

Supplementary Table S6

Event 1 – LINC00665 (GO)

ONTOLOGY	ID	Description	setSize	enrichmentScore	NES	pvalue	p.adjust	qvalues	rank	leading edge
BP	GO:0051270	regulation of cellular component movement	784	-0.3745	-1.5961	1.2657E-04	2.5244E-02	2.3044E-02	2208	tags=25%, list=15%, signal=22%
BP	GO:0071345	cellular response to cytokine stimulus	790	-0.3800	-1.6198	1.2666E-04	2.5244E-02	2.3044E-02	1898	tags=20%, list=13%, signal=19%
BP	GO:0035295	tube development	776	-0.4379	-1.8656	1.2671E-04	2.5244E-02	2.3044E-02	1776	tags=24%, list=12%, signal=23%
BP	GO:1902533	positive regulation of intracellular signal transduction	780	-0.3372	-1.4367	1.2677E-04	2.5244E-02	2.3044E-02	1788	tags=17%, list=12%, signal=16%
BP	GO:0040012	regulation of locomotion	773	-0.3844	-1.6375	1.2679E-04	2.5244E-02	2.3044E-02	2208	tags=26%, list=15%, signal=23%
BP	GO:0060284	regulation of cell development	787	-0.3649	-1.5551	1.2679E-04	2.5244E-02	2.3044E-02	2702	tags=25%, list=18%, signal=21%
BP	GO:0051960	regulation of nervous system development	782	-0.3612	-1.5390	1.2687E-04	2.5244E-02	2.3044E-02	2657	tags=24%, list=18%, signal=21%
BP	GO:0009790	embryo development	762	-0.3519	-1.4974	1.2711E-04	2.5244E-02	2.3044E-02	2201	tags=21%, list=15%, signal=19%
BP	GO:0002684	positive regulation of immune system process	725	-0.3545	-1.5038	1.2776E-04	2.5244E-02	2.3044E-02	1898	tags=20%, list=13%, signal=19%
BP	GO:0051093	negative regulation of developmental process	721	-0.3945	-1.6722	1.2793E-04	2.5244E-02	2.3044E-02	2288	tags=25%, list=16%, signal=22%
BP	GO:0050767	regulation of neurogenesis	698	-0.3771	-1.5972	1.2807E-04	2.5244E-02	2.3044E-02	2657	tags=25%, list=18%, signal=22%
BP	GO:2000145	regulation of cell motility	714	-0.3968	-1.6811	1.2819E-04	2.5244E-02	2.3044E-02	2208	tags=26%, list=15%, signal=23%
MF	GO:0060089	molecular transducer activity	691	-0.3747	-1.5850	1.2837E-04	2.5244E-02	2.3044E-02	2000	tags=25%, list=14%, signal=22%
BP	GO:0098657	import into cell	677	-0.3750	-1.5837	1.2898E-04	2.5244E-02	2.3044E-02	2286	tags=22%, list=16%, signal=20%
BP	GO:0030334	regulation of cell migration	674	-0.4051	-1.7107	1.2912E-04	2.5244E-02	2.3044E-02	2208	tags=27%, list=15%, signal=24%
BP	GO:0050776	regulation of immune response	674	-0.3482	-1.4702	1.2912E-04	2.5244E-02	2.3044E-02	1898	tags=13%, signal=18%
BP	GO:0008284	positive regulation of cell proliferation	633	-0.3595	-1.5121	1.2937E-04	2.5244E-02	2.3044E-02	2277	tags=23%, list=16%, signal=20%
BP	GO:0035239	tube morphogenesis	631	-0.4426	-1.8610	1.2942E-04	2.5244E-02	2.3044E-02	2198	tags=29%, list=15%, signal=26%
MF	GO:0038023	signaling receptor activity	645	-0.3825	-1.6105	1.2943E-04	2.5244E-02	2.3044E-02	1846	tags=24%, list=13%, signal=22%
BP	GO:0098609	cell-cell adhesion	628	-0.4009	-1.6855	1.2950E-04	2.5244E-02	2.3044E-02	2101	tags=26%, list=14%, signal=24%
BP	GO:0031344	regulation of cell projection organization	598	-0.3612	-1.5132	1.3094E-04	2.5244E-02	2.3044E-02	2225	tags=20%, list=15%, signal=18%
BP	GO:0032101	regulation of response to external stimulus	560	-0.4129	-1.7238	1.3115E-04	2.5244E-02	2.3044E-02	2200	tags=26%, list=15%, signal=23%
BP	GO:0006897	endocytosis	585	-0.3838	-1.6056	1.3120E-04	2.5244E-02	2.3044E-02	1921	tags=19%, list=13%, signal=17%
BP	GO:0120035	regulation of plasma membrane bounded cell projection organization	590	-0.3600	-1.5066	1.3135E-04	2.5244E-02	2.3044E-02	2225	tags=20%, list=15%, signal=18%
BP	GO:0007186	G protein-coupled receptor signaling pathway	573	-0.3804	-1.5893	1.3137E-04	2.5244E-02	2.3044E-02	1880	tags=22%, list=13%, signal=20%
BP	GO:0072358	cardiovascular system development	552	-0.4572	-1.9063	1.3142E-04	2.5244E-02	2.3044E-02	2188	tags=29%, list=15%, signal=26%
BP	GO:0070848	response to growth factor	572	-0.3544	-1.4802	1.3153E-04	2.5244E-02	2.3044E-02	1977	tags=21%, list=14%, signal=19%
BP	GO:0001944	vasculature development	544	-0.4580	-1.9097	1.3158E-04	2.5244E-02	2.3044E-02	2188	tags=29%, list=15%, signal=26%
BP	GO:0045596	negative regulation of cell differentiation	543	-0.3629	-1.5126	1.3160E-04	2.5244E-02	2.3044E-02	2307	tags=25%, list=16%, signal=22%
CC	GO:0009986	cell surface	536	-0.4762	-1.9827	1.3201E-04	2.5244E-02	2.3044E-02	2139	tags=32%, list=15%, signal=28%
BP	GO:0019221	cytokine-mediated signaling pathway	524	-0.3573	-1.4852	1.3235E-04	2.5244E-02	2.3044E-02	1720	tags=19%, list=12%, signal=18%
BP	GO:0001568	blood vessel development	518	-0.4620	-1.9185	1.3256E-04	2.5244E-02	2.3044E-02	2188	tags=30%, list=15%, signal=27%
BP	GO:0008285	negative regulation of cell proliferation	521	-0.3564	-1.4804	1.3266E-04	2.5244E-02	2.3044E-02	2198	tags=23%, list=15%, signal=21%
BP	GO:0030155	regulation of cell adhesion	506	-0.4309	-1.7866	1.3293E-04	2.5244E-02	2.3044E-02	2416	tags=30%, list=16%, signal=26%
MF	GO:0004888	transmembrane signaling receptor activity	512	-0.3866	-1.6037	1.3294E-04	2.5244E-02	2.3044E-02	1563	tags=27%, list=11%, signal=25%
BP	GO:0009611	response to wounding	496	-0.3779	-1.5636	1.3358E-04	2.5244E-02	2.3044E-02	2401	tags=27%, list=16%, signal=24%
BP	GO:0007264	small GTPase mediated signal transduction	486	-0.3682	-1.5213	1.3405E-04	2.5244E-02	2.3044E-02	3011	tags=30%, list=21%, signal=25%
BP	GO:0006954	inflammatory response	468	-0.4458	-1.8372	1.3504E-04	2.5244E-02	2.3044E-02	1900	tags=26%, list=13%, signal=23%
BP	GO:0042330	taxis	451	-0.4452	-1.8298	1.3546E-04	2.5244E-02	2.3044E-02	2200	tags=28%, list=15%, signal=24%
BP	GO:0048514	blood vessel morphogenesis	451	-0.4750	-1.9522	1.3546E-04	2.5244E-02	2.3044E-02	2188	tags=31%, list=15%, signal=27%
BP	GO:0006935	chemotaxis	449	-0.4458	-1.8306	1.3552E-04	2.5244E-02	2.3044E-02	2200	tags=28%, list=15%, signal=24%
BP	GO:0046649	lymphocyte activation	441	-0.4190	-1.7180	1.3561E-04	2.5244E-02	2.3044E-02	2032	tags=25%, list=14%, signal=23%
BP	GO:0022604	regulation of cell morphogenesis	430	-0.4013	-1.6429	1.3578E-04	2.5244E-02	2.3044E-02	2375	tags=24%, list=16%, signal=21%
BP	GO:0030855	epithelial cell differentiation	422	-0.3838	-1.5689	1.3622E-04	2.5244E-02	2.3044E-02	1977	tags=23%, list=14%, signal=21%
BP	GO:0007265	Ras protein signal transduction	375	-0.3947	-1.5974	1.3897E-04	2.5244E-02	2.3044E-02	3011	tags=30%, list=21%, signal=24%
BP	GO:0050865	regulation of cell activation	374	-0.4122	-1.6676	1.3897E-04	2.5244E-02	2.3044E-02	2288	tags=28%, list=16%, signal=25%
BP	GO:0001525	angiogenesis	381	-0.4636	-1.8771	1.3916E-04	2.5244E-02	2.3044E-02	2172	tags=31%, list=15%, signal=27%
BP	GO:0002694	regulation of leukocyte activation	344	-0.4069	-1.6341	1.3994E-04	2.5244E-02	2.3044E-02	2012	tags=26%, list=14%, signal=23%
BP	GO:0009617	response to bacterium	356	-0.4071	-1.6384	1.4004E-04	2.5244E-02	2.3044E-02	2619	tags=31%, list=18%, signal=26%

CC	GO:0098552	side of membrane	338	-0.4184	-1.6777	1.4045E-04	2.5244E-02	2.3044E-02	1744 tags=22%, list=12%, signal=20%
BP	GO:0043062	extracellular structure organization	317	-0.4309	-1.7170	1.4154E-04	2.5244E-02	2.3044E-02	2274 tags=34%, list=16%, signal=29%
BP	GO:0036293	response to decreased oxygen levels	302	-0.4063	-1.6119	1.4241E-04	2.5244E-02	2.3044E-02	1843 tags=17%, list=13%, signal=15%
BP	GO:0042110	T cell activation	304	-0.4358	-1.7296	1.4253E-04	2.5244E-02	2.3044E-02	2012 tags=28%, list=14%, signal=24%
BP	GO:0051056	regulation of small GTPase mediated signal transduction	286	-0.4320	-1.7068	1.4269E-04	2.5244E-02	2.3044E-02	3000 tags=34%, list=20%, signal=27%
BP	GO:0001666	response to hypoxia	292	-0.4162	-1.6480	1.4271E-04	2.5244E-02	2.3044E-02	1843 tags=17%, list=13%, signal=15%
BP	GO:0045785	positive regulation of cell adhesion	291	-0.4348	-1.7208	1.4273E-04	2.5244E-02	2.3044E-02	2340 tags=31%, list=16%, signal=27%
BP	GO:0050900	leukocyte migration	281	-0.5136	-2.0261	1.4284E-04	2.5244E-02	2.3044E-02	1895 tags=35%, list=13%, signal=31%
BP	GO:0002768	immune response-regulating cell surface receptor signaling pathway	284	-0.4227	-1.6691	1.4288E-04	2.5244E-02	2.3044E-02	2619 tags=25%, list=18%, signal=21%
BP	GO:0010721	negative regulation of cell development	280	-0.4445	-1.7530	1.4302E-04	2.5244E-02	2.3044E-02	2241 tags=28%, list=15%, signal=24%
BP	GO:0030198	extracellular matrix organization	280	-0.4396	-1.7338	1.4302E-04	2.5244E-02	2.3044E-02	2274 tags=36%, list=16%, signal=31%
BP	GO:0022407	regulation of cell-cell adhesion	272	-0.4324	-1.7003	1.4329E-04	2.5244E-02	2.3044E-02	2416 tags=31%, list=16%, signal=26%
BP	GO:0040013	negative regulation of locomotion	261	-0.4636	-1.8161	1.4333E-04	2.5244E-02	2.3044E-02	2263 tags=30%, list=15%, signal=26%
BP	GO:0051961	negative regulation of nervous system development	265	-0.4595	-1.8024	1.4388E-04	2.5244E-02	2.3044E-02	2241 tags=29%, list=15%, signal=25%
BP	GO:0051271	negative regulation of cellular component movement	252	-0.4691	-1.8300	1.4393E-04	2.5244E-02	2.3044E-02	2263 tags=30%, list=15%, signal=26%
BP	GO:0050768	negative regulation of neurogenesis	245	-0.4576	-1.7803	1.4411E-04	2.5244E-02	2.3044E-02	2241 tags=29%, list=15%, signal=25%
BP	GO:0042063	gliogenesis	243	-0.5054	-1.9648	1.4430E-04	2.5244E-02	2.3044E-02	2562 tags=36%, list=17%, signal=30%
BP	GO:1901342	regulation of vasculature development	241	-0.4667	-1.8123	1.4472E-04	2.5244E-02	2.3044E-02	2147 tags=30%, list=15%, signal=26%
BP	GO:0032102	negative regulation of response to external stimulus	239	-0.4555	-1.7680	1.4484E-04	2.5244E-02	2.3044E-02	2263 tags=36%, list=15%, signal=29%
BP	GO:0072001	renal system development	230	-0.4457	-1.7236	1.4579E-04	2.5244E-02	2.3044E-02	2129 tags=32%, list=15%, signal=28%
BP	GO:2000146	negative regulation of cell motility	221	-0.4670	-1.7994	1.4631E-04	2.5244E-02	2.3044E-02	2263 tags=29%, list=15%, signal=24%
BP	GO:0001822	kidney development	216	-0.4415	-1.6979	1.4635E-04	2.5244E-02	2.3044E-02	2129 tags=31%, list=15%, signal=27%
BP	GO:0007159	leukocyte cell-cell adhesion	220	-0.4478	-1.7245	1.4641E-04	2.5244E-02	2.3044E-02	2251 tags=30%, list=15%, signal=26%
BP	GO:0098742	cell-cell adhesion via plasma-membrane adhesion molecules	218	-0.4561	-1.7547	1.4652E-04	2.5244E-02	2.3044E-02	2091 tags=30%, list=14%, signal=26%
CC	GO:0030667	secretory granule membrane	219	-0.4507	-1.7348	1.4656E-04	2.5244E-02	2.3044E-02	2283 tags=29%, list=16%, signal=25%
BP	GO:0045765	regulation of angiogenesis	213	-0.4969	-1.9074	1.4669E-04	2.5244E-02	2.3044E-02	2003 tags=31%, list=14%, signal=27%
MF	GO:0048018	receptor ligand activity	213	-0.4391	-1.6854	1.4669E-04	2.5244E-02	2.3044E-02	1526 tags=23%, list=10%, signal=21%
BP	GO:0030336	negative regulation of cell migration	212	-0.4724	-1.8130	1.4676E-04	2.5244E-02	2.3044E-02	2263 tags=29%, list=15%, signal=25%
BP	GO:0006909	phagocytosis	214	-0.4771	-1.8315	1.4680E-04	2.5244E-02	2.3044E-02	2626 tags=34%, list=18%, signal=28%
BP	GO:0060326	cell chemotaxis	179	-0.4928	-1.8549	1.5122E-04	2.5244E-02	2.3044E-02	2135 tags=32%, list=15%, signal=28%
CC	GO:0009897	external side of plasma membrane	177	-0.4998	-1.8778	1.5161E-04	2.5244E-02	2.3044E-02	2225 tags=36%, list=15%, signal=31%
BP	GO:0050730	regulation of peptidyl-tyrosine phosphorylation	177	-0.5070	-1.9046	1.5161E-04	2.5244E-02	2.3044E-02	2883 tags=35%, list=20%, signal=28%
BP	GO:0030595	leukocyte chemotaxis	129	-0.5592	-2.0163	1.5706E-04	2.5244E-02	2.3044E-02	1233 tags=23%, list=8%, signal=21%
BP	GO:0042552	myelination	120	-0.5764	-2.0563	1.5838E-04	2.5244E-02	2.3044E-02	1758 tags=33%, list=12%, signal=30%
BP	GO:0007272	ensheathment of neurons	122	-0.5791	-2.0686	1.5848E-04	2.5244E-02	2.3044E-02	1758 tags=30%, list=12%, signal=27%
BP	GO:0008366	axon ensheathment	122	-0.5791	-2.0686	1.5848E-04	2.5244E-02	2.3044E-02	1758 tags=30%, list=12%, signal=27%
BP	GO:0097529	myeloid leukocyte migration	122	-0.5687	-2.0314	1.5848E-04	2.5244E-02	2.3044E-02	1475 tags=35%, list=10%, signal=32%
CC	GO:0070821	tertiary granule membrane	50	-0.6609	-2.0571	1.6992E-04	2.5842E-02	2.3590E-02	1402 tags=38%, list=10%, signal=34%
BP	GO:0050922	negative regulation of chemotaxis	47	-0.6662	-2.0534	1.7065E-04	2.5842E-02	2.3590E-02	2199 tags=49%, list=15%, signal=42%
BP	GO:0014003	oligodendrocyte development	40	-0.6975	-2.0861	1.7129E-04	2.5842E-02	2.3590E-02	973 tags=38%, list=7%, signal=35%
CC	GO:0043209	myelin sheath	43	-0.7426	-2.2490	1.7141E-04	2.5842E-02	2.3590E-02	1419 tags=47%, list=10%, signal=42%
BP	GO:0072577	endothelial cell apoptotic process	39	-0.7216	-2.1445	1.7200E-04	2.5842E-02	2.3590E-02	489 tags=18%, list=3%, signal=17%
BP	GO:2000351	regulation of endothelial cell apoptotic process	34	-0.7350	-2.1186	1.7504E-04	2.5842E-02	2.3590E-02	489 tags=21%, list=3%, signal=20%
BP	GO:0072678	T cell migration	35	-0.7020	-2.0319	1.7544E-04	2.5842E-02	2.3590E-02	1131 tags=20%, list=8%, signal=18%
BP	GO:0072160	nephron tubule epithelial cell differentiation	10	-0.8997	-1.9850	1.8491E-04	2.6948E-02	2.4600E-02	1370 tags=80%, list=9%, signal=73%
MF	GO:0004965	G protein-coupled GABA receptor activity	3	-0.9888	-1.6295	1.9720E-04	2.6972E-02	2.4622E-02	26 tags=67%, list=0%, signal=67%
MF	GO:0019763	immunoglobulin receptor activity	3	-0.9868	-1.6262	1.9720E-04	2.6972E-02	2.4622E-02	150 tags=100%, list=1%, signal=99%
CC	GO:0038039	G protein-coupled receptor heterodimeric complex	3	-0.9888	-1.6295	1.9720E-04	2.6972E-02	2.4622E-02	26 tags=67%, list=0%, signal=67%
BP	GO:0046121	deoxyribonucleoside catabolic process	3	-0.9892	-1.6303	1.9720E-04	2.6972E-02	2.4622E-02	100 tags=67%, list=1%, signal=66%
MF	GO:0047391	alkylglycerophosphoethanolamine phosphodiesterase activity	3	-0.9872	-1.6269	1.9720E-04	2.6972E-02	2.4622E-02	102 tags=67%, list=1%, signal=66%

BP	GO:2000698	positive regulation of epithelial cell differentiation involved in kidney de	3	-0.9929	-1.6363	1.9720E-04	2.6972E-02	2.4622E-02	108 tags=100%, list=1%, signal=99%
BP	GO:0070426	positive regulation of nucleotide-binding oligomerization domain conta	3	0.9895	1.6361	2.0280E-04	2.6972E-02	2.4622E-02	5 tags=67%, list=0%, signal=67%
BP	GO:0070434	positive regulation of nucleotide-binding oligomerization domain conta	3	0.9895	1.6361	2.0280E-04	2.6972E-02	2.4622E-02	5 tags=67%, list=0%, signal=67%
BP	GO:0090063	positive regulation of microtubule nucleation	3	0.9885	1.6345	2.0280E-04	2.6972E-02	2.4622E-02	5 tags=67%, list=0%, signal=67%
BP	GO:0010968	regulation of microtubule nucleation	5	0.9761	1.8403	2.0899E-04	2.7528E-02	2.5129E-02	5 tags=40%, list=0%, signal=40%
BP	GO:0060700	regulation of ribonuclease activity	8	0.9396	2.0022	2.1538E-04	2.8028E-02	2.5585E-02	167 tags=38%, list=1%, signal=37%
BP	GO:0097201	negative regulation of transcription from RNA polymerase II promoter	12	0.8952	2.1309	2.1687E-04	2.8028E-02	2.5585E-02	6 tags=25%, list=0%, signal=25%
MF	GO:0044183	protein binding involved in protein folding	20	0.9151	2.4721	2.2477E-04	2.8681E-02	2.6182E-02	86 tags=25%, list=1%, signal=25%
BP	GO:0051085	chaperone cofactor-dependent protein refolding	28	0.8842	2.5762	2.3073E-04	2.8681E-02	2.6182E-02	143 tags=25%, list=1%, signal=25%
BP	GO:0042026	protein refolding	32	0.8434	2.5270	2.3223E-04	2.8681E-02	2.6182E-02	136 tags=19%, list=1%, signal=19%
CC	GO:0008180	COP9 signalosome	33	0.8750	2.6387	2.3240E-04	2.8681E-02	2.6182E-02	86 tags=12%, list=1%, signal=12%
BP	GO:0051084	'de novo' posttranslational protein folding	33	0.8695	2.6220	2.3240E-04	2.8681E-02	2.6182E-02	143 tags=21%, list=1%, signal=21%
BP	GO:006458	'de novo' protein folding	37	0.8657	2.6598	2.3540E-04	2.8793E-02	2.6284E-02	143 tags=22%, list=1%, signal=21%
BP	GO:0061077	chaperone-mediated protein folding	53	0.8517	2.8099	2.4319E-04	2.9385E-02	2.6825E-02	145 tags=21%, list=1%, signal=21%
BP	GO:0045597	positive regulation of cell differentiation	772	-0.3401	-1.4484	2.5397E-04	2.9385E-02	2.6825E-02	2157 tags=22%, list=15%, signal=19%
BP	GO:0042327	positive regulation of phosphorylation	759	-0.3426	-1.4574	2.5439E-04	2.9385E-02	2.6825E-02	1788 tags=17%, list=12%, signal=15%
BP	GO:1900034	regulation of cellular response to heat	79	0.6908	2.4430	2.5523E-04	2.9385E-02	2.6825E-02	206 tags=13%, list=1%, signal=13%
BP	GO:0001934	positive regulation of protein phosphorylation	716	-0.3444	-1.4596	2.5595E-04	2.9385E-02	2.6825E-02	1876 tags=17%, list=13%, signal=16%
MF	GO:0008289	lipid binding	557	-0.3559	-1.4854	2.6236E-04	2.9385E-02	2.6825E-02	1990 tags=19%, list=14%, signal=17%
BP	GO:0045664	regulation of neuron differentiation	570	-0.3485	-1.4552	2.6316E-04	2.9385E-02	2.6825E-02	2241 tags=21%, list=15%, signal=18%
BP	GO:0071363	cellular response to growth factor stimulus	549	-0.3530	-1.4713	2.6337E-04	2.9385E-02	2.6825E-02	2157 tags=23%, list=15%, signal=20%
MF	GO:0051082	unfolded protein binding	108	0.7366	2.7379	2.6532E-04	2.9385E-02	2.6825E-02	1516 tags=24%, list=10%, signal=22%
MF	GO:0031072	heat shock protein binding	109	0.6405	2.3822	2.6631E-04	2.9385E-02	2.6825E-02	1449 tags=21%, list=10%, signal=19%
BP	GO:0048729	tissue morphogenesis	499	-0.3562	-1.4747	2.6688E-04	2.9385E-02	2.6825E-02	2198 tags=23%, list=15%, signal=20%
BP	GO:0034605	cellular response to heat	118	0.6705	2.5249	2.6867E-04	2.9385E-02	2.6825E-02	206 tags=10%, list=1%, signal=10%
BP	GO:0061564	axon development	436	-0.3703	-1.5168	2.7163E-04	2.9385E-02	2.6825E-02	2201 tags=22%, list=15%, signal=19%
BP	GO:2000147	positive regulation of cell motility	408	-0.3739	-1.5230	2.7420E-04	2.9385E-02	2.6825E-02	2340 tags=27%, list=16%, signal=24%
BP	GO:0009408	response to heat	149	0.6163	2.3872	2.8137E-04	2.9385E-02	2.6825E-02	604 tags=13%, list=4%, signal=13%
BP	GO:0070482	response to oxygen levels	321	-0.4058	-1.6194	2.8197E-04	2.9385E-02	2.6825E-02	1843 tags=17%, list=13%, signal=15%
BP	GO:0051249	regulation of lymphocyte activation	282	-0.4128	-1.6292	2.8576E-04	2.9385E-02	2.6825E-02	2012 tags=26%, list=14%, signal=23%
BP	GO:0018212	peptidyl-tyrosine modification	269	-0.4310	-1.6933	2.8657E-04	2.9385E-02	2.6825E-02	1720 tags=21%, list=12%, signal=19%
CC	GO:0045177	apical part of cell	262	-0.4385	-1.7188	2.8682E-04	2.9385E-02	2.6825E-02	1544 tags=24%, list=11%, signal=22%
BP	GO:0006986	response to unfolded protein	161	0.6215	2.4285	2.8719E-04	2.9385E-02	2.6825E-02	143 tags=9%, list=1%, signal=9%
BP	GO:0018108	peptidyl-tyrosine phosphorylation	266	-0.4309	-1.6911	2.8732E-04	2.9385E-02	2.6825E-02	1720 tags=21%, list=12%, signal=19%
CC	GO:0044450	microtubule organizing center part	160	0.5575	2.1764	2.8744E-04	2.9385E-02	2.6825E-02	1706 tags=14%, list=12%, signal=13%
BP	GO:0035966	response to topologically incorrect protein	182	0.6034	2.3926	2.9647E-04	2.9833E-02	2.7233E-02	143 tags=8%, list=1%, signal=8%
BP	GO:0019882	antigen processing and presentation	187	-0.4610	-1.7451	3.0003E-04	2.9833E-02	2.7233E-02	1736 tags=17%, list=12%, signal=15%
BP	GO:0070661	leukocyte proliferation	188	-0.4786	-1.8124	3.0048E-04	2.9833E-02	2.7233E-02	2288 tags=36%, list=16%, signal=30%
BP	GO:0010001	glial cell differentiation	186	-0.4708	-1.7808	3.0053E-04	2.9833E-02	2.7233E-02	2646 tags=35%, list=18%, signal=29%
BP	GO:0006457	protein folding	194	0.6522	2.6012	3.0303E-04	2.9865E-02	2.7262E-02	358 tags=10%, list=2%, signal=10%
BP	GO:0009266	response to temperature stimulus	202	0.5287	2.1165	3.0941E-04	3.0033E-02	2.7416E-02	610 tags=12%, list=4%, signal=12%
BP	GO:0044344	cellular response to fibroblast growth factor stimulus	107	-0.5371	-1.8896	3.2041E-04	3.0033E-02	2.7416E-02	1484 tags=20%, list=10%, signal=18%
BP	GO:0071774	response to fibroblast growth factor	110	-0.5449	-1.9179	3.2056E-04	3.0033E-02	2.7416E-02	528 tags=20%, list=4%, signal=19%
BP	GO:0055123	digestive system development	102	-0.5693	-1.9847	3.2201E-04	3.0033E-02	2.7416E-02	1211 tags=28%, list=8%, signal=26%
BP	GO:0048565	digestive tract development	94	-0.5876	-2.0264	3.2237E-04	3.0033E-02	2.7416E-02	1211 tags=30%, list=8%, signal=28%
BP	GO:0021782	glial cell development	101	-0.5235	-1.8225	3.2253E-04	3.0033E-02	2.7416E-02	1758 tags=32%, list=12%, signal=28%
BP	GO:0014013	regulation of gliogenesis	96	-0.5313	-1.8375	3.2263E-04	3.0033E-02	2.7416E-02	2530 tags=40%, list=17%, signal=33%
BP	GO:0006959	humoral immune response	92	-0.5621	-1.9331	3.2326E-04	3.0033E-02	2.7416E-02	1122 tags=26%, list=8%, signal=24%
BP	GO:0048709	oligodendrocyte differentiation	86	-0.5665	-1.9317	3.2446E-04	3.0033E-02	2.7416E-02	973 tags=28%, list=7%, signal=26%
BP	GO:0097530	granulocyte migration	70	-0.6067	-2.0040	3.3031E-04	3.0368E-02	2.7722E-02	1233 tags=29%, list=8%, signal=26%

BP	GO:0072676	lymphocyte migration	53	-0.6193	-1.9442	3.3956E-04	3.0805E-02	2.8121E-02	1131 tags=17%, list=8%, signal=16%
BP	GO:1990266	neutrophil migration	53	-0.6266	-1.9669	3.3956E-04	3.0805E-02	2.8121E-02	1184 tags=30%, list=8%, signal=28%
BP	GO:0035329	hippo signaling	33	-0.6947	-1.9912	3.5094E-04	3.1628E-02	2.8872E-02	1767 tags=39%, list=12%, signal=35%
MF	GO:0019864	IgG binding	6	-0.9638	-1.8783	3.8045E-04	3.3849E-02	3.0899E-02	329 tags=83%, list=2%, signal=81%
BP	GO:0009887	animal organ morphogenesis	766	-0.3247	-1.3826	3.8052E-04	3.3849E-02	3.0899E-02	2201 tags=23%, list=15%, signal=20%
CC	GO:0000139	Golgi membrane	653	-0.3369	-1.4198	3.8800E-04	3.4292E-02	3.1303E-02	2906 tags=22%, list=20%, signal=18%
BP	GO:0061047	positive regulation of branching involved in lung morphogenesis	4	0.9764	1.7445	4.0601E-04	3.5542E-02	3.2445E-02	239 tags=75%, list=2%, signal=74%
BP	GO:0040017	positive regulation of locomotion	433	-0.3678	-1.5061	4.0733E-04	3.5542E-02	3.2445E-02	2340 tags=22%, list=16%, signal=23%
CC	GO:0098589	membrane region	273	-0.4006	-1.5757	4.3005E-04	3.7244E-02	3.3998E-02	1734 tags=24%, list=12%, signal=22%
BP	GO:0001655	urogenital system development	255	-0.4327	-1.6894	4.3228E-04	3.7244E-02	3.3998E-02	2129 tags=31%, list=15%, signal=27%
BP	GO:0098656	anion transmembrane transport	206	-0.4358	-1.6691	4.4248E-04	3.7884E-02	3.4583E-02	2273 tags=29%, list=16%, signal=25%
BP	GO:0045665	negative regulation of neuron differentiation	194	-0.4362	-1.6587	4.4763E-04	3.8087E-02	3.4768E-02	2241 tags=29%, list=15%, signal=25%
BP	GO:0032943	mononuclear cell proliferation	172	-0.4709	-1.7622	4.5683E-04	3.8188E-02	3.4861E-02	2288 tags=35%, list=16%, signal=30%
MF	GO:0051787	misfolded protein binding	24	0.8479	2.3916	4.5704E-04	3.8188E-02	3.4861E-02	359 tags=21%, list=2%, signal=20%
BP	GO:0046651	lymphocyte proliferation	170	-0.4728	-1.7668	4.5718E-04	3.8188E-02	3.4861E-02	2288 tags=35%, list=16%, signal=30%
BP	GO:0070663	regulation of leukocyte proliferation	140	-0.5051	-1.8410	4.6758E-04	3.8294E-02	3.4957E-02	2288 tags=39%, list=16%, signal=33%
BP	GO:0032944	regulation of mononuclear cell proliferation	134	-0.4977	-1.8052	4.6831E-04	3.8294E-02	3.4957E-02	2288 tags=39%, list=16%, signal=33%
BP	GO:0002685	regulation of leukocyte migration	132	-0.4925	-1.7817	4.7015E-04	3.8294E-02	3.4957E-02	2200 tags=33%, list=15%, signal=28%
BP	GO:0050670	regulation of lymphocyte proliferation	133	-0.4951	-1.7921	4.7118E-04	3.8294E-02	3.4957E-02	2288 tags=38%, list=16%, signal=33%
BP	GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	125	-0.5146	-1.8455	4.7408E-04	3.8294E-02	3.4957E-02	2856 tags=38%, list=20%, signal=31%
BP	GO:0045766	positive regulation of angiogenesis	124	-0.5208	-1.8642	4.7521E-04	3.8294E-02	3.4957E-02	1879 tags=35%, list=13%, signal=30%
CC	GO:0042581	specific granule	109	-0.5018	-1.7653	4.8023E-04	3.8472E-02	3.5119E-02	2494 tags=35%, list=17%, signal=29%
BP	GO:0030316	osteoclast differentiation	68	-0.5597	-1.8415	4.9636E-04	3.8814E-02	3.5432E-02	3708 tags=54%, list=25%, signal=41%
BP	GO:2000117	negative regulation of cysteine-type endopeptidase activity	65	-0.5820	-1.9029	4.9817E-04	3.8814E-02	3.5432E-02	412 tags=15%, list=3%, signal=15%
CC	GO:0035579	specific granule membrane	66	-0.5952	-1.9462	4.9975E-04	3.8814E-02	3.5432E-02	2728 tags=44%, list=19%, signal=36%
BP	GO:0043154	negative regulation of cysteine-type endopeptidase activity involved in	61	-0.6061	-1.9595	5.0100E-04	3.8814E-02	3.5432E-02	412 tags=16%, list=3%, signal=16%
BP	GO:0071621	granulocyte chemotaxis	61	-0.6035	-1.9510	5.0100E-04	3.8814E-02	3.5432E-02	1233 tags=28%, list=8%, signal=26%
BP	GO:0009247	glycolipid biosynthetic process	60	-0.5928	-1.9116	5.0150E-04	3.8814E-02	3.5432E-02	1971 tags=23%, list=13%, signal=20%
MF	GO:0005215	transporter activity	797	-0.3211	-1.3692	5.0665E-04	3.8992E-02	3.5594E-02	2231 tags=20%, list=15%, signal=18%
CC	GO:0012506	vesicle membrane	651	-0.3324	-1.4006	5.1740E-04	3.9164E-02	3.5751E-02	1494 tags=15%, list=10%, signal=14%
BP	GO:1901137	carbohydrate derivative biosynthetic process	646	-0.3315	-1.3957	5.1847E-04	3.9164E-02	3.5751E-02	2796 tags=22%, list=19%, signal=19%
BP	GO:0009607	response to biotic stimulus	603	-0.3377	-1.4154	5.2315E-04	3.9164E-02	3.5751E-02	1842 tags=19%, list=13%, signal=17%
CC	GO:0030141	secretory granule	596	-0.3372	-1.4128	5.2377E-04	3.9164E-02	3.5751E-02	1421 tags=18%, list=10%, signal=17%
BP	GO:0043207	response to external biotic stimulus	575	-0.3440	-1.4374	5.2604E-04	3.9164E-02	3.5751E-02	1768 tags=19%, list=12%, signal=17%
BP	GO:0051707	response to other organism	575	-0.3440	-1.4374	5.2604E-04	3.9164E-02	3.5751E-02	1768 tags=19%, list=12%, signal=17%
CC	GO:0005814	centriole	119	0.6013	2.2695	5.3879E-04	3.9897E-02	3.6420E-02	5 tags=3%, list=0%, signal=3%
MF	GO:0042379	chemokine receptor binding	17	-0.8005	-1.9983	5.4456E-04	3.9916E-02	3.6438E-02	44 tags=24%, list=0%, signal=23%
BP	GO:0051272	positive regulation of cellular component movement	422	-0.3678	-1.5036	5.4488E-04	3.9916E-02	3.6438E-02	2340 tags=27%, list=16%, signal=23%
BP	GO:0030335	positive regulation of cell migration	398	-0.3719	-1.5119	5.4968E-04	4.0053E-02	3.6563E-02	2340 tags=27%, list=16%, signal=24%
BP	GO:1903044	protein localization to membrane raft	8	-0.9125	-1.9130	5.5981E-04	4.0576E-02	3.7040E-02	2 tags=25%, list=0%, signal=25%
BP	GO:0035967	cellular response to topologically incorrect protein	147	0.5416	2.0897	5.6449E-04	4.0700E-02	3.7153E-02	120 tags=4%, list=1%, signal=4%
CC	GO:0098857	membrane microdomain	266	-0.4033	-1.5827	5.7463E-04	4.1064E-02	3.7486E-02	1734 tags=25%, list=12%, signal=22%
CC	GO:0045121	membrane raft	265	-0.4046	-1.5871	5.7564E-04	4.1064E-02	3.7486E-02	1734 tags=25%, list=12%, signal=22%
BP	GO:0002250	adaptive immune response	239	-0.4297	-1.6680	5.7937E-04	4.1124E-02	3.7540E-02	2317 tags=32%, list=16%, signal=27%
BP	GO:0046578	regulation of Ras protein signal transduction	198	-0.4316	-1.6454	5.9453E-04	4.1982E-02	3.8323E-02	2619 tags=31%, list=18%, signal=26%
BP	GO:0003373	dynamin family protein polymerization involved in membrane fission	4	0.9725	1.7377	6.0901E-04	4.2566E-02	3.8856E-02	129 tags=50%, list=1%, signal=50%
BP	GO:0003374	dynamin family protein polymerization involved in mitochondrial fission	4	0.9725	1.7377	6.0901E-04	4.2566E-02	3.8856E-02	129 tags=50%, list=1%, signal=50%
BP	GO:0001763	morphogenesis of a branching structure	145	-0.4799	-1.7584	6.1833E-04	4.2781E-02	3.9053E-02	2201 tags=40%, list=15%, signal=34%
BP	GO:0048015	phosphatidylinositol-mediated signaling	145	-0.4791	-1.7555	6.1833E-04	4.2781E-02	3.9053E-02	3134 tags=38%, list=21%, signal=30%
BP	GO:1904018	positive regulation of vasculature development	141	-0.4914	-1.7925	6.2267E-04	4.2864E-02	3.9129E-02	1879 tags=33%, list=13%, signal=29%

