

In vivo Monitoring of Transcriptional Dynamics After Lower-Limb Muscle Injury Enables Quantitative Classification of Healing

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Supplementary Materials

Text S1: Transcriptional Signatures of Inflammation and Immune System Detected in Early Period

Text S2: Transcriptional Signatures Associated With Injured Muscle Tissue Extracellular Matrix

Text S3: Injured Muscle Tissue Microenvironment Regulates Existing and Invading Cellular Migration, Proliferation, Differentiation and Phenotype

Text S4: Activation of Muscle Repair Machinery

Text S5: Late Transcriptional Programs Activated in Response to Traumatic LLMI

Fig. S1. Immuno-histological analysis of muscle after cryo-injury.

Fig. S2. a) Example of reproducibility from RNA-Seq datasets. Biological replicates of *in vivo* isolated RNA samples from 24 hours after injury. Sequencing libraries were prepared from the isolated RNA and a strong correlation ($R^2 = 0.95$) was observed for two representative examples. b) Validation of RNA-Seq data with qPCR comparing the injured versus uninjured samples for the 3 hour time point. c) Validation of RNA-Seq data with qPCR comparing the injured versus uninjured samples for the 10 hour time point. d) Validation of RNA-Seq data with qPCR comparing the injured versus uninjured samples for the 24 hour time point.

Fig. S3. Number of differentially expressed genes.

Fig. S4. Gene Sets Activated Early After Injury (3-24 hrs) a) Enriched KEGG pathways from differentially expressed genes for the early time points (3-24 hrs). The size of the circle corresponds to the number of significant genes with each enriched pathway. b) Heatmap of genes associated metabolism expressed in the early time period. c) Gene expression profile of Arginase 1 (Arg1), which is a molecule emitted by type 2 macrophages to balance inflammatory reactive-oxygen species present in the injured tissue. Red-Injured, Blue-Uninjured

Fig. S5. Examples of alternative splicing in immune network of genes.

Fig. S6. Genes associated with hematopoietic activation, proliferation and anti-inflammatory cytokines activated in early & middle periods.

Fig. S7. Gene sets associated with extra-cellular matrix remodeling & satellite cell activation.

Fig. S8. a) Enriched KEGG pathways from differentially expressed genes for the late time points. The size of the circle corresponds to the number of significant genes with each enriched pathway. b) Heatmaps of gene sets activated in late period categorized by function.

Fig. S9. Area plots of FDR values for Gene Annotation (GO) clusters over time. GO terms were separated into major functional categories, and the IQR was computed for the terms in each group. The grey lines indicate the 25th and 75th percentiles, red lines denote the 25% of gene FDR values, the blue line denotes the median FDR value, and the green line denotes the 75% for FDR.

Fig. S10. Pathway-level scoring results for test datasets from PCA and the timepoint signatures methods. a) Principal component analysis. b) Normalized time point signatures method applied to mean pathway expression values. Timepoint signatures for 6 test samples and a truth training sample. The green curve indicates the control sample that was misclassified by the algorithm at the pathway level. Time point signatures for the 9 time points (blue lines) as well as 6 test samples (red and green lines).

Fig. S11. Differentially expressed gene pathways in injured samples over time.

Table S1. Significant GO clusters (FDR <0.05) identified for differentially expressed genes through the DAVID annotation tool. Each tab represents the annotations derived for each timepoint, clustered by function and sorted by FDR value from most to least significant.

Table S2: KEGG pathways identified for differentially expressed genes (FDR < 0.05). Pathways are listed for each timepoint and sorted by FDR value from most to least significant.

Table S3. Significant GO clusters identified from the 168h time point that were obtained from differentially expressed genes that were determined to contribute the largest variance at that time point.

Text S1: Transcriptional Signatures of Inflammation and Immune System Detected in Early Period

Pro-inflammatory cytokines and chemotactic protein members: IL-1 β , IL-6, IL-18, Tnf α , Osm, Ccl2, Ccr2, Cxcr2, Trem2, S100a8, FDR=2.21e-22 - GO:0034097, response to cytokine

Anti-inflammatory genes: Socs3, IL-1rn, IL-4 α , IL-10 α , IL-13 α 1, FDR=4.31e-10 - GO:0050728, negative regulation of inflammatory response

Invading immune cell genes: Cd68, Ly6c, Cd14, Cd163, Mrc1, Ptprc, Cd24a, Cd63, Itgam, Clec7a, Ltf, Irf7, Hp, FDR=7.6e-7 - GO:0050900, leukocyte migration involved in inflammatory response

Cytokines and chemokines: Ym1, S100a9, Spp1, Ccr1, Ccl3, Ccl11, Lcn2, Cxcl5, Ccl12, FDR=3.8e-44 - GO:0001816, cytokine production, FDR=9.05e-14 - GO:0032602, chemokine production

Signaling lymphocytic activation molecule family: Slamf7, Slamf8, Ly9, FDR=3.44e-16 - GO:0046649, lymphocyte activation

Pro-apoptotic loci: Casp1, Casp4, Casp8, Apaf1, Fas, FDR=1.40e-9 - GO:2001235, positive regulation of apoptotic signaling pathway

Anti-apoptotic loci: Xiap, Birc3, Birc5, Api5, Bax, Mcl1, Bcl2l1, FDR=2.17e-23 - GO:0043066, negative regulation of apoptotic process

Text S2: Transcriptional Signatures Associated With Injured Muscle Tissue Extracellular Matrix

Structural components of extra-cellular matrix (ECM) remodeling: Colla1, Colla2, Col3a1, Col5a1, Col5a2, Col5a3, Col6a1, Col6a2, Col6a3, Eln, FDR=4.19e-111 - GO:0016043, cellular component organization

Connective tissue: Fbn1, Ctgf, Has1, Hbegf, Fn1, Sparc, Tnc, FDR=6.65e-14 - GO:0061448, connective tissue development

ECM cross-linking enzymes: Lox, Loxl1, Loxl2, Plod3, Leprel2, P4hb

Small leucine-rich proteoglycans: Dcn, Bgn, Kera, Vcan, Lum, Ogn, FDR=3.69e-28 - GO:0036211, protein modification process

Adhesive glycoproteins: Pcolce, Itbpbp1, Lgals1, Dpt, Postn, Emilin2, Efemp2, Igfbp7, FDR=3.36e-16 - GO:0043062, extracellular structure organization

Tgf- β superfamily: Tgf- β i, Tgf- β r1, Tgf- β r2, Tgf- β 1

Formation and stabilization of blood vessels and arterial repair: Ang, Angpt2, Angptl1, Angptl4, Angptl7, Cthrc1, Aif1, FDR=3.12e-10 - GO:0001525, angiogenesis

Contractile fibers: ActB, Actg, Capg, Arpc3, Cotl1, Tln1, Tagln, Vcl, RhoA, FDR=7.8e-5 - GO:0030833, regulate actin filament polymerization, FDR=1.5e-3 - GO:0032273, positive regulation of protein polymerization

Integrin-associated genes: Itga5, Itga7, Itgam, Itgav, Itgb1, Itgb2, FDR=3.34e-5 - GO:0007229, integrin-mediated signaling pathway

Mmps, Adams and Timps: Mmp2, Mmp3, Mmp8, Mmp14, Mmp19, Adam8, Adam15, Adam19, Timp1, Timp2, FDR=6.83e-8 - GO:0048771, tissue remodeling

Text S3: Injured Muscle Tissue Changes from Pro- to Anti-Inflammatory States Several Days After Injury

Innate immunity and microbial recognition: Tlr1, Tlr7, Tlr8, FDR=0.003 - GO:0034121, regulation of toll-like receptor signaling pathway

Antigen presentation and hematopoietic activation and proliferation: Ptprc, IL-21r, IL-17ra, Vav1, Lyz2, Csf1r, Csf2rb, Csf2ra, Il3ra, Il5ra, Ifi204, Aif1, FDR=1.4e-8 - GO:0042110, T cell activation, FDR=8.18e-19 - GO:0030097, Haematopoiesis

Anti-inflammatory cytokines: IL-1rl1, Il-4ra, IL-10 α , Msr1, IL-13ra1, S100a9, FDR=2.9e-10 - KEGG mmu04630, cytokine-cytokine receptor interaction, FDR=9e-3 - GO:0010934, macrophage cytokine production

Phagocytic and complement cascade genes: Cyba, Ncf1, Ncf2, Ncf4, C1qa, C1qb, C1qc, C1ra, C1s, FDR=3.37e-8 - GO:0006956, complement activation, FDR=7e-6 - GO:0006909, phagocytosis

Notch signaling: Dll1, Notch2, Myc, Rbpj, Cdkn1a, FDR = 3.69e-18, GO:0002684, positive regulation of immune system process

Bone morphogenetic proteins: Bmp1, Bmp4, FDR = 0.08, GO:0005125, cytokine activity

Actively proliferating cells: Cdk1, FDR = 9.63e-9, GO:0007049, cell cycle

Text S4: Activation of Muscle Repair Machinery

Satellite cell markers: CD34, Itga7, Itgb1, Sdc3, Sdc4, Sdcbp, Cav1, Cxcr4, Cdh15, Ly6a, FDR=4.933e-5 - GO:0007519, muscle tissue development

Muscle-fusion genes: Tmem8c, Cdh15, Capn2, Capns1, Myof, Cav3, Itgb1, Vcam1, Itga4, FDR=2.5e-6 - GO:0098602, single organism cell adhesion

Basement membrane genes: Col4a1, Col4a2, Dysf, Trim72, Lamc2, Cav3, Ahnak, Anxa1, Anxa2, Anxa5, FDR=4.78e-9 - GO:0061024, membrane organization

Muscle-specific actins, myosins, troponins, and tropomyosins: Actl9, Clrn1, Myh3, Myl4, Myl6b, Cald1, Tpm4, Tnni1, Tnni3, Tnnt1, Tnnt2, Tnnc1, Tpm3, Des, Vim

Transcription factors: Itgb2, Rrad, Fos, JunB, FosB, Pbx2, Pbx3, Dusp5, Myc, BMyc, Mt3, Egr1, Egr2, Sgms2, Runx1, Grn, Pdlim3, Csrp3, Usf1, Arid5b, Naca, Ankrd1, Ankrd2, Atf3, Atf4, Atf6, Xbp1, Tead4, Nfe2l2, FDR=2.46e-10 - GO:0006351, transcription, DNA-templated

Text S5: Late Transcriptional Programs Activated in Response to Traumatic LLMI

Chemotaxis genes: Ccl6, Ccl8, Ccl9, Cxcl16, Fcer1g, Fcgr3, FDR=1.9e-5

Mast cell activation: Fyb, Fcer1g, Fcgr3, Fcgr2b, Lat2, Lcp2, FDR=3.33e-5 - GO:0045576, mast cell activation

Fc receptors: Fcer1g, Fcgr1, Fcgr3, Fcgr2b, Clec7a, Colec12, Hck, Sirpa, Slc11a1, Vav1, FDR=0.035 for KEGG mmu04664, Fc epsilon RI signaling pathway.

Lectins: Clec12a, Clec4a1, Clec4a2, Clec4a3, Clec4n, Clec7a, Clec10a.

Collagen fibril organization: Adamts14, Col3a1, Col5a1, Col5a2, Dpt, Lox, and Anxa2, FDR = 1e-7)

ECM receptors: VLA proteins ($\alpha 2$, $\alpha 5$, $\alpha 8$, $\alpha 9$, $\alpha 10$, $\alpha 11$), cytoadhesins ($\beta 3$, A11- β), and proteoglycans (Cd44, Sdc3, Sv2), KEGG ECM-receptor interaction pathway, FDR = $5.7e-7$

Angiogenesis genes: Col4a1, Col4a2, Robo4, Vash1, Sema5a, Sox18, GO:0001525, FDR = $3.24e-14$

Muscle contraction and muscle system processes: Cacna1s, Myom1, Myh2, Myh4, Myh7, Nos1, Kcnma1, Ryr1, Trim63, FDR= $6.7e-4$ and $1.6e-3$, respectively.

Ossification regulation: Gpnmb, Bglap, Sparc, Spp1, Runx2, Bmp1, Bmp5, Smad1

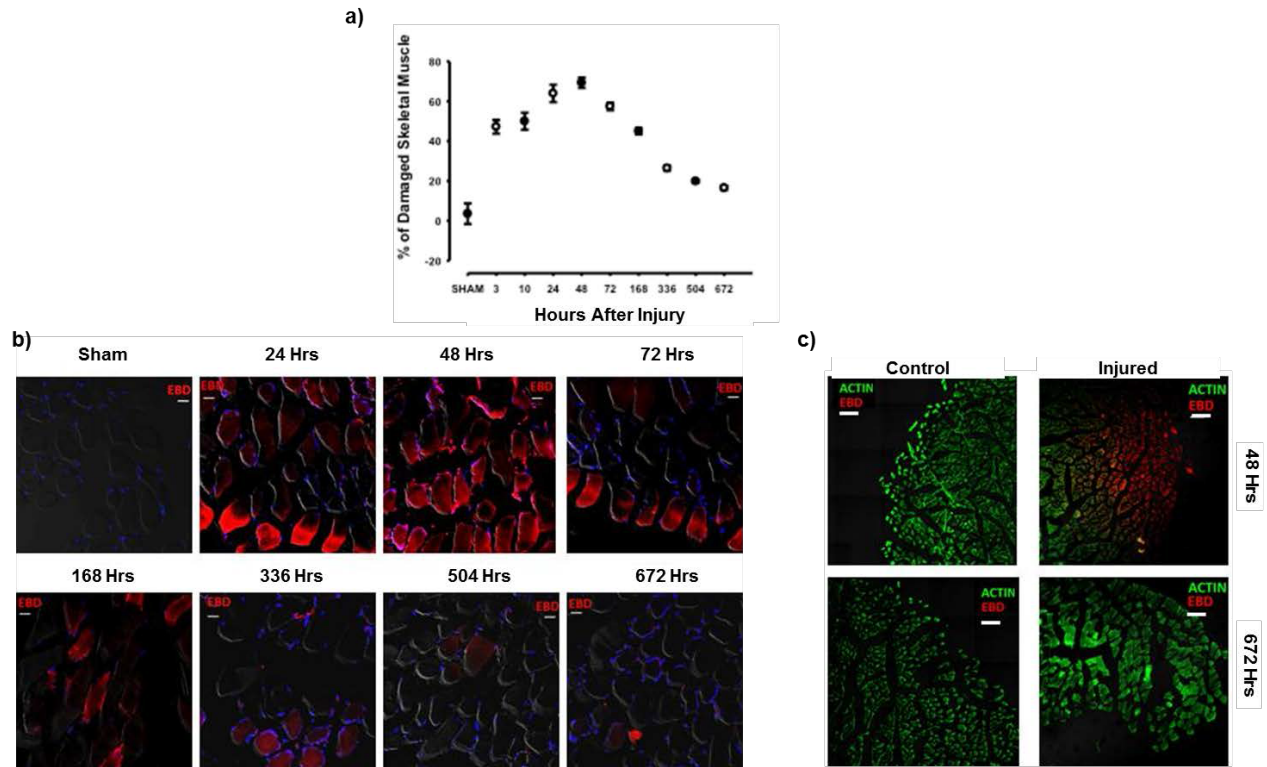


Fig. S1. Immuno-histological analysis of muscle after cryo-injury. a) Quantitative analysis of immuno-histological images revealed a gradual increase in tissue damage until 48 hours, indicating secondary damage to the muscle tissue occurred after the initial cryo-injury. b) Representative histological images of the injured TA stained with Evans Blue Dye (EBD – red) and DNA (blue) after several time points. c) Representative immuno-histological images at 48 hours and 672 hours after injury, whereby the green is stained for actin and red is stained for evans blue dye.

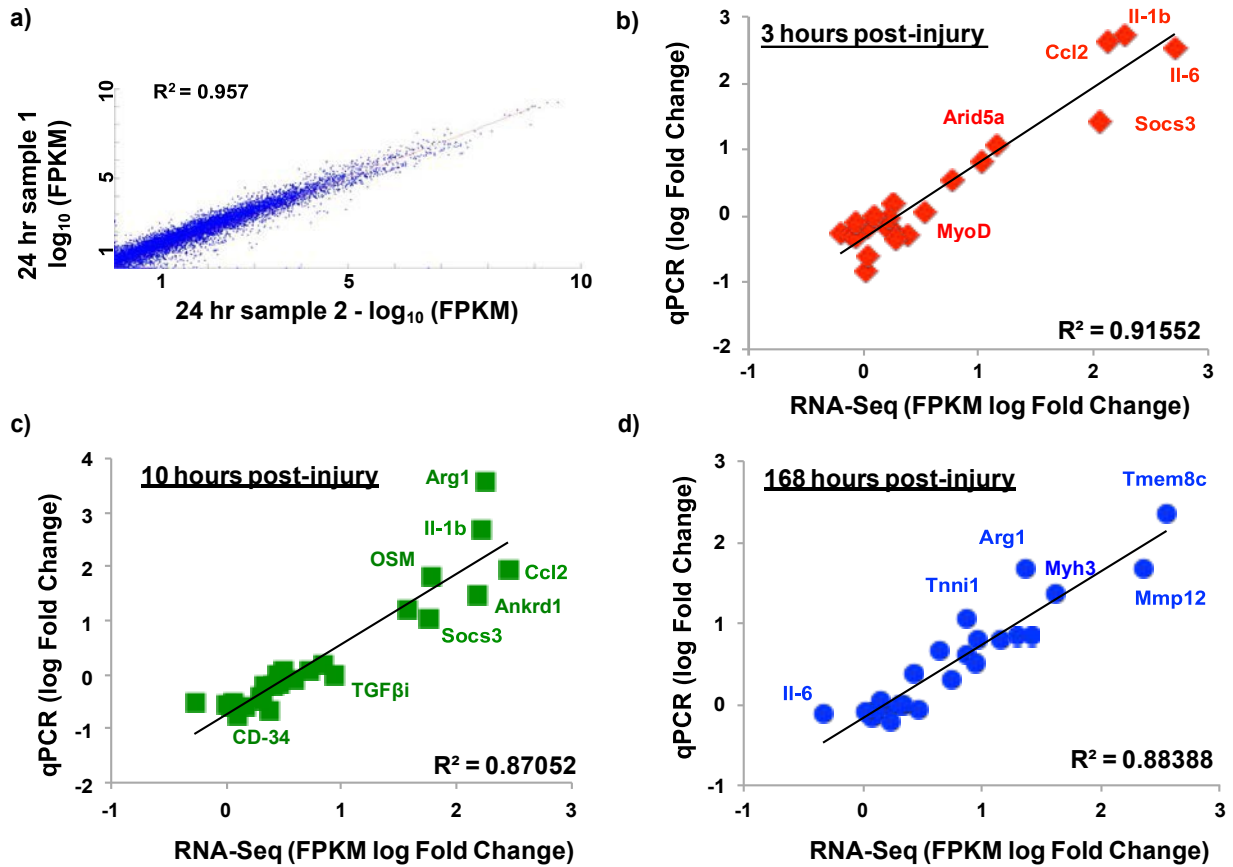


Fig. S2. a) Example of reproducibility from RNA-Seq datasets. Biological replicates of *in vivo* isolated RNA samples from 24 hours after injury. Sequencing libraries were prepared from the isolated RNA and a strong correlation ($R^2 = 0.95$) was observed for two representative examples. b) Validation of RNA-Seq data with qPCR comparing the injured versus uninjured samples for the 3 hour time point. c) Validation of RNA-Seq data with qPCR comparing the injured versus uninjured samples for the 10 hour time point. d) Validation of RNA-Seq data with qPCR comparing the injured versus uninjured samples for the 168 hr time point.

