

Supplementary Material

Supplementary Tables

Table S1: Ten most significantly upregulated and downregulated genes in AMs from wild type (WT) mice.

### 1.12E.03 expressed sequence AV27808 Source MGI Symbol.Acc MGI 2410 ### 1.78E.03 Symbol.Acc MGI 2410 ### 1.78E.03 Symbol.Acc MGI 2410 ### 1.78E.03 Symbol.Acc MGI 2417289 ### 1.78E.03 Symbol.Acc MGI 2417489 ### 1.78E.03 Symbol.Acc MGI 241749 ###	omparison (WT time course)	Gene name	Gene expression	FDR	Gene description
Color					
Cut/2019	_	Ggt1	_	1.79E-04	
178E-04 178E-05 178E		C1qc		3.82E-03	
Alexanormal		Cd209a		1.79E-04	
1,32E-133 lipase, lamily member N Source MIG Symbol Acc MIG 197106		Heph	Unregulation	1.14E-03	hephaestin [Source:MGI Symbol;Acc:MGI:1332240]
1.12E-03		Lipn	- Opregulation		lipase, family member N [Source:MGl Symbol;Acc:MGl:1917416]
Fam19a5 Cospb5 Cospb6					immunoglobulin heavy constant mu [Source:MGI Symbol;Acc:MGI:96448]
Swints vs 4wks	_	AI427809		1.12E-03	expressed sequence Al427809 [Source:MGI Symbol;Acc:MGI:2140270]
### Swiss vs 4wks ### Cappil		Fam19a5		1.78E-03	
Camba Camb	Overlan van Averlan	Osbpl5		3.99E-04	oxysterol binding protein-like 5 [Source:MGI Symbol;Acc:MGI:1930265]
207E-03 Rho GTPase activating protein 29 [Source MIGI Symbol.Acc MIGI 24	8WKS VS 4WKS	Gm26742		2.29E-05	predicted gene, 26742 [Source:MGl Symbol;Acc:MGl:5477236]
Spirit 2 Sash Sas		Gm3235		7.11E-03	predicted gene 3235 [Source:MGI Symbol;Acc:MGI:3781413]
Sash1		Arhgap29		2.07E-03	Rho GTPase activating protein 29 [Source:MGl Symbol;Acc:MGl:2443818]
Pixmb1		Spink2			serine peptidase inhibitor, Kazal type 2 [Source:MGl Symbol;Acc:MGl:1917232]
Smad6	_				SAM and SH3 domain containing 1 [Source:MGI Symbol;Acc:MGI:1917347]
Lritm2	_		Downregulation		
Since-12 Symbol Acc. MGI 289174	_	Smad6	_		
1,86E-05 Insulin-like growth factor 2 mRNA brinding protein 3 [Source.MGI Symbol.Acc.MGI 1937Acc.MGI 1937Acc.M		Lrrtm2		3.15E-02	
Symbol Acc.Mici 1890359 Ggft		Fmr1nb		4.22E-02	Fmr1 neighbor [Source:MGl Symbol;Acc:MGl:2672032]
Ggff		Igf2bp3		1.86E-05	
Heph Ca209a Palagard A 48E-02 phospholipase Ag. group IID Source MGI Symbol Acc. MGI: 1332240] 5 83E-05 CD209a artigen Source MGI Symbol Acc. MGI: 157942] 4 48E-02 phospholipase Ag. group IID Source MGI Symbol Acc. MGI: 1921998] 1 4 68E-02 phospholipase Ag. group IID Source MGI Symbol Acc. MGI: 1921998] 4 68E-02 phospholipase Ag. group IID Source MGI Symbol Acc. MGI: 1921998] 4 68E-02 phosphol Acc. MGI: 1921998] 4 68E-03 phosphol Acc. MGI: 1921998] 4 68E-03 phosphol Acc. MGI: 19219998] 4 68E-03 phosphol Acc. MGI: 19219998] 4 68E-03 phosphol Acc. MGI: 192299 4 68E-03 ph		Gat1		6.72F-05	
Same			_		
Pla2g2d Slam/8 Fam19a5 Upregulation Upreg			Upregulation		
Fam19a5		Pla2g2d		4.48E-02	phospholipase A2, group IID [Source:MGI Symbol;Acc:MGI:1341796]
Hmcn1 Surfe MG Symbol Acc MG 1246182		Slamf8		1.18E-03	SLAM family member 8 [Source:MGI Symbol;Acc:MGI:1921998]
Hmcn1 3.85E-04 hemicentin [Source.IMG :27895047] 1.06E-03 somatostatin receptor 5 [Source.IMG :27895047] 1.06E-03 somatostatin receptor 6 [Source.IMG :37894282] 1.06E-03 somatostatin receptor 6 [Source.IMG :37894282] 1.06E-03 somatostatin receptor 1 [Source.IMG :37894282] 1.06E-03 somatostatin receptor 1 [Source.IMG :37894282] 1.06E-04 symbol.Acc.IMG :1341295 marily with sequence similarity 20, member C [Source.IMG :37804283] 2.26E-02 talin 2 [Source.IMG :578963] 2.26E-02 talin 2 [Source.IMG :57799] redicted gene 15530 [Source.IMG :577078] redicted gene, 26584 [Source.IMG :577078] redicted gene, 26584 [Source.IMG :577078] 3.24E-03 predicted gene, 26584 [Source.IMG :577078] redicted gene, 26584 [Source.IMG :57708] redicted gene, 26584 [Source.IMG :57707] redicted		Fam19a5		4.67E-04	
Satr5 Tirl 9.17E-04 toll-like receptor 5 [Source:MGI Symbol,Acc:MGI:894282] 9.17E-04 toll-like receptor 1 [Source:MGI Symbol,Acc:MGI:1341295] 3.12E-04 family with sequence similarity 20, member C [Source:MGI Symbol,Acc:MGI:1341295] family with sequence similarity 20, member C [Source:MGI Symbol,Acc:MGI:1917799] 2.08E-02 toll-like 2.08E-03 predicted gene; 2.6584 [Source:MGI Symbol,Acc:MGI:5477078] 2.08E-02 predicted gene; 2.6584 [Source:MGI Symbol,Acc:MGI:5477078] predicted gene; 2.6584 [Source:MGI Symbol,Acc:MGI:3782978] 6.34E-03 predicted gene; 2.6584 [Source:MGI Symbol,Acc:MGI:3782978] 6.34E-03 predicted gene; 2.6584 [Source:MGI Symbol,Acc:MGI:2782978] 4.52E-03 serine peptidase inhibitor, Kazal type 2 [Source:MGI Symbol,Acc:MGI:47829] 2.04E-02 RAB36, member RAS oncogene family [Source:MGI Symbol,Acc:MGI:48846] 1.57E-02 SAM and SH3 domain containing 1 [Source:MGI Symbol,Acc:MGI:48846] 4.14E-05 symbol,Acc:MGI:48846] 4.14E-05 symbol,Acc:MGI:488464] 2.41E-05 pemicentary and symbol,Acc:MGI:4886647] 2.63E-03 japase, family member N [Source:MGI Symbol,Acc:MGI:49769] 4.56E-03 gamma-glutamyltransferase 1 [Source:MGI Symbol,Acc:MGI:49769] 4.56E-03 stearoyl-Coenzyme A desaturase 1 [Source:MGI Symbol,Acc:MGI:198726] 4.56E-03 stearoyl-Coenzyme A desaturase 1 [Source:MGI Symbol,Acc:MGI:1989726] 4.56E-03 stearoyl-Coenzyme A des	_	Uman1			
