071479	cellular response to ionizing radiation	67	12	3.81	3.60E-04	5.49E-03
GO:0031330	negative regulation of cellular catabolic process	221	26	12.58	3.60E-04	5.49E-03
GO:0008202	steroid metabolic process	308	33	17.53	3.60E-04	5.49E-03
GO:0032210	regulation of telomere maintenance via telomerase	49	10	2.79	3.70E-04	5.62E-03
GO:0030194	positive regulation of blood coagulation	25	7	1.42	3.70E-04	5.62E-03

Supplementary Table S2A: Significant gene ontology categories for expressed genes in MKs

GO.ID	Term	Annotated	Significant	Expected	pval	qval
GO:1900048	positive regulation of hemostasis	25	7	1.42	3.70E-04	5.62E-03
GO:1903321	negative regulation of protein modification by small protein conjugation or removal	77	13	4.38	3.70E-04	5.62E-03
GO:0009889	regulation of biosynthetic process	3824	261	217.71	3.80E-04	5.76E-03
GO:0051051	negative regulation of transport	468	45	26.64	4.00E-04	6.05E-03
GO:0017001	antibiotic catabolic process	41	9	2.33	4.10E-04	6.16E-03
GO:0090382	phagosome maturation	41	9	2.33	4.10E-04	6.16E-03
GO:0007154	cell communication	5575	365	317.39	4.10E-04	6.16E-03
GO:0055072	iron ion homeostasis	68	12	3.87	4.10E-04	6.16E-03
GO:0009895	negative regulation of catabolic process	260	29	14.8	4.10E-04	6.16E-03
GO:0045070	positive regulation of viral genome replication	33	8	1.88	4.20E-04	6.30E-03
GO:0051301	cell division	537	50	30.57	4.20E-04	6.30E-03
GO:0097305	response to alcohol	224	26	12.75	4.40E-04	6.59E-03
GO:0043112	receptor metabolic process	165	21	9.39	4.50E-04	6.71E-03
GO:0009966	regulation of signal transduction	3047	213	173.47	4.50E-04	6.71E-03
GO:0019216	regulation of lipid metabolic process	377	38	21.46	4.50E-04	6.71E-03
GO:0006606	protein import into nucleus	99	15	5.64	4.60E-04	6.85E-03
GO:0031397	negative regulation of protein ubiquitination	69	12	3.93	4.70E-04	6.98E-03
GO:0009605	response to external stimulus	2119	155	120.64	4.70E-04	6.98E-03
GO:0032069	regulation of nuclease activity	19	6	1.08	4.80E-04	7.07E-03
GO:0006735	NADH regeneration	26	7	1.48	4.80E-04	7.07E-03
GO:0050820	positive regulation of coagulation	26	7	1.48	4.80E-04	7.07E-03
GO:0061621	canonical glycolysis	26	7	1.48	4.80E-04	7.07E-03
GO:0061718	glucose catabolic process to pyruvate	26	7	1.48	4.80E-04	7.07E-03
GO:1904951	positive regulation of establishment of protein localization	418	41	23.8	4.80E-04	7.07E-03
GO:0071806	protein transmembrane transport	42	9	2.39	4.90E-04	7.21E-03
GO:0070670	response to interleukin-4	34	8	1.94	5.20E-04	7.61E-03
GO:0072595	maintenance of protein localization in organelle	34	8	1.94	5.20E-04	7.61E-03
GO:0044794	positive regulation by host of viral process	13	5	0.74	5.20E-04	7.61E-03
GO:0071801	regulation of podosome assembly	13	5	0.74	5.20E-04	7.61E-03
GO:0010822	positive regulation of mitochondrion organization	111	16	6.32	5.30E-04	7.74E-03
GO:0050793	regulation of developmental process	2427	174	138.17	5.40E-04	7.86E-03
GO:0034381	plasma lipoprotein particle clearance	70	12	3.99	5.40E-04	7.86E-03
GO:0034502	protein localization to chromosome	70	12	3.99	5.40E-04	7.86E-03
GO:0033044	regulation of chromosome organization	290	31	16.51	5.60E-04	8.13E-03
GO:0048878	chemical homeostasis	960	79	54.65	5.60E-04	8.13E-03
GO:0097006	regulation of plasma lipoprotein particle levels	101	15	5.75	5.70E-04	8.26E-03
GO:0071363	cellular response to growth factor stimulus	643	57	36.61	5.80E-04	8.40E-03
GO:0006596	polyamine biosynthetic process	8	4	0.46	6.10E-04	8.80E-03
GO:0060316	positive regulation of ryanodine-sensitive calcium-release channel activity	8	4	0.46	6.10E-04	8.80E-03
GO:0075713	establishment of integrated proviral latency	8	4	0.46	6.10E-04	8.80E-03
GO:0034314	Arp2/3 complex-mediated actin nucleation	27	7	1.54	6.20E-04	8.89E-03
GO:0061615	glycolytic process through fructose-6-phosphate	27	7	1.54	6.20E-04	8.89E-03
GO:0061620	glycolytic process through glucose-6-phosphate	27	7	1.54	6.20E-04	8.89E-03
GO:0071480	cellular response to gamma radiation	27	7	1.54	6.20E-04	8.89E-03
GO:0007339	binding of sperm to zona pellucida	35	8	1.99	6.40E-04	9.17E-03
GO:0050865	regulation of cell activation	506	47	28.81	6.50E-04	9.29E-03
GO:0000715	nucleotide-excision repair, DNA damage recognition	20	6	1.14	6.50E-04	9.29E-03
GO:2000058	regulation of ubiquitin-dependent protein catabolic process	124	17	7.06	6.60E-04	9.42E-03
GO:0097711	ciliary basal body-plasma membrane docking	92	14	5.24	6.70E-04	9.55E-03
GO:0006875	cellular metal ion homeostasis	439	42	24.99	6.90E-04	9.82E-03
GO:0032204	regulation of telomere maintenance	72	12	4.1	7.00E-04	9.82E-03
GO:0006952	defense response	1512	115	86.08	7.00E-04	9.82E-03
GO:0000028	ribosomal small subunit assembly	4	3	0.23	7.00E-04	9.82E-03
GO:0005997	xylulose metabolic process	4	3	0.23	7.00E-04	9.82E-03
GO:0030043	actin filament fragmentation	4	3	0.23	7.00E-04	9.82E-03
GO:0051343	positive regulation of cyclic-nucleotide phosphodiesterase activity	4	3	0.23	7.00E-04	9.82E-03
GO:0071787	endoplasmic reticulum tubular network formation	4	3	0.23	7.00E-04	9.82E-03
GO:0090666	scaRNA localization to Cajal body	4	3	0.23	7.00E-04	9.82E-03
GO:1905908	positive regulation of amyloid fibril formation	4	3	0.23	7.00E-04	9.82E-03
GO:2000152	regulation of ubiquitin-specific protease activity	4	3	0.23	7.00E-04	9.82E-03
GO:0090199	regulation of release of cytochrome c from mitochondria	44	9	2.5	7.00E-04	9.82E-03
GO:0050684	regulation of mRNA processing	103	15	5.86	7.10E-04	9.91E-03
GO:0030521	androgen receptor signaling pathway	53	10	3.02	7.10E-04	9.91E-03
GO:1901135	carbohydrate derivative metabolic process	1057	85	60.18	7.10E-04	9.91E-03
GO:0051346	negative regulation of hydrolase activity	386	38	21.98	7.10E-04	9.91E-03
GO:0031468	nuclear envelope reassembly	14	5	0.8	7.70E-04	1.07E-02
GO:0043558	regulation of translational initiation in response to stress	14	5	0.8	7.70E-04	1.07E-02
GO:0051280	negative regulation of release of sequestered calcium ion into cytosol	14	5	0.8	7.70E-04	1.07E-02
GO:0042542	response to hydrogen peroxide	137	18	7.8	7.70E-04	1.07E-02
GO:0046782	regulation of viral transcription	63	11	3.59	7.70E-04	1.07E-02
GO:0046596	regulation of viral entry into host cell	28	7	1.59	7.80E-04	1.08E-02
GO:0090383	phagosome acidification	28	7	1.59	7.80E-04	1.08E-02
GO:0045595	regulation of cell differentiation	1703	127	96.95	7.90E-04	1.09E-02
GO:0023052	signaling	5555	361	316.25	8.20E-04	1.13E-02
GO:0007006	mitochondrial membrane organization	94	14	5.35	8.40E-04	1.16E-02
GO:0055065	metal ion homeostasis	499	46	28.41	8.60E-04	1.18E-02
GO:0032928	regulation of superoxide anion generation	21	6	1.2	8.70E-04	1.20E-02
GO:0036473	cell death in response to oxidative stress	84	13	4.78	8.80E-04	1.21E-02
GO:0070848	response to growth factor	669	58	38.09	9.00E-04	1.23E-02
GO:0018208	peptidyl-proline modification	37	8	2.11	9.40E-04	1.28E-02

Supplementary Table S2A: Significant gene ontology categories for expressed genes in MKs

GO.ID	Term	Annotated	Significant	Expected	pval	qval
GO:0032506	cytokinetic process	37	8	2.11	9.40E-04	1.28E-02
GO:0023051	regulation of signaling	3400	232	193.57	9.40E-04	1.28E-02
GO:0006468	protein phosphorylation	1727	128	98.32	9.50E-04	1.30E-02
GO:0032446	protein modification by small protein conjugation	816	68	46.46	9.70E-04	1.32E-02
GO:0050690	regulation of defense response to virus by virus	29	7	1.65	9.80E-04	1.33E-02
GO:0061462	protein localization to lysosome	29	7	1.65	9.80E-04	1.33E-02
GO:1902230	negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage	29	7	1.65	9.80E-04	1.33E-02
GO:0010950	positive regulation of endopeptidase activity	152	19	8.65	1.03E-03	1.39E-02
GO:0051017	actin filament bundle assembly	129	17	7.34	1.03E-03	1.39E-02
GO:0061572	actin filament bundle organization	129	17	7.34	1.03E-03	1.39E-02
GO:0019043	establishment of viral latency	9	4	0.51	1.04E-03	1.40E-02
GO:0071803	positive regulation of podosome assembly	9	4	0.51	1.04E-03	1.40E-02
GO:1904667	negative regulation of ubiquitin protein ligase activity	9	4	0.51	1.04E-03	1.40E-02
GO:0030518	intracellular steroid hormone receptor signaling pathway	118	16	6.72	1.05E-03	1.41E-02
GO:0032502	developmental process	5591	362	318.3	1.07E-03	1.44E-02
GO:0051284	positive regulation of sequestering of calcium ion	15	5	0.85	1.10E-03	1.47E-02
GO:1990000	amyloid fibril formation	15	5	0.85	1.10E-03	1.47E-02
GO:0019220	regulation of phosphate metabolic process	1562	117	88.93	1.10E-03	1.47E-02
GO:0010324	membrane invagination	56	10	3.19	1.11E-03	1.49E-02
GO:0033622	integrin activation	22	6	1.25	1.14E-03	1.52E-02
GO:0042255	ribosome assembly	22	6	1.25	1.14E-03	1.52E-02
GO:0051174	regulation of phosphorus metabolic process	1564	117	89.04	1.15E-03	1.53E-02
GO:0019674	NAD metabolic process	66	11	3.76	1.16E-03	1.54E-02
GO:1900024	regulation of substrate adhesion-dependent cell spreading	47	9	2.68	1.16E-03	1.54E-02
GO:0000413	protein peptidyl-prolyl isomerization	30	7	1.71	1.22E-03	1.62E-02
GO:0032435	negative regulation of proteasomal ubiquitin-dependent protein catabolic process	30	7	1.71	1.22E-03	1.62E-02
GO:0006888	ER to Golgi vesicle-mediated transport	166	20	9.45	1.22E-03	1.62E-02
GO:0032434	regulation of proteasomal ubiquitin-dependent protein catabolic process	98	14	5.58	1.27E-03	1.68E-02
GO:0032392	DNA geometric change	77	12	4.38	1.29E-03	1.71E-02
GO:0006839	mitochondrial transport	191	22	10.87	1.30E-03	1.72E-02
GO:1903201	regulation of oxidative stress-induced cell death	67	11	3.81	1.31E-03	1.73E-02
GO:0044344	cellular response to fibroblast growth factor stimulus	132	17	7.51	1.34E-03	1.77E-02
GO:0035036	sperm-egg recognition	48	9	2.73	1.36E-03	1.78E-02
GO:1901799	negative regulation of proteasomal protein catabolic process	48	9	2.73	1.36E-03	1.78E-02
GO:0007584	response to nutrient	204	23	11.61	1.36E-03	1.78E-02
GO:2001236	regulation of extrinsic apoptotic signaling pathway	144	18	8.2	1.38E-03	1.81E-02
GO:0010646	regulation of cell communication	3358	228	191.18	1.39E-03	1.82E-02
GO:0006289	nucleotide-excision repair	99	14	5.64	1.41E-03	1.84E-02
GO:0010038	response to metal ion	320	32	18.22	1.41E-03	1.84E-02
GO:0099131	ATP hydrolysis coupled ion transmembrane transport	23	6	1.31	1.46E-03	1.90E-02
GO:0098662	inorganic cation transmembrane transport	583	51	33.19	1.49E-03	1.93E-02
GO:0032801	receptor catabolic process	31	7	1.76	1.49E-03	1.93E-02
GO:0035088	establishment or maintenance of apical/basal cell polarity	31	7	1.76	1.49E-03	1.93E-02
GO:0061245	establishment or maintenance of bipolar cell polarity	31	7	1.76	1.49E-03	1.93E-02
GO:0010557	positive regulation of macromolecule biosynthetic process	1607	119	91.49	1.50E-03	1.95E-02
GO:0051049	regulation of transport	1670	123	95.08	1.52E-03	1.97E-02
GO:0051444	negative regulation of ubiquitin-protein transferase activity	16	5	0.91	1.52E-03	1.97E-02
GO:1901617	organic hydroxy compound biosynthetic process	231	25	13.15	1.54E-03	1.99E-02
GO:0010639	negative regulation of organelle organization	322	32	18.33	1.56E-03	2.01E-02
GO:0007566	embryo implantation	49	9	2.79	1.58E-03	2.04E-02
GO:0006396	RNA processing	1102	86	62.74	1.63E-03	2.10E-02
GO:0006066	alcohol metabolic process	323	32	18.39	1.64E-03	2.11E-02
GO:0009162	deoxyribonucleoside monophosphate metabolic process	10	4	0.57	1.66E-03	2.12E-02
GO:0019042	viral latency	10	4	0.57	1.66E-03	2.12E-02
GO:0019321	pentose metabolic process	10	4	0.57	1.66E-03	2.12E-02
GO:0032070	regulation of deoxyribonuclease activity	10	4	0.57	1.66E-03	2.12E-02
GO:0035646	endosome to melanosome transport	10	4	0.57	1.66E-03	2.12E-02
GO:0043485	endosome to pigment granule transport	10	4	0.57	1.66E-03	2.12E-02
GO:0048757	pigment granule maturation	10	4	0.57	1.66E-03	2.12E-02
GO:0060315	negative regulation of ryanodine-sensitive calcium-release channel activity	10	4	0.57	1.66E-03	2.12E-02
GO:0006801	superoxide metabolic process	59	10	3.36	1.68E-03	2.13E-02
GO:0032418	lysosome localization	59	10	3.36	1.68E-03	2.13E-02
GO:0140029	exocytic process	59	10	3.36	1.68E-03	2.13E-02
GO:0007021	tubulin complex assembly	5	3	0.28	1.69E-03	2.13E-02
GO:0010572	positive regulation of platelet activation	5	3	0.28	1.69E-03	2.13E-02
GO:0031536	positive regulation of exit from mitosis	5	3	0.28	1.69E-03	2.13E-02
GO:0044501	modulation of signal transduction in other organism	5	3	0.28	1.69E-03	2.13E-02
GO:0052250	modulation of signal transduction in other organism involved in symbiotic interaction	5	3	0.28	1.69E-03	2.13E-02
GO:1902177	positive regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	5	3	0.28	1.69E-03	2.13E-02
GO:0051101	regulation of DNA binding	112	15	6.38	1.69E-03	2.13E-02
GO:0009725	response to hormone	880	71	50.1	1.78E-03	2.24E-02
GO:0070647	protein modification by small protein conjugation or removal	970	77	55.22	1.80E-03	2.26E-02
GO:0051656	establishment of organelle localization	420	39	23.91	1.82E-03	2.28E-02
GO:0010823	negative regulation of mitochondrion organization	50	9	2.85	1.83E-03	2.29E-02
GO:0045807	positive regulation of endocytosis	136	17	7.74	1.85E-03	2.32E-02
GO:0000303	response to superoxide	24	6	1.37	1.86E-03	2.32E-02
GO:0090662	ATP hydrolysis coupled transmembrane transport	24	6	1.37	1.86E-03	2.32E-02
GO:1902410	mitotic cytokinetic process	24	6	1.37	1.86E-03	2.32E-02
GO:0016050	vesicle organization	260	27	14.8	1.88E-03	2.34E-02
GO:0033143	regulation of intracellular steroid hormone receptor signaling pathway	70	11	3.99	1.89E-03	2.35E-02

