

Table SI. Sequences of primers used for reverse transcription-quantitative PCR.

Gene	Sequence (5'-3')
PTGS2	F: ATTAACGAAGCATCCACAGA R: GGTGAATGTTTGCCTTAGG
HMOX1	F: ATTCTCTGGCTGGCTTC R: CCGTGCAACAAGGATACT
TNFSF18	F: CTTCACTCTGCTCACCTT R: TGACTACAAGAGGCAATGG
THEMIS2	F: CTGTCTTCCTCATCTCTGTAG R: AAGGCCTAAGGTTGTGTTT
TRIM21	F: ATGTTGATGGTGAAGTACT R: TCTACTCCTTCTCTGAATGTG
IL6	F: GGCACCTCAGATTGTTGT R: TAGTGCCTAACGCTCATACT
NLRC5	F: AAGGACAGGTGGAGGTAG R: AGTGTGACAGAGCCATTC
SECTM1	F: CTGAACTGGAGTGTGTCTG R: ATGGAACCACCTCACCTC
CXCL11	F: ACTGGTGCTACTAATTTGGT R: TTACGGTGGAGACATTGAC
CEBPB	F: TCTCTGCTTCTCCCTCTG

	R: GCCCGTAGGAACATCTTTA
ATP13A2-M	F: AGGAAGGGCACATTGGTGTA
ATP13A2-AS	F: CTAGCACGCTCATTGGTGTA
ATP13A2-M/AS	R: TGCCCAACTACGAGAACACC
SIGIRR-M/AS	F: GCCTCGAAGAATCAGCATG
SIGIRR-AS	R: ACAGCTTCCGACTCCTTCCT
SIGIRR-M	R: CGGCTCCGTGACTCCTTCCT
CTNNB1-M/AS	F: CCAGGTGACAGCAATCAG
CTNNB1-AS	R: GACAATACAGCTAAAGGATG
CTNNB1-M	R: ATGTACTCCTAAAGGATG
HDAC7-M/AS	F: GGCAGGAAGAGGGGAGTGT
HDAC7-AS	R: TGGGCTCGGAGGCTGACAGTGA
HDAC7-M	R: CCCTGCCAGGGCTGACAGTGA
IL32-M/AS	F: GCTCCTTGAACCTTTGGC
IL32-AS	R: TCGACATCACCATTGGGCCTT
IL32-M	R: TATGGCCTGGTGCATTGGGCCTT
GAPDH	F: GGTCGGAGTCAACGGATTTG R: GGAAGATGGTGATGGGATTTTC

HDAC7, histone deacetylase 7; HMOX1, heme oxygenase 1; PTGS2, prostaglandin-endoperoxide synthase 2; CTNNB1, catenin β 1F; forward; R, reverse; TNFSF18, TNF ligand superfamily member 18; THEMIS2, Thymocyte-Expressed Molecule involved In Selection Protein 2, ; SECTM1, Secreted and transmembrane protein 1 ; CXCL11, C-X-C motif chemokine 11; SIGIRR-M/AS, single immunoglobulin and toll-interleukin 1 receptor domain .

Table SII. Gene Ontology biological processes for downregulated genes.

Term	ID	Input no.	Background	P-value	Corrected	Input	URL
transmembrane transport	GO:005508	5	578	1.81×10^{-5}	1.88×10^{-5}	FXYD2,Sodium/potassium-transporting ATPase subunit gamma,cDNA FLJ51453, highly similar to Aquaporin-1	amigo.geneontology.org/amigo/term/GO:0055085
signal transduction	GO:000716	6	1045	1.88×10^{-5}	1.88×10^{-5}	Growth/differentiation factor 3, acid-sensing ion channel 1	amigo.geneontology.org/amigo/term/GO:0007165

Statistical analysis was performed using hypergeometric test and false discovery rate correction was performed using the Benjamini and Hochberg method.

Table SIII. Gene Ontology biological processes for upregulated genes.

Term	ID	Input num	Backgroun	P-Value	Corrected	Input	URL
defense response to virus	GO:005160	21	145	0	0	OAS1 IFIT	amigo.geneontology.org/amigo/term/GO:0051607
type I interferon-mediated signaling pathway	GO:006033	12	65	4.35×10^{-13}	1.04×10^{-11}	IFITM1 MX	amigo.geneontology.org/amigo/term/GO:0060337
response to virus	GO:000961	14	114	1.57×10^{-12}	2.51×10^{-11}	RSAD2 DDX	amigo.geneontology.org/amigo/term/GO:0009615
negative regulation of viral genome replication	GO:004507	9	34	1.23×10^{-11}	1.47×10^{-10}	IFITM1 AP	amigo.geneontology.org/amigo/term/GO:0045071
cytokine-mediated signaling pathway	GO:001922	16	229	2.21×10^{-10}	2.12×10^{-9}	IL20RA IL	amigo.geneontology.org/amigo/term/GO:0019221
inflammatory response	GO:000695	15	307	1.04×10^{-7}	8.33×10^{-7}	PTGS2 AOC	amigo.geneontology.org/amigo/term/GO:0006954
positive regulation of transcription from RNA polymerase II promoter	GO:004594	23	749	1.97×10^{-7}	1.35×10^{-6}	IL23A DDI	amigo.geneontology.org/amigo/term/GO:0045944
negative regulation of type I interferon production	GO:003248	5	32	8.87×10^{-5}	5.32×10^{-5}	NLRC5 DDX	amigo.geneontology.org/amigo/term/GO:0032480
ion transport	GO:000681	9	163	1.58×10^{-5}	8.44×10^{-5}	SLC22A20	amigo.geneontology.org/amigo/term/GO:0006811
innate immune response	GO:004508	19	754	4.18×10^{-5}	0.000201	DDX58 TLR	amigo.geneontology.org/amigo/term/GO:0045087
response to endoplasmic reticulum stress	GO:003497	5	48	6.72×10^{-5}	0.000293	CEBPB DDI	amigo.geneontology.org/amigo/term/GO:0034976
cell surface receptor signaling pathway	GO:000716	8	160	9.58×10^{-5}	0.000383	LAMA1 IFI	amigo.geneontology.org/amigo/term/GO:0007166

endoplasmic reticulum unfolded protein response	GO:003096	6	84	0.000106	0.000391	DDIT3 ASN	amigo.geneontology.org/amigo/term/GO:0030968
response to mechanical stimulus	GO:000961	5	54	0.000119	0.000408	RCAN1 IL6	amigo.geneontology.org/amigo/term/GO:0009612
positive regulation of NF-kappaB transcription factor activity	GO:005109	7	127	0.000145	0.000463	AMH TNFSF	amigo.geneontology.org/amigo/term/GO:0051092
negative regulation of NF-kappaB transcription factor activity	GO:003208	5	63	0.000248	0.000744	NLRC5 KLF	amigo.geneontology.org/amigo/term/GO:0032088
cell-cell signaling	GO:000726	9	237	0.000283	0.000768	AMH STC2	amigo.geneontology.org/amigo/term/GO:0007267
GTP catabolic process	GO:000618	7	142	0.000288	0.000768	RERG RRAD	amigo.geneontology.org/amigo/term/GO:0006184
cellular response to lipopolysaccharide	GO:007122	5	83	0.000888	0.002243	IL6 NR1D1	amigo.geneontology.org/amigo/term/GO:0071222
signal transduction	GO:000716	20	1045	0.001	0.002399	GEM IL5RA	amigo.geneontology.org/amigo/term/GO:0007165
small GTPase mediated signal transduction	GO:000726	10	348	0.001159	0.002571	RERG RAB3	amigo.geneontology.org/amigo/term/GO:0007264
immune response	GO:000695	12	476	0.001179	0.002571	OAS1 CEBP	amigo.geneontology.org/amigo/term/GO:0006955
transmembrane transport	GO:005508	13	578	0.002053	0.004284	TAP1 ATP2	amigo.geneontology.org/amigo/term/GO:0055085
positive regulation of I-kappaB kinase/NF-kappaB cascade	GO:004312	6	153	0.002544	0.005088	HMOX1 BIR	amigo.geneontology.org/amigo/term/GO:0043123
negative regulation of transcription, DNA-dependent	GO:004589	11	464	0.003038	0.005833	CEBPB CIA	amigo.geneontology.org/amigo/term/GO:0045892