BP	GO:0008360	regulation of cell shape	129	-0.5004	-1.8043	6.2824E-04	4.3031E-02	3.9281E-02	2259 tags=31%, list=15%, signal=26%
BP	GO:0070665	positive regulation of leukocyte proliferation	83	-0.5466	-1.8526	6.5317E-04	4.4140E-02	4.0294E-02	1949 tags=33%, list=13%, signal=28%
BP	GO:0032946	positive regulation of mononuclear cell proliferation	80	-0.5481	-1.8471	6.5552E-04	4.4140E-02	4.0294E-02	1949 tags=32%, list=13%, signal=28%
BP	GO:0098840	protein transport along microtubule	15	0.8466	2.1397	6.5732E-04	4.4140E-02	4.0294E-02	7 tags=13%, list=0%, signal=13%
BP	GO:0099118	microtubule-based protein transport	15	0.8466	2.1397	6.5732E-04	4.4140E-02	4.0294E-02	7 tags=13%, list=0%, signal=13%
BP	GO:0048589	developmental growth	528	-0.3465	-1.4411	6.6173E-04	4.4219E-02	4.0366E-02	2201 tags=22%, list=15%, signal=20%
BP	GO:0031102	neuron projection regeneration	51	-0.6119	-1.9116	6.7866E-04	4.5025E-02	4.1102E-02	978 tags=24%, list=7%, signal=22%
BP	GO:0035904	aorta development	47	-0.6306	-1.9438	6.8259E-04	4.5025E-02	4.1102E-02	2376 tags=47%, list=16%, signal=39%
BP	GO:0030593	neutrophil chemotaxis	46	-0.6404	-1.9629	6.8364E-04	4.5025E-02	4.1102E-02	1184 tags=33%, list=8%, signal=30%
CC	GO:0031012	extracellular matrix	370	-0.3798	-1.5356	6.9377E-04	4.5473E-02	4.1511E-02	1695 tags=25%, list=12%, signal=23%
BP	GO:0006688	glycosphingolipid biosynthetic process	24	-0.7366	-1.9819	7.1098E-04	4.6380E-02	4.2338E-02	546 tags=33%, list=4%, signal=32%
BP	GO:0035587	purinergic receptor signaling pathway	20	-0.7641	-1.9790	7.2033E-04	4.6767E-02	4.2692E-02	1392 tags=55%, list=10%, signal=50%
BP	GO:0002237	response to molecule of bacterial origin	229	-0.4276	-1.6533	7.2939E-04	4.7132E-02	4.3025E-02	2224 tags=27%, list=15%, signal=23%
BP	GO:0071356	cellular response to tumor necrosis factor	199	-0.4264	-1.6266	7.4140E-04	4.7558E-02	4.3414E-02	1107 tags=14%, list=8%, signal=13%
BP	GO:0072182	regulation of nephron tubule epithelial cell differentiation	8	-0.9033	-1.8937	7.4641E-04	4.7558E-02	4.3414E-02	108 tags=75%, list=1%, signal=74%
BP	GO:2000696	regulation of epithelial cell differentiation involved in kidney developme	8	-0.9033	-1.8937	7.4641E-04	4.7558E-02	4.3414E-02	108 tags=75%, list=1%, signal=74%
BP	GO:0048017	inositol lipid-mediated signaling	148	-0.4741	-1.7388	7.7592E-04	4.9210E-02	4.4921E-02	3134 tags=38%, list=21%, signal=30%
BP	GO:0061138	morphogenesis of a branching epithelium	135	-0.4712	-1.7110	7.8162E-04	4.9343E-02	4.5043E-02	2188 tags=40%, list=15%, signal=34%
BP	GO:0071346	cellular response to interferon-gamma	128	-0.4852	-1.7472	7.8555E-04	4.9363E-02	4.5062E-02	2184 tags=33%, list=15%, signal=28%

Event 1 – LINC00665 (KEGG)

ID	Description	setSize	enrichmentScore	NES	pvalue	p.adjust	qvalues	rank	leading_edge
hsa04933	AGE-RAGE signaling pathway in diabetic complications	90	-0.6016	-2.0596	1.5969E-04	6.9084E-03	5.5447E-03	1799	tags=28%, list=12%, signal=25%
hsa05140	Leishmaniasis	58	-0.6488	-2.0727	1.6431E-04	6.9084E-03	5.5447E-03	1252	tags=36%, list=9%, signal=33%
hsa05323	Rheumatoid arthritis	56	-0.6878	-2.1862	1.6434E-04	6.9084E-03	5.5447E-03	1233	tags=32%, list=8%, signal=30%
hsa04640	Hematopoietic cell lineage	51	-0.6902	-2.1612	1.6540E-04	6.9084E-03	5.5447E-03	1046	tags=45%, list=7%, signal=42%
hsa05150	Staphylococcus aureus infection	39	-0.6561	-1.9466	1.6801E-04	6.9084E-03	5.5447E-03	1122	tags=49%, list=8%, signal=45%
hsa05219	Bladder cancer	35	-0.7352	-2.1312	1.6969E-04	6.9084E-03	5.5447E-03	920	tags=26%, list=6%, signal=24%
hsa04061	Viral protein interaction with cytokine and cytokine receptor	29	-0.6990	-1.9575	1.7044E-04	6.9084E-03	5.5447E-03	1689	tags=45%, list=12%, signal=40%
hsa05162	Measles	100	0.6102	2.2409	2.7248E-04	6.9084E-03	5.5447E-03	167	tags=8%, list=1%, signal=8%
hsa04915	Estrogen signaling pathway	104	0.6059	2.2379	2.7510E-04	6.9084E-03	5.5447E-03	194	tags=7%, list=1%, signal=7%
hsa03040	Spliceosome	129	0.6975	2.6439	2.8450E-04	6.9084E-03	5.5447E-03	86	tags=5%, list=1%, signal=5%
hsa04141	Protein processing in endoplasmic reticulum	158	0.6133	2.3891	2.9231E-04	6.9084E-03	5.5447E-03	928	tags=9%, list=6%, signal=9%
hsa05020	Prion disease	223	0.4744	1.9246	3.1037E-04	6.9084E-03	5.5447E-03	246	tags=4%, list=2%, signal=4%
hsa04514	Cell adhesion molecules	108	-0.5309	-1.8696	3.1299E-04	6.9084E-03	5.5447E-03	1532	tags=36%, list=10%, signal=33%
hsa04666	Fc gamma R-mediated phagocytosis	88	-0.5214	-1.7784	3.2087E-04	6.9084E-03	5.5447E-03	2814	tags=39%, list=19%, signal=31%
hsa04670	Leukocyte transendothelial migration	85	-0.5428	-1.8437	3.2134E-04	6.9084E-03	5.5447E-03	1799	tags=27%, list=12%, signal=24%
hsa05142	Chagas disease	82	-0.5427	-1.8300	3.2415E-04	6.9084E-03	5.5447E-03	1252	tags=17%, list=9%, signal=16%
hsa04062	Chemokine signaling pathway	129	-0.4877	-1.7609	4.6246E-04	8.3123E-03	6.6714E-03	1829	tags=20%, list=12%, signal=18%
hsa04621	NOD-like receptor signaling pathway	128	-0.4849	-1.7481	4.6339E-04	8.3123E-03	6.6714E-03	1361	tags=16%, list=9%, signal=14%
hsa04145	Phagosome	118	-0.5013	-1.7881	4.6519E-04	8.3123E-03	6.6714E-03	1022	tags=25%, list=7%, signal=23%
hsa04657	IL-17 signaling pathway	57	-0.6102	-1.9456	4.9221E-04	8.3123E-03	6.6714E-03	176	tags=14%, list=1%, signal=14%
hsa04213	Longevity regulating pathway - multiple species	57	0.7426	2.4786	5.1190E-04	8.3123E-03	6.6714E-03	206	tags=9%, list=1%, signal=9%
hsa05135	Yersinia infection	120	-0.4852	-1.7357	6.1939E-04	9.6005E-03	7.7053E-03	1799	tags=17%, list=12%, signal=15%
hsa05146	Amoebiasis	71	-0.5393	-1.7792	6.4988E-04	9.6351E-03	7.7331E-03	1637	tags=28%, list=11%, signal=25%
hsa05130	Pathogenic Escherichia coli infection	158	-0.4413	-1.6338	9.1172E-04	1.2954E-02	1.0397E-02	1898	tags=27%, list=13%, signal=23%
hsa05145	Toxoplasmosis	91	0.6020	2.1744	1.0712E-03	1.4612E-02	1.1727E-02	86	tags=5%, list=1%, signal=5%
hsa04151	PI3K-Akt signaling pathway	264	-0.3898	-1.5262	1.2955E-03	1.6991E-02	1.3637E-02	2673	tags=28%, list=18%, signal=23%
hsa04512	ECM-receptor interaction	69	-0.5320	-1.7462	1.4610E-03	1.8402E-02	1.4769E-02	1042	tags=36%, list=7%, signal=34%
hsa05205	Proteoglycans in cancer	174	-0.4191	-1.5686	1.5110E-03	1.8402E-02	1.4769E-02	1827	tags=22%, list=12%, signal=20%
hsa04510	Focal adhesion	176	-0.4166	-1.5623	2.1075E-03	2.4781E-02	1.9889E-02	2467	tags=25%, list=17%, signal=21%
hsa04612	Antigen processing and presentation	54	0.6915	2.2915	2.2750E-03	2.5859E-02	2.0755E-02	86	tags=11%, list=1%, signal=11%
hsa04380	Osteoclast differentiation	98	-0.4687	-1.6250	2.6933E-03	2.9626E-02	2.3778E-02	2530	tags=34%, list=17%, signal=28%
hsa04144	Endocytosis	232	0.4273	1.7406	2.8029E-03	2.9868E-02	2.3972E-02	304	tags=3%, list=2%, signal=3%
hsa03320	PPAR signaling pathway	55	-0.5488	-1.7380	2.9698E-03	2.9963E-02	2.4048E-02	3383	tags=49%, list=23%, signal=38%
hsa04015	Rap1 signaling pathway	180	-0.4063	-1.5277	3.0008E-03	2.9963E-02	2.4048E-02	1829	tags=23%, list=12%, signal=20%
hsa05144	Malaria	33	-0.6229	-1.7839	3.0753E-03	2.9963E-02	2.4048E-02	1252	tags=39%, list=9%, signal=36%
hsa04060	Cytokine-cytokine receptor interaction	109	-0.4557	-1.6063	3.4391E-03	3.2576E-02	2.6145E-02	1582	tags=24%, list=11%, signal=21%
hsa05163	Human cytomegalovirus infection	182	-0.4046	-1.5238	3.7380E-03	3.4451E-02	2.7650E-02	1746	tags=24%, list=12%, signal=22%
hsa05416	Viral myocarditis	46	-0.5583	-1.7132	4.6784E-03	4.1982E-02	3.3695E-02	1686	tags=39%, list=12%, signal=35%
hsa04072	Phospholipase D signaling pathway	130	-0.4274	-1.5464	5.3854E-03	4.7088E-02	3.7793E-02	3005	tags=30%, list=21%, signal=24%
hsa00100	Steroid biosynthesis	15	-0.7375	-1.7793	5.8803E-03	4.9599E-02	3.9808E-02	2981	tags=67%, list=20%, signal=53%
hsa04010	MAPK signaling pathway	249	0.4033	1.6527	6.0858E-03	4.9599E-02	3.9808E-02	595	tags=6%, list=4%, signal=6%
hsa00565	Ether lipid metabolism	35	-0.5946	-1.7236	6.1089E-03	4.9599E-02	3.9808E-02	2601	tags=43%, list=18%, signal=35%

Event 1 – LINC00665 (Hallmark)

ID	Description	setSize	enrichmentScore	NES	pvalue	p.adjust	qvalues	rank	leading_edge
HALLMARK_IL2_STAT5_SIGNALING	HALLMARK_IL2_STAT5_SIGNALING	156	-0.4978	-1.8321	1.5263E-04	2.5904E-03	1.8542E-03	2475	tags=35%, list=17%, signal=29%
HALLMARK_INFLAMMATORY_RESPONSE	HALLMARK_INFLAMMATORY_RESPONSE	141	-0.6180	-2.2503	1.5314E-04	2.5904E-03	1.8542E-03	2000	tags=43%, list=14%, signal=38%
HALLMARK_ALLOGRAFT_REJECTION	HALLMARK_ALLOGRAFT_REJECTION	123	-0.5135	-1.8364	1.5642E-04	2.5904E-03	1.8542E-03	2741	tags=39%, list=19%, signal=32%
HALLMARK_COAGULATION	HALLMARK_COAGULATION	87	-0.5253	-1.7846	6.3969E-04	7.9962E-03	5.7236E-03	1331	tags=25%, list=9%, signal=23%
HALLMARK_TNFA_SIGNALING_VIA_NFKB	HALLMARK_TNFA_SIGNALING_VIA_NFKB	170	-0.4345	-1.6188	1.3550E-03	1.1995E-02	8.5857E-03	796	tags=20%, list=5%, signal=19%
HALLMARK_COMPLEMENT	HALLMARK_COMPLEMENT	157	-0.4417	-1.6272	1.6743E-03	1.1995E-02	8.5857E-03	1612	tags=25%, list=11%, signal=22%
HALLMARK_IL6_JAK_STAT3_SIGNALING	HALLMARK_IL6_JAK_STAT3_SIGNALING	55	-0.5844	-1.8428	1.6733E-03	1.1995E-02	8.5857E-03	2633	tags=47%, list=17%, signal=39%
HALLMARK_ANGIOGENESIS	HALLMARK_ANGIOGENESIS	27	-0.6716	-1.8401	3.3410E-03	2.0105E-02	1.4391E-02	2274	tags=44%, list=16%, signal=38%
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	175	-0.4124	-1.5421	3.6188E-03	2.0105E-02	1.4391E-02	1686	tags=29%, list=12%, signal=26%
HALLMARK_INTERFERON_GAMMA_RESPONSE	HALLMARK_INTERFERON_GAMMA_RESPONSE	172	-0.4020	-1.5013	5.6980E-03	2.8490E-02	2.0393E-02	1894	tags=30%, list=13%, signal=27%
HALLMARK_ESTROGEN_RESPONSE_EARLY	HALLMARK_ESTROGEN_RESPONSE_EARLY	157	-0.4051	-1.4923	7.4581E-03	3.3901E-02	2.4266E-02	2193	tags=26%, list=15%, signal=22%

Event 2 – NSUN4 (GO)

ONTOLOGY	ID	Description	setSize	enrichmentScore	NES	pvalue	p.adjust	qvalues	rank	leading_edge
BP	GO:0035295	tube development	791	-0.3904	-1.8377	1.0520E-04	9.3680E-03	8.1490E-03	3295	tags=31%, list=22%, signal=26%
MF	GO:0043565	sequence-specific DNA binding	769	-0.3130	-1.4718	1.0526E-04	9.3680E-03	8.1490E-03	3043	tags=25%, list=20%, signal=21%
BP	GO:0040012	regulation of locomotion	790	-0.3730	-1.7553	1.0529E-04	9.3680E-03	8.1490E-03	3608	tags=34%, list=24%, signal=27%
BP	GO:0009887	animal organ morphogenesis	780	-0.3347	-1.5739	1.0531E-04	9.3680E-03	8.1490E-03	3516	tags=33%, list=23%, signal=27%
BP	GO:0002684	positive regulation of immune system process	753	-0.3806	-1.7877	1.0549E-04	9.3680E-03	8.1490E-03	2053	tags=22%, list=13%, signal=20%
CC	GO:0009503	secretory vesicle	750	-0.3416	-1.6043	1.0555E-04	9.3680E-03	8.1490E-03	1800	tags=17%, list=12%, signal=16%
BP	GO:0006887	exocytosis	745	-0.3598	-1.6889	1.0560E-04	9.3680E-03	8.1490E-03	2971	tags=26%, list=19%, signal=22%
BP	GO:0051093	negative regulation of developmental process	733	-0.3150	-1.4782	1.0571E-04	9.3680E-03	8.1490E-03	3056	tags=26%, list=20%, signal=22%
MF	GO:0060089	molecular transducer activity	732	-0.3860	-1.8112	1.0578E-04	9.3680E-03	8.1490E-03	2536	tags=26%, list=17%, signal=23%
BP	GO:2000145	regulation of cell motility	731	-0.3742	-1.7553	1.0584E-04	9.3680E-03	8.1490E-03	3608	tags=34%, list=24%, signal=27%
BP	GO:0050776	regulation of immune response	703	-0.3778	-1.7693	1.0598E-04	9.3680E-03	8.1490E-03	2053	tags=22%, list=13%, signal=20%
BP	GO:0098657	import into cell	693	-0.3672	-1.7187	1.0619E-04	9.3680E-03	8.1490E-03	3338	tags=29%, list=22%, signal=24%
BP	GO:0030334	regulation of cell migration	688	-0.3866	-1.8083	1.0629E-04	9.3680E-03	8.1490E-03	3608	tags=35%, list=24%, signal=28%
BP	GO:0048534	hematopoietic or lymphoid organ development	688	-0.3203	-1.4981	1.0629E-04	9.3680E-03	8.1490E-03	3208	tags=27%, list=21%, signal=22%
MF	GO:0038023	signaling receptor activity	685	-0.3986	-1.8640	1.0644E-04	9.3680E-03	8.1490E-03	2536	tags=27%, list=17%, signal=23%
BP	GO:0043069	negative regulation of programmed cell death	687	-0.3255	-1.5220	1.0644E-04	9.3680E-03	8.1490E-03	2431	tags=20%, list=16%, signal=18%
BP	GO:0033993	response to lipid	680	-0.3511	-1.6414	1.0646E-04	9.3680E-03	8.1490E-03	2227	tags=22%, list=15%, signal=20%
MF	GO:0044212	transcription regulatory region DNA binding	675	-0.3284	-1.5350	1.0647E-04	9.3680E-03	8.1490E-03	3043	tags=27%, list=20%, signal=23%
MF	GO:0011067	regulatory region nucleic acid binding	676	-0.3281	-1.5335	1.0652E-04	9.3680E-03	8.1490E-03	3043	tags=27%, list=20%, signal=23%
BP	GO:0043066	negative regulation of apoptotic process	672	-0.3311	-1.5463	1.0664E-04	9.3680E-03	8.1490E-03	2431	tags=21%, list=16%, signal=18%
BP	GO:0045055	regulated exocytosis	653	-0.3826	-1.7840	1.0683E-04	9.3680E-03	8.1490E-03	2971	tags=28%, list=19%, signal=24%
BP	GO:0035239	tube morphogenesis	641	-0.4286	-1.9968	1.0699E-04	9.3680E-03	8.1490E-03	3598	tags=36%, list=24%, signal=29%
BP	GO:0098609	cell-cell adhesion	646	-0.3894	-1.8147	1.0699E-04	9.3680E-03	8.1490E-03	3045	tags=31%, list=20%, signal=26%
BP	GO:0009607	response to biotic stimulus	630	-0.4429	-2.0611	1.0733E-04	9.3680E-03	8.1490E-03	2077	tags=24%, list=14%, signal=21%
MF	GO:1990837	sequence-specific double-stranded DNA binding	624	-0.3306	-1.5380	1.0737E-04	9.3680E-03	8.1490E-03	3043	tags=27%, list=20%, signal=22%
CC	GO:0030141	secretory granule	613	-0.3872	-1.7996	1.0753E-04	9.3680E-03	8.1490E-03	1794	tags=19%, list=12%, signal=18%
BP	GO:0045087	innate immune response	613	-0.4230	-1.9660	1.0753E-04	9.3680E-03	8.1490E-03	2077	tags=24%, list=14%, signal=23%
BP	GO:0030029	actin filament-based process	618	-0.3293	-1.5305	1.0756E-04	9.3680E-03	8.1490E-03	3693	tags=32%, list=24%, signal=25%
BP	GO:0043207	response to external biotic stimulus	601	-0.4476	-2.0772	1.0790E-04	9.3680E-03	8.1490E-03	2077	tags=24%, list=14%, signal=22%
BP	GO:0051707	response to other organism	601	-0.4476	-2.0772	1.0790E-04	9.3680E-03	8.1490E-03	2077	tags=24%, list=14%, signal=22%
BP	GO:0043086	negative regulation of catalytic activity	595	-0.3312	-1.5365	1.0813E-04	9.3680E-03	8.1490E-03	2496	tags=19%, list=16%, signal=17%
BP	GO:0006897	endocytosis	597	-0.3859	-1.7901	1.0815E-04	9.3680E-03	8.1490E-03	2886	tags=26%, list=19%, signal=22%
BP	GO:0032101	regulation of response to external stimulus	586	-0.4445	-2.0605	1.0827E-04	9.3680E-03	8.1490E-03	2167	tags=26%, list=14%, signal=23%
MF	GO:0000976	transcription regulatory region sequence-specific DNA binding	581	-0.3413	-1.5813	1.0828E-04	9.3680E-03	8.1490E-03	3043	tags=28%, list=20%, signal=23%
BP	GO:0024443	leukocyte mediated immunity	575	-0.4528	-2.0967	1.0837E-04	9.3680E-03	8.1490E-03	1805	tags=23%, list=12%, signal=21%
BP	GO:0030162	regulation of proteolysis	563	-0.3816	-1.6716	1.0892E-04	9.3680E-03	8.1490E-03	2479	tags=23%, list=16%, signal=20%
BP	GO:0072358	cardiovascular system development	562	-0.4452	-2.0578	1.0896E-04	9.3680E-03	8.1490E-03	3295	tags=33%, list=22%, signal=27%
BP	GO:0031347	regulation of defense response	559	-0.3723	-1.7198	1.0898E-04	9.3680E-03	8.1490E-03	2134	tags=22%, list=14%, signal=19%
BP	GO:0050778	positive regulation of immune response	561	-0.3579	-1.6538	1.0898E-04	9.3680E-03	8.1490E-03	2053	tags=21%, list=13%, signal=19%
CC	GO:0009986	cell surface	560	-0.4075	-1.8828	1.0900E-04	9.3680E-03	8.1490E-03	3502	tags=36%, list=23%, signal=29%
BP	GO:0019444	vasculature development	555	-0.4471	-2.0648	1.0903E-04	9.3680E-03	8.1490E-03	3295	tags=33%, list=22%, signal=27%
BP	GO:0001816	cytokine production	556	-0.4230	-1.9533	1.0911E-04	9.3680E-03	8.1490E-03	2134	tags=24%, list=14%, signal=21%
BP	GO:0019221	cytokine-mediated signaling pathway	547	-0.4699	-2.1683	1.0919E-04	9.3680E-03	8.1490E-03	2288	tags=27%, list=15%, signal=24%
MF	GO:0010112	RNA polymerase II regulatory region DNA binding	545	-0.3479	-1.6033	1.0921E-04	9.3680E-03	8.1490E-03	3043	tags=28%, list=20%, signal=23%
MF	GO:0044888	transmembrane signaling receptor activity	545	-0.3901	-1.7998	1.0921E-04	9.3680E-03	8.1490E-03	2530	tags=27%, list=17%, signal=23%
BP	GO:0002263	cell activation involved in immune response	543	-0.4325	-1.9953	1.0924E-04	9.3680E-03	8.1490E-03	1988	tags=23%, list=13%, signal=20%
BP	GO:0000977	RNA polymerase II regulatory region sequence-specific DNA binding	540	-0.3479	-1.6044	1.0927E-04	9.3680E-03	8.1490E-03	3043	tags=35%, list=20%, signal=29%
MF	GO:0002366	leukocyte activation involved in immune response	539	-0.4349	-2.0052	1.0931E-04	9.3680E-03	8.1490E-03	1988	tags=23%, list=13%, signal=21%
BP	GO:0008285	negative regulation of cell proliferation	531	-0.3866	-1.6985	1.0937E-04	9.3680E-03	8.1490E-03	3041	tags=29%, list=20%, signal=24%
BP	GO:0015688	blood vessel development	528	-0.4492	-2.0692	1.0948E-04	9.3680E-03	8.1490E-03	3295	tags=33%, list=22%, signal=27%
BP	GO:0030155	regulation of cell adhesion	522	-0.3917	-1.8034	1.0954E-04	9.3680E-03	8.1490E-03	3197	tags=31%, list=21%, signal=25%
CC	GO:0070161	anchoring junction	517	-0.3719	-1.7107	1.0966E-04	9.3680E-03	8.1490E-03	3050	tags=28%, list=20%, signal=23%
BP	GO:0009611	response to wounding	508	-0.4204	-1.9329	1.0975E-04	9.3680E-03	8.1490E-03	3210	tags=32%, list=21%, signal=26%
BP	GO:0001817	regulation of cytokine production	500	-0.4045	-1.8573	1.0989E-04	9.3680E-03	8.1490E-03	2053	tags=23%, list=13%, signal=20%
BP	GO:0002274	myeloid leukocyte activation	505	-0.4528	-2.0801	1.0990E-04	9.3680E-03	8.1490E-03	2971	tags=32%, list=19%, signal=27%
CC	GO:0005912	adherens junction	506	-0.3731	-1.7139	1.0996E-04	9.3680E-03	8.1490E-03	3130	tags=28%, list=20%, signal=23%
BP	GO:0006954	inflammatory response	491	-0.5241	-2.4036	1.1024E-04	9.3680E-03	8.1490E-03	1805	tags=29%, list=12%, signal=26%
BP	GO:0042330	taxis	471	-0.4275	-1.9563	1.1052E-04	9.3680E-03	8.1490E-03	3177	tags=33%, list=21%, signal=27%
BP	GO:0008935	chemotaxis	469	-0.4285	-1.9606	1.1060E-04	9.3680E-03	8.1490E-03	3177	tags=33%, list=21%, signal=27%
BP	GO:0048514	blood vessel morphogenesis	461	-0.4817	-2.1092	1.1100E-04	9.3680E-03	8.1490E-03	3343	tags=35%, list=22%, signal=28%
BP	GO:0046649	lymphocyte activation	450	-0.3539	-1.6166	1.1102E-04	9.3680E-03	8.1490E-03	2648	tags=25%, list=17%, signal=21%
MF	GO:0050839	cell adhesion molecule binding	458	-0.3870	-1.7663	1.1132E-04	9.3680E-03	8.1490E-03	2239	tags=22%, list=15%, signal=19%
BP	GO:0002253	activation of immune response	449	-0.3917	-1.7876	1.1138E-04	9.3680E-03	8.1490E-03	2236	tags=24%, list=15%, signal=21%
BP	GO:0040017	positive regulation of locomotion	444	-0.4127	-1.8823	1.1143E-04	9.3680E-03	8.1490E-03	3605	tags=36%, list=24%, signal=28%
BP	GO:0002444	myeloid leukocyte mediated immunity	443	-0.4347	-1.9822	1.1151E-04	9.3680E-03	8.1490E-03	1794	tags=21%, list=12%, signal=19%
BP	GO:0002275	myeloid cell activation involved in immune response	437	-0.4436	-2.0197	1.1193E-04	9.3680E-03	8.1490E-03	1794	tags=22%, list=12%, signal=20%
BP	GO:0051272	positive regulation of cellular component movement	433	-0.4259	-1.9381	1.1204E-04	9.3680E-03	8.1490E-03	3605	tags=36%, list=24%, signal=29%
BP	GO:0030855	epithelial cell differentiation	430	-0.4058	-1.8447	1.1221E-04	9.3680E-03	8.1490E-03	3272	tags=36%, list=21%, signal=29%
BP	GO:0043299	leukocyte degranulation	430	-0.4399	-2.0000	1.1221E-04	9.3680E-03	8.1490E-03	1794	tags=21%, list=12%, signal=19%
BP	GO:0048598	embryonic morphogenesis	422	-0.3536	-1.6056	1.1265E-04	9.3680E-03	8.1490E-03	3259	tags=32%, list=21%, signal=26%
BP	GO:2000147	positive regulation of cell motility	419	-0.4227	-1.9183	1.1279E-04	9.3680E-03	8.1490E-03	3605	tags=36%, list=24%, signal=28%
BP	GO:0042060	wound healing	418	-0.4327	-1.9628	1.1282E-04	9.3680E-03	8.1490E-03	2517	tags=32%, list=16%, signal=28%
BP	GO:0036230	granulocyte activation	402	-0.4548	-2.0589	1.1322E-04	9.3680E-03	8.1490E-03	1794	tags=22%, list=12%, signal=20%
BP	GO:0002446	neutrophil mediated immunity	399	-0.4493	-2.0339	1.1324E-04	9.3680E-03	8.1490E-03	1794	tags=22%, list=12%, signal=20%
BP	GO:0042119	neutrophil activation	398	-0.4576	-2.0711	1.1326E-04	9.3680E-03	8.1490E-03	1794	tags=22%, list=12%, signal=20%
BP	GO:0030335	positive regulation of cell migration	406	-0.4244	-1.9219	1.1333E-04	9.3680E-03	8.1490E-03	3605	tags=36%, list=24%, signal=28%
BP	GO:0001525	angiogenesis	392	-0.4780	-2.1599	1.1351E-04	9.3680E-03	8.1490E-03	3295	tags=35%, list=22%, signal=28%
BP	GO:0002283	neutrophil activation involved in immune response	391	-0.4500	-2.0330	1.1355E-04	9.3680E-03	8.1490E-03	1794	tags=22%, list=12%, signal=20%
MF	GO:0000987	proximal promoter sequence-specific DNA binding	390	-0.3721	-1.6802	1.1374E-04	9.3680E-03	8.1490E-03	3031	tags=30%, list=20%, signal=25%
CC	GO:0043312	neutrophil degranulation	390	-0.4511	-2.0367	1.1374E-04	9.3680E-03	8.1490E-03	1794	tags=22%, list=12%, signal=20%
BP	GO:0030055	cell-substrate junction	384	-0.3914	-1.7653	1.1387E-04	9.3680E-03	8.1490E-03	2751	tags=27%, list=18%, signal=23%
CC	GO:0005924	cell-substrate adherens junction	382	-0.3878	-1.7483	1.1388E-04	9.3680E-03	8.1490E-03	2751	tags=27%, list=18%, signal=22%
MF	GO:0000978	RNA polymerase II proximal promoter sequence-specific DNA binding	381	-0.3685	-1.6610	1.1392E-04	9.3680E-03	8.1490E-03	3031	tags=30%, list=20%, signal=25%
CC	GO:0005925	focal adhesion	380	-0.3927	-1.7695	1.1395E-04	9.3680E-03	8.1490E-03	2751	tags=27%, list=18%, signal=23%
BP	GO:0001501	skeletal system development	374	-0.3662	-1.6492	1.1408E-04	9.3680E-03	8.1490E-03	3187	tags=31%, list=21%, signal=25%
BP	GO:0009617	response to bacterium	376	-0.4749	-2.1387	1.1410E-04	9.3680E-03	8.1490E-03	2055	tags=26%, list=13%, signal=23%
CC	GO:0031012	extracellular matrix	375	-0.4564	-2.0547	1.1425E-04	9.3680E-03	8.1490E-03	1963	tags=28%, list=13%, signal=25%
BP	GO:0048871	multicellular organismal homeostasis	356	-0.3663	-1.6421	1.1538E-04	9.3680E-03	8.1490E-03	2154	tags=22%, list=14%, signal=20%
BP	GO:0050878	regulation of body fluid levels	350	-0.4049	-1.8127	1.1553E-0				

