

Supplementary Table 1: GSEA analysis of MMP9

ONTOLOGY	ID	Description	NES	p. adjust
CC	G0:0000313	organellar ribosome	-3.1418	1.83E-08
CC	G0:0000315	organellar large ribosomal subunit	-2.88566	1.83E-08
BP	G0:0002181	cytoplasmic translation	-2.57005	1.83E-08
MF	G0:0003735	structural constituent of ribosome	-3.18548	1.83E-08
MF	G0:0004672	protein kinase activity	1.871607	1.83E-08
CC	G0:0005743	mitochondrial inner membrane	-2.84039	1.83E-08
CC	G0:0005759	mitochondrial matrix	-2.95753	1.83E-08
CC	G0:0005761	mitochondrial ribosome	-3.1418	1.83E-08
CC	G0:0005762	mitochondrial large ribosomal subunit	-2.88566	1.83E-08
CC	G0:0005766	primary lysosome	2.393632	1.83E-08
CC	G0:0005840	ribosome	-3.13584	1.83E-08
BP	G0:0006364	rRNA processing	-2.90774	1.83E-08
BP	G0:0006399	tRNA metabolic process	-2.60846	1.83E-08
BP	G0:0006400	tRNA modification	-2.55163	1.83E-08
BP	G0:0006412	translation	-2.34153	1.83E-08
BP	G0:0008033	tRNA processing	-2.59288	1.83E-08
BP	G0:0009451	RNA modification	-2.42086	1.83E-08
CC	G0:0015934	large ribosomal subunit	-3.02732	1.83E-08
CC	G0:0015935	small ribosomal subunit	-2.88537	1.83E-08
BP	G0:0016072	rRNA metabolic process	-2.86455	1.83E-08
MF	G0:0019843	rRNA binding	-2.71656	1.83E-08
CC	G0:0019866	organelle inner membrane	-2.63897	1.83E-08
BP	G0:0022613	ribonucleoprotein complex biogenesis	-2.76941	1.83E-08
CC	G0:0022626	cytosolic ribosome	-2.6595	1.83E-08
CC	G0:0030667	secretory granule membrane	2.663124	1.83E-08
CC	G0:0030684	preribosome	-2.73745	1.83E-08
BP	G0:0032543	mitochondrial translation	-2.68829	1.83E-08
BP	G0:0034470	ncRNA processing	-2.90632	1.83E-08
BP	G0:0034660	ncRNA metabolic process	-2.79547	1.83E-08
CC	G0:0035579	specific granule membrane	2.602711	1.83E-08
BP	G0:0042254	ribosome biogenesis	-2.89679	1.83E-08
BP	G0:0042273	ribosomal large subunit biogenesis	-2.59149	1.83E-08
CC	G0:0042581	specific granule	2.840897	1.83E-08
CC	G0:0042582	azurophil granule	2.393632	1.83E-08
CC	G0:0044391	ribosomal subunit	-3.25617	1.83E-08
CC	G0:0070820	tertiary granule	2.716115	1.83E-08
CC	G0:0098798	mitochondrial protein-containing complex	-3.13504	1.83E-08
CC	G0:0098800	inner mitochondrial membrane protein complex	-2.53824	1.83E-08
BP	G0:0140053	mitochondrial gene expression	-2.72961	1.83E-08
MF	G0:0140098	catalytic activity, acting on RNA	-2.30829	1.83E-08
MF	G0:0140640	catalytic activity, acting on a nucleic acid	-2.32027	1.83E-08
CC	G0:1904724	tertiary granule lumen	2.679315	1.83E-08
MF	G0:0004674	protein serine/threonine kinase activity	1.992636	2.19E-08
BP	G0:0006909	phagocytosis	2.122914	5.05E-08
CC	G0:0000314	organellar small ribosomal subunit	-2.62342	5.39E-08
CC	G0:0005763	mitochondrial small ribosomal subunit	-2.62342	5.39E-08
BP	G0:0046777	protein autophosphorylation	2.065987	7.19E-08
CC	G0:0101002	ficolin-1-rich granule	2.21615	8.21E-08
CC	G0:0034774	secretory granule lumen	1.97181	9.60E-08
BP	G0:0060627	regulation of vesicle-mediated transport	1.786017	2.30E-07
BP	G0:0022618	ribonucleoprotein complex assembly	-2.20524	2.76E-07

BP	G0:0042274	ribosomal small subunit biogenesis	-2.44379	2.76E-07
CC	G0:0060205	cytoplasmic vesicle lumen	1.927211	2.78E-07
BP	G0:0042326	negative regulation of phosphorylation	1.906118	2.78E-07
BP	G0:0045936	negative regulation of phosphate metabolism	1.87912	3.79E-07
CC	G0:0035580	specific granule lumen	2.464857	4.72E-07
MF	G0:0140101	catalytic activity, acting on a tRNA	-2.35435	5.18E-07
BP	G0:1901137	carbohydrate derivative biosynthetic process	-1.76481	5.60E-07
BP	G0:0006457	protein folding	-2.12247	5.84E-07
CC	G0:0045335	phagocytic vesicle	2.201523	5.84E-07
CC	G0:0031983	vesicle lumen	1.923364	1.06E-06
BP	G0:0010563	negative regulation of phosphorus metabolism	1.866495	1.06E-06
CC	G0:0022625	cytosolic large ribosomal subunit	-2.42952	1.06E-06
BP	G0:0000045	autophagosome assembly	2.385561	1.07E-06
BP	G0:0006281	DNA repair	-1.81816	1.27E-06
BP	G0:0071216	cellular response to biotic stimulus	1.974642	1.49E-06
MF	G0:0051082	unfolded protein binding	-2.23475	1.59E-06
BP	G0:0042255	ribosome assembly	-2.42201	2.00E-06
BP	G0:0002274	myeloid leukocyte activation	2.034659	2.27E-06
BP	G0:0090305	nucleic acid phosphodiester bond hydrolysis	-2.00854	2.33E-06
MF	G0:0106310	protein serine kinase activity	1.845897	2.75E-06
BP	G0:0071826	ribonucleoprotein complex subunit organization	-2.12902	2.93E-06
BP	G0:1905037	autophagosome organization	2.334594	3.16E-06
BP	G0:0055086	nucleobase-containing small molecule metabolism	-1.74432	3.36E-06
BP	G0:0007033	vacuole organization	2.080705	3.53E-06
MF	G0:0000049	tRNA binding	-2.38292	4.07E-06
BP	G0:0006520	cellular amino acid metabolic process	-1.97055	4.16E-06
CC	G0:0022627	cytosolic small ribosomal subunit	-2.45298	4.39E-06
BP	G0:0007015	actin filament organization	1.762569	4.62E-06
MF	G0:0016874	ligase activity	-2.20518	4.76E-06
BP	G0:1990266	neutrophil migration	2.169276	6.06E-06
BP	G0:0002446	neutrophil mediated immunity	2.479644	6.14E-06
BP	G0:0007005	mitochondrion organization	-1.77852	6.14E-06
BP	G0:0010256	endomembrane system organization	1.756471	6.15E-06
MF	G0:0043021	ribonucleoprotein complex binding	-2.13037	6.43E-06
BP	G0:0006914	autophagy	1.719871	6.78E-06
BP	G0:0061919	process utilizing autophagic mechanism	1.719871	6.78E-06
BP	G0:0046112	nucleobase biosynthetic process	-2.3705	6.81E-06
CC	G0:0009295	nucleoid	-2.42565	6.92E-06
CC	G0:0042645	mitochondrial nucleoid	-2.42565	6.92E-06
MF	G0:0140097	catalytic activity, acting on DNA	-1.98105	6.93E-06
BP	G0:0045333	cellular respiration	-2.00286	7.99E-06
MF	G0:0051536	iron-sulfur cluster binding	-2.28786	8.18E-06
MF	G0:0051540	metal cluster binding	-2.28786	8.18E-06
BP	G0:0030490	maturation of SSU-rRNA	-2.44406	8.28E-06
BP	G0:0046148	pigment biosynthetic process	-2.27535	1.17E-05
BP	G0:0000470	maturation of LSU-rRNA	-2.34581	1.20E-05
BP	G0:0000959	mitochondrial RNA metabolic process	-2.40362	1.20E-05
BP	G0:0009113	purine nucleobase biosynthetic process	-2.29191	1.22E-05
BP	G0:0071900	regulation of protein serine/threonine kinase activity	1.76182	1.46E-05
BP	G0:1990542	mitochondrial transmembrane transport	-2.21283	1.51E-05
BP	G0:0001933	negative regulation of protein phosphorylation	1.824032	1.66E-05
BP	G0:0009060	aerobic respiration	-2.03826	1.69E-05
CC	G0:0101003	ficolin-1-rich granule membrane	2.291021	1.83E-05
BP	G0:0018105	peptidyl-serine phosphorylation	1.79262	1.93E-05

BP	G0:0018209	peptidyl-serine modification	1.795117	2.02E-05
BP	G0:0001510	RNA methylation	-2.29296	2.03E-05
BP	G0:0009124	nucleoside monophosphate biosynthetic process	-2.35473	2.20E-05
CC	G0:0035577	azurophil granule membrane	2.300048	2.20E-05
BP	G0:0042119	neutrophil activation	2.411261	2.21E-05
CC	G0:0030670	phagocytic vesicle membrane	2.231986	2.49E-05
BP	G0:0043405	regulation of MAP kinase activity	1.963448	2.51E-05
BP	G0:0030335	positive regulation of cell migration	1.652308	2.53E-05
BP	G0:0019221	cytokine-mediated signaling pathway	1.681346	2.98E-05
BP	G0:0006887	exocytosis	1.747649	3.06E-05
MF	G0:0004518	nuclease activity	-1.94278	3.26E-05
MF	G0:0003779	actin binding	1.694688	3.26E-05
BP	G0:0050900	leukocyte migration	1.736761	3.41E-05
BP	G0:0097530	granulocyte migration	2.034757	3.41E-05
CC	G0:0070821	tertiary granule membrane	2.271012	3.43E-05
BP	G0:0036230	granulocyte activation	2.364487	3.43E-05
BP	G0:0008154	actin polymerization or depolymerization	1.924532	3.47E-05
CC	G0:0031252	cell leading edge	1.714834	3.63E-05
BP	G0:0009123	nucleoside monophosphate metabolic process	-2.22289	3.86E-05
MF	G0:0051539	4 iron, 4 sulfur cluster binding	-2.35679	3.96E-05
CC	G0:0032040	small-subunit processome	-2.34272	4.37E-05
BP	G0:0043254	regulation of protein-containing complex	1.733563	4.76E-05
MF	G0:0016741	transferase activity, transferring one-carbon	-1.99152	4.88E-05
MF	G0:0035325	Toll-like receptor binding	2.265701	5.93E-05
BP	G0:0072522	purine-containing compound biosynthetic process	-1.98431	6.21E-05
MF	G0:0008173	RNA methyltransferase activity	-2.30187	6.25E-05
BP	G0:1901293	nucleoside phosphate biosynthetic process	-1.84922	6.67E-05
BP	G0:0071219	cellular response to molecule of bacterial origin	1.890053	6.67E-05
BP	G0:0030488	tRNA methylation	-2.31278	6.67E-05
BP	G0:0009156	ribonucleoside monophosphate biosynthetic process	-2.30082	7.27E-05
CC	G0:0005770	late endosome	1.798062	8.46E-05
BP	G0:0040017	positive regulation of locomotion	1.608126	8.46E-05
BP	G0:0042742	defense response to bacterium	1.784606	8.46E-05
CC	G0:0030139	endocytic vesicle	1.734837	8.46E-05
BP	G0:0030041	actin filament polymerization	1.916477	8.46E-05
CC	G0:0016605	PML body	2.023992	9.32E-05
BP	G0:0009117	nucleotide metabolic process	-1.66825	9.32E-05
BP	G0:0030099	myeloid cell differentiation	1.702287	9.67E-05
BP	G0:0043410	positive regulation of MAPK cascade	1.646829	9.67E-05
BP	G0:0072521	purine-containing compound metabolic process	-1.72021	0.00010071
CC	G0:0005746	mitochondrial respirasome	-2.09924	0.00010071
BP	G0:0046390	ribose phosphate biosynthetic process	-1.91324	0.000100841
BP	G0:0009165	nucleotide biosynthetic process	-1.86506	0.000106691
BP	G0:0006839	mitochondrial transport	-1.85683	0.000107001
BP	G0:0044089	positive regulation of cellular component	1.630238	0.000107001
BP	G0:0006260	DNA replication	-1.77913	0.000107536
BP	G0:0002532	production of molecular mediator involved in	2.124073	0.000107536
BP	G0:0006164	purine nucleotide biosynthetic process	-1.91672	0.000110871
BP	G0:0002237	response to molecule of bacterial origin	1.714438	0.000119917
BP	G0:0016050	vesicle organization	1.731629	0.000119917
BP	G0:0009260	ribonucleotide biosynthetic process	-1.90155	0.000120154
BP	G0:1901605	alpha-amino acid metabolic process	-1.91086	0.000120196
BP	G0:0032496	response to lipopolysaccharide	1.69291	0.000124116
BP	G0:0051272	positive regulation of cellular component	1.58033	0.000127486

BP	G0:0016236	macroautophagy	1.753427	0.000127486
BP	G0:0043068	positive regulation of programmed cell death	1.586073	0.000128526
MF	G0:0004527	exonuclease activity	-2.14053	0.000128526
BP	G0:2000147	positive regulation of cell motility	1.59485	0.000131088
CC	G0:0030686	90S preribosome	-2.29809	0.000134131
MF	G0:0035091	phosphatidylinositol binding	1.758232	0.000140388
BP	G0:0002221	pattern recognition receptor signaling pathway	1.905224	0.000140486
BP	G0:0045055	regulated exocytosis	1.792633	0.000142502
CC	G0:0005758	mitochondrial intermembrane space	-2.06051	0.000148467
BP	G0:0006753	nucleoside phosphate metabolic process	-1.66279	0.000158467
CC	G0:0005769	early endosome	1.657843	0.000158467
BP	G0:0042773	ATP synthesis coupled electron transport	-2.07792	0.000164162
BP	G0:0042775	mitochondrial ATP synthesis coupled electron transport	-2.07792	0.000164162
BP	G0:0002283	neutrophil activation involved in immune response	2.275753	0.000166065
BP	G0:0051640	organelle localization	1.601088	0.00016959
CC	G0:0015629	actin cytoskeleton	1.606263	0.00016959
BP	G0:0030593	neutrophil chemotaxis	2.05764	0.000170516
BP	G0:0070302	regulation of stress-activated protein kinase activity	1.840013	0.000178633
MF	G0:0090079	translation regulator activity, nucleic acid dependent	-2.03317	0.000183608
MF	G0:0005543	phospholipid binding	1.616037	0.000184651
BP	G0:0002377	immunoglobulin production	-1.95221	0.000184651
BP	G0:0071621	granulocyte chemotaxis	1.981826	0.000184651
BP	G0:0009161	ribonucleoside monophosphate metabolic process	-2.12587	0.000184651
BP	G0:0002224	toll-like receptor signaling pathway	1.96239	0.000184651
BP	G0:0051493	regulation of cytoskeleton organization	1.612013	0.000192814
BP	G0:1902532	negative regulation of intracellular signaling	1.622039	0.000203436
CC	G0:0098803	respiratory chain complex	-2.03281	0.000224332
CC	G0:0070469	respirasome	-2.05887	0.000235171
BP	G0:1902903	regulation of supramolecular fiber organization	1.661111	0.00023906
BP	G0:1903530	regulation of secretion by cell	1.52351	0.000241366
BP	G0:0050732	negative regulation of peptidyl-tyrosine phosphorylation	2.154891	0.000255704
CC	G0:0031301	integral component of organelle membrane	-1.69638	0.000264241
BP	G0:0072593	reactive oxygen species metabolic process	1.75586	0.000281813
CC	G0:0000228	nuclear chromosome	-1.85104	0.000281813
BP	G0:0033108	mitochondrial respiratory chain complex assembly	-2.12035	0.000281813
BP	G0:0006403	RNA localization	-1.84891	0.000286677
BP	G0:0032635	interleukin-6 production	1.929065	0.000286677
BP	G0:0032675	regulation of interleukin-6 production	1.929065	0.000286677
BP	G0:0000462	maturation of SSU-rRNA from tricistronic transcript	-2.20481	0.000297188
MF	G0:0008168	methyltransferase activity	-1.90881	0.000317218
MF	G0:0051087	chaperone binding	-1.99369	0.000322237
BP	G0:0043312	neutrophil degranulation	2.165933	0.000327149
BP	G0:0090501	RNA phosphodiester bond hydrolysis	-1.94107	0.000327149
BP	G0:0000154	rRNA modification	-2.20699	0.000333476
BP	G0:0006310	DNA recombination	-1.76934	0.000334243
CC	G0:0005742	mitochondrial outer membrane translocase	-2.18888	0.000341251
BP	G0:0019646	aerobic electron transport chain	-2.05857	0.000341251
CC	G0:0005776	autophagosome	2.020098	0.000341251
BP	G0:0002381	immunoglobulin production involved in immune response	-2.04729	0.000350363
MF	G0:0023023	MHC protein complex binding	-2.19561	0.000351993
BP	G0:0006284	base-excision repair	-2.15655	0.000351993
CC	G0:0030427	site of polarized growth	1.830076	0.000354264
BP	G0:0097529	myeloid leukocyte migration	1.791869	0.000357239
BP	G0:1904874	positive regulation of telomerase RNA localization	-2.24232	0.000357239

BP	G0:0006911	phagocytosis, engulfment	2.155477	0.000361506
BP	G0:0050727	regulation of inflammatory response	1.652319	0.000361506
BP	G0:0071222	cellular response to lipopolysaccharide	1.829448	0.000361745
BP	G0:0031400	negative regulation of protein modification	1.586024	0.000370282
BP	G0:0062208	positive regulation of pattern recognition	2.222234	0.000371326
BP	G0:1903305	regulation of regulated secretory pathway	1.866149	0.000373417
CC	G0:0032592	integral component of mitochondrial membrane	-2.02651	0.000384107
BP	G0:1901607	alpha-amino acid biosynthetic process	-2.04645	0.000403421
BP	G0:0072350	tricarboxylic acid metabolic process	-2.17537	0.000403421
BP	G0:0006626	protein targeting to mitochondrion	-1.9986	0.000405453
BP	G0:0017157	regulation of exocytosis	1.755863	0.000405453
BP	G0:0030833	regulation of actin filament polymerization	1.803277	0.00040564
BP	G0:0031065	positive regulation of histone deacetylation	2.231854	0.000417864
MF	G0:0140297	DNA-binding transcription factor binding	1.595936	0.000432666
CC	G0:0031970	organelle envelope lumen	-1.97771	0.000436548
BP	G0:0006144	purine nucleobase metabolic process	-2.16115	0.000455229
BP	G0:1904816	positive regulation of protein localization	-2.19841	0.000464997
CC	G0:0010008	endosome membrane	1.563324	0.000471234
BP	G0:0099024	plasma membrane invagination	2.067718	0.000473783
BP	G0:0022900	electron transport chain	-1.84299	0.000473783
BP	G0:0002764	immune response-regulating signaling pathway	1.584815	0.000482468
BP	G0:0009126	purine nucleoside monophosphate metabolic process	-2.16753	0.000489151
BP	G0:0060326	cell chemotaxis	1.671592	0.000498435
BP	G0:0043299	leukocyte degranulation	2.055039	0.000500777
BP	G0:0052547	regulation of peptidase activity	1.550773	0.000505751
BP	G0:2000377	regulation of reactive oxygen species metabolism	1.817386	0.000507005
BP	G0:0019693	ribose phosphate metabolic process	-1.64101	0.000508803
BP	G0:0070129	regulation of mitochondrial translation	-2.1515	0.000513272
BP	G0:0032103	positive regulation of response to external stimulus	1.596006	0.000513272
BP	G0:0006163	purine nucleotide metabolic process	-1.64324	0.000518196
CC	G0:0101031	chaperone complex	-2.16118	0.000525588
MF	G0:0004386	helicase activity	-1.85546	0.000525588
BP	G0:0051258	protein polymerization	1.701905	0.000525588
MF	G0:0003954	NADH dehydrogenase activity	-2.15471	0.000525588
BP	G0:0016311	dephosphorylation	1.598829	0.000525588
BP	G0:2000379	positive regulation of reactive oxygen species metabolism	2.048182	0.000534345
BP	G0:0051091	positive regulation of DNA-binding transcription factor activity	1.690464	0.0005579
BP	G0:0070585	protein localization to mitochondrion	-1.91042	0.000565594
BP	G0:0032535	regulation of cellular component size	1.592451	0.000577582
CC	G0:1904813	ficolin-1-rich granule lumen	1.868146	0.000577582
BP	G0:0022904	respiratory electron transport chain	-1.96687	0.000588843
BP	G0:0044283	small molecule biosynthetic process	-1.55233	0.000588843
CC	G0:0030426	growth cone	1.79668	0.000600155
BP	G0:0090066	regulation of anatomical structure size	1.524567	0.000606828
BP	G0:0070498	interleukin-1-mediated signaling pathway	2.199569	0.000613881
BP	G0:0050863	regulation of T cell activation	-1.64588	0.000650266
BP	G0:1901657	glycosyl compound metabolic process	-1.9441	0.000663448
MF	G0:0008757	S-adenosylmethionine-dependent methyltransferase activity	-1.94673	0.00067837
BP	G0:0032956	regulation of actin cytoskeleton organization	1.625678	0.000683448
BP	G0:0002444	myeloid leukocyte mediated immunity	1.90032	0.000715411
BP	G0:0031098	stress-activated protein kinase signaling pathway	1.698542	0.00071783
MF	G0:0004722	protein serine/threonine phosphatase activity	1.915231	0.000720059
BP	G0:0045088	regulation of innate immune response	1.728427	0.000724406
BP	G0:0042554	superoxide anion generation	2.126683	0.000724406

BP	GO:0006790	sulfur compound metabolic process	-1.64249	0.000728806
BP	GO:2000785	regulation of autophagosome assembly	2.136051	0.000731777
BP	GO:0002534	cytokine production involved in inflammation	2.051225	0.000734741
BP	GO:1900015	regulation of cytokine production involved in inflammation	2.051225	0.000734741
BP	GO:0038127	ERBB signaling pathway	1.864189	0.00073635
MF	GO:0015453	oxidoreduction-driven active transmembrane transport	-2.05102	0.000778933
BP	GO:0000469	cleavage involved in rRNA processing	-2.14495	0.000781418
BP	GO:0010257	NADH dehydrogenase complex assembly	-2.13326	0.000781745
BP	GO:0032981	mitochondrial respiratory chain complex I	-2.13326	0.000781745
BP	GO:0110053	regulation of actin filament organization	1.696039	0.000788225
BP	GO:0052548	regulation of endopeptidase activity	1.584602	0.00080212
BP	GO:0000387	spliceosomal snRNP assembly	-2.14704	0.00080212
MF	GO:0050136	NADH dehydrogenase (quinone) activity	-2.13427	0.00080212
BP	GO:0043065	positive regulation of apoptotic process	1.511577	0.000813095
BP	GO:0072655	establishment of protein localization to organelle	-1.90996	0.000813095
MF	GO:0009055	electron transfer activity	-1.88745	0.000813095
BP	GO:0032271	regulation of protein polymerization	1.730935	0.000828504
BP	GO:0051014	actin filament severing	2.184756	0.000828504
BP	GO:0042440	pigment metabolic process	-1.96327	0.000847876
CC	GO:0030687	preribosome, large subunit precursor	-2.13195	0.000878973
BP	GO:0006261	DNA-dependent DNA replication	-1.89102	0.000885436
BP	GO:0051403	stress-activated MAPK cascade	1.678204	0.000886424
BP	GO:0006220	pyrimidine nucleotide metabolic process	-2.10549	0.000886424
CC	GO:0031968	organelle outer membrane	-1.73733	0.000886424
BP	GO:0030595	leukocyte chemotaxis	1.72289	0.000901448
BP	GO:0006541	glutamine metabolic process	-2.16216	0.000915726
MF	GO:0016860	intramolecular oxidoreductase activity	-2.0956	0.000915726
BP	GO:0043407	negative regulation of MAP kinase activity	2.042072	0.000929034
BP	GO:0009620	response to fungus	2.068812	0.000929034
BP	GO:0071375	cellular response to peptide hormone stimulation	1.646802	0.000929034
BP	GO:0006470	protein dephosphorylation	1.629801	0.000929034
CC	GO:0019867	outer membrane	-1.75259	0.000930425
BP	GO:0050852	T cell receptor signaling pathway	-1.88791	0.00094786
BP	GO:0032970	regulation of actin filament-based process	1.572893	0.000958495
BP	GO:0009595	detection of biotic stimulus	2.102982	0.000994566
BP	GO:0050851	antigen receptor-mediated signaling pathway	-1.73382	0.001060304
CC	GO:0005741	mitochondrial outer membrane	-1.76417	0.001080221
BP	GO:0002440	production of molecular mediator of immune response	-1.71911	0.001086847
BP	GO:0000963	mitochondrial RNA processing	-2.11647	0.001125725
CC	GO:0098573	intrinsic component of mitochondrial membrane	-1.96961	0.001125725
CC	GO:0098799	outer mitochondrial membrane protein complex	-2.11535	0.001149407
BP	GO:0006221	pyrimidine nucleotide biosynthetic process	-2.1322	0.00115951
BP	GO:0031334	positive regulation of protein-containing complex assembly	1.699337	0.001166465
BP	GO:0009127	purine nucleoside monophosphate biosynthesis	-2.14702	0.001180605
BP	GO:0050870	positive regulation of T cell activation	-1.70423	0.001190904
CC	GO:0120114	Sm-like protein family complex	-1.93602	0.00119644
BP	GO:0010324	membrane invagination	2.026608	0.001210904
BP	GO:0043087	regulation of GTPase activity	1.594849	0.001227463
BP	GO:1904814	regulation of protein localization to chromosome	-2.16267	0.001227641
BP	GO:0062207	regulation of pattern recognition receptor activity	1.938823	0.001244572
BP	GO:0009152	purine ribonucleotide biosynthetic process	-1.78949	0.001259931
BP	GO:0009611	response to wounding	1.481949	0.001259931
BP	GO:0002275	myeloid cell activation involved in immune response	1.922473	0.001265913
BP	GO:0071901	negative regulation of protein serine/threonine phosphorylation	1.819186	0.001279169