12wks vs 4 wks	_				
Tam20c	_				
12wks vs 4 wks					
2.08E-02 predicted gene, 26584 Source:MGI Symbol,Acc:MGI:5477078]	12wks vs 4 wks				Symbol;Acc:MGI:2136853]
Spink2	_				
Cspg4 Spink2 Downregulation A:5E-03 Serine peptidase inhibitor, Kazal type 2 [Source:MGl Symbol;Acc:MGl:218 4:5E-03 Serine peptidase inhibitor, Kazal type 2 [Source:MGl Symbol;Acc:MGl:1921 4:5E-03 Serine peptidase inhibitor, Kazal type 2 [Source:MGl Symbol;Acc:MGl:1921 1:0E-02 RAB36 RiKEN cDNA 4933400F21 gene [Source:MGl Symbol;Acc:MGl:1921 1:0E-02 RAB36, member RAS oncogene family [Source:MGl Symbol;Acc:MGl:1921 1:0E-02 SAM and SH3 domain containing 1 [Source:MGl Symbol;Acc:MGl:1921 1:0E-03 Symbol;Acc:MGl:1890359] 4:14E-05 Symbol;Acc:MGl:1890359] 2:70E-03 nephroblastoma overexpressed gene [Source:MGl Symbol;Acc:MGl:1917416] 2:63E-03 Sipase, family member N [Source:MGl Symbol;Acc:MGl:1917416] 4:56E-03 Spamma-glutamyltransferase 1 [Source:MGl Symbol;Acc:MGl:95706] 4:56E-03 Spamma-glutamyltransferase 1 [Source:MGl Symbol;Acc:MGl:1917416] 4:56E-03 Spamma-glutamyltransferase 1 [Source:	_				
Spink2 4933400F21Rik 2.04E-02 RIKEN cDNA 4933400F21 gene [Source:MGI Symbol;Acc:MGI:1921 1.10E-02 RAB36 member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1921 1.10E-02 RAB36, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1921 1.10E-02 SAM and SH3 domain containing 1 [Source:MGI Symbol;Acc:MGI:1921 1.10E-03 Symbol;Acc:MGI:1980359] 2.70E-03 nephroblastoma overexpressed gene [Source:MGI Symbol;Acc:MGI:1980369] 2.41E-05 hemicentin 1 [Source:MGI Symbol;Acc:MGI:1917416] 2.63E-03 iipase, family member N [Source:MGI Symbol;Acc:MGI:1917416] 4.56E-03 gamma-glutamyltransferase 1 [Source:MGI Symbol;Acc:MGI:1917416] 4.56E-03 gamma-glutamyltransferase 1 [Source:MGI Symbol;Acc:MGI:1917416] 6.07E-03 expressed sequence Al427809 [Source:MGI Symbol;Acc:MGI:2157942] 0.05bpl5 1.12E-03 oxysterol binding protein 2 [Source:MGI Symbol;Acc:MGI:193024] 1.12E-03 oxysterol binding protein 2 [Source:MGI Symbol;Acc:MGI:193024] 1.46E-02 epithelial membrane protein 2 [Source:MGI Symbol;Acc:MGI:19872] 2.08E-05 major facilitator superfamily domain containing 6 [Source:MGI Symbol;Acc:MGI:19872] 7.73E-03 chondroitin sulfate proteoglycan 4 [Source:MGI Symbol;Acc:MGI:216777] 7.73E-03 chondroitin sulfate proteoglycan 4 [Source:MGI Symbol;Acc:MGI:2167977] 7.73E-03 chondroitin sulfate proteoglycan 4 [So	_				
Downregulation 2.04E-02 RIKEN cDNA 4933400F21 gene [Source:MGI Symbol;Acc:MGI:1921	_		-		1 21 1
Rab36		•	Downregulation		
1.57E-02 SAM and SH3 domain containing 1 [Source:MGI Symbol;Acc:MGI:18 1972bp3 4.14E-05 5ymbol;Acc:MGI:1890359] 4.14E-05 5ymbol;Acc:MGI:1890359] 2.70E-03 6phroblastoma overexpressed gene [Source:MGI Symbol;Acc:MGI:1890359] 2.70E-03 6phroblastoma overexpressed gene [Source:MGI Symbol;Acc:MGI:2685047] 2.63E-03 5phroblastoma overexpressed gene [Source:MGI Symbol;Acc:MGI:1917416] 2.63E-03 5phroblastoma overexpressed gene [Source:MGI Symbol;Acc:MGI:1917416] 4.56E-03 5phroblastoma overexpressed gene [Source:MGI Symbol;Acc:MGI:1917416]					RAB36, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1924127]
19f2bp3		Sash1			SAM and SH3 domain containing 1 [Source:MGI Symbol;Acc:MGI:1917347]
Nov 2.70E-03 nephroblastoma overexpressed gene [Source:MGl Symbol;Acc:MGl Symbol;Ac		laf2hn3		4 14E 05	
Hmcn1	_		_		· · ·
Lipn Ggt1 Heph Al427809 Cd209a Osbpl5 Scd1 Emp2 Misd6 40wks vs 4wks Lipn Lipn Al427809 Csgd4 Lipn Al427809 Cd209a Cospg4 Lipn Al427809 Cd209a Cospg4 Lipn Al427809 Cd209a Al487E-05 Cd209a Aligner [Source:MGl Symbol;Acc:MGl:21402 Cd209a Aligner [Source:MGl Symbol;Acc:MGl:21402 Cd209a Cd209a Cd209a Aligner [Source:MGl Symbol;Acc:MGl:21402 Cd209a Aligner [Source:MGl Symbol;Acc:MGl:193024 Alexe-Ose epithelial membrane protein 2 [Source:MGl Symbol;Acc:MGl:109872 Aligner [Source:MGl Symbol;Acc:MGl:109872 Cospg4 Aligner [Source:MGl Symbol;Acc:MGl:104082 Cospg4 Aligner [Source:MGl Symbol;Acc:MGl:104082 Cospg4 Aligner [Source:MGl Symbol;Acc:MGl:104082 Cospg4 Aligner [Source:MGl Symbol;Acc:MGl:104082 Cospg4 Aligner [Source:MGl S					
