

Supplementary Table 14. *Enriched pathways of Pattern III genes* . Columns are the same as Table S10.

path	desc	p	m	P	M	nrich	log2FC	pval	fdr
GO:0018108	peptidyl-tyrosine phosphorylation	6	100	161	17583	6.55	2.71	3.71E-05	1.41E-02
GO:0018212	peptidyl-tyrosine modification	6	100	163	17583	6.47	2.69	4.02E-05	1.46E-02
GO:0030534	adult behavior	5	100	143	17583	6.15	2.62	1.66E-04	2.73E-02
GO:0030162	regulation of proteolysis	12	100	711	17583	2.97	1.57	1.93E-04	2.73E-02
GO:0030155	regulation of cell adhesion	12	100	778	17583	2.71	1.44	4.58E-04	2.73E-02
GO:0051246	regulation of protein metabolic process	26	100	2494	17583	1.83	0.87	5.62E-04	2.73E-02
GO:0031399	regulation of protein modification process	18	100	1495	17583	2.12	1.08	6.88E-04	2.73E-02
GO:0007626	locomotory behavior	5	100	195	17583	4.51	2.17	8.66E-04	2.73E-02
GO:0045862	positive regulation of proteolysis	7	100	359	17583	3.43	1.78	1.02E-03	2.73E-02
GO:0030198	extracellular matrix organization	6	100	278	17583	3.79	1.92	1.05E-03	2.73E-02
GO:0043062	extracellular structure organization	6	100	279	17583	3.78	1.92	1.07E-03	2.73E-02
GO:0045229	external encapsulating structure organization	6	100	281	17583	3.75	1.91	1.12E-03	2.73E-02
GO:0080090	regulation of primary metabolic process	47	100	5782	17583	1.43	0.52	1.17E-03	2.73E-02
GO:0051171	regulation of nitrogen compound metabolic process	46	100	5628	17583	1.44	0.52	1.21E-03	2.73E-02
GO:0048193	Golgi vesicle transport	6	100	291	17583	3.63	1.86	1.36E-03	2.73E-02
GO:0010810	regulation of cell-substrate adhesion	5	100	215	17583	4.09	2.03	1.43E-03	2.73E-02
GO:1901215	negative regulation of neuron death	5	100	215	17583	4.09	2.03	1.43E-03	2.73E-02
GO:0045785	positive regulation of cell adhesion	8	100	474	17583	2.97	1.57	1.52E-03	2.73E-02
GO:0051173	positive regulation of nitrogen compound metabolic process	29	100	3112	17583	1.64	0.71	1.76E-03	2.73E-02
GO:0010468	regulation of gene expression	40	100	4813	17583	1.46	0.55	2.17E-03	2.73E-02
GO:0044089	positive regulation of cellular component biogenesis	8	100	503	17583	2.80	1.48	2.27E-03	2.73E-02
GO:0010556	regulation of macromolecule biosynthetic process	34	100	3907	17583	1.53	0.61	2.33E-03	2.73E-02
GO:0060255	regulation of macromolecule metabolic process	48	100	6147	17583	1.37	0.46	2.61E-03	2.73E-02
GO:0010604	positive regulation of macromolecule metabolic process	31	100	3487	17583	1.56	0.64	2.66E-03	2.73E-02
GO:0031325	positive regulation of cellular metabolic process	28	100	3060	17583	1.61	0.69	2.81E-03	2.73E-02
GO:0009410	response to xenobiotic stimulus	7	100	424	17583	2.90	1.54	2.88E-03	2.73E-02
GO:0051094	positive regulation of developmental process	15	100	1317	17583	2.00	1.00	3.02E-03	2.73E-02
GO:1903320	regulation of protein modification by small protein conjugati	5	100	251	17583	3.50	1.81	3.11E-03	2.73E-02

GO:0051247	positive regulation of protein metabolic process	16	100	1449	17583	1.94	0.96	3.18E-03	2.73E-02
GO:0051090	regulation of DNA-binding transcription factor activity	7	100	434	17583	2.84	1.50	3.32E-03	2.73E-02
