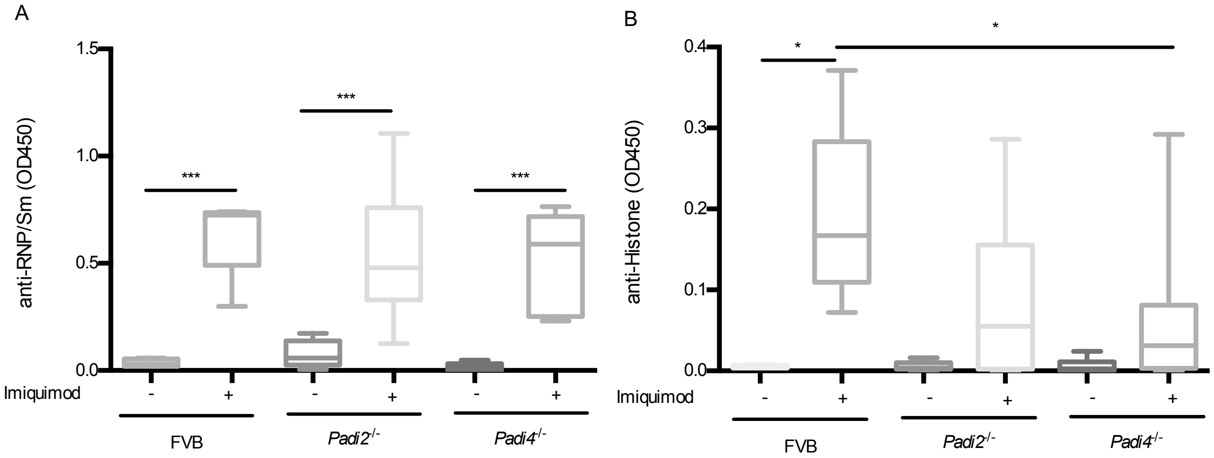
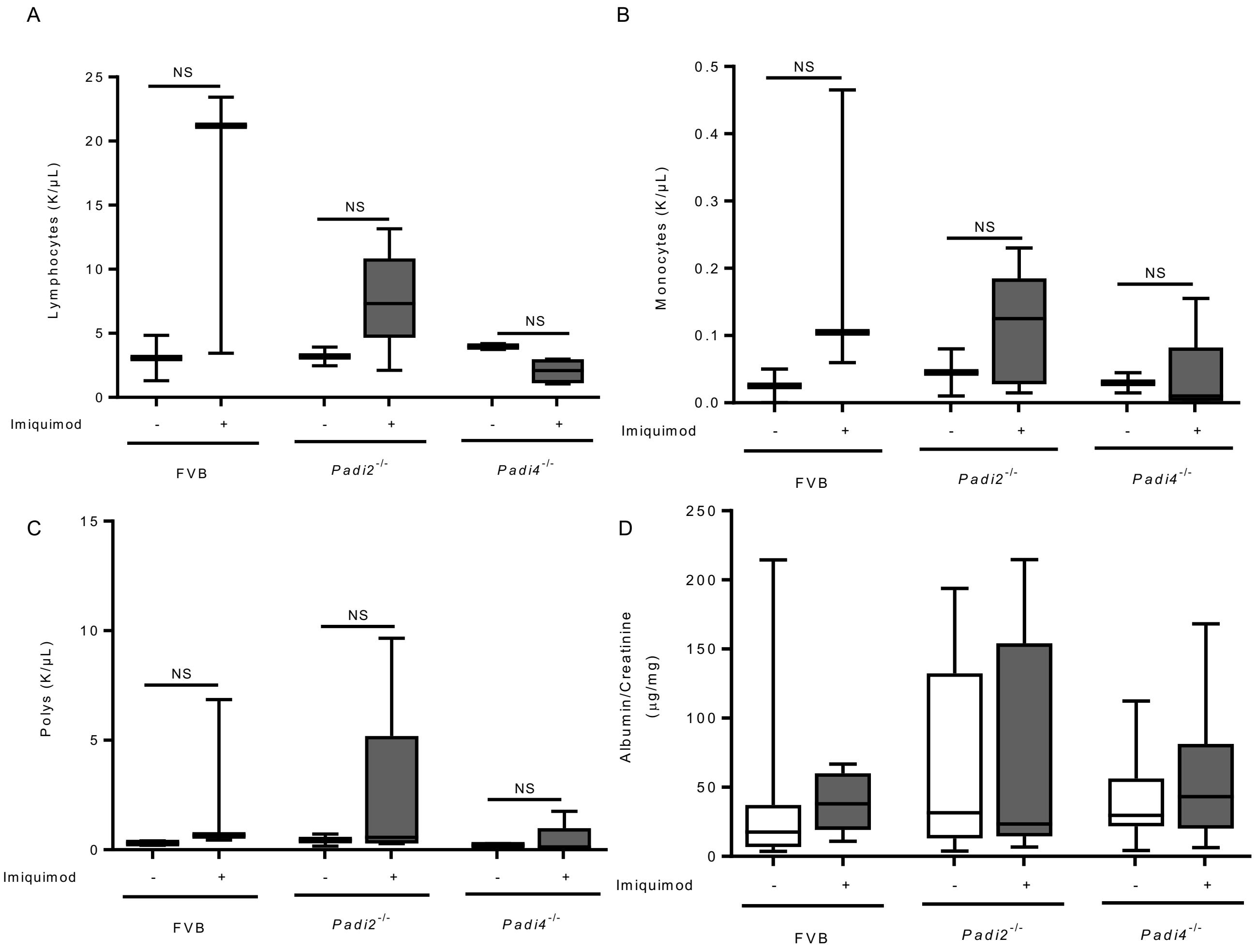
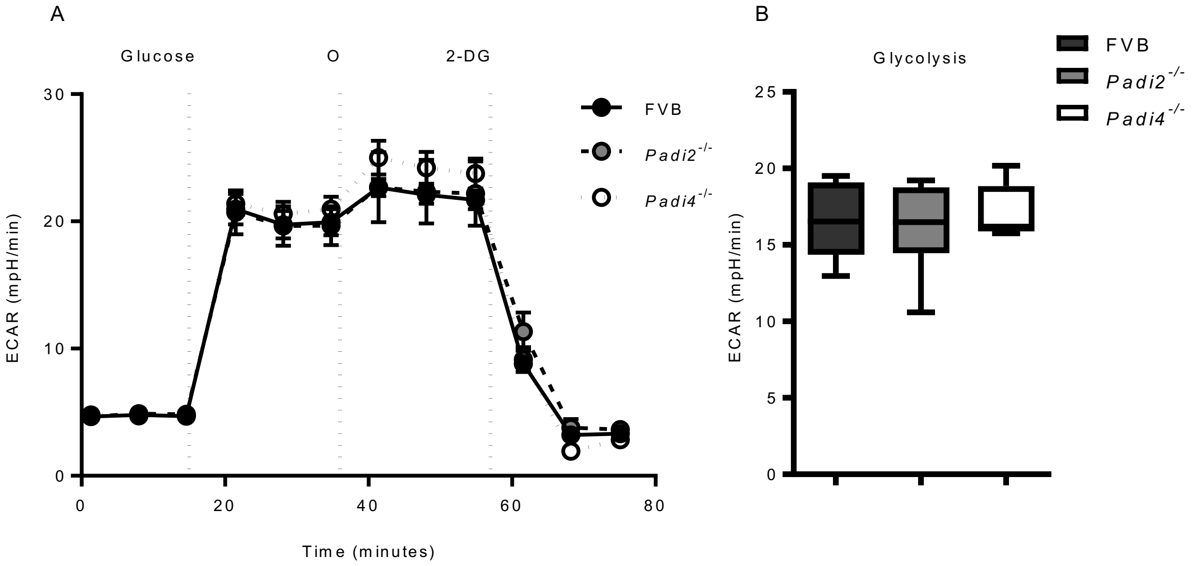
Supplemental Data



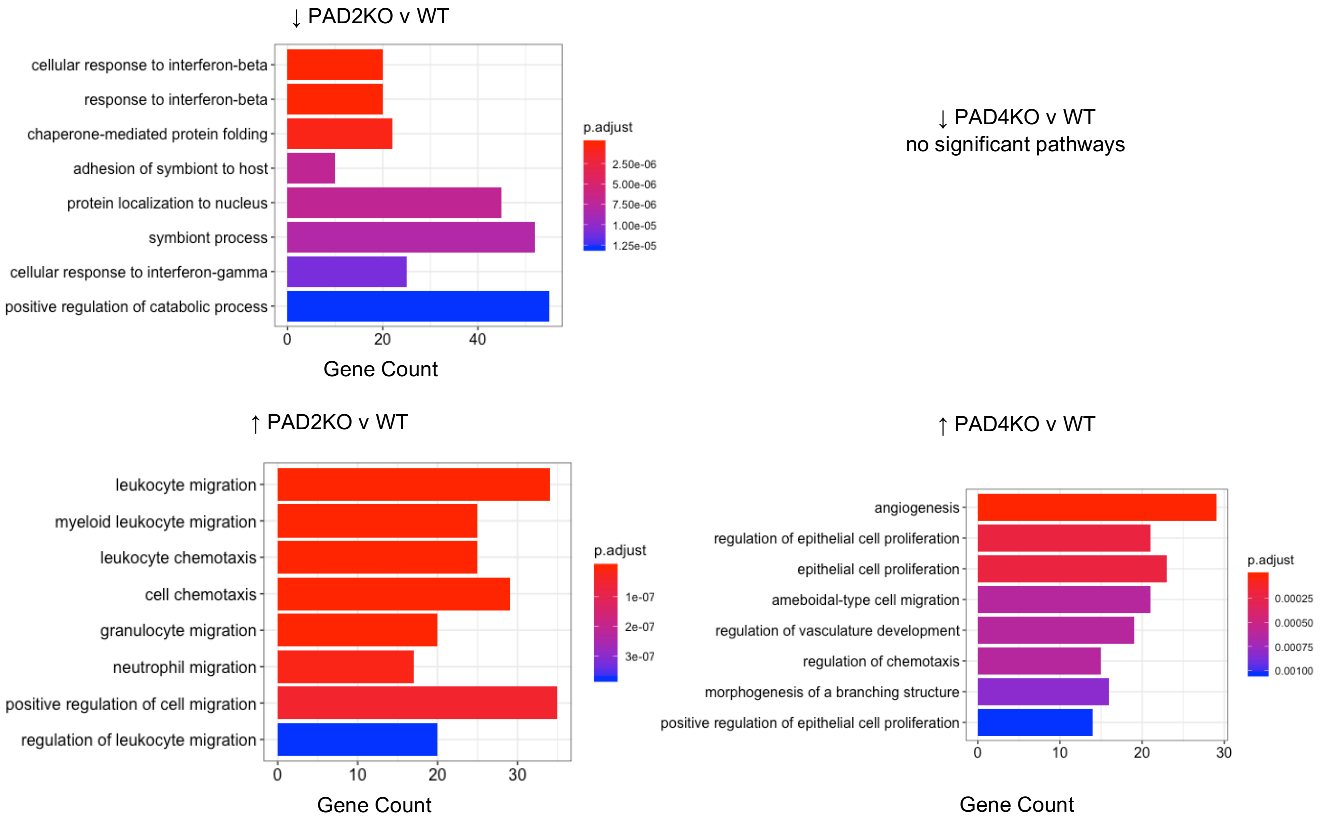
Supplemental Figure 1. Anti-RNP/Sm **(A)** and anti-histone **(B)** Ab quantification at euthanasia in serum of FVB, Padi2$^{-/-}$ and Pad4$^{-/-}$ mice in the presence and absence of imiquimod in vivo exposure. Box-and-whisker plots show median, lower and upper quartiles, and minimum and maximum optical density (OD) values at 450 of 5-10 mice/group**;** * $p<0.05$; *** $p<0.001$. Statistical analysis was performed by 2-tailed Mann-Whitney test.



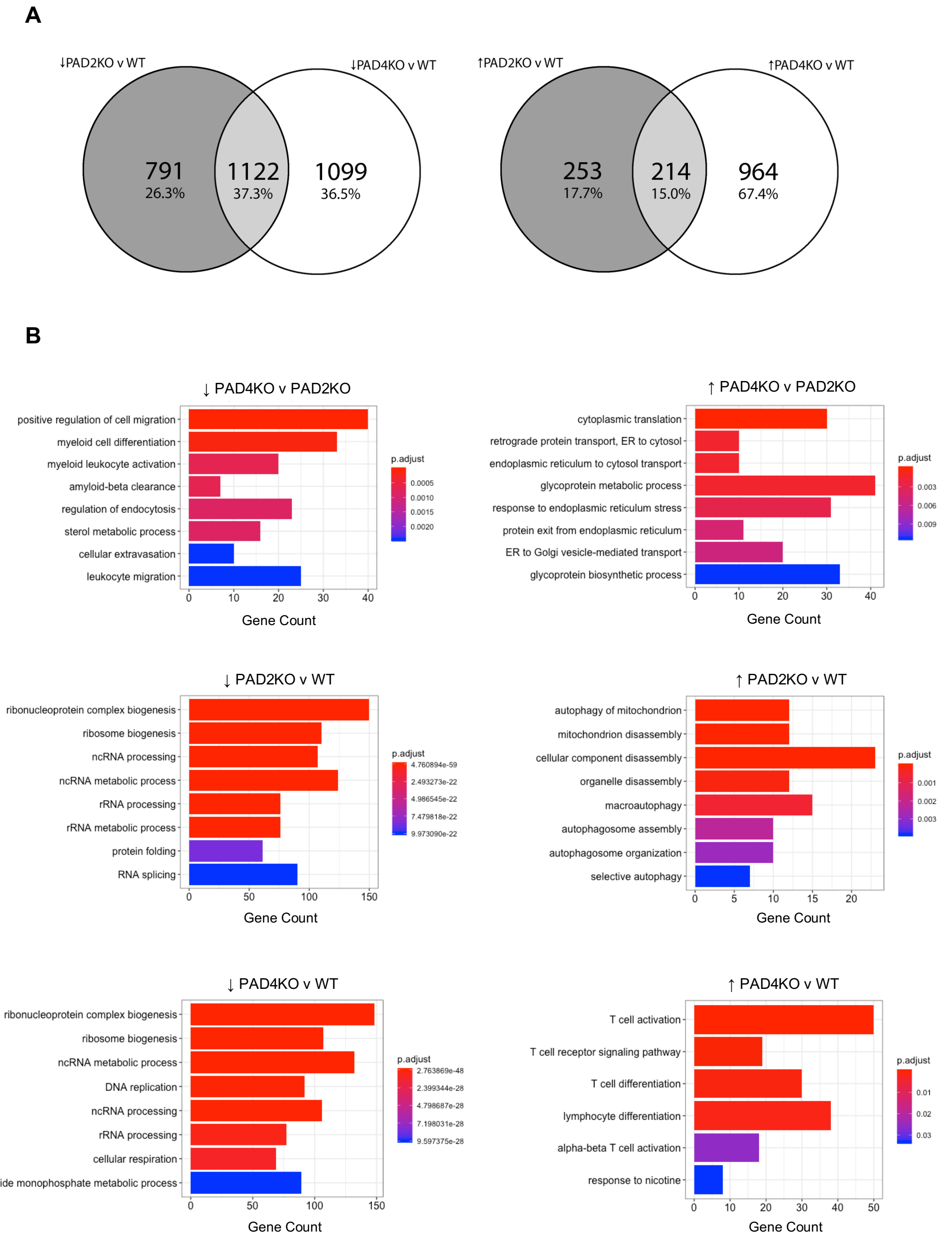
Supplemental Figure 2. Blood and urine analysis of Imiquimod-treated mice. A-C. Whole blood was isolated from naïve and Imiquimod-treated FVB, Padi2$^{-/-}$, and Padi4$^{-/-}$ mice and the frequency of lymphocytes **(A)**, monocytes **(B)**, and neutrophils **(C)** was measured in 3-5 mice/group. NS = not significant. **D.** Analysis of albumin: creatinine ratio at euthanasia following in vivo Imiquimod treatment of FVB, Padi2$^{-/-}$, and Padi4$^{-/-}$ mice; n = 8 mice/group. All differences were not statistically significant. Box-and-whisker plots show median, lower and upper quartiles, and minimum and maximum values. Statistical analysis was performed by 2-tailed Mann-Whitney test.



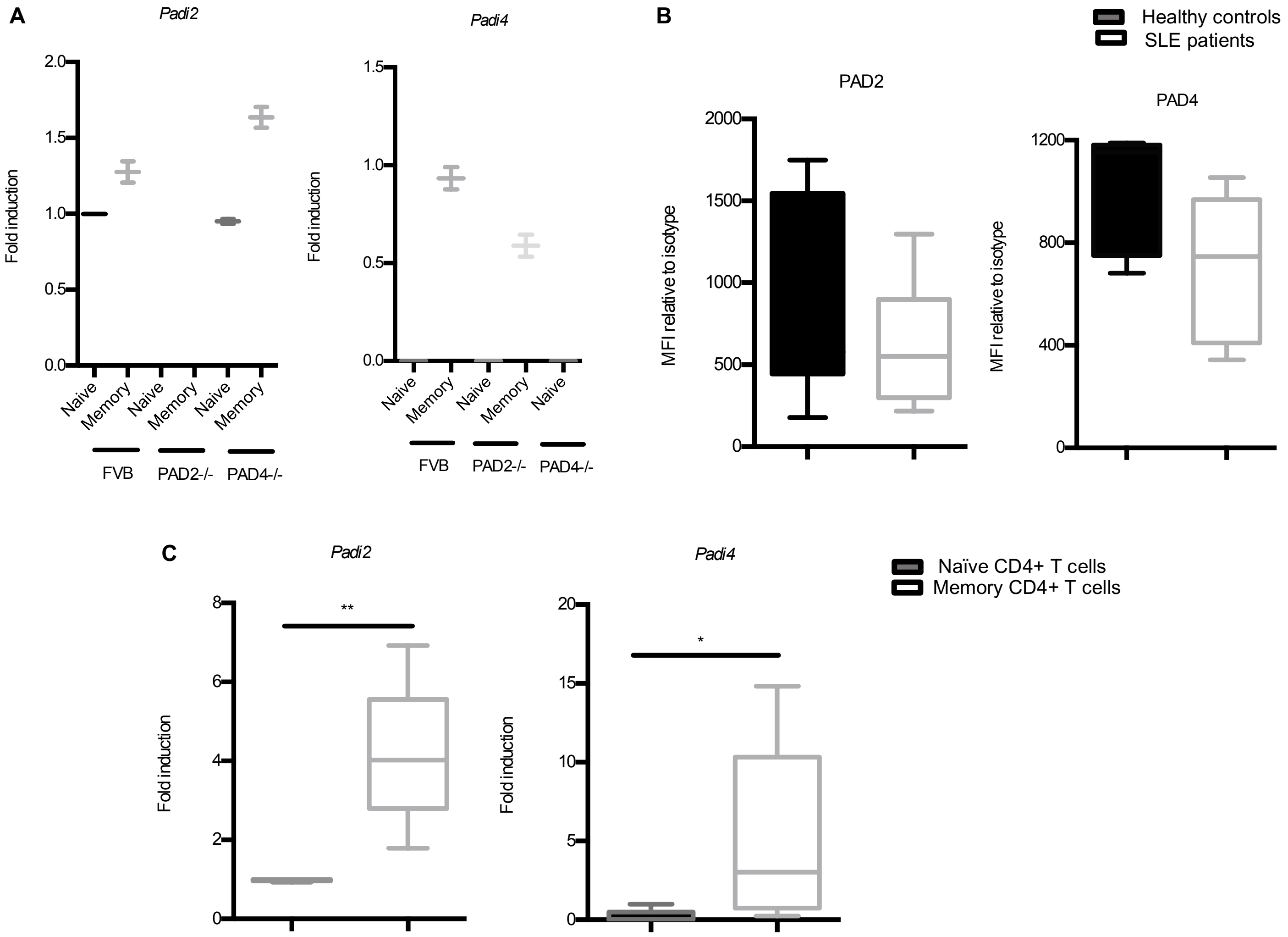
Supplemental Figure 3. Glycolytic function of FVB, *Padi2$^{-/-}$*, and *Padi4$^{-/-}$* neutrophils. Bone marrow neutrophils of untreated FVB, *Padi2$^{-/-}$*, and *Padi4$^{-/-}$* mice were tested by the extracellular flux assay **(A)** to determine their glycolytic function **(B)** ,as measured by the Extracellular Acidification Rate (ECAR). Data are shown as mean +/- SEM in **A**. In B, data are shown as box-and-whisker plots that show median, lower and upper quartiles, and minimum and maximum values of ECAR. Assay is representative of three independent experiments. O: oligomycin; 2-DG: 2-Deoxy-D-glucose. Statistical analysis was performed by 2-tailed Mann-Whitney test.



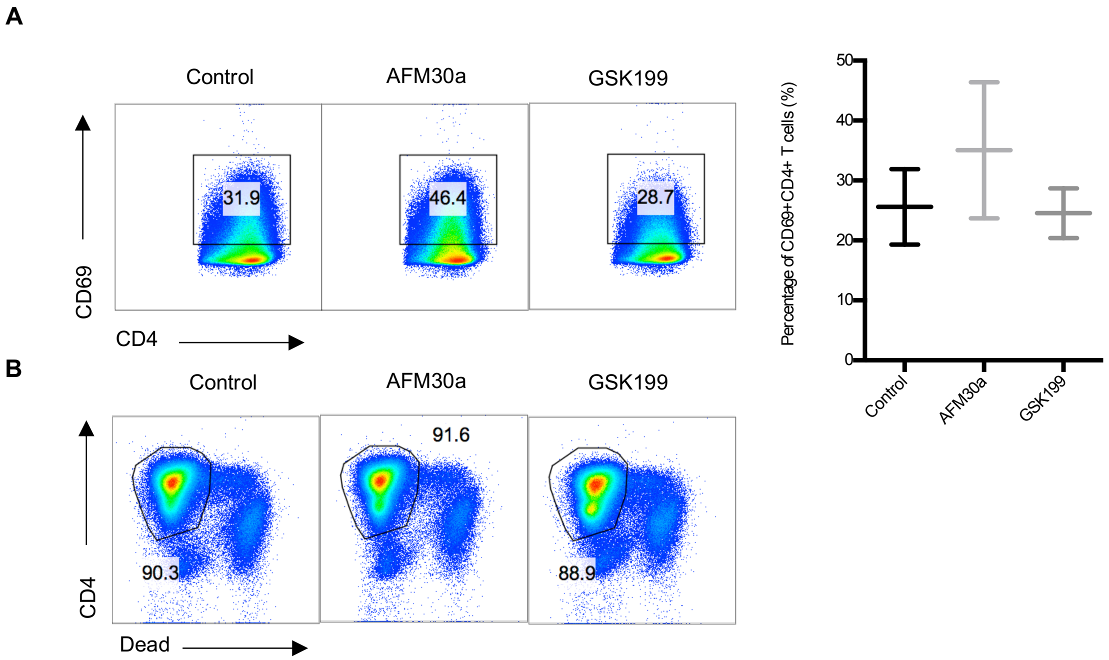
Supplemental Figure 4. Gene ontology biological pathway analysis of significant genes between Padi2$^{-/-}$ or Padi4$^{-/-}$ lymph nodes and wild-type (WT) lymph nodes; n=4 mice/group. Statistical analysis of functional profiles for genes and related pathways was performed using the clusterProfiler package in RStudio. P values are depicted in the boxes next to the graphics.



Supplemental Figure 5. (A) Venn Diagrams depicting the number of genes significantly upregulated and downregulated in Padi2$^{-/-}$ and Padi4$^{-/-}$ spleens (n=3/group) following in vivo imiquimod exposure, as compared to wild-type FVB spleens (WT, n=3) following imiquimod treatment. Differential expression was calculated using an ANOVA test on normalized gene counts. Genes with p-value < 0.05 were considered significant. **(B)** Gene ontology biological pathway analysis of significant genes between Padi2$^{-/-}$, Padi4$^{-/-}$, and WT spleens. P values are depicted in the boxes next to the graphics. Statistical analysis of functional profiles for genes and related pathways was performed using the clusterProfiler package in RStudio.



Supplemental Figure 6. Memory CD4+ T cells exhibit increased levels of PAD2 and PAD4 compared to naïve CD4+ T cells. (A) Naïve and memory T cells were purified from Imiquimod-treated WT, Padi2$^{-/-}$, and Padi4$^{-/-}$ FVB splenocytes by cell sorting. Gene expression levels of *padi2* and *padi4* were determined and box-and-whisker plots show median, lower and upper quartiles, and minimum and maximum values of mRNA fold induction when compared to naïve FVB T cells; n=2; **(B)** Box-and-whisker plots show median, lower and upper quartiles, and minimum and maximum values of fluorescence intensity of PAD2 and PAD4 relative to isotype controls in CD4+ T cells in 9 healthy controls and 6 SLE subjects (for PAD2) and 5 controls and 5 SLE subjects (for PAD4). There were no statistically significant differences between SLE and controls. **(C)** mRNA from naïve T cells (CD4+CD45RA+CD45RO-) and memory T cells (CD4+CD45RA-CD45RO+) was purified and gene expression levels of *PADI2* and *PADI4* were determined. Box-and-whisker plots show median, lower and upper quartiles, and minimum and maximum values of mRNA fold induction when compared to naïve CD4+ T cells in 5 healthy controls.* $p<0.05$; **<0.01. Statistical analysis was performed by 2-tailed Mann-Whitney test.



Supplemental Figure 7. Effect of PAD inhibitors on human CD4+ T cell activation and apoptosis. Healthy control CD4+ T cells were activated with anti-CD3 and anti-CD28 Abs for 5 days in the presence or absence of the PAD2 inhibitor AFM30a or the PAD4 inhibitor GSK199. CD4+ T cell activation (CD69 cell surface expression) and apoptosis were quantified by FACS. N=2/condition. Representative dot plots are displayed. Box-and-whisker plots show median, lower and upper quartiles, and minimum and maximum values of % of CD69-positive CD4 T cells.