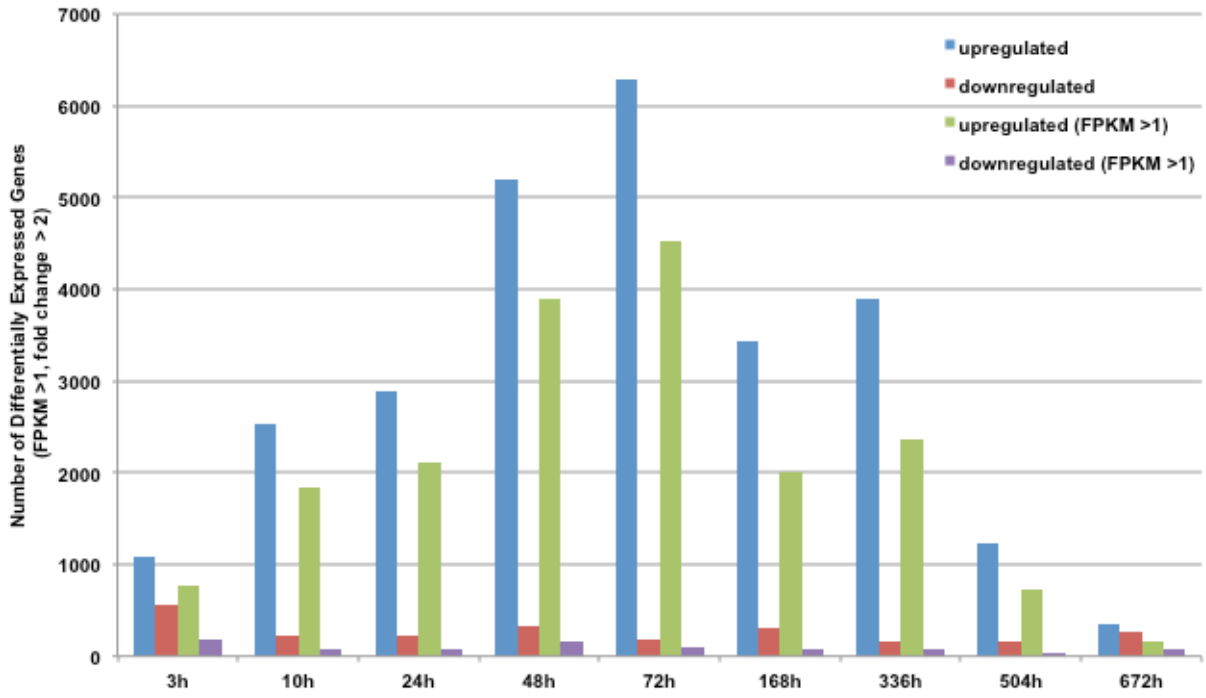


Fig. S3. Number of differentially expressed genes

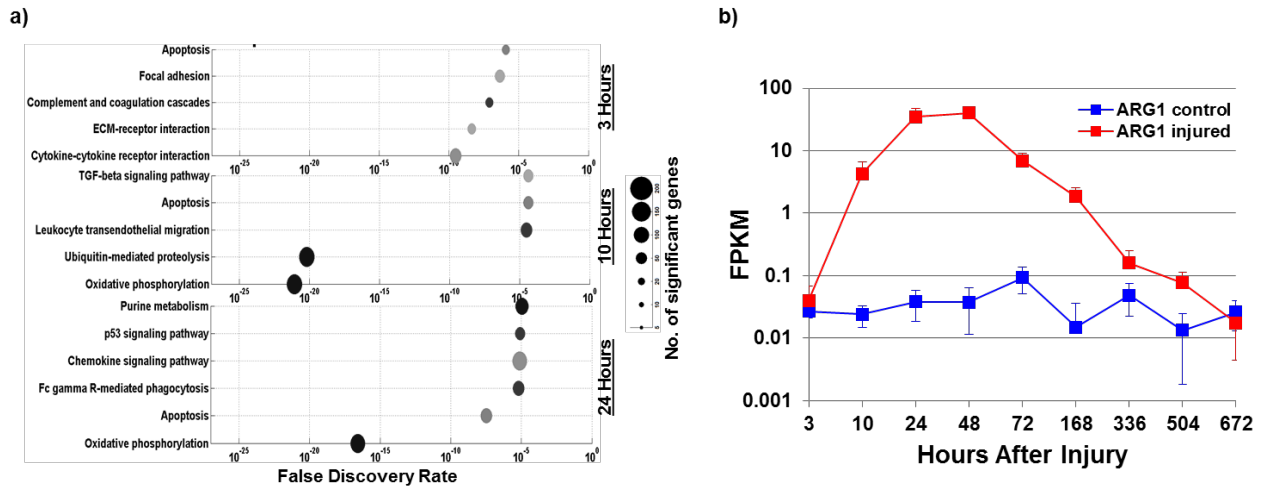


Fig. S4. Gene Sets Activated Early After Injury (3-24 hrs) a) Enriched KEGG pathways from differentially expressed genes for the early time points (3-24 hrs). The size of the circle corresponds to the number of significant genes with each enriched pathway. b) Heatmap of genes associated metabolism expressed in the early time period. c) Gene expression profile of Arginase 1 (Arg1), which is a molecule emitted by type 2 macrophages to balance inflammatory reactive-oxygen species present in the injured tissue. Red-Injured, Blue-Uninjured.

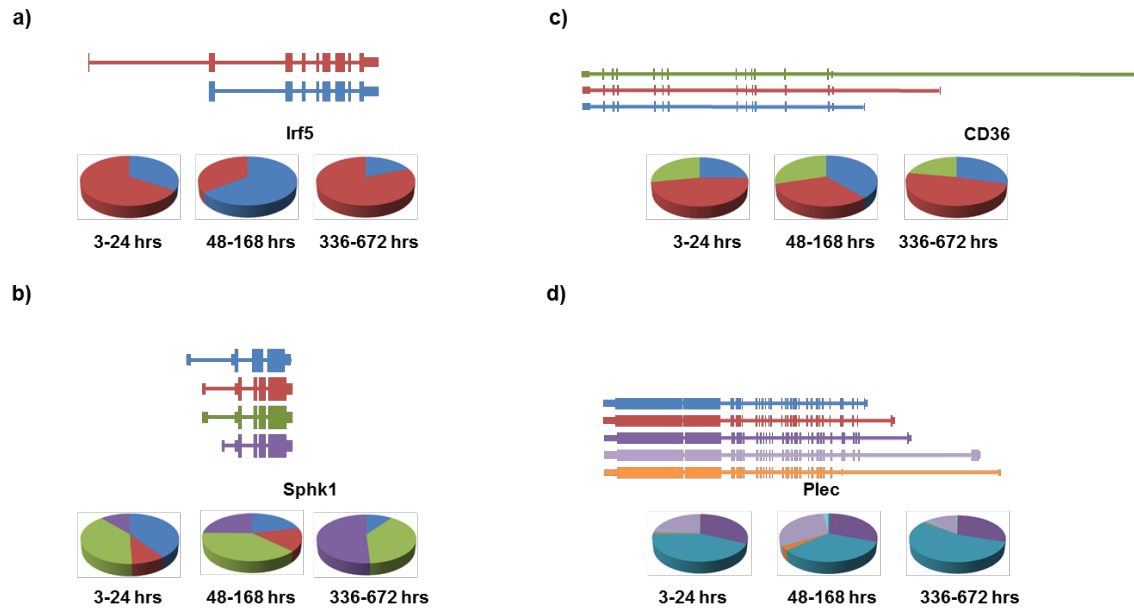


Fig. S5. Examples of alternative splicing in immune network of genes as determined by Cufflinks.

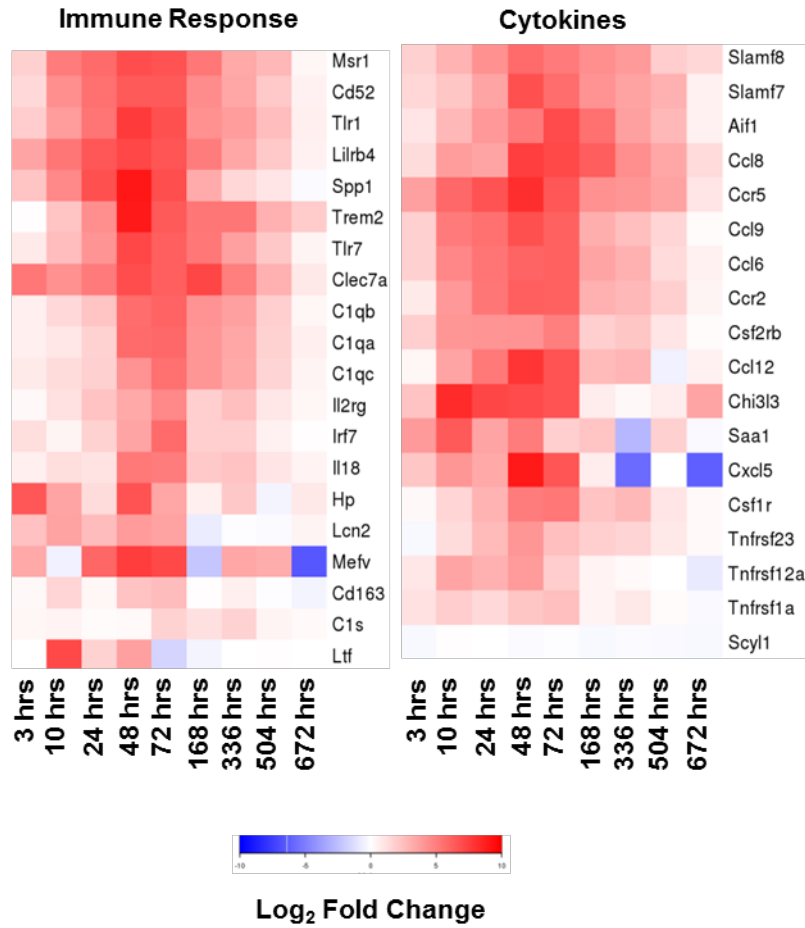


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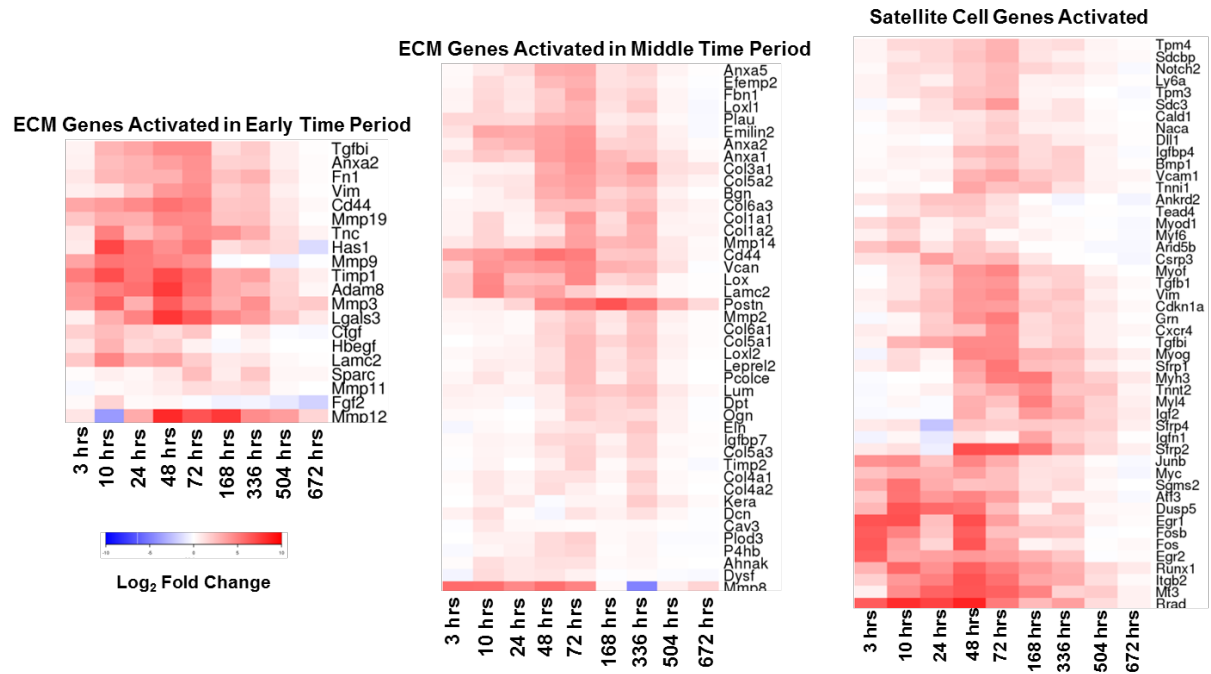


Fig. S7. Gene sets associated with extra-cellular matrix remodeling & satellite cell activation

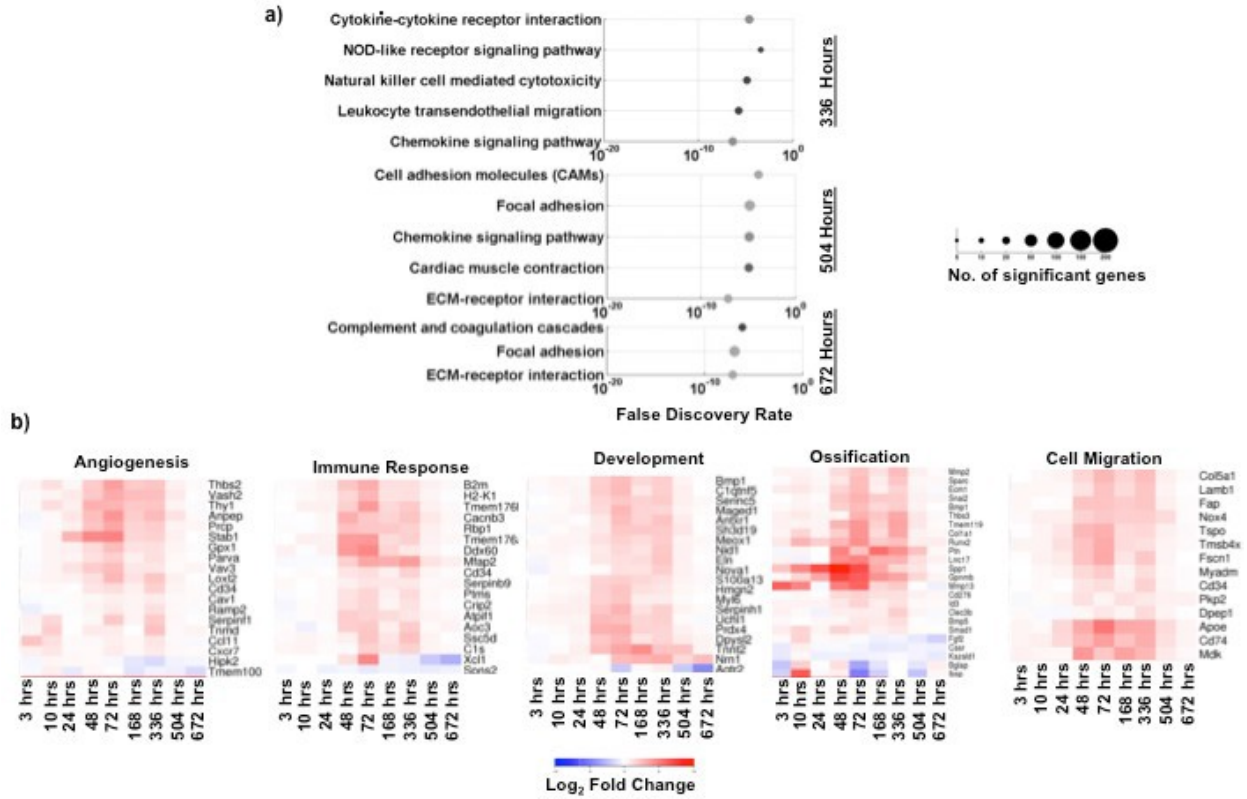


Fig. S8. a) Enriched KEGG pathways from differentially expressed genes for the late time points. The size of the circle corresponds to the number of significant genes with each enriched pathway. b) Heatmaps of gene sets activated in late period categorized by function.