BP	G0:0016197	endosomal transport	1.711728	0.001299564
BP	G0:0050804	modulation of chemical synaptic transmission	1.526537	0.001299564
BP	G0:0099177	regulation of trans-synaptic signaling	1.526537	0.001299564
CC	G0:0035578	azurophil granule lumen	1.914455	0.001299564
BP	G0:0032872	regulation of stress-activated MAPK cascade	1.762975	0.001306362
BP	G0:0018210	peptidyl-threonine modification	1.824757	0.001309456
MF	G0:0050135	NAD(P)+ nucleosidase activity	2.149477	0.001321361
MF	G0:0061809	NAD+ nucleotidase, cyclic ADP-ribose generated	2.149477	0.001321361
BP	G0:1902563	regulation of neutrophil activation	2.082041	0.001334668
BP	G0:0070431	nucleotide-binding oligomerization domain	2.101336	0.001334668
BP	G0:0033673	negative regulation of kinase activity	1.690798	0.001334668
CC	G0:0045121	membrane raft	1.578364	0.00134416
CC	G0:0098857	membrane microdomain	1.578364	0.00134416
CC	G0:0005774	vacuolar membrane	1.576053	0.001351193
BP	G0:0031663	lipopolysaccharide-mediated signaling pathway	1.971801	0.001395624
MF	G0:0016655	oxidoreductase activity, acting on NAD(P)-	-2.01887	0.001464406
BP	G0:0070525	tRNA threonylcarbamoyladenosine metabolic	-2.09001	0.001522279
CC	G0:0005767	secondary lysosome	2.116527	0.001526447
BP	G0:0090670	RNA localization to Cajal body	-2.09496	0.001526447
BP	G0:0090671	telomerase RNA localization to Cajal body	-2.09496	0.001526447
BP	G0:0090672	telomerase RNA localization	-2.09496	0.001526447
BP	G0:0090685	RNA localization to nucleus	-2.09496	0.001526447
BP	G0:1904872	regulation of telomerase RNA localization	-2.09496	0.001526447
CC	G0:0005925	focal adhesion	1.520852	0.001532652
BP	G0:0030832	regulation of actin filament length	1.75267	0.001532652
BP	G0:0009067	aspartate family amino acid biosynthetic	-2.11969	0.001532652
MF	G0:0016614	oxidoreductase activity, acting on CH-OH	-1.75726	0.001570712
BP	G0:0008064	regulation of actin polymerization or depoly	1.775403	0.001648776
CC	G0:0042575	DNA polymerase complex	-2.07391	0.001672345
BP	G0:0051092	positive regulation of NF-kappaB transcription	1.730777	0.001676175
BP	G0:1903039	positive regulation of leukocyte cell-cell	-1.62553	0.001706348
MF	G0:0008408	3'-5' exonuclease activity	-2.0353	0.001709321
MF	G0:0051020	GTPase binding	1.593732	0.001717655
MF	G0:0008137	NADH dehydrogenase (ubiquinone) activity	-2.0685	0.001721622
MF	G0:0008135	translation factor activity, RNA binding	-1.95115	0.001805121
BP	G0:0031349	positive regulation of defense response	1.597226	0.001835818
BP	G0:0000723	telomere maintenance	-1.80061	0.001845028
BP	G0:0032637	interleukin-8 production	1.895059	0.001906039
BP	G0:0006469	negative regulation of protein kinase acti	1.65904	0.001939927
BP	G0:0009167	purine ribonucleoside monophosphate meta	-2.08569	0.001942535
BP	G0:0034134	toll-like receptor 2 signaling pathway	2.117138	0.001972598
MF	G0:0031267	small GTPase binding	1.609863	0.001997547
BP	G0:0007173	epidermal growth factor receptor signaling	1.806624	0.002024544
BP	G0:0002218	activation of innate immune response	1.99227	0.002025172
BP	G0:0033674	positive regulation of kinase activity	1.499417	0.002052033
BP	G0:0006091	generation of precursor metabolites and c	-1.53805	0.00207858
BP	G0:0000027	ribosomal large subunit assembly	-2.12275	0.002089502
BP	G0:0044743	protein transmembrane import into intrace	-2.08087	0.002101774
MF	G0:0017069	snRNA binding	-2.04004	0.002101774
BP	G0:0034135	regulation of toll-like receptor 2 signal	2.044908	0.002105417
MF	G0:0004721	phosphoprotein phosphatase activity	1.680964	0.002117068
BP	G0:0009259	ribonucleotide metabolic process	-1.60107	0.002135449
BP	G0:0046328	regulation of JNK cascade	1.730048	0.002135759
BP	G0:0006271	DNA strand elongation involved in DNA repl	-2.11708	0.00217407

BP	G0:0015980	energy derivation by oxidation of organic	-1.62147	0.002181185
BP	G0:0000466	maturation of 5.8S rRNA from tricistronic	-2.06946	0.002181185
MF	G0:0016791	phosphatase activity	1.601935	0.002258337
CC	G0:0019898	extrinsic component of membrane	1.578597	0.002269514
CC	G0:0005666	RNA polymerase III complex	-2.0611	0.002276087
CC	G0:0031304	intrinsic component of mitochondrial inner	-2.03972	0.002281652
CC	G0:0031305	integral component of mitochondrial inner	-2.03972	0.002281652
MF	G0:0140657	ATP-dependent activity	-1.50468	0.002303307
BP	G0:0002755	MyD88-dependent toll-like receptor signal	2.12604	0.002310194
BP	G0:0000272	polysaccharide catabolic process	2.082381	0.002310194
CC	G0:0031300	intrinsic component of organelle membrane	-1.59215	0.002310442
BP	G0:0045862	positive regulation of proteolysis	1.549187	0.002313741
MF	G0:0061629	RNA polymerase II-specific DNA-binding tti	1.573998	0.002332784
BP	G0:0016482	cytosolic transport	1.774754	0.00235148
BP	G0:0072527	pyrimidine-containing compound metabolic	-1.8718	0.00235148
BP	G0:0044264	cellular polysaccharide metabolic process	1.846007	0.002374269
BP	G0:0006119	oxidative phosphorylation	-1.84535	0.002408318
BP	G0:0051547	regulation of keratinocyte migration	2.062254	0.002426473
MF	G0:0016835	carbon-oxygen lyase activity	-1.874	0.002455782
BP	G0:1901223	negative regulation of NIK/NF-kappaB sign	2.099684	0.002505109
CC	G0:0030027	lamellipodium	1.654183	0.002505109
BP	G0:0051090	regulation of DNA-binding transcription tti	1.494517	0.00256043
MF	G0:0052650	NADP-retinol dehydrogenase activity	-2.10365	0.00256043
MF	G0:0016616	oxidoreductase activity, acting on the Cl	-1.77108	0.00257532
MF	G0:0016779	nucleotidyltransferase activity	-1.82944	0.002615402
CC	G0:0005657	replication fork	-1.92747	0.002629335
BP	G0:0043112	receptor metabolic process	1.700301	0.002658656
BP	G0:0072594	establishment of protein localization to	-1.53315	0.002698644
CC	G0:0030055	cell-substrate junction	1.50629	0.002708331
BP	G0:0002758	innate immune response-activating signal	2.061946	0.002720112
BP	G0:0032757	positive regulation of interleukin-8 prod	1.930916	0.002720112
BP	G0:0031123	RNA 3'-end processing	-1.83804	0.002763968
CC	G0:0005747	mitochondrial respiratory chain complex I	-2.02421	0.002763968
CC	G0:0030964	NADH dehydrogenase complex	-2.02421	0.002763968
CC	G0:0045271	respiratory chain complex I	-2.02421	0.002763968
BP	G0:0045056	transcytosis	2.07229	0.002763968
BP	G0:0043547	positive regulation of GTPase activity	1.631514	0.002766878
BP	G0:0006487	protein N-linked glycosylation	-1.9361	0.002766878
BP	G0:0002250	adaptive immune response	-1.52477	0.002805388
MF	G0:0051287	NAD binding	-1.88858	0.002900207
BP	G0:0001819	positive regulation of cytokine productio	1.488522	0.002966831
BP	G0:0032200	telomere organization	-1.80668	0.002998358
BP	G0:0030150	protein import into mitochondrial matrix	-2.09325	0.00300476
MF	G0:0008175	tRNA methyltransferase activity	-2.10235	0.003103002
BP	G0:0032677	regulation of interleukin-8 production	1.894627	0.003128158
BP	G0:0007034	vacuolar transport	1.722143	0.003142667
CC	G0:0061702	inflammasome complex	2.042538	0.003157392
CC	G0:0097525	spliceosomal snRNP complex	-1.92942	0.003216744
MF	G0:0008484	sulfuric ester hydrolase activity	2.079145	0.003216744
MF	G0:0023026	MHC class II protein complex binding	-2.07111	0.003238885
BP	G0:0044247	cellular polysaccharide catabolic proces	2.093553	0.003238885
MF	G0:0004065	arylsulfatase activity	2.044259	0.003254159
MF	G0:0016887	ATP hydrolysis activity	-1.5845	0.003304147
BP	G0:0030837	negative regulation of actin filament pol	1.962945	0.003319083



BP	G0:2000116	regulation of cysteine-type endopeptidase	1.621395	0.003338796
BP	G0:0009303	rRNA transcription	-2.03635	0.003390261
BP	G0:0065002	intracellular protein transmembrane trans	-1.9802	0.003405199
BP	G0:0043300	regulation of leukocyte degranulation	1.96941	0.003461727
CC	G0:1990204	oxidoreductase complex	-1.8207	0.003461727
BP	G0:0016054	organic acid catabolic process	-1.62182	0.003482659
BP	G0:0009251	glucan catabolic process	2.033453	0.003537835
BP	G0:0032273	positive regulation of protein polymeriza	1.739247	0.003537835
BP	G0:0071496	cellular response to external stimulus	1.564868	0.003543454
BP	G0:0010950	positive regulation of endopeptidase acti	1.679678	0.003583193
BP	G0:0070943	neutrophil-mediated killing of symbiont	2.008668	0.003607897
BP	G0:0006488	dolichol-linked oligosaccharide biosynthe	-2.01772	0.003778636
BP	G0:0046395	carboxylic acid catabolic process	-1.60702	0.003778636
BP	G0:0045005	DNA-dependent DNA replication maintenanc	-2.009	0.003778636
BP	G0:0006490	oligosaccharide-lipid intermediate biosyr	-2.02091	0.003798997
BP	G0:0002833	positive regulation of response to biotic	1.658506	0.003798997
BP	G0:0010952	positive regulation of peptidase activity	1.621468	0.003830166
MF	G0:1901981	phosphatidylinositol phosphate binding	1.692051	0.003840331
MF	G0:0005347	ATP transmembrane transporter activity	-2.02678	0.003848942
BP	G0:0071806	protein transmembrane transport	-1.91158	0.003866765
BP	G0:0071347	cellular response to interleukin-1	1.773309	0.003933444
BP	G0:0044262	cellular carbohydrate metabolic process	1.549376	0.003933444
BP	G0:0008286	insulin receptor signaling pathway	1.773683	0.003953667
CC	G0:0098562	cytoplasmic side of membrane	1.595854	0.003987533
BP	G0:0006801	superoxide metabolic process	1.927348	0.004037952
BP	G0:1903532	positive regulation of secretion by cell	1.566103	0.004047864
CC	G0:0005765	lysosomal membrane	1.493676	0.004061124
CC	G0:0098852	lytic vacuole membrane	1.493676	0.004061124
BP	G0:0009150	purine ribonucleotide metabolic process	-1.56103	0.004115116
BP	G0:0006691	leukotriene metabolic process	2.027168	0.004210819
BP	G0:0072528	pyrimidine-containing compound biosynthe	-1.99586	0.004226759
BP	G0:0070202	regulation of establishment of protein lo	-2.02434	0.004226759
BP	G0:0070203	regulation of establishment of protein lo	-2.02434	0.004226759
BP	G0:0048771	tissue remodeling	1.656052	0.004256845
BP	G0:1903405	protein localization to nuclear body	-2.02209	0.004256845
BP	G0:1904867	protein localization to Cajal body	-2.02209	0.004256845
BP	G0:1904869	regulation of protein localization to Ca	-2.02209	0.004256845
BP	G0:1904871	positive regulation of protein localizati	-2.02209	0.004256845
BP	G0:0042060	wound healing	1.466169	0.004316169
BP	G0:0048260	positive regulation of receptor-mediated	1.869799	0.004316169
BP	G0:0006120	mitochondrial electron transport, NADH t	-1.95586	0.004316169
BP	G0:0018107	peptidyl-threonine phosphorylation	1.73649	0.004339959
BP	G0:0009112	nucleobase metabolic process	-1.98812	0.004339959
BP	G0:0002220	innate immune response activating cell s	2.017976	0.004347131
MF	G0:0005078	MAP-kinase scaffold activity	1.994451	0.004351191
BP	G0:0007178	transmembrane receptor protein serine/thr	1.521991	0.004416961
BP	G0:0002501	peptide antigen assembly with MHC protei	-2.00445	0.004452125
BP	G0:0007041	lysosomal transport	1.763845	0.004452125
BP	G0:0043038	amino acid activation	-1.96405	0.004452125
CC	G0:0031234	extrinsic component of cytoplasmic side	1.764339	0.00445727
MF	G0:0046332	SMAD binding	1.838511	0.00451172
BP	G0:0051251	positive regulation of lymphocyte activat	-1.54827	0.004626614
BP	G0:0001818	negative regulation of cytokine producti	1.540854	0.004626614
BP	G0:0034142	toll-like receptor 4 signaling pathway	1.967629	0.004680935

CC	G0:0043596	nuclear replication fork	-2.01226	0.004712892
BP	G0:0009066	aspartate family amino acid metabolic proc	-1.94357	0.004712892
BP	G0:0002831	regulation of response to biotic stimulus	1.498906	0.004832606
BP	G0:0044282	small molecule catabolic process	-1.51102	0.00488138
MF	G0:0043022	ribosome binding	-1.89202	0.004883459
MF	G0:0003953	NAD <sup>+</sup> nucleosidase activity	1.990393	0.004990955
BP	G0:1902115	regulation of organelle assembly	1.635686	0.004990955
BP	G0:0045860	positive regulation of protein kinase acti	1.464015	0.005011393
BP	G0:0010506	regulation of autophagy	1.537751	0.005042598
BP	G0:0097320	plasma membrane tubulation	2.040595	0.005042598
BP	G0:0006099	tricarboxylic acid cycle	-1.97071	0.005042598
BP	G0:0051648	vesicle localization	1.649527	0.005128117
MF	G0:0005096	GTPase activator activity	1.4922	0.005165174
BP	G0:0045921	positive regulation of exocytosis	1.799933	0.005217055
BP	G0:0005976	polysaccharide metabolic process	1.784586	0.005225322
BP	G0:0090322	regulation of superoxide metabolic proces	1.989028	0.005249006
MF	G0:0045182	translation regulator activity	-1.76375	0.005252244
BP	G0:0002399	MHC class II protein complex assembly	-1.98754	0.005252244
BP	G0:0002503	peptide antigen assembly with MHC class I	-1.98754	0.005252244
MF	G0:0003899	DNA-directed 5'-3' RNA polymerase activit	-1.96093	0.005331057
BP	G0:0034121	regulation of toll-like receptor signalin	1.848708	0.005346999
BP	G0:0070199	establishment of protein localization to	-1.99215	0.005419035
BP	G0:0032928	regulation of superoxide anion generatio	1.994794	0.005572808
BP	G0:0016226	iron-sulfur cluster assembly	-2.00744	0.005605994
BP	G0:0031163	metallo-sulfur cluster assembly	-2.00744	0.005605994
BP	G0:0045058	T cell selection	-1.84514	0.005643614
BP	G0:0043648	dicarboxylic acid metabolic process	-1.77101	0.005644197
BP	G0:1902622	regulation of neutrophil migration	1.95512	0.005677356
BP	G0:0002449	lymphocyte mediated immunity	-1.56756	0.005705587
BP	G0:0043620	regulation of DNA-templated transcription	1.862974	0.005705587
BP	G0:0030100	regulation of endocytosis	1.561704	0.005705587
BP	G0:0002223	stimulatory C-type lectin receptor signal	2.041361	0.005705587
BP	G0:1990840	response to lectin	2.041361	0.005705587
BP	G0:1990858	cellular response to lectin	2.041361	0.005705587
CC	G0:0030133	transport vesicle	1.471539	0.0057352
BP	G0:0033044	regulation of chromosome organization	-1.65732	0.005776779
BP	G0:0045807	positive regulation of endocytosis	1.758856	0.005899026
MF	G0:0003955	NAD(P)H dehydrogenase (quinone) activity	-1.98875	0.005966244
BP	G0:0051047	positive regulation of secretion	1.502341	0.006007138
BP	G0:1901186	positive regulation of ERBB signaling pat	1.932953	0.006097913
MF	G0:0008186	ATP-dependent activity, acting on RNA	-1.79281	0.006097913
BP	G0:0038066	p38MAPK cascade	1.918226	0.006097913
BP	G0:1901653	cellular response to peptide	1.463127	0.006097913
BP	G0:0050832	defense response to fungus	1.917586	0.006154093
BP	G0:0006417	regulation of translation	-1.52834	0.006173395
BP	G0:0051549	positive regulation of keratinocyte migræ	1.96845	0.006298012
BP	G0:0007007	inner mitochondrial membrane organizatio	-1.95444	0.00637881
BP	G0:0033002	muscle cell proliferation	1.584776	0.006454259
BP	G0:0051656	establishment of organelle localization	1.47979	0.006454259
MF	G0:0030695	GTPase regulator activity	1.456776	0.006454259
MF	G0:0060589	nucleoside-triphosphatase regulator activ	1.456776	0.006454259
BP	G0:0009168	purine ribonucleoside monophosphate biosy	-1.97595	0.006454259
CC	G0:0042613	MHC class II protein complex	-1.97635	0.006454259
BP	G0:1990776	response to angiotensin	1.984586	0.006547032

BP	G0:0051347	positive regulation of transferase activi	1.404129	0.006548476
CC	G0:0005775	vacuolar lumen	1.668347	0.006607291
BP	G0:0022616	DNA strand elongation	-2.01597	0.006632594
BP	G0:0032611	interleukin-1 beta production	1.755927	0.006671286
BP	G0:0032651	regulation of interleukin-1 beta producti	1.755927	0.006671286
MF	G0:0030275	LRR domain binding	2.008569	0.006698155
MF	G0:0034062	5'-3' RNA polymerase activity	-1.93765	0.006785255
MF	G0:0097747	RNA polymerase activity	-1.93765	0.006785255
MF	G0:0004536	deoxyribonuclease activity	-1.90485	0.00688161
BP	G0:0071706	tumor necrosis factor superfamily cytokin	1.621954	0.00688161
BP	G0:1903555	regulation of tumor necrosis factor super	1.621954	0.00688161
BP	G0:1902905	positive regulation of supramolecular fil	1.585908	0.00688161
BP	G0:0043628	ncRNA 3'-end processing	-1.93268	0.006942854
BP	G0:1900076	regulation of cellular response to insuli	1.849582	0.006942854
MF	G0:0003724	RNA helicase activity	-1.774	0.006942854
BP	G0:0009265	2'-deoxyribonucleotide biosynthetic proc	-1.98527	0.006949298
BP	G0:0046385	deoxyribose phosphate biosynthetic proces	-1.98527	0.006949298
BP	G0:0070570	regulation of neuron projection regenerat	1.961106	0.006949298
BP	G0:1903037	regulation of leukocyte cell-cell adhesio	-1.50002	0.006949298
BP	G0:0043406	positive regulation of MAP kinase activit	1.689965	0.006956326
MF	G0:0038187	pattern recognition receptor activity	1.974427	0.006961686
BP	G0:0010975	regulation of neuron projection developme	1.433412	0.007051325
MF	G0:0003697	single-stranded DNA binding	-1.6943	0.007063352
BP	G0:1905114	cell surface receptor signaling pathway	1.399925	0.007088562
BP	G0:0045730	respiratory burst	1.912902	0.007088562
BP	G0:0051961	negative regulation of nervous system dev	1.643358	0.007093939
BP	G0:0045061	thymic T cell selection	-1.92237	0.007113473
BP	G0:0060284	regulation of cell development	1.411176	0.007178689
BP	G0:1990173	protein localization to nucleoplasm	-1.98893	0.007179109
BP	G0:0010592	positive regulation of lamellipodium ass	2.007008	0.007187834
BP	G0:1903557	positive regulation of tumor necrosis fac	1.720017	0.007335283
BP	G0:0043374	CD8-positive, alpha-beta T cell different	-2.01397	0.007381541
BP	G0:0043409	negative regulation of MAPK cascade	1.586044	0.007403845
BP	G0:0071902	positive regulation of protein serine/thr	1.551397	0.0074299
CC	G0:0030532	small nuclear ribonucleoprotein complex	-1.83591	0.007446169
BP	G0:0007254	JNK cascade	1.608704	0.00747625
MF	G0:0042578	phosphoric ester hydrolase activity	1.469854	0.00747625
BP	G0:0006302	double-strand break repair	-1.58008	0.007730085
BP	G0:0035994	response to muscle stretch	1.96249	0.007858397
BP	G0:0042769	DNA damage response, detection of DNA dar	-2.00162	0.007973749
MF	G0:0016790	thiolester hydrolase activity	-1.92425	0.00801868
BP	G0:0032869	cellular response to insulin stimulus	1.574597	0.00801868
BP	G0:0010591	regulation of lamellipodium assembly	1.86984	0.008038424
BP	G0:0062125	regulation of mitochondrial gene expressi	-1.94601	0.008053784
BP	G0:0034123	positive regulation of toll-like receptor	1.948733	0.008454452
CC	G0:0031011	Ino80 complex	-1.95802	0.008551537
BP	G0:0008652	cellular amino acid biosynthetic process	-1.74247	0.008658627
BP	G0:0032612	interleukin-1 production	1.703854	0.008658627
BP	G0:0032652	regulation of interleukin-1 production	1.703854	0.008658627
CC	G0:0034719	SMN-Sm protein complex	-1.95135	0.008680025
BP	G0:0045089	positive regulation of innate immune res	1.631322	0.008728957
BP	G0:0006397	mRNA processing	-1.49451	0.008728957
BP	G0:0009116	nucleoside metabolic process	-1.82994	0.008747656
BP	G0:0046501	protoporphyrinogen IX metabolic process	-1.9727	0.008755841

