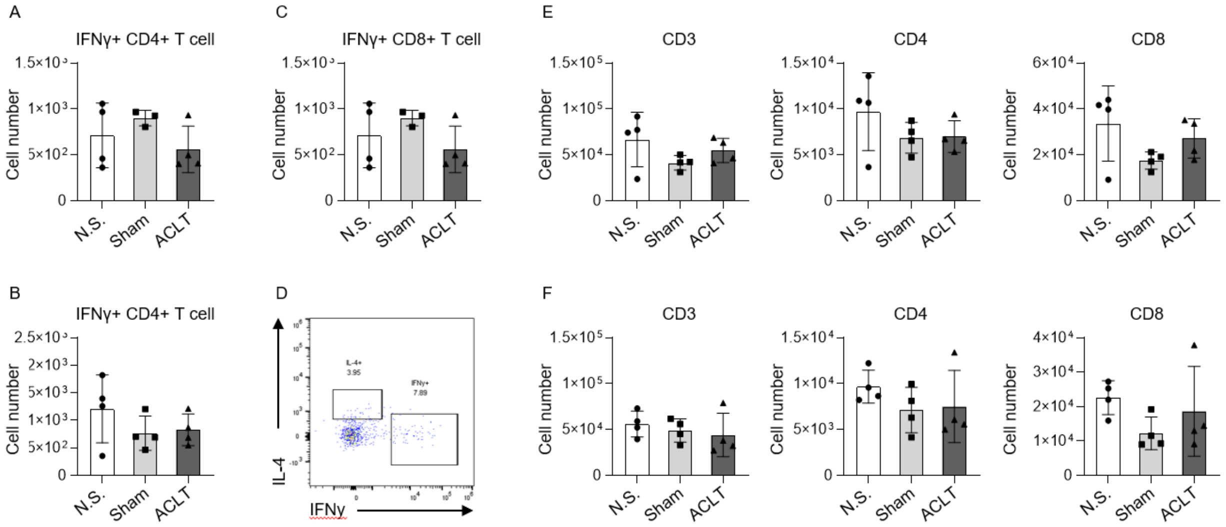
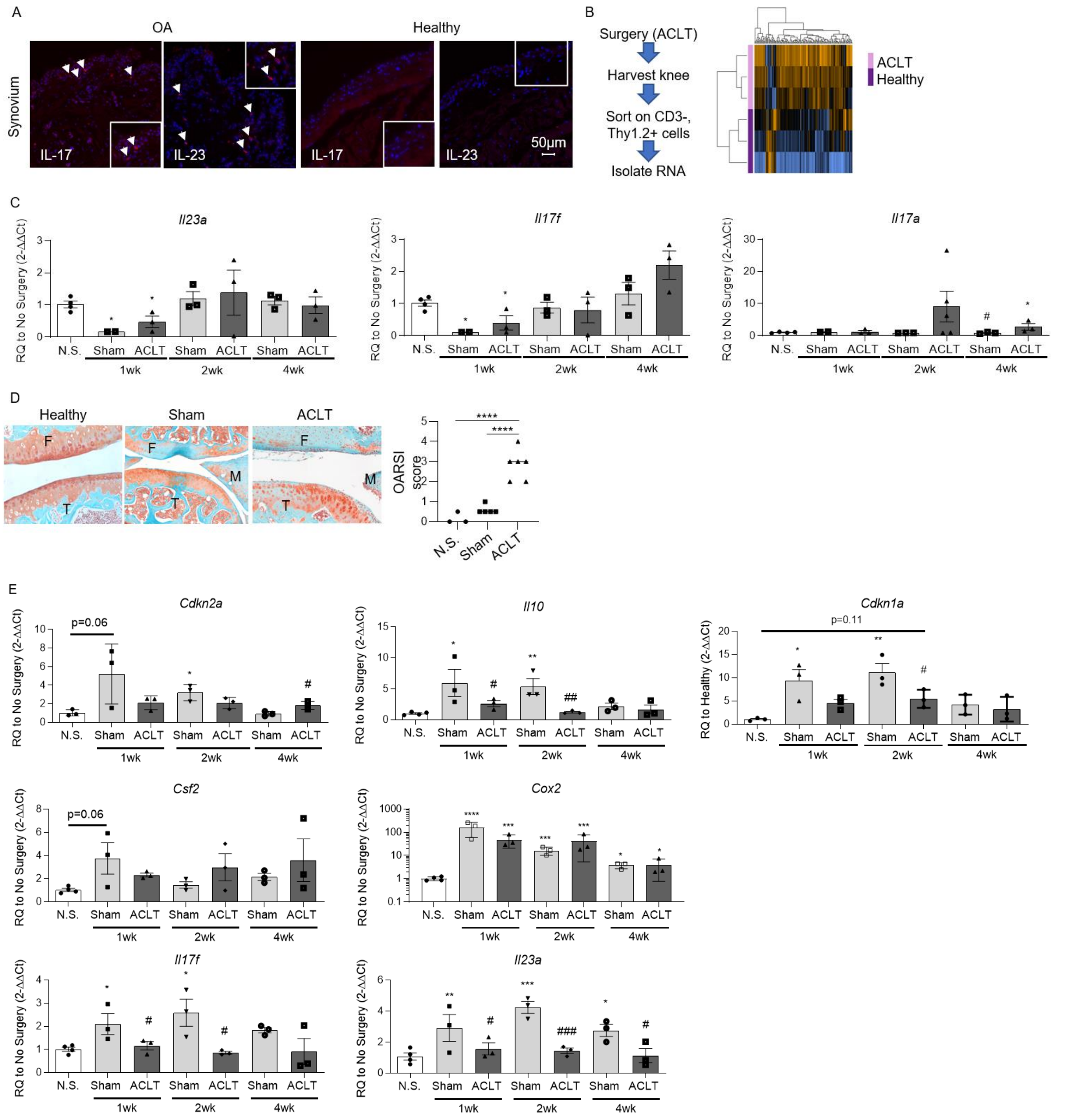
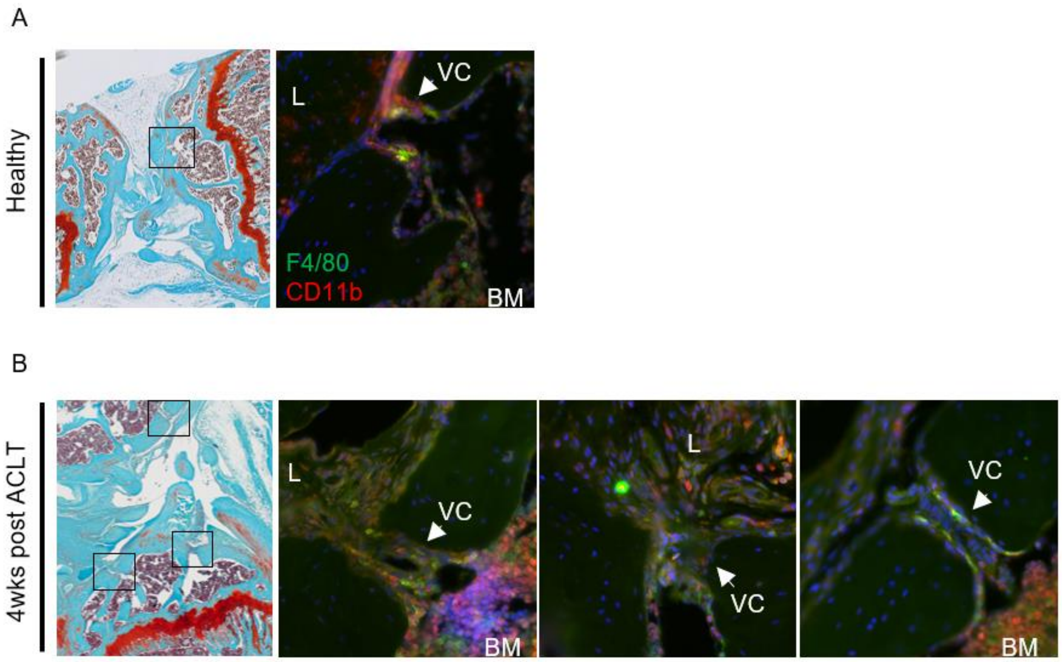


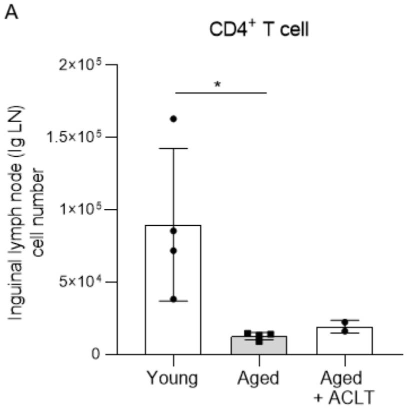
Supplemental Figure 1. No lymphoid cell number changes are observed in the joint 2-and-4 weeks post ACLT. Numbers of IFNγ+ CD4+ T cells in the joint are similar to no surgery at 1 week (A), 2 weeks (B), and 4 weeks (C). (D) is an example dot plot from an ACLT joint 2 weeks post surgery demonstrating the low number of IL-4+ cells (30) for quantitation. This sample is representative of most joint samples for IL-4 levels. Lymphoid cell numbers in the joint are similar to no surgery at 2 weeks (E) and 4 weeks (F) post surgery.



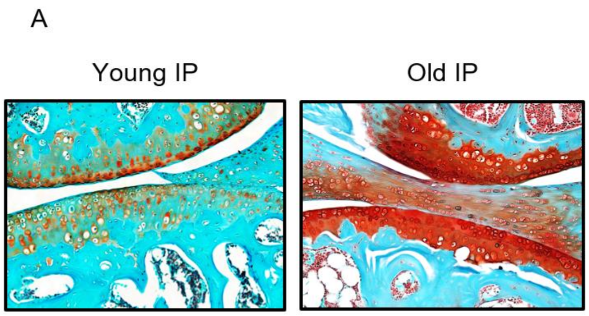
Supplemental Figure 2. (A) Immunofluorescence of human healthy and OA synovium. Only OA tissue exhibits IL-17 and IL-23 staining. Joint and inguinal lymph node post injury gene expression, flow cytometry, and immunohistochemistry characterization. (B) Nanostring pathway analysis of ILCs sorted from 2wk post ACLT vs no surgery joints. (C) Inguinal lymph node PCR from young mice with sham or ACLT 1, 2, and 4 wks post surgery (n=3). Stars represent significance compared to the no surgery group, pound signs indicate significance compared to opposite surgical group, and when p is indicated numerically, groups being compared are specified with a line. Groups are only statistically compared within each time point. (D) OARSI scores and representative images of sham joints 4wks post surgery. E. Whole joint PCR from young mice with sham or ACLT 1, 2, and 4 wks post surgery (n=3). Same statistical scheme as used in C. *p<0.05, **p <0.01, ***p<0.001 and ****p<0.001.



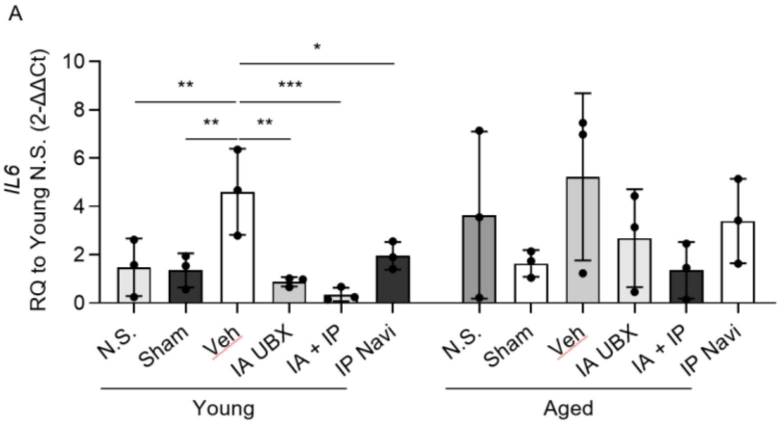
Supplemental Figure 3. Vascular channels change with joint trauma. Joints were sectioned and regions with ligaments insertions were imaged to identify vascular channels. Vascular channel=VC. Bone marrow=BM. Ligament=L. In healthy joints (A) F4/80$^+$ CD11b$^+$ cells are identified lining the walls of the vascular channels. In mice that have undergone ACLT (B) F4/80$^+$ CD11b$^+$ cells traffic through these vascular channels. More vascular channels were observed in ACLT joints than in healthy joints.



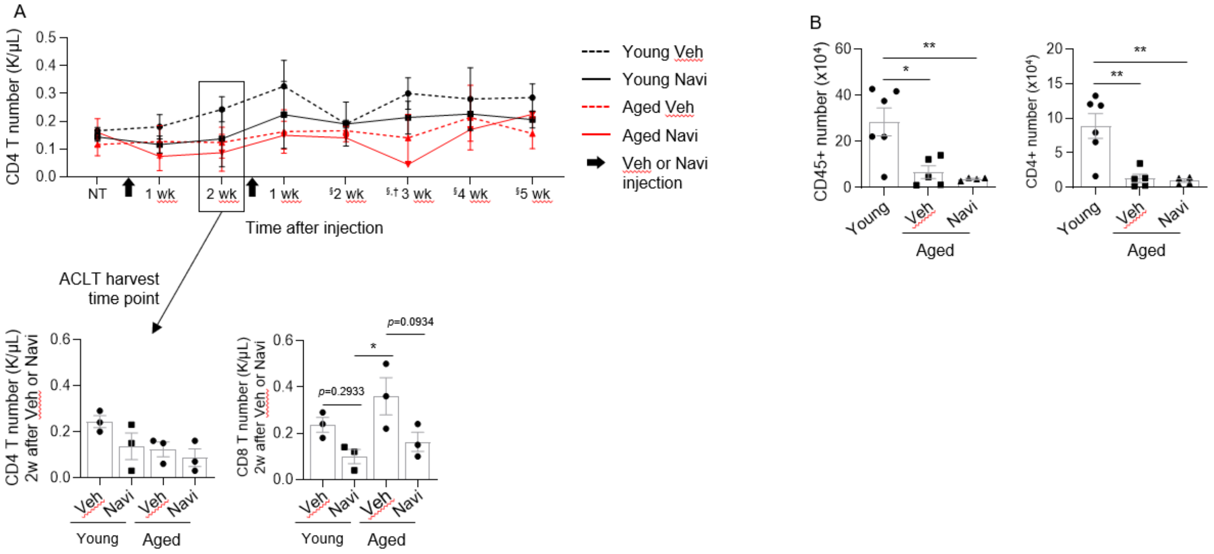
Supplemental Figure 4. Aging decreases lymph node lymphoid cell number. (A) Inguinal lymph node total CD4^{+} T cell number in aged vs young mice. *p<0.05.



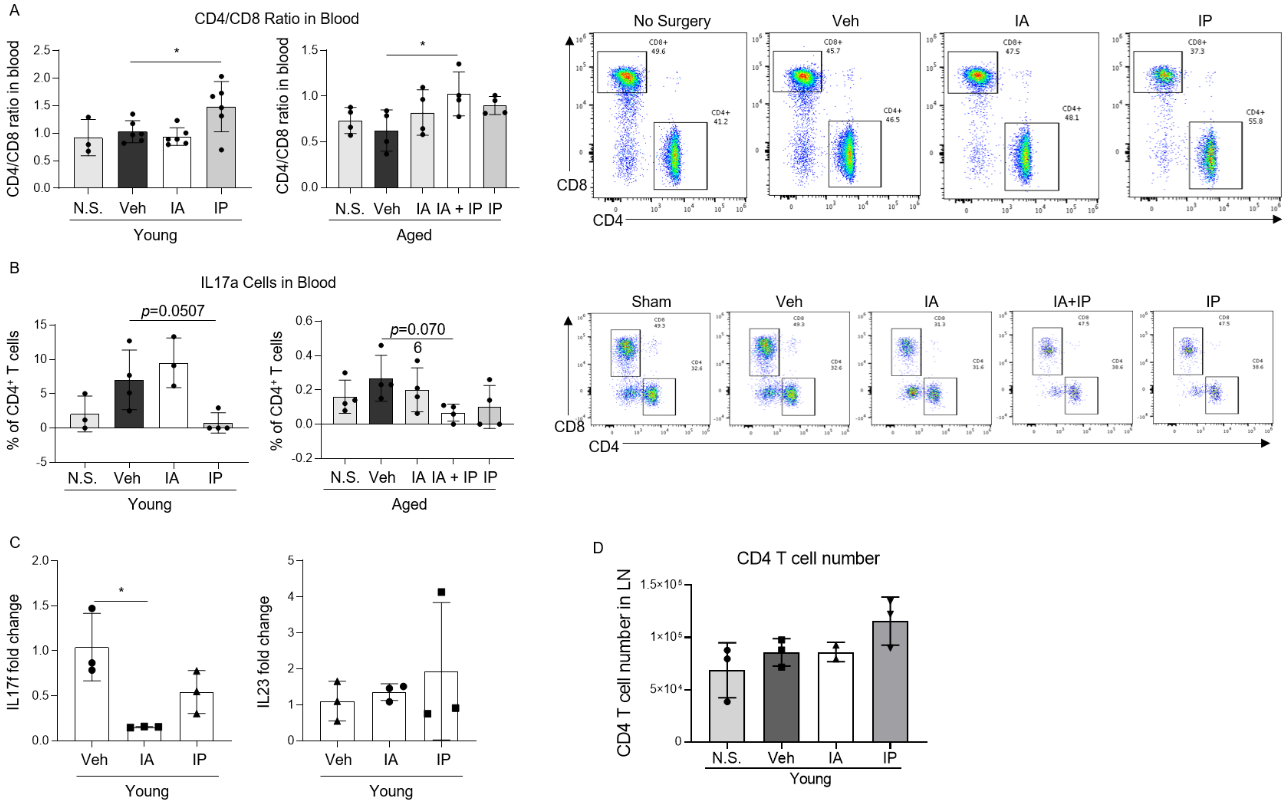
Supplemental Figure 5. Senolytic treatment of senescent cells enhances repair and decreases Th17 signature. (A) Representative histological images of systemic Navitoclax treatment in young and aged animal increase the cartilage repair.



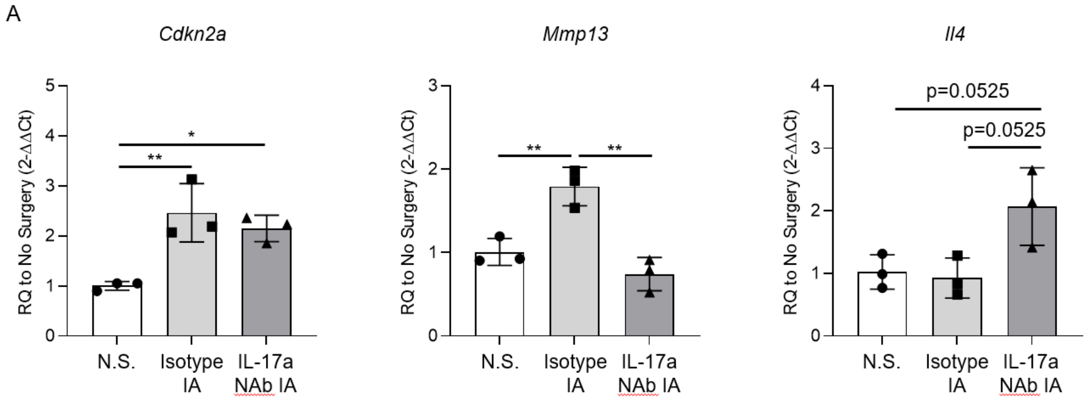
Supplemental Figure 6. SASP factor Il6 expression. (A) Quantification of mRNA expression of Il6 in articular joints before and after senolytic treatment in young and aged mice. *$p<0.05$, **$p<0.01$, and ***$p<0.001$. Experimental groups are compared to the control group (Veh).



