

Table SI. Detailed information about GO and KEGG terms.

Group ID	Category	Term	Description	LogP	Log (q-value)	InTerm_InList
1_Summary	GO Biological Process	GO:0006954	Inflammatory response	-21.1336	-16.870	87/715
1_Member	GO Biological Process	GO:0006954	Inflammatory response	-21.1336	-16.870	87/715
1_Member	GO Biological Process	GO:0032101	Regulation of response to external stimulus	-15.6467	-11.986	82/792
1_Member	GO Biological Process	GO:0050727	Regulation of inflammatory response	-15.0181	-11.533	51/363
1_Member	GO Biological Process	GO:0031347	Regulation of defense response	-14.7909	-11.431	71/649
1_Member	GO Biological Process	GO:0050729	Positive regulation of inflammatory response	-10.5187	-7.824	26/142
1_Member	GO Biological Process	GO:0031349	Positive regulation of defense response	-9.96988	-7.360	43/370
1_Member	GO Biological Process	GO:0032103	Positive regulation of response to external stimulus	-9.18573	-6.715	38/319
1_Member	GO Biological Process	GO:0001816	Cytokine production	-9.02427	-6.574	67/788
1_Member	GO Biological Process	GO:0001817	Regulation of cytokine production	-8.05278	-5.749	60/709
1_Member	GO Biological Process	GO:0001819	Positive regulation of cytokine production	-6.83102	-4.701	42/454
2_Summary	GO Biological Process	GO:0008285	Negative regulation of cell proliferation	-20.3324	-16.370	84/692
2_Member	GO Biological Process	GO:0008285	Negative regulation of cell proliferation	-20.3324	-16.370	84/692

2_Member	GO Biological Process	GO:0010942	Positive regulation of cell death	-9.24347	-6.759	63/710
			Positive regulation of programmed cell			
			death	-9.10997	-6.653	59/648
2_Member	GO Biological Process	GO:0043068				
2_Member	GO Biological Process	GO:0043065	Positive regulation of apoptotic process	-8.81152	-6.400	58/643
3_Summary	GO Biological Process	GO:0001503	Ossification	-18.0479	-14.262	58/393
3_Member	GO Biological Process	GO:0001503	Ossification	-18.0479	-14.262	58/393
3_Member	GO Biological Process	GO:0001649	Osteoblast differentiation	-11.4336	-8.602	33/207
3_Member	GO Biological Process	GO:0030278	Regulation of ossification	-10.4013	-7.740	34/238
3_Member	GO Biological Process	GO:0031214	Biominerale tissue development	-9.8581	-7.267	27/163
3_Member	GO Biological Process	GO:0030282	Bone mineralization	-9.79458	-7.213	23/120
3_Member	GO Biological Process	GO:0045667	Regulation of osteoblast differentiation	-6.77178	-4.649	21/145
3_Member	GO Biological Process	GO:0045778	Positive regulation of ossification	-5.77566	-3.816	16/102
			Regulation of biominerale tissue			
			development	-5.31724	-3.477	15/98
3_Member	GO Biological Process	GO:0070167	Positive regulation of osteoblast			
			differentiation	-4.88449	-3.141	12/70
3_Member	GO Biological Process	GO:0045669				
3_Member	GO Biological Process	GO:0030500	Regulation of bone mineralization	-4.2295	-2.600	12/81

4_Summary	GO Biological Process	GO:0042330	Taxis	-15.3748	-11.811	69/603
4_Member	GO Biological Process	GO:0042330	Taxis	-15.3748	-11.811	69/603
4_Member	GO Biological Process	GO:0006935	Chemotaxis	-14.9445	-11.526	68/600
4_Member	GO Biological Process	GO:0048858	Cell projection morphogenesis	-5.18231	-3.371	52/709
			Plasma membrane bounded cell projection			
4_Member	GO Biological Process	GO:0120039	morphogenesis	-4.94665	-3.185	51/704
4_Member	GO Biological Process	GO:0048812	Neuron projection morphogenesis	-4.86392	-3.122	50/690
4_Member	GO Biological Process	GO:0032990	Cell part morphogenesis	-4.79923	-3.065	52/732
			Positive regulation of nervous system			
4_Member	GO Biological Process	GO:0051962	development	-4.38573	-2.726	47/662
			Regulation of neuron projection			
4_Member	GO Biological Process	GO:0010975	development	-3.91323	-2.335	43/615
4_Member	GO Biological Process	GO:0061564	Axon development	-3.89296	-2.322	38/521
4_Member	GO Biological Process	GO:0050769	Positive regulation of neurogenesis	-3.70215	-2.166	41/590
4_Member	GO Biological Process	GO:0010720	Positive regulation of cell development	-3.64498	-2.121	45/672
4_Member	GO Biological Process	GO:0007411	Axon guidance	-3.60923	-2.095	22/248
4_Member	GO Biological Process	GO:0097485	Neuron projection guidance	-3.56026	-2.056	22/250