CC	G0:0031143	pseudopodium	1.987914	0.00880674
BP	G0:0008333	endosome to lysosome transport	1.876489	0.00880674
CC	G0:0140534	endoplasmic reticulum protein-containing	-1.66898	0.009200633
MF	G0:0015926	glucosidase activity	1.951371	0.009266957
BP	G0:0006898	receptor-mediated endocytosis	1.512745	0.009378258
BP	G0:0070131	positive regulation of mitochondrial tran	-1.94809	0.009417066
BP	G0:0032490	detection of molecule of bacterial origin	1.933152	0.009420273
BP	G0:0043650	dicarboxylic acid biosynthetic process	-1.94319	0.009510171
BP	G0:0070304	positive regulation of stress-activated p	1.67607	0.009524178
BP	G0:0010657	muscle cell apoptotic process	1.793938	0.009635864
BP	G0:0032494	response to peptidoglycan	1.931635	0.009710795
BP	G0:0051546	keratinocyte migration	1.945646	0.009719182
CC	G0:0009898	cytoplasmic side of plasma membrane	1.568371	0.009719182
BP	G0:0110096	cellular response to aldehyde	-1.98872	0.009719182
CC	G0:0030496	midbody	1.597945	0.009794951
CC	G0:0071013	catalytic step 2 spliceosome	-1.79148	0.009794951
MF	G0:0031369	translation initiation factor binding	-1.91207	0.009794951
MF	G0:0003712	transcription coregulator activity	1.428847	0.009958397
BP	G0:0006073	cellular glucan metabolic process	1.778678	0.00996749
BP	G0:0044042	glucan metabolic process	1.778678	0.00996749
CC	G0:1902911	protein kinase complex	1.741636	0.00996749
CC	G0:0017053	transcription repressor complex	1.817934	0.010106699
BP	G0:0032259	methylation	-1.52143	0.010295859
CC	G0:0005938	cell cortex	1.45716	0.010370292
BP	G0:0032760	positive regulation of tumor necrosis fac	1.666897	0.010538512
BP	G0:1903358	regulation of Golgi organization	1.931112	0.010550851
BP	G0:0002090	regulation of receptor internalization	1.809511	0.010576223
BP	G0:0051249	regulation of lymphocyte activation	-1.4555	0.010629402
BP	G0:0032640	tumor necrosis factor production	1.579673	0.010629402
BP	G0:0032680	regulation of tumor necrosis factor produ	1.579673	0.010629402
BP	G0:0030838	positive regulation of actin filament pol	1.70322	0.010691929
MF	G0:0016836	hydro-lyase activity	-1.78196	0.010781718
BP	G0:0000460	maturation of 5.8S rRNA	-1.8937	0.010781718
MF	G0:0051015	actin filament binding	1.571129	0.010781718
BP	G0:0043281	regulation of cysteine-type endopeptidase	1.555049	0.010793486
BP	G0:0098581	detection of external biotic stimulus	1.96645	0.010793486
BP	G0:0031623	receptor internalization	1.663599	0.011016656
BP	G0:0006298	mismatch repair	-1.9042	0.011016656
BP	G0:0031669	cellular response to nutrient levels	1.565924	0.011021507
BP	G0:0031331	positive regulation of cellular catabolic	1.413148	0.011021507
CC	G0:0005736	RNA polymerase I complex	-1.9363	0.011021507
BP	G0:0048259	regulation of receptor-mediated endocytos	1.683441	0.011037765
BP	G0:0042116	macrophage activation	1.691953	0.011074037
BP	G0:0035872	nucleotide-binding domain, leucine rich	1.977725	0.011081271
BP	G0:0043434	response to peptide hormone	1.432315	0.011097594
BP	G0:0007249	I-kappaB kinase/NF-kappaB signaling	1.496667	0.011162919
CC	G0:0005884	actin filament	1.686155	0.01119248
BP	G0:0051051	negative regulation of transport	1.431281	0.01119248
BP	G0:0006637	acyl-CoA metabolic process	-1.69595	0.01119248
BP	G0:0035383	thioester metabolic process	-1.69595	0.01119248
CC	G0:0005732	sno(s)RNA-containing ribonucleoprotein co	-1.92188	0.01123863
BP	G0:0018108	peptidyl-tyrosine phosphorylation	1.430291	0.01124474
BP	G0:0038061	NIK/NF-kappaB signaling	1.630624	0.011247755
BP	G0:0060560	developmental growth involved in morphoge	1.493017	0.011300155

BP	G0:0042987	amyloid precursor protein catabolic process	1.791009	0.011317049
BP	G0:0050768	negative regulation of neurogenesis	1.624004	0.011317049
BP	G0:0097479	synaptic vesicle localization	1.838896	0.011341929
MF	G0:0044183	protein folding chaperone	-1.93237	0.011341929
BP	G0:0070942	neutrophil mediated cytotoxicity	1.94517	0.01134476
BP	G0:0010608	posttranscriptional regulation of gene expression	-1.43609	0.011552691
BP	G0:0070423	nucleotide-binding oligomerization domain	1.959949	0.011697519
CC	G0:0019897	extrinsic component of plasma membrane	1.58446	0.011720513
BP	G0:0032733	positive regulation of interleukin-10 production	1.865941	0.011744175
BP	G0:1901214	regulation of neuron death	1.471518	0.011821835
BP	G0:0002886	regulation of myeloid leukocyte mediated	1.781397	0.011845146
CC	G0:0098978	glutamatergic synapse	1.439683	0.011878105
BP	G0:0051348	negative regulation of transferase activity	1.491211	0.011878105
BP	G0:0045069	regulation of viral genome replication	-1.70258	0.011878105
MF	G0:0017070	U6 snRNA binding	-1.95542	0.011903979
BP	G0:0002526	acute inflammatory response	1.633487	0.011904931
MF	G0:0016796	exonuclease activity, active with either	-1.7717	0.01197339
BP	G0:0002433	immune response-regulating cell surface	1.908202	0.011982407
BP	G0:0038096	Fc-gamma receptor signaling pathway involving	1.908202	0.011982407
BP	G0:0031167	rRNA methylation	-1.94232	0.012281026
BP	G0:0070944	neutrophil-mediated killing of bacterium	1.927412	0.01228393
BP	G0:0044546	NLRP3 inflammasome complex assembly	1.969052	0.01228393
BP	G0:0140632	inflammasome complex assembly	1.969052	0.01228393
BP	G0:0030177	positive regulation of Wnt signaling pathway	1.57849	0.012320803
BP	G0:0010659	cardiac muscle cell apoptotic process	1.908835	0.012353558
BP	G0:0001890	placenta development	1.557777	0.012449647
BP	G0:0006779	porphyrin-containing compound biosynthesis	-1.8894	0.012495566
BP	G0:0033014	tetrapyrrole biosynthetic process	-1.8894	0.012495566
BP	G0:0010660	regulation of muscle cell apoptotic process	1.735534	0.01270072
CC	G0:0001401	SAM complex	-1.93907	0.01270072
CC	G0:0140275	MIB complex	-1.93907	0.01270072
BP	G0:0032868	response to insulin	1.493148	0.013011014
BP	G0:0002573	myeloid leukocyte differentiation	1.536938	0.013121095
BP	G0:0051650	establishment of vesicle localization	1.592235	0.013131967
BP	G0:0008380	RNA splicing	-1.48111	0.013320332
BP	G0:0022409	positive regulation of cell-cell adhesion	-1.48897	0.013322004
BP	G0:0032874	positive regulation of stress-activated MAPK	1.608418	0.013322004
BP	G0:0098543	detection of other organism	1.94919	0.013322004
BP	G0:0032418	lysosome localization	1.733452	0.013322004
BP	G0:0098781	ncRNA transcription	-1.83697	0.013333358
BP	G0:0030308	negative regulation of cell growth	1.520732	0.01343686
MF	G0:0008094	ATP-dependent activity, acting on DNA	-1.6965	0.013668633
MF	G0:0016922	nuclear receptor binding	1.613052	0.013712947
BP	G0:0009142	nucleoside triphosphate biosynthetic process	-1.76106	0.013712947
MF	G0:0005149	interleukin-1 receptor binding	1.886067	0.013932294
BP	G0:0051054	positive regulation of DNA metabolic process	-1.56058	0.014008455
BP	G0:0018212	peptidyl-tyrosine modification	1.432553	0.014008455
BP	G0:0036257	multivesicular body organization	1.892164	0.014056084
BP	G0:0033013	tetrapyrrole metabolic process	-1.72413	0.014080744
BP	G0:0042790	nucleolar large rRNA transcription by RNA polymerase	-1.94718	0.014089664
BP	G0:0016049	cell growth	1.407371	0.014119791
BP	G0:0007032	endosome organization	1.764266	0.01416304
BP	G0:0051346	negative regulation of hydrolase activity	1.399894	0.01416304
BP	G0:0000966	RNA 5'-end processing	-1.89824	0.014218338

BP	G0:0046033	AMP metabolic process	-1.8996	0.014218338
BP	G0:0051098	regulation of binding	1.429966	0.014218338
BP	G0:0006112	energy reserve metabolic process	1.694672	0.01430083
BP	G0:0032715	negative regulation of interleukin-6 prod	1.833268	0.01430083
BP	G0:0042110	T cell activation	-1.42709	0.01430083
CC	G0:0005777	peroxisome	-1.60312	0.014486384
CC	G0:0042579	microbody	-1.60312	0.014486384
BP	G0:0070997	neuron death	1.428241	0.014486384
MF	G0:0036041	long-chain fatty acid binding	1.915817	0.014684855
BP	G0:0002639	positive regulation of immunoglobulin pro	-1.81416	0.014702817
BP	G0:0032731	positive regulation of interleukin-1 beta	1.766497	0.014702817
BP	G0:0031668	cellular response to extracellular stimul	1.479212	0.014778765
BP	G0:0009062	fatty acid catabolic process	-1.68704	0.014899158
BP	G0:1902683	regulation of receptor localization to sy	1.92931	0.014915404
MF	G0:0016780	phosphotransferase activity, for other su	-1.88964	0.014915404
BP	G0:0032102	negative regulation of response to exter	1.400727	0.014915404
CC	G0:0000428	DNA-directed RNA polymerase complex	-1.66704	0.014961228
BP	G0:1902745	positive regulation of lamellipodium orga	1.888511	0.015393947
BP	G0:0009896	positive regulation of catabolic process	1.395277	0.015448955
CC	G0:0000421	autophagosome membrane	1.828886	0.015448955
BP	G0:0043414	macromolecule methylation	-1.50505	0.015448955
CC	G0:0005744	TIM23 mitochondrial import inner membran	-1.89555	0.015448955
CC	G0:0030666	endocytic vesicle membrane	1.52625	0.015448955
BP	G0:0001525	angiogenesis	1.370193	0.015448955
BP	G0:0002183	cytoplasmic translational initiation	-1.89127	0.01546116
BP	G0:0090312	positive regulation of protein deacetyl	1.876699	0.015480205
BP	G0:0050854	regulation of antigen receptor-mediated	-1.76196	0.015480205
MF	G0:0019205	nucleobase-containing compound kinase act	-1.81961	0.015480205
BP	G0:0043368	positive T cell selection	-1.82201	0.015480205
BP	G0:0018279	protein N-linked glycosylation via aspara	-1.87923	0.015576523
BP	G0:0006188	IMP biosynthetic process	-1.90677	0.015585926
BP	G0:0042407	crisetae formation	-1.93064	0.01569355
BP	G0:1901184	regulation of ERBB signaling pathway	1.707892	0.015793279
BP	G0:0010665	regulation of cardiac muscle cell apopto	1.818727	0.01581736
BP	G0:0014855	striated muscle cell proliferation	1.756283	0.015932966
BP	G0:0006631	fatty acid metabolic process	-1.43878	0.015996347
BP	G0:0009612	response to mechanical stimulus	1.49301	0.015996347
BP	G0:0015931	nucleobase-containing compound transport	-1.54615	0.016009994
MF	G0:0016651	oxidoreductase activity, acting on NAD(P)	-1.71311	0.016009994
BP	G0:0010833	telomere maintenance via telomere length	-1.73852	0.01601607
BP	G0:0097581	lamellipodium organization	1.705264	0.016020337
CC	G0:0005685	U1 snRNP	-1.8812	0.016042798
BP	G0:0000054	ribosomal subunit export from nucleus	-1.89819	0.016042798
BP	G0:0033750	ribosome localization	-1.89819	0.016042798
BP	G0:0034502	protein localization to chromosome	-1.67085	0.016042798
BP	G0:0002637	regulation of immunoglobulin production	-1.71247	0.016042798
BP	G0:0022411	cellular component disassembly	1.376154	0.016042798
BP	G0:0002263	cell activation involved in immune respon	1.419753	0.016046609
BP	G0:0002708	positive regulation of lymphocyte mediat	-1.61124	0.016341847
BP	G0:0090151	establishment of protein localization to	-1.87165	0.016376165
BP	G0:0070200	establishment of protein localization to	-1.89209	0.016376165
BP	G0:0099504	synaptic vesicle cycle	1.506293	0.016403309
BP	G0:0005977	glycogen metabolic process	1.706534	0.016417015
BP	G0:0038094	Fc-gamma receptor signaling pathway	1.869183	0.016421824

BP	G0:0006783	heme biosynthetic process	-1.85181	0.016555005
BP	G0:0044088	regulation of vacuole organization	1.873317	0.016555005
MF	G0:0004812	aminoacyl-tRNA ligase activity	-1.88762	0.016597048
BP	G0:0006418	tRNA aminoacylation for protein translati	-1.88762	0.016597048
MF	G0:0016875	ligase activity, forming carbon-oxygen bc	-1.88762	0.016597048
BP	G0:0008360	regulation of cell shape	1.565176	0.016660588
BP	G0:0046459	short-chain fatty acid metabolic process	-1.88973	0.016693969
MF	G0:0008649	rRNA methyltransferase activity	-1.88486	0.016693969
MF	G0:0140102	catalytic activity, acting on a rRNA	-1.88486	0.016693969
BP	G0:0031333	negative regulation of protein-containin	1.58768	0.016905207
BP	G0:0045123	cellular extravasation	1.717557	0.016993267
BP	G0:0098927	vesicle-mediated transport between endosc	1.867701	0.017032443
CC	G0:0000781	chromosome, telomeric region	-1.59907	0.017038186
BP	G0:1901216	positive regulation of neuron death	1.641253	0.017075475
BP	G0:0016071	mRNA metabolic process	-1.37647	0.017075475
BP	G0:1900225	regulation of NLRP3 inflammasome complex	1.866518	0.01721321
BP	G0:0019068	virion assembly	1.866025	0.01721321
MF	G0:0017124	SH3 domain binding	1.571928	0.017551457
BP	G0:0031346	positive regulation of cell projection on	1.426514	0.017569369
BP	G0:0034143	regulation of toll-like receptor 4 signa	1.886642	0.017596209
BP	G0:0005980	glycogen catabolic process	1.890256	0.017624347
BP	G0:0010658	striated muscle cell apoptotic process	1.867342	0.01779256
BP	G0:0010662	regulation of striated muscle cell apopt	1.768505	0.017855166
MF	G0:0016829	lyase activity	-1.55734	0.017965453
BP	G0:0060969	negative regulation of gene silencing	1.859778	0.018178494
BP	G0:0099003	vesicle-mediated transport in synapse	1.506449	0.018384105
BP	G0:1901659	glycosyl compound biosynthetic process	-1.87923	0.018416905
MF	G0:0102991	myristoyl-CoA hydrolase activity	-1.92049	0.018591056
BP	G0:0016358	dendrite development	1.469019	0.018591056
BP	G0:0045580	regulation of T cell differentiation	-1.59446	0.018688543
BP	G0:0006379	mRNA cleavage	-1.85554	0.018728511
BP	G0:0034471	ncRNA 5'-end processing	-1.87462	0.018728511
BP	G0:0009147	pyrimidine nucleoside triphosphate metab	-1.935	0.018751488
BP	G0:0009130	pyrimidine nucleoside monophosphate biosy	-1.91	0.018999259
BP	G0:0051494	negative regulation of cytoskeleton organ	1.580677	0.019084819
BP	G0:0046514	ceramide catabolic process	1.859513	0.019115975
BP	G0:1901361	organic cyclic compound catabolic proces	-1.39943	0.019115975
BP	G0:0032732	positive regulation of interleukin-1 procl	1.697277	0.01915586
BP	G0:0042982	amyloid precursor protein metabolic proc	1.696551	0.01915586
MF	G0:0070182	DNA polymerase binding	-1.86678	0.019207935
BP	G0:0043525	positive regulation of neuron apoptotic p	1.751966	0.019233359
CC	G0:0005819	spindle	1.424452	0.019371749
BP	G0:0034248	regulation of cellular amide metabolic pr	-1.43473	0.019589823
BP	G0:2001233	regulation of apoptotic signaling pathway	1.402804	0.019666249
BP	G0:0060263	regulation of respiratory burst	1.844947	0.019666249
BP	G0:0034655	nucleobase-containing compound catabolic	-1.44536	0.019666249
BP	G0:0006766	vitamin metabolic process	-1.61631	0.019804379
BP	G0:0045646	regulation of erythrocyte differentiation	1.84809	0.019832485
BP	G0:0060828	regulation of canonical Wnt signaling pat	1.489581	0.019927926
BP	G0:0019884	antigen processing and presentation of ex	-1.7559	0.020099353
MF	G0:0003995	acyl-CoA dehydrogenase activity	-1.86588	0.020415949
CC	G0:0030014	CCR4-NOT complex	1.871204	0.020528891
BP	G0:0031638	zymogen activation	1.728074	0.020551016
BP	G0:0022604	regulation of cell morphogenesis	1.408946	0.020629642

BP	GO:0043951	negative regulation of cAMP-mediated signaling	1.868918	0.021164049
BP	GO:1901652	response to peptide	1.351543	0.021269566
BP	GO:0043144	sno(s)RNA processing	-1.89951	0.021562979
BP	GO:0045637	regulation of myeloid cell differentiation	1.482471	0.021562979
BP	GO:2001020	regulation of response to DNA damage stimulus	-1.51472	0.021598952
BP	GO:0043039	tRNA aminoacylation	-1.90492	0.021829237
BP	GO:0006287	base-excision repair, gap-filling	-1.90136	0.021844113
MF	GO:0106306	protein serine phosphatase activity	1.678357	0.02194679
MF	GO:0106307	protein threonine phosphatase activity	1.678357	0.02194679
BP	GO:0031063	regulation of histone deacetylation	1.872434	0.02199972
BP	GO:0038093	Fc receptor signaling pathway	1.773992	0.022037169
BP	GO:0050806	positive regulation of synaptic transmission	1.520874	0.022153385
BP	GO:0048588	developmental cell growth	1.510777	0.022189096
MF	GO:0003729	mRNA binding	-1.46788	0.022189096
BP	GO:1900744	regulation of p38MAPK cascade	1.829966	0.022241535
BP	GO:0032508	DNA duplex unwinding	-1.64309	0.022244927
BP	GO:0007159	leukocyte cell-cell adhesion	-1.4209	0.022305766
BP	GO:0022617	extracellular matrix disassembly	1.694695	0.022406134
BP	GO:0030522	intracellular receptor signaling pathway	1.431474	0.022524567
BP	GO:1902743	regulation of lamellipodium organization	1.763557	0.022530399
MF	GO:0005536	glucose binding	1.846334	0.022643758
MF	GO:0043539	protein serine/threonine kinase activation	1.774756	0.022767251
MF	GO:0019003	GDP binding	1.660817	0.022767251
BP	GO:0046323	glucose import	1.74375	0.022767251
BP	GO:0030217	T cell differentiation	-1.45151	0.023195824
MF	GO:0047617	acyl-CoA hydrolase activity	-1.85733	0.023195824
BP	GO:0048661	positive regulation of smooth muscle cell proliferation	1.647082	0.023195824
BP	GO:1903034	regulation of response to wounding	1.542025	0.023225133
MF	GO:0030515	snoRNA binding	-1.78943	0.023231342
BP	GO:0050729	positive regulation of inflammatory response	1.55397	0.023261967
BP	GO:0090263	positive regulation of canonical Wnt signaling	1.640642	0.023266043
BP	GO:0071559	response to transforming growth factor beta	1.412164	0.023273598
CC	GO:0005667	transcription regulator complex	1.375462	0.023321318
CC	GO:0005643	nuclear pore	-1.70011	0.023497004
BP	GO:1900017	positive regulation of cytokine production	1.819963	0.023541004
MF	GO:0008138	protein tyrosine/serine/threonine phosphorylation	1.748286	0.023564084
BP	GO:1903649	regulation of cytoplasmic transport	1.827094	0.023700433
BP	GO:0048659	smooth muscle cell proliferation	1.489675	0.023796088
BP	GO:1904667	negative regulation of ubiquitin protein ligase activity	-1.8901	0.023950929
BP	GO:0030656	regulation of vitamin metabolic process	-1.85348	0.024017208
BP	GO:0048167	regulation of synaptic plasticity	1.513851	0.024106558
MF	GO:0016813	hydrolase activity, acting on carbon-nitrogen bonds, except amide bonds	1.838942	0.024106558
BP	GO:0001959	regulation of cytokine-mediated signaling pathway	1.531972	0.024122423
BP	GO:0009267	cellular response to starvation	1.537455	0.024723915
BP	GO:0071356	cellular response to tumor necrosis factor	1.467375	0.024725957
CC	GO:0030894	replisome	-1.88945	0.024982556
BP	GO:0033194	response to hydroperoxide	1.842033	0.025053293
BP	GO:0120032	regulation of plasma membrane bounded cell-cell junction assembly	1.511175	0.025053293
BP	GO:0042102	positive regulation of T cell proliferation	-1.62048	0.02506531
BP	GO:0036490	regulation of translation in response to stress	1.857234	0.025414834
BP	GO:0045022	early endosome to late endosome transport	1.75215	0.025414834
CC	GO:0036452	ESCRT complex	1.844821	0.025495611
MF	GO:0015399	primary active transmembrane transporter activity	-1.53218	0.025536373
BP	GO:0051052	regulation of DNA metabolic process	-1.43313	0.025748541