A	_		_		
Heph Al427809 Cd209a Upregulation Osbpl5 Scd1 Emp2 Misd6 40wks vs 4wks Pkdcc Cgg4 Degulation 1.85E-02 hephaestin [Source:MGl Symbol;Acc:MGl:1332240] hephaestin [Source:MGl Symbol;Acc:MGl:21402] he		<u> </u>	†		
Al427809 Cd209a Upregulation Upregulation Upregulation Upregulation Upregulation 6.07E-03 expressed sequence Al427809 [Source:MGI Symbol;Acc:MGI:21402 9.40E-03 CD209a antigen [Source:MGI Symbol;Acc:MGI:2157942] 0xysterol binding protein-like 5 [Source:MGI Symbol;Acc:MGI:193028 4.87E-05 stearoyl-Coenzyme A desaturase 1 [Source:MGI Symbol;Acc:MGI:193028 4.87E-05 stearoyl-Coenzyme A desaturase 1 [Source:MGI Symbol;Acc:MGI:19872 Misd6 2.08E-05 Symbol;Acc:MGI:1922925] 40wks vs 4wks Pkdcc 1.06E-02 T.73E-03 chondroitin sulfate proteoglycan 4 [Source:MGI Symbol;Acc:MGI:21402 expressed sequence Al427809 [Source:MGI Symbol;Acc:MGI:21402 9.40E-03 cymsterol binding protein-like 5 [Source:MGI Symbol;Acc:MGI:193028 4.87E-05 stearoyl-Coenzyme A desaturase 1 [Source:MGI Symbol;Acc:MGI:19282925] Symbol;Acc:MGI:1922925] 40wks vs 4wks Pkdcc 1.06E-02 CD209a antigen [Source:MGI Symbol;Acc:MGI:193028] 1.12E-03 cymsterol binding protein-like 5 [Source:MGI Symbol;Acc:MGI:193028] 4.87E-05 stearoyl-Coenzyme A desaturase 1 [Source:MGI Symbol;Acc:MGI:19282925] 5.08E-05 Symbol;Acc:MGI:1922925] 7.73E-03 chondroitin sulfate proteoglycan 4 [Source:MGI Symbol;Acc:MGI:214077]					
Osbpl5 Scd1 Scd1 Scd1 Scd1 Scd1 Scd1 Scd1 Scd1					expressed sequence Al427809 [Source:MGI Symbol;Acc:MGI:2140270]
Scd1 4.87E-05 stearoyl-Coenzyme A desaturase 1 [Source:MGI Symbol;Acc::MGI:99872 Mfsd6		Cd209a	Upregulation	9.40E-03	CD209a antigen [Source:MGl Symbol;Acc:MGl:2157942]
Emp2 1.46E-02 epithelial membrane protein 2 [Source:MGI Symbol;Acc:MGI:109872 Misd6 2.08E-05 major facilitator superfamily domain containing 6 [Source:MGI Symbol;Acc:MGI:1922925] 40wks vs 4wks Pkdcc 1.06E-02 protein kinase domain containing, cytoplasmic [Source:MGI Symbol;Acc:MGI:2147077] Cspg4 7.73E-03 chondroitin sulfate proteoglycan 4 [Source:MGI Symbol;Acc:MGI:218		Osbpl5		1.12E-03	oxysterol binding protein-like 5 [Source:MGI Symbol;Acc:MGI:1930265]
Misd6 2.08E-05 major facilitator superfamily domain containing 6 [Source:MGl Symbol:Acc:MGl:1922925] 40wks vs 4wks Pkdcc 1.06E-02 T.73E-03 major facilitator superfamily domain containing 6 [Source:MGl Symbol:Acc:MGl:1922925] protein kinase domain containing, cytoplasmic [Source:MGl Symbol:Acc:MGl:2147077] Cspg4 7.73E-03 chondroitin sulfate proteoglycan 4 [Source:MGl Symbol;Acc:MGl:218		Scd1		4.87E-05	stearoyl-Coenzyme A desaturase 1 [Source:MGl Symbol;Acc:MGl:98239]
40wks vs 4wks Pkdcc 1.06E-02 Symbol;Acc:MGI:1922925] protein kinase domain containing, cytoplasmic [Source:MGI Symbol;Acc:MGI:2147077] Cspg4 7.73E-03 chondroitin sulfate proteoglycan 4 [Source:MGI Symbol;Acc:MGI:218		Emp2		1.46E-02	epithelial membrane protein 2 [Source:MGl Symbol;Acc:MGl:1098726]
40wks vs 4wks Pkdcc 1.06E-02 protein kinase domain containing, cytoplasmic [Source:MGl Symbol;Acc:MGl:2147077] Cspg4 7.73E-03 chondroitin sulfate proteoglycan 4 [Source:MGl Symbol;Acc:MGl:218		Mfsd6		2.08E-05	
Symbol;Acc:MGI:2147077] Cspg4 7.73E-03 chondroitin sulfate proteoglycan 4 [Source:MGI Symbol;Acc:MGI:218	40wke ve 4wke				
		Pkdcc		1.06E-02	Symbol;Acc:MGI:2147077]
Gm9725 1.82E-02 predicted gene 9725 [Source:MGI Symbol:Acc:MGI:3646552]	_				chondroitin sulfate proteoglycan 4 [Source:MGI Symbol;Acc:MGI:2153093]
	_		-		
	<u> </u>	Spink2	-	5.83E-03	serine peptidase inhibitor, Kazal type 2 [Source:MGI Symbol;Acc:MGI:1917232]
Nfatc2 Downregulation Downregulation 3.66E-02 Symbol;Acc:MGI:102463]		Nfatc2	Downregulation	3.66E-02	nuclear factor of activated T cells, cytoplasmic, calcineurin dependent 2 [Source:MGI Symbol:Acc:MGI:102463]
Smad6 3.13E-03 SMAD family member 6 [Source:MGI Symbol;Acc:MGI:1336883]		Smad6		3.13E-03	
Micall2 2.56E-02 MICAL-like 2 [Source:MGI Symbol;Acc:MGI:2444818]		Micall2		2.56E-02	MICAL-like 2 [Source:MGI Symbol;Acc:MGI:2444818]
Sash1 9.79E-03 SAM and SH3 domain containing 1 [Source:MGI Symbol;Acc:MGI:19		Sash1		9.79E-03	SAM and SH3 domain containing 1 [Source:MGl Symbol;Acc:MGl:1917347]
		Nov		6.86E-03	nephroblastoma overexpressed gene [Source:MGI Symbol;Acc:MGI:109185]
lgf2bp3 3.30E-05 insulin-like growth factor 2 mRNA binding protein 3 [Source:MGI Symbol:Acc:MGI:1890359]		lgf2bp3		3.30E-05	