Supplemental Table 1: Most Significantly Regulated Genes in Lymph Nodes (LN)

Cutoffs: $p < 0.05$, $|FC| > 1.5$, log2(rpkm) >1

Supplemental Table 1A. PAD4KO v PAD2KO in LN

Lymph Nodes – PAD4KO v PAD2KO mice					
Gene Symbol	Fold-Change	Gene Symbol	Fold-Change	Gene Symbol	Fold-Change
Cd209f	12.6241	Lrig1	1.64613	Clec4a2	-1.74249
Cd209b	8.18346	Procr	1.63619	Msrb1	-1.76693
Cbr2	5.967	Tagln	1.63463	Mtus1	-1.77084
Marco	5.67595	Tgfbr3	1.62276	Lilr4b	-1.77783
Cd209d	5.45845	Chordc1	1.62236	Lilra6	-1.77789
Cd207	4.91288	Laptm4b	1.61533	Rab3d	-1.77899
Postn	3.8611	Hsp90ab1	1.60706	Cxcr2	-1.78081
Hspa1b	3.44918	Gpd2	1.60695	5031425E22Rik	-1.78931
Siglec1	3.35415	Hpgd	1.59979	Gsr	-1.79427
Timd4	3.22364	Bcl2	1.59405	Crb3	-1.80463
Lyve1	2.94731	Rgs16	1.58818	Emilin2	-1.80727
Ccl12	2.79457	Meox2	1.58528	Mmp11	-1.81357
Cpe	2.79064	Gpr183	1.57631	Il1f9	-1.82583
Dab2	2.74371	Dglucy	1.57521	Sirpb1a	-1.82966
C6	2.59164	Rab7b	1.57456	Cfi	-1.83039
Gbp2b	2.51024	Gnb4	1.57052	6430548M08Rik	-1.83509
Retnla	2.42715	Cacybp	1.56977	Pilrb1	-1.8469
Sh3gl3	2.42604	Cd86	1.56771	Ckap4	-1.85469
Mcpt4	2.39147	Ttc3	1.55645	Bhlha15	-1.85983
Hsph1	2.28914	Slc45a3	1.55488	Alpl	-1.87884
Cma1	2.28832	Ccdc163	1.55418	Socs3	-1.88249
Cyp4b1	2.27767	Chst10	1.54997	Il18rap	-1.8964
Gm13546	2.20782	Rab3ip	1.54682	Cpxm1	-1.91129
Adam23	2.14632	Pdpn	1.54154	Alox5ap	-1.9121
Ccl7	2.11933	Smc4	1.54113	Gm5150	-1.92188
Eomes	2.11726	Frmd6	1.53579	Clmp	-1.94281
Ltc4s	2.09308	Stip1	1.53557	Bhlhe41	-2.00261
Cdkn2a	2.08654	Gypc	1.53408	Gpihbp1	-2.05301
Fxyd6	2.08253	Slc10a6	1.53374	Rbp7	-2.05481
Jam3	2.05636	Mtss1	1.53201	Pglyrp1	-2.07985
Tnc	2.05202	Clec4n	1.52474	Clec7a	-2.08626
Tnfsf11	2.04462	Stk32c	1.52469	Xbp1	-2.09421
Clec10a	1.99598	P4ha1	1.52301	Pilra	-2.14335

Tnfrsf9	1.99446	Hoxd8	1.52162	Slc16a3	-2.24022
Dnaja1	1.99324	Gprasp1	1.51964	Gda	-2.39085
Trat1	1.98755	Cnrip1	1.51481	Csf3r	-2.40629
Xcr1	1.95373	Banp	1.51122	Pygl	-2.5332
Hyi	1.94847	Il2ra	1.50662	C5ar1	-2.60668
P2ry6	1.94306	Gbp7	1.50621	Anxa1	-2.62845
Mir1982	1.91905	Ccnd1	1.5062	Asprv1	-2.76729
Dnase1l3	1.91904	Akap2	1.5025	Mcemp1	-2.90054
Tmem2	1.90684	1700097N02Rik	1.5022	Fcna	-3.08493
Cish	1.89102	Capn5	-1.5094	Ccl6	-3.18701
Cldn5	1.88602	Slc2a3	-1.51312	Saa3	-3.24187
Tspan7	1.85659	Fgr	-1.5205	Hdc	-3.27481
Ccl8	1.81904	Kif1b	-1.52108	Cd5l	-3.28124
Hspa4l	1.81438	Gadd45a	-1.53359	Pi16	-3.3819
Rtn1	1.81398	Snhg3	-1.5494	C7	-3.49854
Ndn	1.81182	Edem2	-1.55669	Fpr2	-3.79485
Csf1	1.80267	Ubiad1	-1.56462	Clec4d	-3.86134
Aif1	1.79844	Prdm1	-1.56765	Fpr1	-4.24931
Btnl2	1.796	Hid1	-1.57226	Slpi	-4.39499
Mcoln2	1.7796	Atp9a	-1.57251	Chil1	-5.28809
Dnajb1	1.7759	Arl11	-1.57615	Mmp9	-6.57291
Itm2a	1.76899	Cd14	-1.57905	Mpo	-6.62246
Clca3a1	1.7654	Mmp2	-1.58028	Prtn3	-6.80247
Naaa	1.76234	1600010M07Rik	-1.58136	Chil3	-6.97426
Dnajb4	1.76013	Cd300lf	-1.58548	Gm5483	-7.06553
Ift80	1.75529	Rasgrp4	-1.58612	Ifitm6	-7.12512
Arhgef10	1.75409	Isg20	-1.58707	Hp	-7.18132
Cyp1b1	1.74098	Ccpg1	-1.59026	S100a9	-7.21976
Tubb2b	1.74013	Trp53inp1	-1.59545	Stfa2l1	-7.22052
Ltbp2	1.73689	Adpgk	-1.59712	Elane	-7.55101
Plekhg5	1.73272	Siglece	-1.60049	Lcn2	-7.72252
Fmo1	1.73015	Dhrs3	-1.609	S100a8	-7.72793
Stab1	1.71821	Sort1	-1.61006	Ngp	-7.79541
Bok	1.70764	Pla2g7	-1.61686	Wfdc21	-8.25511
Crtam	1.697	Card9	-1.61807	Camp	-8.33219
Idi1	1.68628	Apobr	-1.62295	Mmp8	-8.43321
Pdlim4	1.67067	Hist2h2aa1	-1.62362	Retnlg	-8.86636
Fam174b	1.66974	Pfkfb4	-1.63082	Ltf	-8.97689
Mgl2	1.66019	Erlec1	-1.671		

Msr1	1.6565	S100a6	-1.67727		
Itgb3	1.65501	Hk3	-1.6795		
Hsp90aa1	1.65398	Trpt1	-1.68399		
Enpp2	1.65348	Gpr160	-1.69578		
Sulf2	1.64786	Adgrg5	-1.7138		
P2ry10	1.6464	Igsf6	-1.72774		

Supplemental Table 1B. PAD2KO v WT in LN

Lymph Nodes - PAD2KO v FVB (WT) mice					
Gene Symbol	Fold-Change	Gene Symbol	Fold-Change	Gene Symbol	Fold-Change
Retnlg	15.0385	Sgk1	1.55601	Gm12505	-1.6025
Wfdc21	11.8642	Pla2g7	1.5534	Foxn3	-1.606
S100a8	11.2142	Gm11423	1.55178	Tgtp1	-1.6087
S100a9	10.6032	Ifitm1	1.55021	Myo1e	-1.6103
Camp	10.3066	Flot1	1.54875	Ankrd37	-1.6137
Ifitm6	10.0003	H1f0	1.54693	Serpina3g	-1.6196
Ngp	9.60969	Gstp3	1.53422	Gbp9	-1.6326
Mpo	9.35721	Cd7	1.53377	Rassf4	-1.6357
Prtn3	9.28623	Gadd45g	1.53284	P2ry10	-1.6395
Mmp9	8.25985	Emilin2	1.53159	Ccdc50	-1.6416
Lcn2	8.03324	Trpt1	1.52969	Cxcl9	-1.6423
Gm5483	7.98411	2310010J17Rik	1.51928	Chordc1	-1.6435
Chil3	7.93292	Tox2	1.51664	Bank1	-1.6521
Ltf	7.8313	Upp1	1.51309	Fbn1	-1.6594
Elane	7.6717	Sema3f	1.51079	Irf8	-1.6621
Stfa2l1	6.08169	Ccl9	1.50921	Fcrl5	-1.6642
Hp	5.57892	Palm	1.50797	Gnb4	-1.6677
Chil1	4.48952	Pfkfb4	1.5077	H2-Q6	-1.6806
Mcemp1	3.86739	Tmem150a	1.50368	Hsp90ab1	-1.6849
Saa3	3.84476	Slc15a4	-1.5004	Fcrla	-1.6905
Asprv1	2.93879	Chst10	-1.5018	Hspa4l	-1.699
Ccl6	2.81648	Hsp90aa1	-1.5022	4930431F12Rik	-1.6996
Anxa1	2.78645	Cdkn1a	-1.5032	Cttnbp2nl	-1.7085
Fpr2	2.69031	Aida	-1.5035	Cd72	-1.7086
Pi16	2.67559	Irf1	-1.5046	Abhd2	-1.7089
Csf3r	2.67231	Mbd4	-1.5048	Igtp	-1.7114
Clec7a	2.63699	Sod3	-1.5081	Slc9a7	-1.7127
Fpr1	2.59993	St13	-1.5103	Gbp11	-1.7148
Pglyrp1	2.46307	Lama4	-1.5137	Ccl8	-1.7185
Fcna	2.35765	Txndc16	-1.5145	Irgm1	-1.7197
C5ar1	2.28738	Mob1a	-1.5153	Dnaja1	-1.7199
Slc16a3	2.20308	Gm6377	-1.518	Tagln	-1.7256
Gda	2.19524	Ly75	-1.5193	Zfp318	-1.7266
Il18rap	2.18637	Cryab	-1.5193	Gbp4	-1.7269
Socs3	2.16756	6530403H02Rik	-1.5227	Pik3ap1	-1.7469
Oosp1	2.16075	Narf	-1.523	Ms4a1	-1.7494

F13a1	2.06247	Uba6	-1.5235	Gbp8	-1.7555
Cebpd	2.0293	Slamf8	-1.5265	Myh11	-1.7608
Gsr	1.93927	Arap2	-1.5265	Tpm2	-1.7633
Dhrs3	1.90571	Clec4a1	-1.5271	Itgae	-1.7716
6430548M08Rik	1.89451	Oas1a	-1.528	Serpina3f	-1.7755
Mtus1	1.89037	Vhl	-1.5354	Adgre1	-1.7959
Dusp1	1.88292	Gbp2	-1.5357	B3gnt5	-1.8217
Pygl	1.88017	Stip1	-1.5369	Gpd2	-1.825
Cxcr2	1.87756	Ifi47	-1.5388	Pde3b	-1.8268
Msrb1	1.86401	Tnfrsf9	-1.5405	Irgm2	-1.8452
Bst1	1.85713	Rtp4	-1.5408	Ifit3	-1.8482
Alox5ap	1.84745	Phf11b	-1.5427	Sh3bp4	-1.8547
Rasgrp4	1.82776	Irf7	-1.5431	Dnase1l3	-1.875
Rab3d	1.82261	Sesn3	-1.5433	Gm4951	-1.8784
Lgals3	1.80033	Itpr1	-1.5436	Stat1	-1.9072
Cebpb	1.79106	Slc15a2	-1.5439	Gm12250	-1.9174
Lrg1	1.7882	Clec4a3	-1.5448	Xcr1	-1.9268
Itih3	1.77654	Cd37	-1.5469	Gvin1	-1.9431
Lyz1	1.73676	Ifi30	-1.5481	Gm4070	-1.9444
Arap3	1.73651	Banp	-1.5493	Gm17644	-1.9557
Ddit4	1.72716	Zfp46	-1.5506	Col6a3	-1.9746
Ace	1.72481	Btnl2	-1.5545	Ccl3	-1.9908
Hist2h2aa1	1.70933	Btla	-1.558	Ms4a4c	-1.9911
Il1f9	1.68538	Gucy1a1	-1.5609	4930470H14Rik	-2.0092
Adgrg5	1.67542	A430078G23Rik	-1.5629	Pfkfb3	-2.0101
Tha1	1.67322	Hspb1	-1.5631	Acta2	-2.029
S100a6	1.65467	Gpc6	-1.5654	Gbp2b	-2.1596
B430306N03Rik	1.65181	A530032D15Rik	-1.5659	Ccl5	-2.1623
Pilra	1.64991	Klhl28	-1.5678	Cdkn2b	-2.2161
Grrp1	1.64812	Serpina3i	-1.5683	Dusp4	-2.2271
Adpgk	1.63314	Hvcn1	-1.5703	Tgtp2	-2.2518
Gpr160	1.62756	Gbp7	-1.5708	Gbp6	-2.2682
Matk	1.62427	Gbp5	-1.571	Iigp1	-2.2971
Card9	1.62251	Cdkn2a	-1.5763	Mreg	-2.3052
Fosl2	1.61451	Tnfrsf1b	-1.5816	Fcmr	-2.3133
Hist1h1c	1.60389	H2-DMa	-1.584	Arhgap22	-2.3544
Arl11	1.59886	P4ha1	-1.5864	Hsph1	-2.3707
Lyz2	1.5979	Vim	-1.5884	Col14a1	-2.5766
Ier3	1.59706	Nid2	-1.589	Gbp10	-2.759

Klrc1	1.59638	Pdcd4	-1.5896	Postn	-2.7603
Atp9a	1.59412	Tnfrsf13c	-1.5908	Cd209f	-3.0028
Gpr83	1.59396	Fcrl1	-1.5912	Hspa1b	-3.0501
Kif1b	1.58851	Gm1966	-1.5942	Ptn	-3.4278
Vegfa	1.57498	Itgb3	-1.5949		
Igsf6	1.56626	Havcr2	-1.5969		

Supplemental Table 1C. PAD4KO v WT in LN

Lymph Nodes - PAD2KO v FVB (WT) mice					
Gene Symbol	Fold-Change	Gene Symbol	Fold-Change	Gene Symbol	Fold-Change
Cd209f	4.20406	Oit1	1.74866	Mgmt	1.5068
Cd209b	3.54736	Cebpd	1.74119	Grrp1	1.50673
Cbr2	3.29483	Galnt18	1.73936	Adamts2	-1.545
Folr2	3.1578	Clec10a	1.73856	Ipp	-1.5458
Marco	3.13578	Gpr182	1.71542	Clec4a1	-1.555
Lyve1	2.95566	Gmpr	1.71024	Pltp	-1.5759
Timd4	2.60579	Tsc22d3	1.70112	Themis2	-1.6339
C6	2.40547	Tnc	1.69303	Zbtb8a	-1.6685
Cox4i2	2.38791	AU021092	1.643	Col6a3	-1.6806
Tpsb2	2.31528	Ch25h	1.63919	Snhg3	-1.6885
Mcpt4	2.31152	Tspan7	1.6367	Thbs2	-1.7122
Stab2	2.18135	Tnfsf11	1.61357	Cxcr3	-1.741
Cpe	2.17196	Ltbp2	1.60126	Fcrl5	-1.7526
Sh3gl3	2.15794	Tmem2	1.5958	Bhlhe41	-1.8102
Ednrb	2.11958	Chst4	1.59408	Zfp46	-1.8165
Siglec1	2.09128	Lrg1	1.59324	Fabp4	-2.0202
Ccl12	2.0598	Pkdcc	1.59214	Cd5l	-2.1869
Dab2	1.97491	Plcd1	1.5882	C7	-2.2218
Hyi	1.94556	Ubd	1.58411	Wisp2	-2.3593
Cyp4b1	1.89848	Nr4a1	1.57822	Hba-a1	-3.536
Hoxd9	1.89498	Phldb2	1.57106	Hba-a2	-3.5701
Clca3a1	1.89407	Bok	1.56539	Hbb-bs	-3.7028
Mcoln2	1.88011	Shank3	1.55371	Hbb-b1	-3.7418
Ptprk	1.80128	Ramp2	1.54134	Hbb-b2	-3.7622
Jam3	1.79317	Cd59a	1.53112	Hbb-bt	-3.7622
Hyal2	1.77976	Egfl7	1.51146	Gm48909	-6.2098

Supplemental Table 2: Most Significantly Regulated Genes in Spleens

Cutoffs: $p < 0.05$, $|FC| > 1.5$, $\log2(rpkm) > 1$

Supplemental Table 2A. PAD4KO v PAD2KO Spleens

Spleens – PAD4KO v PAD2KO mice					
Gene Symbol	Fold-Change	Gene Symbol	Fold-Change	Gene Symbol	Fold-Change
Mzb1	2.38891	Ppp3cc	1.64561	Lrp1	-1.52113
Fkbp11	2.30048	Hsp90b1	1.64327	Cd99l2	-1.53031
Endou	2.28788	Edem1	1.64126	Nfix	-1.53286
Dapl1	2.2854	Pdia4	1.64064	Plscr1	-1.5509
Alpl	2.2785	Ms4a1	1.63651	Usp46	-1.56119
Erdr1	2.27287	Ifi214	1.63399	Wipi1	-1.56556
Mir6240	2.23511	Itm2a	1.62829	Gabarapl1	-1.56843
Gm15674	2.20374	Btla	1.609	Tuba4a	-1.56949
Cd8b1	2.17881	Mapk11	1.60402	Slc2a3	-1.57303
Bhlha15	2.17712	Gm12505	1.60383	Slc16a3	-1.57705
Derl3	2.15813	Xbp1	1.6	Tpcn1	-1.58198
Jchain	2.15654	Cd79a	1.59581	Ssx2ip	-1.60165
Stac2	2.1025	Ly6d	1.58865	Rab38	-1.60783
Sdc1	2.0373	E330020D12Rik	1.58818	Ampd3	-1.61747
Fcer2a	2.03421	Ccr7	1.58682	Rnd1	-1.62041
Lars2	2.00629	Faah	1.58585	Itgam	-1.62108
Id3	1.97457	Trp53inp1	1.58574	Ctnnd1	-1.63104
Mir6236	1.9634	Gm19585	1.58563	Atpif1	-1.63916
Ubxn11	1.93138	Sh2b2	1.58418	Lpcat2	-1.64365
Hid1	1.92481	Dennd5b	1.58049	Hmgb3	-1.64641
Ffar1	1.90815	Spib	1.57699	Gas7	-1.6509
Tmsb15b1	1.90253	Fcrla	1.57566	Nt5dc2	-1.65793
Neil1	1.88359	Clcf1	1.57394	Acsl1	-1.65868
Eaf2	1.86611	Ero1lb	1.5713	Rab3d	-1.66934
Dusp4	1.85735	St14	1.57021	Slc40a1	-1.67391
Creld2	1.85155	Blnk	1.56775	Tnfrsf21	-1.68039
Epcam	1.84976	Egr3	1.55708	Dhrs13	-1.69182
Slamf7	1.83859	Ephx1	1.55702	Il18bp	-1.69669
Cd8a	1.83079	Fcrl1	1.55576	Itga5	-1.70119
Creb3l2	1.81917	Gm8369	1.55378	Mvb12b	-1.70175
Prr5	1.8153	Hyi	1.55304	Cpd	-1.70344
Myl4	1.81338	Irf4	1.54699	Eef2k	-1.70957
Cd55	1.81263	Fam169b	1.54458	Ubiad1	-1.71076

Fcmr	1.80823	Iqcb1	1.54324	Kit	-1.72682
Pou2af1	1.80779	Klhdc1	1.54165	Hacd1	-1.72821
Cd79b	1.80689	Rab30	1.54108	Csf2rb	-1.73558
Rn45s	1.80152	Atat1	1.53816	Arap3	-1.74292
Lax1	1.79359	N4bp3	1.53715	Rnasel	-1.75028
Pon3	1.79234	Zfp318	1.53116	Osgin1	-1.76787
C1qb	1.77956	Mtss1	1.53003	Prkar2b	-1.77361
Il12a	1.77901	Rabep2	1.52833	Emilin2	-1.77915
Txndc11	1.77042	Hook1	1.52741	Parvb	-1.79596
Bhlhe41	1.76749	Ada	1.52704	Arhgap23	-1.8226
Tubb2b	1.76379	Bcl9l	1.52701	Ptafr	-1.83587
Enpp1	1.76075	B3gnt5	1.52475	Muc13	-1.84759
Txndc5	1.75871	Gpr183	1.52353	Aunip	-1.8573
Sfn	1.74498	Fut8	1.5197	Mxd1	-1.8627
Cd19	1.73815	Smagp	1.51952	Svip	-1.86738
Pafah1b3	1.73722	Gabre	1.51665	Tnfaip2	-1.87361
Sbk1	1.73332	Man1a	1.51506	Atp9a	-1.88226
Bcar3	1.72756	Neurl2	1.51105	Tceal8	-1.88336
Tram2	1.72155	Haao	1.511	Srxn1	-1.92036
St8sia6	1.70979	Scimp	1.50933	Adam8	-1.92334
Chst3	1.70809	Tnfrsf13b	1.50879	Fads2	-1.98603
Blk	1.70493	Fchsd2	1.50791	Csf2rb2	-1.99246
Amigo2	1.69575	Klk8	1.50551	Cxcr2	-2.03333
Zfp296	1.69059	Tmsb15l	1.5044	Snhg3	-2.09558
St6gal1	1.68608	Arrdc4	-1.50116	Man1c1	-2.15256
Bend5	1.67534	St3gal4	-1.50131	Tbxas1	-2.18446
Prdx4	1.67355	Fam234b	-1.50512	Gda	-2.19228
Zcchc18	1.66115	Ccne2	-1.50546	Dhrs3	-2.21341
Hmces	1.65782	Golim4	-1.50659	St3gal5	-2.23084
Fam214a	1.65698	Igf1r	-1.51303	Saa3	-4.32218
Rras2	1.64921	1700037H04Rik	-1.51625	Rn4.5s	-4.68754

Supplemental Table 2B. PAD2KO v WT Spleens

Spleens - PAD2KO v FVB (WT) mice					
Gene Symbol	Fold-Change	Gene Symbol	Fold-Change	Gene Symbol	Fold-Change
Cd8a	2.08688	Gm11346	1.5534	Creld2	-1.54149
Gpcpd1	2.00124	Klhl25	1.55185	Sdhaf3	-1.54264
Cd8b1	1.98811	Adrb2	1.53178	Pecr	-1.57096
Gda	1.95211	Tcp11l2	1.52852	Ddit4	-1.57609
Cmas	1.88452	Fkbp5	1.52744	Srm	-1.60281
Tbcel	1.83279	Ap4b1	1.52085	Tram2	-1.61144
Dhrs3	1.82382	Afmid	1.51683	Sdc1	-1.62913
Ier3	1.80307	Ypel3	1.50311	Cenpv	-1.67058
Fam214b	1.77377	Hsph1	-1.50325	Derl3	-1.67306
Atp9a	1.73349	Per1	-1.50823	Alpl	-1.76373
Ctsw	1.62056	Sik1	-1.51017	Fkbp11	-1.76666
Clcn6	1.61171	Creb3l2	-1.51071	Prdx4	-1.77304
Arl4c	1.58826	Pla2g12a	-1.52592	Bhlha15	-1.78039
Trat1	1.57258	Ccdc117	-1.52829	Fabp5	-1.80078
Bnip3l	1.56383	Tubb2b	-1.53149	Erdr1	-1.95031

Supplemental Table 2C. PAD4KO v WT Spleens

Spleens - PAD4KO v FVB (WT) mice					
Gene Symbol	Fold-Change	Gene Symbol	Fold-Change	Gene Symbol	Fold-Change
Cd8b1	4.33173	Add3	1.50499	Nme4	-1.66776
Cd8a	3.82064	Trp53inp1	1.50152	Sdc3	-1.66936
Dapl1	3.20223	A430078G23Rik	1.50017	Il18bp	-1.67231
Mir1982	2.41005	Gins2	-1.50104	Lhpp	-1.68505
Id3	2.33883	Fanci	-1.50159	Csf2rb2	-1.69241
Trat1	2.05317	Rcc1	-1.50292	Cdc6	-1.69275
Ctsw	2.01997	Skp2	-1.50299	Mlkl	-1.6956
Fcer2a	2.01814	Slc40a1	-1.50319	Akap1	-1.69609
Txk	1.97244	Tamm41	-1.50425	Thop1	-1.69706
Fabp4	1.95199	Wdr12	-1.50544	Chaf1b	-1.6974
Klrd1	1.93298	Eef1e1	-1.50549	Tmem107	-1.70431
Gm15674	1.92782	Gm9199	-1.50564	Prkar2b	-1.70529
Ubxn11	1.92646	Fads1	-1.50577	Smyd2	-1.70912
Arl4c	1.90281	Ddias	-1.50677	Dusp1	-1.71542
Gm11346	1.88406	Pola2	-1.50718	Mtfp1	-1.73011
Ccr7	1.88157	Nolc1	-1.50764	Sqle	-1.73121
S1pr1	1.86638	Lyrm4	-1.50772	Ccne2	-1.73443
Als2cl	1.86283	Mcm10	-1.50834	Tnfaip2	-1.73503
Klk8	1.86039	Ptov1	-1.50926	Nfix	-1.73515
Nsg2	1.8513	Ctnnd1	-1.50968	Recql4	-1.74816
Mir142b	1.81985	Magohb	-1.51079	Gss	-1.76136
Epcam	1.79315	Fdps	-1.51434	Itga5	-1.76491
Sit1	1.78995	Rrm1	-1.51444	Pla2g12a	-1.76699
Sfn	1.78537	Cdk6	-1.51516	Scd2	-1.77266
Sidt1	1.76572	Cmss1	-1.5156	Dnph1	-1.77719
Fkbp5	1.74909	Lyar	-1.51691	Usp46	-1.78019
Cd55	1.73247	Hdgf	-1.51858	Hspd1	-1.78378
Eaf2	1.72577	Coq7	-1.51946	Tspan4	-1.79472
Gpcpd1	1.7181	Cdc25a	-1.5197	Selenbp1	-1.79514
Chst3	1.69167	Lefty1	-1.5231	Pawr	-1.80963
Scml4	1.69063	Hnrnpll	-1.52401	Dhcr24	-1.8201
Clec2i	1.67936	Exosc2	-1.52406	Pop1	-1.8279
Egr3	1.67298	Hk1	-1.5246	Eng	-1.83231
Arhgef18	1.67282	Agpat5	-1.52956	Ccne1	-1.83361
Bcl2	1.67133	Hsph1	-1.52975	Parvb	-1.84165
Cirbp	1.67016	Srm	-1.53026	Minpp1	-1.84626
Faah	1.66577	Exo1	-1.53322	Ssx2ip	-1.85337

Fcmr	1.66428	Cacybp	-1.53394	Egfl7	-1.87593
Dusp4	1.65249	Slc25a13	-1.53494	Clca3a1	-1.90732
Cd79b	1.64077	Amd1	-1.5364	Svip	-1.92892
Cd7	1.63435	Ybx3	-1.53671	Cited4	-1.93592
Rab30	1.63255	Zmynd19	-1.53833	Rab38	-1.9749
Satb1	1.63207	Idi1	-1.53981	Rgs12	-1.98544
Itm2a	1.62852	Comt	-1.54096	Lmna	-1.98848
Lef1	1.62203	Fbxo10	-1.54207	Sept8	-1.99375
Afmid	1.61896	Nasp	-1.54376	Ryk	-2.0085
Bend5	1.61754	Bysl	-1.54403	C1qtnf12	-2.01736
Pim2	1.61035	Nefh	-1.54521	Sox12	-2.02124
Cers4	1.6098	Ctsl	-1.54587	Mthfd1	-2.03581
Il12a	1.60948	Tmem41a	-1.54734	Nt5dc2	-2.03891
Fam214a	1.59548	Ppp2r1b	-1.55029	Tceal8	-2.04938
Il7r	1.5951	Ammecr1	-1.55104	Mt1	-2.05877
Gm20337	1.58708	Chchd6	-1.5522	Pfkm	-2.06042
Cbx7	1.56268	A730008H23Rik	-1.55529	Bag2	-2.06117
Ppic	1.56237	Retsat	-1.55896	Ccnb1ip1	-2.0716
Mzb1	1.56139	Orc2	-1.55945	Rangrf	-2.08839
Osbpl5	1.55832	Trip6	-1.55955	Cd59a	-2.08888
Ppcs	1.55732	C1qbp	-1.56085	Hmgb3	-2.0977
Pgam2	1.55462	Slc19a1	-1.56318	Oaf	-2.09775
Lax1	1.55443	Tmem97	-1.56544	Slc39a8	-2.12469
Lat	1.55146	Ldlr	-1.56755	Cpd	-2.13908
Izumo4	1.54635	Gabarapl1	-1.56791	Smo	-2.1651
Snn	1.54518	Dnajb1	-1.5697	Tfr2	-2.1658
Arl4d	1.54092	Eif2ak2	-1.57252	Sdsl	-2.18768
Gm12505	1.54037	Amd2	-1.57908	Mcrip2	-2.2505
Tnfrsf26	1.53851	B3gnt7	-1.58539	Aunip	-2.29225
Fam169b	1.53834	Eif2b3	-1.58971	Steap3	-2.30713
Krtcap3	1.53638	Hebp1	-1.5908	Gdf3	-2.30934
Hid1	1.53351	Orc1	-1.60668	Myh10	-2.31995
St8sia6	1.53247	Hsp90aa1	-1.61449	Sec14l2	-2.32216
Haao	1.53162	Stard10	-1.62077	Mns1	-2.345
N4bp3	1.52685	Ctps	-1.62085	Snhg3	-2.40586
Usp28	1.52341	Kdelc1	-1.62379	Man1c1	-2.4755
Hyi	1.52316	Cenpp	-1.62653	Hacd1	-2.5203
Klf2	1.5221	Timm8a1	-1.62695	Atp1b2	-2.57301
B3gnt5	1.52189	Ttll12	-1.62995	Bex4	-2.66347
Pdlim4	1.52099	Per1	-1.63475	Fads2	-2.79613
Sytl3	1.51451	Cdkn1a	-1.64662	Pklr	-2.79992

Bcl9l	1.51294	Atpif1	-1.64985	Mt2	-2.83873
Gm8369	1.51225	Syce2	-1.65053	Fabp5	-2.97759
Gabre	1.51213	Uck2	-1.65797	Podxl	-4.42543
Otud1	1.5059	Acss2	-1.66492	Rn4.5s	-5.44583

Supplemental Table 3: Pathway Analysis of Differentially Regulated Genes in Lymph Nodes (LN)

Supplemental Table 3A. PAD4KO vs PAD2KO LN Downregulated Pathways

ID	Description	p.adjust	Count
GO:0050900	leukocyte migration	3.44E-07	29
GO:0097529	myeloid leukocyte migration	1.17E-06	21
GO:0002446	neutrophil mediated immunity	2.79E-05	9
GO:0097530	granulocyte migration	2.90E-05	16
GO:0030595	leukocyte chemotaxis	5.42E-05	19
GO:0060326	cell chemotaxis	0.000161911	22
GO:0030574	collagen catabolic process	0.000346065	7
GO:0042119	neutrophil activation	0.000733099	7
GO:0060191	regulation of lipase activity	0.00119089	10
GO:0030100	regulation of endocytosis	0.00119089	19
GO:0032963	collagen metabolic process	0.001249041	11
GO:0050764	regulation of phagocytosis	0.001249041	11
GO:1990266	neutrophil migration	0.001249041	12
GO:0002444	myeloid leukocyte mediated immunity	0.001345366	11
GO:0036230	granulocyte activation	0.001345366	7
GO:0071621	granulocyte chemotaxis	0.001360234	12
GO:0051004	regulation of lipoprotein lipase activity	0.002928604	5
GO:0072677	eosinophil migration	0.003023985	6
GO:0051852	disruption by host of symbiont cells	0.003495817	5
GO:0051873	killing by host of symbiont cells	0.003495817	5
GO:0030335	positive regulation of cell migration	0.003495817	27
GO:0031640	killing of cells of other organism	0.003495817	7
GO:0044364	disruption of cells of other organism	0.003495817	7
GO:0050663	cytokine secretion	0.003495817	16
GO:0030593	neutrophil chemotaxis	0.003925276	10
GO:1901342	regulation of vasculature development	0.004544395	20
GO:0050765	negative regulation of phagocytosis	0.004977149	5
GO:0051006	positive regulation of lipoprotein lipase activity	0.006072111	4
GO:0001525	angiogenesis	0.006225661	26
GO:0051047	positive regulation of secretion	0.006225661	26
GO:0051818	disruption of cells of other organism involved in symbiotic interaction	0.007093499	5
GO:0051883	killing of cells in other organism involved in symbiotic interaction	0.007093499	5
GO:0042742	defense response to bacterium	0.007093499	24