Supplementary Table S2A: Significant gene ontology categories for expressed genes in MKs

GO.ID	Term	Annotated	Significant	Expected	pval	qval
GO:0002437	inflammatory response to antigenic stimulus	41	8	2.33	1.91E-03	2.37E-02
GO:0036498	IRE1-mediated unfolded protein response	60	10	3.42	1.91E-03	2.37E-02
GO:0002009	morphogenesis of an epithelium	506	45	28.81	2.01E-03	2.49E-02
GO:0033138	positive regulation of peptidyl-serine phosphorylation	81	12	4.61	2.02E-03	2.50E-02
GO:0001101	response to acid chemical	314	31	17.88	2.03E-03	2.51E-02
GO:0043555	regulation of translation in response to stress	17	5	0.97	2.06E-03	2.54E-02
GO:0045947	negative regulation of translational initiation	17	5	0.97	2.06E-03	2.54E-02
GO:0048025	negative regulation of mRNA splicing, via spliceosome	17	5	0.97	2.06E-03	2.54E-02
GO:1902165	regulation of intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	17	5	0.97	2.06E-03	2.54E-02
GO:0030218	erythrocyte differentiation	103	14	5.86	2.07E-03	2.55E-02
GO:0048545	response to steroid hormone	355	34	20.21	2.10E-03	2.58E-02
GO:0071902	positive regulation of protein serine/threonine kinase activity	302	30	17.19	2.16E-03	2.65E-02
GO:0071774	response to fibroblast growth factor	138	17	7.86	2.17E-03	2.66E-02
GO:0006487	protein N-linked glycosylation	61	10	3.47	2.17E-03	2.66E-02
GO:0006007	glucose catabolic process	33	7	1.88	2.20E-03	2.68E-02
GO:0061077	chaperone-mediated protein folding	33	7	1.88	2.20E-03	2.68E-02
GO:0072665	protein localization to vacuole	33	7	1.88	2.20E-03	2.68E-02
GO:0090322	regulation of superoxide metabolic process	33	7	1.88	2.20E-03	2.68E-02
GO:1901030	positive regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling...	33	7	1.88	2.20E-03	2.68E-02
GO:0009891	positive regulation of biosynthetic process	1735	126	98.78	2.21E-03	2.69E-02
GO:0030834	regulation of actin filament depolymerization	42	8	2.39	2.24E-03	2.72E-02
GO:0016567	protein ubiquitination	740	61	42.13	2.25E-03	2.73E-02
GO:0071417	cellular response to organonitrogen compound	538	47	30.63	2.30E-03	2.79E-02
GO:0070997	neuron death	330	32	18.79	2.31E-03	2.80E-02
GO:2001020	regulation of response to DNA damage stimulus	175	20	9.96	2.32E-03	2.81E-02
GO:0000305	response to oxygen radical	25	6	1.42	2.33E-03	2.81E-02
GO:0050686	negative regulation of mRNA processing	25	6	1.42	2.33E-03	2.81E-02
GO:0060765	regulation of androgen receptor signaling pathway	25	6	1.42	2.33E-03	2.81E-02
GO:1900739	regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	25	6	1.42	2.33E-03	2.81E-02
GO:1900740	positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling...	25	6	1.42	2.33E-03	2.81E-02
GO:0031328	positive regulation of cellular biosynthetic process	1707	124	97.18	2.37E-03	2.85E-02
GO:0031100	animal organ regeneration	72	11	4.1	2.39E-03	2.87E-02
GO:0048678	response to axon injury	72	11	4.1	2.39E-03	2.87E-02
GO:0072332	intrinsic apoptotic signaling pathway by p53 class mediator	72	11	4.1	2.39E-03	2.87E-02
GO:0006469	negative regulation of protein kinase activity	213	23	12.13	2.40E-03	2.87E-02
GO:0033993	response to lipid	846	68	48.16	2.43E-03	2.90E-02
GO:0006879	cellular iron ion homeostasis	52	9	2.96	2.43E-03	2.90E-02
GO:1903312	negative regulation of mRNA metabolic process	62	10	3.53	2.46E-03	2.94E-02
GO:0043436	oxoacid metabolic process	1027	80	58.47	2.47E-03	2.95E-02
GO:0000041	transition metal ion transport	83	12	4.73	2.49E-03	2.95E-02
GO:0030901	midbrain development	83	12	4.73	2.49E-03	2.95E-02
GO:0031532	actin cytoskeleton reorganization	83	12	4.73	2.49E-03	2.95E-02
GO:0002679	respiratory burst involved in defense response	11	4	0.63	2.49E-03	2.95E-02
GO:0043476	pigment accumulation	11	4	0.63	2.49E-03	2.95E-02
GO:0043482	cellular pigment accumulation	11	4	0.63	2.49E-03	2.95E-02
GO:0090151	establishment of protein localization to mitochondrial membrane	11	4	0.63	2.49E-03	2.95E-02
GO:0007044	cell-substrate junction assembly	94	13	5.35	2.52E-03	2.98E-02
GO:0006082	organic acid metabolic process	1043	81	59.38	2.52E-03	2.98E-02
GO:0006464	cellular protein modification process	3563	238	202.85	2.56E-03	3.02E-02
GO:0036211	protein modification process	3563	238	202.85	2.56E-03	3.02E-02
GO:1990090	cellular response to nerve growth factor stimulus	43	8	2.45	2.62E-03	3.08E-02
GO:1900026	positive regulation of substrate adhesion-dependent cell spreading	34	7	1.94	2.63E-03	3.09E-02
GO:0033157	regulation of intracellular protein transport	202	22	11.5	2.65E-03	3.11E-02
GO:0071214	cellular response to abiotic stimulus	293	29	16.68	2.68E-03	3.14E-02
GO:0104004	cellular response to environmental stimulus	293	29	16.68	2.68E-03	3.14E-02
GO:0030220	platelet formation	18	5	1.02	2.72E-03	3.17E-02
GO:0032516	positive regulation of phosphoprotein phosphatase activity	18	5	1.02	2.72E-03	3.17E-02
GO:0036344	platelet morphogenesis	18	5	1.02	2.72E-03	3.17E-02
GO:0042276	error-prone translesion synthesis	18	5	1.02	2.72E-03	3.17E-02
GO:0071243	cellular response to arsenic-containing substance	18	5	1.02	2.72E-03	3.17E-02
GO:0010810	regulation of cell-substrate adhesion	190	21	10.82	2.75E-03	3.20E-02
GO:2001237	negative regulation of extrinsic apoptotic signaling pathway	95	13	5.41	2.77E-03	3.22E-02
GO:0097191	extrinsic apoptotic signaling pathway	203	22	11.56	2.82E-03	3.28E-02
GO:0015949	nucleobase-containing small molecule interconversion	26	6	1.48	2.89E-03	3.36E-02
GO:0030193	regulation of blood coagulation	74	11	4.21	2.98E-03	3.46E-02
GO:0051052	regulation of DNA metabolic process	363	34	20.67	3.02E-03	3.49E-02
GO:0007179	transforming growth factor beta receptor signaling pathway	179	20	10.19	3.02E-03	3.49E-02
GO:0034383	low-density lipoprotein particle clearance	44	8	2.5	3.04E-03	3.51E-02
GO:0046364	monosaccharide biosynthetic process	85	12	4.84	3.05E-03	3.52E-02
GO:1904029	regulation of cyclin-dependent protein kinase activity	85	12	4.84	3.05E-03	3.52E-02
GO:0050900	leukocyte migration	391	36	22.26	3.08E-03	3.55E-02
GO:0045860	positive regulation of protein kinase activity	475	42	27.04	3.09E-03	3.56E-02
GO:0015682	ferric iron transport	35	7	1.99	3.13E-03	3.59E-02
GO:0033572	transferrin transport	35	7	1.99	3.13E-03	3.59E-02
GO:0051973	positive regulation of telomerase activity	35	7	1.99	3.13E-03	3.59E-02
GO:0072512	trivalent inorganic cation transport	35	7	1.99	3.13E-03	3.59E-02
GO:0006620	posttranslational protein targeting to endoplasmic reticulum membrane	6	3	0.34	3.23E-03	3.68E-02
GO:0032415	regulation of sodium:proton antiporter activity	6	3	0.34	3.23E-03	3.68E-02
GO:0034112	positive regulation of homotypic cell-cell adhesion	6	3	0.34	3.23E-03	3.68E-02
GO:1902416	positive regulation of mRNA binding	6	3	0.34	3.23E-03	3.68E-02

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GO.ID	Term	Annotated	Significant	Expected	pval	qval
GO:1905323	telomerase holoenzyme complex assembly	6	3	0.34	3.23E-03	3.68E-02
GO:1905475	regulation of protein localization to membrane	168	19	9.56	3.31E-03	3.76E-02
GO:0051279	regulation of release of sequestered calcium ion into cytosol	75	11	4.27	3.31E-03	3.76E-02
GO:1900046	regulation of hemostasis	75	11	4.27	3.31E-03	3.76E-02
GO:0098655	cation transmembrane transport	665	55	37.86	3.39E-03	3.85E-02
GO:0048513	animal organ development	3201	215	182.24	3.39E-03	3.85E-02
GO:0050867	positive regulation of cell activation	298	29	16.97	3.43E-03	3.88E-02
GO:0033673	negative regulation of kinase activity	232	24	13.21	3.43E-03	3.88E-02
GO:0006520	cellular amino acid metabolic process	325	31	18.5	3.43E-03	3.88E-02
GO:0019430	removal of superoxide radicals	19	5	1.08	3.52E-03	3.97E-02
GO:0030042	actin filament depolymerization	45	8	2.56	3.52E-03	3.97E-02
GO:0006739	NADP metabolic process	27	6	1.54	3.53E-03	3.97E-02
GO:0045197	establishment or maintenance of epithelial cell apical/basal polarity	27	6	1.54	3.53E-03	3.97E-02
GO:0051385	response to mineralocorticoid	27	6	1.54	3.53E-03	3.97E-02
GO:0005513	detection of calcium ion	12	4	0.68	3.57E-03	4.00E-02
GO:0006595	polyamine metabolic process	12	4	0.68	3.57E-03	4.00E-02
GO:0051238	sequestering of metal ion	12	4	0.68	3.57E-03	4.00E-02
GO:0051645	Golgi localization	12	4	0.68	3.57E-03	4.00E-02
GO:0007160	cell-matrix adhesion	207	22	11.78	3.58E-03	4.01E-02
GO:0002694	regulation of leukocyte activation	465	41	26.47	3.62E-03	4.05E-02
GO:1901654	response to ketone	182	20	10.36	3.66E-03	4.09E-02
GO:0045652	regulation of megakaryocyte differentiation	76	11	4.33	3.68E-03	4.10E-02
GO:1905897	regulation of response to endoplasmic reticulum stress	76	11	4.33	3.68E-03	4.10E-02
GO:0042769	DNA damage response, detection of DNA damage	36	7	2.05	3.70E-03	4.10E-02
GO:0043403	skeletal muscle tissue regeneration	36	7	2.05	3.70E-03	4.10E-02
GO:0048488	synaptic vesicle endocytosis	36	7	2.05	3.70E-03	4.10E-02
GO:0140238	presynaptic endocytosis	36	7	2.05	3.70E-03	4.10E-02
GO:1905521	regulation of macrophage migration	36	7	2.05	3.70E-03	4.10E-02
GO:0044087	regulation of cellular component biogenesis	817	65	46.51	3.80E-03	4.21E-02
GO:0007569	cell aging	110	14	6.26	3.82E-03	4.23E-02
GO:0006281	DNA repair	453	40	25.79	3.92E-03	4.33E-02
GO:1901983	regulation of protein acetylation	66	10	3.76	3.94E-03	4.35E-02
GO:0071496	cellular response to external stimulus	301	29	17.14	3.95E-03	4.36E-02
GO:0001932	regulation of protein phosphorylation	1246	93	70.94	3.97E-03	4.38E-02
GO:0006415	translational termination	99	13	5.64	3.98E-03	4.38E-02
GO:0043270	positive regulation of ion transport	248	25	14.12	4.02E-03	4.42E-02
GO:0000731	DNA synthesis involved in DNA repair	46	8	2.62	4.05E-03	4.45E-02
GO:1990089	response to nerve growth factor	46	8	2.62	4.05E-03	4.45E-02
GO:1900407	regulation of cellular response to oxidative stress	77	11	4.38	4.08E-03	4.48E-02
GO:1903749	positive regulation of establishment of protein localization to mitochondrion	56	9	3.19	4.09E-03	4.48E-02
GO:0010256	endomembrane system organization	343	32	19.53	4.17E-03	4.57E-02
GO:0007050	cell cycle arrest	223	23	12.7	4.27E-03	4.67E-02
GO:0019985	translesion synthesis	37	7	2.11	4.35E-03	4.75E-02
GO:1903146	regulation of autophagy of mitochondrion	37	7	2.11	4.35E-03	4.75E-02
GO:0009988	cell-cell recognition	67	10	3.81	4.40E-03	4.80E-02
GO:0008630	intrinsic apoptotic signaling pathway in response to DNA damage	89	12	5.07	4.48E-03	4.87E-02
GO:0000717	nucleotide-excision repair, DNA duplex unwinding	20	5	1.14	4.48E-03	4.87E-02
GO:0010801	negative regulation of peptidyl-threonine phosphorylation	20	5	1.14	4.48E-03	4.87E-02
GO:0032986	protein-DNA complex disassembly	20	5	1.14	4.48E-03	4.87E-02
GO:1903322	positive regulation of protein modification by small protein conjugation or removal	112	14	6.38	4.50E-03	4.88E-02
GO:0050818	regulation of coagulation	78	11	4.44	4.51E-03	4.89E-02
GO:0030705	cytoskeleton-dependent intracellular transport	148	17	8.43	4.52E-03	4.89E-02
GO:0042325	regulation of phosphorylation	1377	101	78.39	4.56E-03	4.93E-02
GO:0051291	protein heterooligomerization	124	15	7.06	4.57E-03	4.94E-02
GO:0098660	inorganic ion transmembrane transport	660	54	37.57	4.58E-03	4.95E-02

Supplementary Table S2B: Significant gene ontology categories for expressed genes in platelets