Table S2: Upregulated and downregulated gene sets in WT AMs.

Comparison (WT) Pathway ID	Set Size	Mean Log FC	FDR	GO: Biological pro Comparison (WT		Set Size	lean Log F	FDI
wks vs 4wks	GO:0042277 peptide binding	153	4.129	8.39E-03	8wks vs 4wks	GO:0045087 innate immune response	422	4.921	2.518
WK3 V3 4WK3	GO:0033218 amide binding	179	3.956	1.27E-02	12wks vs 4wks	GO:0045087 innate immune response	422	6.790	5.516
	GO:0004872 receptor activity	371	3.849	1.54E-02		GO:0043207 response to external biotic stimulus	469	5.490	3.63
	GO:0005198 structural molecule activity	309	3.520	3.89E-02		GO:0051707 response to other organism	469	5.490	3.63
	GO:0008009 chemokine activity	19	3.515	3.89E-02		GO:0098542 defense response to other organism	279	5.466	3.63
	GO:0016491 oxidoreductase activity	478	3.389	4.68E-02		GO:0009607 response to biotic stimulus	495	5.421	3.63
	GO:0022891 substrate-specific transmembrane transp	384	3.377	4.68E-02		GO:0002252 immune effector process	443	5.136	1.38
	GO:0003735 structural constituent of ribosome	143	-4.419	6.90E-03		GO:0034341 response to interferon-gamma	63	4.723	1.44
2wks vs 4wks	GO:0042277 peptide binding	153	3.612	4.84E-02		GO:0050776 regulation of immune response	426	4.630	2.15
2WK5 V5 4WK5	GO:0033218 amide binding	179	3.556	4.84E-02		GO:0001817 regulation of cytokine production	389	4.513	2.15
	<u> </u>	371				• .	227		
	GO:0004872 receptor activity		3.522	4.84E-02		GO:0002250 adaptive immune response		4.392	2.83
	GO:0003735 structural constituent of ribosome	143	-5.506	4.86E-05		GO:0009617 response to bacterium	290	4.392	2.83
)wks vs 4wks	GO:0003735 structural constituent of ribosome	143	-5.506	1.04E-03		GO:0034097 response to cytokine	465	4.366	2.83
						GO:0001816 cytokine production	430	4.253	4.27
EGG disease						GO:0002443 leukocyte mediated immunity	208	4.202	5.57
omparison (WT) Pathway_ID	Set Size	Mean Log FC	FDR		GO:0009615 response to virus	187	4.151	6.57
8wks vs 4wks	mmu05169 Epstein-Barr virus infection	167	3.865	1.19E-02		GO:0002460 adaptive immune response based on some	169	4.077	6.57
	mmu05164 Influenza A	125	3.543	1.19E-02		GO:0051607 defense response to virus	154	4.075	7.99
	mmu05150 Staphylococcus aureus infection	31	2.617	3.54E-02		GO:0019882 antigen processing and presentation	71	4.066	7.99
	mmu05162 Measles	93	2.442	4.69E-02		GO:0042742 defense response to bacterium	111	4.035	7.99
	mmu05016 Huntington's disease	152	3.381	1.19E-02		GO:0050778 positive regulation of immune response	337	4.023	9.6
	mmu05320 Autoimmune thyroid disease	26	3.330	1.19E-02		GO:0035456 response to interferon-beta	36	3.830	9.8
	mmu04932 Non-alcoholic fatty liver disease (NAFLD)	127	3.287	1.19E-02		GO:0001819 positive regulation of cytokine production	262	3.823	1.6
	mmu05330 Allograft rejection	27	3.188	1.19E-02		GO:0002449 lymphocyte mediated immunity	157	3.753	2.1
	mmu04940 Type I diabetes mellitus	30	3.165	1.50E-02		GO:0071345 cellular response to cytokine stimulus	393	3.693	2.3
	mmu05332 Graft-versus-host disease	27	2.488	4.69E-02		GO:0050865 regulation of cell activation	331	3.658	2.6
	mmu05416 Viral myocarditis	48	-2.654	3.51E-02		GO:0048002 antigen processing and presentation of pe		3.602	3.0
	mmu05168 Herpes simplex infection	158	-3.117	1.19E-02		GO:0002694 regulation of leukocyte activation	310	3.572	3.2
12wks vs 4wks	mmu05169 Epstein-Barr virus infection	167	4,202	1.29F-03		GO:0071346 cellular response to interferon-gamma	50	3.571	3.6
.2	mmu05164 Influenza A	125	3.472	6.41E-03		GO:0006954 inflammatory response	348	3.529	4.0
	mmu05168 Herpes simplex infection	158	3.228	7.88E-03		GO:0045088 regulation of innate immune response	188	3.509	4.1
	mmu05416 Viral myocarditis	48	3.220	7.88E-03		GO:0050801 ion homeostasis	376	3.572	3.2
	•	31	3.215				466	3.472	4.2
	mmu05150 Staphylococcus aureus infection			9.13E-03		GO:0019725 cellular homeostasis			
	mmu05162 Measles	93	2.668	2.61E-02		GO:0098771 inorganic ion homeostasis	346	3.460	4.2
	mmu05167 Kaposi's sarcoma-associated herpesvirus ii	149	2.526	3.31E-02		GO:0006820 anion transport	241	3.421	4.2
	mmu05203 Viral carcinogenesis	167	2.486	3.31E-02		GO:0050867 positive regulation of cell activation	197	3.396	4.5
	mmu05152 Tuberculosis	128	2.426	3.51E-02		GO:0034220 ion transmembrane transport	346	3.379	4.85
	mmu05134 Legionellosis	51	2.320	4.25E-02		GO:0055080 cation homeostasis	337	3.376	4.85
	mmu05160 Hepatitis C	116	2.290	4.25E-02		GO:0006412 translation	493	-4.102	4.85
	mmu05145 Toxoplasmosis	79	2.220	4.96E-02					
	mmu05330 Allograft rejection	27	3.711	6.41E-03	KEGG metabolisr	n			
	mmu05320 Autoimmune thyroid disease	26	3.523	7.88E-03	Comparison (WT) Pathway_ID	Set Size	lean Log F	F
	mmu04940 Type I diabetes mellitus	30	3.309	7.88E-03	8wks vs 4wks	mmu04612 Antigen processing and presentation	55	4.090	3.55
	mmu05332 Graft-versus-host disease	27	3.203	9.13E-03		mmu04145 Phagosome	120	4.095	3.55
	mmu05322 Systemic lupus erythematosus	52	2.556	3.31E-02		mmu04514 Cell adhesion molecules (CAMs)	60	3.690	7.70
	mmu05020 Prion diseases	24	2.545	3.51E-02		mmu03010 Ribosome	133	-5.213	5.3
	mmu05418 Fluid shear stress and atherosclerosis	94	2.363	3.98E-02	12wks vs 4wks	mmu04612 Antigen processing and presentation	55	4.176	3.7
	mmu04932 Non-alcoholic fatty liver disease (NAFLD)	127	-3.205	7.88E-03		mmu00100 Steroid biosynthesis	15	3.831	1.4
	mmu05016 Huntington's disease	152	-3,594	6.41E-03		mmu04145 Phagosome	120	3,640	1.2
10wks vs 4wks	mmu05169 Epstein-Barr virus infection	167	3.405	2.60E-02		mmu04514 Cell adhesion molecules (CAMs)	60	3.556	1.4
	mmu05164 Influenza A	125	3.253	2.60E-02		mmu03050 Proteasome	44	3.058	4.8
	mmu05168 Herpes simplex infection	158	3.185	2.60E-02		mmu00190 Oxidative phosphorylation	112	-3.079	4.2
	mmu05150 Staphylococcus aureus infection	31	2.726	3.57E-02		mmu03010 Ribosome	133		3.6
		31 48			40wks vs 4wks			-6.223	
	mmu05416 Viral myocarditis		2.636	3.57E-02	HUWKS VS 4WKS	mmu04612 Antigen processing and presentation	55	3.784	1.5
	mmu05167 Kaposi's sarcoma-associated herpesvirus ii	149	2.562	3.60E-02		mmu04145 Phagosome	120	3.383	3.2
	mmu05162 Measles	93	2.546	3.57E-02		mmu04514 Cell adhesion molecules (CAMs)	60	3.280	3.2
	mmu05016 Huntington's disease	152	3.294	2.60E-02		mmu00100 Steroid biosynthesis	15	-3.127	4.3
	mmu05320 Autoimmune thyroid disease	26	2.971	2.60E-02		mmu03010 Ribosome	133	-5.590	9.5
	mmu04932 Non-alcoholic fatty liver disease (NAFLD)	127	2.806	3.57E-02					
	mmu04940 Type I diabetes mellitus	30	2.796	3.57E-02					
	mmu05322 Systemic lupus erythematosus	52	2.469	3.72E-02					
	mmu05332 Graft-versus-host disease	27	-2.573	3.57E-02					
	mmu05330 Allograft rejection	27	-2.949	2.60E-02					