BP	G0:0071560	cellular response to transforming growth	1.420781	0.025774787
BP	G0:1902904	negative regulation of supramolecular fil	1.546003	0.025779437
BP	G0:2001238	positive regulation of extrinsic apopto	1.733987	0.025859254
BP	G0:0032755	positive regulation of interleukin-6 pro	1.629171	0.025864981
BP	G0:0045648	positive regulation of erythrocyte differ	1.809209	0.026058752
BP	G0:0048489	synaptic vesicle transport	1.717717	0.02617882
BP	G0:0006270	DNA replication initiation	-1.77539	0.026386877
CC	G0:0005782	peroxisomal matrix	-1.6897	0.026514982
CC	G0:0031907	microbody lumen	-1.6897	0.026514982
BP	G0:0060759	regulation of response to cytokine stimu	1.538237	0.026576895
MF	G0:0004540	ribonuclease activity	-1.61595	0.026795383
MF	G0:0008106	alcohol dehydrogenase (NADP+) activity	-1.84412	0.026795383
BP	G0:0061418	regulation of transcription from RNA poly	1.837954	0.026961127
CC	G0:0150034	distal axon	1.413317	0.027043322
BP	G0:0046697	decidualization	1.843895	0.027069836
BP	G0:0071396	cellular response to lipid	1.336123	0.027133707
BP	G0:1901888	regulation of cell junction assembly	1.459654	0.027318608
BP	G0:0045742	positive regulation of epidermal growth	1.817302	0.027318608
BP	G0:0009064	glutamine family amino acid metabolic pro	-1.62947	0.027318608
BP	G0:0006312	mitotic recombination	-1.87152	0.027414368
BP	G0:0006413	translational initiation	-1.63646	0.027431949
BP	G0:0032930	positive regulation of superoxide anion	1.876364	0.02746492
MF	G0:0004519	endonuclease activity	-1.59425	0.02746492
BP	G0:0060491	regulation of cell projection assembly	1.503293	0.027525655
BP	G0:0030032	lamellipodium assembly	1.665972	0.027525655
BP	G0:0016575	histone deacetylation	1.580899	0.027539036
BP	G0:0071428	rRNA-containing ribonucleoprotein comple	-1.87663	0.027539036
CC	G0:0001726	ruffle	1.538404	0.028002926
BP	G0:0006476	protein deacetylation	1.579842	0.028002926
BP	G0:0045453	bone resorption	1.634386	0.028002926
MF	G0:0016702	oxidoreductase activity, acting on single	1.820069	0.02816865
BP	G0:0044275	cellular carbohydrate catabolic process	1.766339	0.02816865
BP	G0:0007006	mitochondrial membrane organization	-1.58635	0.028244759
BP	G0:0050869	negative regulation of B cell activation	1.732388	0.028276594
MF	G0:0016290	palmitoyl-CoA hydrolase activity	-1.83235	0.028284585
BP	G0:0045727	positive regulation of translation	-1.57442	0.028345106
BP	G0:0002366	leukocyte activation involved in immune	1.428556	0.028393324
BP	G0:0050830	defense response to Gram-positive bacteri	1.598413	0.028434226
CC	G0:0001772	immunological synapse	-1.73836	0.028514486
BP	G0:0046034	ATP metabolic process	-1.45175	0.028621865
BP	G0:0002396	MHC protein complex assembly	-1.88946	0.028632186
BP	G0:0032272	negative regulation of protein polymeriza	1.665688	0.028636673
BP	G0:0002700	regulation of production of molecular mec	-1.50274	0.028720478
BP	G0:0061025	membrane fusion	1.54753	0.029200421
BP	G0:0044270	cellular nitrogen compound catabolic pro	-1.39723	0.029249546
BP	G0:0046700	heterocycle catabolic process	-1.38011	0.029249546
BP	G0:0051873	killing by host of symbiont cells	1.806257	0.029567709
BP	G0:0051883	killing of cells in other organism invol	1.806257	0.029567709
BP	G0:0009063	cellular amino acid catabolic process	-1.57172	0.029567709
BP	G0:0034219	carbohydrate transmembrane transport	1.544857	0.029746034
CC	G0:0042788	polysomal ribosome	-1.79239	0.029800854
BP	G0:0061077	chaperone-mediated protein folding	-1.68241	0.030020537
BP	G0:0051056	regulation of small GTPase mediated sign	1.373732	0.030058521
BP	G0:1902570	protein localization to nucleolus	-1.86638	0.030086265

BP	G0:1901222	regulation of NIK/NF-kappaB signaling	1.562875	0.03014193
BP	G0:0051016	barbed-end actin filament capping	1.832442	0.03014193
BP	G0:0032613	interleukin-10 production	1.671072	0.030302567
BP	G0:0032653	regulation of interleukin-10 production	1.671072	0.030302567
CC	G0:0005635	nuclear envelope	-1.35461	0.030379624
BP	G0:0009110	vitamin biosynthetic process	-1.88529	0.030379624
BP	G0:0014856	skeletal muscle cell proliferation	1.817208	0.030379624
BP	G0:0007179	transforming growth factor beta receptor	1.469562	0.030424087
BP	G0:0014831	gastro-intestinal system smooth muscle cell	1.804914	0.030514021
BP	G0:0006360	transcription by RNA polymerase I	-1.70258	0.030736744
CC	G0:0034708	methyltransferase complex	-1.60648	0.031086498
BP	G0:0120034	positive regulation of plasma membrane bound	1.605478	0.03109884
MF	G0:0016798	hydrolase activity, acting on glycosyl bonds	1.49059	0.031144855
MF	G0:0016879	ligase activity, forming carbon-nitrogen bonds	-1.79412	0.031260324
CC	G0:0000177	cytoplasmic exosome (RNase complex)	-1.86116	0.031387721
BP	G0:0042058	regulation of epidermal growth factor receptor	1.655496	0.031509535
BP	G0:2000269	regulation of fibroblast apoptotic process	1.823673	0.031658831
BP	G0:0060291	long-term synaptic potentiation	1.610359	0.031658831
CC	G0:0005681	spliceosomal complex	-1.51864	0.031666844
BP	G0:0008645	hexose transmembrane transport	1.558324	0.031694442
BP	G0:0045600	positive regulation of fat cell differentiation	1.69045	0.03172819
MF	G0:0030295	protein kinase activator activity	1.608539	0.03186803
CC	G0:1905368	peptidase complex	-1.58926	0.03186803
BP	G0:0019439	aromatic compound catabolic process	-1.38158	0.031989848
BP	G0:0006903	vesicle targeting	1.780807	0.031989848
BP	G0:0000478	endonucleolytic cleavage involved in rRNA	-1.82709	0.031989848
BP	G0:0000479	endonucleolytic cleavage of tricistronic	-1.82709	0.031989848
MF	G0:0015605	organophosphate ester transmembrane transport	-1.78402	0.031989848
MF	G0:0005546	phosphatidylinositol-4,5-bisphosphate binding	1.652117	0.03227822
BP	G0:0009220	pyrimidine ribonucleotide biosynthetic process	-1.78873	0.032435749
BP	G0:0015749	monosaccharide transmembrane transport	1.549803	0.032435749
BP	G0:0097028	dendritic cell differentiation	1.739073	0.032455755
MF	G0:0030374	nuclear receptor coactivator activity	1.786528	0.03252122
BP	G0:0062197	cellular response to chemical stress	1.341719	0.033052659
CC	G0:0030880	RNA polymerase complex	-1.60617	0.033229747
BP	G0:1901606	alpha-amino acid catabolic process	-1.60328	0.033729792
BP	G0:0016064	immunoglobulin mediated immune response	-1.50515	0.033955086
CC	G0:0000178	exosome (RNase complex)	-1.78347	0.033955086
BP	G0:0098789	pre-mRNA cleavage required for polyadenylation	-1.80364	0.033955086
BP	G0:1904385	cellular response to angiotensin	1.786981	0.033955086
MF	G0:0003743	translation initiation factor activity	-1.74651	0.034121181
BP	G0:0007264	small GTPase mediated signal transduction	1.332947	0.034283997
BP	G0:0009148	pyrimidine nucleoside triphosphate biosynthesis	-1.81561	0.034369404
BP	G0:0071897	DNA biosynthetic process	-1.513	0.034409613
BP	G0:1903307	positive regulation of regulated secretory	1.695983	0.034555996
BP	G0:0090502	RNA phosphodiester bond hydrolysis, endonuclease	-1.63903	0.034597335
BP	G0:0007004	telomere maintenance via telomerase	-1.66268	0.034660453
MF	G0:0061659	ubiquitin-like protein ligase activity	1.38995	0.034768042
BP	G0:0019724	B cell mediated immunity	-1.51701	0.0348047
BP	G0:0070391	response to lipoteichoic acid	1.826274	0.0348047
BP	G0:0071223	cellular response to lipoteichoic acid	1.826274	0.0348047
BP	G0:0014841	skeletal muscle satellite cell proliferation	1.792325	0.034945564
BP	G0:0061099	negative regulation of protein tyrosine phosphorylation	1.757328	0.035064647
BP	G0:0002863	positive regulation of inflammatory response	-1.79656	0.03521035

MF	G0:0005158	insulin receptor binding	1.77349	0.035214757
MF	G0:0046965	retinoid X receptor binding	1.81299	0.035229495
BP	G0:0006278	RNA-dependent DNA biosynthetic process	-1.63097	0.035263114
BP	G0:0035601	protein deacylation	1.523181	0.035263114
BP	G0:1990089	response to nerve growth factor	1.64633	0.035302259
BP	G0:0002431	Fc receptor mediated stimulatory signaling	1.741468	0.035311871
BP	G0:0090022	regulation of neutrophil chemotaxis	1.746649	0.035392742
BP	G0:0009263	deoxyribonucleotide biosynthetic process	-1.84393	0.035462249
BP	G0:0002312	B cell activation involved in immune response	-1.60562	0.035576167
BP	G0:0019217	regulation of fatty acid metabolic process	1.617231	0.035603084
BP	G0:0051205	protein insertion into membrane	-1.81065	0.035951324
MF	G0:0030544	Hsp70 protein binding	-1.78199	0.035977685
MF	G0:0016776	phosphotransferase activity, phosphate group	-1.8151	0.036116673
BP	G0:0071800	podosome assembly	1.780567	0.036139634
CC	G0:1905354	exoribonuclease complex	-1.86197	0.036180572
BP	G0:0031589	cell-substrate adhesion	1.354972	0.036556973
BP	G0:2001056	positive regulation of cysteine-type endopeptidase activity	1.525607	0.036556973
BP	G0:0002694	regulation of leukocyte activation	-1.33278	0.036556973
BP	G0:0050657	nucleic acid transport	-1.51175	0.036556973
BP	G0:0050658	RNA transport	-1.51175	0.036556973
BP	G0:1990090	cellular response to nerve growth factor	1.621159	0.03659681
MF	G0:0003713	transcription coactivator activity	1.388356	0.036636725
BP	G0:0046330	positive regulation of JNK cascade	1.574503	0.036785933
BP	G0:0045017	glycerolipid biosynthetic process	1.439723	0.036843406
MF	G0:0019209	kinase activator activity	1.567029	0.036843406
BP	G0:0051385	response to mineralocorticoid	-1.75594	0.036843406
BP	G0:0090503	RNA phosphodiester bond hydrolysis, exonuclease	-1.75566	0.036843406
CC	G0:0055029	nuclear DNA-directed RNA polymerase complex	-1.6187	0.03707562
BP	G0:0032957	inositol trisphosphate metabolic process	1.820164	0.03707562
BP	G0:0014909	smooth muscle cell migration	1.602209	0.03707562
MF	G0:0016701	oxidoreductase activity, acting on single donors with NAD, NADP, flavin, ferredoxin, or flavin mononucleotide as acceptor	1.813266	0.037182894
MF	G0:0004529	exodeoxyribonuclease activity	-1.77066	0.037353764
MF	G0:0016895	exodeoxyribonuclease activity, producing 5' phosphate	-1.77066	0.037353764
BP	G0:0070555	response to interleukin-1	1.493826	0.037452916
BP	G0:0046631	alpha-beta T cell activation	-1.52579	0.037484472
BP	G0:0036258	multivesicular body assembly	1.803949	0.037484472
MF	G0:0016765	transferase activity, transferring alkyl groups	-1.67666	0.037565056
BP	G0:0046635	positive regulation of alpha-beta T cell activation	-1.62342	0.03773305
BP	G0:0010721	negative regulation of cell development	1.459441	0.03784085
CC	G0:0009897	external side of plasma membrane	-1.40873	0.03784085
BP	G0:2001236	regulation of extrinsic apoptotic signaling pathway	1.489621	0.037883505
BP	G0:0034762	regulation of transmembrane transport	1.293509	0.038338372
BP	G0:0050856	regulation of T cell receptor signaling pathway	-1.75733	0.038338372
MF	G0:0016289	CoA hydrolase activity	-1.82392	0.038388814
MF	G0:0000149	SNARE binding	1.510013	0.038527461
BP	G0:0030010	establishment of cell polarity	1.491289	0.038953232
BP	G0:1903036	positive regulation of response to wounding	1.609129	0.039025873
BP	G0:0021700	developmental maturation	1.365273	0.040299356
BP	G0:0043122	regulation of I-kappaB kinase/NF-kappaB signaling pathway	1.403074	0.040299356
BP	G0:0060070	canonical Wnt signaling pathway	1.366266	0.040369025
BP	G0:0043302	positive regulation of leukocyte degranulation	1.752403	0.040600986
BP	G0:0090311	regulation of protein deacetylation	1.726982	0.040692926
BP	G0:0016485	protein processing	1.421868	0.040937534
BP	G0:0046040	IMP metabolic process	-1.79555	0.040988333

BP	G0:0150115	cell-substrate junction organization	1.514712	0.041131493
BP	G0:0071353	cellular response to interleukin-4	-1.71463	0.041131493
BP	G0:0051223	regulation of protein transport	1.323707	0.041131493
BP	G0:0050764	regulation of phagocytosis	1.578687	0.04119919
BP	G0:0009163	nucleoside biosynthetic process	-1.82848	0.041215005
BP	G0:0034404	nucleobase-containing small molecule biosynthesis	-1.82848	0.041215005
BP	G0:0070741	response to interleukin-6	1.721947	0.041588102
BP	G0:0071985	multivesicular body sorting pathway	1.683465	0.041926947
BP	G0:0071027	nuclear RNA surveillance	-1.81982	0.042686729
BP	G0:0071028	nuclear mRNA surveillance	-1.81982	0.042686729
BP	G0:0060964	regulation of gene silencing by miRNA	1.714896	0.042760733
BP	G0:0034612	response to tumor necrosis factor	1.44698	0.043035579
MF	G0:0002020	protease binding	1.475891	0.043121257
CC	G0:0098687	chromosomal region	-1.40082	0.043413381
BP	G0:0046394	carboxylic acid biosynthetic process	-1.41486	0.043441851
BP	G0:0090092	regulation of transmembrane receptor protein tyrosine kinase activity	1.389949	0.043449504
BP	G0:0007611	learning or memory	1.405419	0.043449504
CC	G0:1905369	endopeptidase complex	-1.62511	0.043499051
BP	G0:0006506	GPI anchor biosynthetic process	-1.74294	0.043548822
BP	G0:0043393	regulation of protein binding	1.445754	0.043548822
BP	G0:0044403	biological process involved in symbiotic nitrogen fixation	1.37701	0.043548822
BP	G0:0045861	negative regulation of proteolysis	1.345108	0.043620154
BP	G0:0002697	regulation of immune effector process	1.346466	0.043920692
MF	G0:0003756	protein disulfide isomerase activity	-1.807	0.04395076
CC	G0:0005847	mRNA cleavage and polyadenylation specificity factor activity	-1.80794	0.04395076
MF	G0:0016864	intramolecular oxidoreductase activity, trans	-1.807	0.04395076
BP	G0:0070665	positive regulation of leukocyte proliferation	-1.43727	0.044002567
BP	G0:0048291	isotype switching to IgG isotypes	-1.78856	0.044006865
MF	G0:0030674	protein-macromolecule adaptor activity	1.376843	0.044013305
BP	G0:0051236	establishment of RNA localization	-1.48948	0.044013305
BP	G0:0036037	CD8-positive, alpha-beta T cell activation	-1.76876	0.044020057
BP	G0:0051222	positive regulation of protein transport	1.393029	0.044138517
BP	G0:0031279	regulation of cyclase activity	1.649354	0.04422401
BP	G0:0090141	positive regulation of mitochondrial fission	-1.7867	0.044256933
BP	G0:0045070	positive regulation of viral genome replication	-1.77231	0.044256933
BP	G0:0007040	lysosome organization	1.583423	0.044256933
BP	G0:0080171	lytic vacuole organization	1.583423	0.044256933
MF	G0:0004683	calmodulin-dependent protein kinase activity	1.720659	0.044447559
BP	G0:0006778	porphyrin-containing compound metabolic process	-1.65274	0.044455271
BP	G0:0106106	cold-induced thermogenesis	1.416603	0.044479104
BP	G0:0120161	regulation of cold-induced thermogenesis	1.416603	0.044479104
BP	G0:0046324	regulation of glucose import	1.628432	0.04461493
BP	G0:0031647	regulation of protein stability	1.34794	0.04461493
BP	G0:0000375	RNA splicing, via transesterification reaction	-1.4267	0.044793508
BP	G0:0060419	heart growth	1.559458	0.044844899
BP	G0:0098926	postsynaptic signal transduction	1.706862	0.044896849
BP	G0:0034122	negative regulation of toll-like receptor signaling pathway	1.715021	0.04500708
BP	G0:0042362	fat-soluble vitamin biosynthetic process	-1.80728	0.045325682
BP	G0:0099116	tRNA 5'-end processing	-1.80714	0.045325682
BP	G0:0016053	organic acid biosynthetic process	-1.41013	0.045334532
MF	G0:0019199	transmembrane receptor protein kinase activity	1.423682	0.045482314
BP	G0:0099565	chemical synaptic transmission, postsynaptic	1.497963	0.045585085
CC	G0:0098685	Schaffer collateral - CA1 synapse	1.576732	0.045607751
MF	G0:0043560	insulin receptor substrate binding	1.74409	0.045607751

BP	G0:0019395	fatty acid oxidation	-1.55268	0.045607751
BP	G0:0055017	cardiac muscle tissue growth	1.535606	0.045607751
BP	G0:1904659	glucose transmembrane transport	1.502748	0.045694331
BP	G0:0006361	transcription initiation from RNA polymer	-1.7778	0.045943149
BP	G0:0006979	response to oxidative stress	1.331715	0.046001115
MF	G0:0031435	mitogen-activated protein kinase kinase	1.783879	0.046001115
BP	G0:0043555	regulation of translation in response to	1.782637	0.046001115
BP	G0:0071025	RNA surveillance	-1.78099	0.046244713
CC	G0:0005793	endoplasmic reticulum-Golgi intermediate	1.476117	0.046313663
CC	G0:0070382	exocytic vesicle	1.399368	0.046424878
BP	G0:0022407	regulation of cell-cell adhesion	-1.32701	0.046603438
BP	G0:0000028	ribosomal small subunit assembly	-1.72859	0.046603438
MF	G0:0043024	ribosomal small subunit binding	-1.72631	0.046603438
BP	G0:0050728	negative regulation of inflammatory respo	1.47454	0.046660892
BP	G0:1900078	positive regulation of cellular response	1.735502	0.046663393
BP	G0:0048660	regulation of smooth muscle cell prolifera	1.478428	0.047323703
BP	G0:0014812	muscle cell migration	1.622582	0.047323703
BP	G0:0009141	nucleoside triphosphate metabolic proces	-1.55037	0.047323703
BP	G0:0045619	regulation of lymphocyte differentiation	-1.47103	0.047453824
BP	G0:0006605	protein targeting	-1.43033	0.047721104
BP	G0:0044706	multi-multicellular organism process	1.37395	0.047746507
BP	G0:0001522	pseudouridine synthesis	-1.80174	0.047746507
MF	G0:0009982	pseudouridine synthase activity	-1.80174	0.047746507
BP	G0:0140029	exocytic process	1.605909	0.047835034
CC	G0:0043601	nuclear replisome	-1.76758	0.047848231
BP	G0:0030098	lymphocyte differentiation	-1.3608	0.047903314
BP	G0:0140112	extracellular vesicle biogenesis	1.717935	0.047916343
BP	G0:1904356	regulation of telomere maintenance via te	-1.66495	0.047989942
BP	G0:0051693	actin filament capping	1.633509	0.048226871
BP	G0:0031640	killing of cells of other organism	1.572315	0.048226871
CC	G0:0002102	podosome	1.707691	0.048526195
BP	G0:0097202	activation of cysteine-type endopeptidas	1.754078	0.048638482
BP	G0:0002696	positive regulation of leukocyte activati	-1.39108	0.048638482
BP	G0:0033865	nucleoside bisphosphate metabolic proces	-1.55025	0.048638482
BP	G0:0033875	ribonucleoside bisphosphate metabolic pro	-1.55025	0.048638482
BP	G0:0034032	purine nucleoside bisphosphate metabolic	-1.55025	0.048638482
BP	G0:0009086	methionine biosynthetic process	-1.7631	0.048851496
BP	G0:0016045	detection of bacterium	1.752455	0.049034676
BP	G0:0033539	fatty acid beta-oxidation using acyl-CoA	-1.76934	0.049132526
BP	G0:0035112	genitalia morphogenesis	1.776279	0.049322637
MF	G0:0019887	protein kinase regulator activity	1.445378	0.049452385
BP	G0:1902624	positive regulation of neutrophil migrati	1.751608	0.049620434
BP	G0:0090407	organophosphate biosynthetic process	-1.3395	0.049620434
CC	G0:0042405	nuclear inclusion body	1.730851	0.049725712
BP	G0:0010939	regulation of necrotic cell death	1.694343	0.049773996
BP	G0:0001893	maternal placenta development	1.667911	0.049773996
MF	G0:1902936	phosphatidylinositol bisphosphate bindin	1.569493	0.049773996
BP	G0:0002204	somatic recombination of immunoglobulin	-1.67838	0.049773996
BP	G0:0002208	somatic diversification of immunoglobulin	-1.67838	0.049773996
BP	G0:0045190	isotype switching	-1.67838	0.049773996
BP	G0:0007009	plasma membrane organization	1.513416	0.049784219
BP	G0:0061760	antifungal innate immune response	1.771605	0.049784219
BP	G0:0002753	cytoplasmic pattern recognition receptor	1.660377	0.049885398

ID	Description	NES	p. adjust
hsa03008	Ribosome biogenesis in eukaryotes	-2.60742	1.67E-08
hsa03010	Ribosome	-3.17607	1.67E-08
hsa04062	Chemokine signaling pathway	2.068376	4.30E-07
hsa04144	Endocytosis	1.999805	4.93E-07
hsa05135	Yersinia infection	2.116084	1.60E-06
hsa04140	Autophagy - animal	2.135355	2.82E-06
hsa05417	Lipid and atherosclerosis	1.919522	3.73E-06
hsa05131	Shigellosis	1.963015	5.31E-06
hsa05130	Pathogenic Escherichia coli infection	1.948429	5.72E-06
hsa05152	Tuberculosis	1.958181	5.72E-06
hsa04380	Osteoclast differentiation	2.073692	7.59E-06
hsa04666	Fc gamma R-mediated phagocytosis	2.084913	1.41E-05
hsa05132	Salmonella infection	1.848891	1.43E-05
hsa05332	Graft-versus-host disease	-2.27558	2.58E-05
hsa04010	MAPK signaling pathway	1.744597	2.58E-05
hsa04910	Insulin signaling pathway	1.978818	3.46E-05
hsa04670	Leukocyte transendothelial migration	1.982706	3.81E-05
hsa05167	Kaposi sarcoma-associated herpesvirus infection	1.837231	4.25E-05
hsa05330	Allograft rejection	-2.23756	5.24E-05
hsa03030	DNA replication	-2.24828	6.74E-05
hsa04621	NOD-like receptor signaling pathway	1.861818	7.31E-05
hsa04613	Neutrophil extracellular trap formation	1.929574	0.000108605
hsa01240	Biosynthesis of cofactors	-1.93385	0.000108605
hsa05134	Legionellosis	2.069067	0.00014478
hsa01200	Carbon metabolism	-1.93135	0.000241428
hsa05163	Human cytomegalovirus infection	1.679353	0.000251503
hsa04722	Neurotrophin signaling pathway	1.869587	0.000266966
hsa04068	FoxO signaling pathway	1.807813	0.000529446
hsa05320	Autoimmune thyroid disease	-1.98978	0.000569291
hsa05211	Renal cell carcinoma	1.981019	0.000656545
hsa00280	Valine, leucine and isoleucine degradation	-1.9931	0.000656545
hsa01230	Biosynthesis of amino acids	-1.95319	0.000656545
hsa04620	Toll-like receptor signaling pathway	1.80071	0.000656545
hsa04360	Axon guidance	1.649339	0.000668843
hsa03410	Base excision repair	-2.03435	0.00077144
hsa00620	Pyruvate metabolism	-1.9666	0.000938575
hsa00510	N-Glycan biosynthesis	-2.01975	0.000953878
hsa01232	Nucleotide metabolism	-1.9236	0.001003254
hsa05215	Prostate cancer	1.843717	0.001223018
hsa00270	Cysteine and methionine metabolism	-1.97534	0.001255089
hsa00020	Citrate cycle (TCA cycle)	-1.97671	0.001296859
hsa00190	Oxidative phosphorylation	-1.77951	0.00130223
hsa04940	Type I diabetes mellitus	-1.9798	0.00130223
hsa04071	Sphingolipid signaling pathway	1.776057	0.001431091
hsa05161	Hepatitis B	1.702399	0.001457527
hsa05205	Proteoglycans in cancer	1.642974	0.001457527
hsa04612	Antigen processing and presentation	-1.83819	0.001550377
hsa04146	Peroxisome	-1.83458	0.001598681
hsa04926	Relaxin signaling pathway	1.70784	0.001867863
hsa05340	Primary immunodeficiency	-1.96591	0.001909709
hsa04810	Regulation of actin cytoskeleton	1.611408	0.00227271
hsa05014	Amyotrophic lateral sclerosis	-1.53536	0.00229666
hsa01210	2-Oxocarboxylic acid metabolism	-1.97015	0.002743493