4_Member	GO Biological Process	GO:0045664	Regulation of neuron differentiation	-3.44603	-1.959	50/787
4_Member	GO Biological Process	GO:0007409	Axonogenesis	-3.01435	-1.635	33/480
4_Member	GO Biological Process	GO:0010976	Positive regulation of neuron projection development	-2.9043	-1.553	27/372
4_Member	GO Biological Process	GO:0031344	Regulation of cell projection organization	-2.83794	-1.502	48/797
4_Member	GO Biological Process	GO:0048667	Cell morphogenesis involved in neuron differentiation	-2.70292	-1.406	40/643
4_Member	GO Biological Process	GO:0045666	Positive regulation of neuron differentiation	-2.56106	-1.307	31/472
4_Member	GO Biological Process	GO:0031346	Positive regulation of cell projection organization	-2.49289	-1.254	31/477
4_Member	GO Biological Process	GO:0120035	Regulation of plasma membrane bounded cell projection organization	-2.26933	-1.095	45/788
4_Member	GO Biological Process	GO:0050770	Regulation of axonogenesis	-2.19342	-1.038	16/207
4_Member	GO Biological Process	GO:1902667	Regulation of axon guidance	-2.1447	-0.999	6/45
5_Summary	GO Biological Process	GO:0048514	Blood vessel morphogenesis	-14.3371	-11.028	69/632
5_Member	GO Biological Process	GO:0048514	Blood vessel morphogenesis	-14.3371	-11.028	69/632

5_Member	GO Biological Process	GO:0072358	Cardiovascular system development	-14.0633	-10.800	78/780
5_Member	GO Biological Process	GO:0001944	Vasculature development	-13.9759	-10.792	77/767
5_Member	GO Biological Process	GO:0001568	Blood vessel development	-13.626	-10.509	74/731
5_Member	GO Biological Process	GO:0001525	Angiogenesis	-12.9973	-9.938	59/521
5_Member	GO Biological Process	GO:1901342	Regulation of vasculature development	-9.17231	-6.709	40/348
5_Member	GO Biological Process	GO:0045765	Regulation of angiogenesis	-7.82863	-5.539	35/312
5_Member	GO Biological Process	GO:1904018	Positive regulation of vasculature development	-6.98469	-4.825	26/206
5_Member	GO Biological Process	GO:0001667	Ameboidal-type cell migration	-6.95034	-4.801	40/417
5_Member	GO Biological Process	GO:0045766	Positive regulation of angiogenesis	-6.67673	-4.571	24/186
5_Member	GO Biological Process	GO:0010631	Epithelial cell migration	-5.18894	-3.375	28/287
5_Member	GO Biological Process	GO:0090132	Epithelium migration	-5.1318	-3.333	28/289
5_Member	GO Biological Process	GO:0090130	Tissue migration	-5.07531	-3.291	28/291
5_Member	GO Biological Process	GO:0043542	Endothelial cell migration	-3.91087	-2.334	20/204
5_Member	GO Biological Process	GO:0010634	Positive regulation of epithelial cell migration	-3.76144	-2.213	16/147
5_Member	GO Biological Process	GO:0010632	Regulation of epithelial cell migration	-3.20071	-1.779	20/231

5_Member	GO Biological Process	GO:0010595	Positive regulation of endothelial cell migration	-2.29331	-1.113	10/100
5_Member	GO Biological Process	GO:0010594	Regulation of endothelial cell migration	-2.0069	-0.897	13/162
6_Summary	GO Biological Process	GO:0043062	Extracellular structure organization	-14.0214	-10.800	46/319
6_Member	GO Biological Process	GO:0043062	Extracellular structure organization	-14.0214	-10.800	46/319
6_Member	GO Biological Process	GO:0030198	Extracellular matrix organization	-13.0501	-9.963	41/275
6_Member	Reactome Gene Sets	R-MMU-1474244	Extracellular matrix organization	-9.68019	-7.116	35/266
6_Member	Reactome Gene Sets	R-MMU-1474290	Collagen formation	-6.40485	-4.336	15/81
6_Member	Reactome Gene Sets	R-MMU-2022090	Assembly of collagen fibrils and other multimeric structures	-5.86305	-3.883	12/57
6_Member	Reactome Gene Sets	R-MMU-1650814	Collagen biosynthesis and modifying enzymes	-2.74592	-1.442	8/59
6_Member	KEGG Pathway	mmu04974	Protein digestion and absorption	-2.62601	-1.349	10/90
7_Summary	GO Biological Process	GO:1903047	Mitotic cell cycle process	-13.741	-10.592	70/665
7_Member	GO Biological Process	GO:1903047	Mitotic cell cycle process	-13.741	-10.592	70/665
7_Member	GO Biological Process	GO:0140014	Mitotic nuclear division	-11.8117	-8.929	38/261
7_Member	Reactome Gene Sets	R-MMU-69278	Cell cycle, mitotic	-10.1983	-7.569	53/513