GO:0051187	cofactor catabolic process	0.007093499	7
GO:0002685	regulation of leukocyte migration	0.007093499	14
GO:0061365	positive regulation of triglyceride lipase activity	0.007093499	4
GO:0070943	neutrophil mediated killing of symbiont cell	0.007093499	4
GO:0006909	phagocytosis	0.008850817	19
GO:0045806	negative regulation of endocytosis	0.009216829	7
GO:0045765	regulation of angiogenesis	0.009216829	18
GO:0043312	neutrophil degranulation	0.009216829	4
GO:1904018	positive regulation of vasculature development	0.009216829	14
GO:0045088	regulation of innate immune response	0.009572405	16
GO:0009100	glycoprotein metabolic process	0.009790119	19
GO:0001819	positive regulation of cytokine production	0.010103049	22
GO:0055078	sodium ion homeostasis	0.011500851	7
GO:0070942	neutrophil mediated cytotoxicity	0.011500851	4
GO:0045766	positive regulation of angiogenesis	0.011500851	13
GO:1901222	regulation of NIK/NF-kappaB signaling	0.011500851	9
GO:0007159	leukocyte cell-cell adhesion	0.011829823	18
GO:0002548	monocyte chemotaxis	0.012093649	7
GO:0044117	growth of symbiont in host	0.013822292	5
GO:0051851	modification by host of symbiont morphology or physiology	0.013822292	8
GO:0001503	ossification	0.013976672	20
GO:0051817	modification of morphology or physiology of other organism involved in symbiotic interaction	0.01433019	9
GO:0046394	carboxylic acid biosynthetic process	0.01433019	19
GO:0035821	modification of morphology or physiology of other organism	0.01433019	12
GO:0016053	organic acid biosynthetic process	0.01433019	19
GO:0043901	negative regulation of multi-organism process	0.01433019	13
GO:0045123	cellular extravasation	0.01433019	7
GO:0071674	mononuclear cell migration	0.01433019	8
GO:0046456	icosanoid biosynthetic process	0.01433019	6
GO:0038061	NIK/NF-kappaB signaling	0.014802901	9
GO:0002263	cell activation involved in immune response	0.015224914	16
GO:0072672	neutrophil extravasation	0.015224914	4
GO:0002687	positive regulation of leukocyte migration	0.015224914	11
GO:0043900	regulation of multi-organism process	0.015224914	21
GO:0044110	growth involved in symbiotic interaction	0.015249227	5
GO:0044116	growth of symbiont involved in interaction with host	0.015249227	5
GO:0050707	regulation of cytokine secretion	0.015249227	13
GO:0001906	cell killing	0.015249227	11

GO:0009101	glycoprotein biosynthetic process	0.015441364	16
GO:0015711	organic anion transport	0.015441364	21
GO:0051702	interaction with symbiont	0.015793845	8
GO:0097006	regulation of plasma lipoprotein particle levels	0.016222919	7
GO:0002283	neutrophil activation involved in immune response	0.017201449	4
GO:1905153	regulation of membrane invagination	0.017201449	4
GO:0006887	exocytosis	0.018535993	18
GO:0006022	aminoglycan metabolic process	0.020205432	9
GO:0006486	protein glycosylation	0.020751631	13
GO:0043413	macromolecule glycosylation	0.020751631	13
GO:0010832	negative regulation of myotube differentiation	0.020751631	4
GO:0055075	potassium ion homeostasis	0.021590032	5
GO:0006691	leukotriene metabolic process	0.025588329	4
GO:0042110	T cell activation	0.026425234	23
GO:0050878	regulation of body fluid levels	0.026689858	18
GO:0050830	defense response to Gram-positive bacterium	0.027293321	10
GO:0060142	regulation of syncytium formation by plasma membrane fusion	0.02745673	5
GO:1901570	fatty acid derivative biosynthetic process	0.02745673	6
GO:0002366	leukocyte activation involved in immune response	0.027716312	15
GO:1903305	regulation of regulated secretory pathway	0.027716312	10
GO:0031349	positive regulation of defense response	0.028050073	17
GO:0002526	acute inflammatory response	0.028766668	10
GO:0006575	cellular modified amino acid metabolic process	0.028766668	11
GO:0051148	negative regulation of muscle cell differentiation	0.028766668	6
GO:0007200	phospholipase C-activating G-protein coupled receptor signaling pathway	0.029028063	9
GO:0034381	plasma lipoprotein particle clearance	0.029120483	5
GO:0043299	leukocyte degranulation	0.029702977	7
GO:0070085	glycosylation	0.030015465	13
GO:0019233	sensory perception of pain	0.030015465	10
GO:0050777	negative regulation of immune response	0.030015465	11
GO:0044403	symbiont process	0.031502449	18
GO:0044130	negative regulation of growth of symbiont in host	0.031586344	4
GO:1901223	negative regulation of NIK/NF-kappaB signaling	0.031586344	4
GO:0052547	regulation of peptidase activity	0.031653915	20
GO:0007596	blood coagulation	0.031653915	11
GO:0006690	icosanoid metabolic process	0.031653915	9
GO:1903532	positive regulation of secretion by cell	0.032538214	21
GO:0048147	negative regulation of fibroblast proliferation	0.033883141	5

GO:0007599	hemostasis	0.033883141	11
GO:0032635	interleukin-6 production	0.03407355	10
GO:0044126	regulation of growth of symbiont in host	0.035281995	4
GO:0048245	eosinophil chemotaxis	0.035281995	4
GO:0002274	myeloid leukocyte activation	0.035576031	12
GO:0050817	coagulation	0.035838805	11
GO:0051154	negative regulation of striated muscle cell differentiation	0.036612579	5
GO:0042107	cytokine metabolic process	0.037148805	9
GO:0046631	alpha-beta T cell activation	0.037801087	10
GO:0030336	negative regulation of cell migration	0.037981062	14
GO:0045071	negative regulation of viral genome replication	0.037981062	6
GO:0060193	positive regulation of lipase activity	0.037981062	6
GO:0000272	polysaccharide catabolic process	0.038923435	4
GO:0044146	negative regulation of growth of symbiont involved in interaction with host	0.038923435	4
GO:0001655	urogenital system development	0.042323094	17
GO:0022407	regulation of cell-cell adhesion	0.04264864	18
GO:0009620	response to fungus	0.043267507	5
GO:0030204	chondroitin sulfate metabolic process	0.044140914	4
GO:0044144	modulation of growth of symbiont involved in interaction with host	0.044140914	4
GO:0071677	positive regulation of mononuclear cell migration	0.044140914	4
GO:0017157	regulation of exocytosis	0.044407789	12
GO:0001867	complement activation, lectin pathway	0.044407789	3
GO:1904152	regulation of retrograde protein transport, ER to cytosol	0.044407789	3
GO:0002443	leukocyte mediated immunity	0.044528968	21
GO:0045055	regulated exocytosis	0.045060982	12
GO:0022409	positive regulation of cell-cell adhesion	0.045060982	13
GO:0030193	regulation of blood coagulation	0.047855921	7
GO:1900046	regulation of hemostasis	0.047855921	7
GO:1903307	positive regulation of regulated secretory pathway	0.048426651	6
GO:0046942	carboxylic acid transport	0.049059384	15

Supplemental Table 3B. PAD4KO vs PAD2KO LN Upregulated Pathways

ID	Description	p.adjust	Count
GO:0042026	protein refolding	5.04E-05	11
GO:0061077	chaperone-mediated protein folding	5.04E-05	19
GO:0006457	protein folding	0.0001105	31
GO:0006458	'de novo' protein folding	0.00012141	15
GO:0051085	chaperone cofactor-dependent protein refolding	0.00034764	11
GO:0051084	'de novo' posttranslational protein folding	0.000435	12
GO:0040013	negative regulation of locomotion	0.01431144	37
GO:0008380	RNA splicing	0.01431144	42
GO:0051271	negative regulation of cellular component movement	0.01805105	35
GO:0009266	response to temperature stimulus	0.02205756	23
GO:1903900	regulation of viral life cycle	0.02205756	21
GO:0034605	cellular response to heat	0.02205756	13
GO:0048588	developmental cell growth	0.02205756	30
GO:0045116	protein neddylation	0.02205756	7
GO:0050922	negative regulation of chemotaxis	0.02205756	11
GO:1901379	regulation of potassium ion transmembrane transport	0.02327747	14
GO:0016049	cell growth	0.02327747	51
GO:0048738	cardiac muscle tissue development	0.0238478	30
GO:0010769	regulation of cell morphogenesis involved in differentiation	0.02946935	36
GO:0043401	steroid hormone mediated signaling pathway	0.0314402	22
GO:0019058	viral life cycle	0.032779	25
GO:0060039	pericardium development	0.03367826	8
GO:0007409	axonogenesis	0.03414326	47
GO:0014706	striated muscle tissue development	0.03414326	44
GO:0001654	eye development	0.03414326	41
GO:0003229	ventricular cardiac muscle tissue development	0.03597355	12
GO:0055010	ventricular cardiac muscle tissue morphogenesis	0.03735252	11
GO:0061564	axon development	0.03735252	49
GO:0009408	response to heat	0.03735252	16
GO:0035051	cardiocyte differentiation	0.03735252	22
GO:0043266	regulation of potassium ion transport	0.03735252	16
GO:0055008	cardiac muscle tissue morphogenesis	0.03735252	13
GO:0045666	positive regulation of neuron differentiation	0.03735252	44
GO:0060537	muscle tissue development	0.03735252	45
GO:0006997	nucleus organization	0.03735252	18
GO:2000146	negative regulation of cell motility	0.03735252	30

GO:1990138	neuron projection extension	0.03769913	23
GO:0009755	hormone-mediated signaling pathway	0.0381171	24
GO:0050792	regulation of viral process	0.0381171	23
GO:0016032	viral process	0.0381171	31
GO:0048644	muscle organ morphogenesis	0.0381171	15
GO:0044403	symbiont process	0.0381171	37
GO:0051052	regulation of DNA metabolic process	0.0381171	42
GO:0097485	neuron projection guidance	0.04427685	26
GO:0060415	muscle tissue morphogenesis	0.04427685	14

Supplemental Table 3C. PAD2KO vs WT LN Downregulated Pathways

ID	Description	p.adjust	Count
GO:0035458	cellular response to interferon-beta	1.33E-10	20
GO:0035456	response to interferon-beta	2.29E-08	20
GO:0061077	chaperone-mediated protein folding	6.68E-07	22
GO:0044406	adhesion of symbiont to host	7.21E-06	10
GO:0034504	protein localization to nucleus	7.21E-06	45
GO:0044403	symbiont process	8.25E-06	52
GO:0071346	cellular response to interferon-gamma	1.10E-05	25
GO:0009896	positive regulation of catabolic process	1.29E-05	55
GO:0042832	defense response to protozoan	1.84E-05	13
GO:0006458	'de novo' protein folding	2.36E-05	16
GO:0031331	positive regulation of cellular catabolic process	2.37E-05	48
GO:0034341	response to interferon-gamma	2.38E-05	27
GO:0001562	response to protozoan	6.64E-05	13
GO:0016032	viral process	0.00010758	41
GO:0000209	protein polyubiquitination	0.0001128	32
GO:0042026	protein refolding	0.0001128	10
GO:0051607	defense response to virus	0.0001128	35
GO:0019058	viral life cycle	0.00015509	32
GO:0009615	response to virus	0.00019178	39
GO:0045089	positive regulation of innate immune response	0.00031623	32
GO:0006457	protein folding	0.00037449	30
GO:0045088	regulation of innate immune response	0.00044011	36
GO:0044419	interspecies interaction between organisms	0.00052823	52
GO:0016482	cytosolic transport	0.00102665	24
GO:0032607	interferon-alpha production	0.00105055	10
GO:0051085	chaperone cofactor-dependent protein refolding	0.0014533	10
GO:0042176	regulation of protein catabolic process	0.00150747	45
GO:0002218	activation of innate immune response	0.00166761	24
GO:0050792	regulation of viral process	0.00166761	28
GO:0051084	'de novo' posttranslational protein folding	0.00166761	11
GO:0031349	positive regulation of defense response	0.00166976	41
GO:1900180	regulation of protein localization to nucleus	0.00166976	22
GO:0006606	protein import into nucleus	0.00166976	26
GO:1990173	protein localization to nucleoplasm	0.00173287	6
GO:0051170	import into nucleus	0.0024682	26
GO:0060760	positive regulation of response to cytokine stimulus	0.00259533	12

GO:1903900	regulation of viral life cycle	0.00349171	23
GO:0032647	regulation of interferon-alpha production	0.00383387	9
GO:0006403	RNA localization	0.00383387	28
GO:0046931	pore complex assembly	0.00383387	7
GO:0006913	nucleocytoplasmic transport	0.00416368	39
GO:1903901	negative regulation of viral life cycle	0.00417515	16
GO:0034605	cellular response to heat	0.00417515	14
GO:0051169	nuclear transport	0.00417515	39
GO:0048525	negative regulation of viral process	0.00450741	18
GO:1903311	regulation of mRNA metabolic process	0.0046115	30
GO:0045732	positive regulation of protein catabolic process	0.00506696	29
GO:0017038	protein import	0.00516804	30
GO:0043903	regulation of symbiosis, encompassing mutualism through parasitism	0.00516804	30
GO:0032386	regulation of intracellular transport	0.00647662	48
GO:0006914	autophagy	0.00657888	44
GO:0061919	process utilizing autophagic mechanism	0.00657888	44
GO:0034655	nucleobase-containing compound catabolic process	0.00691512	46
GO:0002221	pattern recognition receptor signaling pathway	0.00799972	20
GO:0002758	innate immune response-activating signal transduction	0.00992624	20
GO:0051865	protein autoubiquitination	0.0115926	13
GO:0072594	establishment of protein localization to organelle	0.0119969	48
GO:0009988	cell-cell recognition	0.01308314	13
GO:1900182	positive regulation of protein localization to nucleus	0.01308314	15
GO:0043900	regulation of multi-organism process	0.01441041	45
GO:0044270	cellular nitrogen compound catabolic process	0.01474911	48
GO:0010833	telomere maintenance via telomere lengthening	0.01596638	14
GO:0001961	positive regulation of cytokine-mediated signaling pathway	0.01621675	10
GO:0045785	positive regulation of cell adhesion	0.01621675	43
GO:0070203	regulation of establishment of protein localization to telomere	0.01621675	5
GO:0045862	positive regulation of proteolysis	0.01799746	37
GO:0000723	telomere maintenance	0.01911661	19
GO:0032200	telomere organization	0.0229647	19
GO:0022407	regulation of cell-cell adhesion	0.0229647	41
GO:0032727	positive regulation of interferon-alpha production	0.0229647	7
GO:0032206	positive regulation of telomere maintenance	0.0229647	11
GO:0070202	regulation of establishment of protein localization to chromosome	0.02514077	5
GO:0006278	RNA-dependent DNA biosynthetic process	0.02514077	12
GO:0007004	telomere maintenance via telomerase	0.02514077	12
GO:0050821	protein stabilization	0.02546185	22

GO:2000573	positive regulation of DNA biosynthetic process	0.02615839	13
GO:0051236	establishment of RNA localization	0.02715751	22
GO:0046700	heterocycle catabolic process	0.0292052	47
GO:0051028	mRNA transport	0.0292052	17
GO:2000641	regulation of early endosome to late endosome transport	0.02936235	6
GO:1903362	regulation of cellular protein catabolic process	0.03029599	28
GO:0009266	response to temperature stimulus	0.03033156	22
GO:0019439	aromatic compound catabolic process	0.03033156	48
GO:0035036	sperm-egg recognition	0.03348563	10
GO:1903037	regulation of leukocyte cell-cell adhesion	0.03348563	32
GO:0044772	mitotic cell cycle phase transition	0.03348563	39
GO:0046822	regulation of nucleocytoplasmic transport	0.03363522	18
GO:0034122	negative regulation of toll-like receptor signaling pathway	0.03393223	8
GO:0042147	retrograde transport, endosome to Golgi	0.03427103	13
GO:0009408	response to heat	0.03441159	16
GO:0043901	negative regulation of multi-organism process	0.03498	24
GO:0030889	negative regulation of B cell proliferation	0.03559719	6
GO:0033160	positive regulation of protein import into nucleus, translocation	0.03559719	6
GO:1901998	toxin transport	0.03559719	9
GO:0008380	RNA splicing	0.03606846	40
GO:1904589	regulation of protein import	0.03642187	13
GO:0002224	toll-like receptor signaling pathway	0.03816944	15
GO:0006308	DNA catabolic process	0.03836431	8
GO:0071897	DNA biosynthetic process	0.04020791	21
GO:0001819	positive regulation of cytokine production	0.04020791	43
GO:0043254	regulation of protein complex assembly	0.04135262	45
GO:0060759	regulation of response to cytokine stimulus	0.04228583	16
GO:1901990	regulation of mitotic cell cycle phase transition	0.04256847	30
GO:0034121	regulation of toll-like receptor signaling pathway	0.04256847	11
GO:0042326	negative regulation of phosphorylation	0.04256847	47
GO:0061136	regulation of proteasomal protein catabolic process	0.04256847	22
GO:0060402	calcium ion transport into cytosol	0.04256847	20
GO:0007339	binding of sperm to zona pellucida	0.04505181	9
GO:0007159	leukocyte cell-cell adhesion	0.04505181	34
GO:0002507	tolerance induction	0.04505181	7
GO:0045956	positive regulation of calcium ion-dependent exocytosis	0.04505181	7
GO:0030522	intracellular receptor signaling pathway	0.04529431	25
GO:1901361	organic cyclic compound catabolic process	0.0463688	49
GO:0071901	negative regulation of protein serine/threonine kinase activity	0.04677067	16

GO:1903039	positive regulation of leukocyte cell-cell adhesion	0.047405	24
GO:0043401	steroid hormone mediated signaling pathway	0.04826689	21
GO:0033627	cell adhesion mediated by integrin	0.04826689	10
GO:0000075	cell cycle checkpoint	0.04906392	23
GO:0050870	positive regulation of T cell activation	0.04906392	23
GO:0042306	regulation of protein import into nucleus	0.04994757	12
GO:1903829	positive regulation of cellular protein localization	0.04994757	37
GO:0010498	proteasomal protein catabolic process	0.04994757	45

Supplemental Table 3D. PAD2KO vs WT LN Upregulated Pathways

ID	Description	p.adjust	Count
GO:0050900	leukocyte migration	2.47E-12	34
GO:0097529	myeloid leukocyte migration	3.65E-11	25
GO:0030595	leukocyte chemotaxis	1.41E-10	25
GO:0060326	cell chemotaxis	2.22E-10	29
GO:0097530	granulocyte migration	8.36E-10	20
GO:1990266	neutrophil migration	2.01E-08	17
GO:0030335	positive regulation of cell migration	4.80E-08	35
GO:0002685	regulation of leukocyte migration	3.78E-07	20
GO:0001819	positive regulation of cytokine production	1.19E-06	29
GO:0071621	granulocyte chemotaxis	1.57E-06	15
GO:0072672	neutrophil extravasation	2.19E-06	7
GO:0002687	positive regulation of leukocyte migration	4.96E-06	16
GO:0050727	regulation of inflammatory response	2.54E-05	23
GO:0006022	aminoglycan metabolic process	2.74E-05	13
GO:0002446	neutrophil mediated immunity	3.85E-05	8
GO:0030593	neutrophil chemotaxis	3.85E-05	12
GO:0007159	leukocyte cell-cell adhesion	3.85E-05	22
GO:0045766	positive regulation of angiogenesis	8.54E-05	16
GO:0042107	cytokine metabolic process	0.00010403	13
GO:0050920	regulation of chemotaxis	0.00011816	17
GO:0031640	killing of cells of other organism	0.00013648	8
GO:0044364	disruption of cells of other organism	0.00013648	8
GO:0032103	positive regulation of response to external stimulus	0.00017715	20
GO:0022407	regulation of cell-cell adhesion	0.00017715	23
GO:1904018	positive regulation of vasculature development	0.00020787	16
GO:0045123	cellular extravasation	0.00020787	9
GO:0002688	regulation of leukocyte chemotaxis	0.00026735	12
GO:0001525	angiogenesis	0.00029002	27
GO:0032637	interleukin-8 production	0.00058898	9
GO:1903037	regulation of leukocyte cell-cell adhesion	0.00095291	18
GO:0022408	negative regulation of cell-cell adhesion	0.00095291	14
GO:0051051	negative regulation of transport	0.00095308	26
GO:0042742	defense response to bacterium	0.00105704	24
GO:1901222	regulation of NIK/NF-kappaB signaling	0.00105704	10
GO:0051852	disruption by host of symbiont cells	0.00113478	5
GO:0051873	killing by host of symbiont cells	0.00113478	5

GO:0002444	myeloid leukocyte mediated immunity	0.0011885	10
GO:0042119	neutrophil activation	0.00120046	6
GO:0042089	cytokine biosynthetic process	0.00136219	11
GO:0042110	T cell activation	0.00136219	25
GO:0001818	negative regulation of cytokine production	0.00149301	16
GO:0031349	positive regulation of defense response	0.00150554	19
GO:0038061	NIK/NF-kappaB signaling	0.00150645	10
GO:1903555	regulation of tumor necrosis factor superfamily cytokine production	0.00160283	12
GO:0019221	cytokine-mediated signaling pathway	0.00160283	21
GO:0032677	regulation of interleukin-8 production	0.0016286	8
GO:1903510	mucopolysaccharide metabolic process	0.0016286	8
GO:0045765	regulation of angiogenesis	0.00165277	18
GO:0001906	cell killing	0.00165277	12
GO:0050663	cytokine secretion	0.00165277	15
GO:0071706	tumor necrosis factor superfamily cytokine production	0.0017191	12
GO:0050863	regulation of T cell activation	0.00177626	18
GO:0034614	cellular response to reactive oxygen species	0.00177626	12
GO:1902622	regulation of neutrophil migration	0.00188028	7
GO:0070301	cellular response to hydrogen peroxide	0.00197753	9
GO:0036230	granulocyte activation	0.00225299	6
GO:0060142	regulation of syncytium formation by plasma membrane fusion	0.00225299	6
GO:0030203	glycosaminoglycan metabolic process	0.00226356	9
GO:0051818	disruption of cells of other organism involved in symbiotic interaction	0.00226356	5
GO:0051883	killing of cells in other organism involved in symbiotic interaction	0.00226356	5
GO:0030100	regulation of endocytosis	0.00227521	16
GO:1901570	fatty acid derivative biosynthetic process	0.00252469	7
GO:0035710	CD4-positive, alpha-beta T cell activation	0.00255608	9
GO:0070943	neutrophil mediated killing of symbiont cell	0.00263473	4
GO:0002693	positive regulation of cellular extravasation	0.00269792	5
GO:0045806	negative regulation of endocytosis	0.00272022	7
GO:0002690	positive regulation of leukocyte chemotaxis	0.00317822	9
GO:0002526	acute inflammatory response	0.00335291	11
GO:0032963	collagen metabolic process	0.00335291	9
GO:0007200	phospholipase C-activating G-protein coupled receptor signaling pathway	0.00335291	10
GO:0002430	complement receptor mediated signaling pathway	0.00342644	4
GO:1901298	regulation of hydrogen peroxide-mediated programmed cell death	0.00342644	4
GO:1901342	regulation of vasculature development	0.00342644	18
GO:0052547	regulation of peptidase activity	0.00358	21

GO:0050777	negative regulation of immune response	0.00358	12
GO:0042542	response to hydrogen peroxide	0.00358	10
GO:0051897	positive regulation of protein kinase B signaling	0.00358	9
GO:0001667	ameboidal-type cell migration	0.00358	20
GO:0007162	negative regulation of cell adhesion	0.00369517	16
GO:0002548	monocyte chemotaxis	0.00369517	7
GO:0032680	regulation of tumor necrosis factor production	0.00369517	11
GO:0042092	type 2 immune response	0.00369517	6
GO:0032635	interleukin-6 production	0.00406916	11
GO:0032640	tumor necrosis factor production	0.00406916	11
GO:0019370	leukotriene biosynthetic process	0.00406916	4
GO:0043117	positive regulation of vascular permeability	0.00406916	4
GO:0070942	neutrophil mediated cytotoxicity	0.00406916	4
GO:0002274	myeloid leukocyte activation	0.00430289	13
GO:0038083	peptidyl-tyrosine autophosphorylation	0.00430289	7
GO:0071674	mononuclear cell migration	0.00446275	8
GO:0002695	negative regulation of leukocyte activation	0.00451829	12
GO:0044117	growth of symbiont in host	0.00461202	5
GO:0072677	eosinophil migration	0.00461202	5
GO:0050729	positive regulation of inflammatory response	0.00482296	10
GO:1903038	negative regulation of leukocyte cell-cell adhesion	0.00482296	10
GO:0001503	ossification	0.00485743	19
GO:0046456	icosanoid biosynthetic process	0.00490529	6
GO:0010421	hydrogen peroxide-mediated programmed cell death	0.00492813	4
GO:0097468	programmed cell death in response to reactive oxygen species	0.00492813	4
GO:0000302	response to reactive oxygen species	0.00523545	13
GO:0010466	negative regulation of peptidase activity	0.00586227	15
GO:0044110	growth involved in symbiotic interaction	0.00612447	5
GO:0044116	growth of symbiont involved in interaction with host	0.00612447	5
GO:0045446	endothelial cell differentiation	0.00653493	9
GO:0000768	syncytium formation by plasma membrane fusion	0.00777411	7
GO:1901224	positive regulation of NIK/NF-kappaB signaling	0.00777411	7
GO:0002691	regulation of cellular extravasation	0.00837433	5
GO:0045926	negative regulation of growth	0.00837433	15
GO:0042088	T-helper 1 type immune response	0.00852147	6
GO:0050830	defense response to Gram-positive bacterium	0.00866955	10
GO:0048259	regulation of receptor-mediated endocytosis	0.00881276	8
GO:0006949	syncytium formation	0.00898384	7
GO:0002828	regulation of type 2 immune response	0.0092301	5

GO:0048841	regulation of axon extension involved in axon guidance	0.0092301	5
GO:0002367	cytokine production involved in immune response	0.0092301	8
GO:0002523	leukocyte migration involved in inflammatory response	0.0093955	4
GO:0045064	T-helper 2 cell differentiation	0.0093955	4
GO:0002292	T cell differentiation involved in immune response	0.0093955	7
GO:0050866	negative regulation of cell activation	0.00952837	12
GO:0051224	negative regulation of protein transport	0.00952837	12
GO:0051048	negative regulation of secretion	0.00984721	14
GO:0035821	modification of morphology or physiology of other organism	0.00994626	11
GO:0050868	negative regulation of T cell activation	0.01050958	9
GO:0050707	regulation of cytokine secretion	0.0106769	12
GO:0002443	leukocyte mediated immunity	0.0106769	21
GO:1904950	negative regulation of establishment of protein localization	0.01102824	12
GO:0006691	leukotriene metabolic process	0.01102824	4
GO:0003158	endothelium development	0.01145383	9
GO:0050829	defense response to Gram-negative bacterium	0.01145383	9
GO:0042130	negative regulation of T cell proliferation	0.01235031	7
GO:0046394	carboxylic acid biosynthetic process	0.01258357	17
GO:0016053	organic acid biosynthetic process	0.01291549	17
GO:0030278	regulation of ossification	0.01336754	13
GO:0034599	cellular response to oxidative stress	0.0134192	14
GO:0051817	modification of morphology or physiology of other organism involved in symbiotic interaction	0.01348655	8
GO:0046631	alpha-beta T cell activation	0.01349803	10
GO:2000514	regulation of CD4-positive, alpha-beta T cell activation	0.01356519	6
GO:0002369	T cell cytokine production	0.01371053	5
GO:0048846	axon extension involved in axon guidance	0.01371053	5
GO:1902284	neuron projection extension involved in neuron projection guidance	0.01371053	5
GO:0051250	negative regulation of lymphocyte activation	0.01371053	10
GO:0032102	negative regulation of response to external stimulus	0.01371053	16
GO:0006898	receptor-mediated endocytosis	0.01418494	12
GO:0051851	modification by host of symbiont morphology or physiology	0.01446981	7
GO:0044130	negative regulation of growth of symbiont in host	0.01472006	4
GO:1901223	negative regulation of NIK/NF-kappaB signaling	0.01472006	4
GO:0002366	leukocyte activation involved in immune response	0.01587061	14
GO:0060485	mesenchyme development	0.01587061	14
GO:0072593	reactive oxygen species metabolic process	0.01587061	14
GO:0031348	negative regulation of defense response	0.01683096	12
GO:0002683	negative regulation of immune system process	0.01683096	20