negative regulation of neuron apoptotic process	GO:004352	5	124	0.005148	0.009504	NR4A2 NR4	amigo.geneontology.org/amigo/term/GO:0043524
negative regulation of cell proliferation	GO:000828	9	378	0.00698	0.012408	PTGS2 RER	amigo.geneontology.org/amigo/term/GO:0008285
positive regulation of apoptotic process	GO:004306	7	294	0.016679	0.028593	PTGS2 GAD	amigo.geneontology.org/amigo/term/GO:0043065
cellular nitrogen compound metabolic process	GO:003464	5	185	0.025477	0.041289	PSAT1 CTH	amigo.geneontology.org/amigo/term/GO:0034641
cell differentiation	GO:003015	8	395	0.025806	0.041289	SLC7A5 ET	amigo.geneontology.org/amigo/term/GO:0030154
angiogenesis	GO:000152	5	206	0.037897	0.058678	PTGS2 HMO	amigo.geneontology.org/amigo/term/GO:0001525
blood coagulation	GO:000759	8	469	0.060103	0.090155	ACTN2 F3	amigo.geneontology.org/amigo/term/GO:0007596
negative regulation of apoptotic process	GO:004306	8	475	0.063751	0.092729	CTH TNFSF	amigo.geneontology.org/amigo/term/GO:0043066
negative regulation of transcription from RNA polymerase II promoter	GO:000012	9	565	0.067433	0.0952	HDAC9 JDP	amigo.geneontology.org/amigo/term/GO:0000122
transcription from RNA polymerase II promoter	GO:000636	7	407	0.073433	0.100708	CEBPB ETV	amigo.geneontology.org/amigo/term/GO:0006366
axon guidance	GO:000741	6	334	0.0799	0.106534	LAMA1 NR4	amigo.geneontology.org/amigo/term/GO:0007411
cell proliferation	GO:000828	6	344	0.089035	0.115505	IL5RA DDI	amigo.geneontology.org/amigo/term/GO:0008283
apoptotic process	GO:000691	9	605	0.093589	0.118217	GADD45B B	amigo.geneontology.org/amigo/term/GO:0006915
response to drug	GO:004249	5	305	0.139019	0.171101	IL6 PTGS2	amigo.geneontology.org/amigo/term/GO:0042495

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positive regulation of transcription, DNA-dependent	GO:004589	7	503	0.165451	0.198541	DDIT3 FOS	amigo.geneontology.org/ami go/term/GO:0045893
viral reproduction	GO:001603	7	555	0.230048	0.269325	DDX58 HPX	amigo.geneontology.org/ami go/term/GO:0016032
cellular protein metabolic process	GO:004426	6	530	0.338747	0.379338	STX1A GCN	amigo.geneontology.org/ami go/term/GO:0044267
positive regulation of cell proliferation	GO:000828	5	429	0.339824	0.379338	IL6 IL11	amigo.geneontology.org/ami go/term/GO:0008284
cell adhesion	GO:000715	5	445	0.368324	0.401808	LAMA1 AOC	amigo.geneontology.org/ami go/term/GO:0007155
small molecule metabolic process	GO:004428	14	1413	0.387023	0.412825	STX1A PTG	amigo.geneontology.org/ami go/term/GO:0044281
transcription, DNA-dependent	GO:000635	17	1857	0.500992	0.522775	ZNF844 CI	amigo.geneontology.org/ami go/term/GO:0006351
gene expression	GO:001046	6	672	0.561886	0.573841	NR4A2 NR4	amigo.geneontology.org/ami go/term/GO:0010467
regulation of transcription, DNA-dependent	GO:000635	10	1305	0.742111	0.742111	CEBPB DDI	amigo.geneontology.org/ami go/term/GO:0006355

Statistical analysis was performed using the hypergeometric test and false discovery rate correction was performed using the Benjamini and Hochberg method.

Table SIV. KEGG pathways of upregulated genes.

Term	ID	Input num	Backgroun	P-Value	Corrected	Input	URL
Cytokine-	hsa04060	15	265	3.55E-06	0.000628	IL20RA AM	http://www.genome.jp/kegg-bin/show_pathway?hsa04060/hsa:53832%09red/hsa:3568%09red/hsa:51561%09red/hsa:8995%09red/hsa:3569%09red/hsa:6373%09red/hsa:3456%09red/hsa:3589%09red/hsa:3627%09red/hsa:3576%09red/hsa:3624%09red/hsa:3552%09red/hsa:268%09red/hsa:2826%09red/hsa:4804%09red
Influenza	hsa05164	11	176	3.19E-05	0.00282	IL6 DDX58	http://www.genome.jp/kegg-bin/show_pathway?hsa05164/hsa:3569%09red/hsa:3552%09red/hsa:7098%09red/hsa:4599%09red/hsa:3456%09red/hsa:23586%09red/hsa:3627%09red/hsa:3576%09red/hsa:4938%09red/hsa:4939%09red/hsa:91543%09red
Toll-like	hsa04620	8	106	0.00011	0.004963	FOS CXCL8	http://www.genome.jp/kegg-bin/show_pathway?hsa04620/hsa:54106%09red/hsa:3569%09red/hsa:7098%09red/hsa:6373%09red/hsa:3456%09red/hsa:3627%09red/hsa:3576%09red/hsa:2353%09red
Measles	hsa05162	9	136	0.000112	0.004963	IL6 DDX58	http://www.genome.jp/kegg-bin/show_pathway?hsa05162/hsa:54106%09red/hsa:3552%09red/hsa:7128%09red/hsa:3569%09red/hsa:4599%09red/hsa:3456%09red/hsa:4938%09red/hsa:4939%09red/hsa:23586%09red
Transcrip	hsa05202	10	180	0.000198	0.007018	CEBPB DDI	http://www.genome.jp/kegg-bin/show_pathway?hsa05202/hsa:3569%09red/hsa:330%09red/hsa:8900%09red/hsa:4804%09red/hsa:3576%09red/hsa:8013%09red/hsa:1051%09red/hsa:51513%09red/hsa:1649%09red/hsa:26471%09red
Herpes si	hsa05168	10	186	0.000259	0.007637	TAP1 IL6	http://www.genome.jp/kegg-bin/show_pathway?hsa05168/hsa:3569%09red/hsa:330%09red/hsa:8900%09red/hsa:4804%09red/hsa:3576%09red/hsa:8013%09red/hsa:1051%09red/hsa:51513%09red/hsa:1649%09red/hsa:26471%09red

							168/hsa:54106%09red/hsa:6890%09red/hsa:3569%09red/hsa:7098%09red/hsa:3456%09red/hsa:4938%09red/hsa:3434%09red/hsa:4939%09red/hsa:23586%09red/hsa:2353%09red
TNF signa	hsa04668	7	110	0.000846	0.021381	CEBPB FOS	http://www.genome.jp/kegg-bin/show_pathway?hsa04668/hsa:3569%09red/hsa:330%09red/hsa:7128%09red/hsa:5743%09red/hsa:3627%09red/hsa:1051%09red/hsa:2353%09red
Rheumatoi	hsa05323	6	91	0.001669	0.0367	IL23A FOS	http://www.genome.jp/kegg-bin/show_pathway?hsa05323/hsa:3569%09red/hsa:51561%09red/hsa:3589%09red/hsa:3576%09red/hsa:3552%09red/hsa:2353%09red
NF-kappa	hsa04064	6	93	0.001866	0.0367	PTGS2 DDX	http://www.genome.jp/kegg-bin/show_pathway?hsa04064/hsa:7128%09red/hsa:5743%09red/hsa:3576%09red/hsa:4616%09red/hsa:23586%09red/hsa:330%09red
Glycine,	hsa00260	4	40	0.002261	0.040024	PSAT1 AOC	http://www.genome.jp/kegg-bin/show_pathway?hsa00260/hsa:8639%09red/hsa:26227%09red/hsa:29968%09red/hsa:1491%09red
Hepatitis	hsa05160	7	133	0.002545	0.040949	DDX58 CXC	http://www.genome.jp/kegg-bin/show_pathway?hsa05160/hsa:7098%09red/hsa:3456%09red/hsa:4938%09red/hsa:3576%09red/hsa:3434%09red/hsa:4939%09red/hsa:23586%09red
RIG-I-lik	hsa04622	5	70	0.00289	0.042631	CXCL10 DD	http://www.genome.jp/kegg-bin/show_pathway?hsa04622/hsa:79132%09red/hsa:3456%09red/hsa:3627%09red/hsa:3576%09red/hsa:23586%09red
Pertussis	hsa05133	5	75	0.003901	0.053115	IL6 IL1A	http://www.genome.jp/kegg-bin/show_pathway?hsa05133/hsa:3569%09red/hsa:51561%09red/hsa:2353%09red/hsa:3552%09red/hsa:3576%09red
Hepatitis	hsa05161	7	146	0.00428	0.054108	DDX58 CCN	http://www.genome.jp/kegg-bin/show_pathway?hsa05161/hsa:7098%09red/hsa:3456%09red/hsa:4938%09red/hsa:3576%09red/hsa:3434%09red/hsa:4939%09red/hsa:23586%09red