BP	GO:0052547	regulation of peptidase activity	304	-0.3983	-1.7632	1.1805E-04	9.3680E-03	8.1490E-03	2473 tags=25%, list=16%, signal=21%
BP	GO:0045785	positive regulation of cell adhesion	299	-0.3745	-1.6549	1.1830E-04	9.3680E-03	8.1490E-03	3197 tags=30%, list=21%, signal=24%
BP	GO:0031589	cell-substrate adhesion	295	-0.4439	-1.9602	1.1832E-04	9.3680E-03	8.1490E-03	3756 tags=42%, list=25%, signal=33%
BP	GO:0050900	leukocyte migration	295	-0.5393	-2.3813	1.1832E-04	9.3680E-03	8.1490E-03	1748 tags=28%, list=11%, signal=25%
CC	GO:0062023	collagen-containing extracellular matrix	298	-0.4656	-2.0566	1.1844E-04	9.3680E-03	8.1490E-03	1963 tags=30%, list=13%, signal=27%
BP	GO:0098542	defense response to other organism	287	-0.4814	-2.1203	1.1876E-04	9.3680E-03	8.1490E-03	1803 tags=24%, list=12%, signal=22%
BP	GO:0030198	extracellular matrix organization	282	-0.4851	-2.1319	1.1918E-04	9.3680E-03	8.1490E-03	2317 tags=36%, list=15%, signal=31%
BP	GO:0052548	regulation of endopeptidase activity	282	-0.4074	-1.7906	1.1918E-04	9.3680E-03	8.1490E-03	2473 tags=26%, list=16%, signal=22%
CC	GO:0098589	membrane region	276	-0.3788	-1.6616	1.1970E-04	9.3680E-03	8.1490E-03	3197 tags=30%, list=21%, signal=25%
MF	GO:0001228	DNA-binding transcription activator activity, RNA polymerase II	274	-0.3952	-1.7327	1.1989E-04	9.3680E-03	8.1490E-03	3043 tags=31%, list=20%, signal=26%
BP	GO:0019058	viral life cycle	271	-0.3950	-1.7300	1.2024E-04	9.3680E-03	8.1490E-03	2663 tags=24%, list=17%, signal=20%
BP	GO:0002697	regulation of immune effector process	269	-0.4346	-1.9005	1.2053E-04	9.3680E-03	8.1490E-03	2052 tags=25%, list=13%, signal=22%
CC	GO:0098857	membrane microdomain	269	-0.3811	-1.6665	1.2053E-04	9.3680E-03	8.1490E-03	3197 tags=31%, list=21%, signal=25%
CC	GO:0045121	membrane raft	268	-0.3774	-1.6492	1.2069E-04	9.3680E-03	8.1490E-03	3197 tags=31%, list=21%, signal=25%
CC	GO:0031983	vesicle lumen	259	-0.4244	-1.8481	1.2143E-04	9.3680E-03	8.1490E-03	1064 tags=14%, list=7%, signal=13%
BP	GO:0034330	cell junction organization	254	-0.3990	-1.7359	1.2149E-04	9.3680E-03	8.1490E-03	3690 tags=38%, list=24%, signal=29%
BP	GO:0050727	regulation of inflammatory response	254	-0.4933	-2.1459	1.2149E-04	9.3680E-03	8.1490E-03	2134 tags=29%, list=14%, signal=25%
CC	GO:0030139	endocytic vesicle	255	-0.3966	-1.7261	1.2151E-04	9.3680E-03	8.1490E-03	2830 tags=27%, list=18%, signal=22%
MF	GO:0004175	endopeptidase activity	258	-0.3814	-1.6602	1.2160E-04	9.3680E-03	8.1490E-03	2047 tags=20%, list=13%, signal=18%
CC	GO:0060205	cytoplasmic vesicle lumen	258	-0.4254	-1.8515	1.2160E-04	9.3680E-03	8.1490E-03	1064 tags=14%, list=7%, signal=13%
BP	GO:0002250	adaptive immune response	251	-0.5279	-2.2926	1.2174E-04	9.3680E-03	8.1490E-03	1944 tags=31%, list=13%, signal=28%
BP	GO:1901342	regulation of vasculature development	249	-0.4987	-2.1629	1.2206E-04	9.3680E-03	8.1490E-03	3278 tags=36%, list=21%, signal=29%
BP	GO:0042063	gliogenesis	244	-0.4064	-1.7596	1.2226E-04	9.3680E-03	8.1490E-03	3163 tags=34%, list=21%, signal=27%
BP	GO:0050817	coagulation	245	-0.4268	-1.8488	1.2226E-04	9.3680E-03	8.1490E-03	3295 tags=32%, list=22%, signal=25%
BP	GO:0007599	hemostasis	247	-0.4241	-1.8377	1.2228E-04	9.3680E-03	8.1490E-03	3295 tags=32%, list=22%, signal=25%
CC	GO:0034774	secretory granule lumen	247	-0.4149	-1.7981	1.2228E-04	9.3680E-03	8.1490E-03	1794 tags=18%, list=12%, signal=16%
BP	GO:0007596	blood coagulation	243	-0.4295	-1.8586	1.2244E-04	9.3680E-03	8.1490E-03	3295 tags=32%, list=22%, signal=26%
BP	GO:0009615	response to virus	240	-0.4171	-1.8017	1.2302E-04	9.3680E-03	8.1490E-03	2131 tags=23%, list=14%, signal=20%
BP	GO:0002237	response to molecule of bacterial origin	236	-0.5018	-2.1654	1.2314E-04	9.3680E-03	8.1490E-03	2055 tags=28%, list=13%, signal=25%
BP	GO:0003098	lymphocyte differentiation	235	-0.4086	-1.7628	1.2317E-04	9.3680E-03	8.1490E-03	3197 tags=31%, list=21%, signal=25%
BP	GO:0007159	leukocyte cell-cell adhesion	232	-0.4179	-1.7998	1.2356E-04	9.3680E-03	8.1490E-03	1838 tags=21%, list=12%, signal=18%
CC	GO:0030687	secretory granule membrane	230	-0.4523	-1.9467	1.2359E-04	9.3680E-03	8.1490E-03	2830 tags=34%, list=18%, signal=28%
BP	GO:0032496	response to lipopolysaccharide	224	-0.5094	-2.1845	1.2424E-04	9.3680E-03	8.1490E-03	2055 tags=27%, list=13%, signal=24%
BP	GO:0034612	response to tumor necrosis factor	222	-0.4537	-1.9435	1.2464E-04	9.3680E-03	8.1490E-03	2274 tags=24%, list=15%, signal=21%
BP	GO:0045765	regulation of angiogenesis	222	-0.5080	-2.1758	1.2464E-04	9.3680E-03	8.1490E-03	3278 tags=37%, list=21%, signal=29%
BP	GO:0006909	phagocytosis	217	-0.4215	-1.8031	1.2475E-04	9.3680E-03	8.1490E-03	3465 tags=38%, list=23%, signal=30%
BP	GO:0032103	positive regulation of response to external stimulus	215	-0.4760	-2.0351	1.2484E-04	9.3680E-03	8.1490E-03	2167 tags=28%, list=14%, signal=25%
BP	GO:0006898	receptor-mediated endocytosis	214	-0.4734	-2.0229	1.2489E-04	9.3680E-03	8.1490E-03	1429 tags=17%, list=9%, signal=16%
BP	GO:0051091	positive regulation of DNA-binding transcription factor activity	214	-0.3987	-1.7035	1.2489E-04	9.3680E-03	8.1490E-03	2964 tags=30%, list=19%, signal=25%
BP	GO:0007162	negative regulation of cell adhesion	211	-0.4071	-1.7359	1.2530E-04	9.3680E-03	8.1490E-03	3177 tags=34%, list=21%, signal=27%
BP	GO:0071356	cellular response to tumor necrosis factor	206	-0.4409	-1.8746	1.2552E-04	9.3680E-03	8.1490E-03	2274 tags=24%, list=15%, signal=21%
BP	GO:0072593	reactive oxygen species metabolic process	205	-0.4029	-1.7109	1.2593E-04	9.3680E-03	8.1490E-03	2966 tags=32%, list=19%, signal=26%
BP	GO:0018181	negative regulation of cytokine production	198	-0.4234	-1.7932	1.2609E-04	9.3680E-03	8.1490E-03	1976 tags=25%, list=13%, signal=22%
BP	GO:0097191	extrinsic apoptotic signaling pathway	193	-0.4415	-1.8655	1.2639E-04	9.3680E-03	8.1490E-03	1922 tags=38%, list=13%, signal=34%
BP	GO:0016485	protein processing	191	-0.4320	-1.8210	1.2734E-04	9.3680E-03	8.1490E-03	2014 tags=25%, list=13%, signal=22%
BP	GO:0060326	cell chemotaxis	190	-0.5491	-2.3119	1.2770E-04	9.3680E-03	8.1490E-03	1872 tags=28%, list=12%, signal=25%
BP	GO:0010001	glial cell differentiation	187	-0.4252	-1.7867	1.2791E-04	9.3680E-03	8.1490E-03	3140 tags=36%, list=21%, signal=29%
CC	GO:0009897	external side of plasma membrane	185	-0.4333	-1.8183	1.2819E-04	9.3680E-03	8.1490E-03	3251 tags=37%, list=21%, signal=29%
BP	GO:0007160	cell-matrix adhesion	182	-0.4756	-1.9934	1.2821E-04	9.3680E-03	8.1490E-03	3756 tags=42%, list=25%, signal=32%
BP	GO:0051607	defense response to virus	177	-0.4721	-1.9738	1.2832E-04	9.3680E-03	8.1490E-03	2288 tags=28%, list=15%, signal=24%
BP	GO:0035966	response to topologically incorrect protein	184	-0.4672	-1.9594	1.2842E-04	9.3680E-03	8.1490E-03	1846 tags=17%, list=12%, signal=15%
BP	GO:0002460	adaptive immune response based on somatic recombination of	172	-0.5360	-2.2292	1.2990E-04	9.3680E-03	8.1490E-03	2014 tags=33%, list=13%, signal=29%
BP	GO:0009612	response to mechanical stimulus	172	-0.4372	-1.8182	1.2990E-04	9.3680E-03	8.1490E-03	2209 tags=27%, list=14%, signal=24%
BP	GO:0030217	T cell differentiation	168	-0.4346	-1.8050	1.2997E-04	9.3680E-03	8.1490E-03	2643 tags=27%, list=17%, signal=23%
BP	GO:0006986	response to unfolded protein	163	-0.5030	-2.0822	1.3019E-04	9.3680E-03	8.1490E-03	1846 tags=18%, list=12%, signal=16%
BP	GO:0071216	cellular response to biotic stimulus	163	-0.5052	-2.0910	1.3019E-04	9.3680E-03	8.1490E-03	1846 tags=25%, list=12%, signal=22%
BP	GO:0002064	epithelial cell development	165	-0.4674	-1.9365	1.3041E-04	9.3680E-03	8.1490E-03	3109 tags=40%, list=20%, signal=32%
BP	GO:0050920	regulation of chemotaxis	160	-0.4777	-1.9717	1.3074E-04	9.3680E-03	8.1490E-03	2167 tags=28%, list=14%, signal=24%
BP	GO:0031099	regeneration	157	-0.4307	-1.7736	1.3087E-04	9.3680E-03	8.1490E-03	2847 tags=34%, list=19%, signal=28%
BP	GO:0002449	lymphocyte mediated immunity	155	-0.5285	-2.1738	1.3108E-04	9.3680E-03	8.1490E-03	1889 tags=32%, list=12%, signal=28%
BP	GO:0035967	cellular response to topologically incorrect protein	149	-0.4624	-1.8916	1.3238E-04	9.3680E-03	8.1490E-03	1846 tags=17%, list=12%, signal=15%
BP	GO:0034341	response to interferon-gamma	147	-0.5972	-2.4414	1.3238E-04	9.3680E-03	8.1490E-03	2628 tags=41%, list=17%, signal=35%
BP	GO:0001763	morphogenesis of a branching structure	148	-0.4477	-1.8298	1.3245E-04	9.3680E-03	8.1490E-03	3295 tags=37%, list=22%, signal=29%
BP	GO:1904018	positive regulation of vasculature development	145	-0.5689	-2.3218	1.3256E-04	9.3680E-03	8.1490E-03	3278 tags=41%, list=21%, signal=32%
BP	GO:0010466	negative regulation of peptidase activity	144	-0.4777	-1.9480	1.3261E-04	9.3680E-03	8.1490E-03	1794 tags=22%, list=12%, signal=20%
BP	GO:0071219	cellular response to molecule of bacterial origin	142	-0.5241	-2.1340	1.3263E-04	9.3680E-03	8.1490E-03	1459 tags=25%, list=10%, signal=23%
MF	GO:0005126	cytokine receptor binding	143	-0.4460	-1.8173	1.3264E-04	9.3680E-03	8.1490E-03	1802 tags=19%, list=12%, signal=17%
BP	GO:0010951	negative regulation of endopeptidase activity	139	-0.4786	-1.9436	1.3314E-04	9.3680E-03	8.1490E-03	1794 tags=22%, list=12%, signal=20%
BP	GO:0061138	morphogenesis of a branching epithelium	138	-0.4721	-1.9139	1.3373E-04	9.3680E-03	8.1490E-03	3295 tags=40%, list=22%, signal=32%
BP	GO:0026885	regulation of leukocyte migration	137	-0.5069	-2.0538	1.3376E-04	9.3680E-03	8.1490E-03	1748 tags=26%, list=11%, signal=23%
BP	GO:0030595	leukocyte chemotaxis	137	-0.5598	-2.2679	1.3376E-04	9.3680E-03	8.1490E-03	1748 tags=28%, list=11%, signal=25%
BP	GO:0071346	cellular response to interferon-gamma	133	-0.5791	-2.3360	1.3425E-04	9.3680E-03	8.1490E-03	2628 tags=39%, list=17%, signal=33%
BP	GO:0071222	cellular response to lipopolysaccharide	135	-0.5328	-2.1517	1.3450E-04	9.3680E-03	8.1490E-03	1803 tags=26%, list=12%, signal=23%
BP	GO:2001236	regulation of extrinsic apoptotic signaling pathway	135	-0.4890	-1.9751	1.3450E-04	9.3680E-03	8.1490E-03	3673 tags=43%, list=24%, signal=33%
BP	GO:0034620	cellular response to unfolded protein	130	-0.5089	-2.0469	1.3479E-04	9.3680E-03	8.1490E-03	1846 tags=20%, list=12%, signal=18%
BP	GO:1903034	regulation of response to wounding	129	-0.4803	-1.9301	1.3490E-04	9.3680E-03	8.1490E-03	2031 tags=27%, list=13%, signal=24%
BP	GO:0045766	positive regulation of angiogenesis	128	-0.5732	-2.3007	1.3523E-04	9.3680E-03	8.1490E-03	3343 tags=43%, list=22%, signal=34%
BP	GO:0051092	positive regulation of NF-kappaB transcription factor activity	127	-0.4648	-1.8623	1.3576E-04	9.3680E-03	8.1490E-03	2236 tags=28%, list=15%, signal=24%
BP	GO:0097529	myeloid leukocyte migration	127	-0.5455	-2.1856	1.3576E-04	9.3680E-03	8.1490E-03	1748 tags=27%, list=11%, signal=24%
BP	GO:0048771	tissue remodeling	123	-0.4697	-1.8743	1.3630E-04	9.3680E-03	8.1490E-03	3581 tags=46%, list=23%, signal=36%
CC	GO:0070820	tertiary granule	124	-0.5175	-2.0655	1.3657E-04	9.3680E-03	8.1490E-03	2052 tags=32%, list=13%, signal=28%
MF	GO:0005201	extracellular matrix structural constituent	122	-0.4683	-1.8648	1.3691E-04	9.3680E-03	8.1490E-03	2683 tags=37%, list=18%, signal=31%
CC	GO:0042581	specific granule	116	-0.5589	-2.2112	1.3749E-04	9.3680E-03	8.1490E-03	1988 tags=32%, list=13%, signal=28%
MF	GO:0005178	integrin binding	113	-0.5881	-2.3188	1.3791E-04	9.3680E-03	8.1490E-03	1937 tags=34%, list=13%, signal=30%
MF	GO:0019838	growth factor binding	112	-0.4873	-1.9193	1.3835E-04	9.3680E-03	8.1490E-03	2476 tags=36%, list=16%, signal=30%
BP	GO:0042742	defense response to bacterium	108	-0.5003	-1.9632	1.3858E-04	9.3680E-03	8.1490E-03	1803 tags=25%, list=12%, signal=22%
BP	GO:0030260	entry into host cell	106	-0.5093	-1.9934	1.3875E-04	9.3680E-03	8.1490E-03	1639 tags=23%, list=11%, signal=20%
BP	GO:0044409	entry into host	106	-0.5093	-1.9934	1.3875E-04	9.3680E-03	8.1490E-03	1639 tags=23%, list=11%, signal=20%
BP	GO:0051806	entry into cell of other organism involved in symbiotic interaction	106	-0.5093	-1.9934	1.3875E-04	9.3680E-03	8.1490E-03	1639 tags=23%, list=11%, signal=20%
BP	GO:0051828	entry into other organism involved in symbiotic interaction	106	-0.5093	-1.9934	1.3875E-04	9.3680E-03	8.1490E-03	1639 tags=23%, list=11%, signal=20%
BP	GO:0003158	endothelium development	105	-0.5313	-2.0759	1.3924E-04	9.3680E-03	8.1490E-03	3251 tags=42%, list=21%, signal=33%
BP	GO:0021782	glial cell development	101	-0.5180	-2.0078	1.4059E-04	9.3680E-03	8.1490E-03	3412 tags=46%, list=22%, signal=36%
BP	GO:0006959	humoral immune response	100	-0.6288	-2.4349	1.40			

MF	GO:0005125	cytokine activity	81	-0.5550	-2.0770	1.4510E-04	9.3680E-03	8.1490E-03	1243 tags=25%, list=8%, signal=23%
BP	GO:1903317	regulation of protein maturation	80	-0.5701	-2.1285	1.4541E-04	9.3680E-03	8.1490E-03	2433 tags=40%, list=16%, signal=34%
BP	GO:0002688	regulation of leukocyte chemotaxis	78	-0.5300	-1.9709	1.4616E-04	9.3680E-03	8.1490E-03	1748 tags=27%, list=11%, signal=24%
BP	GO:0070613	regulation of protein processing	78	-0.5837	-2.1707	1.4616E-04	9.3680E-03	8.1490E-03	2433 tags=41%, list=16%, signal=35%
BP	GO:0016064	immunoglobulin mediated immune response	77	-0.5836	-2.1677	1.4626E-04	9.3680E-03	8.1490E-03	1604 tags=39%, list=10%, signal=35%
BP	GO:0019724	B cell mediated immunity	77	-0.5836	-2.1677	1.4626E-04	9.3680E-03	8.1490E-03	1604 tags=39%, list=10%, signal=35%
BP	GO:0034340	response to type I interferon	75	-0.5882	-2.1768	1.4669E-04	9.3680E-03	8.1490E-03	2274 tags=44%, list=15%, signal=38%
BP	GO:0060333	interferon-gamma-mediated signaling pathway	75	-0.5671	-2.4317	1.4669E-04	9.3680E-03	8.1490E-03	1335 tags=36%, list=9%, signal=33%
BP	GO:0032963	collagen metabolic process	76	-0.5605	-2.0767	1.4680E-04	9.3680E-03	8.1490E-03	2538 tags=38%, list=17%, signal=32%
BP	GO:0097530	granulocyte migration	73	-0.6856	-2.5255	1.4708E-04	9.3680E-03	8.1490E-03	1745 tags=38%, list=11%, signal=34%
BP	GO:0045069	regulation of viral genome replication	74	-0.5396	-1.9875	1.4717E-04	9.3680E-03	8.1490E-03	1253 tags=22%, list=8%, signal=20%
BP	GO:0060337	type I interferon signaling pathway	71	-0.5855	-2.1460	1.4802E-04	9.3680E-03	8.1490E-03	2274 tags=45%, list=15%, signal=39%
BP	GO:0071357	cellular response to type I interferon	71	-0.5855	-2.1460	1.4802E-04	9.3680E-03	8.1490E-03	2274 tags=45%, list=15%, signal=39%
MF	GO:0044252	serine-type endopeptidase activity	70	-0.5850	-2.1380	1.4835E-04	9.3680E-03	8.1490E-03	2047 tags=34%, list=13%, signal=30%
BP	GO:0042089	cytokine biosynthetic process	70	-0.5549	-2.0281	1.4835E-04	9.3680E-03	8.1490E-03	1803 tags=29%, list=12%, signal=25%
BP	GO:0042107	cytokine metabolic process	70	-0.5549	-2.0281	1.4835E-04	9.3680E-03	8.1490E-03	1803 tags=29%, list=12%, signal=25%
BP	GO:0042116	macrophage activation	67	-0.5578	-2.0286	1.4865E-04	9.3680E-03	8.1490E-03	2838 tags=43%, list=19%, signal=35%
BP	GO:0048525	negative regulation of viral process	67	-0.6055	-2.2018	1.4865E-04	9.3680E-03	8.1490E-03	3392 tags=54%, list=22%, signal=42%
BP	GO:0048708	astrocyte differentiation	67	-0.5521	-2.0079	1.4865E-04	9.3680E-03	8.1490E-03	2622 tags=39%, list=17%, signal=32%
BP	GO:1903305	negative regulation of response to wounding	67	-0.5761	-2.0948	1.4865E-04	9.3680E-03	8.1490E-03	1157 tags=24%, list=8%, signal=22%
BP	GO:0002286	T cell activation involved in immune response	64	-0.6182	-2.2257	1.5006E-04	9.3681E-03	8.1492E-03	2139 tags=38%, list=14%, signal=32%
CC	GO:0072562	blood microparticle	64	-0.7171	-2.5815	1.5006E-04	9.3681E-03	8.1492E-03	1012 tags=39%, list=7%, signal=37%
BP	GO:0071621	granulocyte chemotaxis	63	-0.6839	-2.4551	1.5069E-04	9.3681E-03	8.1492E-03	1050 tags=32%, list=7%, signal=30%
BP	GO:0002673	regulation of acute inflammatory response	57	-0.5792	-2.0442	1.5368E-04	9.3717E-03	8.1523E-03	1744 tags=37%, list=11%, signal=33%
BP	GO:1903901	negative regulation of viral life cycle	57	-0.5972	-2.1077	1.5368E-04	9.3717E-03	8.1523E-03	1672 tags=33%, list=11%, signal=30%
BP	GO:0072676	lymphocyte migration	56	-0.6034	-2.1238	1.5399E-04	9.3717E-03	8.1523E-03	1744 tags=23%, list=11%, signal=21%
BP	GO:1990266	neutrophil migration	56	-0.7493	-2.6375	1.5399E-04	9.3717E-03	8.1523E-03	1745 tags=46%, list=11%, signal=41%
BP	GO:0032637	interleukin-8 production	53	-0.6977	-2.4330	1.5485E-04	9.3717E-03	8.1523E-03	1692 tags=40%, list=11%, signal=35%
BP	GO:0072376	protein activation cascade	50	-0.6706	-2.3151	1.5571E-04	9.3717E-03	8.1523E-03	1586 tags=48%, list=10%, signal=43%
CC	GO:0031093	platelet alpha granule lumen	49	-0.5996	-2.0613	1.5623E-04	9.3717E-03	8.1523E-03	1430 tags=31%, list=9%, signal=28%
BP	GO:0030593	neutrophil chemotaxis	48	-0.7380	-2.5253	1.5686E-04	9.3717E-03	8.1523E-03	1050 tags=38%, list=7%, signal=35%
BP	GO:0032677	regulation of interleukin-8 production	48	-0.6853	-2.3448	1.5686E-04	9.3717E-03	8.1523E-03	1933 tags=38%, list=13%, signal=33%
BP	GO:0045123	cellular extravasation	44	-0.6558	-2.2135	1.5848E-04	9.3900E-03	8.1682E-03	1198 tags=27%, list=8%, signal=25%
BP	GO:0045071	negative regulation of viral genome replication	42	-0.6380	-2.1314	1.6028E-04	9.3900E-03	8.1682E-03	1253 tags=36%, list=8%, signal=33%
BP	GO:1990868	response to chemokine	42	-0.6891	-2.3021	1.6028E-04	9.3900E-03	8.1682E-03	1678 tags=31%, list=11%, signal=28%
BP	GO:1990869	cellular response to chemokine	42	-0.6891	-2.3021	1.6028E-04	9.3900E-03	8.1682E-03	1678 tags=31%, list=11%, signal=28%
BP	GO:0002920	regulation of humoral immune response	39	-0.7227	-2.3757	1.6200E-04	9.3900E-03	8.1682E-03	1586 tags=51%, list=10%, signal=46%
CC	GO:0035580	specific granule lumen	39	-0.6413	-2.1079	1.6200E-04	9.3900E-03	8.1682E-03	1962 tags=28%, list=13%, signal=25%
BP	GO:0006956	complement activation	38	-0.7733	-2.5303	1.6236E-04	9.3900E-03	8.1682E-03	1586 tags=58%, list=10%, signal=52%
BP	GO:0032964	collagen biosynthetic process	35	-0.6405	-2.0629	1.6329E-04	9.3900E-03	8.1682E-03	2268 tags=40%, list=15%, signal=34%
BP	GO:0070098	chemokine-mediated signaling pathway	35	-0.7195	-2.3175	1.6329E-04	9.3900E-03	8.1682E-03	1678 tags=37%, list=11%, signal=33%
BP	GO:0050907	detection of chemical stimulus involved in sensory perception	34	-0.6450	-2.0657	1.6426E-04	9.3963E-03	8.1737E-03	2647 tags=65%, list=17%, signal=50%
BP	GO:0032757	positive regulation of interleukin-8 production	33	-0.7253	-2.3075	1.6493E-04	9.3963E-03	8.1737E-03	1933 tags=42%, list=13%, signal=37%
BP	GO:0030449	regulation of complement activation	31	-0.7856	-2.4655	1.6675E-04	9.3963E-03	8.1737E-03	1586 tags=58%, list=10%, signal=52%
BP	GO:2000257	regulation of protein activation cascade	31	-0.7856	-2.4655	1.6675E-04	9.3963E-03	8.1737E-03	1586 tags=58%, list=10%, signal=52%
BP	GO:0002455	humoral immune response mediated by circulating immunoglobulin	29	-0.8042	-2.4929	1.6681E-04	9.3963E-03	8.1737E-03	1497 tags=69%, list=10%, signal=62%
BP	GO:0071622	regulation of granulocyte chemotaxis	28	-0.7092	-2.1749	1.6793E-04	9.4209E-03	8.1951E-03	1433 tags=36%, list=9%, signal=32%
BP	GO:0061756	leukocyte adhesion to vascular endothelial cell	26	-0.7315	-2.1978	1.7056E-04	9.4852E-03	8.2510E-03	1191 tags=35%, list=8%, signal=32%
BP	GO:1902622	regulation of neutrophil migration	23	-0.8027	-2.3540	1.7170E-04	9.4852E-03	8.2510E-03	1744 tags=57%, list=11%, signal=50%
BP	GO:0006953	acute-phase response	24	-0.7368	-2.1796	1.7182E-04	9.4852E-03	8.2510E-03	780 tags=29%, list=5%, signal=28%
BP	GO:0048247	lymphocyte chemotaxis	24	-0.7453	-2.2045	1.7182E-04	9.4852E-03	8.2510E-03	1744 tags=38%, list=11%, signal=33%
BP	GO:0006958	complement activation, classical pathway	21	-0.8303	-2.3796	1.7373E-04	9.5150E-03	8.2769E-03	1497 tags=71%, list=10%, signal=65%
BP	GO:0090022	regulation of neutrophil chemotaxis	19	-0.7946	-2.2267	1.7443E-04	9.5150E-03	8.2769E-03	1433 tags=47%, list=9%, signal=43%
BP	GO:1902624	positive regulation of neutrophil migration	19	-0.8096	-2.2689	1.7443E-04	9.5150E-03	8.2769E-03	1744 tags=63%, list=11%, signal=56%
MF	GO:0042379	chemokine receptor binding	18	-0.8054	-2.2301	1.7513E-04	9.5157E-03	8.2776E-03	1050 tags=33%, list=7%, signal=31%
BP	GO:0071624	positive regulation of granulocyte chemotaxis	16	-0.8148	-2.1937	1.7794E-04	9.5926E-03	8.3444E-03	1433 tags=56%, list=9%, signal=51%
BP	GO:0090023	positive regulation of neutrophil chemotaxis	16	-0.8148	-2.1937	1.7794E-04	9.5926E-03	8.3444E-03	1433 tags=56%, list=9%, signal=51%
MF	GO:0008009	chemokine activity	12	-0.8813	-2.1971	1.8560E-04	9.9667E-03	8.6698E-03	1050 tags=50%, list=7%, signal=47%
BP	GO:0002523	leukocyte migration involved in inflammatory response	10	-0.8841	-2.1117	1.8678E-04	9.9911E-03	8.6911E-03	531 tags=60%, list=3%, signal=58%
MF	GO:0030492	hemoglobin binding	3	-0.9904	-1.6736	1.9861E-04	1.0583E-02	9.2060E-02	151 tags=100%, list=1%, signal=96%
BP	GO:0097250	mitochondrial respiratory chain supercomplex assembly	3	0.9743	1.6673	2.0133E-04	1.0646E-02	9.2060E-02	396 tags=100%, list=3%, signal=97%
BP	GO:1903999	negative regulation of eating behavior	3	0.9750	1.6805	2.0133E-04	1.0646E-02	9.2060E-02	159 tags=67%, list=1%, signal=66%
BP	GO:0008628	hormone-mediated apoptotic signaling pathway	4	0.9828	1.8410	2.0354E-04	1.0722E-02	9.3266E-02	32 tags=50%, list=0%, signal=50%
MF	GO:0008121	ubiquinol-cytochrome-c reductase activity	8	0.9139	2.1406	2.0982E-04	1.0883E-02	9.4667E-03	1324 tags=100%, list=9%, signal=91%
MF	GO:0016679	oxidoreductase activity, acting on diphenols and related substrates	8	0.9139	2.1406	2.0982E-04	1.0883E-02	9.4667E-03	1324 tags=100%, list=9%, signal=91%
MF	GO:0016681	oxidoreductase activity, acting on diphenols and related substrates	8	0.9139	2.1406	2.0982E-04	1.0883E-02	9.4667E-03	1324 tags=100%, list=9%, signal=91%
MF	GO:0030627	pre-mRNA 5'-splice site binding	9	0.9124	2.2196	2.1191E-04	1.0883E-02	9.4667E-03	356 tags=78%, list=2%, signal=76%
BP	GO:0030097	hemopoiesis	663	-0.3154	-1.4722	2.1324E-04	1.0883E-02	9.4667E-03	3208 tags=26%, list=21%, signal=22%
BP	GO:0008284	positive regulation of cell proliferation	650	-0.3083	-1.4367	2.1402E-04	1.0883E-02	9.4667E-03	3206 tags=28%, list=21%, signal=23%
BP	GO:0045187	regulation of circadian sleep/wake cycle, sleep	10	0.8463	2.1152	2.1515E-04	1.0883E-02	9.4667E-03	53 tags=30%, list=0%, signal=30%
CC	GO:0045277	respiratory chain complex IV	10	0.8849	2.2118	2.1515E-04	1.0883E-02	9.4667E-03	1712 tags=90%, list=11%, signal=80%
CC	GO:0005750	mitochondrial respiratory chain complex III	11	0.8587	2.2149	2.1538E-04	1.0883E-02	9.4667E-03	1494 tags=82%, list=10%, signal=74%
CC	GO:0045275	respiratory chain complex III	11	0.8587	2.2149	2.1538E-04	1.0883E-02	9.4667E-03	1494 tags=82%, list=10%, signal=74%
BP	GO:0006122	mitochondrial electron transport, ubiquinol to cytochrome c	12	0.8777	2.3286	2.1673E-04	1.0883E-02	9.4667E-03	1494 tags=92%, list=10%, signal=83%
BP	GO:0010942	positive regulation of cell death	579	-0.3276	-1.5175	2.1676E-04	1.0883E-02	9.4667E-03	2497 tags=21%, list=16%, signal=18%
BP	GO:0070848	response to growth factor	570	-0.3196	-1.4798	2.1685E-04	1.0883E-02	9.4667E-03	3590 tags=31%, list=23%, signal=24%
BP	GO:0071363	cellular response to growth factor stimulus	555	-0.3228	-1.4907	2.1805E-04	1.0904E-02	9.4848E-03	3590 tags=31%, list=23%, signal=24%
BP	GO:0071396	cellular response to lipid	457	-0.3396	-1.5510	2.2232E-04	1.0968E-02	9.5407E-03	2492 tags=24%, list=16%, signal=21%
BP	GO:0000395	mRNA 5'-splice site recognition	14	0.8067	2.2424	2.2331E-04	1.0968E-02	9.5407E-03	356 tags=50%, list=2%, signal=49%
MF	GO:0005184	neuropeptide hormone activity	14	0.8599	2.3903	2.2331E-04	1.0968E-02	9.5407E-03	288 tags=64%, list=2%, signal=63%
BP	GO:0006123	mitochondrial electron transport, cytochrome c to oxygen	14	0.8339	2.3180	2.2331E-04	1.0968E-02	9.5407E-03	1712 tags=79%, list=11%, signal=70%
BP	GO:0019646	aerobic electron transport chain	14	0.8339	2.3180	2.2331E-04	1.0968E-02	9.5407E-03	1712 tags=79%, list=11%, signal=70%
BP	GO:0050865	regulation of cell activation	388	-0.3534	-1.5953	2.2753E-04	1.1086E-02	9.6431E-03	3197 tags=29%, list=21%, signal=24%
CC	GO:0005911	cell-cell junction	366	-0.3467	-1.5566	2.2957E-04	1.1086E-02	9.6431E-03	3157 tags=29%, list=21%, signal=23%
MF	GO:0004129	cytochrome-c oxidase activity	17	0.8290	2.4282	2.2973E-04	1.1086E-02	9.6431E-03	1712 tags=71%, list=11%, signal=63%
MF	GO:0015002	heme-copper terminal oxidase activity	17	0.8290	2.4282	2.2973E-04	1.1086E-02	9.6431E-03	1712 tags=71%, list=11%, signal=63%
MF	GO:0016676	oxidoreductase activity, acting on a heme group of donors, oxygen	17	0.8290	2.4282	2.2973E-04	1.1086E-02	9.6431E-03	1712 tags=71%, list=11%, signal=63%
CC	GO:0005753	mitochondrial proton-transporting ATP synthase complex	18	0.7788	2.3184	2.3299E-04	1.1165E-02	9.7122E-03	1770 tags=72%, list=12%, signal=64%
MF	GO:0016675	oxidoreductase activity, acting on a heme group of donors	18	0.7993	2.3797	2.3299E-04	1.1165E-02	9.7122E-03	1712 tags=67%, list=11%, signal=59%
CC	GO:0070099	cytochrome complex	21	0.8448	2.6291	2.3552E-04	1.1247E-02	9.7835E-03	1712 tags=76%, list=11%, signal=68%
BP	GO:0050673	epithelial cell proliferation	301	-0.3671	-1.6233	2.3643E-04	1.1252E-02	9.7878E-03	3279 tags=31%, list=21%, signal=25%
CC	GO:0005685	U1 snRNP	25	0.7314	2.3901	2.4062E-04	1.1411E-02	9.9267E-03	2116 tags=56%, list=19%, signal=48%
CC	GO:0000314	organellar small ribosomal subunit	28	0.6827	2.2922	2.4710E-04	1.1555E-02		