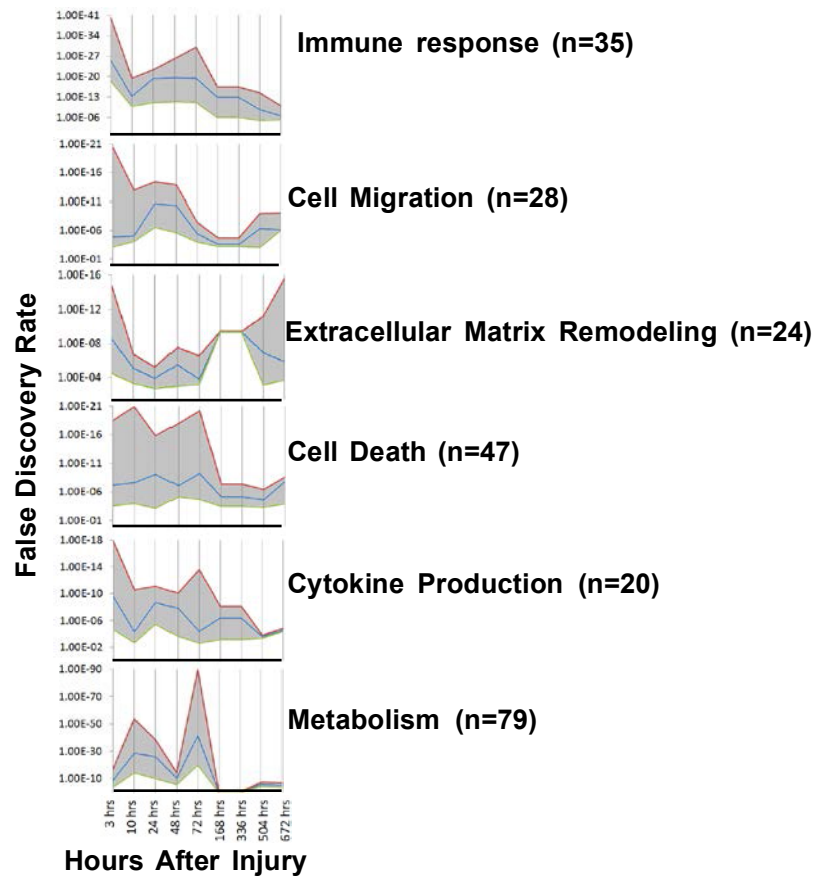


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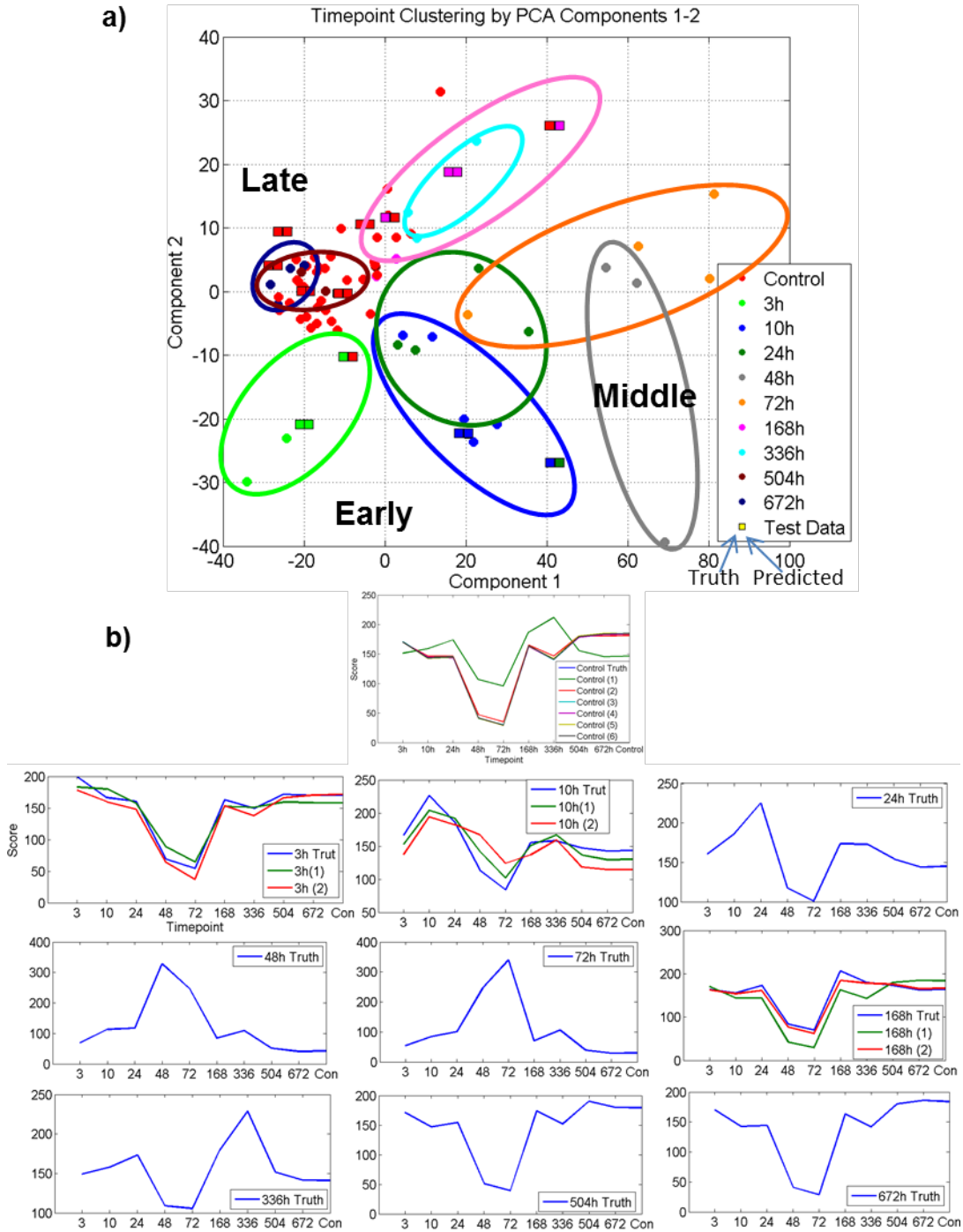


Fig. S10. Pathway-level scoring results for test datasets from PCA and the timepoint signatures methods. a) Principal component analysis. b) Normalized time point signatures method applied to mean pathway expression values. The top panel represents the timepoint signatures obtained for the uninjured control datasets for 6 test samples and a truth training sample. The green curve indicates the control sample that was misclassified by the algorithm at the pathway level. The next panels are derived from time point signatures for the 9 time points (blue lines) as well as 6 test samples (red and green lines).



Fig. S11. Differentially expressed gene pathways in injured samples over time.

GOTERM_BP_FAT	GO:0007155~cell adhesion	76	7.01	5.20E-11	PVR, NR2P, CADM3, ATP1B2, CLDN5, POSTN, DDR2, TGFBR2, CCRF1, CD44, CD93, CTGF, TGFBI, CSF3R, ZYX, ADAM8, COL1A2, BOC, CYR61, ICAM1, PDPN, PCOH47, MYH9, SRPA, BCL2L11, CD84, HES1, TNFAIP6, CD33, VCAN, LAMC2, DCBLD2, ITGAL, TNFRSF12A, TNC, NEDD9, ITGB2, SOX9, CDH4, ITGAM, ITGBL1, VCAM1, CD9, PVRL3, AGT, COMP, MYBPH, COL6A2, COL6A1, THBS1, SELPLG, THBS2, THBS3, FN1, THBS4, DPT, SPP1, COL18A1, PTPRC, SELP, SVEP1, TNXB, PLEK, SELL, PCDH12, NID1, ITGA3, ITGAA, EMLIN2, COL18A1, LAMA4, COL14A1, SNEI1, ITGAS, CLEC7A, BMPRI3	823	561	13588	2.24	1.57E-07	0.00	9.36E-08
GOTERM_BP_FAT	GO:0022610~biological adhesion	76	7.01	5.65E-11	PVR, NR2P, CADM3, ATP1B2, CLDN5, POSTN, DDR2, TGFBR2, CCRF1, CD44, CD93, CTGF, TGFBI, CSF3R, ZYX, ADAM8, COL1A2, BOC, CYR61, ICAM1, PDPN, PCOH47, MYH9, SRPA, BCL2L11, CD84, HES1, TNFAIP6, CD33, VCAN, LAMC2, DCBLD2, ITGAL, TNFRSF12A, TNC, NEDD9, ITGB2, SOX9, CDH4, ITGAM, ITGBL1, VCAM1, CD9, PVRL3, AGT, COMP, MYBPH, COL6A2, COL6A1, THBS1, SELPLG, THBS2, THBS3, FN1, THBS4, DPT, SPP1, COL18A1, PTPRC, SELP, SVEP1, TNXB, PLEK, SELL, PCDH12, NID1, ITGA3, ITGAA, EMLIN2, COL18A1, LAMA4, COL14A1, SNEI1, ITGAS, CLEC7A, BMPRI3	823	562	13588	2.23	1.70E-07	0.00	1.02E-07
Annotation Cluster 8 Category	Enrichment Score: 5.794336180757243	Count %	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_MF_FAT	GO:0008009~chemokine activity	14	1.29	1.36E-07	CXCL1, CCL3, CCL2, CXCL2, CXCL9, CCL8, PP4, CCL7, CCL6, CCL24, CCL11, CXCL14, PPPB, CXCL16	788	38	13288	6.21	1.16E-04	0.00	2.10E-04
GOTERM_MF_FAT	GO:0042379~chemokine receptor binding	14	1.29	1.93E-07	CXCL1, CCL3, CCL2, CXCL2, CXCL9, CCL8, PP4, CCL7, CCL6, CCL24, CCL11, CXCL14, PPPB, CXCL16	788	39	13288	6.05	1.65E-04	0.00	2.99E-04
Annotation Cluster 9 Category	Enrichment Score: 5.746125904859628	Count %	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0006915~apoptosis	56	5.17	1.28E-06	RASSF5, CSRN1, CASP12, SULF1, APAF1, DRAM1, PDCD7	823	465	13588	1.99	0.003849547	0.00	0.002303428
GOTERM_BP_FAT	GO:0016265~death	60	5.54	1.93E-06	NUAK2, NFKB1, CXCR2, TGFBR2, SHB, TMEM173, CASP4, BAG3, CASP8, FAS, CASP1, MYC, BCL10, LTBR, NLRP3, BCL2L11, DDIT4, OSM, TNFRSF10B, RIPK1, GADD45G, RIPK3, TNFAIP3, EIF2AK2, GADD45B, PPP1R15A, PEG3, MCL1, LITAF, TNFRSF12A, PML, STK17B, ARF6, IRAK3, TNFRSF1A, PRUNE2, IRAK3, PEG10, COMP, MAP3K1, SHSAS, ZC3H12A, FGL2, INPP5D, SRGN, PHLDA1, CFLAR, ACTC1, BIRC3, NFKB1L1, CIDEC, NRAA2, BIRC3, NFKB1L1, CIDEC, RASSF5, CSRN1, SULF1, CASP12, APAF1, DRAM1, PDCD7	823	519	13588	1.91	0.005805099	0.00	0.003476951
GOTERM_BP_FAT	GO:0008219~cell death	59	5.44	1.93E-06	NUAK2, NFKB1, CXCR2, TGFBR2, SHB, TMEM173, CASP4, BAG3, CASP8, FAS, CASP1, MYC, BCL10, LTBR, NLRP3, BCL2L11, DDIT4, OSM, TNFRSF10B, RIPK1, GADD45G, RIPK3, TNFAIP3, EIF2AK2, GADD45B, PPP1R15A, PEG3, MCL1, LITAF, TNFRSF12A, PML, STK17B, ARF6, IRAK3, TNFRSF1A, PRUNE2, IRAK3, PEG10, COMP, MAP3K1, SHSAS, ZC3H12A, FGL2, INPP5D, SRGN, PHLDA1, CFLAR, LY2Z, ACTC1, BIRC3, NFKB1L1, CIDEC, RASSF5, CSRN1, SULF1, CASP12, APAF1, DRAM1, PDCD7	823	507	13588	1.92	0.005808084	0.00	0.003478744
GOTERM_BP_FAT	GO:0012501~programmed cell death	56	5.17	2.18E-06	NUAK2, NFKB1, CXCR2, TGFBR2, SHB, TMEM173, CASP4, BAG3, CASP8, FAS, CASP1, MYC, BCL10, LTBR, NLRP3, BCL2L11, DDIT4, OSM, TNFRSF10B, RIPK1, GADD45G, RIPK3, TNFAIP3, EIF2AK2, GADD45B, PPP1R15A, PEG3, MCL1, LITAF, TNFRSF12A, PML, STK17B, ARF6, IRAK3, TNFRSF1A, PRUNE2, IRAK3, PEG10, COMP, MAP3K1, SHSAS, ZC3H12A, FGL2, INPP5D, SRGN, PHLDA1, CFLAR, ACTC1, BIRC3, NFKB1L1, CIDEC, RASSF5, CSRN1, CASP12, SULF1, APAF1, DRAM1, PDCD7	823	473	13588	1.95	0.006542704	0.00	0.003920182
Annotation Cluster 10 Category	Enrichment Score: 4.535473351581223	Count %	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0010941~regulation of cell death	66	6.09	3.28E-07	NUAK2, FOXO1, PNP, TGFBR2, BDNF, CASP4, APOE, BAG3, HMOX1, CHST11, CASP8, FAS, CASP1, MYC, BCL10, PM1, NLRP3, BCL2L11, ADRB2, HIF1A, TNFRSF10B, BTG2, BTG1, RIPK3, IFIH1, FGFRL3, MCL1, PML, STK17B, HSPA1A, HSPA1B, NR3C1, SOX9, CD74, ADA, GCHI, IRAK3, ALDH3A3, AGT, SHSAS, BCL3, FCER1G, INPP5D, SKI1, ANGPTL4, SPP1, BMP4, COL18A1, CFLAR, PTPRC, PTPN6, KLF10, TGFBR1, SPHK1, NRAA2, BIRC3, NFKB1L1, FCGR3, CIDEC, NOTCH2, CDKN1A, NUPR1, CASP12, APAF1, ID3, PDCD7, IFI204	823	563	13588	1.94	9.88E-04	0.00	5.91E-04
GOTERM_BP_FAT	GO:0042081~regulation of apoptosis	65	6.00	3.70E-07	NUAK2, FOXO1, PNP, TGFBR2, BDNF, CASP4, APOE, BAG3, HMOX1, CHST11, CASP8, FAS, CASP1, MYC, BCL10, PM1, NLRP3, BCL2L11, ADRB2, HIF1A, TNFRSF10B, BTG2, BTG1, RIPK3, IFIH1, FGFRL3, MCL1, PML, STK17B, HSPA1A, HSPA1B, NR3C1, SOX9, CD74, ADA, GCHI, IRAK3, ALDH3A3, AGT, SHSAS, BCL3, FCER1G, INPP5D, SKI1, ANGPTL4, SPP1, COL18A1, CFLAR, PTPRC, PTPN6, KLF10, TGFBR1, SPHK1, NRAA2, BIRC3, NFKB1L1, FCGR3, CIDEC, NOTCH2, CDKN1A, NUPR1, CASP12, APAF1, ID3, PDCD7, IFI204	823	553	13588	1.94	0.001115723	0.00	6.67E-04

GOTERM_BP_FAT	GO:0051173	positive regulation of nitrogen compound metabolic process	121	4.22	2.33E-06	MYO01, THRB, TGF03, TLK2, TLK4, PNP, TGF01, CTED2, KDM1A, MYO08, TRP63, RARA, RARB, BCL10, REL, SIK2, ARNTL, SIK4, MED13, PPARGC1B, PTH4, HOKD9, HIF1A, ZFP462, JUN, VEGFA, SIK1, VGLL2, NFE2L2, FUS, HMGB2, ADORA2B, CYTL1, SOX4, ITGB2, SFP11, SOX9, PLAGL1, SLC11A1, TEAD4, AGRN, RUNX1, RUNX2, TRP53, BMP4, KLF5, KLF6, BMP2, ESRRB, EPAS1, IZFP1, MAFB, MAML1, SMAD5, CREBBP, NR4A2, ESRG, NR4A1, SMAD3, SMAD1, NR4A3, KLF15, TEAD3, SREBF2, ATF4, SALL4, EAF1, CSRN1P, KLF2, KLF4, PPARA, CHURC1, FOXK1, ELF4, FOS, SDFR, GUCY1A3, YAP1, MYC, FGF2, RHOG, SERTAD1, EGR1, AR, EGR2, HSP90AA1, TOPORS, HMGA1, SMO, MURC, CAND1, FOXC1, INGS, ABLUM2, GLI2, ABLUM3, NUPFP1, PRDM16, TNFRSF1A, REL, NFAT3, BCL3, MYOG, PTK3, CEPBA, BCKDHA, MYF6, PTPRC, IL6, CEPBB, CEPBD, TBX1, AFF1, STAT3, IRF8, IRF1, PPK1, RBM14, RBM15, NFIA, ARAP1	2080	526	13588	1.50	9.57E-03	2.67E-04	4.34E-03
GOTERM_BP_FAT	GO:0045941	positive regulation of transcription from RNA polymerase II promoter	89	3.10	2.36E-06	MYO01, THRB, TGF03, TGF01, CTED2, KDM1A, MYO08, TRP63, RARA, RARB, BCL10, REL, SIK2, ARNTL, SIK4, MED13, PPARGC1B, HOKD9, HIF1A, ZFP462, JUN, VEGFA, SIK1, VGLL2, NFE2L2, FUS, HMGB2, CYTL1, SOX4, SFP11, SOX9, PLAGL1, SLC11A1, TNFRSF1A, TEAD4, NFAT3, BCL3, MYOG, AGRN, RUNX1, RUNX2, BMP4, CEPBA, TRP53, KLF6, BMP2, ESRRB, IL6, CEPBB, IZFP1, EPAS1, MAFB, CEPBD, MAML1, CREBBP, SMAD5, NR4A2, SMAD3, NR4A1, TBX1, NR4A3, SMAD1, TEAD3, SREBF2, ATF4, SALL4, EAF1, CSRN1P, IRF1, PPK1, RBM14, RBM15, NFIA, ARAP1	2080	358	13588	1.62	9.72E-03	2.64E-04	4.41E-03
GOTERM_BP_FAT	GO:0045941	positive regulation of transcription	111	3.87	2.96E-06	MYO01, THRB, TGF03, TGF01, CTED2, KDM1A, MYO08, TRP63, RARA, RARB, BCL10, REL, SIK2, ARNTL, SIK4, MED13, PPARGC1B, HOKD9, HIF1A, ZFP462, JUN, VEGFA, SIK1, VGLL2, NFE2L2, FUS, HMGB2, CYTL1, SOX4, SFP11, SOX9, PLAGL1, SLC11A1, TEAD4, AGRN, RUNX1, RUNX2, TRP53, BMP4, KLF5, KLF6, ESRB, BMP2, EPAS1, IZFP1, MAFB, MAML1, SMAD5, CREBBP, NR4A2, ESRG, NR4A1, SMAD3, SMAD1, NR4A3, KLF15, TEAD3, SREBF2, ATF4, SALL4, EAF1, CSRN1P, KLF2, KLF4, PPARA, CHURC1, FOXK1, ELF4, FOS, SDFR, YAP1, FGF2, MYC, RHOG, SERTAD1, EGR1, AR, EGR2, TOPORS, HMGA1, SMO, MURC, CAND1, FOXC1, INGS, ABLUM2, ABLUM1, GLI2, NUPFP1, PRDM16, TNFRSF1A, REL, NFAT3, BCL3, MYOG, CEPBA, BCKDHA, MYF6, IL6, CEPBB, CEPBD, TBX1, AFF1, STAT3, IRF8, IRF1, PPK1, RBM14, RBM15, NFIA, ARAP1	2080	475	13588	1.53	1.21E-02	2.98E-04	5.52E-03
GOTERM_BP_FAT	GO:0010628	positive regulation of gene expression	113	3.94	3.77E-06	MYO01, THRB, TGF03, TGF01, CTED2, KDM1A, MYO08, TRP63, RARA, RARB, BCL10, REL, SIK2, ARNTL, SIK4, MED13, PPARGC1B, HOKD9, HIF1A, ZFP462, JUN, VEGFA, SIK1, VGLL2, NFE2L2, FUS, HMGB2, CYTL1, SOX4, SFP11, SOX9, PLAGL1, SLC11A1, TEAD4, AGRN, RUNX1, RUNX2, TRP53, BMP4, KLF5, KLF6, ESRB, BMP2, EPAS1, IZFP1, MAFB, MAML1, SMAD5, CREBBP, NR4A2, ESRG, NR4A1, SMAD3, SMAD1, NR4A3, KLF15, TEAD3, SREBF2, ATF4, SALL4, EAF1, CSRN1P, KLF2, KLF4, PPARA, CHURC1, FOXK1, ELF4, FOS, SDFR, YAP1, MYC, FGF2, RHOG, SERTAD1, EGR1, AR, EGR2, TOPORS, HMGA1, SMO, MURC, CAND1, FOXC1, INGS, ABLUM2, ABLUM1, GLI2, NUPFP1, PRDM16, TNFRSF1A, REL, NFAT3, BCL3, MYOG, CEPBA, BCKDHA, MYF6, IL6, CEPBB, CEPBD, TBX1, AFF1, STAT3, IRF8, IRF1, PPK1, RBM14, RBM15, NFIA, ARAP1	2080	488	13588	1.51	1.54E-02	3.38E-04	7.02E-03
GOTERM_BP_FAT	GO:0006357	regulation of transcription from RNA polymerase II promoter	136	4.74	5.27E-06	MYO01, THRB, TGF03, TGF01, CTED2, KDM1A, MYO08, TRP63, RARA, RARB, BCL10, REL, SIK2, ARNTL, SIK4, MED13, PPARGC1B, HOKD9, HIF1A, ZFP462, JUN, VEGFA, SIK1, VGLL2, NFE2L2, FUS, HMGB2, ADORA2B, CYTL1, SOX4, SFP11, SOX9, PLAGL1, SLC11A1, TEAD4, AGRN, RUNX1, RUNX2, TRP53, BMP4, KLF5, KLF6, ESRB, BMP2, EPAS1, IZFP1, MAFB, MAML1, SMAD5, CREBBP, NR4A2, ESRG, NR4A1, SMAD3, SMAD1, NR4A3, KLF15, TEAD3, SREBF2, ATF4, SALL4, EAF1, CSRN1P, KLF2, KLF4, PPARA, CHURC1, FOXK1, ELF4, FOS, SDFR, YAP1, MYC, FGF2, RHOG, SERTAD1, EGR1, AR, EGR2, TOPORS, HMGA1, SMO, MURC, CAND1, FOXC1, INGS, ABLUM2, ABLUM1, GLI2, NUPFP1, PRDM16, TNFRSF1A, REL, NFAT3, BCL3, MYOG, CEPBA, BCKDHA, MYF6, IL6, CEPBB, CEPBD, TBX1, AFF1, STAT3, IRF8, IRF1, PPK1, RBM14, RBM15, NFIA, ARAP1	2080	616	13588	1.44	2.15E-02	4.10E-04	9.82E-03
GOTERM_BP_FAT	GO:0045935	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic proc	116	4.04	6.74E-06	MYO01, THRB, TGF03, TGF01, CTED2, KDM1A, MYO08, TRP63, RARA, RARB, BCL10, REL, SIK2, ARNTL, SIK4, MED13, PPARGC1B, PTH4, HOKD9, HIF1A, ZFP462, JUN, VEGFA, SIK1, VGLL2, NFE2L2, FUS, HMGB2, ADORA2B, CYTL1, SOX4, SFP11, SOX9, PLAGL1, SLC11A1, TEAD4, AGRN, RUNX1, RUNX2, TRP53, BMP4, KLF5, KLF6, ESRB, BMP2, EPAS1, IZFP1, MAFB, MAML1, SMAD5, CREBBP, NR4A2, ESRG, NR4A1, SMAD3, SMAD1, NR4A3, KLF15, TEAD3, SREBF2, ATF4, SALL4, EAF1, CSRN1P, KLF2, KLF4, PPARA, CHURC1, FOXK1, ELF4, FOS, SDFR, YAP1, MYC, FGF2, RHOG, SERTAD1, EGR1, AR, EGR2, TOPORS, HMGA1, SMO, MURC, CAND1, FOXC1, INGS, ABLUM2, ABLUM1, GLI2, NUPFP1, PRDM16, TNFRSF1A, REL, NFAT3, BCL3, MYOG, CEPBA, BCKDHA, MYF6, PTPRC, IL6, CEPBB, CEPBD, TBX1, AFF1, STAT3, IRF8, IRF1, PPK1, RBM14, RBM15, NFIA, ARAP1	2080	510	13588	1.49	2.74E-02	5.06E-04	1.26E-02
GOTERM_BP_FAT	GO:0010557	positive regulation of macromolecule biosynthetic process	119	4.15	9.65E-06	MYO01, THRB, TGF03, TGF01, CTED2, KDM1A, MYO08, TRP63, RARA, RARB, BCL10, REL, SIK2, ARNTL, SIK4, MED13, PPARGC1B, HOKD9, HIF1A, ZFP462, JUN, VEGFA, SIK1, VGLL2, NFE2L2, FUS, HMGB2, ADORA2B, CYTL1, SOX4, SFP11, SOX9, PLAGL1, SLC11A1, TEAD4, AGRN, RUNX1, RUNX2, TRP53, BMP4, KLF5, KLF6, ESRB, BMP2, EPAS1, IZFP1, MAFB, MAML1, SMAD5, CREBBP, NR4A2, ESRG, NR4A1, SMAD3, SMAD1, NR4A3, KLF15, TEAD3, SREBF2, ATF4, SALL4, EAF1, CSRN1P, KLF2, KLF4, PPARA, CHURC1, FOXK1, ELF4, FOS, SDFR, YAP1, MYC, FGF2, RHOG, SERTAD1, EGR1, AR, EGR2, TOPORS, HMGA1, SMO, MURC, CAND1, FOXC1, EFS2, SERP1, INGS, ABLUM2, GLI2, ABLUM3, NUPFP1, PRDM16, TNFRSF1A, REL, NFAT3, BCL3, MYOG, CEPBA, BCKDHA, MYF6, IL6, CEPBB, CEPBD, TBX1, AFF1, STAT3, IRF8, IRF1, PPK1, RBM14, RBM15, NFIA, ARAP1	2080	530	13588	1.47	3.91E-02	6.87E-04	1.80E-02