							161/hsa:3569%09red/hsa:8900%09red/hsa:7098%09red/hsa:3456%09red/hsa:3576%09red/hsa:23586%09red/hsa:2353%09red
NOD-like	hsa04621	4	57	0.008154	0.096216	IL6 CXCL8	http://www.genome.jp/kegg-bin/show_pathway?hsa04621/hsa:3569%09red/hsa:330%09red/hsa:7128%09red/hsa:3576%09red
Cytosolic	hsa04623	4	64	0.012177	0.127262	IL6 CXCL1	http://www.genome.jp/kegg-bin/show_pathway?hsa04623/hsa:3569%09red/hsa:3456%09red/hsa:3627%09red/hsa:23586%09red
Prion dis	hsa05020	3	35	0.012665	0.127262	IL6 IL1A	http://www.genome.jp/kegg-bin/show_pathway?hsa05020/hsa:3569%09red/hsa:735%09red/hsa:3552%09red
Amoebiasi	hsa05146	5	100	0.012942	0.127262	IL6 LAMA1	http://www.genome.jp/kegg-bin/show_pathway?hsa05146/hsa:284217%09red/hsa:3569%09red/hsa:735%09red/hsa:88%09red/hsa:3576%09red
Chagas di	hsa05142	5	104	0.015134	0.140982	IL6 IFNB1	http://www.genome.jp/kegg-bin/show_pathway?hsa05142/hsa:54106%09red/hsa:3456%09red/hsa:2353%09red/hsa:3576%09red/hsa:3569%09red
Selenocom	hsa00450	2	17	0.023104	0.196136	CTH TXNRD	http://www.genome.jp/kegg-bin/show_pathway?hsa00450/hsa:7296%09red/hsa:1491%09red
Jak-STAT	hsa04630	6	158	0.02327	0.196136	IL20RA IL	http://www.genome.jp/kegg-bin/show_pathway?hsa04630/hsa:53832%09red/hsa:3568%09red/hsa:51561%09red/hsa:3569%09red/hsa:3456%09red/hsa:3589%09red
Malaria	hsa05144	3	49	0.030987	0.238036	IL6 CXCL8	http://www.genome.jp/kegg-bin/show_pathway?hsa05144/hsa:54106%09red/hsa:3576%09red/hsa:3569%09red
One carbo	hsa00670	2	20	0.031413	0.238036	ALDH1L2 M	http://www.genome.jp/kegg-bin/show_pathway?hsa00670/hsa:10797%09red/hsa:160428%09red
Salmonell	hsa05132	4	86	0.032276	0.238036	IL6 IL1A	http://www.genome.jp/kegg-bin/show_pathway?hsa05132/hsa:3569%09red/hsa:330%09red/hsa:7128%09red/hsa:3576%09red

							132/hsa:3569%09red/hsa:2353%09red/hsa:3576%09red/hsa:3552%09red
Hematopoi	hsa04640	4	88	0.034707	0.245727	IL6 IL11	http://www.genome.jp/kegg-bin/show_pathway?hsa04640/hsa:3568%09red/hsa:3569%09red/hsa:3589%09red/hsa:3552%09red
Tuberculo	hsa05152	6	179	0.03946	0.268629	CEBPB IL2	http://www.genome.jp/kegg-bin/show_pathway?hsa05152/hsa:54106%09red/hsa:51561%09red/hsa:3569%09red/hsa:3456%09red/hsa:1051%09red/hsa:3552%09red
Systemic	hsa05322	5	136	0.041869	0.274472	HIST1H2AE	http://www.genome.jp/kegg-bin/show_pathway?hsa05322/hsa:88%09red/hsa:735%09red/hsa:8334%09red/hsa:6737%09red/hsa:3012%09red
AGE-RAGE	hsa04933	4	101	0.053054	0.335375	IL6 IL1A	http://www.genome.jp/kegg-bin/show_pathway?hsa04933/hsa:3569%09red/hsa:3552%09red/hsa:2152%09red/hsa:3576%09red
Non-alcohol	hsa04932	5	151	0.06057	0.369686	IL6 IL1A	http://www.genome.jp/kegg-bin/show_pathway?hsa04932/hsa:3569%09red/hsa:3552%09red/hsa:56901%09red/hsa:3576%09red/hsa:1649%09red
Inflammat	hsa05321	3	66	0.06503	0.377349	IL6 IL1A	http://www.genome.jp/kegg-bin/show_pathway?hsa05321/hsa:3569%09red/hsa:51561%09red/hsa:3552%09red
Insulin r	hsa04931	4	109	0.066523	0.377349	PCK2 IL6	http://www.genome.jp/kegg-bin/show_pathway?hsa04931/hsa:3569%09red/hsa:57761%09red/hsa:5106%09red/hsa:5837%09red
Butirosin	hsa00524	1	5	0.068221	0.377349	HKDC1	http://www.genome.jp/kegg-bin/show_pathway?hsa00524/hsa:80201%09red
Apoptosis	hsa04215	2	33	0.077688	0.41669	BIRC3 NGF	http://www.genome.jp/kegg-bin/show_pathway?hsa04215/hsa:4804%09red/hsa:330%09red
Vitamin B	hsa00750	1	6	0.081302	0.420229	PSAT1	http://www.genome.jp/kegg-bin/show_pathway?hsa00750

							750/hsa:29968%09red
Leishmani	hsa05140	3	74	0.08516	0.420229	PTGS2 IL1	http://www.genome.jp/kegg-bin/show_pathway?hsa05140/hsa:5743%09red/hsa:2353%09red/hsa:3552%09red
African t	hsa05143	2	35	0.086003	0.420229	IL6 TLR9	http://www.genome.jp/kegg-bin/show_pathway?hsa05143/hsa:54106%09red/hsa:3569%09red
Biosynthe	hsa01230	3	75	0.087845	0.420229	PSAT1 CTH	http://www.genome.jp/kegg-bin/show_pathway?hsa01230/hsa:26227%09red/hsa:29968%09red/hsa:1491%09red
Pathways	hsa05200	9	397	0.103908	0.476638	LAMA1 FOS	http://www.genome.jp/kegg-bin/show_pathway?hsa05200/hsa:8900%09red/hsa:3569%09red/hsa:330%09red/hsa:5743%09red/hsa:2250%09red/hsa:3576%09red/hsa:284217%09red/hsa:9170%09red/hsa:2353%09red
PI3K-Akt	hsa04151	8	341	0.105022	0.476638	PCK2 LAMA	http://www.genome.jp/kegg-bin/show_pathway?hsa04151/hsa:3569%09red/hsa:3456%09red/hsa:2250%09red/hsa:5106%09red/hsa:54541%09red/hsa:284217%09red/hsa:9170%09red/hsa:4804%09red
TGF-beta	hsa04350	3	84	0.113542	0.502421	INHBA FST	http://www.genome.jp/kegg-bin/show_pathway?hsa04350/hsa:268%09red/hsa:10468%09red/hsa:3624%09red
Graft-ver	hsa05332	2	42	0.116981	0.504046	IL6 IL1A	http://www.genome.jp/kegg-bin/show_pathway?hsa05332/hsa:3569%09red/hsa:3552%09red
Small cel	hsa05222	3	86	0.119604	0.504046	LAMA1 BIR	http://www.genome.jp/kegg-bin/show_pathway?hsa05222/hsa:284217%09red/hsa:5743%09red/hsa:330%09red
Apoptosis	hsa04210	4	140	0.13326	0.548537	GADD45B D	http://www.genome.jp/kegg-bin/show_pathway?hsa04210/hsa:2353%09red/hsa:330%09red/hsa:4616%09red/hsa:1649%09red