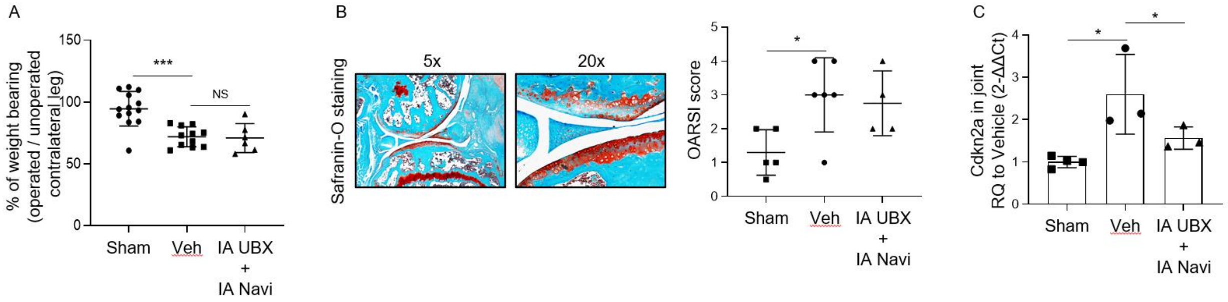
Supplemental Figure 7. Effect of senolytic treatment on lymphoid cells. (A) Effect of Navitoclax on blood T cell numbers after Vehicle or Navi treatment. N=2 for Young Veh and Aged Navi for the time points marked with §. N=2 for Aged Veh for the time point marked with †. N=3 for the rest of time points for all groups. *p<0.05. (B) Effect of Navitoclax on inguinal lymph nodal CD45 and CD4 cells 2 weeks after treatment. *p<0.05, and **p <0.01.



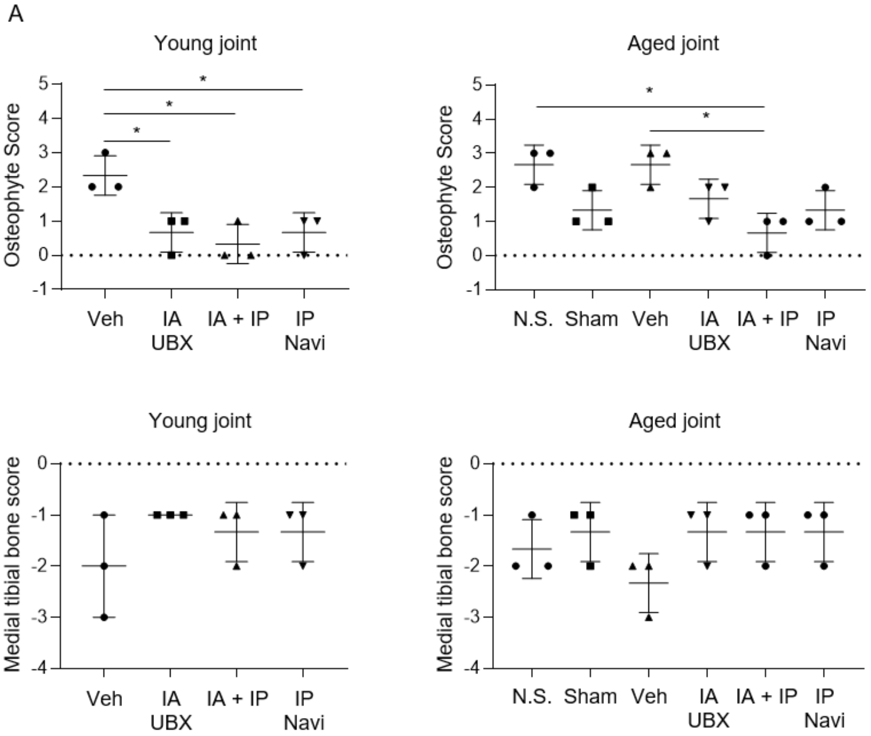
Supplemental Figure 8. Systemic senolytic treatment in ACL transected mice induces systemic immune changes. (A) CD4/CD8 ratio change in young and aged mice after treatments, and corresponding flow plots. (B) IL17a cell percentage in blood, and corresponding flow plots. (C) IL17f and IL23 fold change in young animal inguinal lymph nodes. **p*<0.05. Experimental groups are compared to the control group (Veh). (D) Quantified CD4+T cell numbers from inguinal lymph nodes of young mice; n=2-3 for each group. **p*<0.05. ****p*<0.001.



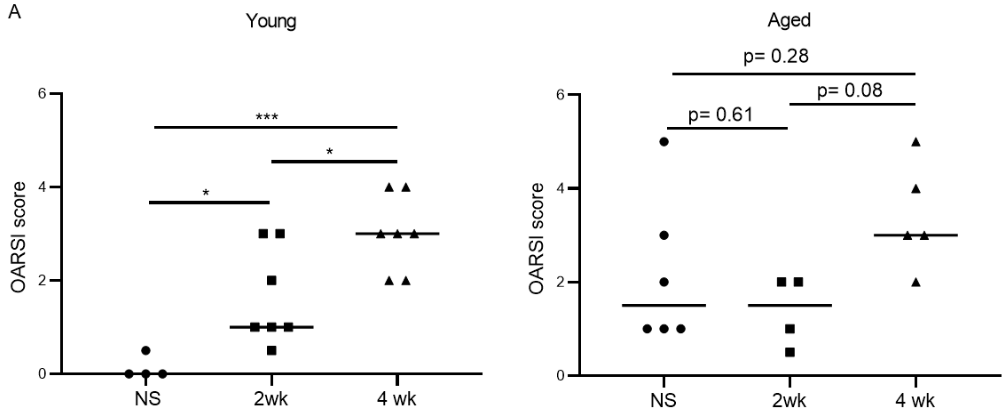
Supplemental Figure 9. IL-17 neutralization effects on joint gene expression. (A) Whole joint gene expression in young mice 4wks post ACLT with either isotype or IL-17 Nab administered (n=3). **p*<0.05, and ***p* <0.01.



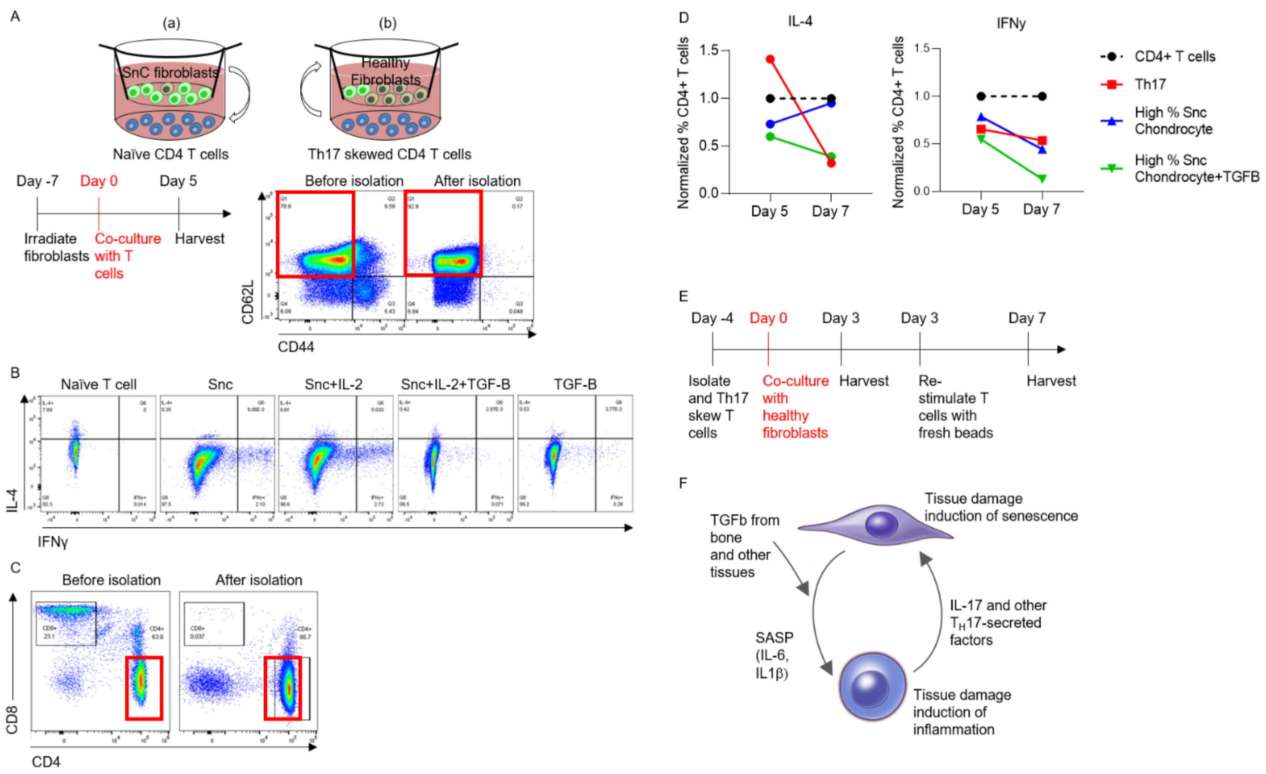
Supplemental Figure 10. Combined intra-articular treatment with navitoclax and UBX0101 does not enhance joint repair in aged mice. (A) Weight bearing of IA both group (IA injection of both UBX + Navi), (B) Representative images of Saf-O staining of IA both group joints, and OARSI score of IA both group joints. (C) CDKN2a gene expression of IA both group joints. Mice are age 76 weeks in all panels. ***p<0.001. Experimental groups are compared to the control group (Veh).



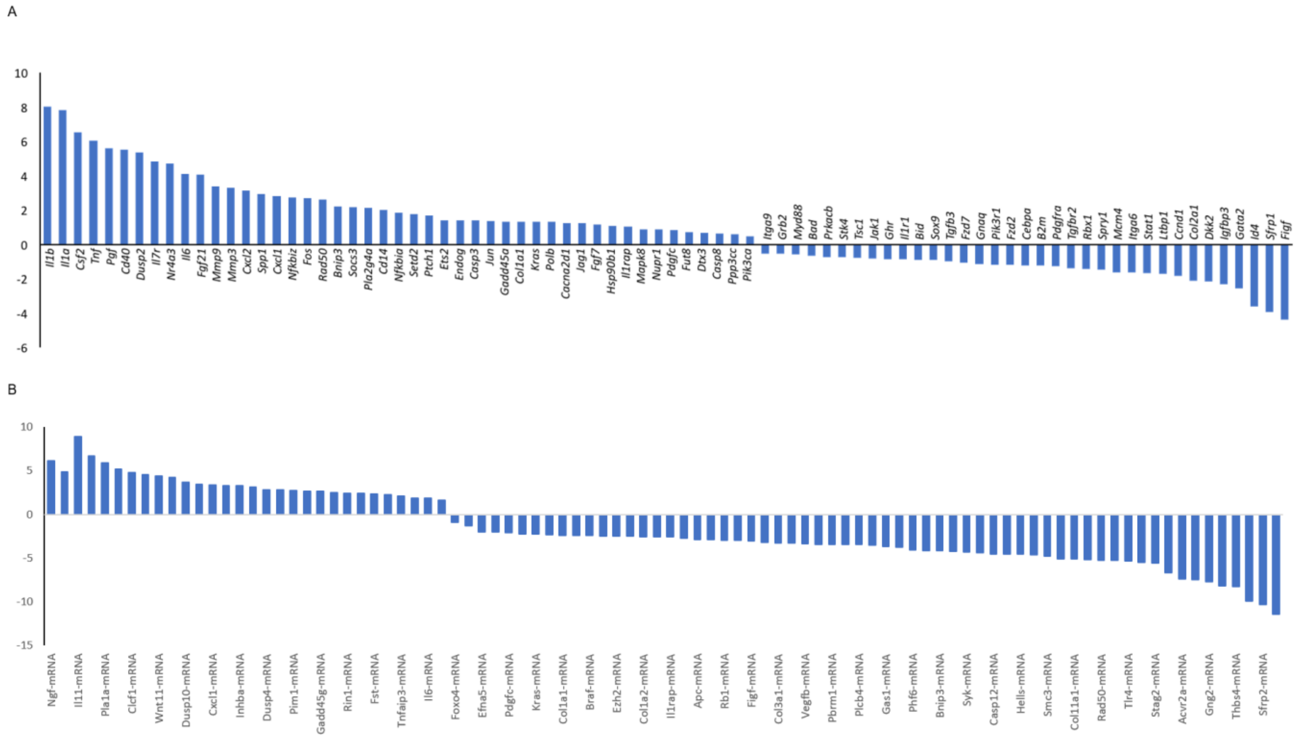
Supplemental Figure 11. (A) Osteophyte scoring on young and aged joints with IA UBX0101, IP navitoclax, or combined IA UBX0101 and IP navitoclax treatment after ACLT. *$p<0.05$. Experimental groups are compared to the control group (Veh).



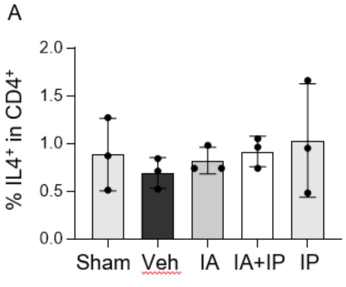
Supplemental Figure 12. ACLT induces joint damage as early as two weeks post injury. (A) Young or aged (76 weeks old) mice underwent ACL transection and were subsequently scored for cartilage damage using OARSI scoring at 2 and 4-weeks post ACLT. Mice 2wks post injury received no treatment or joint injections while mice 4wks post ACLT received one saline injection at 2wks post ACLT. *p<0.05. ***p<0.001.



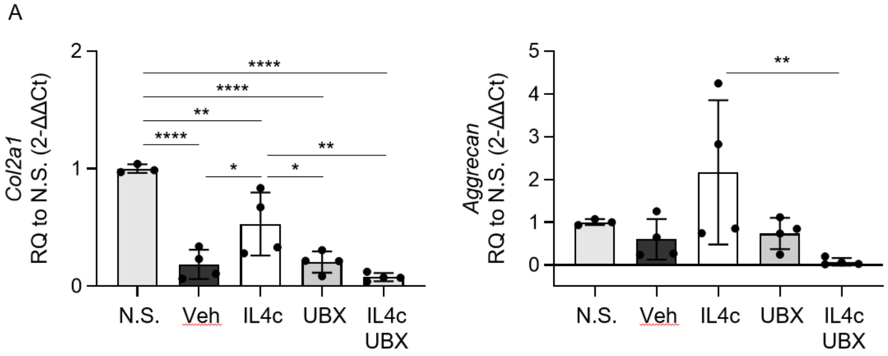
Supplemental Figure 13. Th17-senescent cell in vitro studies. (A) (a and b) Schematic of experimental set-up for in vitro experiments in figure 3 panels a and b. Experimental scheme and naïve CD4 T cell isolation from pooled lymph nodes before and after MACS isolation of naïve CD4 T cells. (B) Representative flow plots for IFNy quantification (C) Human CD4 T cell isolation from PMBCs. Left is PMBC, right is after MACS isolation of CD4 T cells. (D) Quantification of IL-4 and IFNy from human T cells after co-culture with Snc OA chondrocytes. Percentage of IL-4 or IFNy expressing CD4$^+$ T cells were normalized to the control CD4$^+$ T cell group within each time point. (E) Experimental scheme for Th17 cell co-culture with healthy fibroblasts. (F) Schematic of Th17 differentiation in the context of joint damage. Tissue damage induces senescent cell development, which supplies IL-6 and IL-1B needed for Th17 differentiation. Bone and other tissues provide TGFB, which is also needed for inducing Th17 differentiation. IL-17 and other factors secreted from Th17 cells then promote stromal cell senescence.



Supplemental Figure 14. Nanostring profiling of Th17 and irradiation induced senescence. (A) Complete list of significantly regulated genes in fibroblasts co-cultured with Th17 cells compared to normal fibroblasts. (B) Significantly regulated genes in irradiated fibroblasts compared to normal fibroblasts.



Supplemental Figure 15. Senolytic treatment does not enhance IL-4 protein levels. (A) Percentage of IL4+ cells in CD4+ T cells in inguinal lymph nodes in aged animals with senolytic treatment.



Supplemental Figure 16. Effect of IL-4 supplement in aged mice after ACL transection. (A) Whole joint gene expression 4 weeks after ACLT surgery. Surgery groups were treated with either Veh, IL-4 complex (IL4c), UBX or IL4c+UBX 2 weeks after ACLT surgery. *$p<0.05$, **$p<0.01$, ***$p<0.001$ and ****$p<0.001$.