Gene	Accession	Protein	Start	End	Score	E-value	Score	E-value	Score	E-value
GOTERM_MF_FAT	GO:0032557	purine ribonucleotide binding	356	12.46	4.82E-11	1.36	6.82E-08	1.70E-08	7.95E-08	
GOTERM_MF_FAT	GO:0000169	nucleotide binding	413	14.46	7.12E-11	1.30	1.01E-06	1.68E-07	1.17E-06	
GOTERM_MF_FAT	GO:0030054	adenyl nucleotide binding	295	10.33	9.02E-08	1.32	1.28E-04	1.59E-05	1.49E-04	
GOTERM_MF_FAT	GO:0001883	purine nucleotide binding	296	10.36	1.32E-07	1.31	1.87E-04	1.70E-05	2.74E-04	

IQGAP2, ARHGAP15, TBC1D19, IQGAP1, TBC1D16, HMMH1, ARHGAP22, ARHGAP20, RINI, TIAM2,
ARHGAP1, RANBP1, ARHGAP11A, ARHGAP9, SCS, ARHGAP28, SIPA1L1, TWI1, ARHGAP25, ARHGAP30,
ACAP1, RINI, RIN3, ARFGAP2, ARHGAP2, ARFGAP3, RAPIGAP, TBC1D9, GFSM3, SIPA1, MYO9B,
FAM138, ADAP1, DOCK2, RGS12, GMP, GFSM1, RASA3, ARHGDA, ARHGDB, TBC1D2, TBC1D2B,
TBC1D10C, ABR, TBC1D10A, RGS18, RGS16, RACGAP1, RGS14, USPNL, ADAP2, RGS2, CHML, GRTF1,

GOTERM_MF_FAT GO:0005096-GTPase activator activity

56 1.96

3.05E-07 SH3BP1, ARAP1

1935 192 13288

2.00 4.32E-04

2.70E-05

5.03E-04

Annotation Cluster 19	Enrichment Score: 3.3671298805420657	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0016791~phosphatase activity	50	2.32	2.99E-05	PP1PSK2, PGAM1, PTPN22, PGAM2, PPP5K1, NTSC, PTPRL, PPP2C2, FBP2, PPP3B3A, LPIN2, PTPRO, LPIN3, PPM3A, PPM1L, PPM3A, PPM3B, NTSCLA, RBCK333ZORR, PPK3E1, PPM3A, AC2, PTP2B, PPK3C, PPK3CA, NPFSO, PPTC7, PTPN7, PTPN6, PTPN8, PTPN9, PTPN18, PTPN3, PTPN4, PTPR4, EPM2A, EPHK2, DUSP23, ATP1A1, BPGM, PTPN12, DUSP5, DUSP4, DUSP28, PTP4A3, DUSP26, PTPN1, PMPRT1, DUSP8, DUSP6	1524	238	13288	1.83	3.77E-02	1.54E-03	4.88E-02
Annotation Cluster 25	Enrichment Score: 2.4724967356094183	Count <th>%</th> <th>PValue</th> <th>Genes</th> <th>List Total</th> <th>Pop Hits</th> <th>Pop Total</th> <th>Fold Enrichment</th> <th>Bonferroni</th> <th>Benjamini</th> <th>FDR</th>	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006631~fatty acid metabolic process	48	2.23	1.46E-05	MHO5A, PINKA3, SLC71A1, PPARA, ACOY1, ACAD8, ECH1, CPT2, STAT5B, NDUFA8, ECHS1, CD74, HADHA, HADHB, SC4MDL, FAB1, ELOVL1, PRKAR2B, TNFRSF1A, ALOX5AP, PRKAA2, ELOVL6, HADH, HPGDS, GHR, ACSL5, SCD1, CPT1B, ACAA2, SCD2, ACAD4, TBXAS1, NCF1, ALDH5A1, ACADS, PDPE, FADS1, PRKAR2, EPHK2, FADS3, CROT, PTHN, CPT1A, BRCA1, ACADVL, ALOX5, AACS, DEGS1	1594	184	13588	2.22	5.31E-04	1.12E-05	2.68E-04
Annotation Cluster 27	Enrichment Score: 2.4478334888926443	Count <th>%</th> <th>PValue</th> <th>Genes</th> <th>List Total</th> <th>Pop Hits</th> <th>Pop Total</th> <th>Fold Enrichment</th> <th>Bonferroni</th> <th>Benjamini</th> <th>FDR</th>	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0051130~positive regulation of cellular component organization	32	1.49	2.08E-05	FMNL, PLK4, FCGR2B, TPRP, CFL1, CLEC7A	1594	122	13588	2.24	7.30E-02	1.26E-03	3.83E-02
Annotation Cluster 27	Enrichment Score: 2.4478334888926443	Count <th>%</th> <th>PValue</th> <th>Genes</th> <th>List Total</th> <th>Pop Hits</th> <th>Pop Total</th> <th>Fold Enrichment</th> <th>Bonferroni</th> <th>Benjamini</th> <th>FDR</th>	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0051493~regulation of cytoskeleton organization	29	1.35	5.90E-06	LIMA1, CAPZL, ARPC5, VILL, DSTN, ACTR3, ARPC1, ARPC2, RHOA, RANBP1, SKA1, SYNPO, TES, DBNL, ARHGFE2, CDC8BA, PLEK, CEP192, MYO1F, TMSB10, MID1P1, FMN1, ARPC1B, PLK4, CORO1A, CFL1	1594	99	13588	2.50	2.12E-02	4.29E-04	1.08E-02
Annotation Cluster 30	Enrichment Score: 2.3517354573541587	Count <th>%</th> <th>PValue</th> <th>Genes</th> <th>List Total</th> <th>Pop Hits</th> <th>Pop Total</th> <th>Fold Enrichment</th> <th>Bonferroni</th> <th>Benjamini</th> <th>FDR</th>	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0032956~regulation of actin cytoskeleton organization	21	0.98	8.63E-06	DBNL, LIMA1, CDC8BA, PLEK, CAPZL, MYO1F, TMSB10, ARPC5, VILL, DSTN, ACTR3, FMN1, ARPC1B, CORO1A, ARPC3, ARPC2, CFL1, CAPG, RHOA, TMSB4X, SYNPO	1594	60	13588	2.98	3.09E-02	6.04E-04	1.59E-02
Annotation Cluster 30	Enrichment Score: 2.3517354573541587	Count <th>%</th> <th>PValue</th> <th>Genes</th> <th>List Total</th> <th>Pop Hits</th> <th>Pop Total</th> <th>Fold Enrichment</th> <th>Bonferroni</th> <th>Benjamini</th> <th>FDR</th>	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0032970~regulation of actin filament-based process	21	0.98	1.14E-05	CORO1A, ARPC3, ARPC2, CFL1, CAPG, RHOA, TMSB4X, SYNPO	1594	61	13588	2.93	4.08E-02	7.56E-04	2.10E-02
Annotation Cluster 30	Enrichment Score: 2.3517354573541587	Count <th>%</th> <th>PValue</th> <th>Genes</th> <th>List Total</th> <th>Pop Hits</th> <th>Pop Total</th> <th>Fold Enrichment</th> <th>Bonferroni</th> <th>Benjamini</th> <th>FDR</th>	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0033043~regulation of organelle organization	38	1.77	1.37E-05	LIMA1, LST1, CAPZ1, ARPC5, TGF1, VILL, DSTN, ACTR3, CLU7, ARPC1, ARPC2, RHOA, RANBP1, SKA1, TES, SYNPO, TRPS3, DBNL, ARHGFE2, CDC8BA, PLEK, CEP192, NUSAP1, MYO1F, TMSB10, HERC2, MID1P1, UBE2B, FMN1, ARPC1B, CORO1A, PLK4, YWHAH, MAD2L1, CFL1, CAPG, TMSB4X, STMN1	1594	154	13588	2.10	4.88E-02	8.77E-04	2.53E-02
Annotation Cluster 32	Enrichment Score: 2.1864103669617593	Count <th>%</th> <th>PValue</th> <th>Genes</th> <th>List Total</th> <th>Pop Hits</th> <th>Pop Total</th> <th>Fold Enrichment</th> <th>Bonferroni</th> <th>Benjamini</th> <th>FDR</th>	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0030095~GTPase regulator activity	70	3.25	1.14E-05	RASGEF1B, ARHGAP18, IQGAP2, ARHGAP15, RGL1, IQGAP1, TRC1D16, HMHA1, ARHGAP22, DMXL2, ARHGAP20, RINL, ARHGAP1, RANBP1, ARHGAP11A, DOCK10, DOCK11, DAR2IP, ARHGFE2, MADD, ARHGFE6, RAB11L1, ARHGAP2B, PSD4, ARHGFE9, ECT2, WAS, THY1, ARHGAP25, ARHGAP30, MAP4K4, RIN2, SRGAP3, RIN1, FGD2, ARFGAP3, TRC1D9, GPSM3, CYTH4, MAFK1, MYO9B, ADAF1, DOCK2, RASGRP3, GMP, SOS2, RASAL3, IQSEC3, RASA3, RAP1GAP2, FGD3, ARHGDI4, ARHGDI8, OBSLN, TRC1D2B, VAV3, ABR, EXPH5, RGS18, DOCK8, RGS16, RACGAP1, DOCK5, VAV1, RGS14, ADAP2, RGS2, SH3BP1, ARAP1, BCAR3	1524	361	13288	1.69	1.45E-02	7.32E-04	1.86E-02
Annotation Cluster 32	Enrichment Score: 2.1864103669617593	Count <th>%</th> <th>PValue</th> <th>Genes</th> <th>List Total</th> <th>Pop Hits</th> <th>Pop Total</th> <th>Fold Enrichment</th> <th>Bonferroni</th> <th>Benjamini</th> <th>FDR</th>	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0060589~nucleoside-triphosphatase regulator activity	70	3.25	2.01E-05	SH3BP1, ARAP1, BCAR3	1524	367	13288	1.66	2.55E-02	1.07E-03	3.27E-02
Annotation Cluster 58	Enrichment Score: 1.561380646898854	Count <th>%</th> <th>PValue</th> <th>Genes</th> <th>List Total</th> <th>Pop Hits</th> <th>Pop Total</th> <th>Fold Enrichment</th> <th>Bonferroni</th> <th>Benjamini</th> <th>FDR</th>	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0002684~positive regulation of immune system process	50	2.32	8.11E-07	IL18, STAT5B, HPS1, TLR2, PTPN22, TLR4, C1QC, PNP, TLR8, TGF1, B2M, CFP, KLH6, MYD88, HSP90AA1, IYIN, NFKB1, CD40, THY1, CD1A, C1QB, LAT2, CD19, H2-AA, ITGAL, LARA, UNC93B1, IL7R, ADA, CD74, SLC11A1, FCER1G, IL2RG, SH2B2, NPFSO, THBS1, PTPN6, PTPN8, CARD9, H2-M1, IKZF1, CFB, FCGR1, FCGR3, CORO1A, CDKN1A, PLCG2, CLEC7A, H2-DMA, SASH3	1594	206	13588	2.07	2.95E-03	8.94E-05	1.49E-03
Annotation Cluster 69	Enrichment Score: 1.2861838620748725	Count <th>%</th> <th>PValue</th> <th>Genes</th> <th>List Total</th> <th>Pop Hits</th> <th>Pop Total</th> <th>Fold Enrichment</th> <th>Bonferroni</th> <th>Benjamini</th> <th>FDR</th>	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0044271~nitrogen compound biosynthetic process	61	2.84	2.55E-05	ADCY7, ATP1B3, HPRT, ATP1B2, LQHD, PNP, MTHFD1L, ANK1, GOT1, HDC, IMPDH1, ATP5K, ATR8B4, HSP90AA1, FCO1, ATPV5D, PADI2, PADI4, ATPV5A, NME1, AUK, RIN2, ATRPC1, ASL1, BCAT1, ALDH1B1, BCAT2, SRM, NAGS, ASNSD1, ASNS, ADN1, CMPK1, ADA, TVMS, ATPVOE, ALDH4A1, DCTD, TCIRG1, CEPBA, ODC1, ADSSL1, NOS1, NPR2, ATP1A1, ATP13A3, AMPD2, AMPD3, MMA8, ATP13A4, APR1, AMPD1, ADH1, P2RX4, ATPV0E2, ADCY9, ATP2A2, SLC7A2, PHGDH, PSAT1, ATRPA1	1594	302	13588	1.72	8.85E-02	1.47E-03	4.68E-02
Annotation Cluster 69	Enrichment Score: 1.2861838620748725	Count <th>%</th> <th>PValue</th> <th>Genes</th> <th>List Total</th> <th>Pop Hits</th> <th>Pop Total</th> <th>Fold Enrichment</th> <th>Bonferroni</th> <th>Benjamini</th> <th>FDR</th>	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0009081~branched chain fatty amino acid metabolic process	10	0.46	1.06E-05	BCAT1, BCKDHA, ALDH1A1, BCKDK, BCAT2, STAT5B, BCKDHB, HIBADH, GHR, AUH	1594	15	13588	5.68	3.77E-02	7.12E-04	1.94E-02

Gene	Accession	Protein	Start	End	Score	Start	End	Score	Start	End	Score
GOTERM_MF_FAT	GO:0032557	ribonucleotide binding	349	12.28	2.89E-16						
GOTERM_MF_FAT	GO:0017076	purine nucleotide binding	358	12.60	1.12E-09						
GOTERM_MF_FAT	GO:0000166	nucleotide binding	397	13.97	3.73E-08						
GOTERM_MF_FAT	GO:0005244	ATP binding	270	9.50	1.51E-06						
GOTERM_MF_FAT	GO:0032559	adenyl ribonucleotide binding	271	9.54	2.85E-06						