GO:0006869	lipid transport	0.01683096	16
GO:0044126	regulation of growth of symbiont in host	0.01697106	4
GO:0048245	eosinophil chemotaxis	0.01697106	4
GO:0002791	regulation of peptide secretion	0.01710639	21
GO:0071347	cellular response to interleukin-1	0.01710639	7
GO:0002263	cell activation involved in immune response	0.0175267	14
GO:1902624	positive regulation of neutrophil migration	0.01832277	5
GO:0048762	mesenchymal cell differentiation	0.01894408	12
GO:0051702	interaction with symbiont	0.01894408	7
GO:0032372	negative regulation of sterol transport	0.01894408	3
GO:0032375	negative regulation of cholesterol transport	0.01894408	3
GO:0052803	imidazole-containing compound metabolic process	0.01894408	3
GO:0097084	vascular smooth muscle cell development	0.01894408	3
GO:0044146	negative regulation of growth of symbiont involved in interaction with host	0.01894408	4
GO:0048843	negative regulation of axon extension involved in axon guidance	0.01894408	4
GO:0009620	response to fungus	0.01964084	5
GO:0051047	positive regulation of secretion	0.01996531	21
GO:0097237	cellular response to toxic substance	0.02153837	10
GO:0050710	negative regulation of cytokine secretion	0.02153837	6
GO:0009611	response to wounding	0.02153837	20
GO:0044144	modulation of growth of symbiont involved in interaction with host	0.02153837	4
GO:0071677	positive regulation of mononuclear cell migration	0.02153837	4
GO:1902668	negative regulation of axon guidance	0.02153837	4
GO:0030308	negative regulation of cell growth	0.02162202	11
GO:0007009	plasma membrane organization	0.02230251	7
GO:0001655	urogenital system development	0.02273769	16
GO:1903531	negative regulation of secretion by cell	0.02273811	12
GO:0019730	antimicrobial humoral response	0.02287234	8
GO:0045088	regulation of innate immune response	0.02287234	13
GO:0030517	negative regulation of axon extension	0.02287234	5
GO:0090279	regulation of calcium ion import	0.02287234	5
GO:0001867	complement activation, lectin pathway	0.02310816	3
GO:0046642	negative regulation of alpha-beta T cell proliferation	0.02310816	3
GO:0032675	regulation of interleukin-6 production	0.02344193	9
GO:0030574	collagen catabolic process	0.02367623	4
GO:1901739	regulation of myoblast fusion	0.02367623	4
GO:0032945	negative regulation of mononuclear cell proliferation	0.02397711	7
GO:0050672	negative regulation of lymphocyte proliferation	0.02397711	7

GO:0042060	wound healing	0.02397711	16
GO:1902667	regulation of axon guidance	0.02442301	5
GO:0007229	integrin-mediated signaling pathway	0.02540157	7
GO:0001909	leukocyte mediated cytotoxicity	0.02555642	8
GO:0019233	sensory perception of pain	0.02605092	9
GO:0050709	negative regulation of protein secretion	0.02605092	9
GO:0050832	defense response to fungus	0.02605092	4
GO:0072606	interleukin-8 secretion	0.02605092	4
GO:2000515	negative regulation of CD4-positive, alpha-beta T cell activation	0.02605092	4
GO:0006953	acute-phase response	0.02605092	5
GO:0031952	regulation of protein autophosphorylation	0.02605092	5
GO:1903039	positive regulation of leukocyte cell-cell adhesion	0.02668788	11
GO:0001781	neutrophil apoptotic process	0.02741618	3
GO:0045414	regulation of interleukin-8 biosynthetic process	0.02741618	3
GO:0070664	negative regulation of leukocyte proliferation	0.02741618	7
GO:0050708	regulation of protein secretion	0.02741618	19
GO:0050921	positive regulation of chemotaxis	0.02741618	9
GO:0050670	regulation of lymphocyte proliferation	0.02789017	12
GO:0032757	positive regulation of interleukin-8 production	0.02789017	5
GO:0044419	interspecies interaction between organisms	0.02829575	18
GO:0045861	negative regulation of proteolysis	0.02843037	16
GO:0009065	glutamine family amino acid catabolic process	0.02847905	4
GO:0030212	hyaluronan metabolic process	0.02847905	4
GO:0044403	symbiont process	0.02886465	16
GO:0042129	regulation of T cell proliferation	0.02886465	10
GO:0032944	regulation of mononuclear cell proliferation	0.02900481	12
GO:0070997	neuron death	0.02929565	17
GO:0071675	regulation of mononuclear cell migration	0.0296772	5
GO:0002286	T cell activation involved in immune response	0.0303064	8
GO:0022409	positive regulation of cell-cell adhesion	0.03069899	12
GO:0009063	cellular amino acid catabolic process	0.03109529	7
GO:0002237	response to molecule of bacterial origin	0.03109529	17
GO:0060143	positive regulation of syncytium formation by plasma membrane fusion	0.03138538	4
GO:0051271	negative regulation of cellular component movement	0.03138538	14
GO:0006979	response to oxidative stress	0.03138538	17
GO:0097164	ammonium ion metabolic process	0.03138538	10
GO:0032494	response to peptidoglycan	0.03138538	3
GO:0042228	interleukin-8 biosynthetic process	0.03138538	3

GO:0045628	regulation of T-helper 2 cell differentiation	0.03138538	3
GO:0030098	lymphocyte differentiation	0.03139834	17
GO:0050728	negative regulation of inflammatory response	0.03139834	9
GO:0051896	regulation of protein kinase B signaling	0.03139834	9
GO:1903036	positive regulation of response to wounding	0.03139834	6
GO:0070555	response to interleukin-1	0.03139834	7
GO:0042098	T cell proliferation	0.03311948	11
GO:0030217	T cell differentiation	0.03311948	13
GO:0045669	positive regulation of osteoblast differentiation	0.03311948	6
GO:0072001	renal system development	0.03311948	14
GO:0097193	intrinsic apoptotic signaling pathway	0.03311948	14
GO:0002792	negative regulation of peptide secretion	0.03311948	9
GO:0042036	negative regulation of cytokine biosynthetic process	0.03311948	4
GO:0045742	positive regulation of epidermal growth factor receptor signaling pathway	0.03311948	4
GO:0051354	negative regulation of oxidoreductase activity	0.03311948	4
GO:0010876	lipid localization	0.03368025	16
GO:0070663	regulation of leukocyte proliferation	0.03431015	12
GO:0045619	regulation of lymphocyte differentiation	0.03431015	10
GO:0050922	negative regulation of chemotaxis	0.03522775	5
GO:0002829	negative regulation of type 2 immune response	0.0357546	3
GO:0018119	peptidyl-cysteine S-nitrosylation	0.0357546	3
GO:0021534	cell proliferation in hindbrain	0.0357546	3
GO:0050755	chemokine metabolic process	0.0357546	3
GO:0070486	leukocyte aggregation	0.0357546	3
GO:0043114	regulation of vascular permeability	0.03632377	4
GO:2000116	regulation of cysteine-type endopeptidase activity	0.03814306	12
GO:0051346	negative regulation of hydrolase activity	0.0382161	17
GO:0044282	small molecule catabolic process	0.03886443	14
GO:0017015	regulation of transforming growth factor beta receptor signaling pathway	0.03903059	7
GO:0043900	regulation of multi-organism process	0.03966591	17
GO:0043062	extracellular structure organization	0.03966591	13
GO:0042554	superoxide anion generation	0.03996584	4
GO:1901186	positive regulation of ERBB signaling pathway	0.03996584	4
GO:0006023	aminoglycan biosynthetic process	0.03996584	5
GO:0015711	organic anion transport	0.04187227	17
GO:0017014	protein nitrosylation	0.04187227	3
GO:0032717	negative regulation of interleukin-8 production	0.04187227	3
GO:0060840	artery development	0.04229609	7

GO:1903844	regulation of cellular response to transforming growth factor beta stimulus	0.04229609	7
GO:0070371	ERK1 and ERK2 cascade	0.04313646	15
GO:0070528	protein kinase C signaling	0.04386173	4
GO:0040013	negative regulation of locomotion	0.04537621	14
GO:0032720	negative regulation of tumor necrosis factor production	0.04591325	5
GO:0048247	lymphocyte chemotaxis	0.04591325	5
GO:0046777	protein autophosphorylation	0.04816889	12
GO:0051402	neuron apoptotic process	0.04820821	13
GO:0046640	regulation of alpha-beta T cell proliferation	0.04827373	4
GO:0042035	regulation of cytokine biosynthetic process	0.04857571	7
GO:0048261	negative regulation of receptor-mediated endocytosis	0.04857571	3
GO:0055078	sodium ion homeostasis	0.04872789	5
GO:1903556	negative regulation of tumor necrosis factor superfamily cytokine production	0.04872789	5

Supplemental Table 3E. PAD4KO vs WT LN Downregulated Pathways

ID	**Description**	**p.adjust**	**Count**
N/A			

Supplemental Table 3F. PAD4KO vs WT LN Upregulated Pathways

ID	Description	p.adjust	Count
GO:0001525	angiogenesis	7.73E-06	29
GO:0050678	regulation of epithelial cell proliferation	0.00021978	21
GO:0050673	epithelial cell proliferation	0.00021978	23
GO:0001667	ameboidal-type cell migration	0.00062387	21
GO:1901342	regulation of vasculature development	0.00062387	19
GO:0050920	regulation of chemotaxis	0.00062387	15
GO:0001763	morphogenesis of a branching structure	0.00082788	16
GO:0050679	positive regulation of epithelial cell proliferation	0.00103503	14
GO:0001936	regulation of endothelial cell proliferation	0.00130414	11
GO:0045765	regulation of angiogenesis	0.00186799	17
GO:0001938	positive regulation of endothelial cell proliferation	0.00198538	9
GO:0090130	tissue migration	0.00202991	16
GO:0001935	endothelial cell proliferation	0.00246964	11
GO:0040013	negative regulation of locomotion	0.00246964	17
GO:0060326	cell chemotaxis	0.00246964	16
GO:0050900	leukocyte migration	0.00279894	17
GO:0061138	morphogenesis of a branching epithelium	0.00283271	14
GO:0030595	leukocyte chemotaxis	0.00311987	13
GO:0060560	developmental growth involved in morphogenesis	0.00321957	15
GO:0030335	positive regulation of cell migration	0.00335966	22
GO:0010631	epithelial cell migration	0.00400359	15
GO:0090132	epithelium migration	0.00417627	15
GO:0043542	endothelial cell migration	0.00642977	12
GO:0030336	negative regulation of cell migration	0.00642977	14
GO:0048568	embryonic organ development	0.00642977	21
GO:1904018	positive regulation of vasculature development	0.00889804	12
GO:1905330	regulation of morphogenesis of an epithelium	0.00889804	9
GO:0051271	negative regulation of cellular component movement	0.00889804	15
GO:2000146	negative regulation of cell motility	0.01001865	14
GO:2000027	regulation of organ morphogenesis	0.01154033	12
GO:0048705	skeletal system morphogenesis	0.01667737	13
GO:0010632	regulation of epithelial cell migration	0.01667737	12
GO:0060840	artery development	0.01667737	8
GO:0001505	regulation of neurotransmitter levels	0.01667737	15
GO:0006027	glycosaminoglycan catabolic process	0.01667737	4
GO:0060841	venous blood vessel development	0.01667737	4

GO:0048562	embryonic organ morphogenesis	0.01878163	15
GO:0060485	mesenchyme development	0.02609616	13
GO:0035904	aorta development	0.03460614	6
GO:0002687	positive regulation of leukocyte migration	0.03460614	9
GO:0001501	skeletal system development	0.03460614	19
GO:0002688	regulation of leukocyte chemotaxis	0.03460614	8
GO:0003231	cardiac ventricle development	0.04332921	9
GO:0045766	positive regulation of angiogenesis	0.04332921	10
GO:0010594	regulation of endothelial cell migration	0.04502115	9
GO:0032757	positive regulation of interleukin-8 production	0.04502115	5
GO:1905517	macrophage migration	0.04502115	5
GO:0008015	blood circulation	0.04502115	18
GO:0048845	venous blood vessel morphogenesis	0.04502115	3
GO:0097529	myeloid leukocyte migration	0.04730914	10
GO:0003013	circulatory system process	0.04730914	18

Supplemental Table 4: Pathway Analysis of Differentially Regulated Genes in Spleen

Supplemental Table 4A. PAD4KO vs PAD2KO Spleen Downregulated Pathways

ID	Description	p.adjust	Count
GO:0030335	positive regulation of cell migration	2.52E-05	40
GO:0030099	myeloid cell differentiation	8.09E-05	33
GO:0002274	myeloid leukocyte activation	0.00067592	20
GO:0097242	amyloid-beta clearance	0.00067592	7
GO:0030100	regulation of endocytosis	0.00083639	23
GO:0016125	sterol metabolic process	0.00085047	16
GO:0045123	cellular extravasation	0.00245999	10
GO:0050900	leukocyte migration	0.00245999	25
GO:0008203	cholesterol metabolic process	0.0041467	14
GO:1990778	protein localization to cell periphery	0.0041467	23
GO:0031589	cell-substrate adhesion	0.00426787	24
GO:0002573	myeloid leukocyte differentiation	0.00426787	19
GO:0072659	protein localization to plasma membrane	0.00441872	21
GO:1902652	secondary alcohol metabolic process	0.00448256	14
GO:0006898	receptor-mediated endocytosis	0.00448256	18
GO:0043112	receptor metabolic process	0.00448256	17
GO:0002693	positive regulation of cellular extravasation	0.00544324	6
GO:0072657	protein localization to membrane	0.00544324	31
GO:0043254	regulation of protein complex assembly	0.00557405	29
GO:0008202	steroid metabolic process	0.00564988	22
GO:0002685	regulation of leukocyte migration	0.00564988	17
GO:0031623	receptor internalization	0.00644953	12
GO:0006066	alcohol metabolic process	0.00707384	21
GO:0002687	positive regulation of leukocyte migration	0.00900244	14
GO:0007265	Ras protein signal transduction	0.00953769	28
GO:0000082	G1/S transition of mitotic cell cycle	0.01016012	16
GO:0034105	positive regulation of tissue remodeling	0.0108105	7
GO:0032528	microvillus organization	0.01269481	6
GO:1901615	organic hydroxy compound metabolic process	0.01275649	28
GO:1903362	regulation of cellular protein catabolic process	0.01298528	18
GO:0120031	plasma membrane bounded cell projection assembly	0.01367598	30
GO:0002275	myeloid cell activation involved in immune response	0.01385794	10
GO:0042176	regulation of protein catabolic process	0.01385794	24
GO:0006644	phospholipid metabolic process	0.01470396	23

GO:0000422	autophagy of mitochondrion	0.01471	10
GO:0061726	mitochondrion disassembly	0.01471	10
GO:1900221	regulation of amyloid-beta clearance	0.01471	4
GO:0007160	cell-matrix adhesion	0.01471	16
GO:0034330	cell junction organization	0.01471	18
GO:0044843	cell cycle G1/S phase transition	0.01471	16
GO:0007229	integrin-mediated signaling pathway	0.01471	10
GO:0045637	regulation of myeloid cell differentiation	0.01471	17
GO:0043299	leukocyte degranulation	0.01486024	9
GO:0002691	regulation of cellular extravasation	0.01548071	6
GO:0045807	positive regulation of endocytosis	0.01800612	14
GO:1901653	cellular response to peptide	0.01807126	19
GO:0031272	regulation of pseudopodium assembly	0.01807126	4
GO:0061337	cardiac conduction	0.01807126	8
GO:0010256	endomembrane system organization	0.01948362	23
GO:0030301	cholesterol transport	0.01970794	9
GO:2000406	positive regulation of T cell migration	0.01970794	6
GO:0002761	regulation of myeloid leukocyte differentiation	0.02018537	12
GO:0032869	cellular response to insulin stimulus	0.02018537	15
GO:0015918	sterol transport	0.02018537	9
GO:0048872	homeostasis of number of cells	0.02018537	21
GO:0048771	tissue remodeling	0.02075975	15
GO:0097006	regulation of plasma lipoprotein particle levels	0.02135783	8
GO:0001781	neutrophil apoptotic process	0.02135783	4
GO:1902622	regulation of neutrophil migration	0.02135783	7
GO:0007264	small GTPase mediated signal transduction	0.02135783	29
GO:0006338	chromatin remodeling	0.02253944	13
GO:0034394	protein localization to cell surface	0.02277089	8
GO:0034113	heterotypic cell-cell adhesion	0.02312543	7
GO:0006650	glycerophospholipid metabolic process	0.0238942	16
GO:0071375	cellular response to peptide hormone stimulus	0.0238942	17
GO:0097164	ammonium ion metabolic process	0.0246789	14
GO:0097530	granulocyte migration	0.0246789	12
GO:0031269	pseudopodium assembly	0.02607446	4
GO:0032868	response to insulin	0.02607446	16
GO:0002262	myeloid cell homeostasis	0.02642398	14
GO:0009311	oligosaccharide metabolic process	0.02649567	8
GO:0045454	cell redox homeostasis	0.02649567	8
GO:0035794	positive regulation of mitochondrial membrane permeability	0.02649567	6

GO:0046470	phosphatidylcholine metabolic process	0.02649567	6
GO:2000403	positive regulation of lymphocyte migration	0.02649567	6
GO:0034103	regulation of tissue remodeling	0.02649567	9
GO:0072593	reactive oxygen species metabolic process	0.02922949	18
GO:0009312	oligosaccharide biosynthetic process	0.02970402	6
GO:0006887	exocytosis	0.02970402	21
GO:0022411	cellular component disassembly	0.02970402	22
GO:0014831	gastro-intestinal system smooth muscle contraction	0.03003762	4
GO:0044772	mitotic cell cycle phase transition	0.03250656	22
GO:0086065	cell communication involved in cardiac conduction	0.03260814	6
GO:1905710	positive regulation of membrane permeability	0.03260814	6
GO:0016126	sterol biosynthetic process	0.03507178	7
GO:2000008	regulation of protein localization to cell surface	0.03507178	6
GO:2000404	regulation of T cell migration	0.03507178	6
GO:0031268	pseudopodium organization	0.03507178	4
GO:0045655	regulation of monocyte differentiation	0.03507178	4
GO:0071404	cellular response to low-density lipoprotein particle stimulus	0.03507178	4
GO:0072672	neutrophil extravasation	0.03507178	4
GO:0090136	epithelial cell-cell adhesion	0.03507178	4
GO:0097529	myeloid leukocyte migration	0.03507178	14
GO:1903008	organelle disassembly	0.03507178	10
GO:0045576	mast cell activation	0.03507178	8
GO:0090257	regulation of muscle system process	0.03613152	16
GO:0051258	protein polymerization	0.03940494	18
GO:2000377	regulation of reactive oxygen species metabolic process	0.03940494	14
GO:0044770	cell cycle phase transition	0.03946281	23
GO:0045453	bone resorption	0.04045652	8
GO:0030316	osteoclast differentiation	0.04061941	10
GO:0042119	neutrophil activation	0.04061941	5
GO:0097345	mitochondrial outer membrane permeabilization	0.04061941	5
GO:0097503	sialylation	0.04061941	4
GO:1903363	negative regulation of cellular protein catabolic process	0.04215174	8
GO:1990266	neutrophil migration	0.04215174	10
GO:0097035	regulation of membrane lipid distribution	0.04489489	6
GO:0016236	macroautophagy	0.04647401	14
GO:0002444	myeloid leukocyte mediated immunity	0.04788371	9
GO:0030033	microvillus assembly	0.04892125	4
GO:0001525	angiogenesis	0.04892125	27

Supplemental Table 4B. PAD4KO vs PAD2KO Spleen Upregulated Pathways

ID	Description	p.adjust	Count
GO:0002181	cytoplasmic translation	5.85E-11	30
GO:0030970	retrograde protein transport, ER to cytosol	0.00130777	10
GO:1903513	endoplasmic reticulum to cytosol transport	0.00130777	10
GO:0009100	glycoprotein metabolic process	0.00136661	41
GO:0034976	response to endoplasmic reticulum stress	0.00275731	31
GO:0032527	protein exit from endoplasmic reticulum	0.00466117	11
GO:0006888	ER to Golgi vesicle-mediated transport	0.00521749	20
GO:0009101	glycoprotein biosynthetic process	0.01135024	33
GO:0035966	response to topologically incorrect protein	0.01855026	20
GO:0006986	response to unfolded protein	0.01855026	18
GO:0042255	ribosome assembly	0.02117709	14
GO:0042254	ribosome biogenesis	0.02164022	34
GO:0030968	endoplasmic reticulum unfolded protein response	0.02875764	13
GO:0042274	ribosomal small subunit biogenesis	0.03581896	14
GO:0006486	protein glycosylation	0.03863127	25
GO:0043413	macromolecule glycosylation	0.03863127	25
GO:0070085	glycosylation	0.03863127	26
GO:0000028	ribosomal small subunit assembly	0.04011946	7
GO:0006465	signal peptide processing	0.04011946	6
GO:0006613	cotranslational protein targeting to membrane	0.04011946	6
GO:0035967	cellular response to topologically incorrect protein	0.04125542	16
GO:0036503	ERAD pathway	0.04125542	15
GO:1904152	regulation of retrograde protein transport, ER to cytosol	0.04348275	5
GO:0034620	cellular response to unfolded protein	0.04779348	14

Supplemental Table 4C. PAD2KO vs WT Spleen Downregulated Pathways

ID	Description	p.adjust	Count
GO:0022613	ribonucleoprotein complex biogenesis	4.76E-59	150
GO:0042254	ribosome biogenesis	3.94E-46	110
GO:0034470	ncRNA processing	1.11E-36	107
GO:0034660	ncRNA metabolic process	3.03E-35	124
GO:0006364	rRNA processing	6.53E-33	76
GO:0016072	rRNA metabolic process	3.83E-28	76
GO:0006457	protein folding	8.49E-22	61
GO:0008380	RNA splicing	9.97E-22	90
GO:0006397	mRNA processing	6.04E-21	99
GO:0022618	ribonucleoprotein complex assembly	6.92E-21	65
GO:0071826	ribonucleoprotein complex subunit organization	2.56E-20	66
GO:0009123	nucleoside monophosphate metabolic process	5.92E-19	70
GO:0072594	establishment of protein localization to organelle	5.92E-19	94
GO:0045333	cellular respiration	3.91E-18	52
GO:0009161	ribonucleoside monophosphate metabolic process	4.70E-18	67
GO:0009141	nucleoside triphosphate metabolic process	8.83E-18	70
GO:0042273	ribosomal large subunit biogenesis	1.30E-17	37
GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	2.85E-17	64
GO:0000398	mRNA splicing, via spliceosome	2.85E-17	64
GO:0009167	purine ribonucleoside monophosphate metabolic process	2.98E-17	65
GO:0000375	RNA splicing, via transesterification reactions	3.26E-17	64
GO:0009126	purine nucleoside monophosphate metabolic process	3.41E-17	65
GO:0009144	purine nucleoside triphosphate metabolic process	4.41E-17	66
GO:0006413	translational initiation	4.70E-17	41
GO:0006403	RNA localization	1.04E-16	55
GO:0009205	purine ribonucleoside triphosphate metabolic process	1.04E-16	64
GO:0009199	ribonucleoside triphosphate metabolic process	2.44E-16	64
GO:0006091	generation of precursor metabolites and energy	7.84E-16	76
GO:0140053	mitochondrial gene expression	1.74E-15	37
GO:0015980	energy derivation by oxidation of organic compounds	7.44E-15	61
GO:0032543	mitochondrial translation	1.04E-14	31
GO:0061077	chaperone-mediated protein folding	1.64E-14	31
GO:0046034	ATP metabolic process	3.83E-14	56
GO:0070585	protein localization to mitochondrion	3.88E-13	45
GO:0006839	mitochondrial transport	5.87E-13	60
GO:0072655	establishment of protein localization to mitochondrion	6.61E-13	44

GO:0009124	nucleoside monophosphate biosynthetic process	2.09E-12	42
GO:0006399	tRNA metabolic process	2.52E-12	45
GO:0009060	aerobic respiration	2.59E-12	29
GO:0010498	proteasomal protein catabolic process	2.67E-12	81
GO:0006626	protein targeting to mitochondrion	7.92E-12	40
GO:0000470	maturation of LSU-rRNA	9.15E-12	18
GO:0017038	protein import	1.06E-11	51
GO:0042775	mitochondrial ATP synthesis coupled electron transport	1.06E-11	25
GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process	1.10E-11	72
GO:1990542	mitochondrial transmembrane transport	1.78E-11	26
GO:1904874	positive regulation of telomerase RNA localization to Cajal body	2.12E-11	13
GO:0022904	respiratory electron transport chain	2.26E-11	29
GO:0006119	oxidative phosphorylation	2.77E-11	30
GO:0002181	cytoplasmic translation	3.59E-11	32
GO:0009156	ribonucleoside monophosphate biosynthetic process	4.11E-11	39
GO:0033108	mitochondrial respiratory chain complex assembly	4.84E-11	28
GO:0042274	ribosomal small subunit biogenesis	4.84E-11	28
GO:0034655	nucleobase-containing compound catabolic process	5.09E-11	73
GO:0042773	ATP synthesis coupled electron transport	5.32E-11	25
GO:0022900	electron transport chain	1.15E-10	29
GO:0006417	regulation of translation	2.56E-10	72
GO:0019693	ribose phosphate metabolic process	2.56E-10	78
GO:0009127	purine nucleoside monophosphate biosynthetic process	3.04E-10	37
GO:0009168	purine ribonucleoside monophosphate biosynthetic process	3.04E-10	37
GO:0009259	ribonucleotide metabolic process	4.42E-10	76
GO:0015931	nucleobase-containing compound transport	5.94E-10	44
GO:0006163	purine nucleotide metabolic process	6.04E-10	76
GO:0010608	posttranscriptional regulation of gene expression	7.39E-10	79
GO:0009150	purine ribonucleotide metabolic process	9.48E-10	74
GO:0000387	spliceosomal snRNP assembly	9.63E-10	17
GO:0030150	protein import into mitochondrial matrix	9.64E-10	13
GO:1904872	regulation of telomerase RNA localization to Cajal body	9.64E-10	13
GO:0006605	protein targeting	1.51E-09	60
GO:0006099	tricarboxylic acid cycle	1.70E-09	16
GO:0050657	nucleic acid transport	2.06E-09	38
GO:0050658	RNA transport	2.06E-09	38
GO:0090670	RNA localization to Cajal body	2.54E-09	13
GO:0090671	telomerase RNA localization to Cajal body	2.54E-09	13
GO:0090672	telomerase RNA localization	2.54E-09	13

GO:0090685	RNA localization to nucleus	2.54E-09	13
GO:0071806	protein transmembrane transport	2.60E-09	21
GO:0034248	regulation of cellular amide metabolic process	2.70E-09	74
GO:0072521	purine-containing compound metabolic process	2.94E-09	79
GO:0010257	NADH dehydrogenase complex assembly	3.15E-09	19
GO:0032981	mitochondrial respiratory chain complex I assembly	3.15E-09	19
GO:0009142	nucleoside triphosphate biosynthetic process	3.16E-09	36
GO:0051236	establishment of RNA localization	3.32E-09	38
GO:0009145	purine nucleoside triphosphate biosynthetic process	3.34E-09	34
GO:0044270	cellular nitrogen compound catabolic process	3.34E-09	73
GO:0006401	RNA catabolic process	4.89E-09	47
GO:0046700	heterocycle catabolic process	6.23E-09	73
GO:0006458	'de novo' protein folding	8.15E-09	20
GO:0042255	ribosome assembly	1.07E-08	24
GO:0009206	purine ribonucleoside triphosphate biosynthetic process	1.12E-08	33
GO:0065002	intracellular protein transmembrane transport	1.21E-08	20
GO:0006402	mRNA catabolic process	1.38E-08	42
GO:0090501	RNA phosphodiester bond hydrolysis	1.42E-08	24
GO:0006101	citrate metabolic process	1.63E-08	16
GO:0015985	energy coupled proton transport, down electrochemical gradient	1.72E-08	14
GO:0015986	ATP synthesis coupled proton transport	1.72E-08	14
GO:0006913	nucleocytoplasmic transport	1.88E-08	56
GO:0009201	ribonucleoside triphosphate biosynthetic process	1.99E-08	33
GO:0051169	nuclear transport	2.10E-08	56
GO:0019439	aromatic compound catabolic process	2.31E-08	73
GO:1990173	protein localization to nucleoplasm	3.29E-08	9
GO:0044743	protein transmembrane import into intracellular organelle	3.39E-08	17
GO:0030490	maturation of SSU-rRNA	3.55E-08	20
GO:1901361	organic cyclic compound catabolic process	5.82E-08	75
GO:0051186	cofactor metabolic process	5.88E-08	73
GO:0006520	cellular amino acid metabolic process	9.85E-08	50
GO:0006732	coenzyme metabolic process	1.35E-07	54
GO:0000460	maturation of 5.8S rRNA	1.59E-07	15
GO:0009451	RNA modification	1.69E-07	31
GO:0072350	tricarboxylic acid metabolic process	1.85E-07	16
GO:0034976	response to endoplasmic reticulum stress	2.02E-07	43
GO:0000469	cleavage involved in rRNA processing	2.16E-07	13
GO:0036503	ERAD pathway	3.35E-07	25
GO:0008033	tRNA processing	4.28E-07	28