S. Table 1 Mouse GO Th17 compared to healthy fibroblasts_downregulated

Annotation Cluster 1	Enrichment Score: 7.029864357839707				
Category	Term	PValue	Genes	Fold Enric	Bonferroni
UP_KEYWORDS	Signal	1.44E-08	FGFR2, TSPAN7, IGF1, GAS1, VEGFB, ACVR2A, ITGA6, SFRP1, SFRP2, COMP, NTRK2, EFNA5, NGFR, IGFBP3, LFNG, CSF1R	4.204039	9.38E-07
UP_KEYWORDS	Disulfide bond	2.73E-08	FGFR2, IGF1, VEGFB, ACVR2A, ITGA6, SFRP1, SFRP2, COMP, NTRK2, EFNA5, NGFR, IGFBP3, LFNG, CSF1R	5.349417	1.77E-06
UP_SEQ_FEATURE	disulfide bond	4.28E-07	FGFR2, VEGFB, ACVR2A, SFRP1, ITGA6, SFRP2, COMP, NTRK2, IGF1, EFNA5, NGFR, IGFBP3, CSF1R	4.90996	4.37E-05
UP_SEQ_FEATURE	signal peptide	4.51E-07	FGFR2, VEGFB, ACVR2A, SFRP1, ITGA6, SFRP2, COMP, NTRK2, IGF1, EFNA5, GAS1, NGFR, IGFBP3, CSF1R	4.248399	4.60E-05

Annotation Cluster 2	Enrichment Score: 6.350258440433879				
Category	Term	PValue	Genes	Fold Enric	Bonferroni
UP_KEYWORDS	Signal	1.44E-08	FGFR2, TSPAN7, IGF1, GAS1, VEGFB, ACVR2A, ITGA6, SFRP1, SFRP2, COMP, NTRK2, EFNA5, NGFR, IGFBP3, LFNG, CSF1R	4.204039	9.38E-07
UP_KEYWORDS	Glycoprotein	3.12E-07	FGFR2, TSPAN7, GAS1, VEGFB, ACVR2A, ITGA6, SFRP1, COMP, NTRK2, EFNA5, NGFR, IGFBP3, LFNG, CSF1R	4.380493	2.03E-05
UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	1.97E-05	FGFR2, ACVR2A, SFRP1, ITGA6, COMP, NTRK2, TSPAN7, EFNA5, GAS1, NGFR, IGFBP3, LFNG, CSF1R	3.458883	0.002012

Annotation Cluster 3	Enrichment Score: 4.638878204897676				
Category	Term	PValue	Genes	Fold Enric	Bonferroni
GOTERM_BP_DIRECT	GO:0008284~positive regulation of cell proliferation	6.59E-06	FGFR2, SFRP1, SFRP2, NTRK2, IGF1, GAS1, CSF1R	12.97396	0.003551

GOTERM_BP_DIRECT	GO:0050680~negative regulation of epithelial cell proliferation	3.95E-05	FGFR2, SFRP1, SFRP2, GAS1	55.80864	0.02113
GOTERM_BP_DIRECT	GO:0050679~positive regulation of epithelial cell proliferation	4.65E-05	FGFR2, SFRP1, IGF1, GAS1	52.87135	0.024802
Annotation Cluster 4	Enrichment Score: 4.3541011898918525				
Category	Term	PValue	Genes	Fold Enricl	Bonferroni
KEGG_PATHWAY	mmu04151:PI3K-Akt signaling pathway	2.94E-07	FGFR2, VEGFB, ITGA6, COMP, IGF1, EFNA5, NGFR, PIK3R1, CSF1R	10.95584	2.77E-05
KEGG_PATHWAY	mmu04015:Rap1 signaling pathway	4.14E-06	FGFR2, VEGFB, IGF1, EFNA5, NGFR, PIK3R1, CSF1R	13.97638	3.89E-04
KEGG_PATHWAY	mmu04014:Ras signaling pathway	6.13E-06	FGFR2, VEGFB, IGF1, EFNA5, NGFR, PIK3R1, CSF1R	13.06089	5.77E-04
GOTERM_BP_DIRECT	GO:0030335~positive regulation of cell migration	8.44E-04	ITGA6, IGF1, PIK3R1, CSF1R	19.7942	0.366194
KEGG_PATHWAY	mmu04510:Focal adhesion	9.21E-04	VEGFB, ITGA6, COMP, IGF1, PIK3R1	10.32072	0.082966
KEGG_PATHWAY	mmu05200:Pathways in cancer	0.00129	FGFR2, VEGFB, ITGA6, IGF1, PIK3R1, CSF1R	6.490295	0.114242
Annotation Cluster 5	Enrichment Score: 3.4286934471703976				
Category	Term	PValue	Genes	Fold Enricl	Bonferroni
GOTERM_BP_DIRECT	GO:0043410~positive regulation of MAPK cascade	2.32E-06	FGFR2, NTRK2, IGF1, NGFR, IGFBP3	48.29594	0.001252
GOTERM_BP_DIRECT	GO:0007623~circadian rhythm	0.004534	NTRK2, IGF1, NGFR	27.90432	0.914028

GOTERM_BP_DIRECT	GO:0007399~nervous system development	0.00492	NTRK2, IGF1, EFNA5, NGFR	10.65841	0.930286
Annotation Cluster 6	Enrichment Score: 3.340610858924582				
Category	Term	PValue	Genes	Fold Enrich	Bonferroni
UP_KEYWORDS	Developmental protein	7.43E-05	VEGFB, SFRP1, SFRP2, NTRK2, EFNA5, NGFR, LFNG	8.56126	0.004821
UP_KEYWORDS	Differentiation	1.16E-04	VEGFB, SFRP1, SFRP2, NTRK2, EFNA5, NGFR	11.08685	0.007525
GOTERM_BP_DIRECT	GO:0007275~multicellular organism development	2.41E-04	VEGFB, SFRP1, SFRP2, NTRK2, EFNA5, NGFR, LFNG	6.833711	0.121862
GOTERM_BP_DIRECT	GO:0030154~cell differentiation	5.92E-04	VEGFB, SFRP1, SFRP2, NTRK2, EFNA5, NGFR	7.72735	0.273492
UP_KEYWORDS	Neurogenesis	0.016112	NTRK2, EFNA5, NGFR	14.49819	0.6521
Annotation Cluster 7	Enrichment Score: 2.471996764501841				
Category	Term	PValue	Genes	Fold Enrich	Bonferroni
GOTERM_BP_DIRECT	GO:0008285~negative regulation of cell proliferation	2.11E-05	FGFR2, SFRP1, SFRP2, IGF1, IGFBP3, CSF1R	15.69618	0.011328
GOTERM_BP_DIRECT	GO:0050732~negative regulation of peptidyl-tyrosine phosphorylation	1.12E-04	SFRP1, SFRP2, IGF1	177.2745	0.058798
GOTERM_BP_DIRECT	GO:0045600~positive regulation of fat cell differentiation	9.53E-04	SFRP1, SFRP2, IGF1	61.5034	0.40251
GOTERM_BP_DIRECT	GO:0030307~positive regulation of cell growth	0.003174	SFRP1, SFRP2, IGF1	33.48519	0.820323
GOTERM_CC_DIRECT	GO:0005576~extracellular region	0.003609	FGFR2, VEGFB, SFRP1, SFRP2, COMP, IGF1, IGFBP3	4.132285	0.253885

GOTERM_BP_DIRECT	GO:0001649~osteoblast differentiation	0.004952	SFRP1, IGF1, IGFBP3	26.66962	0.931468
UP_KEYWORDS	Secreted	0.008507	VEGFB, SFRP1, SFRP2, COMP, IGF1, IGFBP3	4.250508	0.426112
GOTERM_CC_DIRECT	GO:0005615~extracellular space	0.009599	VEGFB, SFRP1, SFRP2, COMP, IGF1, IGFBP3	4.128359	0.54216
GOTERM_BP_DIRECT	GO:0010629~negative regulation of gene expression	0.025175	SFRP1, SFRP2, IGF1	11.37233	0.999999
GOTERM_CC_DIRECT	GO:0070062~extracellular exosome	0.724182	SFRP1, COMP, IGFBP3	1.161005	1
Annotation Cluster 8	Enrichment Score: 2.208186783569238				
Category	Term	PValue	Genes	Fold Enricł	Bonferroni
KEGG_PATHWAY	mmu05200:Pathways in cancer	0.00129	FGFR2, VEGFB, ITGA6, IGF1, PIK3R1, CSF1R	6.490295	0.114242
GOTERM_BP_DIRECT	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	0.001773	FGFR2, ACVR2A, ITGA6, SFRP2, IGF1, PIK3R1	6.057621	0.616461
KEGG_PATHWAY	mmu04550:Signaling pathways regulating pluripotency of stem cells	0.003197	FGFR2, ACVR2A, IGF1, PIK3R1	12.38486	0.259891
KEGG_PATHWAY	mmu05215:Prostate cancer	0.015746	FGFR2, IGF1, PIK3R1	14.56629	0.775052
KEGG_PATHWAY	mmu04810:Regulation of actin cytoskeleton	0.079067	FGFR2, ITGA6, PIK3R1	6.017997	0.999566
Annotation Cluster 9	Enrichment Score: 2.063396684684468				
Category	Term	PValue	Genes	Fold Enricł	Bonferroni

GOTERM_BP_DIRECT	GO:0006468~protein phosphorylation	9.33E-06	FGFR2, ACVR2A, MAP3K1, NTRK2, IGFBP3, PIK3R1, CSF1R	12.20814	0.005028
GOTERM_CC_DIRECT	GO:0009986~cell surface	1.40E-05	FGFR2, ACVR2A, SFRP1, ITGA6, NTRK2, NGFR, CSF1R	11.51653	0.001132
UP_KEYWORDS	Kinase	1.77E-04	FGFR2, ACVR2A, MAP3K1, NTRK2, PIK3R1, CSF1R	10.13028	0.011464
GOTERM_MF_DIRECT	GO:0016301~kinase activity	3.56E-04	FGFR2, ACVR2A, MAP3K1, NTRK2, PIK3R1, CSF1R	8.628091	0.037405
INTERPRO	IPR000719:Protein kinase, catalytic domain	8.95E-04	FGFR2, ACVR2A, MAP3K1, NTRK2, CSF1R	10.52325	0.070783
INTERPRO	IPR011009:Protein kinase-like domain	0.00119	FGFR2, ACVR2A, MAP3K1, NTRK2, CSF1R	9.747255	0.093001
GOTERM_MF_DIRECT	GO:0004714~transmembrane receptor protein tyrosine kinase activity	0.001241	FGFR2, NTRK2, CSF1R	53.84568	0.124455
UP_KEYWORDS	Transferase	0.001288	FGFR2, ACVR2A, MAP3K1, NTRK2, LFNG, PIK3R1, CSF1R	5.051868	0.080343
UP_SEQ_FEATURE	domain:Protein kinase	0.001337	FGFR2, ACVR2A, MAP3K1, NTRK2, CSF1R	9.442231	0.127534
GOTERM_MF_DIRECT	GO:0004672~protein kinase activity	0.001473	FGFR2, ACVR2A, MAP3K1, NTRK2, CSF1R	9.126386	0.145886
GOTERM_BP_DIRECT	GO:0016310~phosphorylation	0.002175	FGFR2, ACVR2A, MAP3K1, NTRK2, CSF1R	8.207153	0.691497
INTERPRO	IPR020635:Tyrosine-protein kinase, catalytic domain	0.002244	FGFR2, NTRK2, CSF1R	40.14425	0.168252
UP_SEQ_FEATURE	binding site:ATP	0.002315	FGFR2, ACVR2A, MAP3K1, NTRK2, CSF1R	8.13036	0.210517
INTERPRO	IPR008266:Tyrosine-protein kinase, active site	0.003329	FGFR2, NTRK2, CSF1R	32.8453	0.239228
UP_KEYWORDS	Tyrosine-protein kinase	0.003573	FGFR2, NTRK2, CSF1R	31.69073	0.207595

INTERPRO	IPR017441:Protein kinase, ATP binding site	0.00458	FGFR2, MAP3K1, NTRK2, CSF1R	11.00401	0.313697
UP_SEQ_FEATURE	active site:Proton acceptor	0.004709	FGFR2, ACVR2A, MAP3K1, NTRK2, CSF1R	6.676056	0.382124
SMART	SM00219:TyrKc	0.005863	FGFR2, NTRK2, CSF1R	24.13194	0.121355
GOTERM_MF_DIRECT	GO:0004713~protein tyrosine kinase activity	0.006061	FGFR2, NTRK2, CSF1R	24.0303	0.478224
GOTERM_MF_DIRECT	GO:0042803~protein homodimerization activity	0.006416	FGFR2, VEGFB, NTRK2, NGFR, CSF1R	6.072821	0.497776
INTERPRO	IPR001245:Serine-threonine/tyrosine-protein kinase catalytic domain	0.006447	FGFR2, NTRK2, CSF1R	23.39341	0.41161
UP_SEQ_FEATURE	domain:Ig-like C2-type 1	0.007552	FGFR2, NTRK2, CSF1R	21.54545	0.538478
UP_SEQ_FEATURE	domain:Ig-like C2-type 2	0.007663	FGFR2, NTRK2, CSF1R	21.38346	0.543703
GOTERM_MF_DIRECT	GO:0016740~transferase activity	0.011116	FGFR2, ACVR2A, MAP3K1, NTRK2, LFNG, CSF1R	3.950634	0.697631
GOTERM_BP_DIRECT	GO:0046777~protein autophosphorylation	0.012538	FGFR2, NTRK2, CSF1R	16.46812	0.998901
GOTERM_BP_DIRECT	GO:0001934~positive regulation of protein phosphorylation	0.012668	ACVR2A, PIK3R1, CSF1R	16.37862	0.998977
UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	0.013615	FGFR2, ACVR2A, MAP3K1, NTRK2, CSF1R	4.922118	0.752968
INTERPRO	IPR003598:Immunoglobulin subtype 2	0.018589	FGFR2, NTRK2, CSF1R	13.43671	0.785322
UP_SEQ_FEATURE	topological domain:Extracellular	0.018684	FGFR2, ACVR2A, ITGA6, NTRK2, TSPAN7, NGFR, CSF1R	2.941489	0.853949
UP_KEYWORDS	ATP-binding	0.020178	FGFR2, ACVR2A, MAP3K1, NTRK2, CSF1R	4.378886	0.7342

UP_KEYWORDS	Nucleotide-binding	0.045484	FGFR2, ACVR2A, MAP3K1, NTRK2, CSF1R	3.402749	0.951482
SMART	SM00408:IGc2	0.046193	FGFR2, NTRK2, CSF1R	8.077221	0.64671
UP_KEYWORDS	Receptor	0.048042	FGFR2, ACVR2A, ITGA6, NTRK2, NGFR, CSF1R	2.740951	0.959247
GOTERM_BP_DIRECT	GO:0010628~positive regulation of gene expression	0.053101	FGFR2, NTRK2, PIK3R1	7.553049	1
GOTERM_MF_DIRECT	GO:0005524~ATP binding	0.053144	FGFR2, ACVR2A, MAP3K1, NTRK2, CSF1R	3.215734	0.9971
UP_KEYWORDS	Immunoglobulin domain	0.054902	FGFR2, NTRK2, CSF1R	7.445016	0.974533
INTERPRO	IPR003599:Immunoglobulin subtype	0.074108	FGFR2, NTRK2, CSF1R	6.277383	0.998189
KEGG_PATHWAY	mmu04010:MAPK signaling pathway	0.104663	FGFR2, MAP3K1, NTRK2	5.106906	0.999969
GOTERM_MF_DIRECT	GO:0000166~nucleotide binding	0.111309	FGFR2, ACVR2A, MAP3K1, NTRK2, CSF1R	2.503157	0.999997
UP_KEYWORDS	Ubl conjugation	0.113048	FGFR2, NTRK2, PIK3R1, CSF1R	3.172583	0.999589
UP_KEYWORDS	Cell membrane	0.165319	FGFR2, ITGA6, NTRK2, EFNA5, GAS1, CSF1R	1.905322	0.999992
SMART	SM00409:IG	0.169195	FGFR2, NTRK2, CSF1R	3.773528	0.983057
INTERPRO	IPR007110:Immunoglobulin-like domain	0.190942	FGFR2, NTRK2, CSF1R	3.534439	1
INTERPRO	IPR013783:Immunoglobulin-like fold	0.249226	FGFR2, NTRK2, CSF1R	2.958766	1
GOTERM_CC_DIRECT	GO:0005737~cytoplasm	0.601574	FGFR2, ACVR2A, MAP3K1, NTRK2, IGF1, NGFR, PIK3R1	1.092429	1
Annotation Cluster 10	Enrichment Score: 1.8193059244053358				
Category	Term	PValue	Genes	Fold Enrich	Bonferroni
GOTERM_CC_DIRECT	GO:0009986~cell surface	1.40E-05	FGFR2, ACVR2A, SFRP1, ITGA6, NTRK2, NGFR, CSF1R	11.51653	0.001132
UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	1.97E-05	FGFR2, ACVR2A, SFRP1, ITGA6, COMP, NTRK2, TSPAN7, EFNA5, GAS1, NGFR, IGFBP3, LFNG, CSF1R	3.458883	0.002012

GOTERM_CC_DIRECT	GO:0005886~plasma membrane	0.005059	FGFR2, ACVR2A, SFRP1, ITGA6, NTRK2, IGF1, EFNA5, GAS1, NGFR, PIK3R1, CSF1R	2.335507	0.336899
GOTERM_CC_DIRECT	GO:0016020~membrane	0.00717	FGFR2, VEGFB, ACVR2A, ITGA6, MAP3K1, NTRK2, TSPAN7, EFNA5, GAS1, NGFR, LFNG, PIK3R1, CSF1R	1.922399	0.441724
UP_SEQ_FEATURE	topological domain:Cytoplasmic	0.016563	FGFR2, ACVR2A, ITGA6, NTRK2, TSPAN7, NGFR, LFNG, CSF1R	2.633333	0.817966
UP_SEQ_FEATURE	topological domain:Extracellular	0.018684	FGFR2, ACVR2A, ITGA6, NTRK2, TSPAN7, NGFR, CSF1R	2.941489	0.853949
UP_KEYWORDS	Receptor	0.048042	FGFR2, ACVR2A, ITGA6, NTRK2, NGFR, CSF1R	2.740951	0.959247
GOTERM_CC_DIRECT	GO:0016021~integral component of membrane	0.059403	FGFR2, ACVR2A, SFRP1, ITGA6, SFRP2, NTRK2, TSPAN7, NGFR, LFNG, PIK3R1, CSF1R	1.655025	0.99299
GOTERM_CC_DIRECT	GO:0005887~integral component of plasma membrane	0.080416	FGFR2, NTRK2, TSPAN7, NGFR	3.676171	0.998876
UP_KEYWORDS	Membrane	0.10416	FGFR2, ACVR2A, ITGA6, NTRK2, TSPAN7, EFNA5, GAS1, NGFR, LFNG, PIK3R1, CSF1R	1.512211	0.999215
UP_SEQ_FEATURE	transmembrane region	0.115732	FGFR2, ACVR2A, ITGA6, NTRK2, TSPAN7, NGFR, LFNG, CSF1R	1.758813	0.999996
UP_KEYWORDS	Transmembrane helix	0.15371	FGFR2, ACVR2A, ITGA6, NTRK2, TSPAN7, NGFR, LFNG, PIK3R1, CSF1R	1.548452	0.999981
UP_KEYWORDS	Transmembrane	0.155423	FGFR2, ACVR2A, ITGA6, NTRK2, TSPAN7, NGFR, LFNG, PIK3R1, CSF1R	1.544667	0.999983
UP_KEYWORDS	Cell membrane	0.165319	FGFR2, ITGA6, NTRK2, EFNA5, GAS1, CSF1R	1.905322	0.999992

Annotation Cluster 11	Enrichment Score: 1.110395136017742				
Category	Term	PValue	Genes	Fold Enrich	Bonferroni
KEGG_PATHWAY	mmu05200:Pathways in cancer	0.00129	FGFR2, VEGFB, ITGA6, IGF1, PIK3R1, CSF1R	6.490295	0.114242
UP_KEYWORDS	Cell membrane	0.165319	FGFR2, ITGA6, NTRK2, EFNA5, GAS1, CSF1R	1.905322	0.999992
UP_KEYWORDS	Alternative splicing	0.324713	FGFR2, VEGFB, ITGA6, NTRK2, IGF1, EFNA5	1.498662	1
UP_SEQ_FEATURE	splice variant	0.522521	FGFR2, VEGFB, ITGA6, NTRK2, IGF1, EFNA5	1.212535	1