MAPK sign	hsa04010	6	255	0.147746	0.591048	DDIT3 FOS	http://www.genome.jp/kegg-bin/show_pathway?hsa04010/hsa:3552%09red/hsa:2250%09red/hsa:1649%09red/hsa:4616%09red/hsa:2353%09red/hsa:23162%09red
Intestina	hsa04672	2	49	0.150266	0.591048	IL6 CCR10	http://www.genome.jp/kegg-bin/show_pathway?hsa04672/hsa:3569%09red/hsa:2826%09red
mTOR sign	hsa04150	4	154	0.169916	0.653808	SLC3A2 SL	http://www.genome.jp/kegg-bin/show_pathway?hsa04150/hsa:8140%09red/hsa:83667%09red/hsa:54541%09red/hsa:6520%09red
HIF-1 sig	hsa04066	3	103	0.175451	0.660739	HKDC1 IL6	http://www.genome.jp/kegg-bin/show_pathway?hsa04066/hsa:3569%09red/hsa:80201%09red/hsa:3162%09red
Legionell	hsa05134	2	55	0.1801	0.664119	IL6 CXCL8	http://www.genome.jp/kegg-bin/show_pathway?hsa05134/hsa:3569%09red/hsa:3576%09red
Starch an	hsa00500	2	57	0.19024	0.687195	HKDC1 PYG	http://www.genome.jp/kegg-bin/show_pathway?hsa00500/hsa:80201%09red/hsa:5837%09red
Carbon me	hsa01200	3	113	0.211165	0.741755	HKDC1 PSA	http://www.genome.jp/kegg-bin/show_pathway?hsa01200/hsa:80201%09red/hsa:26227%09red/hsa:29968%09red
Phenylala	hsa00360	1	17	0.213726	0.741755	AOC3	http://www.genome.jp/kegg-bin/show_pathway?hsa00360/hsa:8639%09red
Synaptic	hsa04721	2	63	0.221071	0.752493	STX1A UNC	http://www.genome.jp/kegg-bin/show_pathway?hsa04721/hsa:23025%09red/hsa:6804%09red
Shigellos	hsa05131	2	65	0.231447	0.764435	CXCL8 ELM	http://www.genome.jp/kegg-bin/show_pathway?hsa05131/hsa:79767%09red/hsa:3576%09red
Amphetami	hsa05031	2	67	0.241855	0.764435	STX1A FOS	http://www.genome.jp/kegg-bin/show_pathway?hsa05031/hsa:2353%09red/hsa:6804%09red
Central c	hsa05230	2	67	0.241855	0.764435	HKDC1 SLC	http://www.genome.jp/kegg-bin/show_pathway?hsa05230/hsa:80201%09red/hsa:8140%09red

Glycolysi	hsa00010	2	67	0.241855	0.764435	PCK2 HKDC	http://www.genome.jp/kegg-bin/show_pathway?hsa00010/hsa:80201%09red/hsa:5106%09red
Steroid b	hsa00100	1	20	0.246437	0.765252	CEL	http://www.genome.jp/kegg-bin/show_pathway?hsa00100/hsa:1056%09red
p53 signa	hsa04115	2	69	0.252285	0.769905	GADD45B S	http://www.genome.jp/kegg-bin/show_pathway?hsa04115/hsa:4616%09red/hsa:83667%09red
Chemokine	hsa04062	4	187	0.267327	0.781476	CXCL11 CX	http://www.genome.jp/kegg-bin/show_pathway?hsa04062/hsa:6373%09red/hsa:3627%09red/hsa:3576%09red/hsa:2826%09red
B cell re	hsa04662	2	73	0.273175	0.781476	IFITM1 FO	http://www.genome.jp/kegg-bin/show_pathway?hsa04662/hsa:2353%09red/hsa:8519%09red
Proximal	hsa04964	1	23	0.277801	0.781476	PCK2	http://www.genome.jp/kegg-bin/show_pathway?hsa04964/hsa:5106%09red
Mismatch	hsa03430	1	23	0.277801	0.781476	RPA4	http://www.genome.jp/kegg-bin/show_pathway?hsa03430/hsa:29935%09red
Arrhythmo	hsa05412	2	74	0.278398	0.781476	ACTN2 DSP	http://www.genome.jp/kegg-bin/show_pathway?hsa05412/hsa:88%09red/hsa:1832%09red
Osteoclas	hsa04380	3	132	0.282568	0.781476	IL1A IFNB	http://www.genome.jp/kegg-bin/show_pathway?hsa04380/hsa:3456%09red/hsa:2353%09red/hsa:3552%09red
FoxO sign	hsa04068	3	134	0.290245	0.79036	PCK2 IL6	http://www.genome.jp/kegg-bin/show_pathway?hsa04068/hsa:3569%09red/hsa:4616%09red/hsa:5106%09red
Complemen	hsa04610	2	79	0.304462	0.816513	C9 F3	http://www.genome.jp/kegg-bin/show_pathway?hsa04610/hsa:735%09red/hsa:2152%09red
Insulin s	hsa04910	3	139	0.309503	0.817643	PCK2 HKDC	http://www.genome.jp/kegg-bin/show_pathway?hsa04910/hsa:80201%09red/hsa:5106%09red/hsa:5837%09red

Dorso-ven	hsa04320	1	28	0.327227	0.824537	ETV7	http://www.genome.jp/kegg-bin/show_pathway?hsa04320/hsa:51513%09red
Homologou	hsa03440	1	29	0.336702	0.824537	RPA4	http://www.genome.jp/kegg-bin/show_pathway?hsa03440/hsa:29935%09red
Pentose p	hsa00030	1	29	0.336702	0.824537	RBKS	http://www.genome.jp/kegg-bin/show_pathway?hsa00030/hsa:64080%09red
Citrate c	hsa00020	1	30	0.346046	0.824537	PCK2	http://www.genome.jp/kegg-bin/show_pathway?hsa00020/hsa:5106%09red
GABAergic	hsa04727	2	88	0.350902	0.824537	SLC6A13 G	http://www.genome.jp/kegg-bin/show_pathway?hsa04727/hsa:6540%09red/hsa:2564%09red
Circadian	hsa04710	1	31	0.355259	0.824537	NR1D1	http://www.genome.jp/kegg-bin/show_pathway?hsa04710/hsa:9572%09red
Galactose	hsa00052	1	31	0.355259	0.824537	HKDC1	http://www.genome.jp/kegg-bin/show_pathway?hsa00052/hsa:80201%09red
Mucin typ	hsa00512	1	31	0.355259	0.824537	GCNT4	http://www.genome.jp/kegg-bin/show_pathway?hsa00512/hsa:51301%09red
beta-Alan	hsa00410	1	31	0.355259	0.824537	AOC3	http://www.genome.jp/kegg-bin/show_pathway?hsa00410/hsa:8639%09red
Protein d	hsa04974	2	90	0.361095	0.824537	SLC3A2 SL	http://www.genome.jp/kegg-bin/show_pathway?hsa04974/hsa:6543%09red/hsa:6520%09red
Fructose	hsa00051	1	33	0.373302	0.824537	HKDC1	http://www.genome.jp/kegg-bin/show_pathway?hsa00051/hsa:80201%09red
SNARE int	hsa04130	1	34	0.382135	0.824537	STX1A	http://www.genome.jp/kegg-bin/show_pathway?hsa04130/hsa:6804%09red
Oxytocin	hsa04921	3	158	0.382732	0.824537	RCAN1 PTG	http://www.genome.jp/kegg-bin/show_pathway?hsa04921/hsa:1827%09red/hsa:5743%09red/hsa:2353%09red
Circadian	hsa04713	2	95	0.386312	0.824537	RASD1 FOS	http://www.genome.jp/kegg-bin/show_pathway?hsa04713/hsa:9572%09red/hsa:2353%09red