MF	GO:0008137	NADH dehydrogenase (ubiquinone) activity	36	0.7851	2.8173	2.5780E-04	1.1713E-02	1.0189E-02	2167 tags=83%, list=14%, signal=72%
MF	GO:0050136	NADH dehydrogenase (quinone) activity	36	0.7851	2.8173	2.5780E-04	1.1713E-02	1.0189E-02	2167 tags=83%, list=14%, signal=72%
CC	GO:0016323	basolateral plasma membrane	166	-0.4296	-1.7826	2.6018E-04	1.1713E-02	1.0189E-02	3499 tags=35%, list=23%, signal=27%
BP	GO:007007	inner mitochondrial membrane organization	39	0.6785	2.4878	2.6116E-04	1.1713E-02	1.0189E-02	3312 tags=79%, list=22%, signal=52%
CC	GO:0031304	intrinsic component of mitochondrial inner membrane	39	0.6078	2.2284	2.6116E-04	1.1713E-02	1.0189E-02	5151 tags=79%, list=34%, signal=53%
CC	GO:0031305	integral component of mitochondrial inner membrane	39	0.6078	2.2284	2.6116E-04	1.1713E-02	1.0189E-02	5151 tags=79%, list=34%, signal=53%
CC	GO:0005747	mitochondrial respiratory chain complex I	40	0.7835	2.8903	2.6151E-04	1.1713E-02	1.0189E-02	2252 tags=82%, list=15%, signal=71%
CC	GO:0030964	NADH dehydrogenase complex	40	0.7835	2.8903	2.6151E-04	1.1713E-02	1.0189E-02	2252 tags=82%, list=15%, signal=71%
CC	GO:0045271	respiratory chain complex I	40	0.7835	2.8903	2.6151E-04	1.1713E-02	1.0189E-02	2252 tags=82%, list=15%, signal=71%
BP	GO:0050663	cytokine secretion	154	-0.4268	-1.7541	2.6226E-04	1.1713E-02	1.0189E-02	2031 tags=24%, list=13%, signal=21%
CC	GO:0016469	proton-transporting two-sector ATPase complex	41	0.6172	2.2886	2.6539E-04	1.1815E-02	1.0278E-02	2546 tags=63%, list=17%, signal=53%
MF	GO:0005179	hormone activity	43	0.5524	2.0732	2.6752E-04	1.1872E-02	1.0327E-02	566 tags=33%, list=4%, signal=31%
BP	GO:0006120	mitochondrial electron transport, NADH to ubiquinone	44	0.7428	2.7973	2.7086E-04	1.1981E-02	1.0422E-02	2941 tags=84%, list=19%, signal=68%
MF	GO:0003743	translation initiation factor activity	46	0.5332	2.0344	2.7181E-04	1.1985E-02	1.0426E-02	5189 tags=70%, list=34%, signal=46%
MF	GO:0016655	oxidoreductase activity, acting on NAD(P)H, quinone or similar	48	0.7232	2.7877	2.7571E-04	1.2118E-02	1.0541E-02	2167 tags=69%, list=14%, signal=59%
BP	GO:1903900	regulation of viral life cycle	112	-0.4841	-1.9064	2.7670E-04	1.2123E-02	1.0546E-02	1717 tags=23%, list=11%, signal=21%
BP	GO:0061041	regulation of wound healing	103	-0.4890	-1.9025	2.8003E-04	1.2187E-02	1.0601E-02	1933 tags=27%, list=13%, signal=24%
BP	GO:0010257	NADH dehydrogenase complex assembly	55	0.7376	2.9288	2.8313E-04	1.2187E-02	1.0601E-02	2830 tags=78%, list=18%, signal=64%
CC	GO:0022625	cytosolic large ribosomal subunit	56	0.5432	2.1568	2.8313E-04	1.2187E-02	1.0601E-02	4152 tags=62%, list=27%, signal=45%
BP	GO:0032981	mitochondrial respiratory chain complex I assembly	55	0.7376	2.9288	2.8313E-04	1.2187E-02	1.0601E-02	2830 tags=78%, list=18%, signal=64%
MF	GO:0017171	serine hydrolase activity	93	-0.5282	-2.0210	2.8437E-04	1.2187E-02	1.0601E-02	2047 tags=29%, list=13%, signal=26%
BP	GO:0005079	positive regulation of inflammatory response	93	-0.5173	-1.9792	2.8437E-04	1.2187E-02	1.0601E-02	1838 tags=29%, list=12%, signal=26%
BP	GO:0006521	regulation of cellular amino acid metabolic process	54	0.5210	2.0534	2.8490E-04	1.2187E-02	1.0601E-02	3044 tags=57%, list=20%, signal=46%
CC	GO:0000315	organellar large ribosomal subunit	57	0.6048	2.4234	2.8612E-04	1.2187E-02	1.0601E-02	3881 tags=67%, list=25%, signal=50%
CC	GO:0005762	mitochondrial large ribosomal subunit	57	0.6048	2.4234	2.8612E-04	1.2187E-02	1.0601E-02	3881 tags=67%, list=25%, signal=50%
BP	GO:2001237	negative regulation of extrinsic apoptotic signaling pathway	87	-0.5324	-2.0164	2.8699E-04	1.2187E-02	1.0601E-02	1902 tags=29%, list=12%, signal=25%
BP	GO:0072181	neurotrophin signaling pathway	58	0.5079	2.0418	2.8952E-04	1.2257E-02	1.0662E-02	2874 tags=47%, list=19%, signal=38%
BP	GO:0000245	spliceosomal complex assembly	60	0.4917	1.9931	2.9265E-04	1.2314E-02	1.0712E-02	3012 tags=35%, list=20%, signal=28%
CC	GO:0000502	proteasome complex	60	0.4742	1.9220	2.9265E-04	1.2314E-02	1.0712E-02	3044 tags=55%, list=20%, signal=44%
CC	GO:1905369	endopeptidase complex	61	0.4798	1.9524	2.9481E-04	1.2364E-02	1.0756E-02	3044 tags=56%, list=20%, signal=45%
CC	GO:0032592	integral component of mitochondrial membrane	63	0.5235	2.1464	2.9709E-04	1.2364E-02	1.0756E-02	3433 tags=54%, list=22%, signal=42%
CC	GO:0098803	respiratory chain complex	63	0.7819	3.2058	2.9709E-04	1.2364E-02	1.0756E-02	2252 tags=79%, list=15%, signal=68%
CC	GO:0097525	spliceosomal snRNP complex	62	0.5863	2.3925	2.9744E-04	1.2364E-02	1.0756E-02	2465 tags=44%, list=16%, signal=37%
CC	GO:0098573	intrinsic component of mitochondrial membrane	64	0.5226	2.1521	2.9958E-04	1.2393E-02	1.0780E-02	3433 tags=53%, list=22%, signal=41%
BP	GO:0042273	ribosomal large subunit biogenesis	66	0.5279	2.1867	3.0349E-04	1.2393E-02	1.0780E-02	3426 tags=55%, list=22%, signal=43%
CC	GO:0030532	small nuclear ribonucleoprotein complex	68	0.5546	2.3149	3.0377E-04	1.2393E-02	1.0780E-02	2683 tags=43%, list=18%, signal=35%
CC	GO:0015935	small ribosomal subunit	67	0.5014	2.0817	3.0534E-04	1.2393E-02	1.0780E-02	4365 tags=66%, list=29%, signal=47%
CC	GO:0005746	mitochondrial respiratory chain	69	0.7627	3.1907	3.0618E-04	1.2393E-02	1.0780E-02	2252 tags=74%, list=15%, signal=63%
MF	GO:0004896	cytokine receptor activity	54	-0.5715	-2.0011	3.0807E-04	1.2393E-02	1.0780E-02	1506 tags=28%, list=10%, signal=25%
BP	GO:0061045	negative regulation of wound healing	54	-0.5664	-1.9832	3.0807E-04	1.2393E-02	1.0780E-02	1035 tags=22%, list=7%, signal=21%
BP	GO:0009060	aerobic respiration	72	0.5509	3.2357	3.0836E-04	1.2393E-02	1.0780E-02	2278 tags=40%, list=15%, signal=34%
BP	GO:0061418	regulation of transcription from RNA polymerase II promoter in	72	0.4519	1.9077	3.0836E-04	1.2393E-02	1.0780E-02	2405 tags=40%, list=16%, signal=34%
CC	GO:0030684	peribosome	74	0.4339	1.8394	3.1182E-04	1.2393E-02	1.0780E-02	5089 tags=61%, list=33%, signal=41%
BP	GO:0031145	anaphase-promoting complex-dependent catabolic process	74	0.5563	2.3583	3.1182E-04	1.2393E-02	1.0780E-02	3540 tags=66%, list=23%, signal=51%
CC	GO:0005758	mitochondrial intermembrane space	73	0.4857	2.0528	3.1221E-04	1.2393E-02	1.0780E-02	4528 tags=60%, list=30%, signal=43%
BP	GO:0042773	ATP synthesis coupled electron transport	76	0.7454	3.1729	3.1348E-04	1.2393E-02	1.0780E-02	2167 tags=74%, list=14%, signal=62%
CC	GO:0070469	respiratory chain	76	0.7457	3.1742	3.1348E-04	1.2393E-02	1.0780E-02	2389 tags=74%, list=16%, signal=62%
BP	GO:0042775	mitochondrial ATP synthesis coupled electron transport	75	0.7437	3.1541	3.1397E-04	1.2393E-02	1.0780E-02	2167 tags=73%, list=14%, signal=63%
MF	GO:0008135	translation factor activity, RNA binding	77	0.4299	1.8329	3.1596E-04	1.2393E-02	1.0780E-02	5198 tags=56%, list=34%, signal=37%
CC	GO:0120114	Sm-like protein family complex	77	0.5519	2.3534	3.1596E-04	1.2393E-02	1.0780E-02	2683 tags=44%, list=18%, signal=37%
BP	GO:0060548	negative regulation of cell death	762	-0.3102	-1.4575	3.1636E-04	1.2393E-02	1.0780E-02	2431 tags=20%, list=16%, signal=18%
BP	GO:0010972	negative regulation of G2/M transition of mitotic cell cycle	78	0.5162	2.2090	3.1646E-04	1.2393E-02	1.0780E-02	3099 tags=49%, list=20%, signal=39%
BP	GO:0002520	immune system development	734	-0.3069	-1.4398	3.1723E-04	1.2393E-02	1.0780E-02	3208 tags=26%, list=21%, signal=21%
CC	GO:0031970	organellar envelope lumen	82	0.4616	1.9936	3.1969E-04	1.2393E-02	1.0780E-02	4528 tags=59%, list=30%, signal=41%
CC	GO:1905368	peptidase complex	82	0.4569	1.9735	3.1969E-04	1.2393E-02	1.0780E-02	2405 tags=46%, list=16%, signal=39%
MF	GO:0016651	oxidoreductase activity, acting on NAD(P)H	84	0.5673	2.4587	3.2446E-04	1.2393E-02	1.0780E-02	2167 tags=52%, list=14%, signal=45%
BP	GO:0030195	negative regulation of blood coagulation	36	-0.6208	-2.0096	3.2664E-04	1.2393E-02	1.0780E-02	527 tags=22%, list=3%, signal=22%
BP	GO:1900447	negative regulation of hemostasis	36	-0.6208	-2.0096	3.2664E-04	1.2393E-02	1.0780E-02	527 tags=22%, list=3%, signal=22%
BP	GO:0097435	supramolecular fiber organization	553	-0.3214	-1.4840	3.2730E-04	1.2393E-02	1.0780E-02	2768 tags=24%, list=18%, signal=20%
BP	GO:0030036	actin cytoskeleton organization	548	-0.3144	-1.4505	3.2762E-04	1.2393E-02	1.0780E-02	3654 tags=31%, list=24%, signal=25%
BP	GO:0033108	mitochondrial respiratory chain complex assembly	86	0.6723	2.9207	3.2895E-04	1.2393E-02	1.0780E-02	3580 tags=73%, list=23%, signal=56%
BP	GO:0048729	tissue morphogenesis	509	-0.3161	-1.4532	3.2934E-04	1.2393E-02	1.0780E-02	3331 tags=30%, list=22%, signal=24%
CC	GO:0000313	organellar ribosome	87	0.6249	2.7226	3.2971E-04	1.2393E-02	1.0780E-02	3619 tags=67%, list=24%, signal=51%
CC	GO:0005761	mitochondrial ribosome	87	0.6249	2.7226	3.2971E-04	1.2393E-02	1.0780E-02	3619 tags=67%, list=24%, signal=51%
BP	GO:0031146	SCF-dependent proteasomal ubiquitin-dependent protein catab	87	0.4778	2.0818	3.2971E-04	1.2393E-02	1.0780E-02	4068 tags=56%, list=27%, signal=42%
BP	GO:0070126	mitochondrial translational termination	89	0.6576	2.8808	3.3113E-04	1.2393E-02	1.0780E-02	3619 tags=69%, list=24%, signal=53%
MF	GO:0009055	electron transfer activity	88	0.5016	2.1918	3.3135E-04	1.2393E-02	1.0780E-02	2167 tags=47%, list=14%, signal=40%
BP	GO:0070125	mitochondrial translational elongation	88	0.6555	2.8644	3.3135E-04	1.2393E-02	1.0780E-02	3881 tags=70%, list=25%, signal=53%
BP	GO:1902750	negative regulation of cell cycle G2/M phase transition	88	0.4685	2.0472	3.3135E-04	1.2393E-02	1.0780E-02	3099 tags=45%, list=20%, signal=36%
CC	GO:1902004	oxidoreductase complex	88	0.6450	2.8185	3.3135E-04	1.2393E-02	1.0780E-02	2252 tags=58%, list=15%, signal=50%
BP	GO:1904036	negative regulation of epithelial cell apoptotic process	30	-0.6640	-2.0711	3.3400E-04	1.2458E-02	1.0837E-02	348 tags=37%, list=2%, signal=36%
MF	GO:0015078	proton transmembrane transporter activity	93	0.4661	2.0581	3.3681E-04	1.2529E-02	1.0899E-02	2023 tags=40%, list=13%, signal=35%
BP	GO:1900542	mitochondrial transmembrane transport	92	0.4778	2.1024	3.3772E-04	1.2529E-02	1.0899E-02	3225 tags=47%, list=21%, signal=37%
BP	GO:0006614	SRP-dependent cotranslational protein targeting to membrane	96	0.5305	2.3534	3.3990E-04	1.2544E-02	1.0912E-02	4356 tags=62%, list=28%, signal=45%
BP	GO:0002757	immune response-activating signal transduction	401	-0.3434	-1.5544	3.3994E-04	1.2544E-02	1.0912E-02	2274 tags=22%, list=15%, signal=19%
BP	GO:0022904	respiratory electron transport chain	95	0.7090	3.1352	3.4130E-04	1.2561E-02	1.0926E-02	2012 tags=64%, list=13%, signal=56%
CC	GO:0022626	cytosolic ribosome	99	0.4576	2.0404	3.4329E-04	1.2600E-02	1.0961E-02	4356 tags=59%, list=28%, signal=42%
BP	GO:0006613	cotranslational protein targeting to membrane	100	0.5224	2.3302	3.4530E-04	1.2639E-02	1.0995E-02	4356 tags=61%, list=28%, signal=44%
BP	GO:0002694	regulation of leukocyte activation	358	-0.3471	-1.5559	3.4618E-04	1.2639E-02	1.0995E-02	3197 tags=31%, list=21%, signal=25%
BP	GO:0006415	translational termination	102	0.6297	2.8193	3.4722E-04	1.2644E-02	1.0999E-02	3619 tags=66%, list=24%, signal=50%
CC	GO:0015934	large ribosomal subunit	112	0.5694	2.5906	3.6049E-04	1.3030E-02	1.1335E-02	4152 tags=64%, list=27%, signal=47%
MF	GO:0018488	complement binding	14	-0.8158	-2.1193	3.6206E-04	1.3030E-02	1.1335E-02	531 tags=50%, list=3%, signal=48%
CC	GO:0071682	endocytic vesicle lumen	14	-0.8207	-2.1322	3.6206E-04	1.3030E-02	1.1335E-02	800 tags=36%, list=5%, signal=34%
CC	GO:0098800	inner mitochondrial membrane protein complex	111	0.7236	3.2831	3.6271E-04	1.3030E-02	1.1335E-02	2830 tags=71%, list=18%, signal=58%
BP	GO:0045047	protein targeting to ER	109	0.4982	2.2493	3.6298E-04	1.3030E-02	1.1335E-02	4356 tags=60%, list=28%, signal=43%
BP	GO:0072599	establishment of protein localization to endoplasmic reticulum	113	0.4992	2.2729	3.6350E-04	1.3030E-02	1.1335E-02	4356 tags=59%, list=28%, signal=43%
BP	GO:0042730	fibrinolysis	13	-0.8377	-2.1341	3.6590E-04	1.3068E-02	1.1367E-02	293 tags=38%, list=2%, signal=38%
BP	GO:0006119	oxidative phosphorylation	116	0.6786	3.1064	3.6643E-04	1.3068E-02	1.1367E-02	2167 tags=63%, list=14%, signal=54%
BP	GO:1902600	proton transmembrane transport	114	0.4229	1.9241	3.6792E-04	1.3087E-02	1.1384E-02	2603 tags=39%, list=17%, signal=33%
MF	GO:0140101	catalytic activity, acting on a tRNA	120	0.4434	2.0401	3.7272E-04	1.3153E-02	1.1442E-02	5293 tags=53%, list=35%, signal=35%
BP	GO:0008033	tRNA processing	124	0.3956	1.8285	3.7313E-04	1.3153E-02	1.1442E-02	5330 tags=51%, list=35%, signal=33%
BP	GO:0002827	positive regulation of T-helper 1 type immune response	11	-0.8400	-2.0479	3.7320E-04	1.3153E-02	1.1442E-02	333 tags=36%, list=2%, signal=36%
BP	GO:0007249	I-kappaB kinase/NF-kappaB signaling	220	-0.3914					

MF	GO:0003735	structural constituent of ribosome	149	0.5999	2.8528	4.0866E-04	1.4100E-02	1.2265E-02	4365 tags=68%, list=29%, signal=49%
BP	GO:0022900	electron transport chain	146	0.5693	2.6904	4.1051E-04	1.4128E-02	1.2290E-02	2071 tags=51%, list=14%, signal=45%
BP	GO:0002285	lymphocyte activation involved in immune response	117	-0.4726	-1.8717	4.1231E-04	1.4155E-02	1.2313E-02	1944 tags=27%, list=13%, signal=24%
CC	GO:0005751	mitochondrial respiratory chain complex IV	8	0.8837	2.0697	4.1964E-04	1.4371E-02	1.2501E-02	1712 tags=88%, list=11%, signal=78%
BP	GO:0040007	growth	787	-0.3043	-1.4316	4.2163E-04	1.4403E-02	1.2529E-02	3383 tags=28%, list=22%, signal=23%
MF	GO:0002020	protease binding	99	-0.4859	-1.8773	4.2319E-04	1.4404E-02	1.2529E-02	2957 tags=33%, list=19%, signal=27%
BP	GO:0002576	platelet degranulation	98	-0.4866	-1.8774	4.2373E-04	1.4404E-02	1.2529E-02	1509 tags=26%, list=10%, signal=23%
BP	GO:0140053	mitochondrial gene expression	161	0.5381	2.5869	4.2808E-04	1.4511E-02	1.2623E-02	4888 tags=66%, list=32%, signal=46%
BP	GO:0045333	cellular respiration	162	0.5951	2.8639	4.2900E-04	1.4511E-02	1.2623E-02	2278 tags=49%, list=15%, signal=42%
BP	GO:0006413	translational initiation	175	0.3622	1.7658	4.2428E-04	1.4931E-02	1.2988E-02	5527 tags=64%, list=36%, signal=41%
BP	GO:0034109	homotypic cell-cell adhesion	66	-0.5411	-1.9593	4.4729E-04	1.5051E-02	1.3093E-02	3025 tags=44%, list=20%, signal=35%
CC	GO:0044391	ribosomal subunit	176	0.5401	2.6306	4.4823E-04	1.5051E-02	1.3093E-02	4365 tags=65%, list=29%, signal=47%
BP	GO:0006399	tRNA metabolic process	186	0.4191	2.0582	4.5600E-04	1.5273E-02	1.3286E-02	5330 tags=52%, list=35%, signal=34%
BP	GO:0002690	positive regulation of leukocyte chemotaxis	58	-0.5590	-1.9797	4.5816E-04	1.5273E-02	1.3286E-02	1748 tags=28%, list=11%, signal=25%
BP	GO:0033627	cell adhesion mediated by integrin	58	-0.5589	-1.9795	4.5816E-04	1.5273E-02	1.3286E-02	1621 tags=26%, list=11%, signal=23%
BP	GO:1902041	regulation of extrinsic apoptotic signaling pathway via death do	51	-0.5720	-1.9795	4.6678E-04	1.5423E-02	1.3416E-02	2428 tags=39%, list=16%, signal=33%
CC	GO:0045299	proton-transporting ATP synthase complex	19	0.7686	2.3217	4.6849E-04	1.5423E-02	1.3416E-02	1770 tags=68%, list=12%, signal=61%
BP	GO:0060780	positive regulation of response to cytokine stimulus	49	-0.5718	-1.9657	4.6868E-04	1.5423E-02	1.3416E-02	1692 tags=29%, list=11%, signal=25%
BP	GO:0070527	platelet aggregation	49	-0.5773	-1.9845	4.6868E-04	1.5423E-02	1.3416E-02	1509 tags=31%, list=10%, signal=26%
BP	GO:0042776	mitochondrial ATP synthesis coupled proton transport	21	0.7291	2.2689	4.7103E-04	1.5423E-02	1.3416E-02	2841 tags=71%, list=19%, signal=68%
BP	GO:0004856	embryonic organ development	297	-0.3654	-1.6148	4.7276E-04	1.5423E-02	1.3416E-02	2791 tags=27%, list=18%, signal=24%
MF	GO:0051537	2 iron, 2 sulfur cluster binding	20	0.7203	2.2027	4.7304E-04	1.5423E-02	1.3416E-02	2219 tags=60%, list=15%, signal=51%
BP	GO:0048545	response to steroid hormone	300	-0.3628	-1.6039	4.7315E-04	1.5423E-02	1.3416E-02	3445 tags=33%, list=23%, signal=26%
BP	GO:0015985	energy coupled proton transport, down electrochemical gradien	22	0.7142	2.2512	4.7382E-04	1.5423E-02	1.3416E-02	2841 tags=68%, list=19%, signal=56%
BP	GO:0015986	ATP synthesis coupled proton transport	22	0.7142	2.2512	4.7382E-04	1.5423E-02	1.3416E-02	2841 tags=68%, list=19%, signal=56%
CC	GO:0044455	mitochondrial membrane part	194	0.6332	3.1165	4.7619E-04	1.5463E-02	1.3451E-02	3433 tags=64%, list=22%, signal=50%
CC	GO:005732	small nuclear ribonucleoprotein complex	25	0.6682	2.1836	4.8123E-04	1.5590E-02	1.3562E-02	2757 tags=52%, list=18%, signal=43%
BP	GO:0043624	cellular protein complex disassembly	202	0.4098	2.0268	4.8685E-04	1.5736E-02	1.3688E-02	3881 tags=47%, list=25%, signal=36%
BP	GO:0014002	astrocyte development	34	-0.6332	-2.0280	4.9277E-04	1.5881E-02	1.3815E-02	2622 tags=44%, list=17%, signal=37%
BP	GO:0006364	rRNA processing	208	0.3790	1.8834	4.9407E-04	1.5881E-02	1.3815E-02	5278 tags=59%, list=34%, signal=39%
BP	GO:1902042	negative regulation of extrinsic apoptotic signaling pathway via	33	-0.6494	-2.0660	4.9480E-04	1.5881E-02	1.3815E-02	2132 tags=45%, list=14%, signal=39%
BP	GO:0070371	ERK1 and ERK2 cascade	218	-0.3841	-1.6440	4.9807E-04	1.5927E-02	1.3855E-02	1184 tags=15%, list=8%, signal=14%
BP	GO:0008544	epidermis development	212	-0.3849	-1.6425	5.0044E-04	1.5927E-02	1.3855E-02	3243 tags=33%, list=21%, signal=26%
BP	GO:0034329	cell junction assembly	212	-0.3843	-1.6397	5.0044E-04	1.5927E-02	1.3855E-02	3673 tags=37%, list=24%, signal=28%
CC	GO:0005840	ribosome	215	0.4985	2.4877	5.0201E-04	1.5927E-02	1.3855E-02	3619 tags=53%, list=24%, signal=41%
CC	GO:0044445	cytosolic part	215	0.3744	1.8684	5.0201E-04	1.5927E-02	1.3855E-02	4356 tags=47%, list=28%, signal=34%
BP	GO:0043122	regulation of I-kappaB kinase/NF-kappaB signaling	195	-0.4000	-1.6909	5.0601E-04	1.6017E-02	1.3933E-02	2917 tags=30%, list=19%, signal=24%
BP	GO:0051701	interaction with host	171	-0.4122	-1.7135	5.1975E-04	1.6402E-02	1.4268E-02	2171 tags=21%, list=14%, signal=18%
BP	GO:0022618	ribonucleoprotein complex assembly	128	0.3727	1.8736	5.2056E-04	1.6402E-02	1.4268E-02	4890 tags=47%, list=32%, signal=33%
BP	GO:0018194	tissue homeostasis	258	-0.4154	-1.7117	5.2356E-04	1.6445E-02	1.4305E-02	2053 tags=23%, list=13%, signal=20%
BP	GO:0035455	response to interferon-alpha	18	-0.7615	-2.1084	5.2539E-04	1.6445E-02	1.4305E-02	427 tags=33%, list=3%, signal=32%
BP	GO:0006839	mitochondrial transport	231	0.3266	1.6466	5.2549E-04	1.6445E-02	1.4305E-02	3387 tags=39%, list=22%, signal=30%
BP	GO:0030278	regulation of ossification	152	-0.4230	-1.7344	5.2743E-04	1.6468E-02	1.4326E-02	3093 tags=40%, list=20%, signal=32%
BP	GO:0070555	response to interleukin-1	148	-0.4259	-1.7409	5.2980E-04	1.6472E-02	1.4329E-02	1049 tags=13%, list=7%, signal=12%
BP	GO:0015980	energy derivation by oxidation of organic compounds	234	0.4696	2.3696	5.2994E-04	1.6472E-02	1.4329E-02	4033 tags=53%, list=26%, signal=39%
CC	GO:0098794	mitochondrial protein complex	236	0.6588	3.3273	5.3163E-04	1.6488E-02	1.4342E-02	2857 tags=61%, list=19%, signal=50%
BP	GO:0071826	ribonucleoprotein complex subunit organization	242	0.3822	1.9359	5.4025E-04	1.6717E-02	1.4542E-02	3309 tags=35%, list=22%, signal=28%
BP	GO:0016072	rRNA metabolic process	243	0.3444	1.7442	5.4496E-04	1.6825E-02	1.4636E-02	5278 tags=55%, list=17%, signal=36%
BP	GO:0061061	muscle structure development	497	-0.3171	-1.4555	5.4945E-04	1.6881E-02	1.4684E-02	3008 tags=28%, list=20%, signal=23%
BP	GO:0043039	tRNA aminoacylation	48	0.4952	1.9088	5.5142E-04	1.6881E-02	1.4684E-02	5794 tags=69%, list=38%, signal=43%
BP	GO:0043901	negative regulation of multi-organism process	113	-0.4650	-1.8336	5.5165E-04	1.6881E-02	1.4684E-02	3392 tags=38%, list=22%, signal=30%
BP	GO:0048754	branching morphogenesis of an epithelial tube	113	-0.4663	-1.8387	5.5165E-04	1.6881E-02	1.4684E-02	3806 tags=44%, list=25%, signal=33%
BP	GO:0043038	amino acid activation	49	0.4966	1.9214	5.5540E-04	1.6958E-02	1.4752E-02	5794 tags=69%, list=38%, signal=43%
BP	GO:0002764	immune response-regulating signaling pathway	426	-0.3301	-1.5000	5.6173E-04	1.7095E-02	1.4871E-02	2274 tags=21%, list=17%, signal=19%
CC	GO:0015629	actin cytoskeleton	424	-0.3313	-1.5049	5.6237E-04	1.7095E-02	1.4871E-02	3310 tags=30%, list=22%, signal=24%
BP	GO:0046034	ATP metabolic process	254	0.4335	2.2043	5.6465E-04	1.7127E-02	1.4898E-02	2167 tags=39%, list=14%, signal=34%
CC	GO:0000151	ubiquitin ligase complex	256	0.2984	1.5198	5.6818E-04	1.7196E-02	1.4959E-02	4409 tags=38%, list=29%, signal=28%
MF	GO:0051536	iron-sulfur cluster binding	60	0.4687	1.8999	5.8531E-04	1.7572E-02	1.5285E-02	2243 tags=32%, list=15%, signal=27%
MF	GO:0051540	metal cluster binding	60	0.4687	1.8999	5.8531E-04	1.7572E-02	1.5285E-02	2243 tags=32%, list=15%, signal=27%
MF	GO:0001847	opsin receptor activity	4	-0.9611	-1.7611	5.8951E-04	1.7572E-02	1.5285E-02	384 tags=75%, list=3%, signal=73%
BP	GO:0019755	one-carbon compound transport	4	-0.9609	-1.7607	5.8951E-04	1.7572E-02	1.5285E-02	263 tags=75%, list=2%, signal=74%
BP	GO:0001682	regulation of progesterone biosynthetic process	4	-0.9646	-1.7675	5.8951E-04	1.7572E-02	1.5285E-02	102 tags=50%, list=1%, signal=50%
BP	GO:0000554	regulation of T-helper 1 cell cytokine production	4	-0.9619	-1.7625	5.8951E-04	1.7572E-02	1.5285E-02	285 tags=75%, list=2%, signal=74%
BP	GO:0000556	positive regulation of T-helper 1 cell cytokine production	4	-0.9619	-1.7625	5.8951E-04	1.7572E-02	1.5285E-02	285 tags=75%, list=2%, signal=74%
BP	GO:0071496	cellular response to external stimulus	284	-0.3647	-1.6044	5.9503E-04	1.7698E-02	1.5395E-02	2541 tags=24%, list=17%, signal=20%
BP	GO:0042035	regulation of cytokine biosynthetic process	63	-0.5482	-1.9679	6.0277E-04	1.7890E-02	1.5562E-02	1803 tags=29%, list=12%, signal=25%
BP	GO:1904035	regulation of epithelial cell apoptotic process	59	-0.5527	-1.9638	6.0827E-04	1.8015E-02	1.5671E-02	2307 tags=32%, list=15%, signal=27%
BP	GO:0009205	purine ribonucleoside triphosphate metabolic process	282	0.4314	2.2257	6.2073E-04	1.8344E-02	1.5957E-02	2969 tags=43%, list=19%, signal=36%
BP	GO:0042254	ribosome biogenesis	283	0.4035	2.0799	6.2344E-04	1.8385E-02	1.5993E-02	5278 tags=60%, list=34%, signal=40%
BP	GO:0009167	purine ribonucleoside monophosphate metabolic process	284	0.4211	2.1716	6.2539E-04	1.8403E-02	1.6008E-02	2969 tags=42%, list=19%, signal=34%
BP	GO:1901532	regulation of hematopoietic progenitor cell differentiation	76	0.4206	1.7904	6.2696E-04	1.8410E-02	1.6014E-02	2405 tags=38%, list=16%, signal=32%
BP	GO:0009126	purine nucleoside monophosphate metabolic process	285	0.4205	2.1679	6.2972E-04	1.8452E-02	1.6051E-02	2969 tags=42%, list=19%, signal=34%
BP	GO:0009199	ribonucleoside triphosphate metabolic process	287	0.4282	2.2115	6.3211E-04	1.8483E-02	1.6078E-02	2969 tags=43%, list=19%, signal=35%
BP	GO:0009144	purine nucleoside triphosphate metabolic process	289	0.4309	2.2248	6.3654E-04	1.8573E-02	1.6156E-02	2969 tags=43%, list=19%, signal=36%
BP	GO:0001022	negative regulation of transcription by RNA polymerase II	661	-0.3019	-1.4086	6.4041E-04	1.8637E-02	1.6212E-02	3041 tags=24%, list=20%, signal=26%
BP	GO:0032984	protein-containing complex disassembly	298	0.3319	1.7257	6.4144E-04	1.8637E-02	1.6212E-02	3891 tags=39%, list=25%, signal=29%
BP	GO:0051345	positive regulation of hydrolase activity	632	-0.3022	-1.4066	6.4392E-04	1.8651E-02	1.6225E-02	3331 tags=27%, list=22%, signal=22%
BP	GO:0009161	ribonucleoside monophosphate metabolic process	295	0.4232	2.1947	6.4516E-04	1.8651E-02	1.6225E-02	2293 tags=37%, list=15%, signal=32%
BP	GO:0090150	establishment of protein localization to membrane	300	0.3120	1.6230	6.4599E-04	1.8651E-02	1.6225E-02	4152 tags=42%, list=27%, signal=31%
BP	GO:0061900	glial cell activation	38	-0.6139	-2.0088	6.4946E-04	1.8712E-02	1.6277E-02	2838 tags=47%, list=19%, signal=39%
BP	GO:0009141	nucleoside triphosphate metabolic process	307	0.4353	2.2696	6.5488E-04	1.8805E-02	1.6358E-02	2969 tags=43%, list=19%, signal=36%
BP	GO:0051216	cartilage development	155	-0.4144	-1.7048	6.5539E-04	1.8805E-02	1.6358E-02	2975 tags=32%, list=19%, signal=26%
BP	GO:0002181	cytoplasmic translation	89	0.4040	1.7698	6.6225E-04	1.8962E-02	1.6495E-02	5131 tags=60%, list=34%, signal=40%
BP	GO:0070741	response to interleukin-6	31	-0.6525	-2.0478	6.6700E-04	1.9022E-02	1.6547E-02	1802 tags=29%, list=12%, signal=26%
BP	GO:0006520	cellular amino acid metabolic process	312	0.3033	1.5813	6.6711E-04	1.9022E-02	1.6547E-02	2422 tags=27%, list=16%, signal=23%
BP	GO:0009123	nucleoside monophosphate metabolic process	313	0.4255	2.2172	6.7340E-04	1.9162E-02	1.6669E-02	2691 tags=39%, list=18%, signal=33%
BP	GO:0000375	RNA splicing, via transesterification reactions	317	0.2973	1.5499	6.7843E-04	1.9212E-02	1.6713E-02	4649 tags=37%, list=30%, signal=26%
BP	GO:0000377	RNA splicing, via transesterification reactions with bulged ader	314	0.2965	1.5448	6.7935E-04	1.9212E-02	1.6713E-02	4649 tags=37%, list=30%, signal=26%
BP	GO:0000398	mRNA splicing, via spliceosome	314	0.2965	1.5448	6.7935E-04	1.9212E-02	1.6713E-02	4649 tags=37%, list=30%, signal=26%
CC	GO:0043235	receptor complex	304	-0.3509	-1.5532	7.0830E-04	1.9894E-02	1.7306E-02	3279 tags=29%, list=21%, signal=23%
BP	GO:1901293	nucleoside phosphate biosynthetic process	330	0.2732	1.4289	7.0872E-04	1.9894E-02	1.7306E-02	3250 tags=30%, list=21%, signal=24%
BP	GO:0046718	viral entry into host cell	94	-0.4886	-1.8746	7.0892E-04	1.9894E-02	1.7306E-02	2620 tags=32%, list=17%, signal=27%
BP	GO:0009165	nucleotide biosynthetic process	328</						