S. Table 1 Mouse GO Th17 compared to healthy fibroblasts_upregulated

Annotation Cluster 1	Enrichment Score: 4.3928215226419995				
Category	Term	PValue	Genes	Fold Enrich	Bonferroni
UP_KEYWORDS	Growth factor	2.34E-09	CXCL1, LIF, INHBA, IL6, PGF, FGF2, IL11, NGF	34.8454	2.34E-07
GOTERM_MF_DIRECT	GO:0008083~growth factor activity	3.51E-08	CXCL1, LIF, INHBA, IL6, PGF, FGF2, IL11, NGF	23.47653	5.23E-06
GOTERM_CC_DIRECT	GO:0005615~extracellular space	5.38E-07	CXCL1, IL6, WNT5B, PGF, TNC, MMP9, MMP3, IL11, LIF, INHBA, CLCF1, HSPB1, WNT11, FGF2, NGF	4.902427	4.41E-05
UP_KEYWORDS	Secreted	5.44E-07	CXCL1, IL6, WNT5B, PGF, TNC, MMP9, MMP3, IL11, LIF, INHBA, CLCF1, PLA1A, WNT11, FGF2, NGF	4.924369	5.44E-05
GOTERM_CC_DIRECT	GO:0005576~extracellular region	3.38E-06	CXCL1, IL6, WNT5B, PGF, TNC, MMP9, MMP3, IL11, LIF, INHBA, CLCF1, PLA1A, WNT11, FGF2, NGF	4.206075	2.77E-04
GOTERM_MF_DIRECT	GO:0005102~receptor binding	3.58E-06	LIF, DVL3, INHBA, IL6, WNT5B, CLCF1, WNT11, FGF2, NGF	9.295169	5.34E-04
GOTERM_MF_DIRECT	GO:0005125~cytokine activity	8.61E-06	CXCL1, LIF, INHBA, IL6, CLCF1, FGF2, IL11	13.91862	0.001282
UP_SEQ_FEATURE	signal peptide	0.001423	CXCL1, CACNA2D1, IL6, WNT5B, PGF, TNC, MMP9, MMP3, IL11, LIF, INHBA, CLCF1, CSF2RB, PLA1A, WNT11, NGF	2.306274	0.246792
UP_KEYWORDS	Disulfide bond	0.001989	CXCL1, CACNA2D1, IL6, WNT5B, PGF, MMP9, TNC, MMP3, LIF, INHBA, CSF2RB, PLA1A, WNT11, NGF	2.478998	0.180568
UP_KEYWORDS	Signal	0.00798	CXCL1, CACNA2D1, IL6, WNT5B, PGF, TNC, MMP9, MMP3, IL11, LIF, INHBA, CLCF1, CSF2RB, PLA1A, WNT11, NGF	1.948213	0.551225
UP_KEYWORDS	Glycoprotein	0.011342	CACNA2D1, WNT5B, PGF, MMP9, TNC, MMP3, LIF, INHBA, CLCF1, CSF2RB, CREB3L1, PLA1A, WNT11, NGF	2.029984	0.680395
UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	0.032568	CACNA2D1, WNT5B, PGF, MMP9, TNC, MMP3, LIF, INHBA, CLCF1, CSF2RB, CREB3L1, PLA1A, WNT11, NGF	1.769352	0.998625

UP_SEQ_FEATURE	disulfide bond	0.03747	CXCL1, LIF, INHBA, IL6, PGF, MMP9, TNC, CSF2RB, PLA1A, MMP3, NGF	1.973426	0.999499
Annotation Cluster 2	**Enrichment Score: 3.297593221134542**				
Category	Term	PValue	Genes	Fold Enricl	Bonferroni
KEGG_PATHWAY	mmu04668:TNF signaling pathway	3.13E-09	CXCL1, LIF, FOS, IL6, SOCS3, MMP9, NFKBIA, CREB3L1, TNFAIP3, MMP3	17.20967	4.14E-07
KEGG_PATHWAY	mmu05164:Influenza A	0.011562	PRKCA, IL6, HSPA2, SOCS3, NFKBIA	5.484952	0.784574
KEGG_PATHWAY	mmu04931:Insulin resistance	0.019165	IL6, SOCS3, NFKBIA, CREB3L1	6.821286	0.922255
KEGG_PATHWAY	mmu05168:Herpes simplex infection	0.092929	FOS, IL6, SOCS3, NFKBIA	3.607411	0.999997
Annotation Cluster 3	**Enrichment Score: 2.7755941169736236**				
Category	**Term**	**PValue**	**Genes**	**Fold Enricl**	**Bonferroni**
KEGG_PATHWAY	mmu04916:Melanogenesis	1.47E-04	PRKCA, DVL3, WNT5B, LEF1, CREB3L1, WNT11	11.36881	0.019218
GOTERM_BP_DIRECT	GO:0001649~osteoblast differentiation	0.001984	TNC, LEF1, CREB3L1, WNT11	15.61148	0.769549
GOTERM_MF_DIRECT	GO:0044212~transcription regulatory region DNA binding	0.016156	FOS, LEF1, CREB3L1, WNT11	7.30493	0.911695
Annotation Cluster 4	**Enrichment Score: 2.636553309813029**				
Category	**Term**	**PValue**	**Genes**	**Fold Enricl**	**Bonferroni**
GOTERM_MF_DIRECT	GO:0005125~cytokine activity	8.61E-06	CXCL1, LIF, INHBA, IL6, CLCF1, FGF2, IL11	13.91862	0.001282
UP_KEYWORDS	Cytokine	4.18E-04	CXCL1, LIF, IL6, CLCF1, IL11	13.82927	0.040973
GOTERM_BP_DIRECT	GO:0046888~negative regulation of hormone secretion	4.27E-04	LIF, IL6, IL11	94.50523	0.270646
INTERPRO	IPR009079:Four-helical cytokine-like, core	7.33E-04	LIF, IL6, CLCF1, IL11	22.0788	0.09486

KEGG_PATHWAY	mmu04630:Jak-STAT signaling pathway	8.60E-04	LIF, IL6, SOCS3, PIM1, CSF2RB, IL11	7.762153	0.107321
KEGG_PATHWAY	mmu04060:Cytokine-cytokine receptor interaction	0.001426	CXCL1, LIF, INHBA, IL6, CLCF1, CSF2RB, IL11	5.426023	0.171709
GOTERM_BP_DIRECT	GO:0042517~positive regulation of tyrosine phosphorylation of Stat3 protein	0.001996	LIF, IL6, CLCF1	44.10244	0.771541
GOTERM_BP_DIRECT	GO:0033138~positive regulation of peptidyl-serine phosphorylation	0.011656	LIF, IL6, IL11	17.87937	0.999827
INTERPRO	IPR012351:Four-helical cytokine, core	0.012673	LIF, IL6, CLCF1	17.12361	0.823528
GOTERM_BP_DIRECT	GO:0050731~positive regulation of peptidyl-tyrosine phosphorylation	0.020993	LIF, IL6, IL11	13.09973	1
GOTERM_BP_DIRECT	GO:0043410~positive regulation of MAPK cascade	0.022172	LIF, IL6, IL11	12.72186	1
GOTERM_BP_DIRECT	GO:0006955~immune response	0.121302	CXCL1, LIF, IL6	4.86424	1

Annotation Cluster 5 **Enrichment Score: 2.4746683250657333**

Category	**Term**	**PValue**	**Genes**	**Fold Enricl**	**Bonferroni**
GOTERM_BP_DIRECT	GO:0045766~positive regulation of angiogenesis	1.45E-04	PRKCA, PGF, MMP9, HSPB1, FGF2	18.22415	0.101437
KEGG_PATHWAY	mmu04151:PI3K-Akt signaling pathway	3.70E-04	PRKCA, IL6, PGF, TNC, NR4A1, CREB3L1, FGF2, DDIT4, NGF	4.809881	0.047696
GOTERM_BP_DIRECT	GO:0001938~positive regulation of endothelial cell proliferation	4.36E-04	PRKCA, PGF, NR4A1, FGF2	26.32981	0.275242
KEGG_PATHWAY	mmu04014:Ras signaling pathway	0.001072	PRKCA, REL, PGF, RIN1, PLA1A, FGF2, NGF	5.73405	0.132048
UP_KEYWORDS	Angiogenesis	0.019593	PRKCA, PGF, FGF2	13.60256	0.861757

GOTERM_BP_DIRECT	GO:0001525~angiogenesis	0.097874	PRKCA, PGF, FGF2	5.535871	1
KEGG_PATHWAY	mmu04015:Rap1 signaling pathway	0.099149	PRKCA, PGF, FGF2, NGF	3.506269	0.999999

Annotation Cluster 6 **Enrichment Score: 2.388996644745089**

Category	**Term**	**PValue**	**Genes**	**Fold Enricl**	**Bonferroni**
UP_KEYWORDS	Extracellular matrix	7.66E-04	WNT5B, MMP9, TNC, WNT11, MMP3	11.76959	0.073784
GOTERM_BP_DIRECT	GO:0030335~positive regulation of cell migration	0.001027	PRKCA, WNT5B, LEF1, WNT11, MMP3	10.86267	0.53209
GOTERM_CC_DIRECT	GO:0005578~proteinaceous extracellular matrix	0.003457	WNT5B, MMP9, TNC, WNT11, MMP3	7.77769	0.247206
GOTERM_CC_DIRECT	GO:0031012~extracellular matrix	0.020341	MMP9, TNC, HSPB1, MMP3	6.687755	0.814592
KEGG_PATHWAY	mmu05205:Proteoglycans in cancer	0.020509	PRKCA, WNT5B, MMP9, WNT11, FGF2	4.620329	0.935132

Annotation Cluster 7 Enrichment Score: 2.384409938694051

Category	Term	PValue	Genes	Fold Enricl	Bonferroni
KEGG_PATHWAY	mmu04310:Wnt signaling pathway	7.84E-05	PRKCA, DVL3, WNT5B, LEF1, WNT11, FOSL1, NFATC1	9.312749	0.010297
KEGG_PATHWAY	mmu04916:Melanogenesis	1.47E-04	PRKCA, DVL3, WNT5B, LEF1, CREB3L1, WNT11	11.36881	0.019218
KEGG_PATHWAY	mmu04550:Signaling pathways regulating pluripotency of stem cells	6.87E-04	LIF, DVL3, INHBA, WNT5B, WNT11, FGF2	8.155885	0.08671
GOTERM_BP_DIRECT	GO:0030335~positive regulation of cell migration	0.001027	PRKCA, WNT5B, LEF1, WNT11, MMP3	10.86267	0.53209
KEGG_PATHWAY	mmu05217:Basal cell carcinoma	0.002691	DVL3, WNT5B, LEF1, WNT11	13.89521	0.299271
GOTERM_MF_DIRECT	GO:0005109~frizzled binding	0.00342	DVL3, WNT5B, WNT11	33.59307	0.399791
UP_KEYWORDS	Wnt signaling pathway	0.003676	DVL3, WNT5B, LEF1, WNT11	12.57206	0.308072
GOTERM_BP_DIRECT	GO:0016055~Wnt signaling pathway	0.011558	DVL3, WNT5B, LEF1, WNT11	8.282148	0.999814

GOTERM_BP_DIRECT	GO:0060070~canonical Wnt signaling pathway	0.016551	DVL3, LEF1, WNT11	14.86599	0.999996
GOTERM_BP_DIRECT	GO:0090090~negative regulation of canonical Wnt signaling pathway	0.021383	WNT5B, LEF1, WNT11	12.97131	1
UP_KEYWORDS	Developmental protein	0.027624	DVL3, WNT5B, PGF, CREB3L1, WNT11, FGF2	3.40064	0.939264
KEGG_PATHWAY	mmu04390:Hippo signaling pathway	0.043193	DVL3, WNT5B, LEF1, WNT11	4.969149	0.997057
GOTERM_BP_DIRECT	GO:0007275~multicellular organism development	0.074936	DVL3, WNT5B, PGF, CREB3L1, WNT11, FGF2	2.571571	1
Annotation Cluster 8	Enrichment Score: 2.3427938579208942				
Category	Term	PValue	Genes	Fold Enrich	Bonferroni
GOTERM_MF_DIRECT	GO:0001077~transcriptional activator activity, RNA polymerase II core promoter proximal region sequence-specific binding	3.21E-05	FOS, LEF1, NR4A1, CREB3L1, HMGA2, FOSL1, NFATC1	11.0318	0.004767
INTERPRO	IPR004827:Basic-leucine zipper domain	0.004938	FOS, CREB3L1, FOSL1	27.90515	0.489971
SMART	SM00338:BRLZ	0.011912	FOS, CREB3L1, FOSL1	17.52101	0.380811
UP_SEQ_FEATURE	domain:Leucine-zipper	0.022849	FOS, CREB3L1, FOSL1	12.50833	0.989946
UP_SEQ_FEATURE	DNA-binding region:Basic motif	0.044818	FOS, CREB3L1, FOSL1	8.659615	0.999891
Annotation Cluster 9	Enrichment Score: 2.2669436192051693				
Category	Term	PValue	Genes	Fold Enrich	Bonferroni
INTERPRO	IPR008343:Mitogen-activated protein (MAP) kinase phosphatase	1.64E-04	DUSP5, DUSP4, DUSP10	150.6878	0.022047

GOTERM_MF_DIRECT	GO:0017017~MAP kinase tyrosine/serine/threonine phosphatase activity	3.93E-04	DUSP5, DUSP4, DUSP10	98.19512	0.056953
INTERPRO	IPR001763:Rhodanese-like domain	9.88E-04	DUSP5, DUSP4, DUSP10	62.78659	0.125809
INTERPRO	IPR024950:Dual specificity phosphatase	0.001651	DUSP5, DUSP4, DUSP10	48.60897	0.201217
INTERPRO	IPR020422:Dual specificity phosphatase, subgroup, catalytic domain	0.002102	DUSP5, DUSP4, DUSP10	43.05366	0.248837
SMART	SM00450:RHOD	0.002502	DUSP5, DUSP4, DUSP10	38.85093	0.095362
INTERPRO	IPR000340:Dual specificity phosphatase, catalytic domain	0.002738	DUSP5, DUSP4, DUSP10	37.67195	0.311283
GOTERM_MF_DIRECT	GO:0008138~protein tyrosine/serine/threonine phosphatase activity	0.003784	DUSP5, DUSP4, DUSP10	31.91341	0.431559
SMART	SM00195:DSPc	0.005743	DUSP5, DUSP4, DUSP10	25.53061	0.205763
INTERPRO	IPR016130:Protein-tyrosine phosphatase, active site	0.008861	DUSP5, DUSP4, DUSP10	20.64217	0.701948
INTERPRO	IPR000387:Protein-tyrosine/Dual specificity phosphatase	0.011076	DUSP5, DUSP4, DUSP10	18.37656	0.780121
GOTERM_MF_DIRECT	GO:0004725~protein tyrosine phosphatase activity	0.020807	DUSP5, DUSP4, DUSP10	13.16017	0.956411
UP_KEYWORDS	Protein phosphatase	0.022063	DUSP5, DUSP4, DUSP10	12.76548	0.892575
GOTERM_BP_DIRECT	GO:0016311~dephosphorylation	0.024199	DUSP5, DUSP4, DUSP10	12.13829	1
GOTERM_MF_DIRECT	GO:0016791~phosphatase activity	0.029935	DUSP5, DUSP4, DUSP10	10.81811	0.989202
GOTERM_MF_DIRECT	GO:0004721~phosphoprotein phosphatase activity	0.040364	DUSP5, DUSP4, DUSP10	9.183716	0.997843
UP_KEYWORDS	Hydrolase	0.066808	DUSP5, DUSP4, MMP9, DUSP10, PLA1A, TNFAIP3, MMP3	2.352488	0.999007

Annotation Cluster 10	Enrichment Score: 2.246166125995958				
Category	Term	PValue	Genes	Fold Enricl	Bonferroni
GOTERM_BP_DIRECT	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	1.29E-08	IL6, NFKBIA, NR4A1, LEF1, HMGA2, IL11, LIF, INHBA, FOS, REL, CREB3L1, FOSL1, FGF2, ETV4, NFATC1	6.648609	9.53E-06
GOTERM_MF_DIRECT	GO:0001077~transcriptional activator activity, RNA polymerase II core promoter proximal region sequence-specific binding	3.21E-05	FOS, LEF1, NR4A1, CREB3L1, HMGA2, FOSL1, NFATC1	11.0318	0.004767
UP_KEYWORDS	Nucleus	2.99E-04	PRKCA, NFKBIZ, PIM1, DUSP10, NFKBIA, NR4A1, LEF1, LIG4, HMGA2, FOS, DUSP4, REL, CREB3L1, HSPB1, TNFAIP3, FOSL1, FGF2, ETV4, NFATC1	2.318095	0.029441
GOTERM_MF_DIRECT	GO:0043565~sequence-specific DNA binding	5.26E-04	FOS, REL, LEF1, NR4A1, CREB3L1, FOSL1, ETV4, NFATC1	5.377721	0.07538
UP_KEYWORDS	DNA-binding	0.001596	FOS, REL, LEF1, NR4A1, CREB3L1, HMGA2, TNFAIP3, FOSL1, ETV4, NFATC1	3.448695	0.147598
GOTERM_BP_DIRECT	GO:0006357~regulation of transcription from RNA polymerase II promoter	0.001739	FOS, NFKBIZ, INHBA, LEF1, FOSL1, NFATC1	6.665356	0.723776
GOTERM_CC_DIRECT	GO:0005667~transcription factor complex	0.001882	FOS, REL, LEF1, NR4A1, NFATC1	9.205056	0.143129
GOTERM_MF_DIRECT	GO:0003700~transcription factor activity, sequence-specific DNA binding	0.003583	FOS, REL, LEF1, NR4A1, CREB3L1, FOSL1, ETV4, NFATC1	3.85515	0.414198
GOTERM_CC_DIRECT	GO:0005634~nucleus	0.005544	PRKCA, NFKBIZ, PIM1, DUSP10, NFKBIA, LEF1, NR4A1, LIG4, HMGA2, MMP3, FOS, DUSP4, REL, HSPA2, HSPB1, CREB3L1, TNFAIP3, FOSL1, FGF2, ETV4, NFATC1	1.714994	0.366124
GOTERM_MF_DIRECT	GO:0003677~DNA binding	0.007482	FOS, REL, LEF1, NR4A1, CREB3L1, LIG4, HMGA2, TNFAIP3, FOSL1, ETV4, NFATC1	2.534182	0.673416

GOTERM_MF_DIRECT	GO:0008134~transcription factor binding	0.007606	FOS, PIM1, LEF1, NR4A1, NFATC1	6.220939	0.679444
GOTERM_MF_DIRECT	GO:0000978~RNA polymerase II core promoter proximal region sequence-specific DNA binding	0.00899	FOS, LEF1, FOSL1, ETV4, NFATC1	5.926354	0.73959
GOTERM_MF_DIRECT	GO:0000977~RNA polymerase II regulatory region sequence-specific DNA binding	0.014038	REL, LEF1, FOSL1, NFATC1	7.701578	0.878344
GOTERM_MF_DIRECT	GO:0003682~chromatin binding	0.021513	FOS, REL, LEF1, CREB3L1, NFATC1	4.565581	0.960853
UP_KEYWORDS	Activator	0.023715	NFKBIZ, LEF1, CREB3L1, ETV4, NFATC1	4.432458	0.909288
UP_KEYWORDS	Transcription regulation	0.036043	NFKBIZ, REL, LEF1, NR4A1, CREB3L1, HMGA2, ETV4, NFATC1	2.459903	0.974545
UP_KEYWORDS	Transcription	0.041957	NFKBIZ, REL, LEF1, NR4A1, CREB3L1, HMGA2, ETV4, NFATC1	2.380509	0.986244
GOTERM_BP_DIRECT	GO:0006355~regulation of transcription, DNA-templated	0.057428	FOS, NFKBIZ, REL, LEF1, NR4A1, CREB3L1, HMGA2, FOSL1, ETV4, NFATC1	1.935166	1
GOTERM_BP_DIRECT	GO:0006351~transcription, DNA-templated	0.117251	NFKBIZ, REL, LEF1, NR4A1, CREB3L1, HMGA2, ETV4, NFATC1	1.871722	1
GOTERM_BP_DIRECT	GO:0000122~negative regulation of transcription from RNA polymerase II promoter	0.217659	REL, LEF1, HMGA2, NFATC1	2.419887	1
UP_KEYWORDS	Alternative splicing	0.767575	NFKBIZ, CACNA2D1, TNC, LEF1, CREB3L1, HSPB1, ETV4, NFATC1	0.926002	1
UP_SEQ_FEATURE	splice variant	0.913982	NFKBIZ, CACNA2D1, TNC, PIM1, LEF1, CREB3L1, HSPB1, NFATC1	0.767939	1
Annotation Cluster 11	Enrichment Score: 2.1054837611080806				
Category	Term	PValue	Genes	Fold Enricl	Bonferroni
KEGG_PATHWAY	mmu05134:Legionellosis	0.00314	CXCL1, IL6, HSPA2, NFKBIA	13.16389	0.339742