Table S3: Ten most significantly upregulated and downregulated genes in AMs from Scgb1a1-knockout (KO) mice.

comparison (KO time course)	Gene name	Gene expression	FDR	Gene description
	Uty		4.38E-03	ubiquitously transcribed tetratricopeptide repeat gene, Y chromosome [Source:MGl Symbol;Acc:MGl:894810]
	Eif2s3y	-	1.02E-02	eukaryotic translation initiation factor 2, subunit 3, structural gene Y-linked [Source:MGI Symbol;Acc:MGI:1349430]
	Ddx3y	-	4.15E-03	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked [Source:MGl Symbol;Acc:MGl:1349406]
	Slamf8	-	2.74E-03	SLAM family member 8 [Source:MGI Symbol;Acc:MGI:1921998]
	Sstr5		2.06E-02	somatostatin receptor 5 [Source:MGI Symbol;Acc:MGI:894282]
•	Acod1	- Upregulation -	1.24E-03	aconitate decarboxylase 1 [Source:MGl Symbol;Acc:MGl:103206]
•	Ggt1	-	1.91E-03	gamma-glutamyltransferase 1 [Source:MGl Symbol;Acc:MGl:95706]
•	Cd209a	-	1.72E-03	CD209a antigen [Source:MGl Symbol;Acc:MGl:2157942]
	Kdm5d	-	3.98E-03	lysine (K)-specific demethylase 5D [Source:MGl Symbol;Acc:MGl:99780]
	Spic	-	2.49E-05	Spi-C transcription factor (Spi-1/PU.1 related) [Source:MGI Symbol;Acc:MGI:1341168]
8wks vs 4wks	Zfp979		3.42E-02	zinc finger protein 979 [Source:MGl Symbol;Acc:MGl:2148252]
	Zfp119b	-	2.36E-02	zinc finger protein 119b [Source:MGl Symbol;Acc:MGl:2385323]
	Gm13369	-	5.64E-03	predicted gene 13369 [Source:MGI Symbol;Acc:MGI:3651010]
	Tln2	-	1.78E-02	
	Gm28286	-	2.03E-02	predicted gene 28286 [Source:MGI Symbol;Acc:MGI:5578992]
•	Cspg4	- Downregulation -	3.21E-03	chondroitin sulfate proteoglycan 4 [Source:MGI Symbol;Acc:MGI:2153093]
	Adcy4	-	4.55E-02	
	Smad6		3.38E-03	
	lgf2bp3	-	3.62E-04	insulin-like growth factor 2 mRNA binding protein 3 [Source:MGI Symbol;Acc:MGI:1890359]
	Fhdc1	-	4.14E-02	FH2 domain containing 1 [Source:MGI Symbol;Acc:MGI:2684972]
	Uty		3.29E-03	ubiquitously transcribed tetratricopeptide repeat gene, Y chromosome [Source:MGI Symbol;Acc:MGI:894810]
	Ddx3y	-	7.17E-03	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked [Source:MGI Symbol;Acc:MGI:1349406]
	Eif2s3y		2.33E-02	eukaryotic translation initiation factor 2, subunit 3, structural gene Y-linked [Source:MGI Symbol;Acc:MGI:1349430]
	Cd209a		1.29E-03	CD209a antigen [Source:MGI Symbol;Acc:MGI:2157942]
	Slamf8		1.82E-02	
	Kdm5d			lysine (K)-specific demethylase 5D [Source:MGI Symbol;Acc:MGI:99780]
	Acod1		6.08E-03	
			1.58E-02	
	Cd40		1.01E-03	
	A1427809		9.54E-03	expressed sequence Al427809 [Source:MGI Symbol;Acc:MGI:2140270]
12wks vs 4 wks	Esrrg		1.90E-02	estrogen-related receptor gamma [Source:MGI Symbol;Acc:MGI:1347056]
	Sash1		3.39E-02	SAM and SH3 domain containing 1 [Source:MGI Symbol;Acc:MGI:1917347]
	Cspg4	_	7.67E-04	chondroitin sulfate proteoglycan 4 [Source:MGI Symbol;Acc:MGI:2153093]
	E330009J07Rik		1.06E-04	
	Dusp1		3.22E-03	dual specificity phosphatase 1 [Source:MGl Symbol;Acc:MGl:105120]
	Sik1	- Downregulation -	5.85E-03	
	E230001N04Rik		3.23E-03	RIKEN cDNA E230001N04 gene [Source:MGI Symbol;Acc:MGI:2443549]
	lgf2bp3		1.06E-04	insulin-like growth factor 2 mRNA binding protein 3 [Source:MGl Symbol;Acc:MGl:1890359]
	Nov		1.18E-02	nephroblastoma overexpressed gene [Source:MGl Symbol;Acc:MGl:109185]
	Smad6		2.54E-04	SMAD family member 6 [Source:MGl Symbol;Acc:MGl:1336883]
	Tln2		1.37E-04	talin 2 [Source:MGl Symbol;Acc:MGl:1917799]
	Pla2g2d		7.02E-04	phospholipase A2, group IID [Source:MGI Symbol;Acc:MGI:1341796]
	BC051142		3.92E-08	cDNA sequence BC051142 [Source:MGl Symbol;Acc:MGl:3039565]
	Ccdc7a	_	6.58E-06	coiled-coil domain containing 7A [Source:MGI Symbol;Acc:MGI:1921953]
	Hmcn1		8.08E-08	hemicentin 1 [Source:MGI Symbol;Acc:MGI:2685047]
	A1427809	- Upregulation -	1.60E-05	expressed sequence Al427809 [Source:MGl Symbol;Acc:MGl:2140270]
	C130026I21Rik	- Opregulation	8.72E-07	RIKEN cDNA C130026l21 gene [Source:MGl Symbol;Acc:MGl:3612702]
	Uty	-	3.15E-03	ubiquitously transcribed tetratricopeptide repeat gene, Y chromosome [Source:MGl Symbol;Acc:MGl:894810]
	Esrrg	-	1.04E-04	estrogen-related receptor gamma [Source:MGl Symbol;Acc:MGl:1347056]
•	Lipn	-	7.86E-05	lipase, family member N [Source:MGI Symbol;Acc:MGI:1917416]
40udeo vo 4::-t	Dpysl3		9.99E-05	dihydropyrimidinase-like 3 [Source:MGl Symbol;Acc:MGl:1349762]
40wks vs 4wks	Zfp979		1.56E-04	zinc finger protein 979 [Source:MGI Symbol;Acc:MGI:2148252]
•	Zfp979	-	1.56E-04	zinc finger protein 979 [Source:MGI Symbol;Acc:MGI:2148252]
•	Cd93	-	9.68E-06	CD93 antigen [Source:MGI Symbol;Acc:MGI:106664]
•	Sik1		4.10E-03	
	Fhdc1	-	1.63E-02	
	Hfm1	- Downregulation -	1.99E-02	
	Arhgap29	-	4.29E-05	
	Smad6	=	2.39E-05	
		-	2.39E-05 2.16E-06	EGF-like and EMI domain containing 1 [Source:MGI Symbol:Acc:MGI:1922990]
	Egfem1			

Table S4: Up-regulated and downregulated gene sets in KO AMs.