GO:0030036	actin cytoskeleton organization	8	100	539	17583	2.61	1.38	3.59E-03	2.73E-02
GO:0044087	regulation of cellular component biogenesis	12	100	981	17583	2.15	1.10	3.68E-03	2.73E-02
GO:0048522	positive regulation of cellular process	44	100	5593	17583	1.38	0.47	3.81E-03	2.73E-02
GO:0006338	chromatin remodeling	6	100	354	17583	2.98	1.58	4.08E-03	2.73E-02
GO:0090092	regulation of transmembrane receptor protein serine/threor	5	100	274	17583	3.21	1.68	4.76E-03	2.73E-02
GO:0050804	modulation of chemical synaptic transmission	7	100	462	17583	2.66	1.41	4.83E-03	2.73E-02
GO:0099177	regulation of trans-synaptic signaling	7	100	463	17583	2.66	1.41	4.90E-03	2.73E-02
GO:0016043	cellular component organization	43	100	5509	17583	1.37	0.46	5.09E-03	2.73E-02
GO:0009893	positive regulation of metabolic process	32	100	3796	17583	1.48	0.57	5.39E-03	2.73E-02
GO:0022407	regulation of cell-cell adhesion	7	100	477	17583	2.58	1.37	5.83E-03	2.79E-02
GO:0048871	multicellular organismal homeostasis	8	100	581	17583	2.42	1.28	5.84E-03	2.79E-02
GO:0009889	regulation of biosynthetic process	34	100	4122	17583	1.45	0.54	5.85E-03	2.80E-02
GO:0051172	negative regulation of nitrogen compound metabolic proces	22	100	2357	17583	1.64	0.71	6.03E-03	2.89E-02
GO:0071840	cellular component organization or biogenesis	44	100	5719	17583	1.35	0.44	6.04E-03	2.89E-02
GO:0042592	homeostatic process	15	100	1417	17583	1.86	0.90	6.12E-03	2.93E-02
GO:0031323	regulation of cellular metabolic process	43	100	5561	17583	1.36	0.44	6.14E-03	2.94E-02
GO:0036211	protein modification process	24	100	2645	17583	1.60	0.67	6.17E-03	2.95E-02
GO:0009892	negative regulation of metabolic process	26	100	2934	17583	1.56	0.64	6.17E-03	2.95E-02
GO:0051130	positive regulation of cellular component organization	12	100	1058	17583	1.99	1.00	6.88E-03	3.24E-02
GO:0030029	actin filament-based process	8	100	600	17583	2.34	1.23	7.15E-03	3.37E-02
GO:0006468	protein phosphorylation	9	100	712	17583	2.22	1.15	7.26E-03	3.41E-02
GO:0006355	regulation of DNA-templated transcription	29	100	3420	17583	1.49	0.58	7.44E-03	3.41E-02
GO:0051252	regulation of RNA metabolic process	31	100	3724	17583	1.46	0.55	7.50E-03	3.41E-02
GO:1903506	regulation of nucleic acid-templated transcription	29	100	3422	17583	1.49	0.58	7.50E-03	3.41E-02
GO:0071705	nitrogen compound transport	16	100	1581	17583	1.78	0.83	7.60E-03	3.41E-02
GO:2001141	regulation of RNA biosynthetic process	29	100	3431	17583	1.49	0.57	7.79E-03	3.41E-02
GO:0000122	negative regulation of transcription by RNA polymerase II	11	100	959	17583	2.02	1.01	8.17E-03	3.41E-02
GO:0042325	regulation of phosphorylation	13	100	1207	17583	1.89	0.92	8.26E-03	3.41E-02
GO:0031326	regulation of cellular biosynthetic process	33	100	4057	17583	1.43	0.52	8.32E-03	3.41E-02

GO:0010605	negative regulation of macromolecule metabolic process	24	100	2717	17583	1.55	0.64	8.67E-03	3.41E-02
GO:0043412	macromolecule modification	25	100	2865	17583	1.53	0.62	8.76E-03	3.41E-02