BP	GO:0034314	Arp2/3 complex-mediated actin nucleation	32	0.5509	1.9171	7.5738E-04	2.0905E-02	1.8185E-02	2635 tags=38%, list=17%, signal=31%
BP	GO:0045596	negative regulation of cell differentiation	551	-0.3086	-1.4243	7.6411E-04	2.1049E-02	1.8310E-02	3006 tags=27%, list=20%, signal=23%
BP	GO:0035744	T-helper 1 cell cytokine production	5	-0.9375	-1.8292	7.7354E-04	2.1185E-02	1.8429E-02	285 tags=60%, list=2%, signal=59%
MF	GO:0045236	CXCR chemokine receptor binding	5	-0.9320	-1.8183	7.7354E-04	2.1185E-02	1.8429E-02	6 tags=40%, list=0%, signal=40%
BP	GO:0045292	mRNA cis splicing, via spliceosome	37	0.5364	1.9373	7.7519E-04	2.1185E-02	1.8429E-02	356 tags=19%, list=2%, signal=19%
BP	GO:0070432	regulation of nucleotide-binding oligomerization domain contain	6	-0.9218	-1.8917	7.7519E-04	2.1185E-02	1.8429E-02	348 tags=50%, list=2%, signal=49%
BP	GO:0060759	regulation of response to cytokine stimulus	145	-0.4210	-1.7183	7.9533E-04	2.1693E-02	1.8870E-02	2236 tags=25%, list=15%, signal=21%
BP	GO:2000852	regulation of corticosterone secretion	4	0.9477	1.7753	8.1417E-04	2.2135E-02	1.9255E-02	18 tags=50%, list=0%, signal=50%
BP	GO:0006418	tRNA aminoacylation for protein translation	45	0.4865	1.8451	8.1477E-04	2.2135E-02	1.9255E-02	5794 tags=67%, list=38%, signal=42%
CC	GO:0042383	sarcolemma	121	-0.4443	-1.7682	8.2091E-04	2.2258E-02	1.9362E-02	3155 tags=32%, list=21%, signal=26%
BP	GO:0032570	response to progesterone	33	-0.6364	-2.0248	8.2467E-04	2.2302E-02	1.9400E-02	3367 tags=61%, list=22%, signal=47%
BP	GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic pr	389	0.2764	1.4727	8.2576E-04	2.2302E-02	1.9400E-02	4519 tags=40%, list=30%, signal=29%
BP	GO:0022407	regulation of cell-cell adhesion	283	-0.3574	-1.5717	8.3353E-04	2.2468E-02	1.9544E-02	2986 tags=30%, list=20%, signal=25%
BP	GO:0006065	protein targeting	397	0.3006	1.6031	8.4602E-04	2.2726E-02	1.9769E-02	4166 tags=41%, list=27%, signal=30%
BP	GO:0030856	regulation of epithelial cell differentiation	99	-0.4707	-1.8188	8.4638E-04	2.2726E-02	1.9769E-02	1925 tags=25%, list=13%, signal=22%
MF	GO:0003690	double-stranded DNA binding	699	-0.2995	-1.4022	8.4890E-04	2.2746E-02	1.9786E-02	3659 tags=30%, list=24%, signal=24%
BP	GO:0051604	protein maturation	254	-0.3633	-1.5805	8.5044E-04	2.2746E-02	1.9786E-02	2014 tags=21%, list=13%, signal=19%
CC	GO:0005743	mitochondrial inner membrane	414	0.5181	2.7766	8.6505E-04	2.3071E-02	2.0069E-02	3619 tags=54%, list=24%, signal=42%
MF	GO:0044183	protein binding involved in protein folding	20	-0.7206	-2.0489	8.6595E-04	2.3071E-02	2.0069E-02	49 tags=25%, list=0%, signal=25%
BP	GO:0071260	cellular response to mechanical stimulus	69	-0.5264	-1.9205	8.9074E-04	2.3686E-02	2.0604E-02	2209 tags=36%, list=14%, signal=31%
CC	GO:0032432	actin filament bundle	65	-0.5311	-1.9180	8.9579E-04	2.3775E-02	2.0681E-02	1500 tags=36%, list=10%, signal=35%
BP	GO:0045116	protein neddylation	15	0.7444	2.1113	9.8827E-04	2.3795E-02	2.0699E-02	3792 tags=93%, list=25%, signal=70%
BP	GO:0010310	regulation of hydrogen peroxide metabolic process	15	-0.7812	-2.0663	9.0106E-04	2.3823E-02	2.0732E-02	116 tags=13%, list=1%, signal=13%
BP	GO:0006612	protein targeting to membrane	182	0.3313	1.6218	9.0827E-04	2.3956E-02	2.0839E-02	4402 tags=47%, list=29%, signal=34%
BP	GO:0072666	Rho protein signal transduction	171	-0.4070	-1.6919	9.0956E-04	2.3956E-02	2.0839E-02	2789 tags=30%, list=18%, signal=25%
MF	GO:0071855	neuropeptide receptor binding	16	0.7199	2.0709	9.1283E-04	2.3996E-02	2.0874E-02	288 tags=44%, list=2%, signal=43%
BP	GO:0033238	regulation of cellular amine metabolic process	69	0.4346	1.8180	9.1855E-04	2.4070E-02	2.0938E-02	3187 tags=51%, list=21%, signal=40%
BP	GO:0006091	generation of precursor metabolites and energy	432	0.3809	2.0486	9.1912E-04	2.4070E-02	2.0938E-02	2900 tags=36%, list=19%, signal=30%
BP	GO:0011885	endothelial cell development	54	-0.5511	-1.9295	9.2421E-04	2.4157E-02	2.1014E-02	3251 tags=46%, list=21%, signal=37%
BP	GO:0097201	negative regulation of transcription from RNA polymerase II pro	12	-0.8101	-2.0196	9.2799E-04	2.4210E-02	2.1060E-02	75 tags=33%, list=0%, signal=33%
BP	GO:2000377	regulation of reactive oxygen species metabolic process	140	-0.4262	-1.7329	9.3023E-04	2.4223E-02	2.1071E-02	1802 tags=36%, list=12%, signal=32%
CC	GO:0005759	mitochondrial matrix	435	0.3771	2.0251	9.4251E-04	2.4450E-02	2.1269E-02	4048 tags=43%, list=26%, signal=32%
BP	GO:0071674	mononuclear cell migration	47	-0.5721	-1.9504	9.4251E-04	2.4450E-02	2.1269E-02	1748 tags=30%, list=11%, signal=26%
CC	GO:0005838	proteasome regulatory particle	20	0.6760	2.0672	9.4607E-04	2.4489E-02	2.1303E-02	3044 tags=65%, list=20%, signal=52%
BP	GO:0009790	embryo development	768	-0.2951	-1.3874	9.4757E-04	2.4489E-02	2.1303E-02	3494 tags=29%, list=23%, signal=23%
BP	GO:010498	proteasomal protein catabolic process	440	0.2622	1.4105	9.5147E-04	2.4544E-02	2.1351E-02	4519 tags=40%, list=30%, signal=29%
BP	GO:0022613	ribonucleoprotein complex biogenesis	445	0.3931	2.1150	9.5969E-04	2.4710E-02	2.1495E-02	4898 tags=51%, list=32%, signal=35%
BP	GO:0011961	positive regulation of cytokine-mediated signaling pathway	42	-0.6004	-2.0057	9.6169E-04	2.4712E-02	2.1497E-02	1692 tags=29%, list=11%, signal=25%
BP	GO:0038033	positive regulation of endothelial cell chemotaxis by VEGF-acti	5	-0.9289	-1.8124	9.6693E-04	2.4712E-02	2.1497E-02	565 tags=40%, list=4%, signal=39%
MF	GO:0050542	icosanoid binding	5	-0.9232	-1.8012	9.6693E-04	2.4712E-02	2.1497E-02	239 tags=60%, list=2%, signal=59%
MF	GO:0050544	arachidonic acid binding	5	-0.9232	-1.8012	9.6693E-04	2.4712E-02	2.1497E-02	239 tags=60%, list=2%, signal=59%
BP	GO:0042108	positive regulation of cytokine biosynthetic process	40	-0.5971	-1.9713	9.7119E-04	2.4775E-02	2.1552E-02	1802 tags=30%, list=12%, signal=27%
BP	GO:0050777	negative regulation of immune response	103	-0.4681	-1.8212	9.8012E-04	2.4951E-02	2.1705E-02	2052 tags=26%, list=13%, signal=23%
BP	GO:0090130	tissue migration	241	-0.3700	-1.5988	9.8172E-04	2.4951E-02	2.1705E-02	3196 tags=29%, list=21%, signal=24%
BP	GO:0071757	heterophilic cell-cell adhesion via plasma membrane cell adhes	33	-0.6310	-2.0075	9.8961E-04	2.5071E-02	2.1809E-02	1760 tags=30%, list=12%, signal=27%
BP	GO:0022612	gland morphogenesis	96	-0.4757	-1.8291	9.9150E-04	2.5071E-02	2.1809E-02	3272 tags=45%, list=21%, signal=35%
BP	GO:009150	purine ribonucleotide metabolic process	453	0.3759	2.0239	9.9502E-04	2.5071E-02	2.1809E-02	3250 tags=39%, list=21%, signal=32%
BP	GO:0071704	cytochrome complex assembly	31	0.5629	1.9437	9.9875E-04	2.5071E-02	2.1809E-02	4924 tags=74%, list=32%, signal=50%
CC	GO:0046540	U4/U6 x U5 tri-snRNP complex	31	0.5696	1.9669	9.9875E-04	2.5071E-02	2.1809E-02	2386 tags=45%, list=16%, signal=38%
CC	GO:0075266	spliceosomal tri-snRNP complex	31	0.5696	1.9669	9.9875E-04	2.5071E-02	2.1809E-02	2386 tags=45%, list=16%, signal=38%
MF	GO:0061135	endopeptidase regulator activity	91	-0.4818	-1.8379	9.9914E-04	2.5071E-02	2.1809E-02	800 tags=16%, list=5%, signal=16%
BP	GO:0042476	odontogenesis	90	-0.4803	-1.8275	1.0021E-03	2.5101E-02	2.1835E-02	2814 tags=37%, list=18%, signal=30%
BP	GO:0051085	chaperone cofactor-dependent protein refolding	28	-0.6559	-2.0116	1.0076E-03	2.5158E-02	2.1884E-02	75 tags=18%, list=0%, signal=18%
CC	GO:0019866	organelle inner membrane	460	0.4923	2.6536	1.0081E-03	2.5158E-02	2.1884E-02	3619 tags=51%, list=24%, signal=40%
BP	GO:2001234	negative regulation of apoptotic signaling pathway	193	-0.3899	-1.6473	1.0111E-03	2.5189E-02	2.1911E-02	1902 tags=20%, list=12%, signal=18%
BP	GO:0009262	deoxyribonucleotide metabolic process	33	0.5419	1.9062	1.0155E-03	2.5252E-02	2.1966E-02	3176 tags=55%, list=21%, signal=43%
BP	GO:0061036	positive regulation of cartilage development	25	-0.6642	-1.9801	1.0263E-03	2.5476E-02	2.2161E-02	2382 tags=44%, list=16%, signal=37%
BP	GO:0034001	axis elongation	24	-0.6728	-1.9901	1.0309E-03	2.5507E-02	2.2188E-02	1493 tags=42%, list=10%, signal=38%
CC	GO:0072588	box H/ACA RNP complex	7	0.8634	1.9375	1.0328E-03	2.5507E-02	2.2188E-02	1263 tags=57%, list=8%, signal=52%
BP	GO:0035934	corticosterone secretion	5	0.8947	1.7950	1.0350E-03	2.5507E-02	2.2188E-02	18 tags=40%, list=0%, signal=40%
BP	GO:1903998	regulation of eating behavior	5	0.8952	1.7959	1.0350E-03	2.5507E-02	2.2188E-02	159 tags=40%, list=1%, signal=40%
BP	GO:0009259	ribonucleotide metabolic process	466	0.3774	2.0335	1.0384E-03	2.5546E-02	2.2222E-02	3250 tags=39%, list=21%, signal=31%
BP	GO:0007005	mitochondrion organization	474	0.3799	2.0510	1.0515E-03	2.5822E-02	2.2462E-02	2900 tags=37%, list=19%, signal=31%
BP	GO:0022411	cellular component disassembly	473	0.2490	1.3435	1.0560E-03	2.5830E-02	2.2470E-02	3187 tags=29%, list=21%, signal=24%
BP	GO:0002674	negative regulation of acute inflammatory response	9	0.8386	2.0401	1.0595E-03	2.5830E-02	2.2470E-02	677 tags=33%, list=4%, signal=34%
BP	GO:0002825	regulation of T-helper 1 type immune response	17	-0.7645	-2.0842	1.0621E-03	2.5830E-02	2.2470E-02	507 tags=35%, list=3%, signal=34%
BP	GO:0051195	negative regulation of cofactor metabolic process	17	-0.7611	-2.0751	1.0621E-03	2.5830E-02	2.2470E-02	2374 tags=53%, list=2%, signal=45%
CC	GO:001725	stress fiber	59	-0.5334	-1.8953	1.0645E-03	2.5830E-02	2.2470E-02	2759 tags=39%, list=18%, signal=32%
CC	GO:0097517	contractile actin filament bundle	59	-0.5334	-1.8953	1.0645E-03	2.5830E-02	2.2470E-02	2759 tags=39%, list=18%, signal=32%
BP	GO:0019693	ribose phosphate metabolic process	484	0.3707	2.0083	1.0650E-03	2.5830E-02	2.2470E-02	3250 tags=38%, list=21%, signal=31%
BP	GO:0006163	purine nucleotide metabolic process	476	0.3753	2.0262	1.0776E-03	2.6091E-02	2.2696E-02	3250 tags=39%, list=21%, signal=31%
MF	GO:0004930	G protein-coupled receptor activity	267	-0.3625	-1.5839	1.0859E-03	2.6246E-02	2.2831E-02	2508 tags=28%, list=16%, signal=24%
BP	GO:0050678	regulation of epithelial cell proliferation	255	-0.3609	-1.5708	1.0936E-03	2.6385E-02	2.2952E-02	3849 tags=36%, list=25%, signal=27%
BP	GO:0007006	mitochondrial membrane organization	116	0.3714	1.7002	1.0993E-03	2.6477E-02	2.3032E-02	2941 tags=38%, list=19%, signal=31%
BP	GO:0072521	purine-containing compound metabolic process	503	0.3738	2.0309	1.1099E-03	2.6639E-02	2.3173E-02	3250 tags=38%, list=21%, signal=31%
BP	GO:0072594	establishment of protein localization to organelle	503	0.2796	1.5191	1.1099E-03	2.6639E-02	2.3173E-02	4227 tags=40%, list=28%, signal=30%
BP	GO:0061614	pr-miRNA transcription by RNA polymerase II	41	-0.5864	-1.9503	1.1229E-03	2.6904E-02	2.3403E-02	2742 tags=44%, list=18%, signal=36%
BP	GO:0019079	viral genome replication	98	-0.4669	-1.8015	1.1299E-03	2.7027E-02	2.3510E-02	2185 tags=23%, list=14%, signal=20%
BP	GO:1903428	positive regulation of reactive oxygen species biosynthetic pro	40	-0.5925	-1.9560	1.1331E-03	2.7054E-02	2.3534E-02	1564 tags=38%, list=10%, signal=34%
BP	GO:0050819	negative regulation of coagulation	38	-0.6014	-1.9680	1.1365E-03	2.7091E-02	2.3566E-02	527 tags=21%, list=3%, signal=20%
BP	GO:0034660	ncRNA metabolic process	523	0.3184	1.7391	1.1442E-03	2.7206E-02	2.3666E-02	4785 tags=43%, list=31%, signal=31%
BP	GO:0007009	plasma membrane organization	90	-0.4745	-1.8055	1.1453E-03	2.7206E-02	2.3666E-02	4004 tags=47%, list=26%, signal=35%
BP	GO:0042493	response to drug	795	-0.2916	-1.3730	1.1567E-03	2.7428E-02	2.3859E-02	2578 tags=22%, list=17%, signal=19%
MF	GO:0042498	threonine-type endopeptidase activity	18	0.6914	2.0584	1.1650E-03	2.7530E-02	2.3948E-02	2803 tags=89%, list=18%, signal=73%
MF	GO:0070003	threonine-type peptidase activity	18	0.6914	2.0584	1.1650E-03	2.7530E-02	2.3948E-02	2803 tags=89%, list=18%, signal=73%
BP	GO:0042088	T-helper 1 type immune response	31	-0.6377	-2.0015	1.1673E-03	2.7535E-02	2.3952E-02	507 tags=35%, list=3%, signal=34%
BP	GO:0060348	bone development	167	-0.4087	-1.6976	1.1691E-03	2.7535E-02	2.3952E-02	3187 tags=34%, list=21%, signal=27%
BP	GO:0002548	monocyte chemotaxis	28	-0.6531	-2.0027	1.1755E-03	2.7605E-02	2.4013E-02	62 tags=25%, list=0%, signal=25%
BP	GO:2000379	positive regulation of reactive oxygen species metabolic proces	73	-0.5060	-1.8639	1.1766E-03	2.7605E-02	2.4013E-02	1692 tags=30%, list=11%, signal=27%
BP	GO:0051346	negative regulation of hydrolase activity	310	-0.3446	-1.5276	1.1781E-03	2.7605E-02	2.4013E-02	1966 tags=17%, list=13%, signal=15%
CC	GO:0042641	actomyosin	71	-0.5179	-1.8982	1.1841E-03	2.7687E-02	2.4084E-02	2759 tags=38%, list=18%, signal=31%
CC	GO:0031091	platelet alpha granule	67	-0.5259	-1.9123	1.1892E-03	2.7687E-02	2.4084E-02	1430 tags=27%, list=9%, signal=24%
BP	GO:0070426	positive regulation of nucleotide-binding oligomerization domain	3	-0.9799	-1.6558	1.1917E-03	2.7687E-02	2.4084E-02	49 tags=67%, list=

MF	GO:0016491	oxidoreductase activity	571	0.2736	1.5086	1.2594E-03	2.8969E-02	2.5200E-02	2372 tags=26%, list=16%, signal=23%
BP	GO:001952	regulation of cell-matrix adhesion	95	-0.4624	-1.7771	1.2726E-03	2.9224E-02	2.5421E-02	3177 tags=36%, list=21%, signal=29%
BP	GO:0006412	translation	574	0.3169	1.7462	1.2853E-03	2.9467E-02	2.5633E-02	4951 tags=49%, list=32%, signal=34%
MF	GO:0030414	peptidase inhibitor activity	87	-0.4740	-1.7952	1.2914E-03	2.9521E-02	2.5680E-02	1311 tags=22%, list=9%, signal=20%
BP	GO:0006376	mRNA splice site selection	37	0.5211	1.8820	1.2920E-03	2.9521E-02	2.5680E-02	3012 tags=38%, list=20%, signal=30%
BP	GO:0044743	protein transmembrane import into intracellular organelle	39	0.5114	1.8750	1.3058E-03	2.9788E-02	2.5912E-02	3387 tags=46%, list=22%, signal=36%
CC	GO:0055684	U2-type spliceosome complex	85	0.4017	1.7413	1.3119E-03	2.9877E-02	2.5990E-02	4649 tags=48%, list=30%, signal=34%
BP	GO:1904019	epithelial cell apoptotic process	77	-0.4981	-1.8499	1.3164E-03	2.9929E-02	2.6035E-02	2307 tags=47%, list=15%, signal=40%
BP	GO:0006753	nucleoside phosphate metabolic process	598	0.3779	2.0894	1.3333E-03	3.2655E-02	2.6327E-02	3225 tags=37%, list=21%, signal=31%
BP	GO:0002430	complement receptor mediated signaling pathway	8	-0.8712	-1.9418	1.3369E-03	3.2966E-02	2.6354E-02	1010 tags=62%, list=7%, signal=58%
BP	GO:0009117	nucleotide metabolic process	593	0.3753	2.0731	1.3441E-03	3.3060E-02	2.6409E-02	3225 tags=37%, list=21%, signal=30%
BP	GO:0043043	peptide biosynthetic process	593	0.3140	1.7341	1.3441E-03	3.3060E-02	2.6409E-02	4951 tags=49%, list=32%, signal=34%
BP	GO:0050691	regulation of defense response to virus by host	26	-0.6517	-1.9581	1.3645E-03	3.0770E-02	2.6766E-02	1672 tags=35%, list=11%, signal=31%
BP	GO:1902749	regulation of cell cycle G2/M phase transition	187	0.3153	1.5496	1.3736E-03	3.0926E-02	2.6902E-02	3099 tags=32%, list=20%, signal=26%
BP	GO:0070372	regulation of ERK1 and ERK2 cascade	202	-0.3800	-1.6126	1.3840E-03	3.1108E-02	2.7061E-02	1184 tags=14%, list=8%, signal=13%
BP	GO:0034103	regulation of tissue remodeling	54	-0.5453	-1.9093	1.3863E-03	3.1110E-02	2.7062E-02	3243 tags=44%, list=21%, signal=35%
BP	GO:0000904	cell morphogenesis involved in differentiation	637	-0.2968	-1.3823	1.3920E-03	3.1172E-02	2.7116E-02	3809 tags=33%, list=25%, signal=26%
BP	GO:0061077	chaperone-mediated protein folding	53	-0.5507	-1.9202	1.3936E-03	3.1172E-02	2.7116E-02	249 tags=19%, list=2%, signal=19%
CC	GO:0055839	proteasome core complex	18	0.6835	2.0349	1.3979E-03	3.1219E-02	2.7157E-02	2803 tags=83%, list=18%, signal=68%
CC	GO:0031966	mitochondrial membrane	612	0.4411	2.4369	1.4104E-03	3.1447E-02	2.7355E-02	3580 tags=47%, list=23%, signal=37%
BP	GO:0150076	neuroinflammatory response	47	-0.5652	-1.9270	1.4138E-03	3.1470E-02	2.7375E-02	2838 tags=43%, list=19%, signal=35%
BP	GO:0031623	receptor internalization	93	-0.4646	-1.7776	1.4219E-03	3.1599E-02	2.7488E-02	1417 tags=17%, list=9%, signal=16%
BP	GO:0051458	corticotropin secretion	5	0.8891	1.7837	1.4490E-03	3.2150E-02	2.7967E-02	28 tags=40%, list=0%, signal=40%
BP	GO:0032102	negative regulation of response to external stimulus	252	-0.3603	-1.5652	1.4606E-03	3.2355E-02	2.8145E-02	2876 tags=25%, list=19%, signal=21%
BP	GO:0009636	response to toxic substance	400	-0.3264	-1.4778	1.4716E-03	3.2547E-02	2.8312E-02	2462 tags=21%, list=16%, signal=18%
BP	GO:1903053	regulation of extracellular matrix organization	34	-0.6104	-1.9549	1.4783E-03	3.2644E-02	2.8396E-02	3187 tags=59%, list=21%, signal=47%
BP	GO:0032609	interferon-gamma production	64	-0.5281	-1.9011	1.5006E-03	3.3083E-02	2.8778E-02	1388 tags=28%, list=9%, signal=26%
MF	GO:0061134	peptidase regulator activity	122	-0.4323	-1.7215	1.5060E-03	3.3117E-02	2.8808E-02	1966 tags=21%, list=13%, signal=19%
BP	GO:0042475	odontogenesis of dentin-containing tooth	63	-0.5225	-1.8756	1.5069E-03	3.3117E-02	2.8808E-02	2966 tags=38%, list=19%, signal=31%
BP	GO:0009266	response to temperature stimulus	205	-0.3803	-1.6146	1.5111E-03	3.3156E-02	2.8842E-02	1842 tags=16%, list=12%, signal=14%
BP	GO:0017144	drug metabolic process	648	0.2622	1.4541	1.5221E-03	3.3343E-02	2.9005E-02	2691 tags=29%, list=18%, signal=25%
BP	GO:0048608	reproductive structure development	309	-0.3398	-1.5058	1.5334E-03	3.3538E-02	2.9174E-02	3397 tags=28%, list=22%, signal=22%
BP	GO:0010968	regulation of microtubule nucleation	5	-0.9166	-1.7884	1.5471E-03	3.3784E-02	2.9388E-02	49 tags=60%, list=0%, signal=60%
CC	GO:0050740	mitochondrial envelope	652	0.4427	2.4544	1.5552E-03	3.3908E-02	2.9496E-02	3580 tags=47%, list=23%, signal=37%
BP	GO:0051952	regulation of amine transport	73	0.3995	1.6887	1.5610E-03	3.3946E-02	2.9529E-02	653 tags=19%, list=4%, signal=18%
BP	GO:0070585	protein localization to mitochondrion	131	0.3498	1.6275	1.5619E-03	3.3946E-02	2.9529E-02	3402 tags=43%, list=22%, signal=34%
BP	GO:0045066	regulatory T cell differentiation	19	-0.7143	-2.0018	1.5699E-03	3.4012E-02	2.9586E-02	1669 tags=47%, list=11%, signal=42%
BP	GO:0045589	regulation of regulatory T cell differentiation	19	-0.7143	-2.0018	1.5699E-03	3.4012E-02	2.9586E-02	1669 tags=47%, list=11%, signal=42%
BP	GO:0046631	alpha-beta T cell activation	90	-0.4658	-1.7725	1.5748E-03	3.4042E-02	2.9613E-02	2890 tags=32%, list=19%, signal=26%
BP	GO:0048143	astrocyte activation	18	-0.7270	-2.0130	1.5762E-03	3.4042E-02	2.9613E-02	2031 tags=61%, list=13%, signal=53%
BP	GO:0030185	nitric oxide transport	3	-0.9658	-1.6320	1.5889E-03	3.4171E-02	2.9725E-02	527 tags=100%, list=3%, signal=97%
BP	GO:1902623	negative regulation of neutrophil migration	3	-0.9665	-1.6331	1.5889E-03	3.4171E-02	2.9725E-02	42 tags=67%, list=0%, signal=66%
BP	GO:0034333	adherens junction assembly	84	-0.4789	-1.8031	1.5896E-03	3.4171E-02	2.9725E-02	3449 tags=40%, list=23%, signal=32%
CC	GO:0012506	vesicle membrane	664	-0.2935	-1.3704	1.5988E-03	3.4316E-02	2.9851E-02	2842 tags=23%, list=19%, signal=19%
BP	GO:0019599	regulation of cytokine-mediated signaling pathway	134	-0.4221	-1.7037	1.6129E-03	3.4511E-02	3.0021E-02	2236 tags=25%, list=15%, signal=21%
BP	GO:0055086	nucleobase-containing small molecule metabolic process	668	0.3597	1.9982	1.6129E-03	3.4511E-02	3.0021E-02	3225 tags=36%, list=21%, signal=29%
BP	GO:0006949	syncytium formation	40	-0.5861	-1.9348	1.6186E-03	3.4580E-02	3.0081E-02	3056 tags=50%, list=20%, signal=40%
BP	GO:0070559	chromosome segregation	243	0.2841	1.4387	1.6349E-03	3.4873E-02	3.0336E-02	3624 tags=32%, list=24%, signal=25%
BP	GO:0030168	platelet activation	120	-0.4359	-1.7345	1.6396E-03	3.4919E-02	3.0376E-02	3295 tags=33%, list=22%, signal=26%
BP	GO:0051084	'de novo' posttranslational protein folding	33	-0.6087	-1.9367	1.6493E-03	3.5073E-02	3.0510E-02	75 tags=15%, list=0%, signal=15%
BP	GO:0010700	negative regulation of norepinephrine secretion	5	0.8862	1.7778	1.6560E-03	3.5160E-02	3.0585E-02	218 tags=40%, list=1%, signal=39%
CC	GO:0005902	microvillus	61	-0.5256	-1.8763	1.6641E-03	3.5225E-02	3.0642E-02	3235 tags=41%, list=21%, signal=32%
MF	GO:0016209	antioxidant activity	61	-0.5217	-1.8624	1.6641E-03	3.5225E-02	3.0642E-02	961 tags=20%, list=6%, signal=19%
BP	GO:0050792	regulation of viral process	167	-0.3944	-1.6381	1.6888E-03	3.5691E-02	3.1047E-02	3392 tags=32%, list=22%, signal=25%
CC	GO:0000276	mitochondrial proton-transporting ATP synthase complex, coupled	9	0.7942	1.9322	1.6953E-03	3.5774E-02	3.1120E-02	2546 tags=89%, list=17%, signal=74%
BP	GO:0007265	Ras protein signal transduction	385	-0.3258	-1.4690	1.7117E-03	3.6067E-02	3.1374E-02	3316 tags=28%, list=22%, signal=23%
BP	GO:0070424	regulation of nucleotide-binding oligomerization domain containing	8	-0.8475	-1.8889	1.7189E-03	3.6155E-02	3.1451E-02	348 tags=38%, list=2%, signal=37%
CC	GO:0045263	protein-transporting ATP synthase complex, coupling factor F1c	10	0.7741	1.9347	1.7212E-03	3.6155E-02	3.1451E-02	2546 tags=80%, list=17%, signal=67%
MF	GO:0048666	endopeptidase inhibitor activity	84	-0.4777	-1.7987	1.7341E-03	3.6358E-02	3.1627E-02	800 tags=15%, list=5%, signal=15%
BP	GO:0010389	regulation of G2/M transition of mitotic cell cycle	172	0.3299	1.6060	1.7361E-03	3.6358E-02	3.1627E-02	3099 tags=33%, list=20%, signal=27%
BP	GO:0043604	amide biosynthetic process	713	0.2967	1.6542	1.7452E-03	3.6493E-02	3.1745E-02	4951 tags=47%, list=32%, signal=33%
BP	GO:0045926	negative regulation of growth	202	-0.3774	-1.6016	1.7614E-03	3.6768E-02	3.1984E-02	3417 tags=33%, list=22%, signal=26%
BP	GO:0006518	peptide metabolic process	715	0.2621	1.4611	1.7637E-03	3.6768E-02	3.1984E-02	4951 tags=46%, list=32%, signal=33%
MF	GO:0035662	Toll-like receptor 4 binding	4	-0.9392	-1.7210	1.7685E-03	3.6813E-02	3.2023E-02	193 tags=75%, list=1%, signal=74%
CC	GO:1990234	transferase complex	704	0.2489	1.3840	1.7730E-03	3.6852E-02	3.2057E-02	4234 tags=35%, list=28%, signal=26%
MF	GO:0005044	scavenger receptor activity	37	-0.5877	-1.9140	1.7939E-03	3.7173E-02	3.2336E-02	1427 tags=46%, list=9%, signal=42%
BP	GO:0017001	antibiotic catabolic process	37	-0.5894	-1.9194	1.7939E-03	3.7173E-02	3.2336E-02	2374 tags=38%, list=16%, signal=32%
BP	GO:0016567	protein ubiquitination	732	0.2330	1.2979	1.8248E-03	3.7758E-02	3.2845E-02	4415 tags=36%, list=29%, signal=27%
MF	GO:0036002	pre-mRNA binding	40	0.5026	1.8541	1.8305E-03	3.7819E-02	3.2898E-02	423 tags=20%, list=3%, signal=19%
BP	GO:0006617	SRP-dependent cotranslational protein targeting to membrane	8	0.8169	1.9132	1.8884E-03	3.8956E-02	3.3887E-02	1691 tags=75%, list=11%, signal=67%
BP	GO:0070199	establishment of protein localization to chromosome	22	0.6268	1.9757	1.8953E-03	3.9040E-02	3.3960E-02	3728 tags=59%, list=24%, signal=45%
BP	GO:0030199	collagen fibril organization	43	-0.5742	-1.9274	1.9157E-03	3.9402E-02	3.4275E-02	2277 tags=40%, list=15%, signal=34%
BP	GO:0019355	endothelial cell proliferation	115	-0.4368	-1.7286	1.9202E-03	3.9435E-02	3.4304E-02	1802 tags=23%, list=12%, signal=21%
BP	GO:0010727	negative regulation of hydrogen peroxide metabolic process	7	-0.8731	-1.8686	1.9376E-03	3.9675E-02	3.4513E-02	2 tags=57%, list=0%, signal=57%
MF	GO:0042609	CD4 receptor binding	7	-0.8716	-1.8656	1.9376E-03	3.9675E-02	3.4513E-02	1443 tags=71%, list=9%, signal=65%
BP	GO:0060602	branch elongation of an epithelium	16	-0.7448	-2.0054	1.9573E-03	3.9977E-02	3.4775E-02	1493 tags=50%, list=10%, signal=45%
BP	GO:0060351	cartilage development involved in endochondral bone morphogenesis	35	-0.5907	-1.9027	1.9595E-03	3.9977E-02	3.4775E-02	1273 tags=34%, list=8%, signal=32%
CC	GO:0017266	ruffle	160	-0.3944	-1.6277	1.9610E-03	3.9977E-02	3.4775E-02	2885 tags=29%, list=19%, signal=24%
BP	GO:0042743	hydrogen peroxide metabolic process	34	-0.5946	-1.9041	1.9711E-03	4.0122E-02	3.4902E-02	654 tags=18%, list=4%, signal=17%
BP	GO:0050866	negative regulation of cell activation	139	-0.4126	-1.6757	1.9971E-03	4.0591E-02	3.5310E-02	2052 tags=22%, list=13%, signal=19%
BP	GO:0019334	positive regulation of protein phosphorylation	739	-0.2875	-1.3490	2.0080E-03	4.0731E-02	3.5431E-02	3413 tags=27%, list=22%, signal=22%
BP	GO:0070200	establishment of protein localization to telomere	14	0.7163	1.9911	2.0098E-03	4.0731E-02	3.5431E-02	3728 tags=79%, list=24%, signal=59%
BP	GO:0055114	oxidation-reduction process	793	0.2704	1.5189	2.0161E-03	4.0799E-02	3.5490E-02	2471 tags=26%, list=16%, signal=23%
BP	GO:0022410	circadian sleep/wake cycle process	15	0.7089	2.0107	2.0211E-03	4.0839E-02	3.5526E-02	273 tags=27%, list=2%, signal=26%
BP	GO:0051459	regulation of corticotropin secretion	4	0.9321	1.7461	2.0354E-03	4.1068E-02	3.5725E-02	28 tags=50%, list=0%, signal=50%
BP	GO:0002693	positive regulation of cellular extravasation	12	-0.7907	-1.9712	2.0416E-03	4.1132E-02	3.5780E-02	839 tags=50%, list=5%, signal=47%
BP	GO:0002367	cytokine production involved in immune response	75	-0.4912	-1.8175	2.0537E-03	4.1159E-02	3.5803E-02	2053 tags=29%, list=13%, signal=26%
BP	GO:0042033	chemokine biosynthetic process	10	-0.8160	-1.9490	2.0545E-03	4.1159E-02	3.5803E-02	1433 tags=40%, list=9%, signal=36%
BP	GO:0050755	chemokine metabolic process	10	-0.8160	-1.9490	2.0545E-03	4.1159E-02	3.5803E-02	1433 tags=40%, list=9%, signal=36%
BP	GO:0034605	cellular response to heat	119	-0.4326	-1.7198	2.0548E-03	4.1159E-02	3.5803E-02	1842 tags=18%, list=12%, signal=16%
CC	GO:0035579	specific granule membrane	70	-0.5009	-1.8306	2.0768E-03	4.1457E-02	3.6063E-02	1748 tags=33%, list=11%, signal=29%
BP	GO:0044106	cellular amine metabolic process	101	0.3756	1.6786	2.0768E-03	4.1457E-02	3.6063E-02	3044 tags=45%, list=20%, signal=36%
BP	GO:0032680	regulation of tumor necrosis factor production	108	-					