GO.ID	Term	Annotated	Significant	Expected	pval	qval
GO:0045055	regulated exocytosis	724	86	20.06	1.00E-30	5.48E-27
GO:0006887	exocytosis	809	90	22.42	1.00E-30	5.48E-27
GO:0016192	vesicle-mediated transport	1728	135	47.89	1.50E-30	5.48E-27
GO:0051179	localization	5680	260	157.41	6.60E-24	1.81E-20
GO:0006810	transport	4395	220	121.8	8.50E-24	1.86E-20
GO:0051234	establishment of localization	4501	223	124.74	1.30E-23	2.37E-20
GO:0001775	cell activation	1268	102	35.14	1.70E-23	2.66E-20
GO:0002576	platelet degranulation	118	31	3.27	5.50E-22	7.53E-19
GO:0042060	wound healing	522	61	14.47	6.50E-22	7.91E-19
GO:0009611	response to wounding	630	66	17.46	4.70E-21	5.15E-18
GO:0046903	secretion	1493	107	41.38	9.40E-21	9.36E-18
GO:0032940	secretion by cell	1368	101	37.91	1.80E-20	1.64E-17
GO:0007596	blood coagulation	317	45	8.79	1.10E-19	9.27E-17
GO:0007599	hemostasis	321	45	8.9	1.80E-19	1.41E-16
GO:0050817	coagulation	322	45	8.92	2.10E-19	1.53E-16
GO:0002446	neutrophil mediated immunity	475	54	13.16	6.50E-19	4.19E-16
GO:0042119	neutrophil activation	475	54	13.16	6.50E-19	4.19E-16
GO:0043312	neutrophil degranulation	461	53	12.78	8.50E-19	5.18E-16
GO:0002283	neutrophil activation involved in immune response	464	53	12.86	1.10E-18	6.34E-16
GO:0036230	granulocyte activation	482	54	13.36	1.30E-18	7.12E-16
GO:0002274	myeloid leukocyte activation	618	61	17.13	3.30E-18	1.72E-15
GO:0002444	myeloid leukocyte mediated immunity	522	55	14.47	9.60E-18	4.76E-15
GO:0043299	leukocyte degranulation	505	54	14	1.00E-17	4.76E-15
GO:0070527	platelet aggregation	56	20	1.55	1.50E-17	6.85E-15
GO:0002275	myeloid cell activation involved in immune response	515	54	14.27	2.40E-17	1.05E-14
GO:0030168	platelet activation	145	29	4.02	3.90E-17	1.64E-14
GO:0051641	cellular localization	2356	131	65.29	4.30E-16	1.75E-13
GO:0034109	homotypic cell-cell adhesion	74	21	2.05	4.80E-16	1.88E-13
GO:0002376	immune system process	2684	142	74.38	9.80E-16	3.70E-13
GO:0050878	regulation of body fluid levels	475	49	13.16	1.60E-15	5.84E-13
GO:0002263	cell activation involved in immune response	651	58	18.04	2.60E-15	9.19E-13
GO:0002443	leukocyte mediated immunity	713	61	19.76	2.90E-15	9.93E-13
GO:0002366	leukocyte activation involved in immune response	648	57	17.96	8.00E-15	2.66E-12
GO:0045321	leukocyte activation	1122	78	31.09	2.60E-14	8.38E-12
GO:0002252	immune effector process	1076	75	29.82	7.80E-14	2.44E-11
GO:0034613	cellular protein localization	1442	90	39.96	1.10E-13	3.35E-11
GO:0070727	cellular macromolecule localization	1449	90	40.16	1.40E-13	4.15E-11
GO:0008104	protein localization	2265	121	62.77	1.70E-13	4.90E-11
GO:0033036	macromolecule localization	2563	131	71.03	3.10E-13	8.71E-11
GO:0065008	regulation of biological quality	3417	160	94.7	3.80E-13	1.04E-10
GO:0044419	interspecies interaction between organisms	873	64	24.19	7.50E-13	2.00E-10
GO:0098657	import into cell	660	54	18.29	8.20E-13	2.14E-10
GO:0044403	symbiont process	831	62	23.03	8.40E-13	2.14E-10
GO:0046907	intracellular transport	1421	87	39.38	9.10E-13	2.27E-10
GO:0006897	endocytosis	586	50	16.24	1.30E-12	3.17E-10
GO:0072657	protein localization to membrane	511	46	14.16	1.70E-12	4.05E-10
GO:0009056	catabolic process	2172	114	60.19	3.70E-12	8.63E-10
GO:0051649	establishment of localization in cell	1773	99	49.14	4.40E-12	1.00E-09
GO:0044248	cellular catabolic process	1926	104	53.38	8.30E-12	1.86E-09
GO:0006413	translational initiation	170	25	4.71	8.50E-12	1.86E-09
GO:0022607	cellular component assembly	2516	125	69.73	1.00E-11	2.15E-09
GO:0050896	response to stimulus	7976	290	221.04	1.40E-11	2.95E-09
GO:0016032	viral process	772	56	21.39	3.70E-11	7.65E-09
GO:0044085	cellular component biogenesis	2682	129	74.33	4.00E-11	8.12E-09
GO:0090150	establishment of protein localization to membrane	262	30	7.26	4.60E-11	9.17E-09
GO:0070887	cellular response to chemical stimulus	2925	137	81.06	4.90E-11	9.59E-09
GO:0006955	immune response	1823	98	50.52	5.20E-11	1.00E-08
GO:0051128	regulation of cellular component organization	2181	111	60.44	5.50E-11	1.04E-08
GO:0032879	regulation of localization	2500	122	69.28	6.70E-11	1.24E-08
GO:0033365	protein localization to organelle	742	54	20.56	7.50E-11	1.37E-08
GO:0071702	organic substance transport	2270	113	62.91	1.40E-10	2.47E-08
GO:0071840	cellular component organization or biogenesis	5415	214	150.07	1.40E-10	2.47E-08
GO:0016043	cellular component organization	5288	210	146.55	1.60E-10	2.78E-08
GO:0072594	establishment of protein localization to organelle	423	38	11.72	1.80E-10	3.08E-08
GO:0070972	protein localization to endoplasmic reticulum	117	19	3.24	5.00E-10	8.43E-08
GO:0050790	regulation of catalytic activity	1987	101	55.07	5.80E-10	9.63E-08
GO:0071705	nitrogen compound transport	1907	98	52.85	6.30E-10	1.03E-07
GO:0045184	establishment of protein localization	1691	90	46.86	6.70E-10	1.08E-07
GO:1901575	organic substance catabolic process	1800	94	49.88	6.80E-10	1.08E-07
GO:0006950	response to stress	3494	152	96.83	6.90E-10	1.08E-07
GO:0030036	actin cytoskeleton organization	526	42	14.58	7.30E-10	1.13E-07
GO:0051716	cellular response to stimulus	6378	239	176.76	9.30E-10	1.42E-07
GO:0042886	amide transport	1649	88	45.7	9.50E-10	1.43E-07
GO:0009057	macromolecule catabolic process	1136	68	31.48	1.10E-09	1.63E-07
GO:0045047	protein targeting to ER	97	17	2.69	1.20E-09	1.75E-07
GO:0006605	protein targeting	337	32	9.34	1.30E-09	1.87E-07
GO:0006996	organelle organization	3069	137	85.05	1.40E-09	1.99E-07
GO:0060341	regulation of cellular localization	807	54	22.36	1.60E-09	2.25E-07
GO:0015031	protein transport	1589	85	44.04	1.80E-09	2.50E-07
GO:0030029	actin filament-based process	629	46	17.43	1.90E-09	2.60E-07

Supplementary Table S2B: Significant gene ontology categories for expressed genes in platelets

GO.ID	Term	Annotated	Significant	Expected	pval	qval
GO:0015833	peptide transport	1620	86	44.9	2.00E-09	2.71E-07
GO:0072599	establishment of protein localization to endoplasmic reticulum	101	17	2.8	2.30E-09	3.07E-07
GO:0006886	intracellular protein transport	778	52	21.56	3.50E-09	4.62E-07
GO:0006614	SRP-dependent cotranslational protein targeting to membrane	92	16	2.55	4.20E-09	5.48E-07
GO:0006613	cotranslational protein targeting to membrane	95	16	2.63	6.90E-09	8.90E-07
GO:0097435	supramolecular fiber organization	512	39	14.19	1.10E-08	1.40E-06
GO:0065003	protein-containing complex assembly	1579	82	43.76	1.40E-08	1.76E-06
GO:0065009	regulation of molecular function	2860	126	79.26	2.10E-08	2.62E-06
GO:0050789	regulation of biological process	10213	336	283.04	2.80E-08	3.41E-06
GO:0061024	membrane organization	664	45	18.4	2.80E-08	3.41E-06
GO:0042221	response to chemical	4227	169	117.14	3.00E-08	3.61E-06
GO:0043933	protein-containing complex subunit organization	1858	91	51.49	3.20E-08	3.81E-06
GO:0006612	protein targeting to membrane	151	19	4.18	3.80E-08	4.48E-06
GO:0051049	regulation of transport	1670	84	46.28	3.90E-08	4.55E-06
GO:0021762	substantia nigra development	37	10	1.03	4.30E-08	4.91E-06
GO:0006909	phagocytosis	236	24	6.54	4.30E-08	4.91E-06
GO:1903827	regulation of cellular protein localization	474	36	13.14	4.60E-08	5.20E-06
GO:0048519	negative regulation of biological process	5075	194	140.65	4.70E-08	5.26E-06
GO:0043085	positive regulation of catalytic activity	1223	67	33.89	5.20E-08	5.76E-06
GO:0097581	lamellipodium organization	70	13	1.94	5.40E-08	5.92E-06
GO:0050794	regulation of cellular process	9281	311	257.21	5.60E-08	6.08E-06
GO:0008154	actin polymerization or depolymerization	155	19	4.3	5.90E-08	6.34E-06
GO:0048523	negative regulation of cellular process	4237	168	117.42	6.40E-08	6.81E-06
GO:0051246	regulation of protein metabolic process	2465	111	68.31	6.50E-08	6.85E-06
GO:0051704	multi-organism process	2290	105	63.46	6.70E-08	6.99E-06
GO:0055080	cation homeostasis	553	39	15.33	9.00E-08	9.30E-06
GO:0009719	response to endogenous stimulus	1488	76	41.24	1.10E-07	1.13E-05
GO:0098869	cellular oxidant detoxification	88	14	2.44	1.30E-07	1.32E-05
GO:0008219	cell death	2061	96	57.12	1.40E-07	1.41E-05
GO:0098771	inorganic ion homeostasis	565	39	15.66	1.60E-07	1.55E-05
GO:0008064	regulation of actin polymerization or depolymerization	133	17	3.69	1.60E-07	1.55E-05
GO:0043112	receptor metabolic process	165	19	4.57	1.60E-07	1.55E-05
GO:0019080	viral gene expression	182	20	5.04	1.60E-07	1.55E-05
GO:0030832	regulation of actin filament length	134	17	3.71	1.80E-07	1.72E-05
GO:0009894	regulation of catabolic process	853	51	23.64	1.80E-07	1.72E-05
GO:0097190	apoptotic signaling pathway	546	38	15.13	1.90E-07	1.80E-05
GO:0044265	cellular macromolecule catabolic process	931	54	25.8	2.00E-07	1.86E-05
GO:0051493	regulation of cytoskeleton organization	438	33	12.14	2.00E-07	1.86E-05
GO:0032268	regulation of cellular protein metabolic process	2287	103	63.38	2.30E-07	2.12E-05
GO:0030003	cellular cation homeostasis	488	35	13.52	2.80E-07	2.56E-05
GO:0048518	positive regulation of biological process	5298	197	146.83	3.20E-07	2.87E-05
GO:0010324	membrane invagination	56	11	1.55	3.20E-07	2.87E-05
GO:0055076	transition metal ion homeostasis	95	14	2.63	3.40E-07	3.00E-05
GO:0032880	regulation of protein localization	921	53	25.52	3.40E-07	3.00E-05
GO:0009636	response to toxic substance	471	34	13.05	3.60E-07	3.13E-05
GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	110	15	3.05	3.60E-07	3.13E-05
GO:0071310	cellular response to organic substance	2428	107	67.29	3.70E-07	3.14E-05
GO:0098609	cell-cell adhesion	726	45	20.12	3.70E-07	3.14E-05
GO:0065007	biological regulation	10751	345	297.95	3.70E-07	3.14E-05
GO:1990748	cellular detoxification	96	14	2.66	3.90E-07	3.29E-05
GO:0010035	response to inorganic substance	497	35	13.77	4.40E-07	3.68E-05
GO:0010033	response to organic substance	2960	124	82.03	5.00E-07	4.15E-05
GO:0006873	cellular ion homeostasis	501	35	13.88	5.30E-07	4.37E-05
GO:0140029	exocytic process	59	11	1.64	5.50E-07	4.50E-05
GO:0006936	muscle contraction	331	27	9.17	5.80E-07	4.71E-05
GO:0099024	plasma membrane invagination	48	10	1.33	6.10E-07	4.92E-05
GO:0060548	negative regulation of cell death	942	53	26.11	6.80E-07	5.44E-05
GO:0043254	regulation of protein complex assembly	376	29	10.42	7.10E-07	5.64E-05
GO:0006826	iron ion transport	49	10	1.36	7.50E-07	5.91E-05
GO:0006914	autophagy	442	32	12.25	7.60E-07	5.91E-05
GO:0061919	process utilizing autophagic mechanism	442	32	12.25	7.60E-07	5.91E-05
GO:0098754	detoxification	102	14	2.83	8.30E-07	6.41E-05
GO:0012501	programmed cell death	1938	89	53.71	8.50E-07	6.47E-05
GO:0032956	regulation of actin cytoskeleton organization	277	24	7.68	8.50E-07	6.47E-05
GO:0007229	integrin-mediated signaling pathway	88	13	2.44	8.70E-07	6.58E-05
GO:0043281	regulation of cysteine-type endopeptidase activity involved in apoptotic process	184	19	5.1	8.80E-07	6.61E-05
GO:0006915	apoptotic process	1797	84	49.8	9.10E-07	6.74E-05
GO:0050801	ion homeostasis	629	40	17.43	9.10E-07	6.74E-05
GO:0007015	actin filament organization	299	25	8.29	9.70E-07	7.13E-05
GO:1905475	regulation of protein localization to membrane	168	18	4.66	1.00E-06	7.31E-05
GO:0051336	regulation of hydrolase activity	1086	58	30.1	1.10E-06	7.88E-05
GO:0006518	peptide metabolic process	755	45	20.92	1.10E-06	7.88E-05
GO:0046916	cellular transition metal ion homeostasis	76	12	2.11	1.10E-06	7.88E-05
GO:0010941	regulation of cell death	1558	75	43.18	1.30E-06	9.25E-05
GO:0055065	metal ion homeostasis	499	34	13.83	1.40E-06	9.77E-05
GO:1902905	positive regulation of supramolecular fiber organization	172	18	4.77	1.40E-06	9.77E-05
GO:1902903	regulation of supramolecular fiber organization	285	24	7.9	1.40E-06	9.77E-05
GO:0033043	regulation of organelle organization	1071	57	29.68	1.50E-06	1.03E-04
GO:0044093	positive regulation of molecular function	1536	74	42.57	1.50E-06	1.03E-04
GO:0006446	regulation of translational initiation	66	11	1.83	1.80E-06	1.23E-04

Supplementary Table S2B: Significant gene ontology categories for expressed genes in platelets