GO:0034504	protein localization to nucleus	5.49E-07	49
GO:0071824	protein-DNA complex subunit organization	5.98E-07	41
GO:0000956	nuclear-transcribed mRNA catabolic process	6.14E-07	27
GO:0071166	ribonucleoprotein complex localization	6.75E-07	22
GO:0051123	RNA polymerase II transcriptional preinitiation complex assembly	6.79E-07	13
GO:1901293	nucleoside phosphate biosynthetic process	7.26E-07	53
GO:0070897	DNA-templated transcriptional preinitiation complex assembly	8.72E-07	14
GO:0045727	positive regulation of translation	1.12E-06	28
GO:0065004	protein-DNA complex assembly	1.45E-06	36
GO:0000338	protein deneddylation	1.51E-06	8
GO:0000463	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	1.53E-06	9
GO:0030433	ubiquitin-dependent ERAD pathway	1.53E-06	20
GO:0090305	nucleic acid phosphodiester bond hydrolysis	1.86E-06	29
GO:0009165	nucleotide biosynthetic process	2.13E-06	51
GO:0051028	mRNA transport	2.35E-06	26
GO:0071426	ribonucleoprotein complex export from nucleus	2.45E-06	21
GO:0006281	DNA repair	3.35E-06	65
GO:0019081	viral translation	3.79E-06	9
GO:0090151	establishment of protein localization to mitochondrial membrane	3.79E-06	9
GO:0010499	proteasomal ubiquitin-independent protein catabolic process	3.93E-06	12
GO:0006754	ATP biosynthetic process	3.99E-06	27
GO:0044282	small molecule catabolic process	5.56E-06	49
GO:0000413	protein peptidyl-prolyl isomerization	7.16E-06	13
GO:0006405	RNA export from nucleus	7.19E-06	23
GO:0006611	protein export from nucleus	7.52E-06	28
GO:0006888	ER to Golgi vesicle-mediated transport	1.01E-05	26
GO:2000278	regulation of DNA biosynthetic process	1.04E-05	25
GO:0071897	DNA biosynthetic process	1.04E-05	31
GO:1904816	positive regulation of protein localization to chromosome, telomeric region	1.26E-05	8
GO:0018205	peptidyl-lysine modification	1.43E-05	52
GO:2000573	positive regulation of DNA biosynthetic process	1.54E-05	19
GO:0019080	viral gene expression	1.77E-05	17
GO:0072522	purine-containing compound biosynthetic process	1.83E-05	44
GO:0051168	nuclear export	2.07E-05	30
GO:0006418	tRNA aminoacylation for protein translation	2.24E-05	15
GO:0006220	pyrimidine nucleotide metabolic process	2.37E-05	12
GO:0035966	response to topologically incorrect protein	2.44E-05	27
GO:0034250	positive regulation of cellular amide metabolic process	2.56E-05	28

GO:0006164	purine nucleotide biosynthetic process	2.64E-05	43
GO:0009108	coenzyme biosynthetic process	2.67E-05	32
GO:0000466	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	2.76E-05	10
GO:0042451	purine nucleoside biosynthetic process	2.76E-05	10
GO:0046129	purine ribonucleoside biosynthetic process	2.76E-05	10
GO:0006733	oxidoreduction coenzyme metabolic process	3.01E-05	30
GO:0000462	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	3.09E-05	13
GO:0009260	ribonucleotide biosynthetic process	3.11E-05	43
GO:0043648	dicarboxylic acid metabolic process	3.13E-05	22
GO:0090502	RNA phosphodiester bond hydrolysis, endonucleolytic	3.28E-05	11
GO:0018279	protein N-linked glycosylation via asparagine	3.31E-05	12
GO:0006986	response to unfolded protein	3.40E-05	24
GO:0070203	regulation of establishment of protein localization to telomere	3.78E-05	7
GO:0075522	IRES-dependent viral translational initiation	3.78E-05	7
GO:0050821	protein stabilization	3.79E-05	30
GO:0046390	ribose phosphate biosynthetic process	4.04E-05	43
GO:0042026	protein refolding	4.39E-05	10
GO:0018196	peptidyl-asparagine modification	4.74E-05	12
GO:0043039	tRNA aminoacylation	4.84E-05	15
GO:0070198	protein localization to chromosome, telomeric region	4.86E-05	11
GO:0043248	proteasome assembly	5.42E-05	8
GO:1901070	guanosine-containing compound biosynthetic process	5.42E-05	8
GO:1904814	regulation of protein localization to chromosome, telomeric region	5.42E-05	8
GO:0006367	transcription initiation from RNA polymerase II promoter	5.42E-05	17
GO:0043484	regulation of RNA splicing	5.71E-05	25
GO:0043038	amino acid activation	6.19E-05	15
GO:0016054	organic acid catabolic process	6.69E-05	36
GO:0046395	carboxylic acid catabolic process	6.69E-05	36
GO:0070199	establishment of protein localization to chromosome	6.75E-05	10
GO:0009152	purine ribonucleotide biosynthetic process	6.75E-05	41
GO:0006606	protein import into nucleus	6.87E-05	30
GO:0006338	chromatin remodeling	8.03E-05	28
GO:0070202	regulation of establishment of protein localization to chromosome	8.72E-05	7
GO:1903311	regulation of mRNA metabolic process	9.07E-05	36
GO:0042455	ribonucleoside biosynthetic process	9.08E-05	12
GO:0031647	regulation of protein stability	9.73E-05	40
GO:0070200	establishment of protein localization to telomere	0.00010074	8
GO:0033119	negative regulation of RNA splicing	0.00010085	11

GO:0051085	chaperone cofactor-dependent protein refolding	0.00010085	11
GO:0007006	mitochondrial membrane organization	0.00010142	21
GO:0006221	pyrimidine nucleotide biosynthetic process	0.00010142	10
GO:0051170	import into nucleus	0.00010931	30
GO:0032259	methylation	0.00014241	48
GO:0006278	RNA-dependent DNA biosynthetic process	0.00014338	16
GO:0007004	telomere maintenance via telomerase	0.00014338	16
GO:0050684	regulation of mRNA processing	0.00014669	24
GO:0016032	viral process	0.00014829	42
GO:0048024	regulation of mRNA splicing, via spliceosome	0.00015402	19
GO:0034404	nucleobase-containing small molecule biosynthetic process	0.00015402	30
GO:0009163	nucleoside biosynthetic process	0.00016586	12
GO:0051084	'de novo' posttranslational protein folding	0.00016586	12
GO:1903320	regulation of protein modification by small protein conjugation or removal	0.00017184	35
GO:0018208	peptidyl-proline modification	0.00017184	13
GO:0000966	RNA 5'-end processing	0.00017184	8
GO:0006613	cotranslational protein targeting to membrane	0.00017184	8
GO:0006487	protein N-linked glycosylation	0.00018325	18
GO:0006352	DNA-templated transcription, initiation	0.00018917	21
GO:1901607	alpha-amino acid biosynthetic process	0.0002658	16
GO:0006084	acetyl-CoA metabolic process	0.00027602	11
GO:0009147	pyrimidine nucleoside triphosphate metabolic process	0.00029607	8
GO:1901659	glycosyl compound biosynthetic process	0.00029706	12
GO:0043467	regulation of generation of precursor metabolites and energy	0.00030289	21
GO:0044403	symbiont process	0.00030289	49
GO:0031503	protein-containing complex localization	0.00032037	32
GO:0099116	tRNA 5'-end processing	0.00033804	7
GO:0034502	protein localization to chromosome	0.00037761	18
GO:0000027	ribosomal large subunit assembly	0.00038901	12
GO:0016999	antibiotic metabolic process	0.00042491	23
GO:0008652	cellular amino acid biosynthetic process	0.00047591	16
GO:1901605	alpha-amino acid metabolic process	0.00047925	32
GO:0009063	cellular amino acid catabolic process	0.00048897	19
GO:1902600	proton transmembrane transport	0.00048897	19
GO:0006473	protein acetylation	0.00055873	30
GO:0006400	tRNA modification	0.00056925	16
GO:0000478	endonucleolytic cleavage involved in rRNA processing	0.00059911	7
GO:0034471	ncRNA 5'-end processing	0.00059911	7

GO:0045899	positive regulation of RNA polymerase II transcriptional preinitiation complex assembly	0.00059911	7
GO:0072528	pyrimidine-containing compound biosynthetic process	0.00061436	10
GO:0000723	telomere maintenance	0.00061644	23
GO:0051188	cofactor biosynthetic process	0.00062971	34
GO:0018195	peptidyl-arginine modification	0.00070305	9
GO:0045047	protein targeting to ER	0.00070305	9
GO:0048025	negative regulation of mRNA splicing, via spliceosome	0.00070305	9
GO:0002183	cytoplasmic translational initiation	0.00071876	8
GO:0071428	rRNA-containing ribonucleoprotein complex export from nucleus	0.00071876	8
GO:0032200	telomere organization	0.00078455	23
GO:0050685	positive regulation of mRNA processing	0.0008275	10
GO:0009083	branched-chain amino acid catabolic process	0.00100243	7
GO:0072524	pyridine-containing compound metabolic process	0.00104115	25
GO:0006637	acyl-CoA metabolic process	0.00105668	17
GO:0035383	thioester metabolic process	0.00105668	17
GO:0001682	tRNA 5'-leader removal	0.00114927	6
GO:0001731	formation of translation preinitiation complex	0.00114927	6
GO:0006105	succinate metabolic process	0.00114927	6
GO:0006183	GTP biosynthetic process	0.00114927	6
GO:0070131	positive regulation of mitochondrial translation	0.00114927	6
GO:0046496	nicotinamide nucleotide metabolic process	0.00120232	24
GO:0031396	regulation of protein ubiquitination	0.00128504	29
GO:0030970	retrograde protein transport, ER to cytosol	0.00136592	9
GO:1903513	endoplasmic reticulum to cytosol transport	0.00136592	9
GO:0009069	serine family amino acid metabolic process	0.00140712	11
GO:0032527	protein exit from endoplasmic reticulum	0.00140712	11
GO:1900182	positive regulation of protein localization to nucleus	0.00141227	17
GO:0043414	macromolecule methylation	0.00143893	39
GO:0019362	pyridine nucleotide metabolic process	0.00148352	24
GO:0010833	telomere maintenance via telomere lengthening	0.00152259	16
GO:0009070	serine family amino acid biosynthetic process	0.00152259	7
GO:0045898	regulation of RNA polymerase II transcriptional preinitiation complex assembly	0.00152259	7
GO:0046131	pyrimidine ribonucleoside metabolic process	0.00152259	8
GO:0048026	positive regulation of mRNA splicing, via spliceosome	0.00152259	8
GO:0070841	inclusion body assembly	0.00152259	8
GO:0072527	pyrimidine-containing compound metabolic process	0.00165061	13
GO:0061136	regulation of proteasomal protein catabolic process	0.00179147	27
GO:0009394	2'-deoxyribonucleotide metabolic process	0.00180575	9

GO:0019692	deoxyribose phosphate metabolic process	0.00180575	9
GO:0050686	negative regulation of mRNA processing	0.00184759	10
GO:0000245	spliceosomal complex assembly	0.00191512	12
GO:0001824	blastocyst development	0.00191512	19
GO:0006090	pyruvate metabolic process	0.00191512	19
GO:0016570	histone modification	0.00192168	55
GO:0006086	acetyl-CoA biosynthetic process from pyruvate	0.00194829	6
GO:0006122	mitochondrial electron transport, ubiquinol to cytochrome c	0.00194829	6
GO:1900180	regulation of protein localization to nucleus	0.00197564	22
GO:0016569	covalent chromatin modification	0.002099	56
GO:0000028	ribosomal small subunit assembly	0.00211532	8
GO:0060261	positive regulation of transcription initiation from RNA polymerase II promoter	0.00211532	8
GO:0043543	protein acylation	0.00213162	33
GO:0006635	fatty acid beta-oxidation	0.00215445	15
GO:0000054	ribosomal subunit export from nucleus	0.00223988	7
GO:0009218	pyrimidine ribonucleotide metabolic process	0.00223988	7
GO:0033750	ribosome localization	0.00223988	7
GO:1902176	negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	0.00223988	7
GO:0072599	establishment of protein localization to endoplasmic reticulum	0.00232813	9
GO:0009408	response to heat	0.00240188	19
GO:0007339	binding of sperm to zona pellucida	0.00265397	11
GO:0009119	ribonucleoside metabolic process	0.00266517	16
GO:0045862	positive regulation of proteolysis	0.0026778	42
GO:0006289	nucleotide-excision repair	0.00277572	13
GO:0010501	RNA secondary structure unwinding	0.00277572	12
GO:0070646	protein modification by small protein removal	0.00281008	23
GO:0006302	double-strand break repair	0.00292703	29
GO:0000479	endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	0.00312635	6
GO:0006415	translational termination	0.00312635	6
GO:0006614	SRP-dependent cotranslational protein targeting to membrane	0.00312635	6
GO:0010918	positive regulation of mitochondrial membrane potential	0.00312635	6
GO:0072593	reactive oxygen species metabolic process	0.00314565	36
GO:0006120	mitochondrial electron transport, NADH to ubiquinone	0.00324587	7
GO:0070129	regulation of mitochondrial translation	0.00324587	7
GO:0072329	monocarboxylic acid catabolic process	0.00327935	20
GO:0070972	protein localization to endoplasmic reticulum	0.00330302	12
GO:0051881	regulation of mitochondrial membrane potential	0.003308	15

GO:1903313	positive regulation of mRNA metabolic process	0.003308	15
GO:0009116	nucleoside metabolic process	0.00345103	18
GO:2001243	negative regulation of intrinsic apoptotic signaling pathway	0.00345103	18
GO:0031123	RNA 3'-end processing	0.00346993	17
GO:0046165	alcohol biosynthetic process	0.00363121	20
GO:0009132	nucleoside diphosphate metabolic process	0.00379023	19
GO:0070584	mitochondrion morphogenesis	0.00379887	8
GO:1904292	regulation of ERAD pathway	0.00379887	8
GO:0032210	regulation of telomere maintenance via telomerase	0.00392304	12
GO:0008637	apoptotic mitochondrial changes	0.00404093	20
GO:0006790	sulfur compound metabolic process	0.00437566	36
GO:0033120	positive regulation of RNA splicing	0.00447533	10
GO:1901068	guanosine-containing compound metabolic process	0.00447533	10
GO:0097193	intrinsic apoptotic signaling pathway	0.00450191	39
GO:0006475	internal protein amino acid acetylation	0.0045217	24
GO:0009081	branched-chain amino acid metabolic process	0.0045217	7
GO:0006406	mRNA export from nucleus	0.00463574	12
GO:0032206	positive regulation of telomere maintenance	0.00463574	12
GO:0071427	mRNA-containing ribonucleoprotein complex export from nucleus	0.00463574	12
GO:0043628	ncRNA 3'-end processing	0.00488486	9
GO:0010821	regulation of mitochondrion organization	0.00497311	29
GO:0044770	cell cycle phase transition	0.00501074	48
GO:0046128	purine ribonucleoside metabolic process	0.00521065	13
GO:0001510	RNA methylation	0.0061827	13
GO:0000154	rRNA modification	0.0061949	9
GO:0009262	deoxyribonucleotide metabolic process	0.0061949	9
GO:0032212	positive regulation of telomere maintenance via telomerase	0.0061949	9
GO:0045070	positive regulation of viral genome replication	0.0061949	9
GO:0009200	deoxyribonucleoside triphosphate metabolic process	0.00625381	7
GO:0046051	UTP metabolic process	0.00631258	5
GO:0018394	peptidyl-lysine acetylation	0.00644133	24
GO:0007007	inner mitochondrial membrane organization	0.00654565	8
GO:1901998	toxin transport	0.00669438	10
GO:0035036	sperm-egg recognition	0.0067468	11
GO:0046132	pyrimidine ribonucleoside biosynthetic process	0.00698917	6
GO:0051131	chaperone-mediated protein complex assembly	0.00698917	6
GO:0090083	regulation of inclusion body assembly	0.00698917	6
GO:0044419	interspecies interaction between organisms	0.00725188	50
GO:0044772	mitotic cell cycle phase transition	0.00730121	44

GO:1901606	alpha-amino acid catabolic process	0.00739797	15
GO:0032434	regulation of proteasomal ubiquitin-dependent protein catabolic process	0.00740553	20
GO:0048193	Golgi vesicle transport	0.00750327	34
GO:0006260	DNA replication	0.00756197	35
GO:0009062	fatty acid catabolic process	0.00794011	17
GO:1903050	regulation of proteolysis involved in cellular protein catabolic process	0.00801298	28
GO:1903362	regulation of cellular protein catabolic process	0.0081541	31
GO:0060260	regulation of transcription initiation from RNA polymerase II promoter	0.00832305	8
GO:1901657	glycosyl compound metabolic process	0.00904182	20
GO:0016573	histone acetylation	0.00916349	22
GO:0042278	purine nucleoside metabolic process	0.00940589	13
GO:0048524	positive regulation of viral process	0.00951263	15
GO:0006607	NLS-bearing protein import into nucleus	0.00994996	6
GO:0006744	ubiquinone biosynthetic process	0.00994996	6
GO:0009220	pyrimidine ribonucleotide biosynthetic process	0.00994996	6
GO:1901663	quinone biosynthetic process	0.00994996	6
GO:0009265	2'-deoxyribonucleotide biosynthetic process	0.01001749	5
GO:0046385	deoxyribose phosphate biosynthetic process	0.01001749	5
GO:1904152	regulation of retrograde protein transport, ER to cytosol	0.01001749	5
GO:0000060	protein import into nucleus, translocation	0.01023812	12
GO:0006213	pyrimidine nucleoside metabolic process	0.01047497	8
GO:1902175	regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	0.01047497	8
GO:0050792	regulation of viral process	0.01064031	26
GO:0051054	positive regulation of DNA metabolic process	0.01067988	32
GO:0051052	regulation of DNA metabolic process	0.01130505	49
GO:1904358	positive regulation of telomere maintenance via telomere lengthening	0.01143599	9
GO:0032204	regulation of telomere maintenance	0.01197158	15
GO:1903829	positive regulation of cellular protein localization	0.01269722	42
GO:0033044	regulation of chromosome organization	0.01291927	41
GO:0000288	nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	0.01297865	11
GO:0006310	DNA recombination	0.01299195	32
GO:0051262	protein tetramerization	0.01324858	24
GO:0019395	fatty acid oxidation	0.01350462	17
GO:1904356	regulation of telomere maintenance via telomere lengthening	0.01357385	12
GO:0042176	regulation of protein catabolic process	0.01357385	43
GO:0006085	acetyl-CoA biosynthetic process	0.01357385	6
GO:0006743	ubiquinone metabolic process	0.01357385	6
GO:0046134	pyrimidine nucleoside biosynthetic process	0.01357385	6

GO:0018393	internal peptidyl-lysine acetylation	0.01371855	22
GO:0043094	cellular metabolic compound salvage	0.01408609	7
GO:0000963	mitochondrial RNA processing	0.01495652	5
GO:0009208	pyrimidine ribonucleoside triphosphate metabolic process	0.01495652	5
GO:0009219	pyrimidine deoxyribonucleotide metabolic process	0.01495652	5
GO:0031125	rRNA 3'-end processing	0.01495652	5
GO:0034982	mitochondrial protein processing	0.01495652	5
GO:1904294	positive regulation of ERAD pathway	0.01495652	5
GO:1905214	regulation of RNA binding	0.01495652	5
GO:0033143	regulation of intracellular steroid hormone receptor signaling pathway	0.01530125	14
GO:0046039	GTP metabolic process	0.01597308	8
GO:0070670	response to interleukin-4	0.01597308	8
GO:2000144	positive regulation of DNA-templated transcription, initiation	0.01597308	8
GO:0034440	lipid oxidation	0.01611787	17
GO:0035967	cellular response to topologically incorrect protein	0.01611787	17
GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	0.01630563	9
GO:2000142	regulation of DNA-templated transcription, initiation	0.01630563	9
GO:0030518	intracellular steroid hormone receptor signaling pathway	0.01634995	18
GO:0007030	Golgi organization	0.01642529	19
GO:0017148	negative regulation of translation	0.01829091	30
GO:0008631	intrinsic apoptotic signaling pathway in response to oxidative stress	0.01865377	10
GO:0006414	translational elongation	0.0192841	14
GO:1903312	negative regulation of mRNA metabolic process	0.0192841	14
GO:0005996	monosaccharide metabolic process	0.01937821	32
GO:1903364	positive regulation of cellular protein catabolic process	0.01944484	20
GO:0008299	isoprenoid biosynthetic process	0.01944484	8
GO:0009266	response to temperature stimulus	0.01944484	23
GO:0006006	glucose metabolic process	0.01974415	26
GO:2001252	positive regulation of chromosome organization	0.02014141	24
GO:0006997	nucleus organization	0.0215003	19
GO:0009166	nucleotide catabolic process	0.0215003	19
GO:0090503	RNA phosphodiester bond hydrolysis, exonucleolytic	0.02153898	5
GO:0051438	regulation of ubiquitin-protein transferase activity	0.02161358	10
GO:0001836	release of cytochrome c from mitochondria	0.02283665	12
GO:0017004	cytochrome complex assembly	0.02375774	8
GO:0006103	2-oxoglutarate metabolic process	0.02375774	6
GO:0016226	iron-sulfur cluster assembly	0.02375774	6
GO:0031163	metallo-sulfur cluster assembly	0.02375774	6
GO:0044843	cell cycle G1/S phase transition	0.02414173	26

GO:0006479	protein methylation	0.02489883	24
GO:0008213	protein alkylation	0.02489883	24
GO:0051196	regulation of coenzyme metabolic process	0.02509557	10
GO:0009988	cell-cell recognition	0.02576286	12
GO:0034249	negative regulation of cellular amide metabolic process	0.02581058	31
GO:2001242	regulation of intrinsic apoptotic signaling pathway	0.02594601	23
GO:2000058	regulation of ubiquitin-dependent protein catabolic process	0.02596048	21
GO:1901292	nucleoside phosphate catabolic process	0.02679703	20
GO:0031365	N-terminal protein amino acid modification	0.02760181	7
GO:0034508	centromere complex assembly	0.02760181	7
GO:0006270	DNA replication initiation	0.02826034	8
GO:0006890	retrograde vesicle-mediated transport, Golgi to ER	0.02826034	8
GO:0006107	oxaloacetate metabolic process	0.02978971	5
GO:0006544	glycine metabolic process	0.02978971	5
GO:0009148	pyrimidine nucleoside triphosphate biosynthetic process	0.02978971	5
GO:0009263	deoxyribonucleotide biosynthetic process	0.02978971	5
GO:0043280	positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	0.0302575	18
GO:0019430	removal of superoxide radicals	0.03028915	6
GO:0035384	thioester biosynthetic process	0.03028915	6
GO:0071616	acyl-CoA biosynthetic process	0.03028915	6
GO:1901800	positive regulation of proteasomal protein catabolic process	0.0304111	16
GO:0007059	chromosome segregation	0.0307495	38
GO:0035304	regulation of protein dephosphorylation	0.03244359	14
GO:0008654	phospholipid biosynthetic process	0.03331563	22
GO:0030488	tRNA methylation	0.0336315	7
GO:0034661	ncRNA catabolic process	0.0336315	7
GO:0019318	hexose metabolic process	0.03483844	28
GO:0032436	positive regulation of proteasomal ubiquitin-dependent protein catabolic process	0.03590768	14
GO:0034620	cellular response to unfolded protein	0.03590768	14
GO:0010822	positive regulation of mitochondrion organization	0.03612619	20
GO:0000959	mitochondrial RNA metabolic process	0.03655232	9
GO:0016073	snRNA metabolic process	0.03655232	9
GO:0016925	protein sumoylation	0.03655232	9
GO:0000082	G1/S transition of mitotic cell cycle	0.03655232	24
GO:1900408	negative regulation of cellular response to oxidative stress	0.03771576	10
GO:0045838	positive regulation of membrane potential	0.03826764	6
GO:0070861	regulation of protein exit from endoplasmic reticulum	0.03826764	6
GO:0090150	establishment of protein localization to membrane	0.03922414	26

GO:0000729	DNA double-strand break processing	0.03941604	5
GO:0006123	mitochondrial electron transport, cytochrome c to oxygen	0.03941604	5
GO:0006999	nuclear pore organization	0.03941604	5
GO:0019646	aerobic electron transport chain	0.03941604	5
GO:0042407	cristae formation	0.03941604	5
GO:0046112	nucleobase biosynthetic process	0.03941604	5
GO:1905897	regulation of response to endoplasmic reticulum stress	0.04000798	12
GO:0000305	response to oxygen radical	0.04000798	7
GO:0071353	cellular response to interleukin-4	0.04000798	7
GO:1990748	cellular detoxification	0.04000798	7
GO:1903052	positive regulation of proteolysis involved in cellular protein catabolic process	0.04194518	17
GO:0031331	positive regulation of cellular catabolic process	0.04194518	38
GO:2000060	positive regulation of ubiquitin-dependent protein catabolic process	0.04304579	15
GO:1901617	organic hydroxy compound biosynthetic process	0.0432581	27
GO:1903322	positive regulation of protein modification by small protein conjugation or removal	0.04422425	18
GO:0035307	positive regulation of protein dephosphorylation	0.04593962	8
GO:0000055	ribosomal large subunit export from nucleus	0.04637922	4
GO:0006241	CTP biosynthetic process	0.04637922	4
GO:0031468	nuclear envelope reassembly	0.04637922	4
GO:0035246	peptidyl-arginine N-methylation	0.04637922	4
GO:0035247	peptidyl-arginine omega-N-methylation	0.04637922	4
GO:0046036	CTP metabolic process	0.04637922	4
GO:1902415	regulation of mRNA binding	0.04637922	4
GO:0006165	nucleoside diphosphate phosphorylation	0.04637922	14
GO:0051289	protein homotetramerization	0.04637922	14
GO:0071450	cellular response to oxygen radical	0.04637922	6
GO:0071451	cellular response to superoxide	0.04637922	6
GO:1901658	glycosyl compound catabolic process	0.04637922	6
GO:2000377	regulation of reactive oxygen species metabolic process	0.04870008	24
GO:0006261	DNA-dependent DNA replication	0.04872221	19

Supplemental Table 4D. PAD2KO vs WT Spleen Upregulated Pathways

ID	Description	p.adjust	Count
GO:0000422	autophagy of mitochondrion	2.52E-05	12
GO:0061726	mitochondrion disassembly	2.52E-05	12
GO:0022411	cellular component disassembly	4.16E-05	23
GO:1903008	organelle disassembly	0.00015145	12
GO:0016236	macroautophagy	0.00057481	15
GO:0000045	autophagosome assembly	0.00224488	10
GO:1905037	autophagosome organization	0.00283378	10
GO:0061912	selective autophagy	0.00386692	7
GO:0098780	response to mitochondrial depolarisation	0.00687118	5
GO:0000423	mitophagy	0.00800345	5
GO:2000377	regulation of reactive oxygen species metabolic process	0.02289363	12
GO:0016239	positive regulation of macroautophagy	0.02289363	7
GO:0032984	protein-containing complex disassembly	0.03964501	12
GO:0043243	positive regulation of protein complex disassembly	0.03964501	5
GO:0045926	negative regulation of growth	0.03964501	14