GO:0019222	regulation of metabolic process	49	100	6669	17583	1.29	0.37	9.06E-03	3.41E-02
GO:0048468	cell development	20	100	2160	17583	1.63	0.70	9.23E-03	3.41E-02
GO:0031331	positive regulation of cellular catabolic process	6	100	413	17583	2.55	1.35	9.25E-03	3.41E-02
GO:0022409	positive regulation of cell-cell adhesion	5	100	316	17583	2.78	1.48	9.34E-03	3.41E-02
GO:0009628	response to abiotic stimulus	12	100	1106	17583	1.91	0.93	9.81E-03	3.41E-02
GO:1901214	regulation of neuron death	5	100	320	17583	2.75	1.46	9.90E-03	3.41E-02
GO:1903131	mononuclear cell differentiation	5	100	325	17583	2.71	1.44	1.06E-02	3.41E-02
GO:0048731	system development	29	100	3507	17583	1.45	0.54	1.06E-02	3.41E-02
GO:0045597	positive regulation of cell differentiation	10	100	873	17583	2.01	1.01	1.07E-02	3.41E-02
GO:0007010	cytoskeleton organization	13	100	1247	17583	1.83	0.87	1.08E-02	3.41E-02
GO:0010558	negative regulation of macromolecule biosynthetic process	15	100	1510	17583	1.75	0.80	1.10E-02	3.41E-02
GO:0010557	positive regulation of macromolecule biosynthetic process	18	100	1920	17583	1.65	0.72	1.12E-02	3.41E-02
GO:0035556	intracellular signal transduction	15	100	1517	17583	1.74	0.80	1.15E-02	3.44E-02
GO:0048518	positive regulation of biological process	46	100	6241	17583	1.30	0.37	1.15E-02	3.46E-02
GO:0016310	phosphorylation	10	100	897	17583	1.96	0.97	1.29E-02	3.85E-02
GO:0030097	hemopoiesis	8	100	663	17583	2.12	1.09	1.32E-02	3.93E-02
GO:0019219	regulation of nucleobase-containing compound metabolic p	32	100	4030	17583	1.40	0.48	1.35E-02	3.99E-02
GO:0022008	neurogenesis	13	100	1281	17583	1.78	0.84	1.35E-02	4.00E-02
GO:0043161	proteasome-mediated ubiquitin-dependent protein cataboli	5	100	345	17583	2.55	1.35	1.39E-02	4.07E-02
GO:0042327	positive regulation of phosphorylation	9	100	789	17583	2.01	1.00	1.42E-02	4.07E-02
GO:0019538	protein metabolic process	31	100	3891	17583	1.40	0.49	1.43E-02	4.07E-02
GO:0031346	positive regulation of cell projection organization	5	100	347	17583	2.53	1.34	1.43E-02	4.07E-02
GO:0007275	multicellular organism development	31	100	3903	17583	1.40	0.48	1.49E-02	4.07E-02
GO:0031327	negative regulation of cellular biosynthetic process	15	100	1566	17583	1.68	0.75	1.52E-02	4.07E-02
GO:0045786	negative regulation of cell cycle	5	100	352	17583	2.50	1.32	1.53E-02	4.07E-02
GO:0045892	negative regulation of DNA-templated transcription	13	100	1303	17583	1.75	0.81	1.55E-02	4.07E-02
GO:0045595	regulation of cell differentiation	15	100	1570	17583	1.68	0.75	1.55E-02	4.07E-02
GO:1903507	negative regulation of nucleic acid-templated transcription	13	100	1305	17583	1.75	0.81	1.56E-02	4.07E-02
GO:1902679	negative regulation of RNA biosynthetic process	13	100	1307	17583	1.75	0.81	1.58E-02	4.07E-02

GO:0030182	neuron differentiation	11	100	1052	17583	1.84	0.88	1.61E-02	4.07E-02
GO:0006996	organelle organization	25	100	3011	17583	1.46	0.55	1.63E-02	4.07E-02
GO:1903037	regulation of leukocyte cell-cell adhesion	5	100	361	17583	2.44	1.28	1.71E-02	4.09E-02
GO:0009890	negative regulation of biosynthetic process	15	100	1596	17583	1.65	0.72	1.79E-02	4.27E-02
GO:0001932	regulation of protein phosphorylation	11	100	1068	17583	1.81	0.86	1.80E-02	4.29E-02
GO:0006357	regulation of transcription by RNA polymerase II	22	100	2592	17583	1.49	0.58	1.81E-02	4.32E-02
GO:0051098	regulation of binding	5	100	368	17583	2.39	1.26	1.86E-02	4.44E-02
GO:0071363	cellular response to growth factor stimulus	6	100	475	17583	2.22	1.15	1.87E-02	4.46E-02
GO:0023051	regulation of signaling	27	100	3352	17583	1.42	0.50	1.89E-02	4.51E-02
GO:0071345	cellular response to cytokine stimulus	8	100	705	17583	2.00	1.00	1.89E-02	4.52E-02
GO:0007267	cell-cell signaling	11	100	1077	17583	1.80	0.84	1.91E-02	4.54E-02
GO:0018193	peptidyl-amino acid modification	9	100	828	17583	1.91	0.93	1.93E-02	4.60E-02
GO:0010646	regulation of cell communication	27	100	3362	17583	1.41	0.50	1.96E-02	4.67E-02
GO:0031400	negative regulation of protein modification process	6	100	480	17583	2.20	1.14	1.97E-02	4.68E-02
GO:0048666	neuron development	9	100	832	17583	1.90	0.93	1.99E-02	4.71E-02
GO:0001934	positive regulation of protein phosphorylation	8	100	711	17583	1.98	0.98	1.99E-02	4.71E-02
GO:0010498	proteasomal protein catabolic process	5	100	376	17583	2.34	1.23	2.04E-02	4.71E-02
GO:0019220	regulation of phosphate metabolic process	13	100	1355	17583	1.69	0.75	2.10E-02	4.71E-02
GO:0051174	regulation of phosphorus metabolic process	13	100	1356	17583	1.69	0.75	2.11E-02	4.71E-02
GO:0031401	positive regulation of protein modification process	10	100	967	17583	1.82	0.86	2.14E-02	4.71E-02
GO:0007610	behavior	7	100	603	17583	2.04	1.03	2.16E-02	4.71E-02
GO:0009891	positive regulation of biosynthetic process	18	100	2055	17583	1.54	0.62	2.18E-02	4.71E-02
GO:0006351	DNA-templated transcription	7	100	606	17583	2.03	1.02	2.21E-02	4.71E-02
GO:0043170	macromolecule metabolic process	42	100	5792	17583	1.28	0.35	2.23E-02	4.71E-02
GO:0097659	nucleic acid-templated transcription	7	100	607	17583	2.03	1.02	2.23E-02	4.71E-02
GO:0009991	response to extracellular stimulus	6	100	497	17583	2.12	1.09	2.33E-02	4.85E-02
GO:0031324	negative regulation of cellular metabolic process	19	100	2218	17583	1.51	0.59	2.37E-02	4.95E-02
GO:0032774	RNA biosynthetic process	7	100	617	17583	1.99	1.00	2.43E-02	5.07E-02
GO:0071407	cellular response to organic cyclic compound	6	100	502	17583	2.10	1.07	2.44E-02	5.08E-02
GO:0009966	regulation of signal transduction	24	100	2966	17583	1.42	0.51	2.45E-02	5.10E-02
GO:0014070	response to organic cyclic compound	9	100	864	17583	1.83	0.87	2.50E-02	5.20E-02

GO:0016192	vesicle-mediated transport	13	100	1387	17583	1.65	0.72	2.51E-02	5.20E-02
GO:0048699	generation of neurons	11	100	1121	17583	1.73	0.79	2.51E-02	5.22E-02
GO:0070848	response to growth factor	6	100	506	17583	2.08	1.06	2.53E-02	5.26E-02
GO:0051248	negative regulation of protein metabolic process	10	100	994	17583	1.77	0.82	2.56E-02	5.30E-02
GO:0045937	positive regulation of phosphate metabolic process	9	100	867	17583	1.83	0.87	2.56E-02	5.30E-02
GO:0010562	positive regulation of phosphorus metabolic process	9	100	867	17583	1.83	0.87	2.56E-02	5.30E-02
GO:0051128	regulation of cellular component organization	20	100	2384	17583	1.48	0.56	2.58E-02	5.34E-02
GO:0071702	organic substance transport	17	100	1956	17583	1.53	0.61	2.66E-02	5.34E-02
GO:0009896	positive regulation of catabolic process	6	100	512	17583	2.06	1.04	2.68E-02	5.34E-02
GO:0032103	positive regulation of response to external stimulus	6	100	518	17583	2.04	1.03	2.83E-02	5.36E-02
GO:0002521	leukocyte differentiation	5	100	406	17583	2.17	1.11	2.84E-02	5.38E-02
GO:0007167	enzyme-linked receptor protein signaling pathway	7	100	637	17583	1.93	0.95	2.87E-02	5.44E-02
GO:0051254	positive regulation of RNA metabolic process	16	100	1833	17583	1.53	0.62	2.90E-02	5.50E-02
GO:0051253	negative regulation of RNA metabolic process	13	100	1416	17583	1.61	0.69	2.93E-02	5.54E-02
GO:0046903	secretion	6	100	524	17583	2.01	1.01	2.99E-02	5.65E-02
GO:0052547	regulation of peptidase activity	5	100	412	17583	2.13	1.09	3.02E-02	5.70E-02
GO:0032940	secretion by cell	5	100	412	17583	2.13	1.09	3.02E-02	5.70E-02
GO:1903508	positive regulation of nucleic acid-templated transcription	15	100	1700	17583	1.55	0.63	3.02E-02	5.70E-02
GO:0045893	positive regulation of DNA-templated transcription	15	100	1700	17583	1.55	0.63	3.02E-02	5.70E-02
GO:0006810	transport	29	100	3800	17583	1.34	0.42	3.07E-02	5.79E-02
GO:1902680	positive regulation of RNA biosynthetic process	15	100	1706	17583	1.55	0.63	3.11E-02	5.86E-02
GO:0048519	negative regulation of biological process	38	100	5250	17583	1.27	0.35	3.13E-02	5.90E-02
GO:0031328	positive regulation of cellular biosynthetic process	17	100	2016	17583	1.48	0.57	3.46E-02	6.09E-02
GO:0050793	regulation of developmental process	20	100	2459	17583	1.43	0.52	3.49E-02	6.14E-02
GO:0042391	regulation of membrane potential	5	100	427	17583	2.06	1.04	3.50E-02	6.16E-02
GO:0033036	macromolecule localization	19	100	2323	17583	1.44	0.52	3.66E-02	6.43E-02
GO:0045935	positive regulation of nucleobase-containing compound me	17	100	2034	17583	1.47	0.56	3.73E-02	6.49E-02
GO:0034097	response to cytokine	8	100	800	17583	1.76	0.81	3.83E-02	6.49E-02
GO:0007399	nervous system development	18	100	2189	17583	1.45	0.53	3.86E-02	6.49E-02
GO:0048523	negative regulation of cellular process	34	100	4675	17583	1.28	0.35	3.89E-02	6.49E-02
GO:0016567	protein ubiquitination	7	100	681	17583	1.81	0.85	4.02E-02	6.65E-02

GO:0070887	cellular response to chemical stimulus	19	100	2350	17583	1.42	0.51	4.06E-02	6.73E-02
GO:0000226	microtubule cytoskeleton organization	6	100	561	17583	1.88	0.91	4.09E-02	6.76E-02
GO:0051960	regulation of nervous system development	5	100	454	17583	1.94	0.95	4.50E-02	7.13E-02
GO:0006511	ubiquitin-dependent protein catabolic process	6	100	574	17583	1.84	0.88	4.53E-02	7.17E-02
GO:0002831	regulation of response to biotic stimulus	5	100	455	17583	1.93	0.95	4.54E-02	7.19E-02
GO:0001775	cell activation	7	100	702	17583	1.75	0.81	4.66E-02	7.38E-02
GO:0007155	cell adhesion	9	100	963	17583	1.64	0.72	4.71E-02	7.45E-02
GO:0046649	lymphocyte activation	5	100	460	17583	1.91	0.93	4.74E-02	7.49E-02
GO:0045321	leukocyte activation	6	100	580	17583	1.82	0.86	4.74E-02	7.49E-02
GO:2000026	regulation of multicellular organismal development	12	100	1374	17583	1.54	0.62	4.75E-02	7.51E-02
GO:0019941	modification-dependent protein catabolic process	6	100	584	17583	1.81	0.85	4.89E-02	7.64E-02
GO:0099536	synaptic signaling	5	100	464	17583	1.89	0.92	4.90E-02	7.64E-02
GO:0051234	establishment of localization	29	100	3956	17583	1.29	0.37	4.97E-02	7.64E-02
GO:0045944	positive regulation of transcription by RNA polymerase II	11	100	1246	17583	1.55	0.63	5.01E-02	7.65E-02
GO:0031667	response to nutrient levels	5	100	467	17583	1.88	0.91	5.03E-02	7.68E-02
GO:0010720	positive regulation of cell development	5	100	467	17583	1.88	0.91	5.03E-02	7.68E-02
GO:0061024	membrane organization	8	100	844	17583	1.67	0.74	5.08E-02	7.75E-02
GO:0140352	export from cell	5	100	472	17583	1.86	0.90	5.25E-02	7.99E-02
GO:0006796	phosphate-containing compound metabolic process	15	100	1826	17583	1.44	0.53	5.26E-02	8.01E-02
GO:0043632	modification-dependent macromolecule catabolic process	6	100	596	17583	1.77	0.82	5.34E-02	8.12E-02
GO:0045934	negative regulation of nucleobase-containing compound m	13	100	1541	17583	1.48	0.57	5.34E-02	8.13E-02
GO:0060284	regulation of cell development	8	100	856	17583	1.64	0.72	5.46E-02	8.21E-02
GO:0045184	establishment of protein localization	11	100	1264	17583	1.53	0.61	5.48E-02	8.21E-02
GO:0065009	regulation of molecular function	20	100	2588	17583	1.36	0.44	5.57E-02	8.25E-02
GO:0006325	chromatin organization	6	100	608	17583	1.74	0.80	5.82E-02	8.60E-02
GO:0006793	phosphorus metabolic process	15	100	1852	17583	1.42	0.51	5.84E-02	8.63E-02
GO:0044092	negative regulation of molecular function	9	100	1004	17583	1.58	0.66	5.92E-02	8.74E-02
GO:0043065	positive regulation of apoptotic process	5	100	488	17583	1.80	0.85	5.98E-02	8.75E-02
GO:0006807	nitrogen compound metabolic process	45	100	6674	17583	1.19	0.25	6.07E-02	8.75E-02
GO:0032446	protein modification by small protein conjugation	7	100	751	17583	1.64	0.71	6.41E-02	9.21E-02
GO:0030030	cell projection organization	10	100	1158	17583	1.52	0.60	6.44E-02	9.26E-02

GO:0000278	mitotic cell cycle	6	100	624	17583	1.69	0.76	6.50E-02	9.31E-02
GO:0043068	positive regulation of programmed cell death	5	100	503	17583	1.75	0.81	6.71E-02	9.44E-02
GO:0008104	protein localization	15	100	1892	17583	1.39	0.48	6.82E-02	9.58E-02
GO:0071396	cellular response to lipid	5	100	508	17583	1.73	0.79	6.97E-02	9.78E-02
GO:0070727	cellular macromolecule localization	15	100	1898	17583	1.39	0.47	6.97E-02	9.79E-02
GO:0010629	negative regulation of gene expression	8	100	900	17583	1.56	0.64	7.03E-02	9.84E-02
GO:0015031	protein transport	10	100	1176	17583	1.50	0.58	7.03E-02	9.84E-02
GO:0007417	central nervous system development	9	100	1041	17583	1.52	0.60	7.18E-02	9.88E-02
GO:0034330	cell junction organization	5	100	512	17583	1.72	0.78	7.18E-02	9.88E-02
GO:0043086	negative regulation of catalytic activity	6	100	640	17583	1.65	0.72	7.23E-02	9.95E-02
GO:0016070	RNA metabolic process	13	100	1619	17583	1.41	0.50	7.42E-02	1.02E-01
GO:0051640	organelle localization	5	100	517	17583	1.70	0.77	7.45E-02	1.02E-01
GO:0051603	proteolysis involved in protein catabolic process	6	100	645	17583	1.64	0.71	7.47E-02	1.03E-01
GO:0044265	cellular macromolecule catabolic process	7	100	786	17583	1.57	0.65	7.89E-02	1.06E-01
GO:0051240	positive regulation of multicellular organismal process	12	100	1492	17583	1.41	0.50	8.01E-02	1.08E-01
GO:0060627	regulation of vesicle-mediated transport	5	100	528	17583	1.67	0.74	8.06E-02	1.09E-01
GO:0120035	regulation of plasma membrane bounded cell projection org	6	100	658	17583	1.60	0.68	8.11E-02	1.09E-01
GO:0051493	regulation of cytoskeleton organization	5	100	529	17583	1.66	0.73	8.11E-02	1.09E-01
GO:0031329	regulation of cellular catabolic process	7	100	797	17583	1.54	0.63	8.39E-02	1.11E-01
GO:0042221	response to chemical	27	100	3828	17583	1.24	0.31	8.47E-02	1.12E-01
GO:0048856	anatomical structure development	35	100	5143	17583	1.20	0.26	8.59E-02	1.14E-01
GO:0009967	positive regulation of signal transduction	12	100	1511	17583	1.40	0.48	8.65E-02	1.14E-01
GO:1901564	organonitrogen compound metabolic process	34	100	4982	17583	1.20	0.26	8.69E-02	1.14E-01
GO:0050778	positive regulation of immune response	6	100	671	17583	1.57	0.65	8.78E-02	1.15E-01
GO:0031344	regulation of cell projection organization	6	100	672	17583	1.57	0.65	8.83E-02	1.15E-01
GO:0098609	cell-cell adhesion	5	100	543	17583	1.62	0.70	8.93E-02	1.17E-01
GO:0051179	localization	31	100	4502	17583	1.21	0.28	8.99E-02	1.17E-01
GO:0044238	primary metabolic process	47	100	7194	17583	1.15	0.20	9.02E-02	1.18E-01
GO:0000904	cell morphogenesis involved in differentiation	5	100	551	17583	1.60	0.67	9.41E-02	1.22E-01
GO:0007507	heart development	5	100	555	17583	1.58	0.66	9.66E-02	1.25E-01
GO:0060322	head development	7	100	826	17583	1.49	0.58	9.81E-02	1.25E-01

GO:0070925	organelle assembly	7	100	827	17583	1.49	0.57	9.86E-02	1.26E-01
GO:0007166	cell surface receptor signaling pathway	16	100	2149	17583	1.31	0.39	9.88E-02	1.26E-01
GO:0051336	regulation of hydrolase activity	8	100	968	17583	1.45	0.54	9.94E-02	1.27E-01
GO:0120036	plasma membrane bounded cell projection organization	9	100	1112	17583	1.42	0.51	1.00E-01	1.28E-01
GO:0008285	negative regulation of cell population proliferation	6	100	698	17583	1.51	0.60	1.03E-01	1.30E-01
GO:0051345	positive regulation of hydrolase activity	5	100	565	17583	1.56	0.64	1.03E-01	1.30E-01
GO:0065008	regulation of biological quality	20	100	2788	17583	1.26	0.33	1.04E-01	1.31E-01
GO:0010942	positive regulation of cell death	5	100	569	17583	1.55	0.63	1.06E-01	1.33E-01
GO:0051641	cellular localization	19	100	2639	17583	1.27	0.34	1.06E-01	1.34E-01
GO:0051249	regulation of lymphocyte activation	5	100	577	17583	1.52	0.61	1.11E-01	1.38E-01
GO:0010467	gene expression	16	100	2186	17583	1.29	0.36	1.11E-01	1.38E-01
GO:0071310	cellular response to organic substance	13	100	1728	17583	1.32	0.40	1.11E-01	1.39E-01
GO:0009719	response to endogenous stimulus	11	100	1431	17583	1.35	0.43	1.12E-01	1.40E-01
GO:0009894	regulation of catabolic process	8	100	995	17583	1.41	0.50	1.13E-01	1.40E-01
GO:0023052	signaling	34	100	5106	17583	1.17	0.23	1.15E-01	1.42E-01
GO:0043549	regulation of kinase activity	6	100	723	17583	1.46	0.55	1.18E-01	1.45E-01
GO:0050865	regulation of cell activation	6	100	723	17583	1.46	0.55	1.18E-01	1.45E-01
GO:0048609	multicellular organismal reproductive process	7	100	869	17583	1.42	0.50	1.21E-01	1.49E-01
GO:0044237	cellular metabolic process	42	100	6489	17583	1.14	0.19	1.23E-01	1.50E-01
GO:0071495	cellular response to endogenous stimulus	9	100	1166	17583	1.36	0.44	1.26E-01	1.53E-01
GO:0071704	organic substance metabolic process	48	100	7534	17583	1.12	0.16	1.26E-01	1.54E-01
GO:0032501	multicellular organismal process	41	100	6337	17583	1.14	0.19	1.28E-01	1.55E-01
GO:0051241	negative regulation of multicellular organismal process	8	100	1028	17583	1.37	0.45	1.30E-01	1.57E-01
GO:0048583	regulation of response to stimulus	27	100	4008	17583	1.18	0.24	1.31E-01	1.58E-01
GO:0090304	nucleic acid metabolic process	16	100	2247	17583	1.25	0.32	1.33E-01	1.60E-01
GO:0070647	protein modification by small protein conjugation or removal	7	100	893	17583	1.38	0.46	1.36E-01	1.62E-01
GO:0051239	regulation of multicellular organismal process	19	100	2734	17583	1.22	0.29	1.38E-01	1.64E-01
GO:0048513	animal organ development	20	100	2895	17583	1.21	0.28	1.38E-01	1.65E-01
GO:0022402	cell cycle process	7	100	899	17583	1.37	0.45	1.39E-01	1.66E-01
GO:0016477	cell migration	7	100	900	17583	1.37	0.45	1.40E-01	1.67E-01
GO:0030163	protein catabolic process	6	100	760	17583	1.39	0.47	1.42E-01	1.69E-01

GO:0030154	cell differentiation	24	100	3556	17583	1.19	0.25	1.43E-01	1.70E-01
GO:0033043	regulation of organelle organization	9	100	1199	17583	1.32	0.40	1.44E-01	1.70E-01
GO:0048878	chemical homeostasis	7	100	908	17583	1.36	0.44	1.45E-01	1.71E-01
GO:0032504	multicellular organism reproduction	7	100	910	17583	1.35	0.44	1.46E-01	1.73E-01
GO:0044093	positive regulation of molecular function	11	100	1513	17583	1.28	0.35	1.50E-01	1.76E-01
GO:0048869	cellular developmental process	24	100	3579	17583	1.18	0.24	1.51E-01	1.77E-01
GO:0050776	regulation of immune response	7	100	920	17583	1.34	0.42	1.53E-01	1.78E-01
GO:0007420	brain development	6	100	778	17583	1.36	0.44	1.54E-01	1.80E-01
GO:0050790	regulation of catalytic activity	13	100	1838	17583	1.24	0.31	1.58E-01	1.84E-01
GO:0023056	positive regulation of signaling	12	100	1684	17583	1.25	0.33	1.59E-01	1.84E-01
GO:0010647	positive regulation of cell communication	12	100	1685	17583	1.25	0.32	1.59E-01	1.85E-01
GO:0007154	cell communication	34	100	5269	17583	1.13	0.18	1.60E-01	1.86E-01
GO:1902531	regulation of intracellular signal transduction	12	100	1699	17583	1.24	0.31	1.66E-01	1.92E-01
GO:0003006	developmental process involved in reproduction	7	100	944	17583	1.30	0.38	1.69E-01	1.94E-01