hsa04935 Growth hormone synthesis, secretion and action	1.67491	0.003445845
hsa05310 Asthma	-1.8884	0.003445845
hsa05020 Prion disease	-1.55724	0.003548798
hsa00230 Purine metabolism	-1.66488	0.003874134
hsa04662 B cell receptor signaling pathway	1.745775	0.004120228
hsa00630 Glyoxylate and dicarboxylate metabolism	-1.91781	0.004120228
hsa05220 Chronic myeloid leukemia	1.696445	0.004229077
hsa04931 Insulin resistance	1.683945	0.004229077
hsa05100 Bacterial invasion of epithelial cells	1.775038	0.004294641
hsa03420 Nucleotide excision repair	-1.85881	0.004342512
hsa05012 Parkinson disease	-1.55509	0.004865191
hsa03018 RNA degradation	-1.7741	0.005087597
hsa04110 Cell cycle	-1.63444	0.005584101
hsa04510 Focal adhesion	1.523282	0.005667805
hsa05140 Leishmaniasis	1.779401	0.005730375
hsa04928 Parathyroid hormone synthesis, secretion and action	1.595994	0.005749578
hsa04668 TNF signaling pathway	1.639969	0.005749578
hsa05142 Chagas disease	1.635852	0.006151579
hsa04672 Intestinal immune network for IgA production	-1.8057	0.006151579
hsa05235 PD-L1 expression and PD-1 checkpoint pathway in canc	1.638081	0.006151579
hsa05322 Systemic lupus erythematosus	-1.80593	0.006151579
hsa05416 Viral myocarditis	-1.75682	0.006192817
hsa05221 Acute myeloid leukemia	1.742481	0.006726442
hsa04664 Fc epsilon RI signaling pathway	1.724545	0.006950197
hsa03430 Mismatch repair	-1.89187	0.007225348
hsa04625 C-type lectin receptor signaling pathway	1.626186	0.007660931
hsa05170 Human immunodeficiency virus 1 infection	1.508034	0.007660931
hsa03013 Nucleocytoplasmic transport	-1.63539	0.007901943
hsa04520 Adherens junction	1.719249	0.008239661
hsa04012 ErbB signaling pathway	1.635693	0.009328305
hsa00062 Fatty acid elongation	-1.84424	0.009392366
hsa00500 Starch and sucrose metabolism	1.807843	0.009392366
hsa04657 IL-17 signaling pathway	1.596672	0.009752266
hsa05214 Glioma	1.6042	0.012163067
hsa04964 Proximal tubule bicarbonate reclamation	-1.8272	0.012483731
hsa03040 Spliceosome	-1.57365	0.012947273
hsa04611 Platelet activation	1.544252	0.013522315
hsa04915 Estrogen signaling pathway	1.46619	0.014191291
hsa03020 RNA polymerase	-1.80513	0.014287869
hsa04658 Th1 and Th2 cell differentiation	-1.56551	0.014287869
hsa03060 Protein export	-1.73161	0.014287869
hsa00562 Inositol phosphate metabolism	1.626801	0.01471108
hsa04330 Notch signaling pathway	1.643085	0.01471108
hsa05162 Measles	1.512134	0.01484314
hsa03460 Fanconi anemia pathway	-1.70312	0.016383516
hsa04610 Complement and coagulation cascades	1.589898	0.016383516
hsa05120 Epithelial cell signaling in Helicobacter pylori inf	1.616525	0.016395365
hsa05133 Pertussis	1.596499	0.016784772
hsa04150 mTOR signaling pathway	1.498761	0.016784772
hsa05212 Pancreatic cancer	1.544841	0.017125664
hsa04622 RIG-I-like receptor signaling pathway	1.601814	0.017870754
hsa00563 Glycosylphosphatidylinositol (GPI)-anchor biosynthes	-1.71412	0.018352249
hsa05171 Coronavirus disease - COVID-19	-1.40514	0.018466123
hsa04066 HIF-1 signaling pathway	1.517704	0.018753592

hsa04936 Alcoholic liver disease	1.483994	0.018938496
hsa05231 Choline metabolism in cancer	1.497537	0.019170195
hsa04210 Apoptosis	1.435798	0.019214748
hsa05223 Non-small cell lung cancer	1.580789	0.019214748
hsa05219 Bladder cancer	1.659469	0.019427011
hsa04145 Phagosome	1.425662	0.019427011
hsa01522 Endocrine resistance	1.476741	0.019427011
hsa04370 VEGF signaling pathway	1.559494	0.019723832
hsa05213 Endometrial cancer	1.554586	0.020022148
hsa04713 Circadian entrainment	1.501002	0.020655921
hsa05418 Fluid shear stress and atherosclerosis	1.419844	0.021679855
hsa04726 Serotonergic synapse	1.451655	0.02202587
hsa04064 NF-kappa B signaling pathway	1.488656	0.0235571
hsa05160 Hepatitis C	1.421436	0.023570315
hsa04015 Rap1 signaling pathway	1.403192	0.023570315
hsa00600 Sphingolipid metabolism	1.627284	0.023720414
hsa04070 Phosphatidylinositol signaling system	1.486859	0.023720414
hsa04120 Ubiquitin mediated proteolysis	-1.46699	0.025253344
hsa00513 Various types of N-glycan biosynthesis	-1.67889	0.025714432
hsa05164 Influenza A	1.390739	0.026614969
hsa00640 Propanoate metabolism	-1.60287	0.027674995
hsa04917 Prolactin signaling pathway	1.535434	0.027674995
hsa04912 GnRH signaling pathway	1.434856	0.028691129
hsa04720 Long-term potentiation	1.571626	0.029341071
hsa05207 Chemical carcinogenesis - receptor activation	1.394872	0.029341071
hsa00250 Alanine, aspartate and glutamate metabolism	-1.62295	0.029853713
hsa00071 Fatty acid degradation	-1.61342	0.029982882
hsa01521 EGFR tyrosine kinase inhibitor resistance	1.462491	0.031116511
hsa04921 Oxytocin signaling pathway	1.36424	0.032176654
hsa03250 Viral life cycle - HIV-1	1.539467	0.033026667
hsa01212 Fatty acid metabolism	-1.52718	0.034123938
hsa05166 Human T-cell leukemia virus 1 infection	-1.3532	0.034619527
hsa05016 Huntington disease	-1.31819	0.035526647
hsa00970 Aminoacyl-tRNA biosynthesis	-1.65643	0.036264652
hsa04932 Non-alcoholic fatty liver disease	-1.36577	0.041898115
hsa04919 Thyroid hormone signaling pathway	1.447655	0.041898115
hsa04371 Apelin signaling pathway	1.398367	0.041898115
hsa05321 Inflammatory bowel disease	-1.53925	0.043918692
hsa05202 Transcriptional misregulation in cancer	1.329303	0.044016262
hsa04024 cAMP signaling pathway	1.290588	0.045217232
hsa05210 Colorectal cancer	1.40134	0.048032531
hsa00450 Selenocompound metabolism	-1.55318	0.049116386



Supplementary Table 2: GSEA analysis of TGFBR3

ONTOLOGY ID	Description	NES	p. adjust
CC	G0:00003:organellar ribosome	2.612293	2.85E-08
BP	G0:00021:cytoplasmic translation	2.629894	2.85E-08
MF	G0:00037:structural constituent of ribosome	2.680175	2.85E-08
CC	G0:00057:mitochondrial inner membrane	2.071033	2.85E-08
CC	G0:00057:mitochondrial matrix	2.298291	2.85E-08
CC	G0:00057:mitochondrial ribosome	2.612293	2.85E-08
CC	G0:00058:ribosome	2.713538	2.85E-08
BP	G0:00063:rRNA processing	2.499351	2.85E-08
BP	G0:00063:tRNA metabolic process	2.413463	2.85E-08
BP	G0:00064:translation	2.277351	2.85E-08
BP	G0:00094:RNA modification	2.426652	2.85E-08
CC	G0:00159:large ribosomal subunit	2.519822	2.85E-08
BP	G0:00160:rRNA metabolic process	2.422192	2.85E-08
CC	G0:00198:organelle inner membrane	1.974234	2.85E-08
BP	G0:00226:ribonucleoprotein complex biogenesis	2.432245	2.85E-08
CC	G0:00226:cytosolic ribosome	2.473463	2.85E-08
CC	G0:00306:secretory granule membrane	-2.55935	2.85E-08
BP	G0:00344:ncRNA processing	2.561562	2.85E-08
BP	G0:00346:ncRNA metabolic process	2.499737	2.85E-08
BP	G0:00422:ribosome biogenesis	2.5093	2.85E-08
CC	G0:00425:specific granule	-2.74916	2.85E-08
CC	G0:00443:ribosomal subunit	2.764404	2.85E-08
CC	G0:00708:tertiary granule	-2.59352	2.85E-08
CC	G0:00987:mitochondrial protein-containing complex	2.408812	2.85E-08
BP	G0:01400:mitochondrial gene expression	2.468948	2.85E-08
MF	G0:01400:catalytic activity, acting on RNA	2.19432	2.85E-08
MF	G0:01406:catalytic activity, acting on a nucleic acid	2.221907	2.85E-08
CC	G0:00159:small ribosomal subunit	2.448753	6.44E-08
CC	G0:00355:specific granule membrane	-2.51752	9.37E-08
BP	G0:00325:mitochondrial translation	2.458651	1.63E-07
MF	G0:00167:transferase activity, transferring one-carbon group	2.165742	1.63E-07
CC	G0:19047:tertiary granule lumen	-2.62582	2.79E-07
MF	G0:00081:methyltransferase activity	2.168171	5.25E-07
BP	G0:00064:tRNA modification	2.408459	7.05E-07
CC	G0:00057:primary lysosome	-2.16915	9.50E-07
CC	G0:00425:azurophil granule	-2.16915	9.50E-07
MF	G0:01401:catalytic activity, acting on a tRNA	2.322695	1.04E-06
BP	G0:00080:tRNA processing	2.281759	1.11E-06
MF	G0:00037:mRNA binding	1.935886	3.57E-06
CC	G0:00347:secretory granule lumen	-1.82542	4.64E-06
CC	G0:00355:specific granule lumen	-2.42031	7.58E-06
BP	G0:00160:mRNA metabolic process	1.694913	8.70E-06
MF	G0:01406:ATP-dependent activity	1.728896	1.05E-05
MF	G0:00081:RNA methyltransferase activity	2.391205	1.05E-05
BP	G0:00322:methylation	1.870259	1.18E-05
CC	G0:00602:cytoplasmic vesicle lumen	-1.80468	1.26E-05
CC	G0:00319:vesicle lumen	-1.79602	1.26E-05
CC	G0:00226:cytosolic large ribosomal subunit	2.243658	2.19E-05
BP	G0:19011:carbohydrate derivative biosynthetic process	1.678136	2.28E-05
CC	G0:01010:ficolin-1-rich granule	-1.97819	2.43E-05
BP	G0:00015:RNA methylation	2.301766	2.50E-05

BP	G0:00064	regulation of translation	1.783519	4.28E-05
BP	G0:00434	macromolecule methylation	1.881515	4.44E-05
CC	G0:00003	organellar large ribosomal subunit	2.234325	4.47E-05
CC	G0:00057	(mitochondrial large ribosomal subunit	2.234325	4.47E-05
MF	G0:00087	S-adenosylmethionine-dependent methyltransferase activity	2.100635	4.91E-05
BP	G0:00606	regulation of vesicle-mediated transport	-1.5653	5.59E-05
BP	G0:00226	ribonucleoprotein complex assembly	2.010215	6.05E-05
BP	G0:00106	(posttranscriptional regulation of gene expression	1.701948	6.05E-05
MF	G0:00167	nucleotidyltransferase activity	2.059973	9.81E-05
BP	G0:00069	phagocytosis	-1.82026	0.000106
BP	G0:00342	regulation of cellular amide metabolic process	1.693855	0.000116
BP	G0:00718	ribonucleoprotein complex subunit organization	1.966981	0.000126
MF	G0:00043	helicase activity	1.965998	0.000129
CC	G0:00453	phagocytic vesicle	-1.96583	0.000145
MF	G0:00168	ATP hydrolysis activity	1.804965	0.000149
MF	G0:01400	catalytic activity, acting on DNA	1.860155	0.000163
BP	G0:00063	mRNA processing	1.732871	0.000177
BP	G0:00422	ribosomal large subunit biogenesis	2.160773	0.000181
CC	G0:00708	tertiary granule membrane	-2.18095	0.000273
BP	G0:00313	regulation of protein ubiquitination	1.834652	0.000273
BP	G0:00062	DNA repair	1.655212	0.00028
BP	G0:00083	RNA splicing	1.717709	0.000288
BP	G0:00422	ribosomal small subunit biogenesis	2.116762	0.000303
MF	G0:00198	rRNA binding	2.127536	0.000316
BP	G0:00003	RNA splicing, via transesterification reactions	1.801559	0.000322
BP	G0:00003	RNA splicing, via transesterification reactions with	1.77887	0.000379
BP	G0:00003	mRNA splicing, via spliceosome	1.77887	0.000379
CC	G0:00616	transferase complex, transferring phosphorus-containing	1.782696	0.000468
CC	G0:00003	organellar small ribosomal subunit	2.168346	0.000468
CC	G0:00057	(mitochondrial small ribosomal subunit	2.168346	0.000468
BP	G0:00326	interleukin-6 production	-1.90819	0.00057
BP	G0:00326	regulation of interleukin-6 production	-1.90819	0.00057
BP	G0:00324	response to lipopolysaccharide	-1.61138	0.00057
CC	G0:00057	early endosome	-1.58319	0.00057
MF	G0:00081	tRNA methyltransferase activity	2.175989	0.000597
BP	G0:00009	mitochondrial RNA metabolic process	2.219936	0.000701
MF	G0:00080	ATP-dependent activity, acting on DNA	1.956604	0.000701
BP	G0:00725	establishment of protein localization to organelle	1.630398	0.000701
BP	G0:00703	response to lipoteichoic acid	-2.27748	0.000701
BP	G0:00712	cellular response to lipoteichoic acid	-2.27748	0.000701
CC	G0:00301	transport vesicle	-1.55181	0.00074
BP	G0:00507	positive regulation of inflammatory response	-1.85845	0.00074
MF	G0:00037	double-stranded RNA binding	2.054628	0.000903
CC	G0:00100	endosome membrane	-1.49953	0.000984
BP	G0:00022	response to molecule of bacterial origin	-1.61742	0.001111
MF	G0:00353	Toll-like receptor binding	-2.27457	0.001132
CC	G0:01010	(ficolin-1-rich granule membrane	-2.15351	0.001132
CC	G0:00056	spliceosomal complex	1.797557	0.001138
CC	G0:00226	cytosolic small ribosomal subunit	2.107901	0.001211
BP	G0:00311	RNA 3'-end processing	1.972092	0.00127
BP	G0:00309	positive regulation of vascular endothelial growth factor	-2.29389	0.00127
CC	G0:00058	centrosome	1.559342	0.00127
BP	G0:00062	DNA replication	1.70252	0.00127
BP	G0:00000	ribosomal subunit export from nucleus	2.078593	0.00127

BP	G0:00337	ribosome localization	2.078593	0.00127
CC	G0:00308	RNA polymerase complex	1.922264	0.001293
BP	G0:00327	positive regulation of interleukin-6 production	-1.98773	0.001456
CC	G0:00550	nuclear DNA-directed RNA polymerase complex	1.975089	0.001515
BP	G0:00070	mitochondrion organization	1.592448	0.001654
BP	G0:00064	RNA localization	1.79124	0.001654
BP	G0:00192	cytokine-mediated signaling pathway	-1.50302	0.001686
BP	G0:19046	negative regulation of ubiquitin protein ligase activity	2.090477	0.001796
BP	G0:00304	tRNA methylation	2.06775	0.001831
MF	G0:00430	ribonucleoprotein complex binding	1.852943	0.00186
BP	G0:00309	regulation of vascular endothelial growth factor production	-2.22968	0.001875
CC	G0:00004	DNA-directed RNA polymerase complex	1.967831	0.002088
CC	G0:00355	azurophil granule membrane	-2.09225	0.002088
BP	G0:20003	regulation of reactive oxygen species metabolic process	-1.75832	0.002088
BP	G0:00510	positive regulation of DNA metabolic process	1.728517	0.002142
BP	G0:00507	regulation of inflammatory response	-1.57903	0.002187
MF	G0:00036	single-stranded DNA binding	1.835602	0.002329
MF	G0:00381	pattern recognition receptor activity	-2.25055	0.002353
CC	G0:00306	phagocytic vesicle membrane	-1.97252	0.002389
CC	G0:00988	inner mitochondrial membrane protein complex	1.827278	0.002601
MF	G0:00000	tRNA binding	1.994499	0.002777
BP	G0:19033	regulation of protein modification by small protein	1.706116	0.002818
MF	G0:00038	DNA-directed 5'-3' RNA polymerase activity	2.059923	0.002818
BP	G0:00508	antigen receptor-mediated signaling pathway	1.737762	0.002832
BP	G0:00322	telomere organization	1.826071	0.002832
CC	G0:00057	mitochondrial outer membrane	1.710937	0.002968
BP	G0:00711	DNA conformation change	1.732575	0.002968
CC	G0:00306	preribosome	1.973982	0.003069
BP	G0:00525	regulation of peptidase activity	-1.48542	0.003254
BP	G0:00718	protein-DNA complex subunit organization	1.737036	0.003331
BP	G0:00509	detection of stimulus involved in sensory perception	-1.46164	0.003344
BP	G0:00070	vacuole organization	-1.71334	0.003405
BP	G0:00714	rRNA-containing ribonucleoprotein complex export	12.044916	0.003448
CC	G0:00058	polysome	1.948621	0.003448
BP	G0:00327	positive regulation of interleukin-8 production	-2.024	0.003481
CC	G0:00057	vacuolar membrane	-1.49543	0.003554
BP	G0:00508	positive regulation of T cell activation	1.655404	0.003796
BP	G0:00453	cellular respiration	1.679277	0.003872
MF	G0:00340	5'-3' RNA polymerase activity	2.078574	0.003872
MF	G0:00977	RNA polymerase activity	2.078574	0.003872
BP	G0:00622	regulation of pattern recognition receptor signaling	-1.86624	0.003872
MF	G0:00016	ATPase activator activity	2.079943	0.003872
CC	G0:00301	endocytic vesicle	-1.53223	0.003937
BP	G0:00007	telomere maintenance	1.825963	0.004001
BP	G0:00068	mitochondrial transport	1.68338	0.004076
BP	G0:00725	reactive oxygen species metabolic process	-1.60316	0.004163
BP	G0:00525	regulation of endopeptidase activity	-1.46634	0.004616
CC	G0:01201	Sm-like protein family complex	1.902235	0.004616
BP	G0:00326	regulation of interleukin-8 production	-1.88631	0.004622
BP	G0:00022	myeloid leukocyte activation	-1.58348	0.004761
BP	G0:00422	ribosome assembly	1.948245	0.00487
BP	G0:00508	T cell receptor signaling pathway	1.794581	0.004912
BP	G0:00650	protein-DNA complex assembly	1.832353	0.00492
BP	G0:00326	interleukin-8 production	-1.87178	0.00492

BP	G0:00436:ncRNA 3'-end processing	2.006465	0.005348
CC	G0:00056:replication fork	1.97868	0.005372
BP	G0:00025:acute inflammatory response	-1.77714	0.005398
BP	G0:19033:regulation of cellular protein catabolic process	1.615432	0.005541
BP	G0:00510:positive regulation of NF-kappaB transcription factor activity	-1.66999	0.005616
BP	G0:00457:positive regulation of translation	1.803493	0.005627
BP	G0:00161:endosomal transport	-1.60755	0.005663
BP	G0:19035:regulation of secretion by cell	-1.39803	0.005663
BP	G0:00160:carbohydrate catabolic process	-1.66724	0.005663
CC	G0:00347:methyltransferase complex	1.841781	0.005847
BP	G0:00063:DNA recombination	1.632436	0.005859
BP	G0:00430:amino acid activation	2.012728	0.006088
BP	G0:00063:chromatin organization	1.549482	0.006149
BP	G0:00325:DNA duplex unwinding	1.844246	0.006443
CC	G0:00056:RNA polymerase III complex	2.012854	0.006443
BP	G0:00434:positive regulation of MAPK cascade	-1.41635	0.006489
BP	G0:00300:lymphocyte differentiation	1.549613	0.006677
CC	G0:00057:lysosomal membrane	-1.5024	0.006677
CC	G0:00988:lytic vacuole membrane	-1.5024	0.006677
BP	G0:00069:acute-phase response	-1.9885	0.006894
BP	G0:00062:DNA-dependent DNA replication	1.75562	0.007021
BP	G0:00096:response to wounding	-1.37799	0.007021
BP	G0:00091:purine nucleobase biosynthetic process	1.949258	0.007058
BP	G0:00027:positive regulation of natural killer cell mediated cytotoxicity	1.948803	0.007317
BP	G0:00063:transcription by RNA polymerase III	1.956057	0.007327
BP	G0:00346:nucleobase-containing compound catabolic process	1.526104	0.007342
BP	G0:00711:ribonucleoprotein complex localization	1.904191	0.007401
BP	G0:00427:defense response to bacterium	-1.50915	0.00745
MF	G0:00170:structural constituent of nuclear pore	2.028302	0.007508
BP	G0:20003:positive regulation of reactive oxygen species metabolism	-1.91775	0.007597
BP	G0:00108:telomere maintenance via telomere lengthening	1.856562	0.008063
MF	G0:00081:N-methyltransferase activity	1.823995	0.008187
CC	G0:00150:Cajal body	1.922828	0.008187
BP	G0:00170:protein import	1.657988	0.008211
BP	G0:00508:regulation of T cell activation	1.561714	0.008276
BP	G0:00510:regulation of DNA metabolic process	1.552138	0.008649
BP	G0:00304:maturation of SSU-rRNA	1.961566	0.008922
BP	G0:00512:positive regulation of lymphocyte activation	1.532842	0.009302
BP	G0:00158:peptide transport	-1.5617	0.009539
BP	G0:20005:positive regulation of DNA biosynthetic process	1.854199	0.009539
CC	G0:00319:organelle outer membrane	1.645768	0.009539
BP	G0:00400:negative regulation of multicellular organism growth	1.91868	0.010148
BP	G0:00165:histone modification	1.511384	0.010333
MF	G0:01406:ATP-dependent chromatin remodeler activity	1.971687	0.01035
BP	G0:00001:rRNA modification	1.966769	0.01035
BP	G0:00447:cell cycle phase transition	1.489067	0.010456
BP	G0:00022:pattern recognition receptor signaling pathway	-1.65124	0.010466
BP	G0:00162:iron-sulfur cluster assembly	1.989298	0.010476
BP	G0:00311:metallo-sulfur cluster assembly	1.989298	0.010476
BP	G0:00428:amide transport	-1.50396	0.010546
BP	G0:00427:DNA damage response, detection of DNA damage	1.957143	0.010918
CC	G0:00198:outer membrane	1.660674	0.010918
BP	G0:19030:positive regulation of leukocyte cell-cell adhesion	1.584474	0.010952
CC	G0:19048:ficolin-1-rich granule lumen	-1.63642	0.010985