KEGG_PATHWAY	mmu04621:NOD-like receptor signaling pathway	0.00314	CXCL1, IL6, NFKBIA, TNFAIP3	13.16389	0.339742
KEGG_PATHWAY	mmu05164:Influenza A	0.011562	PRKCA, IL6, HSPA2, SOCS3, NFKBIA	5.484952	0.784574
KEGG_PATHWAY	mmu05162:Measles	0.033203	IL6, HSPA2, NFKBIA, TNFAIP3	5.517217	0.988405
Annotation Cluster 12	Enrichment Score: 1.9600844654307423				
Category	Term	PValue	Genes	Fold Enric	Bonferroni
GOTERM_BP_DIRECT	GO:0008285~negative regulation of cell proliferation	0.001503	PRKCA, LIF, INHBA, IL6, FOSL1, FGF2	6.891006	0.67085
GOTERM_BP_DIRECT	GO:0048661~positive regulation of smooth muscle cell proliferation	0.013524	PRKCA, IL6, FGF2	16.53841	0.999957
GOTERM_BP_DIRECT	GO:0070374~positive regulation of ERK1 and ERK2 cascade	0.064836	PRKCA, IL6, FGF2	7.037623	1
Annotation Cluster 13	Enrichment Score: 1.7672878620366368				
Category	Term	PValue	Genes	Fold Enric	Bonferroni
KEGG_PATHWAY	mmu05161:Hepatitis B	9.52E-05	PRKCA, FOS, IL6, MMP9, NFKBIA, CREB3L1, NFATC1	8.993819	0.012485
KEGG_PATHWAY	mmu05168:Herpes simplex infection	0.092929	FOS, IL6, SOCS3, NFKBIA	3.607411	0.999997
KEGG_PATHWAY	mmu04620:Toll-like receptor signaling pathway	0.096586	FOS, IL6, NFKBIA	5.571843	0.999998
KEGG_PATHWAY	mmu05142:Chagas disease (American trypanosomiasis)	0.09983	FOS, IL6, NFKBIA	5.463651	0.999999
Annotation Cluster 14	Enrichment Score: 1.6694518425935816				
Category	Term	PValue	Genes	Fold Enric	Bonferroni

KEGG_PATHWAY	mmu05161:Hepatitis B	9.52E-05	PRKCA, FOS, IL6, MMP9, NFKBIA, CREB3L1, NFATC1	8.993819	0.012485
KEGG_PATHWAY	mmu04380:Osteoclast differentiation	0.003978	FOS, SOCS3, NFKBIA, FOSL1, NFATC1	7.443864	0.409153
BIOCARTA	m_tcrPathway:T Cell Receptor Signaling Pathway	0.012678	PRKCA, FOS, NFKBIA, NFATC1	7.323864	0.690819
BIOCARTA	m_cdmacPathway:Cadmium induces DNA synthesis and proliferation in macrophages	0.013811	PRKCA, FOS, NFKBIA	15.10547	0.721814
KEGG_PATHWAY	mmu04921:Oxytocin signaling pathway	0.042485	PRKCA, FOS, CACNA2D1, NFATC1	5.002276	0.996755
KEGG_PATHWAY	mmu04662:B cell receptor signaling pathway	0.051019	FOS, NFKBIA, NFATC1	8.039373	0.999005
BIOCARTA	m_bcrPathway:BCR Signaling Pathway	0.057219	PRKCA, FOS, NFATC1	7.108456	0.995576
BIOCARTA	m_gpcrPathway:Signaling Pathway from G-Protein Families	0.057219	PRKCA, FOS, NFATC1	7.108456	0.995576
KEGG_PATHWAY	mmu04024:cAMP signaling pathway	0.081979	FOS, NFKBIA, CREB3L1, NFATC1	3.80884	0.999988
KEGG_PATHWAY	mmu04660:T cell receptor signaling pathway	0.096586	FOS, NFKBIA, NFATC1	5.571843	0.999998
BIOCARTA	m_keratinocytePathway:Keratinocyte Differentiation	0.116105	PRKCA, FOS, NFKBIA	4.738971	0.999988
Annotation Cluster 15	Enrichment Score: 1.4442820906558291				
Category	Term	PValue	Genes	Fold Enrich	Bonferroni
KEGG_PATHWAY	mmu05161:Hepatitis B	9.52E-05	PRKCA, FOS, IL6, MMP9, NFKBIA, CREB3L1, NFATC1	8.993819	0.012485
KEGG_PATHWAY	mmu05031:Amphetamine addiction	0.047164	PRKCA, FOS, CREB3L1	8.399345	0.9983
KEGG_PATHWAY	mmu04725:Cholinergic synapse	0.116493	PRKCA, FOS, CREB3L1	4.980142	1

KEGG_PATHWAY	mmu04728:Dopaminergic synapse	0.1535	PRKCA, FOS, CREB3L1	4.199672	1
GOTERM_CC_DIRECT	GO:0005783~endoplasmic reticulum	0.748245	PRKCA, FOS, CREB3L1	1.114626	1
Annotation Cluster 16	Enrichment Score: 1.335702433107032				
Category	Term	PValue	Genes	Fold Enric	Bonferroni
UP_SEQ_FEATURE	metal ion-binding site:Calcium 3; via carbonyl oxygen	9.35E-04	PRKCA, MMP9, MMP3	64.32857	0.169803
UP_SEQ_FEATURE	metal ion-binding site:Calcium 3	0.002042	PRKCA, MMP9, MMP3	43.57742	0.334152
UP_SEQ_FEATURE	metal ion-binding site:Calcium 2; via carbonyl oxygen	0.0029	PRKCA, MMP9, MMP3	36.51081	0.438975
UP_SEQ_FEATURE	metal ion-binding site:Calcium 1	0.004644	PRKCA, MMP9, MMP3	28.74255	0.603965
UP_SEQ_FEATURE	metal ion-binding site:Calcium 2	0.006995	PRKCA, MMP9, MMP3	23.29138	0.752654
GOTERM_BP_DIRECT	GO:0006915~apoptotic process	0.036483	PRKCA, PIM1, NR4A1, TNFAIP3, DDIT4	3.868635	1
GOTERM_CC_DIRECT	GO:0043234~protein complex	0.127605	PRKCA, MMP9, NFKBIA, MMP3	3.130892	0.999986
UP_KEYWORDS	Calcium	0.178148	PRKCA, CACNA2D1, MMP9, MMP3	2.675554	1
GOTERM_MF_DIRECT	GO:0008270~zinc ion binding	0.231012	PRKCA, MMP9, NR4A1, TNFAIP3, MMP3	1.979126	1
UP_KEYWORDS	Metal-binding	0.391169	PRKCA, CACNA2D1, MMP9, PIM1, NR4A1, LIG4, TNFAIP3, MMP3	1.303495	1
UP_KEYWORDS	Zinc	0.51349	PRKCA, MMP9, NR4A1, TNFAIP3, MMP3	1.317701	1
UP_KEYWORDS	Zinc-finger	0.773209	PRKCA, NR4A1, TNFAIP3	1.060391	1
GOTERM_MF_DIRECT	GO:0046872~metal ion binding	0.808263	PRKCA, CACNA2D1, MMP9, NR4A1, LIG4, TNFAIP3, MMP3	0.887805	1

Annotation Cluster 17	Enrichment Score: 0.9401008508974922				
Category	Term	PValue	Genes	Fold Enrich	Bonferroni
GOTERM_BP_DIRECT	GO:0008283~cell proliferation	0.012607	PIM1, LIG4, HMGA2, DDIT4	8.018625	0.999915
UP_KEYWORDS	Cell cycle	0.302996	PIM1, LIG4, HMGA2	2.650978	1
GOTERM_BP_DIRECT	GO:0007049~cell cycle	0.395951	PIM1, LIG4, HMGA2	2.154842	1

Annotation Cluster 18	Enrichment Score: 0.534160811306344				
Category	Term	PValue	Genes	Fold Enrich	Bonferroni
UP_KEYWORDS	Hydrolase	0.066808	DUSP5, DUSP4, MMP9, DUSP10, PLA1A, TNFAIP3, MMP3	2.352488	0.999007
GOTERM_MF_DIRECT	GO:0008270~zinc ion binding	0.231012	PRKCA, MMP9, NR4A1, TNFAIP3, MMP3	1.979126	1
UP_KEYWORDS	Protease	0.247788	MMP9, TNFAIP3, MMP3	3.061831	1
GOTERM_MF_DIRECT	GO:0016787~hydrolase activity	0.272762	DUSP4, MMP9, DUSP10, PLA1A, TNFAIP3, MMP3	1.66541	1
GOTERM_MF_DIRECT	GO:0008233~peptidase activity	0.332293	MMP9, TNFAIP3, MMP3	2.473908	1
GOTERM_BP_DIRECT	GO:0006508~proteolysis	0.370491	MMP9, TNFAIP3, MMP3	2.273322	1
UP_KEYWORDS	Zinc	0.51349	PRKCA, MMP9, NR4A1, TNFAIP3, MMP3	1.317701	1
GOTERM_MF_DIRECT	GO:0046872~metal ion binding	0.808263	PRKCA, CACNA2D1, MMP9, NR4A1, LIG4, TNFAIP3, MMP3	0.887805	1

Annotation Cluster 19	Enrichment Score: 0.3494247586609406				
Category	Term	PValue	Genes	Fold Enrich	Bonferroni
UP_KEYWORDS	Methylation	0.239062	DVL3, HSPA2, RIN1, HSPB1	2.304878	1
UP_KEYWORDS	Cytoskeleton	0.57048	HSPA2, RIN1, HSPB1	1.54661	1
GOTERM_CC_DIRECT	GO:0005856~cytoskeleton	0.656107	HSPA2, RIN1, HSPB1	1.324933	1

Annotation Cluster 20	Enrichment Score: 0.20317962059120928				
Category	Term	PValue	Genes	Fold Enrich	Bonferroni

UP_SEQ_FEATURE	binding site:ATP	0.361391	PRKCA, PIM1, LIG4	2.317153	1
UP_KEYWORDS	ATP-binding	0.43463	PRKCA, HSPA2, PIM1, LIG4	1.623392	1
UP_KEYWORDS	Nucleotide-binding	0.607193	PRKCA, HSPA2, PIM1, LIG4	1.261507	1
GOTERM_MF_DIRECT	GO:0005524~ATP binding	0.683485	PRKCA, HSPA2, PIM1, LIG4	1.129429	1
GOTERM_MF_DIRECT	GO:0000166~nucleotide binding	0.945955	PRKCA, HSPA2, LIG4	0.659368	1
GOTERM_CC_DIRECT	GO:0005886~plasma membrane	0.979263	PRKCA, PIM1, NFKBIA, RIN1, HSPB1, LIG4	0.605109	1
Annotation Cluster 21	Enrichment Score: 7.100104747328335E-4				
Category	Term	PValue	Genes	Fold Enricl	Bonferroni
UP_SEQ_FEATURE	topological domain:Cytoplasmic	0.990623	CACNA2D1, CSF2RB, CREB3L1	0.469063	1
UP_SEQ_FEATURE	transmembrane region	0.999695	CACNA2D1, CSF2RB, CREB3L1	0.313288	1
UP_KEYWORDS	Membrane	0.999934	PRKCA, CACNA2D1, PIM1, RIN1, CSF2RB, CREB3L1	0.382244	1
UP_KEYWORDS	Transmembrane helix	0.999992	CACNA2D1, CSF2RB, CREB3L1	0.239192	1
UP_KEYWORDS	Transmembrane	0.999992	CACNA2D1, CSF2RB, CREB3L1	0.238607	1
GOTERM_CC_DIRECT	GO:0016021~integral component of membrane	0.999999	CACNA2D1, CSF2RB, CREB3L1	0.214401	1

S. Table 2 Mouse GO IR compared to healthy fibroblasts_downregulated

Annotation Cluster 1	Enrichment Score:				
Category	Term	PValue	Genes	Fold Enricl	Bonferroni
UP_SEQ_FEATURE	propeptide:N-terminal propeptide	6.71E-08	COL3A1, COL1A2, COL1A1, COL11A1	414.069	1.11E-05
UP_SEQ_FEATURE	propeptide:C-terminal propeptide	1.17E-07	COL3A1, COL1A2, COL1A1, COL11A1	354.9163	1.93E-05
UP_SEQ_FEATURE	domain:Fibrillar collagen NC1	4.01E-07	COL3A1, COL1A2, COL1A1, COL11A1	248.4414	6.61E-05
INTERPRO	IPR000885:Fibrillar collagen, C-	4.11E-07	COL3A1, COL1A2, COL1A1, COL11A1	249.6242	4.65E-05
GOTERM_BP_DIRECT	GO:0030199~collagen fibril	4.22E-07	SFRP2, COL3A1, COL1A2, COL1A1, COL11A1	77.2735	2.61E-04
SMART	SM00038:COLFI	1.75E-06	COL3A1, COL1A2, COL1A1, COL11A1	151.6364	7.17E-05
KEGG_PATHWAY	mmu04510:Focal adhesion	3.94E-06	VEGFB, BRAF, COL3A1, COL1A2, PDGFC, COL1A1, COL11A1, THBS4	11.00877	4.76E-04
KEGG_PATHWAY	mmu05146:Amoebiasis	3.81E-05	PLCB4, COL3A1, COL1A2, TLR4, COL1A1, COL11A1	14.60779	0.0046
GOTERM_MF_DIRECT	GO:0005201~extracellular matrix structural constituent	4.22E-05	COL3A1, COL1A2, COL1A1, COL11A1	56.73496	0.005386
KEGG_PATHWAY	mmu04611:Platelet activation	6.55E-05	PLCB4, COL3A1, COL1A2, COL1A1, COL11A1, SYK	13.04665	0.007899
INTERPRO	IPR008160:Collagen triple helix	1.65E-04	COL3A1, COL1A2, COL1A1, COL11A1	36.12982	0.018441
UP_KEYWORDS	Collagen	1.73E-04	COL3A1, COL1A2, COL1A1, COL11A1	35.57647	0.018173
GOTERM_MF_DIRECT	GO:0048407~platelet-derived growth factor binding	1.74E-04	COL3A1, COL1A2, COL1A1	145.3833	0.022063
UP_KEYWORDS	Hydroxylation	1.92E-04	COL3A1, COL1A2, COL1A1, COL11A1	34.36364	0.020119
KEGG_PATHWAY	mmu04512:ECM-receptor	1.97E-04	COL3A1, COL1A2, COL1A1, COL11A1, THBS4	16.18476	0.023603
UP_KEYWORDS	Extracellular matrix	2.18E-04	COL3A1, COL1A2, COL1A1, COL11A1, THBS4	16.08511	0.022813
GOTERM_CC_DIRECT	GO:0005581~collagen trimer	2.45E-04	COL3A1, COL1A2, COL1A1, COL11A1	31.58554	0.027529
UP_SEQ_FEATURE	region of interest:Triple-helical	3.51E-04	COL3A1, COL1A1, COL11A1	103.5172	0.056294
GOTERM_CC_DIRECT	GO:0031012~extracellular matrix	8.66E-04	COL3A1, COL1A2, COL1A1, COL11A1, THBS4	11.14626	0.094067
UP_KEYWORDS	Secreted	9.53E-04	VEGFB, SFRP2, COL3A1, IL1RAP, COL1A2, PDGFC, COL1A1, COL11A1, THBS4	4.037982	0.096147
GOTERM_CC_DIRECT	GO:0005578~proteinaceous extracellular matrix	0.001132	COL3A1, COL1A2, COL1A1, COL11A1, THBS4	10.37025	0.121142
GOTERM_BP_DIRECT	GO:0071230~cellular response to amino acid stimulus	0.001346	COL3A1, COL1A2, PDGFC, COL1A1	17.59805	0.564964
GOTERM_CC_DIRECT	GO:0005576~extracellular region	0.003066	VEGFB, SFRP2, COL3A1, IL1RAP, COL1A2, PDGFC, COL1A1, COL11A1, THBS4	3.36486	0.295372
KEGG_PATHWAY	mmu04974:Protein digestion and	0.003111	COL3A1, COL1A2, COL1A1, COL11A1	12.94781	0.314124

GOTERM_BP_DIRECT	GO:0001568~blood vessel	0.005763	COL3A1, COL1A2, COL1A1	25.46761	0.971896
GOTERM_BP_DIRECT	GO:0001501~skeletal system	0.012692	COL3A1, COL1A2, COL1A1	16.89907	0.999627
UP_KEYWORDS	Calcium	0.02019	COL3A1, COL1A2, COL1A1, COL11A1, THBS4	4.570738	0.884911
GOTERM_CC_DIRECT	GO:0005615~extracellular space	0.02049	VEGFB, SFRP2, COL3A1, COL1A2, PDGFC, COL1A1, THBS4	3.050399	0.905595
UP_KEYWORDS	Metal-binding	0.13205	ACVR2A, BRAF, COL3A1, COL1A2, COL1A1, COL11A1, RAD50, PHF6	1.781443	1
GOTERM_MF_DIRECT	GO:0046872~metal ion binding	0.317813	ACVR2A, BRAF, COL3A1, COL1A2, COL1A1, COL11A1, RAD50, PHF6	1.386667	1
Annotation Cluster 2	Enrichment Score: 3.242989941052708				
Category	Term	PValue	Genes	Fold Enric	Bonferroni
GOTERM_BP_DIRECT	GO:0050680~negative regulation of epithelial cell proliferation	2.05E-04	SFRP2, RB1, GAS1, APC	33.48519	0.119192
GOTERM_BP_DIRECT	GO:0007050~cell cycle arrest	2.91E-04	RB1, GAS1, FOXO4, APC	29.76461	0.164579
GOTERM_BP_DIRECT	GO:0008285~negative regulation of cell proliferation	0.003124	SFRP2, PBRM1, RB1, FOXO4, APC	7.84809	0.855414
Annotation Cluster 3	Enrichment Score: 3.1525466853972954				
Category	Term	PValue	Genes	Fold Enric	Bonferroni
KEGG_PATHWAY	mmu04151:PI3K-Akt signaling pathway	6.39E-09	VEGFB, KRAS, COL3A1, COL1A2, TLR4, PDGFC, GNG2, EFNA5, COL1A1, COL11A1, THBS4, SYK	9.738525	7.73E-07
KEGG_PATHWAY	mmu04510:Focal adhesion	3.94E-06	VEGFB, BRAF, COL3A1, COL1A2, PDGFC, COL1A1, COL11A1, THBS4	11.00877	4.76E-04
UP_KEYWORDS	Secreted	9.53E-04	VEGFB, SFRP2, COL3A1, IL1RAP, COL1A2, PDGFC, COL1A1, COL11A1, THBS4	4.037982	0.096147
UP_KEYWORDS	Disulfide bond	0.001049	VEGFB, ACVR2A, SFRP2, COL3A1, IL1RAP, COL1A2, TLR4, PDGFC, EFNA5, COL1A1, COL11A1, THBS4	2.903969	0.105281