Supplemental Table 4E. PAD4KO vs WT spleen Downregulated Pathways

ID	Description	p.adjust	Count
GO:0022613	ribonucleoprotein complex biogenesis	2.76E-48	148
GO:0042254	ribosome biogenesis	7.03E-37	107
GO:0034660	ncRNA metabolic process	2.77E-33	132
GO:0006260	DNA replication	6.46E-30	92
GO:0034470	ncRNA processing	6.46E-30	106
GO:0006364	rRNA processing	3.94E-29	77
GO:0045333	cellular respiration	9.33E-29	69
GO:0009123	nucleoside monophosphate metabolic process	9.60E-28	89
GO:0009161	ribonucleoside monophosphate metabolic process	5.61E-27	86
GO:0016072	rRNA metabolic process	6.61E-27	80
GO:0009167	purine ribonucleoside monophosphate metabolic process	3.87E-26	84
GO:0009126	purine nucleoside monophosphate metabolic process	4.91E-26	84
GO:0009141	nucleoside triphosphate metabolic process	1.86E-25	88
GO:0006397	mRNA processing	2.05E-25	116
GO:0006261	DNA-dependent DNA replication	3.85E-25	59
GO:0006281	DNA repair	5.63E-25	115
GO:0008380	RNA splicing	5.71E-25	103
GO:0009144	purine nucleoside triphosphate metabolic process	2.16E-24	83
GO:0009199	ribonucleoside triphosphate metabolic process	2.32E-24	82
GO:0009205	purine ribonucleoside triphosphate metabolic process	3.39E-24	81
GO:0006403	RNA localization	1.38E-23	69
GO:0072594	establishment of protein localization to organelle	1.60E-23	111
GO:0000375	RNA splicing, via transesterification reactions	6.69E-23	78
GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	2.34E-22	77
GO:0000398	mRNA splicing, via spliceosome	2.34E-22	77
GO:0006091	generation of precursor metabolites and energy	6.17E-22	94
GO:0015980	energy derivation by oxidation of organic compounds	1.66E-21	77
GO:0046034	ATP metabolic process	1.26E-20	71
GO:0006913	nucleocytoplasmic transport	2.73E-18	82
GO:0051169	nuclear transport	3.30E-18	82
GO:0019693	ribose phosphate metabolic process	4.99E-18	104
GO:0009060	aerobic respiration	6.97E-18	37
GO:0009259	ribonucleotide metabolic process	1.99E-17	101
GO:0071826	ribonucleoprotein complex subunit organization	4.65E-17	66
GO:0022618	ribonucleoprotein complex assembly	5.08E-17	64
GO:0140053	mitochondrial gene expression	9.43E-17	41

GO:0006163	purine nucleotide metabolic process	9.45E-17	100
GO:0017038	protein import	1.04E-16	64
GO:0009150	purine ribonucleotide metabolic process	3.19E-16	97
GO:0072521	purine-containing compound metabolic process	3.31E-16	105
GO:0006119	oxidative phosphorylation	3.14E-15	37
GO:0051186	cofactor metabolic process	8.44E-15	99
GO:0032543	mitochondrial translation	9.12E-15	33
GO:0034655	nucleobase-containing compound catabolic process	9.12E-15	89
GO:0006457	protein folding	9.12E-15	55
GO:0022904	respiratory electron transport chain	1.07E-14	35
GO:1904874	positive regulation of telomerase RNA localization to Cajal body	1.56E-14	15
GO:0006839	mitochondrial transport	2.33E-14	68
GO:0050657	nucleic acid transport	3.77E-14	49
GO:0050658	RNA transport	3.77E-14	49
GO:0006270	DNA replication initiation	4.08E-14	22
GO:0042773	ATP synthesis coupled electron transport	4.68E-14	30
GO:0042775	mitochondrial ATP synthesis coupled electron transport	4.68E-14	29
GO:0015931	nucleobase-containing compound transport	4.85E-14	55
GO:0051236	establishment of RNA localization	8.22E-14	49
GO:0022900	electron transport chain	8.77E-14	35
GO:0070585	protein localization to mitochondrion	1.86E-13	49
GO:0006413	translational initiation	2.61E-13	39
GO:0034504	protein localization to nucleus	2.62E-13	68
GO:0072655	establishment of protein localization to mitochondrion	2.76E-13	48
GO:0046700	heterocycle catabolic process	2.76E-13	92
GO:0044270	cellular nitrogen compound catabolic process	3.23E-13	91
GO:0009124	nucleoside monophosphate biosynthetic process	6.37E-13	46
GO:0071897	DNA biosynthetic process	7.06E-13	47
GO:0019439	aromatic compound catabolic process	1.89E-12	92
GO:0009156	ribonucleoside monophosphate biosynthetic process	2.61E-12	44
GO:1901361	organic cyclic compound catabolic process	4.02E-12	95
GO:0006732	coenzyme metabolic process	4.82E-12	70
GO:0006099	tricarboxylic acid cycle	5.19E-12	19
GO:0033108	mitochondrial respiratory chain complex assembly	6.40E-12	31
GO:1904872	regulation of telomerase RNA localization to Cajal body	6.52E-12	15
GO:0006611	protein export from nucleus	6.65E-12	41
GO:1990542	mitochondrial transmembrane transport	7.94E-12	28
GO:0006101	citrate metabolic process	9.25E-12	20
GO:0006520	cellular amino acid metabolic process	9.25E-12	64

GO:0051052	regulation of DNA metabolic process	1.18E-11	84
GO:0006302	double-strand break repair	1.34E-11	51
GO:0009127	purine nucleoside monophosphate biosynthetic process	1.63E-11	42
GO:0009168	purine ribonucleoside monophosphate biosynthetic process	1.63E-11	42
GO:0000723	telomere maintenance	1.91E-11	39
GO:0090670	RNA localization to Cajal body	2.40E-11	15
GO:0090671	telomerase RNA localization to Cajal body	2.40E-11	15
GO:0090672	telomerase RNA localization	2.40E-11	15
GO:0090685	RNA localization to nucleus	2.40E-11	15
GO:0072350	tricarboxylic acid metabolic process	2.49E-11	21
GO:0032200	telomere organization	3.21E-11	39
GO:0051028	mRNA transport	3.31E-11	36
GO:0006626	protein targeting to mitochondrion	3.31E-11	42
GO:0006399	tRNA metabolic process	7.89E-11	46
GO:0042273	ribosomal large subunit biogenesis	7.94E-11	31
GO:0006401	RNA catabolic process	8.77E-11	55
GO:0051168	nuclear export	9.38E-11	43
GO:0071166	ribonucleoprotein complex localization	1.03E-10	29
GO:0051170	import into nucleus	1.51E-10	45
GO:0006733	oxidoreduction coenzyme metabolic process	1.89E-10	43
GO:0044770	cell cycle phase transition	2.61E-10	77
GO:0044772	mitotic cell cycle phase transition	3.62E-10	72
GO:0006310	DNA recombination	3.89E-10	56
GO:0071426	ribonucleoprotein complex export from nucleus	4.31E-10	28
GO:0051188	cofactor biosynthetic process	7.19E-10	52
GO:1901293	nucleoside phosphate biosynthetic process	8.39E-10	66
GO:0006606	protein import into nucleus	8.97E-10	43
GO:0009142	nucleoside triphosphate biosynthetic process	9.10E-10	40
GO:2000278	regulation of DNA biosynthetic process	1.01E-09	34
GO:0006405	RNA export from nucleus	1.07E-09	31
GO:0009108	coenzyme biosynthetic process	1.29E-09	44
GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process	1.35E-09	74
GO:0007059	chromosome segregation	1.41E-09	66
GO:0010498	proteasomal protein catabolic process	1.66E-09	82
GO:0051054	positive regulation of DNA metabolic process	2.15E-09	54
GO:0009165	nucleotide biosynthetic process	2.23E-09	64
GO:0009145	purine nucleoside triphosphate biosynthetic process	2.66E-09	37
GO:0010257	NADH dehydrogenase complex assembly	4.24E-09	20
GO:0032981	mitochondrial respiratory chain complex I assembly	4.24E-09	20

GO:0009201	ribonucleoside triphosphate biosynthetic process	4.24E-09	37
GO:0007006	mitochondrial membrane organization	6.96E-09	30
GO:0009206	purine ribonucleoside triphosphate biosynthetic process	8.50E-09	36
GO:0065004	protein-DNA complex assembly	8.97E-09	44
GO:2000573	positive regulation of DNA biosynthetic process	1.39E-08	25
GO:0006458	'de novo' protein folding	1.47E-08	21
GO:0045786	negative regulation of cell cycle	1.58E-08	80
GO:0022616	DNA strand elongation	2.62E-08	14
GO:0061077	chaperone-mediated protein folding	3.82E-08	25
GO:0000724	double-strand break repair via homologous recombination	3.86E-08	31
GO:0000725	recombinational repair	3.86E-08	31
GO:0006402	mRNA catabolic process	4.02E-08	45
GO:0043039	tRNA aminoacylation	6.72E-08	20
GO:0000387	spliceosomal snRNP assembly	7.65E-08	16
GO:0071824	protein-DNA complex subunit organization	8.34E-08	47
GO:0043038	amino acid activation	1.00E-07	20
GO:0048024	regulation of mRNA splicing, via spliceosome	1.15E-07	26
GO:0033044	regulation of chromosome organization	1.27E-07	63
GO:0006418	tRNA aminoacylation for protein translation	1.29E-07	19
GO:0034404	nucleobase-containing small molecule biosynthetic process	1.39E-07	40
GO:0046390	ribose phosphate biosynthetic process	1.79E-07	54
GO:0000819	sister chromatid segregation	2.10E-07	41
GO:0010499	proteasomal ubiquitin-independent protein catabolic process	2.14E-07	14
GO:0009116	nucleoside metabolic process	2.34E-07	28
GO:0043484	regulation of RNA splicing	2.43E-07	32
GO:0031503	protein-containing complex localization	2.63E-07	43
GO:0009260	ribonucleotide biosynthetic process	3.09E-07	53
GO:0000075	cell cycle checkpoint	3.40E-07	41
GO:0072522	purine-containing compound biosynthetic process	4.58E-07	53
GO:0098813	nuclear chromosome segregation	4.97E-07	51
GO:0070202	regulation of establishment of protein localization to chromosome	5.30E-07	9
GO:0006164	purine nucleotide biosynthetic process	6.11E-07	52
GO:0006790	sulfur compound metabolic process	6.11E-07	52
GO:0043248	proteasome assembly	6.99E-07	10
GO:0050684	regulation of mRNA processing	7.09E-07	31
GO:0006284	base-excision repair	7.21E-07	17
GO:0009119	ribonucleoside metabolic process	7.64E-07	24
GO:0042274	ribosomal small subunit biogenesis	7.64E-07	24
GO:1903311	regulation of mRNA metabolic process	8.54E-07	45

GO:0006605	protein targeting	8.92E-07	59
GO:0006338	chromatin remodeling	9.10E-07	35
GO:0000470	maturation of LSU-rRNA	1.17E-06	14
GO:0071806	protein transmembrane transport	1.20E-06	19
GO:0000070	mitotic sister chromatid segregation	1.29E-06	35
GO:0006120	mitochondrial electron transport, NADH to ubiquinone	1.40E-06	11
GO:0030150	protein import into mitochondrial matrix	1.40E-06	11
GO:0009451	RNA modification	1.40E-06	32
GO:0010212	response to ionizing radiation	1.40E-06	32
GO:0009152	purine ribonucleotide biosynthetic process	1.54E-06	50
GO:0046496	nicotinamide nucleotide metabolic process	1.54E-06	33
GO:0072524	pyridine-containing compound metabolic process	1.66E-06	34
GO:1904816	positive regulation of protein localization to chromosome, telomeric region	1.71E-06	9
GO:2001020	regulation of response to DNA damage stimulus	1.73E-06	40
GO:0006754	ATP biosynthetic process	1.92E-06	30
GO:0007007	inner mitochondrial membrane organization	1.98E-06	13
GO:0044743	protein transmembrane import into intracellular organelle	1.99E-06	16
GO:0019362	pyridine nucleotide metabolic process	2.14E-06	33
GO:0043648	dicarboxylic acid metabolic process	2.14E-06	26
GO:0030490	maturation of SSU-rRNA	2.21E-06	19
GO:0016999	antibiotic metabolic process	2.28E-06	30
GO:0032259	methylation	2.46E-06	59
GO:0032392	DNA geometric change	3.00E-06	14
GO:0090329	regulation of DNA-dependent DNA replication	3.16E-06	17
GO:1901990	regulation of mitotic cell cycle phase transition	3.25E-06	49
GO:0070199	establishment of protein localization to chromosome	3.30E-06	12
GO:0090305	nucleic acid phosphodiester bond hydrolysis	3.66E-06	31
GO:0006271	DNA strand elongation involved in DNA replication	3.86E-06	10
GO:0006607	NLS-bearing protein import into nucleus	3.86E-06	10
GO:0070203	regulation of establishment of protein localization to telomere	3.91E-06	8
GO:1990173	protein localization to nucleoplasm	3.91E-06	8
GO:1901657	glycosyl compound metabolic process	3.91E-06	30
GO:0006406	mRNA export from nucleus	4.22E-06	18
GO:0032206	positive regulation of telomere maintenance	4.22E-06	18
GO:0065002	intracellular protein transmembrane transport	4.22E-06	18
GO:0071427	mRNA-containing ribonucleoprotein complex export from nucleus	4.22E-06	18
GO:0050821	protein stabilization	4.39E-06	35
GO:0000154	rRNA modification	4.51E-06	14

GO:0090501	RNA phosphodiester bond hydrolysis	4.52E-06	22
GO:0034502	protein localization to chromosome	4.79E-06	23
GO:0033120	positive regulation of RNA splicing	5.45E-06	15
GO:0009132	nucleoside diphosphate metabolic process	5.67E-06	27
GO:0042278	purine nucleoside metabolic process	6.24E-06	20
GO:0046394	carboxylic acid biosynthetic process	6.40E-06	59
GO:0000460	maturation of 5.8S rRNA	6.95E-06	14
GO:0016053	organic acid biosynthetic process	7.03E-06	59
GO:0006275	regulation of DNA replication	7.12E-06	29
GO:0006743	ubiquinone metabolic process	7.81E-06	10
GO:0071478	cellular response to radiation	9.01E-06	33
GO:0008637	apoptotic mitochondrial changes	9.30E-06	28
GO:0046128	purine ribonucleoside metabolic process	9.30E-06	19
GO:0015985	energy coupled proton transport, down electrochemical gradient	9.34E-06	12
GO:0015986	ATP synthesis coupled proton transport	9.34E-06	12
GO:0000956	nuclear-transcribed mRNA catabolic process	9.96E-06	27
GO:0042455	ribonucleoside biosynthetic process	1.03E-05	14
GO:0090151	establishment of protein localization to mitochondrial membrane	1.04E-05	9
GO:1901070	guanosine-containing compound biosynthetic process	1.04E-05	9
GO:1904814	regulation of protein localization to chromosome, telomeric region	1.04E-05	9
GO:0006278	RNA-dependent DNA biosynthetic process	1.20E-05	19
GO:0007004	telomere maintenance via telomerase	1.20E-05	19
GO:0050685	positive regulation of mRNA processing	1.28E-05	13
GO:1901987	regulation of cell cycle phase transition	1.38E-05	51
GO:0042255	ribosome assembly	1.41E-05	21
GO:0032508	DNA duplex unwinding	1.51E-05	12
GO:0097193	intrinsic apoptotic signaling pathway	1.55E-05	52
GO:0009314	response to radiation	1.63E-05	64
GO:1900180	regulation of protein localization to nucleus	1.65E-05	29
GO:0010833	telomere maintenance via telomere lengthening	1.77E-05	21
GO:0009163	nucleoside biosynthetic process	2.23E-05	14
GO:0042407	cristae formation	2.25E-05	9
GO:0070200	establishment of protein localization to telomere	2.25E-05	9
GO:0018205	peptidyl-lysine modification	2.32E-05	57
GO:0051123	RNA polymerase II transcriptional preinitiation complex assembly	2.41E-05	12
GO:0071103	DNA conformation change	2.61E-05	40
GO:0043414	macromolecule methylation	2.70E-05	49
GO:0006103	2-oxoglutarate metabolic process	2.75E-05	10
GO:0032204	regulation of telomere maintenance	2.75E-05	22

GO:0017004	cytochrome complex assembly	2.92E-05	13
GO:1901068	guanosine-containing compound metabolic process	3.16E-05	14
GO:0009411	response to UV	3.25E-05	30
GO:0006744	ubiquinone biosynthetic process	4.50E-05	9
GO:1901663	quinone biosynthetic process	4.50E-05	9
GO:0048025	negative regulation of mRNA splicing, via spliceosome	4.50E-05	11
GO:1901659	glycosyl compound biosynthetic process	4.50E-05	14
GO:1901605	alpha-amino acid metabolic process	5.35E-05	38
GO:0010608	posttranscriptional regulation of gene expression	5.69E-05	72
GO:0031647	regulation of protein stability	5.69E-05	45
GO:0010822	positive regulation of mitochondrion organization	5.98E-05	30
GO:0010821	regulation of mitochondrion organization	5.98E-05	38
GO:0006090	pyruvate metabolic process	6.55E-05	24
GO:0033045	regulation of sister chromatid segregation	6.58E-05	21
GO:0000463	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	6.59E-05	8
GO:0000469	cleavage involved in rRNA processing	7.12E-05	11
GO:2001252	positive regulation of chromosome organization	7.20E-05	34
GO:0048285	organelle fission	7.24E-05	71
GO:0034248	regulation of cellular amide metabolic process	7.60E-05	68
GO:0000338	protein deneddylation	8.06E-05	7
GO:0000466	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	8.06E-05	10
GO:0042451	purine nucleoside biosynthetic process	8.06E-05	10
GO:0046129	purine ribonucleoside biosynthetic process	8.06E-05	10
GO:0048026	positive regulation of mRNA splicing, via spliceosome	8.06E-05	10
GO:0009147	pyrimidine nucleoside triphosphate metabolic process	8.16E-05	9
GO:0006220	pyrimidine nucleotide metabolic process	8.24E-05	12
GO:1904358	positive regulation of telomere maintenance via telomere lengthening	8.67E-05	13
GO:0006417	regulation of translation	8.91E-05	63
GO:0009185	ribonucleoside diphosphate metabolic process	8.91E-05	22
GO:0009408	response to heat	8.91E-05	24
GO:0051983	regulation of chromosome segregation	8.91E-05	24
GO:0031570	DNA integrity checkpoint	9.91E-05	26
GO:0000245	spliceosomal complex assembly	0.00010258	15
GO:0016570	histone modification	0.00010258	67
GO:0006734	NADH metabolic process	0.00010543	11
GO:0000462	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	0.00012013	13
GO:0051084	'de novo' posttranslational protein folding	0.00012013	13

GO:0016569	covalent chromatin modification	0.00013157	68
GO:0140014	mitotic nuclear division	0.00013422	46
GO:0010948	negative regulation of cell cycle process	0.00013694	40
GO:0009135	purine nucleoside diphosphate metabolic process	0.00013812	21
GO:0009179	purine ribonucleoside diphosphate metabolic process	0.00013812	21
GO:0000280	nuclear division	0.00014292	64
GO:0070198	protein localization to chromosome, telomeric region	0.00015841	11
GO:0044843	cell cycle G1/S phase transition	0.00016344	36
GO:0009262	deoxyribonucleotide metabolic process	0.0001683	12
GO:0070897	DNA-templated transcriptional preinitiation complex assembly	0.0001683	12
GO:0046031	ADP metabolic process	0.00017874	20
GO:0006273	lagging strand elongation	0.0001841	7
GO:0046040	IMP metabolic process	0.0001841	7
GO:0000082	G1/S transition of mitotic cell cycle	0.00020762	34
GO:0007093	mitotic cell cycle checkpoint	0.00020974	27
GO:0044786	cell cycle DNA replication	0.0002247	13
GO:0050686	negative regulation of mRNA processing	0.00023737	12
GO:0033047	regulation of mitotic sister chromatid segregation	0.0002396	18
GO:0006999	nuclear pore organization	0.0002396	8
GO:0007091	metaphase/anaphase transition of mitotic cell cycle	0.0002396	16
GO:0044282	small molecule catabolic process	0.00026361	49
GO:0000077	DNA damage checkpoint	0.00027678	24
GO:0031123	RNA 3'-end processing	0.00028415	21
GO:0097327	response to antineoplastic agent	0.00029427	18
GO:0001836	release of cytochrome c from mitochondria	0.00030092	17
GO:0010965	regulation of mitotic sister chromatid separation	0.00030092	16
GO:0044784	metaphase/anaphase transition of cell cycle	0.00030092	16
GO:0006221	pyrimidine nucleotide biosynthetic process	0.0003018	10
GO:0033119	negative regulation of RNA splicing	0.00032875	11
GO:0051085	chaperone cofactor-dependent protein refolding	0.00032875	11
GO:0034644	cellular response to UV	0.00033361	19
GO:0090199	regulation of release of cytochrome c from mitochondria	0.0003417	14
GO:0060249	anatomical structure homeostasis	0.00037132	56
GO:0009200	deoxyribonucleoside triphosphate metabolic process	0.00037402	9
GO:0006122	mitochondrial electron transport, ubiquinol to cytochrome c	0.00037843	7
GO:0045930	negative regulation of mitotic cell cycle	0.00040075	39
GO:0046039	GTP metabolic process	0.00046696	11
GO:0016126	sterol biosynthetic process	0.00046751	15
GO:1904356	regulation of telomere maintenance via telomere lengthening	0.00046882	16

GO:0051262	protein tetramerization	0.00049246	31
GO:0006575	cellular modified amino acid metabolic process	0.0005239	30
GO:1903313	positive regulation of mRNA metabolic process	0.0005241	18
GO:0006633	fatty acid biosynthetic process	0.00055094	26
GO:0006333	chromatin assembly or disassembly	0.00055094	29
GO:0051306	mitotic sister chromatid separation	0.00057985	16
GO:0046131	pyrimidine ribonucleoside metabolic process	0.00058037	9
GO:1901292	nucleoside phosphate catabolic process	0.00060406	27
GO:0044272	sulfur compound biosynthetic process	0.00062973	18
GO:1903320	regulation of protein modification by small protein conjugation or removal	0.00064081	37
GO:0034508	centromere complex assembly	0.00064369	10
GO:0090502	RNA phosphodiester bond hydrolysis, endonucleolytic	0.00064369	10
GO:0000959	mitochondrial RNA metabolic process	0.00067282	13
GO:0070646	protein modification by small protein removal	0.00067976	27
GO:0000054	ribosomal subunit export from nucleus	0.00068271	8
GO:0006085	acetyl-CoA biosynthetic process	0.00068271	8
GO:0009218	pyrimidine ribonucleotide metabolic process	0.00068271	8
GO:0033750	ribosome localization	0.00068271	8
GO:0072330	monocarboxylic acid biosynthetic process	0.00068854	40
GO:1905818	regulation of chromosome separation	0.00069554	16
GO:0034250	positive regulation of cellular amide metabolic process	0.00076149	27
GO:1900182	positive regulation of protein localization to nucleus	0.00080047	19
GO:0009166	nucleotide catabolic process	0.00082597	25
GO:0008535	respiratory chain complex IV assembly	0.00085641	9
GO:0042026	protein refolding	0.00085641	9
GO:0032212	positive regulation of telomere maintenance via telomerase	0.00085641	11
GO:0000086	G2/M transition of mitotic cell cycle	0.00085764	23
GO:0006289	nucleotide-excision repair	0.00088097	15
GO:0009394	2'-deoxyribonucleotide metabolic process	0.00089157	10
GO:0019692	deoxyribose phosphate metabolic process	0.00089157	10
GO:0009895	negative regulation of catabolic process	0.00092097	43
GO:1903829	positive regulation of cellular protein localization	0.00093505	52
GO:0006367	transcription initiation from RNA polymerase II promoter	0.00103249	16
GO:0034599	cellular response to oxidative stress	0.00104515	41
GO:0044839	cell cycle G2/M phase transition	0.00105508	25
GO:0001522	pseudouridine synthesis	0.00107138	8
GO:0006825	copper ion transport	0.00107138	8
GO:0000060	protein import into nucleus, translocation	0.00107142	15

GO:0000726	non-recombinational repair	0.00107142	13
GO:0045727	positive regulation of translation	0.00108185	24
GO:0032210	regulation of telomere maintenance via telomerase	0.00108875	14
GO:0006631	fatty acid metabolic process	0.00109447	56
GO:0031497	chromatin assembly	0.00118262	25
GO:0009263	deoxyribonucleotide biosynthetic process	0.00119764	7
GO:0016074	snoRNA metabolic process	0.00119764	7
GO:0019081	viral translation	0.00119764	7
GO:0045899	positive regulation of RNA polymerase II transcriptional preinitiation complex assembly	0.00119764	7
GO:0006213	pyrimidine nucleoside metabolic process	0.00121307	10
GO:0007098	centrosome cycle	0.00121491	24
GO:0006479	protein methylation	0.00123512	31
GO:0008213	protein alkylation	0.00123512	31
GO:0008630	intrinsic apoptotic signaling pathway in response to DNA damage	0.00124735	23
GO:0006303	double-strand break repair via nonhomologous end joining	0.00125831	12
GO:0031023	microtubule organizing center organization	0.00131265	25
GO:0046822	regulation of nucleocytoplasmic transport	0.00137365	24
GO:0046434	organophosphate catabolic process	0.00140308	33
GO:1903312	negative regulation of mRNA metabolic process	0.00141174	18
GO:0008033	tRNA processing	0.00141724	23
GO:0033617	mitochondrial respiratory chain complex IV assembly	0.00160082	8
GO:0071428	rRNA-containing ribonucleoprotein complex export from nucleus	0.00160082	8
GO:0072527	pyrimidine-containing compound metabolic process	0.00162817	14
GO:0010390	histone monoubiquitination	0.00162817	10
GO:0032435	negative regulation of proteasomal ubiquitin-dependent protein catabolic process	0.00162817	10
GO:0033260	nuclear DNA replication	0.00162817	10
GO:0072528	pyrimidine-containing compound biosynthetic process	0.00162817	10
GO:0043543	protein acylation	0.00163833	37
GO:1902653	secondary alcohol biosynthetic process	0.00164481	13
GO:2001022	positive regulation of response to DNA damage stimulus	0.00168529	19
GO:0007088	regulation of mitotic nuclear division	0.00175777	29
GO:0006979	response to oxidative stress	0.00179163	56
GO:0033157	regulation of intracellular protein transport	0.00180323	43
GO:0000096	sulfur amino acid metabolic process	0.00190041	11
GO:0043467	regulation of generation of precursor metabolites and energy	0.00192265	21
GO:0046132	pyrimidine ribonucleoside biosynthetic process	0.00192265	7
GO:0051131	chaperone-mediated protein complex assembly	0.00192265	7
GO:0071482	cellular response to light stimulus	0.00194384	20

GO:0006997	nucleus organization	0.00194384	24
GO:0006183	GTP biosynthetic process	0.00199382	6
GO:0009396	folic acid-containing compound biosynthetic process	0.00199382	6
GO:2001233	regulation of apoptotic signaling pathway	0.00202133	57
GO:0030433	ubiquitin-dependent ERAD pathway	0.00202133	16
GO:1901991	negative regulation of mitotic cell cycle phase transition	0.00216663	26
GO:0001510	RNA methylation	0.00222301	15
GO:0035384	thioester biosynthetic process	0.00230549	8
GO:0071616	acyl-CoA biosynthetic process	0.00230549	8
GO:0042398	cellular modified amino acid biosynthetic process	0.00243077	11
GO:2001243	negative regulation of intrinsic apoptotic signaling pathway	0.0025684	20
GO:0044403	symbiont process	0.00258498	51
GO:0009063	cellular amino acid catabolic process	0.00258498	19
GO:0046939	nucleotide phosphorylation	0.00258498	19
GO:0008608	attachment of spindle microtubules to kinetochore	0.00285497	10
GO:0043628	ncRNA 3'-end processing	0.00285497	10
GO:0051053	negative regulation of DNA metabolic process	0.00289951	25
GO:0006282	regulation of DNA repair	0.00292803	20
GO:0031330	negative regulation of cellular catabolic process	0.00297122	36
GO:0009220	pyrimidine ribonucleotide biosynthetic process	0.0029718	7
GO:0042559	pteridine-containing compound biosynthetic process	0.0029718	7
GO:0045898	regulation of RNA polymerase II transcriptional preinitiation complex assembly	0.0029718	7
GO:0046931	pore complex assembly	0.0029718	7
GO:0010332	response to gamma radiation	0.00303926	13
GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	0.00306918	11
GO:0016032	viral process	0.00307974	42
GO:0051345	positive regulation of hydrolase activity	0.00332936	67
GO:0000963	mitochondrial RNA processing	0.00340757	6
GO:0006086	acetyl-CoA biosynthetic process from pyruvate	0.00340757	6
GO:0009208	pyrimidine ribonucleoside triphosphate metabolic process	0.00340757	6
GO:0033240	positive regulation of cellular amine metabolic process	0.00340757	6
GO:0034982	mitochondrial protein processing	0.00340757	6
GO:0097329	response to antimetabolite	0.00340757	6
GO:1902570	protein localization to nucleolus	0.00340757	6
GO:1905214	regulation of RNA binding	0.00340757	6
GO:0042176	regulation of protein catabolic process	0.00346718	51
GO:0006084	acetyl-CoA metabolic process	0.00362745	10
GO:0045070	positive regulation of viral genome replication	0.00362745	10