							713/hsa:51655%09red/hsa:2353%09red
Tyrosine	hsa00350	1	35	0.390845	0.824537	AOC3	http://www.genome.jp/kegg-bin/show_pathway?hsa00350/hsa:8639%09red
Alanine,	hsa00250	1	35	0.390845	0.824537	ASNS	http://www.genome.jp/kegg-bin/show_pathway?hsa00250/hsa:440%09red
Pancreati	hsa04972	2	96	0.391306	0.824537	CEL ATP2A	http://www.genome.jp/kegg-bin/show_pathway?hsa04972/hsa:1056%09red/hsa:487%09red
DNA repli	hsa03030	1	36	0.399433	0.829657	RPA4	http://www.genome.jp/kegg-bin/show_pathway?hsa03030/hsa:29935%09red
Primary i	hsa05340	1	37	0.407901	0.829657	TAP1	http://www.genome.jp/kegg-bin/show_pathway?hsa05340/hsa:6890%09red
Retrograd	hsa04723	2	101	0.416	0.829657	GABRE PTG	http://www.genome.jp/kegg-bin/show_pathway?hsa04723/hsa:5743%09red/hsa:2564%09red
cGMP-PKG	hsa04022	3	167	0.416951	0.829657	MEF2B SLC	http://www.genome.jp/kegg-bin/show_pathway?hsa04022/hsa:487%09red/hsa:6543%09red/hsa:100271849%09red
Glucagon	hsa04922	2	102	0.42088	0.829657	PCK2 PYGM	http://www.genome.jp/kegg-bin/show_pathway?hsa04922/hsa:5106%09red/hsa:5837%09red
Nicotine	hsa05033	1	40	0.432603	0.829657	GABRE	http://www.genome.jp/kegg-bin/show_pathway?hsa05033/hsa:2564%09red
Pyruvate	hsa00620	1	40	0.432603	0.829657	PCK2	http://www.genome.jp/kegg-bin/show_pathway?hsa00620/hsa:5106%09red
Pyrimidin	hsa00240	2	105	0.435397	0.829657	CMPK2 TXN	http://www.genome.jp/kegg-bin/show_pathway?hsa00240/hsa:7296%09red/hsa:129607%09red
Bladder c	hsa05219	1	41	0.440609	0.829657	CXCL8	http://www.genome.jp/kegg-bin/show_pathway?hsa05219/hsa:3576%09red
Fat diges	hsa04975	1	41	0.440609	0.829657	CEL	http://www.genome.jp/kegg-bin/show_pathway?hsa04975/hsa:1056%09red

Porphyrin	hsa00860	1	42	0.448502	0.834602	HMOX1	http://www.genome.jp/kegg-bin/show_pathway?hsa00860/hsa:3162%09red
Alcoholis	hsa05034	3	179	0.461605	0.834602	HIST1H2AE	http://www.genome.jp/kegg-bin/show_pathway?hsa05034/hsa:9734%09red/hsa:8334%09red/hsa:3012%09red
Type I di	hsa04940	1	44	0.463959	0.834602	IL1A	http://www.genome.jp/kegg-bin/show_pathway?hsa04940/hsa:3552%09red
Proteasom	hsa03050	1	44	0.463959	0.834602	PSMB9	http://www.genome.jp/kegg-bin/show_pathway?hsa03050/hsa:5698%09red
ABC trans	hsa02010	1	45	0.471526	0.834602	TAP1	http://www.genome.jp/kegg-bin/show_pathway?hsa02010/hsa:6890%09red
Cysteine	hsa00270	1	45	0.471526	0.834602	CTH	http://www.genome.jp/kegg-bin/show_pathway?hsa00270/hsa:1491%09red
Carbohydr	hsa04973	1	46	0.478988	0.839414	HKDC1	http://www.genome.jp/kegg-bin/show_pathway?hsa04973/hsa:80201%09red
Nucleotid	hsa03420	1	47	0.486345	0.840068	RPA4	http://www.genome.jp/kegg-bin/show_pathway?hsa03420/hsa:29935%09red
Amino sug	hsa00520	1	48	0.493599	0.840068	HKDC1	http://www.genome.jp/kegg-bin/show_pathway?hsa00520/hsa:80201%09red
Type II d	hsa04930	1	48	0.493599	0.840068	HKDC1	http://www.genome.jp/kegg-bin/show_pathway?hsa04930/hsa:80201%09red
Toxoplasm	hsa05145	2	119	0.500447	0.843611	LAMA1 BIR	http://www.genome.jp/kegg-bin/show_pathway?hsa05145/hsa:284217%09red/hsa:330%09red
Ovarian s	hsa04913	1	50	0.507805	0.845423	PTGS2	http://www.genome.jp/kegg-bin/show_pathway?hsa04913/hsa:5743%09red
Mineral a	hsa04978	1	52	0.521615	0.845423	HMOX1	http://www.genome.jp/kegg-bin/show_pathway?hsa04978/hsa:3162%09red
AMPK sign	hsa04152	2	124	0.522513	0.845423	PCK2 CCNA	http://www.genome.jp/kegg-bin/show_pathway?hsa04152/hsa:3162%09red

							152/hsa:8900%09red/hsa:5106%09red
Cell cycl	hsa04110	2	124	0.522513	0.845423	GADD45B C	http://www.genome.jp/kegg-bin/show_pathway?hsa04110/hsa:8900%09red/hsa:4616%09red
Autoimmun	hsa05320	1	54	0.535043	0.845423	TG	http://www.genome.jp/kegg-bin/show_pathway?hsa05320/hsa:7038%09red
Epstein-B	hsa05169	3	201	0.539396	0.845423	DDX58 TNF	http://www.genome.jp/kegg-bin/show_pathway?hsa05169/hsa:8900%09red/hsa:7128%09red/hsa:23586%09red
Fanconi a	hsa03460	1	55	0.541616	0.845423	RPA4	http://www.genome.jp/kegg-bin/show_pathway?hsa03460/hsa:29935%09red
Focal adh	hsa04510	3	203	0.546157	0.845423	LAMA1 BIR	http://www.genome.jp/kegg-bin/show_pathway?hsa04510/hsa:284217%09red/hsa:330%09red/hsa:88%09red
Regulatio	hsa04923	1	56	0.548097	0.845423	PTGS2	http://www.genome.jp/kegg-bin/show_pathway?hsa04923/hsa:5743%09red
Viral car	hsa05203	3	205	0.55286	0.845423	HDAC9 ACT	http://www.genome.jp/kegg-bin/show_pathway?hsa05203/hsa:8900%09red/hsa:88%09red/hsa:9734%09red
Acute mye	hsa05221	1	57	0.554487	0.845423	CCNA1	http://www.genome.jp/kegg-bin/show_pathway?hsa05221/hsa:8900%09red
Glyceroli	hsa00561	1	59	0.567	0.845423	CEL	http://www.genome.jp/kegg-bin/show_pathway?hsa00561/hsa:1056%09red
Natural k	hsa04650	2	135	0.568745	0.845423	IFNB1 ULB	http://www.genome.jp/kegg-bin/show_pathway?hsa04650/hsa:3456%09red/hsa:80329%09red
Rap1 sign	hsa04015	3	211	0.572624	0.845423	LPAR2 FGF	http://www.genome.jp/kegg-bin/show_pathway?hsa04015/hsa:9170%09red/hsa:4804%09red/hsa:2250%09red
VEGF sign	hsa04370	1	61	0.579166	0.845423	PTGS2	http://www.genome.jp/kegg-bin/show_pathway?hsa04370/hsa:5743%09red
Colorecta	hsa05210	1	62	0.585121	0.845423	FOS	http://www.genome.jp/kegg-bin/show_pathway?hsa05210/hsa:8900%09red/hsa:5106%09red