UP_SEQ_FEATURE	signal peptide	0.00141	COL3A1, TLR4, GAS1, VEGFB, ACVR2A, SFRP2, IL1RAP, COL1A2, EFNA5, PDGFC, COL1A1, COL11A1, THBS4	2.584617	0.207704
UP_KEYWORDS	Glycoprotein	0.001548	COL3A1, EZH2, TLR4, GAS1, VEGFB, ACVR2A, IL1RAP, COL1A2, EFNA5, PDGFC, COL1A1, COL11A1, THBS4	2.576147	0.1514
UP_KEYWORDS	Signal	0.002171	COL3A1, TLR4, GAS1, RB1, VEGFB, ACVR2A, SFRP2, IL1RAP, COL1A2, EFNA5, PDGFC, COL1A1, COL11A1, THBS4	2.329738	0.205752
GOTERM_CC_DIRECT	GO:0005576~extracellular region	0.003066	VEGFB, SFRP2, COL3A1, IL1RAP, COL1A2, PDGFC, COL1A1, COL11A1, THBS4	3.36486	0.295372
GOTERM_CC_DIRECT	GO:0005615~extracellular space	0.02049	VEGFB, SFRP2, COL3A1, COL1A2, PDGFC, COL1A1, THBS4	3.050399	0.905595
UP_SEQ_FEATURE	disulfide bond	0.033027	VEGFB, ACVR2A, SFRP2, COL3A1, IL1RAP, TLR4, PDGFC, EFNA5, THBS4	2.227064	0.996079
UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	0.084944	ACVR2A, IL1RAP, COL1A2, TLR4, PDGFC, EFNA5, COL1A1, GAS1, COL11A1, THBS4	1.743204	1
Annotation Cluster 4	Enrichment Score: 2.5122576737300997				
Category	Term	PValue	Genes	Fold Enrich	Bonferroni
GOTERM_BP_DIRECT	GO:0051781~positive regulation of cell division	5.03E-05	VEGFB, PDGFC, THBS4, APC	53.5763	0.030608
UP_KEYWORDS	Mitogen	9.68E-04	VEGFB, PDGFC, THBS4	63	0.097573
UP_KEYWORDS	Growth factor	0.011442	VEGFB, PDGFC, THBS4	17.85827	0.704729
GOTERM_CC_DIRECT	GO:0005615~extracellular space	0.02049	VEGFB, SFRP2, COL3A1, COL1A2, PDGFC, COL1A1, THBS4	3.050399	0.905595
GOTERM_MF_DIRECT	GO:0008083~growth factor activity	0.024053	VEGFB, PDGFC, THBS4	12.03172	0.955686
Annotation Cluster 5	Enrichment Score: 2.134573188535231				
Category	Term	PValue	Genes	Fold Enrich	Bonferroni

KEGG_PATHWAY	mmu04014:Ras signaling pathway	8.83E-04	VEGFB, KRAS, PDGFC, GNG2, EFNA5, FOXO4	7.463367	0.101389
UP_SEQ_FEATURE	propeptide:Removed in mature form	0.005848	KRAS, GNG2, EFNA5, GAS1	10.43871	0.620052
UP_KEYWORDS	Lipoprotein	0.076431	KRAS, GNG2, EFNA5, GAS1	3.876923	0.999781
Annotation Cluster 6	Enrichment Score: 2.1001117789576402				
Category	Term	PValue	Genes	Fold Enricl	Bonferroni
UP_KEYWORDS	Cell cycle	1.19E-04	RB1, GAS1, FOXO4, STAG2, RAD50, SMC3, HELLS	8.453674	0.012563
GOTERM_BP_DIRECT	GO:0007049~cell cycle	3.64E-04	RB1, GAS1, FOXO4, STAG2, RAD50, SMC3, HELLS	6.871553	0.201721
GOTERM_CC_DIRECT	GO:0000775~chromosome, centromeric region	0.001151	STAG2, SMC3, HELLS, PHF6	18.59291	0.123002
GOTERM_MF_DIRECT	GO:0003682~chromatin binding	0.00703	EZH2, PBRM1, STAG2, SMC3, HELLS	6.239628	0.59465
GOTERM_BP_DIRECT	GO:0051301~cell division	0.021545	RB1, STAG2, SMC3, HELLS	6.446346	0.999999
UP_KEYWORDS	Mitosis	0.043086	STAG2, SMC3, HELLS	8.756757	0.990613
KEGG_PATHWAY	mmu04110:Cell cycle	0.065175	RB1, STAG2, SMC3	6.891577	0.999713
GOTERM_BP_DIRECT	GO:0007067~mitotic nuclear division	0.072428	STAG2, SMC3, HELLS	6.527798	1
UP_KEYWORDS	Cell division	0.081513	STAG2, SMC3, HELLS	6.096774	0.999878
Annotation Cluster 7	Enrichment Score: 2.062838212952619				
Category	Term	PValue	Genes	Fold Enricl	Bonferroni
GOTERM_CC_DIRECT	GO:0000775~chromosome, centromeric region	0.001151	STAG2, SMC3, HELLS, PHF6	18.59291	0.123002
GOTERM_CC_DIRECT	GO:0005694~chromosome	0.001548	EZH2, STAG2, RAD50, SMC3, PHF6	9.526163	0.16186
UP_KEYWORDS	Chromosome	0.001732	EZH2, STAG2, RAD50, SMC3, PHF6	9.242054	0.167868
GOTERM_MF_DIRECT	GO:0003682~chromatin binding	0.00703	EZH2, PBRM1, STAG2, SMC3, HELLS	6.239628	0.59465
UP_KEYWORDS	Centromere	0.012674	STAG2, SMC3, PHF6	16.92537	0.741272

GOTERM_CC_DIRECT	GO:0005634~nucleus	0.0141	BRAF, EZH2, BNIP3, RB1, FOXO4, SMC3, RAD50, PLCB4, CASP12, PBRM1, PDGFC, STAG2, HELLS, SYK, APC, PHF6	1.742216	0.801874
GOTERM_CC_DIRECT	GO:0005654~nucleoplasm	0.019873	EZH2, PBRM1, BNIP3, FOXO4, STAG2, RAD50, SMC3, PHF6	2.709664	0.898569
UP_KEYWORDS	Nucleus	0.049023	BRAF, EZH2, PBRM1, PDGFC, RB1, FOXO4, STAG2, RAD50, SMC3, HELLS, PHF6	1.834142	0.995147
UP_KEYWORDS	Phosphoprotein	0.072031	BRAF, EZH2, BNIP3, RB1, FOXO4, SMC3, RAD50, CASP12, PBRM1, COL1A1, STAG2, HELLS, SYK, APC, PHF6	1.488775	0.999638

Annotation Cluster 8 Enrichment Score: 1.922270358680305

Category	Term	PValue	Genes	Fold Enrich	Bonferroni
KEGG_PATHWAY	mmu04014:Ras signaling pathway	8.83E-04	VEGFB, KRAS, PDGFC, GNG2, EFNA5, FOXO4	7.463367	0.101389
UP_KEYWORDS	Developmental protein	0.007336	VEGFB, SFRP2, PDGFC, EFNA5, FOXO4, HELLS	4.647541	0.541815
GOTERM_BP_DIRECT	GO:0007275~multicellular organism development	0.022452	VEGFB, SFRP2, PDGFC, EFNA5, FOXO4, HELLS	3.51448	0.999999
GOTERM_BP_DIRECT	GO:0030154~cell differentiation	0.034637	VEGFB, BRAF, SFRP2, EFNA5, FOXO4	3.863675	1
UP_KEYWORDS	Differentiation	0.04857	VEGFB, SFRP2, EFNA5, FOXO4	4.681115	0.994895

Annotation Cluster 9 Enrichment Score: 1.7765422608708206

Category	Term	PValue	Genes	Fold Enrich	Bonferroni
KEGG_PATHWAY	mmu05218:Melanoma	0.001683	KRAS, BRAF, PDGFC, RB1	16.04799	0.18442
KEGG_PATHWAY	mmu05200:Pathways in cancer	0.001691	VEGFB, PLCB4, KRAS, BRAF, GNG2, RB1, APC	5.048008	0.185183
KEGG_PATHWAY	mmu05215:Prostate cancer	0.003111	KRAS, BRAF, PDGFC, RB1	12.94781	0.314124
KEGG_PATHWAY	mmu05219:Bladder cancer	0.008311	KRAS, BRAF, RB1	20.84282	0.635715
KEGG_PATHWAY	mmu05213:Endometrial cancer	0.013137	KRAS, BRAF, APC	16.43376	0.798128
KEGG_PATHWAY	mmu05223:Non-small cell lung cancer	0.015132	KRAS, BRAF, RB1	15.25992	0.841965
KEGG_PATHWAY	mmu05210:Colorectal cancer	0.019485	KRAS, BRAF, APC	13.35243	0.907534
KEGG_PATHWAY	mmu05214:Glioma	0.020062	KRAS, BRAF, RB1	13.14701	0.913893

KEGG_PATHWAY	mmu05212:Pancreatic cancer	0.020062	KRAS, BRAF, RB1	13.14701	0.913893
KEGG_PATHWAY	mmu05220:Chronic myeloid leukemia	0.0243	KRAS, BRAF, RB1	11.86883	0.949035
KEGG_PATHWAY	mmu04810:Regulation of actin cytoskeleton	0.034081	KRAS, BRAF, PDGFC, APC	5.349331	0.98494
UP_KEYWORDS	Methylation	0.122646	KRAS, BRAF, GNG2, RB1	3.15	0.999999
UP_KEYWORDS	Cytoplasm	0.689339	KRAS, BRAF, PDGFC, FOXO4, SYK, APC	1.029973	1
Annotation Cluster 10	Enrichment Score: 1.7294883617400314				
Category	Term	PValue	Genes	Fold Enricl	Bonferroni
KEGG_PATHWAY	mmu04015:Rap1 signaling pathway	6.49E-04	VEGFB, PLCB4, KRAS, BRAF, PDGFC, EFNA5	7.986501	0.075599
KEGG_PATHWAY	mmu05200:Pathways in cancer	0.001691	VEGFB, PLCB4, KRAS, BRAF, GNG2, RB1, APC	5.048008	0.185183
KEGG_PATHWAY	mmu04726:Serotonergic synapse	0.009628	PLCB4, KRAS, BRAF, GNG2	8.631874	0.689844
KEGG_PATHWAY	mmu04730:Long-term depression	0.017797	PLCB4, KRAS, BRAF	14.00911	0.886141
KEGG_PATHWAY	mmu04720:Long-term potentiation	0.020646	PLCB4, KRAS, BRAF	12.94781	0.919888
KEGG_PATHWAY	mmu04062:Chemokine signaling pathway	0.027542	PLCB4, KRAS, BRAF, GNG2	5.813303	0.965929
GOTERM_BP_DIRECT	GO:0007165~signal transduction	0.047147	KRAS, BRAF, IL1RAP, TLR4, GNG2, SMC3	2.881594	1
KEGG_PATHWAY	mmu04725:Cholinergic synapse	0.055309	PLCB4, KRAS, GNG2	7.562439	0.998977
UP_KEYWORDS	Methylation	0.122646	KRAS, BRAF, GNG2, RB1	3.15	0.999999
KEGG_PATHWAY	mmu05034:Alcoholism	0.148177	KRAS, BRAF, GNG2	4.230473	1
Annotation Cluster 11	Enrichment Score: 1.4428988027085192				
Category	Term	PValue	Genes	Fold Enricl	Bonferroni
GOTERM_BP_DIRECT	GO:0051276~chromosome organization	0.001685	RAD50, SMC3, APC	47.58421	0.647234
GOTERM_BP_DIRECT	GO:0006974~cellular response to DNA damage stimulus	0.145236	RAD50, SMC3, APC	4.305238	1

UP_KEYWORDS	Coiled coil	0.191751	PLCB4, PBRM1, STAG2, RAD50, SMC3, HELLS, APC	1.720416	1

Annotation Cluster 12 Enrichment Score: 1.0575525256474256

Category	Term	PValue	Genes	Fold Enrich	Bonferroni
UP_KEYWORDS	Innate immunity	0.037822	IL1RAP, TLR4, SYK	9.410788	0.983209
UP_KEYWORDS	Immunity	0.092638	IL1RAP, TLR4, SYK	5.65586	0.999967
GOTERM_BP_DIRECT	GO:0002376~immune system process	0.125109	IL1RAP, TLR4, SYK	4.721149	1
GOTERM_BP_DIRECT	GO:0045087~innate immune response	0.134267	IL1RAP, TLR4, SYK	4.5205	1

Annotation Cluster 13 Enrichment Score: 1.0419788437733186

Category	Term	PValue	Genes	Fold Enrich	Bonferroni
UP_KEYWORDS	Acetylation	0.00399	KRAS, BRAF, PBRM1, GNG2, RB1, FOXO4, STAG2, RAD50, SMC3, PHF6, APC	2.66112	0.345467
UP_KEYWORDS	Chromatin regulator	0.046431	EZH2, PBRM1, RB1	8.4	0.993524
UP_KEYWORDS	Nucleus	0.049023	BRAF, EZH2, PBRM1, PDGFC, RB1, FOXO4, STAG2, RAD50, SMC3, HELLS, PHF6	1.834142	0.995147
GOTERM_BP_DIRECT	GO:0016569~covalent chromatin modification	0.067498	EZH2, PBRM1, RB1	6.797744	1
UP_KEYWORDS	Transcription regulation	0.075341	EZH2, PBRM1, RB1, FOXO4, HELLS, PHF6	2.521401	0.999752
UP_KEYWORDS	Transcription	0.08417	EZH2, PBRM1, RB1, FOXO4, HELLS, PHF6	2.440022	0.99991
GOTERM_MF_DIRECT	GO:0019899~enzyme binding	0.133177	RB1, FOXO4, PHF6	4.543229	1
GOTERM_BP_DIRECT	GO:0006351~transcription, DNA-templated	0.178965	EZH2, PBRM1, RB1, FOXO4, HELLS, PHF6	1.918515	1
GOTERM_BP_DIRECT	GO:0006355~regulation of transcription, DNA-templated	0.299104	EZH2, PBRM1, RB1, FOXO4, HELLS, PHF6	1.586836	1
UP_KEYWORDS	DNA-binding	0.33751	PBRM1, RB1, FOXO4, PHF6	1.885287	1
GOTERM_MF_DIRECT	GO:0003677~DNA binding	0.369165	PBRM1, RB1, FOXO4, RAD50, PHF6	1.574265	1

Annotation Cluster 14 Enrichment Score: 0.9202226534608133

Category	Term	PValue	Genes	Fold Enric	Bonferroni
UP_KEYWORDS	Cell membrane	0.039925	KRAS, BRAF, IL1RAP, TLR4, PDGFC, GNG2, EFNA5, GAS1, SYK, APC	2.011173	0.986684
GOTERM_CC_DIRECT	GO:0005886~plasma membrane	0.081136	ACVR2A, KRAS, BRAF, IL1RAP, TLR4, PDGFC, GNG2, EFNA5, GAS1, STAG2, SYK, APC	1.613623	0.999935
GOTERM_CC_DIRECT	GO:0016020~membrane	0.109983	BRAF, BNIP3, TLR4, GAS1, RAD50, VEGFB, ACVR2A, KRAS, IL1RAP, GNG2, EFNA5, PDGFC, STAG2, APC, SYK	1.40483	0.999998
UP_KEYWORDS	Membrane	0.585233	ACVR2A, KRAS, BRAF, IL1RAP, BNIP3, TLR4, PDGFC, GNG2, EFNA5, GAS1, SYK, APC	1.0448	1

Annotation Cluster 15 Enrichment Score: 0.8645895536634423

Category	Term	PValue	Genes	Fold Enric	Bonferroni
UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	0.015224	ACVR2A, BRAF, RAD50, SMC3, HELLS, SYK	3.869803	0.920439
UP_KEYWORDS	Nucleotide-binding	0.021528	ACVR2A, KRAS, BRAF, RAD50, SMC3, HELLS, SYK	3.017104	0.900426
UP_KEYWORDS	ATP-binding	0.027686	ACVR2A, BRAF, RAD50, SMC3, HELLS, SYK	3.327953	0.94901
KEGG_PATHWAY	mmu04650:Natural killer cell mediated cytotoxicity	0.048509	KRAS, BRAF, SYK	8.138624	0.997563
GOTERM_MF_DIRECT	GO:0000166~nucleotide binding	0.094989	ACVR2A, KRAS, BRAF, RAD50, SMC3, HELLS, SYK	2.102652	0.999997
GOTERM_MF_DIRECT	GO:0005524~ATP binding	0.100074	ACVR2A, BRAF, RAD50, SMC3, HELLS, SYK	2.315328	0.999999
INTERPRO	IPR027417:P-loop containing nucleoside triphosphate hydrolase	0.134397	KRAS, RAD50, SMC3, HELLS	3.020755	1
GOTERM_MF_DIRECT	GO:0004674~protein serine/threonine kinase activity	0.158419	ACVR2A, BRAF, SYK	4.076168	1
INTERPRO	IPR000719:Protein kinase, catalytic domain	0.163284	ACVR2A, BRAF, SYK	3.998835	1
UP_SEQ_FEATURE	domain:Protein kinase	0.182951	ACVR2A, BRAF, SYK	3.711774	1

INTERPRO	IPR011009:Protein kinase-like domain	0.18393	ACVR2A, BRAF, SYK	3.703957	1
GOTERM_MF_DIRECT	GO:0004672~protein kinase activity	0.220436	ACVR2A, BRAF, SYK	3.285499	1
UP_KEYWORDS	Kinase	0.228361	ACVR2A, BRAF, SYK	3.207921	1
UP_SEQ_FEATURE	binding site:ATP	0.229176	ACVR2A, BRAF, SYK	3.196073	1
GOTERM_BP_DIRECT	GO:0006468~protein phosphorylation	0.235711	ACVR2A, BRAF, SYK	3.139236	1
GOTERM_BP_DIRECT	GO:0016310~phosphorylation	0.257275	ACVR2A, BRAF, SYK	2.954575	1
UP_SEQ_FEATURE	active site:Proton acceptor	0.303073	ACVR2A, BRAF, SYK	2.624381	1
GOTERM_MF_DIRECT	GO:0016301~kinase activity	0.30928	ACVR2A, BRAF, SYK	2.588427	1
UP_KEYWORDS	Transferase	0.355473	ACVR2A, BRAF, EZH2, SYK	1.828295	1
GOTERM_MF_DIRECT	GO:0016740~transferase activity	0.447634	ACVR2A, BRAF, EZH2, SYK	1.580254	1
Annotation Cluster 16	Enrichment Score: 0.021827864066571737				
Category	Term	PValue	Genes	Fold Enrich	Bonferroni
UP_KEYWORDS	Receptor	0.862946	ACVR2A, IL1RAP, TLR4	0.867968	1
UP_SEQ_FEATURE	topological domain:Extracellular	0.882021	ACVR2A, IL1RAP, TLR4	0.825935	1
UP_SEQ_FEATURE	topological domain:Cytoplasmic	0.951958	ACVR2A, IL1RAP, TLR4	0.646983	1
UP_SEQ_FEATURE	transmembrane region	0.977845	ACVR2A, IL1RAP, BNIP3, TLR4	0.576163	1
GOTERM_CC_DIRECT	GO:0016021~integral component of membrane	0.997353	ACVR2A, SFRP2, IL1RAP, BNIP3, TLR4	0.476447	1
UP_KEYWORDS	Transmembrane helix	0.997678	ACVR2A, IL1RAP, BNIP3, TLR4	0.43586	1
UP_KEYWORDS	Transmembrane	0.997735	ACVR2A, IL1RAP, BNIP3, TLR4	0.434795	1