BP	GO:2001233	regulation of apoptotic signaling pathway	347	-0.3302	-1.4777	2.1970E-03	4.3316E-02	3.7680E-02	2444 tags=21%, list=16%, signal=18%
BP	GO:0060562	epithelial tube morphogenesis	247	-0.3573	-1.5482	2.2010E-03	4.3333E-02	3.7695E-02	3822 tags=37%, list=25%, signal=28%
BP	GO:0002865	negative regulation of acute inflammatory response to ant	4	0.9168	1.7175	2.2390E-03	4.4017E-02	3.8290E-02	677 tags=75%, list=4%, signal=72%
BP	GO:0010718	positive regulation of epithelial to mesenchymal transition	41	-0.5674	-1.8871	2.2457E-03	4.4088E-02	3.8351E-02	1902 tags=32%, list=12%, signal=28%
MF	GO:0004867	serine-type endopeptidase inhibitor activity	40	-0.5784	-1.9093	2.2661E-03	4.4416E-02	3.8637E-02	598 tags=25%, list=4%, signal=24%
BP	GO:0045073	regulation of chemokine biosynthetic process	9	-0.8302	-1.9187	2.2714E-03	4.4416E-02	3.8637E-02	1433 tags=44%, list=9%, signal=40%
BP	GO:0019692	deoxyribose phosphate metabolic process	32	0.5199	1.8094	2.2722E-03	4.4416E-02	3.8637E-02	3176 tags=50%, list=21%, signal=40%
BP	GO:0007369	gastrulation	129	-0.4173	-1.6768	2.2933E-03	4.4766E-02	3.8941E-02	3605 tags=37%, list=24%, signal=29%
BP	GO:0072655	establishment of protein localization to mitochondrion	128	0.3424	1.5878	2.3015E-03	4.4863E-02	3.9026E-02	3402 tags=42%, list=22%, signal=33%
MF	GO:0070492	oligosaccharide binding	6	-0.8829	-1.8119	2.3256E-03	4.5259E-02	3.9370E-02	876 tags=67%, list=6%, signal=63%
CC	GO:0005814	centriole	119	-0.4282	-1.7023	2.3288E-03	4.5259E-02	3.9370E-02	1792 tags=15%, list=12%, signal=13%
BP	GO:0045619	regulation of lymphocyte differentiation	115	-0.4337	-1.7164	2.3316E-03	4.5259E-02	3.9370E-02	2549 tags=28%, list=17%, signal=23%
BP	GO:0043542	endothelial cell migration	172	-0.3914	-1.6277	2.3383E-03	4.5324E-02	3.9426E-02	3031 tags=28%, list=20%, signal=23%
BP	GO:1903555	regulation of tumor necrosis factor superfamily cytokine p	111	-0.4374	-1.7226	2.3464E-03	4.5418E-02	3.9509E-02	1793 tags=25%, list=12%, signal=22%
CC	GO:0030659	cytoplasmic vesicle membrane	645	-0.2926	-1.3637	2.3532E-03	4.5459E-02	3.9544E-02	2842 tags=23%, list=19%, signal=19%
BP	GO:0010499	proteasomal ubiquitin-independent protein catabolic process	21	0.6208	1.9319	2.3552E-03	4.5459E-02	3.9544E-02	2803 tags=71%, list=18%, signal=58%
BP	GO:0048521	negative regulation of behavior	11	0.7561	1.9504	2.3692E-03	4.5666E-02	3.9724E-02	159 tags=36%, list=1%, signal=36%
BP	GO:0070198	protein localization to chromosome, telomeric region	24	0.6025	1.9452	2.3912E-03	4.6026E-02	4.0038E-02	4615 tags=71%, list=30%, signal=60%
BP	GO:1902036	regulation of hematopoietic stem cell differentiation	64	0.4279	1.7618	2.3966E-03	4.6067E-02	4.0073E-02	3171 tags=45%, list=21%, signal=36%
BP	GO:0098813	nuclear chromosome segregation	199	0.3027	1.4959	2.4038E-03	4.6141E-02	4.0137E-02	3624 tags=34%, list=24%, signal=26%
BP	GO:0002479	antigen processing and presentation of exogenous peptide	66	0.4211	1.7441	2.4279E-03	4.6539E-02	4.0483E-02	2405 tags=39%, list=16%, signal=33%
BP	GO:0000768	syncytium formation by plasma membrane fusion	38	-0.5782	-1.8918	2.4355E-03	4.6554E-02	4.0496E-02	3056 tags=66%, list=20%, signal=53%
BP	GO:0140253	cell-cell fusion	38	-0.5782	-1.8918	2.4355E-03	4.6554E-02	4.0496E-02	3056 tags=66%, list=20%, signal=53%
BP	GO:0002695	negative regulation of leukocyte activation	121	-0.4221	-1.6800	2.4627E-03	4.7010E-02	4.0893E-02	2052 tags=24%, list=13%, signal=21%
BP	GO:0061458	reproductive system development	312	-0.3346	-1.4842	2.4697E-03	4.7078E-02	4.0952E-02	3397 tags=28%, list=22%, signal=22%
BP	GO:1904407	positive regulation of nitric oxide metabolic process	33	-0.5928	-1.8860	2.4740E-03	4.7095E-02	4.0967E-02	1564 tags=33%, list=10%, signal=30%
BP	GO:0045080	positive regulation of chemokine biosynthetic process	8	-0.8365	-1.8645	2.4828E-03	4.7197E-02	4.1056E-02	1433 tags=50%, list=9%, signal=45%
MF	GO:0008233	peptidase activity	408	-0.3180	-1.4405	2.4926E-03	4.7319E-02	4.1162E-02	2484 tags=20%, list=16%, signal=17%
MF	GO:0003823	antigen binding	30	-0.6132	-1.9125	2.5050E-03	4.7489E-02	4.1309E-02	2691 tags=53%, list=18%, signal=44%
CC	GO:0101003	ficolin-1-rich granule membrane	48	-0.5499	-1.8817	2.5098E-03	4.7514E-02	4.1332E-02	2582 tags=46%, list=17%, signal=38%
BP	GO:1903589	positive regulation of blood vessel endothelial cell proliferation i	6	-0.8805	-1.8069	2.5194E-03	4.7630E-02	4.1433E-02	81 tags=50%, list=1%, signal=50%
BP	GO:0008380	RNA splicing	397	0.2489	1.3274	2.5381E-03	4.7918E-02	4.1683E-02	4649 tags=35%, list=30%, signal=25%
BP	GO:0051187	cofactor catabolic process	43	-0.5619	-1.8860	2.5543E-03	4.8158E-02	4.1892E-02	1503 tags=28%, list=10%, signal=25%
BP	GO:0043588	skin development	184	-0.3860	-1.6190	2.5684E-03	4.8358E-02	4.2066E-02	3025 tags=32%, list=20%, signal=26%
BP	GO:0042769	DNA damage response, detection of DNA damage	36	0.5064	1.8170	2.5780E-03	4.8432E-02	4.2130E-02	3897 tags=53%, list=25%, signal=39%
BP	GO:1904816	positive regulation of protein localization to chromosome, telom	10	0.7616	1.9034	2.5818E-03	4.8432E-02	4.2130E-02	3498 tags=90%, list=23%, signal=69%
BP	GO:0060349	bone morphogenesis	87	-0.4604	-1.7437	2.5829E-03	4.8432E-02	4.2130E-02	3187 tags=38%, list=21%, signal=30%
BP	GO:0043900	regulation of multi-organism process	310	-0.3349	-1.4846	2.5919E-03	4.8536E-02	4.2220E-02	3392 tags=28%, list=22%, signal=22%
BP	GO:0071706	tumor necrosis factor superfamily cytokine production	115	-0.4306	-1.7040	2.6060E-03	4.8597E-02	4.2274E-02	1793 tags=24%, list=12%, signal=22%
BP	GO:0008535	respiratory chain complex IV assembly	22	0.6217	1.9594	2.6060E-03	4.8597E-02	4.2274E-02	4756 tags=73%, list=31%, signal=60%
BP	GO:0006458	'de novo' protein folding	37	-0.5799	-1.8885	2.6093E-03	4.8597E-02	4.2274E-02	75 tags=14%, list=0%, signal=13%
BP	GO:0072678	T cell migration	37	-0.5755	-1.8743	2.6093E-03	4.8597E-02	4.2274E-02	614 tags=16%, list=4%, signal=16%
MF	GO:0046933	proton-transporting ATP synthase activity, rotational mechanis	14	0.6978	1.9398	2.6798E-03	4.9843E-02	4.3358E-02	2546 tags=64%, list=17%, signal=54%
BP	GO:0046632	alpha-beta T cell differentiation	65	-0.5050	-1.8238	2.6874E-03	4.9917E-02	4.3422E-02	2890 tags=34%, list=19%, signal=28%

Event 2 – NSUN4 (KEGG)

ID	Description	setSize	enrichmentScore	NES	pvalue	p.adjust	qvalues	rank	leading_edge
hsa04010	MAPK signaling pathway	252	-0.4258	-1.8478	1.2228E-04	2.5430E-03	1.8081E-03	1751	tags=21%, list=11%, signal=19%
hsa05417	Lipid and atherosclerosis	169	-0.5415	-2.2465	1.2967E-04	2.5430E-03	1.8081E-03	1500	tags=20%, list=10%, signal=18%
hsa05164	Influenza A	125	-0.5002	-1.9971	1.3454E-04	2.5430E-03	1.8081E-03	2213	tags=28%, list=14%, signal=24%
hsa04060	Cytokine-cytokine receptor interaction	122	-0.6313	-2.5121	1.3519E-04	2.5430E-03	1.8081E-03	1269	tags=30%, list=8%, signal=28%
hsa04514	Cell adhesion molecules	112	-0.5368	-2.1089	1.3712E-04	2.5430E-03	1.8081E-03	2690	tags=42%, list=18%, signal=35%
hsa05162	Measles	102	-0.5088	-1.9732	1.3856E-04	2.5430E-03	1.8081E-03	2213	tags=25%, list=14%, signal=21%
hsa04933	AGE-RAGE signaling pathway in diabetic complications	91	-0.5475	-2.0875	1.4096E-04	2.5430E-03	1.8081E-03	2917	tags=36%, list=19%, signal=30%
hsa04668	TNF signaling pathway	92	-0.5707	-2.1769	1.4098E-04	2.5430E-03	1.8081E-03	1191	tags=24%, list=8%, signal=22%
hsa05142	Chagas disease	84	-0.5217	-1.9633	1.4271E-04	2.5430E-03	1.8081E-03	560	tags=19%, list=4%, signal=18%
hsa04064	NF-kappa B signaling pathway	76	-0.6834	-2.5289	1.4436E-04	2.5430E-03	1.8081E-03	1692	tags=30%, list=11%, signal=27%
hsa04512	ECM-receptor interaction	72	-0.5381	-1.9733	1.4524E-04	2.5430E-03	1.8081E-03	1996	tags=33%, list=13%, signal=29%
hsa05146	Amoebiasis	72	-0.5816	-2.1330	1.4524E-04	2.5430E-03	1.8081E-03	1191	tags=26%, list=8%, signal=24%
hsa05133	Pertussis	61	-0.6802	-2.4216	1.4817E-04	2.5430E-03	1.8081E-03	1422	tags=36%, list=9%, signal=33%
hsa05323	Rheumatoid arthritis	59	-0.6493	-2.2976	1.4925E-04	2.5430E-03	1.8081E-03	1184	tags=32%, list=8%, signal=30%
hsa04612	Antigen processing and presentation	54	-0.6450	-2.2494	1.4977E-04	2.5430E-03	1.8081E-03	367	tags=26%, list=2%, signal=25%
hsa04657	IL-17 signaling pathway	57	-0.6093	-2.1413	1.5008E-04	2.5430E-03	1.8081E-03	1191	tags=23%, list=8%, signal=21%
hsa04610	Complement and coagulation cascades	51	-0.7307	-2.5186	1.5172E-04	2.5430E-03	1.8081E-03	1012	tags=49%, list=14%, signal=46%
hsa05134	Legionellosis	51	-0.7635	-2.6317	1.5172E-04	2.5430E-03	1.8081E-03	540	tags=25%, list=4%, signal=25%
hsa05150	Staphylococcus aureus infection	43	-0.7923	-2.6385	1.5494E-04	2.5430E-03	1.8081E-03	1012	tags=58%, list=7%, signal=54%
hsa04061	Viral protein interaction with cytokine and cytokine receptor	33	-0.7559	-2.3907	1.5997E-04	2.5430E-03	1.8081E-03	1155	tags=39%, list=8%, signal=36%
hsa05144	Malaria	36	-0.8008	-2.5648	1.6075E-04	2.5430E-03	1.8081E-03	1198	tags=58%, list=8%, signal=54%
hsa05143	African trypanosomiasis	26	-0.7187	-2.1573	1.6359E-04	2.5430E-03	1.8081E-03	1161	tags=42%, list=8%, signal=39%
hsa05169	Epstein-Barr virus infection	165	-0.4286	-1.7755	2.5930E-04	3.5041E-03	2.4914E-03	1955	tags=24%, list=13%, signal=21%
hsa05202	Transcriptional misregulation in cancer	143	-0.4543	-1.8472	2.6417E-04	3.5041E-03	2.4914E-03	2135	tags=26%, list=14%, signal=22%
hsa05145	Toxoplasmosis	93	-0.5093	-1.9468	2.8114E-04	3.5041E-03	2.4914E-03	1335	tags=20%, list=9%, signal=19%
hsa03050	Proteasome	43	0.6473	2.4310	2.8185E-04	3.5041E-03	2.4914E-03	3044	tags=67%, list=20%, signal=54%
hsa05322	Systemic lupus erythematosus	83	-0.5039	-1.8934	2.8543E-04	3.5041E-03	2.4914E-03	1220	tags=29%, list=8%, signal=27%
hsa05412	Arrhythmogenic right ventricular cardiomyopathy	66	-0.5370	-1.9336	2.9612E-04	3.5041E-03	2.4914E-03	3079	tags=36%, list=20%, signal=29%
hsa05140	Leishmaniasis	60	-0.5679	-2.0174	2.9713E-04	3.5041E-03	2.4914E-03	1500	tags=32%, list=10%, signal=29%
hsa04260	Cardiac muscle contraction	63	0.4944	2.0214	3.0826E-04	3.5142E-03	2.4985E-03	1712	tags=38%, list=11%, signal=34%
hsa00190	Oxidative phosphorylation	104	0.7325	3.2721	3.6324E-04	3.9101E-03	2.7801E-03	2023	tags=72%, list=13%, signal=63%
hsa03010	Ribosome	125	0.5883	2.6995	3.8926E-04	3.9101E-03	2.7801E-03	4356	tags=66%, list=28%, signal=48%
hsa04723	Retrograde endocannabinoid signaling	125	0.4275	1.9617	3.8926E-04	3.9101E-03	2.7801E-03	2167	tags=35%, list=14%, signal=30%
hsa05017	Spinocerebellar ataxia	130	0.3921	1.8101	3.9841E-04	3.9101E-03	2.7801E-03	2412	tags=35%, list=16%, signal=29%
hsa04932	Non-alcoholic fatty liver disease	133	0.4523	2.0990	4.0016E-04	3.9101E-03	2.7801E-03	2006	tags=44%, list=13%, signal=39%
hsa05415	Diabetic cardiomyopathy	163	0.4998	2.3898	4.3384E-04	4.1215E-03	2.9303E-03	2083	tags=45%, list=14%, signal=40%
hsa05208	Chemical carcinogenesis - reactive oxygen species	182	0.4867	2.3689	4.5005E-04	4.1599E-03	2.9576E-03	2083	tags=42%, list=14%, signal=37%
hsa04714	Thermogenesis	199	0.4960	2.4385	4.7962E-04	4.3165E-03	3.0690E-03	1770	tags=37%, list=12%, signal=33%
hsa05012	Parkinson disease	219	0.5545	2.7643	5.0582E-04	4.3756E-03	3.1110E-03	2955	tags=56%, list=19%, signal=46%
hsa05020	Prion disease	223	0.4067	2.0292	5.1177E-04	4.3756E-03	3.1110E-03	2167	tags=46%, list=14%, signal=40%
hsa05418	Fluid shear stress and atherosclerosis	119	-0.4561	-1.8098	5.4171E-04	4.5187E-03	3.2127E-03	1500	tags=20%, list=10%, signal=18%
hsa05016	Huntington disease	260	0.5013	2.5497	5.6465E-04	4.5979E-03	3.2690E-03	2237	tags=46%, list=15%, signal=40%
hsa05014	Amyotrophic lateral sclerosis	308	0.4350	2.2519	6.4392E-04	5.1214E-03	3.6412E-03	3222	tags=45%, list=21%, signal=37%
hsa05010	Alzheimer disease	319	0.4365	2.2675	6.7431E-04	5.2412E-03	3.7264E-03	2167	tags=38%, list=14%, signal=33%
hsa05022	Pathways of neurodegeneration - multiple diseases	399	0.4090	2.1719	7.9114E-04	6.0127E-03	4.2749E-03	2412	tags=37%, list=16%, signal=32%
hsa04620	Toll-like receptor signaling pathway	71	-0.5108	-1.8700	8.7070E-04	6.4735E-03	4.6026E-03	842	tags=23%, list=6%, signal=21%
hsa05205	Proteoglycans in cancer	178	-0.4066	-1.6975	1.0263E-03	7.4680E-03	5.3096E-03	3343	tags=37%, list=22%, signal=29%
hsa04640	Hematopoietic cell lineage	54	-0.5505	-1.9200	1.0484E-03	7.4697E-03	5.3108E-03	1621	tags=33%, list=11%, signal=30%
hsa04380	Osteoclast differentiation	101	-0.4593	-1.7769	1.3902E-03	9.4740E-03	6.7359E-03	2968	tags=33%, list=19%, signal=27%
hsa04080	Neuroactive ligand-receptor interaction	192	0.3199	1.5653	1.4052E-03	9.4740E-03	6.7359E-03	524	tags=15%, list=3%, signal=15%
hsa04510	Focal adhesion	180	-0.3991	-1.6682	1.4128E-03	9.4740E-03	6.7359E-03	3824	tags=38%, list=25%, signal=29%
hsa04915	Estrogen signaling pathway	104	-0.4509	-1.7536	1.5175E-03	9.9802E-03	7.0958E-03	3408	tags=34%, list=22%, signal=26%
hsa03008	Ribosome biogenesis in eukaryotes	74	0.4353	1.8341	1.6202E-03	1.0455E-02	7.4334E-03	4328	tags=50%, list=28%, signal=36%
hsa04151	PI3K-Akt signaling pathway	272	-0.3566	-1.5575	1.6929E-03	1.0721E-02	7.6228E-03	3474	tags=31%, list=23%, signal=25%
hsa05321	Inflammatory bowel disease	37	-0.5959	-1.9215	1.7575E-03	1.0928E-02	7.7699E-03	1191	tags=32%, list=8%, signal=30%
hsa05219	Bladder cancer	35	-0.5966	-1.9048	2.2439E-03	1.3637E-02	9.6958E-03	927	tags=17%, list=6%, signal=16%
hsa05414	Dilated cardiomyopathy	78	-0.4739	-1.7623	2.3012E-03	1.3637E-02	9.6958E-03	3730	tags=42%, list=24%, signal=32%
hsa05171	Coronavirus disease - COVID-19	179	-0.3886	-1.6229	2.3127E-03	1.3637E-02	9.6958E-03	1329	tags=17%, list=9%, signal=16%
hsa04621	NOD-like receptor signaling pathway	132	-0.4189	-1.6850	2.4035E-03	1.3932E-02	9.9057E-03	2338	tags=31%, list=15%, signal=27%
hsa05206	MicroRNAs in cancer	147	-0.3989	-1.6275	2.5036E-03	1.4120E-02	1.0039E-02	3137	tags=32%, list=21%, signal=26%
hsa04218	Cellular senescence	138	-0.4106	-1.6616	2.5256E-03	1.4120E-02	1.0039E-02	1236	tags=17%, list=8%, signal=15%
hsa05163	Human cytomegalovirus infection	184	-0.3821	-1.6014	2.5598E-03	1.4120E-02	1.0039E-02	3933	tags=36%, list=26%, signal=27%
hsa00230	Purine metabolism	109	0.3494	1.5750	2.9466E-03	1.5996E-02	1.1373E-02	4348	tags=44%, list=28%, signal=32%
hsa00970	Aminoacyl-tRNA biosynthesis	44	0.4695	1.7708	3.6900E-03	1.9719E-02	1.4020E-02	5030	tags=57%, list=33%, signal=38%
hsa00900	Terpenoid backbone biosynthesis	20	0.5976	1.8500	3.9264E-03	2.0659E-02	1.4688E-02	4390	tags=70%, list=29%, signal=50%
hsa04213	Longevity regulating pathway - multiple species	57	-0.4999	-1.7570	4.2023E-03	2.1776E-02	1.5482E-02	3507	tags=39%, list=23%, signal=30%
hsa05310	Asthma	12	-0.7556	-1.8750	4.7932E-03	2.4467E-02	1.7396E-02	367	tags=42%, list=2%, signal=41%
hsa05410	Hypertrophic cardiomyopathy	72	-0.4639	-1.7014	4.9383E-03	2.4837E-02	1.7659E-02	3185	tags=39%, list=21%, signal=31%
hsa04120	Ubiquitin mediated proteolysis	125	0.3253	1.4927	5.0603E-03	2.5082E-02	1.7833E-02	4484	tags=43%, list=29%, signal=31%
hsa05130	Pathogenic Escherichia coli infection	162	-0.3776	-1.5590	5.3434E-03	2.6106E-02	1.8561E-02	2186	tags=21%, list=14%, signal=18%
hsa04630	JAK-STAT signaling pathway	93	-0.4317	-1.6500	6.0444E-03	2.8857E-02	2.0517E-02	2918	tags=27%, list=19%, signal=22%
hsa04670	Leukocyte transendothelial migration	87	-0.4352	-1.6484	6.0752E-03	2.8857E-02	2.0517E-02	4290	tags=47%, list=28%, signal=34%
hsa04062	Chemokine signaling pathway	131	-0.3947	-1.5862	6.4034E-03	3.0000E-02	2.1329E-02	3286	tags=29%, list=21%, signal=23%
hsa05135	Yersinia infection	122	-0.3986	-1.5860	6.6243E-03	3.0615E-02	2.1767E-02	2213	tags=22%, list=14%, signal=19%
hsa05332	Graft-versus-host disease	19	-0.6560	-1.8301	6.9198E-03	3.1554E-02	2.2435E-02	367	tags=32%, list=2%, signal=31%
hsa05161	Hepatitis B	135	-0.3850	-1.5550	7.6882E-03	3.4597E-02	2.4598E-02	2918	tags=28%, list=19%, signal=23%
hsa00072	Synthesis and degradation of ketone bodies	9	0.7295	1.7838	7.9964E-03	3.5517E-02	2.5252E-02	2335	tags=56%, list=15%, signal=47%
hsa05152	Tuberculosis	135	-0.3824	-1.5447	8.2185E-03	3.6035E-02	2.5620E-02	2288	tags=27%, list=15%, signal=23%
hsa04115	p53 signaling pathway	65	-0.4555	-1.6378	1.0207E-02	4.4188E-02	3.1417E-02	1167	tags=18%, list=8%, signal=17%
hsa05167	Kaposi sarcoma-associated herpesvirus infection	157	-0.3632	-1.4941	1.0844E-02	4.6358E-02	3.2960E-02	2984	tags=24%, list=20%, signal=20%

Event 2 – NSUN4 (Hallmark)

ID	Description	setSize	enrichmentScore	NES	pvalue	p.adjust	qvalues	rank	leading_edge
HALLMARK_HYPOXIA	HALLMARK_HYPOXIA	179	-0.5245	-2.2024	1.2908E-04	6.7985E-04	3.1488E-04	2223	tags=29%, list=15%, signal=25%
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	177	-0.5473	-2.2962	1.2922E-04	6.7985E-04	3.1488E-04	2204	tags=35%, list=14%, signal=30%
HALLMARK_INTERFERON_GAMMA_RESPONSE	HALLMARK_INTERFERON_GAMMA_RESPONSE	177	-0.6195	-2.5991	1.2922E-04	6.7985E-04	3.1488E-04	2575	tags=45%, list=17%, signal=38%
HALLMARK_TNFA_SIGNALING_VIA_NFKB	HALLMARK_TNFA_SIGNALING_VIA_NFKB	173	-0.5811	-2.4280	1.3045E-04	6.7985E-04	3.1488E-04	2284	tags=41%, list=15%, signal=35%
HALLMARK_APICAL_JUNCTION	HALLMARK_APICAL_JUNCTION	166	-0.4716	-1.9629	1.3068E-04	6.7985E-04	3.1488E-04	3278	tags=39%, list=21%, signal=31%
HALLMARK_IL2_STAT5_SIGNALING	HALLMARK_IL2_STAT5_SIGNALING	161	-0.4645	-1.9244	1.3165E-04	6.7985E-04	3.1488E-04	2549	tags=32%, list=17%, signal=27%
HALLMARK_COMPLEMENT	HALLMARK_COMPLEMENT	159	-0.4949	-2.0468	1.3201E-04	6.7985E-04	3.1488E-04	1803	tags=26%, list=12%, signal=24%
HALLMARK_INFLAMMATORY_RESPONSE	HALLMARK_INFLAMMATORY_RESPONSE	151	-0.6183	-2.5431	1.3229E-04	6.7985E-04	3.1488E-04	1384	tags=30%, list=9%, signal=28%
HALLMARK_APOPTOSIS	HALLMARK_APOPTOSIS	142	-0.4913	-2.0042	1.3340E-04	6.7985E-04	3.1488E-04	2186	tags=28%, list=14%, signal=24%
HALLMARK_INTERFERON_ALPHA_RESPONSE	HALLMARK_INTERFERON_ALPHA_RESPONSE	91	-0.6642	-2.5408	1.4236E-04	6.7985E-04	3.1488E-04	2575	tags=51%, list=17%, signal=42%
HALLMARK_IL6_JAK_STAT3_SIGNALING	HALLMARK_IL6_JAK_STAT3_SIGNALING	60	-0.6681	-2.3791	1.4957E-04	6.7985E-04	3.1488E-04	1331	tags=40%, list=9%, signal=37%
HALLMARK_COAGULATION	HALLMARK_COAGULATION	90	-0.5259	-2.0076	2.8690E-04	1.1954E-03	5.5367E-04	3167	tags=42%, list=21%, signal=34%
HALLMARK_ESTROGEN_RESPONSE_EARLY	HALLMARK_ESTROGEN_RESPONSE_EARLY	159	-0.4508	-1.8646	3.9604E-04	1.5232E-03	7.0550E-04	3180	tags=45%, list=21%, signal=36%
HALLMARK_OXIDATIVE_PHOSPHORYLATION	HALLMARK_OXIDATIVE_PHOSPHORYLATION	189	0.6243	3.0320	4.6598E-04	1.5591E-03	7.2210E-04	2083	tags=52%, list=14%, signal=46%
HALLMARK_MYC_TARGETS_V1	HALLMARK_MYC_TARGETS_V1	192	0.4879	2.3741	4.6773E-04	1.5591E-03	7.2210E-04	4312	tags=56%, list=28%, signal=41%
HALLMARK_P53_PATHWAY	HALLMARK_P53_PATHWAY	184	-0.4206	-1.7711	6.4193E-04	2.0060E-03	9.2911E-04	3661	tags=38%, list=24%, signal=29%
HALLMARK_MYOGENESIS	HALLMARK_MYOGENESIS	160	-0.4199	-1.7377	7.9114E-04	2.3269E-03	1.0777E-03	2799	tags=38%, list=18%, signal=31%
HALLMARK_DNA_REPAIR	HALLMARK_DNA_REPAIR	142	0.3476	1.6259	1.1971E-03	3.3254E-03	1.5402E-03	4214	tags=45%, list=28%, signal=33%
HALLMARK_SPERMATOGENESIS	HALLMARK_SPERMATOGENESIS	86	0.3931	1.6987	1.2941E-03	3.4055E-03	1.5773E-03	3614	tags=38%, list=24%, signal=29%
HALLMARK_APICAL_SURFACE	HALLMARK_APICAL_SURFACE	32	-0.6199	-1.9380	1.6181E-03	4.0453E-03	1.8736E-03	2835	tags=38%, list=19%, signal=31%
HALLMARK_E2F_TARGETS	HALLMARK_E2F_TARGETS	173	0.3200	1.5442	1.7123E-03	4.0770E-03	1.8883E-03	3348	tags=34%, list=22%, signal=26%
HALLMARK_ESTROGEN_RESPONSE_LATE	HALLMARK_ESTROGEN_RESPONSE_LATE	158	-0.3990	-1.6481	2.1144E-03	4.8056E-03	2.2257E-03	3180	tags=33%, list=21%, signal=26%
HALLMARK_KRAS_SIGNALING_UP	HALLMARK_KRAS_SIGNALING_UP	166	-0.3964	-1.6498	2.2216E-03	4.8297E-03	2.2369E-03	2103	tags=27%, list=14%, signal=23%
HALLMARK_TGF_BETA_SIGNALING	HALLMARK_TGF_BETA_SIGNALING	52	-0.5127	-1.7753	3.5136E-03	7.3200E-03	3.3903E-03	3137	tags=38%, list=21%, signal=31%
HALLMARK_ALLOGRAFT_REJECTION	HALLMARK_ALLOGRAFT_REJECTION	129	-0.4001	-1.6067	5.0402E-03	1.0072E-02	4.6650E-03	1433	tags=21%, list=9%, signal=19%
HALLMARK_FATTY_ACID_METABOLISM	HALLMARK_FATTY_ACID_METABOLISM	128	0.3288	1.5165	5.2376E-03	1.0072E-02	4.6650E-03	2422	tags=28%, list=16%, signal=24%
HALLMARK_PROTEIN_SECRETION	HALLMARK_PROTEIN_SECRETION	89	0.3417	1.4853	1.3063E-02	2.4191E-02	1.1204E-02	5861	tags=55%, list=38%, signal=34%
HALLMARK_UV_RESPONSE_UP	HALLMARK_UV_RESPONSE_UP	142	-0.3540	-1.4444	2.2412E-02	4.0021E-02	1.8536E-02	1495	tags=15%, list=10%, signal=14%