Set Size Mean Log F

4.961

4.578

4.578

4.514

4.485

4.056

4.002

3.963

4.078

3.917

3.771

3.766

3.711 3.807 3.674

3.640

3.627

3.646

4.650

4.155

4.155

4.168

4.146

4.026

422

469

469

279

443

495

71

426

154

63

208

389

227

466

422

469

279

443

495

_	CO	Dial	 	nathways

8wks vs 4wks GO:0045087 innate immune response

GO:0043207 response to external biotic stimulus

GO:0098542 defense response to other organism

GO:0019882 antigen processing and presentation

GO:0048002 antigen processing and presentation

GO:0001819 positive regulation of cytokine produc

GO:0043207 response to external biotic stimulus

GO:0098542 defense response to other organism

GO:0050776 regulation of immune response

GO:0034341 response to interferon-gamma

GO:0002443 leukocyte mediated immunity

GO:0002250 adaptive immune response

GO:0051707 response to other organism

GO:0002252 immune effector process

GO:0009607 response to biotic stimulus

GO:0009617 response to bacterium

GO:0019725 cellular homeostasis

12wks vs 4wks GO:0045087 innate immune response

GO:0001817 regulation of cytokine production

GO:0051707 response to other organism

GO:0002252 immune effector process

GO:0009615 response to virus

GO:0009607 response to biotic stimulus

GO:0051607 defense response to virus

Comparison (WT; Pathway ID

	c. KEGG disea	se
C FDR	Comparison (W	1Pathway_ID
2.09E-03	8wks vs 4wks	mmu05416 \
3.98E-03		mmu05164 I
3.98E-03		mmu05169 I
3.98E-03		mmu05152
3.98E-03		mmu05145
2.19E-02		mmu05168 I
2.28E-02		mmu05330 /
2.28E-02		mmu05322
2.28E-02		mmu05150
2.28E-02		mmu05320 /
3.62E-02		mmu05332
3.62E-02		mmu04940
4.22E-02		mmu05310 /
4.22E-02	12wks vs 4wks	mmu05416 \
4.22E-02		mmu05150
4.22E-02		mmu05164 I

4.22E-02

9.27E-03 1.78E-02

1.78E-02

1.78E-02

1.78E-02

2.42E-02

	mmu05169 Epstein-Barr virus infection	167	3.05	1.25E-02
	mmu05152 Tuberculosis	128	3.15	1.36E-02
	mmu05145 Toxoplasmosis	79	2.83	4.35E-02
	mmu05168 Herpes simplex infection	158	2.45	4.35E-02
	mmu05330 Allograft rejection	27	4.15	7.76E-03
	mmu05322 Systemic lupus erythematosu	52	3.76	8.32E-03
	mmu05150 Staphylococcus aureus infecti	31	3.34	9.39E-03
	mmu05320 Autoimmune thyroid disease	26	3.34	1.03E-02
	mmu05332 Graft-versus-host disease	27	3.21	1.25E-02
	mmu04940 Type I diabetes mellitus	30	2.66	3.32E-02
	mmu05310 Asthma	11	2.48	4.35E-02
12wks vs 4wks	mmu05416 Viral myocarditis	48	3.38	1.59E-02
	mmu05150 Staphylococcus aureus infecti	31	3.37	1.59E-02
	mmu05164 Influenza A	125	2.92	2.28E-02
	mmu05169 Epstein-Barr virus infection	167	2.88	2.28E-02
	mmu05152 Tuberculosis	128	2.76	2.60E-02
	mmu05145 Toxoplasmosis	79	2.49	4.39E-02
	mmu05330 Allograft rejection	27	3.74	1.59E-02
	mmu05322 Systemic lupus erythematosu	52	3.28	1.59E-02
	mmu05320 Autoimmune thyroid disease	26	3.12	2.28E-02

mmu05332 Graft-versus-host disease

mmu05150 Staphylococcus aureus infecti

mmu05169 Epstein-Barr virus infection

mmu05322 Systemic lupus erythematosu

mmu05320 Autoimmune thyroid disease

mmu05332 Graft-versus-host disease

mmu04940 Type I diabetes mellitus

mmu05310 Asthma

mmu05164 Influenza A

mmu05330 Allograft rejection

mmu05416 Viral myocarditis

mmu05164 Influenza A

Set Size Mean Log FC

3.45

3.29

48

125

27 30

11

48

31

125

167

27

52

26

2.95

2.83

2.99

4.11

3.74

3.40

3.49

4.67

3.81

3.49

FDR

8.32E-03

1.25E-02

2.54E-02 2.71E-02

3.80E-02

5.29E-03

6.14E-03

7.13E-03

7.13E-03

1.97E-03

6 14F-03 6.70E-03

9.98E-03

b. KEGG metab	olism			
Comparison (WT	; Pathway_ID	Set Size	Mean Log FC	FDR
8wks vs 4wks	mmu04514 Cell adhesion molecules (CAMs)	60	4.048	1.14E-02
	mmu04612 Antigen processing and presentation	55	3.873	1.14E-02
12wks vs 4wks	mmu04514 Cell adhesion molecules (CAMs)	60	3.795	2.65E-02
	mmu04612 Antigen processing and presentation	55	3.616	2.65E-02
40wks vs 4wks	mmu04514 Cell adhesion molecules (CAMs)	60	4.270	5.94E-03
	mmu04612 Antigen processing and presentation	55	-3.614	1.97E-02

Table S5: Ten most significantly upregulated and downregulated genes in WT and KO AMs.