BP	G0:00712:cellular response to molecule of bacterial origin	-1.59154	0.011115
BP	G0:00066:protein targeting	1.556152	0.011271
MF	G0:00046:protein serine/threonine kinase activity	-1.43398	0.011314
MF	G0:00706:proteasome binding	1.95494	0.011314
BP	G0:00021:cytoplasmic translational initiation	1.957502	0.011314
MF	G0:00170:snRNA binding	1.957708	0.011314
BP	G0:00301:water homeostasis	-1.8561	0.011314
BP	G0:00906:RNA localization to Cajal body	1.945722	0.011314
BP	G0:00906:telomerase RNA localization to Cajal body	1.945722	0.011314
BP	G0:00906:telomerase RNA localization	1.945722	0.011314
BP	G0:00906:RNA localization to nucleus	1.945722	0.011314
BP	G0:19048:regulation of telomerase RNA localization to Cajal body	1.945722	0.011314
BP	G0:00032:ventricular septum development	1.889372	0.011314
BP	G0:00071:leukocyte cell-cell adhesion	1.509629	0.011314
CC	G0:00986:chromosomal region	1.539158	0.01165
CC	G0:00975:spliceosomal snRNP complex	1.826787	0.011727
BP	G0:00059:monosaccharide metabolic process	-1.51431	0.011781
BP	G0:00065:cellular amino acid metabolic process	1.587605	0.011982
BP	G0:00066:acyl-CoA metabolic process	1.771238	0.012483
BP	G0:00353:thioester metabolic process	1.771238	0.012483
BP	G0:00069:autophagy	-1.387	0.012802
BP	G0:00619:process utilizing autophagic mechanism	-1.387	0.012802
BP	G0:19030:regulation of leukocyte cell-cell adhesion	1.533208	0.012802
MF	G0:00046:protein kinase activity	-1.34728	0.012832
BP	G0:00509:leukocyte migration	-1.39197	0.012923
BP	G0:00466:alpha-beta T cell activation	1.667162	0.013309
BP	G0:00714:ribonucleoprotein complex export from nucleus	1.871443	0.013398
BP	G0:19035:positive regulation of tumor necrosis factor superfamily 1 signaling pathway	-1.66652	0.01357
BP	G0:00465:negative regulation of viral entry into host cell	-2.07407	0.01357
BP	G0:00182:peptidyl-lysine modification	1.52701	0.01357
BP	G0:00461:purine ribonucleoside metabolic process	1.894182	0.013612
BP	G0:00712:cellular response to biotic stimulus	-1.51953	0.013612
BP	G0:00025:myeloid leukocyte differentiation	-1.50593	0.013612
BP	G0:00703:regulation of ERK1 and ERK2 cascade	-1.45324	0.013612
BP	G0:01200:plasma membrane bounded cell projection assembly	1.493475	0.013612
BP	G0:00009:mitochondrial RNA processing	1.936073	0.013612
CC	G0:00166:PML body	-1.66497	0.013963
BP	G0:00457:respiratory burst	-2.01036	0.014232
BP	G0:20000:regulation of ubiquitin-dependent protein catabolism	1.656666	0.014233
BP	G0:00511:nuclear export	1.696931	0.014241
BP	G0:00015:pseudouridine synthesis	1.92872	0.014301
MF	G0:00099:pseudouridine synthase activity	1.92872	0.014301
BP	G0:00300:lamellipodium assembly	1.768526	0.014301
BP	G0:00466:alpha-beta T cell differentiation	1.689557	0.014613
BP	G0:00323:DNA geometric change	1.778282	0.014862
BP	G0:00346:response to tumor necrosis factor	-1.50653	0.014862
BP	G0:00068:receptor-mediated endocytosis	-1.49335	0.014903
BP	G0:19030:regulation of proteolysis involved in cellular protein catabolism	1.608829	0.015195
BP	G0:00712:cellular response to lipopolysaccharide	-1.56296	0.015282
CC	G0:00057:late endosome	-1.51674	0.015581
BP	G0:00430:tRNA aminoacylation	1.949178	0.015581
BP	G0:00459:positive regulation of natural killer cell mediated cytotoxicity	1.932547	0.015746
BP	G0:00090:aerobic respiration	1.656183	0.015746
BP	G0:00070:vacuolar transport	-1.63227	0.015746

BP	G0:00342:negative regulation of cellular amide metabolic p	1.623982	0.015787
BP	G0:00725:purine-containing compound biosynthetic process	1.651646	0.016067
MF	G0:00900:translation regulator activity, nucleic acid bind	1.770518	0.016067
BP	G0:00985:detection of external biotic stimulus	-2.01876	0.016088
BP	G0:00650:intracellular protein transmembrane transport	1.834087	0.016103
BP	G0:00300:cell projection assembly	1.457101	0.016136
BP	G0:00027:regulation of peptide secretion	-1.46359	0.016832
CC	G0:00355:azurophil granule lumen	-1.7701	0.016832
BP	G0:00064:translational initiation	1.723199	0.016859
CC	G0:00057:vacuolar lumen	-1.56988	0.017122
BP	G0:00381:ERBB signaling pathway	-1.61864	0.01754
BP	G0:00027:peptide secretion	-1.50111	0.017649
BP	G0:00070:telomere maintenance via telomerase	1.799078	0.017711
BP	G0:00302:T cell differentiation	1.53883	0.017714
MF	G0:00081:translation factor activity, RNA binding	1.783448	0.017714
BP	G0:00071:epidermal growth factor receptor signaling pathway	-1.62533	0.017738
BP	G0:00550:nucleobase-containing small molecule metabolic pro	1.425079	0.017747
BP	G0:00096:response to mechanical stimulus	-1.50232	0.017747
BP	G0:00076:sensory perception of chemical stimulus	-1.35773	0.017747
BP	G0:00061:mitochondrial electron transport, NADH to ubiquin	1.86252	0.017747
BP	G0:00027:immune response-regulating cell surface receptor	1.548283	0.017863
BP	G0:00102:NADH dehydrogenase complex assembly	1.84833	0.017871
BP	G0:00329:mitochondrial respiratory chain complex I assembly	1.84833	0.017871
MF	G0:00515:iron-sulfur cluster binding	1.794784	0.01803
MF	G0:00515:metal cluster binding	1.794784	0.01803
CC	G0:00427:polysomal ribosome	1.86902	0.018318
BP	G0:00062:RNA-dependent DNA biosynthetic process	1.742375	0.018469
BP	G0:00621:regulation of mitochondrial gene expression	1.854891	0.018573
BP	G0:00427:ATP synthesis coupled electron transport	1.75028	0.018624
BP	G0:00427:mitochondrial ATP synthesis coupled electron trans	1.75028	0.018624
MF	G0:00048:aminoacyl-tRNA ligase activity	1.914745	0.018979
BP	G0:00064:tRNA aminoacylation for protein translation	1.914745	0.018979
MF	G0:00168:ligase activity, forming carbon-oxygen bonds	1.914745	0.018979
BP	G0:00064:protein folding	1.577543	0.018979
BP	G0:00330:regulation of chromosome organization	1.623186	0.018979
MF	G0:00510:chaperone binding	1.692075	0.018979
BP	G0:00717:tumor necrosis factor superfamily cytokine produc	-1.55685	0.018979
BP	G0:19035:regulation of tumor necrosis factor superfamily cy	-1.55685	0.018979
BP	G0:00514:regulation of ubiquitin-protein transferase activ	1.803547	0.019046
BP	G0:00095:detection of chemical stimulus	-1.36592	0.019046
BP	G0:00508:protein stabilization	1.577496	0.019161
BP	G0:00509:detection of chemical stimulus involved in sensory	-1.38313	0.019551
BP	G0:00380:NIK/NF-kappaB signaling	-1.59408	0.019551
BP	G0:00069:nucleocytoplasmic transport	1.515921	0.019551
BP	G0:00511:nuclear transport	1.515921	0.019551
BP	G0:00096:response to fungus	-1.79601	0.019598
BP	G0:00301:extracellular matrix organization	-1.43484	0.019646
BP	G0:00611:regulation of proteasomal protein catabolic proces	1.616988	0.019679
BP	G0:00326:interleukin-1 production	-1.61639	0.019805
BP	G0:00326:regulation of interleukin-1 production	-1.61639	0.019805
BP	G0:00511:glucose 6-phosphate metabolic process	-2.04069	0.019901
BP	G0:00421:T cell activation	1.420223	0.019901
BP	G0:00975:lamellipodium organization	1.729934	0.019911
BP	G0:00702:necrotic cell death	-1.83013	0.020196

MF	G0:00451	translation regulator activity	1.696708	0.020567
BP	G0:00066	NLS-bearing protein import into nucleus	1.920498	0.020784
BP	G0:00321	negative regulation of response to external stimulus	-1.38472	0.020784
BP	G0:00159	nucleobase-containing compound transport	1.568916	0.020784
MF	G0:00423	histone binding	1.574508	0.020861
BP	G0:00447	mitotic cell cycle phase transition	1.474571	0.020862
BP	G0:00160	snRNA metabolic process	1.845707	0.020869
BP	G0:00615	macrophage proliferation	-1.98702	0.021264
BP	G0:20000	negative regulation of ubiquitin-dependent protein catabolic process	1.865444	0.021264
BP	G0:00713	cellular response to tumor necrosis factor	-1.46972	0.021264
BP	G0:00703	ERK1 and ERK2 cascade	-1.43106	0.021376
BP	G0:00425	superoxide anion generation	-1.93079	0.021386
BP	G0:00109	positive regulation of peptidase activity	-1.50616	0.021882
BP	G0:00314	regulation of mRNA 3'-end processing	1.885433	0.021882
BP	G0:00510	positive regulation of secretion	-1.4294	0.021882
BP	G0:00076	sensory perception of smell	-1.37994	0.021882
BP	G0:00068	exocytosis	-1.4042	0.021882
BP	G0:00313	positive regulation of protein ubiquitination	1.650307	0.021882
BP	G0:00091	glycoprotein biosynthetic process	1.467248	0.022036
CC	G0:00002	nuclear chromosome	1.618597	0.022095
BP	G0:00461	nucleobase biosynthetic process	1.873925	0.022095
BP	G0:00229	respiratory electron transport chain	1.713405	0.022268
BP	G0:00025	production of molecular mediator involved in inflammation	-1.69575	0.022762
BP	G0:00322	positive regulation of telomere maintenance	1.838589	0.022957
MF	G0:01063	protein serine kinase activity	-1.37396	0.022957
BP	G0:00509	detection of chemical stimulus involved in sensory perception of smell	-1.38971	0.022957
BP	G0:00455	regulation of T cell differentiation	1.599022	0.022957
BP	G0:00064	RNA catabolic process	1.54591	0.022957
BP	G0:00109	regulation of necrotic cell death	-1.93436	0.022957
BP	G0:00066	protein targeting to mitochondrion	1.67848	0.022957
BP	G0:00342	positive regulation of cellular amide metabolic process	1.630139	0.022961
MF	G0:00168	ligase activity	1.661329	0.022975
BP	G0:00995	chemical synaptic transmission, postsynaptic	-1.63634	0.023052
BP	G0:00316	regulation of protein stability	1.496438	0.023052
BP	G0:00064	regulation of translational fidelity	1.873832	0.023166
CC	G0:00057	mitochondrial respiratory chain complex I	1.80169	0.023392
CC	G0:00309	NADH dehydrogenase complex	1.80169	0.023392
CC	G0:00452	respiratory chain complex I	1.80169	0.023392
BP	G0:00512	regulation of lymphocyte activation	1.427776	0.023392
BP	G0:00467	heterocycle catabolic process	1.443384	0.02341
CC	G0:00312	anchored component of membrane	-1.53636	0.02349
BP	G0:00004	maturation of LSU-rRNA	1.864305	0.023593
BP	G0:00022	natural killer cell mediated immunity	1.743862	0.023636
BP	G0:00095	detection of biotic stimulus	-1.96184	0.023861
BP	G0:00508	regulation of antigen receptor-mediated signaling	1.762465	0.023872
BP	G0:00326	tumor necrosis factor production	-1.52924	0.024427
BP	G0:00326	regulation of tumor necrosis factor production	-1.52924	0.024427
CC	G0:00305	small nuclear ribonucleoprotein complex	1.754131	0.024525
BP	G0:00465	regulation of viral entry into host cell	-1.90848	0.024786
BP	G0:00324	regulation of proteasomal ubiquitin-dependent protein catabolic process	1.630845	0.026294
BP	G0:00457	negative regulation of cell cycle	1.477271	0.026912
BP	G0:00712	cellular response to mechanical stimulus	-1.68499	0.027028
BP	G0:20003	positive regulation of endothelial cell apoptotic process	1.893688	0.027028
BP	G0:00989	postsynaptic actin cytoskeleton organization	-1.95298	0.027028

BP	G0:19001	extracellular regulation of signal transduction	-1.95247	0.027028
BP	G0:19001	extracellular negative regulation of signal transduction	-1.95247	0.027028
BP	G0:00990	plasma membrane invagination	-1.7019	0.027028
BP	G0:00324	negative regulation of proteasomal ubiquitin-dependent proteolysis	1.856577	0.027028
BP	G0:00000	ribosomal large subunit assembly	1.867489	0.027028
BP	G0:19039	negative regulation of viral life cycle	-1.915	0.027028
MF	G0:00082	protein methyltransferase activity	1.708546	0.027383
CC	G0:00019	uropod	-2.0182	0.027383
CC	G0:00312	cell trailing edge	-2.0182	0.027383
MF	G0:01202	acyl-CoA binding	1.870055	0.028173
BP	G0:19025	regulation of neutrophil activation	-2.01469	0.028173
BP	G0:00070	lysosomal transport	-1.60403	0.028653
BP	G0:00432	leukocyte degranulation	-1.71579	0.029248
BP	G0:00452	external encapsulating structure organization	-1.42669	0.029248
BP	G0:00423	keratan sulfate metabolic process	-1.9685	0.02954
BP	G0:00430	positive regulation of programmed cell death	-1.309	0.02954
MF	G0:00037	RNA helicase activity	1.697023	0.029615
MF	G0:00036	DNA helicase activity	1.714078	0.030148
MF	G0:00501	NADH dehydrogenase (quinone) activity	1.87414	0.030256
CC	G0:00315	microvillus membrane	-1.90032	0.030456
BP	G0:00900	regulation of peptide transport	-1.48757	0.030519
BP	G0:00725	purine-containing compound metabolic process	1.436936	0.030519
BP	G0:00430	extracellular structure organization	-1.43014	0.03061
BP	G0:19033	positive regulation of protein modification by small molecule	1.605786	0.030643
BP	G0:00331	mitochondrial respiratory chain complex assembly	1.689648	0.030876
BP	G0:19905	mitochondrial transmembrane transport	1.744277	0.030886
BP	G0:00513	kinetochore organization	1.828437	0.031197
BP	G0:00327	positive regulation of tumor necrosis factor production	-1.6238	0.031336
BP	G0:00064	mRNA catabolic process	1.546311	0.031409
MF	G0:00049	olfactory receptor activity	-1.3511	0.031414
BP	G0:00321	positive regulation of response to external stimulus	-1.36744	0.031414
BP	G0:00194	aromatic compound catabolic process	1.402098	0.031418
BP	G0:00196	aerobic electron transport chain	1.722794	0.031418
BP	G0:00481	regulation of synaptic plasticity	-1.49251	0.031418
MF	G0:00168	isomerase activity	1.615787	0.031418
BP	G0:00063	chromatin remodeling	1.585768	0.031418
BP	G0:00902	regulation of peptide hormone secretion	-1.45727	0.031418
BP	G0:00064	protein methylation	1.596417	0.031527
BP	G0:00082	protein alkylation	1.596417	0.031527
CC	G0:00007	condensed chromosome	1.537047	0.031716
BP	G0:00000	G1/S transition of mitotic cell cycle	1.55407	0.031716
BP	G0:00506	nucleic acid transport	1.574732	0.031716
BP	G0:00506	RNA transport	1.574732	0.031716
CC	G0:00421	T cell receptor complex	1.879053	0.031716
CC	G0:00007	chromosome, centromeric region	1.538974	0.032637
BP	G0:00091	purine ribonucleotide biosynthetic process	1.573066	0.032804
BP	G0:00507	regulation of phagocytosis	-1.62	0.032804
BP	G0:00341	regulation of toll-like receptor signaling pathway	-1.66455	0.033121
MF	G0:00551	ubiquitin-protein transferase regulator activity	1.803816	0.034087
BP	G0:00083	endosome to lysosome transport	-1.82963	0.034087
BP	G0:00300	peptide hormone secretion	-1.43917	0.034087
MF	G0:00037	transcription coregulator activity	1.398887	0.034098
BP	G0:00600	excitatory postsynaptic potential	-1.55372	0.034202
BP	G0:00327	positive regulation of interleukin-1 production	-1.65787	0.034282



BP	G0:00456:regulation of lymphocyte differentiation	1.517291 0.034568
MF	G0:00037:translation initiation factor activity	1.790164 0.03487
BP	G0:20012:positive regulation of chromosome organization	1.680386 0.034931
CC	G0:00080:synaptic vesicle	-1.41938 0.034931
CC	G0:00017:immunological synapse	1.788947 0.034997
BP	G0:00603:cell chemotaxis	-1.39766 0.035232
BP	G0:00362:granulocyte activation	-1.82713 0.035232
BP	G0:00714:cellular response to external stimulus	-1.39979 0.035315
BP	G0:00345:centromere complex assembly	1.826041 0.036273
BP	G0:00361:cellular response to platelet-derived growth factor	1.785329 0.036273
BP	G0:00985:detection of other organism	-1.94676 0.036273
MF	G0:00510:unfolded protein binding	1.620385 0.03635
CC	G0:00092:nucleoid	1.799681 0.03635
CC	G0:00426:mitochondrial nucleoid	1.799681 0.03635
CC	G0:00704:respirasome	1.658227 0.03635
BP	G0:00421:neutrophil activation	-1.90941 0.03635
BP	G0:00070:lysosome organization	-1.70873 0.03635
BP	G0:00801:lytic vacuole organization	-1.70873 0.03635
BP	G0:19031:mononuclear cell differentiation	1.416788 0.03635
BP	G0:00433:regulation of leukocyte degranulation	-1.81972 0.03635
MF	G0:00039:NADH dehydrogenase activity	1.799153 0.03635
BP	G0:00452:mRNA cis splicing, via spliceosome	1.808774 0.036481
CC	G0:00057:mitochondrial respirasome	1.638039 0.036571
BP	G0:00180:peptidyl-lysine methylation	1.651982 0.036625
BP	G0:00349:histone lysine methylation	1.651982 0.036625
BP	G0:00332:response to vitamin D	-1.79931 0.036625
BP	G0:00028:negative regulation of response to biotic stimulus	-1.53923 0.036981
BP	G0:00326:interleukin-1 beta production	-1.55667 0.037343
BP	G0:00326:regulation of interleukin-1 beta production	-1.55667 0.037343
BP	G0:00336:cell-cell adhesion mediated by integrin	1.855766 0.037343
BP	G0:00061:oxidative phosphorylation	1.700726 0.037343
BP	G0:00701:positive regulation of mitochondrial translation	1.790969 0.037381
BP	G0:00063:DNA-templated transcription, initiation	1.646241 0.037381
BP	G0:00705:protein localization to mitochondrion	1.608576 0.037461
BP	G0:19011:regulation of ERBB signaling pathway	-1.64801 0.03806
BP	G0:00701:regulation of mitochondrial translation	1.858693 0.038149
BP	G0:00420:regulation of epidermal growth factor receptor signaling	-1.64458 0.038149
BP	G0:00510:positive regulation of DNA-binding transcription factor activity	-1.43377 0.038286
BP	G0:00064:regulation of translational initiation	1.65191 0.038794
BP	G0:00024:immune response-activating cell surface receptor signaling	1.505796 0.038794
BP	G0:00027:immune response-activating signal transduction	1.505796 0.038794
BP	G0:00512:establishment of RNA localization	1.589566 0.038927
BP	G0:19048:positive regulation of telomerase RNA localization	1.821215 0.038992
BP	G0:00468:hormone secretion	-1.37994 0.039143
MF	G0:00170:U6 snRNA binding	1.819722 0.03931
CC	G0:00314:cullin-RING ubiquitin ligase complex	1.575607 0.039554
MF	G0:00166:oxidoreductase activity, acting on NAD(P)H, quinone	1.701269 0.039813
BP	G0:00027:regulation of natural killer cell mediated immunity	1.736683 0.040407
CC	G0:00710:catalytic step 2 spliceosome	1.695098 0.040407
BP	G0:00305:leukocyte chemotaxis	-1.39608 0.040924
MF	G0:00081:ATP-dependent activity, acting on RNA	1.680876 0.04101
BP	G0:00480:vascular endothelial growth factor receptor signaling	-1.72795 0.041416
BP	G0:00726:establishment of protein localization to mitochondrion	1.562095 0.041776
BP	G0:00508:multicellular organismal water homeostasis	-1.70375 0.041817

BP	G0:00723:signal transduction by p53 class mediator	1.574618	0.041852
BP	G0:00065:GPI anchor metabolic process	1.728899	0.041852
BP	G0:00306:regulation of vitamin metabolic process	1.784448	0.041973
BP	G0:20012:positive regulation of extrinsic apoptotic signal	-1.77672	0.042161
BP	G0:00340:stress granule assembly	1.787221	0.042174
BP	G0:00361:response to platelet-derived growth factor	1.803531	0.042303
BP	G0:00442:cellular nitrogen compound catabolic process	1.397621	0.042395
BP	G0:00161:snRNA processing	1.791346	0.042571
BP	G0:00171:negative regulation of translation	1.584208	0.042571
CC	G0:00357:ribonucleoprotein granule	1.455017	0.042571
BP	G0:00159:energy derivation by oxidation of organic compound	1.461899	0.042957
CC	G0:00056:nuclear envelope	1.404096	0.042974
MF	G0:00336:sialic acid binding	-1.84891	0.042974
BP	G0:19012:regulation of NIK/NF-kappaB signaling	-1.60332	0.043079
BP	G0:00229:electron transport chain	1.54731	0.043086
BP	G0:00061:purine nucleotide biosynthetic process	1.548693	0.043181
BP	G0:00514:negative regulation of ubiquitin-protein transferase	1.797897	0.043181
BP	G0:19046:regulation of ubiquitin protein ligase activity	1.784806	0.0435
BP	G0:00196:ribose phosphate metabolic process	1.402825	0.0435
MF	G0:00039:NAD(P)H dehydrogenase (quinone) activity	1.781602	0.043935
BP	G0:00507:regulation of peptidyl-tyrosine phosphorylation	-1.40256	0.043948
CC	G0:00056:U2 snRNP	1.794924	0.044544
BP	G0:00301:sphingolipid catabolic process	-1.83704	0.044692
BP	G0:00002:protein polyubiquitination	1.475424	0.044776
BP	G0:00523:modulation by symbiont of entry into host	-1.77075	0.044776
BP	G0:00600:regulation of postsynaptic membrane potential	-1.47499	0.044776
BP	G0:00901:establishment of protein localization to membrane	1.491984	0.044776
CC	G0:00056:U2-type spliceosomal complex	1.663068	0.044778
BP	G0:00024:neutrophil mediated immunity	-1.85584	0.044778
BP	G0:00300:myeloid cell differentiation	-1.34674	0.044778
BP	G0:00018:NK T cell differentiation	1.769919	0.044778
MF	G0:00055:GTP binding	1.417068	0.044778
MF	G0:00019:retinoic acid binding	-1.8385	0.044823
BP	G0:00165:histone methylation	1.591241	0.044823
BP	G0:00430:positive regulation of apoptotic process	-1.27811	0.04483
MF	G0:00515:4 iron, 4 sulfur cluster binding	1.765784	0.045061
BP	G0:00450:regulated exocytosis	-1.3939	0.045335
BP	G0:20002:regulation of DNA biosynthetic process	1.610298	0.045335
BP	G0:00322:positive regulation of actin filament bundle assembly	1.681071	0.0454
BP	G0:00463:ribose phosphate biosynthetic process	1.527169	0.0454
BP	G0:00027:MyD88-dependent toll-like receptor signaling pathway	-1.82514	0.0454
BP	G0:19050:autophagosome organization	-1.61928	0.0454
BP	G0:00086:carbohydrate transport	-1.46495	0.0454
BP	G0:00063:transcription by RNA polymerase I	1.710575	0.04544
BP	G0:00062:base-excision repair	1.734123	0.04544
BP	G0:00514:regulation of stress fiber assembly	1.611789	0.045789
BP	G0:00092:ribonucleotide biosynthetic process	1.511387	0.045789
BP	G0:00338:nucleoside bisphosphate biosynthetic process	1.621971	0.045789
BP	G0:00340:ribonucleoside bisphosphate biosynthetic process	1.621971	0.045789
BP	G0:00340:purine nucleoside bisphosphate biosynthetic process	1.621971	0.045789
MF	G0:00081:NADH dehydrogenase (ubiquinone) activity	1.819035	0.045885
CC	G0:00703:exocytic vesicle	-1.42258	0.046736
BP	G0:00103:membrane invagination	-1.6203	0.047239
BP	G0:00352:ionotropic glutamate receptor signaling pathway	-1.81789	0.047239