S. Table 2 Mouse GO IR compared to healthy fibroblasts_upregulated

Annotation Cluster 1	Enrichment Score: 3.207551267604257				
Category	Term	PValue	Genes	Fold Enrich	Bonferroni
UP_KEYWORDS	Growth factor	8.99E-07	CXCL1, INHBA, IL6, NGF, IL11	59.52756	4.94E-05
UP_KEYWORDS	Secreted	1.83E-06	CXCL1, INHBA, IL6, CLCF1, FST, PLA1A, WNT11, NGF, IL11	8.075964	1.00E-04
GOTERM_MF_DIRECT	GO:0008083~growth factor activity	4.30E-06	CXCL1, INHBA, IL6, NGF, IL11	40.10575	2.62E-04
GOTERM_CC_DIRECT	GO:0005576~extracellular region	7.22E-06	CXCL1, INHBA, IL6, CLCF1, FST, PLA1A, WNT11, NGF, IL11	6.72972	1.88E-04
GOTERM_MF_DIRECT	GO:0005125~cytokine activity	2.00E-05	CXCL1, INHBA, IL6, CLCF1, IL11	27.17445	0.00122
UP_KEYWORDS	Cytokine	2.29E-04	CXCL1, IL6, CLCF1, IL11	30.24	0.012511
GOTERM_MF_DIRECT	GO:0005102~receptor binding	2.54E-04	INHBA, IL6, CLCF1, WNT11, NGF	14.11489	0.015392
GOTERM_CC_DIRECT	GO:0005615~extracellular space	3.48E-04	CXCL1, INHBA, IL6, CLCF1, WNT11, NGF, IL11	6.100798	0.009013
KEGG_PATHWAY	mmu04060:Cytokine-cytokine receptor interaction	7.46E-04	CXCL1, INHBA, IL6, CLCF1, IL11	10.59366	0.038789
UP_SEQ_FEATURE	signal peptide	9.02E-04	CXCL1, INHBA, IL6, CLCF1, FST, PLA1A, WNT11, NGF, IL11	3.459411	0.049253
INTERPRO	IPR009079:Four-helical cytokine-like, core	0.001698	IL6, CLCF1, IL11	45.26154	0.081447
UP_KEYWORDS	Signal	0.002414	CXCL1, INHBA, IL6, CLCF1, FST, PLA1A, WNT11, NGF, IL11	2.995378	0.12449
UP_KEYWORDS	Disulfide bond	0.00757	CXCL1, INHBA, IL6, FST, PLA1A, WNT11, NGF	3.387964	0.341603
GOTERM_BP_DIRECT	GO:0008284~positive regulation of cell proliferation	0.007618	IL6, CLCF1, NGF, IL11	8.896433	0.917953
UP_SEQ_FEATURE	disulfide bond	0.035235	CXCL1, INHBA, IL6, FST, PLA1A, NGF	2.870438	0.865842
UP_KEYWORDS	Glycoprotein	0.071248	INHBA, CLCF1, FST, PLA1A, WNT11, NGF	2.377982	0.982841
UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	0.125099	INHBA, CLCF1, FST, PLA1A, WNT11, NGF	2.022116	0.999438
GOTERM_BP_DIRECT	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	0.178087	INHBA, IL6, IL11	3.634573	1

Annotation Cluster 2	Enrichment Score: 2.858676753889115				
Category	Term	PValue	Genes	Fold Enricl	Bonferroni
GOTERM_MF_DIRECT	GO:0005102~receptor binding	2.54E-04	INHBA, IL6, CLCF1, WNT11, NGF	14.11489	0.015392
GOTERM_CC_DIRECT	GO:0005615~extracellular space	3.48E-04	CXCL1, INHBA, IL6, CLCF1, WNT11, NGF, IL11	6.100798	0.009013
GOTERM_BP_DIRECT	GO:0043065~positive regulation of apoptotic process	0.001971	IL6, GADD45G, WNT11, NGF	14.39363	0.47544
GOTERM_BP_DIRECT	GO:0010628~positive regulation of gene expression	0.003239	INHBA, IL6, WNT11, NGF	12.08488	0.65382
GOTERM_BP_DIRECT	GO:0045893~positive regulation of transcription, DNA-templated	0.009004	INHBA, IL6, PIM1, WNT11	8.371296	0.948061

Annotation Cluster 3	Enrichment Score: 1.891029378739467				
Category	Term	PValue	Genes	Fold Enricl	Bonferroni
KEGG_PATHWAY	mmu04621:NOD-like receptor signaling pathway	0.004638	CXCL1, IL6, TNFAIP3	26.98596	0.218389
KEGG_PATHWAY	mmu04668:TNF signaling pathway	0.016207	CXCL1, IL6, TNFAIP3	14.11193	0.579369
GOTERM_BP_DIRECT	GO:0006954~inflammatory response	0.02824	CXCL1, IL6, TNFAIP3	10.51279	0.999915

Annotation Cluster 4	Enrichment Score: 0.9077843484664367				
Category	Term	PValue	Genes	Fold Enricl	Bonferroni
UP_KEYWORDS	Apoptosis	0.035572	GADD45G, PIM1, TNFAIP3	9.276074	0.863589
GOTERM_BP_DIRECT	GO:0006915~apoptotic process	0.070289	GADD45G, PIM1, TNFAIP3	6.344561	1
GOTERM_MF_DIRECT	GO:0005515~protein binding	0.214551	IL6, CLCF1, GADD45G, PIM1, WNT11, TNFAIP3	1.705376	1
GOTERM_CC_DIRECT	GO:0005634~nucleus	0.435854	DUSP4, FST, GADD45G, PIM1, DUSP10, TNFAIP3	1.306662	1

Annotation Cluster 5	Enrichment Score: 0.7673855924904919

Category	Term	PValue	Genes	Fold Enrich	Bonferroni
UP_KEYWORDS	Hydrolase	0.076071	DUSP4, DUSP10, PLA1A, TNFAIP3	3.674362	0.987114
GOTERM_MF_DIRECT	GO:0016787~hydrolase activity	0.118836	DUSP4, DUSP10, PLA1A, TNFAIP3	3.034747	0.999555
UP_KEYWORDS	Nucleus	0.551668	DUSP4, PIM1, DUSP10, TNFAIP3	1.333921	1

Annotation Cluster 6	Enrichment Score: 0.19357586408446692				
Category	Term	PValue	Genes	Fold Enrich	Bonferroni
UP_KEYWORDS	Cytoplasm	0.529924	PIM1, DUSP10, RIN1, TNFAIP3	1.373297	1
UP_KEYWORDS	Nucleus	0.551668	DUSP4, PIM1, DUSP10, TNFAIP3	1.333921	1
UP_KEYWORDS	Phosphoprotein	0.898217	DUSP4, PIM1, RIN1, TNFAIP3	0.794013	1

S. Table 3 Mouse GO TH17 compared to IR_upregulated

Annotation Cluster 1	Enrichment Score: 5.38189138476703				
Category	Term	PValue	Genes	Fold Enric	Bonferroni
GOTERM_BP_DIRECT	GO:0051781~positive regulation of cell division	5.32E-08	PGF, IL1B, PDGFC, IL1A, THBS4, APC	57.40317	4.31E-05
UP_KEYWORDS	Mitogen	5.19E-07	PGF, IL1B, PDGFC, IL1A, THBS4	75	6.38E-05
GOTERM_BP_DIRECT	GO:0045766~positive regulation of angiogenesis	0.002589	PGF, MMP9, IL1B, IL1A	14.23219	0.877473
Annotation Cluster 2	Enrichment Score: 5.282045892666902				
Category	Term	PValue	Genes	Fold Enric	Bonferroni
UP_KEYWORDS	Growth factor	2.80E-09	CXCL1, LIF, CSF2, IL6, PGF, PDGFC, BMP5, THBS4	34.01575	3.45E-07
UP_KEYWORDS	Secreted	1.39E-08	CXCL1, CSF2, IL6, TNF, PGF, MMP9, MMP3, LIF, IL1RAP, IL1B, PDGFC, COL1A1, IL1A, BMP5, CD14, THBS4, SPP1	5.448071	1.71E-06
GOTERM_CC_DIRECT	GO:0005576~extracellular region	2.49E-08	CXCL1, CSF2, IL6, TNF, PGF, MMP9, MMP3, LIF, HSP90B1, IL1RAP, IL1B, PDGFC, COL1A1, IL1A, BMP5, CD14, THBS4, SPP1	4.806943	2.82E-06
GOTERM_MF_DIRECT	GO:0008083~growth factor activity	4.20E-08	CXCL1, LIF, CSF2, IL6, PGF, PDGFC, BMP5, THBS4	22.91757	5.47E-06
GOTERM_CC_DIRECT	GO:0005615~extracellular space	1.58E-07	CXCL1, CSF2, IL6, TNF, PGF, MMP9, MMP3, LIF, IL1B, PDGFC, COL1A1, IL1A, BMP5, CD14, THBS4,	4.980243	1.79E-05
UP_KEYWORDS	Disulfide bond	5.42E-05	CXCL1, CSF2, IL6, TNF, PGF, MMP9, TLR4, MMP3, LIF, HSP90B1, IL1RAP, PDGFC, COL1A1, BMP5, CD14, THBS4, CSF1R	2.93854	0.006642
UP_SEQ_FEATURE	disulfide bond	1.78E-04	CXCL1, CSF2, IL6, TNF, PGF, MMP9, TLR4, MMP3, LIF, HSP90B1, IL1RAP, PDGFC, BMP5, CD14, THBS4, CSF1R	2.800428	0.038438
UP_KEYWORDS	Glycoprotein	5.87E-04	CSF2, TNF, PGF, MMP9, TLR4, MMP3, LIF, HSP90B1, IL1RAP, PDGFC, COL1A1, IL1A, BMP5, CD14, THBS4, CSF1R, SPP1	2.406291	0.069685
UP_SEQ_FEATURE	signal peptide	6.01E-04	CXCL1, CSF2, IL6, PGF, MMP9, TLR4, MMP3, LIF, HSP90B1, IL1RAP, PDGFC, COL1A1, BMP5, CD14, THBS4, CSF1R, SPP1	2.39065	0.123903

UP_KEYWORDS	Signal	0.001391	CXCL1, CSF2, IL6, PGF, MMP9, TLR4, MMP3, LIF, HSP90B1, ENDOG, IL1RAP, PDGFC, COL1A1, BMP5, CD14, THBS4, CSF1R, SPP1	2.139555	0.15732
UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	0.002584	CSF2, TNF, PGF, MMP9, TLR4, MMP3, LIF, HSP90B1, IL1RAP, PDGFC, COL1A1, IL1A, BMP5, CD14, THBS4, CSF1R, SPP1	2.096096	0.433995
Annotation Cluster 3	Enrichment Score: 3.6147870774603135				
Category	Term	PValue	Genes	Fold Enric	Bonferroni
KEGG_PATHWAY	mmu04668:TNF signaling pathway	1.28E-10	CXCL1, LIF, FOS, CSF2, IL6, CASP3, TNF, SOCS3, MMP9, IL1B, MMP3	18.93063	1.73E-08
UP_KEYWORDS	Cytokine	2.37E-09	CXCL1, LIF, CSF2, IL6, TNF, IL1B, BMP5, IL1A, SPP1	24.3	2.91E-07
GOTERM_BP_DIRECT	GO:0006954~inflammatory response	3.62E-09	CXCL1, NFKBIZ, IL6, TNF, IL1RAP, IL1B, TLR4, CD14, IL1A, CSF1R, SPP1	13.76675	2.93E-06
KEGG_PATHWAY	mmu05134:Legionellosis	1.30E-08	CXCL1, IL6, CASP3, TNF, IL1B, BNIP3, TLR4, CD14	26.32777	1.75E-06
GOTERM_MF_DIRECT	GO:0005125~cytokine activity	3.03E-08	CXCL1, LIF, CSF2, IL6, TNF, IL1B, BMP5, IL1A, SPP1	17.46929	3.94E-06
KEGG_PATHWAY	mmu05133:Pertussis	8.27E-08	FOS, IL6, CASP3, TNF, IL1B, TLR4, CD14, IL1A	20.2795	1.12E-05
KEGG_PATHWAY	mmu05132:Salmonella infection	1.20E-07	CXCL1, FOS, CSF2, IL6, IL1B, TLR4, CD14, IL1A	19.23952	1.62E-05
GOTERM_BP_DIRECT	GO:0008285~negative regulation of cell proliferation	1.54E-07	LIF, IL6, TNF, CDKN2C, IL1B, PBRM1, BMP5, IL1A, CSF1R, APC	11.21156	1.25E-04
KEGG_PATHWAY	mmu05323:Rheumatoid arthritis	1.70E-07	FOS, CSF2, IL6, TNF, IL1B, TLR4, MMP3, IL1A	18.30101	2.29E-05
GOTERM_BP_DIRECT	GO:0019221~cytokine-mediated signaling pathway	8.90E-07	IL6, KRAS, SOCS3, IL1RAP, IL1B, IL1A, CSF1R	20.64155	7.21E-04
KEGG_PATHWAY	mmu05146:Amoebiasis	1.94E-06	CSF2, IL6, CASP3, TNF, IL1B, TLR4, COL1A1, CD14	12.82635	2.62E-04
KEGG_PATHWAY	mmu04640:Hematopoietic cell lineage	4.33E-06	CSF2, IL6, TNF, IL1B, CD14, IL1A, CSF1R	15.44821	5.85E-04
GOTERM_BP_DIRECT	GO:0032755~positive regulation of interleukin-6 production	5.69E-06	IL6, TNF, IL1B, TLR4, IL1A	41.39652	0.0046
KEGG_PATHWAY	mmu04620:Toll-like receptor signaling pathway	1.18E-05	FOS, IL6, TNF, IL1B, TLR4, CD14, SPP1	13.00097	0.001593
GOTERM_BP_DIRECT	GO:0046330~positive regulation of JNK cascade	1.87E-05	TNF, IL1B, TLR4, GADD45A, IL1A	30.7517	0.015047

KEGG_PATHWAY	mmu04060:Cytokine-cytokine receptor interaction	2.75E-05	CXCL1, LIF, CSF2, IL6, TNF, IL1RAP, IL1B, IL1A, CSF1R	6.976315	0.003707
GOTERM_BP_DIRECT	GO:0010628~positive regulation of gene expression	2.84E-05	LIF, CSF2, IL6, KRAS, TNF, IL1B, TLR4, IL1A	8.632056	0.022767
GOTERM_BP_DIRECT	GO:0006955~immune response	3.17E-05	CXCL1, LIF, CSF2, IL6, TNF, IL1B, IL1A	11.07966	0.025338
GOTERM_BP_DIRECT	GO:0031663~lipopolysaccharide-mediated signaling pathway	4.65E-05	TNF, IL1B, TLR4, CD14	55.55146	0.036995
GOTERM_BP_DIRECT	GO:0070374~positive regulation of ERK1 and ERK2 cascade	6.37E-05	IL6, IL1B, TLR4, PDGFC, IL1A, CSF1R	13.74012	0.050301
KEGG_PATHWAY	mmu05144:Malaria	1.04E-04	IL6, TNF, IL1B, TLR4, THBS4	19.54014	0.013877
GOTERM_BP_DIRECT	GO:0051092~positive regulation of NF-kappaB transcription factor activity	1.07E-04	KRAS, TNF, IL1RAP, IL1B, TLR4	19.7488	0.082689
GOTERM_BP_DIRECT	GO:0045429~positive regulation of nitric oxide biosynthetic process	1.44E-04	IL6, TNF, IL1B, TLR4	38.26878	0.109892
GOTERM_BP_DIRECT	GO:0032729~positive regulation of interferon-gamma production	2.21E-04	TNF, IL1B, TLR4, CD14	33.11722	0.164167
KEGG_PATHWAY	mmu05321:Inflammatory bowel disease (IBD)	2.32E-04	IL6, TNF, IL1B, TLR4, IL1A	15.89706	0.030882
KEGG_PATHWAY	mmu05152:Tuberculosis	2.65E-04	IL6, CASP3, TNF, IL1B, TLR4, CD14, IL1A	7.460782	0.035172
KEGG_PATHWAY	mmu05140:Leishmaniasis	3.18E-04	FOS, TNF, IL1B, TLR4, IL1A	14.65511	0.042072
KEGG_PATHWAY	mmu04380:Osteoclast differentiation	4.53E-04	FOS, TNF, SOCS3, IL1B, IL1A, CSF1R	8.932636	0.059334
KEGG_PATHWAY	mmu05020:Prion diseases	6.38E-04	IL6, CASP12, IL1B, IL1A	22.73762	0.08258
GOTERM_MF_DIRECT	GO:0005149~interleukin-1 receptor binding	7.17E-04	IL1RAP, IL1B, IL1A	73.30252	0.088987
GOTERM_BP_DIRECT	GO:0042346~positive regulation of NF-kappaB import into nucleus	8.37E-04	TNF, IL1B, TLR4	67.97744	0.492523
GOTERM_BP_DIRECT	GO:0032722~positive regulation of chemokine production	9.29E-04	IL6, TNF, TLR4	64.57857	0.528872
GOTERM_BP_DIRECT	GO:0032874~positive regulation of stress-activated MAPK cascade	9.29E-04	IL1B, TLR4, IL1A	64.57857	0.528872
GOTERM_BP_DIRECT	GO:0032496~response to lipopolysaccharide	0.00101	CXCL1, FOS, TNF, IL1B, TLR4	10.927	0.558786
KEGG_PATHWAY	mmu04932:Non-alcoholic fatty liver disease (NAFLD)	0.001229	IL6, CASP3, TNF, SOCS3, IL1B, IL1A	7.168867	0.152965