GO.ID	Term	Annotated	Significant	Expected	pval	qval
GO:0044267	cellular protein metabolic process	4512	170	125.04	1.80E-06	1.23E-04
GO:0030032	lamellipodium assembly	54	10	1.5	1.90E-06	1.29E-04
GO:0071495	cellular response to endogenous stimulus	1243	63	34.45	2.00E-06	1.34E-04
GO:0006898	receptor-mediated endocytosis	233	21	6.46	2.20E-06	1.47E-04
GO:0048857	neural nucleus development	55	10	1.52	2.30E-06	1.53E-04
GO:0055072	iron ion homeostasis	68	11	1.88	2.40E-06	1.57E-04
GO:0010506	regulation of autophagy	294	24	8.15	2.40E-06	1.57E-04
GO:0051051	negative regulation of transport	468	32	12.97	2.60E-06	1.69E-04
GO:0007010	cytoskeleton organization	1038	55	28.77	2.60E-06	1.69E-04
GO:0048878	chemical homeostasis	960	52	26.6	2.70E-06	1.74E-04
GO:0048522	positive regulation of cellular process	4675	174	129.56	2.80E-06	1.79E-04
GO:0043069	negative regulation of programmed cell death	860	48	23.83	3.00E-06	1.91E-04
GO:0031329	regulation of cellular catabolic process	760	44	21.06	3.10E-06	1.96E-04
GO:0060627	regulation of vesicle-mediated transport	450	31	12.47	3.20E-06	2.02E-04
GO:0032970	regulation of actin filament-based process	320	25	8.87	3.30E-06	2.07E-04
GO:0097193	intrinsic apoptotic signaling pathway	259	22	7.18	3.40E-06	2.12E-04
GO:0043066	negative regulation of apoptotic process	839	47	23.25	3.50E-06	2.17E-04
GO:0051130	positive regulation of cellular component organization	1102	57	30.54	3.60E-06	2.22E-04
GO:0052548	regulation of endopeptidase activity	343	26	9.51	3.70E-06	2.27E-04
GO:0030041	actin filament polymerization	132	15	3.66	3.80E-06	2.31E-04
GO:0042592	homeostatic process	1632	76	45.23	3.90E-06	2.36E-04
GO:0010942	positive regulation of cell death	668	40	18.51	4.00E-06	2.41E-04
GO:0019725	cellular homeostasis	768	44	21.28	4.10E-06	2.46E-04
GO:2001242	regulation of intrinsic apoptotic signaling pathway	150	16	4.16	4.20E-06	2.50E-04
GO:0040012	regulation of locomotion	950	51	26.33	4.40E-06	2.58E-04
GO:0030833	regulation of actin filament polymerization	117	14	3.24	4.40E-06	2.58E-04
GO:0032386	regulation of intracellular transport	368	27	10.2	4.40E-06	2.58E-04
GO:0019083	viral transcription	169	17	4.68	4.70E-06	2.73E-04
GO:0003012	muscle system process	436	30	12.08	4.70E-06	2.73E-04
GO:0051247	positive regulation of protein metabolic process	1443	69	39.99	4.80E-06	2.77E-04
GO:0043067	regulation of programmed cell death	1445	69	40.05	5.00E-06	2.87E-04
GO:0030162	regulation of proteolysis	650	39	18.01	5.10E-06	2.91E-04
GO:0006875	cellular metal ion homeostasis	439	30	12.17	5.40E-06	3.07E-04
GO:0019220	regulation of phosphate metabolic process	1562	73	43.29	5.50E-06	3.11E-04
GO:0044270	cellular nitrogen compound catabolic process	604	37	16.74	5.60E-06	3.15E-04
GO:2001233	regulation of apoptotic signaling pathway	373	27	10.34	5.70E-06	3.17E-04
GO:0051174	regulation of phosphorus metabolic process	1564	73	43.34	5.70E-06	3.17E-04
GO:0016477	cell migration	1312	64	36.36	5.90E-06	3.25E-04
GO:0110053	regulation of actin filament organization	209	19	5.79	5.90E-06	3.25E-04
GO:0032535	regulation of cellular component size	289	23	8.01	6.00E-06	3.29E-04
GO:0030334	regulation of cell migration	831	46	23.03	6.10E-06	3.33E-04
GO:2000116	regulation of cysteine-type endopeptidase activity	210	19	5.82	6.30E-06	3.42E-04
GO:0030838	positive regulation of actin filament polymerization	75	11	2.08	6.50E-06	3.51E-04
GO:0051640	organelle localization	584	36	16.18	6.60E-06	3.55E-04
GO:1901565	organonitrogen compound catabolic process	1045	54	28.96	6.80E-06	3.64E-04
GO:0034655	nucleobase-containing compound catabolic process	562	35	15.57	7.10E-06	3.78E-04
GO:0031324	negative regulation of cellular metabolic process	2250	96	62.36	7.20E-06	3.81E-04
GO:0030100	regulation of endocytosis	252	21	6.98	7.60E-06	4.00E-04
GO:0019068	virion assembly	38	8	1.05	7.70E-06	4.04E-04
GO:0051050	positive regulation of transport	891	48	24.69	7.80E-06	4.07E-04
GO:1901564	organonitrogen compound metabolic process	5942	209	164.67	7.90E-06	4.10E-04
GO:0015669	gas transport	19	6	0.53	8.70E-06	4.50E-04
GO:0051235	maintenance of location	275	22	7.62	8.90E-06	4.58E-04
GO:1903828	negative regulation of cellular protein localization	108	13	2.99	9.00E-06	4.61E-04
GO:0006911	phagocytosis, engulfment	39	8	1.08	9.40E-06	4.79E-04
GO:0042981	regulation of apoptotic process	1419	67	39.33	1.00E-05	5.07E-04
GO:0043269	regulation of ion transport	598	36	16.57	1.10E-05	5.50E-04
GO:0006879	cellular iron ion homeostasis	52	9	1.44	1.10E-05	5.50E-04
GO:1901700	response to oxygen-containing compound	1481	69	41.04	1.10E-05	5.50E-04
GO:0010959	regulation of metal ion transport	344	25	9.53	1.20E-05	5.84E-04
GO:0030335	positive regulation of cell migration	480	31	13.3	1.20E-05	5.84E-04
GO:0090066	regulation of anatomical structure size	411	28	11.39	1.20E-05	5.84E-04
GO:0000956	nuclear-transcribed mRNA catabolic process	181	17	5.02	1.20E-05	5.84E-04
GO:0051248	negative regulation of protein metabolic process	1039	53	28.79	1.20E-05	5.84E-04
GO:0007155	cell adhesion	1259	61	34.89	1.20E-05	5.84E-04
GO:0040017	positive regulation of locomotion	529	33	14.66	1.30E-05	6.19E-04
GO:1903034	regulation of response to wounding	164	16	4.54	1.30E-05	6.19E-04
GO:2000145	regulation of cell motility	883	47	24.47	1.30E-05	6.19E-04
GO:0048870	cell motility	1431	67	39.66	1.30E-05	6.19E-04
GO:0051674	localization of cell	1431	67	39.66	1.30E-05	6.19E-04
GO:0051172	negative regulation of nitrogen compound metabolic process	2105	90	58.34	1.40E-05	6.50E-04
GO:0097237	cellular response to toxic substance	222	19	6.15	1.40E-05	6.50E-04
GO:0019538	protein metabolic process	5028	181	139.34	1.40E-05	6.50E-04
GO:0052547	regulation of peptidase activity	370	26	10.25	1.40E-05	6.50E-04
GO:0022610	biological adhesion	1265	61	35.06	1.40E-05	6.50E-04
GO:0055082	cellular chemical homeostasis	630	37	17.46	1.40E-05	6.50E-04
GO:0034329	cell junction assembly	204	18	5.65	1.60E-05	7.40E-04
GO:0030834	regulation of actin filament depolymerization	42	8	1.16	1.70E-05	7.83E-04
GO:0031532	actin cytoskeleton reorganization	83	11	2.3	1.80E-05	8.25E-04
GO:0030163	protein catabolic process	739	41	20.48	1.90E-05	8.64E-04

Supplementary Table S2B: Significant gene ontology categories for expressed genes in platelets

GO.ID	Term	Annotated	Significant	Expected	pval	qval
GO:0048583	regulation of response to stimulus	3919	147	108.61	1.90E-05	8.64E-04
GO:0019439	aromatic compound catabolic process	615	36	17.04	2.00E-05	9.06E-04
GO:0044502	positive regulation of signal transduction in other organism	3	3	0.08	2.10E-05	9.28E-04
GO:0052470	modulation by host of symbiont signal transduction pathway	3	3	0.08	2.10E-05	9.28E-04
GO:0052525	positive regulation by host of symbiont signal transduction pathway	3	3	0.08	2.10E-05	9.28E-04
GO:0052526	positive regulation by organism of signal transduction in other organism involved in symbiotic inter...	3	3	0.08	2.10E-05	9.28E-04
GO:0075205	modulation by host of symbiont cAMP-mediated signal transduction	3	3	0.08	2.10E-05	9.28E-04
GO:0075206	positive regulation by host of symbiont cAMP-mediated signal transduction	3	3	0.08	2.10E-05	9.28E-04
GO:1901361	organic cyclic compound catabolic process	644	37	17.85	2.30E-05	1.01E-03
GO:0051258	protein polymerization	211	18	5.85	2.50E-05	1.07E-03
GO:0043068	positive regulation of programmed cell death	621	36	17.21	2.50E-05	1.07E-03
GO:0034622	cellular protein-containing complex assembly	826	44	22.89	2.50E-05	1.07E-03
GO:0061041	regulation of wound healing	136	14	3.77	2.50E-05	1.07E-03
GO:2000147	positive regulation of cell motility	499	31	13.83	2.50E-05	1.07E-03
GO:0051270	regulation of cellular component movement	959	49	26.58	2.50E-05	1.07E-03
GO:0010951	negative regulation of endopeptidase activity	192	17	5.32	2.60E-05	1.11E-03
GO:0051280	negative regulation of release of sequestered calcium ion into cytosol	14	5	0.39	2.60E-05	1.11E-03
GO:0051345	positive regulation of hydrolase activity	648	37	17.96	2.70E-05	1.14E-03
GO:0006928	movement of cell or subcellular component	1812	79	50.22	2.70E-05	1.14E-03
GO:2001243	negative regulation of intrinsic apoptotic signaling pathway	87	11	2.41	2.80E-05	1.18E-03
GO:0006402	mRNA catabolic process	318	23	8.81	2.80E-05	1.18E-03
GO:0030042	actin filament depolymerization	45	8	1.25	2.90E-05	1.21E-03
GO:1903076	regulation of protein localization to plasma membrane	88	11	2.44	3.10E-05	1.28E-03
GO:0010243	response to organonitrogen compound	886	46	24.55	3.10E-05	1.28E-03
GO:0046700	heterocycle catabolic process	603	35	16.71	3.10E-05	1.28E-03
GO:0043154	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	73	10	2.02	3.10E-05	1.28E-03
GO:0040011	locomotion	1646	73	45.62	3.30E-05	1.35E-03
GO:0007154	cell communication	5575	195	154.5	3.40E-05	1.39E-03
GO:0032270	positive regulation of cellular protein metabolic process	1359	63	37.66	3.40E-05	1.39E-03
GO:0006979	response to oxidative stress	413	27	11.45	3.50E-05	1.42E-03
GO:0031334	positive regulation of protein complex assembly	217	18	6.01	3.60E-05	1.46E-03
GO:0051014	actin filament severing	8	4	0.22	3.70E-05	1.48E-03
GO:0060316	positive regulation of ryanodine-sensitive calcium-release channel activity	8	4	0.22	3.70E-05	1.48E-03
GO:0034330	cell junction organization	259	20	7.18	3.70E-05	1.48E-03
GO:0015671	oxygen transport	15	5	0.42	3.80E-05	1.51E-03
GO:0051284	positive regulation of sequestering of calcium ion	15	5	0.42	3.80E-05	1.51E-03
GO:0043603	cellular amide metabolic process	975	49	27.02	3.90E-05	1.54E-03
GO:0023052	signaling	5555	194	153.95	4.00E-05	1.58E-03
GO:0043549	regulation of kinase activity	764	41	21.17	4.10E-05	1.61E-03
GO:0022411	cellular component disassembly	465	29	12.89	4.30E-05	1.68E-03
GO:0051272	positive regulation of cellular component movement	514	31	14.24	4.40E-05	1.72E-03
GO:0043065	positive regulation of apoptotic process	614	35	17.02	4.60E-05	1.79E-03
GO:0009987	cellular process	14228	418	394.31	4.70E-05	1.81E-03
GO:0044092	negative regulation of molecular function	1010	50	27.99	4.70E-05	1.81E-03
GO:0010562	positive regulation of phosphorus metabolic process	958	48	26.55	5.00E-05	1.92E-03
GO:0045937	positive regulation of phosphate metabolic process	958	48	26.55	5.00E-05	1.92E-03
GO:0045859	regulation of protein kinase activity	695	38	19.26	5.30E-05	2.02E-03
GO:0009605	response to external stimulus	2119	88	58.72	5.30E-05	2.02E-03
GO:0010466	negative regulation of peptidase activity	204	17	5.65	5.50E-05	2.09E-03
GO:0032271	regulation of protein polymerization	165	15	4.57	5.60E-05	2.12E-03
GO:0051924	regulation of calcium ion transport	227	18	6.29	6.50E-05	2.45E-03
GO:0007160	cell-matrix adhesion	207	17	5.74	6.70E-05	2.51E-03
GO:2001234	negative regulation of apoptotic signaling pathway	209	17	5.79	7.50E-05	2.81E-03
GO:0006812	cation transport	947	47	26.24	7.60E-05	2.83E-03
GO:0031399	regulation of protein modification process	1601	70	44.37	7.70E-05	2.86E-03
GO:2000117	negative regulation of cysteine-type endopeptidase activity	81	10	2.24	7.80E-05	2.89E-03
GO:0032269	negative regulation of cellular protein metabolic process	976	48	27.05	7.90E-05	2.91E-03
GO:0010800	positive regulation of peptidyl-threonine phosphorylation	27	6	0.75	7.90E-05	2.91E-03
GO:0045861	negative regulation of proteolysis	296	21	8.2	8.30E-05	3.03E-03
GO:0051343	positive regulation of cyclic-nucleotide phosphodiesterase activity	4	3	0.11	8.30E-05	3.03E-03
GO:1901698	response to nitrogen compound	951	47	26.36	8.40E-05	3.05E-03
GO:0007167	enzyme linked receptor protein signaling pathway	924	46	25.61	8.40E-05	3.05E-03
GO:0045010	actin nucleation	39	7	1.08	8.50E-05	3.07E-03
GO:0044087	regulation of cellular component biogenesis	817	42	22.64	8.60E-05	3.10E-03
GO:1903829	positive regulation of cellular protein localization	297	21	8.23	8.70E-05	3.13E-03
GO:0010038	response to metal ion	320	22	8.87	8.90E-05	3.19E-03
GO:0042325	regulation of phosphorylation	1377	62	38.16	9.20E-05	3.28E-03
GO:0000041	transition metal ion transport	83	10	2.3	9.60E-05	3.40E-03
GO:0030901	midbrain development	83	10	2.3	9.60E-05	3.40E-03
GO:0050900	leukocyte migration	391	25	10.84	9.70E-05	3.43E-03
GO:1903573	negative regulation of response to endoplasmic reticulum stress	40	7	1.11	1.00E-04	3.46E-03
GO:0010523	negative regulation of calcium ion transport into cytosol	18	5	0.5	1.00E-04	3.46E-03
GO:0042176	regulation of protein catabolic process	323	22	8.95	1.00E-04	3.46E-03
GO:0006401	RNA catabolic process	346	23	9.59	1.00E-04	3.46E-03
GO:0006508	proteolysis	1470	65	40.74	1.00E-04	3.46E-03
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	640	35	17.74	1.00E-04	3.46E-03
GO:0045807	positive regulation of endocytosis	136	13	3.77	1.00E-04	3.46E-03
GO:0031333	negative regulation of protein complex assembly	118	12	3.27	1.10E-04	3.76E-03
GO:0031667	response to nutrient levels	441	27	12.22	1.10E-04	3.76E-03
GO:0060315	negative regulation of ryanodine-sensitive calcium-release channel activity	10	4	0.28	1.10E-04	3.76E-03