GO:0034605	cellular response to heat	0.00365142	15
GO:0045454	cell redox homeostasis	0.00365142	15
GO:1901607	alpha-amino acid biosynthetic process	0.00365142	15
GO:0071214	cellular response to abiotic stimulus	0.00375287	42
GO:0104004	cellular response to environmental stimulus	0.00375287	42
GO:0006695	cholesterol biosynthetic process	0.00377544	12
GO:0036503	ERAD pathway	0.00377544	19
GO:0009069	serine family amino acid metabolic process	0.00377544	11
GO:0032781	positive regulation of ATPase activity	0.00377544	11
GO:0010389	regulation of G2/M transition of mitotic cell cycle	0.00384401	17
GO:0043462	regulation of ATPase activity	0.00401012	14
GO:0035518	histone H2A monoubiquitination	0.00436777	7
GO:0046134	pyrimidine nucleoside biosynthetic process	0.00436777	7
GO:0030071	regulation of mitotic metaphase/anaphase transition	0.0043685	13
GO:0046653	tetrahydrofolate metabolic process	0.00448423	8
GO:0016054	organic acid catabolic process	0.00450495	34
GO:0046395	carboxylic acid catabolic process	0.00450495	34
GO:1901661	quinone metabolic process	0.00460082	10
GO:0000027	ribosomal large subunit assembly	0.00473461	11
GO:1901988	negative regulation of cell cycle phase transition	0.00487564	27
GO:2001242	regulation of intrinsic apoptotic signaling pathway	0.0048809	28
GO:1902749	regulation of cell cycle G2/M phase transition	0.00489346	19
GO:1904951	positive regulation of establishment of protein localization	0.00499738	64
GO:0006513	protein monoubiquitination	0.00499738	15
GO:0006165	nucleoside diphosphate phosphorylation	0.00501168	18
GO:0051304	chromosome separation	0.00501168	18
GO:1902099	regulation of metaphase/anaphase transition of cell cycle	0.00520567	13
GO:0006473	protein acetylation	0.00522377	30
GO:0031396	regulation of protein ubiquitination	0.00522377	30
GO:0006760	folic acid-containing compound metabolic process	0.00538667	9
GO:0030497	fatty acid elongation	0.00541647	6
GO:0051985	negative regulation of chromosome segregation	0.00557884	12
GO:0051783	regulation of nuclear division	0.00559982	31
GO:0034243	regulation of transcription elongation from RNA polymerase II promoter	0.00579731	10
GO:0008652	cellular amino acid biosynthetic process	0.00580519	15
GO:0016052	carbohydrate catabolic process	0.0058618	22
GO:1904589	regulation of protein import	0.0058618	16
GO:1902600	proton transmembrane transport	0.00653555	18

GO:0071479	cellular response to ionizing radiation	0.00661357	14
GO:0006368	transcription elongation from RNA polymerase II promoter	0.00677959	12
GO:0006066	alcohol metabolic process	0.00702974	40
GO:0009266	response to temperature stimulus	0.00702974	27
GO:0019674	NAD metabolic process	0.00716937	11
GO:0098754	detoxification	0.00716937	11
GO:0042558	pteridine-containing compound metabolic process	0.00729062	10
GO:0051973	positive regulation of telomerase activity	0.00729062	10
GO:0051291	protein heterooligomerization	0.00768929	27
GO:0046165	alcohol biosynthetic process	0.00789697	21
GO:0006352	DNA-templated transcription, initiation	0.00798946	19
GO:0070584	mitochondrion morphogenesis	0.00813122	8
GO:0010501	RNA secondary structure unwinding	0.00813122	12
GO:0009148	pyrimidine nucleoside triphosphate biosynthetic process	0.00834994	6
GO:0009215	purine deoxyribonucleoside triphosphate metabolic process	0.00834994	6
GO:0050667	homocysteine metabolic process	0.00834994	6
GO:0046605	regulation of centrosome cycle	0.0086888	13
GO:0016073	snRNA metabolic process	0.0086888	11
GO:0016925	protein sumoylation	0.0086888	11
GO:0031952	regulation of protein autophosphorylation	0.0086888	11
GO:0009081	branched-chain amino acid metabolic process	0.0086888	7
GO:0016226	iron-sulfur cluster assembly	0.0086888	7
GO:0031163	metallo-sulfur cluster assembly	0.0086888	7
GO:0090201	negative regulation of release of cytochrome c from mitochondria	0.0086888	7
GO:0007568	aging	0.00917672	35
GO:0045787	positive regulation of cell cycle	0.00968988	48
GO:1903322	positive regulation of protein modification by small protein conjugation or removal	0.00986356	22
GO:0000055	ribosomal large subunit export from nucleus	0.00986356	5
GO:0006241	CTP biosynthetic process	0.00986356	5
GO:0046036	CTP metabolic process	0.00986356	5
GO:0046051	UTP metabolic process	0.00986356	5
GO:0075522	IRES-dependent viral translational initiation	0.00986356	5
GO:2000059	negative regulation of ubiquitin-dependent protein catabolic process	0.01047543	11
GO:0006323	DNA packaging	0.01055027	28
GO:0042770	signal transduction in response to DNA damage	0.01114578	17
GO:0019080	viral gene expression	0.01201231	13
GO:0009083	branched-chain amino acid catabolic process	0.01226526	6
GO:0009151	purine deoxyribonucleotide metabolic process	0.01226526	6

GO:0046112	nucleobase biosynthetic process	0.01226526	6
GO:0071025	RNA surveillance	0.01226526	6
GO:0033046	negative regulation of sister chromatid segregation	0.01266669	11
GO:0120031	plasma membrane bounded cell projection assembly	0.01321221	63
GO:0001701	in utero embryonic development	0.01345187	59
GO:0045739	positive regulation of DNA repair	0.01358807	12
GO:0008053	mitochondrial fusion	0.01373018	8
GO:0010165	response to X-ray	0.01373018	8
GO:0043457	regulation of cellular respiration	0.01373018	8
GO:1901799	negative regulation of proteasomal protein catabolic process	0.01523879	11
GO:0045839	negative regulation of mitotic nuclear division	0.01602551	12
GO:0000491	small nucleolar ribonucleoprotein complex assembly	0.01602551	5
GO:0006105	succinate metabolic process	0.01602551	5
GO:0009209	pyrimidine ribonucleoside triphosphate biosynthetic process	0.01602551	5
GO:0009265	2'-deoxyribonucleotide biosynthetic process	0.01602551	5
GO:0046385	deoxyribose phosphate biosynthetic process	0.01602551	5
GO:0046607	positive regulation of centrosome cycle	0.01602551	5
GO:0070841	inclusion body assembly	0.01607846	7
GO:1901998	toxin transport	0.01652394	10
GO:0009416	response to light stimulus	0.01697763	40
GO:0000966	RNA 5'-end processing	0.01747125	6
GO:2000104	negative regulation of DNA-dependent DNA replication	0.01747125	6
GO:0030488	tRNA methylation	0.01747125	8
GO:0070979	protein K11-linked ubiquitination	0.01747125	8
GO:0090200	positive regulation of release of cytochrome c from mitochondria	0.01747125	8
GO:0072331	signal transduction by p53 class mediator	0.01752655	23
GO:0042866	pyruvate biosynthetic process	0.01762849	15
GO:0006400	tRNA modification	0.0182904	14
GO:0045931	positive regulation of mitotic cell cycle	0.01850418	25
GO:0044773	mitotic DNA damage checkpoint	0.01855703	13
GO:0051193	regulation of cofactor metabolic process	0.01855703	13
GO:0035304	regulation of protein dephosphorylation	0.01893158	16
GO:0006470	protein dephosphorylation	0.01895013	34
GO:0010824	regulation of centrosome duplication	0.01974702	10
GO:0006635	fatty acid beta-oxidation	0.0209245	14
GO:0060261	positive regulation of transcription initiation from RNA polymerase II promoter	0.02105471	7
GO:0016574	histone ubiquitination	0.02105471	11
GO:0051972	regulation of telomerase activity	0.02105471	11

GO:0016125	sterol metabolic process	0.02110464	22
GO:0045005	DNA-dependent DNA replication maintenance of fidelity	0.02121789	9
GO:0007062	sister chromatid cohesion	0.02142488	12
GO:1903902	positive regulation of viral life cycle	0.02142488	12
GO:1990748	cellular detoxification	0.02184403	8
GO:1903747	regulation of establishment of protein localization to mitochondrion	0.02215625	17
GO:0006334	nucleosome assembly	0.02322194	19
GO:0008654	phospholipid biosynthetic process	0.02351553	25
GO:0090342	regulation of cell aging	0.02351553	10
GO:0046599	regulation of centriole replication	0.02377253	6
GO:1902176	negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	0.02377253	6
GO:0031125	rRNA 3'-end processing	0.02390918	5
GO:0031145	anaphase-promoting complex-dependent catabolic process	0.02390918	5
GO:0042440	pigment metabolic process	0.02434214	13
GO:0000380	alternative mRNA splicing, via spliceosome	0.02474582	12
GO:1902652	secondary alcohol metabolic process	0.02535239	21
GO:0007094	mitotic spindle assembly checkpoint	0.02551172	9
GO:0008156	negative regulation of DNA replication	0.02551172	9
GO:0046470	phosphatidylcholine metabolic process	0.02551172	9
GO:0071173	spindle assembly checkpoint	0.02551172	9
GO:0006475	internal protein amino acid acetylation	0.02592296	24
GO:0043524	negative regulation of neuron apoptotic process	0.02634151	26
GO:0006096	glycolytic process	0.02643096	14
GO:0034614	cellular response to reactive oxygen species	0.02643096	23
GO:0006298	mismatch repair	0.02643096	7
GO:0031954	positive regulation of protein autophosphorylation	0.02643096	7
GO:0043094	cellular metabolic compound salvage	0.02643096	7
GO:0046688	response to copper ion	0.02643096	7
GO:0098869	cellular oxidant detoxification	0.02643096	7
GO:0140112	extracellular vesicle biogenesis	0.02643096	7
GO:0034724	DNA replication-independent nucleosome organization	0.02654385	8
GO:0035308	negative regulation of protein dephosphorylation	0.02654385	8
GO:0043487	regulation of RNA stability	0.0268005	17
GO:0031577	spindle checkpoint	0.02712511	10
GO:0033048	negative regulation of mitotic sister chromatid segregation	0.02712511	10
GO:0042771	intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	0.02712511	10
GO:0006637	acyl-CoA metabolic process	0.02769473	15
GO:0035383	thioester metabolic process	0.02769473	15

GO:0090398	cellular senescence	0.02780767	12
GO:0046148	pigment biosynthetic process	0.02785276	11
GO:0006757	ATP generation from ADP	0.02941016	14
GO:0051881	regulation of mitochondrial membrane potential	0.02941016	14
GO:2001234	negative regulation of apoptotic signaling pathway	0.02995791	32
GO:0000302	response to reactive oxygen species	0.03042408	29
GO:0048524	positive regulation of viral process	0.03104067	15
GO:1904424	regulation of GTP binding	0.03104067	6
GO:0046825	regulation of protein export from nucleus	0.03193804	10
GO:0070534	protein K63-linked ubiquitination	0.03193804	10
GO:1900408	negative regulation of cellular response to oxidative stress	0.03234342	11
GO:0007099	centriole replication	0.03234342	8
GO:2000144	positive regulation of DNA-templated transcription, initiation	0.03234342	8
GO:0051402	neuron apoptotic process	0.03234342	38
GO:0008203	cholesterol metabolic process	0.03238551	20
GO:0032434	regulation of proteasomal ubiquitin-dependent protein catabolic process	0.03238551	20
GO:0050792	regulation of viral process	0.03288824	27
GO:0006376	mRNA splice site selection	0.03288824	7
GO:0018195	peptidyl-arginine modification	0.03288824	7
GO:0033522	histone H2A ubiquitination	0.03288824	7
GO:0010918	positive regulation of mitochondrial membrane potential	0.03293072	5
GO:0042761	very long-chain fatty acid biosynthetic process	0.03293072	5
GO:0046033	AMP metabolic process	0.03293072	5
GO:0071027	nuclear RNA surveillance	0.03293072	5
GO:0071028	nuclear mRNA surveillance	0.03293072	5
GO:0090503	RNA phosphodiester bond hydrolysis, exonucleolytic	0.03293072	5
GO:0099116	tRNA 5'-end processing	0.03293072	5
GO:1903362	regulation of cellular protein catabolic process	0.03316087	32
GO:0018394	peptidyl-lysine acetylation	0.03399285	24
GO:0044774	mitotic DNA integrity checkpoint	0.03423299	13
GO:0071174	mitotic spindle checkpoint	0.03514788	9
GO:2000142	regulation of DNA-templated transcription, initiation	0.03514788	9
GO:0043523	regulation of neuron apoptotic process	0.035669	35
GO:0006354	DNA-templated transcription, elongation	0.035669	12
GO:0034728	nucleosome organization	0.0361339	22
GO:0043903	regulation of symbiosis, encompassing mutualism through parasitism	0.03722933	31
GO:1901215	negative regulation of neuron death	0.03749529	32
GO:0048872	homeostasis of number of cells	0.03844397	41
GO:0006335	DNA replication-dependent nucleosome assembly	0.03844397	8

GO:0034723	DNA replication-dependent nucleosome organization	0.03844397	8
GO:0098534	centriole assembly	0.03844397	8
GO:0051298	centrosome duplication	0.03844397	13
GO:1903578	regulation of ATP metabolic process	0.03844397	13
GO:0051383	kinetochore organization	0.0395138	6
GO:1905523	positive regulation of macrophage migration	0.0395138	6
GO:1901214	regulation of neuron death	0.04008021	45
GO:0070206	protein trimerization	0.04040453	12
GO:0045841	negative regulation of mitotic metaphase/anaphase transition	0.0414331	9
GO:0043488	regulation of mRNA stability	0.04180351	15
GO:0042177	negative regulation of protein catabolic process	0.041804	19
GO:0016573	histone acetylation	0.04196452	22
GO:1903900	regulation of viral life cycle	0.04196452	22
GO:0032784	regulation of DNA-templated transcription, elongation	0.042068	10
GO:0033013	tetrapyrrole metabolic process	0.042068	10
GO:0061136	regulation of proteasomal protein catabolic process	0.04328048	25
GO:0044419	interspecies interaction between organisms	0.04385265	52
GO:0032886	regulation of microtubule-based process	0.04421517	31
GO:0000478	endonucleolytic cleavage involved in rRNA processing	0.04485874	5
GO:0006107	oxaloacetate metabolic process	0.04485874	5
GO:0034471	ncRNA 5'-end processing	0.04485874	5
GO:0042921	glucocorticoid receptor signaling pathway	0.04485874	5
GO:0051382	kinetochore assembly	0.04485874	5
GO:1904923	regulation of autophagy of mitochondrion in response to mitochondrial depolarization	0.04485874	5
GO:1903828	negative regulation of cellular protein localization	0.04588153	18
GO:0072525	pyridine-containing compound biosynthetic process	0.04633336	16
GO:0034976	response to endoplasmic reticulum stress	0.0466199	31
GO:1902883	negative regulation of response to oxidative stress	0.04733995	11
GO:0042306	regulation of protein import into nucleus	0.04796599	13
GO:0031572	G2 DNA damage checkpoint	0.04796599	9
GO:1902100	negative regulation of metaphase/anaphase transition of cell cycle	0.04796599	9
GO:2000816	negative regulation of mitotic sister chromatid separation	0.04796599	9
GO:0009066	aspartate family amino acid metabolic process	0.04822175	10
GO:1903050	regulation of proteolysis involved in cellular protein catabolic process	0.04823294	28
GO:0016180	snRNA processing	0.04889511	7
GO:0033233	regulation of protein sumoylation	0.04889511	7
GO:0071480	cellular response to gamma radiation	0.04889511	7
GO:1903955	positive regulation of protein targeting to mitochondrion	0.04936899	14

GO:0019430	removal of superoxide radicals	0.04950199	6
GO:0031440	regulation of mRNA 3'-end processing	0.04950199	6
GO:1990182	exosomal secretion	0.04950199	6
GO:2001235	positive regulation of apoptotic signaling pathway	0.04964703	26
GO:0031398	positive regulation of protein ubiquitination	0.04992443	17
GO:0019359	nicotinamide nucleotide biosynthetic process	0.04992443	15

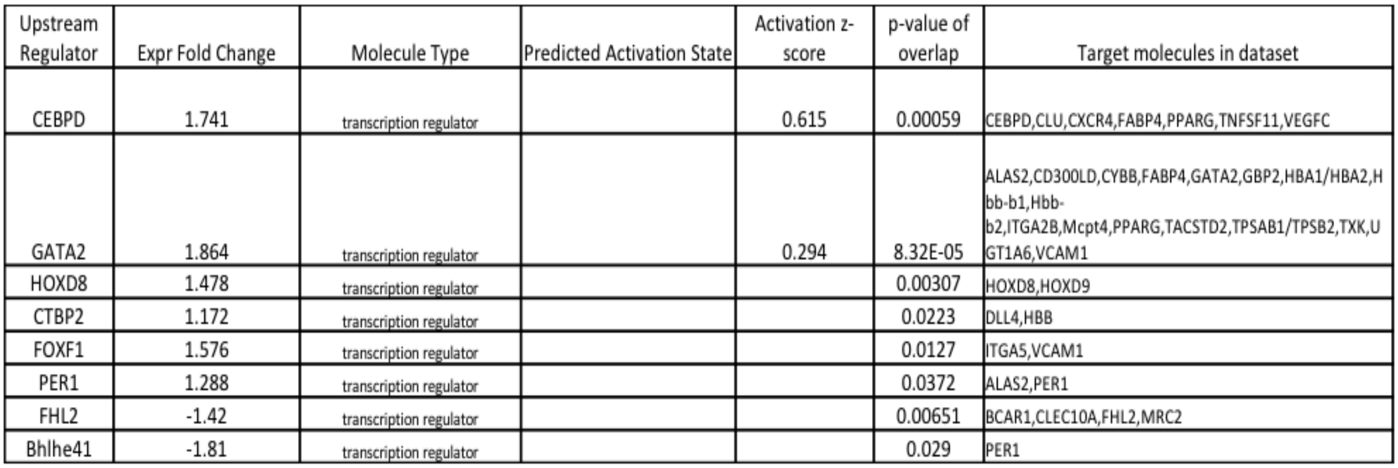
Supplemental Table 4F. PAD4KO vs WT spleen Upregulated Pathways

ID	Description	p.adjust	Count
GO:0042110	T cell activation	3.28E-05	50
GO:0050852	T cell receptor signaling pathway	0.00064206	19
GO:0030217	T cell differentiation	0.00104412	30
GO:0030098	lymphocyte differentiation	0.00171139	38
GO:0046631	alpha-beta T cell activation	0.02563088	18
GO:0035094	response to nicotine	0.03332624	8

Supplemental Table 5: Transcription factor analysis showing differential regulation in lymph nodes of PAD2 KO compared to WT

Upstream Regulator	Expr Fold Change	Molecule Type	Predicted Activation State	Activation z-score	p-value of overlap	Target molecules in dataset
IRF7	-1.543	transcription regulator	Inhibited	-5.583	2.32E-13	CCL5,DNAJA1,FCGR1A,GBP3,GBP4,GBP5,Ifi47,IFIH1,IFIT1B,IFIT2,IFIT3,Igtp,IRF1,IRF7,IRF8,IRF9,IRGM,Irgm1,JAK2,Ly6a (includes others),Ms4a4b (includes others),NAMPT,NT5C3A,OAS1,Oasl2,PARP14,PHF11,PSME1,RTP4,S100A8,STAT1,TDRD7,TNFAIP8,TREX1,TRIM21,Trim30a/Trim30d,USP18
STAT1	-1.907	transcription regulator	Inhibited	-5.237	4.97E-15	APOC2,BATF2,CASP3,CASP8,CCL3L3,CCL5,Ccl8,CD86,CDKN1A,CEBPD,CH25H,Chil3/Chil4,CSF3R,Cxcl9,EIF2AK2,FCGR1A,FURIN,GBP2,GBP3,GBP4,GBP5,GBP6,HAVCR2,HLA-E,ICAM1,IFI30,Ifi47,IFIH1,IFIT1B,IFIT2,IFIT3,IGF1R,Igtp,IL1R1,IRF1,IRF7,IRF8,IRF9,Irgm1,JAK2,LCN2,LY6E,MMP9,OAS1,PSME1,PTN,RTP4,SAMHD1,Serpina3g (includes others),SLAMF8,SLFN12L,SLFN13,SMAGP,SOCS3,STAT1,Tgtp1/Tgtp2,TRAFD1,TRIM21,USP18
IRF1	-1.505	transcription regulator	Inhibited	-2.92	0.00000388	ADAM8,CASP3,CASP8,CCL5,CDKN1A,Cxcl9,CYBB,EIF2AK2,EIF4A3,FPR2,GBP2,Ifi47,IFIH1,IFIT2,IFIT3,IL18,IRF1,IRF7,IRF9,JAK2,MMP9,OAS1,PSME1,STAT1,TRIM21
HSF2	-1.19	transcription regulator	Inhibited	-2.433	0.00000355	CCT2,CCT3,CCT4,CCT7,CCT8,CLU,HSPA1A/HSPA1B,Hspa1b,HSPB1,HSPH1,STAG2
IRF9	-1.421	transcription regulator		-0.664	0.000124	Cxcl9,IFIT2,IFIT3,IRF1,IRF7,IRF8,SOCS3,STAT1,Tgtp1/Tgtp2
MTPN	-1.361	transcription regulator		-0.376	0.0131	ANXA1,CASP3,CASP8,ENG,MTPN,S100A6,S100A8,SERPINE1,TAGLN,TNFRSF1A
CDKN2A	-1.576	transcription regulator		0.015	0.00000064	CASP3,CCL3L3,CCL5,Ccl6,Ccl8,Ccl9,CCNG1,CDCA4,CDKN1A,CDKN2A,CDKN2B,CDKN2D,CEBPB,CEBPD,Cxcl9,CXCR2,DCTN4,DUSP1,FAM111A,GADD45G,GAS7,ITGB3,JAK2,LGALS3,LIN9,MS4A1,NR3C1,PBX3,POLD3,POLK,RBBP7,S100A6,SERPINE1,TNFRSF1A,TNFRSF1B,VEGFA,VIM,XCR1
IRF8	-1.662	transcription regulator		0.105	0.00000456	ADGRE1,BANK1,CASP3,CCL5,Ccl9,CD37,CD86,CDKN1A,CSF3R,Cxcl9,CYBB,ICAM1,IFIT1B,IFIT2,IFIT3,IL18,IRF8,MMP9,MS4A1,OAS1,STAT1,TRIM21
EPAS1	1.262	transcription regulator		0.484	0.0155	ALDOC,CDKN1A,CEBPB,CXCR4,DMXL1,HIST1H1C,INHBB,ITGB3,ITPR1,NAMPT,PDPK1,PFKFB3,PIK3CA,SERPINE1,SF3A3,SLC2A1,SLC2A3,TRIM21,VEGFA
JUND	1.204	transcription regulator		0.647	0.000787	BCL3,CCL5,CDKN2A,CLU,CSTA,CYBB,ITGB4,JUND,MMP9,PLAUR,VEGFA
CREB1	-1.358	transcription regulator		1.042	0.00157	ATF5,CDK14,CDKN1A,CEBPB,CEBPD,CH25H,Chil3/Chil4,CREB1,CXCR4,DUSP1,GADD45A,GADD45G,GDA,GPR83,H2-T22,HLA-A,HMGCR,IER3,IL2RA,IRF7,JPT1,LCN2,MAT2A,MCAM,MCTP1,MYH10,NARF,OPA3,PCK1,PDE3B,PER2,PGM2L1,PIM3,PSEN1,SEMA7A,SGK1,Sik1,SLC2A3,SMS,SRSF10,SRXN1,TOM1,TP53INP2,Tpm4,TRAFD1,UPP1,VEGFA,VIM
VHL	-1.535	transcription regulator		1.163	0.0125	CDKN1A,CLTC,CXCR4,EPAS1,HNRNPA2B1,IER3,MAVS,PFKFB3,RAP1B,SLC16A3,SLC2A1,TAGLN,VEGFA,VIM
CEBPB	1.791	transcription regulator		1.198	0.000000611	ACTA2,AKR1B10,ALOX5AP,APCDD1,ATM,CCL3L3,CCL5,CDKN1A,CDKN2B,CEBPB,CEBPD,CSF3R,CTSC,CXCR4,DHX9,ELANE,GADD45A,HDC,HLA-A,HP,HSP90AA1,HSPA8,HSPD1,ICAM1,IER3,IL1RN,IRF9,LCN2,LYN,PCK1,PLAUR,PRTN3,PTGES,RBBP7,Saa3,SCARB1,SERPINE1,SGK1,SLC38A2,SOCS3,SQOR,TNFRSF1A,TRIB3,UBA2,UPP1,USP33,VIM,ZNF638
BCL3	1.392	transcription regulator		1.253	0.00693	CAMP,CCL5,CD86,Cxcl9,ICAM1,IRF1,PLAUR
CEBPD	2.029	transcription regulator		1.831	0.0171	ALOX5AP,CCL3L3,CEBPB,CEBPD,CLU,CSF3R,CXCR4,HP,MMP8,PRTN3,Saa3
CCAR1	-1.116	transcription regulator			0.0381	CEBPD,EPAS1
TFEC	1.435	transcription regulator			0.000266	COL6A3,CSF3R,F13A1,GBP7,IGF1R,S100A9
TLE1	-1.25	transcription regulator			0.0303	CDKN2A,DUSP1,ROCK2
PAWR	1.187	transcription regulator			0.0143	CCAR1,IL2RA,MAPK1
SIN3A	-1.261	transcription regulator			0.05	CASP3,CCNG2,KLF10,MMP9,S100A9,SERPINE1,TMEM71

Supplemental Table 6: Transcription factor analysis showing differential regulation in lymph nodes of PAD4 KO compared to WT



Upstream Regulator	Expr Fold Change	Molecule Type	Predicted Activation State	Activation z-score	p-value of overlap	Target molecules in dataset
CEBPD	1.741	transcription regulator		0.615	0.00059	CEBPD,CLU,CXCR4,FABP4,PPARG,TNFSF11,VEGFC
GATA2	1.864	transcription regulator		0.294	8.32E-05	ALAS2,CD300LD,CYBB,FABP4,GATA2,GBP2,HBA1/HBA2,Hbb-b1,Hbb-b2,ITGA2B,Mcpt4,PPARG,TACSTD2,TPSAB1/TPSB2,TXK,UGT1A6,VCAM1
HOXD8	1.478	transcription regulator			0.00307	HOXD8,HOXD9
CTBP2	1.172	transcription regulator			0.0223	DLL4,HBB
FOXF1	1.576	transcription regulator			0.0127	ITGA5,VCAM1
PER1	1.288	transcription regulator			0.0372	ALAS2,PER1
FHL2	-1.42	transcription regulator			0.00651	BCAR1,CLEC10A,FHL2,MRC2
Bhlhe41	-1.81	transcription regulator			0.029	PER1

Supplemental Table 7. Transcription factor analysis showing differential regulation in spleens of PAD2 KO compared to WT