Event 3 – SRRM2 (GO)

ONTOLOGY ID	Description	setSize	enrichmentScore	NES	pvalue	p.adjust	qvalues	rank	leading edge
BP	GO:0071345 cellular response to cytokine stimulus	780	0.4317	1.6427	1.0087E-04	2.4720E-02	2.3114E-02	1775	tags=21%, list=12%, signal=19%
BP	GO:0002684 positive regulation of immune system process	716	0.3975	1.5100	1.0112E-04	2.4720E-02	2.3114E-02	1663	tags=17%, list=11%, signal=16%
BP	GO:0050776 regulation of immune response	665	0.3976	1.5074	1.0144E-04	2.4720E-02	2.3114E-02	1188	tags=14%, list=8%, signal=14%
BP	GO:0009607 response to biotic stimulus	595	0.4566	1.7245	1.0217E-04	2.4720E-02	2.3114E-02	1794	tags=23%, list=12%, signal=21%
CC	GO:0030141 secretory granule	589	0.4101	1.5484	1.0222E-04	2.4720E-02	2.3114E-02	1365	tags=15%, list=9%, signal=14%
BP	GO:0045087 innate immune response	582	0.4502	1.6997	1.0223E-04	2.4720E-02	2.3114E-02	1794	tags=22%, list=12%, signal=20%
BP	GO:0043207 response to external biotic stimulus	568	0.4622	1.7436	1.0238E-04	2.4720E-02	2.3114E-02	1794	tags=23%, list=12%, signal=21%
BP	GO:0051707 response to other organism	568	0.4622	1.7436	1.0238E-04	2.4720E-02	2.3114E-02	1794	tags=23%, list=12%, signal=21%
BP	GO:0002443 leukocyte mediated immunity	546	0.4322	1.6287	1.0255E-04	2.4720E-02	2.3114E-02	1191	tags=15%, list=8%, signal=14%
BP	GO:0030162 regulation of proteolysis	546	0.4262	1.6060	1.0255E-04	2.4720E-02	2.3114E-02	1837	tags=18%, list=13%, signal=16%
BP	GO:0032101 regulation of response to external stimulus	553	0.3917	1.4766	1.0255E-04	2.4720E-02	2.3114E-02	1794	tags=21%, list=12%, signal=19%
BP	GO:0019221 cytokine-mediated signaling pathway	518	0.4808	1.8080	1.0287E-04	2.4720E-02	2.3114E-02	1775	tags=24%, list=12%, signal=21%
BP	GO:0002263 cell activation involved in immune response	516	0.4143	1.5576	1.0289E-04	2.4720E-02	2.3114E-02	1191	tags=15%, list=8%, signal=14%
BP	GO:0002366 leukocyte activation involved in immune response	512	0.4155	1.5617	1.0290E-04	2.4720E-02	2.3114E-02	1191	tags=15%, list=8%, signal=14%
BP	GO:0002274 myeloid leukocyte activation	482	0.4475	1.6777	1.0342E-04	2.4720E-02	2.3114E-02	1376	tags=17%, list=10%, signal=16%
BP	GO:0006954 inflammatory response	459	0.4687	1.7542	1.0381E-04	2.4720E-02	2.3114E-02	1794	tags=26%, list=12%, signal=24%
MF	GO:0050839 cell adhesion molecule binding	440	0.4534	1.6936	1.0399E-04	2.4720E-02	2.3114E-02	3409	tags=32%, list=24%, signal=26%
BP	GO:0002253 activation of immune response	429	0.4320	1.6119	1.0416E-04	2.4720E-02	2.3114E-02	1644	tags=18%, list=11%, signal=17%
BP	GO:0002444 myeloid leukocyte mediated immunity	423	0.4248	1.5842	1.0423E-04	2.4720E-02	2.3114E-02	1365	tags=16%, list=9%, signal=15%
BP	GO:0002275 myeloid cell activation involved in immune response	417	0.4309	1.6060	1.0431E-04	2.4720E-02	2.3114E-02	1365	tags=16%, list=9%, signal=15%
BP	GO:0043299 leukocyte degranulation	410	0.4325	1.6105	1.0435E-04	2.4720E-02	2.3114E-02	1365	tags=15%, list=9%, signal=14%
BP	GO:0002446 neutrophil mediated immunity	383	0.4557	1.6897	1.0510E-04	2.4720E-02	2.3114E-02	1365	tags=16%, list=9%, signal=15%
BP	GO:0036230 granulocyte activation	383	0.4792	1.7770	1.0510E-04	2.4720E-02	2.3114E-02	1365	tags=16%, list=9%, signal=15%
BP	GO:0042119 neutrophil activation	380	0.4803	1.7803	1.0515E-04	2.4720E-02	2.3114E-02	1365	tags=16%, list=9%, signal=15%
BP	GO:0002283 neutrophil activation involved in immune response	376	0.4604	1.7063	1.0521E-04	2.4720E-02	2.3114E-02	1365	tags=16%, list=9%, signal=15%
BP	GO:0043312 neutrophil degranulation	375	0.4578	1.6964	1.0522E-04	2.4720E-02	2.3114E-02	1365	tags=16%, list=9%, signal=15%
CC	GO:0031012 extracellular matrix	364	0.4671	1.7295	1.0531E-04	2.4720E-02	2.3114E-02	1819	tags=24%, list=13%, signal=22%
BP	GO:0043062 extracellular structure organization	313	0.4987	1.8314	1.0676E-04	2.4720E-02	2.3114E-02	1819	tags=26%, list=13%, signal=23%
BP	GO:0052547 regulation of peptidase activity	292	0.4636	1.6948	1.0761E-04	2.4720E-02	2.3114E-02	1775	tags=22%, list=12%, signal=19%
CC	GO:0062023 collagen-containing extracellular matrix	288	0.4915	1.7953	1.0762E-04	2.4720E-02	2.3114E-02	1819	tags=27%, list=13%, signal=24%
BP	GO:0030198 extracellular matrix organization	276	0.5203	1.8950	1.0832E-04	2.4720E-02	2.3114E-02	1819	tags=28%, list=13%, signal=25%
BP	GO:0052548 regulation of endopeptidase activity	270	0.4738	1.7227	1.0860E-04	2.4720E-02	2.3114E-02	1775	tags=22%, list=12%, signal=20%
BP	GO:0098542 defense response to other organism	267	0.5084	1.8469	1.0881E-04	2.4720E-02	2.3114E-02	1766	tags=27%, list=12%, signal=24%
BP	GO:0019058 viral life cycle	264	0.4967	1.8014	1.0912E-04	2.4720E-02	2.3114E-02	2510	tags=24%, list=17%, signal=20%
CC	GO:0031983 vesicle lumen	251	0.4681	1.6900	1.0999E-04	2.4720E-02	2.3114E-02	1521	tags=18%, list=11%, signal=16%
CC	GO:0060205 cytoplasmic vesicle lumen	250	0.4700	1.6968	1.1002E-04	2.4720E-02	2.3114E-02	1521	tags=18%, list=11%, signal=16%
BP	GO:0051604 protein maturation	244	0.5132	1.8490	1.1024E-04	2.4720E-02	2.3114E-02	1875	tags=25%, list=13%, signal=22%
CC	GO:0005788 endoplasmic reticulum lumen	233	0.4716	1.6919	1.1088E-04	2.4720E-02	2.3114E-02	2574	tags=30%, list=18%, signal=25%
BP	GO:0009615 response to virus	229	0.5433	1.9465	1.1123E-04	2.4720E-02	2.3114E-02	1427	tags=24%, list=10%, signal=22%
BP	GO:0045861 negative regulation of proteolysis	213	0.4811	1.7139	1.1203E-04	2.4720E-02	2.3114E-02	1876	tags=20%, list=13%, signal=18%
BP	GO:0034612 response to tumor necrosis factor	210	0.5675	2.0193	1.1231E-04	2.4720E-02	2.3114E-02	1775	tags=24%, list=12%, signal=21%
BP	GO:0071356 cellular response to tumor necrosis factor	195	0.5748	2.0318	1.1348E-04	2.4720E-02	2.3114E-02	1775	tags=24%, list=12%, signal=21%
BP	GO:0016485 protein processing	182	0.5543	1.9478	1.1414E-04	2.4720E-02	2.3114E-02	1875	tags=29%, list=13%, signal=26%
BP	GO:0035966 response to topologically incorrect protein	180	0.5631	1.9760	1.1444E-04	2.4720E-02	2.3114E-02	2000	tags=22%, list=14%, signal=19%
BP	GO:0051607 defense response to virus	168	0.5845	2.0405	1.1519E-04	2.4720E-02	2.3114E-02	1380	tags=26%, list=10%, signal=24%
BP	GO:0006986 response to unfolded protein	159	0.5849	2.0293	1.1624E-04	2.4720E-02	2.3114E-02	1942	tags=22%, list=13%, signal=19%
BP	GO:0060759 regulation of response to cytokine stimulus	140	0.5198	1.7777	1.1850E-04	2.4720E-02	2.3114E-02	2159	tags=31%, list=15%, signal=26%
BP	GO:0034341 response to interferon-gamma	139	0.5649	1.9310	1.1858E-04	2.4720E-02	2.3114E-02	1711	tags=30%, list=12%, signal=27%
BP	GO:0010466 negative regulation of peptidase activity	136	0.5399	1.8398	1.1919E-04	2.4720E-02	2.3114E-02	1759	tags=25%, list=12%, signal=22%

BP	GO:0001959	regulation of cytokine-mediated signaling pathway	129	0.5479	1.8582	1.1975E-04	2.4720E-02	2.3114E-02	2159	tags=32%, list=15%, signal=27%
BP	GO:0010951	negative regulation of endopeptidase activity	131	0.5354	1.8169	1.1983E-04	2.4720E-02	2.3114E-02	1759	tags=24%, list=12%, signal=22%
BP	GO:0034620	cellular response to unfolded protein	126	0.5304	1.7946	1.2013E-04	2.4720E-02	2.3114E-02	1942	tags=17%, list=13%, signal=15%
BP	GO:0071347	cellular response to interleukin-1	125	0.5159	1.7446	1.2021E-04	2.4720E-02	2.3114E-02	1621	tags=14%, list=11%, signal=13%
BP	GO:0071346	cellular response to interferon-gamma	127	0.5401	1.8283	1.2025E-04	2.4720E-02	2.3114E-02	1711	tags=28%, list=12%, signal=25%
BP	GO:2001236	regulation of extrinsic apoptotic signaling pathway	127	0.5399	1.8274	1.2025E-04	2.4720E-02	2.3114E-02	2197	tags=27%, list=15%, signal=23%
BP	GO:0034605	cellular response to heat	117	0.5340	1.7940	1.2129E-04	2.4720E-02	2.3114E-02	2258	tags=25%, list=16%, signal=21%
BP	GO:1903900	regulation of viral life cycle	111	0.6040	2.0153	1.2244E-04	2.4720E-02	2.3114E-02	1249	tags=21%, list=9%, signal=19%
MF	GO:0005178	integrin binding	107	0.5533	1.8393	1.2267E-04	2.4720E-02	2.3114E-02	1999	tags=30%, list=14%, signal=26%
BP	GO:0019079	viral genome replication	96	0.6587	2.1579	1.2433E-04	2.4720E-02	2.3114E-02	1233	tags=20%, list=9%, signal=18%
BP	GO:0006959	humoral immune response	88	0.6276	2.0311	1.2579E-04	2.4720E-02	2.3114E-02	1182	tags=32%, list=8%, signal=29%
BP	GO:0002526	acute inflammatory response	87	0.6629	2.1408	1.2620E-04	2.4720E-02	2.3114E-02	1207	tags=37%, list=8%, signal=34%
BP	GO:2001237	negative regulation of extrinsic apoptotic signaling pathway	82	0.6331	2.0274	1.2747E-04	2.4720E-02	2.3114E-02	2104	tags=30%, list=15%, signal=26%
BP	GO:0034340	response to type I interferon	74	0.6723	2.1233	1.2877E-04	2.4720E-02	2.3114E-02	1380	tags=41%, list=10%, signal=37%
BP	GO:1903317	regulation of protein maturation	74	0.6677	2.1090	1.2877E-04	2.4720E-02	2.3114E-02	1814	tags=42%, list=13%, signal=37%
BP	GO:0045069	regulation of viral genome replication	73	0.6866	2.1638	1.2910E-04	2.4720E-02	2.3114E-02	1233	tags=25%, list=9%, signal=23%
BP	GO:0070613	regulation of protein processing	72	0.6665	2.0954	1.2950E-04	2.4720E-02	2.3114E-02	1814	tags=42%, list=13%, signal=37%
BP	GO:0060337	type I interferon signaling pathway	70	0.6806	2.1302	1.2989E-04	2.4720E-02	2.3114E-02	1380	tags=43%, list=10%, signal=39%
BP	GO:0071357	cellular response to type I interferon	70	0.6806	2.1302	1.2989E-04	2.4720E-02	2.3114E-02	1380	tags=43%, list=10%, signal=39%
BP	GO:0097530	granulocyte migration	67	0.6484	2.0163	1.3038E-04	2.4720E-02	2.3114E-02	1104	tags=24%, list=8%, signal=22%
CC	GO:0072562	blood microparticle	61	0.7124	2.1800	1.3217E-04	2.4720E-02	2.3114E-02	1350	tags=44%, list=9%, signal=40%
BP	GO:0071621	granulocyte chemotaxis	58	0.6913	2.1009	1.3275E-04	2.4720E-02	2.3114E-02	987	tags=26%, list=7%, signal=24%
BP	GO:0061077	chaperone-mediated protein folding	52	0.6405	1.9059	1.3510E-04	2.4720E-02	2.3114E-02	2258	tags=38%, list=16%, signal=33%
BP	GO:1990266	neutrophil migration	50	0.6443	1.9051	1.3596E-04	2.4720E-02	2.3114E-02	987	tags=24%, list=7%, signal=22%
BP	GO:0045071	negative regulation of viral genome replication	41	0.6966	1.9956	1.3749E-04	2.4720E-02	2.3114E-02	602	tags=32%, list=4%, signal=30%
BP	GO:0030199	collagen fibril organization	42	0.6933	1.9940	1.3780E-04	2.4720E-02	2.3114E-02	343	tags=26%, list=2%, signal=26%
BP	GO:0030593	neutrophil chemotaxis	43	0.6858	1.9783	1.3785E-04	2.4720E-02	2.3114E-02	987	tags=28%, list=7%, signal=26%
BP	GO:0072577	endothelial cell apoptotic process	36	0.7034	1.9672	1.3955E-04	2.4720E-02	2.3114E-02	68	tags=11%, list=0%, signal=11%
BP	GO:2000351	regulation of endothelial cell apoptotic process	31	0.7233	1.9756	1.4231E-04	2.4886E-02	2.3269E-02	68	tags=13%, list=0%, signal=13%
BP	GO:0071622	regulation of granulocyte chemotaxis	27	0.7543	2.0051	1.4562E-04	2.4989E-02	2.3365E-02	810	tags=30%, list=6%, signal=28%
BP	GO:0002455	humoral immune response mediated by circulating immun	26	0.7847	2.0707	1.4656E-04	2.4989E-02	2.3365E-02	1350	tags=58%, list=9%, signal=52%
BP	GO:0035456	response to interferon-beta	21	0.8105	2.0507	1.4921E-04	2.5126E-02	2.3493E-02	651	tags=43%, list=4%, signal=41%
BP	GO:0001580	detection of chemical stimulus involved in sensory perception o	12	0.8776	1.9774	1.5765E-04	2.6224E-02	2.4520E-02	1415	tags=83%, list=10%, signal=75%
BP	GO:0060700	regulation of ribonuclease activity	8	0.9671	1.9781	1.6295E-04	2.6778E-02	2.5038E-02	232	tags=50%, list=2%, signal=49%
CC	GO:0099503	secretory vesicle	722	0.3730	1.4171	2.0235E-04	3.2857E-02	3.0722E-02	1365	tags=13%, list=9%, signal=12%
BP	GO:0097190	apoptotic signaling pathway	499	0.3848	1.4454	2.0623E-04	3.3094E-02	3.0943E-02	2226	tags=18%, list=15%, signal=16%
BP	GO:0009617	response to bacterium	350	0.4265	1.5771	2.1104E-04	3.3166E-02	3.1011E-02	1794	tags=22%, list=12%, signal=20%
BP	GO:0031589	cell-substrate adhesion	280	0.4350	1.5863	2.1577E-04	3.3166E-02	3.1011E-02	2422	tags=24%, list=17%, signal=21%
BP	GO:0032497	detection of lipopolysaccharide	3	-0.9845	-1.6896	2.2686E-04	3.3166E-02	3.1011E-02	133	tags=100%, list=1%, signal=99%
BP	GO:0097191	extrinsic apoptotic signaling pathway	183	0.4891	1.7196	2.2802E-04	3.3166E-02	3.1011E-02	2226	tags=24%, list=15%, signal=21%
BP	GO:0050792	regulation of viral process	166	0.4981	1.7364	2.3121E-04	3.3166E-02	3.1011E-02	1351	tags=16%, list=9%, signal=15%
BP	GO:0051701	interaction with host	166	0.4937	1.7211	2.3121E-04	3.3166E-02	3.1011E-02	3179	tags=34%, list=22%, signal=27%
MF	GO:0001608	G protein-coupled nucleotide receptor activity	5	-0.9561	-1.8934	2.4120E-04	3.3166E-02	3.1011E-02	641	tags=100%, list=4%, signal=96%
BP	GO:0035589	G protein-coupled purinergic nucleotide receptor signaling pathw	5	-0.9561	-1.8934	2.4120E-04	3.3166E-02	3.1011E-02	641	tags=100%, list=4%, signal=96%
MF	GO:0045028	G protein-coupled purinergic nucleotide receptor activity	5	-0.9561	-1.8934	2.4120E-04	3.3166E-02	3.1011E-02	641	tags=100%, list=4%, signal=96%
BP	GO:0071774	response to fibroblast growth factor	108	0.5454	1.8160	2.4474E-04	3.3166E-02	3.1011E-02	995	tags=14%, list=7%, signal=13%
BP	GO:0044344	cellular response to fibroblast growth factor stimulus	105	0.5394	1.7863	2.4664E-04	3.3166E-02	3.1011E-02	995	tags=13%, list=7%, signal=13%
BP	GO:0051291	protein heterooligomerization	105	0.5353	1.7726	2.4664E-04	3.3166E-02	3.1011E-02	1829	tags=25%, list=13%, signal=22%
BP	GO:0030260	entry into host cell	101	0.5512	1.8149	2.4795E-04	3.3166E-02	3.1011E-02	2460	tags=33%, list=17%, signal=27%
BP	GO:0044409	entry into host	101	0.5512	1.8149	2.4795E-04	3.3166E-02	3.1011E-02	2460	tags=33%, list=17%, signal=27%

BP	GO:0051806	entry into cell of other organism involved in symbiotic inte	101	0.5512	1.8149	2.4795E-04	3.3166E-02	3.1011E-02	2460	tags=33%, list=17%, signal=27%
BP	GO:0051828	entry into other organism involved in symbiotic interaction	101	0.5512	1.8149	2.4795E-04	3.3166E-02	3.1011E-02	2460	tags=33%, list=17%, signal=27%
BP	GO:0021782	glial cell development	100	0.5442	1.7896	2.4802E-04	3.3166E-02	3.1011E-02	2555	tags=39%, list=18%, signal=32%
BP	GO:0060333	interferon-gamma-mediated signaling pathway	72	0.6230	1.9587	2.5900E-04	3.3703E-02	3.1513E-02	1344	tags=33%, list=9%, signal=30%
CC	GO:0001931	uropod	9	-0.8895	-2.0727	2.6178E-04	3.3703E-02	3.1513E-02	1013	tags=44%, list=7%, signal=41%
CC	GO:0031254	cell trailing edge	9	-0.8895	-2.0727	2.6178E-04	3.3703E-02	3.1513E-02	1013	tags=44%, list=7%, signal=41%
BP	GO:0045076	regulation of interleukin-2 biosynthetic process	10	-0.8968	-2.1605	2.6192E-04	3.3703E-02	3.1513E-02	760	tags=60%, list=5%, signal=57%
BP	GO:1903901	negative regulation of viral life cycle	56	0.6503	1.9636	2.6692E-04	3.4026E-02	3.1815E-02	1249	tags=34%, list=9%, signal=31%
BP	GO:0010812	negative regulation of cell-substrate adhesion	52	0.6390	1.9015	2.7020E-04	3.4088E-02	3.1873E-02	2183	tags=23%, list=15%, signal=20%
BP	GO:0042094	interleukin-2 biosynthetic process	13	-0.8964	-2.3212	2.7241E-04	3.4088E-02	3.1873E-02	760	tags=54%, list=5%, signal=51%
BP	GO:0070841	inclusion body assembly	21	0.7719	1.9530	2.9842E-04	3.7004E-02	3.4599E-02	1714	tags=43%, list=12%, signal=38%
BP	GO:0042060	wound healing	400	0.4040	1.5015	3.1417E-04	3.8132E-02	3.5655E-02	1926	tags=20%, list=13%, signal=18%
BP	GO:0097201	negative regulation of transcription from RNA polymerase II prom	12	0.8423	1.8977	3.1531E-04	3.8132E-02	3.5655E-02	106	tags=25%, list=1%, signal=25%
BP	GO:0006825	copper ion transport	13	0.8334	1.9046	3.1591E-04	3.8132E-02	3.5655E-02	1377	tags=38%, list=10%, signal=35%
BP	GO:0042730	fibrinolysis	11	0.8575	1.8919	3.1969E-04	3.8251E-02	3.5765E-02	1021	tags=73%, list=7%, signal=68%
MF	GO:0033038	bitter taste receptor activity	9	0.9029	1.8967	3.2352E-04	3.8372E-02	3.5879E-02	1415	tags=100%, list=10%, signal=90%
BP	GO:0097193	intrinsic apoptotic signaling pathway	246	0.4498	1.6218	3.3043E-04	3.8641E-02	3.6131E-02	2758	tags=23%, list=19%, signal=19%
CC	GO:0034774	secretory granule lumen	239	0.4459	1.6040	3.3146E-04	3.8641E-02	3.6131E-02	1324	tags=15%, list=9%, signal=14%
BP	GO:0035967	cellular response to topologically incorrect protein	145	0.5053	1.7346	3.5415E-04	4.0937E-02	3.8277E-02	2000	tags=17%, list=14%, signal=14%
BP	GO:0050871	positive regulation of B cell activation	51	-0.5720	-2.0277	3.8153E-04	4.3623E-02	4.0788E-02	2351	tags=39%, list=16%, signal=33%
BP	GO:1900034	regulation of cellular response to heat	79	0.5667	1.8080	3.8378E-04	4.3623E-02	4.0788E-02	2258	tags=27%, list=16%, signal=23%
BP	GO:0044419	interspecies interaction between organisms	757	0.3639	1.3838	4.0392E-04	4.5533E-02	4.2574E-02	3460	tags=27%, list=24%, signal=21%
BP	GO:0045055	regulated exocytosis	629	0.3804	1.4391	4.0762E-04	4.5574E-02	4.2612E-02	1365	tags=14%, list=9%, signal=13%
BP	GO:0002764	immune response-regulating signaling pathway	409	0.4021	1.4973	4.1741E-04	4.5865E-02	4.2885E-02	1644	tags=15%, list=11%, signal=14%
BP	GO:0002920	regulation of humoral immune response	36	0.8642	1.8574	4.1864E-04	4.5865E-02	4.2885E-02	1350	tags=44%, list=9%, signal=40%
CC	GO:0098803	respiratory chain complex	63	-0.5099	-1.8689	4.2052E-04	4.5865E-02	4.2885E-02	4583	tags=57%, list=9%, signal=39%
BP	GO:2001233	regulation of apoptotic signaling pathway	337	0.4070	1.5014	4.2368E-04	4.5865E-02	4.2885E-02	2126	tags=18%, list=15%, signal=16%
MF	GO:0045296	cadherin binding	308	0.4161	1.5261	4.2790E-04	4.5957E-02	4.2971E-02	3409	tags=30%, list=24%, signal=23%
CC	GO:0005746	mitochondrial respiratory chain	69	-0.5026	-1.8791	4.3234E-04	4.6071E-02	4.3077E-02	3383	tags=57%, list=23%, signal=44%
BP	GO:0042775	mitochondrial ATP synthesis coupled electron transport	75	-0.5217	-1.9846	4.4783E-04	4.6102E-02	4.3106E-02	4292	tags=57%, list=30%, signal=41%
MF	GO:0008017	microtubule binding	208	0.4576	1.6286	4.4878E-04	4.6102E-02	4.3106E-02	2399	tags=24%, list=17%, signal=20%
BP	GO:0042773	ATP synthesis coupled electron transport	76	-0.5022	-1.9149	4.5106E-04	4.6102E-02	4.3106E-02	4292	tags=57%, list=30%, signal=40%
CC	GO:0070469	respiratory chain	76	-0.5255	-2.0036	4.5106E-04	4.6102E-02	4.3106E-02	3383	tags=59%, list=23%, signal=46%
BP	GO:0036499	PERK-mediated unfolded protein response	19	0.7773	1.9244	4.5181E-04	4.6102E-02	4.3106E-02	1791	tags=37%, list=12%, signal=32%
BP	GO:2001234	negative regulation of apoptotic signaling pathway	186	0.4769	1.6789	4.5636E-04	4.6102E-02	4.3106E-02	2104	tags=20%, list=15%, signal=18%
BP	GO:0035455	response to interferon-alpha	18	0.7826	1.9181	4.5648E-04	4.6102E-02	4.3106E-02	591	tags=33%, list=4%, signal=32%
BP	GO:0043903	regulation of symbiosis, encompassing mutualism through	175	0.4797	1.6796	4.5966E-04	4.6102E-02	4.3106E-02	1351	tags=15%, list=9%, signal=14%
BP	GO:0070555	response to interleukin-1	143	0.4859	1.6665	4.7164E-04	4.6958E-02	4.3906E-02	1621	tags=13%, list=11%, signal=12%
MF	GO:0360441	long-chain fatty acid binding	10	0.8740	1.8840	4.8512E-04	4.7280E-02	4.4208E-02	28	tags=20%, list=0%, signal=20%
CC	GO:0005814	centriole	117	0.5224	1.7551	4.8514E-04	4.7280E-02	4.4208E-02	3217	tags=37%, list=22%, signal=29%
BP	GO:0051238	sequestering of metal ion	9	0.8901	1.8699	4.8528E-04	4.7280E-02	4.4208E-02	570	tags=33%, list=4%, signal=32%
BP	GO:0045086	positive regulation of interleukin-2 biosynthetic process	7	-0.9274	-2.0246	5.0239E-04	4.8095E-02	4.4970E-02	760	tags=71%, list=5%, signal=68%
BP	GO:0022904	respiratory electron transport chain	95	-0.4864	-1.9191	5.0736E-04	4.8095E-02	4.4970E-02	4794	tags=62%, list=33%, signal=42%
BP	GO:0032119	sequestering of zinc ion	6	0.9545	1.8176	5.0925E-04	4.8095E-02	4.4970E-02	28	tags=33%, list=0%, signal=33%
BP	GO:0008625	extrinsic apoptotic signaling pathway via death domain recepto	71	0.5833	1.8303	5.1827E-04	4.8095E-02	4.4970E-02	1984	tags=27%, list=14%, signal=23%
BP	GO:0010286	heat acclimation	4	0.9861	1.6959	5.2210E-04	4.8095E-02	4.4970E-02	57	tags=50%, list=0%, signal=50%
BP	GO:0060699	regulation of endonuclease activity	4	0.9716	1.6710	5.2210E-04	4.8095E-02	4.4970E-02	13	tags=25%, list=0%, signal=25%
BP	GO:0070370	cellular heat acclimation	4	0.9861	1.6959	5.2210E-04	4.8095E-02	4.4970E-02	57	tags=50%, list=0%, signal=50%
BP	GO:0048525	negative regulation of viral process	66	0.5967	1.8513	5.2253E-04	4.8095E-02	4.4970E-02	2510	tags=45%, list=17%, signal=38%
BP	GO:0002757	immune response-activating signal transduction	386	0.4022	1.4918	5.2538E-04	4.8095E-02	4.4970E-02	1644	tags=16%, list=11%, signal=15%
BP	GO:0090063	positive regulation of microtubule nucleation	3	0.9882	1.5839	5.3629E-04	4.8767E-02	4.5598E-02	57	tags=67%, list=0%, signal=66%
CC	GO:0098800	inner mitochondrial membrane protein complex	111	-0.4181	-1.6969	5.4496E-04	4.9165E-02	4.5971E-02	4586	tags=58%, list=32%, signal=40%
BP	GO:0034976	response to endoplasmic reticulum stress	256	0.4317	1.5622	5.4789E-04	4.9165E-02	4.5971E-02	3114	tags=21%, list=21%, signal=17%

Event 3 – SRRM2 (KEGG)

ID	Description	setSize	enrichmentScore	NES	pvalue	p.adjust	qvalues	rank	leading_edge
hsa05417	Lipid and atherosclerosis	160	0.5110	1.7695	1.1592E-04	5.4415E-03	4.7200E-03	1678	tags=20%, list=12%, signal=18%
hsa04621	NOD-like receptor signaling pathway	126	0.5437	1.8348	1.1942E-04	5.4415E-03	4.7200E-03	776	tags=17%, list=5%, signal=17%
hsa05164	Influenza A	120	0.5522	1.8532	1.2029E-04	5.4415E-03	4.7200E-03	1777	tags=28%, list=12%, signal=24%
hsa05162	Measles	98	0.5773	1.8873	1.2343E-04	5.4415E-03	4.7200E-03	2749	tags=33%, list=19%, signal=27%
hsa04933	AGE-RAGE signaling pathway in diabetic complications	88	0.6098	1.9636	1.2549E-04	5.4415E-03	4.7200E-03	749	tags=15%, list=5%, signal=14%
hsa04668	TNF signaling pathway	86	0.5984	1.9214	1.2598E-04	5.4415E-03	4.7200E-03	510	tags=14%, list=4%, signal=14%
hsa05146	Amoebiasis	69	0.6347	1.9717	1.3036E-04	5.4415E-03	4.7200E-03	749	tags=16%, list=5%, signal=15%
hsa04512	ECM-receptor interaction	68	0.6518	2.0195	1.3070E-04	5.4415E-03	4.7200E-03	1819	tags=38%, list=13%, signal=34%
hsa05144	Malaria	31	0.7711	2.0937	1.4362E-04	5.4415E-03	4.7200E-03	810	tags=39%, list=6%, signal=37%
hsa05171	Coronavirus disease - COVID-19	175	0.5002	1.7475	2.2941E-04	7.8229E-03	6.7857E-03	1736	tags=21%, list=12%, signal=19%
hsa04657	IL-17 signaling pathway	55	0.6442	1.9346	2.6781E-04	7.8499E-03	6.8091E-03	1521	tags=25%, list=11%, signal=23%
hsa04610	Complement and coagulation cascades	44	0.6641	1.9165	2.7624E-04	7.8499E-03	6.8091E-03	1021	tags=45%, list=7%, signal=42%
hsa00190	Oxidative phosphorylation	103	-0.5152	-2.0628	5.4054E-04	1.4179E-02	1.2299E-02	4617	tags=64%, list=32%, signal=44%
hsa04022	cGMP-PKG signaling pathway	137	-0.4251	-1.7703	6.4267E-04	1.5609E-02	1.3540E-02	2132	tags=26%, list=15%, signal=23%
hsa05134	Legionellosis	46	0.6387	1.8573	6.8662E-04	1.5609E-02	1.3540E-02	776	tags=26%, list=5%, signal=25%
hsa05168	Herpes simplex virus 1 infection	433	0.3939	1.4641	8.2962E-04	1.7681E-02	1.5337E-02	3733	tags=34%, list=26%, signal=26%
hsa05143	African trypanosomiasis	22	0.7499	1.8998	1.0479E-03	2.1020E-02	1.8233E-02	776	tags=41%, list=5%, signal=39%
hsa05219	Bladder cancer	35	0.6702	1.8580	1.4241E-03	2.6979E-02	2.3402E-02	38	tags=9%, list=0%, signal=9%
hsa04080	Neuroactive ligand-receptor interaction	178	-0.3731	-1.6150	1.5823E-03	2.8398E-02	2.4633E-02	1462	tags=29%, list=10%, signal=27%
hsa04260	Cardiac muscle contraction	59	-0.4829	-1.7582	2.0016E-03	3.4127E-02	2.9603E-02	4256	tags=56%, list=29%, signal=40%
hsa05323	Rheumatoid arthritis	53	0.5957	1.7783	2.4220E-03	3.9328E-02	3.4114E-02	314	tags=15%, list=2%, signal=15%
hsa05133	Pertussis	58	0.5800	1.7536	3.2081E-03	4.9525E-02	4.2959E-02	951	tags=26%, list=7%, signal=24%
hsa00524	Neomycin, kanamycin and gentamicin biosynthesis	4	-0.9206	-1.7006	3.7691E-03	4.9525E-02	4.2959E-02	1084	tags=75%, list=7%, signal=69%
hsa04024	cAMP signaling pathway	171	-0.3430	-1.4764	3.8314E-03	4.9525E-02	4.2959E-02	1705	tags=22%, list=12%, signal=19%
hsa04510	Focal adhesion	175	0.4396	1.5358	3.9000E-03	4.9525E-02	4.2959E-02	2181	tags=21%, list=15%, signal=18%
hsa05418	Fluid shear stress and atherosclerosis	116	0.4801	1.6009	3.9981E-03	4.9525E-02	4.2959E-02	1594	tags=20%, list=11%, signal=18%
hsa00220	Arginine biosynthesis	17	-0.6518	-1.7929	4.0544E-03	4.9525E-02	4.2959E-02	2157	tags=47%, list=15%, signal=40%
hsa05165	Human papillomavirus infection	271	0.4036	1.4613	4.1157E-03	4.9525E-02	4.2959E-02	2957	tags=25%, list=20%, signal=21%
hsa04261	Adrenergic signaling in cardiomyocytes	122	-0.3772	-1.5481	4.2118E-03	4.9525E-02	4.2959E-02	2073	tags=24%, list=14%, signal=21%