Annotation Cluster	Enrichment Score	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006793-phosphorus metabolic process	175	6.16	5.82E-06	RNASEL, PASK, STYX, PKMYT1, TTK, PTPN22, BORC, AURKB, PRKG2, TGFBI, BTK, PRKAR2B, APP, UQCRI0, UQCRI1, MDRF, MAP3K8, MIAL, MAP3K6, MARI, PTPN1, PKCZG, EGFR, TYRO3, MAGO, MYL5A, MYLK2, WNK2, PTPRN, PTPRO, MAP4K4, ACAP1, SLC37A2, DLD, NEK8, ATP5C1, POGFRA, RPK3, MAPK7, EIF2AK2, LRRK1, FGR4, FGR, GNAZ, NEK2, STK10, SSH3, PTK7, ACPS, MAP4K1, CHEK1, EPHB3, SRC, CD74, EPHB2, IRAK4, IRAK3, VRK1, PTP4B, CSF1R, TEC, PTPN7, GPD2, MDR1, FCER1A, PTPN6, GPD1, PTPN18, TADK1, HGF, EPHA2, EPHA3, HBEK, EPHA3, DUSP28, P387, PLK4, PLK3, PAZ2, PLK1, GNA, MERTK, ATP5E, IMPA2, NLUK2, SYNL1, FES, CAMKK1, CAMKK2, CCNE1, SH2D1B1, ATP5L, ATP5O, MASTL, CSK, SIK1, ATP4VDD2, CDK15, ATP5H, CDK14, ATP5K, ATP5I, CDC7, CDK1, LYN, PHKG1, LIMK1, NDUFC2, CDK6, PKDCC, PRK, PRKCD, CDK2, DAPK3, PRKCB, MAST3, OSM, ATP6V1A, CND1, PPM1E, UQCRI, RPK1, PPM1H, CFL1, LCK, PPM1A, BUB1B, PPM1L, PPM1M, MELK, UQCRI, CAMK1D, PK, NDUFB, PML, PPM1A, ATP5G1, HSF1G, GALK2, GALK1, STAF4, PTK2B, PPP3C, BUB1, DCLK1, TES, TCIRG1, PTPRC, ALPK1, PTPRE, FLT3, PDK3, HCK, PTPRA, NDUFA7, AXL, ATP5F1, CDKN3, GSG2, CDC25B, DUSP4, CCNB1, RPS6KA6, DUSP4, RPS6KA4, GCK, PTP4A3, RPS6KA1, FYN, GYK, JAK3, DUSP9, CIT, CCK2B, DUSP6	2002	866	13588	1.37	2.33E-02	2.36E-04	1.08E-02
Annotation Cluster 35	Enrichment Score: 2.5545766691173992											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0033559-unsaturated fatty acid metabolic process	19	0.67	6.23E-07	FCER1A, TBKAS1, PTPG3, NCF1, POPN, FADS1, EPHK2, LTC4S, CD74, GGT5, TNFRSF1A, PTGS, PTGES, ALOX5AP, ALOX5, HPGD, RNPEP, HRGDS, MGS2	2002	36	13588	3.58	2.53E-03	3.05E-05	1.16E-03
GOTERM_BP_FAT	GO:0006690-icosanoid metabolic process	17	0.60	7.22E-06	HPGD, RNPEP, HRGDS, MGS2	2002	34	13588	3.39	2.89E-02	2.76E-04	1.34E-02
Annotation Cluster 40	Enrichment Score: 2.3291168681773002											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0050777-negative regulation of immune response	14	0.49	2.33E-05	PTPRC, PTPN6, IL27RA, IL7R, TGFBI, GPK1, IRAK3, SH2D1B1, FCGR2B, CD59B, PPP3C, INPP5D, KLFB1B, SPN	2002	26	13588	3.65	9.02E-02	8.00E-04	4.33E-02
Annotation Cluster 43	Enrichment Score: 2.1580019024363786											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0031341-regulation of cell killing	16	0.56	5.44E-06	H2-K1, PTPRC, H2-M3, KLRK1, IL7R, CD101, PNP, H2-Q7, B2M, P2RX7, SH2D1B1, TAP2, ULBP1, PPP3CB, KLRK1B, LAG3	2002	30	13588	3.62	2.19E-02	2.23E-04	1.01E-02
GOTERM_BP_FAT	GO:0001910-regulation of leukocyte mediated cytotoxicity	16	0.56	5.44E-06	H2-K1, PTPRC, H2-M3, KLRK1, IL7R, CD101, PNP, H2-Q7, B2M, P2RX7, SH2D1B1, TAP2, ULBP1, PPP3CB, KLRK1B, LAG3	2002	30	13588	3.62	2.19E-02	2.23E-04	1.01E-02
Annotation Cluster 44	Enrichment Score: 2.143499635516042											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0032101-regulation of response to external stimulus	33	1.16	1.87E-05	SBN2, ADORA2B, IL16, C3, TLRA, CXCL12, ADA, GPX1, TNFRSF1A, CD47, NOD2, TNFRSF1B, ADAH, APDH, FCER1G, LBP, THBS1, SPN, CD28, ZFP36, FCER1A, SELP, CLN3, PLEK, CD276, AGER, FCGR1, FCGR3, ANKRD, CD59B, FCGR2B, NPY, FABP7	2002	103	13588	2.17	7.33E-02	6.62E-04	3.49E-02
Annotation Cluster 50	Enrichment Score: 2.0226420719661573											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0015077-monovalent inorganic cation transmembrane transporter activity	33	1.16	1.79E-07	SLC9A9, ATP5E, SLC36A1, COX7B, COX7C, ATP5G1, UQCRI1, COX5A, COX5B, UQCRI, UQCRI0, UQCRI1, COX6B1, ATP5L, ATP5O, COX6B2, ATP5VDD2, ATP5H, ATP5K, ATP5I, TCIRG1, COX7A2, COX8B, COX7A1, ATP5F1, ATP1A3, ATP1A4, COX6C, ATP6V1A, UQCRI, COX6A2, ATP5C1, UQCRI, SLC9A9, ATP5E, SLC36A1, COX7B, COX7C, ATP5G1, UQCRI1, COX5A, COX5B, UQCRI, UQCRI0, UQCRI1, COX6B1, ATP5L, ATP5O, COX6B2, ATP5VDD2, ATP5H, ATP5K, ATP5I, TCIRG1, COX7A2, COX8B, COX7A1, ATP5F1, COX6C, ATP6V1A, UQCRI, COX6A2, ATP5C1, UQCRI	1916	87	13288	2.63	2.37E-04	1.97E-05	2.93E-04
GOTERM_MF_FAT	GO:0015078-hydrogen ion transmembrane transporter activity	31	1.09	4.92E-07	COX7A1, ATP5F1, COX6C, ATP6V1A, UQCRI, COX6A2, ATP5C1, UQCRI	1916	82	13288	2.62	6.51E-04	4.07E-05	8.05E-04

Table S1.F GO Terms upregulated 168 hours post injury

Annotation Cluster 1	Enrichment Score: 14.55639886357477	Term	Count %	PValue	Genes	List Total	Pop Hrs	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0006955	immune response	49	14.16	6.60E-23	LY86, TLR2, CD101, CIQC, TLR7, IL10, CFP, OASL2, AF251705, NCF1, C4B, H2-DMB1, CIQA, CIQB, IL18PP, CCR5, IL18B3, CX3CR1, LILRB4, CCR2, OAS1A, IL12B, OAS1G, CD300LD, CD300LD, CCL2, LST1, CCL3, CCL4, OAS2, CCL7, SLC11A1, GP49A, FCER1G, CD4, CD7, TLR43, MYD1F, CD90C, FCGR1, CD180, CCL17, FCGR3, CCL12, CD300A, PLCG2, IRF8, CLEC7A, XCL1, CD14	249	471	13588	5.68	1.03E-19	1.03E-19	1.10E-19
GOTERM_BP_FAT	GO:0006952	defense response	37	10.69	5.48E-14	LY22, C4B, NCF1, HCK, CAMP, TLR13, SAA3, MYD1F, CDT11, FCGR1, CD180, FCGR3, CCL17, CIQA, CIQB, CCL12, CD86, IRF8, CXCL, CLEC7A, CD14, ORMD2	249	448	13588	4.51	8.55E-11	4.28E-11	9.15E-11
GOTERM_BP_FAT	GO:0006954	inflammatory response	26	7.51	4.19E-13	FCGR1, CD180, FCGR3, CIQA, CCL12, CIQB, CCR5, CCR2, CLEC7A, ORMD2, CD14	249	225	13588	6.31	6.53E-10	2.18E-10	6.99E-10
GOTERM_BP_FAT	GO:0009611	response to wounding	29	8.38	3.92E-11	CCL2, LY86, TLR2, CCL8, ITGB2, CIQC, TLR7, CCL7, CFP, SLC11A1, PYCARD, TFP12, PLK6, GATM, NCF1, C4B, TLR13, SAA3, FCGR1, CD180, FCGR3, CIQA, CIQB, CCL12, CCR5, CCR2, CLEC7A, ORMD2, CD14	249	347	13588	4.56	6.12E-08	1.53E-08	6.55E-08
Annotation Cluster 2	Enrichment Score: 5.49112366075224	Term	Count %	PValue	Genes	List Total	Pop Hrs	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0042742	defense response to bacterium	13	3.76	6.20E-07	LY22, FGR, NCF1, CAMP, HCK, TLR2, MYD1F, FCGR1, IL10, SLC11A1, CCR5, IRF8, FCER1G	249	108	13588	6.37	9.66E-04	6.90E-05	1.03E-03
GOTERM_BP_FAT	GO:0009617	response to bacterium	15	4.34	1.08E-06	LY22, FGR, NCF1, CAMP, HCK, TLR2, MYD1F, FCGR1, IL10, SLC11A1, CCR5, IRF8, PLCG2, FCER1G, CD14	249	157	13588	5.21	1.69E-03	1.13E-04	1.81E-03
Annotation Cluster 3	Enrichment Score: 4.990727463947588	Term	Count %	PValue	Genes	List Total	Pop Hrs	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0001819	positive regulation of cytokine production	11	3.18	1.60E-07	CD83, SLC11A1, KLR1, PYCARD, TLR2, FCER1G, CLEC7A, CASP1, TLR7, SASH3, CD14	249	62	13588	9.68	2.49E-04	2.27E-05	2.67E-04
GOTERM_BP_FAT	GO:0001817	regulation of cytokine production	15	4.34	2.44E-07	TLR2, CD101, TLR7, IL10, FCGR1, SLC11A1, CD83, HMOX1, KLR1, PYCARD, FCER1G, CLEC7A, CASP1, SASH3, CD14	249	139	13588	5.89	3.80E-04	3.16E-05	4.07E-04
Annotation Cluster 4	Enrichment Score: 4.97611947115325	Term	Count %	PValue	Genes	List Total	Pop Hrs	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0042330	taxis	15	4.34	1.08E-08	CX3CR1, CCL2, CCL9, CCL8, ITGB2, CCL7, CCL17, FCGR3, CCL12, CORO1A, RAC2, CX3CR1, FCER1G, XCR1, XCL1	249	109	13588	7.51	1.69E-05	1.88E-06	1.81E-05
GOTERM_BP_FAT	GO:0006933	chemotaxis	15	4.34	1.08E-08	XCL1	249	109	13588	7.51	1.69E-05	1.88E-06	1.81E-05
GOTERM_MF_FAT	GO:0008009	chemokine receptor binding	7	2.02	2.84E-05	PLCG2, CX3CR1, KLR1, FCER1G, CD4, IL12B, HELLS, RHOM, LOP2	214	38	13588	11.44	9.14E-03	1.58E-03	3.84E-02
GOTERM_MF_FAT	GO:0042339	chemokine receptor binding	7	2.02	3.32E-05	CCL12, CCL2, CCL9, CCL8, XCL1, CCL7, CCL17	214	39	13288	11.14	1.07E-02	3.56E-03	4.48E-02
Annotation Cluster 5	Enrichment Score: 4.73436415573175	Term	Count %	PValue	Genes	List Total	Pop Hrs	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0001775	cell activation	24	6.94	1.31E-10	FYB, LST1, PLEK, MYD1F, RORC, ITGB2, SFP1, CD1D1, WAS, FCGR3, CD48, SLC11A1, BCL2A1D, CD86, IL18B3, PLCG2, CX3CR1, KLR1, FCER1G, CD4, IL12B, HELLS, RHOM, LOP2	249	246	13588	5.32	2.04E-07	4.08E-08	2.19E-07
GOTERM_BP_FAT	GO:0045321	leukocyte activation	22	6.36	5.46E-10	FYB, MYD1F, RORC, ITGB2, SFP1, CD1D1, WAS, FCGR3, CD48, SLC11A1, BCL2A1D, CD86, IL18B3, PLCG2, CX3CR1, KLR1, FCER1G, CD4, IL12B, HELLS, RHOM, LOP2	249	219	13588	5.48	8.52E-07	1.42E-07	9.12E-07
GOTERM_BP_FAT	GO:0002274	myeloid leukocyte activation	10	2.89	9.07E-09	FYB, SLC11A1, IL18B3, CX3CR1, MYD1F, FCER1G, SFP1, LOP2, RHOM, FCGR3	249	35	13588	15.59	1.41E-05	1.77E-06	1.51E-05
GOTERM_BP_FAT	GO:0046649	lymphocyte activation	15	4.34	1.09E-05	RORC, ITGB2, SFP1, CD1D1, WAS, CD48, SLC11A1, CD86, BCL2A1D, PLCG2, KLR1, CD4, IL12B, HELLS, RHOM	249	191	13588	4.29	1.68E-02	8.46E-04	1.81E-02
Annotation Cluster 6	Enrichment Score: 4.102642809152643	Term	Count %	PValue	Genes	List Total	Pop Hrs	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0002684	positive regulation of immune system process	21	6.07	1.15E-09	C4B, TLR2, CD1D1, CIQC, FCGR1, FCGR3, C1QA, C1QB, SLC11A1, CD83, BCL2A1D, CORO1A, PLCG2, KLR1, FCER1G, CD4, IL12B, HELLS, CLEC7A, SASH3	249	206	13588	5.56	1.79E-06	2.56E-07	1.92E-06
GOTERM_BP_FAT	GO:0050778	positive regulation of immune response	16	4.62	2.64E-08	C4B, TLR2, CD1D1, CIQC, FCGR1, FCGR3, C1QA, C1QB, SLC11A1, BCL2A1D, PLCG2, KLR1, FCER1G, CLEC7A, SASH3	249	136	13588	6.42	4.11E-05	4.11E-06	4.40E-05
GOTERM_BP_FAT	GO:0045087	innate immune response	13	3.76	5.60E-07	C4B, TLR2, CD1D1, CIQC, FCGR1, FCGR3, C1QA, C1QB, SLC11A1, BCL2A1D, PLCG2, KLR1, FCER1G, CLEC7A, SASH3	249	107	13588	6.63	8.73E-04	6.72E-05	9.35E-04
GOTERM_BP_FAT	GO:0048584	positive regulation of response to stimulus	16	4.62	1.60E-06	FCER1G, CLEC7A, SASH3	249	186	13588	4.69	2.50E-03	1.56E-04	2.68E-03
GOTERM_BP_FAT	GO:0002252	immune effector process	13	3.76	3.24E-06	NCF1, C4B, MYD1F, CIQC, FCGR1, TLR7, FCGR3, C1QA, CFP, SLC11A1, CIQB, IL18B3, FCER1G	249	126	13588	5.63	5.04E-03	2.97E-04	5.41E-03
GOTERM_BP_FAT	GO:0002253	activation of immune response	11	3.18	3.59E-06	C1QA, CFP, CIQB, BCL2A1D, C4B, PLCG2, KLR1, TLR2, FCER1G, CLEC7A, CIQC	249	86	13588	6.98	5.58E-03	3.11E-04	5.99E-03
GOTERM_BP_FAT	GO:0002443	leukocyte mediated immunity	11	3.18	4.91E-06	C1QA, CIQB, SLC11A1, NCF1, C4B, IL18B3, MYD1F, FCER1G, CIQC, FCGR1, FCGR3	249	89	13588	6.74	7.63E-03	4.03E-04	8.20E-03
GOTERM_BP_FAT	GO:0002359	adaptive immune response	10	2.89	2.17E-05	C1QA, CIQB, SLC11A1, IL18B3, C4B, IL18B3, FCER1G, CIQC, FCGR1, FCGR3	249	84	13588	6.50	3.33E-02	1.61E-03	3.63E-02
GOTERM_BP_FAT	GO:0002460	adaptive immune response based on somatic recombination of immune receptors built fr	10	2.89	2.17E-05	C1QA, CIQB, SLC11A1, IL18B3, C4B, IL18B3, FCER1G, CIQC, FCGR1, FCGR3	249	84	13588	6.50	3.33E-02	1.61E-03	3.63E-02
Annotation Cluster 7	Enrichment Score: 3.0962877308218895	Term	Count %	PValue	Genes	List Total	Pop Hrs	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0050778	positive regulation of immune response	16	4.62	2.64E-08	C4B, TLR2, CD1D1, CIQC, FCGR1, FCGR3, C1QA, C1QB, SLC11A1, BCL2A1D, PLCG2, KLR1, FCER1G, CLEC7A, SASH3	249	136	13588	6.42	4.11E-05	4.11E-06	4.40E-05
GOTERM_BP_FAT	GO:0048584	positive regulation of response to stimulus	16	4.62	1.60E-06	FCER1G, CLEC7A, SASH3	249	186	13588	4.69	2.50E-03	1.56E-04	2.68E-03
Annotation Cluster 12	Enrichment Score: 2.1332794229095495	Term	Count %	PValue	Genes	List Total	Pop Hrs	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0006909	phagocytosis	8	2.31	2.77E-05	SLC11A1, HCK, IRF8, FCER1G, CLEC7A, MEGF10, FCGR1, FCGR3	249	49	13588	8.91	4.23E-02	1.96E-03	4.62E-02
Annotation Cluster 13	Enrichment Score: 2.04835886290177	Term	Count %	PValue	Genes	List Total	Pop Hrs	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_MF_FAT	GO:0019955	cytokine binding	11	3.18	1.38E-06	IL18PP, CCR5, CSF2NB2, IL10RA, CCR2, CX3CR1, CSF2NB, IL12B, IL12B, XCR1, CSF2BA	214	88	13288	7.76	4.45E-04	4.45E-04	1.86E-03