7_Member	GO Biological Process	GO:0010564	Regulation of cell cycle process	-9.7596	-7.187	57/591
7_Member	GO Biological Process	GO:0000070	Mitotic sister chromatid segregation	-9.36121	-6.854	25/148
7_Member	Reactome Gene Sets	R-MMU-1640170	Cell cycle	-8.89309	-6.475	55/590
7_Member	GO Biological Process	GO:0051783	Regulation of nuclear division	-8.6775	-6.289	28/196
7_Member	GO Biological Process	GO:0000280	Nuclear division	-8.44701	-6.113	43/414
7_Member	GO Biological Process	GO:0007346	Regulation of mitotic cell cycle	-7.87956	-5.580	50/546
7_Member	GO Biological Process	GO:0048285	Organelle fission	-7.80521	-5.524	45/467
7_Member	GO Biological Process	GO:0007088	Regulation of mitotic nuclear division	-7.68463	-5.413	24/165
7_Member	GO Biological Process	GO:0000819	Sister chromatid segregation	-7.51816	-5.264	25/181
7_Member	GO Biological Process	GO:0045786	Negative regulation of cell cycle	-7.407	-5.173	43/449
7_Member	GO Biological Process	GO:0090068	Positive regulation of cell cycle process	-7.299	-5.081	30/254
7_Member	GO Biological Process	GO:0051983	Regulation of chromosome segregation	-7.02144	-4.855	18/105
7_Member	GO Biological Process	GO:0045930	Negative regulation of mitotic cell cycle	-6.97445	-4.819	28/234
7_Member	GO Biological Process	GO:0051784	Negative regulation of nuclear division	-6.87153	-4.736	14/65
7_Member	GO Biological Process	GO:0030071	Regulation of mitotic metaphase/anaphase transition	-6.83108	-4.701	13/56
7_Member	GO Biological Process	GO:0031577	Spindle checkpoint	-6.6791	-4.571	11/40

7_Member	GO Biological Process	GO:1902099	Regulation of metaphase/anaphase transition of cell cycle	-6.63927	-4.540	13/58
7_Member	GO Biological Process	GO:0007091	Metaphase/anaphase transition of mitotic cell cycle	-6.54658	-4.460	13/59
7_Member	GO Biological Process	GO:0010965	Regulation of mitotic sister chromatid separation	-6.45593	-4.380	13/60
7_Member	GO Biological Process	GO:0044784	Metaphase/anaphase transition of cell cycle	-6.36724	-4.313	13/61
7_Member	GO Biological Process	GO:0045787	Positive regulation of cell cycle	-6.35238	-4.301	35/358
7_Member	GO Biological Process	GO:0045839	Negative regulation of mitotic nuclear division	-6.1314	-4.111	12/54
7_Member	GO Biological Process	GO:0051306	Mitotic sister chromatid separation	-6.11225	-4.095	13/64
7_Member	GO Biological Process	GO:1905818	Regulation of chromosome separation	-6.03073	-4.023	13/65
7_Member	GO Biological Process	GO:0098813	Nuclear chromosome segregation	-5.99456	-3.996	28/261
7_Member	GO Biological Process	GO:0071174	Mitotic spindle checkpoint	-5.92902	-3.940	10/38
7_Member	GO Biological Process	GO:0045841	Negative regulation of mitotic metaphase/anaphase transition	-5.70567	-3.762	10/40
7_Member	Reactome Gene Sets	R-MMU-2500257	Resolution of Sister Chromatid Cohesion	-5.62205	-3.695	17/117

7_Member	GO Biological Process	GO:1902100	Negative regulation of metaphase/anaphase transition of cell cycle	-5.59936	-3.685	10/41
7_Member	GO Biological Process	GO:2000816	Negative regulation of mitotic sister chromatid separation	-5.59936	-3.685	10/41
7_Member	GO Biological Process	GO:0033047	Regulation of mitotic sister chromatid segregation	-5.57418	-3.663	13/71
7_Member	GO Biological Process	GO:0007059	Chromosome segregation	-5.55748	-3.654	31/322
7_Member	GO Biological Process	GO:1905819	Negative regulation of chromosome separation	-5.49638	-3.617	10/42
7_Member	GO Biological Process	GO:0010948	Negative regulation of cell cycle process	-5.38837	-3.533	24/219
7_Member	GO Biological Process	GO:0033048	Negative regulation of mitotic sister chromatid segregation	-5.29966	-3.466	10/44
7_Member	Reactome Gene Sets	R-MMU-68886	M phase	-5.29831	-3.466	35/398
7_Member	GO Biological Process	GO:0007094	Mitotic spindle assembly checkpoint	-5.19045	-3.375	9/36
7_Member	GO Biological Process	GO:0071173	Spindle assembly checkpoint	-5.19045	-3.375	9/36
7_Member	GO Biological Process	GO:0044772	Mitotic cell cycle phase transition	-5.18355	-3.371	33/369