Supplementary Table S2B: Significant gene ontology categories for expressed genes in platelets

GO.ID	Term	Annotated	Significant	Expected	pval	qval
GO:0006937	regulation of muscle contraction	156	14	4.32	1.10E-04	3.76E-03
GO:0007165	signal transduction	5132	179	142.22	1.20E-04	4.05E-03
GO:0051656	establishment of organelle localization	420	26	11.64	1.20E-04	4.05E-03
GO:1905476	negative regulation of protein localization to membrane	29	6	0.8	1.20E-04	4.05E-03
GO:0000910	cytokinesis	138	13	3.82	1.20E-04	4.05E-03
GO:0043043	peptide biosynthetic process	647	35	17.93	1.30E-04	4.36E-03
GO:0019058	viral life cycle	306	21	8.48	1.30E-04	4.36E-03
GO:0045860	positive regulation of protein kinase activity	475	28	13.16	1.50E-04	5.00E-03
GO:0043086	negative regulation of catalytic activity	705	37	19.54	1.50E-04	5.00E-03
GO:0007166	cell surface receptor signaling pathway	2589	101	71.75	1.60E-04	5.25E-03
GO:0032273	positive regulation of protein polymerization	105	11	2.91	1.60E-04	5.25E-03
GO:0006811	ion transport	1405	62	38.94	1.60E-04	5.25E-03
GO:0042327	positive regulation of phosphorylation	896	44	24.83	1.60E-04	5.25E-03
GO:0051016	barbed-end actin filament capping	11	4	0.3	1.60E-04	5.25E-03
GO:1904375	regulation of protein localization to cell periphery	106	11	2.94	1.70E-04	5.54E-03
GO:0048856	anatomical structure development	5235	181	145.08	1.70E-04	5.54E-03
GO:0032801	receptor catabolic process	31	6	0.86	1.80E-04	5.85E-03
GO:0010799	regulation of peptidyl-threonine phosphorylation	44	7	1.22	1.90E-04	6.12E-03
GO:0072659	protein localization to plasma membrane	226	17	6.26	1.90E-04	6.12E-03
GO:1904062	regulation of cation transmembrane transport	292	20	8.09	1.90E-04	6.12E-03
GO:0030193	regulation of blood coagulation	74	9	2.05	2.00E-04	6.33E-03
GO:0002682	regulation of immune system process	1416	62	39.24	2.00E-04	6.33E-03
GO:0022406	membrane docking	145	13	4.02	2.00E-04	6.33E-03
GO:0010572	positive regulation of platelet activation	5	3	0.14	2.00E-04	6.33E-03
GO:0044501	modulation of signal transduction in other organism	5	3	0.14	2.00E-04	6.33E-03
GO:0052250	modulation of signal transduction in other organism involved in symbiotic interaction	5	3	0.14	2.00E-04	6.33E-03
GO:0034766	negative regulation of ion transmembrane transport	91	10	2.52	2.10E-04	6.61E-03
GO:0009892	negative regulation of metabolic process	3025	114	83.83	2.10E-04	6.61E-03
GO:0035722	interleukin-12-mediated signaling pathway	45	7	1.25	2.20E-04	6.85E-03
GO:0033674	positive regulation of kinase activity	511	29	14.16	2.20E-04	6.85E-03
GO:1900046	regulation of hemostasis	75	9	2.08	2.20E-04	6.85E-03
GO:0051338	regulation of transferase activity	854	42	23.67	2.20E-04	6.85E-03
GO:0045936	negative regulation of phosphate metabolic process	538	30	14.91	2.30E-04	7.14E-03
GO:0010563	negative regulation of phosphorus metabolic process	539	30	14.94	2.40E-04	7.39E-03
GO:0005513	detection of calcium ion	12	4	0.33	2.40E-04	7.39E-03
GO:0051702	interaction with symbiont	76	9	2.11	2.40E-04	7.39E-03
GO:0035304	regulation of protein dephosphorylation	129	12	3.58	2.50E-04	7.67E-03
GO:0050849	negative regulation of calcium-mediated signaling	33	6	0.91	2.60E-04	7.94E-03
GO:1901021	positive regulation of calcium ion transmembrane transporter activity	33	6	0.91	2.60E-04	7.94E-03
GO:0051495	positive regulation of cytoskeleton organization	190	15	5.27	2.70E-04	8.20E-03
GO:0007044	cell-substrate junction assembly	94	10	2.61	2.70E-04	8.20E-03
GO:0032502	developmental process	5591	190	154.95	2.80E-04	8.36E-03
GO:0032799	low-density lipoprotein receptor particle metabolic process	22	5	0.61	2.80E-04	8.36E-03
GO:0033622	integrin activation	22	5	0.61	2.80E-04	8.36E-03
GO:0042744	hydrogen peroxide catabolic process	22	5	0.61	2.80E-04	8.36E-03
GO:0060314	regulation of ryanodine-sensitive calcium-release channel activity	22	5	0.61	2.80E-04	8.36E-03
GO:1903077	negative regulation of protein localization to plasma membrane	22	5	0.61	2.80E-04	8.36E-03
GO:0043271	negative regulation of ion transport	131	12	3.63	2.90E-04	8.59E-03
GO:0035303	regulation of dephosphorylation	191	15	5.29	2.90E-04	8.59E-03
GO:0071349	cellular response to interleukin-12	47	7	1.3	2.90E-04	8.59E-03
GO:1901879	regulation of protein depolymerization	62	8	1.72	3.00E-04	8.81E-03
GO:0050818	regulation of coagulation	78	9	2.16	3.00E-04	8.81E-03
GO:0006412	translation	624	33	17.29	3.00E-04	8.81E-03
GO:0009991	response to extracellular stimulus	471	27	13.05	3.10E-04	9.08E-03
GO:0007265	Ras protein signal transduction	303	20	8.4	3.20E-04	9.33E-03
GO:0031623	receptor internalization	96	10	2.66	3.20E-04	9.33E-03
GO:0048584	positive regulation of response to stimulus	2108	84	58.42	3.30E-04	9.57E-03
GO:0070671	response to interleukin-12	48	7	1.33	3.30E-04	9.57E-03
GO:0070201	regulation of establishment of protein localization	681	35	18.87	3.40E-04	9.81E-03
GO:0006098	pentose-phosphate shunt	13	4	0.36	3.40E-04	9.81E-03
GO:0031401	positive regulation of protein modification process	1040	48	28.82	3.50E-04	9.94E-03
GO:0034763	negative regulation of transmembrane transport	115	11	3.19	3.50E-04	9.94E-03
GO:0070838	divalent metal ion transport	425	25	11.78	3.50E-04	9.94E-03
GO:0032989	cellular component morphogenesis	900	43	24.94	3.50E-04	9.94E-03
GO:0009895	negative regulation of catabolic process	260	18	7.21	3.50E-04	9.94E-03
GO:0016050	vesicle organization	260	18	7.21	3.50E-04	9.94E-03
GO:0051239	regulation of multicellular organismal process	2938	110	81.42	3.70E-04	1.04E-02
GO:0031589	cell-substrate adhesion	307	20	8.51	3.70E-04	1.04E-02
GO:0034765	regulation of ion transmembrane transport	427	25	11.83	3.70E-04	1.04E-02
GO:0002687	positive regulation of leukocyte migration	116	11	3.21	3.80E-04	1.07E-02
GO:0072511	divalent inorganic cation transport	428	25	11.86	3.90E-04	1.09E-02
GO:0043604	amide biosynthetic process	767	38	21.26	3.90E-04	1.09E-02
GO:1902956	regulation of mitochondrial electron transport, NADH to ubiquinone	6	3	0.17	4.00E-04	1.12E-02
GO:0045862	positive regulation of proteolysis	309	20	8.56	4.10E-04	1.14E-02
GO:0001934	positive regulation of protein phosphorylation	852	41	23.61	4.20E-04	1.15E-02
GO:0071900	regulation of protein serine/threonine kinase activity	455	26	12.61	4.20E-04	1.15E-02
GO:0009725	response to hormone	880	42	24.39	4.20E-04	1.15E-02
GO:1902229	regulation of intrinsic apoptotic signaling pathway in response to DNA damage	36	6	1	4.20E-04	1.15E-02
GO:0051240	positive regulation of multicellular organismal process	1636	68	45.34	4.20E-04	1.15E-02
GO:0140056	organelle localization by membrane tethering	137	12	3.8	4.30E-04	1.18E-02

Supplementary Table S2B: Significant gene ontology categories for expressed genes in platelets

GO.ID	Term	Annotated	Significant	Expected	pval	qval
GO:1901701	cellular response to oxygen-containing compound	1022	47	28.32	4.40E-04	1.19E-02
GO:0034762	regulation of transmembrane transport	507	28	14.05	4.40E-04	1.19E-02
GO:0048169	regulation of long-term neuronal synaptic plasticity	24	5	0.67	4.40E-04	1.19E-02
GO:1904376	negative regulation of protein localization to cell periphery	24	5	0.67	4.40E-04	1.19E-02
GO:0120031	plasma membrane bounded cell projection assembly	457	26	12.66	4.50E-04	1.21E-02
GO:0048585	negative regulation of response to stimulus	1520	64	42.12	4.50E-04	1.21E-02
GO:0031330	negative regulation of cellular catabolic process	221	16	6.12	4.60E-04	1.24E-02
GO:0071375	cellular response to peptide hormone stimulus	289	19	8.01	4.70E-04	1.26E-02
GO:0043558	regulation of translational initiation in response to stress	14	4	0.39	4.70E-04	1.26E-02
GO:0022898	regulation of transmembrane transporter activity	222	16	6.15	4.80E-04	1.28E-02
GO:1903202	negative regulation of oxidative stress-induced cell death	51	7	1.41	4.80E-04	1.28E-02
GO:1903170	negative regulation of calcium ion transmembrane transport	37	6	1.03	4.90E-04	1.30E-02
GO:0035556	intracellular signal transduction	2450	94	67.9	5.00E-04	1.32E-02
GO:0051346	negative regulation of hydrolase activity	386	23	10.7	5.00E-04	1.32E-02
GO:0006470	protein dephosphorylation	291	19	8.06	5.10E-04	1.34E-02
GO:0007264	small GTPase mediated signal transduction	436	25	12.08	5.10E-04	1.34E-02
GO:0071363	cellular response to growth factor stimulus	643	33	17.82	5.10E-04	1.34E-02
GO:0071417	cellular response to organonitrogen compound	538	29	14.91	5.10E-04	1.34E-02
GO:0036473	cell death in response to oxidative stress	84	9	2.33	5.20E-04	1.35E-02
GO:0048013	ephrin receptor signaling pathway	84	9	2.33	5.20E-04	1.35E-02
GO:0051261	protein depolymerization	84	9	2.33	5.20E-04	1.35E-02
GO:0030194	positive regulation of blood coagulation	25	5	0.69	5.40E-04	1.39E-02
GO:1900048	positive regulation of hemostasis	25	5	0.69	5.40E-04	1.39E-02
GO:0006816	calcium ion transport	388	23	10.75	5.40E-04	1.39E-02
GO:0009967	positive regulation of signal transduction	1500	63	41.57	5.40E-04	1.39E-02
GO:0030031	cell projection assembly	463	26	12.83	5.40E-04	1.39E-02
GO:0001667	ameboidal-type cell migration	413	24	11.45	5.40E-04	1.39E-02
GO:0035306	positive regulation of dephosphorylation	52	7	1.44	5.50E-04	1.41E-02
GO:1900408	negative regulation of cellular response to oxidative stress	52	7	1.44	5.50E-04	1.41E-02
GO:0030099	myeloid cell differentiation	389	23	10.78	5.60E-04	1.43E-02
GO:0030001	metal ion transport	755	37	20.92	5.70E-04	1.44E-02
GO:0008631	intrinsic apoptotic signaling pathway in response to oxidative stress	38	6	1.05	5.70E-04	1.44E-02
GO:0010605	negative regulation of macromolecule metabolic process	2811	105	77.9	5.70E-04	1.44E-02
GO:0051592	response to calcium ion	122	11	3.38	5.80E-04	1.46E-02
GO:0051129	negative regulation of cellular component organization	622	32	17.24	6.00E-04	1.51E-02
GO:0023051	regulation of signaling	3400	123	94.23	6.00E-04	1.51E-02
GO:0014070	response to organic cyclic compound	841	40	23.31	6.20E-04	1.54E-02
GO:0022904	respiratory electron transport chain	86	9	2.38	6.20E-04	1.54E-02
GO:0042246	tissue regeneration	69	8	1.91	6.20E-04	1.54E-02
GO:0061684	chaperone-mediated autophagy	15	4	0.42	6.20E-04	1.54E-02
GO:1990000	amyloid fibril formation	15	4	0.42	6.20E-04	1.54E-02
GO:0016311	dephosphorylation	418	24	11.58	6.40E-04	1.59E-02
GO:0006735	NADH regeneration	26	5	0.72	6.50E-04	1.60E-02
GO:0050820	positive regulation of coagulation	26	5	0.72	6.50E-04	1.60E-02
GO:0061621	canonical glycolysis	26	5	0.72	6.50E-04	1.60E-02
GO:0061718	glucose catabolic process to pyruvate	26	5	0.72	6.50E-04	1.60E-02
GO:0044257	cellular protein catabolic process	599	31	16.6	6.60E-04	1.62E-02
GO:0010647	positive regulation of cell communication	1633	67	45.26	6.70E-04	1.64E-02
GO:0001932	regulation of protein phosphorylation	1246	54	34.53	6.80E-04	1.66E-02
GO:0051342	regulation of cyclic-nucleotide phosphodiesterase activity	7	3	0.19	6.80E-04	1.66E-02
GO:0042775	mitochondrial ATP synthesis coupled electron transport	70	8	1.94	6.90E-04	1.67E-02
GO:0051651	maintenance of location in cell	70	8	1.94	6.90E-04	1.67E-02
GO:1902883	negative regulation of response to oxidative stress	54	7	1.5	6.90E-04	1.67E-02
GO:0080134	regulation of response to stress	1425	60	39.49	7.00E-04	1.69E-02
GO:0051347	positive regulation of transferase activity	575	30	15.94	7.00E-04	1.69E-02
GO:0080135	regulation of cellular response to stress	655	33	18.15	7.10E-04	1.70E-02
GO:1902533	positive regulation of intracellular signal transduction	960	44	26.6	7.10E-04	1.70E-02
GO:0034333	adherens junction assembly	88	9	2.44	7.30E-04	1.75E-02
GO:0023056	positive regulation of signaling	1639	67	45.42	7.40E-04	1.77E-02
GO:0042773	ATP synthesis coupled electron transport	71	8	1.97	7.50E-04	1.79E-02
GO:0035307	positive regulation of protein dephosphorylation	40	6	1.11	7.60E-04	1.81E-02
GO:0032272	negative regulation of protein polymerization	55	7	1.52	7.70E-04	1.82E-02
GO:0051817	modification of morphology or physiology of other organism involved in symbiotic interaction	107	10	2.97	7.70E-04	1.82E-02
GO:0006294	nucleotide-excision repair, preincision complex assembly	27	5	0.75	7.80E-04	1.82E-02
GO:0034314	Arp2/3 complex-mediated actin nucleation	27	5	0.75	7.80E-04	1.82E-02
GO:0061615	glycolytic process through fructose-6-phosphate	27	5	0.75	7.80E-04	1.82E-02
GO:0061620	glycolytic process through glucose-6-phosphate	27	5	0.75	7.80E-04	1.82E-02
GO:0019882	antigen processing and presentation	210	15	5.82	7.80E-04	1.82E-02
GO:0016236	macroautophagy	255	17	7.07	7.80E-04	1.82E-02
GO:0034248	regulation of cellular amide metabolic process	424	24	11.75	7.90E-04	1.84E-02
GO:0030030	cell projection organization	1285	55	35.61	8.10E-04	1.88E-02
GO:1902176	negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	16	4	0.44	8.10E-04	1.88E-02
GO:0010821	regulation of mitochondrion organization	168	13	4.66	8.30E-04	1.92E-02
GO:0051851	modification by host of symbiont morphology or physiology	72	8	2	8.30E-04	1.92E-02
GO:1903902	positive regulation of viral life cycle	56	7	1.55	8.60E-04	1.96E-02
GO:0050793	regulation of developmental process	2427	92	67.26	8.60E-04	1.96E-02
GO:0006119	oxidative phosphorylation	90	9	2.49	8.60E-04	1.96E-02
GO:0002437	inflammatory response to antigenic stimulus	41	6	1.14	8.60E-04	1.96E-02
GO:0042743	hydrogen peroxide metabolic process	41	6	1.14	8.60E-04	1.96E-02
GO:0090382	phagosome maturation	41	6	1.14	8.60E-04	1.96E-02