							210/hsa:2353%09red
Arachidon	hsa00590	1	62	0.585121	0.845423	PTGS2	http://www.genome.jp/kegg-bin/show_pathway?hsa00590/hsa:5743%09red
Signaling	hsa04550	2	142	0.596467	0.845423	INHBA KLF	http://www.genome.jp/kegg-bin/show_pathway?hsa04550/hsa:9314%09red/hsa:3624%09red
Wnt signa	hsa04310	2	143	0.600318	0.845423	NKD1 DKK2	http://www.genome.jp/kegg-bin/show_pathway?hsa04310/hsa:27123%09red/hsa:85407%09red
Phospholi	hsa04072	2	144	0.604142	0.845423	LPAR2 CXC	http://www.genome.jp/kegg-bin/show_pathway?hsa04072/hsa:9170%09red/hsa:3576%09red
Aminoacyl	hsa00970	1	66	0.608119	0.845423	WARS	http://www.genome.jp/kegg-bin/show_pathway?hsa00970/hsa:7453%09red
Epithelia	hsa05120	1	68	0.61914	0.845423	CXCL8	http://www.genome.jp/kegg-bin/show_pathway?hsa05120/hsa:3576%09red
Adipocyto	hsa04920	1	70	0.629854	0.845423	PCK2	http://www.genome.jp/kegg-bin/show_pathway?hsa04920/hsa:5106%09red
Bile secr	hsa04976	1	71	0.635099	0.845423	SLC4A5	http://www.genome.jp/kegg-bin/show_pathway?hsa04976/hsa:57835%09red
Thyroid h	hsa04918	1	71	0.635099	0.845423	TG	http://www.genome.jp/kegg-bin/show_pathway?hsa04918/hsa:7038%09red
Melanoma	hsa05218	1	71	0.635099	0.845423	FGF5	http://www.genome.jp/kegg-bin/show_pathway?hsa05218/hsa:2250%09red
Prolactin	hsa04917	1	72	0.64027	0.845423	FOS	http://www.genome.jp/kegg-bin/show_pathway?hsa04917/hsa:2353%09red
PPAR sign	hsa03320	1	72	0.64027	0.845423	PCK2	http://www.genome.jp/kegg-bin/show_pathway?hsa03320/hsa:5106%09red
Hippo sig	hsa04390	2	154	0.640884	0.845423	NKD1 AMH	http://www.genome.jp/kegg-bin/show_pathway?hsa04390/hsa:268%09red/hsa:85407%09red

Adherens	hsa04520	1	74	0.650396	0.845423	ACTN2	http://www.genome.jp/kegg-bin/show_pathway?hsa04520/hsa:88%09red
Platinum	hsa01524	1	75	0.655352	0.845423	BIRC3	http://www.genome.jp/kegg-bin/show_pathway?hsa01524/hsa:330%09red
Antigen p	hsa04612	1	78	0.669808	0.845423	TAP1	http://www.genome.jp/kegg-bin/show_pathway?hsa04612/hsa:6890%09red
Bacterial	hsa05100	1	78	0.669808	0.845423	ELMO3	http://www.genome.jp/kegg-bin/show_pathway?hsa05100/hsa:79767%09red
Protein p	hsa04141	2	166	0.681417	0.845423	PPP1R15A	http://www.genome.jp/kegg-bin/show_pathway?hsa04141/hsa:23645%09red/hsa:1649%09red
Aldostero	hsa04925	1	81	0.683663	0.845423	NR4A2	http://www.genome.jp/kegg-bin/show_pathway?hsa04925/hsa:4929%09red
EGFR tyro	hsa01521	1	81	0.683663	0.845423	IL6	http://www.genome.jp/kegg-bin/show_pathway?hsa01521/hsa:3569%09red
Alzheimer	hsa05010	2	168	0.687802	0.845423	NDUFA4L2	http://www.genome.jp/kegg-bin/show_pathway?hsa05010/hsa:487%09red/hsa:56901%09red
ECM-recep	hsa04512	1	82	0.688152	0.845423	LAMA1	http://www.genome.jp/kegg-bin/show_pathway?hsa04512/hsa:284217%09red
Chemical	hsa05204	1	82	0.688152	0.845423	PTGS2	http://www.genome.jp/kegg-bin/show_pathway?hsa05204/hsa:5743%09red
Hypertrop	hsa05410	1	83	0.692579	0.845423	IL6	http://www.genome.jp/kegg-bin/show_pathway?hsa05410/hsa:3569%09red
Insulin s	hsa04911	1	85	0.701245	0.85014	STX1A	http://www.genome.jp/kegg-bin/show_pathway?hsa04911/hsa:6804%09red
HTLV-I in	hsa05166	3	259	0.71044	0.850796	IL6 ATF3	http://www.genome.jp/kegg-bin/show_pathway?hsa05166/hsa:467%09red/hsa:3569%09red/hsa:2353%09red
Axon guid	hsa04360	2	176	0.712311	0.850796	RND1 NTNG	http://www.genome.jp/kegg-bin/show_pathway?hsa04360/hsa:27289%09red/hsa:84628%09red

Salivary	hsa04970	1	89	0.71786	0.850796	STATH	http://www.genome.jp/kegg-bin/show_pathway?hsa04970/hsa:6779%09red
Calcium s	hsa04020	2	180	0.723958	0.850796	SLC8A2 AT	http://www.genome.jp/kegg-bin/show_pathway?hsa04020/hsa:487%09red/hsa:6543%09red
Morphine	hsa05032	1	91	0.72582	0.850796	GABRE	http://www.genome.jp/kegg-bin/show_pathway?hsa05032/hsa:2564%09red
Longevity	hsa04211	1	94	0.737347	0.858621	SESN2	http://www.genome.jp/kegg-bin/show_pathway?hsa04211/hsa:83667%09red
Endocrine	hsa01522	1	97	0.748393	0.859531	FOS	http://www.genome.jp/kegg-bin/show_pathway?hsa01522/hsa:2353%09red
Progester	hsa04914	1	98	0.751972	0.859531	CCNA1	http://www.genome.jp/kegg-bin/show_pathway?hsa04914/hsa:8900%09red
Estrogen	hsa04915	1	99	0.7555	0.859531	FOS	http://www.genome.jp/kegg-bin/show_pathway?hsa04915/hsa:2353%09red
Huntingto	hsa05016	2	193	0.759121	0.859531	NDUFA4L2	http://www.genome.jp/kegg-bin/show_pathway?hsa05016/hsa:25981%09red/hsa:56901%09red
Choline m	hsa05231	1	101	0.762409	0.859531	FOS	http://www.genome.jp/kegg-bin/show_pathway?hsa05231/hsa:2353%09red
cAMP sign	hsa04024	2	199	0.774018	0.859567	AMH FOS	http://www.genome.jp/kegg-bin/show_pathway?hsa04024/hsa:268%09red/hsa:2353%09red
T cell re	hsa04660	1	105	0.775651	0.859567	FOS	http://www.genome.jp/kegg-bin/show_pathway?hsa04660/hsa:2353%09red
Metabolic	hsa01100	15	1241	0.77701	0.859567	PCK2 PTGS	http://www.genome.jp/kegg-bin/show_pathway?hsa01100/hsa:64080%09red/hsa:51301%09red/hsa:56901%09red/hsa:10797%09red/hsa:5837%09red/hsa:1056%09red/hsa:5743%09red/hsa:80201%09red/hsa:5106%09red/hsa:26227%09red/hsa:29968%09red/hsa:129607%09red/hsa:440%09red/hsa:8639%09red/hsa:1491%09red