7_Member	GO Biological Process	GO:0033046	Negative regulation of sister chromatid segregation	-5.11426	-3.321	10/46
7_Member	GO Biological Process	GO:0044770	Cell cycle phase transition	-5.06246	-3.280	35/408
7_Member	GO Biological Process	GO:0045931	Positive regulation of mitotic cell cycle	-4.97457	-3.208	20/172
7_Member	GO Biological Process	GO:0051985	Negative regulation of chromosome segregation	-4.93908	-3.182	10/48
7_Member	Reactome Gene Sets	R-MMU-9648025	EML4 and NUDC in mitotic spindle formation	-4.89085	-3.144	15/106
7_Member	GO Biological Process	GO:0033045	Regulation of sister chromatid segregation	-4.74148	-3.012	13/84
7_Member	Reactome Gene Sets	R-MMU-141424	Amplification of signal from the kinetochores	-4.41409	-2.746	13/90
7_Member	Reactome Gene Sets	R-MMU-141444	Amplification of signal from unattached kinetochores via a MAD2 inhibitory signal	-4.41409	-2.746	13/90
7_Member	Reactome Gene Sets	R-MMU-68877	Mitotic Prometaphase	-4.40779	-2.743	20/188
7_Member	GO Biological Process	GO:0007093	Mitotic cell cycle checkpoint	-4.40302	-2.740	16/130
7_Member	Reactome Gene Sets	R-MMU-69618	Mitotic Spindle Checkpoint	-4.26482	-2.628	14/106
7_Member	Reactome Gene Sets	R-MMU-195258	RHO GTPase Effectors	-4.22786	-2.599	27/307

7_Member	GO Biological Process	GO:0051304	Chromosome separation	-4.16352	-2.542	13/95
7_Member	GO Biological Process	GO:1901987	Regulation of cell cycle phase transition	-4.03685	-2.440	26/298
7_Member	GO Biological Process	GO:1901990	Regulation of mitotic cell cycle phase transition	-3.99617	-2.404	24/266
7_Member	GO Biological Process	GO:1901991	Negative regulation of mitotic cell cycle phase transition	-3.93821	-2.355	16/142
7_Member	GO Biological Process	GO:1901988	Negative regulation of cell cycle phase transition	-3.89756	-2.324	17/158
7_Member	Reactome Gene Sets	R-MMU-5663220	RHO GTPases Activate Formins	-3.80715	-2.252	15/131
7_Member	GO Biological Process	GO:0000075	Cell cycle checkpoint	-3.68627	-2.153	18/180
7_Member	GO Biological Process	GO:0051129	negative regulation of cellular component organization	-3.62667	-2.110	50/773
7_Member	Reactome Gene Sets	R-MMU-194315	Signaling by Rho GTPases	-3.30169	-1.848	31/424
7_Member	Reactome Gene Sets	R-MMU-68882	Mitotic Anaphase	-3.10437	-1.706	19/218
7_Member	GO Biological Process	GO:0045840	Positive regulation of mitotic nuclear division	-3.09123	-1.696	9/65
7_Member	Reactome Gene Sets	R-MMU-2555396	Mitotic Metaphase and Anaphase	-3.08043	-1.688	19/219

7_Member	GO Biological Process	GO:0051785	Positive regulation of nuclear division	-2.97578	-1.610	10/81
7_Member	Reactome Gene Sets	R-MMU-2467813	Separation of Sister Chromatids	-2.76716	-1.450	16/181
			Positive regulation of mitotic cell cycle			
7_Member	GO Biological Process	GO:1901992	phase transition	-2.66231	-1.375	10/89
			Negative regulation of chromosome			
7_Member	GO Biological Process	GO:2001251	organization	-2.35247	-1.159	13/147
			Negative regulation of organelle			
7_Member	GO Biological Process	GO:0010639	organization	-2.2352	-1.070	27/416
			Positive regulation of cell cycle phase			
7_Member	GO Biological Process	GO:1901989	transition	-2.20318	-1.045	10/103
8_Summary	KEGG Pathway	mmu04668	TNF signaling pathway	-12.6246	-9.592	25/107
8_Member	KEGG Pathway	mmu04668	TNF signaling pathway	-12.6246	-9.592	25/107
8_Member	KEGG Pathway	mmu04657	IL-17 signaling pathway	-10.5975	-7.878	21/91
8_Member	GO Biological Process	GO:0002237	Response to molecule of bacterial origin	-7.6528	-5.385	40/393
8_Member	GO Biological Process	GO:0032496	Response to lipopolysaccharide	-7.28037	-5.067	38/374
			Cellular response to molecule of bacterial			
8_Member	GO Biological Process	GO:0071219	origin	-5.70494	-3.762	30/301