Table S1.6 GO Terms upregulated 336 hours post injury

Annotation Cluster 1	Enrichment Score: 14.55639806357477	Term	Count %	PValue	Genes	List Total	Pop Hrs	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0006955	immune response	49	14.16	6.60E-23	LY86, TLR2, CD101, C1QC, TLR7, IL10, CFP, OASL2, AF251705, NCF1, C4B, H2-DMB1, C1QA, C1QB, IL18PP, CCR5, IL18R3, CX3CR1, LILRB4, CCR2, OAS1A, IL12B, OAS1G, CD300LD, CD300LD, CCL2, LST1, CCL3, CCL4, OAS2, CCL7, SLC11A1, GP49A, FCER1G, CD4, CD7, TLR43, MYD1F, CD90C, FCGR1, CD180, CCL17, FCGR3, CCL12, CD300A, PLCG2, IRF8, CLEC7A, XCL1, CD14	249	471	13588	5.68	1.03E-19	1.03E-19	1.10E-19
GOTERM_BP_FAT	GO:0006952	defense response	37	10.69	5.48E-14	CCL2, C4B, NCF1, HCK, CAMP, TLR13, SAA3, MYD1F, CDT11, FCGR1, CD180, FCGR3, CCL17, C1QA, C1QB, CCL12, CD86, IRF8, CXCL, CLEC7A, CD14, OMS4	249	448	13588	4.51	8.55E-11	4.28E-11	9.15E-11
GOTERM_BP_FAT	GO:0006954	inflammatory response	26	7.51	4.19E-13	FCGR1, CD180, FCGR3, C1QA, CCL12, C1QB, CCR5, CCR2, CLEC7A, OMS2, CD14	249	225	13588	6.31	6.53E-10	2.18E-10	6.99E-10
GOTERM_BP_FAT	GO:0009611	response to wounding	29	8.38	3.92E-11	CCL2, LY86, TLR2, CCL8, ITGB2, C1QC, TLR7, CCL7, CFP, SLC11A1, PYCARD, TFP12, PLK1, GATM, NCF1, C4B, TLR13, SAA3, FCGR1, CD180, FCGR3, C1QA, C1QB, CCL12, CCR5, CCR2, CLEC7A, OMS2, CD14	249	347	13588	4.56	6.12E-08	1.53E-08	6.55E-08
Annotation Cluster 2	Enrichment Score: 5.49112366075224	Term	Count %	PValue	Genes	List Total	Pop Hrs	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0042742	defense response to bacterium	13	3.76	6.20E-07	LY22, FGR, NCF1, CAMP, HCK, TLR2, MYD1F, FCGR1, IL10, SLC11A1, CCR5, IRF8, FCER1G	249	108	13588	6.57	9.66E-04	6.90E-05	1.03E-03
GOTERM_BP_FAT	GO:0009617	response to bacterium	15	4.34	1.08E-06	LY22, FGR, NCF1, CAMP, HCK, TLR2, MYD1F, FCGR1, IL10, SLC11A1, CCR5, IRF8, PLCG2, FCER1G, CD14	249	157	13588	5.21	1.69E-03	1.13E-04	1.81E-03
Annotation Cluster 3	Enrichment Score: 4.990727463947588	Term	Count %	PValue	Genes	List Total	Pop Hrs	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0001819	positive regulation of cytokine production	11	3.18	1.60E-07	CD83, SLC11A1, KLR1, PYCARD, TLR2, FCER1G, CLEC7A, CASP1, TLR7, SASH3, CD14	249	62	13588	9.68	2.49E-04	2.27E-05	2.67E-04
GOTERM_BP_FAT	GO:0001817	regulation of cytokine production	15	4.34	2.44E-07	TLR2, CD101, TLR7, IL10, FCGR1, SLC11A1, CD83, HMOX1, KLR1, PYCARD, FCER1G, CLEC7A, CASP1, SASH3, CD14	249	139	13588	5.89	3.80E-04	3.16E-05	4.07E-04
Annotation Cluster 4	Enrichment Score: 4.97611947115325	Term	Count %	PValue	Genes	List Total	Pop Hrs	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0042330	taxis	15	4.34	1.08E-08	CX3CR1, CCL2, CCL9, CCL8, ITGB2, CCL7, CCL17, FCGR3, CCL12, CORO1A, RAC2, CX3CR1, FCER1G, XCR1, XCL1	249	109	13588	7.51	1.69E-05	1.88E-06	1.81E-05
GOTERM_BP_FAT	GO:0006933	chemotaxis	15	4.34	1.08E-08	XCL1	249	109	13588	7.51	1.69E-05	1.88E-06	1.81E-05
GOTERM_MF_FAT	GO:0008009	chemokine receptor binding	7	2.02	2.84E-05	PLCG2, CX3CR1, KLR1, FCER1G, CD4, IL12B, HELLS, RHOH, LOP2	214	38	13588	11.44	9.14E-03	1.58E-03	3.84E-02
GOTERM_MF_FAT	GO:0042339	chemokine receptor binding	7	2.02	3.32E-05	CCL12, CCL9, CCL8, XCL1, CCL7, CCL17	214	39	13288	11.14	1.07E-02	3.56E-03	4.48E-02
Annotation Cluster 5	Enrichment Score: 4.73436415573175	Term	Count %	PValue	Genes	List Total	Pop Hrs	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0001775	cell activation	24	6.94	1.31E-10	FYB, LST1, PLEK, MYD1F, RORC, ITGB2, SFP1, CD1D1, WAS, FCGR3, CD48, SLC11A1, BCL2A1D, CD86, IL18R3, PLCG2, CX3CR1, KLR1, FCER1G, CD4, IL12B, HELLS, RHOH, LOP2	249	246	13588	5.32	2.04E-07	4.08E-08	2.19E-07
GOTERM_BP_FAT	GO:0045321	leukocyte activation	22	6.36	3.46E-10	FYB, MYD1F, RORC, ITGB2, SFP1, CD1D1, WAS, FCGR3, CD48, SLC11A1, BCL2A1D, CD86, IL18R3, PLCG2, CX3CR1, KLR1, FCER1G, CD4, IL12B, HELLS, RHOH, LOP2	249	219	13588	5.48	8.52E-07	1.42E-07	9.12E-07
GOTERM_BP_FAT	GO:0002274	myeloid leukocyte activation	10	2.89	9.07E-09	FYB, SLC11A1, IL18R3, CX3CR1, MYD1F, FCER1G, SFP1, LOP2, RHOH, FCGR3	249	35	13588	15.59	1.41E-05	1.77E-06	1.51E-05
GOTERM_BP_FAT	GO:0046649	lymphocyte activation	15	4.34	1.09E-05	RORC, ITGB2, SFP1, CD1D1, WAS, CD48, SLC11A1, CD86, BCL2A1D, PLCG2, KLR1, CD4, IL12B, HELLS, RHOH	249	191	13588	4.29	1.68E-02	8.46E-04	1.81E-02
Annotation Cluster 6	Enrichment Score: 4.102642809152643	Term	Count %	PValue	Genes	List Total	Pop Hrs	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0002684	positive regulation of immune system process	21	6.07	1.15E-09	C4B, TLR2, CD1D1, C1QC, FCGR1, FCGR3, C1QA, C1QB, SLC11A1, CD83, BCL2A1D, CORO1A, PLCG2, KLR1, FCER1G, CD4, IL12B, CLEC7A, SASH3	249	206	13588	5.56	1.79E-06	2.56E-07	1.92E-06
GOTERM_BP_FAT	GO:0050778	positive regulation of immune response	16	4.62	2.64E-08	C4B, TLR2, CD1D1, C1QC, FCGR1, FCGR3, C1QA, CFP, C1QB, SLC11A1, BCL2A1D, PLCG2, KLR1, FCER1G, CLEC7A, SASH3	249	136	13588	6.42	4.11E-05	4.11E-06	4.40E-05
GOTERM_BP_FAT	GO:0045087	innate immune response	13	3.76	5.60E-07	C4B, TLR2, CD1D1, C1QC, FCGR1, FCGR3, C1QA, CFP, C1QB, SLC11A1, BCL2A1D, PLCG2, KLR1, FCER1G, CLEC7A, SASH3	249	107	13588	6.63	8.73E-04	6.72E-05	9.35E-04
GOTERM_BP_FAT	GO:0048584	positive regulation of response to stimulus	16	4.62	1.60E-06	FCER1G, CLEC7A, SASH3	249	186	13588	4.69	2.50E-03	1.56E-04	2.68E-03
GOTERM_BP_FAT	GO:0002252	immune effector process	13	3.76	3.24E-06	NCF1, C4B, MYD1F, C1QC, FCGR1, TLR7, FCGR3, C1QA, CFP, SLC11A1, C1QB, IL18R3, FCER1G	249	126	13588	5.63	5.04E-03	2.97E-04	5.41E-03
GOTERM_BP_FAT	GO:0002253	activation of immune response	11	3.18	3.59E-06	C1QA, CFP, C1QB, BCL2A1D, C4B, PLCG2, KLR1, TLR2, FCER1G, CLEC7A, C1QC	249	86	13588	6.98	5.58E-03	3.11E-04	5.99E-03
GOTERM_BP_FAT	GO:0002443	leukocyte mediated immunity	11	3.18	4.91E-06	C1QA, C1QB, SLC11A1, NCF1, C4B, IL18R3, MYD1F, FCER1G, C1QC, FCGR1, FCGR3	249	89	13588	6.74	7.63E-03	4.03E-04	8.20E-03
GOTERM_BP_FAT	GO:0002359	adaptive immune response	10	2.89	2.17E-05	C1QA, C1QB, SLC11A1, IL18R3, C4B, IL18R3, FCER1G, C1QC, FCGR1, FCGR3	249	84	13588	6.50	3.33E-02	1.61E-03	3.63E-02
GOTERM_BP_FAT	GO:0002460	adaptive immune response based on somatic recombination of immune receptors built fr	10	2.89	2.17E-05	C1QA, C1QB, SLC11A1, IL18R3, C4B, IL18R3, FCER1G, C1QC, FCGR1, FCGR3	249	84	13588	6.50	3.33E-02	1.61E-03	3.63E-02
Annotation Cluster 7	Enrichment Score: 3.0962877308218895	Term	Count %	PValue	Genes	List Total	Pop Hrs	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0050778	positive regulation of immune response	16	4.62	2.64E-08	C4B, TLR2, CD1D1, C1QC, FCGR1, FCGR3, C1QA, CFP, C1QB, SLC11A1, BCL2A1D, PLCG2, KLR1, FCER1G, CLEC7A, SASH3	249	136	13588	6.42	4.11E-05	4.11E-06	4.40E-05
GOTERM_BP_FAT	GO:0048584	positive regulation of response to stimulus	16	4.62	1.60E-06	C4B, TLR2, CD1D1, C1QC, FCGR1, FCGR3, C1QA, CFP, C1QB, SLC11A1, BCL2A1D, PLCG2, KLR1, FCER1G, CLEC7A, SASH3	249	186	13588	4.69	2.50E-03	1.56E-04	2.68E-03
Annotation Cluster 12	Enrichment Score: 2.1332794229095495	Term	Count %	PValue	Genes	List Total	Pop Hrs	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0006909	phagocytosis	8	2.31	2.77E-05	SLC11A1, HCK, IRF8, FCER1G, CLEC7A, MEGF10, FCGR1, FCGR3	249	49	13588	8.91	4.23E-02	1.96E-03	4.62E-02
Annotation Cluster 13	Enrichment Score: 2.04835886290177	Term	Count %	PValue	Genes	List Total	Pop Hrs	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_MF_FAT	GO:0019955	cytokine binding	11	3.18	1.38E-06	IL18PP, CCR5, CSF2NB2, IL10RA, CCR2, CX3CR1, CSF2NB, IL12B, IL12B, XCR1, CSF2BA	214	88	13288	7.76	4.45E-04	4.45E-04	1.86E-03

Table S2.A KEGG pathways significant at 3 hours

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
KEGG_PATHWAY	mmu04060:Cytokine-cytokine receptor interaction	49	4.52	2.96E-10	OSMR, CXCR2, IL17RA, TGF2, CXCR4, IL1RAP, CSF3R, CSF2RB, IL1B, FAS, IL13RA1, CSF2RA, EGFR, LTBR, INHBB, OSM, TNFRSF10B, PPBP, CCR2, PDGFRA, CXCL1, CSF3, IL1R2, CCL3, IL1R1, CCL2, CSF2RB2, TNFRSF12A, CSF1, CCR1, IL4RA, CXCL2, CXCL9, CCL9, PF4, CNTFR, CCL7, CCL6, CCL24, TNFRSF1A, TNFRSF1B, IL10RA, BMP2, TGFBR1, TGFBR2, CCL11, CXCL14, CXCL16, BMPR1B	434	244	5738	2.66	4.88E-08	4.88E-08	3.59E-07
KEGG_PATHWAY	mmu04512:ECM-receptor interaction	25	2.31	4.36E-09	TNC, COL3A1, SDC4, SDC2, CD44, COMP, COL6A2, COL6A1, COL11A2, THBS1, THBS2, THBS3, THBS4, SPP1, FN1, TNXB, COL4A1, ITGA3, ITGA4, COL5A2, LAMA4, ITGA5, COL1A2, LAMC2, COL1A1	434	83	5738	3.98	7.20E-07	3.60E-07	5.30E-06
KEGG_PATHWAY	mmu04610:Complement and coagulation cascades	22	2.03	7.69E-08	PLAT, C7, C5AR1, MASP1, C3, C4B, CFB, F13A1, SERPING1, C15, C1QC, PLAUR, C1QA, C1QB, C1RA, THBD, F3, SERPINE1, CFH, CFD, PROS1, PLAU	434	75	5738	3.88	1.27E-05	4.23E-06	9.33E-05
KEGG_PATHWAY	mmu04510:Focal adhesion	37	3.41	4.52E-07	MYL2, PGF, TNC, COL3A1, RAC2, COMP, COL6A2, COL6A1, PIK3R5, ZYX, PAK1, COL11A2, THBS1, THBS2, THBS3, FN1, SPP1, THBS4, ACTB, EGFR, COL4A1, TNXB, ACTN1, ITGA3, ITGA4, FLNC, BIRC3, FLNB, COL5A2, LAMA4, ITGA5, FYN, PDGFRA, COL1A2, RAP1B, LAMC2, COL1A1	434	198	5738	2.47	7.45E-05	1.86E-05	5.48E-04
KEGG_PATHWAY	mmu04210:Apoptosis	22	2.03	1.18E-06	CFLAR, IL1R1, CSF2RB2, RELA, NFKBIA, NFKB1, BIRC3, PRKAR2B, TNFRSF1A, IRAK3, TNFRSF10B, MYD88, RIPK1, IL1RAP, CASP8, CASP12, IL1B, CSF2RB, PIK3R5, FAS, APAF1, MAP3K14	434	87	5738	3.34	1.95E-04	3.89E-05	1.43E-03
KEGG_PATHWAY	mmu04062:Chemokine signaling pathway	33	3.04	4.28E-06	CXCL1, ADCY4, CCL3, CCL2, GNAI3, CCR1, CXCL2, CCL9, CXCL9, NFKBIA, NFKB1, CXCR2, PF4, GNG11, CCL7, CCL6, CCL24, RAC2, TIAM1, PTK2B, CXCR4, PIK3R5, PAK1, LYN, RELA, STAT3, STAT2, CCL11, PPBP, CXCL14, CXCL16, CCR2, RAP1B	434	182	5738	2.40	7.05E-04	1.18E-04	5.19E-03
KEGG_PATHWAY	mmu04010:MAPK signaling pathway	41	3.78	1.37E-05	IL1R2, IL1R1, FGFR3, MRAS, DUSP10, HSPA1A, NFKB1, HSPA1B, TGFB2, FOS, TNFRSF1A, BDNF, RAC2, HSPA2, MAP3K2, MAP3K1, JUND, MAP3K8, IL1B, FAS, PAK1, RAPGEF2, MYC, EGFR, RELA, TGFBR1, TGFBR2, IL1B, FAS, PAK1, RAPGEF2, MYC, EGFR, RELA, TGFBR1, TGFBR2, IL1B, FAS, PAK1, RAPGEF2, MAP4K4, DUSP2, GADD45G, NTRK2, PDGFRA, HSPB1, RAP1B, GADD45B, MAP3K14, GADD45A, CD14, PLA2G4E	434	265	5738	2.05	2.26E-03	3.23E-04	1.66E-02