Supplementary Table S2B: Significant gene ontology categories for expressed genes in platelets

GO.ID	Term	Annotated	Significant	Expected	pval	qval
GO:0006796	phosphate-containing compound metabolic process	2879	106	79.79	9.00E-04	2.05E-02
GO:0090087	regulation of peptide transport	665	33	18.43	9.10E-04	2.06E-02
GO:0098655	cation transmembrane transport	665	33	18.43	9.10E-04	2.06E-02
GO:0050865	regulation of cell activation	506	27	14.02	9.20E-04	2.08E-02
GO:0043388	positive regulation of DNA binding	57	7	1.58	9.60E-04	2.17E-02
GO:0032409	regulation of transporter activity	237	16	6.57	9.70E-04	2.19E-02
GO:0030837	negative regulation of actin filament polymerization	42	6	1.16	9.90E-04	2.23E-02
GO:0070848	response to growth factor	669	33	18.54	1.01E-03	2.27E-02
GO:0043280	positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	111	10	3.08	1.03E-03	2.30E-02
GO:1901699	cellular response to nitrogen compound	589	30	16.32	1.03E-03	2.30E-02
GO:0043555	regulation of translation in response to stress	17	4	0.47	1.04E-03	2.31E-02
GO:0045947	negative regulation of translational initiation	17	4	0.47	1.04E-03	2.31E-02
GO:0071824	protein-DNA complex subunit organization	216	15	5.99	1.04E-03	2.31E-02
GO:0090257	regulation of muscle system process	239	16	6.62	1.06E-03	2.35E-02
GO:0006596	polyamine biosynthetic process	8	3	0.22	1.07E-03	2.35E-02
GO:0098974	postsynaptic actin cytoskeleton organization	8	3	0.22	1.07E-03	2.35E-02
GO:1904714	regulation of chaperone-mediated autophagy	8	3	0.22	1.07E-03	2.35E-02
GO:1905446	regulation of mitochondrial ATP synthesis coupled electron transport	8	3	0.22	1.07E-03	2.35E-02
GO:0038093	Fc receptor signaling pathway	173	13	4.79	1.08E-03	2.37E-02
GO:0051279	regulation of release of sequestered calcium ion into cytosol	75	8	2.08	1.09E-03	2.37E-02
GO:1901019	regulation of calcium ion transmembrane transporter activity	75	8	2.08	1.09E-03	2.37E-02
GO:0061136	regulation of proteasomal protein catabolic process	152	12	4.21	1.09E-03	2.37E-02
GO:0032870	cellular response to hormone stimulus	618	31	17.13	1.09E-03	2.37E-02
GO:0051693	actin filament capping	29	5	0.8	1.10E-03	2.38E-02
GO:1902230	negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage	29	5	0.8	1.10E-03	2.38E-02
GO:1990778	protein localization to cell periphery	263	17	7.29	1.10E-03	2.38E-02
GO:0000302	response to reactive oxygen species	218	15	6.04	1.14E-03	2.46E-02
GO:0035821	modification of morphology or physiology of other organism	153	12	4.24	1.15E-03	2.48E-02
GO:0016049	cell growth	436	24	12.08	1.15E-03	2.48E-02
GO:0006793	phosphorus metabolic process	2901	106	80.4	1.17E-03	2.51E-02
GO:0043434	response to peptide hormone	386	22	10.7	1.18E-03	2.51E-02
GO:0042177	negative regulation of protein catabolic process	113	10	3.13	1.18E-03	2.51E-02
GO:1905477	positive regulation of protein localization to membrane	113	10	3.13	1.18E-03	2.51E-02
GO:0002433	immune response-regulating cell surface receptor signaling pathway involved in phagocytosis	76	8	2.11	1.18E-03	2.51E-02
GO:0038096	Fc-gamma receptor signaling pathway involved in phagocytosis	76	8	2.11	1.18E-03	2.51E-02
GO:0016310	phosphorylation	2075	80	57.51	1.24E-03	2.63E-02
GO:0048193	Golgi vesicle transport	290	18	8.04	1.26E-03	2.67E-02
GO:1903169	regulation of calcium ion transmembrane transport	134	11	3.71	1.26E-03	2.67E-02
GO:0002685	regulation of leukocyte migration	176	13	4.88	1.27E-03	2.68E-02
GO:0010543	regulation of platelet activation	30	5	0.83	1.28E-03	2.69E-02
GO:0010922	positive regulation of phosphatase activity	30	5	0.83	1.28E-03	2.69E-02
GO:0000902	cell morphogenesis	818	38	22.67	1.29E-03	2.71E-02
GO:0032387	negative regulation of intracellular transport	60	7	1.66	1.30E-03	2.71E-02
GO:0019682	glyceraldehyde-3-phosphate metabolic process	18	4	0.5	1.31E-03	2.71E-02
GO:0030220	platelet formation	18	4	0.5	1.31E-03	2.71E-02
GO:0032516	positive regulation of phosphoprotein phosphatase activity	18	4	0.5	1.31E-03	2.71E-02
GO:0036344	platelet morphogenesis	18	4	0.5	1.31E-03	2.71E-02
GO:0042276	error-prone translesion synthesis	18	4	0.5	1.31E-03	2.71E-02
GO:0070987	error-free translesion synthesis	18	4	0.5	1.31E-03	2.71E-02
GO:0071243	cellular response to arsenic-containing substance	18	4	0.5	1.31E-03	2.71E-02
GO:0019722	calcium-mediated signaling	177	13	4.91	1.33E-03	2.74E-02
GO:0120036	plasma membrane bounded cell projection organization	1254	53	34.75	1.33E-03	2.74E-02
GO:0038094	Fc-gamma receptor signaling pathway	78	8	2.16	1.40E-03	2.88E-02
GO:0010921	regulation of phosphatase activity	157	12	4.35	1.44E-03	2.96E-02
GO:0002504	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	97	9	2.69	1.47E-03	3.01E-02
GO:0010256	endomembrane system organization	343	20	9.51	1.48E-03	3.03E-02
GO:0006904	vesicle docking involved in exocytosis	31	5	0.86	1.50E-03	3.05E-02
GO:0010039	response to iron ion	31	5	0.86	1.50E-03	3.05E-02
GO:0046685	response to arsenic-containing substance	31	5	0.86	1.50E-03	3.05E-02
GO:0042542	response to hydrogen peroxide	137	11	3.8	1.51E-03	3.06E-02
GO:0002431	Fc receptor mediated stimulatory signaling pathway	79	8	2.19	1.53E-03	3.08E-02
GO:0007045	cell-substrate adherens junction assembly	79	8	2.19	1.53E-03	3.08E-02
GO:0048041	focal adhesion assembly	79	8	2.19	1.53E-03	3.08E-02
GO:0008360	regulation of cell shape	117	10	3.24	1.53E-03	3.08E-02
GO:0033157	regulation of intracellular protein transport	202	14	5.6	1.54E-03	3.10E-02
GO:1903050	regulation of proteolysis involved in cellular protein catabolic process	180	13	4.99	1.55E-03	3.11E-02
GO:0045714	regulation of low-density lipoprotein particle receptor biosynthetic process	9	3	0.25	1.57E-03	3.13E-02
GO:0071281	cellular response to iron ion	9	3	0.25	1.57E-03	3.13E-02
GO:1901844	regulation of cell communication by electrical coupling involved in cardiac conduction	9	3	0.25	1.57E-03	3.13E-02
GO:0001558	regulation of cell growth	370	21	10.25	1.59E-03	3.17E-02
GO:0051156	glucose 6-phosphate metabolic process	19	4	0.53	1.62E-03	3.22E-02
GO:0010638	positive regulation of organelle organization	553	28	15.33	1.64E-03	3.26E-02
GO:0010646	regulation of cell communication	3358	119	93.06	1.68E-03	3.32E-02
GO:0022604	regulation of cell morphogenesis	397	22	11	1.68E-03	3.32E-02
GO:0061061	muscle structure development	608	30	16.85	1.68E-03	3.32E-02
GO:0048524	positive regulation of viral process	99	9	2.74	1.70E-03	3.35E-02
GO:0055114	oxidation-reduction process	860	39	23.83	1.73E-03	3.39E-02
GO:0030835	negative regulation of actin filament depolymerization	32	5	0.89	1.73E-03	3.39E-02
GO:1901020	negative regulation of calcium ion transmembrane transporter activity	32	5	0.89	1.73E-03	3.39E-02
GO:0098662	inorganic cation transmembrane transport	583	29	16.16	1.77E-03	3.46E-02

Supplementary Table S2B: Significant gene ontology categories for expressed genes in platelets

GO.ID	Term	Annotated	Significant	Expected	pval	qval
GO:0032781	positive regulation of ATPase activity	47	6	1.3	1.80E-03	3.50E-02
GO:0048260	positive regulation of receptor-mediated endocytosis	47	6	1.3	1.80E-03	3.50E-02
GO:0031099	regeneration	183	13	5.07	1.80E-03	3.50E-02
GO:0051223	regulation of protein transport	639	31	17.71	1.84E-03	3.58E-02
GO:0031669	cellular response to nutrient levels	206	14	5.71	1.85E-03	3.59E-02
GO:0034599	cellular response to oxidative stress	277	17	7.68	1.92E-03	3.72E-02
GO:0071902	positive regulation of protein serine/threonine kinase activity	302	18	8.37	1.98E-03	3.81E-02
GO:0000715	nucleotide-excision repair, DNA damage recognition	20	4	0.55	1.98E-03	3.81E-02
GO:0000717	nucleotide-excision repair, DNA duplex unwinding	20	4	0.55	1.98E-03	3.81E-02
GO:0010801	negative regulation of peptidyl-threonine phosphorylation	20	4	0.55	1.98E-03	3.81E-02
GO:0006007	glucose catabolic process	33	5	0.91	2.00E-03	3.84E-02
GO:0051452	intracellular pH reduction	48	6	1.33	2.01E-03	3.84E-02
GO:1901653	cellular response to peptide	352	20	9.76	2.01E-03	3.84E-02
GO:1903362	regulation of cellular protein catabolic process	208	14	5.76	2.03E-03	3.88E-02
GO:0002684	positive regulation of immune system process	955	42	26.47	2.07E-03	3.95E-02
GO:0065004	protein-DNA complex assembly	186	13	5.15	2.08E-03	3.96E-02
GO:0051881	regulation of mitochondrial membrane potential	65	7	1.8	2.09E-03	3.96E-02
GO:1904427	positive regulation of calcium ion transmembrane transport	65	7	1.8	2.09E-03	3.96E-02
GO:0034097	response to cytokine	1104	47	30.6	2.17E-03	4.11E-02
GO:0030836	positive regulation of actin filament depolymerization	10	3	0.28	2.19E-03	4.12E-02
GO:0045713	low-density lipoprotein particle receptor biosynthetic process	10	3	0.28	2.19E-03	4.12E-02
GO:0099188	postsynaptic cytoskeleton organization	10	3	0.28	2.19E-03	4.12E-02
GO:0007162	negative regulation of cell adhesion	257	16	7.12	2.23E-03	4.16E-02
GO:0045851	pH reduction	49	6	1.36	2.23E-03	4.16E-02
GO:0002351	serotonin production involved in inflammatory response	3	2	0.08	2.26E-03	4.16E-02
GO:0002442	serotonin secretion involved in inflammatory response	3	2	0.08	2.26E-03	4.16E-02
GO:0002554	serotonin secretion by platelet	3	2	0.08	2.26E-03	4.16E-02
GO:0010710	regulation of collagen catabolic process	3	2	0.08	2.26E-03	4.16E-02
GO:0015684	ferrous iron transport	3	2	0.08	2.26E-03	4.16E-02
GO:0016480	negative regulation of transcription by RNA polymerase III	3	2	0.08	2.26E-03	4.16E-02
GO:0019322	pentose biosynthetic process	3	2	0.08	2.26E-03	4.16E-02
GO:0031509	telomeric heterochromatin assembly	3	2	0.08	2.26E-03	4.16E-02
GO:0097577	sequestering of iron ion	3	2	0.08	2.26E-03	4.16E-02
GO:1902958	positive regulation of mitochondrial electron transport, NADH to ubiquinone	3	2	0.08	2.26E-03	4.16E-02
GO:1903874	ferrous iron transmembrane transport	3	2	0.08	2.26E-03	4.16E-02
GO:1904715	negative regulation of chaperone-mediated autophagy	3	2	0.08	2.26E-03	4.16E-02
GO:0032388	positive regulation of intracellular transport	188	13	5.21	2.28E-03	4.19E-02
GO:0006734	NADH metabolic process	34	5	0.94	2.29E-03	4.20E-02
GO:0099003	vesicle-mediated transport in synapse	166	12	4.6	2.30E-03	4.21E-02
GO:0046034	ATP metabolic process	235	15	6.51	2.39E-03	4.35E-02
GO:0002082	regulation of oxidative phosphorylation	21	4	0.58	2.39E-03	4.35E-02
GO:0051125	regulation of actin nucleation	21	4	0.58	2.39E-03	4.35E-02
GO:0048869	cellular developmental process	3826	132	106.03	2.42E-03	4.38E-02
GO:0002478	antigen processing and presentation of exogenous peptide antigen	167	12	4.63	2.42E-03	4.38E-02
GO:0006457	protein folding	167	12	4.63	2.42E-03	4.38E-02
GO:0000422	autophagy of mitochondrion	50	6	1.39	2.48E-03	4.47E-02
GO:0061726	mitochondrion disassembly	50	6	1.39	2.48E-03	4.47E-02
GO:1903201	regulation of oxidative stress-induced cell death	67	7	1.86	2.48E-03	4.47E-02
GO:0051250	negative regulation of lymphocyte activation	125	10	3.46	2.51E-03	4.52E-02
GO:2001235	positive regulation of apoptotic signaling pathway	168	12	4.66	2.54E-03	4.56E-02
GO:0043666	regulation of phosphoprotein phosphatase activity	105	9	2.91	2.55E-03	4.57E-02
GO:0015682	ferric iron transport	35	5	0.97	2.61E-03	4.66E-02
GO:0033572	transferrin transport	35	5	0.97	2.61E-03	4.66E-02
GO:0072512	trivalent inorganic cation transport	35	5	0.97	2.61E-03	4.66E-02
GO:0042493	response to drug	910	40	25.22	2.65E-03	4.72E-02
GO:0034332	adherens junction organization	126	10	3.49	2.66E-03	4.73E-02
GO:0071345	cellular response to cytokine stimulus	1027	44	28.46	2.67E-03	4.73E-02
GO:0032101	regulation of response to external stimulus	767	35	21.26	2.67E-03	4.73E-02
GO:0019884	antigen processing and presentation of exogenous antigen	169	12	4.68	2.67E-03	4.73E-02
GO:1903747	regulation of establishment of protein localization to mitochondrion	68	7	1.88	2.71E-03	4.79E-02
GO:0030705	cytoskeleton-dependent intracellular transport	148	11	4.1	2.79E-03	4.92E-02
GO:0043244	regulation of protein complex disassembly	87	8	2.41	2.82E-03	4.97E-02