8_Member	GO Biological Process	GO:0071396	Cellular response to lipid	-5.33829	-3.489	48/626
8_Member	GO Biological Process	GO:0071216	Cellular response to biotic stimulus	-5.06125	-3.280	30/324
8_Member	GO Biological Process	GO:0071222	Cellular response to lipopolysaccharide	-5.04729	-3.268	28/292
8_Member	KEGG Pathway	mmu04621	NOD-like receptor signaling pathway	-3.0815	-1.688	16/169
9_Summary	GO Biological Process	GO:0033002	Muscle cell proliferation	-12.5743	-9.566	37/235
9_Member	GO Biological Process	GO:0033002	Muscle cell proliferation	-12.5743	-9.566	37/235
9_Member	GO Biological Process	GO:0048659	Smooth muscle cell proliferation	-11.6767	-8.812	30/169
9_Member	GO Biological Process	GO:0048660	Regulation of smooth muscle cell proliferation	-11.3339	-8.533	29/163
9_Member	GO Biological Process	GO:0048661	Positive regulation of smooth muscle cell proliferation	-7.70285	-5.427	19/106
9_Member	GO Biological Process	GO:1904705	Regulation of vascular smooth muscle cell proliferation	-7.13627	-4.952	13/53
9_Member	GO Biological Process	GO:1990874	Vascular smooth muscle cell proliferation	-7.03208	-4.862	13/54
9_Member	GO Biological Process	GO:0014909	Smooth muscle cell migration	-5.54887	-3.647	15/94
9_Member	GO Biological Process	GO:1904707	Positive regulation of vascular smooth muscle cell proliferation	-5.30042	-3.466	9/35

9_Member	GO Biological Process	GO:0014812	Muscle cell migration	-4.79121	-3.060	15/108
			Regulation of smooth muscle cell			
9_Member	GO Biological Process	GO:0014910	migration	-4.68472	-2.964	13/85
			Positive regulation of smooth muscle cell			
9_Member	GO Biological Process	GO:0014911	migration	-3.93388	-2.353	10/62
			Positive regulation of cellular component			
10_Summary	GO Biological Process	GO:0051272	movement	-12.5143	-9.530	63/595
			Positive regulation of cellular component			
10_Member	GO Biological Process	GO:0051272	movement	-12.5143	-9.530	63/595
10_Member	GO Biological Process	GO:2000147	Positive regulation of cell motility	-12.133	-9.206	61/576
10_Member	GO Biological Process	GO:0040017	Positive regulation of locomotion	-12.1263	-9.206	63/607
10_Member	GO Biological Process	GO:0030335	Positive regulation of cell migration	-11.8847	-8.983	59/553
10_Member	GO Biological Process	GO:0002685	Regulation of leukocyte migration	-8.61642	-6.245	29/210
10_Member	GO Biological Process	GO:0002687	Positive regulation of leukocyte migration	-7.16361	-4.972	22/150
10_Member	GO Biological Process	GO:0050920	Regulation of chemotaxis	-7.05723	-4.884	27/218
10_Member	GO Biological Process	GO:0002688	Regulation of leukocyte chemotaxis	-5.03091	-3.255	16/116
10_Member	GO Biological Process	GO:0050921	Positive regulation of chemotaxis	-3.90211	-2.327	16/143

10_Member	GO Biological Process	GO:0002690	Positive regulation of leukocyte chemotaxis	-3.77831	-2.227	12/90
11_Summary	GO Biological Process	GO:0023014	Signal transduction by protein phosphorylation	-12.1293	-9.206	75/799
11_Member	GO Biological Process	GO:0023014	Signal transduction by protein phosphorylation	-12.1293	-9.206	75/799
11_Member	GO Biological Process	GO:0070371	ERK1 and ERK2 cascade	-11.4358	-8.602	43/334
11_Member	GO Biological Process	GO:0000165	MAPK cascade	-11.4148	-8.599	72/776
11_Member	GO Biological Process	GO:0043408	Regulation of MAPK cascade	-11.1466	-8.361	68/720
11_Member	GO Biological Process	GO:0070372	Regulation of ERK1 and ERK2 cascade	-10.4911	-7.808	40/315
11_Member	GO Biological Process	GO:0043410	Positive regulation of MAPK cascade	-9.41428	-6.884	52/523
11_Member	GO Biological Process	GO:0070374	Positive regulation of ERK1 and ERK2 cascade	-9.19025	-6.715	31/224
11_Member	GO Biological Process	GO:0051345	Positive regulation of hydrolase activity	-2.14675	-0.999	32/525
12_Summary	GO Biological Process	GO:0050900	Leukocyte migration	-10.964	-8.192	43/345
12_Member	GO Biological Process	GO:0050900	Leukocyte migration	-10.964	-8.192	43/345
12_Member	GO Biological Process	GO:0060326	Cell chemotaxis	-10.5555	-7.849	39/300
12_Member	GO Biological Process	GO:1990868	Response to chemokine	-8.9667	-6.530	17/71