Upstream Regulator	Expr Fold Change	Molecule Type	Predicted Activation State	Activation z-score	p-value of overlap	Target molecules in dataset
MYCN	1.981	transcription regulator	Inhibited	-5.989	1.76E-12	ABCE1,ABCF2,APEX1,CCNH,CDK7,CDKN1B,COL8A1,EEF1A1,EEF1G,EEF2,EIF3C,EIF4A1,EIF4G2,EIF5A,EZH1,GAPDH,HDAC2,HMGA1,HSP90AB1,HSPD1,JARID2,KLK3,LDHA,MAGT1,MYCN,NACA,NBN,NCL,NME1,NPM1,PDIA4,PHB,PHGDH,POLR2L,PSMA7,PSMB6,PSMB7,RBBP4,RBBP7,RFC3,RPL10,RPL13,RPL18,RPL24,RPL26,RPL27,RPL28,RPL3,RPL31,RPL35,RPL4,RPL41,RPL6,RPL8,RPLP0,RPS17,RPS19,RPS2,RPS26,RPS6,RPS8,TPI1,TUBA1B,TUBB,TUFM,UBE2V2,WDR5,ZFAND5
MYCBP	-1.262	transcription regulator	Inhibited	-2	0.00254	CDK4,EIF2A,LDHA,NCL
MAFA	-2.106	transcription regulator		-1.96	0.0174	DDIT3,GSTA5,Ins1,TNF
SIRT2	-1.125	transcription regulator		-1.633	0.00785	CDKN1B,IDI1,MVD,MVK,SC5D,SQLE
COPS5	-1.229	transcription regulator		-1.408	0.0328	AIMP1,CDKN1B,GPS1,IFNAR1,RARS
DNAJB6	1.05	transcription regulator		-0.555	0.00425	CDKN1B,DKK1,KISS1,NPM1,SNAI2,TNF
CREM	-1.182	transcription regulator		-0.305	0.00392	ADRB2,BHLHE40,CAMK4,CD8A,CD8B,CIART,COL8A1,CREM,CYP51A1,DUSP1,GPR19,HMGCS1,HSPA4,IDI1,Ins1,IRAK1,MVK,NR4A1,PACRGL,PDXK,PER1,RYR2,SERTAD1,SIAH2,Sik1,TNF
KLF3	1.22	transcription regulator		0.295	0.0125	ABHD14B,BCL2L2,CCT3,CDKN2D,CIRBP,DRG1,EIF2B1,EIF5A,ELOF1,EPRS,GSTP1,HBP1,HM13,HNRNPF,HYPK,JAK2,KBTBD2,KCNK6,MAK16,MIF,MRPL3,MRPL34,MSTO1,MTCH2,NSUN2,NUDT8,POP5,PSMB2,PSMC5,PSMD7,RNF167,Rpl29 (includes others),RUVBL1,SCCPDH,SDC1,SEC24D,SGK1,SSSCA1,TATDN2,THYN1,TP53I13,TUBA1A,VEGFB,VPS50,YTHDF1,ZCCHC17
E2F6	-1.192	transcription regulator		1.406	0.00645	CDC25A,DHFR,GINS2,MCM5,PCLAF,POLA2,RBBP4,RBBP8,RPA2,RYR2,STAG3,UXT,WDR36
RRP1B	-1.235	transcription regulator			0.00106	CASP3,CDKN2D,DHFR,EIF3H,HAT1,HSP90AA1,HSP90AB1,MCM5,RPA1,RPA2,RPL13,RPL14,RPL27,RPL6,Rplp1 (includes others),RPS19,RPS26,RPS8,RRP1B,TUBG1,VEGFC
GTF2F2	-1.255	transcription regulator			0.027	CYC1,TBP
SERTAD1	1.147	transcription regulator			0.027	CDK4,SET
GTF2H1	-1.221	transcription regulator			0.000946	CCNH,DHFR,TBP

Supplemental Table 8. Transcription factor analysis showing differential regulation in spleens of PAD4 KO compared to WT

Upstream Regulator	Expr Fold Change	Molecule Type	Predicted Activation State	Activation z-score	p-value of overlap	Target molecules in dataset
NFE2L2	-1.173	transcription regulator	Inhibited	-6.222	1.06E-10	ABCC4,Acp5,ACSL5,ARHGEF3,ATP6V0D2,B4GALNT1,BCL2,Calm1 (includes others),CCT3,CCT7,CD8B,CDC34,CDKN1A,Ces1g,CHORDC1,CLPP,COPS5,COQ7,CUL1,Cyp2a12/Cyp2a22,CYP4A22,DCSTAMP,DYNLL1,EIF2S1,EIF3C,EIF3G,EIF4G2,ESD,ETV6,FABP4,FGF13,FKBP5,GAS2,GSPT1,GSS,GSTO1,GSTP1,HACD3,HAX1,HPRT1,HSP90AA1,HSP90AB1,HSPA9,IDE,KCNMB4,KIFC2,KLK3,LMNA,M6PR,ME1,MOGS,MORF4L2,MRPS18B,MSMO1,Mt1,NARS,NAT8B,NCKAP1,NFE2L2,NRSN1,OAT,PCBP1,PPARGC1A,PREP,PSAT1,PSMA1,PSMA4,PSMA5,PSMA6,PSMA7,PSMB2,PSMB3,PSMB4,PSMB5,PSMB6,PSMC1,PSMC3,PSMD1,PSMD11,PSMD12,PSMD13,PSMD14,PSMD3,PSMD5,PSMD7,RAN,RARS,RBBP7,RGS11,RUVBL1,SCARB1,SERINC3,SHC1,SNAI2,Snrpa (includes others),SOD1,SOD2,SQSTM1,STIP1,TKT,TNF,TPI1,TXNRD1,UBE2K,UGT2B28,USP14,VCP
PPARGC1A	1.722	transcription regulator	Inhibited	-4.278	0.00195	ACACA,ACAT1,ATP5F1A,ATP5F1B,ATP5PO,BCAT2,CDKN1A,COX5A,Cox5b,COX7B,CPT1A,CS,CYCS,DLAT,FABP4,FBXO32,Gk,GOT2,IDH3A,KYAT3,LDHA,LDLR,MCM3,MCM4,MCM5,MCM6,MDH2,ME1,MFN2,MSMO1,NDUFS1,NDUFV2,NEFH,NRF1,NSDHL,PACSIN2,PDK2,PPARGC1A,PRDX3,PRKAA2,SCARB1,SCO2,SDHA,SLC25A20,SOD1,SOD2,STAC2,TNF,TXN2,TYR,UQCRFS1
CCNE1	-1.834	transcription regulator	Inhibited	-3.13	0.000373	CCNA2,CCNE1,CDC45,CDC6,CDK2,CDKN1A,MCM2,MCM4,mir-142,PCNA,PCYT1A
E2F3	-1.356	transcription regulator	Inhibited	-2.483	0.000000165	CCNA2,CCND3,CCNE1,CDC25A,CDC45,CDC6,CDCA4,CDK2,CDKN1A,COL18A1,CSHL1,CTNND1,DHFR,E2F3,ECE1,EZH2,FAM46A,HIST1H4B,HIST3H2A,HMGB2,HSPD1,ID3,MAD2L1,MCM10,MCM2,MCM3,MCM4,MCM5,MCM6,MCM7,MYB,MYBL2,NUCKS1,ORC1,PCNA,PIN1,POLA1,POLA2,PPP1R13B,PPP1R8,PTGER3,Raet1d/Raet1e,RRM1,RRM2,TAF6L,TERT,TK1,TMPO,TNFAIP2,TOPBP1,UXT
NRF1	-1.151	transcription regulator	Inhibited	-2.414	0.0000184	ATP1B1,COX5A,Cox5b,COX6B1,COX7A2,COX7B,Cox7c,COX8A,CYCS,ESM1,IDE,KIF17,MOGS,Mt1,PPRC1,SDHA,SDHD,TFB1M,TOMM20,VDAC1
TFDP1	-1.394	transcription regulator	Inhibited	-2.213	0.0454	CASP3,CCND3,CCNE1,CDC6,CDKN1A,DHFR,MYB,MYBL2,RANBP1
KLF5	-1.788	transcription regulator	Inhibited	-2.179	0.209	CDKN1A,CDKN1B,CTNNB1,DUSP1,E2F3,GPSM1,ILK,KLF5,PCNA,WNT10A
MYCBP	-1.121	transcription regulator	Inhibited	-2	0.00913	CDK4,EIF2A,LDHA,NCL
MAX	-1.136	transcription regulator		-1.516	0.0000128	APEX1,CBX5,CDC25A,CDK4,CDKN1A,CDKN1B,CYCS,DHFR,DKC1,EZH1,EZH2,FADS2,FBXO32,HDAC2,HMGA1,ID2,JARID2,MTHFD1,NCL,NPM1,RBBP4,RBBP7,RBBP8,RCC1,SERINC3,TERT,WRN,YBX1
Tcf7	1.443	transcription regulator		-1.124	0.00635	BCL2,CD3E,GATA3,IL17A,IL7R,KIT,Klra7 (includes others),LEF1,TNF
COPS5	-1.314	transcription regulator		0.113	0.0108	CCNE1,CD247,CDKN1A,CDKN1B,GPS1,IFNAR1,RARS
RUVBL1	-1.375	transcription regulator		0.378	0.043	CYP4F3,EMC9,KDM4B,KIFC2,MCM3,MCM4,METTL23,NUCKS1,NUDCD2,PCNA
UXT	-1.209	transcription regulator	Activated	2.007	0.0264	CCNA2,CDC6,CHEK1,FKBP5,GTSE1,HUS1,KLK3,PSMD5,SORD
ID2	-1.216	transcription regulator	Activated	2.025	0.0022	BCL2,BCL3,CCNE1,CCNE2,CCR10,CCR7,CCR9,CDC6,CDK20,CDK4,CDKN1A,CSF1,CTNNB1,DUSP1,DUSP22,DUSP4,FLT3LG,G6PC3,HES5,HOMER2,IL7R,IRF6,MAF,MYB,NR4A1,PIK3IP1,PTPN22,PTPN3,RAP1GAP,RAPGEF4,SELL,SLAMF1,STAT4,Tcf7,TGFBR3,TRAF4,TUBA1A,ZBTB16
ID3	2.339	transcription regulator	Activated	2.324	0.00253	BCL2,BCL3,CCNE1,CCNE2,CCR10,CCR7,CCR9,CDC6,CDK20,CDKN1A,CDKN1B,CSF1,DUSP1,DUSP22,DUSP4,ELOVL6,FLT3LG,G6PC3,GNL3,HES5,HOMER2,ID3,IL7R,IRF6,MAF,MYB,NR4A1,PIK3IP1,PREP,PTPN22,PTPN3,RAP1GAP,RAPGEF4,SELL,SLAMF1,STAT4,TGFBR3,TRAF4,ZBTB16
LEF1	1.622	transcription regulator	Activated	2.395	0.538	BCL2,CASP3,CDKN1A,GATA3,IL7R,LCK,LEF1,MSX2,SGK1
HDAC1	-1.163	transcription regulator	Activated	2.593	0.000196	Acp5,AMPD3,APEX1,CCNA2,CCNE1,CCNE2,CD27,CDC25A,CDC6,CDK2,CDKN1A,CDKN1B,CENPX,CSHL1,DHFR,DUSP1,EGR1,FABP4,GABARAPL1,GSTP1,HBE1,HBG2,IL17A,KLK3,LAT,LIG1,MAD1L1,MCM10,MCM3,MCM5,MCM7,Meis1,Mt1,Mt2,MYBL2,NASP,NCL,NEFH,PCYT1A,POLD2,POLL,PPARGC1A,PRIM2,RAD54L,RBBP7,RECQL4,RRM2,SATB1,SGK1,SLC35D1,SMN1/SMN2,SNAI2,SQSTM1,TERT,THEMIS,TNF,TUBB3,UHRF1
HDAC2	-1.261	transcription regulator	Activated	2.889	0.00826	APEX1,CCNE2,CD27,CDK2,CDKN1A,CDKN1B,EGR1,FCER2,GABARAPL1,LAT,LIG1,MCM10,MCM3,MCM5,MCM7,Mt2,NASP,POLD2,POLL,PRIM2,RAD54L,RBBP7,SATB1,SLC35D1,SMN1/SMN2,SQSTM1,TERT,THEMIS,TNF
E2F6	-1.411	transcription regulator	Activated	3	2.42E-09	CBX5,CCNE1,CDC25A,CDC45,CDC6,DCTN4,DHFR,GINS2,GJA1,GMNN,LIG1,MCM2,MCM3,MCM5,POLA2,RAD51AP1,RBBP4,RBBP8,RFC4,RPA2,RRM2,SMC1A,SRSF1,USP47,UXT,VKORC1L1,WDR36,ZNF451
RRP1B	-1.295	transcription regulator			0.000136	CASP3,CCNA2,CCND3,CCNE1,CDC20,CDC6,CDKN1A,CHEK1,DHFR,EXO1,FANCB,FEN1,HAT1,HDAC11,HSP90AA1,HSP90AB1,MCM2,MCM3,MCM4,MCM5,MCM6,ORC1,PCNA,PDGFC,RPA1,RPA2,RRP1B,TOPBP1,TUBG1
CBX4	1.192	transcription regulator			0.00357	CCNE1,CDC25A,CDC6,DHFR,MCM3,ORC1,POLA1
GTF2H4	-1.269	transcription regulator			0.0215	CDK4,NCL,TERT
Bhlhe41	1.439	transcription regulator			0.0193	CENPX,PER1

Supplemental Table 9. Transcription factor analysis showing differential regulation in lymph nodes of PAD2 KO compared to PAD4 KO

Upstream Regulator	Expr Fold Change	Molecule Type	Predicted Activation State	Activation z-score	p-value of overlap	Target molecules in dataset
IRF7	1.336	transcription regulator	Activated	2.696	0.0165	CD69,DNAJA1,GBP3,GBP4,Ifi47,IFIT1,IL33,IRF7,IRF9,ISG20,Ly6a (includes others),NAMPT,NRAP,NT5C3A,OAS1,OASL,PARP14,PELI1,PSME1,PSME2,RSAD2,S100A8,XAF1
FOXL2	2.922	transcription regulator	Activated	2.442	0.0412	BMP2,CDKN2A,CH25H,FST,NR5A2,OSR2,PRTN3,RSPO3,SERPINB2,SMAD6
NKX2-5	11.815	transcription regulator		1.951	0.0481	ANKRD1,BCL2,GATA4,MYLK,NKX2-5,NR5A2,STIP1
ETV1	2.299	transcription regulator		1.387	0.0399	ACSL3,HPSE,ITGB3,PLAUR,VIM
NDN	1.812	transcription regulator		1.387	0.00625	CDKN1A,CDKN2A,DLK1,PPARG,SYP
LHX1	-2.731	transcription regulator		1.315	0.00618	CCAR1,DAB1,Fxyd2,GAD1,GGT1,Hsd3b4 (includes others),LRRC19,Ly6a (includes others),MEP1B,PCP4,PDPN,PKDCC,SLC16A12,SLC32A1,SOSTDC1,SOX17,TMEM229A
GATA4	2.338	transcription regulator		1.23	0.0482	ACTN2,ANKRD1,ASPRV1,BCL2,CORIN,DAB2,EMX2,EPHB1,FSHR,GATA4,INHBB,IRF6,LOR,LTBP2,NKX2-5,NR5A2,POSTN,PRDM1,RARB,TAGLN,VCAM1,VIM
FOSB	2.493	transcription regulator		0.881	0.000463	CCND1,CCR4,FOLR2,FOSB,HPGD,LOR,MMP2,MMP9,PPARG,SERPINB2
CREB1	1.327	transcription regulator		0.734	1.66E-08	AK4,ATF5,BCL2,BHLHE22,CAMK4,CAMKV,CAPN5,CCND1,Ccnjl,CDA,CDH8,CDKN1A,CH25H,CHGB,Chil3/Chil4,CLMP,COL24A1,CREB1,CREM,CSRP2,EDIL3,ERC2,FGF19,FOSB,FRMD6,GAD1,GADD45A,GADD45G,GDA,GFRA1,GPR12,GPR63,GRIA3,HPGD,HTR2A,IDI1,IL2RA,IRF7,ITGBL1,KCNIP2,KLF5,LAPTM4B,LCN2,LOR,MAT2A,MCAM,mir-132,MTSS1,NAB2,NARF,NECTIN3,NKAIN2,NOS1,NR4A2,OMG,OPA3,OTOF,PAM,PER1,PGM2L1,PLPPR1,PPARG,PTPRR,Retnla,RFX4,ROBO1,RRAS2,SCN3B,SGK1,SLC17A6,SLC2A3,SLC32A1,SLC8A2,SMAD6,SMS,SORCS3,STC1,TCEAL6,TNFSF11,TOM1,TP53INP2,Tpm4,UCP1,UPP1,VGF,VIM,Zfp948,ZFPM2
CDKN2A	2.087	transcription regulator		0.524	0.0163	A2M,BCL2,CASP3,CCL2,Ccl6,Ccl7,Ccl8,Ccl9,CCND1,CCR4,CDCA4,CDKN1A,CDKN2A,CDKN2D,CXCL14,CXCR2,FHL2,FST,GADD45G,GFRA2,HACD3,ITGB3,LGALS3,MMP2,PBX3,POLK,PPFIBP1,RAB27A,S100A6,SOX17,TNFRSF1B,TOB2,TP53INP1,TSG101,VIM,XCR1
CREM	1.276	transcription regulator		0.514	0.00962	BCL2,CAMK4,CAMP,CCND1,CD86,CH25H,CREM,FASLG,FRMD6,FSHR,GPD2,IDI1,KLF5,LOR,NAB2,NOS1,NR4A2,PER1,RARB,SMC4,Zfp948,ZNRF4
GATA6	1.603	transcription regulator		0.498	0.00053	ASPRV1,ATP6V0A1,CD5L,CDKN1A,Chil3/Chil4,CLEC10A,COL4A2,COX5A,DAB2,DCBLD2,DLK1,EMX2,Fcna,FKBP14,GATA4,GATA6,IRF6,LOR,LYVE1,MARCO,MYLK,NR5A2,PRDM1,PTGES,RARB,Saa3,SLPI,SOX17,SOX7,TAGLN
EOMES	2.117	transcription regulator		0.307	0.0207	ANXA1,BHLHE22,C3orf58,CDH8,EOMES,FASLG,FOXC1,Klra7 (includes others),LHX1,PDPN,PRDM1,ROBO2,SATB2,SOX17,TMEM2,WNT3
PRDM1	-1.568	transcription regulator		0.282	0.00647	ALPL,ARG2,ATP9A,CA9,CD86,CHI3L1,F5,FGR,GAD1,Gm14685 (includes others),GPAT3,GPR84,HIST2H2AA3/HIST2H2AA4,ID3,IL18RAP,KHDRBS3,KLRC1,LRRN1,NLRP12,NLRP3,PRDM1,PROX1,RGS18,RSAD2,S100A8,S100A9,SERPINB3,SMPDL3B,ST14,UHRF2,XBP1
IRF6	1.553	transcription regulator		-0.02	0.00743	CCL2,CD14,ENPP2,FPR2,LCN2,NLRP3,NR4A2,PLA2G2D,PTGES
HOXD8	1.522	transcription regulator		-0.022	0.000662	CDKN2A,HOXD10,HOXD8,PROX1
SOX17	-1.484	transcription regulator		-0.64	0.0487	CCND1,COL4A2,GATA4,GATA6,PROM1,SOX7
FHL2	-1.342	transcription regulator		-0.714	0.00936	CCND1,Chil3/Chil4,CLDN5,CLEC10A,FASLG,FHL2,IBSP,IL13,MPO,TAGLN
KLF5	-1.511	transcription regulator		-1.227	0.0397	CCND1,CDKN1A,KLF5,MMP9,PPARG,PTGES,S100A9,TAGLN,WFS1
MEOX2	1.585	transcription regulator		-1.281	0.00444	CCL2,CD69,CDKN1A,CDKN2D,ID3,ITGB3,LRP1,VCAM1,VEGFC
GATA2	1.558	transcription regulator	Inhibited	-2.957	2.64E-15	ALOX5,AQP9,ARPP21,Bex6,BPIFB1,CAMP,CCND1,Ccnjl,CCR3,CD177,CD69,CDKN1A,CEBPE,CELSR3,CHI3L1,CHST13,CLEC4E,CLEC4G,CMA1,Cma2/Mcpt9,CSTA,CTSG,Cym,Cyp2c40 (includes others),DLK1,Ear2 (includes others),ELANE,EPX,FCN1,FGD4,GATA2,GDA,GFRA1,Gm9733,GP5,GPR141,Grifin,HDC,IL13,ITGA2B,KHDRBS3,LCN2,LTB4R,LTF,Ly6a (includes others),MCEMP1,Mcpt4,Mcpt8,MGST1,MMP2,MPO,MRGPRX3,MS4A3,NFE2,Ngp,OLFM4,PDE9A,PPARG,PRSS3,Prss34,PRTN3,RAB44,RETNLB,Retnlg,RGS18,RXRG,S100A8,S100A9,SERPINB10,SERPINB2,SNTG2,Stfa1 (includes others),Stfa2/Stfa2l1,SYTL3,TAC3,TACSTD2,TGFBR3,TMEM40,TRAT1,TREM3,TREML1,UGT1A6,VCAM1,Wfdc21
CEBPE	-6.756	transcription regulator	Inhibited	-3.054	9.32E-12	ALOX5AP,BCL2,CAMP,Ccl7,Ccl9,CD14,CLEC10A,CSF3R,ELANE,EPX,F7,IL1RN,LCN2,LTF,LYZ,MMP2,MMP8,MMP9,Ngp,Orm1 (includes others),Retnla,Retnlg,SERPINB2
KLF10	1.345	transcription regulator			0.0496	BCL2,CCND1,CDKN1A,ITGAD

Supplemental Table 10. Transcription factor analysis showing differential regulation in spleens of PAD2 KO compared to PAD4 KO

Upstream Regulator	Expr Fold Change	Molecule Type	Predicted Activation State	Activation z-score	p-value of overlap	Target molecules in dataset
XBP1	1.6	transcription regulator	Activated	6.105	7.45E-24	ADAM10,APP,ARCN1,ARFGAP3,ATF6B,BCL2,BECN1,BHLHA15,COG6,COPE,COPZ1,DAD1,DNAJB11,DNAJC10,DNAJC3,EDEM1,EDEM2,EIF2AK3,ERLEC1,ERO1B,ERP44,FKBP11,FKBP2,GORASP2,HM13,HSP90B1,HSPA13,IRF4,LMAN1,LMAN2,MAFA,P3H1,PCYT1A,PDIA4,PDIA6,POU2AF1,PPIB,PRDM1,RAB3A,RABAC1,RCN3,RPN1,S1PR1,SDF2L1,SEC11C,SEC23B,SEC24D,SEC61A1,SEC61B,SERP1,SERPINA1,SPCS2,SPCS3,SRP9,SRPRA,SRPRB,SSR2,SSR3,SSR4,STARD5,STX5,SYVN1,TFDP1,TXNDC11,TXNDC5,USO1,WFS1,WNT10B,XBP1,YIPF5
MYCN	-2.036	transcription regulator	Activated	5.026	2.62E-11	ABCA6,ABCA7,ABCB7,ABCD4,ACTN4,ATXN2,CDKN1A,CDKN1B,COL18A1,COL8A1,DUSP2,E2F5,EEF1A1,EEF2,EIF4A1,ITGB1,MXI1,MYCN,NME2,NTRK1,P3H1,PDIA4,PHGDH,POLR2L,RBBP4,RPL10,RPL11,RPL12,RPL13,RPL13A,RPL17,RPL18,RPL18A,RPL19,RPL21,RPL27,RPL28,RPL3,RPL35A,RPL4,RPL5,RPL6,RPL7,RPL8,RPL9,RPLP0,RPLP2,RPS13,RPS15,RPS16,RPS19,RPS2,RPS20,RPS24,RPS26,RPS3,RPS5,RPS6,RPS7,RPS8,TUBA1B
IRF4	1.547	transcription regulator	Activated	2.057	0.00136	Acp5,ADA,ALPL,CDK6,ENTPD1,EZR,FCER2,IL12A,IL13,IL17A,IL18RAP,IRF4,ITGB1,MANF,MAPRE1,MS4A1,PIM2,PLSCR1,PPIB,PRDM1,RPL6,SPIB,SUB1,XBP1,ZBTB20
NFE2L2	-1.22	transcription regulator		1.464	0.000000324	Acp5,AGPAT3,ALDH3A1,APBA3,ARHGEF3,BCL2,BDNF,CA11,CD8B,CDKN1A,Ces1g,CLPTM1L,DAD1,DCSTAMP,DNAJB11,DNAJB5,DNAJC3,EIF3E,EPHX1,ETV6,FGF13,G6PD,GAS2,GSS,GSTT2/GSTT2B,HM13,HSP90B1,IL13,IMPDH1,M6PR,MAFG,MEF2C,NAT8B,NFE2L2,NRSN1,OSGIN1,P2RX4,PDIA4,PDIA6,PHGDH,PPARGC1A,PPIB,PRKCB,PSMD1,PSMD5,RACK1,RAN,RPL18,RPLP0,RPS16,SCARB1,SEC61A1,SHC1,SLC35B1,SLC3A1,SLC7A11,SOD2,SOD3,SRXN1,TALDO1,TBRG1,TBXAS1,TKT,TXNRD1,UBE2K,USO1,USP14,XBP1
CTNNB1	-1.086	transcription regulator		1.369	0.0182	ABCD4,ACTN4,APOD,APP,ARFGAP3,BCL2,CBLN1,CCNE2,CD44,CDKN1A,CDKN1B,CELSR1,CNR1,CPSF4,CRIP1,CTNNA1,CTNNB1,DBH,DKK1,EDIL3,EMX2,ENPP1,EPCAM,EPHB2,FCAMR,FGD2,GAP43,GTPBP6,HILPDA,HOXA5,HP1BP3,ID3,IFT57,IL13,IL17A,IRF4,IRF8,ITGB1,ITGB2,JCHAIN,KIT,KLF5,LEF1,MLLT6,MMP3,MTMR7,MYCN,MYL4,NAP1L5,NOP53,NOX1,NR5A2,NR6A1,Oog1 (includes others),OSBPL1A,PCCA,PDAP1,PIK3R1,PPP1R13B,PRDM1,RAB18,RAB3A,RAI14,RGN,Saa3,SEC61A1,SERPINA1,SERPINA5,SFN,SH2B2,SLC17A9,SP6,SP7,SYK,TDGF1,TEAD2,TGIF1,TGM1,TUBB2B,UPB1,USO1,USP46,Zfp94,ZP3
SATB1	1.404	transcription regulator		0.841	0.0000138	ACTN1,ARF5,BCL2,BLNK,BTLA,CD40,CD8A,CDKN1A,CTNNA1,DUSP4,GPR18,GPT2,HVCN1,ID3,IL18RAP,IRF8,ITGB1,KLF2,LAX1,MAFA,Meis1,NFE2L2,PIK3IP1,PRKCB,PTGES3,RASGRP2,RPLP0,S1PR1,SELL,TAF4B,TUBA4A,YPEL5
HOXA7	-1.691	transcription regulator		0.618	0.0363	ERG,HOXA7,PTPRCAP,SATB1,TGM1,Tmsb4x (includes others)
MEF2C	1.468	transcription regulator		0.543	0.0338	ACTN2,BDNF,BLK,CASQ2,CDKN1A,ECM2,IRF4,JUND,KCNA5,KLF2,MEF2C,MYL4,POSTN,PPARA,PPARGC1A,SP7,SYK
POU2AF1	1.808	transcription regulator		0.442	0.00754	B4GALT1,BTLA,CCND3,CD79A,CD79B,Crisp1/Crisp3,CTNNA1,ID3,PRDM1,SPIB
RBPJ	-1.212	transcription regulator		0.391	0.0135	CD44,CDCA7,CDKN1A,CDKN1B,CSF1,FGF1,FGF13,GDF5,HES5,IL12A,IL17A,IRF8,LEF1,MAP2K3,MESP2,MIB2,MMP3,PRDM1,SDC1,TDGF1,VEGFC
KLF5	-1.923	transcription regulator		0.209	0.00716	CDKN1A,CDKN1B,Crisp1/Crisp3,CTNNB1,GPSM1,KLF5,PREB,SLC35F6,SORCS2,WFS1,WNT10A
PRDM1	1.396	transcription regulator		0.146	0.0101	ADA,ADAM8,ALPL,ATP9A,CCR7,CD19,CD44,CD79A,F9,FCER2,FGR,Gm14685 (includes others),HLA-DQA1,ID3,IGF1R,IL17A,IL18RAP,IRF4,IRF8,ITGA4,JCHAIN,NPAS1,PRDM1,PROX1,SELL,SLC16A5,SPIB,ST14,TNFAIP6,TNFRSF13B,XBP1
SPIB	1.577	transcription regulator		-0.008	0.0227	BLNK,CD200,EPCAM,IFNA4,IRF4,KIT,LILRB3,MEF2C,Mucl1/Mucl2,P2RY10,P2RY6,PRDM1,XBP1
ID3	1.975	transcription regulator		-0.247	0.000155	BCL2,BLK,CBFA2T3,CCNE2,CCR10,CCR7,CD44,CD79A,CDKN1A,CDKN1B,CSF1,DTX2,DUSP4,HES5,ID3,IFI16,IRF4,IRF6,IRF8,MYB,PIK3IP1,PIK3R1,PRDM1,PTPN22,PTPN3,RAP1GAP,RAPGEF4,SELL,STAT4,TNFSF14,ZBTB16
SIAH2	1.329	transcription regulator			0.0363	ANGPT1,DDT,DHCR24,FGF1,SIAH2,TINF2
DEK	-1.251	transcription regulator			0.0373	BIRC3,LEF1,PRDX6

Supplemental Table 11. Summary of the major findings in this study.

Mouse		FVB	Pad2i-/-	Pad4i-/-
	<u>In vivo Imiquimod-induced Model</u>			
	Splenomegaly			↓ *
	Anti-ds-DNA Ab		↓	↓
	Anti-histone Ab			↓
	Type 1 Interferon response		↓	↓
	C3 deposition in kidney			↓
	IgG deposition in kidney			↓
	Endothelial dysfunction			↓
	<u>In vitro</u>			
	Cit-H3 containing NETs	Yes	Yes	No
	IFN-γ levels in CD4+ T cells under Th1 polarizing conditions		↓	
	IL-17A levels in CD4+ T cells under Th17 polarizing conditions		↓	↓
		Ifng	IFN-γ	
Human	PAD2 inhibitor AFM30a	↓	↓	
	PAD4 inhibitor GSK199	↓	↓	

*Compared with Imiquimod-treated FVB mice.