Supplementary Table S3: eQTLs significant in both Platelets and MKs

			MK		Platelet		
Chromosome	**Position**	**Gene**	**Beta**	**q-value**	**Beta**	**q-value**	**GTEx eGene?**
1	12043717	MFN2	-0.35	3.4E-33	-1.68	2.3E-133	No
1	25561667	TMEM50A	0.17	9.6E-05	0.24	8.6E-10	Yes
1	25561667	RHD	0.65	1.0E-22	0.54	7.9E-37	Yes
1	28219658	RPA2	-0.28	4.1E-07	-0.26	4.5E-13	Yes
1	38465315	FHL3	-0.32	2.9E-09	-1.47	2.5E-110	Yes
1	39662654	MACF1	0.20	1.0E-05	0.11	1.2E-08	No
1	45476663	UROD	0.31	1.4E-16	0.38	4.9E-55	Yes
1	110236383	GSTM1	-1.45	5.5E-17	-0.82	9.1E-31	Not available
1	110282972	GSTM3	0.51	6.2E-28	0.17	1.3E-07	Yes
1	156869714	PEAR1	0.12	3.6E-02	0.18	1.5E-09	No
2	36808350	FEZ2	0.17	4.0E-03	0.14	2.4E-07	No
2	65283972	CEP68	-0.35	2.6E-26	-0.32	1.5E-63	Yes
2	224874874	SERPINE2	0.52	2.2E-12	0.52	3.2E-95	Yes
2	242645466	ING5	0.70	1.1E-63	0.51	8.9E-129	No
3	15308409	SH3BP5	-0.92	6.6E-08	-0.64	3.9E-16	No
3	71829242	PROK2	0.50	8.2E-07	0.61	2.8E-45	No
4	25863375	SEL1L3	0.29	8.7E-13	0.40	2.4E-12	Yes
4	38960263	KLHL5	1.02	7.8E-61	1.19	1.5E-91	No
4	39446549	RPL9	-0.53	2.5E-76	-0.31	2.4E-40	Yes
5	148725821	PCYOX1L	0.19	1.6E-15	0.20	3.3E-66	No
5	150157111	SMIM3	-0.37	1.8E-03	-0.41	6.9E-08	No
5	177554780	RMND5B	-0.19	2.2E-05	-0.39	2.7E-36	No
6	2783913	WRNIP1	0.21	9.2E-08	0.35	1.2E-11	No
6	10723193	TMEM14C	0.21	2.2E-03	0.62	8.1E-23	No
6	30457732	HLA-E	-1.36	1.1E-43	-1.54	2.2E-15	No
6	86387888	SNHG5	-1.25	2.5E-169	0.25	2.7E-53	Yes
6	99465262	FBXL4	-0.38	8.8E-41	-0.35	1.6E-148	No
6	139350182	ABRACL	0.13	6.0E-04	0.18	2.0E-25	Yes
6	160211259	MRPL18	-0.12	3.6E-03	-0.33	9.9E-32	Yes
7	642774	LOC101926963	0.46	3.1E-04	0.33	4.0E-12	Not available
7	16791225	TSPAN13	0.24	8.0E-04	0.53	6.7E-24	No
7	128790310	TSPAN33	0.49	9.7E-54	0.12	1.3E-03	No
8	42010602	AP3M2	-0.19	5.9E-14	0.10	2.3E-10	Yes
9	99192919	HABP4	-0.49	4.4E-44	-0.93	4.5E-45	Not available
10	71218646	TSPAN15	-0.55	6.0E-29	-0.38	1.0E-22	No
10	73655350	PSAP	0.23	4.0E-09	0.45	2.8E-40	No
10	121037154	GRK5	0.28	4.2E-04	0.30	2.0E-11	No
11	18537800	TSG101	-0.10	7.6E-09	-0.12	1.3E-28	No
11	65644027	CTSW	-1.13	1.1E-29	0.87	2.7E-53	Yes
11	75897374	WNT11	-0.26	2.9E-06	-0.25	9.2E-22	Yes
12	56435929	RPS26	0.66	1.3E-24	0.54	1.1E-46	Yes
12	122216910	RHOF	0.73	5.3E-12	1.03	3.9E-54	No
14	65796846	FUT8-AS1	-0.50	1.6E-36	-0.20	5.7E-30	Not available
15	28999128	WHAMMP2	0.31	1.7E-15	1.12	7.0E-25	No
15	52498360	LOC100129973	-0.36	7.4E-04	-0.46	7.5E-25	Not available
15	65065920	RBPMS2	-0.49	1.3E-08	-1.48	5.2E-30	Yes
15	80235014	C15orf37	-0.24	2.4E-15	-0.42	4.6E-45	No
15	80447911	FAH	0.16	2.2E-08	0.23	2.4E-18	No
15	99660664	SYNM	0.28	7.5E-05	0.46	5.0E-43	No
16	87892024	SLC7A5	0.35	7.5E-11	0.32	1.7E-55	No
17	73828174	UNC13D	0.24	3.9E-05	0.19	5.2E-10	No
17	80696692	FN3K	0.61	8.3E-35	0.46	4.7E-49	Yes
19	1400866	GAMT	-0.37	4.2E-05	-0.65	1.0E-94	No
19	14492219	CD97	-0.32	2.8E-02	-0.29	3.3E-06	Yes
19	38787965	PPP1R14A	0.27	2.8E-03	0.47	4.6E-26	No
20	633968	SRXN1	-0.21	5.2E-03	-0.30	6.6E-30	Yes
20	33872585	EIF6	0.17	3.1E-03	0.40	7.1E-07	No

Supplementary Table S4: Full results from GWAS catalog lookup of significant eQTL results

Chromosome	Position	eQTL Effect Allele	Gene	eQTL Beta (MK)	eQTL q-value (MK)	eQTL Beta (Platelet)	eQTL q-value (Platelet)	PubMed ID	First Author	Journal	Trait	Strongest Risk Allele	GWAS p-value	GWAS odds ratio or beta	GWAS 95% CI
chr1	25561667	G	TMEM50A	0.17	9.58E-05	0.24	8.59E-10	27863252	Astle WJ	Cell	Plateletcrit	rs55794721-A	7.00E-37	0.05	[0.04-0.055] unit decrease
chr1	25561667	G	RHD	0.65	1.03E-22	0.54	7.88E-37	27863252	Astle WJ	Cell	Plateletcrit	rs55794721-A	7.00E-37	0.05	[0.04-0.055] unit decrease
chr1	156869714	G	PEAR1	0.12	3.62E-02	0.18	1.51E-09	29403010	Kanai M	Nat Genet	Platelet count	rs12041331-?	3.00E-13	0.03	[0.023-0.039] unit increase novel
chr1	156869714	G	PEAR1	0.12	3.62E-02	0.18	1.51E-09	27863252	Astle WJ	Cell	Mean platelet volume	rs12041331-A	6.00E-34	0.08	[0.066-0.091] unit decrease
chr1	156869714	G	PEAR1	0.12	3.62E-02	0.18	1.51E-09	27863252	Astle WJ	Cell	Platelet distribution width	rs12041331-A	2.00E-13	0.05	[0.034-0.06] unit decrease
chr12	122216910	A	TMEM120B	0.36	-	0.24	3.90E-02	27863252	Astle WJ	Cell	Platelet count	rs11553699-G	1.00E-45	0.08	[0.069-0.091] unit decrease
chr12	122216910	A	TMEM120B	0.36	-	0.24	3.90E-02	27863252	Astle WJ	Cell	Plateletcrit	rs11553699-G	6.00E-81	0.11	[0.097-0.12] unit increase
chr12	122216910	A	TMEM120B	0.36	-	0.24	3.90E-02	27863252	Astle WJ	Cell	Mean platelet volume	rs11553699-G	0.00E+00	0.37	[0.35-0.38] unit increase
chr12	122216910	A	TMEM120B	0.36	-	0.24	3.90E-02	27863252	Astle WJ	Cell	Platelet distribution width	rs11553699-G	1.00E-184	0.16	[0.15-0.17] unit increase
chr12	122216910	A	RHOF	0.73	5.33E-12	1.03	3.87E-54	27863252	Astle WJ	Cell	Platelet count	rs11553699-G	1.00E-45	0.08	[0.069-0.091] unit decrease
chr12	122216910	A	RHOF	0.73	5.33E-12	1.03	3.87E-54	27863252	Astle WJ	Cell	Plateletcrit	rs11553699-G	6.00E-81	0.11	[0.097-0.12] unit increase
chr12	122216910	A	RHOF	0.73	5.33E-12	1.03	3.87E-54	27863252	Astle WJ	Cell	Mean platelet volume	rs11553699-G	0.00E+00	0.37	[0.35-0.38] unit increase
chr12	122216910	A	RHOF	0.73	5.33E-12	1.03	3.87E-54	27863252	Astle WJ	Cell	Platelet distribution width	rs11553699-G	1.00E-184	0.16	[0.15-0.17] unit increase
chr2	224874874	G	SERPINE2	0.52	2.22E-12	0.52	3.16E-95	27863252	Astle WJ	Cell	Mean platelet volume	rs13412535-A	2.00E-10	0.03	[0.019-0.036] unit decrease
chr2	224874874	G	SERPINE2	0.52	2.22E-12	0.52	3.16E-95	27989323	Ahola-Olli AV	Am J Hum Genet	Platelet-derived growth factor BB levels	rs13412535-G	2.00E-55	0.34	[0.29-0.38] SD units decrease
chr20	1819280	T	SIRPA	0.21	1.35E-03	-	-	27863252	Astle WJ	Cell	Platelet distribution width	rs156356-C	1.00E-12	0.03	[0.019-0.034] unit increase
chr20	1819280	T	SIRPA	0.21	1.35E-03	-	-	27863252	Astle WJ	Cell	Mean platelet volume	rs156356-C	8.00E-66	0.07	[0.058-0.073] unit increase
chr3	56849749	T	ARHGEF3	0.36	7.46E-24	-	-	29066854	Lin BD	J Hum Genet	Platelet count	rs1354034-?	3.00E-13	-	
chr3	56849749	T	ARHGEF3	0.36	7.46E-24	-	-	22139419	Gieger C	Nature	Mean platelet volume	rs1354034-T	3.00E-69	0.02	[0.021-0.025] ln(fl) increase
chr3	56849749	T	ARHGEF3	0.36	7.46E-24	-	-	22139419	Gieger C	Nature	Platelet count	rs1354034-C	3.00E-54	6.85	[5.98-7.71] 10^9/l increase
chr3	56849749	T	ARHGEF3	0.36	7.46E-24	-	-	27863252	Astle WJ	Cell	Platelet count	rs1354034-C	9.00E-301	0.14	[0.13-0.15] unit increase
chr3	56849749	T	ARHGEF3	0.36	7.46E-24	-	-	26805783	Schick UM	Am J Hum Genet	Platelet count	rs1354034-T	2.00E-13	5.87	[4.3-7.44] unit decrease
chr3	56849749	T	ARHGEF3	0.36	7.46E-24	-	-	27863252	Astle WJ	Cell	Plateletcrit	rs1354034-C	2.00E-21	0.04	[0.028-0.043] unit increase
chr3	56849749	T	ARHGEF3	0.36	7.46E-24	-	-	31217584	Wojcik GL	Nature	Platelet count	rs1354034-?	2.00E-23	5.31	[4.27-6.36] unit increase
chr3	56849749	T	ARHGEF3	0.36	7.46E-24	-	-	23263863	Li J	Hum Mol Genet	Platelet count	rs1354034-C	9.00E-13	11.44	[8.31-14.57] unit increase
chr3	56849749	T	ARHGEF3	0.36	7.46E-24	-	-	23263863	Li J	Hum Mol Genet	Platelet count	rs1354034-T	4.00E-09	9.44	[6.3-12.59] unit decrease
chr3	56849749	T	ARHGEF3	0.36	7.46E-24	-	-	23263863	Li J	Hum Mol Genet	Platelet count	rs1354034-T	1.00E-19	10.44	[8.18-12.69] unit decrease
chr3	56849749	T	ARHGEF3	0.36	7.46E-24	-	-	29403010	Kanai M	Nat Genet	Platelet count	rs1354034-?	5.00E-27	0.05	[0.037-0.054] unit increase novel
chr3	56849749	T	ARHGEF3	0.36	7.46E-24	-	-	24026423	Shameer K	Hum Genet	Platelet count	rs1354034-T	6.00E-24	7.97	[NR] unit increase
chr3	56849749	T	ARHGEF3	0.36	7.46E-24	-	-	24026423	Shameer K	Hum Genet	Mean platelet volume	rs1354034-C	9.00E-34	0.19	[NR] unit decrease
chr3	56849749	T	ARHGEF3	0.36	7.46E-24	-	-	31194788	Read RW	PLoS One	Mean platelet volume	rs1354034-T	2.00E-13	0.15	[0.11-0.2] fL increase
chr3	56849749	T	ARHGEF3	0.36	7.46E-24	-	-	27863252	Astle WJ	Cell	Mean platelet volume	rs1354034-C	0.00E+00	0.23	[0.22-0.24] unit decrease
chr3	122833003	C	PDIA5	0.66	1.21E-92	-	-	27863252	Astle WJ	Cell	Platelet count	rs3804749-T	2.00E-28	0.04	[0.034-0.049] unit decrease
chr3	122833003	C	PDIA5	0.66	1.21E-92	-	-	27863252	Astle WJ	Cell	Plateletcrit	rs3804749-T	7.00E-11	0.02	[0.017-0.032] unit decrease
chr3	122833003	C	PDIA5	0.66	1.21E-92	-	-	27863252	Astle WJ	Cell	Mean platelet volume	rs3804749-T	1.00E-32	0.04	[0.037-0.051] unit increase
chr3	122833003	C	PDIA5	0.66	1.21E-92	-	-	27863252	Astle WJ	Cell	Platelet distribution width	rs3804749-T	5.00E-34	0.04	[0.038-0.052] unit increase
chr4	6883012	C	TBC1D14	0.21	6.08E-05	-	-	25705162	Oh JH	Genomics Inform	Platelet count	rs3733606-G	1.00E-10	5.65	[3.73-7.57] unit decrease
chr7	106372219	C	CCDC71L	0.43	7.34E-20	-	-	22139419	Gieger C	Nature	Mean platelet volume	rs342293-G	7.00E-57	0.02	[0.015-0.019] ln(fl) increase
chr7	106372219	C	CCDC71L	0.43	7.34E-20	-	-	31217584	Wojcik GL	Nature	Platelet count	rs342293-?	4.00E-14	3.96	[2.93-4.99] unit decrease
chr7	106372219	C	CCDC71L	0.43	7.34E-20	-	-	19820697	Soranzo N	Nat Genet	Mean platelet volume	rs342293-G	2.00E-33	0.02	[0.013-0.017] fl increase
chr7	106372219	C	CCDC71L	0.43	7.34E-20	-	-	22423221	Qayyum R	PLoS Genet	Platelet count	rs342293-C	2.00E-08	4.05	[2.64-5.46] 10^L decrease
chr7	106372219	C	CCDC71L	0.43	7.34E-20	-	-	24026423	Shameer K	Hum Genet	Mean platelet volume	rs342293-C	5.00E-22	0.15	[NR] unit decrease
chr7	106372219	C	CCDC71L	0.43	7.34E-20	-	-	19221038	Soranzo N	Blood	Mean platelet volume	rs342293-G	1.00E-24	0.02	[0.014-0.018] log fl increase
chr7	106372219	C	CCDC71L	0.43	7.34E-20	-	-	31194788	Read RW	PLoS One	Mean platelet volume	rs342293-G	7.00E-11	0.13	[0.093-0.172] fL increase
chr7	106372219	C	CCDC71L	0.43	7.34E-20	-	-	27863252	Astle WJ	Cell	Mean platelet volume	rs342293-G	0.00E+00	0.16	[0.15-0.17] unit increase
chr8	144996029	A	PLEC	-0.66	1.65E-13	-	-	27863252	Astle WJ	Cell	Platelet count	rs7833924-G	7.00E-33	0.04	[0.037-0.051] unit increase
chr9	99192919	A	HABP4	-0.49	4.41E-44	-0.93	4.55E-45	27863252	Astle WJ	Cell	Plateletcrit	rs10820606-C	1.00E-21	0.04	[0.033-0.051] unit increase
chr9	99192919	A	HABP4	-0.49	4.41E-44	-0.93	4.55E-45	27863252	Astle WJ	Cell	Platelet count	rs10820606-C	4.00E-30	0.05	[0.041-0.058] unit increase
chr9	99192919	A	HABP4	-0.49	4.41E-44	-0.93	4.55E-45	27863252	Astle WJ	Cell	Platelet distribution width	rs10820606-C	1.00E-39	0.06	[0.048-0.065] unit decrease
chr1	8917102	T	ENO1	-	-	-0.23	2.16E-27	27863252	Astle WJ	Cell	Plateletcrit	rs11121246-G	3.00E-16	0.03	[0.023-0.037] unit increase
chr1	10271688	C	KIF1B	-	-	-0.26	1.54E-19	27863252	Astle WJ	Cell	Mean platelet volume	rs11121529-G	1.00E-44	0.08	[0.067-0.089] unit increase
chr1	202909974	G	ADIPOR1	-	-	0.09	2.90E-03	27863252	Astle WJ	Cell	Mean platelet volume	rs7539542-C	5.00E-12	0.03	[0.02-0.035] unit decrease
chr1	247712303	T	GCSAML	-	-	0.25	5.07E-11	27863252	Astle WJ	Cell	Platelet count	rs41315846-C	2.00E-54	0.06	[0.05-0.065] unit increase
chr1	247712303	T	GCSAML	-	-	0.25	5.07E-11	27863252	Astle WJ	Cell	Plateletcrit	rs41315846-C	9.00E-23	0.04	[0.029-0.044] unit increase
chr1	247712303	T	GCSAML	-	-	0.25	5.07E-11	27863252	Astle WJ	Cell	Mean platelet volume	rs41315846-C	3.00E-54	0.06	[0.05-0.064] unit decrease
chr1	247712303	T	GCSAML	-	-	0.25	5.07E-11	27668658	Iotchkova V	Nat Genet	Cardiometabolic and hematological traits	rs41315846-C	3.00E-34	0.05	[0.04-0.056] unit increase
chr1	247712303	T	GCSAML	-	-	0.25	5.07E-11	27863252	Astle WJ	Cell	Platelet distribution width	rs41315846-C	1.00E-47	0.05	[0.046-0.06] unit decrease
chr11	200343	T	BET1L	-	-	-0.41	5.93E-12	27863252	Astle WJ	Cell	Plateletcrit	rs55966801-C	3.00E-24	0.04	[0.036-0.053] unit increase
chr11	126285301	G	ST3GAL4-AS	-	-	-0.19	2.42E-09	27863252	Astle WJ	Cell	Mean platelet volume	rs7949566-A	3.00E-30	0.04	[0.035-0.049] unit increase
chr11	126285301	G	ST3GAL4-AS	-	-	-0.19	2.42E-09	27863252	Astle WJ	Cell	Platelet distribution width	rs7949566-A	4.00E-13	0.03	[0.019-0.033] unit increase
chr11	126285301	G	ST3GAL4	-	-	-0.42	6.39E-36	27863252	Astle WJ	Cell	Mean platelet volume	rs7949566-A	3.00E-30	0.04	[0.035-0.049] unit increase
chr11	126285301	G	ST3GAL4	-	-	-0.42	6.39E-36	27863252	Astle WJ	Cell	Platelet distribution width	rs7949566-A	4.00E-13	0.03	[0.019-0.033] unit increase
chr15	63341996	T	TPM1	-	-	-0.33	2.70E-28	27863252	Astle WJ	Cell	Platelet count	rs11071720-C	1.00E-35	0.05	[0.042-0.057] unit increase
chr15	63341996	T	TPM1	-	-	-0.33	2.70E-28	19820697	Soranzo N	Nat Genet	Mean platelet volume	rs11071720-T	2.00E-08	0.01	[0.007-0.015] fl increase
chr15	63341996	T	TPM1	-	-	-0.33	2.70E-28	27863252	Astle WJ	Cell	Mean platelet volume	rs11071720-C	4.00E-53	0.06	[0.053-0.068] unit decrease