CC	G0:00310	platelet alpha granule membrane	-1.86972	0.048014
BP	G0:00550	monovalent inorganic cation homeostasis	-1.45278	0.048222
CC	G0:00988	respiratory chain complex	1.634159	0.048222
BP	G0:00700	glycosylation	1.461755	0.048222
BP	G0:00459	positive regulation of transcription by RNA polymerase	1.783692	0.048222
BP	G0:00083	associative learning	-1.58773	0.048222
BP	G0:00463	glucose import	-1.61654	0.048222
BP	G0:00450	DNA-dependent DNA replication maintenance of fidelity	1.740145	0.048222
BP	G0:19019	regulation of cell cycle phase transition	1.421751	0.048222
MF	G0:00480	receptor ligand activity	-1.28555	0.048222
BP	G0:20012	positive regulation of apoptotic signaling pathway	-1.47601	0.048222
BP	G0:00311	rRNA methylation	1.76291	0.048222
BP	G0:00068	superoxide metabolic process	-1.61373	0.04853
BP	G0:00025	cytokine production involved in inflammatory response	-1.71409	0.04853
BP	G0:19000	regulation of cytokine production involved in inflammation	-1.71409	0.04853
BP	G0:20001	regulation of cysteine-type endopeptidase activity	-1.40457	0.04853
BP	G0:00338	nucleoside bisphosphate metabolic process	1.544124	0.04853
BP	G0:00338	ribonucleoside bisphosphate metabolic process	1.544124	0.04853
BP	G0:00340	purine nucleoside bisphosphate metabolic process	1.544124	0.04853
CC	G0:01010	chaperone complex	1.769228	0.048716
MF	G0:00086	rRNA methyltransferase activity	1.757058	0.048716
MF	G0:01401	catalytic activity, acting on a rRNA	1.757058	0.048716
BP	G0:00182	peptidyl-tyrosine modification	-1.31783	0.049643
MF	G0:00037	transcription coactivator activity	1.434258	0.0498
BP	G0:00436	engulfment of apoptotic cell	-1.82787	0.0498
BP	G0:00432	regulation of cysteine-type endopeptidase activity	-1.42618	0.049882
BP	G0:00718	protein transmembrane transport	1.623751	0.04992

ID	Description	NES	p. adjust
hsa03010	Ribosome	2.682161	3.33E-08
hsa04380	Osteoclast differentiation	-2.15244	1.82E-05
hsa03008	Ribosome biogenesis in eukaryotes	2.240244	1.82E-05
hsa05152	Tuberculosis	-1.86382	9.29E-05
hsa05168	Herpes simplex virus 1 infection	1.6624	0.000101
hsa04142	Lysosome	-1.95555	0.000117
hsa05167	Kaposi sarcoma-associated herpesvirus infection	-1.77751	0.00016
hsa04145	Phagosome	-1.8918	0.000193
hsa04613	Neutrophil extracellular trap formation	-1.96325	0.000343
hsa03040	Spliceosome	1.901131	0.00052
hsa03013	Nucleocytoplasmic transport	1.831058	0.001607
hsa03020	RNA polymerase	2.018474	0.001857
hsa05130	Pathogenic Escherichia coli infection	-1.64415	0.001899
hsa00970	Aminoacyl-tRNA biosynthesis	2.041089	0.002404
hsa04910	Insulin signaling pathway	-1.67233	0.003438
hsa03030	DNA replication	1.93906	0.003973
hsa04110	Cell cycle	1.741241	0.004662
hsa04740	Olfactory transduction	-1.43179	0.004842
hsa04620	Toll-like receptor signaling pathway	-1.73715	0.005609
hsa03420	Nucleotide excision repair	1.838431	0.00773
hsa00620	Pyruvate metabolism	1.789766	0.010893
hsa04330	Notch signaling pathway	-1.78003	0.015942
hsa03060	Protein export	1.886577	0.016843
hsa03018	RNA degradation	1.758213	0.016843
hsa04666	Fc gamma R-mediated phagocytosis	-1.67605	0.016843
hsa05132	Salmonella infection	-1.43179	0.016843
hsa04610	Complement and coagulation cascades	-1.66578	0.016843
hsa04062	Chemokine signaling pathway	-1.50034	0.016843
hsa04668	TNF signaling pathway	-1.61924	0.016843
hsa01240	Biosynthesis of cofactors	1.564	0.017977
hsa05340	Primary immunodeficiency	1.777018	0.018288
hsa05417	Lipid and atherosclerosis	-1.42236	0.018964
hsa04080	Neuroactive ligand-receptor interaction	-1.36368	0.018964
hsa04621	NOD-like receptor signaling pathway	-1.52036	0.019571
hsa00563	Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	1.777603	0.019987
hsa00280	Valine, leucine and isoleucine degradation	1.682865	0.019987
hsa04662	B cell receptor signaling pathway	-1.63745	0.019987
hsa04010	MAPK signaling pathway	-1.40411	0.019987
hsa00100	Steroid biosynthesis	1.824813	0.021039
hsa04014	Ras signaling pathway	-1.42436	0.028971
hsa05164	Influenza A	-1.4694	0.031595
hsa04120	Ubiquitin mediated proteolysis	1.536454	0.031866
hsa00600	Sphingolipid metabolism	-1.76792	0.035587
hsa04015	Rap1 signaling pathway	-1.38213	0.035587
hsa05160	Hepatitis C	-1.42892	0.038497
hsa05163	Human cytomegalovirus infection	-1.37956	0.039612
hsa04140	Autophagy - animal	-1.4133	0.043605
hsa04930	Type II diabetes mellitus	-1.6507	0.044905
hsa00270	Cysteine and methionine metabolism	1.611843	0.045035
hsa00510	N-Glycan biosynthesis	1.639136	0.045035
hsa04216	Ferroptosis	1.638455	0.045099
hsa04650	Natural killer cell mediated cytotoxicity	1.49118	0.045459
hsa03430	Mismatch repair	1.701755	0.045459

hsa04625 C-type lectin receptor signaling pathway	-1.47963	0.046403
hsa05134 Legionellosis	-1.60456	0.046774
hsa05133 Pertussis	-1.55543	0.046966
hsa05332 Graft-versus-host disease	1.590134	0.047688

**Supplementary Table 3: GSEA analysis of S100A12**

ONTOLOGY ID	Description	NES	p. adjust
MF	G0:00037:structural constituent of ribosome	-2.52178	4.53E-08
CC	G0:00057:mitochondrial inner membrane	-2.39514	4.53E-08
CC	G0:00057:mitochondrial matrix	-2.44293	4.53E-08
CC	G0:00058:ribosome	-2.42282	4.53E-08
BP	G0:00063:rRNA processing	-2.64504	4.53E-08
BP	G0:00064:translation	-2.01344	4.53E-08
BP	G0:00160:rRNA metabolic process	-2.56589	4.53E-08
CC	G0:00198:organelle inner membrane	-2.22842	4.53E-08
BP	G0:00226:ribonucleoprotein complex biogenesis	-2.3704	4.53E-08
CC	G0:00306:secretory granule membrane	2.153923	4.53E-08
CC	G0:00306:preribosome	-2.8536	4.53E-08
BP	G0:00344:ncRNA processing	-2.54198	4.53E-08
BP	G0:00346:ncRNA metabolic process	-2.42494	4.53E-08
BP	G0:00422:ribosome biogenesis	-2.54058	4.53E-08
CC	G0:00443:ribosomal subunit	-2.56452	4.53E-08
CC	G0:00987:mitochondrial protein-containing complex	-2.57347	4.53E-08
MF	G0:01406:catalytic activity, acting on a nucleic acid	-1.91149	4.53E-08
MF	G0:00198:rRNA binding	-2.64561	7.25E-08
BP	G0:00063:tRNA metabolic process	-2.31403	2.14E-07
CC	G0:00708:tertiary granule	2.248922	2.68E-07
MF	G0:01400:catalytic activity, acting on RNA	-2.01199	2.83E-07
CC	G0:00003:organellar ribosome	-2.46395	4.58E-07
CC	G0:00057:mitochondrial ribosome	-2.46395	4.58E-07
CC	G0:00159:large ribosomal subunit	-2.27566	2.14E-06
BP	G0:00091:nucleoside monophosphate biosynthetic process	-2.59401	2.25E-06
BP	G0:00080:tRNA processing	-2.32236	2.35E-06
BP	G0:00000:autophagosome assembly	2.356707	4.48E-06
CC	G0:00159:small ribosomal subunit	-2.40266	9.69E-06
BP	G0:00325:mitochondrial translation	-2.38176	1.18E-05
BP	G0:00160:vesicle organization	1.889631	1.49E-05
BP	G0:00162:macroautophagy	1.894871	1.54E-05
CC	G0:00425:specific granule	2.102103	1.61E-05
BP	G0:19050:autophagosome organization	2.267778	1.93E-05
BP	G0:20007:regulation of autophagosome assembly	2.408393	3.48E-05
BP	G0:01400:mitochondrial gene expression	-2.28267	4.03E-05
BP	G0:00422:ribosomal large subunit biogenesis	-2.36069	4.62E-05
BP	G0:00091:ribonucleoside monophosphate biosynthetic process	-2.47308	4.62E-05
BP	G0:00550:nucleobase-containing small molecule metabolic process	-1.66068	6.00E-05
CC	G0:00988:inner mitochondrial membrane protein complex	-2.17688	6.30E-05
CC	G0:00320:small-subunit processome	-2.41497	9.77E-05
CC	G0:00057:primary lysosome	2.018059	0.000104
CC	G0:00425:azurophil granule	2.018059	0.000104
BP	G0:00102:endomembrane system organization	1.734242	0.000143
BP	G0:00719:regulation of protein serine/threonine kinase activity	1.740105	0.000222
BP	G0:00067:nucleoside phosphate metabolic process	-1.66589	0.000222
CC	G0:00003:organellar large ribosomal subunit	-2.26954	0.000222
CC	G0:00057:mitochondrial large ribosomal subunit	-2.26954	0.000222
BP	G0:00091:nucleoside monophosphate metabolic process	-2.2254	0.000236
BP	G0:00310:positive regulation of histone deacetylation	2.28656	0.000236
BP	G0:00091:nucleotide metabolic process	-1.64809	0.000285
BP	G0:00091:purine nucleoside monophosphate biosynthetic process	-2.3489	0.000301

BP	G0:00094:RNA modification	-1.98627	0.000384
BP	G0:00903:nucleic acid phosphodiester bond hydrolysis	-1.84517	0.000418
CC	G0:00306:90S preribosome	-2.3214	0.00048
BP	G0:00064:tRNA modification	-2.17735	0.000556
BP	G0:00725:purine-containing compound metabolic process	-1.66801	0.000556
BP	G0:00226:ribonucleoprotein complex assembly	-1.91532	0.000556
MF	G0:01401:catalytic activity, acting on a tRNA	-2.08021	0.000556
BP	G0:00069:autophagy	1.630111	0.000607
BP	G0:00619:process utilizing autophagic mechanism	1.630111	0.000607
BP	G0:00061:purine nucleotide metabolic process	-1.65419	0.000622
BP	G0:00304:maturation of SSU-rRNA	-2.28474	0.000837
MF	G0:00192:nucleobase-containing compound kinase activity	-2.28826	0.00086
CC	G0:00100:endosome membrane	1.592851	0.000997
CC	G0:00306:preribosome, large subunit precursor	-2.29183	0.001258
CC	G0:00226:cytosolic ribosome	-1.97748	0.001331
MF	G0:00430:ribonucleoprotein complex binding	-1.9044	0.001367
BP	G0:19021:regulation of organelle assembly	1.843232	0.001546
BP	G0:00062:pyrimidine nucleotide biosynthetic process	-2.24218	0.00156
BP	G0:00091:purine nucleobase biosynthetic process	-2.228	0.001726
BP	G0:00004:maturation of SSU-rRNA from tricistronic rRNA tra	-2.30745	0.001736
BP	G0:00461:pigment biosynthetic process	-2.09447	0.001736
BP	G0:00060:generation of precursor metabolites and energy	-1.57521	0.001736
BP	G0:00066:NLS-bearing protein import into nucleus	2.165203	0.001817
BP	G0:00422:ribosomal small subunit biogenesis	-2.08539	0.001841
BP	G0:00718:ribonucleoprotein complex subunit organization	-1.84226	0.001841
BP	G0:00071:transmembrane receptor protein serine/threonine k	1.660941	0.001845
BP	G0:00331:mitochondrial respiratory chain complex assembly	-2.10043	0.001908
MF	G0:00000:tRNA binding	-2.2352	0.001974
BP	G0:00622:positive regulation of pattern recognition recept	2.155095	0.001997
BP	G0:00062:pyrimidine nucleotide metabolic process	-2.13564	0.002122
BP	G0:00440:regulation of vacuole organization	2.143875	0.00236
MF	G0:00053:ATP transmembrane transporter activity	-2.19329	0.002637
BP	G0:00023:immunoglobulin production	-1.8527	0.002915
BP	G0:00022:myeloid leukocyte activation	1.679626	0.002915
MF	G0:00197:ubiquitin-like protein transferase activity	1.5909	0.002915
CC	G0:00092:nucleoid	-2.1111	0.002934
CC	G0:00426:mitochondrial nucleoid	-2.1111	0.002934
BP	G0:00070:actin filament organization	1.600024	0.002977
BP	G0:00900:regulation of transmembrane receptor protein seri	1.689892	0.003122
BP	G0:00028:positive regulation of response to biotic stimulus	1.799353	0.00313
BP	G0:00064:regulation of translation	-1.61271	0.00317
CC	G0:00355:specific granule membrane	1.960657	0.003427
BP	G0:00091:ribonucleoside monophosphate metabolic process	-2.03726	0.003427
MF	G0:00192:kinase activator activity	1.884049	0.003554
BP	G0:00433:positive T cell selection	-2.15263	0.0036
CC	G0:00355:azurophil granule membrane	2.084076	0.0036
MF	G0:00039:G protein activity	2.10664	0.003602
BP	G0:00461:nucleobase biosynthetic process	-2.20807	0.003989
BP	G0:00427:defense response to bacterium	1.704697	0.003989
BP	G0:00090:aerobic respiration	-1.77422	0.003989
BP	G0:00021:cytoplasmic translation	-1.85391	0.004103
BP	G0:00341:positive regulation of toll-like receptor signal	2.072177	0.004112
BP	G0:00985:detection of external biotic stimulus	2.108185	0.004289
CC	G0:00453:phagocytic vesicle	1.775562	0.004289

BP	G0:00091	purine nucleoside monophosphate metabolic process	-2.09718	0.004289
MF	G0:00501	NAD(P)+ nucleosidase activity	2.100337	0.004289
MF	G0:00618	NAD+ nucleotidase, cyclic ADP-ribose generating	2.100337	0.004289
CC	G0:00057	early endosome	1.60174	0.004289
CC	G0:00003	organellar small ribosomal subunit	-2.18547	0.004289
CC	G0:00057	mitochondrial small ribosomal subunit	-2.18547	0.004289
MF	G0:00167	phosphotransferase activity, for other substituted	-2.15057	0.004289
BP	G0:01200	regulation of plasma membrane bounded cell projec	1.777668	0.004289
BP	G0:00422	ribosome assembly	-2.11342	0.004289
MF	G0:00435	protein serine/threonine kinase activator activity	2.03278	0.004315
MF	G0:00045	nuclease activity	-1.70438	0.004343
CC	G0:01010	ficolin-1-rich granule	1.749157	0.004358
BP	G0:00196	ribose phosphate metabolic process	-1.56022	0.004514
BP	G0:00095	detection of biotic stimulus	2.109352	0.004514
BP	G0:00072	small GTPase mediated signal transduction	1.519223	0.004565
CC	G0:00226	cytosolic small ribosomal subunit	-2.09145	0.004605
BP	G0:00604	regulation of cell projection assembly	1.772796	0.004651
BP	G0:00106	posttranscriptional regulation of gene expression	-1.54665	0.004891
MF	G0:00515	iron-sulfur cluster binding	-1.97432	0.004891
MF	G0:00515	metal cluster binding	-1.97432	0.004891
MF	G0:00166	oxidoreductase activity, acting on the CH-OH group	-1.79995	0.004891
MF	G0:00039	GTPase activity	1.610058	0.00495
BP	G0:00091	purine ribonucleoside monophosphate biosynthetic p	-2.17819	0.005039
BP	G0:00719	positive regulation of protein serine/threonine k	1.685881	0.0051
CC	G0:00347	secretory granule lumen	1.611183	0.005289
BP	G0:00004	cleavage involved in rRNA processing	-2.1771	0.005289
BP	G0:00092	ribonucleotide metabolic process	-1.56134	0.00557
BP	G0:00712	cellular response to biotic stimulus	1.641524	0.005691
MF	G0:00616	ubiquitin-like protein ligase activity	1.595531	0.00577
BP	G0:00421	neutrophil activation	2.061446	0.00587
BP	G0:00070	vacuole organization	1.758238	0.005911
BP	G0:00060	tricarboxylic acid cycle	-2.12791	0.005965
BP	G0:00313	positive regulation of cellular catabolic process	1.526088	0.005965
BP	G0:19012	nucleoside phosphate biosynthetic process	-1.6686	0.005965
BP	G0:00324	Rap protein signal transduction	2.058076	0.005965
BP	G0:00516	organelle localization	1.518887	0.006017
BP	G0:00725	purine-containing compound biosynthetic process	-1.66231	0.00606
MF	G0:00050	GTPase activator activity	1.543719	0.006179
BP	G0:00453	cellular respiration	-1.69111	0.006193
CC	G0:01010	ficolin-1-rich granule membrane	1.974422	0.006298
BP	G0:00182	peptidyl-threonine modification	1.774579	0.006298
BP	G0:00064	RNA localization	-1.63922	0.006548
BP	G0:00091	nucleotide biosynthetic process	-1.64352	0.006585
BP	G0:00709	neutrophil mediated cytotoxicity	2.055145	0.006588
MF	G0:00166	oxidoreductase activity, acting on CH-OH group of	-1.73136	0.006609
BP	G0:00091	nucleoside triphosphate biosynthetic process	-2.03789	0.006609
BP	G0:00091	purine ribonucleotide metabolic process	-1.53919	0.006628
BP	G0:00023	immunoglobulin production involved in immunoglobu	-1.9459	0.006628
CC	G0:00319	vesicle lumen	1.574061	0.006785
BP	G0:00067	heme biosynthetic process	-2.07748	0.007121
BP	G0:00024	neutrophil mediated immunity	2.03266	0.007155
BP	G0:00513	positive regulation of transferase activity	1.494292	0.007155
BP	G0:00726	establishment of protein localization to mitochon	-1.79504	0.007363
BP	G0:19047	vascular associated smooth muscle cell migration	2.003001	0.007506



CC	G0:00708:tertiary granule membrane	1.90401 0.007506
BP	G0:00065:glutamine metabolic process	-2.08093 0.008088
MF	G0:00900:translation regulator activity, nucleic acid bindi	-1.83317 0.008154
BP	G0:00362:granulocyte activation	2.001588 0.00817
BP	G0:00705:protein localization to mitochondrion	-1.75611 0.008259
BP	G0:00460:ATP metabolic process	-1.62188 0.008309
BP	G0:00450:positive regulation of innate immune response	1.768114 0.008362
BP	G0:00003:spliceosomal snRNP assembly	-2.0879 0.00857
BP	G0:00487:tissue remodeling	1.650586 0.008747
CC	G0:00602:cytoplasmic vesicle lumen	1.583261 0.008876
BP	G0:00002:protein polyubiquitination	1.602344 0.009296
BP	G0:00091:pyrimidine nucleoside triphosphate metabolic proce	-2.06763 0.009307
BP	G0:00102:NADH dehydrogenase complex assembly	-2.00468 0.009416
BP	G0:00329:mitochondrial respiratory chain complex I assembly	-2.00468 0.009416
BP	G0:00105:regulation of autophagy	1.561499 0.009537
MF	G0:00198:protein kinase regulator activity	1.641198 0.009825
BP	G0:00068:mitochondrial transport	-1.5884 0.010072
MF	G0:00048:ubiquitin-protein transferase activity	1.534405 0.01033
CC	G0:00990:vesicle tethering complex	-1.96053 0.010408
BP	G0:00715:response to transforming growth factor beta	1.585503 0.010408
MF	G0:01402:DNA-binding transcription factor binding	1.528228 0.010413
CC	G0:00704:respirasome	-1.84521 0.010413
BP	G0:00709:neutrophil-mediated killing of symbiont cell	2.024604 0.010413
MF	G0:00037:transcription coregulator activity	1.520827 0.010463
BP	G0:00723:tricarboxylic acid metabolic process	-2.08606 0.010525
BP	G0:00450:glycerolipid biosynthetic process	1.63955 0.010546
BP	G0:00450:regulation of innate immune response	1.59527 0.010662
BP	G0:00022:neutrophil activation involved in immune response	2.003637 0.010816
BP	G0:00342:regulation of cellular amide metabolic process	-1.49026 0.010998
CC	G0:00057:mitochondrial respirasome	-1.83617 0.010998
CC	G0:00156:actin cytoskeleton	1.451043 0.010998
MF	G0:00167:phosphotransferase activity, phosphate group as ac	-2.07437 0.010998
MF	G0:00302:protein kinase activator activity	1.808569 0.010998
BP	G0:00344:ncRNA 5'-end processing	-2.09381 0.0112
BP	G0:00163:dephosphorylation	1.539338 0.011625
BP	G0:00070:mitochondrion organization	-1.46798 0.011625
BP	G0:00022:activation of innate immune response	1.894148 0.011625
BP	G0:00725:pyrimidine-containing compound biosynthetic proces	-2.04147 0.011625
BP	G0:00162:regulation of macroautophagy	1.691598 0.011625
BP	G0:00065:protein monoubiquitination	1.904594 0.011774
BP	G0:00985:detection of other organism	1.972313 0.011822
BP	G0:00709:neutrophil-mediated killing of bacterium	1.957925 0.011856
CC	G0:19047:tertiary granule lumen	1.891647 0.011921
BP	G0:00086:phospholipid biosynthetic process	1.569853 0.011964
BP	G0:00424:pigment metabolic process	-1.81743 0.011981
BP	G0:00465:protoporphyrinogen IX metabolic process	-2.09534 0.012334
CC	G0:00424:nuclear inclusion body	1.983736 0.012337
CC	G0:19025:endoribonuclease complex	-2.01202 0.012338
BP	G0:00610:membrane fusion	1.705769 0.012596
MF	G0:01400:catalytic activity, acting on DNA	-1.57251 0.012655
MF	G0:00469:thyroid hormone receptor binding	1.9911 0.012733
MF	G0:00043:helicase activity	-1.67398 0.012773
CC	G0:00057:late endosome	1.561439 0.012829
BP	G0:19016:glycosyl compound metabolic process	-1.77791 0.012839