Table S2.B KEGG pathways significant at 10 hours

Category	Term	Count	%	PValue	Genes	ListTotal	PopHits	PopTotal	FoldEnrichment	Bonferroni	Benjamini	FDR
KEGG_PATHWAY	mmu00190:Oxidative phosphorylation	80	2.10	8.69E-22	ATP5D, UQCRC2, ATP5E, COX11, UQCRC1, COX10, ATP5B, CYC1, NDUFA81, UQCRCF51, COX5A, COX5B, UQCRC2, ATP5E, NDUFS6, NDUFS5, UQCRC10, UQCRC11, NDUFA5, NDUFS8, ATP5L, ATP5O, NDUFS3, ATP5H, NDUFS1, ATP5K, ATP5J, COX15, NDUFB10, NDUFC2, COX42, COX411, ATP5V1H, NDUFC1, NDUFA10, COX6C, NDUFA11, ATP6V1A, UQCRCR, ATP5C1, UQCRCB, NDUFB3, NDUFB4, NDUFB5, NDUFB6, NDUFB7, NDUFB8, NDUFB9, COX7B, COX7C, ATP6V1B2, ATP5G1, COX7A2L, ATP5G3, NDUFB2, COX6B1, NDUFA4, NDUFA5, NDUFAZ, ATP5J2, COX7A2, NDUFA3, NDUFA8, COX7A1, COX8B, NDUFA9, NDUFA6, NDUFA7, ATP5F1, NDUFA1, PPA2, SDHA, NDUFV3, SDHB, ATP6V0E2, NDUFV1, SDHC, NDUFV2, SDHD, ATP5A1	1276	130	5738	2.77	1.64E-19	1.64E-19	1.08E-18
KEGG_PATHWAY	mmu05012:Parkinson's disease	80	2.10	6.54E-21	ATP5D, UQCRC2, ATP5E, SNCAIP, UQCRC1, ATP5B, CYC1, NDUFA81, REST, CLTC, COX5A, UQCRCF51, COX5B, UQCRCQ, NDUFS7, GPX1, NDUFS6, AP2B1, NDUFS5, CASP3, UQCRC10, UQCRC11, NDUFS4, PLCB4, CASP8, NDUFS8, CREB3L2, ATP5O, NDUFS3, ATP5H, NDUFS1, ATP5J, NDUFB10, SLC25A4, SLC25A5, CYCS, NDUFC2, COX42, COX411, NDUFC1, NDUFA10, COX6C, UQCRCR, UBC, ATP5C1, UBB, UQCRCB, NDUFB3, NDUFB4, NDUFB5, NDUFB6, NDUFB7, NDUFB8, NDUFB9, COX7B, COX7C, ATP5G1, COX7A2L, ATP5G3, NDUFB2, COX6B1, NDUFA4, NDUFA5, NDUFAZ, COX7A2, NDUFA3, NDUFA8, COX7A1, COX8B, NDUFA9, NDUFA6, NDUFA7, ATP5F1, UBE2L6, VDACC2, VDACC3, NDUFA1, SDHA, NDUFV3, SDHB, NDUFV1, SDHC, NDUFV2, SDHD, AFAF1, ATP5A1	1276	133	5738	2.70	1.24E-18	6.18E-19	8.12E-18
KEGG_PATHWAY	mmu05016:Huntington's disease	95	2.49	1.19E-18	ATP5D, UQCRC2, ATP5E, UQCRC1, ATP5B, SNCA, CYC1, NDUFA81, UQCRCF51, COX5A, COX5B, UQCRCQ, NDUFS7, NDUFS5, CASP3, UQCRC10, UQCRC11, NDUFS4, PLCB4, CASP8, NDUFS8, CREB3L2, ATP5O, NDUFS3, ATP5H, NDUFS1, ATP5J, NDUFB10, SLC25A4, SLC25A5, TAF4B, CYCS, NDUFC2, COX42, COX411, NDUFC1, NDUFA10, COX6C, UQCRCR, ATP5C1, UQCRCB, NDUFB3, NDUFB4, NDUFB5, NDUFB6, NDUFB7, NDUFB8, NDUFB9, COX7B, COX7C, ATP5G1, COX7A2L, ATP5G3, NDUFB2, POLR2A, TFAM, COX6B1, TGM2, TRP53, NDUFA4, NDUFA5, NDUFAZ, COX7A2, NDUFA3, NDUFA8, COX7A1, COX8B, HTT, NDUFA9, DNALC1, NDUFA6, CREBBP, NDUFA7, ATP5F1, VDACC2, VDACC3, NDUFA1, SOD2, UDUFV3, SDHA, SDHB, SP1, BBC3, NDUFV1, SDHC, BAX, NDUFV2, SDHD, AFAF1, ATP5A1	1276	183	5738	2.33	2.24E-16	7.48E-17	1.47E-15
KEGG_PATHWAY	mmu05010:Alzheimer's disease	93	2.44	1.09E-17	SDHB, LRP1, ATP2A2, ATP2A3, NDUFV1, SDHC, NDUFV2, CASP12, SDHD, AFAF1, ATP5A1, CALM2, PDGFR, PDGFA, PGF, BCAR1, CHAD, VCL, ACTG1, ARHGAP5, PAK2, PAK4, SHC1, ZYX, COL11A2, COL11A1, PRKCA, EGFR, PARVG, ACTN4, BRAF, ROCK1, ROCK2, ACTN1, ACTN2, FLNC, FLNB, FLNA, VASP, VEGFB, CCND1, CCND2, JUN, VEGFA, COL1A2, PDGFR, LAMC2, LAMC1, COL1A1, CAV3, IBSP, MYL2, TNC, COL3A1, ITGB1, ITGB1, PKN, MYL9, IGF1R, DOCK1, LAMB2, RAC2, COMP, ITGB7, ITGB6, COL6A2, PPP1R12A, COL6A1, PIK3R5, THBS1, THBS2, PIK3R1, THBS3, FN1, THBS4, SPP1, PIK3R2, ACTB, COL4A2, COL4A1, FLT1, TNXB, MET, BIRC3, CAPN2, COL5A2, VAV1, KDR, VWF, LAMA4, ITGA5, GRLF1, RAP1B, DIAP1	1276	182	5738	2.30	2.07E-15	5.17E-16	1.36E-14
KEGG_PATHWAY	mmu04510:focal adhesion	82	2.15	1.46E-09	DIET, AC02, SUCLA1, CS, IDH3B, ACYL, DIAT, ODGH, PDHB, IDH3A, SDHA, SDHB, IDH3G, SDHC, DLD, SDHD, IDH2, IDH1, PDHA1, FHL1, SUCLA2, MDH2, MDH1	1276	198	5738	1.86	2.76E-07	5.53E-08	1.82E-06
KEGG_PATHWAY	mmu00020:Citrate cycle (TCA cycle)	23	0.60	8.98E-09	UQCRC2, ATP1B1, UQCRC1, MYL2, ATP1B3, TNNC1, MYL3, ATP1B4, CYC1, COX7B, COX7C, CACNB1, COX7A2L, UQCRCF51, COX5A, COX5B, UQCRCQ, TPM4, TPM3, UQCRC10, UQCRC11, COX6B1, ACTC1, SLC8A1, COX7A2, COX8B, COX7A1, COX42, COX411, MYH7, ATP1A1, COX6C, CACNA2D4, ATP2A2, UQCRCR, UQCRCB, SLC9A1	1276	31	5738	3.34	1.70E-06	2.83E-07	1.11E-05
KEGG_PATHWAY	mmu04260:Cardiac muscle contraction	37	0.97	2.11E-06	IBSP, TNC, NPNT, COL3A1, COL2A1, SDC4, ITGB1, SDC2, CHAD, LAMB2, CD44, COMP, ITGB7, ITGB6, COL6A2, COL6A1, AGRN, COL11A2, THBS1, COL11A1, THBS2, THBS3, FN1, SPP1, THBS4, COL4A2, COL4A1, TNXB, COL5A2, VWF, LAMA4, SDC1, CD36, ITGA5, COL11A2, LAMC2, LAMC1, COL1A1, BCAT2, EHHADH, ECHS1, ACAT1, HADHA, HIBADH, AUH, HADHB, MCCC2, MUT, MCEE, OXCT1, MCC1, ACAD8, HADH, HMGC1, BCKDHA, ACAA2, ACADM, ACADS, DBT, DLD, AOX1, HIBCH, PCCA FGF7, PDGFR, PDGFA, TGFBR3, NFKB2, TGFBR1, PRKX, TGFBR2, MAP3K6, FOS, CASP3, MAP3K5, PAK2, BZ30120H23BK, MAP3K8, FAS, RARGP2, FGF2, MYC, CHUK, MAP2K6, PRKCA, EGFR, BRAF, REL, RELB, PTPRR, ECTS, FLNC, FLNB, FLNA, STK3, MAP4K3, MAP4K4, RASGRF2, ARRB2, RRS2, JUN, GADD45G, PDGFR, HSPB1, MAPK7, MAP3K14, GADD45B, GADD45A, ILIR2, ILIR1, FGF3, MKNK2, DUSP10, MAP4K2, CACNB1, HSPA1A, GNG12, HSPA1B, TNFRSF1A, KRAS, HSPA2, RASGRP3, RAC2, ELK4, MAP3K2, PLA2G12A, JUN, RASGRP2, HSPA8, RASA2, PTPN7, TRP53, TGFBR1, TGFBR2, NR4A1, MAPK11, TAB1, CACNA2D4, RPS6KA5, DUSP5, NRAS, DUSP4, ATF4, PLA2G4A, RPS6KA3, DUSP2, RPS6KA4, DUSP1, RPS6KA2, NTRK2, RAP1B, PLA2G4B, CD14, DUSP7	1276	78	5738	2.13	3.99E-04	5.70E-05	0.002622723
KEGG_PATHWAY	mmu04512:ECM-receptor interaction	38	1.00	4.27E-06	ITGAL, GNAI3, MYL2, GNAI2, MMP9, BCAR1, CLDN5, ITGB2, ITGB1, MMP2, PXN, ITGAM, VCL, MYL9, ACTG1, ARHGAP5, EZR, RAC2, PTK2B, PIK3R5, MSN, PIK3R1, MLLT4, PIK3R2, ACTB, PRKCA, ICAM1, ACTN4, ROCK1, NCF2, NCF1, ROCK2, NCF4, ACTH1, ACTH2, MAPK11, CTNNA1, VAV1, VASP, THY1	1276	83	5738	2.06	8.06E-04	1.01E-04	0.005297508
KEGG_PATHWAY	mmu00280:Valine, leucine and isoleucine degradation	25	0.66	7.94E-06	CYBA, CYBB, RASSF5, PLCG2, GRLF1, RAP1B, JAM2, PDGFR, PGF, PDGFA, MMP9, TGFBR3, FOXO1, MMP2, TGFBR1, TGFBR2, SLC2A1, RALB, CSF3R, RARA, FAS, RARB, EGFR, RET, BCR, BRAF, RPLA, RARG, CTNNA1, VEGFB, JUP, HIF1A, JUN, VEGFA, PDGFR, LAMC2, LAMC1, WNT5A, FGF3, SFP1, BCL2L1, ITGB1, KRAS, LAMB2, RAC2, FH1, RUNX1, AXIN2, CSF1R, FN1, AXIN1, TRP53, BMP4, TCF7, BMP2, EPAS1, TGFBR1, MET, CREBBP, TGFBR2, SMAD3, CBLB, LAMA4, CDKN1A, PLCG2, PPARA, FGF7, NFKB2, FOS, CCNE1, CASP3, CASP8, FGF2, MYC, CSF2RA, CHUK, PRKCA, AR, HSP90A1, CYCS, CDK4, SMO, CCND1, MDM2, WNT11, WNT5A, BID, PML, KIT, TPM3, IGF1R, PIK3R5, PIK3R1, PIK3R2, CEBPA, IL6, COL4A2, COL4A1, MSH2, FZD1, BIRC3, FZD5,	1276	46	5738	2.44	0.001499078	1.67E-04	0.009856236
KEGG_PATHWAY	mmu04010:MAPK signaling pathway	90	2.36	9.02E-06	ITGAL, GNAI3, MYL2, GNAI2, MMP9, BCAR1, CLDN5, ITGB2, ITGB1, MMP2, PXN, ITGAM, VCL, MYL9, ACTG1, ARHGAP5, EZR, RAC2, PTK2B, PIK3R5, MSN, PIK3R1, MLLT4, PIK3R2, ACTB, PRKCA, ICAM1, ACTN4, ROCK1, NCF2, NCF1, ROCK2, NCF4, ACTH1, ACTH2, MAPK11, CTNNA1, VAV1, VASP, THY1	1276	265	5738	1.53	0.001703641	1.70E-04	0.011202286
KEGG_PATHWAY	mmu04670:Leukocyte transendothelial migration	47	1.23	3.16E-05	CYBA, CYBB, RASSF5, PLCG2, GRLF1, RAP1B, JAM2, PDGFR, PGF, PDGFA, MMP9, TGFBR3, FOXO1, MMP2, TGFBR1, TGFBR2, SLC2A1, RALB, CSF3R, RARA, FAS, RARB, EGFR, RET, BCR, BRAF, RPLA, RARG, CTNNA1, VEGFB, JUP, HIF1A, JUN, VEGFA, PDGFR, LAMC2, LAMC1, WNT5A, FGF3, SFP1, BCL2L1, ITGB1, KRAS, LAMB2, RAC2, FH1, RUNX1, AXIN2, CSF1R, FN1, AXIN1, TRP53, BMP4, TCF7, BMP2, EPAS1, TGFBR1, MET, CREBBP, TGFBR2, SMAD3, CBLB, LAMA4, CDKN1A, PLCG2, PPARA, FGF7, NFKB2, FOS, CCNE1, CASP3, CASP8, FGF2, MYC, CSF2RA, CHUK, PRKCA, AR, HSP90A1, CYCS, CDK4, SMO, CCND1, MDM2, WNT11, WNT5A, BID, PML, KIT, TPM3, IGF1R, PIK3R5, PIK3R1, PIK3R2, CEBPA, IL6, COL4A2, COL4A1, MSH2, FZD1, BIRC3, FZD5,	1276	119	5738	1.78	0.005957607	5.43E-04	0.039252385
KEGG_PATHWAY	mmu05200:Pathways in cancer	103	2.70	3.93E-05	STAT3, RALGDS, NRAS, HSP90B1, RASSF5, BAX, RASSF1, JAK1	1276	323	5738	1.43	0.007403353	6.19E-04	0.04881099

Table S2.C KEGG pathways significant at 24 hours

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
KEGG_PATHWAY	mmu00190:Oxidative phosphorylation	76	1.88	2.71E-17	ATP5D, UQCRC2, ATP5E, COX11, COX10, UQCRCF1, COX5A, COX5B, NDUFS7, NDUFS6, NDUFS5, UQCRC10, UQCRC11, NDUFS4, CASP9, APOE, CASP8, NDUFS8, IL1B, ATP5O, NDUFS3, ATP5H, COX17, NDUFS1, ATP5K, ATP5I, NDUFB10, NDUFC2, ATP6V1H, NDUFC1, NDUFA10, ATP6V1D, COX6C, NDUFA11, ATP6V1A, UQCRC4, ATP5C1, UQCRC8, NDUFB3, NDUFB4, NDUFB5, NDUFB6, NDUFB7, NDUFB8, NDUFB9, COX7B, COX7C, ATP5G2, ATP6V1B2, ATP5G1, ATP6V1G1, COX7A2L, NDUFB2, NDUFB6, COX6B1, TCIRG1, NDUFA4, NDUFA5, NDUFA2, ATP5J2, COX7A2, NDUFA3, NDUFA8, COX7A1, COX8B, NDUFA9, NDUFA6, NDUFA7, ATP5F1, LHPP, NDUFA1, PPA2, NDUFV3, ATP6V0E2, ATP6V1E1, SDHC, NDUFV2, SDHD, COX6A2	1355	130	5738	2.48	5.15E-15	5.15E-15	3.37E-14
KEGG_PATHWAY	mmu05010:Alzheimer's disease	87	2.15	1.15E-12	ATP5D, UQCRC2, ATP5E, IDE, COX5A, UQCRCF1, COX5B, NDUFS7, NDUFS6, NDUFS5, APP, CASP3, UQCRC10, UQCRC11, NDUFS4, CASP9, APOE, CASP8, NDUFS8, IL1B, ATP5O, NDUFS3, ATP5H, PLCB2, NDUFS1, ATP5J, NDUFB10, ADAM10, CYCS, NDUFC2, FADD, NDUFC1, NDUFA10, COX6C, UQCRC4, ATP5C1, ERN1, GM12070, EIF2AK3, UQCRC8, BID, NDUFB3, NDUFB4, HSD17B10, NDUFB5, NDUFB6, NDUFB7, NDUFB8, NDUFB9, COX7B, COX7C, MME, ATP5G2, ATP5G1, COX7A2L, NDUFB2, TNFRSF1A, COX6B1, PPP3CB, PPP3CA, GAPDH, NDUFA4, NDUFA5, NDUFA2, COX7A2, NDUFA3, NOS1, NDUFA8, COX7A1, COX8B, NDUFA9, NDUFA6, NDUFA7, ATP5F1, CAPN2, NDUFA1, ITPR1, CAPN1, ATF6	1355	182	5738	2.02	2.19E-10	1.09E-10	1.43E-09
KEGG_PATHWAY	mmu05012:Parkinson's disease	69	1.70	3.01E-12	SDHC, NDUFV2, SDHD, COX6A2, APAF1	1355	133	5738	2.20	5.72E-10	1.91E-10	3.74E-09
KEGG_PATHWAY	mmu05016:Huntington's disease	86	2.12	5.05E-12	HDAC1, BBK1, BAX, NDUFV2, SDHD, COX6A2, APAF1	1355	183	5738	1.99	9.59E-10	2.40E-10	6.27E-09
KEGG_PATHWAY	mmu04210:Apoptosis	45	1.11	3.39E-08	ENDOD, RIFK1, BAX, PRKAR1A, APAF1, MAP3K14, IL3RA	1355	87	5738	2.19	6.44E-06	1.29E-06	4.21E-05
KEGG_PATHWAY	mmu04920:Adipocytokine signaling pathway	35	0.86	1.12E-06	PRKAG3, NFKBIE, STK11, NFKBIA, CAMKK1, CAMKK2, AKT1, TNFRSF1A, TNFRSF1B, SLC2A4, SLC2A1, PRKAA1, PRKAA2, ACSL3, CHUK, ACSL6, ACSL5, AKT2, CPT1B, SOCS3, RXRA, REL, PRKAB2, PRKAB1, RXRG, ADIPOR1, ACAC3, ADIPOQ, IRS1, CPT1A, STAT3, TRADD, PRKCC, NPY, JAK2, MARKSKL1, WASF2, ASAP1, ARPC4, ARFG, ARPC5, AKT3, DOCK2, RAC2, ARPC2, GAB2, ARPC2, GSN, PIKFYVE, PIK3R5, INPP5D, PAK1, AKT2, PRKCA, PIK3CG, PTPRC, VAV3, LYN, PPA2C, LIMK1, NCF1, HCK, SHPK2, PRKCE, FCGR1, WAS, VAV1, PRKCD, VASP, PRKCB, ARPC1B, PLA2G4A, FCGR2B, ARPCS, CFL1, PLCG2, SCIN, MARCKS, PLA2G4E	1355	67	5738	2.21	2.13E-04	3.55E-05	0.001393144
KEGG_PATHWAY	mmu04666:Fc gamma R-mediated phagocytosis	44	1.09	6.54E-06	ADCY2, ADCY7, PREX1, STAT5B, CXCR2, PRKX, AKT1, TIAM2, CXCR4, TIAM1, RHOA, PRKACA, SHC1, PAK1, CSK, PLCB2, CHUK, AKT2, PIK3CG, LYN, NCF1, REL, WAS, PRKCD, HRAS1, PRKCB, ELMO1, GNB2, PPP8R, CCR5, ARRB2, GNB1, CCR2, CXCR1, GNB5, CXCL1, PARD3, CCL3, GNAI3, CCL2, GNAI2, FGR, CCR1, CCL9, NFKBIA, CCL8, PF4, CCL7, CCL6, CCL24, CCL25, DOCK2, KRAS, RAC2, PTK2B, SOS2, PIK3R5, VAV3, HCK, VAV1, STAT3, STAT2, NRAS, CCL12, CXCL14, GNG10, CXCL16, JAK2, RAP1B, GRK5, BID, STEAP3, CHEK1, SFN, RRM2B, PMAIP1, SESN2, CCNG2, CCNE1, CASP3, CASP9, SHISAS, SERPINE1, CASP8, THBS1, TRPS3, CDK1, CYCS, CDK6, CDK4, CDK2, RFWO2, CCND1, CDKN1A, EIZ4, BBK3, CCND2, CD82, RRM2, BAX, GADD45G, APAF1, GADD45A	1355	98	5738	1.90	0.001241374	1.77E-04	0.00812502
KEGG_PATHWAY	mmu04062:Chemokine signaling pathway	70	1.73	7.95E-06	PIK3R5, VAV3, HCK, VAV1, STAT3, STAT2, NRAS, CCL12, CXCL14, GNG10, CXCL16, JAK2, RAP1B, GRK5, BID, STEAP3, CHEK1, SFN, RRM2B, PMAIP1, SESN2, CCNG2, CCNE1, CASP3, CASP9, SHISAS, SERPINE1, CASP8, THBS1, TRPS3, CDK1, CYCS, CDK6, CDK4, CDK2, RFWO2, CCND1, CDKN1A, EIZ4, BBK3, CCND2, CD82, RRM2, BAX, GADD45G, APAF1, GADD45A	1355	182	5738	1.63	0.001508532	1.89E-04	0.009874856
KEGG_PATHWAY	mmu04115:p53 signaling pathway	34	0.84	8.49E-06	BBK3, CCND2, CD82, RRM2, BAX, GADD45G, APAF1, GADD45A	1355	69	5738	2.09	0.001611612	1.79E-04	0.010550125
KEGG_PATHWAY	mmu00230:Purine metabolism	62	1.53	1.10E-05	GDA, ADCY2, GMPR2, ADCY7, PDE3B, PRM1, PRM2, NTSM, NTS5C3, PDE4A, PRIM2, NTS5C2, IMPDH1, NTS5, NTS5, NUDT2, POLR1E, NUDT5, PDE4D, PDE10A, POLR1B, GMPR, NME1, ADK, RRM2, ADSL, PRPS2, XDH, POLR2H, ADSS, ENPP1, POLR2K, NTS5C1A, POLR2L, POLA1, DCK, RRM2B, PFAS, ADA, POLR2A, POLE2, PDE1B, ATIC, NUDT9, ENTPD4, ENTPD1, PAPS1, PAPS2, ADSL1, AK1, POLR3GL, NPR2, AMPD2, AMPD1, APRT, POLR3D, AMPD1, POLD1, PDE7B, PDE2A, POLD1, PAICS, PFCS2, POF, MAMP, STATS5B, FGF13, TGFBI, WNT4, SLC2A1, RALB, CSF1R, RARA, RARB, EGFR, PIK3CG, BCR, RXBA, REL, RXRG, SEK2, FADD, CTNNA1, STK4, CTNNA3, HRAS1, VEGFB, CCDC6, HIF1A, VEGFA, PDGFRA, LAMC2, TRAF1, NFKBIA, SFP1, BCL2L1, ITGB1, RBX1, LAMB2, KRAS, RAC2, FHL1, RUNX1, CSF1R, FNI, TRP53, BMP2, EPAS1, MAP2K2, SMAD3, ITGA3, CDKN1A, CDKN1B, HDAC1, PLCG2, E2F1, PPARG, NFKB2, AKT1, ACVR1B, CCNE1, FOS, CASP3, CASP9, CASP8, RHOA, MYC, CHUK, CSF2RA, AKT2, PRKCA, AR, HSP90AA1, CYCS, CDK6, CDK4, CDK2, PRKCB, DAPK1, SMO, CCND1, WNT1, WNT9A, BID, CCK1B, PML, EGR2, HIF1, ZBTB16, TRAF3, IGF1R, BCL2, SOS2, PIK3R5, CEBPA, IL6, CDL4A2, CDL4A1, VHL, CBL, BIRC3, FZD5, FZD4, STAT3, FZD7, NRAS, HSP90B1, RASSF5, BAK	1355	157	5738	1.67	0.00208012	2.08E-04	0.013620114
KEGG_PATHWAY	mmu05200:Pathways in cancer	109	2.69	2.31E-05	RASSF1, ARAF	1355	323	5738	1.43	0.004375503	3.99E-04	0.028680546