12_Member	GO Biological Process	GO:1990869	Cellular response to chemokine	-8.9667	-6.530	17/71
12_Member	GO Biological Process	GO:0030595	Leukocyte chemotaxis	-8.51997	-6.171	29/212
12_Member	GO Biological Process	GO:0097529	Myeloid leukocyte migration	-7.48657	-5.236	27/208
12_Member	GO Biological Process	GO:0070098	Chemokine-mediated signaling pathway	-7.24247	-5.040	14/61
12_Member	GO Biological Process	GO:1990266	Neutrophil migration	-5.57005	-3.662	17/118
12_Member	GO Biological Process	GO:0097530	Granulocyte migration	-5.51819	-3.635	19/145
12_Member	GO Biological Process	GO:0071621	Granulocyte chemotaxis	-5.46788	-3.597	17/120
12_Member	GO Biological Process	GO:0030593	Neutrophil chemotaxis	-5.37392	-3.522	15/97
12_Member	Reactome Gene Sets	R-MMU-380108	Chemokine receptors bind chemokines	-4.05799	-2.456	10/60
12_Member	Reactome Gene Sets	R-MMU-373076	Class A/1 (Rhodopsin-like receptors)	-3.57382	-2.067	25/301
12_Member	Reactome Gene Sets	R-MMU-375276	Peptide ligand-binding receptors	-3.3977	-1.926	18/190
12_Member	Reactome Gene Sets	R-MMU-418594	G alpha (i) signalling events	-2.92593	-1.571	26/352
12_Member	Reactome Gene Sets	R-MMU-500792	GPCR ligand binding	-2.67447	-1.385	27/386
12_Member	GO Biological Process	GO:0019730	Antimicrobial humoral response	-2.56175	-1.307	13/139
12_Member	GO Biological Process	GO:0031640	Killing of cells of other organism	-2.10089	-0.968	7/60
12_Member	GO Biological Process	GO:0044364	Disruption of cells of other organism	-2.10089	-0.968	7/60
13_Summary	GO Biological Process	GO:0050673	Epithelial cell proliferation	-10.7911	-8.033	49/435

13_Member	GO Biological Process	GO:0050673	Epithelial cell proliferation	-10.7911	-8.033	49/435
13_Member	GO Biological Process	GO:0050678	Regulation of epithelial cell proliferation	-6.98814	-4.825	37/368
13_Member	GO Biological Process	GO:0001935	Endothelial cell proliferation	-5.47326	-3.601	19/146
13_Member	GO Biological Process	GO:0050679	Positive regulation of epithelial cell proliferation	-5.25529	-3.427	23/208
13_Member	GO Biological Process	GO:0001936	Regulation of endothelial cell proliferation	-4.36191	-2.705	16/131
13_Member	GO Biological Process	GO:0001938	Positive regulation of endothelial cell proliferation	-3.73208	-2.190	12/91
14_Summary	GO Biological Process	GO:0001501	Skeletal system development	-10.7493	-8.005	56/542
14_Member	GO Biological Process	GO:0001501	Skeletal system development	-10.7493	-8.005	56/542
14_Member	GO Biological Process	GO:0061448	Connective tissue development	-10.3586	-7.708	38/291
14_Member	GO Biological Process	GO:0051216	Cartilage development	-8.95206	-6.521	30/216
14_Member	GO Biological Process	GO:0098868	Bone growth	-4.93908	-3.182	10/48
14_Member	GO Biological Process	GO:0002062	Chondrocyte differentiation	-4.70417	-2.981	16/123
14_Member	GO Biological Process	GO:0003416	Endochondral bone growth	-4.51769	-2.831	9/43
14_Member	GO Biological Process	GO:0060348	Bone development	-4.25221	-2.620	23/240
14_Member	GO Biological Process	GO:0048705	Skeletal system morphogenesis	-4.04712	-2.448	24/264

14_Member	GO Biological Process	GO:0060351	Cartilage development involved in endochondral bone morphogenesis	-3.11295	-1.710	8/52
14_Member	Reactome Gene Sets	R-MMU-3000178	ECM proteoglycans	-2.93579	-1.576	7/43
14_Member	GO Biological Process	GO:0002063	Chondrocyte development	-2.75864	-1.449	7/46
14_Member	GO Biological Process	GO:0003417	Growth plate cartilage development	-2.63947	-1.358	6/36
14_Member	GO Biological Process	GO:0060350	Endochondral bone morphogenesis	-2.60453	-1.332	9/76
14_Member	GO Biological Process	GO:0060349	Bone morphogenesis	-2.26629	-1.093	11/117
14_Member	GO Biological Process	GO:0003433	Chondrocyte development involved in endochondral bone morphogenesis	-2.04069	-0.921	4/22
15_Summary	GO Biological Process	GO:0071363	Cellular response to growth factor stimulus	-10.6256	-7.894	60/609
15_Member	GO Biological Process	GO:0071363	Cellular response to growth factor stimulus	-10.6256	-7.894	60/609
15_Member	GO Biological Process	GO:0070848	Response to growth factor	-10.2238	-7.584	60/623
15_Member	GO Biological Process	GO:0007178	Transmembrane receptor protein serine/threonine kinase signaling pathway	-7.62527	-5.362	38/363
15_Member	GO Biological Process	GO:0090287	Regulation of cellular response to growth factor stimulus	-6.63839	-4.540	30/272