Cholinerg	hsa04725	1	111	0.794157	0.865822	FOS	http://www.genome.jp/kegg-bin/show_pathway?hsa04725/hsa:2353%09red
Serotoner	hsa04726	1	112	0.797091	0.865822	PTGS2	http://www.genome.jp/kegg-bin/show_pathway?hsa04726/hsa:5743%09red
MicroRNAs	hsa05206	3	299	0.797339	0.865822	PTGS2 DDI	http://www.genome.jp/kegg-bin/show_pathway?hsa05206/hsa:5743%09red/hsa:3162%09red/hsa:54541%09red
Regulatio	hsa04810	2	215	0.809913	0.867774	ACTN2 FGF	http://www.genome.jp/kegg-bin/show_pathway?hsa04810/hsa:88%09red/hsa:2250%09red
Thyroid h	hsa04919	1	118	0.813845	0.867774	RCAN1	http://www.genome.jp/kegg-bin/show_pathway?hsa04919/hsa:1827%09red
Leukocyte	hsa04670	1	118	0.813845	0.867774	ACTN2	http://www.genome.jp/kegg-bin/show_pathway?hsa04670/hsa:88%09red
Neurotrop	hsa04722	1	120	0.819119	0.868168	NGFR	http://www.genome.jp/kegg-bin/show_pathway?hsa04722/hsa:4804%09red
Ras signa	hsa04014	2	228	0.835285	0.880033	FGF5 NGFR	http://www.genome.jp/kegg-bin/show_pathway?hsa04014/hsa:4804%09red/hsa:2250%09red
Dopaminer	hsa04728	1	130	0.843352	0.883274	FOS	http://www.genome.jp/kegg-bin/show_pathway?hsa04728/hsa:2353%09red
Oxidative	hsa00190	1	133	0.849973	0.884972	NDUFA4L2	http://www.genome.jp/kegg-bin/show_pathway?hsa00190/hsa:56901%09red
Ubiquitin	hsa04120	1	137	0.858373	0.887467	BIRC3	http://www.genome.jp/kegg-bin/show_pathway?hsa04120/hsa:330%09red
Tight jun	hsa04530	1	139	0.862397	0.887467	ACTN2	http://www.genome.jp/kegg-bin/show_pathway?hsa04530/hsa:88%09red
Parkinson	hsa05012	1	142	0.868221	0.888296	NDUFA4L2	http://www.genome.jp/kegg-bin/show_pathway?hsa05012/hsa:56901%09red
Cell adhe	hsa04514	1	145	0.873801	0.888867	NTNG2	http://www.genome.jp/kegg-bin/show_pathway?hsa04514/hsa:56901%09red

							514/hsa:84628%09red
Phagosome	hsa04145	1	155	0.890765	0.900945	TAP1	http://www.genome.jp/kegg-bin/show_pathway?hsa04145/hsa:6890%09red
Neuroacti	hsa04080	2	278	0.906917	0.91207	LPAR2 GAB	http://www.genome.jp/kegg-bin/show_pathway?hsa04080/hsa:9170%09red/hsa:2564%09red
Olfactory	hsa04740	1	417	0.997697	0.997697	SLC8A2	http://www.genome.jp/kegg-bin/show_pathway?hsa04740/hsa:6543%09red

Statistical analysis was performed using the hypergeometric test and false discovery rate correction was performed using the Benjamini and Hochberg method. KEGG, Kyoto Encyclopedia of Genes and Genomes.

Table SV. KEGG pathways of downregulated genes.

##Databases: KEGG PATHWAY								
#fg	19							
#bg	7057							
#Term	Database	ID	Input num	Backgro un	P-Value	Corrected	Input	Hyperlink
Salivary	KEGG PATH	hsa04970	3	89	0.001624	0.047109	AQP5 FX YD	http://www.genome.jp/kegg-bin/show_pathway?hsa04970/hsa:486%09red/hsa:362%09red/hsa:2977%09red
Proximal	KEGG PATH	hsa04964	2	23	0.00168	0.047109	FX YD2 AQ P	http://www.genome.jp/kegg-bin/show_pathway?hsa04964/hsa:358%09red/hsa:486%09red
Inflammat	KEGG PATH	hsa04750	3	98	0.002141	0.047109	ASIC1 MAP	http://www.genome.jp/kegg-bin/show_pathway?hsa04750/hsa:40%09red/hsa:41%09red/hsa:5608%09red
Renin sec	KEGG PATH	hsa04924	2	64	0.012537	0.197234	GUCY1A2 A	http://www.genome.jp/kegg-bin/show_pathway?hsa04924/hsa:358%09red/hsa:2977%09red
Bile secr	KEGG PATH	hsa04976	2	71	0.015281	0.197234	FX YD2 AQ P	http://www.genome.jp/kegg-bin/show_pathway?hsa04976/hsa:358%09red/hsa:486%09red
Rap1 sign	KEGG PATH	hsa04015	3	211	0.01793	0.197234	TIAM1 MA P	http://www.genome.jp/kegg-bin/show_pathway?hsa04015/hsa:3815%09red/hsa:7074%09red/hsa:5608%09red
Insulin s	KEGG PATH	hsa04911	2	85	0.021468	0.202416	SNAP25 FX	http://www.genome.jp/kegg-bin/show_pathway?hsa04911/hsa:486%09red/hsa:6616%09red
Glycosami	KEGG PATH	hsa00533	1	15	0.039672	0.327292	CHST6	http://www.genome.jp/kegg-bin/show_pathway?hsa00533/hsa:4166%09red
Histidine	KEGG PATH	hsa00340	1	24	0.062754	0.373643	CARNS1	http://www.genome.jp/kegg-bin/show_pathway?hsa00340/hsa:57571%09red
cGMP-PKG	KEGG PATH	hsa04022	2	167	0.073182	0.373643	GUCY1A2	http://www.genome.jp/kegg-bin/show_pathway?

							F	hsa04022/hsa:486%09red/hsa:2977%09red
beta-Alan	KEGG PATH	hsa00410	1	31	0.080343	0.373643	CARNS1	http://www.genome.jp/kegg-bin/show_pathway?hsa00410/hsa:57571%09red
cAMP sign	KEGG PATH	hsa04024	2	199	0.098899	0.373643	TIAM1 FX	http://www.genome.jp/kegg-bin/show_pathway?hsa04024/hsa:486%09red/hsa:7074%09red
Aldostero	KEGG PATH	hsa04960	1	39	0.100061	0.373643	FXD2	http://www.genome.jp/kegg-bin/show_pathway?hsa04960/hsa:486%09red
Ether lip	KEGG PATH	hsa00565	1	45	0.114586	0.373643	ENP2	http://www.genome.jp/kegg-bin/show_pathway?hsa00565/hsa:5168%09red
Carbohydr	KEGG PATH	hsa04973	1	46	0.116985	0.373643	FXD2	http://www.genome.jp/kegg-bin/show_pathway?hsa04973/hsa:486%09red
Endocrine	KEGG PATH	hsa04961	1	47	0.119378	0.373643	FXD2	http://www.genome.jp/kegg-bin/show_pathway?hsa04961/hsa:486%09red
Ras signa	KEGG PATH	hsa04014	2	228	0.124125	0.373643	TIAM1 KIT	http://www.genome.jp/kegg-bin/show_pathway?hsa04014/hsa:3815%09red/hsa:7074%09red
Arginine	KEGG PATH	hsa00330	1	50	0.12652	0.373643	CARNS1	http://www.genome.jp/kegg-bin/show_pathway?hsa00330/hsa:57571%09red
Amyotroph	KEGG PATH	hsa05014	1	51	0.128889	0.373643	MAP2K6	http://www.genome.jp/kegg-bin/show_pathway?hsa05014/hsa:5608%09red
Mineral a	KEGG PATH	hsa04978	1	52	0.131251	0.373643	FXD2	http://www.genome.jp/kegg-bin/show_pathway?hsa04978/hsa:486%09red
Regulatio	KEGG PATH	hsa04923	1	56	0.14064	0.373643	FABP4	http://www.genome.jp/kegg-bin/show_pathway?hsa04923/hsa:2167%09red
Acute mye	KEGG PATH	hsa05221	1	57	0.142973	0.373643	KIT	http://www.genome.jp/kegg-bin/show_pathway?hsa05221/hsa:3815%09red
Long-term	KEGG PATH	hsa04730	1	60	0.149933	0.373643	GUCY1A2	http://www.genome.jp/kegg-bin/show_pathway?hsa04730/hsa:2977%09red
Synaptic	KEGG PATH	hsa04721	1	63	0.15684	0.373643	SNAP25	http://www.genome.jp/kegg-bin/show_pathway?