Table S2.D KEGG pathways significant at 48 hours

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
KEGG_PATHWAY	mmu00280:Valine, leucine and isoleucine degradation	28		1.30	2.79E-12 ALDH9A1, PCCA	820	46	5738	4.26	4.99E-10	4.99E-10	3.43E-09
KEGG_PATHWAY	mmu05010:Alzheimer's disease	55		2.56	4.10E-08 UQCRC2, UQCRC1, CYC1, NDUFB1, UQCRCF51, NDUFS7, CASP3, NDUFA5, UQCRC11, CASP9, APOE, NDUFS8, CASP8, IL1B, NDUFS3, PLCB2, NDUFS2, NDUFS1, ADAM10, NDUFB10, CYCS, NDUFC1, NDUFA10, ATP5C1, UQCRC8, NDUFB3, BID, CDK5R1, TM4SF19, NDUFB8, NDUFB9, NDUFB2, TNFRSF1A, PPP3CB, PPP3CA, LPL, NDUFA5, NOS1, COX7A1, COX8B, NDUFA8, NDUFA9, NDUFA6, CACNA1S, SDHA, NDUFV3, SDHB, LRP1, ATP2A2, NDUFV1, SDHC, NDUFV2, COX6A2, COX6A1, APAF1	820	182	5738	2.11	7.33E-06	3.67E-06	5.04E-05
KEGG_PATHWAY	mmu05012:Parkinson's disease	44		2.05	6.92E-08 UQCRC2, NDUFB3, UQCRC1, NDUFB8, NDUFB9, CYC1, UCHL1, NDUFB1, PINK1, UQCRCF51, NDUFB2, NDUFS7, CASP3, UQCRC11, NDUFA4, CASP9, NDUFS8, NDUFS3, NDUFS2, NDUFS1, NDUFA5, NDUFB10, NDUFA8, COX8B, COX7A1, NDUFA9, SLC25A5, NDUFA6, CYCS, NDUFC1, NDUFA10, VDCA3, VDCA1, NDUFV3, SDHA, SDHB, NDUFV1, SDHC, NDUFV2, COX6A2, ATP5C1, COX6A1, APAF1, UQCRC8, ITGAL, GNAI3, MYL2, GNAI2, MMP9, ITGB2, ITGAM, VCL, ACTG1, VCAM1, EZR, RAC2, PTK2B, CXCR4, RHOA, PIK3R5, MSN, RHOH, ACTB, PRKCA, PIK3CG, ICAM1, VAV3, NCF2, ACTN4, NCF1, NCF4, ACTN1, MYL12B, VAV1, VASP, THY1, PRKCB, CYBA, CYBB, RASSF5, MAPK12, PLCG2, RAP1B	820	133	5738	2.31	1.24E-05	4.13E-06	8.52E-05
KEGG_PATHWAY	mmu04670:Leukocyte transendothelial migration	39		1.81	5.77E-07 UQCRC2, NDUFB3, UQCRC1, NDUFB8, NDUFB9, CYC1, NDUFB1, UQCRCF51, NDUFB2, NDUFS7, ATP5C1, UQCRC11, NDUFA4, NDUFS8, NDUFS3, NDUFS2, NDUFS1, ATP5K, TCIRG1, NDUFA5, NDUFB10, NDUFA8, COX8B, COX7A1, NDUFA9, SDHC, NDUFV2, COX6A2, ATP5C1, COX6A1, NDUFA10, NDUFV3, SDHA, SDHB, ATP6V1A, ATP6V0E2, NDUFV1, SDHC, NDUFV2, COX6A2, ATP5C1, COX6A1, UQCRCB, SUCLG1, CS, IDH3B, ACLY, DLAT, OGDH, IDH3A, SDHA, SDHB, IDH3G, SDHC, DLD, IDH2, PDHA1, FH1, SUCLA2, MDH1	820	119	5738	2.29	1.03E-04	2.58E-05	7.10E-04
KEGG_PATHWAY	mmu00190:Oxidative phosphorylation	41		1.91	8.65E-07 MARKS11, ARPC4, ARFG, ARPC5, DOCK2, RAC2, ARPC3, GAB2, ARPC2, PIK3R5, INPP5D, PIK3CG, PRKCA, PTPRC, VAV3, LYN, PPA2C, NCF1, LMK1, HCK, SPHK1, VAV1, PRKCD, WAS, FCGR1, VASP, PRKCB, ARPC1B, PLA2G4A, FCGR2B, CFL1, PLCG2, MARCKS	820	130	5738	2.21	1.55E-04	3.10E-05	0.001065029
KEGG_PATHWAY	mmu00020:Citrate cycle (TCA cycle)	17		0.79	9.45E-07 SUCLA2, MDH1	820	31	5738	3.84	1.69E-04	2.82E-05	0.001162609
KEGG_PATHWAY	mmu04666:Fc gamma R-mediated phagocytosis	33		1.53	2.63E-06 ADCY7, STAT5B, CXCR2, PRKX, CXCR4, RHOA, CSK, PLCB2, PIK3CG, LYN, NCF1, PRKCD, WAS, ELMO1, PRKCB, CCR5, PPBP, ARRB2, GNB1, CX3CR1, CCR2, GNAI3, CCL2, GNAI2, FGR, CCR1, CCL9, CCL8, PF4, CCL4, CCL7, CCL6, DOCK2, RAC2, PTK2B, SOS2, PIK3R5, VAV3, HCK, VAV1, STAT3, NRAS, ADCY9, CXCL14, CXCL13, CXCL16, GNG10, JAK2, RAP1B	820	98	5738	2.36	4.71E-04	6.72E-05	0.0032361
KEGG_PATHWAY	mmu04062:Chemokine signaling pathway	49		2.28	9.62E-06 UQCRC2, CLTA, UQCRC1, CYC1, NDUFB1, UQCRCF51, NDUFS7, GPX1, CASP3, NDUFA5, UQCRC11, CASP9, NDUFS8, CASP8, NDUFS3, PLCB2, NDUFS2, NDUFS1, NDUFB10, SLC25A5, CYCS, NDUFC1, NDUFA10, ATP5C1, UQCRC8, NDUFB3, NDUFB8, NDUFB9, NDUFB2, TRP53, NDUFA5, COX7A1, COX8B, NDUFA8, NDUFA9, NDUFA6, VDCA3, SOD2, VDCA1, SDHA, NDUFV3, SDHB, BAX, SDHC, NDUFV1, NDUFV2, COX6A2, COX6A1, APAF1	820	182	5738	1.88	0.001720856	2.15E-04	0.011840157
KEGG_PATHWAY	mmu05016:Huntington's disease	49		2.28	1.13E-05 ALDH6A1, LDHB, ACADM, SUCLG1, ECHS1, ACAT1, HADHA, MUT, ACS1, MCEE, ALDH2, SUCLA2, PCCB, ALDH9A1, PCCA	820	183	5738	1.87	0.002020134	2.25E-04	0.013901248
KEGG_PATHWAY	mmu00640:Propanoate metabolism	15		0.70	2.05E-05	820	30	5738	3.50	0.003656954	3.66E-04	0.025184004

KEGG_PATHWAY	mmu05212:Pancreatic cancer	47	0.65	9.20E-06	E2F1, E2F2, PGF, NFKB1, BCL2L1, TGFBI, TGFBI2, AKT1, ACVR1B, RAC2, CASP9, RAC3, RALB, RALA, PIK3CA, PIK3RS, EGF, FIGF, AKT3, AKT2, PIK3CG, TRP53, EGFR, PLD1, RELA, ARHGGEF6, TGFBR1, PIK3CD, TGFBR2, SMAD4, RAF1, BRCA2, SMAD3, CDK6, STAT1, CDK4, STAT3, RALGDS, RADS1, VEGFB, CCND1, ARAF, VEGFA, MAPK3, MAPK9, MAPK8, IKBKB	2203	72	5738	1.70	0.001774079	9.86E-05	0.011463648
KEGG_PATHWAY	mmu05210:Colorectal cancer	53	0.73	2.43E-05	TGFBI, TGFBI2, AKT1, FOS, ACVR1B, CASP3, CASP9, PIK3CA, MYC, AKT3, AKT2, EGFR, PIK3CG, PIK3CD, CYCS, CCND1, JUN, MAPK3, PDGFRA, MAPK9, MAPK8, GRB2, TCF7L2, RAC2, RAC3, SOS1, BCL2, SOS2, PIK3RS, DVL2, FZD9, TRP53, TCF7, MSH3, MSH2, TGFBR1, TGFBR2, SMAD4, FZD1, RAF1, SMAD3, BIRC5, FZD2, FZD5, APPL1, FZD4, FZD7, RALGDS, FZD6, DVL1, BAX, GSK3B, ARAF	2203	86	5738	1.61	0.004670485	2.46E-04	0.030220506
KEGG_PATHWAY	mmu05220:Chronic myeloid leukemia	48	0.67	2.60E-05	E2F1, E2F2, GRB2, STAT5B, NFKBIA, NFKB1, BCL2L1, TGFBI, TGFBI2, AKT1, ACVR1B, GAB2, SOS1, SOS2, PIK3CA, SHC1, PIK3RS, RUXN1, MYC, AKT3, AKT2, PIK3CG, TRP53, CTBP1, BCR, MAP2K2, RELA, TGFBR1, CBL, PIK3CD, TGFBR2, SMAD4, RAF1, SMAD3, CDK6, MECOM, CDK4, PTPN11, HRAS1, NRAS, CCND1, CDKN1A, HDAC2, HDAC1, ARAF, MAPK3, MDM2, IKBKB	2203	76	5738	1.65	0.005013764	2.51E-04	0.032446929

Table S2.F KEGG pathways significant at 168 hours

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
KEGG_PATHWAY	mmu04062:Chemokine signaling pathway	18		0.65	4.47E-07 CCL2, FGR, NCF1, HCK, CCL9, CCL8, WAS, CCL7, CCL17, PRKCB, CCL12, CCR5, RAC2, CCR2, CX3CR1, PIK3RS, XCL1, XCR1	129	182	5738	4.40	4.78E-05	4.78E-05	5.02E-04
KEGG_PATHWAY	mmu04670:Leukocyte transendothelial migration	14		0.50	1.93E-06 NCF2, NCF1, NCF4, ITGB2, PRKCB, VCAM1, CYBA, CYBB, EZR, RAC2, PLCG2, CLDN2, PIK3RS, RHOH	129	119	5738	5.23	2.06E-04	1.03E-04	0.002168346
KEGG_PATHWAY	mmu04650:Natural killer cell mediated cytotoxicity	13		0.47	1.46E-05 BID, FCGR4, ITGB2, NCR1, PRKCB, FCGR3, CD48, RAC2, PLCG2, FCER1G, PIK3RS, LCP2, TYROBP	129	122	5738	4.74	0.001563801	5.22E-04	0.016439609
KEGG_PATHWAY	mmu05322:Systemic lupus erythematosus	12		0.43	1.55E-05 C1QA, C1QB, C7, CD86, C4B, FCGR4, H2-DMB1, HIST1H4I, C1QC, FCGR1, IL10, FCGR3	129	103	5738	5.18	0.001652768	4.13E-04	0.017375573
KEGG_PATHWAY	mmu04060:Cytokine-cytokine receptor interaction	18		0.65	2.48E-05 CCL2, CSF2RB2, CCL9, CCL8, IL10, CCL7, CCL17, CCL12, CCR5, IL10RA, CCR2, CX3CR1, CSF2RB, IL2RG, IL12B, XCL1, XCR1, CSF2RA	129	244	5738	3.28	0.00265068	5.31E-04	0.027879105

Table S2.G KEGG pathways significant at 336 hours

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
KEGG_PATHWAY	mmu04512:ECM-receptor interaction	18	2.36	7.85E-08	IBSP, TNC, COL3A1, ITGB5, ITGA4, COL5A3, COL5A2, SDC2, COL5A1, CD44, COL1A2, COL6A2, COL6A1, COL1A1, THBS2, THBS3, SPP1, FN1	254	83	5738	4.90	1.08E-05	1.08E-05	9.24E-05
KEGG_PATHWAY	mmu05416:Viral myocarditis	16	2.10	1.24E-05	H2-K1, ITGAL, MYH3, H2-D1, H2-DMB1, ITGB2, MYH7, H2-AB1, MYH8, CD86, H2-EB1, SGCD, H2-AA, MYH13, MYH14, ABL2	254	94	5738	3.85	0.001713391	8.57E-04	0.014623985
KEGG_PATHWAY	mmu04062:Chemokinesignalingpathway	23	3.01	1.34E-05	PARD3, CCL2, ADCY7, NCF1, STASB, CXCL9, CCL9, CCL8, GNG11, PF4, CCL6, CCL12, CCR5, ADCY9, TIAM1, CXCR4, GNG10, CXCL16, GSK3B, CCR2, SOS2, PAK1, SHC2	254	182	5738	2.85	0.001841954	6.14E-04	0.015722211
KEGG_PATHWAY	mmu04510:focal adhesion	24	3.15	1.64E-05	IBSP, FLT1, TNC, COL3A1, ITGB5, ITGA4, COL5A3, COL5A2, COL5A1, GSK3B, BCL2, SOS2, COL6A2, GRLF1, COL1A2, COL6A1, COL1A1, PAK1, EGF, SHC2, THBS2, THBS3, SPP1, FN1	254	198	5738	2.74	0.00258263	5.65E-04	0.019279342

Table S2.H KEGG pathways significant at 504 hours

Category	Term	Count	%	PValue	Genes
KEGG_PATHWAY	mmu04512:ECM-receptor interaction	18	2.36	7.85E-08	IBSP, TNC, COL3A1, ITGB5, ITGA4, COL5A3, COL5A2, SDC2, COL5A1, CD44, COL1A2, COL6A2, COL6A1, COL1A1, THBS2, THBS3, SPP1, FN1
KEGG_PATHWAY	mmu05416:Viral myocarditis	16	2.10	1.24E-05	H2-K1, ITGAL, MYH3, H2-D1, H2-DMB1, ITGB2, MYH7, H2-AB1, MYH8, CD86, H2-EB1, SGCD, H2-AA, MYH13, MYH14, ABL2
KEGG_PATHWAY	mmu04062:Chemokine signaling pathway	23	3.01	1.34E-05	TIAM1, CXCR4, GNG10, CXCL16, GSK3B, CCR2, SOS2, PAK1, SHC2, PARD3, CCL2, ADCY7, NCF1, STAT5B, CXCL9, CCL9, CCL8, GNG11, PF4, CCL6, CCL12, CCR5, ADCY9, IBSP, FLT1, TNC, COL3A1, ITGB5, ITGA4, COL5A3, COL5A2, COL5A1, GSK3B, BCL2, SOS2, COL6A2,
KEGG_PATHWAY	mmu04510:focal adhesion	24	3.15	1.64E-05	GRLF1, COL1A2, COL6A1, COL1A1, PAK1, EGF, SHC2, THBS2, THBS3, SPP1, FN1

Table S2.H KEGG pathways significant at 504 hours

List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
254	83	5738	4.90	1.08E-05	1.08E-05	9.24E-05
254	94	5738	3.85	0.001713391	8.57E-04	0.014623985
254	182	5738	2.85	0.001841954	6.14E-04	0.015722211
254	198	5738	2.74	0.002258263	5.65E-04	0.019279342

Table S2.I KEGG pathways significant at 672 hours

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
KEGG_PATHWAY	mmu04512:ECM-receptor interaction	17		2.51	7.58E-08 IBSP, TNC, COL3A1, ITGA4, COL5A2, SDCC2, COL5A1, CD44, COMP, COL1A2, COL6A2, COL6A1, COL1A1, THBS2, COL11A1, THBS3, FN1	223	83	5738	5.27	1.08E-05	1.08E-05	8.96E-05
KEGG_PATHWAY	mmu04510:Focal adhesion	26		3.85	1.21E-07 IBSP, CAV2, CAV1, MYL2, TNC, COL3A1, BCL2, COMP, COL6A2, COL6A1, PAK1, EGF, COL11A1, THBS2, THBS3, FN1, VAV3, IGF1, ITGA4, COL5A2, COL5A1, PDGFRA, COL1A2, GRLF1, COL1A1, PARVA	223	198	5738	3.38	1.72E-05	8.62E-06	1.44E-04
KEGG_PATHWAY	mmu04610:Complement and coagulation cascades	15		2.22	7.70E-07 C3AR1, CFB, F13A1, SERPING1, C1S, C1QC, C1QA, C1QB, C1RA, CD55, F3, CFH, C2, CFB, PROS1	223	75	5738	5.15	1.09E-04	3.64E-05	9.10E-04

Table S3. Significant GO clusters identified from the 168h time point that were obtained from differentially expressed genes that were determined to contribute the largest variance at that time point.

Cluster 1: Enrichment Score: 11.54				
Annotation	GO Term	Gene Count	P-value	FDR
GOTERM_BP_FAT	vasculature development	85	5.20E-14	9.70E-11
GOTERM_BP_FAT	blood vessel development	83	1.00E-13	1.90E-10
GOTERM_BP_FAT	blood vessel morphogenesis	69	4.30E-12	8.00E-09
GOTERM_BP_FAT	angiogenesis	48	3.00E-09	5.60E-06
Cluster 2: Enrichment Score: 11.31				
Annotation	GO Term	Gene Count	P-value	FDR
GOTERM_CC_FAT	extracellular matrix	100	2.50E-14	3.60E-11
SP_PIR_KEYWORD	extracellular matrix	76	7.40E-14	1.10E-10
GOTERM_CC_FAT	proteinaceous extracellular matrix	96	9.40E-14	1.40E-10
GOTERM_CC_FAT	extracellular region part	179	1.10E-09	1.60E-06
GOTERM_CC_FAT	extracellular matrix part	37	1.50E-08	2.20E-05
Cluster 3: Enrichment Score: 9.38				
Annotation	GO Term	Gene Count	P-value	FDR
KEGG_PATHWAY	lysosome	53	2.40E-12	3.00E-09
SP_PIR_KEYWORD	lysosome	52	5.60E-10	8.30E-07
GOTERM_CC_FAT	lysosome	60	1.00E-09	1.50E-06
GOTERM_CC_FAT	lytic vacuole	60	1.30E-09	1.90E-06
GOTERM_CC_FAT	vacuole	64	6.80E-09	9.90E-06
Cluster 4: Enrichment Score: 7.85				
Annotation	GO Term	Gene Count	P-value	FDR
GOTERM_BP_FAT	vesicle-mediated transport	121	2.70E-10	5.00E-07
GOTERM_BP_FAT	membrane invagination	61	2.10E-09	3.90E-06
GOTERM_BP_FAT	endocytosis	61	2.10E-09	3.90E-06
GOTERM_BP_FAT	membrane organization	76	3.10E-08	5.70E-05
SP_PIR_KEYWORD	endocytosis	31	1.60E-05	2.40E-02
Cluster 5: Enrichment Score: 7.18				
Annotation	GO Term	Gene Count	P-value	FDR
GOTERM_BP_FAT	actin filament-based process	61	1.10E-10	2.00E-07
GOTERM_BP_FAT	actin cytoskeleton organization	57	5.60E-10	1.00E-06
GOTERM_BP_FAT	actin filament organization	23	6.70E-06	1.20E-02
GOTERM_BP_FAT	cytoskeleton organization	76	4.80E-05	8.80E-02