GOTERM_BP_DIRECT	GO:0071222~cellular response to lipopolysaccharide	0.001256	CSF2, IL6, TNF, TLR4, CD14	10.29961	0.638829
GOTERM_BP_DIRECT	GO:0032757~positive regulation of interleukin-8 production	0.001456	TNF, IL1B, TLR4	51.66286	0.692774
KEGG_PATHWAY	mmu04064:NF-kappa B signaling pathway	0.001535	TNF, BCL2A1A, IL1B, TLR4, CD14	9.669349	0.18724
GOTERM_BP_DIRECT	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	0.001541	LIF, FOS, IL6, TNF, ETS2, IL1B, TLR4, BMP5, IL1A	3.894185	0.713167
KEGG_PATHWAY	mmu05164:Influenza A	0.001796	IL6, TNF, SOCS3, IL1B, TLR4, IL1A	6.581943	0.215448
GOTERM_BP_DIRECT	GO:0051091~positive regulation of sequence-specific DNA binding transcription factor activity	0.001824	IL6, TNF, IL1B, TLR4	16.09435	0.772023
BIOCARTA	M_il1rPathway:Signal transduction through IL1R	0.001884	IL6, TNF, IL1RAP, IL1B, IL1A	8.491436	0.131899
KEGG_PATHWAY	mmu05142:Chagas disease (American trypanosomiasis)	0.001915	FOS, IL6, TNF, IL1B, TLR4	9.106086	0.227975
GOTERM_BP_DIRECT	GO:0045840~positive regulation of mitotic nuclear division	0.001959	TNF, IL1B, IL1A	44.53695	0.795754
GOTERM_CC_DIRECT	GO:0045121~membrane raft	0.002118	CASP3, KRAS, TNF, TLR4, CD14	8.934024	0.21307
KEGG_PATHWAY	mmu05332:Graft-versus-host disease	0.002415	IL6, TNF, IL1B, IL1A	14.42964	0.278452
GOTERM_BP_DIRECT	GO:2001240~negative regulation of extrinsic apoptotic signaling pathway in absence of ligand	0.002533	CSF2, TNF, IL1B	39.13853	0.871846
GOTERM_BP_DIRECT	GO:0050715~positive regulation of cytokine secretion	0.002688	TNF, CD14, IL1A	37.98739	0.886955
KEGG_PATHWAY	mmu04621:NOD-like receptor signaling pathway	0.00314	CXCL1, IL6, TNF, IL1B	13.16389	0.345942
KEGG_PATHWAY	mmu05205:Proteoglycans in cancer	0.003785	CASP3, KRAS, TNF, MMP9, TLR4, COL1A1	5.544395	0.400669
KEGG_PATHWAY	mmu05168:Herpes simplex infection	0.004199	FOS, IL6, CASP3, TNF, SOCS3, IL1B	5.411116	0.433403
GOTERM_BP_DIRECT	GO:0043123~positive regulation of I-kappaB kinase/NF-kappaB signaling	0.004648	TNF, IL1B, TLR4, IL1A	11.55769	0.977036
KEGG_PATHWAY	mmu05162:Measles	0.005221	CCNE2, IL6, IL1B, TLR4, IL1A	6.896521	0.506723

BIOCARTA	m_inflamPathway:Cytokines and Inflammatory Response	0.008705	CSF2, IL6, TNF, IL1A	8.622074	0.480949
GOTERM_CC_DIRECT	GO:0009986~cell surface	0.009545	TNF, TLR4, PDGFC, CD14, IL1A, CSF1R	4.465592	0.661697
GOTERM_BP_DIRECT	GO:0043525~positive regulation of neuron apoptotic process	0.010691	CASP3, TNF, IL1B	18.71843	0.999834
GOTERM_BP_DIRECT	GO:0000187~activation of MAPK activity	0.012859	TNF, IL1B, TLR4	16.99436	0.999972
KEGG_PATHWAY	mmu05143:African trypanosomiasis	0.014082	IL6, TNF, IL1B	16.07875	0.852606
BIOCARTA	m_il10Pathway:IL-10 Anti-inflammatory Signaling Pathway	0.016555	IL6, TNF, IL1A	14.01087	0.714083
BIOCARTA	m_hsp27Pathway:Stress Induction of HSP Regulation	0.02236	CASP3, TNF, IL1A	12.00932	0.816586
BIOCARTA	m_erythPathway:Erythrocyte Differentiation Pathway	0.025535	CSF2, IL6, IL1A	11.2087	0.856294
GOTERM_CC_DIRECT	GO:0009897~external side of plasma membrane	0.028187	IL6, TNF, TLR4, CD14	5.907165	0.960479
KEGG_PATHWAY	mmu04940:Type I diabetes mellitus	0.040995	TNF, IL1B, IL1A	9.076711	0.996486
BIOCARTA	m_cytokinePathway:Cytokine Network	0.048012	IL6, TNF, IL1A	8.006211	0.975034
BIOCARTA	m_nfkbpathway:NF-kB Signaling Pathway	0.061191	TNF, TLR4, IL1A	7.005435	0.991224
KEGG_PATHWAY	mmu05010:Alzheimer's disease	0.063668	CASP3, TNF, CASP12, IL1B	4.239217	0.999861
KEGG_PATHWAY	mmu05145:Toxoplasmosis	0.103104	CASP3, TNF, TLR4	5.359582	1
KEGG_PATHWAY	mmu04931:Insulin resistance	0.11142	IL6, TNF, SOCS3	5.115965	1

Annotation Cluster 4	Enrichment Score: 2.603824495595101				
Category	Term	PValue	Genes	Fold Enricl	Bonferroni
GOTERM_BP_DIRECT	GO:0008284~positive regulation of cell proliferation	2.47E-05	LIF, CSF2, PLA2G4A, IL6, KRAS, TNF, PGF, PDGFC, CSF1R	7.148919	0.019815
KEGG_PATHWAY	mmu04014:Ras signaling pathway	0.006301	PLA2G4A, KRAS, PGF, ETS2, PDGFC, CSF1R	4.9149	0.573993
KEGG_PATHWAY	mmu04015:Rap1 signaling pathway	0.099149	KRAS, PGF, PDGFC, CSF1R	3.506269	0.999999

Annotation Cluster 5 Enrichment Score: 2.4083097272040006

Category	Term	PValue	Genes	Fold Enrich	Bonferroni
GOTERM_BP_DIRECT	GO:0006955~immune response	3.17E-05	CXCL1, LIF, CSF2, IL6, TNF, IL1B, IL1A	11.07966	0.025338
INTERPRO	IPR012351:Four-helical cytokine, core	0.013287	LIF, CSF2, IL6	16.71591	0.894296
INTERPRO	IPR009079:Four-helical cytokine-like, core	0.01416	LIF, CSF2, IL6	16.16484	0.908911
KEGG_PATHWAY	mmu04630:Jak-STAT signaling pathway	0.039033	LIF, CSF2, IL6, SOCS3	5.174769	0.995369

Annotation Cluster 6 Enrichment Score: 1.9743105321604364

Category	Term	PValue	Genes	Fold Enrich	Bonferroni
GOTERM_CC_DIRECT	GO:0031012~extracellular matrix	0.00321	HSP90B1, MMP9, COL1A1, MMP3, THBS4	7.961613	0.304601
UP_KEYWORDS	Extracellular matrix	0.008761	MMP9, COL1A1, MMP3, THBS4	9.191489	0.661216
UP_KEYWORDS	Calcium	0.016114	PLA2G4A, HSP90B1, MMP9, COL1A1, MMP3, THBS4	3.917775	0.864411
GOTERM_CC_DIRECT	GO:0005578~proteinaceous extracellular matrix	0.02796	MMP9, COL1A1, MMP3, THBS4	5.925859	0.959422

Annotation Cluster 7 Enrichment Score: 1.9577726206341322

Category	Term	PValue	Genes	Fold Enrich	Bonferroni
KEGG_PATHWAY	mmu04664:Fc epsilon RI signaling pathway	0.00517	CSF2, PLA2G4A, KRAS, TNF	11.03443	0.503302
KEGG_PATHWAY	mmu04660:T cell receptor signaling pathway	0.01528	FOS, CSF2, KRAS, TNF	7.429123	0.874916
KEGG_PATHWAY	mmu04650:Natural killer cell mediated cytotoxicity	0.016945	CSF2, CASP3, KRAS, TNF	7.146109	0.900463

Annotation Cluster 8 Enrichment Score: 1.8334503554017587

Category	Term	PValue	Genes	Fold Enrich	Bonferroni
GOTERM_MF_DIRECT	GO:0002020~protease binding	0.002603	CASP3, TNF, CASP12, APC	14.20106	0.287371
KEGG_PATHWAY	mmu04210:Apoptosis	0.003633	CASP3, TNF, ENDOG, CASP12	12.50569	0.388191

KEGG_PATHWAY	mmu05014:Amyotrophic lateral sclerosis (ALS)	0.028644	CASP3, TNF, CASP12	11.03443	0.980228
GOTERM_BP_DIRECT	GO:0006915~apoptotic process	0.039455	CASP3, TNF, BCL2A1A, CASP12, BNIP3	3.776525	1
KEGG_PATHWAY	mmu05010:Alzheimer's disease	0.063668	CASP3, TNF, CASP12, IL1B	4.239217	0.999861
Annotation Cluster 9	Enrichment Score: 1.7241640153216549				
Category	Term	PValue	Genes	Fold Enric	Bonferroni
KEGG_PATHWAY	mmu04110:Cell cycle	0.003757	CCNE2, CDKN2C, GADD45A, STAG2, SMC3	7.563926	0.398371
UP_KEYWORDS	Cell cycle	0.005199	CCNE2, CDKN2C, LIG4, GADD45A, STAG2, SMC3	5.175719	0.473307
GOTERM_BP_DIRECT	GO:0007049~cell cycle	0.01213	CCNE2, CDKN2C, LIG4, GADD45A, STAG2, SMC3	4.207073	0.999949
UP_KEYWORDS	Cell division	0.029474	CCNE2, LIG4, STAG2, SMC3	5.806452	0.974773
GOTERM_BP_DIRECT	GO:0051301~cell division	0.052508	CCNE2, LIG4, STAG2, SMC3	4.604533	1
UP_KEYWORDS	DNA damage	0.123241	LIG4, GADD45A, SMC3	4.821429	1
Annotation Cluster 10	Enrichment Score: 1.613965559981692				
Category	Term	PValue	Genes	Fold Enric	Bonferroni
KEGG_PATHWAY	mmu05205:Proteoglycans in cancer	0.003785	CASP3, KRAS, TNF, MMP9, TLR4, COL1A1	5.544395	0.400669
UP_KEYWORDS	Polymorphism	0.054808	TNF, MMP9, TLR4	7.751196	0.999025
UP_SEQ_FEATURE	sequence variant	0.069374	TNF, MMP9, TLR4, APC	4.096196	1
Annotation Cluster 11	Enrichment Score: 1.5512630368546512				
Category	Term	PValue	Genes	Fold Enric	Bonferroni
UP_SEQ_FEATURE	short sequence motif:Cell attachment site	0.013301	COL1A1, THBS4, SPP1	16.68293	0.947445
KEGG_PATHWAY	mmu04510:Focal adhesion	0.021861	PGF, PDGFC, COL1A1, THBS4, SPP1	4.531047	0.949409
KEGG_PATHWAY	mmu04512:ECM-receptor interaction	0.076322	COL1A1, THBS4, SPP1	6.394956	0.999978
Annotation Cluster 12	Enrichment Score: 1.2190157642888326				
Category	Term	PValue	Genes	Fold Enric	Bonferroni
UP_KEYWORDS	Zymogen	0.006696	CASP3, MMP9, CASP12, MMP3	10.14085	0.562359

GOTERM_MF_DIRECT	GO:0032403~protein complex binding	0.00971	CASP3, KRAS, MMP9, MMP3, APC	5.80141	0.718748
GOTERM_MF_DIRECT	GO:0004175~endopeptidase activity	0.028464	MMP9, CASP12, MMP3	11.12628	0.976577
UP_KEYWORDS	Protease	0.074212	CASP3, MMP9, CASP12, MMP3	3.98524	0.999924
GOTERM_MF_DIRECT	GO:0004252~serine-type endopeptidase activity	0.088544	CASP3, MMP9, MMP3	5.878032	0.999994
GOTERM_MF_DIRECT	GO:0008233~peptidase activity	0.120434	CASP3, MMP9, CASP12, MMP3	3.220007	1
GOTERM_BP_DIRECT	GO:0006508~proteolysis	0.14461	CASP3, MMP9, CASP12, MMP3	2.958927	1
UP_KEYWORDS	Hydrolase	0.173852	PLA2G4A, CASP3, MMP9, ENDOG, CASP12, MMP3	1.968408	1
GOTERM_MF_DIRECT	GO:0016787~hydrolase activity	0.290242	PLA2G4A, CASP3, MMP9, ENDOG, CASP12, MMP3	1.625757	1
Annotation Cluster 13	Enrichment Score: 0.7639446711951424				
Category	Term	PValue	Genes	Fold Enric	Bonferroni
GOTERM_BP_DIRECT	GO:0051092~positive regulation of NF-kappaB transcription factor activity	1.07E-04	KRAS, TNF, IL1RAP, IL1B, TLR4	19.7488	0.082689
UP_KEYWORDS	Innate immunity	0.009383	IL1RAP, TLR4, CD14, CSF1R	8.962656	0.686357
GOTERM_CC_DIRECT	GO:0009986~cell surface	0.009545	TNF, TLR4, PDGFC, CD14, IL1A, CSF1R	4.465592	0.661697
UP_KEYWORDS	Immunity	0.035645	IL1RAP, TLR4, CD14, CSF1R	5.386534	0.988488
GOTERM_BP_DIRECT	GO:0002376~immune system process	0.055627	IL1RAP, TLR4, CD14, CSF1R	4.496332	1
GOTERM_BP_DIRECT	GO:0045087~innate immune response	0.061758	IL1RAP, TLR4, CD14, CSF1R	4.305238	1
GOTERM_BP_DIRECT	GO:0007165~signal transduction	0.152515	KRAS, TNF, SOCS3, IL1RAP, TLR4, SMC3	2.058281	1
GOTERM_CC_DIRECT	GO:0005886~plasma membrane	0.306227	TNF, TLR4, LIG4, HSP90B1, KRAS, ETS2, IL1RAP, PDGFC, IL1A, CD14, STAG2, CSF1R, APC	1.248637	1
UP_KEYWORDS	Cell membrane	0.530576	KRAS, TNF, IL1RAP, TLR4, PDGFC, CD14, CSF1R, APC	1.149242	1
GOTERM_CC_DIRECT	GO:0016020~membrane	0.749831	TNF, PGF, BNIP3, TLR4, FOS, HSP90B1, KRAS, IL1RAP, PDGFC, STMN1, CD14, STAG2, CSF1R, APC	0.936553	1
UP_SEQ_FEATURE	topological domain:Extracellular	0.892681	TNF, IL1RAP, TLR4, CSF1R	0.778931	1
UP_KEYWORDS	Receptor	0.958207	IL1RAP, TLR4, CSF1R	0.619977	1
UP_SEQ_FEATURE	topological domain:Cytoplasmic	0.965466	TNF, IL1RAP, TLR4, CSF1R	0.610163	1
UP_SEQ_FEATURE	transmembrane region	0.993012	TNF, IL1RAP, BNIP3, TLR4, CSF1R	0.509412	1
UP_KEYWORDS	Membrane	0.997122	KRAS, TNF, IL1RAP, BNIP3, TLR4, PDGFC, CD14, CSF1R, APC	0.559714	1
UP_KEYWORDS	Transmembrane helix	0.99966	TNF, IL1RAP, BNIP3, TLR4, CSF1R	0.389161	1

UP_KEYWORDS	Transmembrane	0.999671	TNF, IL1RAP, BNIP3, TLR4, CSF1R	0.38821	1
GOTERM_CC_DIRECT	GO:0016021~integral component of membrane	0.999959	TNF, IL1RAP, BNIP3, TLR4, CSF1R	0.340319	1
Annotation Cluster 14	Enrichment Score: 0.509790242861469				
Category	Term	PValue	Genes	Fold Enrich	Bonferroni
GOTERM_BP_DIRECT	GO:0007275~multicellular organism development	0.203126	TNF, PGF, PDGFC, STMN1, BMP5	2.091952	1
UP_KEYWORDS	Developmental protein	0.258344	PGF, PDGFC, STMN1, BMP5	2.213115	1
UP_KEYWORDS	Differentiation	0.326621	PGF, STMN1, BMP5	2.50774	1
GOTERM_BP_DIRECT	GO:0030154~cell differentiation	0.533127	PGF, STMN1, BMP5	1.655861	1
Annotation Cluster 15	Enrichment Score: 0.48366828468521184				
Category	Term	PValue	Genes	Fold Enrich	Bonferroni
UP_KEYWORDS	Chromatin regulator	0.085546	KMT2C, PBRM1, SETD2	6	0.999983
GOTERM_BP_DIRECT	GO:0016569~covalent chromatin modification	0.121798	KMT2C, PBRM1, SETD2	4.855532	1
UP_KEYWORDS	Nucleus	0.181677	CCNE2, FOS, NFKBIZ, ETS2, KMT2C, PBRM1, PDGFC, LIG4, SETD2, GADD45A, STAG2, SMC3	1.429202	1
UP_KEYWORDS	Activator	0.311894	NFKBIZ, KMT2C, SETD2	2.596154	1
UP_KEYWORDS	Transcription regulation	0.411349	NFKBIZ, ETS2, KMT2C, PBRM1, SETD2	1.500834	1
UP_KEYWORDS	Transcription	0.436409	NFKBIZ, ETS2, KMT2C, PBRM1, SETD2	1.452394	1
UP_KEYWORDS	DNA-binding	0.561786	FOS, ETS2, KMT2C, PBRM1	1.346633	1
GOTERM_BP_DIRECT	GO:0006355~regulation of transcription, DNA-templated	0.602023	FOS, NFKBIZ, ETS2, KMT2C, PBRM1, SETD2	1.133455	1
GOTERM_BP_DIRECT	GO:0006351~transcription, DNA-templated	0.631194	NFKBIZ, ETS2, KMT2C, PBRM1, SETD2	1.141973	1
GOTERM_MF_DIRECT	GO:0003677~DNA binding	0.643753	FOS, ETS2, KMT2C, PBRM1, LIG4	1.124475	1
Annotation Cluster 16	Enrichment Score: 0.3683211269528496				
Category	Term	PValue	Genes	Fold Enrich	Bonferroni

GOTERM_CC_DIRECT	GO:0005925~focal adhesion	0.195963	HSP90B1, KRAS, LIG4	3.591889	1
UP_SEQ_FEATURE	binding site:ATP	0.373108	HSP90B1, LIG4, CSF1R	2.260637	1
UP_KEYWORDS	Nucleotide-binding	0.392446	HSP90B1, KRAS, LIG4, SMC3, CSF1R	1.539339	1
UP_KEYWORDS	ATP-binding	0.450708	HSP90B1, LIG4, SMC3, CSF1R	1.58474	1
GOTERM_MF_DIRECT	GO:0000166~nucleotide binding	0.681485	HSP90B1, KRAS, LIG4, SMC3, CSF1R	1.072781	1
GOTERM_MF_DIRECT	GO:0005524~ATP binding	0.699734	HSP90B1, LIG4, SMC3, CSF1R	1.102537	1
Annotation Cluster 17	Enrichment Score: 0.1231810958443257				
Category	Term	PValue	Genes	Fold Enrich	Bonferroni
UP_KEYWORDS	Metal-binding	0.590885	PLA2G4A, MMP9, ENDOG, KMT2C, COL1A1, LIG4, MMP3	1.113402	1
GOTERM_MF_DIRECT	GO:0008270~zinc ion binding	0.728182	MMP9, KMT2C, MMP3	1.159203	1
GOTERM_MF_DIRECT	GO:0046872~metal ion binding	0.827141	PLA2G4A, MMP9, ENDOG, KMT2C, COL1A1, LIG4, MMP3	0.866667	1
UP_KEYWORDS	Zinc	0.903552	MMP9, KMT2C, MMP3	0.771796	1