CC	G0:003130intrinsic component of mitochondrial inner membrane	-1.95259	0.012939
CC	G0:003130integral component of mitochondrial inner membrane	-1.95259	0.012939
CC	G0:003067ribonuclease P complex	-2.0794	0.013198
BP	G0:000920ribonucleoside triphosphate biosynthetic process	-1.96009	0.013198
BP	G0:000916nucleoside diphosphate metabolic process	-1.71173	0.013369
BP	G0:000916pyrimidine nucleoside monophosphate biosynthetic process	-2.0772	0.013697
CC	G0:001977proteasome core complex, beta-subunit complex	-2.04508	0.013697
BP	G0:003367positive regulation of kinase activity	1.438061	0.013697
BP	G0:199054mitochondrial transmembrane transport	-1.81417	0.013942
BP	G0:006147regulation of transcription from RNA polymerase II promoter	1.966865	0.013942
CC	G0:001660nuclear speck	1.527316	0.014075
BP	G0:000090tRNA 5'-end processing	-2.06117	0.014326
MF	G0:000818ATP-dependent activity, acting on RNA	-1.80166	0.014454
BP	G0:000628DNA repair	-1.44399	0.01452
BP	G0:009017organelle membrane fusion	1.776891	0.01452
BP	G0:007017regulation of mitochondrial translation	-2.02504	0.014691
BP	G0:011007regulation of actin filament organization	1.561084	0.01472
BP	G0:004367regulation of DNA-templated transcription in response to stress	1.882845	0.01472
BP	G0:009911tRNA 5'-end processing	-2.06519	0.014826
BP	G0:005180protein autoubiquitination	1.82381	0.015029
BP	G0:000610nucleoside diphosphate phosphorylation	-1.73926	0.015101
BP	G0:004340regulation of MAP kinase activity	1.623275	0.01516
BP	G0:000610purine nucleotide biosynthetic process	-1.66001	0.015378
MF	G0:003069GTPase regulator activity	1.46986	0.015378
MF	G0:006058nucleoside-triphosphatase regulator activity	1.46986	0.015378
CC	G0:000579endoplasmic reticulum-Golgi intermediate compartment	1.707877	0.015523
BP	G0:000655cellular amino acid metabolic process	-1.53878	0.015523
BP	G0:001810peptidyl-threonine phosphorylation	1.747765	0.015813
BP	G0:000916purine ribonucleoside monophosphate metabolic process	-2.00385	0.015813
BP	G0:006067regulation of vesicle-mediated transport	1.449626	0.016083
BP	G0:004648glycerolipid metabolic process	1.513209	0.016114
BP	G0:000916pyrimidine nucleoside triphosphate biosynthetic process	-2.04058	0.016114
BP	G0:000222toll-like receptor signaling pathway	1.696926	0.016114
BP	G0:004300regulation of GTPase activity	1.521431	0.01617
CC	G0:009880respiratory chain complex	-1.80641	0.016328
BP	G0:003649regulation of translation in response to endoplasmic reticulum stress	1.925923	0.016406
CC	G0:003049midbody	1.611593	0.016406
BP	G0:001619endosomal transport	1.60379	0.016527
BP	G0:001480muscle cell migration	1.777373	0.016527
BP	G0:007150cellular response to transforming growth factor beta	1.575485	0.016527
BP	G0:003130positive regulation of cell projection organization	1.503754	0.016548
CC	G0:003280plasma membrane bounded cell projection cytoplasmic domain	1.606312	0.016548
MF	G0:001900GDP binding	1.792934	0.016548
CC	G0:003067phagocytic vesicle membrane	1.780251	0.016882
BP	G0:000720Ras protein signal transduction	1.533804	0.016895
CC	G0:006170inflammasome complex	1.970816	0.016993
MF	G0:004633SMAD binding	1.789286	0.017259
BP	G0:005169establishment of organelle localization	1.501602	0.017331
BP	G0:000239MHC class II protein complex assembly	-1.9967	0.017576
BP	G0:000250peptide antigen assembly with MHC class II protein	-1.9967	0.017576
BP	G0:000000ribosomal large subunit assembly	-2.03375	0.017863
BP	G0:000690vesicle fusion	1.714128	0.017863
MF	G0:000377RNA helicase activity	-1.82269	0.018228
MF	G0:0051544 iron, 4 sulfur cluster binding	-1.97213	0.018228

BP	G0:00070:endosome organization	1.789081 0.018313
BP	G0:00303:positive regulation of cell migration	1.434 0.018339
BP	G0:00062:DNA strand elongation involved in DNA replication	-2.02381 0.018451
MF	G0:00087:S-adenosylmethionine-dependent methyltransferase activity	-1.6894 0.018754
BP	G0:00463:ribose phosphate biosynthetic process	-1.61819 0.018754
BP	G0:00004:endonucleolytic cleavage involved in rRNA processing	-2.01005 0.018754
BP	G0:00004:endonucleolytic cleavage of tricistronic rRNA transcripts	-2.01005 0.018754
MF	G0:00616:ubiquitin protein ligase activity	1.548289 0.018907
BP	G0:00108:regulation of sequestering of triglyceride	1.904454 0.018963
BP	G0:00105:regulation of lamellipodium assembly	1.935325 0.019009
BP	G0:00431:receptor metabolic process	1.595897 0.019028
BP	G0:00149:smooth muscle cell migration	1.774956 0.019028
BP	G0:00092:cellular response to starvation	1.662125 0.019028
BP	G0:00300:establishment of cell polarity	1.663246 0.019028
BP	G0:00092:pyrimidine ribonucleoside triphosphate biosynthesis	-2.03845 0.019037
MF	G0:00081:translation factor activity, RNA binding	-1.79811 0.019198
BP	G0:00023:MHC protein complex assembly	-1.94239 0.019198
BP	G0:00092:pyrimidine ribonucleotide biosynthetic process	-2.02025 0.019198
MF	G0:00342:peptide N-acetyltransferase activity	1.929031 0.019198
MF	G0:00617:peptide-lysine-N-acetyltransferase activity	1.929031 0.019198
MF	G0:00154:oxidoreduction-driven active transmembrane transport	-1.8067 0.019204
CC	G0:00442:organelle membrane contact site	1.904388 0.019489
BP	G0:00196:aerobic electron transport chain	-1.80158 0.019757
BP	G0:00022:adaptive immune response	-1.41493 0.01978
MF	G0:00510:chaperone binding	-1.70964 0.01978
MF	G0:00168:ligase activity	-1.69061 0.020272
MF	G0:00230:MHC class II protein complex binding	-1.97749 0.020282
BP	G0:00905:RNA phosphodiester bond hydrolysis, endonucleolytic	-1.81869 0.020338
BP	G0:00464:glycerophospholipid biosynthetic process	1.583616 0.020364
BP	G0:00072:spermatogenesis	1.441714 0.020516
CC	G0:00325:integral component of mitochondrial membrane	-1.75306 0.020912
BP	G0:00714:cellular response to external stimulus	1.497841 0.020912
BP	G0:00025:peptide antigen assembly with MHC protein complex	-2.00731 0.020958
MF	G0:01403:solute:anion antiporter activity	-1.97379 0.020987
BP	G0:01200:plasma membrane bounded cell projection assembly	1.467546 0.021015
BP	G0:00713:cellular response to peptide hormone stimulus	1.472443 0.021656
BP	G0:00469:nucleotide phosphorylation	-1.73198 0.022067
BP	G0:00458:positive regulation of protein kinase activity	1.444451 0.022187
BP	G0:19047:regulation of vascular associated smooth muscle cell	1.9252 0.022512
BP	G0:00459:negative regulation of phosphate metabolic processes	1.432158 0.022512
MF	G0:00167:phosphatase activity	1.506894 0.022512
MF	G0:00090:electron transfer activity	-1.65903 0.023395
MF	G0:00350:phosphatidylinositol binding	1.53516 0.023396
CC	G0:00057:autophagosome	1.74587 0.023752
BP	G0:00900:regulation of anatomical structure size	1.41139 0.023806
BP	G0:00064:translational elongation	-1.84197 0.02386
MF	G0:00323:MHC class II receptor activity	-1.97819 0.02386
MF	G0:00168:carbon-oxygen lyase activity	-1.79917 0.023909
BP	G0:00081:actin polymerization or depolymerization	1.542303 0.024031
CC	G0:00001:ubiquitin ligase complex	1.490619 0.024058
MF	G0:00353:Toll-like receptor binding	1.889401 0.024058
MF	G0:00451:translation regulator activity	-1.67673 0.024058
BP	G0:00445:NLRP3 inflammasome complex assembly	1.867759 0.024058
BP	G0:01406:inflammasome complex assembly	1.867759 0.024058

BP	G0:00440	positive regulation of cellular component biogenesis	1.404845	0.024058
MF	G0:00230	MHC protein complex binding	-1.92105	0.024068
BP	G0:00027	MyD88-dependent toll-like receptor signaling pathway	1.894796	0.024068
BP	G0:00092	ribonucleotide biosynthetic process	-1.62893	0.024157
MF	G0:00037	actin binding	1.430672	0.024248
BP	G0:00430	positive regulation of macrophage activation	1.893517	0.024248
BP	G0:00164	cytosolic transport	1.591205	0.024792
CC	G0:00057	secondary lysosome	1.889675	0.025226
BP	G0:00427	ATP synthesis coupled electron transport	-1.74342	0.025316
BP	G0:00427	mitochondrial ATP synthesis coupled electron transport	-1.74342	0.025316
BP	G0:00482	male gamete generation	1.419219	0.025785
BP	G0:00508	modulation of chemical synaptic transmission	1.458813	0.026276
BP	G0:00991	regulation of trans-synaptic signaling	1.458813	0.026276
BP	G0:00329	regulation of actin cytoskeleton organization	1.457238	0.026564
MF	G0:00055	phospholipid binding	1.443824	0.026693
BP	G0:19016	cellular response to peptide	1.460577	0.026693
BP	G0:19029	negative regulation of autophagosome assembly	1.850549	0.027022
BP	G0:00324	detection of molecule of bacterial origin	1.918932	0.027032
BP	G0:00450	T cell selection	-1.8681	0.027032
BP	G0:00905	RNA phosphodiester bond hydrolysis	-1.6475	0.027032
BP	G0:00450	positive thymic T cell selection	-1.95764	0.027032
BP	G0:00001	rRNA modification	-1.97382	0.027051
CC	G0:00355	specific granule lumen	1.754017	0.027142
MF	G0:00046	protein serine/threonine kinase activity	1.423826	0.027142
BP	G0:00709	protein K48-linked ubiquitination	1.721073	0.02739
BP	G0:00022	pattern recognition receptor signaling pathway	1.590102	0.02739
BP	G0:19016	alpha-amino acid biosynthetic process	-1.73955	0.027848
BP	G0:00158	ATP transport	-1.95582	0.027848
MF	G0:00510	unfolded protein binding	-1.61333	0.027863
BP	G0:00356	protein deacylation	1.643957	0.028175
BP	G0:00975	lamellipodium organization	1.747639	0.02849
BP	G0:00903	positive regulation of protein deacetylation	1.879815	0.028722
BP	G0:00300	cell projection assembly	1.420208	0.028841
MF	G0:00428	histone deacetylase binding	1.649902	0.028908
BP	G0:00621	cellular response to chemical stress	1.490737	0.028982
BP	G0:00165	histone modification	1.437808	0.029044
BP	G0:00182	peptidyl-serine modification	1.440889	0.029226
BP	G0:00009	mitochondrial RNA metabolic process	-1.87777	0.029815
BP	G0:00513	cell division	1.361838	0.029815
MF	G0:00192	kinase regulator activity	1.521814	0.030167
BP	G0:00346	nucleobase-containing compound catabolic process	-1.3917	0.030337
CC	G0:00057	mitochondrial outer membrane translocase complex	-1.92608	0.031067
BP	G0:01061	cold-induced thermogenesis	1.628583	0.031067
BP	G0:01201	regulation of cold-induced thermogenesis	1.628583	0.031067
BP	G0:00071	transforming growth factor beta receptor signaling	1.554562	0.031071
BP	G0:00064	protein dephosphorylation	1.499797	0.031071
BP	G0:00400	positive regulation of locomotion	1.375269	0.03143
BP	G0:00149	regulation of smooth muscle cell migration	1.696475	0.031553
CC	G0:00319	organelle envelope lumen	-1.70494	0.03199
BP	G0:00194	aromatic compound catabolic process	-1.38215	0.03199
MF	G0:00045	exonuclease activity	-1.77267	0.032571
BP	G0:00442	small molecule catabolic process	-1.39703	0.032607
BP	G0:00162	iron-sulfur cluster assembly	-1.95963	0.033155
BP	G0:00311	metallo-sulfur cluster assembly	-1.95963	0.033155

BP	G0:00004	maturacion of 5.8S rRNA from tricistronic rRNA tra	-1.94019	0.033386
BP	G0:00364	PERK-mediated unfolded protein response	1.852876	0.0343
CC	G0:00057	mitochondrial intermembrane space	-1.68728	0.034432
BP	G0:00105	negative regulation of phosphorus metabolic proces	1.426336	0.034432
BP	G0:00093	2'-deoxyribonucleotide metabolic process	-1.86225	0.034432
BP	G0:00467	protein autophosphorylation	1.486681	0.034527
BP	G0:00307	ovulation	1.866163	0.03463
BP	G0:00066	protein targeting to mitochondrion	-1.71115	0.034661
MF	G0:00168	lyase activity	-1.50868	0.034735
BP	G0:00508	positive regulation of antigen receptor-mediated s	-1.85908	0.034735
MF	G0:00512	NAD binding	-1.73726	0.034735
BP	G0:00313	positive regulation of protein ubiquitination	1.6581	0.034739
MF	G0:00045	endonuclease activity	-1.6297	0.034966
BP	G0:00421	heme metabolic process	-1.83026	0.034966
BP	G0:00329	regulation of actin filament-based process	1.449674	0.035147
BP	G0:00725	pyrimidine-containing compound metabolic process	-1.68987	0.035188
BP	G0:00109	negative regulation of protein processing	1.854784	0.035188
BP	G0:19033	negative regulation of protein maturation	1.854784	0.035188
BP	G0:00704	nucleotide-binding oligomerization domain contain	1.838479	0.035245
MF	G0:00037	transcription coactivator activity	1.486472	0.035399
CC	G0:00426	MHC class II protein complex	-1.92684	0.035637
BP	G0:00004	maturacion of 5.8S rRNA	-1.86722	0.035752
BP	G0:00316	response to nutrient levels	1.378099	0.035752
CC	G0:00009	spindle pole	1.5834	0.035752
BP	G0:19027	regulation of lamellipodium organization	1.781551	0.035752
BP	G0:00316	cellular response to nutrient levels	1.529953	0.035761
CC	G0:00306	multimeric ribonuclease P complex	-1.91068	0.036191
MF	G0:00332	ribonuclease P RNA binding	-1.91068	0.036191
MF	G0:00166	oxidoreductase activity, acting on the CH-CH group	-1.72217	0.03633
BP	G0:00063	DNA recombination	-1.48449	0.036443
CC	G0:00985	intrinsic component of mitochondrial membrane	-1.73567	0.036739
BP	G0:00709	protein localization to endoplasmic reticulum	1.737371	0.036836
BP	G0:20001	positive regulation of cell motility	1.378245	0.037112
BP	G0:00159	energy derivation by oxidation of organic compound	-1.45033	0.037112
BP	G0:00335	fatty acid beta-oxidation using acyl-CoA dehydroge	-1.90782	0.037112
MF	G0:00616	RNA polymerase II-specific DNA-binding transcript	1.449888	0.03713
BP	G0:00019	negative regulation of protein phosphorylation	1.411271	0.037233
BP	G0:00987	macromolecule deacylation	1.636549	0.037497
CC	G0:00717	endoplasmic reticulum tubular network	1.836755	0.037749
BP	G0:00431	proteasome-mediated ubiquitin-dependent protein ca	1.422319	0.037749
BP	G0:00316	regulation of protein stability	1.416511	0.037786
BP	G0:00098	positive regulation of catabolic process	1.38557	0.037786
MF	G0:00168	hydro-lyase activity	-1.71802	0.037786
BP	G0:00064	protein deacetylation	1.655682	0.03801
MF	G0:00046	protein kinase activity	1.343259	0.038768
BP	G0:00067	porphyrin-containing compound metabolic process	-1.75624	0.038768
BP	G0:00032	atrial septum development	1.826084	0.038773
CC	G0:19053	peptidase complex	-1.60541	0.039092
CC	G0:00002	nuclear chromosome	-1.45388	0.039092
BP	G0:00713	cellular response to estrogen stimulus	1.852074	0.039426
BP	G0:20001	regulation of establishment of cell polarity	1.802098	0.039475
BP	G0:00436	regulation of transcription from RNA polymerase I	1.804464	0.039566
BP	G0:00508	regulation of T cell activation	-1.42012	0.039566
BP	G0:00381	ERBB signaling pathway	1.583197	0.039679

CC	G0:00312:cell leading edge	1.40324 0.039777
BP	G0:00092:pyrimidine ribonucleoside triphosphate metabolic p	-1.92206 0.039985
BP	G0:00432:regulation of protein-containing complex assembly	1.418116 0.040321
BP	G0:00091:nucleoside triphosphate metabolic process	-1.68704 0.04043
CC	G0:00347:(methyltransferase complex	-1.65286 0.040613
BP	G0:00300:actin filament polymerization	1.483037 0.040849
MF	G0:00171:SH3 domain binding	1.592147 0.040849
BP	G0:00717:endoplasmic reticulum tubular network organization	1.789342 0.042517
BP	G0:00069:phagocytosis	1.437795 0.042651
BP	G0:00096:response to fungus	1.71783 0.042743
BP	G0:00072:female gamete generation	1.580681 0.043043
BP	G0:00421:cellular response to glucose starvation	1.772465 0.043269
BP	G0:00068:exocytosis	1.414076 0.043318
BP	G0:19018:regulation of cell junction assembly	1.493458 0.043487
BP	G0:19013:organic cyclic compound catabolic process	-1.3631 0.043706
MF	G0:00510:GTPase binding	1.429274 0.043724
BP	G0:00435:positive regulation of GTPase activity	1.479268 0.044599
BP	G0:00224:cellular process involved in reproduction in mult	1.408957 0.044925
MF	G0:00042:threonine-type endopeptidase activity	-1.92477 0.044925
BP	G0:00481:Golgi vesicle transport	1.448763 0.045135
BP	G0:00421:T cell activation	-1.30305 0.045264
BP	G0:00450:transcytosis	1.802737 0.045264
BP	G0:20002:regulation of fibroblast apoptotic process	1.821498 0.045264
CC	G0:00319:early endosome membrane	1.523926 0.045264
MF	G0:00044:(histone acetyltransferase activity	1.794891 0.045264
BP	G0:00181:(peptidyl-serine phosphorylation	1.431938 0.045264
BP	G0:00071:(establishment or maintenance of cell polarity	1.488256 0.045264
BP	G0:00064:protein folding	-1.48969 0.045264
MF	G0:00192:(phosphatase regulator activity	1.657818 0.045264
CC	G0:00057:RNA polymerase I complex	-1.88139 0.045915
MF	G0:19019:phosphatidylinositol phosphate binding	1.553799 0.046805
BP	G0:00442:cellular polysaccharide catabolic process	1.77309 0.04706
MF	G0:00045:ribonuclease P activity	-1.95523 0.047068
BP	G0:00360:(positive regulation of transcription from RNA poly	1.831676 0.047068
BP	G0:00091:purine nucleoside triphosphate biosynthetic proces	-1.72577 0.047253
MF	G0:00167:transferase activity, transferring one-carbon grou	-1.53686 0.047279
BP	G0:19027:positive regulation of lamellipodium organization	1.778417 0.048004
CC	G0:00226:cytosolic large ribosomal subunit	-1.69691 0.048443
BP	G0:00016:temperature homeostasis	1.479308 0.048922
BP	G0:00170:regulation of transforming growth factor beta rece	1.565874 0.049263
BP	G0:00901:(negative regulation of transmembrane receptor pro	1.56455 0.049263
BP	G0:00421:macrophage activation	1.611943 0.049263
MF	G0:00312:(small GTPase binding	1.464549 0.049263
BP	G0:00308:regulation of actin filament length	1.503006 0.049263
BP	G0:00067:porphyrin-containing compound biosynthetic proces	-1.82548 0.049263
BP	G0:00330:tetrapyrrole biosynthetic process	-1.82548 0.049263
BP	G0:00433:neutrophil degranulation	1.790979 0.049263
BP	G0:00400:negative regulation of multicellular organism grov	-1.87571 0.049497
BP	G0:00070:(inner mitochondrial membrane organization	-1.81961 0.049729

ID	Description	NES	p. adjust
hsa03010	Ribosome	-2.58096	3.33E-08
hsa01200	Carbon metabolism	-2.26547	4.78E-06
hsa01230	Biosynthesis of amino acids	-2.26078	7.05E-05
hsa03008	Ribosome biogenesis in eukaryotes	-2.21325	0.00033
hsa04144	Endocytosis	1.786221	0.00033
hsa04140	Autophagy - animal	1.930503	0.000468
hsa05012	Parkinson disease	-1.68106	0.000831
hsa05131	Shigellosis	1.741645	0.000867
hsa05332	Graft-versus-host disease	-2.15052	0.001145
hsa01232	Nucleotide metabolism	-1.95875	0.002701
hsa05020	Prion disease	-1.68485	0.002701
hsa05330	Allograft rejection	-2.06344	0.003051
hsa00020	Citrate cycle (TCA cycle)	-2.07694	0.003363
hsa05168	Herpes simplex virus 1 infection	1.495545	0.003961
hsa03410	Base excision repair	-2.05862	0.004666
hsa05320	Autoimmune thyroid disease	-1.89547	0.007442
hsa03030	DNA replication	-1.99252	0.007442
hsa05016	Huntington disease	-1.54125	0.008341
hsa04062	Chemokine signaling pathway	1.607407	0.008681
hsa05416	Viral myocarditis	-1.89999	0.00945
hsa05135	Yersinia infection	1.671975	0.011826
hsa05415	Diabetic cardiomyopathy	-1.56896	0.01199
hsa00230	Purine metabolism	-1.66124	0.012189
hsa00270	Cysteine and methionine metabolism	-1.84265	0.012727
hsa01210	2-Oxocarboxylic acid metabolism	-1.99738	0.012733
hsa04940	Type I diabetes mellitus	-1.83341	0.012733
hsa05022	Pathways of neurodegeneration - multiple diseases	-1.40254	0.012733
hsa03050	Proteasome	-1.81513	0.013866
hsa05208	Chemical carcinogenesis - reactive oxygen species	-1.53197	0.015204
hsa05322	Systemic lupus erythematosus	-1.81847	0.015873
hsa05017	Spinocerebellar ataxia	-1.63425	0.020228
hsa00280	Valine, leucine and isoleucine degradation	-1.77329	0.021375
hsa00630	Glyoxylate and dicarboxylate metabolism	-1.85894	0.021375
hsa04068	FoxO signaling pathway	1.620969	0.022948
hsa05014	Amyotrophic lateral sclerosis	-1.42823	0.022948
hsa05010	Alzheimer disease	-1.40186	0.025876
hsa00620	Pyruvate metabolism	-1.74585	0.026025
hsa05130	Pathogenic Escherichia coli infection	1.516687	0.0281
hsa04071	Sphingolipid signaling pathway	1.604535	0.0281
hsa04146	Peroxisome	-1.6795	0.0281
hsa04115	p53 signaling pathway	1.717898	0.03219
hsa05417	Lipid and atherosclerosis	1.433689	0.036012
hsa05211	Renal cell carcinoma	1.679969	0.037057
hsa04722	Neurotrophin signaling pathway	1.523264	0.037057
hsa00240	Pyrimidine metabolism	-1.668	0.037057
hsa05340	Primary immunodeficiency	-1.75021	0.037057
hsa05212	Pancreatic cancer	1.599671	0.037057
hsa00512	Mucin type O-glycan biosynthesis	1.720685	0.037057
hsa05132	Salmonella infection	1.424703	0.037057
hsa00500	Starch and sucrose metabolism	1.731811	0.037057
hsa00190	Oxidative phosphorylation	-1.57761	0.037057
hsa04666	Fc gamma R-mediated phagocytosis	1.584908	0.037057
hsa01240	Biosynthesis of cofactors	-1.50714	0.037069

hsa04670 Leukocyte transendothelial migration	1.501504	0.044796
hsa05310 Asthma	-1.69375	0.044796
hsa04371 Apelin signaling pathway	1.491177	0.044955
hsa05219 Bladder cancer	1.657883	0.046049
hsa04672 Intestinal immune network for IgA production	-1.67143	0.046715
hsa04658 Th1 and Th2 cell differentiation	-1.55356	0.048234
hsa00562 Inositol phosphate metabolism	1.589676	0.048234



**Supplementary Table 4: Expression levels of 6 genes in normal individuals**

	N1	N2	N3	N4	N5	N6
CEBPG	0.2197154	0.1814453	0.0652913	0.1308191	0.3354173	0.1991273
MMP9	0.0026999	0.1027926	0.0119546	0.0202802	0.0006621	0.0026981
MXD4	0.0002014	0.0124918	0.0032213	0.0206336	3.61E-05	0.0003437
S100A12	0.0345667	0.0266974	0.0186975	0.0128603	0.1645962	0.0208235
SSRP1	0.0002737	0.0233752	0.0041028	0.0073091	0.0003251	0.0010722
TGFBR3	0.8586736	0.1166811	0.3253476	0.5987996	0.3152353	0.1030494

**Supplementary Table 5: Expression levels of 6 genes in patients**

	P1	P2	P3	P4	P5	P6
CEBPG	0.1824038	0.2070555	0.1723662	0.0585383	0.2615602	0.1110688
MMP9	0.0196277	0.0054404	0.0003724	0.0116457	0.0110277	0.0055652
MXD4	0.0001288	0.0001334	8.96E-05	9.07E-05	0.0105758	0.0062842
S100A12	0.0615544	2.7322115	0.3654616	2.6586867	0.0617808	1.6952964
SSRP1	1.76E-05	6.69E-05	0.0005355	0.0009582	0.0018216	0.001718
TGFBR3	0.2843132	0.0821123	0.0823897	0.1027926	0.0719451	0.1907818