Supplementary Table S4: Full results from GWAS catalog lookup of significant eQTL results

Chromosome	**Position**	**eQTL Effect Allele**	**Gene**	**eQTL Beta (MK)**	**eQTL q-value (MK)**	**eQTL Beta (Platelet)**	**eQTL q-value (Platelet)**	**PubMed ID**	**First Author**	**Journal**	**Trait**	**Strongest Risk Allele**	**GWAS p-value**	**GWAS odds ratio or beta**	**GWAS 95% CI**
chr15	63341996	T	TPM1	-	-	-0.33	2.70E-28	27863252	Astle WJ	Cell	Platelet distribution width	rs11071720-C	7.00E-34	0.05	[0.04-0.055] unit decrease
chr2	31477838	G	EHD3	-	-	-0.17	1.61E-06	27863252	Astle WJ	Cell	Platelet count	rs655029-A	9.00E-73	0.07	[0.066-0.081] unit increase
chr2	31477838	G	EHD3	-	-	-0.17	1.61E-06	27863252	Astle WJ	Cell	Plateletcrit	rs655029-A	1.00E-18	0.04	[0.028-0.044] unit increase
chr2	31477838	G	EHD3	-	-	-0.17	1.61E-06	27863252	Astle WJ	Cell	Mean platelet volume	rs655029-A	8.00E-109	0.09	[0.082-0.097] unit decrease
chr2	31477838	G	EHD3	-	-	-0.17	1.61E-06	27863252	Astle WJ	Cell	Platelet distribution width	rs655029-A	2.00E-225	0.13	[0.12-0.14] unit decrease
chr4	6857278	T	TBC1D14	-	-	0.13	2.25E-06	29403010	Kanai M	Nat Genet	Platelet count	rs6836941-?	3.00E-09	0.03	[0.018-0.035] unit decrease novel
chr4	57767327	T	POLR2B	-	-	0.06	5.81E-03	27863252	Astle WJ	Cell	Platelet count	rs7665147-A	2.00E-11	0.03	[0.022-0.041] unit decrease

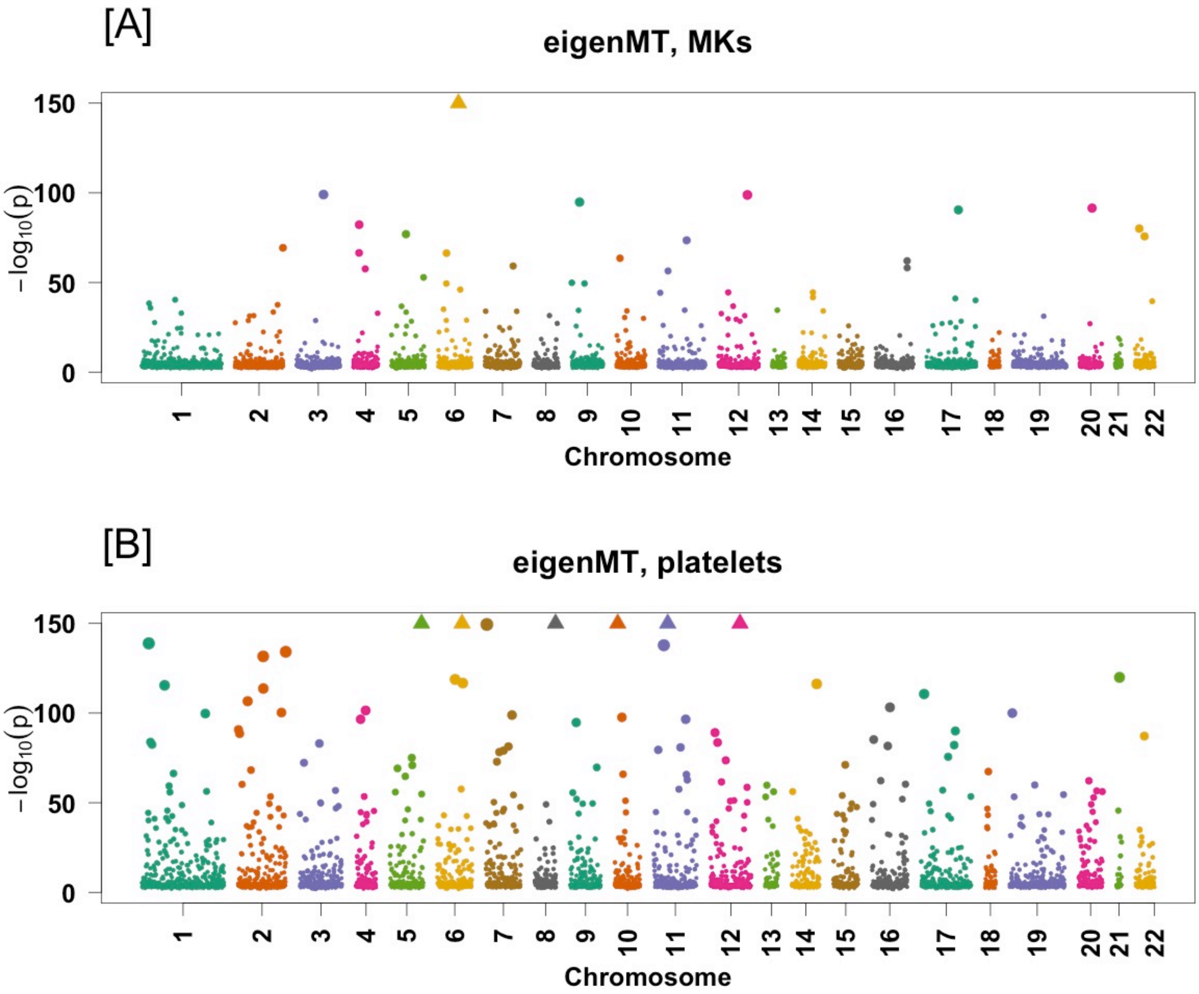
Supplementary Figures

Supplementary Figure legends

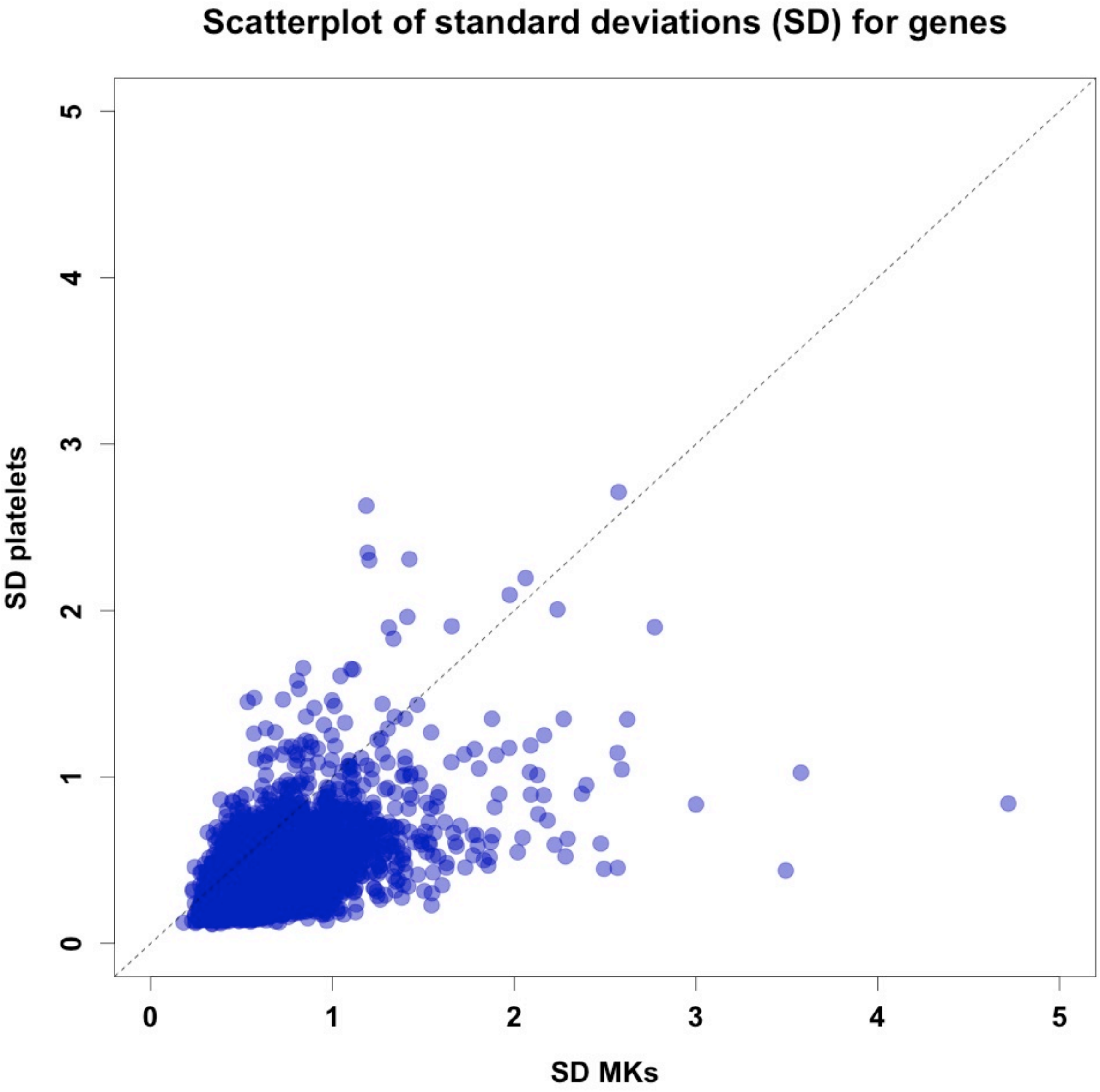
Supplementary Figure S1. Manhattan plots of eQTL results.
Each dot on the two Manhattan plot signifies an eQTL. Genomic coordinates by chromosome are displayed along the x-axis and the negative logarithm of the association p-value for each eQTL is displayed on the y-axis. Results for MKs are displayed in panel (A) and results for platelets are displayed in panel (B). Results are represented by the peak SNP per gene based on eigenMT software. Triangular shaped points indicate that the raw p-values of the corresponding eQTLs was lower than 10^{-150}. Color is used to distinguish between chromosomes.

Supplementary Figure S2. Variability of expressed genes.
Scatterplot of standard deviations among 4,595 expressed genes in MKs and platelets. We observe in 90.75% of genes the standard deviation of expression values is higher in MKs compared to platelets.

Supplementary Figure S1: Manhattan plots of eQTL results.



Supplementary Figure S2. Variability of expressed genes.



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