Event 3 – SRRM2 (Hallmark)

ID	Description	setSize	enrichmentScore	NES	pvalue	p.adjust	qvalues	rank	leading_edge
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	172	0.5436	1.8980	1.1468E-04	1.2531E-03	8.9698E-04	2285	tags=35%, list=16%, signal=30%
HALLMARK_INTERFERON_GAMMA_RESPONSE	HALLMARK_INTERFERON_GAMMA_RESPONSE	171	0.7261	2.5340	1.1476E-04	1.2531E-03	8.9698E-04	1766	tags=54%, list=12%, signal=48%
HALLMARK_COMPLEMENT	HALLMARK_COMPLEMENT	155	0.5414	1.8724	1.1610E-04	1.2531E-03	8.9698E-04	1144	tags=23%, list=8%, signal=21%
HALLMARK_INFLAMMATORY_RESPONSE	HALLMARK_INFLAMMATORY_RESPONSE	138	0.5344	1.8266	1.1776E-04	1.2531E-03	8.9698E-04	1237	tags=24%, list=9%, signal=22%
HALLMARK_INTERFERON_ALPHA_RESPONSE	HALLMARK_INTERFERON_ALPHA_RESPONSE	87	0.7744	2.4996	1.2531E-04	1.2531E-03	8.9698E-04	1661	tags=63%, list=11%, signal=56%
HALLMARK_IL6_JAK_STAT3_SIGNALING	HALLMARK_IL6_JAK_STAT3_SIGNALING	54	0.6086	1.8251	9.2826E-04	7.5702E-03	5.4186E-03	2212	tags=48%, list=15%, signal=41%
HALLMARK_APOPTOSIS	HALLMARK_APOPTOSIS	138	0.4797	1.6397	1.0598E-03	7.5702E-03	5.4186E-03	1694	tags=22%, list=12%, signal=20%
HALLMARK_OXIDATIVE_PHOSPHORYLATION	HALLMARK_OXIDATIVE_PHOSPHORYLATION	189	-0.3430	-1.4956	1.6992E-03	1.0620E-02	7.6018E-03	4623	tags=51%, list=32%, signal=35%
HALLMARK_IL2_STAT5_SIGNALING	HALLMARK_IL2_STAT5_SIGNALING	156	0.4466	1.5452	3.9494E-03	2.1941E-02	1.5705E-02	2092	tags=26%, list=14%, signal=22%
HALLMARK_TNFA_SIGNALING_VIA_NFKB	HALLMARK_TNFA_SIGNALING_VIA_NFKB	165	0.4226	1.4693	9.5788E-03	4.7894E-02	3.4282E-02	1594	tags=24%, list=11%, signal=22%

Event 4 – ELOVL7 (GO)

ONTOLOGY	ID	Description	setSize	enrichmentScore	NES	pvalue	p.adjust	qvalues	rank	leading_edge
BP	GO:0071345	cellular response to cytokine stimulus	788	0.3818	1.5063	1.0442E-04	4.7459E-02	4.5655E-02	2249	tags=23%, list=15%, signal=20%
BP	GO:0009607	response to biotic stimulus	601	0.4593	1.7929	1.0716E-04	4.7459E-02	4.5655E-02	1782	tags=23%, list=12%, signal=21%
BP	GO:0045087	innate immune response	584	0.4202	1.6374	1.0765E-04	4.7459E-02	4.5655E-02	1930	tags=21%, list=13%, signal=19%
BP	GO:0043207	response to external biotic stimulus	573	0.4595	1.7888	1.0784E-04	4.7459E-02	4.5655E-02	1782	tags=23%, list=12%, signal=21%
BP	GO:0051707	response to other organism	573	0.4595	1.7888	1.0784E-04	4.7459E-02	4.5655E-02	1782	tags=23%, list=12%, signal=21%
CC	GO:0009986	cell surface	532	0.4383	1.7003	1.0828E-04	4.7459E-02	4.5655E-02	1591	tags=24%, list=11%, signal=22%
BP	GO:0019221	cytokine-mediated signaling pathway	523	0.4292	1.6632	1.0862E-04	4.7459E-02	4.5655E-02	1946	tags=22%, list=13%, signal=20%
MF	GO:0050839	cell adhesion molecule binding	441	0.4193	1.6102	1.1107E-04	4.7459E-02	4.5655E-02	1961	tags=20%, list=13%, signal=18%
BP	GO:0010721	negative regulation of cell development	280	0.4584	1.7035	1.1761E-04	4.7459E-02	4.5655E-02	1970	tags=24%, list=14%, signal=21%
BP	GO:0098542	defense response to other organism	271	0.5580	2.0674	1.1823E-04	4.7459E-02	4.5655E-02	1407	tags=25%, list=10%, signal=23%
BP	GO:0019058	viral life cycle	264	0.5072	1.8756	1.1841E-04	4.7459E-02	4.5655E-02	1310	tags=15%, list=9%, signal=14%
BP	GO:0051961	negative regulation of nervous system development	265	0.4529	1.6749	1.1846E-04	4.7459E-02	4.5655E-02	2461	tags=27%, list=17%, signal=23%
BP	GO:0050768	negative regulation of neurogenesis	245	0.4664	1.7120	1.1977E-04	4.7459E-02	4.5655E-02	1970	tags=24%, list=14%, signal=21%
BP	GO:0042063	gliogenesis	243	0.4672	1.7139	1.1986E-04	4.7459E-02	4.5655E-02	2040	tags=28%, list=14%, signal=24%
BP	GO:0009615	response to virus	233	0.6077	2.2203	1.2061E-04	4.7459E-02	4.5655E-02	1747	tags=23%, list=12%, signal=25%
BP	GO:0010001	glial cell differentiation	186	0.5056	1.8025	1.2569E-04	4.7459E-02	4.5655E-02	2040	tags=30%, list=14%, signal=26%
BP	GO:0097191	extrinsic apoptotic signaling pathway	186	0.5110	1.8218	1.2569E-04	4.7459E-02	4.5655E-02	2120	tags=26%, list=15%, signal=22%
BP	GO:0035966	response to topologically incorrect protein	182	0.5147	1.8298	1.2639E-04	4.7459E-02	4.5655E-02	1594	tags=13%, list=11%, signal=12%
BP	GO:0043903	regulation of symbiosis, encompassing mutualism through parasitism	176	0.4968	1.7610	1.2687E-04	4.7459E-02	4.5655E-02	999	tags=15%, list=7%, signal=14%
BP	GO:0051607	defense response to virus	171	0.6666	2.3581	1.2713E-04	4.7459E-02	4.5655E-02	1365	tags=29%, list=9%, signal=27%
BP	GO:0050792	regulation of viral process	166	0.5182	1.8287	1.2739E-04	4.7459E-02	4.5655E-02	999	tags=16%, list=7%, signal=15%
BP	GO:0051701	interaction with host	166	0.5099	1.7995	1.2739E-04	4.7459E-02	4.5655E-02	2727	tags=31%, list=19%, signal=25%
BP	GO:0006986	response to unfolded protein	161	0.5493	1.9311	1.2853E-04	4.7459E-02	4.5655E-02	1594	tags=15%, list=11%, signal=13%
BP	GO:0035967	cellular response to topologically incorrect protein	147	0.5078	1.7678	1.3023E-04	4.7459E-02	4.5655E-02	307	tags=6%, list=2%, signal=6%
BP	GO:0034341	response to interferon-gamma	140	0.5312	1.8383	1.3106E-04	4.7459E-02	4.5655E-02	1070	tags=25%, list=7%, signal=23%
BP	GO:2001236	regulation of extrinsic apoptotic signaling pathway	130	0.5502	1.8864	1.3215E-04	4.7459E-02	4.5655E-02	2120	tags=29%, list=15%, signal=25%
BP	GO:0034620	cellular response to unfolded protein	128	0.5418	1.8510	1.3289E-04	4.7459E-02	4.5655E-02	307	tags=7%, list=2%, signal=7%
BP	GO:0007272	ensheathment of neurons	121	0.6283	2.1323	1.3380E-04	4.7459E-02	4.5655E-02	1680	tags=33%, list=12%, signal=29%
BP	GO:0008366	axon ensheathment	121	0.6283	2.1323	1.3380E-04	4.7459E-02	4.5655E-02	1680	tags=33%, list=12%, signal=29%
BP	GO:0034605	cellular response to heat	118	0.5579	1.8891	1.3392E-04	4.7459E-02	4.5655E-02	1566	tags=16%, list=11%, signal=14%
BP	GO:0042552	myelination	119	0.6261	2.1210	1.3399E-04	4.7459E-02	4.5655E-02	1680	tags=33%, list=12%, signal=29%
BP	GO:1903900	regulation of viral life cycle	111	0.6504	2.1884	1.3448E-04	4.7459E-02	4.5655E-02	999	tags=21%, list=7%, signal=19%
BP	GO:0019079	viral genome replication	96	0.6958	2.3006	1.3744E-04	4.7459E-02	4.5655E-02	845	tags=20%, list=6%, signal=19%
BP	GO:2001237	negative regulation of extrinsic apoptotic signaling pathway	84	0.6059	1.9685	1.3916E-04	4.7459E-02	4.5655E-02	2120	tags=33%, list=15%, signal=29%
BP	GO:0034340	response to type I interferon	74	0.7749	2.4656	1.4198E-04	4.7459E-02	4.5655E-02	718	tags=36%, list=5%, signal=35%
BP	GO:0045069	regulation of viral genome replication	73	0.7384	2.3439	1.4223E-04	4.7459E-02	4.5655E-02	845	tags=25%, list=6%, signal=23%
BP	GO:0060337	type I interferon signaling pathway	70	0.7770	2.4480	1.4372E-04	4.7459E-02	4.5655E-02	718	tags=37%, list=5%, signal=35%
BP	GO:0071357	cellular response to type I interferon	70	0.7770	2.4480	1.4372E-04	4.7459E-02	4.5655E-02	718	tags=37%, list=5%, signal=35%
BP	GO:0048525	negative regulation of viral process	66	0.6634	2.0712	1.4468E-04	4.7459E-02	4.5655E-02	999	tags=33%, list=7%, signal=31%
BP	GO:0061077	chaperone-mediated protein folding	53	0.6517	1.9638	1.4730E-04	4.7459E-02	4.5655E-02	1498	tags=25%, list=10%, signal=22%
BP	GO:1903901	negative regulation of viral life cycle	56	0.7511	2.2798	1.4741E-04	4.7459E-02	4.5655E-02	956	tags=36%, list=7%, signal=34%
CC	GO:0043209	myelin sheath	42	0.6820	1.9724	1.5235E-04	4.7459E-02	4.5655E-02	1621	tags=43%, list=11%, signal=38%
BP	GO:0045071	negative regulation of viral genome replication	41	0.7797	2.2446	1.5242E-04	4.7459E-02	4.5655E-02	845	tags=39%, list=6%, signal=37%
BP	GO:0014003	oligodendrocyte development	40	0.6910	1.9784	1.5288E-04	4.7459E-02	4.5655E-02	792	tags=30%, list=5%, signal=28%
CC	GO:0008180	COP9 signalosome	33	0.7362	2.0314	1.5610E-04	4.7459E-02	4.5655E-02	226	tags=9%, list=2%, signal=9%
MF	GO:0044183	protein binding involved in protein folding	20	0.8257	2.0626	1.6351E-04	4.8629E-02	4.6781E-02	422	tags=25%, list=3%, signal=24%

Event 4 – ELOVL7 (KEGG)

ID	Description	setSize	enrichmentScore	NES	pvalue	p.adjust	qvalues	rank	leading_edge
hsa05162	Measles	100	0.6361	2.1002	1.3596E-04	1.7680E-02	1.5391E-02	718	tags=19%, list=5%, signal=18%
hsa05134	Legionellosis	48	0.6844	2.0224	1.4879E-04	1.7680E-02	1.5391E-02	859	tags=25%, list=6%, signal=24%
hsa05168	Herpes simplex virus 1 infection	436	0.3970	1.5194	2.2210E-04	1.7680E-02	1.5391E-02	3115	tags=29%, list=21%, signal=23%
hsa04621	NOD-like receptor signaling pathway	127	0.5339	1.8149	2.6368E-04	1.7680E-02	1.5391E-02	1407	tags=21%, list=10%, signal=19%
hsa04512	ECM-receptor interaction	68	0.5947	1.8583	2.8494E-04	1.7680E-02	1.5391E-02	1644	tags=38%, list=11%, signal=34%
hsa05144	Malaria	33	0.7233	1.9959	3.1109E-04	1.7680E-02	1.5391E-02	1317	tags=52%, list=9%, signal=47%
hsa05164	Influenza A	122	0.5337	1.8071	3.9630E-04	1.9306E-02	1.6806E-02	718	tags=16%, list=5%, signal=15%
hsa05160	Hepatitis C	118	0.5137	1.7317	7.9840E-04	3.4032E-02	2.9625E-02	2458	tags=25%, list=17%, signal=21%
hsa04213	Longevity regulating pathway - multiple species	57	0.6108	1.8547	1.0240E-03	3.8798E-02	3.3774E-02	226	tags=9%, list=2%, signal=9%
hsa05165	Human papillomavirus infection	272	0.4154	1.5357	1.4103E-03	4.8090E-02	4.1863E-02	2120	tags=21%, list=15%, signal=18%

Event 4 – ELOVL7 (Hallmark)

ID	Description	setSize	enrichmentScore	NES	pvalue	p.adjust	qvalues	rank	leading_edge
HALLMARK_INTERFERON_GAMMA_RESPONSE	HALLMARK_INTERFERON_GAMMA_RESPONSE	172	0.6708	2.3790	1.2661E-04	3.2544E-03	2.5350E-03	2026	tags=48%, list=14%, signal=42%
HALLMARK_INTERFERON_ALPHA_RESPONSE	HALLMARK_INTERFERON_ALPHA_RESPONSE	87	0.8144	2.6564	1.3897E-04	3.2544E-03	2.5350E-03	1273	tags=61%, list=9%, signal=56%
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	174	0.4776	1.6956	2.5233E-04	3.2544E-03	2.5350E-03	1644	tags=28%, list=11%, signal=25%
HALLMARK_INFLAMMATORY_RESPONSE	HALLMARK_INFLAMMATORY_RESPONSE	141	0.5136	1.7845	2.6035E-04	3.2544E-03	2.5350E-03	1776	tags=33%, list=12%, signal=29%
HALLMARK_COMPLEMENT	HALLMARK_COMPLEMENT	157	0.4575	1.6090	1.4077E-03	1.4077E-02	1.0965E-02	1700	tags=24%, list=12%, signal=22%

Event 5 – DRC1 (GO)

ONTOLOGY	ID	Description	setSize	enrichmentScore	NES	pvalue	p.adjust	qvalues	rank	leading edge
BP	GO:0051960	regulation of nervous system development	774	0.3248	1.3933	1.7397E-04	4.7142E-02	4.4355E-02	2750	tags=24%, list=19%, signal=21%
BP	GO:0060322	head development	645	0.3564	1.5069	1.7630E-04	4.7142E-02	4.4355E-02	2668	tags=24%, list=18%, signal=20%
BP	GO:0007420	brain development	610	0.3524	1.4844	1.7652E-04	4.7142E-02	4.4355E-02	2668	tags=24%, list=18%, signal=21%
BP	GO:0070848	response to growth factor	561	0.3752	1.5677	1.7899E-04	4.7142E-02	4.4355E-02	1404	tags=14%, list=10%, signal=13%
BP	GO:0071363	cellular response to growth factor stimulus	538	0.3765	1.5665	1.8025E-04	4.7142E-02	4.4355E-02	1404	tags=14%, list=10%, signal=13%
MF	GO:0050839	cell adhesion molecule binding	439	0.3775	1.5448	1.8077E-04	4.7142E-02	4.4355E-02	1835	tags=17%, list=13%, signal=15%
BP	GO:0043062	extracellular structure organization	314	0.4203	1.6624	1.8501E-04	4.7142E-02	4.4355E-02	1368	tags=22%, list=9%, signal=20%
BP	GO:0030198	extracellular matrix organization	277	0.4322	1.6896	1.8512E-04	4.7142E-02	4.4355E-02	1404	tags=23%, list=10%, signal=21%
BP	GO:0051961	negative regulation of nervous system development	263	0.4418	1.7181	1.8615E-04	4.7142E-02	4.4355E-02	2680	tags=26%, list=19%, signal=22%
BP	GO:0098742	cell-cell adhesion via plasma-membrane adhesion molecules	214	0.4686	1.7816	1.8713E-04	4.7142E-02	4.4355E-02	2419	tags=40%, list=17%, signal=34%
BP	GO:0050768	negative regulation of neurogenesis	243	0.4559	1.7546	1.8751E-04	4.7142E-02	4.4355E-02	2680	tags=27%, list=19%, signal=23%
BP	GO:0034612	response to tumor necrosis factor	210	0.4738	1.7949	1.8779E-04	4.7142E-02	4.4355E-02	615	tags=11%, list=4%, signal=11%
BP	GO:0071356	cellular response to tumor necrosis factor	195	0.4848	1.8203	1.8818E-04	4.7142E-02	4.4355E-02	1264	tags=15%, list=9%, signal=14%
MF	GO:0001730	2'-5'-oligoadenylate synthetase activity	3	0.9861	1.5870	1.9113E-04	4.7142E-02	4.4355E-02	205	tags=100%, list=1%, signal=99%
BP	GO:0007156	homophilic cell adhesion via plasma membrane adhesion molecules	145	0.5075	1.8347	1.9175E-04	4.7142E-02	4.4355E-02	2131	tags=41%, list=15%, signal=36%
BP	GO:0001580	detection of chemical stimulus involved in sensory perception of bitter taste	12	0.8758	1.9873	1.9227E-04	4.7142E-02	4.4355E-02	911	tags=67%, list=6%, signal=63%
BP	GO:0030511	positive regulation of transforming growth factor beta receptor signaling pathway	24	0.8042	2.1236	1.9387E-04	4.7142E-02	4.4355E-02	808	tags=17%, list=6%, signal=16%
BP	GO:1903846	positive regulation of cellular response to transforming growth factor beta stimulus	24	0.8042	2.1236	1.9387E-04	4.7142E-02	4.4355E-02	808	tags=17%, list=6%, signal=16%
BP	GO:0055069	zinc ion homeostasis	28	-0.7350	-2.0550	2.0530E-04	4.7142E-02	4.4355E-02	1771	tags=39%, list=12%, signal=35%
BP	GO:0009620	response to fungus	21	-0.8289	-2.1707	2.0644E-04	4.7142E-02	4.4355E-02	704	tags=52%, list=5%, signal=50%
BP	GO:0032602	chemokine production	58	-0.6113	-1.9747	2.0687E-04	4.7142E-02	4.4355E-02	1717	tags=40%, list=12%, signal=35%
BP	GO:0045408	regulation of interleukin-6 biosynthetic process	15	-0.8838	-2.1470	2.0717E-04	4.7142E-02	4.4355E-02	1180	tags=67%, list=8%, signal=61%
BP	GO:0042226	interleukin-6 biosynthetic process	16	-0.8625	-2.1269	2.0738E-04	4.7142E-02	4.4355E-02	1180	tags=62%, list=8%, signal=57%
CC	GO:0045335	phagocytotic vesicle	111	-0.5160	-1.8432	2.0760E-04	4.7142E-02	4.4355E-02	2391	tags=30%, list=17%, signal=25%
BP	GO:0045076	regulation of interleukin-2 biosynthetic process	10	-0.9049	-1.9995	2.0790E-04	4.7142E-02	4.4355E-02	1185	tags=80%, list=8%, signal=74%
BP	GO:0042742	defense response to bacterium	97	-0.5414	-1.8933	2.0851E-04	4.7142E-02	4.4355E-02	1331	tags=42%, list=9%, signal=39%
BP	GO:0022408	negative regulation of cell-cell adhesion	120	-0.5218	-1.8853	2.0877E-04	4.7142E-02	4.4355E-02	1733	tags=33%, list=12%, signal=30%
BP	GO:0032635	interleukin-6 production	99	-0.5122	-1.7957	2.0877E-04	4.7142E-02	4.4355E-02	2190	tags=37%, list=15%, signal=32%
BP	GO:1902107	positive regulation of leukocyte differentiation	98	-0.5166	-1.8084	2.0925E-04	4.7142E-02	4.4355E-02	1479	tags=29%, list=10%, signal=26%
BP	GO:0002399	MHC class II protein complex assembly	3	-0.9922	-1.6376	2.0964E-04	4.7142E-02	4.4355E-02	117	tags=100%, list=1%, signal=99%
BP	GO:0002803	peptide antigen assembly with MHC class II protein complex	3	-0.9922	-1.6376	2.0964E-04	4.7142E-02	4.4355E-02	117	tags=100%, list=1%, signal=99%
MF	GO:0005862	Toll-like receptor 4 binding	3	-0.9933	-1.6394	2.0964E-04	4.7142E-02	4.4355E-02	49	tags=67%, list=0%, signal=66%
BP	GO:0035425	autocrine signalling	6	-0.8412	-1.8273	2.1022E-04	4.7142E-02	4.4355E-02	444	tags=67%, list=3%, signal=65%
BP	GO:0051251	positive regulation of lymphocyte activation	177	-0.4341	-1.6524	2.1124E-04	4.7142E-02	4.4355E-02	1485	tags=28%, list=10%, signal=25%
BP	GO:1903037	regulation of leukocyte cell-cell adhesion	192	-0.4446	-1.7084	2.1231E-04	4.7142E-02	4.4355E-02	1485	tags=29%, list=10%, signal=27%
BP	GO:0002250	adaptive immune response	234	-0.4716	-1.8573	2.1327E-04	4.7142E-02	4.4355E-02	1734	tags=29%, list=12%, signal=26%
BP	GO:0050863	regulation of T cell activation	201	-0.4377	-1.6895	2.1409E-04	4.7142E-02	4.4355E-02	1485	tags=27%, list=10%, signal=25%
BP	GO:0007159	leukocyte cell-cell adhesion	216	-0.4806	-1.8715	2.1501E-04	4.7142E-02	4.4355E-02	1485	tags=30%, list=10%, signal=27%
BP	GO:0022407	regulation of cell-cell adhesion	269	-0.4186	-1.6726	2.1570E-04	4.7142E-02	4.4355E-02	1485	tags=27%, list=10%, signal=24%
BP	GO:0002697	regulation of immune effector process	252	-0.4176	-1.6577	2.1622E-04	4.7142E-02	4.4355E-02	1849	tags=27%, list=13%, signal=21%
BP	GO:0002275	myeloid cell activation involved in immune response	417	-0.4115	-1.7233	2.2168E-04	4.7142E-02	4.4355E-02	2019	tags=25%, list=14%, signal=22%
BP	GO:0042119	neutrophil activation	380	-0.4031	-1.6722	2.2193E-04	4.7142E-02	4.4355E-02	2019	tags=25%, list=14%, signal=22%
BP	GO:0002446	neutrophil mediated immunity	383	-0.4120	-1.7099	2.2207E-04	4.7142E-02	4.4355E-02	2281	tags=27%, list=16%, signal=23%
BP	GO:0036230	granulocyte activation	383	-0.4024	-1.6699	2.2207E-04	4.7142E-02	4.4355E-02	2019	tags=25%, list=14%, signal=22%
BP	GO:0043312	neutrophil degranulation	375	-0.4178	-1.7313	2.2217E-04	4.7142E-02	4.4355E-02	2019	tags=25%, list=14%, signal=22%
BP	GO:0002283	neutrophil activation involved in immune response	376	-0.4162	-1.7247	2.2232E-04	4.7142E-02	4.4355E-02	2019	tags=25%, list=14%, signal=22%
BP	GO:0002444	myeloid leukocyte mediated immunity	423	-0.4084	-1.7117	2.2257E-04	4.7142E-02	4.4355E-02	2019	tags=24%, list=14%, signal=22%
BP	GO:0043299	leukocyte degranulation	410	-0.4145	-1.7326	2.2267E-04	4.7142E-02	4.4355E-02	2019	tags=25%, list=14%, signal=22%
BP	GO:0002253	activation of immune response	429	-0.3535	-1.4838	2.2311E-04	4.7142E-02	4.4355E-02	1843	tags=20%, list=13%, signal=18%
BP	GO:0006954	inflammatory response	459	-0.3804	-1.6064	2.2452E-04	4.7142E-02	4.4355E-02	1388	tags=22%, list=10%, signal=21%
BP	GO:0050778	positive regulation of immune response	532	-0.3764	-1.6099	2.2487E-04	4.7142E-02	4.4355E-02	1843	tags=21%, list=13%, signal=19%
BP	GO:0001816	cytokine production	523	-0.3648	-1.5578	2.2538E-04	4.7142E-02	4.4355E-02	1838	tags=24%, list=13%, signal=21%
BP	GO:0002274	myeloid leukocyte activation	482	-0.3783	-1.6049	2.2619E-04	4.7142E-02	4.4355E-02	1610	tags=23%, list=11%, signal=22%
BP	GO:0001817	regulation of cytokine production	470	-0.3547	-1.5006	2.2635E-04	4.7142E-02	4.4355E-02	2228	tags=28%, list=15%, signal=24%
BP	GO:0002443	leukocyte mediated immunity	546	-0.4105	-1.7574	2.2655E-04	4.7142E-02	4.4355E-02	1864	tags=25%, list=13%, signal=22%
BP	GO:0002366	leukocyte activation involved in immune response	512	-0.3961	-1.6880	2.2701E-04	4.7142E-02	4.4355E-02	1864	tags=23%, list=13%, signal=21%
CC	GO:0000323	lytic vacuole	560	-0.3430	-1.4711	2.2722E-04	4.7142E-02	4.4355E-02	1849	tags=17%, list=13%, signal=16%
BP	GO:0045087	innate immune response	582	-0.3488	-1.5015	2.2743E-04	4.7142E-02	4.4355E-02	1849	tags=23%, list=13%, signal=21%
BP	GO:0002263	cell activation involved in immune response	516	-0.3919	-1.6696	2.2784E-04	4.7142E-02	4.4355E-02	1864	tags=23%, list=13%, signal=20%
MF	GO:0004888	transmembrane signaling receptor activity	506	-0.3385	-1.4402	2.2810E-04	4.7142E-02	4.4355E-02	1479	tags=22%, list=10%, signal=21%
CC	GO:0005764	lysosome	559	-0.3434	-1.4714	2.2836E-04	4.7142E-02	4.4355E-02	1849	tags=17%, list=13%, signal=16%
MF	GO:0060089	molecular transducer activity	679	-0.3325	-1.4461	2.3175E-04	4.7142E-02	4.4355E-02	1555	tags=21%, list=11%, signal=20%
BP	GO:0050776	regulation of immune response	665	-0.3242	-1.4077	2.3191E-04	4.7142E-02	4.4355E-02	1849	tags=21%, list=13%, signal=20%
MF	GO:0038023	signaling receptor activity	634	-0.3430	-1.4832	2.3202E-04	4.7142E-02	4.4355E-02	1555	tags=22%, list=11%, signal=21%
BP	GO:0045055	regulated exocytosis	630	-0.3636	-1.5716	2.3261E-04	4.7142E-02	4.4355E-02	2019	tags=22%, list=14%, signal=20%
BP	GO:0002684	positive regulation of immune system process	717	-0.3172	-1.3846	2.3332E-04	4.7142E-02	4.4355E-02	1486	tags=21%, list=10%, signal=20%
BP	GO:0006887	exocytosis	720	-0.3428	-1.4972	2.3370E-04	4.7142E-02	4.4355E-02	2019	tags=21%, list=14%, signal=19%
BP	GO:0048646	anatomical structure formation involved in morphogenesis	794	-0.3082	-1.3540	2.3502E-04	4.7142E-02	4.4355E-02	1744	tags=21%, list=12%, signal=19%

Event 5 – DRC1 (KEGG)

ID	Description	setSize	enrichmentScore	NES	pvalue	p.adjust	qvalues	rank	leading edge
hsa04672	Intestinal immune network for IgA production	24	-0.7472	-2.0032	2.0653E-04	2.4082E-02	2.1558E-02	1733	tags=67%, list=12%, signal=59%
hsa04270	Vascular smooth muscle contraction	102	-0.5450	-1.9278	2.1093E-04	2.4082E-02	2.1558E-02	1926	tags=27%, list=13%, signal=24%
hsa05152	Tuberculosis	130	-0.5348	-1.9630	2.1186E-04	2.4082E-02	2.1558E-02	890	tags=21%, list=6%, signal=20%
hsa04933	AGE-RAGE signaling pathway in diabetic complication	89	0.5425	1.8234	5.7416E-04	2.8801E-02	2.5782E-02	65	tags=8%, list=0%, signal=8%
hsa04658	Th1 and Th2 cell differentiation	64	-0.5708	-1.8694	6.2526E-04	2.8801E-02	2.5782E-02	1813	tags=31%, list=13%, signal=27%
hsa04659	Th17 cell differentiation	72	-0.5479	-1.8316	6.2578E-04	2.8801E-02	2.5782E-02	1813	tags=33%, list=13%, signal=29%
hsa05140	Leishmaniasis	56	-0.5918	-1.8839	6.2880E-04	2.8801E-02	2.5782E-02	1256	tags=34%, list=9%, signal=31%
hsa04512	ECM-receptor interaction	68	0.5815	1.8669	7.6570E-04	2.8801E-02	2.5782E-02	453	tags=18%, list=3%, signal=17%
hsa05321	Inflammatory bowel disease	32	-0.6523	-1.8588	8.2713E-04	2.8801E-02	2.5782E-02	718	tags=50%, list=5%, signal=48%
hsa04380	Osteoclast differentiation	97	-0.4845	-1.7010	8.4459E-04	2.8801E-02	2.5782E-02	1704	tags=27%, list=12%, signal=24%
hsa05332	Graft-versus-host disease	17	-0.7676	-1.9208	1.4216E-03	4.4070E-02	3.9451E-02	1039	tags=59%, list=7%, signal=55%
hsa05320	Autoimmune thyroid disease	16	-0.7690	-1.8928	1.8412E-03	4.8297E-02	4.3236E-02	1039	tags=62%, list=7%, signal=58%
hsa05330	Allograft rejection	16	-0.7690	-1.8928	1.8412E-03	4.8297E-02	4.3236E-02	1039	tags=62%, list=7%, signal=58%

Event 5 – DRC1 (Hallmark)

ID	Description	setSize	enrichmentScore	NES	pvalue	p.adjust	qvalues	rank	leading edge
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	173	0.4573	1.6946	3.7467E-04	1.8734E-02	1.4198E-02	1187	tags=22%, list=8%, signal=20%
HALLMARK_INTERFERON_GAMMA_RESPONSE	HALLMARK_INTERFERON_GAMMA_RESPONSE	171	0.4351	1.6093	9.3985E-04	1.9048E-02	1.4436E-02	1598	tags=27%, list=11%, signal=24%
HALLMARK_HYPOXIA	HALLMARK_HYPOXIA	170	-0.4256	-1.6124	1.2815E-03	1.9048E-02	1.4436E-02	1386	tags=22%, list=10%, signal=20%
HALLMARK_INTERFERON_ALPHA_RESPONSE	HALLMARK_INTERFERON_ALPHA_RESPONSE	87	0.5184	1.7367	1.9029E-03	1.9048E-02	1.4436E-02	1173	tags=30%, list=8%, signal=28%
HALLMARK_ALLOGRAFT_REJECTION	HALLMARK_ALLOGRAFT_REJECTION	121	-0.4524	-1.6459	1.9048E-03	1.9048E-02	1.4436E-02	1794	tags=29%, list=12%, signal=26%