15_Member	GO Biological Process	GO:0090092	Regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	-4.80326	-3.068	24/237
15_Member	GO Biological Process	GO:0071772	Response to BMP	-3.22601	-1.798	17/180
15_Member	GO Biological Process	GO:0071773	Cellular response to BMP stimulus	-3.22601	-1.798	17/180
15_Member	GO Biological Process	GO:0030509	BMP signaling pathway	-3.0815	-1.688	16/169
15_Member	GO Biological Process	GO:0030510	Regulation of BMP signaling pathway	-2.90807	-1.557	11/97
15_Member	GO Biological Process	GO:0090288	Negative regulation of cellular response to growth factor stimulus	-2.8769	-1.533	14/144
15_Member	GO Biological Process	GO:0090101	Negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	-2.38058	-1.179	11/113
16_Summary	GO Biological Process	GO:0045596	Negative regulation of cell differentiation	-10.4204	-7.748	71/798
16_Member	GO Biological Process	GO:0045596	Negative regulation of cell differentiation	-10.4204	-7.748	71/798
16_Member	GO Biological Process	GO:0010721	Negative regulation of cell development	-4.03731	-2.440	31/385
16_Member	GO Biological Process	GO:0050768	Negative regulation of neurogenesis	-2.24925	-1.081	23/336

16_Member	GO Biological Process	GO:0051961	Negative regulation of nervous system development	-2.14119	-0.996	24/363
17_Summary	GO Biological Process	GO:0097190	Apoptotic signaling pathway	-10.1065	-7.487	59/611
17_Member	GO Biological Process	GO:0097190	Apoptotic signaling pathway	-10.1065	-7.487	59/611
17_Member	GO Biological Process	GO:0097193	Intrinsic apoptotic signaling pathway	-6.37114	-4.313	31/295
17_Member	GO Biological Process	GO:2001233	Regulation of apoptotic signaling pathway	-5.75584	-3.798	37/413
17_Member	GO Biological Process	GO:0008630	Intrinsic apoptotic signaling pathway in response to DNA damage	-5.28183	-3.452	16/111
17_Member	GO Biological Process	GO:2001234	Negative regulation of apoptotic signaling pathway	-4.99037	-3.220	24/231
17_Member	GO Biological Process	GO:2001242	Regulation of intrinsic apoptotic signaling pathway	-2.67127	-1.383	15/168
17_Member	GO Biological Process	GO:2001243	Negative regulation of intrinsic apoptotic signaling pathway	-2.42012	-1.202	10/96
18_Summary	GO Biological Process	GO:0046545	Development of primary female sexual characteristics	-9.94871	-7.348	23/118

18_Member	GO Biological Process	GO:0046545	Development of primary female sexual characteristics	-9.94871	-7.348	23/118
18_Member	GO Biological Process	GO:0008585	Female gonad development	-9.38033	-6.865	22/115
18_Member	GO Biological Process	GO:0048608	Reproductive structure development	-8.58985	-6.225	46/456
18_Member	GO Biological Process	GO:0046660	Female sex differentiation	-8.58219	-6.225	24/149
18_Member	GO Biological Process	GO:0061458	Reproductive system development	-8.46955	-6.131	46/460
18_Member	GO Biological Process	GO:0045137	Development of primary sexual characteristics	-6.41571	-4.343	26/220
18_Member	GO Biological Process	GO:0008406	Gonad development	-6.02332	-4.018	25/216
18_Member	GO Biological Process	GO:0030728	Ovulation	-5.55739	-3.654	8/25
18_Member	GO Biological Process	GO:0001541	Ovarian follicle development	-4.88449	-3.141	12/70
18_Member	GO Biological Process	GO:0022602	Ovulation cycle process	-4.85503	-3.115	10/49
18_Member	GO Biological Process	GO:0042698	Ovulation cycle	-4.67165	-2.955	11/62
18_Member	GO Biological Process	GO:0007548	Sex differentiation	-4.23232	-2.602	26/290
18_Member	GO Biological Process	GO:0007292	Female gamete generation	-3.69325	-2.159	16/149
18_Member	GO Biological Process	GO:0001542	Ovulation from ovarian follicle	-2.79851	-1.473	4/14
19_Summary	GO Biological Process	GO:0048589	Developmental growth	-9.66573	-7.110	69/795