Comparison (KO vs WT)	Gene name	Gene expression		Gene description
	Nuak2	- Upregulation	2.91E-02	NUAK family, SNF1-like kinase, 2 [Source:MGI Symbol;Acc:MGI:1921387]
4wks	Arrdc3	opregulation	2.91E-02	Arrestin domain containing 3 [Source:MGI Symbol;Acc:MGI:2145242]
TWKS	Мус	- Downregulation	3.39E-02	Myelocytomatosis oncogene [Source:MGI Symbol;Acc:MGI:97250]
	KI	Downlegulation	3.39E-02	Klotho [Source:MGI Symbol;Acc:MGI:1101771]
	Herpud1		1.84E-02	Homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain
		-		member 1 Source:MGI Symbol;Acc:MGI:1927406
	Snx27	_	2.31E-02	
	Galnt7		2.42E-02	Polypeptide N-acetylgalactosaminyltransferase 7 [Source:MGI Symbol;Acc:MGI:1349449]
	Cenpf	-	2.91E-02	Centromere protein F [Source:MGI Symbol;Acc:MGI:1313302]
	Cenpe	-		Centromere protein E [Source:MGI Symbol;Acc:MGI:1098230]
	Crip1	Upregulation		Cysteine-rich protein 1 (intestinal) [Source:MGI Symbol;Acc:MGI:88501]
		-		Dna Lheat shock protein family (Hen/III) member R9 [Source:MGI
	Dnajb9	_	2.91E-02	Symbol;Acc:MGI:1351618]
	Runx1		2.91E-02	Runt related transcription factor 1 [Source:MGI Symbol;Acc:MGI:99852]
	Fndc3a	-	3.19E-02	Fibronectin type III domain containing 3A [Source:MGI Symbol;Acc:MGI:1196463]
	Cytip	-	3.48E-02	Cytohesin 1 interacting protein [Source:MGI Symbol;Acc:MGI:2183535]
8wks	Pilra		7 725 03	Paired immunoglobin-like type 2 receptor alpha [Source:MGI Symbol;Acc:MGI:2450529
		_		
	Hdac4	_	2.31E-02	Histone deacetylase 4 [Source:MGI Symbol;Acc:MGI:3036234]
	Rnase6	_	2.31E-02	Ribonuclease, RNase A family, 6 [Source:MGI Symbol;Acc:MGI:1925666]
	Btd	_	2.31E-02	Biotinidase [Source:MGI Symbol;Acc:MGI:1347001]
	Pilrb2	_	2.31F-02	Paired immunoglobin-like type 2 receptor beta 2 [Source:MGI Symbol;Acc:MGI:245053]
		Downregulation		
	Mvk	-		Mevalonate kinase [Source:MGl Symbol;Acc:MGl:107624]
	Arpin	=	2.91E-02	Actin-related protein 2/3 complex inhibitor [Source:MGI Symbol;Acc:MGI:1917670]
	Slc2a6		2.91E-02	Solute carrier family 2 (facilitated glucose transporter), member 6 [Source:MGI Symbol:Acc:MGI:2443286]
		-	0.405.00	mitochondrial calcium uniporter dominant negative heta subunit [Source MG]
	Mcub	_	3.19E-02	Symbol;Acc:MGI:1914065]
	Pagr7		3.19E-02	Progestin and adipoQ receptor family member VII [Source:MGI
	•			Symbol;Acc:MGI:1919154]
	Tmem216	-	2.63E-06	
	Ddx46	_	4.54E-06	
	Acaa1b	_		Acetyl-Coenzyme A acyltransferase 1B [Source:MGl Symbol;Acc:MGl:3605455]
	Gmpr	_	2.79E-05	Guanosine monophosphate reductase [Source:MGI Symbol;Acc:MGI:1913605]
	Tc2n		3.12E-05	Tandem C2 domains, nuclear [Source:MGI Symbol;Acc:MGI:1921663]
	Bzw2	Upregulation	3.73E-05	Basic leucine zipper and W2 domains 2 [Source:MGl Symbol;Acc:MGl:1914162]
	Dennd4a		5.04E-05	DENN/MADD domain containing 4A [Source:MGI Symbol;Acc:MGI:2142979]
	Pparg		5.05E-05	Peroxisome proliferator activated receptor gamma [Source:MGI Symbol;Acc:MGI:9774]
		-		
	Prom1	_		Prominin 1 [Source:MGI Symbol;Acc:MGI:1100886]
	Fabp1		9.26E-05	Fatty acid binding protein 1, liver [Source:MGI Symbol;Acc:MGI:95479]
12wks	Slc3a2		5.47E-07	Solute carrier family 3 (activators of dibasic and neutral amino acid transport), member
	Sc5d	=	5.47E.07	2 [Source:MGI Symbol;Acc:MGI:96955] Sterol-C5-desaturase [Source:MGI Symbol;Acc:MGI:1353611]
	Fdft1	-		
		_		Farnesyl diphosphate farnesyl transferase 1 [Source:MGI Symbol;Acc:MGI:102706]
	Fdps	-	5.47E-07	
	Ninj1	Downregulation	5.47E-07	· · · · · · · · · · · · · · · · · · ·
	Slc2a6	Downlegulation	5.47E-07	Solute carrier family 2 (facilitated glucose transporter), member 6 [Source:MGI
	Zwint	-	6.40E-07	Symbol;Acc:MGI:2443286] ZW10 interactor [Source:MGI Symbol;Acc:MGI:1289227]
		-		Acyl CoA synthetase short chain family member 2 [Source:MG]
	Acss2	_	6.40E-07	Symbol;Acc:MGI:1890410]
	Nampt	-	7.11E-07	Nicotinamide phosphoribosyltransferase [Source:MGl Symbol;Acc:MGl:1929865]
	Msmo1	-	7.66E-07	
	H2-Oa		1.33E-06	Histocompatibility 2, O region alpha locus [Source:MGl Symbol;Acc:MGl:95924]
	Cd209b	-		CD209b antigen [Source:MGI Symbol;Acc:MGI:1916415]
		-		Solute carrier family 1 (dial bigh affinity dutamate transporter), member 3 [Source:MGI
	Slc1a3	_	8.93E-06	Symbol;Acc:MGI:99917]
	Hmcn1	_	3.40E-05	
	H2-DMb1	Upregulation	3.40E-05	Histocompatibility 2, class II, locus Mb1 [Source:MGl Symbol;Acc:MGl:95922]
	Klhl41		1.71E-04	
	4930502E18Rik	-	1.71E-04	
	Zfhx3	-	1.71E-04	
	H2-Eb1	=	1.85E-04	
	Ciita	-	2.04E-04	
40wks				. , , , ,
	Fpr1	_	1.60E-04	
	Emilin1	_	2.84E-04	. , ,
	Fn1	=	3.40E-04	
	Egfem1	_	3.40E-04	EGF-like and EMI domain containing 1 [Source:MGI Symbol;Acc:MGI:1922990]
	Ubl3		6.48E-04	Ubiquitin-like 3 [Source:MGI Symbol;Acc:MGI:1344373]
	Clec4e	Downregulation	8.29E-04	C-type lectin domain family 4, member e [Source:MGI Symbol;Acc:MGI:1861232]
	Tspan32	_	8.82E-04	Tetraspanin 32 [Source:MGI Symbol;Acc:MGI:1350360]
	Inka1	-	1.19E-03	
	Ptgr1	-	1.27E-03	
		-		Protescome (procome macronain) 26S culturit non ATPace 11 [Source MG]
	Psmd11		1.63E-03	Symbol;Acc:MGI:1916327]

Table S6: Upregulated and downregulated gene sets in WT and KO AMs.

GO: Molecular Fun	ction				
Comparison (KO vs WT Pathway_ID			Set Size Mean Log FC		
4wks	GO:0003735 structural constituent of ribosome	143	-4.909	8.52E-04	
8wks	GO:0030545 receptor regulator activity	123	-3.762	2.52E-02	
	GO:0042277 peptide binding	153	-3.936	1.69E-02	
	GO:0008009 chemokine activity	19	-3.935	1.69E-02	
	GO:0003735 structural constituent of ribosome	143	-4 198	1.43F_02	

arison (KO vs	WT Pathway_ID	Set Size	Mean Log FC	FDR
12wks	mmu05012 Parkinson's disease	117	2.581	2.78E-0
	mmu05016 Huntington's disease	152	3.886	2.47E-0
	mmu04932 Non-alcoholic fatty liver disease (NAFLD)	127	2.462	3.60E-0
	mmu05418 Fluid shear stress and atherosclerosis	94	-2.968	1.87E-0
	mmu04940 Type I diabetes mellitus	30	-2.964	1.87E-0
	mmu05320 Autoimmune thyroid disease	26	-2.751	2.45E-0
	mmu05332 Graft-versus-host disease	27	-2.872	1.95E-0
	mmu05330 Allograft rejection	27	-2.989	1.87E-0
	mmu05134 Legionellosis	51	-2.943	1.87E-0
	mmu05167 Kaposi's sarcoma-associated herpesvirus infec	149	-3.534	5.95E-0
	mmu05162 Measles	93	-2.832	1.94E-0
	mmu05169 Epstein-Barr virus infection	167	-4.442	4.53E-0
	mmu05160 Hepatitis C	116	-2.757	1.95E-0
	mmu05168 Herpes simplex infection	158	-3.156	1.30E-0
	mmu05164 Influenza A	125	-3.305	1.04E-0
40wks	mmu05016 Huntington's disease	152	3.046	4.52E-0
	mmu04940 Type I diabetes mellitus	30	2.661	4.70E-0
	mmu05330 Allograft rejection	27	3.027	4.60E-0
	mmu05134 Legionellosis	51	2.723	4.60E-0
	mmu05167 Kaposi's sarcoma-associated herpesvirus infec	149	3.065	4.52E-0
	mmu05168 Herpes simplex infection	158	2.819	4.60E-0
	mmu05164 Influenza A	125	3.000	4.52E-0
	mmu05418 Fluid shear stress and atherosclerosis	94	-2.688	4.60E-0
	mmu05169 Epstein-Barr virus infection	167	-3.417	2.77E-0

Comparison (KO vs WT	Pathway_ID	Set Size	Mean Log FC	FDR
12wks	GO:0045087 innate immune response	422	-5.641	5.59E-0
	GO:0009607 response to biotic stimulus	495	-5.333	8.08E-0
	GO:0043207 response to external biotic stimulus	469	-5.316	8.08E-0
	GO:0051707 response to other organism	469	-5.316	8.08E-0
	GO:0098542 defense response to other organism	279	-5.241	1.13E-0
	GO:0034097 response to cytokine	465	-4.614	1.74E-0
	GO:0001817 regulation of cytokine production	389	-4.592	1.74E-0
	GO:0009617 response to bacterium	290	-4.466	2.75E-0
	GO:0001816 cytokine production	430	-4.427	2.75E-0
	GO:0002252 immune effector process	443	-4.410	2.75E-0
	GO:0006954 inflammatory response	348	-4.206	6.53E-0
	GO:0071345 cellular response to cytokine stimuli	393	-4.077	9.89E-0
	GO:0051607 defense response to virus	154	-3.987	1.43E-0
	GO:0009615 response to virus	187	-3.893	1.86E-0
	GO:0034341 response to interferon-gamma	63	-3.843	3.14E-0
	GO:0042742 defense response to bacterium	111	-3.749	3.18E-0
	GO:0001819 positive regulation of cytokine produ	262	-3.709	3.18E-0
	GO:0006412 translation	493	4.041	1.05E-0
KEGG Metabolism				
Comparison (KO vs WT			Mean Log FC	FDR
4wks	mmu03010 Ribosome	133	-5.421	2.18E-0
8wks	mmu04621 NOD-like receptor signaling pathway	133	-3.300	4.48E-0
		15	-3.432	4.48E-0
	mmu00100 Steroid biosynthesis			
	mmu03010 Ribosome	133	-4.142	3.21E-0
12wks	mmu03010 Ribosome mmu00190 Oxidative phosphorylation	133 112	-4.142 3.124	3.21E-0 2.88E-0
12wks	mmu03010 Ribosome mmu00190 Oxidative phosphorylation mmu03010 Ribosome	133 112 133	-4.142 3.124 5.576	3.21E-0 2.88E-0 1.05E-0
12wks	mmu03010 Ribosome mmu00190 Oxidative phosphorylation mmu03010 Ribosome mmu04978 Mineral absorption	133 112 133 25	-4.142 3.124 5.576 -3.301	3.21E-0 2.88E-0 1.05E-0 2.88E-0
12wks	mmu03010 Ribosome mmu00190 Oxidative phosphorylation mmu03010 Ribosome mmu04978 Mineral absorption mmu03050 Proteasome	133 112 133 25 44	-4.142 3.124 5.576 -3.301 -3.211	3.21E-0 2.88E-0 1.05E-0 2.88E-0 2.88E-0
12wks	mmu03010 Ribosome mmu03010 Ribosome mmu03010 Ribosome mmu03010 Ribosome mmu04978 Milneral absorption mmu03050 Proteasome mmu04612 Antigen processing and presentation	133 112 133 25 44 55	-4.142 3.124 5.576 -3.301 -3.211 -3.401	3.21E-0 2.88E-0 1.05E-0 2.88E-0 2.88E-0 2.14E-0
12wks	mmu03010 Ribosome mmu00190 Oxidative phosphorylation mmu03010 Ribosome mmu04978 Mineral absorption mmu03050 Proteasome mmu04612 Antigen processing and presentation mmu04688 TNF signaling pathway	133 112 133 25 44 55 90	-4.142 3.124 5.576 -3.301 -3.211 -3.401 -3.368	3.21E-0 2.88E-0 1.05E-0 2.88E-0 2.88E-0 2.14E-0 2.14E-0
12wks	mmu03010 Ribosome mmu00190 Oxidative phosphorylation mmu03010 Ribosome mmu04978 Mineral absorption mmu03696 Proteasome mmu04612 Antigen processing and presentation mmu04668 TINE signaling pathway mmu04621 NOD-like receptor signaling pathway	133 112 133 25 44 55 90 133	-4.142 3.124 5.576 -3.301 -3.211 -3.401 -3.368 -4.040	3.21E-0 2.88E-0 1.05E-0 2.88E-0 2.88E-0 2.14E-0 2.14E-0 2.52E-0
12wks	mmu03010 Ribosome mmu00190 Oxidative phosphorylation mmu03010 Ribosome mmu04978 Mineral absorption mmu03050 Proteasome mmu04612 Antigen processing and presentation mmu04688 TNF signaling pathway	133 112 133 25 44 55 90	-4.142 3.124 5.576 -3.301 -3.211 -3.401 -3.368	3.21E-0 2.88E-0 1.05E-0 2.88E-0 2.88E-0 2.14E-0 2.14E-0 2.52E-0 5.18E-0