								hsa04721/hsa:6616%09red
Cytokine-	KEGG PATH	hsa04060	2	265	0.158352	0.373643	INHBB KIT	http://www.genome.jp/kegg-bin/show_pathway?hsa04060/hsa:3815%09red/hsa:3625%09red
Central c	KEGG PATH	hsa05230	1	67	0.165967	0.373643	KIT	http://www.genome.jp/kegg-bin/show_pathway?hsa05230/hsa:3815%09red
Fc epsilo	KEGG PATH	hsa04664	1	68	0.168234	0.373643	MAP2K6	http://www.genome.jp/kegg-bin/show_pathway?hsa04664/hsa:5608%09red
Neuroacti	KEGG PATH	hsa04080	2	278	0.170806	0.373643	RXFP4 NTS	http://www.genome.jp/kegg-bin/show_pathway?hsa04080/hsa:339403%09red/hsa:4923%09red
Thyroid h	KEGG PATH	hsa04918	1	71	0.175001	0.373643	FXVD2	http://www.genome.jp/kegg-bin/show_pathway?hsa04918/hsa:486%09red
PPAR sign	KEGG PATH	hsa03320	1	72	0.177244	0.373643	FABP4	http://www.genome.jp/kegg-bin/show_pathway?hsa03320/hsa:2167%09red
Cardiac m	KEGG PATH	hsa04260	1	78	0.190586	0.373643	FXVD2	http://www.genome.jp/kegg-bin/show_pathway?hsa04260/hsa:486%09red
ECM-recep	KEGG PATH	hsa04512	1	82	0.199366	0.373643	TNR	http://www.genome.jp/kegg-bin/show_pathway?hsa04512/hsa:7143%09red
Taste tra	KEGG PATH	hsa04742	1	83	0.201547	0.373643	ASIC2	http://www.genome.jp/kegg-bin/show_pathway?hsa04742/hsa:40%09red
TGF-beta	KEGG PATH	hsa04350	1	84	0.203723	0.373643	INHBB	http://www.genome.jp/kegg-bin/show_pathway?hsa04350/hsa:3625%09red
Hematopoi	KEGG PATH	hsa04640	1	88	0.212368	0.373643	KIT	http://www.genome.jp/kegg-bin/show_pathway?hsa04640/hsa:3815%09red
Gap junct	KEGG PATH	hsa04540	1	88	0.212368	0.373643	GUCY1A2	http://www.genome.jp/kegg-bin/show_pathway?hsa04540/hsa:2977%09red
Protein d	KEGG PATH	hsa04974	1	90	0.216657	0.373643	FXVD2	http://www.genome.jp/kegg-bin/show_pathway?hsa04974/hsa:486%09red
GnRH sign	KEGG PATH	hsa04912	1	91	0.218793	0.373643	MAP2K6	http://www.genome.jp/kegg-bin/show_pathway?

								hsa04912/hsa:5608%09red
Circadian	KEGG PATH	hsa04713	1	95	0.227283	0.373643	GUCY1A2	http://www.genome.jp/kegg-bin/show_pathway?hsa04713/hsa:2977%09red
Pancreati	KEGG PATH	hsa04972	1	96	0.229392	0.373643	FXYD2	http://www.genome.jp/kegg-bin/show_pathway?hsa04972/hsa:486%09red
PI3K-Akt	KEGG PATH	hsa04151	2	341	0.233244	0.373643	KIT TNR	http://www.genome.jp/kegg-bin/show_pathway?hsa04151/hsa:3815%09red/hsa:7143%09red
Melanogen	KEGG PATH	hsa04916	1	100	0.237773	0.373643	KIT	http://www.genome.jp/kegg-bin/show_pathway?hsa04916/hsa:3815%09red
Toll-like	KEGG PATH	hsa04620	1	106	0.250183	0.384001	MAP2K6	http://www.genome.jp/kegg-bin/show_pathway?hsa04620/hsa:5608%09red
TNF signa	KEGG PATH	hsa04668	1	110	0.258349	0.387524	MAP2K6	http://www.genome.jp/kegg-bin/show_pathway?hsa04668/hsa:5608%09red
Thyroid h	KEGG PATH	hsa04919	1	118	0.27443	0.388226	FXYD2	http://www.genome.jp/kegg-bin/show_pathway?hsa04919/hsa:486%09red
Toxoplasm	KEGG PATH	hsa05145	1	119	0.276417	0.388226	MAP2K6	http://www.genome.jp/kegg-bin/show_pathway?hsa05145/hsa:5608%09red
Vascular	KEGG PATH	hsa04270	1	120	0.278398	0.388226	GUCY1A2	http://www.genome.jp/kegg-bin/show_pathway?hsa04270/hsa:2977%09red
Platelet	KEGG PATH	hsa04611	1	122	0.282346	0.388226	GUCY1A2	http://www.genome.jp/kegg-bin/show_pathway?hsa04611/hsa:2977%09red
Osteoclas	KEGG PATH	hsa04380	1	132	0.301779	0.406479	MAP2K6	http://www.genome.jp/kegg-bin/show_pathway?hsa04380/hsa:5608%09red
Signaling	KEGG PATH	hsa04550	1	142	0.320714	0.419866	INHBB	http://www.genome.jp/kegg-bin/show_pathway?hsa04550/hsa:3625%09red
Phospholi	KEGG PATH	hsa04072	1	144	0.324442	0.419866	KIT	http://www.genome.jp/kegg-bin/show_pathway?hsa04072/hsa:3815%09red
Adrenergi	KEGG PATH	hsa04261	1	149	0.333677	0.423513	FXYD2	http://www.genome.jp/kegg-bin/show_pathway?

								hsa04261/hsa:486%09red
Oxytocin	KEGG PATH	hsa04921	1	158	0.35	0.43585	GUCY1A2	http://www.genome.jp/kegg-bin/show_pathway?hsa04921/hsa:2977%09red
Purine me	KEGG PATH	hsa00230	1	175	0.379805	0.457664	GUCY1A2	http://www.genome.jp/kegg-bin/show_pathway?hsa00230/hsa:2977%09red
Influenza	KEGG PATH	hsa05164	1	176	0.381517	0.457664	MAP2K6	http://www.genome.jp/kegg-bin/show_pathway?hsa05164/hsa:5608%09red
Calcium s	KEGG PATH	hsa04020	1	180	0.388321	0.457664	NTSR1	http://www.genome.jp/kegg-bin/show_pathway?hsa04020/hsa:4923%09red
Chemokine	KEGG PATH	hsa04062	1	187	0.400059	0.463226	TIAM1	http://www.genome.jp/kegg-bin/show_pathway?hsa04062/hsa:7074%09red
Huntingto	KEGG PATH	hsa05016	1	193	0.409949	0.464454	DNAH8	http://www.genome.jp/kegg-bin/show_pathway?hsa05016/hsa:1769%09red
Epstein-B	KEGG PATH	hsa05169	1	201	0.422896	0.464454	MAP2K6	http://www.genome.jp/kegg-bin/show_pathway?hsa05169/hsa:5608%09red
Focal adh	KEGG PATH	hsa04510	1	203	0.42609	0.464454	TNR	http://www.genome.jp/kegg-bin/show_pathway?hsa04510/hsa:7143%09red
Proteogly	KEGG PATH	hsa05205	1	205	0.429268	0.464454	TIAM1	http://www.genome.jp/kegg-bin/show_pathway?hsa05205/hsa:7074%09red
Regulatio	KEGG PATH	hsa04810	1	215	0.444908	0.473612	TIAM1	http://www.genome.jp/kegg-bin/show_pathway?hsa04810/hsa:7074%09red
MAPK sign	KEGG PATH	hsa04010	1	255	0.503501	0.526349	MAP2K6	http://www.genome.jp/kegg-bin/show_pathway?hsa04010/hsa:5608%09red
Endocytos	KEGG PATH	hsa04144	1	260	0.510399	0.526349	KIT	http://www.genome.jp/kegg-bin/show_pathway?hsa04144/hsa:3815%09red
MicroRNAs	KEGG PATH	hsa05206	1	299	0.561169	0.569803	TNR	http://www.genome.jp/kegg-bin/show_pathway?hsa05206/hsa:7143%09red
Pathways	KEGG PATH	hsa05200	1	397	0.667647	0.667647	KIT	genome.jp/kegg-bin/show_pathway?hsa05200/h

								sa:3815%09red
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Statistical analysis was performed using the hypergeometric test and false discovery rate correction was performed using the Benjamini and Hochberg method. KEGG, Kyoto Encyclopedia of Genes and Genomes.