19_Member	GO Biological Process	GO:0048589	Developmental growth	-9.66573	-7.110	69/795
19_Member	GO Biological Process	GO:0040008	Regulation of growth	-9.38995	-6.867	64/721
19_Member	GO Biological Process	GO:0001558	Regulation of cell growth	-9.28296	-6.791	46/434
19_Member	GO Biological Process	GO:0045926	Negative regulation of growth	-8.7566	-6.351	33/260
19_Member	GO Biological Process	GO:0016049	Cell growth	-8.63557	-6.256	50/518
19_Member	GO Biological Process	GO:0030308	Negative regulation of cell growth	-7.47296	-5.227	26/195
19_Member	GO Biological Process	GO:0048638	Regulation of developmental growth	-4.03444	-2.440	32/403
19_Member	GO Biological Process	GO:0048640	Negative regulation of developmental growth	-3.42074	-1.944	14/127
19_Member	GO Biological Process	GO:0048588	Developmental cell growth	-2.52341	-1.278	20/263
20_Summary	GO Biological Process	GO:0098609	Cell-cell adhesion	-9.56105	-7.014	66/748
20_Member	GO Biological Process	GO:0098609	Cell-cell adhesion	-9.56105	-7.014	66/748
20_Member	GO Biological Process	GO:0030155	Regulation of cell adhesion	-9.34215	-6.842	63/706
20_Member	GO Biological Process	GO:0022407	Regulation of cell-cell adhesion	-5.80579	-3.837	37/411
20_Member	GO Biological Process	GO:0002683	Negative regulation of immune system process	-5.73412	-3.783	41/482
20_Member	GO Biological Process	GO:0045785	Positive regulation of cell adhesion	-5.09043	-3.302	36/424

20_Member	GO Biological Process	GO:0007159	Leukocyte cell-cell adhesion	-4.85478	-3.115	30/332
20_Member	GO Biological Process	GO:0007162	Negative regulation of cell adhesion	-4.71285	-2.988	27/288
20_Member	GO Biological Process	GO:0070661	Leukocyte proliferation	-4.32367	-2.673	29/337
20_Member	GO Biological Process	GO:0050865	Regulation of cell activation	-3.94797	-2.363	48/710
20_Member	GO Biological Process	GO:0022409	Positive regulation of cell-cell adhesion	-3.85276	-2.291	23/255
20_Member	GO Biological Process	GO:0022408	Negative regulation of cell-cell adhesion	-3.42545	-1.944	18/189
20_Member	GO Biological Process	GO:0002694	Regulation of leukocyte activation	-3.42368	-1.944	44/668
20_Member	GO Biological Process	GO:0070663	Regulation of leukocyte proliferation	-3.39237	-1.922	21/240
20_Member	GO Biological Process	GO:0050866	Negative regulation of cell activation	-3.35432	-1.889	19/208
20_Member	GO Biological Process	GO:0050863	Regulation of T cell activation	-3.31971	-1.863	25/313
20_Member	GO Biological Process	GO:1903037	Regulation of leukocyte cell-cell adhesion	-3.28243	-1.835	24/297
20_Member	GO Biological Process	GO:0042110	T cell activation	-3.19387	-1.775	35/507
20_Member	GO Biological Process	GO:0002695	Negative regulation of leukocyte activation	-3.03912	-1.655	17/187
20_Member	GO Biological Process	GO:0050670	Regulation of lymphocyte proliferation	-2.91797	-1.564	19/226
20_Member	GO Biological Process	GO:0042098	T cell proliferation	-2.91237	-1.559	18/209
20_Member	GO Biological Process	GO:0032944	Regulation of mononuclear cell proliferation	-2.85097	-1.512	19/229

20_Member	GO Biological Process	GO:0046651	Lymphocyte proliferation	-2.62581	-1.349	23/313
20_Member	GO Biological Process	GO:0050868	Negative regulation of T cell activation	-2.61619	-1.341	12/121
20_Member	GO Biological Process	GO:0042129	Regulation of T cell proliferation	-2.59666	-1.328	15/171
20_Member	GO Biological Process	GO:0032943	Mononuclear cell proliferation	-2.57364	-1.309	23/316
20_Member	GO Biological Process	GO:0051250	Negative regulation of lymphocyte activation	-2.55018	-1.302	14/156
20_Member	GO Biological Process	GO:1903038	Negative regulation of leukocyte cell-cell adhesion	-2.28079	-1.101	12/133
20_Member	GO Biological Process	GO:0042130	Negative regulation of T cell proliferation	-2.20261	-1.045	8/72
20_Member	GO Biological Process	GO:1903039	Positive regulation of leukocyte cell-cell adhesion	-2.13532	-0.993	16/210
20_Member	GO Biological Process	GO:0051249	Regulation of lymphocyte activation	-2.1313	-0.993	34/568
20_Member	GO Biological Process	GO:0070664	Negative regulation of leukocyte proliferation	-2.08396	-0.954	9/91

GO, gene ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes.