

Supplementary Materials:

A Time-Course Study of the Expression Level of Synaptic Plasticity-Associated Genes in Un-Lesioned Spinal Cord and Brain Areas in a Rat Model of Spinal Cord Injury: A Bioinformatic Approach.

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1 Supplementary Tables

1.1 RT² Profiler PCR Array

Supplementary Table S1: PARN-126ZA Genes Array Table.

	Position	Unigene	Refseq	Symbol	Description
0	A01	Rn.42924	NM_019254	Adam10	ADAM metallopeptidase domain 10
1	A02	Rn.214145	NM_001107239	Adcy1	Adenylate cyclase 1 (brain)
2	A03	Rn.10382	NM_017142	Adcy8	Adenylate cyclase 8 (brain)
3	A04	Rn.11422	NM_033230	Akt1	V-akt murine thymoma viral oncogene homolog 1
4	A05	Rn.10086	NM_019361	Arc	Activity-regulated cytoskeleton-associated pro...
5	A06	Rn.11266	NM_012513	Bdnf	Brain-derived neurotrophic factor
6	A07	Rn.107499	NM_012920	Camk2a	Calcium/calmodulin-dependent protein kinase II...
7	A08	Rn.10961	NM_133605	Camk2g	Calcium/calmodulin-dependent protein kinase II...
8	A09	Rn.23200	NM_031333	Cdh2	Cadherin 2
9	A10	Rn.6479	NM_024125	Cebpb	CCAAT/enhancer binding protein (C/EBP), beta
10	A11	Rn.6975	NM_013154	Cebpd	CCAAT/enhancer binding protein (C/EBP), delta
11	A12	Rn.89774	NM_012784	Cnr1	Cannabinoid receptor 1 (brain)
12	B01	Rn.90061	NM_031017	Creb1	CAMP responsive element binding protein 1
13	B02	Rn.10251	NM_001110860	Crem	CAMP responsive element modulator
14	B03	Rn.9765	NM_019621	Dlg4	Discs, large homolog 4 (Drosophila)
15	B04	Rn.9096	NM_012551	Egr1	Early growth response 1
16	B05	Rn.89235	NM_053633	Egr2	Early growth response 2
17	B06	Rn.44371	NM_017086	Egr3	Early growth response 3
18	B07	Rn.31998	NM_019137	Egr4	Early growth response 4
19	B08	Rn.229866	NM_001127319	Ephb2	Eph receptor B2
20	B09	Rn.103750	NM_022197	Fos	FBJ osteosarcoma oncogene
21	B10	Rn.10368	NM_017295	Gabra5	Gamma-aminobutyric acid (GABA) A receptor, alp...
22	B11	Rn.11391	NM_013145	Gnai1	Guanine nucleotide binding protein (G protein)...
23	B12	Rn.29971	NM_031608	Gria1	Glutamate receptor, ionotropic, AMPA 1
24	C01	Rn.91361	NM_017261	Gria2	Glutamate receptor, ionotropic, AMPA 2
25	C02	Rn.74049	NM_032990	Gria3	Glutamate receptor, ionotropic, AMPA 3
26	C03	Rn.10938	NM_017263	Gria4	Glutamate receptor, ionotropic, AMPA 4
27	C04	Rn.9840	NM_017010	Grin1	Glutamate receptor, ionotropic, N-methyl D-asp...
28	C05	Rn.9710	NM_012573	Grin2a	Glutamate receptor, ionotropic, N-methyl D-asp...
29	C06	Rn.9711	NM_012574	Grin2b	Glutamate receptor, ionotropic, N-methyl D-asp...
30	C07	Rn.9709	NM_012575	Grin2c	Glutamate receptor, ionotropic, N-methyl D-asp...
31	C08	Rn.91209	NM_022797	Grin2d	Glutamate receptor, ionotropic, N-methyl D-asp...

Continuation of Table S1

	Position	Unigene	Refseq	Symbol	Description
32	C09	Rn.74240	NM_032069	Grip1	Glutamate receptor interacting protein 1
33	C10	Rn.87787	NM_017011	Grm1	Glutamate receptor, metabotropic 1
34	C11	Rn.9681	NM_001105711	Grm2	Glutamate receptor, metabotropic 2
35	C12	Rn.41715	NM_001105712	Grm3	Glutamate receptor, metabotropic 3
36	D01	Rn.89046	NM_022666	Grm4	Glutamate receptor, metabotropic 4
37	D02	Rn.29972	NM_017012	Grm5	Glutamate receptor, metabotropic 5
38	D03	Rn.10409	NM_031040	Grm7	Glutamate receptor, metabotropic 7
39	D04	Rn.44420	NM_022202	Grm8	Glutamate receptor, metabotropic 8
40	D05	Rn.37500	NM_031707	Homer1	Homer homolog 1 (Drosophila)
41	D06	Rn.228346	NM_178866	Igf1	Insulin-like growth factor 1
42	D07	Rn.9874	NM_017128	Inhba	Inhibin beta-A
43	D08	Rn.93714	NM_021835	Jun	Jun oncogene
44	D09	Rn.15806	NM_021836	Junb	Jun B proto-oncogene
45	D10	Rn.2398	NM_031135	Klf10	Kruppel-like factor 10
46	D11	Rn.34914	NM_053842	Mapk1	Mitogen activated protein kinase 1
47	D12	Rn.10209	NM_031055	Mmp9	Matrix metalloproteinase 9
48	E01	Rn.11283	NM_031521	Ncam1	Neural cell adhesion molecule 1
49	E02	Rn.2411	NM_001276711	Nfkb1	Nuclear factor of kappa light polypeptide gene...
50	E03	Rn.8395	NM_030867	Nfkbib	Nuclear factor of kappa light polypeptide gene...
51	E04	Rn.22168	NM_001277055	Ngf	Nerve growth factor (beta polypeptide)
52	E05	Rn.10980	NM_012610	Ngfr	Nerve growth factor receptor (TNFR superfamily...
53	E06	Rn.10573	NM_052799	Nos1	Nitric oxide synthase 1, neuronal
54	E07	Rn.162101	NM_001034199	Nptx2	Neuronal pentraxin 2
55	E08	Rn.10000	NM_024388	Nr4a1	Nuclear receptor subfamily 4, group A, member 1
56	E09	Rn.9715	NM_031073	Ntf3	Neurotrophin 3
57	E10	Rn.44225	NM_013184	Ntf4	Neurotrophin 4
58	E11	Rn.11246	NM_012731	Ntrk2	Neurotrophic tyrosine kinase, receptor, type 2
59	E12	Rn.23337	NM_022868	Pcdh8	Protocadherin 8
60	F01	Rn.24750	NM_053460	Pick1	Protein interacting with PRKCA 1
61	F02	Rn.34888	NM_017034	Pim1	Pim-1 oncogene
62	F03	Rn.107102	NM_013151	Plat	Plasminogen activator, tissue
63	F04	Rn.11243	NM_013187	Plcg1	Phospholipase C, gamma 1
64	F05	Rn.2024	NM_031527	Ppp1ca	Protein phosphatase 1, catalytic subunit, alph...
65	F06	Rn.1495	NM_022498	Ppp1cc	Protein phosphatase 1, catalytic subunit, gamm...
66	F07	Rn.73852	NM_130403	Ppp1r14a	Protein phosphatase 1, regulatory (inhibitor) ...
67	F08	Rn.1271	NM_017039	Ppp2ca	Protein phosphatase 2, catalytic subunit, alph...
68	F09	Rn.6866	NM_017041	Ppp3ca	Protein phosphatase 3, catalytic subunit, alph...

Continuation of Table S1

	Position	Unigene	Refseq	Symbol	Description
69	F10	Rn.86669	NM_001105713	Prkca	Protein kinase C, alpha
70	F11	Rn.9747	NM_012628	Prkcg	Protein kinase C, gamma
71	F12	Rn.204724	NM_001105731	Prkg1	Protein kinase, cGMP-dependent, type 1
72	G01	Rn.44409	NM_013018	Rab3a	RAB3A, member RAS oncogene family
73	G02	Rn.19480	NM_199267	Rela	V-rel reticuloendotheliosis viral oncogene hom...
74	G03	Rn.98353	NM_080394	Reln	Reelin
75	G04	NaN	XM_003750065	Kif17	Kinesin family member 17
76	G05	Rn.1892	NM_053453	Rgs2	Regulator of G-protein signaling 2
77	G06	Rn.859	NM_013216	Rheb	Ras homolog enriched in brain
78	G07	NaN	NM_001107627	Sirt1	Sirtuin (silent mating type information regula...
79	G08	Rn.1501	NM_001109302	Srf	Serum response factor (c-fos serum response el...
80	G09	Rn.42910	NM_021695	Synpo	Synaptopodin
81	G10	Rn.25754	NM_053819	Timp1	TIMP metalloproteinase inhibitor 1
82	G11	Rn.2275	NM_012675	Tnf	Tumor necrosis factor (TNF superfamily, member 2)
83	G12	Rn.2502	NM_013053	Ywhaq	Tyrosine 3-monooxygenase/tryptophan 5-monooxyg...
84	H01	Rn.94978	NM_031144	Actb	Actin, beta
85	H02	Rn.1868	NM_012512	B2m	Beta-2 microglobulin
86	H03	Rn.47	NM_012583	Hprt1	Hypoxanthine phosphoribosyltransferase 1
87	H04	Rn.107896	NM_017025	Ldha	Lactate dehydrogenase A
88	H05	Rn.973	NM_001007604	Rplp1	Ribosomal protein, large, P1
89	H06	NaN	U26919	RGDC	Rat Genomic DNA Contamination
90	H07	NaN	SA_00104	RTC	Reverse Transcription Control
91	H08	NaN	SA_00104	RTC	Reverse Transcription Control
92	H09	NaN	SA_00104	RTC	Reverse Transcription Control
93	H10	NaN	SA_00103	PPC	Positive PCR Control
94	H11	NaN	SA_00103	PPC	Positive PCR Control
95	H12	NaN	SA_00103	PPC	Positive PCR Control

1.2 GSEA Results Tables

Supplementary Table S2: SC rostral segment early (1 DPL peak) profile GSEA results.

Begin of Table S2								
	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
0	REACTOME_INTERLEUKIN_4_AND_INTERLEUKIN_13_SIGN...	R-RNO-6785807	8	0.922751	2.960325	0.000000	0.001343	0.001
1	REACTOME_SIGNALING_BY_INTERLEUKINS	R-RNO-449147	15	0.590450	2.482950	0.000000	0.022870	0.036
2	HALLMARK_TNFA_SIGNALING_VIA_NFKB	M5890	14	0.591473	2.428519	0.000000	0.020713	0.048
3	GOBP_NEGATIVE_REGULATION_OF_PEPTIDASE_ACTIVITY	GO:0010466	6	0.832010	2.357697	0.000000	0.026939	0.082
4	GOBP_OSTEOCLAST_DIFFERENTIATION	GO:0030316	6	0.807556	2.354578	0.000000	0.021834	0.082
5	REACTOME_TRANSCRIPTIONAL_REGULATION_OF_WHITE_A...	R-RNO-381340	6	0.807932	2.300164	0.000000	0.027823	0.125
6	GOBP_OSSIFICATION	GO:0001503	9	0.624718	2.155755	0.003165	0.069799	0.320
7	GOBP_NEGATIVE_REGULATION_OF_CYSTEINE_TYPE_ENDO...	GO:2000117	5	0.793688	2.100962	0.002740	0.090920	0.439
8	GOBP_MYELOID_LEUKOCYTE_DIFFERENTIATION	GO:0002573	11	0.594451	2.088907	0.003676	0.086556	0.455
9	GOBP_MYELOID_CELL_DIFFERENTIATION	GO:0030099	13	0.502879	2.049608	0.000000	0.097413	0.537
10	GOBP_CYTOKINE_MEDIATED_SIGNALING_PATHWAY	GO:0019221	16	0.477029	2.027812	0.000000	0.101125	0.582
11	GOBP_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	GO:0045670	5	0.768624	1.968335	0.011869	0.129783	0.705
12	GOBP_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENT...	GO:0002761	8	0.575237	1.918722	0.003067	0.159148	0.815
13	GOBP_SKIN_DEVELOPMENT	GO:0043588	5	0.734940	1.912148	0.011905	0.152929	0.824
14	GOBP_RESPONSE_TO_MECHANICAL_STIMULUS	GO:0009612	6	0.682927	1.906121	0.006329	0.146871	0.829
15	REACTOME_DEATH_RECEPTOR_SIGNALING	R-RNO-73887	5	0.737505	1.901219	0.017143	0.141962	0.840
16	GOBP_RESPONSE_TO_ENDOGENOUS_STIMULUS	GO:0009719	34	0.344841	1.889355	0.000000	0.142666	0.855
17	GOBP_POSITIVE_REGULATION_OF_CELL_DIFFERENTIATION	GO:0004597	27	0.368842	1.875748	0.000000	0.145758	0.875
18	GOBP_NEGATIVE_REGULATION_OF_CELL_POPULATION_PR...	GO:0008285	9	0.534148	1.871449	0.007042	0.141389	0.879
19	GOBP_POSITIVE_REGULATION_OF_DEVELOPMENTAL_PROCE...	GO:0051094	32	0.350193	1.864965	0.000000	0.139355	0.882
20	GOBP_IMMUNE_SYSTEM_DEVELOPMENT	GO:0002520	17	0.432172	1.854994	0.004219	0.139355	0.894
21	GOBP_REGULATION_OF_CELL_DIFFERENTIATION	GO:0004595	36	0.329660	1.825157	0.000000	0.156730	0.930
22	GOBP_RESPONSE_TO_CYTOKINE	GO:0034097	23	0.378370	1.813332	0.004484	0.161851	0.948
23	REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM	R-RNO-1280215	21	0.379680	1.812935	0.012195	0.155586	0.948
24	GOBP_INFLAMMATORY_RESPONSE	GO:0006954	12	0.471001	1.808953	0.018939	0.151975	0.950
25	GOBP_NEGATIVE_REGULATION_OF_PROTEOLYSIS	GO:0045861	8	0.548667	1.755278	0.028269	0.194117	0.983
26	GOBP_LEUKOCYTE_DIFFERENTIATION	GO:0002521	15	0.423575	1.754041	0.003953	0.188277	0.984
27	REACTOME_NGIF_STIMULATED_TRANSCRIPTION	R-RNO-9031628	9	0.518987	1.738173	0.023649	0.197365	0.992
28	GOBP_OSTEOBLAST_DIFFERENTIATION	GO:0001649	5	0.664689	1.726725	0.011050	0.201508	0.993
29	GOBP_CELL_POPULATION_PROLIFERATION	GO:0008283	32	0.316965	1.716461	0.005464	0.205741	0.993
30	GOBP_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	GO:1902105	9	0.491450	1.685974	0.036545	0.233448	1.000
31	GOBP_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	GO:00045637	9	0.488989	1.680686	0.032609	0.232190	1.000
32	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	M5930	5	0.650602	1.679643	0.021277	0.226711	1.000
33	GOBP_PRL_MIRNA_TRANSCRIPTION_BY_RNA_POLYMERASE_II	GO:0061614	7	0.543210	1.663227	0.036585	0.238343	1.000
34	GOBP_POSITIVE_REGULATION_OF_BIOSYNTHETIC_PROCESS	GO:0009891	27	0.323659	1.642793	0.017094	0.256950	1.000
35	GOBP_POSITIVE_REGULATION_OF_NUCLEOBASE_CONTAIN...	GO:0045935	28	0.318819	1.635624	0.015000	0.258728	1.000
36	GOBP_POSITIVE_REGULATION_OF_PRL_MIRNA_TRANSCRIP...	GO:1902895	7	0.543210	1.631699	0.024390	0.257242	1.000
37	GOBP_ACTIN_FILAMENT_BASED_PROCESS	GO:0030029	7	0.541508	1.617816	0.022876	0.266744	1.000
38	GOBP_REGULATION_OF_DEFENSE_RESPONSE	GO:0031347	7	0.509083	1.574683	0.042980	0.318328	1.000
39	HALLMARK_HYPOXIA	M5891	5	0.612647	1.565726	0.056886	0.324307	1.000
40	GOBP_NEGATIVE_REGULATION_OF_CELL_DEATH	GO:0060548	22	0.331603	1.557555	0.035176	0.328949	1.000

Continuation of Table S2

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
41	GOBP-INTRINSIC-APOPTOTIC-SIGNALING-PATHWAY	5	0.595854	1.543189	0.045872	0.343915	1.000
42	GOBP-POSITIVE-REGULATION-OF-AXONOGENESIS	5	0.602410	1.536202	0.065527	0.346841	1.000
43	GOBP-REGULATION-OF-HEMOPOIESIS	10	0.424029	1.535530	0.052117	0.340095	1.000
44	GOBP-MULTIMULTICELLULAR-ORGANISM-PROCESS	8	0.471437	1.531031	0.043210	0.339680	1.000
45	GOBP-REGULATION-OF-CELL-SIZE	5	0.590361	1.530751	0.054795	0.332738	1.000
46	GOBP-POSITIVE-REGULATION-OF-TRANSCRIPTION-BY-R...	24	0.310715	1.511869	0.030973	0.355268	1.000
47	GOBP-NEURON-APOPTOTIC-PROCESS	12	0.394737	1.490223	0.060000	0.383582	1.000
48	GOBP-REGULATION-OF-INFLAMMATORY-RESPONSE	7	0.509083	1.488370	0.084112	0.378639	1.000
49	GOBP-REGULATION-OF-CELL-DEATH	34	0.276107	1.488344	0.031963	0.371139	1.000
50	GOBP-POSITIVE-REGULATION-OF-MYELOID-CELL-DIFFE...	7	0.490488	1.482751	0.070968	0.372727	1.000
51	GOBP-POSITIVE-REGULATION-OF-SMOOTH-MUSCLE-CELL...	5	0.566265	1.474395	0.081159	0.379650	1.000
52	HALLMARK-ALLOGRAFT-REJECTION	7	0.497605	1.468273	0.069079	0.383234	1.000
53	GOBP-POSITIVE-REGULATION-OF-PEPTIDYL-TYROSINE...	8	0.462500	1.465458	0.080645	0.381109	1.000
54	GOBP-POSITIVE-REGULATION-OF-CYTOKINE-PRODUCTION	7	0.481481	1.459276	0.066667	0.383954	1.000
55	GOBP-MONONUCLEAR-CELL-DIFFERENTIATION	7	0.481482	1.454565	0.085044	0.384875	1.000
56	GOBP-REGULATION-OF-FAT-CELL-DIFFERENTIATION	6	0.498263	1.425424	0.111765	0.429799	1.000
57	GOBP-LEUKOCYTE-CELL-ADHESION	6	0.500000	1.408764	0.090634	0.454834	1.000
58	GOBP-RESPONSE-TO-NUTRIENT	5	0.536494	1.405000	0.139535	0.454337	1.000
59	GOBP-EPITHELIAL-CELL-DIFFERENTIATION	7	0.453790	1.400421	0.115385	0.455335	1.000
60	GOBP-POSITIVE-REGULATION-OF-MYELOID-LEUKOCYTE...	6	0.503944	1.393833	0.120370	0.460239	1.000
61	GOBP-RESPONSE-TO-REACTIVE-OXYGEN-SPECIES	8	0.423541	1.392840	0.101045	0.454990	1.000
62	GOBP-REGULATION-OF-PEPTIDYL-SERINE-PHOSPHORYLA...	8	0.434007	1.371879	0.110769	0.488968	1.000
63	GOBP-POSITIVE-REGULATION-OF-PEPTIDYL-SERINE-PH...	8	0.434007	1.369715	0.125767	0.486112	1.000
64	GOBP-EMBRYONIC-ORGAN-DEVELOPMENT	7	0.466098	1.369663	0.132911	0.478670	1.000
65	REACTOME-CELLULAR-SENESCENCE	6	0.482887	1.369502	0.125000	0.471748	1.000
66	GOBP-RESPONSE-TO-OXIDATIVE-STRESS	8	0.423541	1.360988	0.102564	0.482503	1.000
67	GOBP-RESPONSE-TO-EXTRACELLULAR-STIMULUS	13	0.339525	1.35283	0.093525	0.480482	1.000
68	GOBP-EMBRYO-DEVELOPMENT	14	0.334556	1.356936	0.106061	0.476183	1.000
69	GOBP-POSITIVE-REGULATION-OF-DEFENSE-RESPONSE	5	0.523801	1.356082	0.119403	0.471085	1.000
70	GOBP-CELLULAR-RESPONSE-TO-EXTERNAL-STIMULUS	10	0.384817	1.346553	0.131673	0.482679	1.000
71	GOBP-NEGATIVE-REGULATION-OF-TRANSCRIPTION-BY-R...	10	0.387147	1.345786	0.136364	0.477689	1.000
72	REACTOME-SENESCENCE-ASSOCIATED-SECRETORY-PHENO...	6	0.482887	1.335211	0.145161	0.490903	1.000
73	GOBP-RHYTHMIC-PROCESS	15	0.322410	1.332421	0.120536	0.489551	1.000
74	GOBP-NEGATIVE-REGULATION-OF-IMMUNE-SYSTEM-PROCESS	5	0.501871	1.329278	0.147929	0.488887	1.000
75	GOBP-RESPONSE-TO-UV	5	0.511987	1.326654	0.165680	0.487851	1.000
76	GOBP-PERIPHERAL-NERVOUS-SYSTEM-DEVELOPMENT	9	0.405063	1.320125	0.127517	0.494279	1.000
77	GOBP-NEGATIVE-REGULATION-OF-HYDROLASE-ACTIVITY	11	0.348567	1.317281	0.115672	0.493901	1.000
78	GOBP-TISSUE-MORPHOGENESIS	7	0.4048729	1.317193	0.161491	0.487898	1.000
79	GOBP-POSITIVE-REGULATION-OF-CELL-CELL-ADHESION	5	0.493976	1.309491	0.140056	0.496777	1.000
80	GOBP-NERVE-DEVELOPMENT	9	0.392405	1.304619	0.154605	0.500199	1.000
81	GOBP-REGULATION-OF-PEPTIDASE-ACTIVITY	10	0.364257	1.298780	0.142415	0.506125	1.000
82	GOBP-NEGATIVE-REGULATION-OF-LOCOMOTION	5	0.496870	1.292414	0.174286	0.512766	1.000
83	GOBP-CELLULAR-RESPONSE-TO-EXTRACELLULAR-STIMULUS	8	0.405901	1.292190	0.160883	0.506961	1.000

Continuation of Table S2

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
84	GOBP-POSITIVE-REGULATION_OF_LEUKOCYTE-CELL...	5	0.493976	1.290738	0.183976	0.503834	1.000
85	GOBP-NEGATIVE-REGULATION_OF_NEURON-APOPTOTIC.P...	8	0.387500	1.288778	0.151515	0.502360	1.000
86	GOBP-REPRODUCTIVE-SYSTEM-DEVELOPMENT	6	0.450016	1.273961	0.166667	0.526424	1.000
87	GOBP-REGULATION_OF_MULTICELLULAR-ORGANISMAL.DE...	31	0.233392	1.270299	0.135678	0.528107	1.000
88	GOBP-POSITIVE-REGULATION_OF_TRANSMEMBRANE-TRAN...	7	0.432099	1.264628	0.179191	0.533287	1.000
89	GOBP-REGULATION_OF_AXONOGENESIS	7	0.432099	1.261935	0.147059	0.533245	1.000
90	GOBP-MEMBRANE-PROTEIN-PROTEOLYSIS	6	0.455071	1.258937	0.179331	0.533337	1.000
91	GOBP-REGULATION_OF_LYMPHOCYTE-ACTIVATION	5	0.493976	1.258292	0.189441	0.529065	1.000
92	GOBP-POSITIVE-REGULATION_OF_HEMOPOIESIS	7	0.412196	1.251139	0.179487	0.538978	1.000
93	GOBP-DEFENSE-RESPONSE	19	0.268609	1.228177	0.200913	0.581761	1.000
94	GOBP-PROTEIN-AUTOPHOSPHORYLATION	5	0.457831	1.225862	0.204748	0.580963	1.000
95	GOBP-HOMEOSTASIS_OF_NUMBER_OF_CELLS	5	0.469880	1.215091	0.229508	0.597441	1.000
96	HALLMARK_UV_RESPONSE_UP	5	0.474630	1.214075	0.218182	0.593256	1.000
97	GOBP-POSITIVE-REGULATION_OF_DEVELOPMENTAL-GROWTH	8	0.382169	1.211029	0.229102	0.594144	1.000
98	GOBP-CELLULAR-RESPONSE_TO_CADMIUM-ION	5	0.470236	1.209200	0.219585	0.591583	1.000
99	GOBP-EPITHELIAL-DEVELOPMENT	15	0.286735	1.201919	0.198606	0.601240	1.000
100	GOBP-APOPTOTIC-SIGNALING-PATHWAY	15	0.291399	1.199184	0.215909	0.600855	1.000
101	GOBP-RESPONSE_TO_NERVE-GROWTH-FACTOR	7	0.395062	1.195291	0.246875	0.604257	1.000
102	GOBP-POSITIVE-REGULATION_OF_PROTEIN-TYROSINE.K...	5	0.445783	1.164471	0.245714	0.669243	1.000
103	GOBP-MUSCLE-CELL-PROLIFERATION	8	0.358376	1.159048	0.273312	0.677999	1.000
104	GOBP-RESPONSE_TO_OXYGEN-CONTAINING-COMPOUND	39	0.204577	1.151828	0.228723	0.688505	1.000
105	GOBP-REGULATION_OF_RECEPTOR-MEDIATED-ENDOCYTOSIS	5	0.445783	1.150438	0.277620	0.685419	1.000
106	GOBP-MORPHOGENESIS_OF_AN_EPITHELIUM	6	0.417905	1.145050	0.286585	0.692153	1.000
107	GOBP-POSITIVE-REGULATION_OF_NERVOUS-SYSTEM.DEV...	12	0.294021	1.139077	0.275735	0.700049	1.000
108	GOBP-APOPTOTIC-PROCESS	35	0.207530	1.134091	0.262136	0.706272	1.000
109	GOBP-REGULATION_OF_PROTEIN-TYROSINE-KINASE-ACT...	5	0.445783	1.132447	0.287791	0.703785	1.000
110	GOBP-RECEPTOR-MEDIATED-ENDOCYTOSIS	6	0.402439	1.130893	0.274510	0.701172	1.000
111	GOBP-REGIONALIZATION	6	0.390244	1.129050	0.285276	0.699698	1.000
112	GOBP-ANIMAL-ORGAN-MORPHOGENESIS	12	0.283743	1.123749	0.271429	0.706669	1.000
113	GOBP-REGULATION_OF_CELLULAR-COMPONENT_SIZE	7	0.367891	1.122414	0.277419	0.704135	1.000
114	GOBP-GLAND-DEVELOPMENT	7	0.372799	1.119691	0.287926	0.705097	1.000
115	GOBP-RESPONSE_TO_GROWTH-FACTOR	18	0.242386	1.117483	0.288793	0.704157	1.000
116	GOBP-CYTOKINE-PRODUCTION	10	0.316989	1.115137	0.310105	0.704038	1.000
117	GOBP-NEUROTROPHIN-SIGNALING-PATHWAY	6	0.390244	1.110732	0.323625	0.708926	1.000
118	GOBP-SPROUTING-ANGIOGENESIS	5	0.433735	1.110017	0.298551	0.704725	1.000
119	GOBP-NEURON-DEATH	18	0.244104	1.105382	0.292079	0.710156	1.000
120	GOBP-POSITIVE-REGULATION_OF_CELL-DEVELOPMENT	12	0.294021	1.104732	0.316406	0.706032	1.000
121	GOBP-POSITIVE-REGULATION_OF_GENE-EXPRESSION	16	0.253048	1.103683	0.297297	0.702819	1.000
122	GOBP-REPRODUCTION	18	0.249701	1.102133	0.311403	0.700433	1.000
123	GOBP-RAS-PROTEIN-SIGNAL-TRANSDUCTION	5	0.421687	1.100958	0.320856	0.697892	1.000
124	GOBP-NEUROTROPHIN-TRK-RECEPTOR-SIGNALING-PATHWAY	6	0.390244	1.100617	0.372781	0.693060	1.000
125	GOBP-POSITIVE-REGULATION_OF_CELL-DEATH	19	0.238123	1.099045	0.275000	0.691025	1.000
126	GOBP-POSITIVE-REGULATION_OF_CATION-TRANSMEMBRAN...	5	0.421687	1.094632	0.326870	0.695733	1.000

Continuation of Table S2

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
127	GOBP-PATTERN-SPECIFICATION-PROCESS	6	0.390244	1.093824	0.308176	0.692185	1.000
128	GOBP-POSITIVE-REGULATION-OF-NEUROGENESIS	12	0.294021	1.081507	0.371025	0.716750	1.000
129	GOBP-CELL-CELL-JUNCTION-ASSEMBLY	5	0.420669	1.078416	0.364742	0.718598	1.000
130	GOBP-RESPONSE-TO-ORGANIC-CYCLIC-COMPOUND	20	0.233652	1.075103	0.328302	0.720624	1.000
131	GOBP-EMBRYO-DEVELOPMENT-ENDING-IN-BIRTH-OR-EGG...	9	0.312711	1.073013	0.358209	0.720005	1.000
132	GOBP-AMEBOIDAL-TYPE-CELL-MIGRATION	11	0.292994	1.070459	0.350000	0.720276	1.000
133	GOBP-POSITIVE-REGULATION-OF-MULTICELLULAR-ORGA...	32	0.206577	1.069789	0.352381	0.716592	1.000
134	GOBP-IN-UTERO-EMBRYONIC-DEVELOPMENT	8	0.327652	1.067714	0.334356	0.716376	1.000
135	GOBP-CELLULAR-RESPONSE-TO-OXYGEN-CONTAINING.CO...	29	0.204257	1.061491	0.378238	0.726085	1.000
136	GOBP-FAT-CELL-DIFFERENTIATION	9	0.312171	1.054375	0.348387	0.737559	1.000
137	GOBP-EXTRINSIC-APOPTOTIC-SIGNALING-PATHWAY	7	0.350570	1.053130	0.346154	0.734964	1.000
138	GOBP-DEFENSE-RESPONSE-TO-OTHER-ORGANISM	9	0.303833	1.046014	0.382838	0.746608	1.000
139	GOBP-REGULATION-OF-CIRCADIAN-RHYTHM	7	0.339959	1.044631	0.362805	0.744492	1.000
140	GOBP-REGULATION-OF-PROTEOLYSIS	12	0.280405	1.040987	0.380952	0.747798	1.000
141	GOBP-CELLULAR-COMPONENT-DISASSEMBLY	6	0.373501	1.038960	0.394659	0.746773	1.000
142	GOBP-RESPONSE-TO-OXYGEN-LEVELS	8	0.332405	1.034402	0.416938	0.752905	1.000
143	GOBP-RECEPTOR-METABOLIC-PROCESS	5	0.397590	1.030348	0.413295	0.757994	1.000
144	GOBP-PEPTIDYL-TYROSINE-MODIFICATION	10	0.284546	1.030200	0.369403	0.752961	1.000
145	GOBP-TUBE-MORPHOGENESIS	15	0.246575	1.028567	0.382470	0.751475	1.000
146	GOBP-POSITIVE-REGULATION-OF-LIPASE-ACTIVITY	5	0.385542	1.024295	0.432353	0.756088	1.000
147	HALLMARK-KRAS-SIGNALING-UP	6	0.366578	1.018665	0.406940	0.763755	1.000
148	GOBP-CELLULAR-RESPONSE-TO-NITROGEN-COMPOUND	20	0.211044	1.012479	0.389830	0.772444	1.000
149	GOBP-RESPONSE-TO-PEPTIDE	18	0.228572	1.010733	0.400844	0.771572	1.000
150	GOBP-NEGATIVE-REGULATION-OF-APOPTOTIC-SIGNALIN...	7	0.324333	1.008630	0.431677	0.771550	1.000
151	GOBP-EPIDERMIS-DEVELOPMENT	5	0.385542	1.005432	0.415954	0.774573	1.000
152	GOBP-RESPONSE-TO-ABIOTIC-STIMULUS	27	0.197061	1.004904	0.463415	0.770655	1.000
153	GOBP-RESPONSE-TO-CADMIUM-ION	6	0.350496	1.003856	0.427350	0.768192	1.000
154	GOBP-REGULATION-OF-NEURON-DIFFERENTIATION	5	0.385542	0.997101	0.419098	0.779806	1.000
155	GOBP-RECEPTOR-INTERNALIZATION	8	0.308742	0.993783	0.432990	0.777463	1.000
156	GOBP-INOSITOL-LIPID-MEDIATED-SIGNALING	11	0.272727	0.992546	0.455149	0.775832	1.000
157	GOBP-NEGATIVE-REGULATION-OF-NEURON-DEATH	28	0.188427	0.992432	0.476190	0.771195	1.000
158	GOBP-COGNITION	6	0.348650	0.991421	0.441176	0.768658	1.000
159	GOBP-RESPONSE-TO-ACID-CHEMICAL	7	0.323984	0.985761	0.435435	0.776903	1.000
160	GOBP-MAINTENANCE-OF-LOCATION	9	0.282733	0.976512	0.447099	0.792714	1.000
161	GOBP-REGULATION-OF-PEPTIDYL-TYROSINE-PHOSPHORY...	6	0.346976	0.974344	0.431818	0.792977	1.000
162	HALLMARK-APOPTOSIS	5	0.385542	0.973536	0.445748	0.790025	1.000
163	GOBP-REGULATION-OF-PHOSPHOLIPASE-C-ACTIVITY	7	0.322147	0.970832	0.492537	0.791073	1.000
164	GOBP-CELLULAR-RESPONSE-TO-ABIOTIC-STIMULUS	6	0.343646	0.966993	0.444785	0.794966	1.000
165	GOBP-SMOOTH-MUSCLE-CELL-PROLIFERATION	14	0.243243	0.965973	0.471483	0.792525	1.000
166	GOBP-BLOOD-VESSEL-MORPHOGENESIS	10	0.269231	0.946946	0.483180	0.831579	1.000
167	GOBP-REGULATION-OF-APOPTOTIC-SIGNALING-PATHWAY	5	0.367759	0.944831	0.493113	0.831490	1.000
168	GOBP-REGULATION-OF-VASCULAR-ASSOCIATED-SMOOTH...	21	0.202991	0.944108	0.551724	0.827934	1.000
169	GOBP-POSITIVE-REGULATION-OF-CELL-POPULATION.PR...						

Continuation of Table S2

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
170	GOBP-NEGATIVE-REGULATION-OF-PROTEIN-METABOLIC...	20	0.206828	0.943682	0.556098	0.824334	1.000
171	GOBP-REGULATION-OF-CELL-DEVELOPMENT	15	0.229179	0.942961	0.526531	0.821382	1.000
172	GOBP-T-CELL-ACTIVATION	8	0.296043	0.942421	0.550769	0.817904	1.000
173	GOBP-POSITIVE-REGULATION-OF-CELL-PROJECTION-OR...	10	0.263454	0.939127	0.545752	0.820297	1.000
174	GOBP-RESPONSE-TO-NITROGEN-COMPOUND	35	0.173399	0.938346	0.541667	0.817325	1.000
175	GOBP-POSITIVE-REGULATION-OF-ORGANELLE-ORGANIZA...	10	0.264193	0.938133	0.511475	0.813289	1.000
176	GOBP-RESPONSE-TO-MOLECULE-OF-BACTERIAL-ORIGIN	13	0.237073	0.938083	0.542636	0.808791	1.000
177	REACTOME-SIGNALING-BY-NTRKS	18	0.206398	0.937190	0.566406	0.806319	1.000
178	GOBP-GLIOGENESIS	12	0.244691	0.937020	0.515464	0.802196	1.000
179	GOBP-RESPONSE-TO-BACTERIUM	13	0.237073	0.928220	0.564000	0.817219	1.000
180	GOBP-CELLULAR-RESPONSE-TO-REACTIVE-OXYGEN-SPECIES	7	0.312426	0.926720	0.544025	0.816003	1.000
181	GOBP-REGULATION-OF-PROTEIN-CATABOLIC-PROCESS	7	0.310043	0.925115	0.538206	0.815394	1.000
182	GOBP-CELLULAR-RESPONSE-TO-BIOTIC-STIMULUS	8	0.282123	0.921191	0.560897	0.819238	1.000
183	GOBP-POSITIVE-REGULATION-OF-CELLULAR-COMPONENT...	9	0.275348	0.909557	0.576369	0.840716	1.000
184	GOBP-CELLULAR-RESPONSE-TO-INORGANIC-SUBSTANCE	11	0.246107	0.905116	0.578740	0.846360	1.000
185	GOBP-CELLULAR-RESPONSE-TO-MOLECULE-OF-BACTERIA...	8	0.282123	0.904349	0.574324	0.843317	1.000
186	GOBP-CARBOHYDRATE-METABOLIC-PROCESS	9	0.265823	0.902198	0.561644	0.843851	1.000
187	GOBP-REGULATION-OF-EXTRINSIC-APOPTOTIC-SIGNALI...	6	0.329268	0.900480	0.534535	0.843186	1.000
188	GOBP-POSITIVE-REGULATION-OF-BINDING	6	0.314323	0.899743	0.593567	0.840011	1.000
189	GOBP-CELLULAR-RESPONSE-TO-CHEMICAL-STRESS	7	0.312426	0.899205	0.586103	0.836582	1.000
190	GOBP-REGULATION-OF-SMALL-MOLECULE-METABOLIC-PR...	9	0.265823	0.897791	0.590476	0.835583	1.000
191	GOBP-CELLULAR-RESPONSE-TO-PEPTIDE	13	0.226667	0.894479	0.581227	0.838232	1.000
192	GOBP-REGULATION-OF-NERVOUS-SYSTEM-DEVELOPMENT	15	0.215999	0.893635	0.624535	0.835723	1.000
193	GOBP-POSITIVE-REGULATION-OF-RESPONSE-TO-EXTERN...	9	0.265249	0.886115	0.610000	0.846711	1.000
194	GOBP-POSITIVE-REGULATION-OF-NEURON-DEATH	5	0.350374	0.871433	0.598214	0.851963	1.000
195	GOBP-REGULATION-OF-EPITHELIAL-CELL-MIGRATION	6	0.301974	0.871433	0.603279	0.869243	1.000
196	GOBP-NEGATIVE-REGULATION-OF-BIOSYNTHETIC-PROCESS	13	0.218566	0.867179	0.616438	0.873859	1.000
197	GOBP-RESPONSE-TO-LIGHT-STIMULUS	11	0.235352	0.861565	0.617857	0.880746	1.000
198	REACTOME-ESR-MEDIATED-SIGNALING	8	0.268343	0.860883	0.637255	0.877862	1.000
199	GOBP-NEGATIVE-REGULATION-OF-NUCLEOBASE-CONTAIN...	13	0.218307	0.860778	0.617761	0.873783	1.000
200	GOBP-ANATOMICAL-STRUCTURE-FORMATION-INVOLVED-I...	20	0.188820	0.859008	0.671296	0.872804	1.000
201	REACTOME-DEVELOPMENTAL-BIOLOGY	22	0.179148	0.858213	0.665158	0.869801	1.000
202	GOBP-NEGATIVE-REGULATION-OF-MOLECULAR-FUNCTION	24	0.174591	0.854855	0.663507	0.872167	1.000
203	REACTOME-EXTRA-NUCLEAR-ESTROGEN-SIGNALING	7	0.280583	0.851443	0.675241	0.875037	1.000
204	REACTOME-SIGNALING-BY-NUCLEAR-RECEPTORS	8	0.268343	0.846029	0.652997	0.881479	1.000
205	GOBP-REGULATION-OF-DEVELOPMENTAL-GROWTH	9	0.247509	0.845564	0.652459	0.878132	1.000
206	GOBP-RESPONSE-TO-LIPID	19	0.186565	0.844920	0.681034	0.875227	1.000
207	GOBP-REGULATION-OF-CELLULAR-COMPONENT-BIOGENESIS	10	0.230795	0.835975	0.686709	0.888405	1.000
208	GOBP-PROTEIN-LOCALIZATION-TO-PLASMA-MEMBRANE	7	0.271605	0.834631	0.681115	0.886700	1.000
209	GOBP-NEGATIVE-REGULATION-OF-CATALYTIC-ACTIVITY	17	0.197492	0.837066	0.691450	0.884383	1.000
210	GOBP-REGULATION-OF-NEUROGENESIS	14	0.204986	0.832092	0.681992	0.883483	1.000
211	GOBP-LEARNING	13	0.214610	0.831109	0.684397	0.881126	1.000
212	REACTOME-NUCLEAR-EVENTS-KINASE-AND-TRANSCRIPTI...	11	0.227933	0.829574	0.682848	0.880018	1.000

Continuation of Table S2

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
213	GOBP-PHAGOCYTOSIS	GO-0006909	5	0.313984	0.823634	0.652661	0.887231	1.000
214	GOBP-GENERATION_OF_PRECURSOR_METABOLITES_AND_E...	GO-0006091	5	0.325301	0.819119	0.666667	0.891227	1.000
215	GOBP-APOPTOTIC-MITOCHONDRIAL-CHANGES	GO-0008637	6	0.280488	0.812946	0.700288	0.898686	1.000
216	GOBP-POSITIVE-REGULATION_OF_CELL-GROWTH	GO-0030307	6	0.289468	0.812719	0.730104	0.894956	1.000
217	GOBP-MITOCHONDRION-ORGANIZATION	GO-0007005	7	0.271605	0.809367	0.739938	0.897279	1.000
218	GOBP-POSITIVE-REGULATION_OF_CELLULAR-COMPONENT...	GO-0051130	24	0.161920	0.804547	0.719298	0.901754	1.000
219	GOBP-RESPONSE_TO-RADIATION	GO-0009314	13	0.202164	0.801178	0.753906	0.903580	1.000
220	GOBP-PROTEIN-MODIFICATION_BY_SMALL-PROTEIN_CON...	GO-0070647	7	0.259259	0.798782	0.723684	0.903603	1.000
221	GOBP-MEMORY	GO-0007613	13	0.197345	0.789150	0.739688	0.916462	1.000
222	GOBP-REGULATION_OF_DNA-BINDING_TRANSCRIPTION_F...	GO-0051090	16	0.182921	0.784759	0.778571	0.920099	1.000
223	GOBP-RESPONSE_TO-INTERLEUKIN_1	GO-0007055	5	0.313845	0.783294	0.744382	0.918634	1.000
224	GOBP-ORGANIC-ACID-METABOLIC-PROCESS	GO-0006082	7	0.259259	0.775646	0.747475	0.927767	1.000
225	GOBP-TISSUE-MIGRATION	GO-0090130	9	0.227848	0.774783	0.778912	0.925098	1.000
226	GOBP-CARBOHYDRATE-DERIVATIVE-METABOLIC-PROCESS	GO-1901135	8	0.238102	0.772809	0.753086	0.924056	1.000
227	GOBP-NEUROINFLAMMATORY_RESPONSE	GO-0150076	5	0.295576	0.766714	0.748447	0.930125	1.000
228	GOBP-TEMPERATURE-HOMEOSTASIS	GO-0001659	5	0.293284	0.765820	0.736842	0.927558	1.000
229	GOBP-NEGATIVE-REGULATION_OF_CATABOLIC-PROCESS	GO-0009895	8	0.234119	0.764973	0.786885	0.924896	1.000
230	GOBP-REGULATION_OF_LIPID-METABOLIC-PROCESS	GO-0019216	7	0.259259	0.763299	0.758278	0.923715	1.000
231	GOBP-PROTEIN_KINASE_B-SIGNALING	GO-0043491	6	0.264584	0.756993	0.776025	0.929676	1.000
232	GOBP-RESPONSE_TO-HORMONE	GO-0009725	20	0.166165	0.753226	0.813853	0.931376	1.000
233	GOBP-REGULATION_OF_IMMUNE-SYSTEM-PROCESS	GO-0002682	21	0.155676	0.744707	0.831818	0.941272	1.000
234	GOBP-PROTEIN_CATABOLIC-PROCESS	GO-0030163	8	0.224278	0.737895	0.778846	0.947455	1.000
235	GOBP-MONOCARBOXYLIC-ACID-METABOLIC-PROCESS	GO-0032787	6	0.256098	0.737115	0.817365	0.944680	1.000
236	GOBP-MONOSACCHARIDE-METABOLIC-PROCESS	GO-0005996	6	0.256098	0.734007	0.782991	0.945105	1.000
237	GOBP-POSITIVE-REGULATION_OF_PHOSPHATIDYLINOSIT...	GO-0014068	5	0.286111	0.732071	0.790055	0.944128	1.000
238	GOBP-TELENCEPHALON-DEVELOPMENT	GO-0021537	7	0.234568	0.726567	0.815534	0.947992	1.000
239	GOBP-BLOOD_VESSEL-ENDOTHELIAL-CELL-MIGRATION	GO-0043534	8	0.225000	0.724806	0.858621	0.946391	1.000
240	GOBP-CELL_JUNCTION_ASSEMBLY	GO-0034329	8	0.225818	0.720379	0.845455	0.948791	1.000
241	GOBP-ENDOTHELIAL-CELL-MIGRATION	GO-0043542	8	0.225000	0.718164	0.869186	0.947988	1.000
242	GOBP-RESPONSE_TO-BIOTIC-STIMULUS	GO-0009607	17	0.157862	0.717363	0.871698	0.945447	1.000
243	GOBP-REGULATION_OF_LIPID-BIOSYNTHETIC-PROCESS	GO-0046890	6	0.256098	0.716666	0.811966	0.942465	1.000
244	GOBP-TRANSMEMBRANE-RECEPTOR_PROTEIN_SERINE_THR...	GO-0007178	6	0.256098	0.716244	0.775000	0.939345	1.000
245	GOBP-GLUCOSE-METABOLIC-PROCESS	GO-0006006	6	0.256098	0.712291	0.833828	0.941003	1.000
246	GOBP-ACTIVATION_OF_PROTEIN_KINASE_ACTIVITY	GO-0032147	10	0.196757	0.711940	0.884615	0.937639	1.000
247	GOBP-TUBE-DEVELOPMENT	GO-0035295	18	0.157401	0.708326	0.889344	0.939202	1.000
248	GOBP-DEVELOPMENTAL-CELL-GROWTH	GO-0048588	5	0.273833	0.701043	0.812680	0.944836	1.000
249	GOBP-NEGATIVE-REGULATION_OF_PROTEIN_CATABOLIC----	GO-0042177	5	0.264669	0.696241	0.865270	0.946683	1.000
250	GOBP-MONAMINE-TRANSPORT	GO-0015844	5	0.264669	0.694773	0.862259	0.944704	1.000
251	GOBP-NEGATIVE-REGULATION_OF_TRANSMEMBRANE_TRAN...	GO-0034763	6	0.246064	0.694754	0.862928	0.940960	1.000
252	GOBP-AXON-DEVELOPMENT	GO-0061564	18	0.153389	0.693965	0.920930	0.938242	1.000
253	GOBP-LIPID-BIOSYNTHETIC-PROCESS	GO-0008610	6	0.256098	0.677422	0.853211	0.955373	1.000
254	REACTOME-ESTROGEN-DEPENDENT_NUCLEAR-EVENTS-DOW...	R-RNO-9634638	5	0.256066	0.673036	0.857143	0.956675	1.000
255	GOBP-INTRACELLULAR-RECEPTOR-SIGNALING-PATHWAY	GO-0030522	5	0.253012	0.669349	0.870523	0.956832	1.000

Continuation of Table S2

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
256	GOBP-PEPTIDYL-SERINE-MODIFICATION	GO-0018209	12	0.172444	0.653322	0.940000	0.970175
257	GOBP-POSITIVE-REGULATION-OF-SMALL-MOLECULE-MET...	GO-0062013	5	0.253012	0.633607	0.904110	0.985770
258	GOBP-REGULATION-OF-BINDING	GO-0051098	11	0.167505	0.628958	0.936396	0.986075
259	GOBP-REGULATION-OF-CELL-CELL-ADHESION	GO-0022407	9	0.185989	0.620166	0.958599	0.989946
260	GOBP-CELL-CELL-ADHESION	GO-0098609	14	0.150142	0.612462	0.962963	0.991996
261	GOBP-ASSOCIATIVE-LEARNING	GO-0008306	7	0.200243	0.603305	0.948640	0.994696
262	GOBP-MUSCLE-STRUCTURE-DEVELOPMENT	GO-0061061	16	0.138889	0.602117	0.953488	0.991787
263	GOBP-EMBRYONIC-MORPHOGENESIS	GO-0048598	6	0.215922	0.598940	0.933526	0.990320
264	GOBP-REGULATION-OF-ANION-TRANSMEMBRANE-TRANSPORT	GO-1903959	5	0.229882	0.586988	0.945860	0.995026
265	HALLMARK-P13K-AKT-MTOR-SIGNALING	M5923	6	0.206315	0.586469	0.960000	0.991653
266	GOBP-PHOSPHATIDYLINOSITOL-3-KINASE-SIGNALING	GO-0014065	7	0.184026	0.575130	0.969789	0.994187
267	GOBP-SMALL-GTPASE-MEDIATED-SIGNAL-TRANSDUCTION	GO-0007264	8	0.175000	0.562528	0.969492	0.993294
268	GOBP-REGULATION-OF-PHOSPHATIDYLINOSITOL-3-KINA...	GO-0014066	6	0.196888	0.561923	0.968116	0.993294
269	GOBP-REGULATION-OF-PHOSPHOLIPASE-ACTIVITY	GO-0010517	6	0.182927	0.523021	0.997167	1.000000
270	GOBP-REGULATION-OF-LIPASE-ACTIVITY	GO-0060191	6	0.182927	0.513614	0.989933	1.000000
271	GOBP-POSITIVE-REGULATION-OF-IMMUNE-SYSTEM-PROCESS	GO-0002684	18	0.116068	0.507689	0.996212	0.999431
272	GOBP-REGULATION-OF-ANATOMICAL-STRUCTURE-SIZE	GO-0090066	10	0.142915	0.500134	0.977860	0.997011
273	GOBP-REGULATION-OF-PROTEIN-BINDING	GO-0043393	7	0.137979	0.422481	1.000000	0.999375
274	GOBP-REGULATION-OF-ANATOMICAL-STRUCTURE-MORPHO...	GO-0022603	17	-0.105904	-0.367504	0.998652	0.999539
275	GOBP-AGING	GO-0007568	13	-0.118336	-0.377863	0.998698	1.000000
276	GOBP-ENZYME-LINKED-RECEPTOR-PROTEIN-SIGNALING...	GO-0007167	24	-0.116853	-0.434821	0.997409	1.000000
277	GOBP-VASCULATURE-DEVELOPMENT	GO-0001944	17	-0.126150	-0.436741	1.000000	1.000000
278	GOBP-CIRCULATORY-SYSTEM-DEVELOPMENT	GO-0072359	21	-0.117975	-0.437028	0.996139	1.000000
279	GOBP-POSITIVE-REGULATION-OF-DNA-BINDING-TRANSC...	GO-0051091	10	-0.154353	-0.450621	0.995575	1.000000
280	GOBP-POSITIVE-REGULATION-OF-GLIOGENESIS	GO-0014015	5	-0.196521	-0.455318	0.993893	1.000000
281	GOBP-REGULATION-OF-GLIOGENESIS	GO-0014013	5	-0.196521	-0.459066	0.994169	1.000000
282	GOBP-NEURON-MIGRATION	GO-0001764	5	-0.202327	-0.469725	0.998440	1.000000
283	GOBP-REGULATION-OF-NEURON-PROJECTION-DEVELOPMENT	GO-0010975	16	-0.146887	-0.489104	0.986486	1.000000
284	REACTOME-CELLULAR-RESPONSES-TO-EXTERNAL-STIMULI	R-RNO-8953897	11	-0.165255	-0.499314	0.983027	1.000000
285	GOBP-CELL-JUNCTION-ORGANIZATION	GO-0034330	19	-0.144928	-0.504704	0.977690	1.000000
286	GOBP-POSITIVE-REGULATION-OF-PROTEIN-PHOSPHORYL...	GO-0001934	22	-0.136159	-0.505624	0.979513	1.000000
287	GOBP-REGULATION-OF-IMMUNE-RESPONSE	GO-0050776	12	-0.164030	-0.506634	0.977654	1.000000
288	GOBP-SYNAPSE-ORGANIZATION	GO-0050808	17	-0.146905	-0.508554	0.979973	1.000000
289	GOBP-POSITIVE-REGULATION-OF-PROTEIN-MODIFICATI...	GO-0031401	22	-0.136159	-0.508561	0.983051	1.000000
290	GOBP-LONG-TERM-SYNAPTIC-DEPRESSION	GO-0060292	5	-0.217440	-0.509775	0.989264	1.000000
291	GOBP-REGULATION-OF-ENDOCYTOSIS	GO-0030100	6	-0.205081	-0.510696	0.973602	1.000000
292	GOBP-REGULATION-OF-PROTEIN-LOCALIZATION-TO-MEM...	GO-1905475	7	-0.204596	-0.519918	0.984849	1.000000
293	GOBP-EPITHELIAL-CELL-PROLIFERATION	GO-0050673	12	-0.173928	-0.533413	0.968320	1.000000
294	GOBP-IMPORT-INTO-CELL	GO-0098657	6	-0.216523	-0.536393	0.964602	1.000000
295	GOBP-REGULATION-OF-PROTEIN-PHOSPHORYLATION	GO-0001932	25	-0.143490	-0.545921	0.955186	1.000000
296	GOBP-REGULATION-OF-PROTEIN-STABILITY	GO-0031647	5	-0.236877	-0.549042	0.976958	1.000000
297	GOBP-POSITIVE-REGULATION-OF-MAP-KINASE-ACTIVITY	GO-0043406	6	-0.222406	-0.549139	0.963415	1.000000
298	REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATION	R-RNO-597592	7	-0.208639	-0.550696	0.952239	1.000000

Continuation of Table S2

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
299	GOBP-ACTIVATION_OF_MAPK_ACTIVITY	6	-0.222406	-0.551998	0.967742	1.000000	1.000
300	GOBP-PURINE-CONTAINING-COMPOUND-METABOLIC-PROCESS	6	-0.223342	-0.553979	0.958209	1.000000	1.000
301	GOBP-RESPONSE-TO-NICOTINE	7	-0.210901	-0.556822	0.959538	1.000000	1.000
302	GOBP-ANION-TRANSMEMBRANE-TRANSPORT	7	-0.215154	-0.557472	0.947368	1.000000	1.000
303	GOBP-RESPONSE-TO-TEMPERATURE-STIMULUS	9	-0.197220	-0.567293	0.959479	1.000000	1.000
304	GOBP-DNA-METABOLIC-PROCESS	6	-0.234427	-0.580471	0.952527	1.000000	1.000
305	GOBP-POSITIVE-REGULATION_OF_PHOSPHORUS-METABOL...	23	-0.155306	-0.586168	0.953488	1.000000	1.000
306	GOBP-MUSCLE-TISSUE-DEVELOPMENT	11	-0.193900	-0.587470	0.942544	1.000000	1.000
307	GOBP-CELLULAR-COMPOONENT-MORPHOGENESIS	25	-0.157655	-0.590751	0.920615	1.000000	1.000
308	GOBP-POSITIVE-REGULATION_OF_PROTEIN_KINASE-ACT...	18	-0.170318	-0.592071	0.944675	1.000000	1.000
309	GOBP-POSITIVE-REGULATION_OF_IMMUNE-RESPONSE	9	-0.207695	-0.593196	0.947826	1.000000	1.000
310	GOBP-SKELETAL-MUSCLE-ORGAN-DEVELOPMENT	5	-0.256647	-0.593414	0.955590	1.000000	1.000
311	GOBP-POSITIVE-REGULATION_OF_NEURON-PROJECTION...	5	-0.205447	-0.596298	0.935664	1.000000	1.000
312	GOBP-FOREBRAIN-DEVELOPMENT	10	-0.203447	-0.596298	0.935664	1.000000	1.000
313	GOBP-CELL-PART-MORPHOGENESIS	25	-0.157655	-0.596462	0.923761	1.000000	1.000
314	GOBP-NEGATIVE-REGULATION_OF_LIPID-METABOLIC-PR...	5	-0.260425	-0.602233	0.933628	1.000000	1.000
315	GOBP-TRANSMEMBRANE-RECEPTOR-PROTEIN-TYROSINE_K...	19	-0.173498	-0.604406	0.920000	1.000000	1.000
316	GOBP-LYMPHOCTEACTIVATION	10	-0.202958	-0.605912	0.924177	1.000000	1.000
317	GOBP-REGULATION_OF-CELLULAR-AMIDE-METABOLIC-PR...	9	-0.213704	-0.606204	0.935574	1.000000	1.000
318	GOBP-REGULATION_OF_PHOSPHORUS-METABOLIC-PROCESS	26	-0.162771	-0.608043	0.920984	1.000000	1.000
319	REACTOME-SIGNALING-BY_NTRK2-TRKB	6	-0.246116	-0.608051	0.908815	1.000000	1.000
320	GOBP-CELL-MORPHOGENESIS	25	-0.157655	-0.608692	0.935317	1.000000	1.000
321	GOBP-POSITIVE-REGULATION_OF-CELL-ADHESION	7	-0.231565	-0.610231	0.923195	1.000000	1.000
322	GOBP-POSITIVE-REGULATION_OF_MAPK-CASCADE	9	-0.216395	-0.610797	0.926934	1.000000	1.000
323	GOBP-NEGATIVE-REGULATION_OF-CELL-DEVELOPMENT	6	-0.247819	-0.614045	0.925595	1.000000	1.000
324	GOBP-ORGANONITROGEN-COMPOUND-CATABOLIC-PROCESS	10	-0.210649	-0.619006	0.940278	1.000000	1.000
325	GOBP-REGULATION_OF-HORMONE-LEVELS	12	-0.200696	-0.621727	0.916103	1.000000	1.000
326	GOBP-RESPONSE-TO-CALCIUM-ION	6	-0.255934	-0.623693	0.911337	1.000000	1.000
327	GOBP-REGULATION_OF-PROTEIN-MODIFICATION-PROCESS	28	-0.162277	-0.623810	0.917092	1.000000	1.000
328	GOBP-POSITIVE-REGULATION_OF-ION-TRANSPORT	17	-0.180748	-0.623969	0.898667	1.000000	1.000
329	GOBP-REGULATION_OF-PROTEIN-KINASE-ACTIVITY	21	-0.174151	-0.625182	0.909574	1.000000	1.000
330	GOBP-POSITIVE-REGULATION_OF-TRANSPORT	26	-0.160936	-0.626176	0.919643	1.000000	1.000
331	GOBP-PEPTIDYL-AMINO-ACID-MODIFICATION	22	-0.168541	-0.627797	0.884566	1.000000	1.000
332	REACTOME-SIGNALING-BY-RECEPTOR-TYROSINE-KINASES	26	-0.164835	-0.635886	0.890703	1.000000	1.000
333	GOBP-POSITIVE-REGULATION_OF-PROTEIN-METABOLIC...	27	-0.164636	-0.636082	0.893484	1.000000	1.000
334	GOBP-EPHRIN-RECEPTOR-SIGNALING-PATHWAY	5	-0.267085	-0.637361	0.913767	1.000000	1.000
335	GOBP-REGULATION_OF-TRANSFERASE-ACTIVITY	21	-0.174151	-0.638531	0.897503	1.000000	1.000
336	GOBP-REGULATION_OF-CELL-ACTIVATION	8	-0.239731	-0.643675	0.890351	1.000000	1.000
337	GOBP-CARDIAC-MUSCLE-TISSUE-DEVELOPMENT	6	-0.257535	-0.644616	0.879822	1.000000	1.000
338	GOBP-MULTICELLULAR-ORGANISMAL-RESPONSE-TO-STRESS	5	-0.279031	-0.647185	0.888719	1.000000	1.000
339	GOBP-RESPONSE-TO-INSULIN	5	-0.280960	-0.647424	0.892097	1.000000	1.000
340	GOBP-AMYLOID-PRECURSOR-PROTEIN-CATABOLIC-PROCESS	5	-0.277078	-0.650088	0.894172	1.000000	1.000
341	GOBP-HEART-DEVELOPMENT	6	-0.257535	-0.651779	0.885587	1.000000	1.000

Continuation of Table S2

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
342	GOBP-AMYLOID-BETA-METABOLIC-PROCESS	GO-0050435	5	-0.277078	-0.651960	0.887879	1.000000
343	GOBP-AMYLOID-PRECURSOR-PROTEIN-METABOLIC-PROCESS	GO-0042982	5	-0.277078	-0.654382	0.875188	1.000000
344	GOBP-PEPTIDYL-LYSINE-MODIFICATION	GO-0018205	5	-0.279765	-0.652523	0.891850	1.000000
345	GOBP-PROTEIN-LOCALIZATION-TO-MEMBRANE	GO-0072687	13	-0.204681	-0.655336	0.882845	1.000000
346	GOBP-CELLULAR-LIPID-METABOLIC-PROCESS	GO-0044255	7	-0.249394	-0.655593	0.880775	1.000000
347	GOBP-ENDOTHELIAL-CELL-PROLIFERATION	GO-0001935	8	-0.233929	-0.655861	0.873381	1.000000
348	GOBP-LIPID-METABOLIC-PROCESS	GO-0006629	10	-0.223034	-0.657325	0.886657	1.000000
349	GOBP-TISSUE-HOMEOSTASIS	GO-0001894	5	-0.280632	-0.659432	0.883686	1.000000
350	GOBP-REGULATION-OF-MUSCLE-CELL-DIFFERENTIATION	GO-0051147	6	-0.264711	-0.665116	0.880060	1.000000
351	GOBP-CELL-ACTIVATION	GO-0001775	22	-0.184767	-0.671771	0.864474	1.000000
352	GOBP-CELLULAR-RESPONSE-TO-ORGANIC-CYCLIC-COMPOUND	GO-0071407	13	-0.208569	-0.671955	0.849007	1.000000
353	GOBP-POSITIVE-REGULATION-OF-TRANSFERASE-ACTIVITY	GO-0051347	19	-0.189698	-0.675121	0.847074	1.000000
354	REACTOME-INFECTIOUS-DISEASE	R-HSA-5663205	12	-0.216988	-0.677693	0.872951	1.000000
355	GOBP-CELLULAR-RESPONSE-TO-HORMONE-STIMULUS	GO-0032870	11	-0.227220	-0.683277	0.850350	1.000000
356	GOBP-REGULATION-OF-LONG-TERM-SYNAPTIC-POTENTIAL...	GO-1900271	6	-0.275500	-0.686393	0.857364	1.000000
357	GOBP-POSITIVE-REGULATION-OF-GROWTH	GO-0045927	9	-0.247927	-0.688416	0.853623	1.000000
358	GOBP-DEVELOPMENTAL-MATURATION	GO-0021700	5	-0.299141	-0.689233	0.858034	1.000000
359	GOBP-ERK1-AND-ERK2-CASCADE	GO-0070371	5	-0.291635	-0.691633	0.867669	1.000000
360	GOBP-CELL-CELL-JUNCTION-ORGANIZATION	GO-0045216	6	-0.280364	-0.693507	0.838710	1.000000
361	GOBP-PEPTIDE-METABOLIC-PROCESS	GO-0006518	11	-0.227051	-0.695085	0.858956	1.000000
362	GOBP-RESPONSE-TO-MONOSACCHARIDE	GO-0034284	6	-0.297300	-0.695934	0.861538	1.000000
363	GOBP-REGULATION-OF-PROTEIN-LOCALIZATION-TO-CEL...	GO-1904375	6	-0.284474	-0.696862	0.859216	1.000000
364	GOBP-REGULATION-OF-CATABOLIC-PROCESS	GO-0009894	13	-0.215512	-0.698101	0.828104	1.000000
365	GOBP-STRIATED-MUSCLE-CELL-DIFFERENTIATION	GO-0051146	9	-0.244568	-0.698942	0.839525	1.000000
366	GOBP-REGULATION-OF-CELLULAR-CATABOLIC-PROCESS	GO-0031329	10	-0.237344	-0.702082	0.850000	1.000000
367	GOBP-NEGATIVE-REGULATION-OF-NERVOUS-SYSTEM-DEV...	GO-0051961	5	-0.297474	-0.702912	0.864742	1.000000
368	GOBP-GLIAL-CELL-DIFFERENTIATION	GO-0010001	10	-0.241437	-0.703706	0.813044	1.000000
369	GOBP-RESPONSE-TO-CARBOHYDRATE	GO-0009743	5	-0.297300	-0.704735	0.840601	1.000000
370	GOBP-MULTICELLULAR-ORGANISMAL-HOMEOSTASIS	GO-0048871	12	-0.232006	-0.707349	0.811554	1.000000
371	REACTOME-DISEASES-OF-SIGNAL-TRANSDUCTION-BY-GR...	R-HSA-5663202	12	-0.227756	-0.707473	0.836364	1.000000
372	GOBP-REGULATION-OF-MITOTIC-CELL-CYCLE	GO-0007346	5	-0.310461	-0.713380	0.811679	1.000000
373	GOBP-RESPONSE-TO-METAL-ION	GO-0010038	15	-0.217060	-0.713842	0.841678	1.000000
374	GOBP-CELLULAR-RESPONSE-TO-DNA-DAMAGE-STIMULUS	GO-0006974	5	-0.308476	-0.714549	0.814590	1.000000
375	GOBP-RESPONSE-TO-STARVATION	GO-0042594	5	-0.311379	-0.717850	0.813814	1.000000
376	GOBP-DEVELOPMENTAL-GROWTH	GO-0048589	10	-0.249504	-0.719140	0.840112	1.000000
377	GOBP-TAXIS	GO-0042330	14	-0.222258	-0.720601	0.817321	1.000000
378	GOBP-DEVELOPMENTAL-PROCESS-INVOLVED-IN-REPRODU...	GO-0003006	11	-0.238661	-0.722136	0.834294	1.000000
379	GOBP-NEUROGENESIS	GO-0022008	41	-0.177027	-0.723212	0.796818	1.000000
380	GOBP-NEGATIVE-REGULATION-OF-SYNAPTIC-TRANSMISSION	GO-0050805	6	-0.293251	-0.725119	0.824060	1.000000
381	GOBP-CELLULAR-RESPONSE-TO-STARVATION	GO-0009267	5	-0.311379	-0.728551	0.822400	1.000000
382	GOBP-POSITIVE-REGULATION-OF-INTRACELLULAR-SIGN...	GO-1902533	14	-0.223275	-0.729047	0.800813	1.000000
383	GOBP-REGULATION-OF-VESICLE-MEDIATED-TRANSPORT	GO-0060627	12	-0.233668	-0.730291	0.813423	1.000000
384	GOBP-RESPONSE-TO-INORGANIC-SUBSTANCE	GO-0010035	19	-0.208714	-0.731355	0.824011	1.000000

Continuation of Table S2

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
385	GOBP-REGULATION-OF-HYDROLASE-ACTIVITY	22	-0.202739	-0.740649	0.791403	1.000000	1.000
386	GOBP-POSITIVE-REGULATION-OF-MOLECULAR-FUNCTION	37	-0.187327	-0.750831	0.764852	1.000000	1.000
387	GOBP-NEGATIVE-REGULATION-OF-SIGNALING	21	-0.208100	-0.751349	0.797635	1.000000	1.000
388	GOBP-RESPONSE-TO-DRUG	11	-0.251497	-0.753562	0.770515	1.000000	1.000
389	GOBP-LONG-TERM-MEMORY	6	-0.303552	-0.754048	0.786687	1.000000	1.000
390	GOBP-SMALL-MOLECULE-BIOSYNTHETIC-PROCESS	5	-0.326053	-0.756275	0.793510	1.000000	1.000
391	GOBP-PROTEIN-MODIFICATION-BY-SMALL-PROTEIN-CON...	6	-0.311944	-0.760384	0.767442	1.000000	1.000
392	GOBP-ORGANOPHOSPHATE-METABOLIC-PROCESS	8	-0.276638	-0.763487	0.756914	1.000000	1.000
393	GOBP-RESPIRATORY-SYSTEM-DEVELOPMENT	6	-0.301638	-0.763542	0.770393	1.000000	1.000
394	GOBP-POSTSYNAPSE-ORGANIZATION	10	-0.262365	-0.765231	0.765739	1.000000	1.000
395	GOBP-PROTEIN-LOCALIZATION-TO-CELL-PERIPHERY	12	-0.247152	-0.768112	0.745179	1.000000	1.000
396	GOBP-POSITIVE-REGULATION-OF-LONG-TERM-SYNAPTIC...	5	-0.331576	-0.771117	0.768049	1.000000	1.000
397	GOBP-REGULATION-OF-ORGANELLE-ORGANIZATION	14	-0.236347	-0.771456	0.756393	1.000000	1.000
398	REACTOME-ANTI-INFLAMMATORY-RESPONSE-FAVOURING...	5	-0.342290	-0.773489	0.769953	1.000000	1.000
399	GOBP-LOCOMOTION	31	-0.198729	-0.773979	0.747112	1.000000	1.000
400	GOBP-MATERNAL-PROCESS-INVOLVED-IN-FEMALE-PREGN...	5	-0.334101	-0.778829	0.735614	1.000000	1.000
401	GOBP-POSITIVE-REGULATION-OF-EPITHELIAL-CELL-MI...	5	-0.338305	-0.781744	0.789474	1.000000	1.000
402	GOBP-BIOLOGICAL-PROCESS-INVOLVED-IN-SYMBIOTIC...	10	-0.271201	-0.782893	0.744681	1.000000	1.000
403	GOBP-NEURON-DIFFERENTIATION	37	-0.195949	-0.784380	0.740050	1.000000	1.000
404	GOBP-REGULATION-OF-SYNAPSE-STRUCTURE-OR-ACTIVITY	11	-0.255691	-0.785471	0.732606	1.000000	1.000
405	GOBP-NEGATIVE-REGULATION-OF-BINDING	6	-0.316559	-0.786286	0.736215	1.000000	1.000
406	GOBP-REGULATION-OF-CELL-PROJECTION-ORGANIZATION	20	-0.220944	-0.788056	0.768725	1.000000	1.000
407	GOBP-EXOCYTOSIS	11	-0.265448	-0.788260	0.758133	1.000000	1.000
408	GOBP-REGULATION-OF-CYSTEINE-TYPE-ENDOPEPTIDASE...	9	-0.284756	-0.795820	0.730994	1.000000	1.000
409	GOBP-ORGANIC-HYDROXY-COMPOUND-METABOLIC-PROCESS	8	-0.289379	-0.798825	0.719168	1.000000	1.000
410	GOBP-BEHAVIOR	33	-0.204091	-0.800811	0.729193	1.000000	1.000
411	GOBP-POSITIVE-REGULATION-OF-APOPTOTIC-SIGNALIN...	5	-0.341606	-0.802040	0.721386	1.000000	1.000
412	GOBP-SMALL-MOLECULE-METABOLIC-PROCESS	16	-0.237436	-0.803595	0.738526	1.000000	1.000
413	GOBP-CYTOSKELETON-ORGANIZATION	11	-0.266359	-0.803693	0.735537	1.000000	1.000
414	GOBP-NUCLEOBASE-CONTAINING-SMALL-MOLECULE-META...	7	-0.312294	-0.804345	0.700590	1.000000	1.000
415	GOBP-ENDOCYTOSIS	8	-0.296944	-0.805204	0.714497	1.000000	1.000
416	GOBP-NEGATIVE-REGULATION-OF-PROTEIN-MODIFICATI...	GO:0031400	-0.271705	-0.806007	0.719323	1.000000	1.000
417	GOBP-REGULATION-OF-CYTOSKELETON-ORGANIZATION	GO:0051493	-0.347092	-0.807242	0.729231	1.000000	1.000
418	GOBP-REGULATION-OF-CELLULAR-PROTEIN-LOCALIZATION	GO:1903827	-0.263226	-0.809202	0.708049	1.000000	1.000
419	GOBP-CELL-MIGRATION	GO:0016477	-0.221668	-0.810406	0.718147	1.000000	1.000
420	GOBP-DENDRITIC-SPINE-MORPHOGENESIS	GO:0060997	-0.342626	-0.812545	0.729521	1.000000	1.000
421	GOBP-MULTI-ORGANISM-PROCESS	GO:0051704	-0.237337	-0.812756	0.712925	1.000000	1.000
422	GOBP-BIOLOGICAL-ADHESION	GO:0022610	-0.238145	-0.814362	0.717131	1.000000	1.000
423	GOBP-REGULATION-OF-CELLULAR-LOCALIZATION	GO:0060341	-0.238145	-0.820208	0.686934	1.000000	1.000
424	REACTOME-ONCOGENIC-MAPK-SIGNALING	R-HSA-680295	-0.356466	-0.820738	0.713202	1.000000	1.000
425	GOBP-MYELOID-LEUKOCYTE-ACTIVATION	GO:0002274	-0.299911	-0.821491	0.701318	1.000000	1.000
426	GOBP-PROTEIN-PHOSPHORYLATION	GO:006468	-0.210224	-0.826240	0.711223	1.000000	1.000
427	GOBP-REGULATION-OF-ORGAN-GROWTH	GO:0046620	-0.367800	-0.836898	0.690402	1.000000	1.000

Continuation of Table S2

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
GOBP-REGULATION-OF-PEPTIDE-SECRETION	GO-0002791	7	-0.323610	-0.838777	0.687407	1.000000	1.000
GOBP-REGULATION-OF-ENDOTHELIAL-CELL-MIGRATION	GO-0010594	5	-0.358628	-0.839037	0.687500	1.000000	1.000
GOBP-RESPONSE-TO-PEPTIDE-HORMONE	GO-0043434	13	-0.266388	-0.846000	0.662873	1.000000	1.000
GOBP-NERVOUS-SYSTEM-PROCESS	GO-0050877	38	-0.208365	-0.846851	0.665446	1.000000	1.000
GOBP-HORMONE-TRANSPORT	GO-0009914	9	-0.300527	-0.853920	0.657593	1.000000	1.000
GOBP-CELL-MORPHOGENESIS-INVOLVED-IN-DIFFERENTI...	GO-0000904	22	-0.232577	-0.858501	0.654568	1.000000	1.000
GOBP-REGULATION-OF-METAL-ION-TRANSPORT	GO-0010959	6	-0.350443	-0.863581	0.665667	1.000000	1.000
GOBP-NEGATIVE-REGULATION-OF-CELLULAR-COMPONENT...	GO-0051129	11	-0.287791	-0.863801	0.644476	1.000000	1.000
GOBP-ORGAN-GROWTH	GO-0035265	5	-0.367800	-0.864454	0.666667	1.000000	1.000
GOBP-CELL-MORPHOGENESIS-INVOLVED-IN-NEURON-DIF...	GO-0048667	22	-0.232577	-0.867671	0.617725	1.000000	1.000
GOBP-POSITIVE-REGULATION-OF-HYDROLASE-ACTIVITY	GO-0051345	16	-0.256692	-0.867713	0.613281	1.000000	1.000
GOBP-IMMUNE-EFFECTOR-PROCESS	GO-0002252	11	-0.285153	-0.873340	0.632737	0.997849	1.000
GOBP-REGULATION-OF-HORMONE-SECRETION	GO-0046883	8	-0.318326	-0.876584	0.625731	0.994141	1.000
REACTOME-EPH-EPHRIN-SIGNALING	R-RNO-2682334	6	-0.354703	-0.877481	0.628571	0.995784	1.000
GOBP-ORGANIC-HYDROXY-COMPOUND-TRANSPORT	GO-0015850	6	-0.344268	-0.878627	0.622388	0.996941	1.000
GOBP-NEGATIVE-REGULATION-OF-RESPONSE-TO-STIMULUS	GO-0048585	16	-0.259419	-0.879063	0.646053	0.999581	1.000
GOBP-ERBB-SIGNALING-PATHWAY	GO-00038127	5	-0.377641	-0.884023	0.623234	0.992558	1.000
GOBP-ORGANONITROGEN-COMPOUND-BIOSYNTHETIC-PROCESS	GO-1901566	13	-0.283564	-0.891715	0.600801	0.979697	1.000
GOBP-POLYSACCHARIDE-METABOLIC-PROCESS	GO-0005976	5	-0.382944	-0.892400	0.615262	0.981657	1.000
GOBP-REGULATION-OF-INTRACELLULAR-SIGNAL-TRANSD...	GO-1902531	21	-0.242174	-0.893651	0.590793	0.982581	1.000
GOBP-POSITIVE-REGULATION-OF-ANION-TRANSPORT	GO-1903793	9	-0.307096	-0.894321	0.577201	0.984660	1.000
GOBP-REGULATION-OF-WNT-SIGNALING-PATHWAY	GO-0030111	5	-0.382454	-0.895705	0.597015	0.985260	1.000
GOBP-REGULATION-OF-RESPONSE-TO-EXTERNAL-STIMULUS	GO-0032101	15	-0.266988	-0.898297	0.588549	0.983143	1.000
GOBP-INSULIN-SECRETION	GO-0030073	7	-0.344258	-0.899369	0.618128	0.984361	1.000
GOBP-AMIDE-BIOSYNTHETIC-PROCESS	GO-0043604	6	-0.370029	-0.899386	0.607784	0.987944	1.000
REACTOME-PLATELET-ACTIVATION-SIGNALING-AND-AGG...	R-HSA-76002	7	-0.346693	-0.901057	0.597365	0.987858	1.000
GOBP-PEPTIDE-HORMONE-SECRETION	GO-0030072	7	-0.344258	-0.901147	0.608504	0.991295	1.000
GOBP-REGULATION-OF-CARBOHYDRATE-METABOLIC-PROCESS	GO-0006109	5	-0.390162	-0.901954	0.605016	0.993180	1.000
GOBP-CHROMATIN-ORGANIZATION	GO-0006325	5	-0.391354	-0.904599	0.582953	0.990804	1.000
GOBP-CARBOHYDRATE-BIOSYNTHETIC-PROCESS	GO-0016051	5	-0.390162	-0.905407	0.570776	0.992856	1.000
GOBP-MULTICELLULAR-ORGANISM-REPRODUCTION	GO-0032504	12	-0.292300	-0.909353	0.555710	0.987683	1.000
GOBP-CELLULAR-RESPONSE-TO-LIPID	GO-0071396	15	-0.280883	-0.909715	0.584131	0.990526	1.000
GOBP-MYOTUBE-DIFFERENTIATION	GO-0014902	5	-0.397590	-0.914068	0.578370	0.984461	1.000
GOBP-MUSCLE-ORGAN-DEVELOPMENT	GO-0007517	9	-0.315704	-0.914258	0.576487	0.987756	1.000
GOBP-POSITIVE-REGULATION-OF-EPITHELIAL-CELL-PR...	GO-0050679	7	-0.352755	-0.914427	0.570381	0.991064	1.000
GOBP-REGULATION-OF-CARBOHYDRATE-BIOSYNTHETIC-P...	GO-0043255	5	-0.390162	-0.918038	0.569733	0.986280	1.000
GOBP-NEGATIVE-REGULATION-OF-CELL-CYCLE	GO-0045786	5	-0.388723	-0.919240	0.587025	0.987321	1.000
GOBP-REGULATION-OF-MAPK-CASCADE	GO-0043468	13	-0.289289	-0.922039	0.553521	0.984860	1.000
GOBP-REGULATION-OF-TRANSMEMBRANE-TRANSPORT	GO-0034702	23	-0.252831	-0.923919	0.560468	0.984233	1.000
GOBP-PEPTIDE-BIOSYNTHETIC-PROCESS	GO-0043043	6	-0.370029	-0.924773	0.549777	0.986246	1.000
REACTOME-EXTRACELLULAR-MATRIX-ORGANIZATION	R-RNO-1474244	5	-0.402623	-0.924862	0.568421	0.989861	1.000
GOBP-POSITIVE-REGULATION-OF-SIGNALING	GO-0023056	34	-0.233837	-0.928207	0.554020	0.985836	1.000
GOBP-ACTIVATION-OF-IMMUNE-RESPONSE	GO-0002253	5	-0.398977	-0.931272	0.562021	0.982758	1.000

Continuation of Table S2

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
471	GOBP-MACROMOLECULE-CATABOLIC-PROCESS	GO-0009057	11	-0.312774	-0.933947	0.543759	0.980494	1.000
472	GOBP-NEGATIVE-REGULATION-OF-DEVELOPMENTAL-PROCESS	GO-0051093	13	-0.294654	-0.939314	0.545076	0.972055	1.000
473	GOBP-DENDRITIC-SPINE-DEVELOPMENT	GO-0060996	6	-0.381641	-0.942065	0.538117	0.969385	1.000
474	GOBP-POSITIVE-REGULATION-OF-SYNAPTIC-TRANSMISSION	GO-0050806	15	-0.275759	-0.945032	0.503365	0.966285	1.000
475	GOBP-NEGATIVE-REGULATION-OF-PHOSPHORUS-METABOLISM	GO-0010563	9	-0.338728	-0.947657	0.524854	0.964151	1.000
476	GOBP-NEGATIVE-REGULATION-OF-CELL-DIFFERENTIATION	GO-0045596	13	-0.294654	-0.948097	0.515646	0.966989	1.000
477	GOBP-CENTRAL-NERVOUS-SYSTEM-NEURON-DIFFERENTIATION	GO-0021953	5	-0.405736	-0.949488	0.541411	0.967592	1.000
478	GOBP-NEURON-DEVELOPMENT	GO-0048666	34	-0.241040	-0.952251	0.532746	0.964906	1.000
479	GOBP-CELLULAR-AMIDE-METABOLIC-PROCESS	GO-0043603	12	-0.308177	-0.954238	0.510578	0.964061	1.000
480	GOBP-POSITIVE-REGULATION-OF-CATALYTIC-ACTIVITY	GO-0043085	29	-0.248073	-0.956300	0.518566	0.963177	1.000
481	GOBP-REGULATION-OF-CELLULAR-COMPONENT-MOVEMENT	GO-0051270	15	-0.286914	-0.957512	0.533153	0.964175	1.000
482	GOBP-REGULATION-OF-NEURONAL-SYNAPTIC-PLASTICITY	GO-0048168	7	-0.358404	-0.958139	0.523169	0.966546	1.000
483	GOBP-NEGATIVE-REGULATION-OF-ION-TRANSPORT	GO-0043271	11	-0.321600	-0.960395	0.514936	0.964994	1.000
484	GOBP-NEGATIVE-REGULATION-OF-INTRACELLULAR-SIGNALING	GO-1902532	7	-0.362562	-0.960469	0.512012	0.968770	1.000
485	GOBP-MUSCLE-CELL-DIFFERENTIATION	GO-0042692	10	-0.323984	-0.961032	0.513630	0.971468	1.000
486	GOBP-REGULATION-OF-MAP-KINASE-ACTIVITY	GO-0043405	9	-0.342459	-0.961560	0.530410	0.974087	1.000
487	GOBP-CIRCADIAN-RHYTHM	GO-0007623	13	-0.305956	-0.963432	0.502688	0.973612	1.000
488	GOBP-ENDOCRINE-SYSTEM-DEVELOPMENT	GO-0035270	6	-0.396638	-0.963598	0.541353	0.977309	1.000
489	GOBP-CALCIUM-MEDIATED-SIGNALING	GO-0019722	10	-0.325941	-0.966247	0.491620	0.974826	1.000
490	GOBP-PEPTIDE-SECRETION	GO-0002790	9	-0.341594	-0.966577	0.502140	0.978166	1.000
491	GOBP-NEURON-PROJECTION-GUIDANCE	GO-0097485	9	-0.337170	-0.970827	0.509573	0.971536	1.000
492	GOBP-POSITIVE-REGULATION-OF-PROTEIN-SERINE-THREONINE-KINASE	GO-0071902	9	-0.342700	-0.972668	0.490701	0.971198	1.000
493	GOBP-RESPONSE-TO-KETONE	GO-1901654	7	-0.375973	-0.972820	0.512195	0.975011	1.000
494	REACTOME-INNATE-IMMUNE-SYSTEM	R-RNO-168249	16	-0.288357	-0.972842	0.496680	0.979170	1.000
495	GOBP-REGULATION-OF-PEPTIDE-HORMONE-SECRETION	GO-0090276	6	-0.395451	-0.974551	0.484756	0.979196	1.000
496	REACTOME-NEUTROPHIL-DEGRANULATION	R-RNO-6798695	6	-0.396667	-0.976684	0.508246	0.978031	1.000
497	GOBP-CELLULAR-CARBOHYDRATE-METABOLIC-PROCESS	GO-0044262	5	-0.419927	-0.978041	0.496979	0.978885	1.000
498	GOBP-RESPONSE-TO-HEAT	GO-0009408	7	-0.372100	-0.978883	0.506667	0.981178	1.000
499	GOBP-LONG-TERM-SYNAPTIC-POTENTIATION	GO-0060291	12	-0.312859	-0.979371	0.481638	0.984255	1.000
500	GOBP-REGULATION-OF-PROTEIN-SERINE-THREONINE-KINASE	GO-0071900	12	-0.316089	-0.979436	0.492997	0.988442	1.000
501	REACTOME-VESICLE-MEDIATED-TRANSPORT	R-RNO-5653656	5	-0.425419	-0.987458	0.467669	0.971921	1.000
502	GOBP-CELL-ACTIVATION-INVOLVED-IN-IMMUNE-RESPONSE	GO-0002263	6	-0.396667	-0.991190	0.488722	0.966459	1.000
503	GOBP-POSITIVE-REGULATION-OF-ESTABLISHMENT-OF-POLARITY	GO-1904951	5	-0.420890	-0.994911	0.482759	0.961393	1.000
504	GOBP-VESICLE-MEDIATED-TRANSPORT-IN-SYNAPSE	GO-0099003	7	-0.382716	-0.994981	0.483533	0.965526	1.000
505	REACTOME-TOLL-LIKE-RECEPTOR-TLR1-TLR2-CASCADE	R-RNO-168179	8	-0.372989	-0.997163	0.484581	0.964256	1.000
506	GOBP-POSITIVE-REGULATION-OF-ENDOTHELIAL-CELL-PROLIFERATION	GO-0001938	6	-0.401205	-0.997302	0.480858	0.968206	1.000
507	GOBP-CIRCULATORY-SYSTEM-PROCESS	GO-0003013	5	-0.430008	-0.997573	0.474654	0.971899	1.000
508	REACTOME-TOLL-LIKE-RECEPTOR-9-TLR9-CASCADE	R-RNO-168138	8	-0.372989	-0.998367	0.464888	0.974219	1.000
509	GOBP-REGULATION-OF-GTPASE-ACTIVITY	GO-0043087	5	-0.425761	-1.001446	0.485075	0.970625	1.000
510	GOBP-REGULATION-OF-GROWTH	GO-0040008	13	-0.310538	-1.002497	0.473538	0.972289	1.000
511	GOBP-MUSCLE-CELL-DEVELOPMENT	GO-0055001	5	-0.437716	-1.003272	0.471212	0.974670	1.000
512	REACTOME-MEMBRANE-TRAFFICKING	R-RNO-199991	5	-0.425419	-1.003789	0.466563	0.977891	1.000
513	GOBP-ANATOMICAL-STRUCTURE-HOMEOSTASIS	GO-0060249	7	-0.384362	-1.004579	0.467262	0.980449	1.000

Continuation of Table S2

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
514	GOBP-RESPONSE.TO.ALKALOID	5	-0.440285	-1.007550	0.465224	0.977129	1.000
515	GOBP-CELLULAR.MACROMOLECULE.LOCALIZATION	20	-0.287657	-1.009095	0.456209	0.977579	1.000
516	GOBP-MYELOID-LEUKOCYTE-MEDIATED-IMMUNITY	6	-0.396667	-1.009402	0.444795	0.981374	1.000
517	REACTOME-TOLL-LIKE-RECEPTOR-CASCADES	8	-0.372989	-1.009612	0.470085	0.985555	1.000
518	GOBP-LEUKOCYTE-MIGRATION	6	-0.406479	-1.009729	0.431085	0.990005	1.000
519	GOBP-POSITIVE-REGULATION-OF-CELLULAR-PROTEIN.L...	7	-0.383383	-1.010994	0.449405	0.991259	1.000
520	GOBP-POSITIVE-REGULATION-OF-PROTEOLYSIS	8	-0.372698	-1.011490	0.463557	0.994639	1.000
521	GOBP-NEURON-PROJECTION-ORGANIZATION	8	-0.368945	-1.014573	0.441595	0.990987	1.000
522	GOBP-PROTEIN-LOCALIZATION.TO-CELL-JUNCTION	6	-0.413131	-1.014950	0.476762	0.994597	1.000
523	GOBP-PROTEIN-DEPHOSPHORYLATION	7	-0.382179	-1.015843	0.442363	0.997053	1.000
524	GOBP-REGULATION-OF-CELL-CYCLE	13	-0.319186	-1.016073	0.444598	1.000000	1.000
525	GOBP-DEPHOSPHORYLATION	7	-0.382179	-1.017675	0.433048	1.000000	1.000
526	GOBP-REGULATION-OF-CELLULAR-RESPONSE.TO-STRESS	9	-0.360298	-1.019560	0.450216	1.000000	1.000
527	GOBP-CELL-PROJECTION-ORGANIZATION	35	-0.256067	-1.019747	0.442211	1.000000	1.000
528	GOBP-REGULATION-OF-RESPONSE.TO-STRESS	19	-0.286207	-1.021829	0.430446	1.000000	1.000
529	GOBP-POSITIVE-REGULATION-OF-PEPTIDASE-ACTIVITY	7	-0.395871	-1.024942	0.430124	1.000000	1.000
530	GOBP-REGULATION-OF-LIPID-LOCALIZATION	5	-0.437572	-1.025840	0.442249	1.000000	1.000
531	REACTOME-MYD88-INDEPENDENT-TLR4-CASCADE	8	-0.372989	-1.027387	0.415473	1.000000	1.000
532	GOBP-ESTABLISHMENT-OF-PROTEIN-LOCALIZATION	17	-0.301025	-1.027400	0.428571	1.000000	1.000
533	GOBP-NEGATIVE-REGULATION-OF-TRANSPORT	13	-0.317179	-1.028373	0.435967	1.000000	1.000
534	GOBP-CELL-GROWTH	10	-0.356386	-1.029903	0.432773	1.000000	1.000
535	GOBP-POSITIVE-REGULATION-OF-CYSTEINE-TYPE-ENDO...	7	-0.392871	-1.032287	0.452489	1.000000	1.000
536	GOBP-REGULATION-OF-NEUROTRANSMITTER-TRANSPORT	6	-0.414634	-1.032350	0.406907	1.000000	1.000
537	REACTOME-LEISHMANIA-INFECTION	10	-0.347032	-1.033476	0.425034	1.000000	1.000
538	REACTOME-NERVOUS-SYSTEM-DEVELOPMENT	14	-0.316682	-1.034492	0.423288	1.000000	1.000
539	REACTOME-MAPK-TARGETS-NUCLEAR-EVENTS-MEDIATED...	5	-0.443061	-1.034742	0.418182	1.000000	1.000
540	GOBP-LEUKOCYTE-MEDIATED-IMMUNITY	8	-0.382515	-1.035226	0.419971	1.000000	1.000
541	GOBP-INTRACELLULAR-TRANSPORT	10	-0.352990	-1.041010	0.437946	1.000000	1.000
542	GOBP-WOUND-HEALING	13	-0.320977	-1.043331	0.402579	1.000000	1.000
543	GOBP-NEGATIVE-REGULATION-OF-PHOSPHORYLATION	7	-0.398240	-1.045222	0.429395	1.000000	1.000
544	GOBP-REGULATION-OF-NERVOUS-SYSTEM-PROCESS	8	-0.386354	-1.045414	0.407143	1.000000	1.000
545	GOBP-IMMUNE-RESPONSE-REGULATING-SIGNALING-PATHWAY	8	-0.386391	-1.050992	0.400875	1.000000	1.000
546	GOBP-CIRCADIAN-REGULATION-OF-GENE-EXPRESSION	5	-0.451813	-1.053837	0.390840	1.000000	1.000
547	GOBP-PROTEOLYSIS	17	-0.306120	-1.056996	0.397919	1.000000	1.000
548	GOBP-REGULATION-OF-TRANSPORTER-ACTIVITY	17	-0.304602	-1.058924	0.400268	1.000000	1.000
549	GOBP-FC-RECEPTOR-SIGNALING-PATHWAY	8	-0.386391	-1.059190	0.402878	1.000000	1.000
550	GOBP-LIPID-LOCALIZATION	10	-0.366699	-1.061920	0.372024	1.000000	1.000
551	GOBP-INTRACELLULAR-PROTEIN-TRANSPORT	8	-0.394335	-1.062952	0.396226	1.000000	1.000
552	GOBP-LIPID-EXPORT-FROM-CELL	5	-0.456163	-1.066032	0.412873	1.000000	1.000
553	REACTOME-INTERFERON-SIGNALING	7	-0.425840	-1.067031	0.391705	1.000000	1.000
554	REACTOME-TRANSCRIPTIONAL-REGULATION-BY-MECP2	6	-0.407407	-1.068152	0.375546	1.000000	1.000
555	GOBP-POSITIVE-REGULATION-OF-SECRETION	6	-0.429704	-1.071394	0.377001	1.000000	1.000
556	REACTOME-CIRCADIAN-CLOCK	5	-0.457831	-1.074296	0.379464	1.000000	1.000

Continuation of Table S2

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
557 GOBP-CELLULAR-RESPONSE-TO-PEPTIDE-HORMONE-STIM...	GO-0071375	9	-0.379408	-1.076934	0.357771	0.998661	1.000
558 GOBP-REGULATION-OF-PROTEIN-LOCALIZATION	GO-0032880	18	-0.313043	-1.077578	0.377238	1.000000	1.000
559 GOBP-CELLULAR-RESPONSE-TO-ALCOHOL	GO-0097306	5	-0.470464	-1.078167	0.399096	1.000000	1.000
560 GOBP-REGULATION-OF-PEPTIDE-TRANSPORT	GO-0090087	10	-0.367655	-1.080792	0.361149	1.000000	1.000
561 GOBP-REGULATION-OF-SYSTEM-PROCESS	GO-0044057	18	-0.310188	-1.083597	0.358768	1.000000	1.000
562 REACTOME-DAG-AND-JP3-SIGNALING	R-RNO-1489509	8	-0.398245	-1.084336	0.355958	1.000000	1.000
563 GOBP-MUSCLE-CONTRACTION	GO-0006936	5	-0.475086	-1.084432	0.360182	1.000000	1.000
564 GOBP-PLATELET-ACTIVATION	GO-0030168	6	-0.439645	-1.085277	0.362952	1.000000	1.000
565 GOBP-SYNAPTIC-SIGNALING	GO-0099536	47	-0.268839	-1.085597	0.375154	1.000000	1.000
566 GOBP-POSITIVE-REGULATION-OF-LOCOMOTION	GO-0040017	11	-0.360755	-1.085955	0.370319	1.000000	1.000
567 REACTOME-L1CAM-INTERACTIONS	R-RNO-373760	5	-0.463606	-1.087414	0.388657	1.000000	1.000
568 GOBP-CARBOHYDRATE-DERIVATIVE-BIOSYNTHETIC-PROCESS	GO-1901137	5	-0.465896	-1.088899	0.350388	1.000000	1.000
569 REACTOME-INTERLEUKIN_I7-SIGNALING	R-RNO-448424	6	-0.439454	-1.088975	0.347181	1.000000	1.000
570 GOBP-REGULATION-OF-NEUROTRANSMITTER-LEVELS	GO-0001505	7	-0.419753	-1.092002	0.350725	1.000000	1.000
571 GOBP-FATTY-ACID-TRANSPORT	GO-0015908	6	-0.445646	-1.105253	0.335294	0.992244	1.000
572 GOBP-NEUROTRANSMITTER-TRANSPORT	GO-0006836	7	-0.419753	-1.105305	0.330484	0.998572	1.000
573 GOBP-GAMETE-GENERATION	GO-0007276	9	-0.386609	-1.107766	0.336662	0.996697	1.000
574 GOBP-REGULATION-OF-MUSCLE-ADAPTATION	GO-0043502	5	-0.481928	-1.109226	0.330769	0.998466	1.000
575 GOBP-HOMEOSTATIC-PROCESS	GO-0042592	31	-0.279633	-1.110197	0.339552	1.000000	1.000
576 REACTOME-RNA-POLYMERASE-III-TRANSCRIPTION	R-RNO-73857	20	-0.310016	-1.111509	0.328125	1.000000	1.000
577 GOBP-MUSCLE-ADAPTATION	GO-0043500	5	-0.481928	-1.115123	0.333866	0.998563	1.000
578 GOBP-PROTEIN-LOCALIZATION-TO-SYNAPSE	GO-0035418	5	-0.476798	-1.116602	0.320669	1.000000	1.000
579 GOBP-NEGATIVE-REGULATION-OF-RESPONSE-TO-EXTERN...	GO-0032102	5	-0.485600	-1.117970	0.324409	1.000000	1.000
580 GOBP-MONOCARBOXYLIC-ACID-TRANSPORT	GO-0015718	5	-0.485881	-1.119902	0.312694	1.000000	1.000
581 GOBP-NEGATIVE-REGULATION-OF-ANION-TRANSPORT	GO-1903792	8	-0.409779	-1.120853	0.338663	1.000000	1.000
582 GOBP-ACIDIC-AMINO-ACID-TRANSPORT	GO-0015800	5	-0.485881	-1.124610	0.302290	1.000000	1.000
583 GOBP-PROTEIN-LOCALIZATION-TO-POSTSYNAPSE	GO-0062237	5	-0.476798	-1.125301	0.302067	1.000000	1.000
584 GOBP-SECRETION	GO-0046903	24	-0.304839	-1.129857	0.301405	0.996688	1.000
585 GOBP-DICARBOXYLIC-ACID-TRANSPORT	GO-0006835	5	-0.485881	-1.130764	0.293395	1.000000	1.000
586 GOBP-REGULATION-OF-CELL-ADHESION	GO-0030155	13	-0.354813	-1.131292	0.293706	1.000000	1.000
587 GOBP-REGULATION-OF-TRANSPORT	GO-0051049	44	-0.278761	-1.131678	0.321770	1.000000	1.000
588 REACTOME-BETA-CATENIN-INDEPENDENT-WNT-SIGNALING	GO-0098660	9	-0.394516	-1.134350	0.302726	1.000000	1.000
589 GOBP-CALCIUM-ION-TRANSPORT-INTO-CYTOSOL	R-RNO-3858494	5	-0.493976	-1.137589	0.287591	1.000000	1.000
590 GOBP-REGULATION-OF-VASCULATURE-DEVELOPMENT	GO-0060402	7	-0.438199	-1.138242	0.293413	1.000000	1.000
591 GOBP-SENSORY-ORGAN-DEVELOPMENT	GO-1901342	5	-0.493884	-1.139157	0.303266	1.000000	1.000
592 REACTOME-RHO-GTPASE-EFFECTORS	GO-0007423	8	-0.417031	-1.139854	0.307359	1.000000	1.000
593 GOBP-CALCIUM-ION-TRANSMEMBRANE-TRANSPORT	R-RNO-195258	9	-0.404701	-1.146367	0.271041	1.000000	1.000
594 GOBP-REGULATION-OF-POSTSYNAPSE-ORGANIZATION	GO-0070588	7	-0.438199	-1.146976	0.296407	1.000000	1.000
595 GOBP-DENDRITE-MORPHOGENESIS	GO-0099175	6	-0.457235	-1.147920	0.295666	1.000000	1.000
596 GOBP-CYTOSOLIC-CALCIUM-ION-TRANSPORT	GO-0048813	7	-0.442763	-1.149962	0.295154	1.000000	1.000
597 GOBP-MUSCLE-SYSTEM-PROCESS	GO-0060401	7	-0.438199	-1.150805	0.300310	1.000000	1.000
598 GOBP-REGULATION-OF-BODY-FLUID-LEVELS	GO-0003012	9	-0.405093	-1.153083	0.287749	1.000000	1.000
599 GOBP-REGULATION-OF-BODY-FLUID-LEVELS	GO-0050878	11	-0.379200	-1.156773	0.297965	1.000000	1.000

Continuation of Table S2

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
600	GOBP-CENTRAL-NERVOUS-SYSTEM-DEVELOPMENT	27	-0.301034	-1.157940	0.303371	1.000000	1.000
601	GOBP-CARBOHYDRATE-HOMEOSTASIS	7	-0.440064	-1.162099	0.263868	1.000000	1.000
602	REACTOME-G-ALPHA-Z-SIGNALING-EVENTS	5	-0.493976	-1.162235	0.267405	1.000000	1.000
603	REACTOME-TRANSCRIPTIONAL-REGULATION-BY-TP53	6	-0.470448	-1.164079	0.276596	1.000000	1.000
604	REACTOME-SIGNALING-BY-RHO-GTPASES-MIRO-GTPASES...	9	-0.404701	-1.166495	0.264012	1.000000	1.000
605	GOBP-CELL-CELL-SIGNALING-BY-WNT	7	-0.436764	-1.168311	0.251841	1.000000	1.000
606	GOBP-COAGULATION	8	-0.423395	-1.169896	0.279494	1.000000	1.000
607	GOBP-RESPONSE-TO-WOUNDING	15	-0.349273	-1.171171	0.272849	1.000000	1.000
608	GOBP-ORGANOPHOSPHATE-BIOSYNTHETIC-PROCESS	5	-0.505945	-1.175941	0.258970	1.000000	1.000
609	GOBP-REGULATION-OF-MUSCLE-SYSTEM-PROCESS	8	-0.434877	-1.175997	0.237313	1.000000	1.000
610	REACTOME-PTEN-REGULATION	5	-0.506090	-1.177432	0.254290	1.000000	1.000
611	GOBP-REGULATION-OF-SYNAPTIC-PLASTICITY	21	-0.325921	-1.177620	0.282638	1.000000	1.000
612	GOBP-SEXUAL-REPRODUCTION	10	-0.398252	-1.179922	0.283804	1.000000	1.000
613	GOBP-CELL-CELL-SIGNALING	56	-0.298321	-1.183036	0.266586	1.000000	1.000
614	GOBP-GROWTH	14	-0.365982	-1.183077	0.272727	1.000000	1.000
615	GOBP-TRANSMEMBRANE-TRANSPORT	27	-0.309359	-1.188971	0.259823	1.000000	1.000
616	GOBP-REGULATION-OF-SYNAPTIC-TRANSMISSION-GLUTA...	12	-0.385135	-1.190906	0.267568	1.000000	1.000
617	GOBP-NUCLEOSIDE-PHOSPHATE-BIOSYNTHETIC-PROCESS	5	-0.505945	-1.192798	0.241538	1.000000	1.000
618	REACTOME-FC-EPSILON-RECEPTOR-FCERL-SIGNALING	7	-0.462802	-1.197427	0.215152	1.000000	1.000
619	REACTOME-G-ALPHA-Q-SIGNALING-EVENTS	6	-0.477054	-1.199992	0.234824	1.000000	1.000
620	GOBP-REGULATION-OF-TRANS-SYNAPTIC-SIGNALING	40	-0.293992	-1.203099	0.240903	1.000000	1.000
621	GOBP-DENDRITE-DEVELOPMENT	10	-0.403987	-1.207640	0.218077	1.000000	1.000
622	GOBP-CHROMOSOME-ORGANIZATION	6	-0.490371	-1.210312	0.232456	1.000000	1.000
623	GOBP-INNATE-IMMUNE-RESPONSE	7	-0.467437	-1.215455	0.232170	1.000000	1.000
624	GOBP-FC-EPSILON-RECEPTOR-SIGNALING-PATHWAY	7	-0.462802	-1.221193	0.243478	0.988504	1.000
625	GOBP-NEGATIVE-REGULATION-OF-CELL-PROJECTION-OR...	5	-0.527500	-1.223418	0.207317	0.989456	1.000
626	GOBP-LOCOMOTORY-BEHAVIOR	8	-0.454188	-1.225827	0.191176	0.989916	1.000
627	REACTOME-TRAFFICKING-OF-GLUR2-CONTAINING-AMPA-...	8	-0.450000	-1.227917	0.176642	0.991887	1.000
628	GOBP-HEAD-DEVELOPMENT	23	-0.330315	-1.227920	0.208333	1.000000	1.000
629	GOBP-SIGNAL-RELEASE	14	-0.379726	-1.236594	0.193681	0.977540	1.000
630	GOBP-REGULATION-OF-SECRETION	14	-0.379856	-1.240428	0.191432	0.972704	1.000
631	GOBP-NEUROTRANSMITTER-SECRETION	6	-0.500000	-1.241094	0.207831	0.980484	1.000
632	GOBP-MALE-GAMETE-GENERATION	5	-0.542169	-1.246496	0.203101	0.969499	1.000
633	GOBP-CELLULAR-MACROMOLECULE-CATABOLIC-PROCESS	5	-0.544343	-1.252644	0.209231	0.955066	1.000
634	GOBP-REGULATION-OF-CELL-CYCLE-PROCESS	5	-0.550414	-1.252782	0.206231	0.965091	1.000
635	GOBP-CELLULAR-RESPONSE-TO-KETONE	5	-0.534818	-1.255053	0.170404	0.966587	1.000
636	GOBP-CHEMICAL-SYNAPTIC-TRANSMISSION-POSTSYNAPTIC	9	-0.451440	-1.267849	0.174962	0.924492	1.000
637	GOBP-RESPONSE-TO-ALCOHOL	11	-0.423741	-1.297619	0.173554	0.819952	1.000
638	GOBP-CELL-CYCLE	21	-0.352648	-1.297864	0.158365	0.828658	1.000
639	GOBP-CALCIUM-ION-TRANSPORT	11	-0.429318	-1.299588	0.150000	0.835324	1.000
640	GOBP-CELL-SURFACE-RECEPTOR-SIGNALING-PATHWAY-I...	15	-0.397237	-1.300695	0.160265	0.837640	1.000
641	GOBP-PROTEIN-LOCALIZATION-TO-ORGANELLE	8	-0.471388	-1.301144	0.167135	0.845867	1.000
642	GOBP-MITOTIC-CELL-CYCLE	10	-0.447847	-1.308137	0.156780	0.829737	1.000

Continuation of Table S2

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
643 REACTOME-HEMOSTASIS	R-RNO-109582	14	-0.403680	-1.309821	0.156000	0.833214	1.000
644 REACTOME-CA-DEPENDENT-EVENTS	R-RNO-111996	8	-0.475000	-1.311256	0.165906	0.838129	1.000
645 GOBP-RESPONSE-TO-TUMOR-NECROSIS-FACTOR	GO-0034612	7	-0.497977	-1.313266	0.152518	0.841031	1.000
646 GOBP-MAPK-CASCADE	GO-0000165	18	-0.379171	-1.316737	0.141145	0.838148	1.000
647 REACTOME-SIGNALING-BY-WNT	R-RNO-195721	7	-0.520046	-1.320924	0.140719	0.831779	1.000
648 GOBP-NUCLEAR-TRANSPORT	GO-0051169	5	-0.560217	-1.323734	0.122807	0.831657	1.000
649 GOBP-MEMBRANE-ORGANIZATION	GO-0061024	12	-0.420784	-1.328571	0.151344	0.823309	1.000
650 GOBP-NEGATIVE-REGULATION-OF-TRANSFERASE-ACTIVITY	GO-0051348	5	-0.571128	-1.330146	0.125937	0.827970	1.000
651 GOBP-ORGANIC-ACID-TRANSPORT	GO-0015849	7	-0.503540	-1.330361	0.141369	0.838356	1.000
652 GOBP-NEGATIVE-REGULATION-OF-KINASE-ACTIVITY	GO-0033673	5	-0.571128	-1.331859	0.120980	0.843636	1.000
653 GOBP-SYNAPTIC-TRANSMISSION-GLUTAMATERGIC	GO-0035249	13	-0.418705	-1.332131	0.160221	0.854343	1.000
654 GOBP-ORGANIC-ANION-TRANSPORT	GO-0015711	6	-0.537694	-1.334938	0.135053	0.854107	1.000
655 GOBP-METAL-ION-TRANSPORT	GO-0030001	11	-0.429318	-1.336007	0.148966	0.861508	1.000
656 GOBP-CARBOXYLIC-ACID-TRANSPORT	GO-0046942	6	-0.537694	-1.338010	0.131148	0.865587	1.000
657 REACTOME-CREB1-PHOSPHORYLATION-THROUGH-NMDA-RE...	R-RNO-442742	8	-0.485388	-1.341865	0.127566	0.862523	1.000
658 GOBP-PROTEIN-TETRAMERIZATION	GO-0051262	5	-0.578313	-1.342770	0.111635	0.871855	1.000
659 REACTOME-CELL-CYCLE-MITOTIC	R-RNO-69278	5	-0.578650	-1.343701	0.134441	0.881371	1.000
660 GOBP-POSTTRANSCRIPTIONAL-REGULATION-OF-GENE-EX...	GO-0010608	8	-0.490146	-1.344707	0.130435	0.890775	1.000
661 GOBP-AMINO-ACID-TRANSPORT	GO-0006865	6	-0.537694	-1.355343	0.102326	0.860527	1.000
662 GOBP-CELLULAR-GLUCOSE-HOMEOSTASIS	GO-0001678	5	-0.592096	-1.362074	0.115152	0.845778	1.000
663 GOBP-ESTABLISHMENT-OF-PROTEIN-LOCALIZATION-TO-...	GO-0072594	5	-0.583592	-1.368286	0.090352	0.833278	1.000
664 GOBP-PROTEIN-COMPLEX-OLIGOMERIZATION	GO-0051259	7	-0.530725	-1.378353	0.127193	0.806843	1.000
665 GOBP-SECOND-MESSENGER-MEDIATED-SIGNALING	GO-0019932	16	-0.413385	-1.381192	0.105820	0.808792	1.000
666 REACTOME-INTRACELLULAR-SIGNALING-BY-SECOND-MES...	R-RNO-9006925	15	-0.417131	-1.381440	0.111842	0.821499	1.000
667 REACTOME-G-PROTEIN-MEDIATED-EVENTS	R-RNO-112040	13	-0.442679	-1.387292	0.100730	0.830294	1.000
668 GOBP-DIVALENT-INORGANIC-CATION-HOMEOSTASIS	GO-0072507	9	-0.481013	-1.382837	0.114441	0.826272	1.000
669 GOBP-REGULATION-OF-ANION-TRANSPORT	GO-0044070	20	-0.386788	-1.396394	0.100000	0.802443	1.000
670 GOBP-REGULATION-OF-CYTOSOLIC-CALCIUM-ION-CONCE...	GO-0051480	13	-0.442679	-1.400049	0.108871	0.800699	1.000
671 GOBP-PROTEIN-CONTAINING-COMPLEX-SUBUNIT-ORGANI...	GO-0043933	15	-0.421908	-1.401436	0.096317	0.810104	1.000
672 REACTOME-NEUREXINS-AND-NEUROLIGINS	R-RNO-6794361	9	-0.493462	-1.402112	0.103448	0.822604	1.000
673 GOBP-METAL-ION-HOMEOSTASIS	GO-0055065	14	-0.436559	-1.406730	0.099329	0.819380	1.000
674 REACTOME-CELL-CYCLE	R-RNO-1640170	6	-0.572810	-1.408553	0.082171	0.827412	1.000
675 GOBP-EXCITATORY-CHEMICAL-SYNAPTIC-TRANSMISSION	GO-0098976	5	-0.599664	-1.408622	0.104596	0.843729	1.000
676 GOBP-NEGATIVE-REGULATION-OF-MULTICELLULAR-ORGA...	GO-0051241	15	-0.420879	-1.409943	0.100271	0.854781	1.000
677 REACTOME-RAS-ACTIVATION-UPON-CA2-INFLUX-THROUG...	R-HSA-442982	6	-0.573171	-1.410257	0.094595	0.871169	1.000
678 GOBP-REGULATION-OF-SIGNALING-RECEPTOR-ACTIVITY	GO-0010469	14	-0.434362	-1.420007	0.098274	0.846374	1.000
679 REACTOME-TRAFFICKING-OF-AMPA-RECEPTORS	R-RNO-399719	11	-0.467532	-1.420179	0.079498	0.863845	1.000
680 REACTOME-CLASS-C-3-METABOTROPIC-GLUTAMATE-PHER...	R-RNO-420499	7	-0.555922	-1.426068	0.084746	0.855601	1.000
681 REACTOME-ASSEMBLY-AND-CELL-SURFACE-PRESENTATIO...	R-RNO-9609736	8	-0.519388	-1.430865	0.074561	0.854270	1.000
682 REACTOME-MAPK-FAMILY-SIGNALING-CASCADES	R-RNO-5683057	12	-0.459035	-1.432120	0.070442	0.868940	1.000
683 GOBP-REGULATION-OF-CATION-CHANNEL-ACTIVITY	R-RNO-2001257	14	-0.434545	-1.433049	0.083333	0.885145	1.000
684 REACTOME-GPCR-LIGAND-BINDING	R-RNO-500792	8	-0.530619	-1.437037	0.077037	0.880155	1.000
685 REACTOME-NEGATIVE-REGULATION-OF-NMDA-RECEPTOR-...	R-HSA-9617324	8	-0.519388	-1.440190	0.089443	0.895385	1.000

Continuation of Table S2

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
686	GOBP-CHEMICAL-HOMEOSTASIS	23	-0.388955	-1.444721	0.078844	0.896240	1.000
687	GOBP-REGULATION_OF_CATION_TRANSMEMBRANE_TRANSPORT	16	-0.428081	-1.460395	0.071146	0.843066	1.000
688	REACTOME-ADAPTIVE-IMMUNE-SYSTEM	9	-0.509115	-1.463810	0.068376	0.850692	1.000
689	GOBP-CATION_TRANSMEMBRANE_TRANSPORT	18	-0.425261	-1.465961	0.058589	0.864340	1.000
690	GOBP-ION-HOMEOSTASIS	16	-0.437862	-1.473055	0.072776	0.854910	1.000
691	GOBP-CELLULAR-COMPONENT-MAINTENANCE	5	-0.627201	-1.477436	0.055046	0.856431	1.000
692	GOBP-SENSORY_PERCEPTION_OF_PAIN	5	-0.635554	-1.487454	0.050671	0.832943	1.000
693	GOBP-ENDOMEMBRANE-SYSTEM_ORGANIZATION	6	-0.603065	-1.493016	0.046990	0.831064	1.000
694	GOBP-RESPONSE_TO_ETHANOL	5	-0.638554	-1.494116	0.048601	0.852698	1.000
695	GOBP-CELLULAR_ION_HOMEOSTASIS	14	-0.466689	-1.521191	0.061026	0.750830	1.000
696	REACTOME-INTEGRATION_OF_ENERGY_METABOLISM	5	-0.661504	-1.539973	0.045741	0.694127	1.000
697	GOBP-REGULATION_OF_MEMBRANE_POTENTIAL	17	-0.450870	-1.544169	0.042497	0.700519	1.000
698	GOBP-G-PROTEIN_COUPLED_GLUTAMATE_RECEPTOR_SIGN...	8	-0.582439	-1.570704	0.026746	0.615723	1.000
699	REACTOME-OPIOID_SIGNALING	12	-0.500000	-1.571680	0.039945	0.636165	1.000
700	GOBP-REGULATION_OF_NEUROTRANSMITTER_RECEPTOR_A...	13	-0.494573	-1.577922	0.040166	0.635698	1.000
701	GOBP-REGULATION_OF_POSTSYNAPTIC_MEMBRANE_POTEN...	14	-0.488935	-1.592668	0.046113	0.606039	1.000
702	REACTOME-LONG-TERM_POTENTIATION	10	-0.546232	-1.608867	0.020576	0.567000	1.000
703	GOBP-CELLULAR_HOMEOSTASIS	18	-0.455897	-1.619541	0.035573	0.551034	1.000
704	REACTOME-SYNAPTIC_ADHESION-LIKE-MOLECULES	9	-0.573582	-1.634053	0.029070	0.521470	1.000
705	GOBP-REGULATION_OF_NMDA_RECEPTOR_ACTIVITY	10	-0.581937	-1.678013	0.011348	0.402719	1.000
706	GOBP-ADENYLATE_CYCLASE-INHIBITING-G-PROTEIN_CO...	5	-0.723347	-1.682956	0.015699	0.410429	1.000
707	GOBP-REGULATION_OF_ION_TRANSPORT	36	-0.419160	-1.686929	0.030265	0.420669	1.000
708	GOBP-G-PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY	18	-0.484188	-1.705699	0.015831	0.388496	1.000
709	REACTOME-PROTEIN-PROTEIN-INTERACTIONS-AT-SYNAPSES	12	-0.549302	-1.712471	0.011299	0.392093	1.000
710	GOBP-ADENYLATE_CYCLASE-MODULATING-G-PROTEIN_CO...	11	-0.567980	-1.724652	0.014306	0.380440	1.000
711	GOBP-NEGATIVE-REGULATION_OF_GENE_EXPRESSION	11	-0.570191	-1.742220	0.008511	0.357916	0.995
712	REACTOME-ACTIVATION_OF_NMDA_RECEPTORS-AND-POST...	16	-0.512241	-1.755589	0.011984	0.344880	0.993
713	GOBP-ADENYLATE_CYCLASE-INHIBITING-G-PROTEIN_CO...	9	-0.614078	-1.767819	0.007143	0.338171	0.992
714	REACTOME-SIGNALING-BY-GPCR	22	-0.483142	-1.772512	0.003916	0.355531	0.991
715	REACTOME-UNBLOCKING_OF_NMDA_RECEPTORS-GLUTAMAT...	12	-0.570093	-1.779374	0.011080	0.368191	0.986
716	REACTOME-G-ALPHA_I-SIGNALING-EVENTS	18	-0.515174	-1.786708	0.010652	0.386627	0.979
717	GOBP-CATION_TRANSPORT	25	-0.477040	-1.795458	0.003876	0.404711	0.972
718	GOBP-IONOTROPIC-GLUTAMATE_RECEPTOR_SIGNALING_P...	9	-0.625297	-1.801502	0.008596	0.440991	0.966
719	GOBP-CELL_CYCLE_PROCESS	11	-0.606056	-1.874702	0.002729	0.267976	0.848
720	REACTOME-NEUROTRANSMITTER_RECEPTORS-AND_POSTSY...	22	-0.510420	-1.905832	0.003802	0.239683	0.748
721	GOBP-SENSORY_PERCEPTION	9	-0.670886	-1.909889	0.001422	0.289396	0.735
722	REACTOME-TRANSMISSION-ACROSS-CHEMICAL-SYNAPSES	23	-0.519574	-1.920571	0.003856	0.325049	0.667
723	REACTOME-NEURONAL-SYSTEM	26	-0.531507	-2.014244	0.001255	0.211187	0.374
724	GOBP-GLUTAMATE_RECEPTOR_SIGNALING_PATHWAY	17	-0.646270	-2.239019	0.000000	0.031969	0.036

End of Table

Supplementary Table S3: SC rostral segment early (8 DPL peak) profile GSEA results.

Begin of Table S3									
	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val	
0	REACTOME_INTERLEUKIN_4_AND_INTERLEUKIN_13_SIGNALING	R-RNO-6785807	8	0.784993	2.518360	0.000000	0.021501	0.015	
1	GOBP_NEGATIVE_REGULATION_OF_PEPTIDASE_ACTIVITY	GO-0010466	6	0.736709	2.130500	0.000000	0.257322	0.298	
2	HALLMARK_TNFA_SIGNALING_VIA_NFKB	M5890	14	0.459459	1.908470	0.004831	0.688131	0.748	
3	GOBP_POSITIVE_REGULATION_OF_CELL_DIFFERENTIATION	GO-0045597	27	0.353574	1.854106	0.000000	0.684561	0.836	
4	GOBP_RESPONSE_TO_ENDOGENOUS_STIMULUS	GO-0009719	34	0.335154	1.838417	0.000000	0.588722	0.856	
5	GOBP_NEGATIVE_REGULATION_OF_CYSTINE_TYPE_ENDOGENOUS_RESPONSE	GO-2000117	5	0.699344	1.801695	0.016892	0.588662	0.902	
6	GOBP_OSTEOCLAST_DIFFERENTIATION	GO-0030316	6	0.622961	1.775699	0.013937	0.575180	0.930	
7	GOBP_LEUKOCYTE_DIFFERENTIATION	GO-0002521	15	0.410959	1.771396	0.021622	0.513138	0.935	
8	GOBP_POSITIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_CONTRACTION	GO-0048661	5	0.674699	1.761438	0.022801	0.479749	0.948	
9	GOBP_CYTOKINE_MEDIATED_SIGNALING_PATHWAY	GO-0019221	16	0.402778	1.742551	0.000000	0.472665	0.961	
10	GOBP_OSTEOBLAST_DIFFERENTIATION	GO-0001649	5	0.674699	1.720435	0.026578	0.478233	0.979	
11	GOBP_DEFENSE_RESPONSE	GO-0006952	19	0.376812	1.704846	0.012379	0.474040	0.984	
12	REACTOME_SIGNALING_BY_INTERLEUKINS	R-RNO-449147	15	0.396585	1.683649	0.023474	0.484422	0.990	
13	GOBP_BLOOD_VESSEL_MORPHOGENESIS	GO-0048514	14	0.405405	1.679468	0.021390	0.455829	0.991	
14	REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM	R-RNO-1280215	21	0.338604	1.648508	0.018405	0.495027	0.996	
15	GOBP_REGULATION_OF_CELL_DIFFERENTIATION	GO-0045595	32	0.300962	1.641018	0.000000	0.481683	0.998	
16	GOBP_POSITIVE_REGULATION_OF_DEVELOPMENTAL_PROCESS	GO-0051094	36	0.300962	1.635074	0.008264	0.468198	0.998	
17	GOBP_REGULATION_OF_HEMOPOIESIS	GO-1903706	10	0.461538	1.626675	0.037975	0.459145	1.000	
18	GOBP_OSSIFICATION	GO-0001503	9	0.481444	1.623824	0.053571	0.439820	1.000	
19	GOBP_CELLULAR_RESPONSE_TO_NITROGEN_COMPOUND	GO-1901699	20	0.333804	1.595932	0.017857	0.476835	1.000	
20	GOBP_MYELOID_CELL_DIFFERENTIATION	GO-0030099	13	0.400000	1.595797	0.051282	0.454274	1.000	
21	GOBP_ANATOMICAL_STRUCTURE_FORMATION_INVOLVED_IN_CELL_DEVELOPMENT	GO-0048646	20	0.336803	1.587974	0.023952	0.449877	1.000	
22	GOBP_CELLULAR_RESPONSE_TO_PEPTIDE	GO-1901653	13	0.386667	1.565440	0.035398	0.481665	1.000	
23	GOBP_PRL_MIRNA_TRANSCRIPTION_BY_RNA_POLYMERASE_II	GO-0061614	7	0.506173	1.561183	0.067568	0.470515	1.000	
24	GOBP_POSITIVE_REGULATION_OF_CYTOKINE_PRODUCTION	GO-0001819	7	0.506173	1.561106	0.045627	0.451695	1.000	
25	GOBP_NEGATIVE_REGULATION_OF_CELL_DEATH	GO-0060548	22	0.318182	1.557852	0.013158	0.441954	1.000	
26	GOBP_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	GO-0045637	9	0.455696	1.555968	0.051724	0.429516	1.000	
27	GOBP_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	GO-1902105	9	0.455696	1.545615	0.029787	0.434428	1.000	
28	GOBP_POSITIVE_REGULATION_OF_PRL_MIRNA_TRANSCRIPTION	GO-1902895	7	0.506173	1.535649	0.054054	0.440023	1.000	
29	GOBP_MONONUCLEAR_CELL_DIFFERENTIATION	GO-1903131	7	0.493827	1.520827	0.040161	0.455997	1.000	
30	GOBP_CELL_POPULATION_PROLIFERATION	GO-0008283	32	0.265636	1.491342	0.042017	0.505450	1.000	
31	HALLMARK_ALLOGRAFT_REJECTION	M5950	7	0.493827	1.488915	0.067857	0.495542	1.000	
32	GOBP_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	GO-0045670	5	0.564178	1.474750	0.083333	0.512239	1.000	
33	GOBP_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENTIATION	GO-0002761	8	0.450000	1.466358	0.092308	0.516134	1.000	
34	GOBP_AMEBOIDAL_TYPE_CELL_MIGRATION	GO-0001667	11	0.389610	1.464363	0.070423	0.505857	1.000	
35	GOBP_RAS_PROTEIN_SIGNAL_TRANSDUCTION	GO-0007265	5	0.578313	1.460845	0.076923	0.490188	1.000	
36	GOBP_NEGATIVE_REGULATION_OF_CELL_POPULATION_PROLIFERATION	GO-0008285	9	0.431277	1.460354	0.073684	0.487369	1.000	
37	GOBP_MYELOID_LEUKOCYTE_DIFFERENTIATION	GO-0002573	11	0.389610	1.443364	0.074890	0.514811	1.000	
38	GOBP_CELLULAR_RESPONSE_TO_OXYGEN_CONTAINING_COMPOUND	GO-1901701	29	0.267083	1.424809	0.043103	0.541622	1.000	
39	REACTOME_TRANSCRIPTIONAL_REGULATION_OF_WHITE_ADIPOCYTE_DIFFERENTIATION	R-RNO-381340	6	0.500000	1.424755	0.073171	0.528197	1.000	
40	GOBP_RESPONSE_TO_MECHANICAL_STIMULUS	GO-0009612	6	0.500000	1.417183	0.103679	0.532377	1.000	

Continuation of Table S3

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
41	GOBP-POSITIVE-REGULATION_OF_TRANSCRIPTION_BY_R...	24	0.282914	1.412818	0.073826	0.530247	1.000
42	GOBP-RESPONSE_TO_PEPTIDE	18	0.309449	1.411098	0.089385	0.521702	1.000
43	GOBP-RESPONSE_TO_CYTOKINE	23	0.279196	1.404905	0.061728	0.523425	1.000
44	REACTOME-DEATH-RECEPTOR-SIGNALING	5	0.534155	1.403333	0.125000	0.515704	1.000
45	GOBP-POSITIVE-REGULATION_OF_MULTICELLULAR_ORGA...	32	0.251094	1.398258	0.076271	0.515165	1.000
46	GOBP-POSITIVE-REGULATION_OF_NUCLEOBASE-CONTAIN...	28	0.261989	1.383227	0.053846	0.538803	1.000
47	GOBP-LEUKOCYTE-CELL-CELL-ADHESION	6	0.500000	1.380752	0.099678	0.533505	1.000
48	GOBP-CELLULAR-RESPONSE_TO_HORMONE-STIMULUS	11	0.376623	1.374529	0.106667	0.536641	1.000
49	GOBP-IMMUNE-SYSTEM-DEVELOPMENT	17	0.316293	1.369192	0.064103	0.538479	1.000
50	GOBP-CYTOKINE-PRODUCTION	10	0.384615	1.363603	0.093220	0.541880	1.000
51	GOBP-NEGATIVE-REGULATION_OF_PROTEOLYSIS	8	0.416564	1.360107	0.109929	0.538666	1.000
52	GOBP-INFLAMMATORY-RESPONSE	12	0.355263	1.345273	0.146667	0.561388	1.000
53	GOBP-POSITIVE-REGULATION_OF_GENE-EXPRESSION	16	0.308092	1.337342	0.080214	0.568983	1.000
54	GOBP-POSITIVE-REGULATION_OF_BIOSYNTHETIC-PROCESS	27	0.247471	1.331844	0.084507	0.572267	1.000
55	GOBP-POSITIVE-REGULATION_OF_MYELOID-CELL-DIFFE...	7	0.444444	1.327102	0.118081	0.573523	1.000
56	GOBP-POSITIVE-REGULATION_OF_HEMOPOIESIS	12	0.343374	1.325744	0.112613	0.557122	1.000
57	GOBP-ANIMAL-ORGAN-MORPHOGENESIS	9	0.379747	1.315879	0.124464	0.570732	1.000
58	GOBP-TISSUE-MIGRATION	8	0.418845	1.312738	0.170040	0.568363	1.000
59	GOBP-CELLULAR-RESPONSE_TO_EXTRACELLULAR-STIMULUS	5	0.506880	1.307240	0.125828	0.572002	1.000
60	HALLMARK-HYPOXIA	10	0.360491	1.305539	0.125561	0.566353	1.000
61	GOBP-CELLULAR-RESPONSE_TO_EXTERNAL-STIMULUS	9	0.379747	1.285547	0.162500	0.605189	1.000
62	GOBP-FAT-CELL-DIFFERENTIATION	21	0.267349	1.284313	0.143713	0.598937	1.000
63	GOBP-POSITIVE-REGULATION_OF_CELL-POPULATION.PR...	5	0.506024	1.282164	0.165079	0.594726	1.000
64	GOBP-REGULATION_OF_ANION-TRANSMEMBRANE-TRANSPORT	33	0.225391	1.267578	0.119266	0.612100	1.000
65	GOBP-POSITIVE-REGULATION_OF_CELL-CELL-ADHESION	5	0.493976	1.271073	0.168498	0.612620	1.000
66	GOBP-PROTEIN-PHOSPHORYLATION	5	0.481928	1.246952	0.190789	0.655338	1.000
67	GOBP-HOMEOSTASIS_OF_NUMBER-OF-CELLS	8	0.375000	1.242722	0.160338	0.656854	1.000
68	GOBP-ENDOTHELIAL-CELL-PROLIFERATION	5	0.493976	1.242314	0.207792	0.648520	1.000
69	GOBP-POSITIVE-REGULATION_OF_LEUKOCYTE-CELL-CEL...	5	0.481928	1.241924	0.210000	0.640357	1.000
70	GOBP-SKIN-DEVELOPMENT	6	0.439024	1.240634	0.204620	0.635096	1.000
71	GOBP-POSITIVE-REGULATION_OF_MYELOID-LEUKOCYTE-...	8	0.375000	1.232408	0.192453	0.646238	1.000
72	GOBP-ENDOTHELIAL-CELL-MIGRATION	9	0.367088	1.231780	0.184874	0.638975	1.000
73	GOBP-DEFENSE-RESPONSE_TO_OTHER-ORGANISM	21	0.255471	1.230069	0.168675	0.634345	1.000
74	GOBP-CIRCULATORY-SYSTEM-DEVELOPMENT	5	0.481928	1.224121	0.215753	0.640098	1.000
75	GOBP-REGULATION_OF_LYMPHOCYTE-ACTIVATION	31	0.222563	1.219608	0.156250	0.643005	1.000
76	GOBP-REGULATION_OF_MULTICELLULAR-ORGANISMAL.DE...	8	0.375000	1.213817	0.191571	0.649382	1.000
77	GOBP-RESPONSE_TO_OXYGEN-LEVELS	11	0.324675	1.211510	0.187192	0.647465	1.000
78	GOBP-NEGATIVE-REGULATION_OF_NEURON-DEATH	8	0.375000	1.213817	0.191571	0.649382	1.000
79	REACTOME-DAG-AND-IP3-SIGNALING	8	0.362500	1.195847	0.219331	0.678175	1.000
80	GOBP-PEPTIDYL-AMINO-ACID-MODIFICATION	22	0.242424	1.194104	0.191489	0.674729	1.000
81	GOBP-EPIDERMIS-DEVELOPMENT	5	0.457831	1.194013	0.227801	0.666829	1.000
82	GOBP-BLOOD-VESSEL-ENDOTHELIAL-CELL-MIGRATION	8	0.375000	1.182722	0.240964	0.687024	1.000
83	GOBP-NEUROTROPHIN-SIGNALING_PATHWAY	6	0.406856	1.173142	0.254902	0.706098	1.000

Continuation of Table S3

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
84	GOBP-MAINTENANCE-OF-LOCATION	7	0.370370	1.155704	0.235294	0.742957	1.000
85	GOBP-NEUROTROPHIN_TRK_RECEPTOR-SIGNALING.PATHWAY	6	0.406856	1.150246	0.270833	0.749556	1.000
86	GOBP-RESPONSE-TO-GROWTH-FACTOR	18	0.252367	1.143544	0.245033	0.758093	1.000
87	GOBP-PROTEIN-MODIFICATION-BY-SMALL-PROTEIN-CON...	7	0.370370	1.137912	0.256917	0.765820	1.000
88	GOBP-POSITIVE-REGULATION-OF-EPITHELIAL-CELL-PR...	7	0.370370	1.137830	0.238636	0.757553	1.000
89	GOBP-RESPONSE-TO-BIOTIC-STIMULUS	17	0.260590	1.133773	0.245714	0.759584	1.000
90	GOBP-RESPONSE-TO-INTERLEUKIN_1	5	0.433735	1.132552	0.318493	0.754552	1.000
91	GOBP-RESPONSE-TO-HORMONE	20	0.234854	1.123023	0.266304	0.772827	1.000
92	GOBP-ACTIN-FILAMENT-BASED-PROCESS	7	0.362602	1.117692	0.286275	0.779794	1.000
93	GOBP-PERIPHERAL-NERVOUS-SYSTEM-DEVELOPMENT	9	0.316456	1.115001	0.229885	0.778519	1.000
94	GOBP-CELLULAR-RESPONSE-TO-ABIOTIC-STIMULUS	7	0.370370	1.114226	0.300752	0.772426	1.000
95	GOBP-CELL-CELL-JUNCTION-ASSEMBLY	5	0.433735	1.111734	0.291096	0.771955	1.000
96	HALLMARK-KRAS-SIGNALING-UP	6	0.378049	1.104313	0.300366	0.783924	1.000
97	GOBP-NEGATIVE-REGULATION-OF-TRANSCRIPTION_BY-R...	10	0.307692	1.103511	0.287611	0.778414	1.000
98	GOBP-TUBE-MORPHOGENESIS	15	0.264046	1.100737	0.322917	0.778284	1.000
99	GOBP-REGULATION-OF-CELL-DEATH	34	0.200167	1.098826	0.307018	0.775653	1.000
100	GOBP-NEGATIVE-REGULATION-OF-PROTEIN-METABOLIC-...	20	0.234273	1.095817	0.328859	0.776192	1.000
101	GOBP-NERVE-DEVELOPMENT	9	0.316456	1.083592	0.333333	0.802992	1.000
102	GOBP-MEMBRANE-PROTEIN-PROTEOLYSIS	6	0.376527	1.081807	0.356115	0.799513	1.000
103	GOBP-POSITIVE-REGULATION-OF-CELLULAR-COMPONENT...	9	0.316456	1.080978	0.313953	0.794155	1.000
104	GOBP-EMBRYO-DEVELOPMENT-ENDING-IN-BIRTH-OR-EGG...	9	0.310423	1.079028	0.333333	0.791668	1.000
105	GOBP-INNATE-IMMUNE-RESPONSE	7	0.358025	1.078314	0.373239	0.786562	1.000
106	GOBP-RESPONSE-TO-EXTRACELLULAR-STIMULUS	13	0.257865	1.072498	0.356436	0.795439	1.000
107	HALLMARK-APOPTOSIS	6	0.378049	1.070394	0.336957	0.794524	1.000
108	GOBP-SPROUTING-ANGIOGENESIS	5	0.409639	1.070221	0.353147	0.787765	1.000
109	GOBP-NEGATIVE-REGULATION-OF-MOLECULAR-FUNCTION	24	0.205784	1.063543	0.373418	0.798017	1.000
110	GOBP-POSITIVE-REGULATION-OF-IMMUNE-SYSTEM-PROCESS	18	0.228571	1.043406	0.407407	0.844361	1.000
111	GOBP-PROTEOLYSIS	17	0.241463	1.042306	0.386740	0.839725	1.000
112	GOBP-REGULATION-OF-EPITHELIAL-CELL-MIGRATION	6	0.365854	1.038968	0.359589	0.842330	1.000
113	GOBP-CELL-JUNCTION-ASSEMBLY	8	0.312500	1.034395	0.377510	0.847999	1.000
114	GOBP-LIPID-BIOSYNTHETIC-PROCESS	6	0.365854	1.033883	0.430034	0.842132	1.000
115	GOBP-POSITIVE-REGULATION-OF-ENDOTHELIAL-CELL-P...	6	0.365854	1.032511	0.362595	0.838798	1.000
116	GOBP-REGULATION-OF-LIPID-BIOSYNTHETIC-PROCESS	6	0.365854	1.032212	0.391608	0.832297	1.000
117	GOBP-ACTIVATION-OF-IMMUNE-RESPONSE	5	0.392890	1.026945	0.431095	0.839562	1.000
118	GOBP-REGULATION-OF-PEPTIDYL-SERINE-PHOSPHORYLA...	8	0.312500	1.026524	0.409420	0.833669	1.000
119	GOBP-LIPID-METABOLIC-PROCESS	10	0.294872	1.024577	0.375546	0.832026	1.000
120	GOBP-REGULATION-OF-FAT-CELL-DIFFERENTIATION	6	0.373094	1.024209	0.394366	0.825967	1.000
121	GOBP-RESPONSE-TO-DRUG	11	0.272727	1.024064	0.412281	0.819641	1.000
122	REACTOME-INTERFERON-SIGNALING	6	0.353659	1.019389	0.449477	0.826180	1.000
123	GOBP-PROTEIN-MODIFICATION-BY-SMALL-PROTEIN-CON...	6	0.365854	1.019260	0.433566	0.819832	1.000
124	GOBP-POSITIVE-REGULATION-OF-AXONOGENESIS	5	0.401522	1.016773	0.409375	0.819567	1.000
125	GOBP-REGULATION-OF-LIPID-METABOLIC-PROCESS	7	0.333333	1.016174	0.396364	0.814257	1.000
126	GOBP-IN-UTERO-EMBRYONIC-DEVELOPMENT	8	0.323991	1.015139	0.419913	0.810562	1.000

Continuation of Table S3

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
127	GOBP-TRANSMEMBRANE.RECEPTOR.PROTEIN.SERINE.THR...	6	0.365854	1.009609	0.439024	0.817176	1.000
128	GOBP-POSITIVE.REGULATION.OF.PEPTIDYL.SERINE.PH...	8	0.312500	1.005618	0.441509	0.821200	1.000
129	GOBP-PROTEIN.KINASE.B.SIGNALING	6	0.365854	1.005044	0.414966	0.816132	1.000
130	GOBP-NEUROINFLAMMATORY.RESPONSE	5	0.385542	1.002477	0.460481	0.816751	1.000
131	GOBP-REGULATION.OF.DEFENSE.RESPONSE	7	0.333333	0.998121	0.393939	0.821904	1.000
132	GOBP-VASCULATURE.DEVELOPMENT	17	0.225352	0.994420	0.434066	0.825485	1.000
133	GOBP-NEGATIVE.REGULATION.OF.NEURON.APOPTOTIC.P...	8	0.312500	0.993219	0.421456	0.822188	1.000
134	GOBP-REGULATION.OF.INFLAMMATORY.RESPONSE	7	0.333333	0.988091	0.438931	0.828629	1.000
135	GOBP-EMBRYO.DEVELOPMENT	14	0.232034	0.974494	0.463918	0.857637	1.000
136	GOBP-NEURON.APOPTOTIC.PROCESS	12	0.252780	0.971368	0.440191	0.859370	1.000
137	REACTOME.SIGNALING.BY.RECEPTOR.TYROSINE.KINASES	26	0.193548	0.965053	0.532787	0.869320	1.000
138	GOBP-ANION-TRANSMEMBRANE-TRANSPORT	7	0.320988	0.965035	0.473485	0.863223	1.000
139	GOBP-REGULATION.OF.PROTEIN.CATABOLIC.PROCESS	7	0.316559	0.964800	0.482490	0.857961	1.000
140	GOBP-PROTEIN.AUTOPHOSPHORYLATION	5	0.327568	0.953968	0.477273	0.879314	1.000
141	GOBP-INTRINSIC.APOPTOTIC.SIGNALING.PATHWAY	5	0.361446	0.950899	0.521127	0.880277	1.000
142	GOBP-POSITIVE.REGULATION.OF.SMALL-MOLECULE.MET...	5	0.361446	0.944578	0.490066	0.888962	1.000
143	GOBP-EMBRYONIC.ORGAN.DEVELOPMENT	7	0.306738	0.943732	0.516484	0.885192	1.000
144	GOBP-RESPONSE.TO.NERVE.GROWTH-FACTOR	7	0.308642	0.939577	0.482759	0.890515	1.000
145	GOBP-MORPHOGENESIS.OF-AN.EPITHELIUM	6	0.339022	0.938117	0.534546	0.887964	1.000
146	GOBP-NEGATIVE.REGULATION.OF.PROTEIN.CATABOLIC....	5	0.360499	0.937439	0.519573	0.883901	1.000
147	GOBP-POSITIVE.REGULATION.OF.LONG-TERM.SYNAPTIC...	5	0.385542	0.937122	0.477663	0.878737	1.000
148	GOBP-POSITIVE.REGULATION.OF.PHOSPHATIDYLINOSIT...	5	0.361446	0.936824	0.526667	0.873723	1.000
149	GOBP-REGULATION.OF.MITOTIC.CELL.CYCLE	5	0.361446	0.932008	0.514469	0.878739	1.000
150	GOBP-CHROMATIN.ORGANIZATION	5	0.361446	0.924508	0.513793	0.891461	1.000
151	GOBP-POSITIVE.REGULATION.OF.EPITHELIAL-CELL.MI...	5	0.361446	0.923452	0.562091	0.888111	1.000
152	GOBP-NEGATIVE.REGULATION.OF.APOPTOTIC-SIGNALIN...	7	0.308642	0.922864	0.540540	0.883827	1.000
153	GOBP-RESPONSE.TO.UV	5	0.361446	0.922388	0.539216	0.878943	1.000
154	GOBP-PROTEIN.CATABOLIC.PROCESS	8	0.275000	0.919328	0.544444	0.879721	1.000
155	GOBP-REGULATION.OF.AXONOGENESIS	7	0.308642	0.917311	0.567164	0.878771	1.000
156	GOBP-RESPONSE.TO.LIPID	19	0.194570	0.912739	0.655405	0.883259	1.000
157	GOBP-EPITHELIAL-CELL.PROLIFERATION	12	0.240703	0.910004	0.537118	0.884419	1.000
158	GOBP-REGULATION.OF.ENDOTHELIAL-CELL.MIGRATION	5	0.361446	0.907882	0.578778	0.884174	1.000
159	GOBP-NEGATIVE.REGULATION.OF.CATALYTIC-ACTIVITY	17	0.197183	0.906013	0.603352	0.882979	1.000
160	GOBP-POSITIVE.REGULATION.OF.DEVELOPMENTAL-GROWTH	8	0.289397	0.903093	0.547085	0.884324	1.000
161	GOBP-INOSITOL.LIPID-MEDIATED.SIGNALING	8	0.280327	0.894555	0.614407	0.898875	1.000
162	GOBP-POSITIVE.REGULATION.OF-CELL.PROJECTION.OR...	10	0.243590	0.891642	0.622407	0.900556	1.000
163	GOBP-NEGATIVE.REGULATION.OF.CATABOLIC.PROCESS	8	0.275000	0.887684	0.598485	0.904326	1.000
164	GOBP-REGULATION.OF-CELL-PROJECTIONS	6	0.308642	0.886693	0.620438	0.900842	1.000
165	GOBP-ORGAN.GROWTH	5	0.344442	0.873389	0.593443	0.921439	1.000
166	GOBP-CELLULAR-RESPONSE.TO-ORGANIC-CYCLIC-COMPOUND	13	0.221033	0.873040	0.609524	0.921276	1.000
167	GOBP-TAXIS	14	0.216216	0.869511	0.616580	0.923763	1.000
168	GOBP-REGULATION.OF.NEURON-DIFFERENTIATION	5	0.330682	0.865395	0.639498	0.927348	1.000
169	GOBP-REGULATION.OF-ORGAN.GROWTH	5	0.344442	0.864631	0.610738	0.923899	1.000

Continuation of Table S3

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
170	GOBP-POSITIVE-REGULATION_OF_DEFENSE-RESPONSE	5	0.325301	0.863089	0.618557	0.921913	1.000
171	GOBP-PEPTIDYL-TYROSINE-MODIFICATION	10	0.243590	0.856718	0.681159	0.930263	1.000
172	GOBP-RESPONSE-TO-NUTRIENT	5	0.326175	0.851056	0.634304	0.937139	1.000
173	GOBP-NEGATIVE-REGULATION_OF_LIPID-METABOLIC-PR...	5	0.325301	0.847292	0.648387	0.940458	1.000
174	GOBP-REGULATION-OF-LIPASE-ACTIVITY	6	0.304877	0.846746	0.646643	0.936306	1.000
175	GOBP-T-CELL-ACTIVATION	8	0.259647	0.844126	0.646586	0.937171	1.000
176	GOBP-MULTI-MULTICELLULAR-ORGANISM-PROCESS	8	0.258645	0.841847	0.665272	0.937014	1.000
177	GOBP-POSITIVE-REGULATION_OF_TRANSMEMBRANE-TRAN...	7	0.279034	0.839617	0.653226	0.935960	1.000
178	GOBP-NEGATIVE-REGULATION_OF_PHOSPHORYLATION	7	0.283951	0.838554	0.681992	0.932837	1.000
179	GOBP-IMMUNE-RESPONSE-REGULATING-SIGNALING-PATHWAY	8	0.258109	0.834987	0.677656	0.934908	1.000
180	REACTOME-CELLULAR-SENESCENCE	6	0.292310	0.831575	0.680000	0.936837	1.000
181	GOBP-RESPONSE-TO-BACTERIUM	13	0.213333	0.826976	0.732394	0.941478	1.000
182	GOBP-CARDIAC-MUSCLE-TISSUE-DEVELOPMENT	6	0.290025	0.822716	0.696864	0.944831	1.000
183	GOBP-NEGATIVE-REGULATION_OF_IMMUNE-SYSTEM-PROCESS	5	0.325301	0.821208	0.654804	0.942627	1.000
184	GOBP-RESPONSE-TO-MOLECULE-OF-BACTERIAL-ORIGIN	13	0.213333	0.820523	0.713568	0.938834	1.000
185	GOBP-REGULATION_OF_DEVELOPMENTAL-GROWTH	9	0.238398	0.817479	0.705628	0.939867	1.000
186	GOBP-FC-RECEPTOR-SIGNALING-PATHWAY	8	0.258109	0.816242	0.697417	0.937375	1.000
187	GOBP-HEART-DEVELOPMENT	6	0.290025	0.812509	0.683453	0.940164	1.000
188	GOBP-POSITIVE-REGULATION_OF_PEPTIDYL-TYROSINE-...	8	0.247860	0.811331	0.710317	0.937216	1.000
189	GOBP-PEPTIDYL-SERINE-MODIFICATION	12	0.210526	0.802020	0.772926	0.950699	1.000
190	REACTOME-DISEASES-OF-SIGNAL-TRANSDUCTION-BY-GR...	12	0.210526	0.801492	0.744186	0.946708	1.000
191	GOBP-LOCOMOTION	31	0.141032	0.800225	0.725000	0.943952	1.000
192	REACTOME-SENESCENCE-ASSOCIATED-SECRETORY-PHENO...	6	0.292310	0.799141	0.732143	0.941095	1.000
193	GOBP-CARBOHYDRATE-DERIVATIVE-METABOLIC-PROCESS	8	0.247846	0.798453	0.726531	0.937532	1.000
194	GOBP-POSITIVE-REGULATION_OF_BINDING	6	0.280488	0.797442	0.665480	0.934412	1.000
195	GOBP-EPITHELIAL-CELL-DIFFERENTIATION	7	0.259573	0.797056	0.704280	0.930468	1.000
196	GOBP-POSITIVE-REGULATION_OF_CELL-DEVELOPMENT	12	0.203559	0.793231	0.719626	0.932833	1.000
197	GOBP-REGULATION-OF-CELL-CELL-ADHESION	9	0.229812	0.790152	0.750000	0.933940	1.000
198	GOBP-POSITIVE-REGULATION_OF_NEUROGENESIS	12	0.203559	0.787728	0.815385	0.933471	1.000
199	HALLMARK-EPITHELIAL-MESENCHYMAL-TRANSITION	5	0.301205	0.785078	0.773026	0.933847	1.000
200	GOBP-POSITIVE-REGULATION_OF_NERVOUS-SYSTEM-DEV...	12	0.203559	0.784173	0.764103	0.930806	1.000
201	GOBP-POSITIVE-REGULATION_OF_LIPASE-ACTIVITY	5	0.301205	0.781320	0.739583	0.931049	1.000
202	GOBP-POSITIVE-REGULATION_OF_NEURON-PROJECTION...	5	0.301205	0.779435	0.733766	0.930320	1.000
203	GOBP-NEGATIVE-REGULATION_OF_HYDROLASE-ACTIVITY	11	0.212303	0.777924	0.787330	0.928315	1.000
204	GOBP-CELLULAR-RESPONSE-TO-INORGANIC-SUBSTANCE	11	0.207792	0.776903	0.786364	0.925378	1.000
205	GOBP-REGULATION-OF-CELL-SIZE	5	0.301205	0.770335	0.718654	0.932304	1.000
206	GOBP-REGULATION-OF-RESPONSE-TO-EXTERNAL-STIMULUS	15	0.178082	0.763231	0.821429	0.939228	1.000
207	GOBP-DEVELOPMENTAL-CELL-GROWTH	5	0.301205	0.763197	0.784195	0.934776	1.000
208	GOBP-NEGATIVE-REGULATION_OF_BIOSYNTHETIC-PROCESS	13	0.185892	0.759040	0.781915	0.937079	1.000
209	REACTOME-NGF-STIMULATED-TRANSCRIPTION	9	0.222405	0.749540	0.809524	0.948400	1.000
210	GOBP-REGULATION-OF-PROTEIN-STABILITY	5	0.280063	0.749381	0.784722	0.944166	1.000
211	GOBP-PHAGOCYTOSIS	5	0.279304	0.748049	0.794212	0.941721	1.000
212	GOBP-POSITIVE-REGULATION_OF_GROWTH	9	0.227577	0.746238	0.809917	0.940095	1.000

Continuation of Table S3

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
213 GOBP-RESPONSE.TO.OXYGEN.CONTAINING.COMPOUND	GO:1901700	39	0.124374	0.739523	0.870690	0.946161	1.000
214 GOBP-REGULATION.OF.PHOSPHOLIPASE.C.ACTIVITY	GO:1900274	5	0.301205	0.738510	0.760656	0.943378	1.000
215 REACTOME.DEVELOPMENTAL.BIOLOGY	R-RNO-1266738	22	0.149855	0.731267	0.844595	0.949794	1.000
216 GOBP-AXON.DEVELOPMENT	GO:0061564	18	0.161514	0.721685	0.921466	0.959240	1.000
217 GOBP-REGULATION.OF.DNA.BINDING.TRANSSCRIPTION.F...	GO:0051090	16	0.165910	0.721324	0.854651	0.955211	1.000
218 GOBP-CELL-CELL.JUNCTION.ORGANIZATION	GO:0045216	6	0.256097	0.720020	0.841060	0.952751	1.000
219 GOBP-TISSUE.MORPHOGENESIS	GO:0048729	7	0.234323	0.719031	0.833333	0.949867	1.000
220 GOBP-CELLULAR.RESPONSE.TO.STARVATION	GO:0009267	5	0.275483	0.715769	0.827119	0.949851	1.000
221 GOBP-ORGANONITROGEN.COMPOUND.CATABOLIC.PROCESS	GO:1901565	10	0.199702	0.709744	0.844156	0.953560	1.000
222 GOBP-NEURON.PROJECTION.GUIDANCE	GO:0097485	9	0.202532	0.701773	0.892857	0.959841	1.000
223 GOBP-RESPONSE.TO.STARVATION	GO:0042594	5	0.275483	0.695740	0.840278	0.963060	1.000
224 GOBP-REPRODUCTIVE.SYSTEM.DEVELOPMENT	GO:0061458	6	0.242811	0.695259	0.894340	0.959418	1.000
225 GOBP-DEVELOPMENTAL.GROWTH	GO:0048589	10	0.187504	0.689377	0.907080	0.962404	1.000
226 GOBP-CELLULAR.RESPONSE.TO.MOLECULE.OF.BACTERIA...	GO:0071219	8	0.213298	0.686701	0.891566	0.961310	1.000
227 GOBP-CELLULAR.RESPONSE.TO.BIOTIC.STIMULUS	GO:0071216	8	0.213298	0.686408	0.893939	0.957451	1.000
228 GOBP-REGULATION.OF.IMMUNE.SYSTEM.PROCESS	GO:0002682	21	0.144975	0.685642	0.913333	0.954190	1.000
229 GOBP-POSITIVE.REGULATION.OF.IMMUNE.RESPONSE	GO:0050778	9	0.202532	0.684082	0.887931	0.952005	1.000
230 GOBP-POSITIVE.REGULATION.OF.RESPONSE.TO.EXTERN...	GO:0032103	9	0.202532	0.682362	0.864407	0.950325	1.000
231 GOBP-GLAND.DEVELOPMENT	GO:0048732	7	0.229132	0.680928	0.887641	0.947834	1.000
232 GOBP-NEURON.DEATH	GO:0070997	18	0.145466	0.671866	0.913793	0.954052	1.000
233 GOBP-RESPONSE.TO.ORGANIC.CYCLIC.COMPOUND	GO:0014070	20	0.144374	0.668537	0.944099	0.953708	1.000
234 REACTOME.POST.TRANSLATIONAL.PROTEIN.MODIFICATION	R-RNO-597592	7	0.222929	0.664100	0.914286	0.954125	1.000
235 GOBP-POSITIVE.REGULATION.OF.CATION.TRANSMEMBR...	GO:1904064	5	0.266763	0.663717	0.898246	0.950521	1.000
236 GOBP-RESPONSE.TO.CADMIUM.ION	GO:0046686	6	0.236588	0.660065	0.887789	0.949980	1.000
237 GOBP-GLIOGENESIS	GO:0042063	12	0.172702	0.656612	0.955285	0.949652	1.000
238 GOBP-RESPONSE.TO.OXIDATIVE.STRESS	GO:0006979	8	0.200000	0.644542	0.911894	0.956871	1.000
239 REACTOME.EXTRACELLULAR.MATRIX.ORGANIZATION	R-RNO-1474244	5	0.253012	0.643903	0.914591	0.953475	1.000
240 GOBP-EXTRINSIC.APOPTOTIC.SIGNALING.PATHWAY	GO:0097191	7	0.213948	0.632606	0.914498	0.959308	1.000
241 GOBP-RESPONSE.TO.REACTIVE.OXYGEN.SPECIES	GO:0000302	8	0.200000	0.631614	0.932075	0.956010	1.000
242 HALLMARK.UV.RESPONSE.UP	M5941	5	0.228916	0.598158	0.954693	0.975470	1.000
243 REACTOME.INFECTIOUS.DISEASE	R-HSA-5663205	12	0.149135	0.566231	0.972973	0.988075	1.000
244 GOBP-NEGATIVE.REGULATION.OF.TRANSMEMBRANE.TRAN...	GO:0034763	6	0.195147	0.548072	0.977273	0.991367	1.000
245 GOBP-TISSUE.HOMEOSTASIS	GO:0001894	5	0.204819	0.536539	0.973077	0.990628	1.000
246 GOBP-ERBB.SIGNALING.PATHWAY	GO:0038127	5	0.192771	0.507811	0.990099	0.993334	1.000
247 GOBP-POSITIVE.REGULATION.OF.CELLULAR.COMPONENT...	GO:0051130	24	-0.109107	-0.384918	0.996499	0.999159	1.000
248 GOBP-RESPONSE.TO.NITROGEN.COMPOUND	GO:1901698	35	-0.114099	-0.425075	0.996652	0.999031	1.000
249 GOBP-REGULATION.OF.CELLULAR.COMPONENT.SIZE	GO:0032535	7	-0.184156	-0.473932	0.991968	0.994017	1.000
250 REACTOME.ESTROGEN.DEPENDENT.NUCLEAR.EVENTS.DOW...	R-RNO-9634638	5	-0.216867	-0.483219	0.986130	0.993909	1.000
251 GOBP-REGIONALIZATION	GO:0003002	6	-0.205458	-0.491284	0.988935	0.993932	1.000
252 GOBP-REGULATION.OF.IMMUNE.RESPONSE	GO:0050776	12	-0.161627	-0.491716	0.980892	0.995929	1.000
253 GOBP-PATTERN.SPECIFICATION.PROCESS	GO:0007389	6	-0.205458	-0.497765	0.992063	0.996338	1.000
254 GOBP-TELENCEPHALON.DEVELOPMENT	GO:0021537	7	-0.201269	-0.500782	0.989026	0.997547	1.000
255 GOBP-CELL-CELL.ADHESION	GO:0008609	14	-0.160845	-0.505760	0.977833	0.998052	1.000

Continuation of Table S3

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
256	GOBP-RESPONSE.TO.ABIOTIC.STIMULUS	27	-0.139435	-0.508388	0.981395	0.999309	1.000
257	GOBP-IMPORT.INTO.CELL	6	-0.212604	-0.516838	0.986188	0.998349	1.000
258	GOBP-EPITHELIUM.DEVELOPMENT	15	-0.164005	-0.518340	0.974296	0.999973	1.000
259	GOBP-POSITIVE.REGULATION.OF.NEURON.DEATH	5	-0.230676	-0.519159	0.979856	1.000000	1.000
260	GOBP-REGULATION.OF.GTPASE.ACTIVITY	5	-0.233002	-0.528485	0.971852	1.000000	1.000
261	GOBP-RESPONSE.TO.LIGHT.STIMULUS	11	-0.181539	-0.530893	0.963589	1.000000	1.000
262	REACTOME.ONCOGENIC.MAPK.SIGNALING	5	-0.234317	-0.530914	0.976261	1.000000	1.000
263	GOBP-TRANSMEMBRANE.RECEPTOR.PROTEIN.TYROSINE.K...	19	-0.158897	-0.531921	0.972941	1.000000	1.000
264	GOBP-EMBRYONIC.MORPHOGENESIS	6	-0.217951	-0.532552	0.983075	1.000000	1.000
265	GOBP-NEGATIVE.REGULATION.OF.NUCLEOBASE.CONTAIN...	13	-0.175333	-0.539493	0.964149	1.000000	1.000
266	GOBP-ENZYME.LINKED.RECEPTOR.PROTEIN.SIGNALING...	24	-0.150104	-0.540346	0.967442	1.000000	1.000
267	GOBP-RESPONSE.TO.NICOTINE	7	-0.215253	-0.541431	0.972259	1.000000	1.000
268	GOBP-NEGATIVE.REGULATION.OF.MULTICELLULAR.ORG...	15	-0.171221	-0.543129	0.972500	1.000000	1.000
269	GOBP-PHOSPHATIDYLINOSITOL.3.KINASE.SIGNALING	7	-0.219319	-0.557360	0.953652	1.000000	1.000
270	GOBP-POSITIVE.REGULATION.OF.ORGANELLE.ORGANIZA...	10	-0.198840	-0.567053	0.951219	1.000000	1.000
271	GOBP-REGULATION.OF.ANATOMICAL.STRUCTURE.SIZE	10	-0.200522	-0.569979	0.937904	1.000000	1.000
272	REACTOME.SIGNALING.BY.NTRK2.TRKB	6	-0.231638	-0.570158	0.957082	1.000000	1.000
273	GOBP-CELLULAR.RESPONSE.TO.REACTIVE.OXYGEN.SPECIES	7	-0.225237	-0.570272	0.954794	1.000000	1.000
274	GOBP-CELLULAR.RESPONSE.TO.CHEMICAL.STRESS	7	-0.225237	-0.572638	0.951743	1.000000	1.000
275	GOBP-RESPONSE.TO.TEMPERATURE.STIMULUS	9	-0.209151	-0.576758	0.959239	1.000000	1.000
276	GOBP-REGULATION.OF.NERVOUS.SYSTEM.DEVELOPMENT	15	-0.181021	-0.580747	0.941323	1.000000	1.000
277	GOBP-MATERNAL.PROCESS.INVOLVED.IN.FEMALE.PREGN...	5	-0.250799	-0.581010	0.949438	1.000000	1.000
278	GOBP-AGING	13	-0.190038	-0.582161	0.945980	1.000000	1.000
279	GOBP-TUBE.DEVELOPMENT	18	-0.174921	-0.582584	0.932845	1.000000	1.000
280	GOBP-CARBOHYDRATE.METABOLIC.PROCESS	9	-0.214767	-0.589052	0.935271	1.000000	1.000
281	GOBP-TEMPERATURE.HOMEOSTASIS	5	-0.255721	-0.589346	0.943870	1.000000	1.000
282	REACTOME.MYD88.INDEPENDENT.TLR4.CASCADE	8	-0.223096	-0.589475	0.952128	1.000000	1.000
283	GOBP-REGULATION.OF.CELL.DEVELOPMENT	15	-0.185295	-0.590447	0.931204	1.000000	1.000
284	GOBP-CELL.ACTIVATION	22	-0.169255	-0.591346	0.935096	1.000000	1.000
285	GOBP-MACROMOLECULE.CATABOLIC.PROCESS	11	-0.207125	-0.592384	0.950943	1.000000	1.000
286	REACTOME.TOLL.LIKE.RECEPTOR.CASCADES	8	-0.223096	-0.593698	0.943122	1.000000	1.000
287	GOBP-APOPTOTIC.PROCESS	35	-0.157896	-0.593930	0.914124	1.000000	1.000
288	REACTOME.TOLL.LIKE.RECEPTOR.TLR1.TLR2.CASCADE	8	-0.223096	-0.595746	0.940781	1.000000	1.000
289	GOBP-REGULATION.OF.NEURON.PROJECTION.DEVELOPMENT	16	-0.183209	-0.597279	0.928922	1.000000	1.000
290	GOBP-DNA.METABOLIC.PROCESS	6	-0.247793	-0.597850	0.933151	1.000000	1.000
291	REACTOME.TOLL.LIKE.RECEPTOR.9.TLR9.CASCADE	8	-0.223096	-0.599521	0.934492	1.000000	1.000
292	GOBP-REGULATION.OF.NEUROGENESIS	14	-0.189992	-0.604027	0.920854	1.000000	1.000
293	GOBP-REGULATION.OF.PROTEIN.SERINE.THREONINE.KI...	12	-0.200390	-0.604047	0.920984	1.000000	1.000
294	GOBP-CELLULAR.COMPONENT.DISASSEMBLY	6	-0.251663	-0.605072	0.935705	1.000000	1.000
295	GOBP.SMALL.MOLECULE.BIOSYNTHETIC.PROCESS	5	-0.264897	-0.605481	0.930595	1.000000	1.000
296	GOBP-REGULATION.OF.SMALL.MOLECULE.METABOLIC.PR...	9	-0.220724	-0.606682	0.919419	1.000000	1.000
297	GOBP-RESPONSE.TO.RADIATION	13	-0.199618	-0.611987	0.925786	1.000000	1.000
298	REACTOME.LEISHMANIA.INFECTION	10	-0.213991	-0.612256	0.926509	1.000000	1.000

Continuation of Table S3

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
299	REACTOME-HEMOSTASIS	14	-0.202156	-0.619065	0.900990	1.000000	1.000
300	GOBP-FORBRAIN-DEVELOPMENT	10	-0.218096	-0.622794	0.911539	1.000000	1.000
301	REACTOME-INTERLEUKIN_17-SIGNALING	6	-0.258818	-0.622892	0.923717	1.000000	1.000
302	GOBP-POSITIVE-REGULATION-OF-CELL-DEATH	19	-0.185289	-0.624362	0.897714	1.000000	1.000
303	GOBP-CIRCADIAN-REGULATION-OF-GENE-EXPRESSION	5	-0.274707	-0.627660	0.927660	1.000000	1.000
304	GOBP-NEGATIVE-REGULATION-OF-LOCOMOTION	5	-0.277471	-0.626907	0.912676	1.000000	1.000
305	REACTOME-SIGNALING-BY-NTRKS	18	-0.189979	-0.628316	0.917476	1.000000	1.000
306	GOBP-REGULATION-OF-INTRACELLULAR-SIGNAL-TRANSD...	21	-0.181653	-0.629324	0.913404	1.000000	1.000
307	GOBP-CELL-PART-MORPHOGENESIS	25	-0.176486	-0.629438	0.911661	1.000000	1.000
308	GOBP-CELL-MORPHOGENESIS	25	-0.176486	-0.632011	0.911935	1.000000	1.000
309	GOBP-MULTICELLULAR-ORGANISMAL-RESPONSE-TO-STRESS	5	-0.276209	-0.634017	0.903930	1.000000	1.000
310	GOBP-APOPTOTIC-SIGNALING-PATHWAY	15	-0.202856	-0.637952	0.898875	1.000000	1.000
311	GOBP-CELLULAR-COMPONENT-MORPHOGENESIS	25	-0.176486	-0.639343	0.893887	1.000000	1.000
312	GOBP-CELLULAR-RESPONSE-TO-CADMIIUMION	5	-0.279725	-0.642169	0.932867	1.000000	1.000
313	REACTOME-LICAM-INTERACTIONS	5	-0.281745	-0.642213	0.891971	1.000000	1.000
314	GOBP-REGULATION-OF-PROTEIN-LOCALIZATION-TO-MEM...	7	-0.256270	-0.649900	0.893960	1.000000	1.000
315	GOBP-REGULATION-OF-LIPID-LOCALIZATION	5	-0.287071	-0.655125	0.900990	1.000000	1.000
316	GOBP-CELLULAR-RESPONSE-TO-DNA-DAMAGE-STIMULUS	5	-0.284945	-0.655841	0.881503	1.000000	1.000
317	GOBP-REGULATION-OF-ANATOMICAL-STRUCTURE-MORPHO...	17	-0.199600	-0.656454	0.893285	1.000000	1.000
318	GOBP-POSITIVE-REGULATION-OF-DNA-BINDING-TRANSC...	10	-0.234812	-0.659850	0.886719	1.000000	1.000
319	GOBP-REGULATION-OF-PHOSPHATIDYLINOSITOL_3-KINA...	6	-0.267683	-0.659917	0.887943	1.000000	1.000
320	GOBP-ORGANIC-HYDROXY-COMPOUND-METABOLIC-PROCESS	8	-0.245539	-0.663838	0.879730	1.000000	1.000
321	GOBP-MUSCLE-TISSUE-DEVELOPMENT	11	-0.227915	-0.664168	0.902188	1.000000	1.000
322	REACTOME-PLATELET-ACTIVATION-SIGNALING-AND-AGG...	7	-0.262887	-0.665760	0.881379	1.000000	1.000
323	GOBP-RECEPTOR-MEDIATED-ENDOCYTOSIS	6	-0.273648	-0.666842	0.895863	1.000000	1.000
324	GOBP-POLYSACCHARIDE-METABOLIC-PROCESS	5	-0.292553	-0.668184	0.888418	1.000000	1.000
325	GOBP-CELLULAR-RESPONSE-TO-LIPID	15	-0.208988	-0.669561	0.865385	1.000000	1.000
326	GOBP-REGULATION-OF-PEPTIDASE-ACTIVITY	10	-0.232725	-0.670308	0.876463	1.000000	1.000
327	GOBP-REGULATION-OF-GLIOGENESIS	5	-0.295102	-0.673243	0.883357	1.000000	1.000
328	GOBP-GLIAL-CELL-DIFFERENTIATION	10	-0.238077	-0.674546	0.858466	1.000000	1.000
329	GOBP-EXOCYTOSIS	11	-0.230807	-0.676119	0.868020	1.000000	1.000
330	GOBP-REGULATION-OF-PROTEOLYSIS	12	-0.225892	-0.678539	0.859395	1.000000	1.000
331	GOBP-NEGATIVE-REGULATION-OF-RESPONSE-TO-STIMULUS	16	-0.210434	-0.678635	0.859069	1.000000	1.000
332	GOBP-REGULATION-OF-WNT-SIGNALING-PATHWAY	5	-0.300503	-0.681691	0.876274	1.000000	1.000
333	GOBP-POSITIVE-REGULATION-OF-GLIOGENESIS	5	-0.295102	-0.683679	0.881924	1.000000	1.000
334	GOBP-INTRACELLULAR-RECEPTOR-SIGNALING-PATHWAY	5	-0.302027	-0.683743	0.881857	1.000000	1.000
335	GOBP-PLATELET-ACTIVATION	6	-0.283390	-0.685073	0.875683	1.000000	1.000
336	GOBP-REGULATION-OF-CIRCADIAN-RHYTHM	7	-0.268253	-0.687284	0.859551	1.000000	1.000
337	GOBP-REGULATION-OF-PROTEIN-LOCALIZATION-TO-CEL...	6	-0.285480	-0.694618	0.857542	1.000000	1.000
338	GOBP-NEGATIVE-REGULATION-OF-RESPONSE-TO-EXTERN...	5	-0.307113	-0.698584	0.849432	1.000000	1.000
339	GOBP-REGULATION-OF-PROTEIN-KINASE-ACTIVITY	21	-0.204638	-0.706512	0.828070	1.000000	1.000
340	GOBP-POSITIVE-REGULATION-OF-APOPTOTIC-SIGNALIN...	5	-0.314914	-0.713002	0.845494	1.000000	1.000
341	GOBP-REGULATION-OF-TRANSFERASE-ACTIVITY	21	-0.204638	-0.713315	0.817527	1.000000	1.000

Continuation of Table S3

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
342	GOBP-MEMORY	GO-0007613	13	-0.233673	-0.714260	0.835600	1.000000	1.000
343	GOBP-GENERATION-OF-PRECURSOR-METABOLITES-AND-E...	GO-0006091	5	-0.314718	-0.717186	0.831697	1.000000	1.000
344	GOBP-NEGATIVE-REGULATION-OF-PHOSPHORUS-METABOL...	GO-0010563	9	-0.262971	-0.718416	0.821935	1.000000	1.000
345	GOBP-COGNITION	GO-0050890	28	-0.198584	-0.720678	0.827546	1.000000	1.000
346	GOBP-FC-EPSILON-RECEPTOR-SIGNALING-PATHWAY	GO-0038095	7	-0.281963	-0.721384	0.834492	1.000000	1.000
347	REACTOME-FC-EPSILON-RECEPTOR-FCER1-SIGNALING	R-RNO-2454202	7	-0.281963	-0.721581	0.818801	1.000000	1.000
348	GOBP-CARBOHYDRATE-BIOSYNTHETIC-PROCESS	GO-0016051	5	-0.323869	-0.722697	0.829912	1.000000	1.000
349	GOBP-RESPONSE-TO-WOUNDING	GO-0009611	15	-0.227930	-0.725898	0.822864	1.000000	1.000
350	GOBP-ERK1-AND-ERK2-CASCADE	GO-0070371	5	-0.322805	-0.727958	0.825648	1.000000	1.000
351	GOBP-PEPTIDE-METABOLIC-PROCESS	GO-0006518	11	-0.246237	-0.728380	0.805447	1.000000	1.000
352	GOBP-REGULATION-OF-MAPK-CASCADE	GO-0043408	13	-0.239447	-0.728918	0.832723	1.000000	1.000
353	REACTOME-CELLULAR-RESPONSES-TO-EXTERNAL-STIMULI	R-RNO-8953897	11	-0.248237	-0.730666	0.825129	1.000000	1.000
354	GOBP-NEGATIVE-REGULATION-OF-ION-TRANSPORT	GO-0043271	11	-0.250337	-0.730796	0.819338	1.000000	1.000
355	GOBP-RESPONSE-TO-ACID-CHEMICAL	GO-0001101	6	-0.295827	-0.731132	0.820690	1.000000	1.000
356	GOBP-RECEPTOR-INTERNALIZATION	GO-0031623	5	-0.318608	-0.732266	0.819820	1.000000	1.000
357	GOBP-REGULATION-OF-CATABOLIC-PROCESS	GO-0009894	13	-0.236000	-0.732349	0.803198	1.000000	1.000
358	GOBP-REGULATION-OF-CARBOHYDRATE-BIOSYNTHETIC-P...	GO-0043255	5	-0.323869	-0.732467	0.800000	1.000000	1.000
359	GOBP-RECEPTOR-METABOLIC-PROCESS	GO-0043112	5	-0.318608	-0.735109	0.796243	1.000000	1.000
360	GOBP-NEGATIVE-REGULATION-OF-PROTEIN-MODIFICATI...	GO-0031400	10	-0.260258	-0.735891	0.807939	1.000000	1.000
361	GOBP-AMYLOID-PRECURSOR-PROTEIN-CATABOLIC-PROCESS	GO-0042987	5	-0.324460	-0.737094	0.810811	1.000000	1.000
362	GOBP-POSITIVE-REGULATION-OF-HYDROLASE-ACTIVITY	GO-0051345	16	-0.227415	-0.738750	0.807692	1.000000	1.000
363	GOBP-REGULATION-OF-PROTEIN-PHOSPHORYLATION	GO-0001932	25	-0.207804	-0.738757	0.791762	1.000000	1.000
364	GOBP-REGULATION-OF-CELLULAR-COMPONENT-BIOGENESIS	GO-0044087	10	-0.263280	-0.739517	0.799228	1.000000	1.000
365	GOBP-REGULATION-OF-APOPTOTIC-SIGNALING-PATHWAY	GO-2001233	10	-0.261930	-0.739953	0.805627	1.000000	1.000
366	GOBP-REGULATION-OF-GROWTH	GO-0040008	13	-0.240030	-0.742395	0.803896	1.000000	1.000
367	GOBP-AMYLOID-BETA-METABOLIC-PROCESS	GO-0050435	5	-0.324460	-0.746784	0.803596	1.000000	1.000
368	GOBP-AMYLOID-PRECURSOR-PROTEIN-METABOLIC-PROCESS	GO-0042982	5	-0.324460	-0.746821	0.802651	1.000000	1.000
369	GOBP-REGULATION-OF-CARBOHYDRATE-METABOLIC-PROCESS	GO-0006109	5	-0.323869	-0.750759	0.773371	1.000000	1.000
370	GOBP-REPRODUCTION	GO-0000003	18	-0.223628	-0.751264	0.790898	1.000000	1.000
371	GOBP-NEGATIVE-REGULATION-OF-NERVOUS-SYSTEM-DEV...	GO-0051961	5	-0.330984	-0.751568	0.787519	1.000000	1.000
372	GOBP-POSITIVE-REGULATION-OF-INTRACELLULAR-SIGN...	GO-1902533	14	-0.237562	-0.751615	0.796548	1.000000	1.000
373	GOBP-POSITIVE-REGULATION-OF-LOCOMOTION	GO-0040017	11	-0.258913	-0.754353	0.795165	1.000000	1.000
374	GOBP-RESPONSE-TO-MONOSACCHARIDE	GO-0034284	5	-0.329580	-0.756305	0.790801	1.000000	1.000
375	GOBP-LIPID-LOCALIZATION	GO-0010876	10	-0.272237	-0.756768	0.766753	1.000000	1.000
376	GOBP-NEGATIVE-REGULATION-OF-ANION-TRANSPORT	GO-1903792	8	-0.281373	-0.762099	0.785034	1.000000	1.000
377	REACTOME-ADAPTIVE-IMMUNE-SYSTEM	R-RNO-1280218	9	-0.278713	-0.764186	0.780355	1.000000	1.000
378	GOBP-REGULATION-OF-HORMONE-LEVELS	GO-0010817	12	-0.252688	-0.764320	0.777070	1.000000	1.000
379	GOBP-NEGATIVE-REGULATION-OF-CELL-DEVELOPMENT	GO-0010721	6	-0.316857	-0.765843	0.759184	1.000000	1.000
380	GOBP-RESPONSE-TO-CARBOHYDRATE	GO-0009743	5	-0.329580	-0.765861	0.796215	1.000000	1.000
381	GOBP-CIRCADIAN-RHYTHM	GO-0007623	13	-0.247202	-0.766661	0.766460	1.000000	1.000
382	GOBP-CELLULAR-CARBOHYDRATE-METABOLIC-PROCESS	GO-0044262	5	-0.342016	-0.773555	0.788489	1.000000	1.000
383	GOBP-MONOAMINE-TRANSPORT	GO-0015844	5	-0.337074	-0.775095	0.749646	1.000000	1.000
384	GOBP-LYMPHOCYTE-ACTIVATION	GO-0046649	10	-0.270374	-0.778554	0.755263	1.000000	1.000

Continuation of Table S3

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
385	GOBP-ORGANIC-HYDROXY-COMPOUND-TRANSPORT	6	-0.321598	-0.780777	0.761636	1.000000	1.000
386	GOBP-REGULATION-OF-CELL-ACTIVATION	8	-0.298521	-0.781291	0.738606	1.000000	1.000
387	GOBP-NEURON-DIFFERENTIATION	37	-0.206484	-0.781932	0.741379	1.000000	1.000
388	GOBP-REGULATION-OF-PEPTIDYL-TYROSINE-PHOSPHORY...	9	-0.287594	-0.782675	0.749340	1.000000	1.000
389	GOBP-MUSCLE-CELL-PROLIFERATION	8	-0.296209	-0.784862	0.765605	1.000000	1.000
390	GOBP-BIOLOGICAL-ADHESION	19	-0.234473	-0.785669	0.736397	1.000000	1.000
391	GOBP-POSITIVE-REGULATION-OF-PHOSPHORUS-METABOL...	23	-0.225402	-0.786456	0.752969	1.000000	1.000
392	GOBP-NEGATIVE-REGULATION-OF-CELLULAR-COMPONENT...	11	-0.265278	-0.788297	0.739355	1.000000	1.000
393	GOBP-REGULATION-OF-RESPONSE-TO-STRESS	19	-0.231922	-0.788348	0.756126	1.000000	1.000
394	GOBP-RESPONSE-TO-TUMOR-NECROSIS-FACTOR	7	-0.303492	-0.788455	0.741287	1.000000	1.000
395	GOBP-CHROMOSOME-ORGANIZATION	6	-0.333024	-0.789546	0.749638	1.000000	1.000
396	REACTOME-ANTI-INFLAMMATORY-RESPONSE-FAVOURING...	5	-0.347893	-0.791148	0.736919	1.000000	1.000
397	GOBP-POSITIVE-REGULATION-OF-TRANSFERASE-ACTIVITY	19	-0.237680	-0.791851	0.746199	1.000000	1.000
398	REACTOME-NEUROUS-SYSTEM-DEVELOPMENT	14	-0.250086	-0.792115	0.737624	1.000000	1.000
399	GOBP-RHYTHMIC-PROCESS	15	-0.246349	-0.792344	0.757463	1.000000	1.000
400	GOBP-LEUKOCYTE-MIGRATION	6	-0.327994	-0.792360	0.741703	1.000000	1.000
401	GOBP-REGULATION-OF-MAP-KINASE-ACTIVITY	9	-0.286182	-0.792552	0.736220	1.000000	1.000
402	GOBP-COAGULATION	8	-0.295169	-0.793318	0.733062	1.000000	1.000
403	GOBP-POSITIVE-REGULATION-OF-ANION-TRANSPORT	9	-0.291891	-0.793514	0.738667	1.000000	1.000
404	GOBP-REGULATION-OF-LONG-TERM-SYNAPTIC-POTENTIA...	6	-0.324315	-0.798614	0.739316	1.000000	1.000
405	GOBP-PROTEIN-LOCALIZATION-TO-PLASMA-MEMBRANE	7	-0.217439	-0.799600	0.722772	1.000000	1.000
406	GOBP-ACTIVATION-OF-PROTEIN-KINASE-ACTIVITY	10	-0.279399	-0.801079	0.738065	1.000000	1.000
407	GOBP-NEGATIVE-REGULATION-OF-CELL-DIFFERENTIATION	13	-0.261246	-0.801478	0.724311	1.000000	1.000
408	GOBP-NEGATIVE-REGULATION-OF-INTRACELLULAR-SIGN...	7	-0.312065	-0.803536	0.724462	1.000000	1.000
409	REACTOME-INNATE-IMMUNE-SYSTEM	16	-0.251708	-0.806745	0.736646	1.000000	1.000
410	GOBP-NEGATIVE-REGULATION-OF-TRANSPORT	13	-0.261116	-0.806812	0.714834	1.000000	1.000
411	GOBP-POSITIVE-REGULATION-OF-MAP-KINASE-ACTIVITY	6	-0.335041	-0.807445	0.738714	1.000000	1.000
412	GOBP-NEGATIVE-REGULATION-OF-DEVELOPMENTAL-PROCESS	13	-0.261246	-0.807637	0.700614	1.000000	1.000
413	GOBP-ACTIVATION-OF-MAPK-ACTIVITY	6	-0.335041	-0.808041	0.697234	1.000000	1.000
414	GOBP-CYTOSOLIC-CALCIUM-ION-TRANSPORT	7	-0.321188	-0.810720	0.722067	1.000000	1.000
415	GOBP-CENTRAL-NERVOUS-SYSTEM-NEURON-DIFFERENTIA...	5	-0.359312	-0.812780	0.695846	1.000000	1.000
416	GOBP-MULTICELLULAR-ORGANISMAL-HOMEOSTASIS	12	-0.267389	-0.812828	0.716113	1.000000	1.000
417	GOBP-LONG-TERM-SYNAPTIC-DEPRESSION	5	-0.360830	-0.815619	0.712857	1.000000	1.000
418	GOBP-REGULATION-OF-EXTRINSIC-APOPTOTIC-SIGNAL...	6	-0.341572	-0.815894	0.710227	1.000000	1.000
419	GOBP-MULTI-ORGANISM-PROCESS	16	-0.256654	-0.818983	0.703202	1.000000	1.000
420	GOBP-CALCIUM-ION-TRANSMEMBRANE-TRANSPORT	7	-0.321188	-0.819381	0.719346	1.000000	1.000
421	GOBP-NEURON-MIGRATION	5	-0.352220	-0.819526	0.702742	1.000000	1.000
422	GOBP-REGULATION-OF-PROTEIN-MODIFICATION-PROCESS	28	-0.220477	-0.819563	0.704307	1.000000	1.000
423	GOBP-REGULATION-OF-CELLULAR-AMIDE-METABOLIC-PR...	9	-0.299826	-0.819862	0.706806	1.000000	1.000
424	GOBP-POSITIVE-REGULATION-OF-CELL-GROWTH	6	-0.303037	-0.820012	0.695890	1.000000	1.000
425	REACTOME-MAPK-TARGETS-NUCLEAR-EVENTS-MEDIATED...	5	-0.364032	-0.820301	0.719054	1.000000	1.000
426	GOBP-REGULATION-OF-VASCULATURE-DEVELOPMENT	5	-0.365558	-0.820559	0.709440	1.000000	1.000
427	GOBP-MEMBRANE-ORGANIZATION	12	-0.280177	-0.824240	0.720099	1.000000	1.000

Continuation of Table S3

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
428	GOBP-CALCIUM-ION-TRANSPORT-INTO-CYTOSOL	GO-0060402	7	-0.321188	-0.824258	0.694102	1.000000	1.000
429	GOBP-BIOLOGICAL-PROCESS-INVOLVED-IN-SYMBIOTIC....	GO-004440	10	-0.296362	-0.826034	0.691275	1.000000	1.000
430	GOBP-REGULATION-OF-PHOSPHORUS-METABOLIC-PROCESS	GO-0051174	26	-0.233215	-0.828515	0.701493	1.000000	1.000
431	GOBP-REGULATION-OF-PROTEIN-TYROSINEKINASE-ACT...	GO-0061097	5	-0.365047	-0.828805	0.697778	1.000000	1.000
432	GOBP-CELLULAR-MACROMOLECULE-CATABOLIC-PROCESS	GO-0044265	5	-0.373494	-0.829246	0.731563	1.000000	1.000
433	GOBP-SMOOTH-MUSCLE-CELL-PROLIFERATION	GO-0048659	6	-0.336269	-0.830615	0.689605	1.000000	1.000
434	GOBP-NEURON-DEVELOPMENT	GO-0048666	34	-0.220567	-0.833480	0.682682	1.000000	1.000
435	GOBP-REGULATION-OF-CYSTEINE-TYPE-ENDOPEPTIDASE...	GO-2000116	9	-0.306778	-0.835725	0.666667	1.000000	1.000
436	GOBP-ORGANIC-ACID-TRANSPORT	GO-0015849	7	-0.334449	-0.838143	0.697260	1.000000	1.000
437	GOBP-REGULATION-OF-RECEPTOR-MEDIATED-ENDOCYTOSIS	GO-0048259	5	-0.365528	-0.839147	0.681159	1.000000	1.000
438	GOBP-LIPID-EXPORT-FROM-CELL	GO-0140353	5	-0.372510	-0.839741	0.677843	1.000000	1.000
439	GOBP-POSITIVE-REGULATION-OF-PROTEIN-TYROSINEK...	GO-0061098	5	-0.365047	-0.839977	0.666179	1.000000	1.000
440	GOBP-RESPONSE-TO-INSULIN	GO-0032868	5	-0.368516	-0.841053	0.666667	1.000000	1.000
441	REACTOME-NUCLEAR-EVENTS-KINASE-AND-TRANSCRIPTI...	R-RNO-198725	11	-0.289384	-0.843772	0.671018	1.000000	1.000
442	GOBP-SMALL-GTPASE-MEDIATED-SIGNAL-TRANSDUCTION	GO-0007264	8	-0.314311	-0.845060	0.672857	1.000000	1.000
443	REACTOME-EXTRA-NUCLEAR-ESTROGEN-SIGNALING	R-RNO-9008391	7	-0.330617	-0.846289	0.677241	1.000000	1.000
444	GOBP-REGULATION-OF-METAL-ION-TRANSPORT	GO-0010959	6	-0.351460	-0.847131	0.695291	1.000000	1.000
445	GOBP-FATTY-ACID-TRANSPORT	GO-0015908	6	-0.351436	-0.851608	0.684432	1.000000	1.000
446	GOBP-REGULATION-OF-CELLULAR-CATABOLIC-PROCESS	GO-0031329	10	-0.300297	-0.851658	0.670935	1.000000	1.000
447	GOBP-POSITIVE-REGULATION-OF-MAPK-CASCADE	GO-0043410	9	-0.312453	-0.852425	0.679296	1.000000	1.000
448	GOBP-POSITIVE-REGULATION-OF-CELL-ADHESION	GO-0045785	7	-0.337509	-0.853958	0.655714	1.000000	1.000
449	REACTOME-CELL-CYCLE-MITOTIC	R-RNO-69278	5	-0.377700	-0.854089	0.672012	1.000000	1.000
450	GOBP-PROTEIN-LOCALIZATION-TO-CELL-JUNCTION	GO-1902414	6	-0.353868	-0.857199	0.675714	1.000000	1.000
451	GOBP-RESPONSE-TO-INORGANIC-SUBSTANCE	GO-0010035	19	-0.253701	-0.857520	0.646635	1.000000	1.000
452	GOBP-REGULATION-OF-CELLULAR-COMPONENT-MOVEMENT	GO-0051270	15	-0.269215	-0.859562	0.635135	1.000000	1.000
453	REACTOME-ESR-MEDIATED-SIGNALING	R-RNO-8939211	8	-0.327527	-0.862059	0.663968	1.000000	1.000
454	GOBP-INORGANIC-ION-TRANSMEMBRANE-TRANSPORT	GO-0098660	9	-0.314256	-0.863061	0.661499	1.000000	1.000
455	GOBP-GROWTH	GO-0040007	14	-0.271291	-0.863402	0.647700	1.000000	1.000
456	GOBP-CELL-MORPHOGENESIS-INVOLVED-IN-NEURON-DIF...	GO-0048667	22	-0.248468	-0.865135	0.661593	1.000000	1.000
457	GOBP-EPHRIN-RECEPTOR-SIGNALING-PATHWAY	GO-0048013	5	-0.371429	-0.866126	0.652299	1.000000	1.000
458	GOBP-CIRCULATORY-SYSTEM-PROCESS	GO-0003013	5	-0.385791	-0.866263	0.632267	1.000000	1.000
459	GOBP-SECRETION	GO-0046903	24	-0.244187	-0.867058	0.647740	1.000000	1.000
460	GOBP-IMMUNE-EFFECTOR-PROCESS	GO-0002252	11	-0.296621	-0.870819	0.627937	1.000000	1.000
461	GOBP-CELL-MORPHOGENESIS-INVOLVED-IN-DIFFERENTI...	GO-0000904	22	-0.248468	-0.872073	0.648585	1.000000	1.000
462	GOBP-CELLULAR-AMIDE-METABOLIC-PROCESS	GO-0043603	12	-0.292983	-0.872282	0.625641	1.000000	1.000
463	GOBP-WOUND-HEALING	GO-0042060	13	-0.287996	-0.872979	0.629032	1.000000	1.000
464	REACTOME-SIGNALING-BY-NUCLEAR-RECEPTORS	R-RNO-9006931	8	-0.327527	-0.873797	0.659489	1.000000	1.000
465	GOBP-PEPTIDYL-LYSINE-MODIFICATION	GO-0018205	5	-0.384058	-0.874839	0.653793	1.000000	1.000
466	GOBP-MUSCLE-STRUCTURE-DEVELOPMENT	GO-0061061	16	-0.270165	-0.875478	0.631579	1.000000	1.000
467	GOBP-REGULATION-OF-PROTEIN-BINDING	GO-0043393	7	-0.348727	-0.876947	0.645333	1.000000	1.000
468	GOBP-NEGATIVE-REGULATION-OF-TRANSFERASE-ACTIVITY	GO-0051348	5	-0.391372	-0.877966	0.651685	1.000000	1.000
469	GOBP-APOPTOTIC-MITOCHONDRIAL-CHANGES	GO-0008637	6	-0.367975	-0.881390	0.615922	1.000000	1.000
470	GOBP-REGULATION-OF-CELL-ADHESION	GO-0030155	13	-0.291838	-0.888093	0.628644	1.000000	1.000

Continuation of Table S3

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
471	GOBP-NEUROGENESIS	GO-0022008	41	-0.233345	-0.888388	0.602941	1.000000	1.000
472	GOBP-POSITIVE-REGULATION-OF-TRANSPORT	GO-0051050	26	-0.252016	-0.890140	0.620023	1.000000	1.000
473	GOBP-RESPONSE-TO-HEAT	GO-0009408	7	-0.354755	-0.893733	0.613423	1.000000	1.000
474	GOBP-NEGATIVE-REGULATION-OF-KINASE-ACTIVITY	GO-0033673	5	-0.391372	-0.900585	0.610795	1.000000	1.000
475	GOBP-CELL-MIGRATION	GO-0016477	22	-0.255407	-0.901862	0.587544	1.000000	1.000
476	GOBP-ANATOMICAL-STRUCTURE-HOMEOSTASIS	GO-0060249	7	-0.358301	-0.906050	0.609418	1.000000	1.000
477	GOBP-CARBOHYDRATE-DERIVATIVE-BIOSYNTHETIC-PROCESS	GO-1901137	5	-0.401259	-0.909092	0.591777	1.000000	1.000
478	GOBP-CELL-PROJECTION-ORGANIZATION	GO-0030030	35	-0.239652	-0.909930	0.586009	1.000000	1.000
479	GOBP-RESPONSE-TO-CALCIUM-ION	GO-0051592	6	-0.375190	-0.910040	0.608696	1.000000	1.000
480	GOBP-PURINE-CONTAINING-COMPOUND-METABOLIC-PROCESS	GO-0072521	6	-0.383959	-0.910331	0.616162	1.000000	1.000
481	GOBP-REGULATION-OF-HYDROLASE-ACTIVITY	GO-0051336	22	-0.264684	-0.911371	0.586493	1.000000	1.000
482	GOBP-INSULIN-SECRETION	GO-0030073	7	-0.359307	-0.911617	0.573351	1.000000	1.000
483	GOBP-NEGATIVE-REGULATION-OF-SYNAPTIC-TRANSMISSION	GO-0050805	6	-0.375991	-0.913455	0.604082	1.000000	1.000
484	GOBP-POSITIVE-REGULATION-OF-PROTEIN-MODIFICATION	GO-0031401	22	-0.264057	-0.914785	0.589327	1.000000	1.000
485	GOBP-ORGANOPHOSPHATE-METABOLIC-PROCESS	GO-0019637	8	-0.343181	-0.916551	0.592593	1.000000	1.000
486	GOBP-AMINO-ACID-TRANSPORT	GO-0006865	6	-0.383968	-0.917194	0.598011	1.000000	1.000
487	GOBP-REGULATION-OF-TRANSPORT	GO-0051049	44	-0.241696	-0.920039	0.573184	1.000000	1.000
488	GOBP-PEPTIDE-HORMONE-SECRETION	GO-0030072	7	-0.359307	-0.920183	0.561570	1.000000	1.000
489	GOBP-DEVELOPMENTAL-PROCESS-INVOLVED-IN-REPRODUCTION	GO-0003006	11	-0.314398	-0.920385	0.602740	1.000000	1.000
490	GOBP-HOMEOSTATIC-PROCESS	GO-0042592	31	-0.251521	-0.922662	0.564825	1.000000	1.000
491	GOBP-MONOCARBOXYLIC-ACID-TRANSPORT	GO-0015718	5	-0.407285	-0.922815	0.603129	1.000000	1.000
492	GOBP-ACIDIC-AMINO-ACID-TRANSPORT	GO-0015800	5	-0.407285	-0.923388	0.577260	1.000000	1.000
493	GOBP-ORGANIC-ANION-TRANSPORT	GO-0015711	6	-0.383968	-0.924567	0.569801	1.000000	1.000
494	GOBP-MAPK-CASCADE	GO-0000165	18	-0.280777	-0.925441	0.574316	1.000000	1.000
495	GOBP-REGULATION-OF-VASCULAR-ASSOCIATED-SMOOTH-MUSCLE-CONTRACTION	GO-1904705	5	-0.401350	-0.926727	0.571429	1.000000	1.000
496	GOBP-REGULATION-OF-CELLULAR-RESPONSE-TO-STRESS	GO-0080135	9	-0.337870	-0.927364	0.572549	1.000000	1.000
497	GOBP-NEGATIVE-REGULATION-OF-CELL-PROJECTION-OR-CELL-ADHESION	GO-0031345	5	-0.410470	-0.928369	0.577746	1.000000	1.000
498	GOBP-POSITIVE-REGULATION-OF-PROTEIN-KINASE-ACTIVITY	GO-0045860	18	-0.277517	-0.929140	0.543165	1.000000	1.000
499	GOBP-POSITIVE-REGULATION-OF-PROTEIN-PHOSPHORYLATION	GO-0001934	22	-0.264057	-0.929198	0.569428	1.000000	1.000
500	GOBP-LONG-TERM-SYNAPTIC-POTENTIATION	GO-0060291	12	-0.309167	-0.930700	0.568354	1.000000	1.000
501	GOBP-DICARBOXYLIC-ACID-TRANSPORT	GO-0006835	5	-0.407285	-0.930833	0.558989	1.000000	1.000
502	GOBP-CARBOXYLIC-ACID-TRANSPORT	GO-0046942	6	-0.383968	-0.932373	0.566334	1.000000	1.000
503	GOBP-REGULATION-OF-CELL-CYCLE	GO-0051726	13	-0.306685	-0.933800	0.549875	1.000000	1.000
504	GOBP-REGULATION-OF-MUSCLE-CELL-DIFFERENTIATION	GO-0051147	6	-0.388416	-0.935434	0.542373	1.000000	1.000
505	GOBP-METAL-ION-HOMEOSTASIS	GO-0055065	14	-0.298810	-0.936538	0.561064	1.000000	1.000
506	HALLMARK-P13K-AKT-MTOR-SIGNALING	M5923	6	-0.388454	-0.938234	0.570850	1.000000	1.000
507	GOBP-ION-HOMEOSTASIS	GO-0050801	16	-0.290152	-0.943794	0.547101	1.000000	1.000
508	GOBP-RESPONSE-TO-PEPTIDE-HORMONE	GO-0043434	13	-0.311954	-0.944205	0.526992	1.000000	1.000
509	GOBP-ASSOCIATIVE-LEARNING	GO-0008306	7	-0.372650	-0.945773	0.567227	1.000000	1.000
510	GOBP-AMIDE-BIOSYNTHETIC-PROCESS	GO-0043604	6	-0.386379	-0.948126	0.537517	1.000000	1.000
511	GOBP-PEPTIDE-BIOSYNTHETIC-PROCESS	GO-0043043	6	-0.386379	-0.952491	0.537827	1.000000	1.000
512	GOBP-POSITIVE-REGULATION-OF-PROTEOLYSIS	GO-0045862	8	-0.362631	-0.953400	0.545455	1.000000	1.000
513	GOBP-SKELETAL-MUSCLE-ORGAN-DEVELOPMENT	GO-0060538	5	-0.412002	-0.953945	0.538244	1.000000	1.000

Continuation of Table S3

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
514	GOBP-INTRACELLULAR-TRANSPORT	GO-0046907	10	-0.334143	-0.956493	0.523377	1.000000	1.000
515	GOBP-NEGATIVE-REGULATION-OF-SIGNALING	GO-0023057	21	-0.281336	-0.961626	0.525822	1.000000	1.000
516	GOBP-EXCITATORY-CHEMICAL-SYNAPTIC-TRANSMISSION	GO-0098976	5	-0.416038	-0.967427	0.497890	1.000000	1.000
517	GOBP-DEVELOPMENTAL-MATURATION	GO-0021700	5	-0.429347	-0.968594	0.526761	1.000000	1.000
518	GOBP-REGULATION-OF-BINDING	GO-0051098	11	-0.328439	-0.968896	0.506953	1.000000	1.000
519	GOBP-ORGANONITROGEN-COMPOUND-BIOSYNTHETIC-PROCESS	GO-1901566	13	-0.315723	-0.969156	0.484549	1.000000	1.000
520	REACTOME-EPHLEPHRIN-SIGNALING	R-RNO-2682334	6	-0.400443	-0.971352	0.516039	1.000000	1.000
521	GOBP-REGULATION-OF-CYTOSKELETON-ORGANIZATION	GO-0051493	5	-0.427073	-0.977426	0.486448	1.000000	1.000
522	REACTOME-NEGATIVE-REGULATION-OF-NMDA-RECEPTOR...	R-HSA-961732	8	-0.376003	-0.978435	0.536521	1.000000	1.000
523	GOBP-BEHAVIOR	GO-0007610	33	-0.264393	-0.980150	0.498294	1.000000	1.000
524	REACTOME-CIRCADIAN-CLOCK	R-HSA-400253	5	-0.433735	-0.987150	0.475728	1.000000	1.000
525	GOBP-ORGANIC-ACID-METABOLIC-PROCESS	GO-0006082	7	-0.390932	-0.988213	0.507483	1.000000	1.000
526	GOBP-VESSICLE-MEDIATED-TRANSPORT-IN-SYNAPSE	GO-0099003	7	-0.389869	-0.989298	0.490566	1.000000	1.000
527	REACTOME-ASSEMBLY-AND-CELL-SURFACE-PRESENTATION...	R-RNO-9609736	8	-0.376003	-0.990208	0.492773	1.000000	1.000
528	GOBP-MUSCLE-ORGAN-DEVELOPMENT	GO-0007517	9	-0.365246	-0.991137	0.494133	1.000000	1.000
529	GOBP-REGULATION-OF-NERVOUS-SYSTEM-PROCESS	GO-0031644	8	-0.380000	-0.992828	0.501971	1.000000	1.000
530	GOBP-STRIATED-MUSCLE-CELL-DIFFERENTIATION	GO-0051146	9	-0.366495	-0.992997	0.487248	1.000000	1.000
531	GOBP-REGULATION-OF-CYTOSOLIC-CALCIUM-ION-CONCE...	GO-0051480	13	-0.328197	-0.993102	0.480601	1.000000	1.000
532	GOBP-CELL-GROWTH	GO-0016049	10	-0.352177	-0.993878	0.484127	1.000000	1.000
533	GOBP-POSITIVE-REGULATION-OF-CYSTEINE-TYPE-ENDO...	GO-2001056	7	-0.396678	-0.996275	0.475661	1.000000	1.000
534	GOBP-CALCIUM-MEDIATED-SIGNALING	GO-0019722	10	-0.354972	-1.004981	0.470361	1.000000	1.000
535	GOBP-MUSCLE-ADAPTATION	GO-0043500	5	-0.439943	-1.005425	0.445714	1.000000	1.000
536	GOBP-REGULATION-OF-MUSCLE-SYSTEM-PROCESS	GO-0090257	8	-0.379538	-1.007587	0.451482	1.000000	1.000
537	GOBP-DIVALENT-INORGANIC-CATION-HOMEOSTASIS	GO-0072507	13	-0.328197	-1.007683	0.454545	1.000000	1.000
538	GOBP-POSITIVE-REGULATION-OF-PEPTIDASE-ACTIVITY	GO-0010952	7	-0.396678	-1.007808	0.454791	1.000000	1.000
539	GOBP-CELLULAR-RESPONSE-TO-PEPTIDE-HORMONE-STIM...	GO-0071375	9	-0.371106	-1.013165	0.485640	1.000000	1.000
540	GOBP-NERVOUS-SYSTEM-PROCESS	GO-0050877	38	-0.268632	-1.014937	0.461197	1.000000	1.000
541	GOBP-PEPTIDE-SECRETION	GO-0002790	9	-0.369285	-1.014989	0.445178	1.000000	1.000
542	GOBP-REGULATION-OF-MUSCLE-ADAPTATION	GO-0043502	5	-0.439943	-1.018549	0.421499	1.000000	1.000
543	REACTOME-G-ALPHA-Q-SIGNALING-EVENTS	R-RNO-416476	6	-0.426040	-1.021899	0.442441	1.000000	1.000
544	GOBP-POSITIVE-REGULATION-OF-PROTEIN-SERINE-THR...	GO-0071902	9	-0.367061	-1.023684	0.435762	1.000000	1.000
545	GOBP-POSITIVE-REGULATION-OF-CATALYTIC-ACTIVITY	GO-0043085	29	-0.278673	-1.024653	0.447545	1.000000	1.000
546	GOBP-REGULATION-OF-HORMONE-SECRETION	GO-0046883	8	-0.380437	-1.024964	0.448461	1.000000	1.000
547	GOBP-POSTTRANSCRIPTIONAL-REGULATION-OF-GENE-EX...	GO-0010608	8	-0.389757	-1.025261	0.446721	1.000000	1.000
548	GOBP-CELLULAR-GLUCOSE-HOMEOSTASIS	GO-0001678	5	-0.440349	-1.025656	0.402878	1.000000	1.000
549	GOBP-METAL-ION-TRANSPORT	GO-0030001	11	-0.355398	-1.025877	0.455458	1.000000	1.000
550	GOBP-REGULATION-OF-SYNAPTIC-PLASTICITY	GO-0048167	21	-0.298522	-1.026806	0.453237	1.000000	1.000
551	GOBP-SMALL-MOLECULE-METABOLIC-PROCESS	GO-0044281	16	-0.317535	-1.028401	0.444578	1.000000	1.000
552	GOBP-RESPONSE-TO-ALKALOID	GO-0043279	5	-0.445783	-1.028599	0.410689	1.000000	1.000
553	GOBP-MUSCLE-CONTRACTION	GO-0006936	5	-0.459507	-1.030296	0.426346	1.000000	1.000
554	GOBP-CELL-CELL-SIGNALING-BY-WNT	GO-0198738	7	-0.401564	-1.030696	0.446575	1.000000	1.000
555	REACTOME-CELL-CYCLE	R-RNO-1640170	6	-0.432403	-1.032565	0.432285	1.000000	1.000
556	GOBP-POSITIVE-REGULATION-OF-ION-TRANSPORT	GO-0043270	17	-0.310225	-1.032943	0.443800	1.000000	1.000

Continuation of Table S3

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
557	GOBP-LONG-TERM-MEMORY	GO-0007616	6	-0.425535	-1.035336	0.434599	1.000000	1.000
558	GOBP-REGULATION-OF-BODY-FLUID-LEVELS	GO-0050878	11	-0.354701	-1.036344	0.434395	1.000000	1.000
559	REACTOME-G-ALPHA-Z-SIGNALING-EVENTS	R-RNO-418597	5	-0.458829	-1.036891	0.416431	1.000000	1.000
560	GOBP-REGULATION-OF-ANION-TRANSPORT	GO-0040470	20	-0.302923	-1.037633	0.421302	1.000000	1.000
561	GOBP-RESPONSE-TO-KETONE	GO-1901654	7	-0.416952	-1.038390	0.424242	1.000000	1.000
562	GOBP-PROTEIN-LOCALIZATION-TO-SYNAPSE	GO-0035418	5	-0.459578	-1.040562	0.423188	1.000000	1.000
563	REACTOME-VESICLE-MEDIATED-TRANSPORT	R-RNO-5653656	5	-0.456478	-1.041515	0.397882	1.000000	1.000
564	GOBP-PROTEIN-LOCALIZATION-TO-MEMBRANE	GO-0042692	13	-0.344106	-1.041710	0.407814	1.000000	1.000
565	GOBP-MUSCLE-CELL-DIFFERENTIATION	GO-0062322	10	-0.369268	-1.042064	0.410622	1.000000	1.000
566	GOBP-HEAD-DEVELOPMENT	GO-0060322	23	-0.296788	-1.042362	0.434579	1.000000	1.000
567	GOBP-ENDOCRINE-SYSTEM-DEVELOPMENT	GO-0035270	6	-0.441807	-1.043165	0.426982	1.000000	1.000
568	GOBP-POSITIVE-REGULATION-OF-SYNAPTIC-TRANSMISSION	GO-0050806	15	-0.324621	-1.043242	0.419512	1.000000	1.000
569	GOBP-TRANSMEMBRANE-TRAFFICKING	GO-0055085	27	-0.293714	-1.044387	0.408884	1.000000	1.000
570	REACTOME-MEMBRANE-TRAFFICKING	R-RNO-199991	5	-0.456478	-1.046892	0.424242	1.000000	1.000
571	GOBP-PROTEIN-LOCALIZATION-TO-POSTSYNAPSE	GO-0062237	5	-0.459578	-1.050103	0.395480	1.000000	1.000
572	GOBP-MONOCARBOXYLIC-ACID-METABOLIC-PROCESS	GO-0032787	6	-0.432593	-1.050564	0.406944	1.000000	1.000
573	GOBP-CALCIUM-ION-TRANSPORT	GO-0006816	11	-0.353398	-1.051212	0.394602	1.000000	1.000
574	GOBP-POSITIVE-REGULATION-OF-MOLECULAR-FUNCTION	GO-0044093	37	-0.275335	-1.051850	0.390190	1.000000	1.000
575	GOBP-CENTRAL-NERVOUS-SYSTEM-DEVELOPMENT	GO-0007417	27	-0.293232	-1.054910	0.401837	1.000000	1.000
576	GOBP-REGULATION-OF-CELL-PROJECTION-ORGANIZATION	GO-0031344	20	-0.303989	-1.055785	0.403129	1.000000	1.000
577	GOBP-DENDRITIC-SPINE-DEVELOPMENT	GO-0060996	6	-0.435566	-1.059645	0.388418	1.000000	1.000
578	REACTOME-BETA-CATENIN-INDEPENDENT-WNT-SIGNALING	R-RNO-3858494	5	-0.464338	-1.059816	0.390244	1.000000	1.000
579	GOBP-DENDRITIC-SPINE-MORPHOGENESIS	GO-0060997	5	-0.468418	-1.060351	0.410587	1.000000	1.000
580	GOBP-HORMONE-TRANSPORT	GO-0009914	9	-0.385155	-1.061188	0.407507	1.000000	1.000
581	GOBP-REGULATION-OF-NEUROTRANSMITTER-TRANSPORT	GO-0051588	6	-0.437356	-1.061976	0.393602	1.000000	1.000
582	GOBP-REGULATION-OF-PEPTIDE-SECRETION	GO-0002791	7	-0.428562	-1.069200	0.383448	1.000000	1.000
583	GOBP-MULTICELLULAR-ORGANISM-REPRODUCTION	GO-0032504	12	-0.353999	-1.066530	0.395379	1.000000	1.000
584	GOBP-ENDOMEMBRANE-SYSTEM-ORGANIZATION	GO-0010256	6	-0.440212	-1.070988	0.386301	1.000000	1.000
585	GOBP-REGULATION-OF-SYSTEM-PROCESS	GO-0044057	18	-0.326021	-1.087235	0.349879	1.000000	1.000
586	GOBP-REGULATION-OF-PEPTIDE-HORMONE-SECRETION	GO-0090276	6	-0.453527	-1.089411	0.340845	1.000000	1.000
587	GOBP-CELL-CYCLE	GO-0007049	21	-0.320869	-1.090761	0.362884	1.000000	1.000
588	GOBP-MUSCLE-SYSTEM-PROCESS	GO-0003012	9	-0.399627	-1.095387	0.350785	1.000000	1.000
589	GOBP-MYELOID-LEUKOCYTE-ACTIVATION	GO-0002274	8	-0.413495	-1.096025	0.359211	1.000000	1.000
590	GOBP-REGULATION-OF-CELLULAR-LOCALIZATION	GO-0060341	17	-0.336435	-1.099643	0.354293	1.000000	1.000
591	GOBP-NEGATIVE-REGULATION-OF-GENE-EXPRESSION	GO-0010629	11	-0.375249	-1.102073	0.355082	1.000000	1.000
592	GOBP-RESPONSE-TO-METAL-ION	GO-0010038	15	-0.344561	-1.103536	0.341104	1.000000	1.000
593	GOBP-MUSCLE-CELL-DEVELOPMENT	GO-0055001	5	-0.482136	-1.104087	0.325037	1.000000	1.000
594	REACTOME-LONG-TERM-POTENTIATION	R-HSA-9620244	10	-0.387434	-1.104610	0.346053	1.000000	1.000
595	GOBP-REGULATION-OF-POSTSYNAPTIC-MEMBRANE-POTEN...	GO-0060078	14	-0.353537	-1.104734	0.336145	1.000000	1.000
596	REACTOME-MAPK-FAMILY-SIGNALING-CASCADES	R-RNO-5683057	12	-0.370644	-1.105365	0.338812	1.000000	1.000
597	REACTOME-PTEN-REGULATION	R-RNO-6807070	5	-0.487796	-1.105616	0.332394	1.000000	1.000
598	GOBP-NUCLEOBASE-CONTAINING-SMALL-MOLECULE-META...	GO-0055086	7	-0.437991	-1.106261	0.336634	1.000000	1.000
599	REACTOME-NEUTROPHIL-DEGRANULATION	R-RNO-6798695	6	-0.461177	-1.114084	0.339489	1.000000	1.000

Continuation of Table S3

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
600	GOBP-MYELOID-LEUKOCYTE-MEDIATED-IMMUNITY	GO-0002444	6	-0.461177	-1.119506	0.331915	1.000000
601	GOBP-CELL_JUNCTION_ORGANIZATION	GO-0034330	19	-0.337812	-1.120207	0.320096	1.000000
602	GOBP-GAMETE-GENERATION	GO-0007276	9	-0.411991	-1.121207	0.345997	1.000000
603	GOBP-CELLULAR-ION-HOMEOSTASIS	GO-0006873	14	-0.358165	-1.123210	0.317897	1.000000
604	GOBP-REGULATION-OF-SYNAPTIC-TRANSMISSION-GLUTA...	GO-0051966	12	-0.381041	-1.124200	0.371132	1.000000
605	REACTOME-TRAFFICKING-OF-GLUR2-CONTAINING-AMPA...	R-RNO-416993	8	-0.430031	-1.126362	0.332414	1.000000
606	GOBP-NEGATIVE-REGULATION-OF-CELL-CYCLE	GO-0045786	5	-0.492412	-1.126754	0.288406	1.000000
607	GOBP-CELLULAR-RESPONSE-TO-ALCOHOL	GO-0097306	5	-0.493793	-1.127890	0.309659	1.000000
608	GOBP-REGULATION-OF-VESICLE-MEDIATED-TRANSPORT	GO-0060627	12	-0.370861	-1.128881	0.316391	1.000000
609	GOBP-CYTOSKELETON-ORGANIZATION	GO-0007010	11	-0.376633	-1.129941	0.304562	1.000000
610	GOBP-PROTEIN-LOCALIZATION-TO-CELL-PERIPHERY	GO-1990778	12	-0.376633	-1.129960	0.319255	1.000000
611	GOBP-SENSORY-ORGAN-DEVELOPMENT	GO-0007423	8	-0.427594	-1.131100	0.311081	1.000000
612	GOBP-POSITIVE-REGULATION-OF-SECRETION	GO-0051047	6	-0.464879	-1.134765	0.314841	1.000000
613	REACTOME-RNA-POLYMERASE-III-TRANSCRIPTION	R-RNO-73857	20	-0.333792	-1.137549	0.301663	1.000000
614	REACTOME-SIGNALING-BY-WNT	R-RNO-195721	7	-0.454792	-1.144613	0.303867	1.000000
615	GOBP-POSITIVE-REGULATION-OF-PROTEIN-METABOLIC...	GO-0051247	27	-0.319058	-1.145538	0.306620	1.000000
616	GOBP-CELLULAR-LIPID-METABOLIC-PROCESS	GO-0044255	7	-0.451062	-1.147858	0.296296	1.000000
617	GOBP-CELL-ACTIVATION-INVOLVED-IN-IMMUNE-RESPONSE	GO-0002263	7	-0.461177	-1.149319	0.289291	1.000000
618	GOBP-CARBOHYDRATE-HOMEOSTASIS	GO-0033500	7	-0.449946	-1.152053	0.306430	1.000000
619	REACTOME-CLASS-C-3-METABOTROPIC-GLUTAMATE-PHER...	R-RNO-420499	7	-0.448677	-1.152288	0.288952	1.000000
620	GOBP-REGULATION-OF-ORGANELLE-ORGANIZATION	GO-0033043	14	-0.363498	-1.152732	0.280247	1.000000
621	GOBP-CHEMICAL-HOMEOSTASIS	GO-0048878	23	-0.330853	-1.154995	0.288235	1.000000
622	GOBP-LEARNING	GO-0007612	13	-0.376278	-1.159820	0.276029	1.000000
623	GOBP-REGULATION-OF-ENDOCYTOSIS	GO-0030100	6	-0.473851	-1.160275	0.280537	1.000000
624	GOBP-CELL-SURFACE-RECEPTOR-SIGNALING-PATHWAY_I...	GO-1905114	15	-0.364596	-1.164498	0.276775	1.000000
625	GOBP-MITOCHONDRION-ORGANIZATION	GO-0007005	7	-0.460814	-1.170978	0.262948	1.000000
626	REACTOME-RAS-ACTIVATION-UPON-CA2-INFLUX-THROUGH...	R-HSA-442982	6	-0.487805	-1.177339	0.251366	1.000000
627	GOBP-SYNAPTIC-SIGNALING	GO-0099536	47	-0.490797	-1.178939	0.258602	1.000000
628	GOBP-GLUCOSE-METABOLIC-PROCESS	GO-0006006	6	-0.490797	-1.180926	0.260388	1.000000
629	GOBP-NUCLEAR-TRANSPORT	GO-0051169	5	-0.511968	-1.188470	0.252427	1.000000
630	GOBP-CELLULAR-HOMEOSTASIS	GO-0019725	18	-0.356988	-1.190694	0.245983	1.000000
631	GOBP-MONOSACCHARIDE-METABOLIC-PROCESS	GO-0005996	6	-0.490797	-1.193563	0.248237	1.000000
632	GOBP-NEUROTRANSMITTER-TRANSPORT	GO-0006836	7	-0.477525	-1.195238	0.244475	1.000000
633	GOBP-REGULATION-OF-NEURONAL-SYNAPTIC-PLASTICITY	GO-0048168	7	-0.470940	-1.204600	0.221477	1.000000
634	GOBP-SECOND-MESSENGER-MEDIATED-SIGNALING	GO-0019932	16	-0.373197	-1.211378	0.233633	1.000000
635	GOBP-INTRACELLULAR-PROTEIN-TRANSPORT	GO-0006886	8	-0.460040	-1.211394	0.210598	1.000000
636	GOBP-POSITIVE-REGULATION-OF-ESTABLISHMENT-OF_P...	GO-1904951	5	-0.531804	-1.212494	0.198847	1.000000
637	GOBP-REGULATION-OF-NEUROTRANSMITTER-LEVELS	GO-0001505	7	-0.477525	-1.212632	0.236016	1.000000
638	GOBP-REGULATION-OF-MEMBRANE-POTENTIAL	GO-0042391	17	-0.367862	-1.214250	0.222089	1.000000
639	GOBP-CHEMICAL-SYNAPTIC-TRANSMISSION-POSTSYNAPTIC	GO-0099565	9	-0.444164	-1.215004	0.241470	1.000000
640	GOBP-POSITIVE-REGULATION-OF-CELLULAR-PROTEIN_L...	GO-1903829	7	-0.477525	-1.223132	0.225585	1.000000
641	GOBP-ENDOCYTOSIS	GO-0006897	8	-0.463492	-1.224305	0.221622	1.000000
642	REACTOME-NEUREXINS-AND-NEUROLIGINS	R-RNO-6794361	9	-0.442768	-1.225097	0.226078	1.000000

Continuation of Table S3

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
643 GOBP-ESTABLISHMENT-OF-PROTEIN-LOCALIZATION	GO-0045184	17	-0.365777	-1.230078	0.207108	1.000000	1.000
644 GOBP-NEGATIVE-REGULATION-OF-BINDING	GO-0051100	6	-0.511318	-1.231544	0.199726	1.000000	1.000
645 GOBP-MALE-GAMETE-GENERATION	GO-0048232	5	-0.542169	-1.235283	0.207232	1.000000	1.000
646 REACTOME-CA-DEPENDENT-EVENTS	R-RNO-111996	8	-0.462500	-1.242206	0.198413	1.000000	1.000
647 GOBP-REGULATION-OF-SECRETION	GO-0051046	14	-0.399329	-1.244348	0.205000	1.000000	1.000
648 REACTOME-SIGNALING-BY-RHO-GTPASES-MIRO-GTPASES...	R-RNO-9716542	9	-0.452156	-1.247256	0.184000	1.000000	1.000
649 GOBP-POSITIVE-REGULATION-OF-SIGNALING	GO-0023056	34	-0.331306	-1.247854	0.210465	1.000000	1.000
650 GOBP-RESPONSE-TO-ETHANOL	GO-0045471	5	-0.548100	-1.250737	0.193687	1.000000	1.000
651 GOBP-NEUROTRANSMITTER-SECRETION	GO-0007269	6	-0.510490	-1.250904	0.180617	1.000000	1.000
652 GOBP-DEPHOSPHORYLATION	GO-0016311	7	-0.490047	-1.251874	0.210235	1.000000	1.000
653 GOBP-SEXUAL-REPRODUCTION	GO-0019953	10	-0.437601	-1.253531	0.199741	1.000000	1.000
654 REACTOME-RHO-GTPASE-EFFECTORS	R-RNO-195258	9	-0.452156	-1.257324	0.187332	1.000000	1.000
655 GOBP-REGULATION-OF-PROTEIN-LOCALIZATION	GO-0032880	18	-0.377804	-1.261681	0.191697	1.000000	1.000
656 GOBP-G-PROTEIN-COUPLED-GLUTAMATE-RECEPTOR-SIGN...	GO-0007216	8	-0.477630	-1.263065	0.165554	1.000000	1.000
657 REACTOME-INTRACELLULAR-SIGNALING-BY-SECOND-MES...	R-RNO-9006925	15	-0.393939	-1.264675	0.193827	1.000000	1.000
658 GOBP-CELLULAR-RESPONSE-TO-KETONE	GO-1901655	5	-0.555812	-1.268112	0.169034	1.000000	1.000
659 GOBP-POSTSYNAPSE-ORGANIZATION	GO-0009173	10	-0.443231	-1.270217	0.179183	1.000000	1.000
660 GOBP-PROTEIN-PHOSPHORYLATION	GO-0006470	7	-0.490047	-1.271305	0.162382	1.000000	1.000
661 REACTOME-TRAFFICKING-OF-AMPA-RECEPTORS	R-RNO-399719	11	-0.441558	-1.274518	0.175796	1.000000	1.000
662 REACTOME-GPCR-LIGAND-BINDING	R-RNO-500792	8	-0.476379	-1.275162	0.177333	1.000000	1.000
663 REACTOME-TRANSCRIPTIONAL-REGULATION-BY-MECP2	R-RNO-8986944	7	-0.493827	-1.276374	0.157895	1.000000	1.000
664 GOBP-NUCLEOSIDE-PHOSPHATE-BIOSYNTHETIC-PROCESS	GO-1901293	5	-0.565559	-1.290962	0.156204	1.000000	1.000
665 GOBP-SYNAPTIC-TRANSMISSION-GLUTAMATERGIC	GO-0035249	13	-0.424684	-1.291277	0.154135	1.000000	1.000
666 GOBP-REGULATION-OF-CELL-CYCLE-PROCESS	GO-0010564	5	-0.560271	-1.292221	0.179379	1.000000	1.000
667 REACTOME-G-PROTEIN-MEDIATED-EVENTS	R-RNO-112040	9	-0.468354	-1.298769	0.150063	1.000000	1.000
668 GOBP-ORGANOPHOSPHATE-BIOSYNTHETIC-PROCESS	GO-0090407	5	-0.565559	-1.303493	0.120235	1.000000	1.000
669 GOBP-REGULATION-OF-TRANS-SYNAPTIC-SIGNALING	GO-0009177	40	-0.347238	-1.307300	0.160398	1.000000	1.000
670 GOBP-SENSORY-PERCEPTION-OF-PAIN	GO-0019233	5	-0.578313	-1.313459	0.143917	1.000000	1.000
671 GOBP-REGULATION-OF-SYNAPSE-STRUCTURE-OR-ACTIVITY	GO-0050803	11	-0.450475	-1.317153	0.141582	1.000000	1.000
672 REACTOME-UNBLOCKING-OF-NMDA-RECEPTORS-GLUTAMAT...	R-RNO-438066	12	-0.446363	-1.319514	0.144686	1.000000	1.000
673 GOBP-LOCOMOTORY-BEHAVIOR	GO-0007626	8	-0.494504	-1.323714	0.128631	1.000000	1.000
674 GOBP-SIGNAL-RELEASE	GO-0023061	14	-0.424209	-1.325561	0.145038	1.000000	1.000
675 GOBP-SYNAPSE-ORGANIZATION	GO-0050808	17	-0.401657	-1.326474	0.150188	1.000000	1.000
676 GOBP-ADENYLATE-CYCLASE-INHIBITING-G-PROTEIN.CO...	GO-0007196	5	-0.580153	-1.327959	0.130127	1.000000	1.000
677 GOBP-CELLULAR-COMPONENT-MAINTENANCE	GO-0043954	5	-0.587260	-1.330923	0.128427	1.000000	1.000
678 GOBP-REGULATION-OF-CELLULAR-PROTEIN-LOCALIZATION	GO-1903827	12	-0.440384	-1.333195	0.137056	1.000000	1.000
679 GOBP-LEUKOCYTE-MEDIATED-IMMUNITY	GO-0002443	8	-0.494080	-1.334947	0.123457	1.000000	1.000
680 REACTOME-CREB1-PHOSPHORYLATION-THROUGH-NMDA.RE...	R-RNO-442742	8	-0.500000	-1.352929	0.128134	1.000000	1.000
681 GOBP-MITOTIC-CELL-CYCLE	GO-0000278	10	-0.482837	-1.360933	0.118100	1.000000	1.000
682 GOBP-ADENYLATE-CYCLASE-INHIBITING-G-PROTEIN.CO...	GO-0007193	9	-0.491023	-1.367327	0.109354	1.000000	1.000
683 REACTOME-TRANSCRIPTIONAL-REGULATION-BY-TP53	R-RNO-3700980	6	-0.565151	-1.375273	0.085135	1.000000	1.000
684 REACTOME-PROTEIN-PROTEIN-INTERACTIONS-AT-SYNAPSES	R-RNO-6794362	12	-0.469600	-1.379378	0.116834	1.000000	1.000
685 GOBP-RESPIRATORY-SYSTEM-DEVELOPMENT	GO-0060541	6	-0.574009	-1.388704	0.097855	1.000000	1.000

Continuation of Table S3

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
686	REACTOME_INTEGRATION_OF_ENERGY_METABOLISM	R-RNO-103685	5	-0.614458	-1.389489	0.095791	1.000000
687	GOBP_CELL_CELL_SIGNALING	GO-0007267	56	-0.376284	-1.403726	0.091620	1.000000
688	GOBP_RESPONSE_TO_ALCOHOL	GO-0097305	11	-0.486403	-1.406502	0.063144	1.000000
689	REACTOME_SYNAPTIC_ADHESION_LIKE_MOLECULES	R-RNO-8849932	9	-0.518656	-1.408335	0.099596	1.000000
690	GOBP_DENDRITE_DEVELOPMENT	GO-0016358	10	-0.506783	-1.414846	0.091731	1.000000
691	GOBP_IONOTROPIC_GLUTAMATE_RECEPTOR_SIGNALING_P...	GO-0035235	9	-0.520588	-1.418908	0.095238	1.000000
692	GOBP_CATION_TRANSPORT	GO-0006812	25	-0.393409	-1.421790	0.068525	1.000000
693	GOBP_NEURON_PROJECTION_ORGANIZATION	GO-0106027	8	-0.535198	-1.424414	0.097754	1.000000
694	GOBP_CATION_TRANSMEMBRANE_TRANSPORT	GO-0098655	18	-0.426629	-1.427653	0.085612	1.000000
695	GOBP_MYOTUBE_DIFFERENTIATION	GO-0014902	5	-0.635713	-1.432647	0.093151	1.000000
696	GOBP_REGULATION_OF_ION_TRANSPORT	GO-0043269	36	-0.379300	-1.434439	0.094145	1.000000
697	GOBP_REGULATION_OF_TRANSMEMBRANE_TRANSPORT	GO-0034762	23	-0.409189	-1.434890	0.082854	1.000000
698	REACTOME_OPIOID_SIGNALING	R-RNO-111885	12	-0.486842	-1.450133	0.080051	1.000000
699	GOBP_REGULATION_OF_PEP_TIDE_TRANSPORT	GO-0090087	10	-0.517736	-1.458708	0.063211	1.000000
700	REACTOME_ACTIVATION_OF_NMDA_RECEPTORS_AND_POST...	R-RNO-442755	16	-0.458006	-1.474546	0.062726	1.000000
701	GOBP_REGULATION_OF_POSTSYNAPSE_ORGANIZATION	GO-0099175	6	-0.610022	-1.500633	0.057103	1.000000
702	GOBP_DENDRITE_MORPHOGENESIS	GO-0048813	7	-0.587217	-1.508011	0.042466	1.000000
703	GOBP_ADENYLATE_CYCLASE_MODULATING_G_PROTEIN_CO...	GO-0007188	11	-0.517337	-1.509981	0.048346	1.000000
704	REACTOME_NEUROTRANSMITTER_RECEPTORS_AND_POSTSY...	R-RNO-112314	22	-0.456908	-1.546301	0.025060	1.000000
705	GOBP_REGULATION_OF_TRANSPORTER_ACTIVITY	GO-0032409	17	-0.466937	-1.552568	0.032927	0.875311
706	GOBP_CELL_CYCLE_PROCESS	GO-0022402	11	-0.546612	-1.584895	0.027379	0.735448
707	REACTOME_SIGNALING_BY_GPCR	R-RNO-372790	22	-0.457918	-1.594328	0.033058	0.726802
708	GOBP_GLUTAMATE_RECEPTOR_SIGNALING_PATHWAY	GO-0007215	17	-0.497391	-1.611705	0.020910	0.679855
709	GOBP_CELLULAR_MACROMOLECULE_LOCALIZATION	GO-0070727	20	-0.466129	-1.617401	0.021557	0.693508
710	GOBP_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY	GO-0007186	18	-0.490504	-1.625658	0.023370	0.697881
711	GOBP_REGULATION_OF_CATION_TRANSMEMBRANE_TRANSPORT	GO-1904062	16	-0.508995	-1.629910	0.021066	0.724018
712	GOBP_PROTEIN_COMPLEX_OLIGOMERIZATION	GO-0051259	7	-0.649794	-1.652536	0.012195	0.656236
713	GOBP_SENSORY_PERCEPTION	GO-0007600	9	-0.607595	-1.660205	0.014286	0.670151
714	GOBP_REGULATION_OF_NMDA_RECEPTOR_ACTIVITY	GO-2000310	10	-0.584148	-1.664863	0.020970	0.706904
715	REACTOME_TRANSMISSION_ACROSS_CHEMICAL_SYNAPSES	R-RNO-112315	23	-0.467033	-1.664978	0.018957	0.777070
716	REACTOME_NEURONAL_SYSTEM	R-RNO-112316	26	-0.466845	-1.684079	0.010490	0.744275
717	REACTOME_G_ALPHA_I_SIGNALING_EVENTS	R-RNO-418594	18	-0.512476	-1.706904	0.019656	0.699389
718	GOBP_PROTEIN_TETRAMERIZATION	GO-0051262	5	-0.759258	-1.739027	0.005690	0.613457
719	GOBP_PROTEIN_CONTAINING_COMPLEX_SUBUNIT_ORGANI...	GO-0043933	15	-0.566463	-1.801572	0.006242	0.417409
720	GOBP_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO...	GO-0072594	5	-0.789795	-1.804116	0.004213	0.487702
721	GOBP_PROTEIN_LOCALIZATION_TO_ORGANELLE	GO-0033365	8	-0.685173	-1.823297	0.004104	0.519052
722	GOBP_REGULATION_OF_SIGNALING_RECEPTOR_ACTIVITY	GO-0010469	14	-0.604349	-1.873540	0.001211	0.431636
723	GOBP_REGULATION_OF_CATION_CHANNEL_ACTIVITY	GO-2001257	14	-0.593628	-1.873590	0.004950	0.647454
724	GOBP_REGULATION_OF_NEUROTRANSMITTER_RECEPTOR_A...	GO-0099601	13	-0.623822	-1.920449	0.000000	0.800690

End of Table

Supplementary Table S4: SC rostral segment late (45 DPL peak) profile GSEA results.

Begin of Table S4									
	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val	
0	GOBP-SYNAPTIC-SIGNALING	GO:0099536	47	0.579961	2.018370	0.001142	0.110040	0.101	
1	GOBP-CELL-CELL-SIGNALING	GO:0007267	56	0.573256	2.007903	0.000000	0.064290	0.117	
2	REACTOME-NEURONAL-SYSTEM	R-RNO-112316	26	0.594129	1.945261	0.000000	0.104607	0.267	
3	GOBP-REGULATION-OF-TRANS-SYNAPTIC-SIGNALING	GO:0099177	40	0.549315	1.942583	0.000000	0.081764	0.277	
4	REACTOME-NEUROTRANSMITTER-RECEPTORS-AND-POSTSY...	R-RNO-112314	22	0.582464	1.874906	0.003788	0.152251	0.520	
5	REACTOME-TRANSMISSION-ACROSS-CHEMICAL-SYNAPSES	R-RNO-112315	23	0.559181	1.809385	0.004878	0.268486	0.775	
6	GOBP-G-PROTEIN-COUPLED-RECEPTOR-SIGNALING-PATHWAY	GO:0007186	18	0.584833	1.792612	0.000000	0.279094	0.825	
7	GOBP-POSITIVE-REGULATION-OF-TRANSMEMBRANE-TRAN...	GO:0034764	7	0.742789	1.775269	0.001497	0.291396	0.877	
8	GOBP-POSITIVE-REGULATION-OF-SIGNALING	GO:0023056	34	0.483082	1.706538	0.008140	0.532927	0.985	
9	GOBP-REGULATION-OF-TRANSPORT	GO:0051049	44	0.481413	1.691242	0.013953	0.551299	0.989	
10	GOBP-CHEMICAL-HOMEOSTASIS	GO:0048878	23	0.525372	1.685761	0.013580	0.527675	0.995	
11	GOBP-GLIOGENESIS	GO:0042063	12	0.604378	1.678670	0.015805	0.512521	0.996	
12	REACTOME-DAG-AND-IP3-SIGNALING	R-RNO-1489509	8	0.686209	1.657882	0.011645	0.575414	1.000	
13	GOBP-CATION-TRANSPORT	GO:0006812	25	0.506346	1.648938	0.017348	0.573248	1.000	
14	REACTOME-ACTIVATION-OF-NMDA-RECEPTORS-AND-POST...	R-RNO-442755	16	0.542285	1.647503	0.020888	0.541463	1.000	
15	GOBP-NEURON-DIFFERENTIATION	GO:0030182	37	0.475443	1.645604	0.012926	0.515312	1.000	
16	REACTOME-SIGNALING-BY-GPCR	R-RNO-372790	22	0.509412	1.644095	0.017789	0.491757	1.000	
17	GOBP-METAL-ION-HOMEOSTASIS	GO:0055065	14	0.562136	1.635932	0.015625	0.499041	1.000	
18	GOBP-REGULATION-OF-POSTSYNAPTIC-MEMBRANE-POTEN...	GO:0060078	14	0.570756	1.633557	0.028683	0.481558	1.000	
19	GOBP-EPITHELIAL-CELL-DIFFERENTIATION	GO:0030855	7	0.678777	1.623725	0.011940	0.47586	1.000	
20	GOBP-MAPK-CASCADE	GO:0000165	18	0.534074	1.622645	0.021330	0.478529	1.000	
21	GOBP-VESICLE-MEDIATED-TRANSPORT-IN-SYNAPSE	GO:0099003	7	0.686091	1.611744	0.016035	0.500597	1.000	
22	GOBP-NEURON-DEVELOPMENT	GO:0048666	34	0.464378	1.610901	0.024706	0.482076	1.000	
23	GOBP-ION-HOMEOSTASIS	GO:0050801	16	0.549220	1.609969	0.019430	0.466643	1.000	
24	GOBP-REGULATION-OF-NEUROTRANSMITTER-TRANSPORT	GO:0051588	6	0.703024	1.606855	0.017699	0.459377	1.000	
25	GOBP-DIVALENT-INORGANIC-CATION-HOMEOSTASIS	GO:0072507	13	0.569745	1.604588	0.026144	0.449745	1.000	
26	GOBP-REGULATION-OF-MEMBRANE-POTENTIAL	GO:0042391	17	0.537767	1.602527	0.022251	0.440312	1.000	
27	GOBP-REGULATION-OF-CYTOSOLIC-CALCIUM-ION-CONCE...	GO:0051480	13	0.569745	1.590337	0.028340	0.468599	1.000	
28	GOBP-CELLULAR-ION-HOMEOSTASIS	GO:0006873	14	0.546138	1.557727	0.036339	0.581443	1.000	
29	GOBP-PROTEIN-PHOSPHORYLATION	GO:0006468	33	0.454898	1.555198	0.026253	0.572667	1.000	
30	GOBP-REGULATION-OF-CIRCADIAN-RHYTHM	GO:0042752	7	0.641028	1.549596	0.041298	0.577128	1.000	
31	GOBP-REGULATION-OF-SYNAPTIC-PLASTICITY	GO:0048167	21	0.491107	1.535360	0.039390	0.623613	1.000	
32	GOBP-POSITIVE-REGULATION-OF-CATION-TRANSMEMBRAN...	GO:1904064	5	0.712489	1.531388	0.042813	0.623568	1.000	
33	REACTOME-TRAFFICKING-OF-AMPA-RECEPTORS	R-RNO-399719	11	0.567396	1.523031	0.051842	0.642349	1.000	
34	GOBP-REGULATION-OF-ANION-TRANSMEMBRANE-TRANSPORT	GO:1903959	5	0.722373	1.520107	0.039557	0.635747	1.000	
35	GOBP-REGULATION-OF-ION-TRANSPORT	GO:0043269	36	0.436332	1.503304	0.038005	0.696873	1.000	
36	GOBP-SIGNAL-RELEASE	GO:0023061	14	0.529178	1.502856	0.043709	0.680147	1.000	
37	GOBP-CELL-PROJECTION-ORGANIZATION	GO:0030030	35	0.428223	1.502620	0.042824	0.663185	1.000	
38	GOBP-PROTEIN-AUTOPHOSPHORYLATION	GO:0046777	5	0.698243	1.502291	0.034226	0.647679	1.000	
39	GOBP-GLUTAMATE-RECEPTOR-SIGNALING-PATHWAY	GO:0007215	17	0.492958	1.501925	0.050378	0.632919	1.000	
40	GOBP-POSITIVE-REGULATION-OF-SYNAPTIC-TRANSMISSION	GO:0050806	15	0.524178	1.498120	0.047493	0.632802	1.000	

Continuation of Table S4

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
41	GOBP-NEUROGENESIS	41	0.424696	1.497123	0.056977	0.622551	1.000
42	GOBP-POSITIVE-REGULATION-OF-LONG-TERM-SYNAPTIC...	5	0.708574	1.495042	0.039334	0.616362	1.000
43	REACTOME-CA-DEPENDENT-EVENTS	8	0.600000	1.490308	0.059972	0.622924	1.000
44	GOBP-FORBRAIN-DEVELOPMENT	10	0.59943	1.483596	0.055021	0.636809	1.000
45	GOBP-REGULATION-OF-NEURON-PROJECTION-DEVELOPMENT	16	0.497489	1.477156	0.051813	0.650835	1.000
46	REACTOME-G-PROTEIN-MEDIATED-EVENTS	10	0.583518	1.474614	0.058156	0.647549	1.000
47	GOBP-REGULATION-OF-SYNAPTIC-TRANSMISSION-GLUTA...	12	0.540506	1.474359	0.069930	0.634990	1.000
48	REACTOME-G-ALPHA1-SIGNALING-EVENTS	18	0.480973	1.470582	0.048114	0.638257	1.000
49	GOBP-REGULATION-OF-NEUROTRANSMITTER-LEVELS	7	0.611760	1.459971	0.064706	0.698906	1.000
50	GOBP-CATION-TRANSMEMBRANE-TRANSPORT	18	0.477400	1.455205	0.059585	0.676904	1.000
51	GOBP-REGULATION-OF-LONG-TERM-SYNAPTIC-POTENTIAL...	6	0.650541	1.454531	0.066971	0.666718	1.000
52	HALLMARK-P13K-AKT-MTOR-SIGNALING	5	0.631691	1.448507	0.079595	0.679976	1.000
53	REACTOME-ANTIINFLAMMATORY-RESPONSEFAVOURING...	6	0.674785	1.445246	0.056782	0.681858	1.000
54	GOBP-REGULATION-OF-MAPK-CASCADE	13	0.508563	1.444475	0.081365	0.672951	1.000
55	GOBP-NEGATIVE-REGULATION-OF-NEURON-DEATH	11	0.529470	1.441110	0.079167	0.674995	1.000
56	GOBP-REGULATION-OF-CELL-PROJECTION-ORGANIZATION	20	0.462295	1.437908	0.063492	0.676172	1.000
57	GOBP-SECRETION	24	0.443305	1.432622	0.067155	0.685987	1.000
58	GOBP-ENDOCRINE-SYSTEM-DEVELOPMENT	6	0.634596	1.428083	0.069630	0.693336	1.000
59	GOBP-NEUROTRANSMITTER-TRANSPORT	7	0.611760	1.426992	0.076923	0.685810	1.000
60	GOBP-LONG-TERM-SYNAPTIC-POTENTIATION	12	0.501933	1.418136	0.099440	0.712403	1.000
61	GOBP-DENDRITIC-SPINE-DEVELOPMENT	6	0.641713	1.417268	0.071429	0.704022	1.000
62	GOBP-POSITIVE-REGULATION-OF-TRANSPERASE-ACTIVITY	19	0.457771	1.415556	0.082310	0.700072	1.000
63	GOBP-REGULATION-OF-NEUROTRANSMITTER-RECEPTOR-A...	13	0.493333	1.411806	0.088235	0.704203	1.000
64	GOBP-SYNAPTIC-TRANSMISSION-GLUTAMATERGIC	13	0.497764	1.408940	0.100134	0.704999	1.000
65	GOBP-EMBRYO-DEVELOPMENT	14	0.493873	1.405106	0.094315	0.710393	1.000
66	REACTOME-PROTEIN-PROTEIN-INTERACTIONS-AT-SYNAPSES	12	0.503261	1.404700	0.088742	0.701685	1.000
67	GOBP-NEUROTRANSMITTER-SECRETION	6	0.623782	1.398775	0.087021	0.715529	1.000
68	REACTOME-UNBLOCKING-OF-NMDA-RECEPTORS-GLUTAMAT...	12	0.501524	1.397337	0.095041	0.710650	1.000
69	GOBP-REGULATION-OF-SYNAPSE-STRUCTURE-OR-ACTIVITY	11	0.514527	1.395172	0.091160	0.709182	1.000
70	GOBP-PROTEIN-KINASE-B-SIGNALING	6	0.608340	1.390999	0.072485	0.716416	1.000
71	GOBP-NEURON-PROJECTION-ORGANIZATION	8	0.554762	1.385954	0.102962	0.727270	1.000
72	GOBP-HOMEOSTATIC-PROCESS	31	0.407834	1.383536	0.109785	0.727190	1.000
73	GOBP-POSITIVE-REGULATION-OF-PHOSPHORUS-METABOL...	23	0.428263	1.383436	0.087871	0.717900	1.000
74	GOBP-INTRACELLULAR-PROTEIN-TRANSPORT	8	0.563900	1.383387	0.092725	0.708518	1.000
75	GOBP-DNA-METABOLIC-PROCESS	6	0.603794	1.380114	0.106782	0.712272	1.000
76	GOBP-POSITIVE-REGULATION-OF-TRANSPORT	26	0.418634	1.379564	0.092121	0.705358	1.000
77	GOBP-FATTY-ACID-TRANSPORT	6	0.613403	1.375902	0.096296	0.710335	1.000
78	GOBP-REGULATION-OF-METAL-ION-TRANSPORT	6	0.613403	1.375902	0.096296	0.710335	1.000
79	REACTOME-OPIOID-SIGNALING	12	0.505538	1.373717	0.117881	0.701432	1.000
80	GOBP-EMBRYO-DEVELOPMENT-ENDING-IN-BIRTH-OR-EGG...	9	0.541671	1.373420	0.096206	0.693914	1.000
81	GOBP-MEMBRANE-ORGANIZATION	12	0.497731	1.369614	0.115127	0.700429	1.000
82	GOBP-CELLULAR-HOMEOSTASIS	18	0.446059	1.366585	0.108005	0.703142	1.000
83	GOBP-DEVELOPMENTAL-MATURATION	5	0.639807	1.363756	0.088647	0.705808	1.000

Continuation of Table S4

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
84	GOBP-REGULATION-OF-CATION-TRANSMEMBRANE-TRANSPORT	16	0.459204	1.360986	0.108639	0.707809	1.000
85	GOBP-REGULATION-OF-CELLULAR-COMPONENT_SIZE	7	0.582271	1.360645	0.108470	0.700857	1.000
86	GOBP-RECEPTOR-MEDIATED-ENDOCYTOSIS	6	0.610298	1.360455	0.111278	0.693533	1.000
87	GOBP-NERVOUS-SYSTEM-PROCESS	38	0.391443	1.354058	0.119952	0.709812	1.000
88	GOBP-INTRACELLULAR-TRANSPORT	10	0.517764	1.345684	0.127778	0.733854	1.000
89	GOBP-GLIAL-CELL-DIFFERENTIATION	10	0.512735	1.343954	0.128671	0.732435	1.000
90	GOBP-REGULATION-OF-SECRETION	14	0.464158	1.343068	0.140000	0.727919	1.000
91	GOBP-PROTEIN-LOCALIZATION-TO-MEMBRANE	13	0.475718	1.334250	0.131169	0.753535	1.000
92	GOBP-MAINTENANCE-OF-LOCATION	7	0.564066	1.334043	0.147661	0.746349	1.000
93	REACTOME-DISEASES-OF-SIGNAL-TRANSDUCTION-BY_GR...	12	0.491715	1.330985	0.128205	0.750687	1.000
94	GOBP-BEHAVIOR	33	0.389457	1.323750	0.132544	0.771390	1.000
95	REACTOME-LONG-TERM-POTENTIATION	10	0.508939	1.323673	0.148611	0.763622	1.000
96	GOBP-ANION-TRANSMEMBRANE-TRANSPORT	7	0.568040	1.323154	0.127168	0.757683	1.000
97	GOBP-CELLULAR-RESPONSE-TO-PEPTIDE	13	0.476672	1.323139	0.148344	0.750026	1.000
98	GOBP-ORGANIC-ACID-TRANSPORT	7	0.558650	1.322334	0.140173	0.745305	1.000
99	GOBP-REGULATION-OF-INTRACELLULAR-SIGNAL-TRANSD...	21	0.422217	1.321694	0.141772	0.740270	1.000
100	GOBP-RECEPTOR-INTERNALIZATION	5	0.620759	1.321207	0.143082	0.734710	1.000
101	GOBP-AMIDE-BIOSYNTHETIC-PROCESS	6	0.591841	1.318286	0.128130	0.738419	1.000
102	GOBP-POSITIVE-REGULATION-OF-PROTEIN-PHOSPHORYL...	22	0.406778	1.318069	0.130923	0.731984	1.000
103	GOBP-POSITIVE-REGULATION-OF-PROTEIN-KINASE-ACT...	18	0.435455	1.316417	0.149808	0.731421	1.000
104	GOBP-REGULATION-OF-ANATOMICAL-STRUCTURE-SIZE	10	0.500570	1.316354	0.155525	0.724622	1.000
105	REACTOME-NEUREXINS-AND-NEUROLIGINS	9	0.520212	1.314834	0.152661	0.723479	1.000
106	GOBP-PEPTIDE-BIOSYNTHETIC-PROCESS	6	0.591841	1.314536	0.151468	0.717611	1.000
107	GOBP-TELENCEPHALON-DEVELOPMENT	7	0.560174	1.312849	0.136364	0.716742	1.000
108	GOBP-POSITIVE-REGULATION-OF-PROTEIN-MODIFICATI...	22	0.406778	1.310951	0.132242	0.716793	1.000
109	GOBP-RESPONSE-TO-HEAT	7	0.549858	1.310516	0.153509	0.711925	1.000
110	GOBP-LOCOMOTORY-BEHAVIOR	8	0.516631	1.306170	0.152661	0.721032	1.000
111	GOBP-POSITIVE-REGULATION-OF-PROTEIN-TYROSINE-K...	5	0.617877	1.304195	0.137255	0.721372	1.000
112	REACTOME-CREB1-PHOSPHORYLATION-THROUGH-NMDA-RE...	8	0.539183	1.300960	0.146240	0.726313	1.000
113	GOBP-REGULATION-OF-PROTEIN-TYROSINE-KINASE-ACT...	5	0.617877	1.300480	0.134884	0.721783	1.000
114	REACTOME-INTRACELLULAR-SIGNALING-BY-SECOND-MES...	15	0.454645	1.297759	0.174373	0.725626	1.000
115	GOBP-RECEPTOR-METABOLIC-PROCESS	5	0.620759	1.296794	0.152239	0.722572	1.000
116	GOBP-CELLULAR-RESPONSE-TO-PEPTIDE-HORMONE-STIM...	9	0.505660	1.295991	0.158996	0.719248	1.000
117	GOBP-CELLULAR-RESPONSE-TO-KETONE	5	0.616481	1.291990	0.154671	0.727216	1.000
118	REACTOME-TRAFFICKING-OF-GLUR2-CONTAINING-AMPA-...	8	0.525000	1.289915	0.156835	0.731842	1.000
119	GOBP-CELLULAR-CARBOHYDRATE-METABOLIC-PROCESS	5	0.610153	1.284127	0.170659	0.742307	1.000
120	GOBP-MULTICELLULAR-ORGANISMAL-RESPONSE-TO-STRESS	5	0.609690	1.283818	0.164274	0.737240	1.000
121	GOBP-INORGANIC-ION-TRANSMEMBRANE-TRANSPORT	9	0.507767	1.283019	0.175732	0.733839	1.000
122	REACTOME-RAS-ACTIVATION-UPON-CA2-INFLUX-THROUG...	6	0.559221	1.280167	0.183976	0.737928	1.000
123	GOBP-REGULATION-OF-CELLULAR-RESPONSE-TO-STRESS	9	0.508009	1.277486	0.170270	0.741338	1.000
124	REACTOME-HEMOSTASIS	14	0.437739	1.276463	0.188602	0.738982	1.000
125	GOBP-CELLULAR-MACROMOLECULE-CATABOLIC-PROCESS	5	0.602410	1.275100	0.176012	0.738070	1.000
126	GOBP-DENDRITIC-SPINE-MORPHOGENESIS	5	0.603090	1.275074	0.158879	0.732388	1.000

Continuation of Table S4

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
127	GOBP-DENDRITE-DEVELOPMENT	GO-0016358	10	0.482082	1.272149	0.176634	0.736172	1.000
128	GOBP-POSITIVE-REGULATION-OF-MAPK-CASCADE	GO-0043410	9	0.497392	1.271583	0.180441	0.732556	1.000
129	GOBP-POSITIVE-REGULATION-OF-PEPTIDYL-TYROSINE...	GO-0050731	8	0.514072	1.271141	0.182584	0.728341	1.000
130	GOBP-GENERATION-OF-PRECURSOR-METABOLITES-AND-E...	GO-0060691	5	0.580669	1.270828	0.189655	0.723808	1.000
131	GOBP-CELL-SURFACE-RECEPTOR-SIGNALING-PATHWAY-I...	GO-1905114	15	0.435118	1.269584	0.161125	0.722606	1.000
132	GOBP-PEPTIDYL-TYROSINE-MODIFICATION	GO-0018212	10	0.486489	1.269439	0.186080	0.717651	1.000
133	REACTOME-G-ALPHA-Z-SIGNALING-EVENTS	R-RNO-418597	5	0.602859	1.267927	0.152568	0.717230	1.000
134	REACTOME-GPCR-LIGAND-BINDING	R-RNO-500792	8	0.510051	1.265641	0.187675	0.719279	1.000
135	GOBP-POLYSACCHARIDE-METABOLIC-PROCESS	GO-0005976	5	0.607272	1.264903	0.158209	0.716380	1.000
136	GOBP-RESPONSE-TO-OXYGEN-LEVELS	GO-0070482	8	0.515302	1.263274	0.172414	0.716545	1.000
137	GOBP-REGULATION-OF-CATION-CHANNEL-ACTIVITY	GO-2001257	14	0.441079	1.261669	0.170410	0.716605	1.000
138	GOBP-POSITIVE-REGULATION-OF-PROTEIN-SERINE-THR...	GO-0071902	5	0.494234	1.261106	0.196676	0.713260	1.000
139	GOBP-REGULATION-OF-CELL-CYCLE-PROCESS	GO-0010564	5	0.594825	1.253227	0.188940	0.733618	1.000
140	GOBP-REGULATION-OF-VESICLE-MEDIATED-TRANSPORT	GO-0060627	12	0.454150	1.252509	0.195448	0.730799	1.000
141	GOBP-METAL-ION-TRANSPORT	GO-0030001	11	0.464498	1.252133	0.182306	0.726764	1.000
142	GOBP-CALCIUM-ION-TRANSPORT	GO-0006816	11	0.464498	1.248122	0.195418	0.734911	1.000
143	GOBP-REGULATION-OF-NMDA-RECEPTOR-ACTIVITY	GO-2000310	10	0.477212	1.246781	0.195155	0.734046	1.000
144	GOBP-SYNAPSE-ORGANIZATION	GO-0050808	17	0.419689	1.245985	0.211068	0.731638	1.000
145	GOBP-G-PROTEIN-COUPLED-GLUTAMATE-RECEPTOR-SIGN...	GO-0007216	8	0.503567	1.243015	0.196078	0.736440	1.000
146	GOBP-CARBOHYDRATE-DERIVATIVE-BIOSYNTHETIC-PROCESS	GO-1901137	5	0.589478	1.238245	0.200949	0.746510	1.000
147	REACTOME-ASSEMBLY-AND-CELL-SURFACE-PRESENTATIO...	R-RNO-9609736	8	0.504520	1.237577	0.204986	0.744476	1.000
148	GOBP-HOMEOSTASIS-OF-NUMBER-OF-CELLS	GO-0048872	5	0.573973	1.237131	0.197819	0.739995	1.000
149	REACTOME-NEGATIVE-REGULATION-OF-NMDA-RECEPTOR...	R-HSA-9617324	8	0.504520	1.236479	0.204578	0.736964	1.000
150	GOBP-PROTEIN-LOCALIZATION-TO-PLASMA-MEMBRANE	GO-0072659	7	0.529955	1.236350	0.235211	0.732559	1.000
151	GOBP-TRANSMEMBRANE-TRANSPORT	GO-0055085	27	0.365599	1.234274	0.219927	0.734088	1.000
152	GOBP-RESPONSE-TO-NERVE-GROWTH-FACTOR	GO-1990089	7	0.519358	1.233172	0.212950	0.732638	1.000
153	GOBP-REGULATION-OF-SIGNALING-RECEPTOR-ACTIVITY	GO-0010469	14	0.431773	1.233082	0.205094	0.728168	1.000
154	REACTOME-CELL-CYCLE-MITOTIC	R-RNO-69278	5	0.578313	1.221772	0.221169	0.759163	1.000
155	GOBP-LEUKOCYTE-MIGRATION	GO-0050900	6	0.539314	1.216719	0.217325	0.769892	1.000
156	REACTOME-CELL-CYCLE	R-RNO-1640170	6	0.539383	1.214278	0.213043	0.772589	1.000
157	GOBP-POSITIVE-REGULATION-OF-EPITHELIAL-CELL-MI...	GO-0010634	5	0.574039	1.207091	0.251149	0.791010	1.000
158	GOBP-REGULATION-OF-RECEPTOR-MEDIATED-ENDOCYTOSIS	GO-0048259	5	0.577510	1.206497	0.250789	0.788136	1.000
159	REACTOME-SIGNALING-BY-WNT	R-RNO-195721	7	0.506173	1.206333	0.243590	0.783780	1.000
160	GOBP-CHEMICAL-SYNAPTIC-TRANSMISSION_POSTSYNAPTIC	GO-0099565	9	0.471181	1.205457	0.235955	0.781809	1.000
161	GOBP-REGULATION-OF-CELL-CELL-ADHESION	GO-0022407	9	0.472497	1.205031	0.239456	0.778373	1.000
162	GOBP-ORGANOPHOSPHATE-BIOSYNTHETIC-PROCESS	GO-0090407	5	0.548784	1.204295	0.228788	0.776065	1.000
163	REACTOME-SYNAPTIC-ADHESION-LIKE-MOLECULES	R-RNO-8849932	9	0.468354	1.202595	0.246238	0.776761	1.000
164	GOBP-MONOCARBOXYLIC-ACID-TRANSPORT	GO-0015718	5	0.553897	1.195709	0.264970	0.794178	1.000
165	GOBP-REGULATION-OF-PHOSPHOLIPASE-C-ACTIVITY	GO-1900274	5	0.557106	1.195374	0.230061	0.790660	1.000
166	HALLMARK-ALLOGRAFT-REJECTION	M5950	7	0.513553	1.195126	0.250737	0.786618	1.000
167	GOBP-IONOTROPIC-GLUTAMATE-RECEPTOR-SIGNALING-P...	GO-0035235	9	0.468354	1.193073	0.235616	0.788203	1.000
168	GOBP-PROTEIN-LOCALIZATION-TO-CELL-PERIPHERY	GO-1990778	12	0.433173	1.189817	0.268358	0.793923	1.000
169	GOBP-REGULATION-OF-RESPONSE-TO-STRESS	GO-0080134	19	0.381756	1.188860	0.249354	0.792258	1.000

Continuation of Table S4

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
170	GOBP-REGULATION-OF-TRANSFERASE-ACTIVITY	21	0.367372	1.185726	0.249357	0.797990	1.000
171	GOBP-REGULATION-OF-CELLULAR-AMIDE-METABOLIC-PR...	9	0.471808	1.184840	0.270604	0.796164	1.000
172	GOBP-POSTTRANSCRIPTIONAL-REGULATION-OF-GENE-EX...	8	0.477916	1.183684	0.251788	0.795305	1.000
173	GOBP-ADENYLATE-CYCLASE-MODULATING-G-PROTEIN-CO...	11	0.435822	1.183207	0.271117	0.792168	1.000
174	GOBP-HORMONE-TRANSPORT	9	0.463124	1.181749	0.249645	0.792226	1.000
175	REACTOME-PLATELET-ACTIVATION-SIGNALING-AND-AGG...	7	0.497009	1.179868	0.236417	0.793585	1.000
176	GOBP-POSTSYNAPSE-ORGANIZATION	10	0.449413	1.178675	0.267930	0.792805	1.000
177	REACTOME-ADAPTIVE-IMMUNE-SYSTEM	9	0.460450	1.177702	0.263523	0.791374	1.000
178	GOBP-NEGATIVE-REGULATION-OF-CELLULAR-COMPONENT...	11	0.428419	1.176470	0.279778	0.790660	1.000
179	REACTOME-INTEGRATION-OF-ENERGY-METABOLISM	5	0.561380	1.172774	0.270016	0.797194	1.000
180	GOBP-NUCLEOSIDE-PHOSPHATE-BIOSYNTHETIC-PROCESS	5	0.549784	1.171665	0.258114	0.796059	1.000
181	GOBP-EPITHELIAL-DEVELOPMENT	15	0.396540	1.169844	0.272727	0.796939	1.000
182	GOBP-POSITIVE-REGULATION-OF-CATALYTIC-ACTIVITY	29	0.342752	1.168338	0.280095	0.797170	1.000
183	GOBP-ACIDIC-AMINO-ACID-TRANSPORT	5	0.553897	1.165902	0.266568	0.800249	1.000
184	GOBP-NEGATIVE-REGULATION-OF-NEURON-APOPTOTIC-P...	8	0.478864	1.163851	0.284900	0.796056	1.000
185	GOBP-POSITIVE-REGULATION-OF-LIPASE-ACTIVITY	5	0.557106	1.164667	0.267647	0.795199	1.000
186	GOBP-REGULATION-OF-PROTEIN-PHOSPHORYLATION	25	0.353012	1.164341	0.297899	0.791923	1.000
187	REACTOME-INTERFERON-SIGNALING	6	0.521953	1.163054	0.273121	0.791801	1.000
188	GOBP-SECOND-MESSENGER-MEDIATED-SIGNALING	16	0.386272	1.162848	0.286632	0.788203	1.000
189	GOBP-PROTEIN-LOCALIZATION-TO-SYNAPSE	5	0.547774	1.162813	0.275148	0.784141	1.000
190	GOBP-REGULATION-OF-PROTEIN-KINASE-ACTIVITY	21	0.367372	1.161385	0.282828	0.784599	1.000
191	GOBP-LIPID-LOCALIZATION	10	0.444690	1.160056	0.279673	0.784614	1.000
192	GOBP-ENDOMEMBRANE-SYSTEM-ORGANIZATION	6	0.504932	1.158611	0.302256	0.784914	1.000
193	GOBP-DICARBOXYLIC-ACID-TRANSPORT	5	0.553897	1.152390	0.273148	0.799763	1.000
194	GOBP-PROTEIN-LOCALIZATION-TO-POSTSYNAPSE	5	0.547774	1.150931	0.292719	0.799718	1.000
195	GOBP-NEGATIVE-REGULATION-OF-LIPID-METABOLIC-PR...	5	0.537670	1.145263	0.299410	0.812103	1.000
196	GOBP-ERBB-SIGNALING-PATHWAY	5	0.542406	1.143138	0.293853	0.814441	1.000
197	GOBP-REGULATION-OF-PROTEIN-MODIFICATION-PROCESS	28	0.343347	1.141716	0.306683	0.814348	1.000
198	GOBP-SENSORY-PERCEPTION	9	0.443038	1.141515	0.295794	0.810846	1.000
199	GOBP-REGULATION-OF-PEPTIDYL-TYROSINE-PHOSPHORY...	9	0.445379	1.141050	0.329496	0.808162	1.000
200	REACTOME-G-ALPHA-Q-SIGNALING-EVENTS	6	0.503150	1.140285	0.294479	0.806429	1.000
201	GOBP-NEGATIVE-REGULATION-OF-PROTEOLYSIS	8	0.456454	1.138464	0.306003	0.807768	1.000
202	GOBP-REGULATION-OF-ANATOMICAL-STRUCTURE-MORPHO...	17	0.378239	1.136317	0.318822	0.809834	1.000
203	GOBP-PROTEIN-CONTAINING-COMPLEX-SUBUNIT-ORGANI...	15	0.387062	1.135811	0.307298	0.807366	1.000
204	GOBP-NEURON-MIGRATION	5	0.541191	1.135138	0.304878	0.805346	1.000
205	GOBP-SENSORY-PERCEPTION-OF-PAIN	5	0.542169	1.134866	0.320840	0.802285	1.000
206	REACTOME-SIGNALING-BY-NTRK2-TRKB	6	0.497214	1.134555	0.305263	0.799438	1.000
207	GOBP-CELL-JUNCTION-ORGANIZATION	19	0.369685	1.133070	0.310038	0.799933	1.000
208	GOBP-REGULATION-OF-CARBOHYDRATE-METABOLIC-PROCESS	5	0.532634	1.131260	0.314985	0.801172	1.000
209	GOBP-GAMETE-GENERATION	9	0.445295	1.130425	0.324728	0.799742	1.000
210	GOBP-CELLULAR-RESPONSE-TO-ALCOHOL	5	0.533158	1.126608	0.320127	0.806980	1.000
211	GOBP-CIRCADIEN-RHYTHM	13	0.392686	1.123823	0.323722	0.811168	1.000
212	GOBP-REGULATION-OF-LIPASE-ACTIVITY	6	0.494158	1.123699	0.337798	0.807673	1.000

Continuation of Table S4

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
213	GOBP-INSULIN-SECRETION	GO-0030073	7	0.475216	1.122864	0.301860	0.806225	1.000
214	GOBP-REGULATION-OF-CARBOHYDRATE-BIOSYNTHETIC.P...	GO-0043255	5	0.532634	1.121811	0.326187	0.805766	1.000
215	GOBP-PEPTIDE-HORMONE-SECRETION	GO-0030072	7	0.475216	1.121725	0.339595	0.802278	1.000
216	GOBP-ENDOCYTOSIS	GO-006897	8	0.456329	1.120751	0.306294	0.801415	1.000
217	GOBP-POSITIVE-REGULATION-OF-NEURON-PROJECTION...	GO-0010976	5	0.529076	1.120034	0.305215	0.799736	1.000
218	GOBP-CELLULAR-RESPONSE-TO-DNA-DAMAGE-STIMULUS	GO-0068974	5	0.529417	1.119047	0.326594	0.798809	1.000
219	GOBP-AXON-DEVELOPMENT	GO-0061564	18	0.372379	1.118752	0.319948	0.795951	1.000
220	GOBP-POSITIVE-REGULATION-OF-CELL-PROJECTION-OR...	GO-0031346	10	0.430290	1.118138	0.338356	0.794043	1.000
221	GOBP-REGULATION-OF-PHOSPHOLIPASE-ACTIVITY	GO-0010517	6	0.494158	1.115957	0.313869	0.796594	1.000
222	GOBP-REGULATION-OF-FAT-CELL-DIFFERENTIATION	GO-0045598	6	0.496602	1.112642	0.323034	0.802203	1.000
223	REACTOME-CLASS-C-3-METABOTROPIC-GLUTAMATE-PHER...	R-RNO-420499	7	0.470785	1.111284	0.326440	0.802371	1.000
224	GOBP-REGULATION-OF-PHOSPHORUS-METABOLIC-PROCESS	GO-0051174	26	0.340835	1.111158	0.335793	0.799064	1.000
225	GOBP-SEXUAL-REPRODUCTION	GO-0019953	10	0.421247	1.110413	0.338398	0.797432	1.000
226	GOBP-POSITIVE-REGULATION-OF-SMALL-MOLECULE-MET...	GO-0062013	5	0.517755	1.105990	0.360414	0.806017	1.000
227	GOBP-CARBOHYDRATE-BIOSYNTHETIC-PROCESS	GO-0016051	5	0.532634	1.105992	0.362170	0.802527	1.000
228	GOBP-CELLULAR-RESPONSE-TO-BIOTIC-STIMULUS	GO-0071216	8	0.449604	1.103410	0.356421	0.806134	1.000
229	GOBP-ACTIVATION-OF-PROTEIN-KINASE-ACTIVITY	GO-0032147	10	0.420417	1.103163	0.363128	0.803325	1.000
230	GOBP-POSITIVE-REGULATION-OF-ION-TRANSPORT	GO-0043270	17	0.357175	1.102194	0.344828	0.802466	1.000
231	GOBP-PEPTIDE-METABOLIC-PROCESS	GO-006518	11	0.404986	1.101216	0.333786	0.801723	1.000
232	REACTOME-EXTRA-NUCLEAR-ESTROGEN-SIGNALING	R-RNO-9008391	7	0.469816	1.099607	0.365639	0.802347	1.000
233	GOBP-PEPTIDYL-AMINO-ACID-MODIFICATION	GO-0018193	22	0.347168	1.098630	0.344516	0.801327	1.000
234	GOBP-PEPTIDYL-SERINE-MODIFICATION	GO-0018209	12	0.400815	1.098596	0.354620	0.798044	1.000
235	GOBP-REGULATION-OF-NERVOUS-SYSTEM-PROCESS	GO-0031644	8	0.448495	1.092099	0.359124	0.801025	1.000
236	GOBP-POSITIVE-REGULATION-OF-INTRACELLULAR-SIGN...	GO-1902533	14	0.386304	1.095641	0.367876	0.799246	1.000
237	GOBP-CARBOXYLIC-ACID-TRANSPORT	GO-0046942	6	0.486287	1.094817	0.364023	0.798153	1.000
238	GOBP-REGULATION-OF-ENDOCYTOSIS	GO-0030100	6	0.488403	1.091068	0.358273	0.804840	1.000
239	GOBP-REGULATION-OF-LYMPHOCYTE-ACTIVATION	GO-0051249	5	0.512694	1.090718	0.376662	0.802491	1.000
240	GOBP-REGULATION-OF-CELLULAR-LOCALIZATION	GO-0060341	17	0.360359	1.08984	0.358974	0.808917	1.000
241	GOBP-CELLULAR-RESPONSE-TO-NITROGEN-COMPOUND	GO-1901699	20	0.347124	1.085746	0.347066	0.808992	1.000
242	GOBP-LIPID-EXPORT-FROM-CELL	GO-0140353	5	0.514408	1.085536	0.377273	0.806267	1.000
243	GOBP-REGULATION-OF-CELL-SIZE	GO-0008361	5	0.507039	1.083736	0.373660	0.807708	1.000
244	GOBP-CELLULAR-RESPONSE-TO-MOLECULE-OF-BACTERIA...	GO-0071219	8	0.449604	1.083038	0.372832	0.806246	1.000
245	GOBP-REGULATION-OF-LIPID-METABOLIC-PROCESS	GO-0019216	7	0.456705	1.082406	0.366197	0.804784	1.000
246	GOBP-AMINO-ACID-TRANSPORT	GO-006865	6	0.486287	1.080411	0.377644	0.806660	1.000
247	GOBP-POSITIVE-REGULATION-OF-PROTEIN-METABOLIC...	GO-0051247	27	0.324883	1.080379	0.387057	0.803481	1.000
248	GOBP-RESPONSE-TO-TEMPERATURE-STIMULUS	GO-0009266	9	0.419237	1.078318	0.365922	0.805461	1.000
249	GOBP-SENSORY-ORGAN-DEVELOPMENT	GO-0007423	8	0.436187	1.078197	0.387955	0.802538	1.000
250	GOBP-ORGANIC-ANION-TRANSPORT	GO-0015711	6	0.436187	1.076716	0.398485	0.803101	1.000
251	GOBP-PHOSPHATIDYLINOSITOL-3-KINASE-SIGNALING	GO-0014065	7	0.460838	1.074921	0.385307	0.804358	1.000
252	REACTOME-ESTROGEN-DEPENDENT-NUCLEAR-EVENTS-DOW...	R-RNO-9634638	5	0.507116	1.072643	0.391097	0.807100	1.000
253	GOBP-NEGATIVE-REGULATION-OF-TRANSMEMBRANE-TRAN...	GO-0034763	6	0.474901	1.072587	0.381657	0.804087	1.000
254	GOBP-ESTABLISHMENT-OF-PROTEIN-LOCALIZATION-TO...	GO-0072594	5	0.498861	1.066284	0.372727	0.816997	1.000
255	GOBP-REGULATION-OF-ENDOTHELIAL-CELL-MIGRATION	GO-0010594	5	0.512557	1.063341	0.387906	0.821107	1.000

Continuation of Table S4

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
256	GOBP-CELL-PART-MORPHOGENESIS	25	0.319443	1.062620	0.387704	0.819715	1.000
257	GOBP-NEGATIVE-REGULATION-OF-PHOSPHORYLATION	7	0.455951	1.062284	0.398827	0.817361	1.000
258	GOBP-NEGATIVE-REGULATION-OF-TRANSFERASE-ACTIVITY	5	0.503944	1.062028	0.377916	0.814830	1.000
259	GOBP-CYTOSOLIC-CALCIUM-ION-TRANSPORT	7	0.446263	1.061413	0.395620	0.813276	1.000
260	GOBP-REGULATION-OF-PROTEIN-LOCALIZATION-TO-MEM...	7	0.458088	1.061076	0.393275	0.810935	1.000
261	GOBP-NEGATIVE-REGULATION-OF-TRANSPORT	13	0.373642	1.060524	0.405333	0.809225	1.000
262	GOBP-PEPTIDE-SECRETION	9	0.415105	1.059109	0.408769	0.809604	1.000
263	GOBP-REGULATION-OF-POSTSYNAPSE-ORGANIZATION	6	0.461052	1.058055	0.381381	0.809335	1.000
264	REACTOME-TRANSCRIPTIONAL-REGULATION-BY-MECP2	7	0.438468	1.057455	0.407895	0.807806	1.000
265	GOBP-REGULATION-OF-HORMONE-SECRETION	8	0.423324	1.057053	0.409692	0.805710	1.000
266	GOBP-ADENYLATE-CYCLASE-INHIBITING-G-PROTEIN.CO...	9	0.413450	1.056288	0.401934	0.804657	1.000
267	GOBP-CENTRAL-NERVOUS-SYSTEM-NEURON-DIFFERENTIA...	5	0.500231	1.056038	0.416918	0.802214	1.000
268	GOBP-NEGATIVE-REGULATION-OF-KINASE-ACTIVITY	5	0.503944	1.054626	0.423304	0.802997	1.000
269	REACTOME-CIRCADIAN-CLOCK	5	0.492116	1.052682	0.407353	0.804726	1.000
270	GOBP-CELLULAR-RESPONSE-TO-HORMONE-STIMULUS	11	0.394869	1.052319	0.429155	0.802596	1.000
271	GOBP-CELLULAR-COMPONENT-MORPHOGENESIS	25	0.319443	1.050897	0.405868	0.803311	1.000
272	GOBP-OSTEOBLAST-DIFFERENTIATION	5	0.507381	1.048911	0.420091	0.805052	1.000
273	GOBP-CALCIUM-ION-TRANSPORT-INTO-CYTOSOL	7	0.446263	1.048042	0.417867	0.804162	1.000
274	GOBP-CALCIUM-ION-TRANSMEMBRANE-TRANSPORT	7	0.446263	1.047815	0.418535	0.801829	1.000
275	GOBP-CELL-MORPHOGENESIS	25	0.319443	1.047670	0.404551	0.799320	1.000
276	GOBP-GLAND-DEVELOPMENT	7	0.439702	1.043832	0.413013	0.805554	1.000
277	GOBP-IN-UTERO-EMBRYONIC-DEVELOPMENT	8	0.425462	1.043619	0.405564	0.803203	1.000
278	REACTOME-BETA-CATENIN-INDEPENDENT-WNT-SIGNALING	5	0.493976	1.043054	0.432229	0.801683	1.000
279	GOBP-REGULATION-OF-CELL-ADHESION	13	0.367387	1.041175	0.435762	0.803407	1.000
280	GOBP-REGULATION-OF-SYSTEM-PROCESS	18	0.338266	1.039680	0.431790	0.804120	1.000
281	GOBP-CELLULAR-RESPONSE-TO-LIPID	15	0.358252	1.034645	0.415894	0.813123	1.000
282	GOBP-REGULATION-OF-NERVOUS-SYSTEM-DEVELOPMENT	15	0.356778	1.032855	0.437018	0.813330	1.000
283	GOBP-CIRCULATORY-SYSTEM-PROCESS	5	0.489964	1.032767	0.426035	0.811723	1.000
284	GOBP-REGULATION-OF-EPITHELIAL-CELL-MIGRATION	6	0.466564	1.032077	0.444444	0.810513	1.000
285	GOBP-PROTEIN-COMPLEX-OLIGOMERIZATION	7	0.434238	1.029524	0.435345	0.813413	1.000
286	GOBP-POSITIVE-REGULATION-OF-CELLULAR-PROTEIN.L...	7	0.441007	1.029496	0.433824	0.810658	1.000
287	GOBP-REGULATION-OF-MAP-KINASE-ACTIVITY	9	0.405286	1.028634	0.435211	0.809717	1.000
288	GOBP-REGULATION-OF-AXONOGENESIS	7	0.427567	1.025789	0.422414	0.813690	1.000
289	GOBP-ORGANONITROGEN-COMPOUND-BIOSYNTHETIC-PROCESS	13	0.360086	1.024842	0.438070	0.813031	1.000
290	GOBP-NEGATIVE-REGULATION-OF-CYSTEINE-TYPE-ENDO...	5	0.481255	1.024445	0.462639	0.811197	1.000
291	GOBP-DENDRITE-MORPHOGENESIS	7	0.403445	1.023566	0.459227	0.810268	1.000
292	GOBP-EXOCYTOSIS	11	0.375334	1.018884	0.440771	0.818217	1.000
293	GOBP-RESPONSE-TO-ALKALOID	5	0.481383	1.017365	0.462250	0.818853	1.000
294	GOBP-CELL-CYCLE-PROCESS	11	0.378601	1.016066	0.443526	0.818965	1.000
295	GOBP-LIPID-METABOLIC-PROCESS	10	0.385587	1.015369	0.455296	0.817715	1.000
296	GOBP-COGNITION	28	0.299733	1.011169	0.477189	0.824596	1.000
297	GOBP-TUBE-DEVELOPMENT	18	0.331817	1.010480	0.452320	0.823419	1.000
298	GOBP-POSITIVE-REGULATION-OF-PHOSPHATIDYLINOSIT...	5	0.465494	1.008740	0.460366	0.824522	1.000

Continuation of Table S4

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
299	GOBP-POSITIVE-REGULATION_OF_CELLULAR_COMPONENT...	9	0.392426	1.008635	0.447405	0.822000	1.000
300	GOBP-REGULATION_OF_HORMONE-LEVELS	12	0.356860	1.006754	0.459060	0.823659	1.000
301	REACTOME-ONCOGENIC_MAPK-SIGNALING	5	0.465580	1.000835	0.472180	0.834454	1.000
302	GOBP-POSITIVE-REGULATION_OF_CELLULAR_COMPONENT...	24	0.302713	1.000670	0.452830	0.832009	1.000
303	GOBP-CELLULAR-AMIDE-METABOLIC-PROCESS	12	0.361094	0.993424	0.480000	0.845442	1.000
304	GOBP-RESPONSE_TO_LIGHT-STIMULUS	11	0.365761	0.990598	0.471523	0.849051	1.000
305	GOBP-CENTRAL-NERVOUS-SYSTEM-DEVELOPMENT	27	0.292388	0.990030	0.492665	0.847575	1.000
306	GOBP-REGULATION_OF_NEURONAL_SYNAPTIC_PLASTICITY	7	0.422088	0.988802	0.491379	0.847695	1.000
307	GOBP-INTRINSIC-APOPTOTIC-SIGNALING-PATHWAY	5	0.463652	0.988014	0.508501	0.846763	1.000
308	HALLMARK_KRAS-SIGNALING_UP	6	0.433197	0.987981	0.487482	0.844079	1.000
309	GOBP-POSITIVE-REGULATION_OF_DEVELOPMENTAL_PROCESS	32	0.284040	0.986006	0.491985	0.845678	1.000
310	GOBP-CALCIUM-MEDIATED-SIGNALING	10	0.368191	0.982802	0.491429	0.850297	1.000
311	GOBP-REGULATION_OF_CELLULAR_CATABOLIC_PROCESS	10	0.374031	0.982715	0.509040	0.847756	1.000
312	GOBP-REGULATION_OF_PEPTIDYL-SERINE-PHOSPHORYLA...	8	0.392795	0.979701	0.480226	0.851731	1.000
313	GOBP-REGULATION_OF_CELLULAR_COMPONENT-BIOGENESIS	10	0.369402	0.978096	0.499320	0.852398	1.000
314	GOBP-ORGAN-GROWTH	5	0.466755	0.972143	0.503748	0.862698	1.000
315	GOBP-REGULATION_OF_PEPTIDE-HORMONE-SECRETION	6	0.428131	0.971854	0.521870	0.860666	1.000
316	GOBP-NEGATIVE-REGULATION_OF_IMMUNE-SYSTEM_PROCESS	5	0.458157	0.969304	0.527048	0.863470	1.000
317	GOBP-REGULATION_OF_ORGANELLE-ORGANIZATION	14	0.335545	0.969083	0.512616	0.861247	1.000
318	GOBP-REGULATION_OF_PEPTIDE-SECRETION	7	0.416168	0.967985	0.520567	0.860940	1.000
319	GOBP-NEGATIVE-REGULATION_OF_ION-TRANSPORT	11	0.360122	0.967908	0.527778	0.858399	1.000
320	GOBP-CELL-MORPHOGENESIS_INVOLVED_IN_DIFFERENTI...	22	0.301922	0.967426	0.513806	0.856782	1.000
321	GOBP-REGULATION_OF_ORGAN-GROWTH	5	0.466755	0.967171	0.530211	0.854660	1.000
322	GOBP-POSITIVE-REGULATION_OF_PEPTIDYL-SERINE_PH...	8	0.392795	0.966916	0.527536	0.852618	1.000
323	GOBP-POSITIVE-REGULATION_OF_DNA-BINDING-TRANSC...	10	0.373826	0.963466	0.526316	0.857296	1.000
324	GOBP-REGULATION_OF_EXTRINSIC-APOPTOTIC-SIGNALI...	6	0.419498	0.960981	0.507225	0.859924	1.000
325	GOBP-POSITIVE-REGULATION_OF_LOCOMOTION	11	0.364375	0.960239	0.519890	0.858813	1.000
326	GOBP-ESTABLISHMENT_OF_PROTEIN-LOCALIZATION	17	0.320294	0.958866	0.507833	0.859066	1.000
327	GOBP-LONG-TERM-MEMORY	6	0.431231	0.957409	0.507983	0.859564	1.000
328	GOBP-REGULATION_OF_MUSCLE-ADAPTATION	5	0.441541	0.956200	0.529687	0.859448	1.000
329	GOBP-REGULATION_OF_ANION-TRANSPORT	20	0.307874	0.955094	0.539702	0.859214	1.000
330	GOBP-CELLULAR_COMPONENT-MAINTENANCE	5	0.451391	0.954875	0.547945	0.856979	1.000
331	GOBP-CELL-MORPHOGENESIS_INVOLVED_IN_NEURON_DIF...	22	0.301922	0.954275	0.522556	0.855636	1.000
332	GOBP-NEGATIVE-REGULATION_OF_PROTEIN-MODIFICATI...	10	0.359998	0.950730	0.530497	0.860453	1.000
333	GOBP-ORGANOPHOSPHATE-METABOLIC-PROCESS	8	0.381223	0.949478	0.544286	0.860540	1.000
334	GOBP-CELLULAR-LIPID-METABOLIC-PROCESS	7	0.401564	0.948976	0.545052	0.859116	1.000
335	GOBP-POSITIVE-REGULATION_OF_DEVELOPMENTAL-GROWTH	8	0.384694	0.946960	0.545953	0.860649	1.000
336	GOBP-REGULATION_OF_MITOTIC-CELL-CYCLE	5	0.448373	0.946857	0.543511	0.858305	1.000
337	GOBP-MEMORY	13	0.334937	0.946478	0.537415	0.856616	1.000
338	GOBP-POSITIVE-REGULATION_OF_GROWTH	9	0.374630	0.941952	0.559829	0.863466	1.000
339	GOBP-DEPHOSPHORYLATION	7	0.400243	0.940883	0.561848	0.863105	1.000
340	GOBP-POSITIVE-REGULATION_OF_MOLECULAR-FUNCTION	37	0.273754	0.940527	0.530374	0.861387	1.000
341	GOBP-PROTEIN-DEPHOSPHORYLATION	7	0.400243	0.940294	0.542222	0.859383	1.000

Continuation of Table S4

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
342	GOBP-REGULATION-OF-PROTEIN-SERINE-THREONINE-KI...	12	0.335194	0.939431	0.549795	0.858598	1.000
343	GOBP-EXCITATORY-CHEMICAL-SYNAPTIC-TRANSMISSION	5	0.445783	0.939274	0.547904	0.856424	1.000
344	GOBP-REGULATION-OF-LIPID-BIOSYNTHETIC-PROCESS	6	0.410809	0.938819	0.540179	0.854936	1.000
345	GOBP-RESPONSE-TO-ETHANOL	5	0.445783	0.936446	0.54217	0.857401	1.000
346	GOBP-REGULATION-OF-PHOSPHATIDYLINOSITOL-3-KINA...	6	0.411724	0.935935	0.562874	0.855933	1.000
347	GOBP-LIPID-BIOSYNTHETIC-PROCESS	6	0.416809	0.932088	0.573082	0.861176	1.000
348	GOBP-POSITIVE-REGULATION-OF-SECRETION	6	0.421156	0.931636	0.574156	0.859581	1.000
349	GOBP-MUSCLE-ADAPTATION	5	0.441541	0.930644	0.567407	0.859074	1.000
350	GOBP-RHYTHMIC-PROCESS	15	0.314720	0.926783	0.565274	0.864203	1.000
351	GOBP-CELL-MIGRATION	22	0.289693	0.920951	0.591811	0.873314	1.000
352	GOBP-NUCLEAR-TRANSPORT	5	0.430060	0.919275	0.581602	0.874196	1.000
353	GOBP-BLOOD-VESSEL-MORPHOGENESIS	14	0.322944	0.917078	0.593540	0.876011	1.000
354	GOBP-MULTICELLULAR-ORGANISM-REPRODUCTION	12	0.332259	0.915927	0.592748	0.875862	1.000
355	GOBP-NEGATIVE-REGULATION-OF-CATABOLIC-PROCESS	8	0.374748	0.914927	0.581259	0.875263	1.000
356	GOBP-PROTEIN-TETRAMERIZATION	5	0.429397	0.913940	0.579186	0.874627	1.000
357	GOBP-HEAD-DEVELOPMENT	23	0.282286	0.911885	0.592040	0.876371	1.000
358	GOBP-ACTIVATION-OF-MAPK-ACTIVITY	6	0.405143	0.910298	0.600587	0.877049	1.000
359	GOBP-POSITIVE-REGULATION-OF-MAP-KINASE-ACTIVITY	6	0.405143	0.908853	0.600592	0.877434	1.000
360	GOBP-CARBOHYDRATE-HOMEOSTASIS	7	0.382980	0.907313	0.610542	0.878056	1.000
361	GOBP-MITOTIC-CELL-CYCLE	10	0.337309	0.905979	0.590723	0.878189	1.000
362	GOBP-REGULATION-OF-DEVELOPMENTAL-GROWTH	9	0.357592	0.905179	0.596467	0.877258	1.000
363	GOBP-INOSITOL-LIPID-MEDIATED-SIGNALING	8	0.362307	0.898399	0.626100	0.887651	1.000
364	GOBP-REGULATION-OF-BODY-FLUID-LEVELS	11	0.339152	0.898375	0.604054	0.885267	1.000
365	GOBP-CIRCULATORY-SYSTEM-DEVELOPMENT	21	0.281467	0.897876	0.628535	0.883741	1.000
366	GOBP-REGULATION-OF-RESPONSE-TO-EXTERNAL-STIMULUS	15	0.314523	0.893867	0.601333	0.888847	1.000
367	GOBP-POSITIVE-REGULATION-OF-LEUKOCYTE-CELL-CEL...	5	0.413723	0.891376	0.619120	0.891125	1.000
368	GOBP-ANIMAL-ORGAN-MORPHOGENESIS	12	0.313849	0.889333	0.601361	0.892675	1.000
369	GOBP-CARBOHYDRATE-DERIVATIVE-METABOLIC-PROCESS	8	0.352983	0.888846	0.598601	0.891260	1.000
370	GOBP-RESPONSE-TO-ACID-CHEMICAL	6	0.392319	0.887978	0.620690	0.890401	1.000
371	GOBP-NEGATIVE-REGULATION-OF-PHOSPHORUS-METABOL...	9	0.344996	0.887420	0.622563	0.889000	1.000
372	GOBP-NEGATIVE-REGULATION-OF-CATALYTIC-ACTIVITY	17	0.297861	0.887089	0.633075	0.887234	1.000
373	GOBP-POSITIVE-REGULATION-OF-EPITHELIAL-CELL-PR...	7	0.374510	0.886607	0.608392	0.885829	1.000
374	GOBP-NEGATIVE-REGULATION-OF-PEPTIDASE-ACTIVITY	6	0.388424	0.884397	0.635240	0.887510	1.000
375	GOBP-ADENYLATE-CYCLASE-INHIBITING-G-PROTEIN-CO...	5	0.421687	0.883349	0.634146	0.887167	1.000
376	GOBP-LEUKOCYTE-CELL-ADHESION	6	0.391994	0.882676	0.626667	0.885989	1.000
377	GOBP-POSITIVE-REGULATION-OF-CELL-CELL-ADHESION	5	0.413723	0.881171	0.640553	0.886386	1.000
378	GOBP-TUBE-MORPHOGENESIS	15	0.307985	0.880239	0.633638	0.885622	1.000
379	GOBP-REGULATION-OF-TRANSMEMBRANE-TRANSPORT	23	0.27304	0.879034	0.648855	0.885538	1.000
380	GOBP-EMBRYONIC-MORPHOGENESIS	6	0.390355	0.875912	0.631741	0.883418	1.000
381	GOBP-POSITIVE-REGULATION-OF-CELL-GROWTH	6	0.392173	0.875654	0.649331	0.881682	1.000
382	GOBP-LEARNING	13	0.307485	0.875688	0.629679	0.884556	1.000
383	GOBP-NEGATIVE-REGULATION-OF-CELL-DEATH	22	0.276307	0.873640	0.655779	0.886143	1.000
384	GOBP-GLUCOSE-METABOLIC-PROCESS	6	0.384855	0.871868	0.637462	0.886835	1.000

Continuation of Table S4

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
385	GOBP-DEVELOPMENTAL-GROWTH	10	0.332129	0.871127	0.630986	0.885912	1.000
386	GOBP-REGULATION-OF-PROTEIN-CATABOLIC-PROCESS	7	0.365255	0.869269	0.637725	0.887061	1.000
387	GOBP-REGULATION-OF-VASCULATURE-DEVELOPMENT	5	0.413688	0.867758	0.654743	0.887240	1.000
388	GOBP-MONOSACCHARIDE-METABOLIC-PROCESS	6	0.384855	0.867737	0.631954	0.884991	1.000
389	GOBP-NEURON-DEATH	18	0.285434	0.866991	0.625160	0.883950	1.000
390	GOBP-AGING	13	0.307029	0.866010	0.630102	0.883489	1.000
391	GOBP-REGULATION-OF-SMALL-MOLECULE-METABOLIC-PR...	9	0.334503	0.862417	0.653740	0.887549	1.000
392	GOBP-NERVE-DEVELOPMENT	9	0.336150	0.861798	0.652531	0.886371	1.000
393	GOBP-POSITIVE-REGULATION-OF-ENDOTHELIAL-CELL-P...	6	0.379955	0.858675	0.655488	0.889613	1.000
394	GOBP-AMEBOIDAL-TYPE-CELL-MIGRATION	11	0.317684	0.856580	0.651260	0.890976	1.000
395	GOBP-PROTEIN-LOCALIZATION-TO-ORGANELLE	8	0.343437	0.855922	0.643478	0.889816	1.000
396	GOBP-SMALL-MOLECULE-METABOLIC-PROCESS	16	0.287356	0.855607	0.660053	0.888114	1.000
397	GOBP-NEGATIVE-REGULATION-OF-ANION-TRANSPORT	8	0.352655	0.855252	0.656077	0.886546	1.000
398	GOBP-NEGATIVE-REGULATION-OF-PROTEIN-METABOLIC-...	20	0.271517	0.854286	0.657071	0.885896	1.000
399	GOBP-REGULATION-OF-PROTEIN-LOCALIZATION	18	0.282815	0.853575	0.665786	0.884927	1.000
400	GOBP-DEFENSE-RESPONSE	19	0.278056	0.850251	0.638821	0.888458	1.000
401	GOBP-PHAGOCYTOSIS	5	0.396903	0.848987	0.666165	0.888355	1.000
402	GOBP-REGULATION-OF-PEPTIDE-TRANSPORT	10	0.323636	0.842469	0.679894	0.896812	1.000
403	GOBP-PATTERN-SPECIFICATION-PROCESS	6	0.373778	0.842069	0.670695	0.895243	1.000
404	GOBP-CELLULAR-MACROMOLECULE-LOCALIZATION	20	0.267745	0.838759	0.678161	0.898730	1.000
405	REACTOME-MAPK-FAMILY-SIGNALING-CASCADES	12	0.302557	0.835967	0.674581	0.901451	1.000
406	GOBP-SPROUTING-ANGIOGENESIS	5	0.388130	0.835963	0.697819	0.899238	1.000
407	GOBP-REGULATION-OF-LIPID-LOCALIZATION	5	0.392034	0.834309	0.712166	0.899959	1.000
408	GOBP-REGULATION-OF-CATABOLIC-PROCESS	13	0.295239	0.832904	0.684070	0.900172	1.000
409	GOBP-REPRODUCTIVE-SYSTEM-DEVELOPMENT	6	0.368967	0.832896	0.686544	0.897986	1.000
410	GOBP-STRIATED-MUSCLE-CELL-DIFFERENTIATION	9	0.331742	0.832790	0.680764	0.895986	1.000
411	GOBP-REGIONALIZATION	6	0.373778	0.831932	0.700880	0.895105	1.000
412	GOBP-REGULATION-OF-TRANSPORTER-ACTIVITY	17	0.275722	0.827846	0.684211	0.899625	1.000
413	GOBP-RESPONSE-TO-ABIOTIC-STIMULUS	27	0.247811	0.826005	0.706897	0.900459	1.000
414	GOBP-RESPONSE-TO-KETONE	7	0.345982	0.824696	0.694524	0.900459	1.000
415	GOBP-REGULATION-OF-CELLULAR-PROTEIN-LOCALIZATION	12	0.292699	0.823316	0.682243	0.900554	1.000
416	GOBP-APOPTOTIC-MITOCHONDRIAL-CHANGES	6	0.363557	0.822225	0.695965	0.900244	1.000
417	GOBP-RESPONSE-TO-MOLECULE-OF-BACTERIAL-ORIGIN	13	0.287963	0.821991	0.693243	0.898432	1.000
418	GOBP-NEGATIVE-REGULATION-OF-SYNAPTIC-TRANSMISSION	6	0.359240	0.821898	0.699708	0.896429	1.000
419	GOBP-RESPONSE-TO-BACTERIUM	13	0.287963	0.819541	0.703655	0.898225	1.000
420	GOBP-REGULATION-OF-PROTEIN-LOCALIZATION-TO-CEL...	6	0.363287	0.817400	0.708093	0.899403	1.000
421	GOBP-RESPONSE-TO-PEPTIDE	18	0.266981	0.812472	0.695652	0.905108	1.000
422	GOBP-NEUROTROPHIN-TRK-RECEPTOR-SIGNALING-PATHWAY	6	0.353369	0.811177	0.713650	0.905158	1.000
423	REACTOME-NEUROUS-SYSTEM-DEVELOPMENT	14	0.281196	0.808416	0.725389	0.907377	1.000
424	GOBP-TRANSMEMBRANE-RECEPTOR-PROTEIN-TYROSINE-K...	19	0.258632	0.805103	0.719059	0.910339	1.000
425	GOBP-REGULATION-OF-PROTEOLYSIS	12	0.289615	0.802187	0.717984	0.912543	1.000
426	GOBP-CELLULAR-RESPONSE-TO-ABIOTIC-STIMULUS	7	0.342142	0.796397	0.736070	0.919340	1.000
427	GOBP-CELL-CELL-ADHESION	14	0.275429	0.796215	0.735294	0.917527	1.000

Continuation of Table S4

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
428	GOBP-NEGATIVE-REGULATION-OF-INTRACELLULAR-SIGN...	7	0.330248	0.796038	0.723781	0.915656	1.000
429	GOBP-NEUTROPHIL-SIGNALING-PATHWAY	6	0.353369	0.795836	0.728083	0.913853	1.000
430	GOBP-LOCOMOTION	31	0.228546	0.794926	0.710145	0.913170	1.000
431	GOBP-NEURON-APOPTOTIC-PROCESS	12	0.291318	0.793906	0.749662	0.912670	1.000
432	GOBP-MATERNAL-PROCESS-INVOLVED-IN-FEMALE-PREGN...	5	0.383593	0.793102	0.759690	0.911813	1.000
433	GOBP-LONG-TERM-SYNAPTIC-DEPRESSION	5	0.374218	0.792976	0.733537	0.909886	1.000
434	GOBP-ENDOTHELIAL-CELL-PROLIFERATION	8	0.319925	0.792224	0.733711	0.908772	1.000
435	GOBP-VASCULATURE-DEVELOPMENT	17	0.263332	0.792031	0.766927	0.906950	1.000
436	GOBP-RESPONSE-TO-NICOTINE	7	0.334449	0.790981	0.739568	0.906530	1.000
437	GOBP-NEGATIVE-REGULATION-OF-LOCOMOTION	5	0.366410	0.789256	0.737313	0.907033	1.000
438	REACTOME-MEMBRANE-TRAFFICKING	5	0.369231	0.789223	0.749254	0.905025	1.000
439	REACTOME-CYTOKINE-SIGNALING-IN-IMMUNE-SYSTEM	21	0.249841	0.788484	0.736709	0.903947	1.000
440	GOBP-RESPONSE-TOLLIPID	19	0.254464	0.787381	0.754057	0.903593	1.000
441	GOBP-FAT-CELL-DIFFERENTIATION	9	0.305997	0.787179	0.745739	0.901899	1.000
442	GOBP-RESPONSE-TO-UV	5	0.377657	0.786718	0.762346	0.900570	1.000
443	GOBP-PROTEIN-CATABOLIC-PROCESS	8	0.317545	0.786464	0.743920	0.898962	1.000
444	GOBP-CELLULAR-RESPONSE-TO-EXTERNAL-STIMULUS	10	0.298457	0.780584	0.762689	0.905507	1.000
445	GOBP-MULTIORGANISM-PROCESS	16	0.264181	0.779939	0.748988	0.904444	1.000
446	REACTOME-VESICLE-MEDIATED-TRANSPORT	5	0.369231	0.774592	0.806748	0.910367	1.000
447	GOBP-NEGATIVE-REGULATION-OF-APOPTOTIC-SIGNALIN...	7	0.327114	0.773537	0.752608	0.909837	1.000
448	GOBP-ERK1-AND-ERK2-CASCADE	5	0.353170	0.763179	0.777778	0.922311	1.000
449	GOBP-MITOCHONDRION-ORGANIZATION	7	0.321620	0.761394	0.763348	0.922786	1.000
450	GOBP-MONOAMINE-TRANSPORT	5	0.354985	0.758311	0.808670	0.925015	1.000
451	GOBP-NUCLEOBASE-CONTAINING-SMALL-MOLECULE-META...	7	0.316438	0.751403	0.763554	0.932782	1.000
452	GOBP-CARBOHYDRATE-METABOLIC-PROCESS	9	0.295179	0.750659	0.797737	0.931750	1.000
453	GOBP-POSITIVE-REGULATION-OF-CELL-ADHESION	7	0.317306	0.747919	0.787143	0.933534	1.000
454	GOBP-RESPONSE-TO-PEPTIDE-HORMONE	13	0.265210	0.745956	0.824866	0.934144	1.000
455	GOBP-NEGATIVE-REGULATION-OF-GENE-EXPRESSION	11	0.280512	0.745796	0.786217	0.932307	1.000
456	GOBP-ORGANONITROGEN-COMPOUND-CATABOLIC-PROCESS	10	0.280737	0.743383	0.776999	0.933534	1.000
457	GOBP-POSITIVE-REGULATION-OF-GENE-EXPRESSION	16	0.248324	0.743059	0.800000	0.931896	1.000
458	GOBP-RESPONSE-TO-ALCOHOL	11	0.271673	0.741108	0.806849	0.932421	1.000
459	GOBP-REGULATION-OF-CELLULAR-COMPONENT-MOVEMENT	15	0.254244	0.740381	0.785252	0.931366	1.000
460	GOBP-PROTEIN-LOCALIZATION-TO-CELL-JUNCTION	6	0.330314	0.738210	0.815267	0.932156	1.000
461	GOBP-MUSCLE-CELL-DIFFERENTIATION	10	0.278407	0.737884	0.792208	0.930573	1.000
462	GOBP-NEGATIVE-REGULATION-OF-SIGNALING	21	0.235383	0.734187	0.814910	0.933425	1.000
463	GOBP-REPRODUCTION	18	0.238262	0.732177	0.817594	0.934133	1.000
464	GOBP-REGULATION-OF-DNA-BINDING-TRANSCRIPTION.F...	16	0.244460	0.730460	0.814474	0.934281	1.000
465	GOBP-MACROMOLECULE-CATABOLIC-PROCESS	11	0.265997	0.728587	0.819293	0.934585	1.000
466	GOBP-EPITHELIAL-CELL-PROLIFERATION	12	0.262624	0.720056	0.804289	0.943584	1.000
467	GOBP-MUSCLE-SYSTEM-PROCESS	9	0.283464	0.719148	0.814111	0.942765	1.000
468	GOBP-ENDOTHELIAL-CELL-MIGRATION	8	0.283447	0.715921	0.812921	0.944675	1.000
469	GOBP-IMPORT-INTO-CELL	6	0.315328	0.713980	0.832836	0.945155	1.000
470	GOBP-REGULATION-OF-GROWTH	13	0.250023	0.713096	0.819135	0.944339	1.000

Continuation of Table S4

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
471 GOBP-REGULATION-OF-CYSTEINE-TYPE-ENDOPEPTIDASE...	GO:2000116	9	0.274191	0.711609	0.807580	0.944224	1.000
472 GOBP-ORGANIC-ACID-METABOLIC-PROCESS	GO:0006082	7	0.300400	0.711585	0.842466	0.942252	1.000
473 GOBP-REGULATION-OF-OSTEOCLAST-DIFFERENTIATION	GO:0045670	5	0.329609	0.710791	0.858859	0.941170	1.000
474 GOBP-POSITIVE-REGULATION-OF-PROTEOLYSIS	GO:0045862	8	0.287312	0.704387	0.835443	0.947084	1.000
475 GOBP-INNATE-IMMUNE-RESPONSE	GO:0045087	7	0.292838	0.703039	0.831625	0.946687	1.000
476 GOBP-CELL-JUNCTION-ASSEMBLY	GO:0034329	8	0.285659	0.701408	0.839650	0.946582	1.000
477 GOBP-EMBRYONIC-ORGAN-DEVELOPMENT	GO:0048568	7	0.303164	0.701267	0.832593	0.944769	1.000
478 GOBP-NEGATIVE-REGULATION-OF-CELL-PROJECTION-OR...	GO:0031345	5	0.332383	0.701176	0.835616	0.942910	1.000
479 GOBP-CELLULAR-RESPONSE-TO-OXYGEN-CONTAINING.CO...	GO:1901701	29	0.210703	0.700410	0.853629	0.941793	1.000
480 GOBP-GROWTH	GO:0040007	14	0.242780	0.697460	0.833333	0.943233	1.000
481 GOBP-BLOOD-VESSEL-ENDOTHELIAL-CELL-MIGRATION	GO:0043534	8	0.283447	0.696388	0.854930	0.942522	1.000
482 GOBP-MONOCARBOXYLIC-ACID-METABOLIC-PROCESS	GO:0032787	6	0.311794	0.695576	0.860058	0.941508	1.000
483 GOBP-TAXIS	GO:0042330	14	0.241473	0.691020	0.853977	0.944647	1.000
484 GOBP-REGULATION-OF-PROTEIN-STABILITY	GO:0031647	5	0.329342	0.690058	0.874807	0.943817	1.000
485 GOBP-CELLULAR-RESPONSE-TO-INORGANIC-SUBSTANCE	GO:0071241	11	0.257611	0.689685	0.863319	0.942304	1.000
486 GOBP-RESPONSE-TO-TUMOR-NECROSIS-FACTOR	GO:0034612	7	0.289646	0.688587	0.865278	0.941703	1.000
487 GOBP-REGULATION-OF-CELL-ACTIVATION	GO:0050865	8	0.284631	0.686618	0.849928	0.941917	1.000
488 GOBP-RESPONSE-TO-BIOTIC-STIMULUS	GO:0009607	17	0.226659	0.686172	0.864474	0.940428	1.000
489 GOBP-CELL-CELL-SIGNALING-BY-WNT	GO:0198738	7	0.292317	0.684920	0.856515	0.939891	1.000
490 GOBP-POSITIVE-REGULATION-OF-RESPONSE-TO-EXTERN...	GO:0032103	9	0.273118	0.683220	0.858543	0.939803	1.000
491 GOBP-BIOLOGICAL-ADHESION	GO:0022610	19	0.219498	0.681910	0.863520	0.939247	1.000
492 GOBP-PURINE-CONTAINING-COMPOUND-METABOLIC-PROCESS	GO:0072521	6	0.308673	0.680787	0.884181	0.938582	1.000
493 GOBP-NEURON-PROJECTION-GUIDANCE	GO:0097485	9	0.273168	0.678164	0.860955	0.939404	1.000
494 GOBP-REGULATION-OF-CYTOSKELETON-ORGANIZATION	GO:0051493	5	0.318758	0.676363	0.883614	0.939333	1.000
495 GOBP-TISSUE-MIGRATION	GO:0090130	9	0.268503	0.672779	0.871191	0.941138	1.000
496 GOBP-INFLAMMATORY-RESPONSE	GO:0006954	12	0.239345	0.666354	0.864792	0.945876	1.000
497 GOBP-POSITIVE-REGULATION-OF-ANION-TRANSPORT	GO:1903793	9	0.254085	0.656929	0.892458	0.953309	1.000
498 GOBP-NEUROINFLAMMATORY-RESPONSE	GO:0150076	5	0.310007	0.654343	0.917169	0.953902	1.000
499 GOBP-CELL-GROWTH	GO:0016049	10	0.247424	0.654113	0.883657	0.952206	1.000
500 GOBP-ORGANIC-HYDROXY-COMPOUND-METABOLIC-PROCESS	GO:1901615	8	0.262385	0.641436	0.903819	0.961834	1.000
501 GOBP-RESPONSE-TO-METAL-ION	GO:0010038	15	0.219218	0.640004	0.921260	0.961229	1.000
502 GOBP-REGULATION-OF-PEPTIDASE-ACTIVITY	GO:0052547	10	0.240018	0.629484	0.899729	0.968847	1.000
503 GOBP-NEGATIVE-REGULATION-OF-HYDROLASE-ACTIVITY	GO:0051346	11	0.230874	0.626295	0.910714	0.969618	1.000
504 GOBP-NEGATIVE-REGULATION-OF-CELL-DEVELOPMENT	GO:0010721	6	0.277700	0.625701	0.917526	0.968202	1.000
505 GOBP-DEVELOPMENTAL-PROCESS-INVOLVED-IN-REPRODU...	GO:0003006	11	0.229732	0.625439	0.907104	0.966469	1.000
506 GOBP-AMYLOID-PRECURSOR-PROTEIN-METABOLIC-PROCESS	GO:0042982	5	0.289564	0.619642	0.938897	0.969280	1.000
507 GOBP-NEGATIVE-REGULATION-OF-NERVOUS-SYSTEM.DEV...	GO:0051961	5	0.289622	0.617231	0.922256	0.969320	1.000
508 GOBP-CARDIAC-MUSCLE-TISSUE-DEVELOPMENT	GO:0048738	6	0.272845	0.611507	0.919075	0.971732	1.000
509 GOBP-ASSOCIATIVE-LEARNING	GO:0008306	7	0.262356	0.608788	0.926362	0.971866	1.000
510 GOBP-MULTICELLULAR-ORGANISM-PROCESS	GO:0044706	8	0.246643	0.607370	0.929972	0.970993	1.000
511 GOBP-AMYLOID-PRECURSOR-PROTEIN-CATABOLIC-PROCESS	GO:0042987	5	0.289564	0.605670	0.937134	0.970265	1.000
512 GOBP-HEART-DEVELOPMENT	GO:0007507	6	0.272845	0.604764	0.935578	0.969093	1.000
513 GOBP-RESPONSE-TO-INORGANIC-SUBSTANCE	GO:0010035	19	0.195394	0.604657	0.935849	0.967278	1.000

Continuation of Table S4

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
514	GOBP-AMYLOID-BETA-METABOLIC-PROCESS	5	0.289564	0.604244	0.940549	0.965700	1.000
515	GOBP-NEGATIVE-REGULATION-OF-MOLECULAR-FUNCTION	24	0.184592	0.603997	0.941038	0.964005	1.000
516	GOBP-REGULATION-OF-MUSCLE-SYSTEM-PROCESS	8	0.243215	0.603157	0.939042	0.962822	1.000
517	GOBP-REGULATION-OF-WNT-SIGNALING-PATHWAY	5	0.281555	0.601814	0.936556	0.961920	1.000
518	GOBP-RESPIRATORY-SYSTEM-DEVELOPMENT	6	0.265806	0.587063	0.957353	0.970165	1.000
519	GOBP-APOPTOTIC-PROCESS	35	0.169580	0.578620	0.957882	0.973673	1.000
520	REACTOME-L1CAM-INTERACTIONS	5	0.271377	0.570881	0.960396	0.976358	1.000
521	GOBP-BIOLOGICAL-PROCESS-INVOLVED-IN-SYMBIOTIC-...	10	0.214721	0.560502	0.946721	0.980197	1.000
522	GOBP-POSITIVE-REGULATION-OF-ORGANELLE-ORGANIZA...	10	0.216285	0.559195	0.945637	0.978978	1.000
523	GOBP-CIRCADIAN-REGULATION-OF-GENE-EXPRESSION	5	0.262878	0.559061	0.973643	0.977172	1.000
524	GOBP-POSITIVE-REGULATION-OF-DEFENSE-RESPONSE	5	0.260620	0.548368	0.977612	0.980835	1.000
525	GOBP-DEFENSE-RESPONSE-TO-OTHER-ORGANISM	5	0.252541	0.536454	0.977811	0.982412	1.000
526	GOBP-REGULATION-OF-NEURON-DIFFERENTIATION	5	0.213048	0.530454	0.977811	0.982412	1.000
527	GOBP-POSITIVE-REGULATION-OF-HYDROLASE-ACTIVITY	16	0.179520	0.531422	0.972863	0.982542	1.000
528	GOBP-REGULATION-OF-HYDROLASE-ACTIVITY	22	0.160603	0.516395	0.973585	0.986325	1.000
529	GOBP-NEGATIVE-REGULATION-OF-PROTEIN-CATABOLIC-...	5	0.239233	0.503173	0.986804	0.988626	1.000
530	GOBP-NEGATIVE-REGULATION-OF-RESPONSE-TO-STIMULUS	16	0.166973	0.500414	0.982984	0.987598	1.000
531	GOBP-RESPONSE-TO-CALCIUM-ION	6	0.210584	0.475114	0.995529	0.992004	1.000
532	GOBP-PROTEOLYSIS	17	0.146049	0.437320	0.996134	0.995953	1.000
533	GOBP-POSITIVE-REGULATION-OF-IMMUNE-RESPONSE	9	-0.188828	-0.575975	0.976510	0.972107	1.000
534	GOBP-RESPONSE-TO-WOUNDING	15	-0.159585	-0.602349	0.981482	0.963180	1.000
535	GOBP-MALE-GAMETE-GENERATION	5	-0.253012	-0.604289	0.949008	0.967070	1.000
536	GOBP-CELLULAR-RESPONSE-TO-ORGANIC-CYCLIC-COMPOUND	13	-0.181751	-0.645069	0.946360	0.942108	1.000
537	GOBP-CYTOKINE-PRODUCTION	10	-0.215426	-0.667603	0.894118	0.925952	1.000
538	GOBP-IMMUNE-EFFECTOR-PROCESS	11	-0.207177	-0.667842	0.904412	0.930700	1.000
539	GOBP-REGULATION-OF-MUSCLE-CELL-DIFFERENTIATION	6	-0.267445	-0.679499	0.869318	0.923287	1.000
540	GOBP-COAGULATION	8	-0.239735	-0.683345	0.856164	0.924074	1.000
541	REACTOME-RNA-POLYMERASE-II-TRANSCRIPTION	20	-0.165242	-0.688255	0.863208	0.923626	1.000
542	REACTOME-SIGNALING-BY-RHO-GTPASES-MIRO-GTPASES...	9	-0.229804	-0.693671	0.855634	0.922112	1.000
543	REACTOME-RHO-GTPASE-EFFECTORS	9	-0.229804	-0.696166	0.876712	0.923845	1.000
544	GOBP-POSITIVE-REGULATION-OF-CYTOKINE-PRODUCTION	7	-0.249042	-0.701150	0.880000	0.922560	1.000
545	GOBP-REGULATION-OF-DEFENSE-RESPONSE	7	-0.259259	-0.705255	0.859060	0.922667	1.000
546	GOBP-ORGANIC-HYDROXY-COMPOUND-TRANSPORT	6	-0.279376	-0.707951	0.854545	0.924173	1.000
547	GOBP-REGULATION-OF-INFLAMMATORY-RESPONSE	7	-0.259259	-0.711584	0.865385	0.924286	1.000
548	GOBP-TEMPERATURE-HOMEOSTASIS	5	-0.305944	-0.725896	0.869048	0.909589	1.000
549	GOBP-WOUND-HEALING	13	-0.213421	-0.748554	0.816794	0.880911	1.000
550	GOBP-MYELOID-LEUKOCYTE-ACTIVATION	8	-0.262500	-0.767898	0.760274	0.855074	1.000
551	GOBP-CELLULAR-RESPONSE-TO-STARVATION	5	-0.323012	-0.770891	0.728022	0.855034	1.000
552	GOBP-NEGATIVE-REGULATION-OF-RESPONSE-TO-EXTERN...	5	-0.323012	-0.773116	0.746988	0.856111	1.000
553	GOBP-NEGATIVE-REGULATION-OF-CELL-DIFFERENTIATION	13	-0.226667	-0.782602	0.784000	0.845644	1.000
554	GOBP-SMALL-MOLECULE-BIOSYNTHETIC-PROCESS	5	-0.323012	-0.784218	0.748538	0.847771	1.000
555	GOBP-RESPONSE-TO-STARVATION	5	-0.331258	-0.791858	0.764205	0.839568	1.000
556	GOBP-EPHRIN-RECEPTOR-SIGNALING-PATHWAY	5	-0.340670	-0.811947	0.704478	0.809923	1.000

Continuation of Table S4

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
557 GOBP-REGULATION-OF-GTPASE-ACTIVITY	GO-0043087	5	-0.343709	-0.820182	0.678873	0.799053	1.000
558 REACTOME-EPH.EPHRIN-SIGNALING	R-RNO-2682334	6	-0.328244	-0.821177	0.625748	0.801913	1.000
559 GOBP-MUSCLE-CELL-PROLIFERATION	GO-0033002	8	-0.284043	-0.821714	0.678689	0.805852	1.000
560 GOBP-NEGATIVE-REGULATION-OF-DEVELOPMENTAL-PROCESS	GO-0051093	13	-0.226667	-0.825767	0.714286	0.803077	1.000
561 GOBP-ACTIVATION-OF-IMMUNE-RESPONSE	GO-0002253	5	-0.337878	-0.830658	0.682584	0.798982	1.000
562 REACTOME-CELLULAR-RESPONSES-TO-EXTERNAL-STIMULI	R-RNO-8953897	11	-0.245370	-0.831103	0.695971	0.803131	1.000
563 GOBP-MUSCLE-CONTRACTION	GO-0006936	5	-0.349398	-0.833371	0.657382	0.804169	1.000
564 GOBP-PLATELET-ACTIVATION	GO-0030168	6	-0.320200	-0.844788	0.647059	0.787952	1.000
565 GOBP-MUSCLE-CELL-DEVELOPMENT	GO-0055001	5	-0.349398	-0.845846	0.636905	0.790722	1.000
566 REACTOME-NEUTROPHIL-DEGRANULATION	R-RNO-6798695	6	-0.329268	-0.849573	0.639437	0.788395	1.000
567 GOBP-MYELOID-LEUKOCYTE-MEDIATED-IMMUNITY	GO-0002444	6	-0.329268	-0.853905	0.635220	0.784900	1.000
568 GOBP-EPIDERMIS-DEVELOPMENT	GO-0008544	5	-0.354236	-0.854984	0.659824	0.788173	1.000
569 GOBP-ANATOMICAL-STRUCTURE-HOMEOSTASIS	GO-0060249	7	-0.315769	-0.856115	0.652038	0.790838	1.000
570 GOBP-MYOTUBE-DIFFERENTIATION	GO-0014902	5	-0.349398	-0.861083	0.622159	0.786448	1.000
571 GOBP-CELL-ACTIVATION-INVOLVED-IN-IMMUNE-RESPONSE	GO-0002263	6	-0.329268	-0.861579	0.613293	0.790653	1.000
572 GOBP-NEGATIVE-REGULATION-OF-MULTICELLULAR-ORGA...	GO-0051241	15	-0.232877	-0.875430	0.626556	0.769383	1.000
573 REACTOME-TOLL-LIKE-RECEPTOR-TLR1-TLR2-CASCADE	R-RNO-168179	8	-0.299598	-0.877066	0.602007	0.771186	1.000
574 GOBP-RESPONSE-TO-INTERLEUKIN-1	GO-0070555	5	-0.375340	-0.879303	0.585987	0.771820	1.000
575 GOBP-REGULATION-OF-PROTEIN-BINDING	GO-0043393	7	-0.318666	-0.879999	0.605863	0.775453	1.000
576 REACTOME-MYD88-INDEPENDENT-TLR4-CASCADE	R-RNO-166166	8	-0.299598	-0.881266	0.600000	0.778104	1.000
577 REACTOME-TOLL-LIKE-RECEPTOR-CASCADES	R-RNO-168898	8	-0.299598	-0.884229	0.585034	0.777513	1.000
578 REACTOME-TOLL-LIKE-RECEPTOR-9-TLR9-CASCADE	R-RNO-168138	8	-0.299598	-0.887034	0.617857	0.776933	1.000
579 HALLMARK-UV-RESPONSE-UP	M5941	5	-0.364515	-0.891458	0.560976	0.773364	1.000
580 GOBP-CELL-ACTIVATION	GO-0001775	22	-0.211768	-0.893785	0.663507	0.774111	1.000
581 GOBP-CELL-CELL-JUNCTION-ASSEMBLY	GO-0007043	5	-0.375193	-0.898075	0.562327	0.771290	1.000
582 GOBP-SMOOTH-MUSCLE-CELL-PROLIFERATION	GO-0048659	6	-0.349740	-0.905414	0.528701	0.761602	1.000
583 REACTOME-INFECTIOUS-DISEASE	R-HSA-5663205	12	-0.269179	-0.906936	0.617021	0.763898	1.000
584 REACTOME-INTERLEUKIN-17-SIGNALING	R-RNO-448424	6	-0.350397	-0.907289	0.563518	0.768446	1.000
585 GOBP-CELL-CELL-JUNCTION-ORGANIZATION	GO-0045216	6	-0.361652	-0.916013	0.516923	0.755710	1.000
586 GOBP-CELL-CYCLE	GO-0007049	21	-0.224069	-0.916324	0.594059	0.760482	1.000
587 GOBP-CELLULAR-GLUCOSE-HOMEOSTASIS	GO-0001678	5	-0.385542	-0.929404	0.530726	0.739660	1.000
588 REACTOME-LEISHMANIA-INFECTION	R-HSA-9658195	10	-0.288306	-0.930093	0.523298	0.743646	1.000
589 GOBP-POSITIVE-REGULATION-OF-APOPTOTIC-SIGNALIN...	GO-2001235	5	-0.385542	-0.936396	0.498507	0.736357	1.000
590 GOBP-SMALL-GTPASE-MEDIATED-SIGNAL-TRANSDUCTION	GO-0007264	8	-0.314810	-0.944682	0.481967	0.724464	1.000
591 GOBP-PROTEIN-MODIFICATION-BY-SMALL-PROTEIN-CON...	GO-0032446	6	-0.372679	-0.958612	0.505119	0.701400	1.000
592 GOBP-POSITIVE-REGULATION-OF-SMOOTH-MUSCLE-CELL...	GO-0048661	5	-0.397089	-0.960690	0.485380	0.702536	1.000
593 GOBP-POSITIVE-REGULATION-OF-ESTABLISHMENT-OF-P...	GO-1904951	5	-0.397590	-0.963172	0.457865	0.702709	1.000
594 GOBP-POSITIVE-REGULATION-OF-CELL-DEATH	GO-0010942	19	-0.237932	-0.965271	0.487562	0.703746	1.000
595 GOBP-LEUKOCYTE-MEDIATED-IMMUNITY	GO-0002443	8	-0.337500	-0.967306	0.465409	0.704833	1.000
596 REACTOME-EXTRACELLULAR-MATRIX-ORGANIZATION	R-RNO-1474244	12	-0.409639	-0.974933	0.465181	0.699370	1.000
597 GOBP-MULTICELLULAR-ORGANISMAL-HOMEOSTASIS	GO-0048871	5	-0.280097	-0.974933	0.471631	0.700343	1.000
598 REACTOME-DEVELOPMENTAL-BIOLOGY	R-RNO-1266738	22	-0.229011	-0.994125	0.464646	0.666714	1.000
599 GOBP-REGULATION-OF-CELL-DEVELOPMENT	GO-0060284	15	-0.275972	-0.996611	0.442623	0.666626	1.000

Continuation of Table S4

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
600 GOBP-RESPONSE.TO.MECHANICAL.STIMULUS	GO-0009612	6	-0.370349	-1.000958	0.401961	0.663296	1.000
601 REACTOME.MAPK.TARGETS.NUCLEAR.EVENTS.MEDIATED....	R-HSA-450282	5	-0.427073	-1.010663	0.404984	0.648941	1.000
602 GOBP-ENZYME.LINKED.RECEPTOR.PROTEIN.SIGNALING....	GO-0007167	24	-0.239507	-1.012965	0.430622	0.649880	1.000
603 GOBP-REGULATION.OF.APOPTOTIC.SIGNALING.PATHWAY	GO-2001233	10	-0.317053	-1.018732	0.400709	0.643467	1.000
604 GOBP-PERIPHERAL.NERVOUS.SYSTEM.DEVELOPMENT	GO-0007422	9	-0.330331	-1.026445	0.401460	0.633681	1.000
605 GOBP-POSITIVE.REGULATION.OF.NEUROGENESIS	GO-0005769	12	-0.306182	-1.031645	0.377863	0.628889	1.000
606 GOBP-POSITIVE.REGULATION.OF.MYELOID.LEUKOCYTE....	GO-0002763	6	-0.400289	-1.033368	0.379009	0.630700	1.000
607 GOBP-REGULATION.OF.NEUROGENESIS	GO-0005767	14	-0.280566	-1.035793	0.404959	0.631054	1.000
608 GOBP-POSITIVE.REGULATION.OF.CELL.DEVELOPMENT	GO-0010720	12	-0.306182	-1.040592	0.374016	0.626372	1.000
609 GOBP-OSTEOCLAST.DIFFERENTIATION	GO-00030316	6	-0.398655	-1.041748	0.368580	0.629273	1.000
610 GOBP-REGULATION.OF.CELL.DEATH	GO-0010941	34	-0.221414	-1.044157	0.424051	0.629500	1.000
611 GOBP-POSITIVE.REGULATION.OF.AXONOGENESIS	GO-0005772	5	-0.432755	-1.044946	0.367953	0.633429	1.000
612 REACTOME.POST.TRANSLATIONAL.PROTEIN.MODIFICATION	R-RNO-597592	7	-0.387151	-1.045708	0.380503	0.637423	1.000
613 GOBP-POSITIVE.REGULATION.OF.NERVOUS.SYSTEM.DEV...	GO-00051962	12	-0.306182	-1.055396	0.384328	0.622745	1.000
614 GOBP-RAS.PROTEIN.SIGNAL.TRANSDUCTION	GO-0007265	5	-0.439391	-1.055553	0.329412	0.628025	1.000
615 REACTOME.DEATH.RECEPTOR.SIGNALING	R-RNO-73887	5	-0.433693	-1.058698	0.345238	0.627034	1.000
616 GOBP-POSITIVE.REGULATION.OF.PEPTIDASE.ACTIVITY	GO-0010952	11	-0.395062	-1.061516	0.338870	0.627181	1.000
617 GOBP-CYTOSKELETON.ORGANIZATION	GO-0007010	7	-0.316087	-1.068483	0.338130	0.619281	1.000
618 GOBP-RESPONSE.TO.NITROGEN.COMPOUND	GO-1901698	35	-0.226016	-1.068676	0.366120	0.624685	1.000
619 GOBP-POSITIVE.REGULATION.OF.CYSTEINE.TYPE.ENDO...	GO-2001056	7	-0.395062	-1.072599	0.356209	0.622193	1.000
620 GOBP-CHROMOSOME.ORGANIZATION	GO-0051276	10	-0.414173	-1.072910	0.346386	0.627431	1.000
621 GOBP-LYMPHOCYTE.ACTIVATION	GO-0046649	6	-0.344968	-1.073802	0.353175	0.631459	1.000
622 GOBP-REGULATION.OF.IMMUNE.SYSTEM.PROCESS	GO-0002682	21	-0.265290	-1.074172	0.363636	0.636818	1.000
623 GOBP-MORPHOGENESIS.OF.AN.EPITHELIUM	GO-0002009	6	-0.400087	-1.075064	0.333333	0.641270	1.000
624 REACTOME.ESR.MEDIATED.SIGNALING	R-RNO-8939211	8	-0.378285	-1.077997	0.348592	0.641440	1.000
625 REACTOME.INNATE.IMMUNE.SYSTEM	R-RNO-168249	16	-0.293349	-1.086835	0.320175	0.628400	1.000
626 GOBP-MEMBRANE.PROTEIN.PROTEOLYSIS	GO-0033619	6	-0.415698	-1.094225	0.355311	0.619253	1.000
627 GOBP-CELLULAR.RESPONSE.TO.CADMIUM.ION	GO-0071276	5	-0.446324	-1.094698	0.312866	0.624410	1.000
628 GOBP-REGULATION.OF.GLIOGENESIS	GO-0014013	5	-0.466353	-1.106269	0.300000	0.606594	1.000
629 REACTOME.SIGNALING.BY.NUCLEAR.RECEPTORS	R-RNO-9006931	8	-0.378285	-1.107596	0.279863	0.610250	1.000
630 GOBP-EXTRINSIC.APOPTOTIC.SIGNALING.PATHWAY	GO-0097191	7	-0.400746	-1.121780	0.296667	0.587415	1.000
631 GOBP-ANATOMICAL.STRUCTURE.FORMATION.INVOLVED.I...	GO-0048646	20	-0.278690	-1.122635	0.290640	0.591693	1.000
632 GOBP-RESPONSE.TO.RADIATION	GO-0009314	13	-0.319042	-1.124602	0.280156	0.594011	1.000
633 GOBP-POSITIVE.REGULATION.OF.GLIOGENESIS	GO-0014015	5	-0.466353	-1.128993	0.277008	0.591486	1.000
634 GOBP-FC.EPSILON.RECEPTOR.SIGNALING.PATHWAY	GO-0038095	7	-0.413386	-1.131829	0.280000	0.592015	1.000
635 REACTOME.PTEN.REGULATION	R-RNO-6807070	18	-0.286606	-1.131897	0.263768	0.598427	1.000
636 GOBP-RESPONSE.TO.GROWTH.FACTOR	GO-0070848	5	-0.479616	-1.138306	0.232877	0.595350	1.000
637 GOBP-POSITIVE.REGULATION.OF.IMMUNE.SYSTEM.PROCESS	GO-0002684	18	-0.291698	-1.137879	0.280374	0.598674	1.000
638 GOBP-RESPONSE.TO.CADMIUM.ION	GO-0046686	6	-0.441754	-1.139080	0.262500	0.602763	1.000
639 REACTOME.TRANSCRIPTIONAL.REGULATION.BY_TP53	R-RNO-3700989	7	-0.413386	-1.142261	0.264151	0.603174	1.000
640 REACTOME.FC.EPSILON.RECEPTOR.FCER1.SIGNALING	R-RNO-2454202	6	-0.413386	-1.142427	0.267516	0.609959	1.000
641 GOBP-POSITIVE.REGULATION.OF.BINDING	GO-0051099	6	-0.451219	-1.147463	0.266862	0.607015	1.000
642 GOBP-OSSIFICATION	GO-0001503	9	-0.366621	-1.148862	0.282609	0.611302	1.000

Continuation of Table S4

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
643	GOBP-CYTOKINE-MEDIATED-SIGNALING-PATHWAY	16	-0.303124	-1.153110	0.230047	0.609363	1.000
644	GOBP-ACTIN-FILAMENT-BASED-PROCESS	7	-0.421261	-1.168487	0.224684	0.583591	1.000
645	GOBP-CELLULAR-COMPONENT-DISSEMBLY	6	-0.455885	-1.169941	0.241477	0.587911	1.000
646	GOBP-CELLULAR-RESPONSE-TO-REACTIVE-OXYGEN-SPECIES	7	-0.417888	-1.174072	0.237342	0.585748	1.000
647	GOBP-RESPONSE-TO-EXTRACELLULAR-STIMULUS	13	-0.339753	-1.177354	0.269373	0.586415	1.000
648	GOBP-RESPONSE-TO-INSULIN	5	-0.488647	-1.179358	0.246106	0.589561	1.000
649	GOBP-TISSUE-HOMEOSTASIS	5	-0.497384	-1.179904	0.240223	0.596054	1.000
650	GOBP-CHROMATIN-ORGANIZATION	5	-0.493709	-1.183317	0.244957	0.596025	1.000
651	GOBP-TISSUE-MORPHOGENESIS	7	-0.436807	-1.187540	0.245734	0.594620	1.000
652	GOBP-CELLULAR-RESPONSE-TO-CHEMICAL-STRESS	7	-0.417888	-1.189496	0.256944	0.598258	1.000
653	GOBP-REGULATION-OF-MULTICELLULAR-ORGANISMAL-DE...	31	-0.255009	-1.198794	0.236559	0.585902	1.000
654	GOBP-POSITIVE-REGULATION-OF-CELL-POPULATION.PR...	21	-0.287913	-1.199113	0.206731	0.593254	1.000
655	GOBP-REGULATION-OF-MYELOID-LEUKOCYTE-DIFFERENT...	8	-0.412065	-1.204109	0.241830	0.590916	1.000
656	REACTOME-SIGNALING-BY-INTERLEUKINS	15	-0.322242	-1.209148	0.181818	0.587908	1.000
657	GOBP-REGULATION-OF-CELL-DIFFERENTIATION	36	-0.249838	-1.216149	0.140449	0.581392	1.000
658	GOBP-POSITIVE-REGULATION-OF-MYELOID-CELL-DIFFE...	7	-0.436005	-1.230284	0.190635	0.559466	1.000
659	GOBP-POSITIVE-REGULATION-OF-MULTICELLULAR-ORGA...	32	-0.271307	-1.248364	0.175325	0.530099	1.000
660	HALLMARK-EPITHELIAL-MESENCHYMAL-TRANSITION	5	-0.536923	-1.250161	0.236760	0.534576	1.000
661	GOBP-POSITIVE-REGULATION-OF-HEMOPOIESIS	7	-0.458349	-1.264510	0.175258	0.512463	1.000
662	GOBP-REGULATION-OF-IMMUNE-RESPONSE	12	-0.369298	-1.266751	0.170455	0.516138	1.000
663	GOBP-PROTEIN-MODIFICATION-BY-SMALL-PROTEIN.CON...	7	-0.475190	-1.279417	0.185668	0.500196	1.000
664	GOBP-CELLULAR-RESPONSE-TO-EXTRACELLULAR-STIMULUS	8	-0.437326	-1.280897	0.165644	0.505768	1.000
665	GOBP-RESPONSE-TO-OXYGEN-CONTAINING-COMPOUND	39	-0.270379	-1.285677	0.099338	0.504316	1.000
666	GOBP-T-CELL-ACTIVATION	8	-0.439503	-1.286534	0.182131	0.510840	1.000
667	GOBP-RESPONSE-TO-ORGANIC-CYCLIC-COMPOUND	20	-0.318332	-1.296448	0.113122	0.498692	1.000
668	GOBP-REGULATION-OF-MYELOID-CELL-DIFFERENTIATION	9	-0.405586	-1.298127	0.157718	0.503615	1.000
669	GOBP-REGULATION-OF-VASCULAR-ASSOCIATED-SMOOTH...	5	-0.549071	-1.306645	0.175385	0.496260	1.000
670	GOBP-MYELOID-LEUKOCYTE-DIFFERENTIATION	11	-0.399629	-1.328862	0.131579	0.462058	1.000
671	GOBP-RESPONSE-TO-HORMONE	20	-0.324517	-1.331026	0.111111	0.466799	1.000
672	GOBP-RESPONSE-TO-CYTOKINE	23	-0.308332	-1.347236	0.091398	0.444507	1.000
673	GOBP-REGULATION-OF-BINDING	11	-0.413449	-1.350367	0.128405	0.447349	1.000
674	GOBP-TRANSMEMBRANE-RECEPTOR-PROTEIN-SERINE.THR...	6	-0.516218	-1.352945	0.109325	0.451276	1.000
675	GOBP-MUSCLE-STRUCTURE-DEVELOPMENT	16	-0.361520	-1.363159	0.105932	0.441367	1.000
676	GOBP-NEGATIVE-REGULATION-OF-BIOSYNTHETIC-PROCESS	13	-0.394169	-1.382312	0.072340	0.416233	1.000
677	GOBP-NEGATIVE-REGULATION-OF-BINDING	6	-0.544758	-1.383101	0.111111	0.423661	1.000
678	GOBP-RESPONSE-TO-OXIDATIVE-STRESS	8	-0.489727	-1.386331	0.126582	0.427093	1.000
679	GOBP-POSITIVE-REGULATION-OF-CELL-DIFFERENTIATION	27	-0.315492	-1.389635	0.070270	0.430220	1.000
680	GOBP-NEGATIVE-REGULATION-OF-NUCLEOBASE-CONTAIN...	13	-0.404594	-1.398318	0.083333	0.423333	1.000
681	REACTOME-SIGNALING-BY-RECEPTOR-TYROSINE-KINASES	26	-0.320548	-1.405331	0.057292	0.420120	1.000
682	GOBP-CELL-POPULATION-PROLIFERATION	32	-0.296713	-1.405551	0.052632	0.429693	1.000
683	GOBP-REGULATION-OF-LEUKOCYTE-DIFFERENTIATION	9	-0.465637	-1.435693	0.058419	0.385548	1.000
684	GOBP-RESPONSE-TO-REACTIVE-OXYGEN-SPECIES	8	-0.489727	-1.443211	0.078550	0.382528	1.000
685	REACTOME-TRANSCRIPTIONAL-REGULATION-OF_WHITE.A...	6	-0.550593	-1.447679	0.087379	0.384890	1.000

Continuation of Table S4

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
686 GOBP-RESPONSE-TO-DRUG	GO-0042493	11	-0.441015	-1.449566	0.090909	0.391519	1.000
687 REACTOME-CELLULAR-SENESCENCE	R-RNO-2559583	6	-0.569835	-1.453079	0.092879	0.395006	1.000
688 REACTOME-SIGNALING-BY-NTRKS	R-RNO-166520	18	-0.375880	-1.453213	0.090129	0.405507	1.000
689 REACTOME-SENESCENCE-ASSOCIATED-SECRETORY-PHENO...	R-RNO-2559582	6	-0.569835	-1.457702	0.098765	0.408737	1.000
690 GOBP-IMMUNE-RESPONSE-REGULATING-SIGNALING-PATHWAY	GO-0002764	8	-0.514187	-1.458344	0.100000	0.419044	1.000
691 GOBP-REGULATION-OF-CELL-CYCLE	GO-0051726	13	-0.410605	-1.475922	0.058577	0.399975	1.000
692 GOBP-RESPONSE-TO-MONOSACCHARIDE	GO-0034284	5	-0.620622	-1.485674	0.073016	0.394405	1.000
693 GOBP-INTRACELLULAR-RECEPTOR-SIGNALING-PATHWAY	GO-0030522	5	-0.621166	-1.493768	0.066852	0.392506	1.000
694 GOBP-FC-RECEPTOR-SIGNALING-PATHWAY	GO-0038093	8	-0.514187	-1.493961	0.025078	0.404713	1.000
695 GOBP-MUSCLE-ORGAN-DEVELOPMENT	GO-0007517	9	-0.489522	-1.494685	0.073801	0.417114	1.000
696 GOBP-RESPONSE-TO-CARBOHYDRATE	GO-0009743	5	-0.620622	-1.495151	0.058140	0.430526	1.000
697 GOBP-REGULATION-OF-HEMOPOIESIS	GO-1903706	10	-0.459472	-1.500683	0.069536	0.435305	1.000
698 GOBP-MUSCLE-TISSUE-DEVELOPMENT	GO-0060537	11	-0.462851	-1.504660	0.040293	0.443553	1.000
699 REACTOME-INTERLEUKIN-4-AND-INTERLEUKIN-13-SIGN...	R-RNO-6785807	8	-0.522996	-1.522088	0.055172	0.425226	1.000
700 GOBP-RESPONSE-TO-NUTRIENT	GO-0007584	5	-0.631836	-1.545407	0.074850	0.396988	1.000
701 GOBP-APOPTOTIC-SIGNALING-PATHWAY	GO-0097190	15	-0.422598	-1.571189	0.035433	0.369499	1.000
702 GOBP-MYELOID-CELL-DIFFERENTIATION	GO-0030099	13	-0.436857	-1.576361	0.037190	0.376092	1.000
703 GOBP-DEVELOPMENTAL-CELL-GROWTH	GO-0048588	5	-0.663419	-1.590167	0.062130	0.369014	1.000
704 GOBP-NEGATIVE-REGULATION-OF-CELL-CYCLE	GO-0045786	5	-0.676551	-1.602648	0.050595	0.365528	1.000
705 GOBP-SKELETAL-MUSCLE-ORGAN-DEVELOPMENT	GO-0060538	5	-0.674408	-1.640210	0.043732	0.321373	0.999
706 GOBP-RESPONSE-TO-ENDOGENOUS-STIMULUS	GO-0009719	34	-0.365070	-1.694751	0.005650	0.259520	0.996
707 GOBP-PEPTIDYL-LYSINE-MODIFICATION	GO-0018205	5	-0.711289	-1.709858	0.022152	0.255432	0.994
708 GOBP-SKIN-DEVELOPMENT	GO-0043588	5	-0.734940	-1.711968	0.040816	0.267747	0.993
709 GOBP-POSITIVE-REGULATION-OF-NEURON-DEATH	GO-1901216	5	-0.733208	-1.733205	0.019417	0.250635	0.985
710 HALLMARK-HYPOXIA	M5891	5	-0.748829	-1.780366	0.012158	0.209527	0.967
711 GOBP-NEGATIVE-REGULATION-OF-CELL-POPULATION-PR...	GO-0008285	9	-0.589598	-1.819714	0.009836	0.178189	0.937
712 REACTOME-NUCLEAR-EVENTS-KINASE-AND-TRANSCRIPTI...	R-RNO-198725	11	-0.558108	-1.851278	0.006873	0.157446	0.896
713 GOBP-NEGATIVE-REGULATION-OF-TRANSCRIPTION-BY-R...	GO-0000122	10	-0.556441	-1.857109	0.007407	0.164463	0.893
714 GOBP-LEUKOCYTE-DIFFERENTIATION	GO-0002521	15	-0.512902	-1.880018	0.004310	0.154865	0.848
715 GOBP-POSITIVE-REGULATION-OF-NUCLEOBASE-CONTAIN...	GO-0045935	28	-0.432931	-1.977779	0.000000	0.082897	0.595
716 REACTOME-NGF-STIMULATED-TRANSCRIPTION	R-RNO-9031628	9	-0.661777	-2.011560	0.014235	0.069736	0.493
717 GOBP-IMMUNE-SYSTEM-DEVELOPMENT	GO-0002520	17	-0.504553	-2.013322	0.000000	0.077424	0.489
718 HALLMARK-APOPTOSIS	M5902	6	-0.792848	-2.064126	0.003185	0.057833	0.346
719 GOBP-POSITIVE-REGULATION-OF-BIOSYNTHETIC-PROCESS	GO-0009891	27	-0.472440	-2.094931	0.000000	0.052790	0.282
720 GOBP-MONONUCLEAR-CELL-DIFFERENTIATION	GO-1903131	7	-0.801532	-2.108012	0.003155	0.057605	0.261
721 GOBP-POSITIVE-REGULATION-OF-TRANSCRIPTION-BY-R...	GO-0045944	24	-0.516244	-2.263185	0.000000	0.013703	0.056
722 GOBP-POSITIVE-REGULATION-OF-PRIMRNA-TRANSCRI...	GO-1902895	7	-0.805455	-2.266591	0.000000	0.017004	0.052
723 GOBP-PRIMRNA-TRANSCRIPTION-BY-RNA-POLYMERASE-II	GO-0061614	7	-0.805455	-2.273288	0.000000	0.022732	0.046
724 HALLMARK-TNFA-SIGNALING-VIA-NFKB	M5890	14	-0.760351	-2.751684	0.000000	0.000000	0.000

End of Table

Supplementary Table S5: SC caudal segment early (1 DPL peak) profile GSEA results.

Begin of Table S5									
	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val	
0	REACTOME_INTERLEUKIN_4_AND_INTERLEUKIN_13_SIGN...	R-RNO-6785807	8	0.900000	2.823968	0.000000	0.000000	0.00000	0.000
1	REACTOME_SIGNALING_BY_INTERLEUKINS	R-RNO-449147	15	0.571289	2.286192	0.003788	0.090280	0.090280	0.118
2	GOBP_CYTOKINE_MEDIATED_SIGNALING_PATHWAY	GO:0019221	16	0.555290	2.273639	0.000000	0.066719	0.066719	0.129
3	GOBP_NEGATIVE_REGULATION_OF_PEPTIDASE_ACTIVITY	GO:0010466	6	0.816037	2.221286	0.000000	0.073200	0.073200	0.185
4	REACTOME_TRANSCRIPTIONAL_REGULATION_OF_WHITE_A...	R-RNO-381340	6	0.764970	2.095562	0.006211	0.152611	0.152611	0.419
5	GOBP_CELLULAR_RESPONSE_TO_EXTERNAL_STIMULUS	GO:0071496	10	0.593990	2.048613	0.000000	0.177395	0.177395	0.537
6	GOBP_NEGATIVE_REGULATION_OF_CELL_POPULATION_PR...	GO:0008285	9	0.620253	2.026670	0.003247	0.176840	0.176840	0.595
7	GOBP_ACTIN_FILAMENT_BASED_PROCESS	GO:0030029	7	0.675066	1.991510	0.005900	0.193944	0.193944	0.679
8	GOBP_NEGATIVE_REGULATION_OF_CYSSTEINE_TYPE_ENDO...	GO:2000117	5	0.789750	1.990752	0.005362	0.173334	0.173334	0.682
9	GOBP_NEGATIVE_REGULATION_OF_LOCOMOTION	GO:0040013	5	0.723951	1.874701	0.008197	0.298478	0.298478	0.877
10	REACTOME_DEATH_RECEPTOR_SIGNALING	R-RNO-73887	5	0.739534	1.873302	0.005479	0.274196	0.274196	0.880
11	GOBP_NEGATIVE_REGULATION_OF_PROTEOLYSIS	GO:0045861	8	0.612182	1.856347	0.006579	0.276496	0.276496	0.906
12	GOBP_RESPONSE_TO_UV	GO:0009411	5	0.727498	1.797517	0.022989	0.348180	0.348180	0.961
13	GOBP_MYELOID_CELL_DIFFERENTIATION	GO:0030099	13	0.475357	1.794794	0.015385	0.328435	0.328435	0.964
14	GOBP_RESPONSE_TO_CYTOKINE	GO:0030497	23	0.392093	1.771658	0.008230	0.344624	0.344624	0.978
15	GOBP_RESPONSE_TO_REACTIVE_OXYGEN_SPECIES	GO:000302	8	0.550213	1.762561	0.018519	0.340836	0.340836	0.982
16	GOBP_RESPONSE_TO_OXIDATIVE_STRESS	GO:0006979	8	0.550213	1.754301	0.018750	0.335511	0.335511	0.984
17	REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM	R-RNO-1280215	21	0.391720	1.739955	0.008403	0.341276	0.341276	0.991
18	GOBP_REGULATION_OF_APOPTOTIC_SIGNALING_PATHWAY	GO:2001233	10	0.500000	1.708110	0.019355	0.381782	0.381782	0.996
19	GOBP_SKIN_DEVELOPMENT	GO:0043588	5	0.686747	1.705049	0.025352	0.367950	0.367950	0.997
20	HALLMARK_ALLOGRAFT_REJECTION	M5950	7	0.566357	1.680803	0.030960	0.396453	0.396453	0.999
21	GOBP_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	GO:0097193	5	0.674699	1.648582	0.033846	0.445877	0.445877	0.999
22	GOBP_APOPTOTIC_SIGNALING_PATHWAY	GO:0097190	15	0.403995	1.641462	0.028455	0.441697	0.441697	0.999
23	GOBP_CELLULAR_RESPONSE_TO_EXTRACELLULAR_STIMULUS	GO:0031668	8	0.526805	1.628601	0.035714	0.450763	0.450763	0.999
24	GOBP_OSSIFICATION	GO:0001503	9	0.482868	1.605176	0.047170	0.484874	0.484874	0.999
25	GOBP_RESPONSE_TO_EXTRACELLULAR_STIMULUS	GO:0009991	13	0.418596	1.598865	0.036232	0.480784	0.480784	0.999
26	HALLMARK_TNFA_SIGNALING_VIA_NFKB	M5890	14	0.413644	1.595161	0.029091	0.471631	0.471631	0.999
27	GOBP_POSITIVE_REGULATION_OF_PRL_MIRNA_TRANSCRI...	GO:1902895	7	0.530135	1.593852	0.043605	0.456894	0.456894	0.999
28	GOBP_MYELOID_LEUKOCYTE_DIFFERENTIATION	GO:0002573	11	0.435931	1.570542	0.058824	0.493213	0.493213	1.000
29	GOBP_RESPONSE_TO_NUTRIENT	GO:0007584	5	0.612976	1.557176	0.060694	0.507076	0.507076	1.000
30	GOBP_NEGATIVE_REGULATION_OF_MOLECULAR_FUNCTION	GO:0044092	24	0.343750	1.554876	0.015625	0.496320	0.496320	1.000
31	GOBP_PRL_MIRNA_TRANSCRIPTION_BY_RNA_POLYMERASE_II	GO:0061614	7	0.530135	1.546847	0.061350	0.498314	0.498314	1.000
32	GOBP_MULTICELLULAR_ORGANISM_PROCESS	GO:0044706	8	0.487356	1.534747	0.055556	0.512907	0.512907	1.000
33	GOBP_IMMUNE_SYSTEM_DEVELOPMENT	GO:0002520	17	0.355993	1.527235	0.055118	0.515177	0.515177	1.000
34	GOBP_POSITIVE_REGULATION_OF_APOPTOTIC_SIGNALIN...	GO:2001235	5	0.602410	1.505491	0.058011	0.551057	0.551057	1.000
35	GOBP_EMBRYONIC_ORGAN_DEVELOPMENT	GO:0048568	7	0.504034	1.501317	0.063063	0.545638	0.545638	1.000
36	GOBP_NEGATIVE_REGULATION_OF_TRANSMEMBRANE_TRAN...	GO:0034763	6	0.536585	1.498759	0.076923	0.536515	0.536515	1.000
37	GOBP_MORPHOGENESIS_OF_AN_EPITHELIUM	GO:0002009	6	0.530992	1.492660	0.062500	0.536384	0.536384	1.000
38	GOBP_POSITIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL...	GO:0003661	5	0.592994	1.488849	0.083102	0.531884	0.531884	1.000
39	GOBP_OSTEOCLAST_DIFFERENTIATION	GO:0030316	6	0.549064	1.484741	0.071207	0.529290	0.529290	1.000
40	GOBP_INFLAMMATORY_RESPONSE	GO:0006954	12	0.411237	1.479026	0.061151	0.530103	0.530103	1.000

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NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
41	GOBP-NEGATIVE-REGULATION-OF-HYDROLASE-ACTIVITY	GO-0051346	11	0.409301	1.471043	0.047273	0.534891
42	GOBP-CYTOSKELETON-ORGANIZATION	GO-0007010	11	0.409713	1.466986	0.056106	0.532329
43	GOBP-NEGATIVE-REGULATION-OF-APOPTOTIC-SIGNALIN...	GO-2001234	7	0.505028	1.461049	0.087097	0.534633
44	GOBP-OSTEOBLAST-DIFFERENTIATION	GO-0001649	5	0.567340	1.452899	0.090361	0.541441
45	GOBP-RESPONSE-TO-CADMIUM-ION	GO-0046686	6	0.523728	1.451341	0.083601	0.534130
46	GOBP-TISSUE-MORPHOGENESIS	GO-0048729	7	0.495947	1.449420	0.097701	0.526783
47	HALLMARK-HYPOXIA	M5891	5	0.560713	1.430652	0.096210	0.560242
48	GOBP-CELLULAR-RESPONSE-TO-CHEMICAL-STRESS	GO-0062197	7	0.480599	1.424055	0.088889	0.566466
49	HALLMARK-APOPTOSIS	M5902	6	0.516166	1.407320	0.078947	0.595930
50	GOBP-NEGATIVE-REGULATION-OF-PHOSPHORUS-METABOL...	GO-0010563	9	0.417722	1.405140	0.114187	0.590142
51	GOBP-CELLULAR-RESPONSE-TO-REACTIVE-OXYGEN-SPECIES	GO-0034614	7	0.480599	1.403380	0.113043	0.583102
52	GOBP-EXTRINSIC-APOPTOTIC-SIGNALING-PATHWAY	GO-0097191	7	0.481481	1.400552	0.103152	0.579550
53	GOBP-POSITIVE-REGULATION-OF-AXONOGENESIS	GO-0050772	5	0.566265	1.399012	0.128527	0.572659
54	GOBP-REGULATION-OF-PEPTIDASE-ACTIVITY	GO-0052547	10	0.410726	1.391193	0.104377	0.582379
55	GOBP-REGULATION-OF-LIPASE-ACTIVITY	GO-0060191	6	0.500000	1.389767	0.109145	0.575741
56	GOBP-CELLULAR-RESPONSE-TO-CADMIUM-ION	GO-0071276	5	0.545887	1.387220	0.123711	0.570731
57	GOBP-SMOOTH-MUSCLE-CELL-PROLIFERATION	GO-0048659	6	0.491024	1.378732	0.112903	0.581253
58	GOBP-NEUROTROPHIN-SIGNALING-PATHWAY	GO-0038179	6	0.500000	1.369896	0.097561	0.592883
59	GOBP-NEUROTROPHIN-TRK-RECEPTOR-SIGNALING-PATHWAY	GO-0048011	6	0.500000	1.367410	0.114114	0.588689
60	GOBP-NEGATIVE-REGULATION-OF-PROTEIN-METABOLIC-...	GO-0051248	20	0.299452	1.356166	0.111111	0.610093
61	GOBP-REGULATION-OF-GTPASE-ACTIVITY	GO-0043087	5	0.530120	1.355659	0.109290	0.601652
62	GOBP-LEUKOCYTE-DIFFERENTIATION	GO-0002521	15	0.344040	1.354841	0.100000	0.594512
63	GOBP-MUSCLE-CELL-PROLIFERATION	GO-0033002	8	0.448356	1.349043	0.129412	0.598568
64	GOBP-REGULATION-OF-PROTEIN-BINDING	GO-0043393	7	0.453202	1.345939	0.123123	0.597514
65	GOBP-NEGATIVE-REGULATION-OF-TRANSCRIPTION-BY-R...	GO-000122	10	0.392040	1.340041	0.128028	0.601577
66	GOBP-REGULATION-OF-PHOSPHOLIPASE-ACTIVITY	GO-0010517	6	0.500000	1.330905	0.162500	0.614208
67	GOBP-MEMBRANE-PROTEIN-PROTEOLYSIS	GO-0033619	6	0.471322	1.325873	0.128743	0.617713
68	GOBP-REGULATION-OF-EXTRINSIC-APOPTOTIC-SIGNALI...	GO-2001236	6	0.475610	1.325399	0.142424	0.610106
69	GOBP-MONOSACCHARIDE-METABOLIC-PROCESS	GO-0005996	6	0.475610	1.317874	0.137026	0.620150
70	GOBP-PROTEOLYSIS	GO-0006508	17	0.318077	1.316853	0.127273	0.613628
71	GOBP-POSITIVE-REGULATION-OF-PEPTIDYL-SERINE-PH...	GO-0033138	8	0.425000	1.316799	0.136519	0.605202
72	GOBP-REGULATION-OF-PEPTIDYL-SERINE-PHOSPHORYLA...	GO-0033135	8	0.425000	1.313251	0.155172	0.605491
73	GOBP-GLUCOSE-METABOLIC-PROCESS	GO-0006006	6	0.475610	1.306552	0.144809	0.613936
74	GOBP-NEGATIVE-REGULATION-OF-CATALYTIC-ACTIVITY	GO-0043086	17	0.317780	1.301923	0.113281	0.616830
75	GOBP-REGULATION-OF-CELL-SIZE	GO-0008361	5	0.502893	1.300239	0.158470	0.613308
76	GOBP-CARBOHYDRATE-METABOLIC-PROCESS	GO-0005975	9	0.392405	1.292990	0.166667	0.625012
77	GOBP-PROTEIN-KINASE-B-SIGNALING	GO-0043491	6	0.475610	1.292642	0.173780	0.617938
78	GOBP-REGULATION-OF-BINDING	GO-0051098	11	0.356158	1.285623	0.134100	0.626709
79	GOBP-POSITIVE-REGULATION-OF-CELL-DIFFERENTIATION	GO-0045597	27	0.261939	1.278710	0.147982	0.634482
80	GOBP-REGULATION-OF-NEURON-DIFFERENTIATION	GO-0045664	5	0.493976	1.272196	0.171254	0.642338
81	GOBP-RESPONSE-TO-MECHANICAL-STIMULUS	GO-0009612	6	0.460386	1.267286	0.214057	0.646325
82	GOBP-REGULATION-OF-PHOSPHOLIPASE-C-ACTIVITY	GO-1900274	5	0.493976	1.266700	0.170520	0.639971
83	GOBP-EPIDERMIS-DEVELOPMENT	GO-0008544	5	0.493976	1.263688	0.161290	0.640731

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NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
84	GOBP-REGULATION-OF-FAT-CELL-DIFFERENTIATION	6	0.457851	1.257120	0.152047	0.649315	1.000
85	GOBP-IMMUNE-RESPONSE-REGULATING-SIGNALING-PATHWAY	8	0.396416	1.251042	0.195286	0.657148	1.000
86	GOBP-POSITIVE-REGULATION-OF-BIOSYNTHETIC-PROCESS	27	0.257470	1.239395	0.187500	0.678835	1.000
87	GOBP-REGULATION-OF-CELL-DIFFERENTIATION	36	0.241848	1.228878	0.195556	0.696463	1.000
88	GOBP-REGULATION-OF-EPITHELIAL-CELL-MIGRATION	6	0.436126	1.224879	0.207207	0.699072	1.000
89	GOBP-REGULATION-OF-CARBOHYDRATE-METABOLIC-PROCESS	5	0.469880	1.220266	0.188679	0.703539	1.000
90	GOBP-REGULATION-OF-ANION-TRANSMEMBRANE-TRANSPORT	5	0.469880	1.219432	0.229692	0.698241	1.000
91	GOBP-POSITIVE-REGULATION-OF-LIPASE-ACTIVITY	5	0.396416	1.211555	0.204204	0.703439	1.000
92	GOBP-FC-RECEPTOR-SIGNALING-PATHWAY	5	0.493976	1.211555	0.220056	0.703966	1.000
93	GOBP-REGULATION-OF-IMMUNE-RESPONSE	12	0.337391	1.209553	0.194030	0.701548	1.000
94	GOBP-REGULATION-OF-VASCULAR-ASSOCIATED-SMOOTH...	5	0.469880	1.204525	0.218329	0.708345	1.000
95	GOBP-CARBOHYDRATE-BIOSYNTHETIC-PROCESS	5	0.469880	1.201346	0.223242	0.709644	1.000
96	GOBP-MAINTENANCE-OF-LOCATION	7	0.419753	1.199787	0.222561	0.706569	1.000
97	GOBP-NEGATIVE-REGULATION-OF-INTRACELLULAR-SIGN...	7	0.407407	1.197808	0.206061	0.704423	1.000
98	GOBP-POSITIVE-REGULATION-OF-DEVELOPMENTAL-GROWTH	8	0.382299	1.194797	0.211480	0.704186	1.000
99	GOBP-POSITIVE-REGULATION-OF-TRANSCRIPTION-BY-R...	24	0.249141	1.191710	0.235808	0.704965	1.000
100	GOBP-DEVELOPMENTAL-CELL-GROWTH	5	0.469880	1.190766	0.229851	0.700547	1.000
101	GOBP-RAS-PROTEIN-SIGNAL-TRANSDUCTION	5	0.469880	1.186071	0.256614	0.705562	1.000
102	GOBP-REGULATION-OF-CARBOHYDRATE-BIOSYNTHETIC-P...	5	0.469880	1.182099	0.241176	0.710046	1.000
103	GOBP-NEGATIVE-REGULATION-OF-PHOSPHORYLATION	7	0.407407	1.178586	0.253049	0.712188	1.000
104	GOBP-RESPONSE-TO-ORGANIC-CYCLOC-COMPOUND	20	0.265083	1.172416	0.232143	0.722585	1.000
105	GOBP-POSITIVE-REGULATION-OF-PHOSPHATIDYLINOSIT...	5	0.469880	1.170439	0.245810	0.721199	1.000
106	GOBP-POSITIVE-REGULATION-OF-NUCLEOBASE-CONTAIN...	28	0.233193	1.167646	0.235577	0.721509	1.000
107	GOBP-CELLULAR-RESPONSE-TO-ABIOTIC-STIMULUS	7	0.411025	1.165801	0.246334	0.719263	1.000
108	GOBP-POSITIVE-REGULATION-OF-IMMUNE-RESPONSE	9	0.357136	1.164353	0.239057	0.716059	1.000
109	GOBP-NEGATIVE-REGULATION-OF-DEVELOPMENTAL-PROCESS	13	0.306667	1.164231	0.242424	0.709890	1.000
110	GOBP-REGULATION-OF-OSTEOCLAST-DIFFERENTIATION	5	0.458364	1.158893	0.271084	0.716530	1.000
111	GOBP-IMPORT-INTO-CELL	6	0.414634	1.156733	0.251429	0.715842	1.000
112	GOBP-REGULATION-OF-PROTEOLYSIS	12	0.330956	1.154072	0.251634	0.716379	1.000
113	GOBP-REGULATION-OF-CELLULAR-COMPONENT-SIZE	7	0.388229	1.151861	0.295385	0.715934	1.000
114	GOBP-NEGATIVE-REGULATION-OF-RESPONSE-TO-EXTERN...	5	0.469880	1.150375	0.306630	0.713777	1.000
115	GOBP-POSITIVE-REGULATION-OF-DEVELOPMENTAL-PROCESS	32	0.222729	1.143297	0.226601	0.726102	1.000
116	GOBP-NEGATIVE-REGULATION-OF-CELL-DIFFERENTIATION	13	0.306667	1.126890	0.292857	0.763295	1.000
117	REACTOME-SENESCENCE-ASSOCIATED-SECRETORY-PHENO...	6	0.405944	1.125761	0.283582	0.759810	1.000
118	GOBP-RESPONSE-TO-ENDOGENOUS-STIMULUS	34	0.224328	1.125598	0.298507	0.753967	1.000
119	GOBP-CELLULAR-COMPONENT-DISASSEMBLY	6	0.417599	1.125341	0.326347	0.748121	1.000
120	GOBP-EMBRYO-DEVELOPMENT	14	0.294001	1.122695	0.300000	0.749103	1.000
121	REACTOME-CELLULAR-SENESCENCE	6	0.405944	1.109476	0.320475	0.777557	1.000
122	REACTOME-ESR-MEDIATED-SIGNALING	8	0.352913	1.107232	0.276873	0.777310	1.000
123	GOBP-CELL-CELL-JUNCTION-ASSEMBLY	5	0.443995	1.106311	0.319149	0.773251	1.000
124	GOBP-POSITIVE-REGULATION-OF_MULTICELLULAR_ORGA...	32	0.214286	1.099257	0.349057	0.785209	1.000
125	GOBP-PHAGOCYTOSIS	5	0.434803	1.095823	0.310541	0.787844	1.000
126	GOBP-POSITIVE-REGULATION-OF_BINDING	6	0.402439	1.085716	0.355685	0.808114	1.000

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NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
127	GOBP-REGULATION-OF-DEVELOPMENTAL-GROWTH	9	0.328853	1.084204	0.329114	0.806226	1.000
128	GOBP-CELLULAR-RESPONSE-TO-ORGANIC-CYCLOC-COMPOUND	13	0.282516	1.082350	0.366667	0.804528	1.000
129	GOBP-REGULATION-OF-INFLAMMATORY-RESPONSE	7	0.366960	1.080222	0.334375	0.803819	1.000
130	GOBP-NEGATIVE-REGULATION-OF-LIPID-METABOLIC-PR...	5	0.428219	1.070865	0.352273	0.823432	1.000
131	GOBP-REGULATION-OF-DEFENSE-RESPONSE	7	0.366960	1.070584	0.359621	0.817805	1.000
132	GOBP-REGULATION-OF-CYSTEINE-TYPE-ENDOPEPTIDASE...	9	0.327677	1.070419	0.373737	0.812002	1.000
133	GOBP-ACTIVATION-OF-IMMUNE-RESPONSE	5	0.422002	1.069992	0.337176	0.806952	1.000
134	GOBP-POSITIVE-REGULATION-OF-ORGANELLE-ORGANIZA...	10	0.320296	1.068884	0.393333	0.803905	1.000
135	REACTOME-SIGNALING-BY-NUCLEAR-RECEPTORS	8	0.352913	1.064179	0.345196	0.809842	1.000
136	REACTOME-ADAPTIVE-IMMUNE-SYSTEM	9	0.329114	1.063166	0.363636	0.806794	1.000
137	GOBP-REGULATION-OF-DNA-BINDING-TRANSCRIPTION-F...	16	0.264118	1.060510	0.376923	0.808698	1.000
138	GOBP-REGULATION-OF-LIPID-LOCALIZATION	5	0.416976	1.056801	0.357143	0.812501	1.000
139	REACTOME-EXTRA-NUCLEAR-ESTROGEN-SIGNALING	7	0.351146	1.042955	0.387302	0.843996	1.000
140	GOBP-NEGATIVE-REGULATION-OF-CELL-DEATH	22	0.227819	1.036211	0.385965	0.855551	1.000
141	GOBP-REGULATION-OF-CELLULAR-AMIDE-METABOLIC-PR...	9	0.305619	1.010975	0.387960	0.917540	1.000
142	GOBP-NEGATIVE-REGULATION-OF-KINASE-ACTIVITY	5	0.397590	1.010869	0.421687	0.911566	1.000
143	GOBP-NEGATIVE-REGULATION-OF-BINDING	6	0.370341	1.010733	0.440341	0.905626	1.000
144	GOBP-ANATOMICAL-STRUCTURE-FORMATION-INVOLVED-I...	20	0.223707	1.009728	0.406250	0.901989	1.000
145	GOBP-POSITIVE-REGULATION-OF-CELL-GROWTH	6	0.365675	1.007472	0.407625	0.902265	1.000
146	GOBP-NEGATIVE-REGULATION-OF-TRANSFERASE-ACTIVITY	5	0.397590	1.007256	0.422222	0.896887	1.000
147	GOBP-MUSCLE-CONTRACTION	5	0.409639	1.007237	0.404070	0.890948	1.000
148	GOBP-CELL-JUNCTION-ASSEMBLY	8	0.327933	1.004022	0.411371	0.893360	1.000
149	GOBP-POSITIVE-REGULATION-OF-SMALL-MOLECULE-MET...	5	0.409639	1.000059	0.422840	0.898774	1.000
150	GOBP-GLAND-DEVELOPMENT	7	0.342857	0.996080	0.450311	0.902788	1.000
151	GOBP-RESPONSE-TO-HORMONE	20	0.221500	0.993601	0.440000	0.904089	1.000
152	GOBP-REGULATION-OF-PROTEIN-CATABOLIC-PROCESS	7	0.334790	0.989675	0.456395	0.908979	1.000
153	HALLMARK-UV-RESPONSE-UP	5	0.386524	0.989075	0.447222	0.904569	1.000
154	GOBP-POSITIVE-REGULATION-OF-MYELOID-LEUKOCYTE-...	6	0.359850	0.981348	0.433048	0.919333	1.000
155	HALLMARK-KRAS-SIGNALING-UP	6	0.357785	0.980052	0.433243	0.916812	1.000
156	GOBP-REPRODUCTIVE-SYSTEM-DEVELOPMENT	15	0.254098	0.978217	0.495968	0.910075	1.000
157	GOBP-EPITHELIAL-DEVELOPMENT	7	0.331437	0.978092	0.464968	0.904734	1.000
158	GOBP-CELLULAR-RESPONSE-TO-OXYGEN-CONTAINING-CO...	29	0.203915	0.977922	0.482143	0.899679	1.000
160	GOBP-POSITIVE-REGULATION-OF-CELLULAR-COMPONENT...	9	0.303320	0.972882	0.490506	0.907061	1.000
161	GOBP-APOPTOTIC-MITOCHONDRIAL-CHANGES	6	0.353659	0.971863	0.463014	0.904296	1.000
162	GOBP-CELLULAR-CARBOHYDRATE-METABOLIC-PROCESS	5	0.374494	0.965481	0.487730	0.916117	1.000
163	GOBP-CELL-POPULATION-PROLIFERATION	32	0.194601	0.957612	0.511521	0.930712	1.000
164	GOBP-REGULATION-OF-MYELOID-CELL-DIFFERENTIATION	9	0.301445	0.956828	0.469055	0.927085	1.000
165	GOBP-REGULATION-OF-MYELOID-LEUKOCYTE-DIFFERENT...	8	0.313217	0.948939	0.518634	0.942771	1.000
166	GOBP-PROTEIN-CATABOLIC-PROCESS	8	0.312081	0.946981	0.520376	0.942308	1.000
167	GOBP-PROTEIN-LOCALIZATION-TO-PLASMA-MEMBRANE	7	0.319858	0.945721	0.505952	0.940621	1.000
168	GOBP-POLYSACCHARIDE-METABOLIC-PROCESS	5	0.373494	0.943741	0.495441	0.940204	1.000
169	GOBP-POSITIVE-REGULATION-OF-CELL-DEATH	19	0.218035	0.941406	0.508130	0.940476	1.000

Continuation of Table S5

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
170	GOBP-INOSITOL-LIPID-MEDIATED-SIGNALING	8	0.298970	0.939988	0.516820	0.938858	1.000
171	GOBP-POSITIVE-REGULATION-OF-GROWTH	9	0.294208	0.937856	0.530945	0.938532	1.000
172	GOBP-POSITIVE-REGULATION-OF-DEFENSE-RESPONSE	5	0.372859	0.933018	0.533333	0.945280	1.000
173	GOBP-LEUKOCYTE-MIGRATION	6	0.338581	0.932096	0.503030	0.941748	1.000
174	GOBP-POSITIVE-REGULATION-OF-TRANSMEMBRANE-TRAN...	7	0.308642	0.927854	0.516820	0.946815	1.000
175	GOBP-NEGATIVE-REGULATION-OF-ION-TRANSPORT	11	0.259740	0.924335	0.527778	0.950346	1.000
176	GOBP-FAT-CELL-DIFFERENTIATION	9	0.277650	0.921036	0.576433	0.953188	1.000
177	GOBP-REGULATION-OF-PROTEIN-LOCALIZATION-TO-CEL...	6	0.336702	0.920154	0.533537	0.949859	1.000
178	GOBP-NEGATIVE-REGULATION-OF-MULTICELLULAR-ORGA...	15	0.233143	0.919272	0.574713	0.946497	1.000
179	GOBP-GENERATION-OF-PRECURSOR-METABOLITES-AND-E...	5	0.373494	0.917577	0.578082	0.945694	1.000
180	GOBP-REGULATION-OF-SMALL-MOLECULE-METABOLIC-PR...	9	0.278481	0.917488	0.518033	0.940662	1.000
181	GOBP-POSITIVE-REGULATION-OF-CELL-DEVELOPMENT	12	0.243084	0.910497	0.565056	0.952963	1.000
182	GOBP-DEVELOPMENTAL-GROWTH	10	0.269419	0.909041	0.537367	0.951648	1.000
183	GOBP-RESPONSE-TO-OXYGEN-CONTAINING-COMPOUND	39	0.176114	0.907330	0.634518	0.950838	1.000
184	GOBP-RESPONSE-TO-LIGHT-STIMULUS	11	0.255317	0.907178	0.580071	0.946049	1.000
185	GOBP-INTRACELLULAR-PROTEIN-TRANSPORT	8	0.287500	0.901398	0.580060	0.955180	1.000
186	HALLMARK-EPITHELIAL-MESENCHYMAL-TRANSITION	M5930	5	0.357522	0.901075	0.582656	0.951018
187	REACTOME-NGF-STIMULATED-TRANSCRIPTION	R-RNO-9031628	9	0.275645	0.896944	0.616129	0.949714
188	GOBP-TISSUE-HOMEOSTASIS	5	0.356290	0.897363	0.557185	0.950637	1.000
189	GOBP-POSITIVE-REGULATION-OF-ION-TRANSPORT	17	0.210952	0.894015	0.607930	0.954024	1.000
190	GOBP-REGULATION-OF-CELL-CYCLE	13	0.241245	0.891463	0.584559	0.954875	1.000
191	GOBP-WOUND-HEALING	13	0.239113	0.891129	0.588679	0.950775	1.000
192	GOBP-ANIMAL-ORGAN-MORPHOGENESIS	12	0.244699	0.890917	0.576779	0.946445	1.000
193	GOBP-POSITIVE-REGULATION-OF-NERVOUS-SYSTEM.DEV...	12	0.243084	0.890763	0.603448	0.941994	1.000
194	GOBP-AGING	13	0.239576	0.888160	0.575290	0.943376	1.000
195	GOBP-POSITIVE-REGULATION-OF-NEUROGENESIS	12	0.243084	0.887733	0.622776	0.939708	1.000
196	REACTOME-ESTROGEN-DEPENDENT-NUCLEAR-EVENTS.DOW...	5	0.352186	0.887601	0.573913	0.935153	1.000
197	GOBP-POSITIVE-REGULATION-OF-ANION-TRANSPORT	9	0.272770	0.886947	0.621212	0.931925	1.000
198	GOBP-POSITIVE-REGULATION-OF-GENE-EXPRESSION	16	0.216239	0.885409	0.593407	0.931099	1.000
199	GOBP-NEGATIVE-REGULATION-OF-IMMUNE-SYSTEM-PROCESS	5	0.350482	0.877843	0.589970	0.943670	1.000
200	GOBP-REGULATION-OF-NERVOUS-SYSTEM-DEVELOPMENT	15	0.219178	0.867559	0.611111	0.963499	1.000
201	GOBP-REGULATION-OF-CELL-DEVELOPMENT	15	0.217715	0.866720	0.666667	0.960601	1.000
202	GOBP-NEGATIVE-REGULATION-OF-CELL-DEVELOPMENT	15	0.219178	0.863752	0.654762	0.962928	1.000
203	GOBP-POSITIVE-REGULATION-OF-CELL-DEVELOPMENT	6	0.317073	0.862027	0.608955	0.962257	1.000
204	GOBP-POSITIVE-REGULATION-OF-CELLULAR-PROTEIN.L...	7	0.283951	0.853302	0.640244	0.976893	1.000
205	GOBP-DEFENSE-RESPONSE	19	0.194489	0.851084	0.678392	0.976831	1.000
206	GOBP-PATTERN-SPECIFICATION-PROCESS	6	0.304878	0.849903	0.677741	0.974819	1.000
207	GOBP-MULTI-ORGANISM-PROCESS	16	0.208726	0.849902	0.690476	0.970160	1.000
208	GOBP-PERIPHERAL-NERVOUS-SYSTEM-DEVELOPMENT	9	0.260110	0.849528	0.660377	0.966426	1.000
209	REACTOME-INFECTIOUS-DISEASE	12	0.227134	0.842919	0.671378	0.976145	1.000
210	GOBP-POSITIVE-REGULATION-OF-NEURON-DEATH	5	0.335224	0.838113	0.634921	0.982171	1.000
211	GOBP-REGIONALIZATION	6	0.304878	0.837841	0.643750	0.978282	1.000
212	GOBP-PROTEIN-MODIFICATION-BY-SMALL-PROTEIN.CON...	7	0.275118	0.835961	0.658892	0.977817	1.000

Continuation of Table S5

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
213 GOBP-PHOSPHATIDYLINOSITOL_3_KINASE-SIGNALING	GO-0014065	7	0.283951	0.835399	0.625369	0.974362	1.000
214 GOBP-NEGATIVE-REGULATION-OF-CATABOLIC-PROCESS	GO-0009895	8	0.273310	0.834456	0.714715	0.972301	1.000
215 GOBP-REGULATION-OF-ANATOMICAL-STRUCTURE-SIZE	GO-0090066	10	0.244660	0.833528	0.676768	0.969872	1.000
216 GOBP-CHROMATIN-ORGANIZATION	GO-0006325	5	0.331573	0.831907	0.654054	0.968753	1.000
217 REACTOME_FC-EPSILON-RECEPTOR_FCERL-SIGNALING	R-RNO-2454202	7	0.283951	0.827759	0.682779	0.968704	1.000
218 GOBP_FC-EPSILON-RECEPTOR-SIGNALING-PATHWAY	GO-0038095	7	0.283951	0.823928	0.706061	0.976878	1.000
219 GOBP-EPHRIN_RECEPTOR-SIGNALING-PATHWAY	GO-0048013	5	0.320222	0.823600	0.659459	0.973131	1.000
220 GOBP-REGULATION-OF-CELLULAR-COMPONENT_BIOGENESIS	GO-0044087	10	0.242218	0.820828	0.687296	0.974718	1.000
221 GOBP-REGULATION-OF-NEUROGENESIS	GO-0050767	14	0.216216	0.820302	0.685121	0.971337	1.000
222 GOBP-NEGATIVE-REGULATION-OF-BIOSYNTHETIC-PROCESS	GO-0009890	13	0.222495	0.819644	0.697318	0.968264	1.000
223 GOBP-NEGATIVE-REGULATION-OF-PROTEIN-MODIFICATION...	GO-0031400	10	0.235815	0.817842	0.693333	0.967258	1.000
224 GOBP-REGULATION-OF-AXONOGENESIS	GO-0050770	7	0.280137	0.817223	0.684848	0.964172	1.000
225 GOBP-REGULATION-OF-HYDROLASE-ACTIVITY	GO-0051336	22	0.181878	0.815166	0.737052	0.964345	1.000
226 GOBP-RESPONSE-TO-WOUNDING	GO-0009611	15	0.196574	0.815110	0.725564	0.960153	1.000
227 GOBP-NEGATIVE-REGULATION-OF-RESPONSE-TO-STIMULUS	GO-0048585	16	0.199906	0.814649	0.710623	0.950822	1.000
228 GOBP-POSITIVE-REGULATION-OF-PEPTIDASE-ACTIVITY	GO-0010952	7	0.267741	0.810088	0.695522	0.961275	1.000
229 GOBP-REGULATION-OF-MULTICELLULAR-ORGANISMAL-DE...	GO-2000026	31	0.161659	0.807526	0.738095	0.962193	1.000
230 HALLMARK_P13K-AKT-MTOR-SIGNALING	M5923	6	0.289532	0.804435	0.696486	0.964217	1.000
231 GOBP-CELLULAR-LIPID-METABOLIC-PROCESS	GO-0044255	7	0.271605	0.797163	0.752443	0.973852	1.000
232 GOBP-NEGATIVE-REGULATION-OF-NEUROUS-SYSTEM-DEV...	GO-0051961	5	0.313253	0.796881	0.692547	0.970271	1.000
233 GOBP-RESPONSE-TO-MOLECULE-OF-BACTERIAL-ORIGIN	GO-0002237	13	0.207770	0.796052	0.749129	0.967679	1.000
234 GOBP-POSITIVE-REGULATION-OF-CELLULAR-COMPONENT...	GO-0051130	24	0.168940	0.795447	0.785088	0.964975	1.000
235 GOBP-RESPONSE-TO-BACTERIUM	GO-0009617	13	0.207770	0.794840	0.796491	0.961974	1.000
236 REACTOME_HEMOSTASIS	R-RNO-109582	14	0.202594	0.793949	0.772908	0.959309	1.000
237 GOBP-CARBOHYDRATE-DERIVATIVE-METABOLIC-PROCESS	GO-1901135	8	0.261345	0.793505	0.736508	0.956158	1.000
238 GOBP-REGULATION-OF-ENDOTHELIAL-CELL-MIGRATION	GO-0010594	5	0.314056	0.791663	0.709677	0.955811	1.000
239 GOBP-ENZYME-LINKED-RECEPTOR-PROTEIN-SIGNALING-...	GO-0007167	24	0.171875	0.788210	0.767857	0.958480	1.000
240 GOBP-ORGANIC-ACID-METABOLIC-PROCESS	GO-0006082	7	0.271605	0.785408	0.723032	0.959606	1.000
241 GOBP-PEPTIDE-BIOSYNTHETIC-PROCESS	GO-0043043	6	0.289471	0.783609	0.716714	0.958802	1.000
242 GOBP-RESPONSE-TO-RADIATION	GO-0009314	13	0.205345	0.783098	0.768683	0.955835	1.000
243 GOBP-MUSCLE-CELL-DEVELOPMENT	GO-0055001	5	0.313253	0.777775	0.729107	0.961726	1.000
244 GOBP-POSITIVE-REGULATION-OF-CYSTEINE-TYPE-ENDO...	GO-2001056	7	0.267741	0.775864	0.783172	0.961099	1.000
245 GOBP-AMIDE-BIOSYNTHETIC-PROCESS	GO-0043604	6	0.289471	0.775495	0.717579	0.957720	1.000
246 GOBP-NEGATIVE-REGULATION-OF-NUCLEOBASE-CONTAIN...	GO-0045934	13	0.204303	0.775257	0.761092	0.954186	1.000
247 GOBP-NEGATIVE-REGULATION-OF-ANION-TRANSPORT	GO-1903792	8	0.250000	0.774839	0.750000	0.951223	1.000
248 GOBP-REPRODUCTION	GO-0000003	18	0.184778	0.770533	0.825203	0.954853	1.000
249 GOBP-EMBRYONIC-MORPHOGENESIS	GO-0048598	6	0.280488	0.764235	0.742690	0.961830	1.000
250 GOBP-LIPID-LOCALIZATION	GO-0010876	10	0.230769	0.760356	0.800725	0.964581	1.000
251 GOBP-NEUROINFLAMMATORY_RESPONSE	GO-0150076	5	0.301644	0.759708	0.760000	0.961775	1.000
252 GOBP-LIPID-BIOSYNTHETIC-PROCESS	GO-0008610	6	0.278771	0.759200	0.787710	0.959081	1.000
253 GOBP-RESPONSE-TO-TUMOR-NECROSIS-FACTOR	GO-0034612	7	0.259052	0.756691	0.800000	0.959142	1.000
254 GOBP-REGULATION-OF-LIPID-BIOSYNTHETIC-PROCESS	GO-0046890	6	0.272642	0.751940	0.760684	0.963120	1.000
255 GOBP-IN-UTERO-EMBRYONIC-DEVELOPMENT	GO-0001701	8	0.246363	0.748104	0.800000	0.965331	1.000

Continuation of Table S5

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
256	GOBP-CELL-GROWTH	10	0.223149	0.747839	0.765151	0.961920	1.000
257	GOBP-INTRACELLULAR-RECEPTOR-SIGNALING-PATHWAY	5	0.294181	0.745583	0.784367	0.961607	1.000
258	GOBP-POSITIVE-REGULATION-OF-PROTEOLYSIS	8	0.243425	0.744545	0.823129	0.959882	1.000
259	GOBP-REGULATION-OF-PHOSPHATIDYLINOSITOL-3-KINA...	6	0.280488	0.743752	0.793313	0.957540	1.000
260	GOBP-MONOCARBOXYLIC-ACID-METABOLIC-PROCESS	6	0.268293	0.739179	0.800000	0.961443	1.000
261	GOBP-NEURON-MIGRATION	5	0.301205	0.738954	0.778393	0.958103	1.000
262	GOBP-POSITIVE-REGULATION-OF-EPITHELIAL-CELL-MI...	5	0.290324	0.736111	0.782967	0.958939	1.000
263	GOBP-REGULATION-OF-GROWTH	13	0.186866	0.731119	0.835125	0.963151	1.000
264	GOBP-RESPONSE-TO-INSULIN	5	0.289157	0.729405	0.788462	0.961919	1.000
265	GOBP-POSITIVE-REGULATION-OF-CELL-POPULATION.PR...	21	0.163806	0.723396	0.81356	0.967522	1.000
266	GOBP-CELLULAR-RESPONSE-TO-BIOTIC-STIMULUS	8	0.225937	0.717785	0.853896	0.971754	1.000
267	GOBP-NERVE-DEVELOPMENT	9	0.215190	0.711452	0.885714	0.976626	1.000
268	GOBP-ORGANONITROGEN-COMPOUND-CATABOLIC-PROCESS	10	0.210715	0.710265	0.856643	0.974580	1.000
269	GOBP-CELLULAR-RESPONSE-TO-STARVATION	5	0.277108	0.704063	0.818444	0.980015	1.000
270	GOBP-CELLULAR-RESPONSE-TO-MOLECULE-OF-BACTERIA...	8	0.225937	0.700387	0.851064	0.981361	1.000
271	GOBP-RESPONSE-TO-STARVATION	5	0.277108	0.697356	0.853731	0.981609	1.000
272	GOBP-PEPTIDE-METABOLIC-PROCESS	11	0.198234	0.697073	0.851711	0.978430	1.000
273	GOBP-RESPONSE-TO-NERVE-GROWTH-FACTOR	7	0.236549	0.696125	0.849398	0.976045	1.000
274	GOBP-MACROMOLECULE-CATABOLIC-PROCESS	11	0.195173	0.694871	0.875912	0.974343	1.000
275	GOBP-REGULATION-OF-ORGAN-GROWTH	5	0.277108	0.694240	0.841945	0.971570	1.000
276	GOBP-ORGAN-GROWTH	5	0.277108	0.692755	0.848315	0.970178	1.000
277	GOBP-POSITIVE-REGULATION-OF-LEUKOCYTE-CELL-CEL...	5	0.269115	0.692685	0.856716	0.966785	1.000
278	GOBP-REGULATION-OF-CYTOSKELETON-ORGANIZATION	5	0.277109	0.685593	0.857143	0.968662	1.000
279	GOBP-ORGANIC-HYDROXY-COMPOUND-METABOLIC-PROCESS	8	0.218368	0.688284	0.854985	0.965549	1.000
280	GOBP-LEUKOCYTE-CELL-CELL-ADHESION	6	0.247227	0.687334	0.870769	0.963218	1.000
281	GOBP-PEPTIDYL-SERINE-MODIFICATION	12	0.184211	0.683352	0.892857	0.964531	1.000
282	GOBP-ANION-TRANSMEMBRANE-TRANSPORT	7	0.234568	0.682120	0.884849	0.962667	1.000
283	GOBP-MATERNAL-PROCESS-INVOLVED-IN-FEMALE-PREGN...	5	0.265060	0.681374	0.859838	0.960348	1.000
284	GOBP-NEGATIVE-REGULATION-OF-NEURON-APOPTOTIC-P...	8	0.212500	0.680021	0.879880	0.958400	1.000
285	REACTOME-SIGNALING-BY-NTRKS	18	0.162836	0.675012	0.917012	0.960637	1.000
286	GOBP-RESPONSE-TO-CALCIUMION	6	0.242185	0.671145	0.900621	0.961645	1.000
287	GOBP-RESPONSE-TO-OXYGEN-LEVELS	8	0.215319	0.669724	0.881789	0.959815	1.000
288	GOBP-REGULATION-OF-PROTEIN-SERINE-THREONINE-KI...	12	0.180421	0.669579	0.885714	0.956583	1.000
289	REACTOME-L1CAM-INTERACTIONS	5	0.265481	0.668440	0.865285	0.954435	1.000
290	GOBP-POSITIVE-REGULATION-OF-CELL-CELL-ADHESION	5	0.269115	0.666356	0.886179	0.953760	1.000
291	GOBP-TRANSMEMBRANE-RECEPTOR-PROTEIN-TYROSINE-K...	19	0.159420	0.666124	0.907258	0.950716	1.000
292	GOBP-ORGANIC-HYDROXY-COMPOUND-TRANSPORT	6	0.240146	0.663121	0.883495	0.950676	1.000
293	GOBP-MITOCHONDRION-ORGANIZATION	7	0.222222	0.661316	0.883436	0.949491	1.000
294	GOBP-BIOLOGICAL-PROCESS-INVOLVED-IN-SYMBIOTIC....	10	0.194383	0.647319	0.919192	0.960717	1.000
295	GOBP-REGULATION-OF-ORGANELLE-ORGANIZATION	14	0.166005	0.645548	0.933566	0.959363	1.000
296	REACTOME-TRANSCRIPTIONAL-REGULATION-BY-TP53	6	0.237742	0.642408	0.921136	0.958962	1.000
297	GOBP-POSITIVE-REGULATION-OF-HYDROLASE-ACTIVITY	16	0.152777	0.633777	0.965780	0.963561	1.000
298	GOBP-SMALL-GTPASE-MEDIATED-SIGNAL-TRANSDUCTION	8	0.200000	0.625020	0.930314	0.967567	1.000

Continuation of Table S5

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
299	GOBP-EMBRYO-DEVELOPMENT-ENDING.IN.BIRTH.OR.EGG...	9	0.191396	0.618590	0.951890	0.969345	1.000
300	GOBP-FATTY-ACID-TRANSPORT	6	0.219512	0.610001	0.949843	0.972896	1.000
301	GOBP-HEART-DEVELOPMENT	6	0.210200	0.604137	0.969040	0.974289	1.000
302	GOBP-GROWTH	14	0.153747	0.598282	0.989437	0.974933	1.000
303	GOBP-REGULATION-OF-MITOTIC-CELL-CYCLE	5	0.234588	0.582728	0.947059	0.980996	1.000
304	GOBP-CELLULAR-AMIDE-METABOLIC-PROCESS	12	0.155332	0.578263	0.982014	0.980063	1.000
305	GOBP-PROTEIN-AUTOPHOSPHORYLATION	5	0.221961	0.570884	0.955182	0.980769	1.000
306	GOBP-CARDIAC-MUSCLE-TISSUE-DEVELOPMENT	6	0.210200	0.569538	0.937500	0.978238	1.000
307	GOBP-CYTOKINE-PRODUCTION	10	0.153846	0.534602	0.990000	0.988565	1.000
308	GOBP-RESPONSE-TO-ACID-CHEMICAL	6	0.189960	0.515294	0.989041	0.990339	1.000
309	GOBP-NEGATIVE-REGULATION-OF-TRANSPORT	13	-0.135637	-0.427250	0.994467	0.996896	1.000
310	GOBP-RESPONSE-TO-KETONE	7	-0.178454	-0.454553	0.994021	0.996023	1.000
311	GOBP-RESPONSE-TO-LIPID	19	-0.134449	-0.464214	0.986505	0.996853	1.000
312	REACTOME-TOLL-LIKE-RECEPTOR-TLR1-TLR2-CASCADE	8	-0.180490	-0.480922	0.989474	0.995826	1.000
313	REACTOME-MYD88-INDEPENDENT-TLR4-CASCADE	8	-0.180490	-0.483036	0.988201	0.997781	1.000
314	REACTOME-TOLL-LIKE-RECEPTOR-CASCADES	8	-0.180490	-0.483477	0.989899	1.000000	1.000
315	REACTOME-TOLL-LIKE-RECEPTOR-9-TLR9-CASCADE	8	-0.180490	-0.483734	0.991241	1.000000	1.000
316	GOBP-POSITIVE-REGULATION-OF-CELL-PROJECTION-OR...	10	-0.177471	-0.502915	0.977974	0.999407	1.000
317	GOBP-POSTTRANSCRIPTIONAL-REGULATION-OF-GENE-EX...	8	-0.187858	-0.507799	0.984127	1.000000	1.000
318	GOBP-REGULATION-OF-MUSCLE-CELL-DIFFERENTIATION	6	-0.211709	-0.512063	0.986466	1.000000	1.000
319	GOBP-POSITIVE-REGULATION-OF-PEPTIDYL-TYROSINE...	8	-0.194058	-0.513289	0.965714	1.000000	1.000
320	GOBP-REGULATION-OF-PROTEIN-STABILITY	5	-0.229634	-0.516532	0.987578	1.000000	1.000
321	GOBP-REGULATION-OF-LYMPHOCYTE-ACTIVATION	5	-0.240510	-0.539624	0.966507	0.997355	1.000
322	GOBP-POSITIVE-REGULATION-OF-ESTABLISHMENT-OF-P...	5	-0.242344	-0.548802	0.970543	0.995105	1.000
323	GOBP-REGULATION-OF-CELL-CELL-ADHESION	9	-0.202706	-0.551777	0.958271	0.997793	1.000
324	GOBP-ACTIVATION-OF-PROTEIN-KINASE-ACTIVITY	11	-0.188793	-0.556301	0.961538	0.998610	1.000
325	GOBP-NEGATIVE-REGULATION-OF-GENE-EXPRESSION	11	-0.190375	-0.561453	0.964865	0.998176	1.000
326	GOBP-MUSCLE-TISSUE-DEVELOPMENT	18	-0.166069	-0.561937	0.949797	1.000000	1.000
327	GOBP-RESPONSE-TO-PEPTIDE	10	-0.201568	-0.565300	0.949852	1.000000	1.000
328	GOBP-LIPID-METABOLIC-PROCESS	12	-0.191124	-0.579049	0.949454	0.997400	1.000
329	GOBP-RESPONSE-TO-METAL-ION	15	-0.172842	-0.568456	0.953947	1.000000	1.000
330	GOBP-REGULATION-OF-CELLULAR-PROTEIN-LOCALIZATION	8	-0.218460	-0.588327	0.943262	0.993426	1.000
331	GOBP-COAGULATION	8	-0.218460	-0.588327	0.943262	0.993426	1.000
332	GOBP-DEVELOPMENTAL-PROCESS-INVOLVED-IN-REPRODU...	11	-0.201896	-0.589013	0.938289	0.995472	1.000
333	GOBP-CELLULAR-RESPONSE-TO-LIPID	15	-0.186212	-0.591105	0.938089	0.996469	1.000
334	GOBP-NEURON-APOPTOTIC-PROCESS	12	-0.195200	-0.593506	0.934752	0.997232	1.000
335	GOBP-NEGATIVE-REGULATION-OF-SIGNALING	21	-0.168633	-0.593890	0.938642	0.999484	1.000
336	GOBP-REGULATION-OF-GLIOGENESIS	5	-0.263896	-0.594080	0.938931	1.000000	1.000
337	GOBP-RESPONSE-TO-GROWTH-FACTOR	18	-0.175529	-0.597909	0.927152	1.000000	1.000
338	GOBP-CELLULAR-RESPONSE-TO-DNA-DAMAGE-STIMULUS	5	-0.262447	-0.598897	0.945652	1.000000	1.000
339	GOBP-NEGATIVE-REGULATION-OF-CELLULAR-COMPONENT...	11	-0.202702	-0.599578	0.922628	1.000000	1.000
340	GOBP-DNA-METABOLIC-PROCESS	6	-0.249659	-0.600673	0.934884	1.000000	1.000
341	GOBP-POSITIVE-REGULATION-OF-GLIOGENESIS	5	-0.263896	-0.602404	0.943164	1.000000	1.000

Continuation of Table S5

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
342	GOBP-ERK1-AND-ERK2-CASCADE	5	-0.271059	-0.603101	0.924471	1.000000	1.000
343	GOBP-POSITIVE-REGULATION-OF-DNA-BINDING-TRANSC...	10	-0.209573	-0.606026	0.928258	1.000000	1.000
344	GOBP-REGULATION-OF-PROTEIN-PHOSPHORYLATION	25	-0.165814	-0.607606	0.916991	1.000000	1.000
345	GOBP-RESPONSE-TO-DRUG	11	-0.208202	-0.614552	0.915954	1.000000	1.000
346	GOBP-REGULATION-OF-PHOSPHORUS-METABOLIC-PROCESS	26	-0.166113	-0.615450	0.921290	1.000000	1.000
347	GOBP-LEARNING	13	-0.198676	-0.616478	0.915160	1.000000	1.000
348	GOBP-ORGANIC-ACID-TRANSPORT	7	-0.241238	-0.619475	0.911544	1.000000	1.000
349	GOBP-ORGANONITROGEN-COMPOUND-BIOSYNTHETIC-PROCESS	13	-0.200773	-0.619753	0.927966	1.000000	1.000
350	GOBP-TRANSMEMBRANE-RECEPTOR-PROTEIN-SERINE-THR...	6	-0.255637	-0.623223	0.910906	1.000000	1.000
351	GOBP-SMALL-MOLECULE-BIOSYNTHETIC-PROCESS	5	-0.273716	-0.625954	0.930269	1.000000	1.000
352	GOBP-REGULATION-OF-TRANSFERASE-ACTIVITY	21	-0.182486	-0.629106	0.919481	1.000000	1.000
353	REACTOME-NUCLEAR-EVENTS-KINASE-AND-TRANSCRIPTI...	11	-0.216813	-0.634729	0.898352	1.000000	1.000
354	GOBP-REGULATION-OF-PEPTIDYL-TYROSINE-PHOSPHORY...	9	-0.226525	-0.635775	0.904286	1.000000	1.000
355	GOBP-REGULATION-OF-PROTEIN-KINASE-ACTIVITY	21	-0.182486	-0.635993	0.909677	1.000000	1.000
356	GOBP-POSITIVE-REGULATION-OF-LOCOMOTION	11	-0.215677	-0.640106	0.895714	1.000000	1.000
357	REACTOME-INTERLEUKIN-17-SIGNALING	6	-0.265749	-0.641903	0.892012	1.000000	1.000
358	GOBP-MUSCLE-STRUCTURE-DEVELOPMENT	16	-0.197464	-0.646219	0.886792	1.000000	1.000
359	GOBP-POSITIVE-REGULATION-OF-PROTEIN-SERINE-THR...	9	-0.242535	-0.648824	0.878437	1.000000	1.000
360	GOBP-ANATOMICAL-STRUCTURE-HOMEOSTASIS	7	-0.252779	-0.649021	0.885246	1.000000	1.000
361	GOBP-NEGATIVE-REGULATION-OF-PROTEIN-CATABOLIC...	5	-0.291270	-0.655322	0.899038	1.000000	1.000
362	GOBP-MONOCARBOXYLIC-ACID-TRANSPORT	5	-0.293809	-0.655807	0.894495	1.000000	1.000
363	GOBP-CELLULAR-RESPONSE-TO-NITROGEN-COMPOUND	20	-0.186747	-0.657272	0.900937	1.000000	1.000
364	GOBP-DICARBOXYLIC-ACID-TRANSPORT	5	-0.293809	-0.666263	0.873684	1.000000	1.000
365	GOBP-REGULATION-OF-PROTEIN-MODIFICATION-PROCESS	28	-0.179845	-0.667107	0.881013	1.000000	1.000
366	REACTOME-EPHLEPHRIN-SIGNALING	6	-0.276592	-0.669302	0.873457	1.000000	1.000
367	GOBP-REGULATION-OF-INTRACELLULAR-SIGNAL-TRANSD...	21	-0.190509	-0.671656	0.879630	1.000000	1.000
368	GOBP-CELLULAR-RESPONSE-TO-KETONE	5	-0.295317	-0.674412	0.875583	1.000000	1.000
369	GOBP-SKELETAL-MUSCLE-ORGAN-DEVELOPMENT	5	-0.302378	-0.676887	0.866373	1.000000	1.000
370	GOBP-MONOAMINE-TRANSPORT	5	-0.298117	-0.677362	0.868657	1.000000	1.000
371	GOBP-ACIDIC-AMINO-ACID-TRANSPORT	5	-0.293809	-0.677600	0.898551	1.000000	1.000
372	GOBP-RESPONSE-TO-INORGANIC-SUBSTANCE	19	-0.196844	-0.677900	0.875170	1.000000	1.000
373	GOBP-MONONUCLEAR-CELL-DIFFERENTIATION	7	-0.270377	-0.678575	0.848921	1.000000	1.000
374	GOBP-POSITIVE-REGULATION-OF-CYTOKINE-PRODUCTION	7	-0.267851	-0.679774	0.873039	1.000000	1.000
375	GOBP-LOCOMOTION	31	-0.183327	-0.680395	0.873724	1.000000	1.000
376	GOBP-CHROMOSOME-ORGANIZATION	6	-0.277617	-0.681208	0.844512	1.000000	1.000
377	GOBP-T-CELL-ACTIVATION	8	-0.263519	-0.683695	0.851485	1.000000	1.000
378	GOBP-RESPONSE-TO-ABIOTIC-STIMULUS	27	-0.184636	-0.683808	0.871665	1.000000	1.000
379	GOBP-RESPONSE-TO-NITROGEN-COMPOUND	35	-0.181536	-0.689073	0.864365	1.000000	1.000
380	GOBP-ERBB-SIGNALING-PATHWAY	5	-0.310468	-0.692087	0.855590	1.000000	1.000
381	GOBP-DEFENSE-RESPONSE-TO-OTHER-ORGANISM	9	-0.257580	-0.699363	0.847645	1.000000	1.000
382	GOBP-CELLULAR-RESPONSE-TO-ALCOHOL	5	-0.310764	-0.702464	0.844720	1.000000	1.000
383	GOBP-AMYLOID-PRECURSOR-PROTEIN-METABOLIC-PROCESS	5	-0.311497	-0.703389	0.848485	1.000000	1.000
384	GOBP-AMYLOID-BETA-METABOLIC-PROCESS	5	-0.311497	-0.703760	0.842795	1.000000	1.000

Continuation of Table S5

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
385 GOBP-CELLULAR-GLUCOSE-HOMEOSTASIS	GO-0001678	5	-0.312020	-0.705921	0.858730	1.000000	1.000
386 GOBP-PEPTIDYL-TYROSINE-MODIFICATION	GO-0018212	10	-0.246353	-0.708059	0.829132	1.000000	1.000
387 GOBP-CIRCULATORY_SYSTEM_PROCESS	GO-0003013	5	-0.308379	-0.709256	0.831832	1.000000	1.000
388 GOBP-ASSOCIATIVE-LEARNING	GO-0008306	7	-0.276491	-0.710629	0.806735	1.000000	1.000
389 GOBP-POSITIVE-REGULATION-OF-CELL-ADHESION	GO-00045785	7	-0.282950	-0.711715	0.823009	1.000000	1.000
390 GOBP-AMYLOID-PRECURSOR-PROTEIN-CATABOLIC-PROCESS	GO-00042987	5	-0.311497	-0.712191	0.825000	1.000000	1.000
391 REACTOME-SIGNALING-BY-NTRK2-TRKB	R-RNO-9006115	6	-0.298219	-0.712497	0.818862	1.000000	1.000
392 GOBP-POSITIVE-REGULATION-OF-PHOSPHORUS-METABOL...	GO-0010562	23	-0.200352	-0.715360	0.832011	1.000000	1.000
393 GOBP-ACTIVATION-OF-MAPK-ACTIVITY	GO-0000187	6	-0.297942	-0.720217	0.827534	1.000000	1.000
394 GOBP-NEGATIVE-REGULATION-OF-NEURON-DEATH	GO-1901215	11	-0.243287	-0.720913	0.820225	1.000000	1.000
395 GOBP-DEPHOSPHORYLATION	GO-0016311	7	-0.289380	-0.721810	0.801161	1.000000	1.000
396 GOBP-REGULATION-OF-ANION-TRANSPORT	GO-0004070	20	-0.207736	-0.722120	0.822493	1.000000	1.000
397 GOBP-SMALL-MOLECULE-METABOLIC-PROCESS	GO-00044281	16	-0.219801	-0.723830	0.806011	1.000000	1.000
398 GOBP-REGULATION-OF-CELLULAR-CATABOLIC-PROCESS	GO-0031329	10	-0.253143	-0.724799	0.829545	1.000000	1.000
399 GOBP-POSITIVE-REGULATION-OF-MAP-KINASE-ACTIVITY	GO-00043406	6	-0.297942	-0.728063	0.808219	1.000000	1.000
400 GOBP-PROTEIN-DEPHOSPHORYLATION	GO-0006470	7	-0.289380	-0.728410	0.810089	1.000000	1.000
401 GOBP-CELL-CYCLE	GO-0007049	21	-0.210750	-0.728811	0.810667	1.000000	1.000
402 GOBP-RESPONSE-TO-BIOTIC-STIMULUS	GO-0009607	17	-0.220579	-0.730327	0.809652	1.000000	1.000
403 GOBP-PLATELET-ACTIVATION	GO-0030168	6	-0.301307	-0.731528	0.820000	1.000000	1.000
404 REACTOME-INNATE-IMMUNE-SYSTEM	R-RNO-168249	16	-0.219605	-0.731597	0.809079	1.000000	1.000
405 GOBP-POSITIVE-REGULATION-OF-PROTEIN-PHOSPHORYL...	GO-0001934	12	-0.207491	-0.733522	0.826087	1.000000	1.000
406 GOBP-MULTICELLULAR-ORGANISM-REPRODUCTION	GO-0032504	22	-0.238146	-0.733641	0.811921	1.000000	1.000
407 GOBP-POSITIVE-REGULATION-OF-PROTEIN-KINASE-ACT...	GO-00045860	18	-0.221264	-0.736282	0.798408	1.000000	1.000
408 GOBP-POSITIVE-REGULATION-OF-PROTEIN-MODIFICATI...	GO-0031401	22	-0.207491	-0.741944	0.809524	1.000000	1.000
409 GOBP-HOMEOSTASIS-OF-NUMBER-OF-CELLS	GO-00048872	5	-0.323521	-0.742061	0.800578	1.000000	1.000
410 GOBP-MUSCLE-CELL-DIFFERENTIATION	GO-00042692	10	-0.262719	-0.746703	0.768202	1.000000	1.000
411 GOBP-RESPONSE-TO-TEMPERATURE-STIMULUS	GO-0009266	9	-0.272981	-0.747637	0.792264	1.000000	1.000
412 REACTOME-MAPK-TARGETS-NUCLEAR-EVENTS-MEDIATED...	R-HSA-450282	5	-0.333901	-0.748503	0.793003	1.000000	1.000
413 GOBP-CELLULAR-RESPONSE-TO-PEPTIDE	GO-1901653	13	-0.241345	-0.749480	0.763636	1.000000	1.000
414 GOBP-CENTRAL-NERVOUS-SYSTEM-NEURON-DIFFERENTIA...	GO-0021953	5	-0.331574	-0.750266	0.812312	1.000000	1.000
415 REACTOME-VESICLE-MEDIATED-TRANSPORT	R-RNO-5653656	5	-0.327005	-0.752737	0.788344	1.000000	1.000
416 REACTOME-EXTRACELLULAR-MATRIX-ORGANIZATION	R-RNO-1474244	5	-0.335918	-0.753219	0.803077	1.000000	1.000
417 REACTOME-SIGNALING-BY-RECEPTOR-TYROSINE-KINASES	R-RNO-9006934	26	-0.204605	-0.755485	0.774667	1.000000	1.000
418 REACTOME-MEMBRANE-TRAFFICKING	R-RNO-199991	5	-0.327005	-0.755781	0.770739	1.000000	1.000
419 REACTOME-SIGNALING-BY-RHO-GTPASES-MIRO-GTPASES...	R-RNO-9716542	9	-0.274540	-0.756500	0.782923	1.000000	1.000
420 GOBP-GAMETE-GENERATION	GO-0007276	9	-0.273948	-0.759876	0.762663	1.000000	1.000
421 GOBP-POSITIVE-REGULATION-OF-CATION-TRANSMEMBR...	GO-1904064	5	-0.333826	-0.760241	0.781011	1.000000	1.000
422 REACTOME-RHO-GTPASE-EFFECTORS	R-RNO-195258	9	-0.274540	-0.761089	0.771852	1.000000	1.000
423 GOBP-LIPID-EXPORT-FROM-CELL	GO-0140353	5	-0.334415	-0.762467	0.780635	1.000000	1.000
424 GOBP-ORGANIC-ANION-TRANSPORT	GO-0015711	16	-0.323244	-0.765635	0.753304	1.000000	1.000
425 GOBP-SYNAPSE-ORGANIZATION	GO-0050808	17	-0.230488	-0.768532	0.769863	1.000000	1.000
426 GOBP-PEPTIDYL-AMINO-ACID-MODIFICATION	GO-0018193	22	-0.220449	-0.769306	0.791281	1.000000	1.000
427 GOBP-APOPTOTIC_PROCESS	GO-0006915	35	-0.200042	-0.771202	0.760870	1.000000	1.000

Continuation of Table S5

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
428 GOBP-REGULATION-OF-CELL-CYCLE-PROCESS	GO-0010564	5	-0.339377	-0.771893	0.780089	1.000000	1.000
429 GOBP-POSITIVE-REGULATION-OF-TRANSFERASE-ACTIVITY	GO-0051347	19	-0.225122	-0.773648	0.768340	1.000000	1.000
430 GOBP-ESTABLISHMENT-OF-PROTEIN-LOCALIZATION-TO-...	GO-0072594	5	-0.338558	-0.776894	0.761610	1.000000	1.000
431 GOBP-AMINO-ACID-TRANSPORT	GO-0068665	6	-0.323244	-0.782134	0.766667	1.000000	1.000
432 GOBP-REGULATION-OF-LIPID-METABOLIC-PROCESS	GO-0019216	7	-0.307048	-0.782303	0.734540	1.000000	1.000
433 GOBP-RESPIRATORY-SYSTEM-DEVELOPMENT	GO-0060541	6	-0.320348	-0.782767	0.746334	1.000000	1.000
434 GOBP-CIRCADIAN-REGULATION-OF-GENE-EXPRESSION	GO-0032922	5	-0.349398	-0.784006	0.728614	1.000000	1.000
435 GOBP-CARBOXYLIC-ACID-TRANSPORT	GO-0046942	6	-0.323244	-0.793120	0.725637	1.000000	1.000
436 GOBP-CELLULAR-RESPONSE-TO-INORGANIC-SUBSTANCE	GO-0071241	11	-0.266601	-0.793193	0.747475	1.000000	1.000
437 GOBP-REGULATION-OF-TRANSMEMBRANE-TRANSPORT	GO-0034762	23	-0.217441	-0.793702	0.730220	1.000000	1.000
438 GOBP-REGULATION-OF-PROTEIN-LOCALIZATION-TO-MEM...	GO-1905475	7	-0.312449	-0.796260	0.731118	1.000000	1.000
439 GOBP-REGULATION-OF-RESPONSE-TO-STRESS	GO-0080134	19	-0.234215	-0.796425	0.733424	1.000000	1.000
440 GOBP-POSITIVE-REGULATION-OF-MOLECULAR-FUNCTION	GO-0044093	37	-0.206058	-0.797471	0.737288	1.000000	1.000
441 GOBP-BIOLOGICAL-ADHESION	GO-0022610	19	-0.236392	-0.803917	0.728972	1.000000	1.000
442 REACTOME-LEISHMANIA-INFECTION	R-HSA-9658195	10	-0.278933	-0.804883	0.691069	1.000000	1.000
443 GOBP-REGULATION-OF-CELL-ADHESION	GO-0030155	13	-0.258851	-0.805770	0.714882	1.000000	1.000
444 GOBP-SENSORY-ORGAN-DEVELOPMENT	GO-0007423	8	-0.307285	-0.807310	0.715318	1.000000	1.000
445 GOBP-MULTICELLULAR-ORGANISMAL-HOMEOSTASIS	GO-0048871	12	-0.264123	-0.808954	0.723202	1.000000	1.000
446 GOBP-REGULATION-OF-RESPONSE-TO-EXTERNAL-STIMULUS	GO-0032101	15	-0.254428	-0.821245	0.700134	1.000000	1.000
447 GOBP-IMMUNE-EFFECTOR-PROCESS	GO-0002252	11	-0.281436	-0.822938	0.686301	1.000000	1.000
448 GOBP-RESPONSE-TO-MONOSACCHARIDE	GO-0034284	5	-0.365476	-0.823316	0.705710	1.000000	1.000
449 GOBP-RHYTHMIC-PROCESS	GO-0048511	15	-0.257778	-0.826658	0.693570	1.000000	1.000
450 GOBP-TELENCEPHALON-DEVELOPMENT	GO-0021537	7	-0.321181	-0.827266	0.679882	1.000000	1.000
451 REACTOME-PLATELET-ACTIVATION-SIGNALING-AND-AGG...	R-HSA-76002	7	-0.317564	-0.827559	0.678211	1.000000	1.000
452 GOBP-REGULATION-OF-IMMUNE-SYSTEM-PROCESS	GO-0002682	21	-0.234910	-0.827626	0.684140	1.000000	1.000
453 GOBP-NEURON-DEATH	GO-0070997	18	-0.239845	-0.829061	0.687500	1.000000	1.000
454 GOBP-CELL-MIGRATION	GO-0016477	22	-0.238468	-0.829568	0.691250	1.000000	1.000
455 GOBP-REGULATION-OF-CELL-DEATH	GO-0010941	34	-0.215446	-0.829630	0.695980	1.000000	1.000
456 GOBP-STRIATED-MUSCLE-CELL-DIFFERENTIATION	GO-0051146	9	-0.304984	-0.830258	0.681223	1.000000	1.000
457 GOBP-RESPONSE-TO-CARBOHYDRATE	GO-0009743	5	-0.365476	-0.833841	0.708649	1.000000	1.000
458 GOBP-TUBE-MORPHOGENESIS	GO-0035239	15	-0.256775	-0.838581	0.658311	1.000000	1.000
459 GOBP-CARBOHYDRATE-HOMEOSTASIS	GO-0033500	7	-0.332355	-0.850939	0.660920	1.000000	1.000
460 GOBP-TISSUE-MIGRATION	GO-0090130	9	-0.309178	-0.851428	0.661383	1.000000	1.000
461 GOBP-MITOTIC-CELL-CYCLE	GO-0000278	10	-0.296632	-0.852302	0.649275	1.000000	1.000
462 REACTOME-CIRCADIAN-CLOCK	R-HSA-400253	5	-0.373494	-0.856573	0.635682	1.000000	1.000
463 GOBP-REGULATION-OF-CATABOLIC-PROCESS	GO-0009894	13	-0.274172	-0.856708	0.641407	1.000000	1.000
464 GOBP-CELL-JUNCTION-ORGANIZATION	GO-0034330	19	-0.249545	-0.856859	0.646277	1.000000	1.000
465 GOBP-REGULATION-OF-ANATOMICAL-STRUCTURE-MORPHO...	GO-0022603	17	-0.262149	-0.860661	0.643048	1.000000	1.000
466 GOBP-CELL-CELL-ADHESION	GO-0098609	14	-0.274765	-0.866736	0.635628	1.000000	1.000
467 GOBP-CELLULAR-RESPONSE-TO-HORMONE-STIMULUS	GO-0032870	11	-0.290648	-0.872792	0.627143	1.000000	1.000
468 GOBP-BLOOD-VESEL-MORPHOGENESIS	GO-0048514	14	-0.279892	-0.872879	0.643855	1.000000	1.000
469 GOBP-REGULATION-OF-NEURONAL-SYNAPTIC-PLASTICITY	GO-0048168	7	-0.335622	-0.874521	0.615942	1.000000	1.000
470 GOBP-NEGATIVE-REGULATION-OF-CELL-PROJECTION-OR...	GO-0031345	5	-0.383003	-0.875758	0.629179	1.000000	1.000

Continuation of Table S5

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
471	GOBP-POSITIVE-REGULATION_OF_IMMUNE-SYSTEM-PROCESS	18	-0.258453	-0.879661	0.632708	1.000000	1.000
472	GOBP-REGULATION_OF_WNT-SIGNALING-PATHWAY	5	-0.395471	-0.884154	0.610687	1.000000	1.000
473	GOBP-REGULATION_OF_MAP-KINASE-ACTIVITY	9	-0.322160	-0.884190	0.598582	1.000000	1.000
474	GOBP-PEPTIDYL-LYSINE-MODIFICATION	5	-0.391495	-0.888295	0.643312	1.000000	1.000
475	GOBP-SEXUAL-REPRODUCTION	10	-0.314355	-0.891089	0.590071	1.000000	1.000
476	GOBP-CALCIUM-MEDIATED-SIGNALING	10	-0.315934	-0.891198	0.611501	1.000000	1.000
477	GOBP-REGULATION_OF_CELLULAR-LOCALIZATION	17	-0.274508	-0.894899	0.609986	1.000000	1.000
478	GOBP-CIRCADIAN-RHYTHM	13	-0.295592	-0.905154	0.577291	0.996750	1.000
479	GOBP-POSITIVE-REGULATION_OF_MAPK-CASCADE	9	-0.325948	-0.907033	0.587798	0.996614	1.000
480	GOBP-REGULATION_OF_CELL-ACTIVATION	8	-0.340617	-0.908737	0.578717	0.996946	1.000
481	GOBP-EPITHELIAL-CELL-PROLIFERATION	12	-0.301305	-0.909481	0.596369	0.999249	1.000
482	GOBP-POSITIVE-REGULATION_OF_PROTEIN-TYROSINE-K...	5	-0.403548	-0.911582	0.591528	0.998459	1.000
483	GOBP-REGULATION_OF_PROTEIN-TYROSINE-KINASE-ACT...	5	-0.403548	-0.915351	0.560676	0.993935	1.000
484	GOBP-REGULATION_OF_MUSCLE-SYSTEM-PROCESS	8	-0.347726	-0.915399	0.568421	0.997964	1.000
485	GOBP-POSITIVE-REGULATION_OF_INTRACELLULAR-SIGN...	14	-0.294460	-0.916403	0.574555	0.999835	1.000
486	GOBP-LYMPHOCTE-ACTIVATION	10	-0.323123	-0.930313	0.552478	0.972004	1.000
487	GOBP-CIRCULATORY-SYSTEM-DEVELOPMENT	21	-0.262992	-0.933827	0.540880	0.967834	1.000
488	GOBP-REGULATION_OF_CIRCADIAN-RHYTHM	7	-0.327184	-0.934106	0.554252	0.971330	1.000
489	GOBP-PROTEIN-PHOSPHORYLATION	33	-0.242364	-0.935852	0.553506	0.971579	1.000
490	GOBP-CELLULAR-MACROMOLECULE-CATABOLIC-PROCESS	5	-0.417827	-0.940497	0.559091	0.964810	1.000
491	GOBP-CELL-CELL-JUNCTION-ORGANIZATION	6	-0.395485	-0.940940	0.538020	0.967831	1.000
492	GOBP-PROTEIN-LOCALIZATION_TO_CELL-PERIPHERY	12	-0.314197	-0.941910	0.542974	0.969608	1.000
493	GOBP-PROTEIN-MODIFICATION_BY_SMALL-PROTEIN.CON...	6	-0.389379	-0.943226	0.554723	0.970605	1.000
494	GOBP-REGULATION_OF_NEURON-PROJECTION-DEVELOPMENT	16	-0.282208	-0.944588	0.521439	0.971559	1.000
495	GOBP-CENTRAL-NERVOUS-SYSTEM-DEVELOPMENT	27	-0.256103	-0.944771	0.550576	0.975309	1.000
496	GOBP-REGULATION_OF-ENDOCYTOSIS	6	-0.398807	-0.946638	0.568862	0.975089	1.000
497	GOBP-AXON-DEVELOPMENT	18	-0.283046	-0.950842	0.543276	0.969301	1.000
498	GOBP-POSITIVE-REGULATION_OF_PROTEIN-METABOLIC...	27	-0.259447	-0.952026	0.543004	0.970694	1.000
499	GOBP-SPROUTING-ANGIOGENESIS	5	-0.420122	-0.955045	0.542768	0.967700	1.000
500	GOBP-PURINE-CONTAINING-COMPOUND-METABOLIC-PROCESS	6	-0.386103	-0.957643	0.537267	0.965856	1.000
501	GOBP-REGULATION_OF_BODY-FLUID-LEVELS	11	-0.326088	-0.959936	0.520115	0.964429	1.000
502	GOBP-EXOCYTOSIS	11	-0.321785	-0.961342	0.516173	0.965223	1.000
503	GOBP-PROTEIN-LOCALIZATION_TO_CELL-JUNCTION	6	-0.402573	-0.971952	0.500768	0.943795	1.000
504	GOBP-REGULATION_OF_SYNAPSE-STRUCTURE_OR-ACTIVITY	11	-0.330094	-0.972336	0.487004	0.947079	1.000
505	GOBP-MALE-GAMETE-GENERATION	5	-0.426195	-0.972425	0.513057	0.951202	1.000
506	GOBP-AMEBODAL-TYPE-CELL-MIGRATION	11	-0.327019	-0.972450	0.503516	0.955485	1.000
507	GOBP-FOREBRAIN-DEVELOPMENT	10	-0.344674	-0.975063	0.516499	0.953487	1.000
508	GOBP-REGULATION_OF_MAPK-CASCADE	13	-0.321373	-0.977187	0.480716	0.952786	1.000
509	GOBP-POSITIVE-REGULATION_OF_TRANSPORT	26	-0.266585	-0.983980	0.498084	0.940118	1.000
510	GOBP-GLIAL-CELL-DIFFERENTIATION	10	-0.346183	-0.986430	0.459459	0.938326	1.000
511	GOBP-RESPONSE_TO-ALCOHOL	11	-0.343565	-0.989141	0.493671	0.936128	1.000
512	GOBP-NEURON-PROJECTION-GUIDANCE	9	-0.353126	-0.990130	0.462774	0.938104	1.000
513	REACTOME-ONCOGENIC_MAPK-SIGNALING	5	-0.440195	-0.996555	0.476831	0.926206	1.000
	R-HSA-6802957						

Continuation of Table S5

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
514 REACTOME_DEVELOPMENTAL_BIOLOGY	R-RNO-1266738	22	-0.281109	-0.998516	0.476821	0.925710	1.000
515 GOBP_ENDOTHELIAL_CELL_MIGRATION	GO-0043542	8	-0.377832	-1.004041	0.476744	0.916032	1.000
516 GOBP_REGULATION_OF_VASCULATURE_DEVELOPMENT	GO-1901342	5	-0.449891	-1.004316	0.425150	0.919721	1.000
517 GOBP_PROTEIN_LOCALIZATION_TO_MEMBRANE	GO-0072657	13	-0.323366	-1.004966	0.464888	0.922488	1.000
518 GOBP_INTRACELLULAR_TRANSPORT	GO-0046907	10	-0.35783	-1.007695	0.448611	0.920180	1.000
519 GOBP_CELLULAR_COMPONENT_MAINTENANCE	GO-0043954	5	-0.433462	-1.007782	0.446617	0.924432	1.000
520 GOBP_MUSCLE_ORGAN_DEVELOPMENT	GO-0007517	9	-0.378375	-1.009409	0.479315	0.924728	1.000
521 GOBP_MUSCLE_SYSTEM_PROCESS	GO-0003012	9	-0.366025	-1.011933	0.449422	0.922697	1.000
522 GOBP_REGULATION_OF_HEMOPOIESIS	GO-1903706	10	-0.360966	-1.019880	0.421127	0.906657	1.000
523 GOBP_BLOOD_VESSEL_ENDOTHELIAL_CELL_MIGRATION	GO-0043534	8	-0.377832	-1.024280	0.443299	0.900035	1.000
524 GOBP_REGULATION_OF_PEPTIDE_SECRETION	GO-0002791	7	-0.395011	-1.025774	0.433934	0.900871	1.000
525 GOBP_POSITIVE_REGULATION_OF_HEMOPOIESIS	GO-1903708	7	-0.410507	-1.030707	0.411504	0.892795	1.000
526 GOBP_EPITHELIAL_CELL_DIFFERENTIATION	GO-0030855	7	-0.400149	-1.035708	0.418262	0.884234	1.000
527 GOBP_NUCLEAR_TRANSPORT	GO-0051169	5	-0.460295	-1.035780	0.429688	0.885527	1.000
528 GOBP_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	GO-1902105	9	-0.371039	-1.036228	0.435821	0.891812	1.000
529 GOBP_LONG_TERM_MEMORY	GO-0007616	6	-0.451417	-1.036466	0.428788	0.895810	1.000
530 GOBP_POSITIVE_REGULATION_OF_NEURON_PROJECTION...	GO-0010976	5	-0.442084	-1.036466	0.431962	0.900404	1.000
531 GOBP_ORGANOPHOSPHATE_METABOLIC_PROCESS	GO-0019637	8	-0.385531	-1.036598	0.442136	0.904717	1.000
532 GOBP_TEMPERATURE_HOMEOSTASIS	GO-0001659	5	-0.455909	-1.037162	0.429675	0.907901	1.000
533 GOBP_CELLULAR_RESPONSE_TO_PEPTIDE_HORMONE_STIM...	GO-0071375	9	-0.377563	-1.038800	0.418571	0.908253	1.000
534 GOBP_CARBOHYDRATE_DERIVATIVE_BIOSYNTHETIC_PROCESS	GO-1901137	5	-0.457765	-1.045399	0.426357	0.895250	1.000
535 GOBP_NUCLEOBASE_CONTAINING_SMALL_MOLECULE_META...	GO-0055086	7	-0.415064	-1.049634	0.425339	0.888533	1.000
536 GOBP_RESPONSE_TO_NICOTINE	GO-0035094	7	-0.407623	-1.049682	0.397644	0.893095	1.000
537 GOBP_TUBE_DEVELOPMENT	GO-0035295	18	-0.310344	-1.051992	0.390789	0.891598	1.000
538 GOBP_MYELOID_LEUKOCYTE_ACTIVATION	GO-0002274	8	-0.389150	-1.053754	0.403400	0.891538	1.000
539 GOBP_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY	GO-0002444	6	-0.445698	-1.054499	0.426829	0.894422	1.000
540 REACTOME_G_ALPHA_Q_SIGNALING_EVENTS	R-RNO-416476	6	-0.439024	-1.056116	0.405286	0.894825	1.000
541 GOBP_CELLULAR_MACROMOLECULE_LOCALIZATION	GO-0070727	20	-0.305042	-1.056512	0.395532	0.898573	1.000
542 GOBP_MEMORY	GO-0007613	13	-0.338720	-1.057839	0.393243	0.899976	1.000
543 GOBP_TRANSMEMBRANE_TRANSPORT	GO-0055085	27	-0.286747	-1.060515	0.377432	0.897526	1.000
544 GOBP_RESPONSE_TO_PEPTIDE_HORMONE	GO-0043434	13	-0.338051	-1.061078	0.396957	0.900942	1.000
545 GOBP_POSITIVE_REGULATION_OF_SIGNALING	GO-0023056	34	-0.277169	-1.063749	0.384324	0.898211	1.000
546 GOBP_REGULATION_OF_LONG_TERM_SYNAPTIC_POTENTIAL...	GO-1900271	6	-0.448094	-1.064461	0.391502	0.901144	1.000
547 REACTOME_CLASS_C_3_METABOTROPIC_GLUTAMATE_PHER...	R-RNO-420499	7	-0.422220	-1.069713	0.386724	0.891695	1.000
548 GOBP_LEUKOCYTE_MEDIATED_IMMUNITY	GO-0002443	8	-0.399168	-1.073443	0.377504	0.886323	1.000
549 GOBP_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	GO-0002263	7	-0.445698	-1.075784	0.395173	0.884776	1.000
550 GOBP_RESPONSE_TO_HEAT	GO-0009408	6	-0.424892	-1.077888	0.387240	0.883886	1.000
551 GOBP_MAPK_CASCADE	GO-0000165	18	-0.320411	-1.078210	0.383091	0.888087	1.000
552 GOBP_NEGATIVE_REGULATION_OF_SYNAPTIC_TRANSMISSION	GO-0050805	6	-0.451107	-1.079409	0.379573	0.889906	1.000
553 GOBP_COGNITION	GO-0050890	28	-0.292021	-1.079725	0.375813	0.894142	1.000
554 GOBP_VASCULATURE_DEVELOPMENT	GO-0001944	17	-0.321373	-1.080094	0.358090	0.898204	1.000
555 REACTOME_CELL_CYCLE	R-RNO-1640170	6	-0.458818	-1.093210	0.372488	0.866146	1.000
556 REACTOME_NEUTROPHIL_DEGRANULATION	R-RNO-6798695	6	-0.445698	-1.096194	0.373457	0.862775	1.000

Continuation of Table S5

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
557	GOBP-REGULATION-OF-PROTEIN-LOCALIZATION	18	-0.323209	-1.09852	0.344737	0.866107	1.000
558	GOBP-NEURON-DIFFERENTIATION	37	-0.287265	-1.101198	0.342172	0.858856	1.000
559	REACTOME-ANTIINFLAMMATORY-RESPONSEFAVOURING...	5	-0.485363	-1.102138	0.328149	0.861456	1.000
560	GOBP-POSITIVE-REGULATION-OF-CATALYTIC-ACTIVITY	29	-0.302869	-1.110952	0.328680	0.841565	1.000
561	GOBP-REGULATION-OF-CELL-PROJECTION-ORGANIZATION	20	-0.323391	-1.111686	0.326746	0.844505	1.000
562	GOBP-REGULATION-OF-SYSTEM-PROCESS	18	-0.333316	-1.114271	0.322709	0.842303	1.000
563	GOBP-REGULATION-OF-PEPTIDE-TRANSPORT	10	-0.385517	-1.116225	0.327485	0.842044	1.000
564	GOBP-GLIOGENESIS	12	-0.373068	-1.116467	0.332402	0.846537	1.000
565	GOBP-INNATE-IMMUNE-RESPONSE	7	-0.438375	-1.119579	0.325000	0.842647	1.000
566	GOBP-REGULATION-OF-TRANSPORTER-ACTIVITY	17	-0.341909	-1.128813	0.322537	0.821601	1.000
567	GOBP-G-PROTEIN-COUPLED-GLUTAMATE-RECEPTOR-SIGN...	8	-0.427473	-1.129670	0.321908	0.824357	1.000
568	GOBP-ENDOTHELIAL-CELL-PROLIFERATION	8	-0.433202	-1.135442	0.313146	0.813446	1.000
569	GOBP-CELL-PROJECTION-ORGANIZATION	35	-0.296628	-1.136528	0.319899	0.815514	1.000
570	GOBP-REGULATION-OF-CELLULAR-RESPONSE-TO-STRESS	9	-0.421220	-1.137814	0.298172	0.817192	1.000
571	GOBP-CELL-ACTIVATION	22	-0.321017	-1.139430	0.302597	0.817760	1.000
572	GOBP-REGULATION-OF-RECEPTOR-MEDIATED-ENDOCYTOSIS	5	-0.510853	-1.146482	0.297297	0.802818	1.000
573	REACTOME-CELLULAR-RESPONSES-TO-EXTERNAL-STIMULI	11	-0.387303	-1.146555	0.283262	0.807904	1.000
574	GOBP-POSITIVE-REGULATION-OF-LONG-TERM-SYNAPTIC...	5	-0.506024	-1.152335	0.281972	0.796545	1.000
575	GOBP-MEMBRANE-ORGANIZATION	12	-0.374581	-1.153745	0.302452	0.797875	1.000
576	GOBP-RESPONSE-TO-INTERLEUKIN_1	5	-0.500691	-1.157027	0.296012	0.793536	1.000
577	GOBP-NEUROUS-SYSTEM-PROCESS	38	-0.301856	-1.157674	0.307039	0.793719	1.000
578	GOBP-NEURON-PROJECTION-ORGANIZATION	8	-0.437919	-1.159113	0.285094	0.798021	1.000
579	GOBP-DENDRITIC-SPINE-MORPHOGENESIS	5	-0.519606	-1.160395	0.254870	0.799598	1.000
580	REACTOME-PTEN-REGULATION	5	-0.513039	-1.163592	0.255952	0.795878	1.000
581	REACTOME-INTERFERON-SIGNALING	6	-0.492042	-1.168554	0.274074	0.786909	1.000
582	GOBP-CELLULAR-COMPONENT-MORPHOGENESIS	25	-0.326232	-1.175816	0.264474	0.771542	1.000
583	GOBP-MUSCLE-ADAPTATION	5	-0.518072	-1.177493	0.248109	0.772226	1.000
584	GOBP-HEAD-DEVELOPMENT	23	-0.335156	-1.178667	0.267097	0.774213	1.000
585	GOBP-REGULATION-OF-MUSCLE-ADAPTATION	5	-0.518072	-1.185143	0.254237	0.760817	1.000
586	GOBP-POSITIVE-REGULATION-OF-RESPONSE-TO-EXTERN...	9	-0.432910	-1.185663	0.261669	0.764520	1.000
587	GOBP-DEVELOPMENTAL-MATURATION	5	-0.519427	-1.188422	0.224299	0.761963	1.000
588	GOBP-CELL-MORPHOGENESIS	25	-0.326232	-1.189264	0.244246	0.765022	1.000
589	GOBP-NEUROGENESIS	41	-0.307241	-1.195564	0.257538	0.751431	1.000
590	GOBP-RESPONSE-TO-ETHANOL	5	-0.518072	-1.198313	0.229299	0.749010	1.000
591	GOBP-CELL-PART-MORPHOGENESIS	25	-0.326232	-1.198929	0.235589	0.752741	1.000
592	GOBP-EXCITATORY-CHEMICAL-SYNAPTIC-TRANSMISSION	5	-0.530120	-1.200816	0.240250	0.752915	1.000
593	GOBP-ADENYLATE-CYCLASE-INHIBITING-G-PROTEIN.CO...	6	-0.524630	-1.205367	0.247774	0.745292	1.000
594	GOBP-REGULATION-OF-PEPTIDE-HORMONE-SECRETION	5	-0.497989	-1.207996	0.251553	0.749738	1.000
595	REACTOME-NEUROUS-SYSTEM-DEVELOPMENT	14	-0.384974	-1.207922	0.230014	0.749408	1.000
596	REACTOME-DISEASES-OF-SIGNAL-TRANSDUCTION-BY-GR...	12	-0.400232	-1.208693	0.232782	0.752815	1.000
597	GOBP-BEHAVIOR	33	-0.313897	-1.209318	0.237009	0.756673	1.000
598	GOBP-INORGANIC-ION-TRANSMEMBRANE-TRANSPORT	9	-0.437255	-1.215031	0.233094	0.745281	1.000
599	REACTOME-INTEGRATION-OF-ENERGY-METABOLISM	5	-0.542169	-1.215428	0.218126	0.749986	1.000

Continuation of Table S5

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
600 REACTOME-SIGNALING-BY-WNT	R-RNO-195721	7	-0.472307	-1.217834	0.244344	0.748684	1.000
601 GOBP-ADENYLATE-CYCLASE-INHIBITING-G-PROTEIN.CO...	GO-0007193	9	-0.442603	-1.225106	0.239377	0.733041	1.000
602 GOBP-MYOTUBE-DIFFERENTIATION	GO-0014902	5	-0.549237	-1.225110	0.213636	0.738988	1.000
603 REACTOME-GPCR-LIGAND-BINDING	R-RNO-500792	8	-0.455445	-1.225461	0.215517	0.743886	1.000
604 GOBP-ORGANOPHOSPHATE-BIOSYNTHETIC-PROCESS	GO-00090407	5	-0.542169	-1.226186	0.198767	0.748003	1.000
605 REACTOME-POST-TRANSLATIONAL-PROTEIN-MODIFICATION	R-RNO-597592	7	-0.483870	-1.228279	0.213333	0.747932	1.000
606 GOBP-DENDRITIC-SPINE-DEVELOPMENT	GO-0060996	6	-0.514146	-1.230799	0.188073	0.746690	1.000
607 GOBP-CELL-CELL-SIGNALING-BY-WNT	GO-0198738	7	-0.485064	-1.233844	0.228826	0.743785	1.000
608 GOBP-HOMEOSTATIC-PROCESS	GO-0042592	31	-0.335645	-1.234088	0.209799	0.749493	1.000
609 REACTOME-CELL-CYCLE-MITOTIC	R-RNO-69278	5	-0.526924	-1.234144	0.211161	0.755827	1.000
610 GOBP-SECOND-MESSENGER-MEDIATED-SIGNALING	GO-0019932	16	-0.378673	-1.238355	0.192513	0.749221	1.000
611 GOBP-NEURON-DEVELOPMENT	GO-0048666	34	-0.320395	-1.241070	0.221656	0.746699	1.000
612 GOBP-NUCLEOSIDE-PHOSPHATE-BIOSYNTHETIC-PROCESS	GO-1901293	5	-0.542169	-1.246884	0.174962	0.734593	1.000
613 GOBP-POSITIVE-REGULATION-OF-EPITHELIAL-CELL-PR...	GO-0050679	7	-0.487329	-1.250135	0.193452	0.731198	1.000
614 GOBP-REGULATION-OF-NERVOUS-SYSTEM-PROCESS	GO-0031644	8	-0.467617	-1.250251	0.229412	0.737421	1.000
615 GOBP-POSTSYNAPSE-ORGANIZATION	GO-0009173	10	-0.437228	-1.256209	0.178470	0.725287	1.000
616 GOBP-REGULATION-OF-SYNAPTIC-TRANSMISSION-GLUTA...	GO-0051966	12	-0.420592	-1.265240	0.184319	0.703253	1.000
617 GOBP-ENDOCRINE-SYSTEM-DEVELOPMENT	GO-0035270	6	-0.526971	-1.268268	0.179941	0.701009	1.000
618 GOBP-NEGATIVE-REGULATION-OF-CELL-CYCLE	GO-0045786	5	-0.559949	-1.269146	0.172956	0.704732	1.000
619 GOBP-CYTOSOLIC-CALCIUM-ION-TRANSPORT	GO-0060401	7	-0.498614	-1.270322	0.185907	0.707914	1.000
620 GOBP-CALCIUM-ION-TRANSPORT-INTO-CYTOSOL	GO-0060402	7	-0.498614	-1.272628	0.179910	0.707091	1.000
621 REACTOME-RNA-POLYMERASE-II-TRANSCRIPTION	R-RNO-73857	20	-0.366685	-1.275771	0.174834	0.703971	1.000
622 REACTOME-BETA-CATENIN-INDEPENDENT-WNT-SIGNALING	R-RNO-3858494	5	-0.572590	-1.282820	0.163110	0.688473	1.000
623 REACTOME-G-ALPHA-Z-SIGNALING-EVENTS	R-RNO-418597	5	-0.561037	-1.292813	0.170370	0.665265	1.000
624 GOBP-PROTEIN-TETRAMERIZATION	GO-0051262	5	-0.566225	-1.295932	0.165877	0.662187	1.000
625 GOBP-CALCIUM-ION-TRANSMEMBRANE-TRANSPORT	GO-0070588	7	-0.498614	-1.301219	0.163447	0.652376	1.000
626 GOBP-PROTEIN-LOCALIZATION-TO-ORGANELLE	GO-0033365	8	-0.480056	-1.301984	0.161337	0.656814	1.000
627 GOBP-REGULATION-OF-VESICLE-MEDIATED-TRANSPORT	GO-0060627	12	-0.428572	-1.304425	0.136620	0.656393	1.000
628 GOBP-PROTEIN-LOCALIZATION-TO-SYNAPSE	GO-0035418	5	-0.576570	-1.305158	0.144578	0.660929	1.000
629 GOBP-LOCOMOTORY-BEHAVIOR	GO-0007626	8	-0.495736	-1.305407	0.152367	0.667054	1.000
630 GOBP-CHEMICAL-HOMEOSTASIS	GO-0048878	23	-0.363951	-1.306546	0.158311	0.670547	1.000
631 GOBP-PROTEIN-LOCALIZATION-TO-POSTSYNAPSE	GO-0062237	5	-0.576570	-1.312490	0.149390	0.659328	1.000
632 GOBP-ENDOMEMBRANE-SYSTEM-ORGANIZATION	GO-0010256	6	-0.559319	-1.325217	0.124615	0.627902	1.000
633 GOBP-REGULATION-OF-NEUROTRANSMITTER-TRANSPORT	GO-0051588	6	-0.548780	-1.327145	0.119084	0.628942	1.000
634 GOBP-REGULATION-OF-POSTSYNAPSE-ORGANIZATION	GO-0009175	6	-0.552741	-1.330497	0.135417	0.626209	1.000
635 GOBP-CELL-MORPHOGENESIS-INVOLVED-IN-NEURON-DIF...	GO-0048667	22	-0.381574	-1.340243	0.136598	0.603951	1.000
636 GOBP-RESPONSE-TO-ALKALOID	GO-0043279	5	-0.588087	-1.347265	0.122388	0.590963	1.000
637 GOBP-REGULATION-OF-HORMONE-LEVELS	GO-0010817	12	-0.461609	-1.351869	0.118384	0.584170	1.000
638 GOBP-LONG-TERM-SYNAPTIC-DEPRESSION	GO-0060292	5	-0.586435	-1.352537	0.125186	0.580058	1.000
639 GOBP-CHEMICAL-SYNAPTIC-TRANSMISSION-POSTSYNAPTIC	GO-0009565	9	-0.484702	-1.352917	0.139130	0.594766	1.000
640 GOBP-CELL-MORPHOGENESIS-INVOLVED-IN-DIFFERENTI...	GO-0000904	22	-0.381574	-1.355580	0.120104	0.594086	1.000
641 GOBP-REGULATION-OF-SIGNALING-RECEPTOR-ACTIVITY	GO-0010469	14	-0.427688	-1.356903	0.132597	0.597431	1.000
642 GOBP-POSITIVE-REGULATION-OF-SYNAPTIC-TRANSMISSION	GO-0050806	15	-0.426335	-1.357025	0.131649	0.604332	1.000

Continuation of Table S5

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
643	GOBP-PEPTIDE-SECRETION	GO-0002790	9	-0.498935	-1.362063	0.134307	0.596917	1.000
644	REACTOME.MAPK.FAMILY.SIGNALING.CASCADES	R-RNO-5683057	12	-0.457009	-1.364161	0.122392	0.597401	1.000
645	GOBP-REGULATION.OF.METAL.ION.TRANSPORT	GO-0010959	6	-0.560813	-1.364759	0.118280	0.602935	1.000
646	GOBP-PROTEIN.COMPLEX.OLIGOMERIZATION	GO-0051259	7	-0.529892	-1.365265	0.113235	0.608957	1.000
647	REACTOME.NEURXINS.AND.NEUROLIGINS	R-RNO-6794361	9	-0.482228	-1.366907	0.129080	0.611609	1.000
648	GOBP-REGULATION.OF.HORMONE.SECRETION	GO-0046883	8	-0.511802	-1.372776	0.114202	0.601206	1.000
649	GOBP-SYNAPTIC.TRANSMISSION.GLUTAMATERGIC	GO-0035249	13	-0.443800	-1.370257	0.124823	0.598654	1.000
650	GOBP-SENSORY.PERCEPTION.OF.PAIN	GO-0019233	5	-0.614458	-1.396832	0.087719	0.545051	1.000
651	GOBP-REGULATION.OF.NEUROTRANSMITTER.LEVELS	GO-0001505	7	-0.555556	-1.396885	0.097451	0.552283	1.000
652	GOBP-POSITIVE.REGULATION.OF.SECRETION	GO-0051047	6	-0.574755	-1.403132	0.090504	0.541878	1.000
653	GOBP-NEUROTRANSMITTER.SECRETION	GO-0007269	6	-0.578100	-1.406550	0.098009	0.539330	1.000
654	GOBP-INSULIN.SECRETION	GO-0030073	7	-0.547623	-1.409727	0.086257	0.537210	1.000
655	GOBP-PEPTIDE.HORMONE.SECRETION	GO-0030072	7	-0.547623	-1.411287	0.098820	0.540121	1.000
656	GOBP-CELL.CYCLE.PROCESS	GO-0022402	11	-0.466999	-1.411327	0.090129	0.547817	1.000
657	GOBP-DENDRITE.DEVELOPMENT	GO-0016358	10	-0.497937	-1.412033	0.102011	0.553785	1.000
658	GOBP-VESSICLE.MEDIATED.TRANSPORT.IN.SYNAPSE	GO-0099003	5	-0.561300	-1.427367	0.092486	0.529765	1.000
659	GOBP-MULTICELLULAR.ORGANISMAL.RESPONSE.TO.STRESS	GO-0035555	7	-0.635554	-1.427392	0.075806	0.524852	1.000
660	GOBP-NEUROTRANSMITTER.TRANSPORT	GO-0006836	7	-0.555556	-1.430385	0.077827	0.524476	1.000
661	GOBP-G.PROTEIN.COUPLED.RECEPTOR.SIGNALING.PATHWAY	GO-0007186	18	-0.431676	-1.440458	0.093915	0.503061	1.000
662	REACTOME.NEGATIVE.REGULATION.OF.NMDA.RECEPTOR....	R-HSA-9617324	8	-0.550000	-1.443245	0.070225	0.503757	1.000
663	GOBP-ESTABLISHMENT.OF.PROTEIN.LOCALIZATION	GO-0045184	17	-0.436434	-1.447617	0.081944	0.500468	1.000
664	GOBP-ENDOCYTOSIS	GO-0006897	8	-0.539662	-1.449498	0.072180	0.503044	1.000
665	GOBP-LONG-TERM.SYNAPTIC.POTENTIATION	GO-0060291	12	-0.488332	-1.453689	0.087500	0.499265	1.000
666	GOBP-REGULATION.OF.SYNAPTIC.PLASTICITY	GO-0048167	21	-0.409889	-1.457786	0.077720	0.495812	1.000
667	GOBP-SECRETION	GO-0046903	24	-0.406812	-1.460529	0.072258	0.496319	1.000
668	REACTOME.ASSEMBLY.AND.CELL.SURFACE.PRESENTATIO....	R-RNO-9609736	8	-0.550000	-1.465975	0.065502	0.489039	1.000
669	GOBP-REGULATION.OF.CATION-TRANSMEMBRANE.TRANSPORT	GO-1904062	16	-0.450802	-1.467663	0.073041	0.492839	1.000
670	GOBP-ADENYLATE.CYCLASE.MODULATING-G.PROTEIN.CO...	GO-0007188	11	-0.502115	-1.474389	0.085795	0.482657	1.000
671	GOBP-POSITIVE.REGULATION.OF.ENDOTHELIAL.CELL.P...	GO-0001938	6	-0.609604	-1.475996	0.060278	0.486982	1.000
672	REACTOME.RAS.ACTIVATION.UPON.CA2.INFLUX.THROUGH...	R-HSA-442982	6	-0.621951	-1.490594	0.060993	0.454215	1.000
673	GOBP-REGULATION.OF.SECRETION	GO-0051046	14	-0.478993	-1.496572	0.055556	0.446908	1.000
674	GOBP-REGULATION.OF.ION.TRANSPORT	GO-0043269	36	-0.385777	-1.508194	0.071960	0.424216	1.000
675	GOBP-CELL.SURFACE.RECEPTOR.SIGNALING.PATHWAY.I...	GO-1905114	15	-0.484886	-1.510771	0.081200	0.426012	1.000
676	GOBP-REGULATION.OF.NEUROTRANSMITTER.RECEPTOR-A...	GO-0099601	13	-0.498644	-1.512563	0.044568	0.430169	1.000
677	GOBP-HORMONE.TRANSPORT	GO-0009914	9	-0.553517	-1.515678	0.044577	0.438114	1.000
678	GOBP-DENDRITE.MORPHOGENESIS	GO-0048813	7	-0.590681	-1.516216	0.044577	0.438114	1.000
679	GOBP-REGULATION.OF.MEMBRANE.POTENTIAL	GO-0042391	17	-0.472290	-1.526963	0.042216	0.418871	1.000
680	GOBP-IONOTROPIC.GLUTAMATE.RECEPTOR.SIGNALING.P...	GO-0035235	9	-0.559075	-1.530844	0.039187	0.417844	1.000
681	GOBP-CELLULAR.HOMEOSTASIS	GO-0019725	18	-0.461519	-1.539590	0.045392	0.403882	1.000
682	REACTOME.SYNAPTIC.ADHESION.LIKE.MOLECULES	R-RNO-8849932	9	-0.561187	-1.549487	0.042433	0.386947	1.000
683	GOBP-ION.HOMEOSTASIS	GO-0050801	16	-0.474224	-1.568573	0.039630	0.348626	1.000
684	GOBP-CALCIUM.ION.TRANSPORT	GO-0006816	11	-0.539376	-1.581617	0.030683	0.326564	1.000
685	GOBP-RECEPTOR.INTERNALIZATION	GO-0031623	5	-0.701972	-1.584845	0.030792	0.327658	1.000

Continuation of Table S5

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
686	GOBP-METAL-ION-TRANSPORT	11	-0.539376	-1.586899	0.037143	0.331651	1.000
687	REACTOME-DAG-AND-IP3-SIGNALING	8	-0.596431	-1.592211	0.030435	0.327938	1.000
688	GOBP-CATION-TRANSMEMBRANE-TRANSPORT	18	-0.475133	-1.596057	0.035620	0.327784	1.000
689	REACTOME-PROTEIN-PROTEIN-INTERACTIONS-AT-SYNAPSES	12	-0.530810	-1.599467	0.032967	0.329218	1.000
690	GOBP-REGULATION-OF-CATION-CHANNEL-ACTIVITY	14	-0.505156	-1.602820	0.025572	0.330627	1.000
691	GOBP-DIVALENT-INORGANIC-CATION-HOMEOSTASIS	13	-0.523379	-1.604957	0.031208	0.335585	1.000
692	GOBP-RECEPTOR-MEDIATED-ENDOCYTOSIS	6	-0.678741	-1.616791	0.018154	0.318780	1.000
693	GOBP-RECEPTOR-METABOLIC-PROCESS	5	-0.701972	-1.624230	0.022157	0.312061	1.000
694	GOBP-REGULATION-OF-TRANS-SYNAPTIC-SIGNALING	40	-0.406844	-1.624587	0.019084	0.321569	1.000
695	REACTOME-LONG-TERM-POTENTIATION	10	-0.574014	-1.626804	0.031944	0.327191	1.000
696	GOBP-REGULATION-OF-CYTOSOLIC-CALCIUM-ION-CONCENTRATION	13	-0.523379	-1.627263	0.030769	0.337165	1.000
697	GOBP-REGULATION-OF-TRANSPORT	44	-0.411581	-1.636704	0.018564	0.326304	1.000
698	GOBP-METAL-ION-HOMEOSTASIS	14	-0.510986	-1.641666	0.025572	0.326857	1.000
699	GOBP-REGULATION-OF-POSTSYNAPTIC-MEMBRANE-POTENTIAL	14	-0.521047	-1.648322	0.018031	0.323010	1.000
700	GOBP-TAXIS	14	-0.530904	-1.664598	0.023546	0.298835	1.000
701	REACTOME-CA-DEPENDENT-EVENTS	8	-0.629874	-1.707873	0.011396	0.223236	0.999
702	GOBP-CELLULAR-ION-HOMEOSTASIS	14	-0.540987	-1.708884	0.009550	0.231082	0.999
703	REACTOME-CREB1-PHOSPHORYLATION-THROUGH-NMDA-RECEPTOR	8	-0.637500	-1.715217	0.014124	0.229466	0.999
704	GOBP-SENSORY PERCEPTION	9	-0.645570	-1.746304	0.011765	0.188347	0.996
705	REACTOME-TRANSCRIPTIONAL-REGULATION-BY-MECP2	7	-0.694299	-1.751326	0.007474	0.190076	0.996
706	REACTOME-OPIOID-SIGNALING	12	-0.581809	-1.752075	0.008658	0.198705	0.996
707	REACTOME-G-PROTEIN-MEDIATED-EVENTS	9	-0.647307	-1.757173	0.004478	0.200199	0.993
708	GOBP-SIGNAL-RELEASE	14	-0.564258	-1.782423	0.004213	0.171940	0.975
709	GOBP-REGULATION-OF-NMDA-RECEPTOR-ACTIVITY	10	-0.632363	-1.791026	0.011577	0.169973	0.969
710	REACTOME-INTRACELLULAR-SIGNALING-BY-SECOND-MESSENGERS	15	-0.555499	-1.805708	0.006739	0.160351	0.952
711	REACTOME-TRAFFICKING-OF-GLUR2-CONTAINING-AMPA-RECEPTORS	8	-0.675187	-1.810510	0.005970	0.165983	0.946
712	GOBP-CATION-TRANSPORT	25	-0.499575	-1.810595	0.005249	0.178624	0.946
713	GOBP-PROTEIN-CONTAINING-COMPLEX-SUBUNIT-ORGANIZATION	15	-0.558366	-1.812063	0.006775	0.191245	0.945
714	GOBP-GLUTAMATE-RECEPTOR-SIGNALING-PATHWAY	17	-0.544366	-1.819266	0.002677	0.195190	0.931
715	REACTOME-UNBLOCKING-OF-NMDA-RECEPTORS-GLUTAMATE	12	-0.603834	-1.824378	0.007022	0.203406	0.924
716	REACTOME-SIGNALING-BY-GPCR	22	-0.517946	-1.829147	0.006502	0.215499	0.919
717	GOBP-SYNAPTIC-SIGNALING	47	-0.482112	-1.862374	0.002436	0.175899	0.821
718	REACTOME-ACTIVATION-OF-NMDA-RECEPTORS-AND-POSTSYNAPTIC-EVENTS	16	-0.611111	-1.969570	0.000000	0.066520	0.439
719	REACTOME-TRAFFICKING-OF-AMPA-RECEPTORS	11	-0.693509	-2.030433	0.000000	0.038970	0.245
720	REACTOME-G-ALPHA-I-SIGNALING-EVENTS	18	-0.618072	-2.109749	0.000000	0.016060	0.092
721	GOBP-CELL-CELL-SIGNALING	56	-0.562372	-2.172927	0.000000	0.009460	0.044
722	REACTOME-NEUROTRANSMITTER-RECEPTORS-AND-POSTSYNAPTIC-EVENTS	22	-0.635336	-2.238737	0.000000	0.006321	0.023
723	REACTOME-TRANSMISSION-ACROSS-CHEMICAL-SYNAPSES	23	-0.652775	-2.334456	0.000000	0.002479	0.006
724	REACTOME-NEURONAL-SYSTEM	26	-0.634596	-2.356828	0.000000	0.003253	0.004

End of Table

Supplementary Table S6: SC caudal segment early (8 DPL peak) profile GSEA results.

Begin of Table S6									
	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val	
0	REACTOME_INTERLEUKIN_4_AND_INTERLEUKIN_13_SIGNALING	R-RNO-6785807	8	0.850000	2.650963	0.000000	0.004133	0.003	
1	GOBP_NEGATIVE_REGULATION_OF_PEPTIDASE_ACTIVITY	GO-0010466	6	0.829268	2.291362	0.000000	0.058247	0.082	
2	GOBP_NEGATIVE_REGULATION_OF_CYSSTEINE_TYPE_ENDO...	GO-2000117	5	0.819277	2.102695	0.003257	0.159675	0.289	
3	REACTOME_DEATH_RECEPTOR_SIGNALING	R-RNO-73887	5	0.843374	2.079119	0.003175	0.142639	0.329	
4	GOBP_CYTOKINE_MEDIATED_SIGNALING_PATHWAY	GO-0019221	16	0.477821	2.072472	0.006757	0.121649	0.346	
5	GOBP_NEGATIVE_REGULATION_OF_PROTEOLYSIS	GO-0045861	8	0.633652	2.050440	0.009132	0.120438	0.397	
6	GOBP_OSTEOLAST_DIFFERENTIATION	GO-0001649	5	0.798331	1.999637	0.013158	0.140692	0.502	
7	GOBP_NEGATIVE_REGULATION_OF_CELL_POPULATION_PR...	GO-0008285	9	0.584956	1.952865	0.018605	0.163842	0.612	
8	REACTOME_SIGNALING_BY_INTERLEUKINS	R-RNO-449147	15	0.475514	1.947926	0.000000	0.148248	0.621	
9	REACTOME_TRANSCRIPTIONAL_REGULATION_OF_WHITE_A...	R-RNO-381340	6	0.709519	1.937768	0.003745	0.141376	0.645	
10	GOBP_POSITIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL...	GO-0048661	5	0.734940	1.884392	0.006431	0.168348	0.737	
11	GOBP_REGULATION_OF_ANION_TRANSMEMBRANE_TRANSPORT	GO-1903959	5	0.722892	1.834365	0.014134	0.201620	0.827	
12	GOBP_MAINTENANCE_OF_LOCATION	GO-0051235	7	0.604938	1.780696	0.019084	0.243920	0.901	
13	GOBP_RESPONSE_TO_CYTOKINE	GO-0034097	23	0.357711	1.722216	0.027027	0.307254	0.952	
14	GOBP_NEGATIVE_REGULATION_OF_MOLECULAR_FUNCTION	GO-0044092	24	0.339218	1.686259	0.015267	0.348070	0.973	
15	GOBP_APOPTOTIC_SIGNALING_PATHWAY	GO-0097190	15	0.410959	1.684289	0.011696	0.329308	0.974	
16	GOBP_PROTEIN_KINASE_B_SIGNALING	GO-0043491	6	0.597551	1.662809	0.032967	0.347823	0.979	
17	GOBP_NEGATIVE_REGULATION_OF_APOPTOTIC_SIGNALIN...	GO-2001234	7	0.543210	1.611342	0.034351	0.428348	0.997	
18	HALLMARK_APOPTOSIS	M5902	6	0.577499	1.608824	0.033210	0.410407	0.998	
19	GOBP_MEMBRANE_PROTEIN_PROTEOLYSIS	GO-0033619	6	0.575726	1.577970	0.053957	0.451800	0.998	
20	GOBP_NEGATIVE_REGULATION_OF_HYDROLASE_ACTIVITY	GO-0051346	11	0.436062	1.573022	0.053097	0.441651	0.998	
21	GOBP_REGULATION_OF_APOPTOTIC_SIGNALING_PATHWAY	GO-2001233	10	0.448718	1.558977	0.025974	0.450405	0.999	
22	GOBP_CARBOHYDRATE_METABOLIC_PROCESS	GO-0005975	9	0.455696	1.549957	0.047170	0.451299	1.000	
23	GOBP_REGULATION_OF_PROTEIN_BINDING	GO-0043393	7	0.518518	1.542498	0.074074	0.447695	1.000	
24	GOBP_LEUKOCYTE_CELL_CELL_ADHESION	GO-0007159	6	0.548780	1.538624	0.063433	0.436162	1.000	
25	REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM	R-RNO-1280215	21	0.321845	1.531217	0.034014	0.434406	1.000	
26	GOBP_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	GO-0097193	5	0.590361	1.529637	0.060284	0.421536	1.000	
27	GOBP_POSITIVE_REGULATION_OF_SMALL_MOLECULE_MET...	GO-0062013	5	0.590361	1.528533	0.050167	0.408780	1.000	
28	GOBP_NEGATIVE_REGULATION_OF_RESPONSE_TO_EXTERN...	GO-0032102	5	0.598862	1.505771	0.062718	0.439577	1.000	
29	GOBP_ACTIN_FILAMENT_BASED_PROCESS	GO-0030029	7	0.493827	1.504634	0.077220	0.427695	1.000	
30	GOBP_RESPONSE_TO_UV	GO-0009411	5	0.590361	1.500342	0.082143	0.421445	1.000	
31	GOBP_NEGATIVE_REGULATION_OF_MULTICELLULAR_ORGA...	GO-0051241	15	0.357820	1.483136	0.061111	0.442787	1.000	
32	GOBP_NEGATIVE_REGULATION_OF_PROTEIN_METABOLIC...	GO-0051248	20	0.304733	1.467683	0.054264	0.462201	1.000	
33	GOBP_NEGATIVE_REGULATION_OF_LOCOMOTION	GO-0040013	5	0.583830	1.450100	0.081356	0.483046	1.000	
34	GOBP_POSITIVE_REGULATION_OF_GENE_EXPRESSION	GO-0006954	16	0.324126	1.442255	0.055901	0.485561	1.000	
35	GOBP_INFLAMMATORY_RESPONSE	GO-0006954	12	0.379522	1.441211	0.060606	0.474136	1.000	
36	GOBP_PRLMIRNA_TRANSCRIPTION_BY_RNA_POLYMERASE_II	GO-0061614	7	0.467470	1.439829	0.072202	0.464377	1.000	
37	GOBP_POSITIVE_REGULATION_OF_CELL_CELL_ADHESION	GO-0022409	5	0.542169	1.425610	0.093023	0.484717	1.000	
38	GOBP_REGULATION_OF_DEFENSE_RESPONSE	GO-0031347	7	0.468013	1.424753	0.082645	0.473571	1.000	
39	GOBP_POSITIVE_REGULATION_OF_AXONOGENESIS	GO-0050772	5	0.555503	1.421564	0.097902	0.468022	1.000	
40	GOBP_CELLULAR_RESPONSE_TO_EXTERNAL_STIMULUS	GO-0071496	10	0.396947	1.410026	0.069149	0.479794	1.000	

Continuation of Table S6

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
41	GOBP-POSITIVE-REGULATION_OF_PRL-MIRNA-TRANSCRIPT...	7	0.467450	1.409578	0.092593	0.469189	1.000
42	GOBP-PROTEOLYSIS	17	0.331716	1.409049	0.076923	0.459111	1.000
43	GOBP-POSITIVE-REGULATION_OF_LEUKOCYTE-CELL-CEL...	5	0.542169	1.406760	0.115523	0.452326	1.000
44	GOBP-POSITIVE-REGULATION_OF_PHOSPHATIDYLINOSIT...	5	0.554217	1.403875	0.120275	0.448688	1.000
45	GOBP-POSITIVE-REGULATION_OF_BINDING	6	0.512195	1.388809	0.125000	0.472215	1.000
46	GOBP-REGULATION_OF_INFLAMMATORY_RESPONSE	7	0.468013	1.387067	0.100746	0.465522	1.000
47	GOBP-REGULATION_OF_BINDING	11	0.390865	1.366613	0.095000	0.496693	1.000
48	GOBP-REGULATION_OF_CELL-CELL-ADHESION	9	0.405063	1.357406	0.102564	0.506228	1.000
49	GOBP-OSSIFICATION	9	0.401897	1.350846	0.120172	0.510587	1.000
50	GOBP-CELLULAR-CARBOHYDRATE-METABOLIC-PROCESS	5	0.518072	1.349536	0.112281	0.503712	1.000
51	GOBP-POSITIVE-REGULATION_OF_CYTOKINE-PRODUCTION	7	0.447422	1.346138	0.116379	0.501258	1.000
52	GOBP-POSITIVE-REGULATION_OF_CELL-DIFFERENTIATION	27	0.257454	1.342514	0.095652	0.498908	1.000
53	GOBP-REGULATION_OF-CARBOHYDRATE-METABOLIC-PROCESS	5	0.518072	1.342408	0.106618	0.490098	1.000
54	GOBP-DEVELOPMENTAL-CELL-GROWTH	5	0.530121	1.339137	0.121094	0.487526	1.000
55	GOBP-REGULATION_OF-CARBOHYDRATE-BIOSYNTHETIC-P...	5	0.518072	1.337963	0.141379	0.481517	1.000
56	GOBP-SMOOTH-MUSCLE-CELL-PROLIFERATION	5	0.487805	1.337529	0.112727	0.474146	1.000
57	GOBP-GENERATION_OF-PRECURSOR-METABOLITES-AND-E...	5	0.518072	1.334865	0.127208	0.471398	1.000
58	GOBP-NEGATIVE-REGULATION_OF-CELL-DEATH	22	0.266423	1.333492	0.098765	0.465792	1.000
59	GOBP-MORPHOGENESIS_OF-AN-EPITHELIUM	6	0.490067	1.330398	0.136842	0.463996	1.000
60	GOBP-RESPONSE-TO-MOLECULE-OF-BACTERIAL-ORIGIN	13	0.333675	1.314412	0.139896	0.489334	1.000
61	GOBP-EXTRINSIC-APOPTOTIC-SIGNALING-PATHWAY	7	0.432099	1.312685	0.150000	0.484675	1.000
62	GOBP-CARBOHYDRATE-BIOSYNTHETIC-PROCESS	5	0.518072	1.310175	0.169935	0.482389	1.000
63	GOBP-POLYSACCHARIDE-METABOLIC-PROCESS	5	0.518072	1.292294	0.153846	0.511206	1.000
64	GOBP-RESPONSE-TO-BACTERIUM	13	0.333675	1.285532	0.146739	0.517268	1.000
65	GOBP-REGULATION_OF-FAT-CELL-DIFFERENTIATION	6	0.464218	1.285140	0.138182	0.510234	1.000
66	GOBP-REGULATION_OF_CELL-DIFFERENTIATION	36	0.227301	1.265996	0.086957	0.543145	1.000
67	GOBP-POSITIVE-REGULATION_OF_DEVELOPMENTAL-PROCESS	32	0.235071	1.263451	0.129032	0.540692	1.000
68	REACTOME-SENESCENCE-ASSOCIATED-SECRETORY-PHENO...	6	0.453492	1.257207	0.198413	0.545614	1.000
69	GOBP-TISSUE-MORPHOGENESIS	7	0.419753	1.247029	0.172662	0.547414	1.000
70	GOBP-REGULATION_OF-GTPASE-ACTIVITY	5	0.481928	1.245655	0.194346	0.549151	1.000
71	GOBP-GLUCOSE-METABOLIC-PROCESS	6	0.439024	1.240985	0.172269	0.551771	1.000
72	GOBP-POSITIVE-REGULATION_OF_DEFENSE-RESPONSE	5	0.488575	1.238543	0.200000	0.549066	1.000
73	GOBP-MYELOID-CELL-DIFFERENTIATION	13	0.300607	1.237936	0.149701	0.542896	1.000
74	GOBP-PERIPHERAL-NERVOUS-SYSTEM-DEVELOPMENT	9	0.355801	1.224405	0.197368	0.564941	1.000
75	GOBP-REGULATION_OF_VASCULAR-ASSOCIATED-SMOOTH...	5	0.481928	1.223218	0.185965	0.560542	1.000
76	GOBP-SKIN-DEVELOPMENT	5	0.491114	1.223002	0.212544	0.554107	1.000
77	GOBP-NEGATIVE-REGULATION_OF_TRANSCRIPTION_BY-R...	10	0.343307	1.207723	0.188776	0.579909	1.000
78	GOBP-MONOSACCHARIDE-METABOLIC-PROCESS	6	0.439024	1.203303	0.210526	0.578745	1.000
79	GOBP-POSITIVE-REGULATION_OF_IMMUNE-RESPONSE	9	0.354107	1.200078	0.232068	0.582966	1.000
80	GOBP-REGULATION_OF-DEVELOPMENTAL-GROWTH	9	0.352055	1.198242	0.247368	0.580520	1.000
81	GOBP-CELLULAR-RESPONSE-TO-MOLECULE-OF-BACTERIA...	8	0.376145	1.195760	0.248927	0.577841	1.000
82	GOBP-CELL-POPULATION-PROLIFERATION	32	0.220748	1.190303	0.157895	0.581657	1.000

Continuation of Table S6

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
84	GOBP-ACTIVATION_OF_IMMUNE_RESPONSE	5	0.473733	1.186214	0.237354	0.586076	1.000
85	GOBP-RESPONSE_TO_MECHANICAL_STIMULUS	6	0.421899	1.180344	0.257143	0.593458	1.000
86	HALLMARK-HYPOXIA	5	0.464336	1.173914	0.239852	0.600206	1.000
87	GOBP-REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING	6	0.426829	1.166786	0.268000	0.609739	1.000
88	GOBP-CELLULAR_RESPONSE_TO_BIOTIC_STIMULUS	8	0.376411	1.161446	0.259574	0.614536	1.000
89	GOBP-RAS_PROTEIN_SIGNAL_TRANSDUCTION	5	0.463971	1.155653	0.278317	0.621031	1.000
90	GOBP-TISSUE_HOMEOSTASIS	5	0.444430	1.154216	0.257840	0.618433	1.000
91	GOBP-REGULATION_OF_LIPID_LOCALIZATION	5	0.469880	1.150313	0.273927	0.621030	1.000
92	GOBP-DEFENSE_RESPONSE_TO_OTHER_ORGANISM	9	0.342538	1.144591	0.270642	0.626987	1.000
93	GOBP-POSITIVE_REGULATION_OF_DEVELOPMENTAL_GROWTH	8	0.360775	1.143424	0.273543	0.622916	1.000
94	GOBP-POSITIVE_REGULATION_OF_BIOSYNTHETIC_PROCESS	27	0.228326	1.140818	0.258064	0.622328	1.000
95	GOBP-IMMUNE_SYSTEM_DEVELOPMENT	17	0.262523	1.140214	0.282209	0.617204	1.000
96	HALLMARK-TNFA_SIGNALING_VIA_NFKB	14	0.278203	1.134372	0.240964	0.624429	1.000
97	GOBP-CARBOHYDRATE_DERIVATIVE_METABOLIC_PROCESS	8	0.355310	1.134310	0.284091	0.618086	1.000
98	HALLMARK-ALLOGRAFT_REJECTION	7	0.376773	1.134252	0.259414	0.611968	1.000
99	GOBP-FC_RECEPTOR_SIGNALING_PATHWAY	8	0.355435	1.129107	0.278481	0.617619	1.000
100	GOBP-REGULATION_OF_IMMUNE_RESPONSE	12	0.295254	1.121226	0.254902	0.631100	1.000
101	GOBP-NEGATIVE_REGULATION_OF_BINDING	6	0.410171	1.120548	0.304833	0.626864	1.000
102	REACTOME-ADAPTIVE_IMMUNE_SYSTEM	9	0.329114	1.118723	0.301653	0.624580	1.000
103	GOBP-CELLULAR_RESPONSE_TO_ORGANIC_CYCLIC_COMPOUND	13	0.285754	1.118335	0.295000	0.619514	1.000
104	GOBP-IMMUNE_RESPONSE_REGULATING_SIGNALING_PATHWAY	GO-00071407	10	0.305326	1.102162	0.302326	0.643152
105	GOBP-REGULATION_OF_CELL_ADHESION	GO-00030155	13	0.280000	1.102162	0.308300	0.625656
106	GOBP-CYTOKINE_PRODUCTION	GO-0001816	10	0.312785	1.096172	0.305936	0.652902
107	GOBP-REGULATION_OF_MULTICELLULAR_ORGANISMAL_DEVELOPMENT	GO-2000026	31	0.202802	1.094705	0.246914	0.651199
108	GOBP-POSITIVE_REGULATION_OF_NUCLEOBASE_CONTAINING	GO-0045935	28	0.205451	1.082979	0.327586	0.670642
109	GOBP-DEVELOPMENTAL_GROWTH	GO-0048589	10	0.305326	1.075151	0.331707	0.683175
110	GOBP-REGULATION_OF_EPITHELIAL_CELL_MIGRATION	GO-0010632	6	0.390244	1.074346	0.329710	0.678917
111	GOBP-RESPONSE_TO_NUTRIENT	GO-0007584	5	0.415962	1.068296	0.392593	0.686907
112	GOBP-REGULATION_OF_ANATOMICAL_STRUCTURE_SIZE	GO-0090066	10	0.310759	1.067914	0.299517	0.681634
113	GOBP-POSITIVE_REGULATION_OF_APOPTOTIC_SIGNALING	GO-2001235	5	0.421687	1.063617	0.389091	0.686629
114	GOBP-REGULATION_OF_LYMPHOCYTE_ACTIVATION	GO-0051249	5	0.421687	1.060266	0.372694	0.689044
115	GOBP-POSITIVE_REGULATION_OF_MULTICELLULAR_ORGANISMAL_DEVELOPMENT	GO-0051240	32	0.196700	1.055915	0.357143	0.693212
116	GOBP-OSTEOCLAST_DIFFERENTIATION	GO-0030316	6	0.375883	1.055669	0.356863	0.687825
117	GOBP-POSITIVE_REGULATION_OF_GROWTH	GO-0045927	9	0.309418	1.052134	0.365546	0.690007
118	GOBP-REGULATION_OF_NERVOUS_SYSTEM_DEVELOPMENT	GO-0051960	15	0.249200	1.044461	0.412587	0.701368
119	GOBP-POSITIVE_REGULATION_OF_PEPTIDYL_SERINE_PHOSPHORYLATION	GO-0033138	8	0.324908	1.041986	0.390438	0.700461
120	GOBP-REGULATION_OF_PEPTIDYL_SERINE_PHOSPHORYLATION	GO-0033135	8	0.324908	1.040885	0.420601	0.696859
121	GOBP-CELLULAR_RESPONSE_TO_OXYGEN-CONTAINING_COMPOUND	GO-1901701	29	0.199997	1.021361	0.387097	0.738433
122	GOBP-REGULATION_OF_MUSCLE_SYSTEM_PROCESS	GO-0090257	8	0.325000	1.021225	0.415638	0.732814
123	GOBP-GLAND_DEVELOPMENT	GO-0048732	7	0.334236	1.007483	0.422925	0.758781
124	GOBP-MONONUCLEAR_CELL_DIFFERENTIATION	GO-1903131	7	0.339976	1.005551	0.451883	0.757515
125	GOBP-INOSITOL_LIPID-MEDIATED_SIGNALING	GO-0048017	8	0.316406	1.002518	0.449393	0.759812
126	GOBP-REGULATION_OF_NEURON_DIFFERENTIATION	GO-0045664	5	0.392180	1.000727	0.425249	0.757867

Continuation of Table S6

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
127	GOBP-REGULATION-OF-PEPTIDYL-TYROSINE-PHOSPHORY...	9	0.299408	0.998255	0.443925	0.758750	1.000
128	GOBP-ORGAN-GROWTH	5	0.381101	0.997915	0.474820	0.753571	1.000
129	GOBP-RESPONSE-TO-ENDOGENOUS-STIMULUS	34	0.183113	0.994952	0.456522	0.754448	1.000
130	GOBP-CELLULAR-RESPONSE-TO-EXTRACELLULAR-STIMULUS	8	0.310091	0.993695	0.453782	0.751206	1.000
131	GOBP-POSITIVE-REGULATION-OF-CELL-GROWTH	6	0.356985	0.991770	0.423077	0.749596	1.000
132	GOBP-NEGATIVE-REGULATION-OF-GENE-EXPRESSION	11	0.272727	0.990087	0.446078	0.748115	1.000
133	GOBP-REGULATION-OF-ENDOTHELIAL-CELL-MIGRATION	5	0.385542	0.989230	0.474747	0.744613	1.000
134	GOBP-REGULATION-OF-MITOTIC-CELL-CYCLE	5	0.385542	0.988099	0.469595	0.741881	1.000
135	GOBP-FAT-CELL-DIFFERENTIATION	9	0.295664	0.986821	0.430380	0.738878	1.000
136	GOBP-REGULATION-OF-NEUROGENESIS	14	0.245709	0.983176	0.480874	0.740571	1.000
137	REACTOME-INFECTIOUS-DISEASE	12	0.263626	0.979187	0.492754	0.743918	1.000
138	GOBP-REGULATION-OF-CELL-DEVELOPMENT	15	0.239794	0.974873	0.479769	0.747772	1.000
139	GOBP-TISSUE-MIGRATION	9	0.291139	0.973249	0.438819	0.746696	1.000
140	GOBP-CHROMATIN-ORGANIZATION	5	0.385542	0.969988	0.468966	0.748869	1.000
141	GOBP-POSITIVE-REGULATION-OF-EPIITHELIAL-CELL-MI...	5	0.385542	0.969252	0.477352	0.745507	1.000
142	GOBP-POSITIVE-REGULATION-OF-TRANSCRIPTION-BY-R...	24	0.203391	0.965913	0.504000	0.748150	1.000
143	GOBP-MUSCLE-CELL-PROLIFERATION	8	0.303707	0.963409	0.483254	0.748472	1.000
144	GOBP-T-CELL-ACTIVATION	8	0.309911	0.961854	0.497817	0.746658	1.000
145	GOBP-REGULATION-OF-ORGAN-GROWTH	5	0.381101	0.953776	0.489796	0.759051	1.000
146	GOBP-PROTEIN-DEPHOSPHORYLATION	7	0.320988	0.950271	0.488722	0.761234	1.000
147	GOBP-DEPHOSPHORYLATION	7	0.320988	0.949025	0.502058	0.758605	1.000
148	GOBP-POSITIVE-REGULATION-OF-CELL-DEVELOPMENT	12	0.245595	0.944240	0.479592	0.764618	1.000
149	GOBP-RESPONSE-TO-INTERLEUKIN-1	5	0.368060	0.942450	0.526882	0.763726	1.000
150	GOBP-REGULATION-OF-CELL-SIZE	5	0.369922	0.937617	0.503472	0.768768	1.000
151	GOBP-NEGATIVE-REGULATION-OF-CATALYTIC-ACTIVITY	17	0.222880	0.937520	0.595376	0.763879	1.000
152	GOBP-POSITIVE-REGULATION-OF-CELL-ADHESION	7	0.320988	0.936632	0.520161	0.760919	1.000
153	REACTOME-INNATE-IMMUNE-SYSTEM	16	0.217631	0.936451	0.564706	0.756687	1.000
154	GOBP-POSITIVE-REGULATION-OF-NERVOUS-SYSTEM.DEV...	12	0.245595	0.923073	0.572770	0.780449	1.000
155	GOBP-BLOOD-VESSEL-ENDOTHELIAL-CELL-MIGRATION	8	0.287500	0.918606	0.557377	0.784430	1.000
156	GOBP-ENDOTHELIAL-CELL-MIGRATION	8	0.287500	0.917486	0.533613	0.781576	1.000
157	GOBP-CELL-GROWTH	10	0.269231	0.916657	0.555556	0.778443	1.000
158	GOBP-POSITIVE-REGULATION-OF-NEUROGENESIS	12	0.245595	0.916609	0.583756	0.773714	1.000
159	HALLMARK-KRAS-SIGNALING-UP	6	0.330454	0.916605	0.549296	0.768887	1.000
160	GOBP-ENDOTHELIAL-CELL-PROLIFERATION	8	0.287500	0.906630	0.611607	0.784658	1.000
161	GOBP-REGULATION-OF-GROWTH	13	0.233078	0.904369	0.573770	0.784084	1.000
162	GOBP-POSITIVE-REGULATION-OF-CELL-POPULATION.PR...	21	0.193309	0.902359	0.580645	0.783720	1.000
163	GOBP-LEUKOCYTE-DIFFERENTIATION	15	0.219425	0.896418	0.618182	0.790412	1.000
164	GOBP-RESPONSE-TO-ORGANIC-CYCLIC-COMPOUND	20	0.193309	0.893317	0.666667	0.791992	1.000
165	GOBP-NEGATIVE-REGULATION-OF-CELL-DEVELOPMENT	6	0.320491	0.880101	0.580000	0.814249	1.000
166	GOBP-REGULATION-OF-IMMUNE-SYSTEM-PROCESS	21	0.182149	0.877930	0.632000	0.814197	1.000
167	GOBP-POSITIVE-REGULATION-OF-PEPTIDYL-TYROSINE....	8	0.282237	0.876676	0.621622	0.811832	1.000
168	GOBP-NEGATIVE-REGULATION-OF-NERVOUS-SYSTEM.DEV...	5	0.333754	0.873836	0.620253	0.812393	1.000
169	GOBP-NEGATIVE-REGULATION-OF-NUCLEOBASE-CONTAIN...	13	0.213333	0.866599	0.679426	0.821534	1.000

Continuation of Table S6

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
170	GOBP-INNATE-IMMUNE-RESPONSE	7	0.289150	0.863453	0.600000	0.823158	1.000
171	GOBP-CELL-CELL-JUNCTION-ASSEMBLY	5	0.352095	0.859633	0.631399	0.825969	1.000
172	GOBP-REGULATION-OF-DNA-BINDING-TRANSCRIPTION-F...	16	0.198823	0.851069	0.684211	0.838673	1.000
173	GOBP-POSITIVE-REGULATION-OF-IMMUNE-SYSTEM-PROCESS	18	0.189856	0.850890	0.685714	0.834365	1.000
174	GOBP-REGULATION-OF-CELLULAR-COMPONENT-SIZE	7	0.282032	0.848047	0.688000	0.834641	1.000
175	GOBP-EPITHELIAL-CELL-PROLIFERATION	12	0.215762	0.847740	0.682796	0.830333	1.000
176	GOBP-GROWTH	14	0.211635	0.846630	0.703911	0.827850	1.000
177	GOBP-NEGATIVE-REGULATION-OF-BIOSYNTHETIC-PROCESS	13	0.213914	0.846260	0.661290	0.823851	1.000
178	GOBP-IN-UTERO-EMBRYONIC-DEVELOPMENT	8	0.268618	0.845298	0.669683	0.820888	1.000
179	GOBP-MYELOID-LEUKOCYTE-DIFFERENTIATION	11	0.222245	0.844695	0.676056	0.817766	1.000
180	GOBP-REGULATION-OF-MYELOID-CELL-DIFFERENTIATION	9	0.234587	0.837252	0.707424	0.825862	1.000
181	GOBP-PEPTIDE-METABOLIC-PROCESS	11	0.223825	0.820233	0.730000	0.853486	1.000
182	GOBP-NEUROTROPHIN-TRK-RECEPTOR-SIGNALING-PATHWAY	6	0.287919	0.811654	0.665427	0.863558	1.000
183	GOBP-POSITIVE-REGULATION-OF-ANION-TRANSPORT	9	0.243544	0.810648	0.722222	0.860938	1.000
184	GOBP-NEUROTROPHIN-SIGNALING-PATHWAY	6	0.287919	0.809990	0.691700	0.857589	1.000
185	GOBP-REGULATION-OF-HEMOPOIESIS	10	0.222658	0.793840	0.781659	0.880720	1.000
186	GOBP-MUSCLE-CONTRACTION	5	0.301205	0.784896	0.752508	0.891388	1.000
187	GOBP-CELLULAR-GLUCOSE-HOMEOSTASIS	5	0.313253	0.781790	0.768212	0.891743	1.000
188	GOBP-NEURON-APOPTOTIC-PROCESS	12	0.202582	0.777287	0.828125	0.894494	1.000
189	GOBP-INTRACELLULAR-RECEPTOR-SIGNALING-PATHWAY	5	0.297755	0.751532	0.767361	0.932543	1.000
190	GOBP-SPROUTING-ANGIOGENESIS	5	0.297211	0.751060	0.781250	0.925888	1.000
191	GOBP-POSITIVE-REGULATION-OF-TRANSMEMBRANE-TRAN...	7	0.254916	0.749835	0.776515	0.925597	1.000
192	GOBP-REGULATION-OF-OSTEOCLAST-DIFFERENTIATION	5	0.291396	0.748408	0.762590	0.922923	1.000
193	GOBP-NEGATIVE-REGULATION-OF-RESPONSE-TO-STIMULUS	16	0.173441	0.743742	0.856287	0.924483	1.000
194	GOBP-CELLULAR-AMIDE-METABOLIC-PROCESS	12	0.194177	0.741730	0.866337	0.922841	1.000
195	GOBP-CELLULAR-RESPONSE-TO-ABIOTIC-STIMULUS	7	0.240240	0.735904	0.827586	0.926570	1.000
196	GOBP-CELLULAR-RESPONSE-TO-LIPID	15	0.178087	0.734421	0.905556	0.924255	1.000
197	GOBP-HOMEOSTASIS-OF-NUMBER-OF-CELLS	5	0.294654	0.725792	0.786260	0.932461	1.000
198	GOBP-PROTEIN-AUTOPHOSPHORYLATION	5	0.277643	0.718271	0.843416	0.937942	1.000
199	GOBP-RESPONSE-TO-TUMOR-NECROSIS-FACTOR	7	0.238818	0.710560	0.872587	0.943498	1.000
200	GOBP-CELLULAR-COMPONENT-DISASSEMBLY	6	0.256098	0.705572	0.843972	0.945202	1.000
201	REACTOME-HEMOSTASIS	14	0.170135	0.696012	0.920455	0.953242	1.000
202	GOBP-EMBRYO-DEVELOPMENT-ENDING-IN-BIRTH-OR-EGG...	9	0.202628	0.687301	0.876068	0.958925	1.000
203	GOBP-POSITIVE-REGULATION-OF-CELL-PROJECTION-OR...	10	0.193454	0.685449	0.892523	0.956550	1.000
204	GOBP-CYTOSKELETON-ORGANIZATION	11	0.183404	0.683791	0.891892	0.953639	1.000
205	GOBP-REGULATION-OF-LEUKOCYTE-DIFFERENTIATION	9	0.202532	0.677548	0.900000	0.956444	1.000
206	GOBP-PROTEIN-MODIFICATION-BY-SMALL-PROTEIN-CON...	7	0.222222	0.674722	0.896414	0.955160	1.000
207	GOBP-POSITIVE-REGULATION-OF-DNA-BINDING-TRANSC...	10	0.184408	0.671541	0.902703	0.954056	1.000
208	GOBP-CELL-CELL-ADHESION	14	0.172325	0.668169	0.937500	0.953535	1.000
209	REACTOME-NGF-STIMULATED-TRANSCRIPTION	9	0.202562	0.664117	0.909091	0.953468	1.000
210	GOBP-LYMPHOCYTE-ACTIVATION	5	0.179889	0.658021	0.935644	0.955209	1.000
211	GOBP-AMYLOID-PRECURSOR-PROTEIN-METABOLIC-PROCESS	5	0.253012	0.652189	0.910714	0.956217	1.000
212	GOBP-AMYLOID-PRECURSOR-PROTEIN-CATABOLIC-PROCESS	5	0.253012	0.646092	0.925267	0.957335	1.000

Continuation of Table S6

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
213	GOBP-AMYLOID-BETA-METABOLIC-PROCESS	GO-0050435	5	0.253012	0.632551	0.928315	0.964982	1.000
214	GOBP-POSITIVE-REGULATION-OF-HEMOPOIESIS	GO-1903708	7	0.197531	0.592621	0.940520	0.988652	1.000
215	GOBP-LONG-TERM-SYNAPTIC-DEPRESSION	GO-0060292	5	0.228916	0.585973	0.962838	0.987705	1.000
216	GOBP-CIRCADIAN-REGULATION-OF-GENE-EXPRESSION	GO-0032922	5	0.216868	0.560846	0.987138	0.994252	1.000
217	GOBP-ANATOMICAL-STRUCTURE-FORMATION-INVOLVED-I...	GO-0048646	20	0.115483	0.553497	0.952537	0.992273	1.000
218	GOBP-RESPONSE-TO-INSULIN	GO-0032868	5	0.216868	0.540678	0.988000	0.991729	1.000
219	GOBP-AMEBOIDAL-TYPE-CELL-MIGRATION	GO-0001667	11	0.121030	0.452301	0.995327	0.999161	1.000
220	GOBP-TUBE-MORPHOGENESIS	GO-0035239	15	-0.132209	-0.405127	0.998767	0.998400	1.000
221	GOBP-REGULATION-OF-RECEPTOR-MEDIATED-ENDOCYTOSIS	GO-0048259	5	-0.194501	-0.430792	0.998615	0.998509	1.000
222	GOBP-PROTEIN-CATABOLIC-PROCESS	GO-0030163	8	-0.173185	-0.447153	0.998706	0.998680	1.000
223	GOBP-BLOOD-VESSEL-MORPHOGENESIS	GO-0048514	14	-0.153097	-0.469870	0.990315	0.997030	1.000
224	GOBP-REGULATION-OF-ENDOCYTOSIS	GO-0030100	6	-0.197535	-0.470647	0.997308	0.998870	1.000
225	GOBP-EPIDERMIS-DEVELOPMENT	GO-0008544	5	-0.209928	-0.470947	0.997319	1.000000	1.000
226	GOBP-RESPONSE-TO-NERVE-GROWTH-FACTOR	GO-1990089	7	-0.198299	-0.488053	0.989218	0.999018	1.000
227	GOBP-NEGATIVE-REGULATION-OF-DEVELOPMENTAL-PROCESS	GO-0051093	13	-0.172485	-0.508365	0.972739	0.995216	1.000
228	GOBP-NEGATIVE-REGULATION-OF-CELL-DIFFERENTIATION	GO-0045596	13	-0.172485	-0.508556	0.980296	0.997156	1.000
229	GOBP-POSITIVE-REGULATION-OF-CELLULAR-COMPONENT...	GO-0044089	9	-0.199390	-0.523379	0.966837	0.993886	1.000
230	GOBP-REGULATION-OF-MYELOID-LEUKOCYTE-DIFFERENT...	GO-0002761	8	-0.204775	-0.530390	0.973958	0.993193	1.000
231	GOBP-NEURON-MIGRATION	GO-0001764	5	-0.240105	-0.531848	0.968792	0.994584	1.000
232	GOBP-REGULATION-OF-CELLULAR-COMPONENT-MOVEMENT	GO-0051270	15	-0.173636	-0.532002	0.969448	0.996552	1.000
233	GOBP-MACROMOLECULE-CATABOLIC-PROCESS	GO-0009057	11	-0.190412	-0.537279	0.968314	0.996250	1.000
234	GOBP-NEGATIVE-REGULATION-OF-INTRACELLULAR-SIGN...	GO-1902532	7	-0.224298	-0.546244	0.969617	0.994337	1.000
235	REACTOME-SIGNALING-BY-RHO-GTPASES-MIRO-GTPASES...	R-RNO-9716542	9	-0.209149	-0.555692	0.969152	0.991834	1.000
236	GOBP-NEGATIVE-REGULATION-OF-NEURON-APOPTOTIC-P...	GO-0043524	8	-0.215662	-0.556955	0.953765	0.993163	1.000
237	REACTOME-RHO-GTPASE-EFFECTORS	R-RNO-195258	9	-0.209149	-0.560037	0.951571	0.993598	1.000
238	GOBP-EMBRYO-DEVELOPMENT	GO-0009790	14	-0.182742	-0.561944	0.963270	0.994562	1.000
239	GOBP-REGULATION-OF-SMALL-MOLECULE-METABOLIC-PR...	GO-0062012	9	-0.214866	-0.565652	0.951507	0.994541	1.000
240	GOBP-PEPTIDYL-LYSINE-MODIFICATION	GO-0018205	5	-0.250422	-0.567693	0.972337	0.995491	1.000
241	GOBP-BIOLOGICAL-PROCESS-INVOLVED-IN-SYMBIOTIC....	GO-0044440	10	-0.204958	-0.571216	0.944862	0.995532	1.000
242	GOBP-POSITIVE-REGULATION-OF-ORGANELLE-ORGANIZA...	GO-0010638	10	-0.209747	-0.574943	0.945083	0.995375	1.000
243	GOBP-RESPONSE-TO-LIPID	GO-0033993	19	-0.177198	-0.586073	0.948538	0.990529	1.000
244	GOBP-REPRODUCTIVE-SYSTEM-DEVELOPMENT	GO-0061458	6	-0.248605	-0.586994	0.962667	0.991971	1.000
245	GOBP-POSITIVE-REGULATION-OF-CELLULAR-COMPONENT...	GO-0051130	24	-0.172410	-0.587822	0.933486	0.993493	1.000
246	GOBP-REGULATION-OF-PROTEIN-CATABOLIC-PROCESS	GO-0042176	7	-0.238198	-0.588718	0.946309	0.995016	1.000
247	GOBP-CHROMOSOME-ORGANIZATION	GO-0051276	6	-0.255983	-0.589788	0.932065	0.996329	1.000
248	GOBP-BIOLOGICAL-ADHESION	GO-0002610	19	-0.183289	-0.592441	0.915677	0.996583	1.000
249	GOBP-PATTERN-SPECIFICATION-PROCESS	GO-0007389	6	-0.252871	-0.593127	0.938005	0.998234	1.000
250	GOBP-REGIONALIZATION	GO-0003002	6	-0.252871	-0.593127	0.938005	0.998234	1.000
251	REACTOME-SIGNALING-BY-RECEPTOR-TYROSINE-KINASES	R-RNO-9006934	26	-0.175447	-0.597356	0.914097	0.999403	1.000
252	GOBP-LIPID-METABOLIC-PROCESS	GO-0006629	15	-0.227896	-0.605589	0.932161	0.995443	1.000
253	GOBP-NEGATIVE-REGULATION-OF-KINASE-ACTIVITY	GO-0033673	5	-0.272806	-0.605905	0.950912	0.997531	1.000
254	GOBP-REGULATION-OF-LIPID-BIOSYNTHETIC-PROCESS	GO-0046890	6	-0.260571	-0.609618	0.936592	0.997014	1.000
255	GOBP-CARBOHYDRATE-HOMEOSTASIS	GO-0033500	7	-0.245852	-0.610074	0.924084	0.998793	1.000

Continuation of Table S6

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
256	GOBP-NEGATIVE-REGULATION-OF-TRANSFERASE-ACTIVITY	5	-0.272896	-0.613962	0.932489	0.997866	1.000
257	GOBP-REGULATION-OF-MUSCLE-CELL-DIFFERENTIATION	6	-0.258661	-0.614355	0.929825	0.999670	1.000
258	GOBP-RESPONSE-TO-KETONE	7	-0.246649	-0.614562	0.916329	1.000000	1.000
259	GOBP-CELL-CELL-JUNCTION-ORGANIZATION	6	-0.259315	-0.616435	0.932705	1.000000	1.000
260	GOBP-NEGATIVE-REGULATION-OF-ANION-TRANSPORT	8	-0.241572	-0.619709	0.915232	1.000000	1.000
261	GOBP-RESPONSE-TO-GROWTH-FACTOR	18	-0.191183	-0.619863	0.914184	1.000000	1.000
262	GOBP-LOCOMOTION	31	-0.175239	-0.621669	0.924208	1.000000	1.000
263	HALLMARK-P13K-AKT-MTOR-SIGNALING	M5923	-0.262890	-0.624989	0.937330	1.000000	1.000
264	GOBP-MUSCLE-CELL-DIFFERENTIATION	10	-0.227547	-0.625683	0.933333	1.000000	1.000
265	GOBP-LIPID-BIOSYNTHETIC-PROCESS	6	-0.260571	-0.627147	0.917469	1.000000	1.000
266	GOBP-NEGATIVE-REGULATION-OF-PROTEIN-MODIFICATION	10	-0.226163	-0.628560	0.920573	1.000000	1.000
267	GOBP-APOPTOTIC-PROCESS	35	-0.174447	-0.633373	0.908197	1.000000	1.000
268	REACTOME-FC-EPSILON-RECEPTOR-FCERL-SIGNALING	R-RNO-2454202	-0.257681	-0.635552	0.910526	1.000000	1.000
269	GOBP-NEUROINFLAMMATORY-RESPONSE	GO-0150076	-0.286797	-0.637802	0.925666	1.000000	1.000
270	GOBP-COAGULATION	GO-0050817	-0.249033	-0.639136	0.917323	1.000000	1.000
271	GOBP-CELLULAR-LIPID-METABOLIC-PROCESS	GO-0044255	-0.264238	-0.642952	0.902145	1.000000	1.000
272	GOBP-REGULATION-OF-VASCULATURE-DEVELOPMENT	GO-1901342	-0.287142	-0.643679	0.917630	1.000000	1.000
273	REACTOME-EXTRACELLULAR-MATRIX-ORGANIZATION	R-RNO-1474244	-0.287071	-0.645639	0.915849	1.000000	1.000
274	GOBP-NEGATIVE-REGULATION-OF-SIGNALING	GO-0023057	-0.193791	-0.648334	0.885514	1.000000	1.000
275	GOBP-REGULATION-OF-NEURON-PROJECTION-DEVELOPMENT	GO-0010975	-0.212260	-0.649270	0.885305	1.000000	1.000
276	GOBP-NEGATIVE-REGULATION-OF-NEURON-DEATH	GO-1901215	-0.231786	-0.650697	0.885101	1.000000	1.000
277	GOBP-FC-EPSILON-RECEPTOR-SIGNALING-PATHWAY	GO-0038095	-0.257681	-0.651763	0.884115	1.000000	1.000
278	GOBP-CELL-MIGRATION	GO-0016477	-0.197845	-0.653618	0.882217	1.000000	1.000
279	GOBP-NEGATIVE-REGULATION-OF-ION-TRANSPORT	GO-0043271	-0.229115	-0.654249	0.892269	1.000000	1.000
280	GOBP-PHAGOCYTOSIS	GO-0006909	-0.293677	-0.655286	0.922644	1.000000	1.000
281	GOBP-POSTTRANSCRIPTIONAL-REGULATION-OF-GENE-EX...	GO-0010608	-0.258709	-0.655638	0.887550	1.000000	1.000
282	GOBP-REGULATION-OF-PROTEIN-TYROSINE-KINASE-ACT...	GO-0061097	-0.298844	-0.659869	0.891929	1.000000	1.000
283	GOBP-POSITIVE-REGULATION-OF-PROTEIN-TYROSINE-K...	GO-0061098	-0.298844	-0.660444	0.891929	1.000000	1.000
284	GOBP-PLATELET-ACTIVATION	GO-0030168	-0.279646	-0.661764	0.903533	1.000000	1.000
285	GOBP-POSITIVE-REGULATION-OF-MYELOID-LEUKOCYTE-...	GO-0002763	-0.277683	-0.663726	0.897849	1.000000	1.000
286	GOBP-REGULATION-OF-ANATOMICAL-STRUCTURE-MORPHO...	GO-0022603	-0.212534	-0.665297	0.880756	1.000000	1.000
287	GOBP-REGULATION-OF-WNT-SIGNALING-PATHWAY	GO-0030111	-0.301835	-0.670719	0.882603	1.000000	1.000
288	REACTOME-NUCLEAR-EVENTS-KINASE-AND-TRANSCRIPTI...	R-RNO-198725	-0.238645	-0.673050	0.884712	1.000000	1.000
289	GOBP-PEPTIDYL-SERINE-MODIFICATION	GO-0018209	-0.227826	-0.673902	0.864634	1.000000	1.000
290	HALLMARK-EPITHELIAL-MESENCHYMAL-TRANSITION	M5930	-0.296845	-0.674608	0.879044	1.000000	1.000
291	GOBP-CELLULAR-RESPONSE-TO-PEPTIDE	GO-1901653	-0.229450	-0.681785	0.868712	1.000000	1.000
292	GOBP-RESPONSE-TO-PEPTIDE	GO-1901652	-0.214231	-0.684356	0.874118	1.000000	1.000
293	GOBP-NEGATIVE-REGULATION-OF-TRANSMEMBRANE-TRAN...	GO-0034763	-0.269125	-0.686373	0.864247	1.000000	1.000
294	REACTOME-LEISHMANIA-INFECTION	R-HSA-9658195	-0.250845	-0.686805	0.864428	1.000000	1.000
295	GOBP-CELL-JUNCTION-ASSEMBLY	GO-0034329	-0.269247	-0.687350	0.870249	1.000000	1.000
296	GOBP-RESPONSE-TO-BIOTIC-STIMULUS	GO-0009607	-0.217569	-0.689466	0.869880	1.000000	1.000
297	GOBP-CELL-CYCLE	GO-0007049	-0.207051	-0.690020	0.853714	1.000000	1.000
298	GOBP-SMALL-MOLECULE-BIOSYNTHETIC-PROCESS	GO-0044283	-0.311213	-0.691045	0.866109	1.000000	1.000

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NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
299 GOBP-PHOSPHATIDYLINOSITOL_3_KINASE_SIGNALING	GO-0014065	7	-0.278522	-0.692001	0.857916	1.000000	1.000
300 GOBP-RECEPTOR-MEDIATED-ENDOCYTOSIS	GO-0006898	6	-0.291085	-0.693525	0.846462	1.000000	1.000
301 GOBP-REGULATION-OF-RESPONSE-TO-STRESS	GO-0080134	19	-0.213301	-0.693768	0.855803	1.000000	1.000
302 GOBP-NEGATIVE-REGULATION-OF-SYNAPTIC-TRANSMISSION	GO-0050805	6	-0.292428	-0.695632	0.857143	1.000000	1.000
303 GOBP-PEPTIDYL-TYROSINE-MODIFICATION	GO-0018212	10	-0.252436	-0.696569	0.840149	1.000000	1.000
304 REACTOME-CELL-CYCLE-MITOTIC	R-RNO-69278	5	-0.314616	-0.702142	0.857531	1.000000	1.000
305 GOBP-ORGANONITROGEN-COMPOUND-BIOSYNTHETIC-PROCESS	GO-1901566	13	-0.234257	-0.704440	0.844282	1.000000	1.000
306 GOBP-CELL-ACTIVATION	GO-0001775	22	-0.212307	-0.705937	0.846336	1.000000	1.000
307 GOBP-NEGATIVE-REGULATION-OF-PHOSPHORUS-METABOLISM	GO-0010563	9	-0.260613	-0.706439	0.822165	1.000000	1.000
308 GOBP-REGULATION-OF-CELL-ACTIVATION	GO-0050865	8	-0.273410	-0.706843	0.864682	1.000000	1.000
309 GOBP-POSITIVE-REGULATION-OF-LOCOMOTION	GO-0040017	11	-0.247204	-0.708535	0.839196	1.000000	1.000
310 GOBP-PROTEIN-MODIFICATION-BY-SMALL-PROTEIN-CONJUGATION	GO-0032446	6	-0.303729	-0.717496	0.822342	1.000000	1.000
311 GOBP-IMPORT-INTO-CELL	GO-0098657	6	-0.303136	-0.718434	0.833333	1.000000	1.000
312 GOBP-ORGANONITROGEN-COMPOUND-CATABOLIC-PROCESS	GO-1901565	10	-0.262245	-0.719173	0.825255	1.000000	1.000
313 GOBP-REGULATION-OF-PHOSPHATIDYLINOSITOL_3_KINASE_ACTIVITY	GO-0014066	6	-0.311008	-0.723242	0.841611	1.000000	1.000
314 GOBP-REGULATION-OF-PROTEIN-MODIFICATION-PROCESS	GO-0031399	28	-0.208360	-0.725342	0.815107	1.000000	1.000
315 GOBP-DEFENSE-RESPONSE	GO-0006952	19	-0.222688	-0.725652	0.822562	1.000000	1.000
316 REACTOME-SIGNALING-BY-NTRKS	R-RNO-166520	18	-0.225937	-0.726817	0.803140	1.000000	1.000
317 GOBP-POSITIVE-REGULATION-OF-EPITHELIAL-CELL-PROLIFERATION	GO-0050679	7	-0.293809	-0.729860	0.814136	1.000000	1.000
318 GOBP-MUSCLE-STRUCTURE-DEVELOPMENT	GO-0061061	16	-0.235574	-0.731154	0.817001	1.000000	1.000
319 GOBP-REGULATION-OF-CELL-DEATH	GO-0010941	34	-0.202377	-0.732338	0.822727	1.000000	1.000
320 GOBP-REGULATION-OF-CELL-CYCLE-PROCESS	GO-0010564	5	-0.322924	-0.733637	0.835022	1.000000	1.000
321 GOBP-REGULATION-OF-CELLULAR-AMIDE-METABOLIC-PROCESS	GO-0034248	9	-0.272273	-0.737085	0.828931	1.000000	1.000
322 GOBP-NEURON-PROJECTION-GUIDANCE	GO-0097485	9	-0.277235	-0.737589	0.832700	1.000000	1.000
323 GOBP-RESPONSE-TO-HORMONE	GO-0009725	20	-0.228754	-0.744769	0.819861	1.000000	1.000
324 GOBP-WOUND-HEALING	GO-0042060	13	-0.254044	-0.745919	0.795620	1.000000	1.000
325 GOBP-REGULATION-OF-CELLULAR-RESPONSE-TO-STRESS	GO-0080135	9	-0.281502	-0.749944	0.787565	1.000000	1.000
326 GOBP-ACTIVATION-OF-PROTEIN-KINASE-ACTIVITY	GO-0032147	10	-0.274616	-0.752277	0.786164	1.000000	1.000
327 GOBP-NEGATIVE-REGULATION-OF-LIPID-METABOLIC-PROCESS	GO-0045833	5	-0.340077	-0.754178	0.804469	1.000000	1.000
328 GOBP-REGULATION-OF-RESPONSE-TO-EXTERNAL-STIMULUS	GO-0032101	15	-0.249899	-0.758116	0.774699	1.000000	1.000
329 GOBP-EPITHELIAL-DEVELOPMENT	GO-0060429	15	-0.245869	-0.761841	0.761336	1.000000	1.000
330 GOBP-NEGATIVE-REGULATION-OF-IMMUNE-SYSTEM-PROCESS	GO-0002683	5	-0.347808	-0.767212	0.803596	1.000000	1.000
331 GOBP-CELLULAR-MACROMOLECULE-CATABOLIC-PROCESS	GO-0044265	5	-0.342446	-0.768822	0.772480	1.000000	1.000
332 GOBP-INTRACELLULAR-PROTEIN-TRANSPORT	GO-0006886	8	-0.295465	-0.767536	0.774366	0.999607	1.000
333 GOBP-RESPONSE-TO-OXYGEN-LEVELS	GO-0070482	8	-0.300775	-0.769724	0.770252	0.998719	1.000
334 REACTOME-TOLL-LIKE-RECEPTOR-CASCADES	R-RNO-168898	8	-0.304442	-0.774192	0.761255	0.994478	1.000
335 GOBP-REGULATION-OF-PHOSPHORUS-METABOLIC-PROCESS	GO-0051174	26	-0.228230	-0.774406	0.767361	0.996698	1.000
336 GOBP-POSITIVE-REGULATION-OF-ENDOTHELIAL-CELL-PROLIFERATION	GO-0001938	6	-0.327253	-0.777736	0.762640	0.994306	1.000
337 GOBP-CELLULAR-RESPONSE-TO-KETONE	GO-1901655	5	-0.352709	-0.778505	0.769441	0.995666	1.000
338 GOBP-REGULATION-OF-AXONOGENESIS	GO-0050770	7	-0.314004	-0.779999	0.760695	0.995861	1.000
339 GOBP-REGULATION-OF-CYTOSKELETON-ORGANIZATION	GO-0051493	5	-0.342908	-0.780034	0.780585	0.998379	1.000
340 GOBP-NUCLEAR-TRANSPORT	GO-0051169	5	-0.353719	-0.780372	0.773040	1.000000	1.000
341 GOBP-NEGATIVE-REGULATION-OF-PROTEIN-CATABOLIC-PROCESS	GO-0042177	5	-0.352341	-0.782753	0.773352	0.999267	1.000

Continuation of Table S6

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
342	REACTOME_MYD88-INDEPENDENT-TLR4-CASCADE	R-RNO-166166	8	-0.304442	-0.784280	0.738562	0.999455	1.000
343	GOBP-POSITIVE-REGULATION-OF-CATION-TRANSMEMBRAN...	GO-1904064	5	-0.348398	-0.787982	0.768377	0.996321	1.000
344	REACTOME-TOLL-LIKE-RECEPTOR-TLR1-TLR2-CASCADE	R-RNO-168179	8	-0.304442	-0.788548	0.753264	0.998053	1.000
345	GOBP-ERBB-SIGNALING-PATHWAY	GO-0038127	5	-0.347093	-0.789239	0.763984	0.999589	1.000
346	GOBP-REGULATION-OF-CELL-CYCLE	GO-0051726	13	-0.270568	-0.789240	0.735802	1.000000	1.000
347	GOBP-NEURON-DEATH	GO-0070997	18	-0.247553	-0.790334	0.752625	1.000000	1.000
348	GOBP-REGULATION-OF-TRANSFERASE-ACTIVITY	GO-0051338	21	-0.239325	-0.791387	0.744509	1.000000	1.000
349	REACTOME-CIRCADIAN-CLOCK	R-HSA-400253	5	-0.361446	-0.792476	0.750341	1.000000	1.000
350	GOBP-CELLULAR-RESPONSE-TO-DNA-DAMAGE-STIMULUS	GO-0006974	5	-0.360847	-0.792881	0.753156	1.000000	1.000
351	GOBP-STRATIATED-MUSCLE-CELL-DIFFERENTIATION	GO-0051146	9	-0.296096	-0.794515	0.752282	1.000000	1.000
352	REACTOME-TOLL-LIKE-RECEPTOR-9-TLR9-CASCADE	R-RNO-168138	8	-0.304442	-0.797109	0.742466	1.000000	1.000
353	GOBP-REGULATION-OF-PROTEIN-LOCALIZATION-TO-CEL...	GO-1904375	6	-0.340436	-0.799511	0.756164	1.000000	1.000
354	GOBP-REGULATION-OF-PROTEIN-KINASE-ACTIVITY	GO-0045859	21	-0.239325	-0.800034	0.732329	1.000000	1.000
355	GOBP-MULTICELLULAR-ORGANISMAL-HOMEOSTASIS	GO-0048871	12	-0.275249	-0.808625	0.722153	0.993261	1.000
356	GOBP-POSITIVE-REGULATION-OF-MYELOID-CELL-DIFFE...	GO-0045639	7	-0.325086	-0.809200	0.730978	0.994966	1.000
357	GOBP-INTRACELLULAR-TRANSPORT	GO-0046907	10	-0.297707	-0.813515	0.725131	0.990314	1.000
358	GOBP-REGULATION-OF-PROTEIN-STABILITY	GO-0031647	5	-0.367587	-0.813727	0.746287	0.992622	1.000
359	REACTOME-TRANSCRIPTIONAL-REGULATION-BY-TP53	R-RNO-3700989	6	-0.344722	-0.814512	0.718291	0.993945	1.000
360	GOBP-REGULATION-OF-LIPASE-ACTIVITY	GO-0060191	6	-0.346693	-0.816252	0.728571	0.993708	1.000
361	GOBP-POSITIVE-REGULATION-OF-PROTEIN-KINASE-ACT...	GO-0045860	18	-0.254491	-0.817105	0.725537	0.994955	1.000
362	GOBP-REGULATION-OF-PHOSPHOLIPASE-ACTIVITY	GO-0010517	8	-0.346693	-0.817347	0.715223	0.997281	1.000
363	GOBP-SMALL-GTPASE-MEDIATED-SIGNAL-TRANSDUCTION	GO-0007264	8	-0.312748	-0.818300	0.722149	0.998404	1.000
364	GOBP-RESPONSE-TO-TEMPERATURE-STIMULUS	GO-0009266	9	-0.309381	-0.818673	0.703608	1.000000	1.000
365	GOBP-TRANSMEMBRANE-RECEPTOR-PROTEIN-TYROSINE_K...	GO-0007169	19	-0.254835	-0.819756	0.731536	1.000000	1.000
366	GOBP-POSITIVE-REGULATION-OF-RESPONSE-TO-EXTERN...	GO-0032103	9	-0.304854	-0.820379	0.730769	1.000000	1.000
367	GOBP-RESPONSE-TO-OXYGEN-CONTAINING-COMPOUND	GO-1901700	39	-0.224616	-0.821895	0.685430	1.000000	1.000
368	REACTOME-MEMBRANE-TRAFFICKING	R-RNO-199991	5	-0.376994	-0.826700	0.710345	0.996976	1.000
369	GOBP-AGING	GO-0007568	13	-0.274892	-0.828709	0.685961	0.996012	1.000
370	GOBP-POSITIVE-REGULATION-OF-ION-TRANSPORT	GO-0043270	17	-0.261551	-0.829262	0.689696	0.997813	1.000
371	GOBP-CARBOHYDRATE-DERIVATIVE-BIOSYNTHETIC-PROCESS	GO-1901137	5	-0.363253	-0.829414	0.709632	1.000000	1.000
372	GOBP-DEVELOPMENTAL-PROCESS-INVOLVED-IN-REPRODU...	GO-0003006	11	-0.295691	-0.83283	0.706186	0.995946	1.000
373	GOBP-NEGATIVE-REGULATION-OF-PHOSPHORYLATION	GO-0042326	7	-0.331776	-0.833539	0.689243	0.998305	1.000
374	GOBP-PEPTIDE-BIOSYNTHETIC-PROCESS	GO-0043043	6	-0.352211	-0.834422	0.701705	0.999518	1.000
375	GOBP-NERVE-DEVELOPMENT	GO-0021675	9	-0.317591	-0.834744	0.683444	1.000000	1.000
376	REACTOME-INTERLEUKIN-17-SIGNALING	R-RNO-448424	6	-0.358449	-0.837367	0.704762	0.999686	1.000
377	GOBP-HEART-DEVELOPMENT	GO-0007507	6	-0.352211	-0.837584	0.692617	1.000000	1.000
378	GOBP-AMIDE-BIOSYNTHETIC-PROCESS	GO-0043604	6	-0.352211	-0.838260	0.689655	1.000000	1.000
379	GOBP-REGULATION-OF-PROTEIN-PHOSPHORYLATION	GO-0001932	25	-0.244811	-0.840052	0.677602	1.000000	1.000
380	GOBP-CARDIAC-MUSCLE-TISSUE-DEVELOPMENT	GO-0048738	6	-0.361401	-0.840901	0.684573	1.000000	1.000
381	GOBP-CELLULAR-RESPONSE-TO-HORMONE-STIMULUS	GO-0032870	11	-0.296515	-0.842400	0.680958	1.000000	1.000
382	GOBP-PEPTIDYL-AMINO-ACID-MODIFICATION	GO-0018193	22	-0.253547	-0.842411	0.666278	1.000000	1.000
383	GOBP-LEUKOCYTE-MIGRATION	GO-0050900	6	-0.360346	-0.843995	0.699864	1.000000	1.000
384	GOBP-MYOTUBE-DIFFERENTIATION	GO-0014902	5	-0.370176	-0.844379	0.686798	1.000000	1.000

Continuation of Table S6

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
385 REACTOME-VESICLE-MEDIATED-TRANSPORT	R-RNO-5653656	5	-0.376994	-0.844526	0.679063	1.000000	1.000
386 GOBP-REGULATION-OF-ANION-TRANSPORT	GO-0044070	20	-0.257561	-0.847894	0.662486	1.000000	1.000
387 GOBP-PROTEIN-LOCALIZATION-TO-CELL-JUNCTION	GO-1902414	6	-0.364239	-0.850727	0.692412	1.000000	1.000
388 GOBP-ANATOMICAL-STRUCTURE-HOMEOSTASIS	GO-0060249	7	-0.348264	-0.852897	0.682825	1.000000	1.000
389 GOBP-LIPID-LOCALIZATION	GO-0010876	10	-0.309666	-0.854643	0.636129	1.000000	1.000
390 REACTOME-INTERFERON-SIGNALING	R-RNO-913531	6	-0.363516	-0.855462	0.685950	1.000000	1.000
391 GOBP-POSITIVE-REGULATION-OF-PROTEIN-PHOSPHORYL...	GO-0001934	22	-0.254643	-0.857540	0.657955	1.000000	1.000
392 GOBP-POSITIVE-REGULATION-OF-PROTEIN-MODIFICATI...	GO-0031401	22	-0.254643	-0.859371	0.677419	1.000000	1.000
393 GOBP-ORGANIC-ACID-METABOLIC-PROCESS	GO-0006082	7	-0.345324	-0.863171	0.652174	0.999751	1.000
394 GOBP-REGULATION-OF-CELLULAR-COMPONENT-BIOGENESIS	GO-0044087	10	-0.318571	-0.863970	0.630295	1.000000	1.000
395 GOBP-IMMUNE-EFFECTOR-PROCESS	GO-0002252	11	-0.308999	-0.865282	0.677096	1.000000	1.000
396 GOBP-RESPONSE-TO-ACID-CHEMICAL	GO-0001101	6	-0.387760	-0.866815	0.649596	1.000000	1.000
397 GOBP-RESPONSE-TO-MONOSACCHARIDE	GO-0034284	5	-0.387760	-0.866815	0.656944	1.000000	1.000
398 GOBP-ANIMAL-ORGAN-MORPHOGENESIS	GO-0009887	12	-0.299789	-0.869346	0.634116	1.000000	1.000
399 GOBP-ORGANIC-HYDROXY-COMPOUND-METABOLIC-PROCESS	GO-1901615	8	-0.335682	-0.871615	0.637076	1.000000	1.000
400 REACTOME-CELL-CYCLE	R-RNO-1640170	6	-0.363415	-0.874535	0.655028	0.997995	1.000
401 GOBP-CELLULAR-RESPONSE-TO-NITROGEN-COMPOUND	GO-1901699	20	-0.274434	-0.877699	0.667845	0.994704	1.000
402 GOBP-DNA-METABOLIC-PROCESS	GO-0006259	6	-0.377127	-0.878980	0.635097	0.995133	1.000
403 GOBP-GAMETE-GENERATION	GO-0007276	9	-0.326947	-0.880208	0.640741	0.995537	1.000
404 GOBP-MONOCARBOXYLIC-ACID-METABOLIC-PROCESS	GO-0032787	6	-0.371294	-0.880307	0.625000	0.998390	1.000
405 GOBP-POSITIVE-REGULATION-OF-NEURON-PROJECTION...	GO-0010976	5	-0.391478	-0.881422	0.629734	0.999122	1.000
406 GOBP-POSITIVE-REGULATION-OF-LIPASE-ACTIVITY	GO-0060193	5	-0.397590	-0.882524	0.628965	0.999964	1.000
407 GOBP-RESPONSE-TO-CARBOHYDRATE	GO-0009743	5	-0.387760	-0.882662	0.645429	1.000000	1.000
408 GOBP-REGULATION-OF-CELLULAR-LOCALIZATION	GO-0060341	17	-0.276841	-0.883352	0.614302	1.000000	1.000
409 GOBP-MITOTIC-CELL-CYCLE	GO-0000278	10	-0.321030	-0.885814	0.628750	1.000000	1.000
410 GOBP-REGULATION-OF-PHOSPHOLIPASE-C-ACTIVITY	GO-1900274	5	-0.397590	-0.887387	0.625683	1.000000	1.000
411 GOBP-TRANSMEMBRANE-RECEPTOR-PROTEIN-SERINE-THR...	GO-0007178	6	-0.380291	-0.893817	0.637097	0.991324	1.000
412 REACTOME-DISEASES-OF-SIGNAL-TRANSDUCTION-BY-GR...	R-HSA-5663202	12	-0.312370	-0.900611	0.601242	0.979409	1.000
413 GOBP-CELLULAR-RESPONSE-TO-PEPTIDE-HORMONE-STIM...	GO-0071375	9	-0.332458	-0.901989	0.607417	0.979582	1.000
414 GOBP-POSITIVE-REGULATION-OF-TRANSFERASE-ACTIVITY	GO-0051347	19	-0.277121	-0.902172	0.590698	0.982344	1.000
415 GOBP-LIPID-EXPORT-FROM-CELL	GO-0140353	5	-0.405131	-0.903079	0.594901	0.983592	1.000
416 GOBP-RECEPTOR-INTERNALIZATION	GO-0031623	5	-0.414102	-0.904008	0.620833	0.984813	1.000
417 GOBP-TUBE-DEVELOPMENT	GO-0033295	18	-0.279044	-0.904037	0.590047	0.987955	1.000
418 GOBP-NEGATIVE-REGULATION-OF-CATABOLIC-PROCESS	GO-0009895	8	-0.357945	-0.904177	0.614474	0.990871	1.000
419 GOBP-CENTRAL-NERVOUS-SYSTEM-NEURON-DIFFERENTIA...	GO-0021953	5	-0.408556	-0.905451	0.596045	0.991274	1.000
420 REACTOME-ONCOGENIC-MAPK-SIGNALING	R-HSA-6802957	5	-0.404445	-0.905885	0.583102	0.993542	1.000
421 GOBP-NEGATIVE-REGULATION-OF-TRANSPORT	GO-0051051	13	-0.307395	-0.906385	0.605875	0.995702	1.000
422 GOBP-CIRCULATORY-SYSTEM-DEVELOPMENT	GO-0072359	21	-0.272697	-0.907594	0.594373	0.996318	1.000
423 GOBP-MUSCLE-CELL-DEVELOPMENT	GO-0055001	5	-0.413976	-0.910006	0.592437	0.993923	1.000
424 GOBP-MALE-GAMETE-GENERATION	GO-0048232	5	-0.406309	-0.910148	0.591922	0.996858	1.000
425 GOBP-RESPONSE-TO-EXTRACELLULAR-STIMULUS	GO-0009991	13	-0.314332	-0.915547	0.602469	0.987841	1.000
426 GOBP-REGULATION-OF-CELLULAR-CATABOLIC-PROCESS	GO-0031329	10	-0.338927	-0.916162	0.609665	0.989733	1.000
427 GOBP-VASCULATURE-DEVELOPMENT	GO-0001944	17	-0.292637	-0.916398	0.580952	0.992532	1.000

Continuation of Table S6

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
428 GOBP-RESPONSE-TO-LIGHT-STIMULUS	GO-0009416	11	-0.324988	-0.916913	0.572660	0.994704	1.000
429 GOBP-NEGATIVE-REGULATION-OF-CELLULAR-COMPONENT...	GO-0051129	11	-0.322351	-0.919128	0.575309	0.992715	1.000
430 GOBP-REGULATION-OF-PROTEOLYSIS	GO-0030162	12	-0.319656	-0.920068	0.577307	0.994136	1.000
431 GOBP-CIRCADIAN-RHYTHM	GO-0007623	13	-0.311067	-0.923193	0.563882	0.990152	1.000
432 GOBP-POSITIVE-REGULATION-OF-PROTEIN-SERINE-THR...	GO-00071902	9	-0.348141	-0.925260	0.581425	0.988661	1.000
433 GOBP-RESPONSE-TO-PEPTIDE-HORMONE	GO-0043434	13	-0.311667	-0.925649	0.591584	0.991215	1.000
434 GOBP-PROTEIN-PHOSPHORYLATION	GO-0006468	33	-0.258178	-0.927232	0.590508	0.991023	1.000
435 GOBP-SMALL-MOLECULE-METABOLIC-PROCESS	GO-0044281	16	-0.301653	-0.929089	0.572491	0.990244	1.000
436 GOBP-CELL-JUNCTION-ORGANIZATION	GO-0034330	19	-0.287178	-0.929359	0.571934	0.993020	1.000
437 GOBP-RESPONSE-TO-CADMIUM-ION	GO-0046686	6	-0.400175	-0.930835	0.566622	0.992912	1.000
438 GOBP-REGULATION-OF-CIRCADIAN-RHYTHM	GO-0042752	7	-0.378874	-0.932605	0.583663	0.992145	1.000
439 GOBP-RESPONSE-TO-WOUNDING	GO-0009611	15	-0.304270	-0.934759	0.559466	0.990324	1.000
440 GOBP-RECEPTOR-METABOLIC-PROCESS	GO-0043112	5	-0.414102	-0.936405	0.567455	0.989864	1.000
441 GOBP-ENZYME-LINKED-RECEPTOR-PROTEIN-SIGNALING...	GO-0007167	24	-0.276629	-0.937168	0.553265	0.991593	1.000
442 GOBP-NEGATIVE-REGULATION-OF-CELL-PROJECTION-OR...	GO-0031345	5	-0.421065	-0.940792	0.554960	0.986027	1.000
443 GOBP-REGULATION-OF-CELLULAR-PROTEIN-LOCALIZATION	GO-1903827	12	-0.323978	-0.941481	0.567183	0.987688	1.000
444 GOBP-RESPONSE-TO-OXIDATIVE-STRESS	GO-0006979	8	-0.368810	-0.941561	0.559740	0.990994	1.000
445 GOBP-APOPTOTIC-MITOCHONDRIAL-CHANGES	GO-0008637	6	-0.400949	-0.941702	0.537212	0.994168	1.000
446 GOBP-POSITIVE-REGULATION-OF-PHOSPHORUS-METABOL...	GO-0010562	23	-0.278474	-0.944471	0.549943	0.991147	1.000
447 GOBP-REGULATION-OF-PROTEIN-SERINE-THREONINE-KI...	GO-0071900	12	-0.327308	-0.946735	0.538365	0.988921	1.000
448 GOBP-POSITIVE-REGULATION-OF-ESTABLISHMENT-OF-P...	GO-1904951	5	-0.422991	-0.947729	0.557065	0.990086	1.000
449 GOBP-REGULATION-OF-PROTEIN-LOCALIZATION-TO-MEM...	GO-1905475	7	-0.379583	-0.948756	0.555108	0.991186	1.000
450 GOBP-REGULATION-OF-LIPID-METABOLIC-PROCESS	GO-0019216	7	-0.384869	-0.949688	0.570470	0.992404	1.000
451 GOBP-REGULATION-OF-CATABOLIC-PROCESS	GO-0009894	13	-0.327352	-0.954400	0.523515	0.984090	1.000
452 GOBP-RESPONSE-TO-HEAT	GO-0009408	7	-0.388747	-0.960420	0.522788	0.972928	1.000
453 GOBP-CELL-CELL-SIGNALING-BY-WNT	GO-0198738	7	-0.382308	-0.961325	0.528571	0.974079	1.000
454 GOBP-RESPONSE-TO-REACTIVE-OXYGEN-SPECIES	GO-0000302	8	-0.368810	-0.961466	0.534301	0.977363	1.000
455 GOBP-REPRODUCTION	GO-0000003	18	-0.298492	-0.963504	0.525120	0.975734	1.000
456 GOBP-RESPONSE-TO-INORGANIC-SUBSTANCE	GO-0010035	19	-0.294584	-0.964646	0.515187	0.976577	1.000
457 GOBP-EMBRYONIC-ORGAN-DEVELOPMENT	GO-0048568	7	-0.387277	-0.966332	0.528121	0.975855	1.000
458 GOBP-MUSCLE-SYSTEM-PROCESS	GO-0003012	9	-0.359911	-0.968518	0.518325	0.973450	1.000
459 GOBP-CELLULAR-RESPONSE-TO-REACTIVE-OXYGEN-SPECIES	GO-0034614	7	-0.393268	-0.969891	0.533424	0.973708	1.000
460 REACTOME-SIGNALING-BY-NTRK2-TRKB	R-RNO-9006115	6	-0.402439	-0.974258	0.500000	0.966161	1.000
461 GOBP-REGULATION-OF-HYDROLASE-ACTIVITY	GO-0051336	22	-0.290844	-0.982034	0.497090	0.950193	1.000
462 GOBP-REGULATION-OF-GLIOGENESIS	GO-0014013	5	-0.447573	-0.987050	0.496393	0.940750	1.000
463 GOBP-CELLULAR-RESPONSE-TO-CHEMICAL-STRESS	GO-0062197	7	-0.450095	-0.990946	0.482260	0.934022	1.000
464 GOBP-ESTABLISHMENT-OF-PROTEIN-LOCALIZATION-TO-...	GO-0072594	5	-0.450095	-0.993776	0.488920	0.930425	1.000
465 GOBP-SECOND-MESSENGER-MEDIATED-SIGNALING	GO-0019932	16	-0.319290	-0.994408	0.467213	0.932373	1.000
466 GOBP-POSITIVE-REGULATION-OF-GLIOGENESIS	GO-0014015	5	-0.447573	-0.995198	0.473907	0.933761	1.000
467 REACTOME-NEUTROPHIL-DEGRANULATION	R-RNO-6798695	6	-0.423572	-0.997711	0.489160	0.935964	1.000
468 GOBP-CELL-ACTIVATION-INVOLVED-IN-IMMUNE-RESPONSE	GO-0002263	6	-0.423572	-0.997711	0.467480	0.934686	1.000
469 GOBP-RESPONSE-TO-METAL-ION	GO-0010038	15	-0.329158	-0.998627	0.476364	0.935914	1.000
470 GOBP-REGULATION-OF-BODY-FLUID-LEVELS	GO-0050878	11	-0.358285	-1.001766	0.459900	0.931155	1.000

Continuation of Table S6

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
471	GOBP-REGULATION-OF-ORGANELLE-ORGANIZATION	GO-0033043	14	-0.337447	-1.009621	0.456368	0.914225	1.000
472	GOBP-FORBRAIN-DEVELOPMENT	GO-0030900	10	-0.363096	-1.009999	0.443717	0.916850	1.000
473	GOBP-RESPONSE-TO-CALCIUMION	GO-0051592	6	-0.434349	-1.011688	0.462888	0.915767	1.000
474	GOBP-ENDOCYTOSIS	GO-006897	8	-0.390666	-1.012205	0.437077	0.918035	1.000
475	GOBP-CIRCULATORY-SYSTEM-PROCESS	GO-0003013	5	-0.455637	-1.012989	0.448324	0.919609	1.000
476	GOBP-LONG-TERM-MEMORY	GO-0007616	6	-0.428579	-1.014406	0.460598	0.919684	1.000
477	GOBP-REGULATION-OF-CELL-PROJECTION-ORGANIZATION	GO-0031344	20	-0.306969	-1.015699	0.458810	0.919795	1.000
478	GOBP-MUSCLE-ORGAN-DEVELOPMENT	GO-0007517	9	-0.373736	-1.017243	0.448539	0.919383	1.000
479	GOBP-RHYTHMIC-PROCESS	GO-0048511	15	-0.329280	-1.017999	0.446321	0.921172	1.000
480	GOBP-MYELOID-LEUKOCYTE-MEDIATED-IMMUNITY	GO-0002444	6	-0.423572	-1.020413	0.418157	0.918178	1.000
481	REACTOME-EXTRA-NUCLEAR-ESTROGEN-SIGNALING	R-RNO-9009391	7	-0.412487	-1.029199	0.421265	0.898100	1.000
482	GOBP-RESPONSE-TO-NICOTINE	GO-0035094	7	-0.416515	-1.031457	0.438896	0.895573	1.000
483	GOBP-TAXIS	GO-0042330	14	-0.339898	-1.031632	0.431373	0.898782	1.000
484	GOBP-REGULATION-OF-HORMONE-LEVELS	GO-0010817	12	-0.355650	-1.034795	0.404177	0.893870	1.000
485	GOBP-SEXUAL-REPRODUCTION	GO-0019953	10	-0.382210	-1.040402	0.419562	0.882369	1.000
486	GOBP-REGULATION-OF-SYNAPSE-STRUCTURE-OR-ACTIVITY	GO-0050803	11	-0.368234	-1.041782	0.404337	0.882305	1.000
487	GOBP-SYNAPSE-ORGANIZATION	GO-0050808	17	-0.330055	-1.043274	0.426887	0.881915	1.000
488	REACTOME-ESR-MEDIATED-SIGNALING	R-RNO-8939211	8	-0.406189	-1.045433	0.425560	0.879882	1.000
489	GOBP-MULTICELLULAR-ORGANISM-REPRODUCTION	GO-0032504	12	-0.364483	-1.047045	0.435961	0.879185	1.000
490	REACTOME-ANTIINFLAMMATORY-RESPONSE-FAVOURING....	R-HSA-9662851	5	-0.476903	-1.047365	0.411189	0.882081	1.000
491	HALLMARK-UV-RESPONSE-UP	M5941	5	-0.471416	-1.049798	0.393162	0.878957	1.000
492	GOBP-PROTEIN-COMPLEX-OLIGOMERIZATION	GO-0051259	7	-0.431281	-1.056544	0.392438	0.864300	1.000
493	GOBP-REGULATION-OF-SYSTEM-PROCESS	GO-0044057	18	-0.335132	-1.060573	0.418632	0.856998	1.000
494	GOBP-POSITIVE-REGULATION-OF-CELLULAR-PROTEIN-L...	GO-1903829	7	-0.430259	-1.062730	0.387399	0.854927	1.000
495	GOBP-PURINE-CONTAINING-COMPOUND-METABOLIC-PROCESS	GO-0072521	6	-0.447672	-1.064219	0.372093	0.854615	1.000
496	GOBP-REGULATION-OF-LONG-TERM-SYNAPTIC-POTENTIAL...	GO-1900271	6	-0.455590	-1.064681	0.401907	0.857136	1.000
497	GOBP-RESPONSE-TO-STARVATION	GO-0042594	5	-0.481524	-1.065815	0.359661	0.857811	1.000
498	REACTOME-SIGNALING-BY-NUCLEAR-RECEPTORS	R-RNO-9006931	8	-0.406189	-1.066692	0.404539	0.859151	1.000
499	REACTOME-PLATELET-ACTIVATION-SIGNALING-AND-AGG...	R-HSA-76002	7	-0.427030	-1.068083	0.389543	0.858916	1.000
500	GOBP-MULTICELLULAR-ORGANISMAL-RESPONSE-TO-STRESS	GO-0033555	5	-0.485190	-1.070182	0.385359	0.856954	1.000
501	GOBP-REGULATION-OF-PEPTIDE-SECRETION	GO-0002791	7	-0.437874	-1.070351	0.357616	0.860265	1.000
502	GOBP-CELLULAR-RESPONSE-TO-STARVATION	GO-0009267	5	-0.481524	-1.075573	0.373427	0.849126	1.000
503	GOBP-PROTEIN-LOCALIZATION-TO-POSTSYNAPSE	GO-0062237	5	-0.486396	-1.076414	0.375000	0.850703	1.000
504	GOBP-REGULATION-OF-PEPTIDE-HORMONE-SECRETION	GO-0090276	6	-0.466019	-1.082574	0.380223	0.837103	1.000
505	REACTOME-CELLULAR-RESPONSES-TO-EXTERNAL-STIMULI	R-RNO-8953897	11	-0.384844	-1.086205	0.361461	0.830562	1.000
506	GOBP-PROTEIN-LOCALIZATION-TO-SYNAPSE	GO-0035418	5	-0.486396	-1.086572	0.337838	0.833343	1.000
507	GOBP-ORGANIC-HYDROXY-COMPOUND-TRANSPORT	GO-0015850	6	-0.456118	-1.096272	0.348361	0.810120	1.000
508	GOBP-POSITIVE-REGULATION-OF-TRANSPORT	GO-0051050	26	-0.322156	-1.099127	0.356902	0.805588	1.000
509	GOBP-REGULATION-OF-PROTEIN-LOCALIZATION	GO-0032880	18	-0.340102	-1.100017	0.345828	0.806796	1.000
510	GOBP-RESPONSE-TO-RADIATION	GO-0009314	13	-0.372167	-1.100361	0.353960	0.809677	1.000
511	GOBP-REGULATION-OF-NERVOUS-SYSTEM-PROCESS	GO-0031644	8	-0.431106	-1.101088	0.364362	0.811578	1.000
512	GOBP-MUSCLE-TISSUE-DEVELOPMENT	GO-0060537	11	-0.388900	-1.101206	0.340768	0.814972	1.000
513	GOBP-EMBRYONIC-MORPHOGENESIS	GO-0048598	6	-0.466873	-1.106211	0.319120	0.804618	1.000

Continuation of Table S6

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
514	GOBP-LEUKOCYTE-MEDIATED-IMMUNITY	GO-0002443	8	-0.430891	-1.108912	0.320704	0.800405	1.000
515	GOBP-MULTIORGANISM-PROCESS	GO-0051704	16	-0.346949	-1.110369	0.336574	0.800216	1.000
516	GOBP-ENDOMEMBRANE-SYSTEM-ORGANIZATION	GO-0010256	6	-0.471879	-1.117926	0.340483	0.783414	1.000
517	GOBP-REGULATION-OF-INTRACELLULAR-SIGNAL-TRANS...	GO-1902531	21	-0.336651	-1.118902	0.336009	0.784286	1.000
518	REACTOME-ESTROGEN-DEPENDENT-NUCLEAR-EVENTS-DOW...	R-RNO-9634638	5	-0.500880	-1.120538	0.307153	0.783573	1.000
519	GOBP-RESPONSE-TO-DRUG	GO-0042493	11	-0.396257	-1.122134	0.311111	0.782897	1.000
520	GOBP-POSITIVE-REGULATION-OF-MAPK-CASCADE	GO-0043410	9	-0.428237	-1.126885	0.317889	0.773680	1.000
521	GOBP-CELLULAR-RESPONSE-TO-ALCOHOL	GO-0097306	5	-0.502900	-1.127052	0.310000	0.777029	1.000
522	GOBP-POSITIVE-REGULATION-OF-INTRACELLULAR-SIGN...	GO-1902533	14	-0.373160	-1.127839	0.303030	0.778727	1.000
523	GOBP-MEMORY	GO-0007613	13	-0.384815	-1.128180	0.321696	0.781634	1.000
524	GOBP-DENDRITIC-SPINE-MORPHOGENESIS	GO-0060997	5	-0.514852	-1.131873	0.296296	0.774994	1.000
525	GOBP-REGULATION-OF-PEPTIDASE-ACTIVITY	GO-0052547	10	-0.412740	-1.136852	0.309278	0.765023	1.000
526	GOBP-POSITIVE-REGULATION-OF-HYDROLASE-ACTIVITY	GO-0051345	16	-0.364479	-1.138746	0.296117	0.763032	1.000
527	GOBP-ACTIVATION-OF-MAPK-ACTIVITY	GO-0000187	6	-0.493880	-1.155529	0.247191	0.720409	1.000
528	GOBP-POSITIVE-REGULATION-OF-MAP-KINASE-ACTIVITY	GO-0043406	6	-0.493880	-1.157169	0.291287	0.719448	1.000
529	GOBP-ERK1-AND-ERK2-CASCADE	GO-0070371	5	-0.519507	-1.160664	0.270572	0.713768	1.000
530	GOBP-NEGATIVE-REGULATION-OF-CELL-CYCLE	GO-0045786	5	-0.520457	-1.160783	0.268428	0.717071	1.000
531	GOBP-ANION-TRANSMEMBRANE-TRANSPORT	GO-0098656	7	-0.467998	-1.166148	0.261905	0.705939	1.000
532	REACTOME-RNA-POLYMERASE-III-TRANSCRIPTION	R-RNO-73857	20	-0.359391	-1.171689	0.247059	0.694306	1.000
533	GOBP-POSITIVE-REGULATION-OF-LONG-TERM-SYNAPTIC...	GO-1900273	5	-0.522369	-1.173691	0.266667	0.692472	1.000
534	GOBP-CELLULAR-COMPONENT-MORPHOGENESIS	GO-0032989	25	-0.345047	-1.174357	0.265143	0.694275	1.000
535	REACTOME-MAPK-TARGETS-NUCLEAR-EVENTS-MEDIATED...	R-HSA-450282	5	-0.528385	-1.176755	0.267908	0.691302	1.000
536	GOBP-CELL-PART-MORPHOGENESIS	GO-0032990	25	-0.345047	-1.179801	0.267717	0.686362	1.000
537	REACTOME-DEVELOPMENTAL-BIOLOGY	R-RNO-1266738	22	-0.354981	-1.183012	0.260718	0.681095	1.000
538	GOBP-CELL-MORPHOGENESIS	GO-0009092	25	-0.345047	-1.184609	0.251995	0.680333	1.000
539	GOBP-REGULATION-OF-PEPTIDE-TRANSPORT	GO-0090087	10	-0.431972	-1.188118	0.246787	0.674382	1.000
540	GOBP-CELL-CYCLE-PROCESS	GO-0022402	11	-0.422034	-1.189070	0.237611	0.675377	1.000
541	GOBP-CELL-MORPHOGENESIS-INVOLVED-IN-NEURON-DIF...	GO-0048667	22	-0.358398	-1.189309	0.254023	0.678480	1.000
542	GOBP-POSITIVE-REGULATION-OF-CELL-DEATH	GO-0010942	19	-0.363029	-1.190170	0.248235	0.679958	1.000
543	GOBP-PROTEIN-LOCALIZATION-TO-ORGANELLE	GO-0033365	8	-0.467929	-1.193822	0.236041	0.673191	1.000
544	GOBP-RESPIRATORY-SYSTEM-DEVELOPMENT	GO-0060541	6	-0.511778	-1.195323	0.221289	0.672861	1.000
545	REACTOME-SIGNALING-BY-WNT	R-RNO-195721	7	-0.482202	-1.196352	0.238411	0.673670	1.000
546	GOBP-CELL-MORPHOGENESIS-INVOLVED-IN-DIFFERENTI...	GO-0000904	22	-0.358398	-1.199990	0.244521	0.667177	1.000
547	GOBP-SKELETAL-MUSCLE-ORGAN-DEVELOPMENT	GO-0060538	5	-0.536128	-1.200111	0.226891	0.670538	1.000
548	GOBP-RESPONSE-TO-ALKALOID	GO-0043279	5	-0.538151	-1.200167	0.216066	0.674179	1.000
549	GOBP-CALCIUM-MEDIATED-SIGNALING	GO-0019722	10	-0.438828	-1.200591	0.243073	0.676715	1.000
550	GOBP-MITOCHONDRION-ORGANIZATION	GO-0007005	7	-0.484528	-1.201357	0.236000	0.678484	1.000
551	REACTOME-POST-TRANSLATIONAL-PROTEIN-MODIFICATION	R-RNO-597592	7	-0.489380	-1.201414	0.218543	0.682158	1.000
552	GOBP-REGULATION-OF-MAP-KINASE-ACTIVITY	GO-0043405	9	-0.453353	-1.202411	0.240602	0.683376	1.000
553	GOBP-CELLULAR-MACROMOLECULE-LOCALIZATION	GO-0070727	20	-0.365628	-1.204134	0.224277	0.682272	1.000
554	GOBP-POSITIVE-REGULATION-OF-PROTEIN-METABOLISM...	GO-0051247	27	-0.345549	-1.205970	0.243820	0.681016	1.000
555	REACTOME-INTEGRATION-OF-ENERGY-METABOLISM	R-RNO-163685	5	-0.542169	-1.209384	0.240331	0.675202	1.000
556	GOBP-TELENCEPHALON-DEVELOPMENT	GO-0021537	7	-0.483254	-1.210240	0.220028	0.676509	1.000

Continuation of Table S6

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
GOBP-PROTEIN_LOCALIZATION_TO_MEMBRANE	GO-0072657	13	-0.412578	-1.215876	0.232360	0.664307	1.000
GOBP-REGULATION_OF_TRANSMEMBRANE_TRANSPORT	GO-0034762	23	-0.357250	-1.218218	0.227950	0.661669	1.000
GOBP-ADENYLATE_CYCLASE_INHIBITING_G_PROTEIN_CO...	GO-0007196	5	-0.554022	-1.220394	0.220816	0.659065	1.000
GOBP-POSITIVE_REGULATION_OF_PROTEOLYSIS	GO-0045862	8	-0.475030	-1.220790	0.232558	0.661975	1.000
GOBP-PROTEIN_LOCALIZATION_TO_PLASMA_MEMBRANE	GO-0072659	7	-0.500420	-1.223316	0.207622	0.659066	1.000
GOBP-INSULIN_SECRETION	GO-0030073	7	-0.494120	-1.224552	0.221614	0.659684	1.000
GOBP-CELLULAR_COMPONENT_MAINTENANCE	GO-0043954	5	-0.544998	-1.224787	0.209497	0.663032	1.000
GOBP-EPITHELIAL_CELL_DIFFERENTIATION	GO-0030855	7	-0.497576	-1.228931	0.201847	0.655568	1.000
GOBP-POSITIVE_REGULATION_OF_PEPTIDASE_ACTIVITY	GO-0010952	7	-0.506670	-1.230211	0.194444	0.656014	1.000
GOBP-REGULATION_OF_MUSCLE_ADAPTATION	GO-0043502	5	-0.550733	-1.233226	0.196453	0.651259	1.000
GOBP-REGULATION_OF_POSTSYNAPSE_ORGANIZATION	GO-0099175	6	-0.524672	-1.233911	0.201072	0.653392	1.000
GOBP-REGULATION_OF_CYSSTEINE_TYPE_ENDOPEPTIDASE...	GO-2000116	9	-0.459510	-1.234881	0.200782	0.654676	1.000
GOBP-CELLULAR_RESPONSE_TO_INORGANIC_SUBSTANCE	GO-0071241	11	-0.440201	-1.238110	0.191011	0.649599	1.000
GOBP-NEURON_DIFFERENTIATION	GO-0030182	37	-0.345350	-1.239698	0.214597	0.649013	1.000
GOBP-MUSCLE_ADAPTATION	GO-0043500	5	-0.550733	-1.241769	0.186969	0.647111	1.000
GOBP-ESTABLISHMENT_OF_PROTEIN_LOCALIZATION	GO-0045184	17	-0.396998	-1.242524	0.197430	0.649090	1.000
GOBP-CHEMICAL_SYNAPTIC_TRANSMISSION_POSTSYNAPTIC	GO-0099565	9	-0.462464	-1.244061	0.199224	0.649076	1.000
GOBP-REGULATION_OF_SYNAPTIC_TRANSMISSION_GLUTA...	GO-0051966	12	-0.436316	-1.247869	0.214724	0.642536	1.000
GOBP-ORGANOPHOSPHATE_METABOLIC_PROCESS	GO-0019637	8	-0.485329	-1.252971	0.182529	0.632291	1.000
GOBP-DENDRITE_DEVELOPMENT	GO-0016358	10	-0.453225	-1.253528	0.186352	0.634851	1.000
GOBP-REGULATION_OF_MAPK_CASCADE	GO-0043408	13	-0.418682	-1.254315	0.186585	0.636952	1.000
GOBP-PEPTIDE_HORMONE_SECRETION	GO-0030072	7	-0.494120	-1.256270	0.206494	0.635683	1.000
REACTOME_BETA_CATENIN_INDEPENDENT_WNT_SIGNALING	R-RNO-3858494	5	-0.566205	-1.256370	0.188406	0.639779	1.000
GOBP-TEMPERATURE_HOMEOSTASIS	GO-0001659	5	-0.560088	-1.259294	0.174221	0.635855	1.000
GOBP-GLIOGENESIS	GO-0042063	12	-0.437677	-1.262367	0.169118	0.631376	1.000
REACTOME_CLASS_C_3_METABOTROPIC_GLUTAMATE_PHER...	R-RNO-420499	7	-0.507326	-1.266290	0.177866	0.624270	1.000
GOBP-POSITIVE_REGULATION_OF_CYSSTEINE_TYPE_ENDO...	GO-2001056	7	-0.506670	-1.271326	0.184426	0.614429	1.000
GOBP-TRANSMEMBRANE_TRANSPORT	GO-0055085	27	-0.361807	-1.275317	0.158427	0.607070	1.000
GOBP-PROTEIN_LOCALIZATION_TO_CELL_PERIPHERY	GO-1990778	12	-0.443422	-1.276364	0.171569	0.608608	1.000
GOBP-CELLULAR_RESPONSE_TO_CADMIUM_ION	GO-0071276	5	-0.577965	-1.279612	0.150815	0.603532	1.000
GOBP-REGULATION_OF_METAL_ION_TRANSPORT	GO-0010959	6	-0.544639	-1.280391	0.149254	0.605753	1.000
GOBP-AXON_DEVELOPMENT	GO-0061564	18	-0.504585	-1.282507	0.164269	0.603810	1.000
GOBP-MYELOID_LEUKOCYTE_ACTIVATION	GO-0002274	8	-0.504585	-1.282507	0.163030	0.596468	1.000
GOBP-POSITIVE_REGULATION_OF_NEURON_DEATH	GO-1901216	5	-0.567978	-1.293057	0.147383	0.582467	1.000
GOBP-DEVELOPMENTAL_MATURATION	GO-0021700	5	-0.58263	-1.299380	0.156425	0.596658	1.000
GOBP-PROTEIN_TETRAMERIZATION	GO-0051262	5	-0.582145	-1.307806	0.135246	0.550919	1.000
REACTOME_G_ALPHA_Q_SIGNALING_EVENTS	R-RNO-416476	6	-0.557530	-1.310865	0.142259	0.546887	1.000
GOBP-CELL_SURFACE_RECEPTOR_SIGNALING_PATHWAY_I...	R-1905114	15	-0.420965	-1.317332	0.142518	0.533561	1.000
GOBP-REGULATION_OF_HORMONE_SECRETION	GO-0046883	8	-0.516624	-1.335001	0.122876	0.491102	1.000
GOBP-REGULATION_OF_TRANSPORTER_ACTIVITY	GO-0032409	17	-0.423584	-1.335864	0.134118	0.492576	1.000
GOBP-POSITIVE_REGULATION_OF_MOLECULAR_FUNCTION	GO-0044093	37	-0.368582	-1.339329	0.138239	0.487289	1.000
GOBP-ORGANOPHOSPHATE_BIOSYNTHETIC_PROCESS	GO-0090407	5	-0.604715	-1.343017	0.105263	0.481612	1.000
GOBP-PEPTIDE_SECRETION	GO-0002790	9	-0.498265	-1.343548	0.120000	0.484215	1.000

Continuation of Table S6

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
600	GOBP-FATTY-ACID-TRANSPORT	GO-0015908	6	-0.565687	-1.343981	0.120596	0.486915	1.000
601	GOBP-POSTSYNAPSE.ORGANIZATION	GO-0099173	10	-0.496171	-1.344516	0.121437	0.489366	1.000
602	GOBP-ORGANIC-ACID-TRANSPORT	GO-0015849	7	-0.543054	-1.347476	0.107143	0.485777	1.000
603	GOBP-NUCLEOSIDE-PHOSPHATE-BIOSYNTHETIC-PROCESS	GO-1901293	5	-0.604715	-1.353237	0.106145	0.474708	1.000
604	GOBP-G-PROTEIN-COUPLED-GLUTAMATE-RECEPTOR-SIGN...	GO-0007216	8	-0.523834	-1.353774	0.120823	0.477042	1.000
605	GOBP-NUCLEOBASE-CONTAINING-SMALL-MOLECULE-META...	GO-0055086	7	-0.555078	-1.354543	0.110067	0.479075	1.000
606	GOBP-MULTI-MULTICELLULAR-ORGANISM-PROCESS	GO-0004706	8	-0.52736	-1.356030	0.115681	0.479252	1.000
607	GOBP-SYNAPTIC-TRANSMISSION-GLUTAMATERGIC	GO-0035249	13	-0.456545	-1.362213	0.117429	0.467853	1.000
608	GOBP-CELL-PROJECTION-ORGANIZATION	GO-0030030	35	-0.373087	-1.362311	0.111849	0.471638	1.000
609	REACTOME-GPCR-LIGAND-BINDING	R-RNO-500792	8	-0.525887	-1.367952	0.094148	0.461421	1.000
610	REACTOME-G-ALPHA-Z-SIGNALING-EVENTS	R-RNO-118597	5	-0.609410	-1.372797	0.091938	0.453698	1.000
611	GOBP-POSITIVE-REGULATION-OF-SECRETION	GO-0051047	6	-0.575026	-1.372858	0.094595	0.457443	1.000
612	GOBP-DICARBOXYLIC-ACID-TRANSPORT	GO-0006835	5	-0.624967	-1.373425	0.083333	0.460011	1.000
613	GOBP-MEMBRANE-ORGANIZATION	GO-0061024	12	-0.475936	-1.377446	0.088418	0.453678	1.000
614	GOBP-GLIAL-CELL-DIFFERENTIATION	GO-0010001	10	-0.501228	-1.380678	0.094994	0.449515	1.000
615	REACTOME-L1CAM-INTERACTIONS	R-RNO-373760	7	-0.628147	-1.382939	0.090909	0.447854	1.000
616	GOBP-DENDRITE-MORPHOGENESIS	GO-0048813	5	-0.554950	-1.383141	0.095176	0.451488	1.000
617	REACTOME-EPH-EPHRIN-SIGNALING	R-RNO-2682334	6	-0.582873	-1.383299	0.102180	0.455286	1.000
618	GOBP-SECRETION	GO-0046903	24	-0.409581	-1.383696	0.109070	0.458414	1.000
619	GOBP-ACIDIC-AMINO-ACID-TRANSPORT	GO-0015800	5	-0.624947	-1.384145	0.090014	0.461625	1.000
620	GOBP-DENDRITIC-SPINE-DEVELOPMENT	GO-0060996	6	-0.576691	-1.388516	0.106901	0.454838	1.000
621	GOBP-NEURON-DEVELOPMENT	GO-0048666	34	-0.385072	-1.388806	0.098324	0.458369	1.000
622	GOBP-AMINO-ACID-TRANSPORT	GO-0006865	6	-0.597876	-1.392111	0.083221	0.454392	1.000
623	GOBP-CARBOXYLIC-ACID-TRANSPORT	GO-0046942	6	-0.597876	-1.395719	0.093623	0.449473	1.000
624	GOBP-HORMONE-TRANSPORT	GO-0009914	9	-0.534973	-1.396604	0.088083	0.451522	1.000
625	GOBP-CALCIUM-ION-TRANSMEMBRANE-TRANSPORT	GO-0070588	7	-0.573322	-1.396796	0.084100	0.455509	1.000
626	GOBP-SENSORY-ORGAN-DEVELOPMENT	GO-0007423	8	-0.539262	-1.400108	0.101935	0.451501	1.000
627	GOBP-MONOCARBOXYLIC-ACID-TRANSPORT	GO-0015718	5	-0.624947	-1.400890	0.084469	0.454094	1.000
628	REACTOME-DAG-AND-IP3-SIGNALING	R-RNO-1489509	8	-0.545640	-1.401913	0.079470	0.456195	1.000
629	GOBP-EXOCYTOSIS	GO-0006887	11	-0.490628	-1.407056	0.082174	0.447395	1.000
630	GOBP-NEURON-PROJECTION-ORGANIZATION	GO-0106027	8	-0.551982	-1.407599	0.089032	0.450853	1.000
631	REACTOME-MAPK-FAMILY-SIGNALING-CASCADES	R-RNO-5683057	12	-0.482904	-1.411985	0.079807	0.444243	1.000
632	GOBP-CYTOSOLIC-CALCIUM-ION-TRANSPORT	GO-0060401	7	-0.573322	-1.414494	0.077446	0.443097	1.000
633	GOBP-REGULATION-OF-ION-TRANSPORT	GO-0043269	36	-0.389808	-1.417684	0.089305	0.440361	1.000
634	GOBP-CATION-TRANSMEMBRANE-TRANSPORT	GO-0098655	18	-0.439388	-1.419000	0.081395	0.441844	1.000
635	GOBP-ORGANIC-ANION-TRANSPORT	GO-0015711	6	-0.597876	-1.421787	0.073370	0.439285	1.000
636	GOBP-HOMEOSTATIC-PROCESS	GO-0042592	31	-0.398999	-1.422121	0.071429	0.443275	1.000
637	GOBP-INORGANIC-ION-TRANSMEMBRANE-TRANSPORT	GO-0098660	9	-0.527261	-1.425988	0.062262	0.438213	1.000
638	GOBP-CELLULAR-HOMEOSTASIS	GO-0019725	18	-0.449661	-1.426856	0.072941	0.440681	1.000
639	REACTOME-NEUROUS-SYSTEM-DEVELOPMENT	R-RNO-9675108	14	-0.475167	-1.428879	0.065296	0.440114	1.000
640	GOBP-CALCIUM-ION-TRANSPORT	GO-0006816	11	-0.502948	-1.429027	0.076826	0.445039	1.000
641	REACTOME-TRANSCRIPTIONAL-REGULATION_BY_MECP2	R-RNO-8986944	7	-0.582810	-1.429380	0.063325	0.449413	1.000
642	GOBP-MONOAMINE-TRANSPORT	GO-0015844	5	-0.645358	-1.434131	0.065278	0.443499	1.000

Continuation of Table S6

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
643	GOBP-IONOTROPIC-GLUTAMATE-RECEPTOR-SIGNALING.P...	GO-0035235	9	-0.537666	-1.437174	0.070000	0.440229	1.000
644	GOBP-REGULATION-OF-VESICLE-MEDIATED-TRANSPORT	GO-0060627	12	-0.495908	-1.437770	0.078205	0.444267	1.000
645	GOBP-CALCIUM-ION-TRANSPORT-INTO-CYTOSOL	GO-0060402	7	-0.573322	-1.438866	0.080537	0.446581	1.000
646	GOBP-CHEMICAL-HOMEOSTASIS	GO-0048878	23	-0.427048	-1.439643	0.084296	0.450087	1.000
647	GOBP-METAL-ION-TRANSPORT	GO-0030001	11	-0.502948	-1.440051	0.069853	0.454836	1.000
648	GOBP-RESPONSE-TO-NITROGEN-COMPOUND	GO-1901698	35	-0.406253	-1.447275	0.076923	0.441411	1.000
649	REACTOME-RAS-ACTIVATION-UPON-CA2-INFLUX-THROUGH...	R-HSA-442982	6	-0.612042	-1.457593	0.065246	0.420542	1.000
650	GOBP-POSITIVE-REGULATION-OF-SIGNALING	GO-0023056	34	-0.406980	-1.458933	0.062084	0.422360	1.000
651	GOBP-LONG-TERM-SYNAPTIC-POTENTIATION	GO-0060291	12	-0.505580	-1.469100	0.058096	0.402125	1.000
652	GOBP-NEUROGENESIS	GO-0022008	41	-0.408275	-1.473300	0.057047	0.396711	1.000
653	GOBP-RESPONSE-TO-ABIOTIC-STIMULUS	GO-0009628	27	-0.420002	-1.473553	0.055866	0.401478	1.000
654	GOBP-VESICLE-MEDIATED-TRANSPORT-IN-SYNAPSE	GO-0099003	7	-0.597739	-1.476885	0.058124	0.398696	1.000
655	GOBP-ADENYLATE-CYCLASE-INHIBITING-G-PROTEIN.CO...	GO-0007193	9	-0.553073	-1.477594	0.073383	0.402464	1.000
656	GOBP-EXCITATORY-CHEMICAL-SYNAPTIC-TRANSMISSION	GO-0098976	5	-0.674349	-1.482913	0.043539	0.394982	1.000
657	GOBP-REGULATION-OF-TRANSPORT	GO-0051049	44	-0.409308	-1.483467	0.060307	0.399382	1.000
658	REACTOME-SYNAPTIC-ADHESION-LIKE-MOLECULES	R-RNO-8849932	9	-0.565946	-1.493910	0.035202	0.378258	1.000
659	REACTOME-TRAFFICKING-OF-GLUR2-CONTAINING-AMPA...	R-RNO-416993	8	-0.584130	-1.494439	0.066225	0.382469	1.000
660	GOBP-RESPONSE-TO-ALCOHOL	GO-0097305	11	-0.532213	-1.496157	0.055696	0.383915	1.000
661	GOBP-METAL-ION-HOMEOSTASIS	GO-0055065	14	-0.497848	-1.499174	0.043742	0.382033	1.000
662	GOBP-EPHRIN-RECEPTOR-SIGNALING-PATHWAY	GO-0040403	5	-0.674042	-1.500579	0.046008	0.384492	1.000
663	GOBP-POSITIVE-REGULATION-OF-CATALYTIC-ACTIVITY	GO-0043085	29	-0.441269	-1.512506	0.043624	0.361039	1.000
664	GOBP-REGULATION-OF-NEUROTRANSMITTER-LEVELS	GO-0001505	7	-0.617669	-1.515815	0.041444	0.358831	1.000
665	GOBP-NEUROTRANSMITTER-TRANSPORT	GO-0008636	7	-0.617669	-1.523413	0.037037	0.347095	1.000
666	GOBP-LOCOMOTORY-BEHAVIOR	GO-0007626	8	-0.578414	-1.531450	0.042581	0.334641	1.000
667	GOBP-MAPK-CASCADE	GO-0000165	18	-0.481307	-1.532718	0.037209	0.337364	1.000
668	GOBP-REGULATION-OF-POSTSYNAPTIC-MEMBRANE-POTEN...	GO-0060078	14	-0.510995	-1.541737	0.035496	0.322805	1.000
669	REACTOME-LONG-TERM-POTENTIATION	R-HSA-9620244	10	-0.564724	-1.545852	0.026718	0.319676	1.000
670	GOBP-MATERNAL-PROCESS-INVOLVED-IN-FEMALE-PREGN...	GO-0060135	5	-0.689626	-1.546167	0.033520	0.324773	1.000
671	REACTOME-NEUREXINS-AND-NEUROLIGINS	R-RNO-6794361	9	-0.583649	-1.553540	0.023622	0.314913	1.000
672	REACTOME-INTRACELLULAR-SIGNALING-BY-SECOND.MES...	R-RNO-9006925	15	-0.508988	-1.557504	0.033175	0.312030	1.000
673	GOBP-PROTEIN-CONTAINING-COMPLEX-SUBUNIT-ORGANI...	GO-0043933	15	-0.514730	-1.562909	0.029976	0.305645	1.000
674	GOBP-HEAD-DEVELOPMENT	GO-0060322	23	-0.459542	-1.562981	0.036047	0.311515	1.000
675	GOBP-NEUROTRANSMITTER-SECRETION	GO-0007269	6	-0.658537	-1.573744	0.031662	0.294132	1.000
676	REACTOME-NEGATIVE-REGULATION-OF-NMDA-RECEPTOR...	R-HSA-961732	8	-0.609517	-1.581282	0.024485	0.283479	1.000
677	REACTOME-ASSEMBLY-AND-CELL-SURFACE-PRESENTATIO...	R-RNO-9609736	8	-0.609517	-1.58045	0.023316	0.281518	1.000
678	REACTOME-PTEN-REGULATION	R-RNO-6807070	5	-0.711373	-1.589450	0.025956	0.278012	1.000
679	GOBP-CENTRAL-NERVOUS-SYSTEM-DEVELOPMENT	GO-0007417	27	-0.459423	-1.595509	0.017026	0.271078	1.000
680	REACTOME-CA-DEPENDENT-EVENTS	R-RNO-111996	8	-0.625000	-1.605423	0.024235	0.256591	1.000
681	GOBP-REGULATION-OF-MEMBRANE-POTENTIAL	GO-0042391	17	-0.504949	-1.608057	0.025731	0.256983	1.000
682	GOBP-ENDOCRINE-SYSTEM-DEVELOPMENT	GO-0035270	6	-0.686349	-1.614611	0.023035	0.249867	1.000
683	GOBP-REGULATION-OF-CYTOSOLIC-CALCIUM-ION-CONCE...	GO-0051480	13	-0.548547	-1.624236	0.020631	0.236795	1.000
684	GOBP-DIVALENT-INORGANIC-CATION-HOMEOSTASIS	GO-0072507	13	-0.548547	-1.626426	0.016867	0.238239	1.000
685	GOBP-REGULATION-OF-CATION-TRANSMEMBRANE-TRANSPORT	GO-1904062	16	-0.522452	-1.630347	0.020457	0.237078	1.000

Continuation of Table S6

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
686	GOBP-ADENYLATE_CYCLASE-MODULATING-G-PROTEIN.CO...	11	-0.575197	-1.631949	0.016049	0.239970	1.000
687	GOBP-REGULATION-OF-NEURONAL-SYNAPTIC-PLASTICITY	7	-0.671868	-1.674084	0.006757	0.174043	0.998
688	GOBP-ION-HOMEOSTASIS	16	-0.534390	-1.674562	0.010883	0.177972	0.998
689	REACTOME-OPIOID-SIGNALING	12	-0.578947	-1.675804	0.016393	0.180725	0.998
690	GOBP-REGULATION-OF-SECRETION	14	-0.552200	-1.683909	0.007168	0.174410	0.997
691	REACTOME-PROTEIN-PROTEIN-INTERACTIONS-AT-SYNAPSES	12	-0.587224	-1.700171	0.011307	0.155660	0.994
692	GOBP-COGNITION	28	-0.488629	-1.713015	0.009091	0.144083	0.992
693	GOBP-REGULATION-OF-CATION-CHANNEL-ACTIVITY	14	-0.574871	-1.714200	0.013018	0.147328	0.991
694	GOBP-ASSOCIATIVE-LEARNING	7	-0.490872	-1.714581	0.006757	0.151709	0.991
695	GOBP-NERVOUS-SYSTEM-PROCESS	38	-0.472666	-1.715893	0.006593	0.155510	0.990
696	REACTOME-G-PROTEIN-MEDIATED-EVENTS	9	-0.632911	-1.717259	0.007595	0.159273	0.989
697	GOBP-G-PROTEIN-COUPLED-RECEPTOR-SIGNALING-PATHWAY	18	-0.547868	-1.728097	0.014286	0.149059	0.981
698	REACTOME-CREB1-PHOSPHORYLATION-THROUGH-NMDA.RE...	8	-0.667485	-1.730324	0.006579	0.151196	0.979
699	GOBP-CATION-TRANSPORT	25	-0.507066	-1.732377	0.012687	0.154251	0.979
700	GOBP-REGULATION-OF-SIGNALING-RECEPTOR-ACTIVITY	14	-0.570295	-1.734783	0.010856	0.156608	0.978
701	GOBP-REGULATION-OF-NMDA-RECEPTOR-ACTIVITY	10	-0.643207	-1.738805	0.009988	0.157851	0.975
702	GOBP-CELLULAR-ION-HOMEOSTASIS	14	-0.586959	-1.749861	0.008373	0.148060	0.967
703	GOBP-POSITIVE-REGULATION-OF-SYNAPTIC-TRANSMISSION	15	-0.568107	-1.752610	0.006024	0.150662	0.961
704	GOBP-GLUTAMATE-RECEPTOR-SIGNALING-PATHWAY	17	-0.547291	-1.760493	0.008304	0.146765	0.952
705	GOBP-REGULATION-OF-NEUROTRANSMITTER-TRANSPORT	6	-0.738216	-1.764317	0.006729	0.149277	0.948
706	REACTOME-UNBLOCKING-OF-NMDA-RECEPTORS-GLUTAMAT...	12	-0.603836	-1.772242	0.004944	0.146428	0.940
707	REACTOME-TRAFFICKING-OF-AMPA-RECEPTORS	11	-0.612620	-1.772307	0.010204	0.154563	0.940
708	GOBP-REGULATION-OF-NEUROTRANSMITTER-RECEPTOR-A...	13	-0.605535	-1.792867	0.002413	0.133359	0.903
709	GOBP-SYNAPTIC-SIGNALING	47	-0.497587	-1.819590	0.005507	0.110527	0.848
710	GOBP-SIGNAL-RELEASE	14	-0.606604	-1.826460	0.003745	0.110375	0.830
711	GOBP-SENSORY-PERCEPTION-OF-PAIN	5	-0.821836	-1.827264	0.002869	0.117237	0.829
712	REACTOME-SIGNALING-BY-GPCR	22	-0.561404	-1.850861	0.003501	0.098777	0.748
713	GOBP-LEARNING	13	-0.623505	-1.856330	0.003676	0.100764	0.722
714	GOBP-BEHAVIOR	33	-0.524783	-1.866342	0.002222	0.100165	0.687
715	REACTOME-ACTIVATION-OF-NMDA-RECEPTORS-AND-POST...	16	-0.606031	-1.902437	0.002331	0.075281	0.550
716	GOBP-REGULATION-OF-SYNAPTIC-PLASTICITY	21	-0.581217	-1.925688	0.001145	0.063086	0.455
717	REACTOME-G-ALPHA-I-SIGNALING-EVENTS	18	-0.611447	-1.954176	0.000000	0.051105	0.361
718	GOBP-CELL-CELL-SIGNALING	56	-0.546936	-1.970412	0.000000	0.047453	0.304
719	GOBP-SENSORY-PERCEPTION	9	-0.748452	-1.978668	0.001295	0.050751	0.278
720	GOBP-REGULATION-OF-TRANS-SYNAPTIC-SIGNALING	40	-0.550881	-2.015969	0.000000	0.036091	0.183
721	GOBP-RESPONSE-TO-ETHANOL	5	-0.920693	-2.053963	0.001368	0.029496	0.128
722	REACTOME-NEUROTRANSMITTER-RECEPTORS-AND-POSTSY...	22	-0.635096	-2.107194	0.000000	0.019659	0.066
723	REACTOME-TRANSMISSION-ACROSS-CHEMICAL-SYNAPSES	23	-0.647100	-2.226893	0.000000	0.004021	0.009
724	REACTOME-NEURONAL-SYSTEM	26	-0.658596	-2.307014	0.000000	0.003537	0.004

End of Table

Supplementary Table S7: SC caudal segment late (45 DPL peak) profile GSEA results.

Begin of Table S7									
	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val	
0	GOBP-REGULATION_OF_TRANSPORT	GO-0051049	44	0.474193	1.889698	0.003604	1.000000	0.789	
1	GOBP-REGULATION_OF_NMDA_RECEPTOR_ACTIVITY	GO-2000310	10	0.663015	1.875735	0.003906	0.697381	0.829	
2	REACTOME_BETA_CATENIN_INDEPENDENT_WNT_SIGNALING	R-RNO-3858494	5	0.831325	1.867099	0.009560	0.499257	0.853	
3	REACTOME_TRAFFICKING_OF_AMPA_RECEPTORS	R-RNO-399719	11	0.586301	1.760962	0.015444	0.925434	0.990	
4	GOBP-POSITIVE_REGULATION_OF_PHOSPHATIDYLINOSIT...	GO-0014068	5	0.760268	1.745467	0.009862	0.828830	0.998	
5	GOBP-REGULATION_OF_SECRETION	GO-0051046	14	0.559599	1.735413	0.011450	0.740975	0.999	
6	REACTOME_CA_DEPENDENT_EVENTS	R-RNO-111996	8	0.634228	1.682862	0.025591	0.927006	1.000	
7	GOBP-REGULATION_OF_ION_TRANSPORT	GO-0043269	36	0.425834	1.674123	0.014440	0.861662	1.000	
8	GOBP_MULTICELLULAR_ORGANISMAL_RESPONSE_TO_STRESS	GO-0033555	5	0.725926	1.662167	0.023438	0.835798	1.000	
9	GOBP-REGULATION_OF_PHOSPHATIDYLINOSITOL_3_KINA...	GO-0014066	6	0.690108	1.649739	0.035055	0.817130	1.000	
10	REACTOME_TRAFFICKING_OF_GLR2_CONTAINING_AMPA...	R-RNO-416993	8	0.622691	1.635950	0.022312	0.814072	1.000	
11	GOBP-SIGNAL_RELEASE	GO-0023061	14	0.507187	1.593127	0.028736	0.977330	1.000	
12	GOBP_NUCLEOSIDE_PHOSPHATE_BIOSYNTHETIC_PROCESS	GO-1901293	5	0.695524	1.581219	0.034682	0.969315	1.000	
13	REACTOME_NEUROTRANSMITTER_RECEPTORS_AND_POSTSY...	R-RNO-112314	22	0.443452	1.577878	0.041353	0.916988	1.000	
14	GOBP-REGULATION_OF_SYNAPTIC_PLASTICITY	GO-0048167	21	0.446175	1.565029	0.041293	0.922754	1.000	
15	GOBP_ORGANOPHOSPHATE_BIOSYNTHETIC_PROCESS	GO-0090407	5	0.695524	1.564679	0.049020	0.866720	1.000	
16	REACTOME_TRANSMISSION_ACROSS_CHEMICAL_SYNAPSES	R-RNO-112315	23	0.425414	1.555688	0.028302	0.857711	1.000	
17	GOBP-REGULATION_OF_ENDOCYTOSIS	GO-0030100	6	0.625754	1.524679	0.072614	0.964385	1.000	
18	GOBP-NEURON_DIFFERENTIATION	GO-0030182	37	0.380794	1.498858	0.039146	1.000000	1.000	
19	GOBP-REGULATION_OF_VESICLE_MEDIATED_TRANSPORT	GO-0060627	12	0.491614	1.475037	0.095517	1.000000	1.000	
20	GOBP-POSITIVE_REGULATION_OF_PEPTIDYL_TYROSINE...	GO-0050731	8	0.568632	1.470524	0.091262	1.000000	1.000	
21	REACTOME_ACTIVATION_OF_NMDA_RECEPTORS_AND_POST...	R-RNO-442755	16	0.445542	1.466909	0.077381	1.000000	1.000	
22	GOBP-POSITIVE_REGULATION_OF_ORGANELLE_ORGANIZA...	GO-0010638	10	0.516408	1.456897	0.081633	1.000000	1.000	
23	GOBP-ENDOCYTOSIS	GO-0006897	8	0.561568	1.456420	0.096457	1.000000	1.000	
24	GOBP-TAXIS	GO-0042330	14	0.445904	1.450670	0.077710	1.000000	1.000	
25	REACTOME_NEURONAL_SYSTEM	R-RNO-112316	26	0.388813	1.445383	0.062030	1.000000	1.000	
26	GOBP-DEVELOPMENTAL_MATURATION	GO-0021700	5	0.644710	1.441076	0.101167	0.989905	1.000	
27	GOBP-REGULATION_OF_NEUROTRANSMITTER_TRANSPORT	GO-0051588	6	0.607224	1.436559	0.108911	0.975692	1.000	
28	GOBP-INSULIN_SECRETION	GO-0030073	7	0.563899	1.429114	0.085828	0.975825	1.000	
29	GOBP-PEPTIDE_HORMONE_SECRETION	GO-0030072	7	0.563899	1.419962	0.116466	0.983538	1.000	
30	GOBP-NEGATIVE_REGULATION_OF_CELL_PROJECTION_OR...	GO-0031345	5	0.638554	1.417892	0.112167	0.960695	1.000	
31	REACTOME_DAG_AND_IP3_SIGNALING	R-RNO-1489509	8	0.542408	1.416519	0.089866	0.936074	1.000	
32	REACTOME_G_PROTEIN_MEDIATED_EVENTS	R-RNO-112040	9	0.518577	1.415466	0.111111	0.912166	1.000	
33	GOBP-CYTOSKELETON_ORGANIZATION	GO-0007010	11	0.469657	1.409864	0.099426	0.908896	1.000	
34	GOBP-SECRETION	GO-0046903	24	0.385010	1.406475	0.095149	0.896980	1.000	
35	GOBP-REGULATION_OF_PEPTIDE_SECRETION	GO-0002791	7	0.549880	1.405874	0.100386	0.874777	1.000	
36	GOBP-NEUROTRANSMITTER_TRANSPORT	GO-0006836	7	0.544502	1.402483	0.105263	0.864331	1.000	
37	GOBP-REGULATION_OF_NEUROTRANSMITTER_LEVELS	GO-0001505	7	0.544502	1.397612	0.130518	0.859994	1.000	
38	GOBP-POSITIVE_REGULATION_OF_PROTEIN_TYROSINE_K...	GO-0061098	5	0.610675	1.392818	0.118321	0.856408	1.000	
39	GOBP-POSITIVE_REGULATION_OF_INTRACELLULAR_SIGN...	GO-1902533	14	0.437784	1.384024	0.097606	0.869543	1.000	
40	GOBP-REGULATION_OF_PEPTIDE_HORMONE_SECRETION	GO-0090276	6	0.583321	1.375093	0.130769	0.883623	1.000	

Continuation of Table S7

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
41	GOBP-REGULATION-OF-PEPTIDYL-TYROSINE-PHOSPHORY...	GO-0050730	9	0.491862	1.372482	0.123753	0.872647	1.000
42	GOBP-REGULATION-OF-RECEPTOR-MEDIATED-ENDOCYTOSIS	GO-0048259	5	0.607019	1.366538	0.135397	0.874096	1.000
43	GOBP-NEUROGENESIS	GO-0022008	41	0.339989	1.360091	0.108893	0.878318	1.000
44	REACTOME-G-ALPHA-Z-SIGNALING-EVENTS	R-RNO-418597	5	0.593937	1.354861	0.131179	0.877576	1.000
45	GOBP-REGULATION-OF-PROTEIN-TYROSINEKINASE-ACT...	GO-0061097	5	0.610675	1.347464	0.177993	0.887397	1.000
46	GOBP-REGULATION-OF-GTPASE-ACTIVITY	GO-0043087	5	0.598252	1.346646	0.150198	0.871155	1.000
47	GOBP-NEURON-MIGRATION	GO-0001764	5	0.598765	1.343552	0.139489	0.863954	1.000
48	GOBP-POSITIVE-REGULATION-OF-MAPK-CASCADE	GO-0043410	9	0.487103	1.343002	0.137363	0.847844	1.000
49	GOBP-NEGATIVE-REGULATION-OF-NEURON-APOPTOTIC_P...	GO-0043524	8	0.504369	1.322774	0.143426	0.904410	1.000
50	GOBP-NEUROTRANSMITTER-SECRETION	GO-0007269	6	0.548844	1.321194	0.156250	0.892574	1.000
51	GOBP-PEPTIDYL-TYROSINE-MODIFICATION	GO-0018212	10	0.467872	1.320888	0.153696	0.876654	1.000
52	GOBP-PHOSPHATIDYLINOSITOL-3-KINASE-SIGNALING	GO-0014065	7	0.528379	1.320437	0.143426	0.861658	1.000
53	GOBP-RECEPTOR-METABOLIC-PROCESS	GO-0043112	5	0.586000	1.316186	0.186180	0.860001	1.000
54	REACTOME-SIGNALING-BY-WNT	R-RNO-195721	7	0.517309	1.311882	0.165339	0.858872	1.000
55	GOBP-PEPTIDE-SECRETION	GO-0002790	9	0.477623	1.306499	0.179630	0.861483	1.000
56	REACTOME-TRANSCRIPTIONAL-REGULATION-BY-MECP2	R-RNO-8986944	7	0.519248	1.300339	0.170000	0.867880	1.000
57	GOBP-CELLULAR-COMPONENT-MAINTENANCE	GO-0043954	5	0.584374	1.299695	0.171598	0.855130	1.000
58	GOBP-POSITIVE-REGULATION-OF-CELLULAR-COMPONENT...	GO-0051130	24	0.365521	1.297990	0.167910	0.846191	1.000
59	GOBP-RECEPTOR-INTERNALIZATION	GO-0031623	5	0.586000	1.292789	0.182353	0.849365	1.000
60	GOBP-DENDRITE-DEVELOPMENT	GO-0016358	10	0.452142	1.292669	0.180608	0.835940	1.000
61	GOBP-REGULATION-OF-CYTOSKELETON-ORGANIZATION	GO-0051493	5	0.567797	1.291066	0.179283	0.827999	1.000
62	GOBP-NEURON-DEVELOPMENT	GO-0048666	34	0.327568	1.286555	0.136525	0.829158	1.000
63	GOBP-POSITIVE-REGULATION-OF-LONG-TERM-SYNAPTIC...	GO-1900273	5	0.579696	1.286023	0.192913	0.818163	1.000
64	GOBP-SYNAPSE-ORGANIZATION	GO-0050808	17	0.390541	1.285465	0.167897	0.807278	1.000
65	GOBP-NEURON-PROJECTION-GUIDANCE	GO-0097485	9	0.467153	1.284936	0.178908	0.796554	1.000
66	GOBP-INTRACELLULAR-TRANSPORT	GO-0046907	10	0.449779	1.279357	0.171429	0.802230	1.000
67	GOBP-POSITIVE-REGULATION-OF-NEURON-PROJECTION...	GO-0010976	5	0.569975	1.273067	0.204159	0.810015	1.000
68	GOBP-REGULATION-OF-PEPTIDE-TRANSPORT	GO-0090087	10	0.447267	1.263074	0.197368	0.829689	1.000
69	GOBP-REGULATION-OF-SYNAPSE-STRUCTURE-OR-ACTIVITY	GO-0050803	11	0.431532	1.257060	0.183236	0.836068	1.000
70	GOBP-RECEPTOR-MEDIATED-ENDOCYTOSIS	GO-0006898	6	0.530409	1.251695	0.212598	0.841390	1.000
71	GOBP-ACTIN-FILAMENT-BASED-PROCESS	GO-0030029	7	0.496472	1.249611	0.213052	0.836102	1.000
72	GOBP-NEGATIVE-REGULATION-OF-NEURON-DEATH	GO-1901215	11	0.433861	1.246519	0.202756	0.833888	1.000
73	GOBP-RESPONSE-TO-STARVATION	GO-0042594	5	0.544196	1.244306	0.225141	0.828896	1.000
74	GOBP-CELL-MIGRATION	GO-0016477	22	0.348876	1.234305	0.197158	0.850003	1.000
75	GOBP-LOCOMOTION	GO-0040011	31	0.323832	1.231782	0.179584	0.846024	1.000
76	GOBP-INOSITOL-LIPID-MEDIATED-SIGNALING	GO-0048017	8	0.462398	1.230176	0.210421	0.839775	1.000
77	GOBP-REGULATION-OF-CATION-CHANNEL-ACTIVITY	GO-2001257	14	0.385089	1.228460	0.181474	0.834055	1.000
78	GOBP-HORMONE-TRANSPORT	GO-0009914	9	0.441635	1.226762	0.215686	0.828657	1.000
79	GOBP-POSITIVE-REGULATION-OF-LIPASE-ACTIVITY	GO-0060193	5	0.536025	1.213444	0.228102	0.859179	1.000
80	GOBP-CELL-PROJECTION-ORGANIZATION	GO-0030030	35	0.308541	1.210015	0.196364	0.859001	1.000
81	GOBP-DICARBOXYLIC-ACID-TRANSPORT	GO-0008835	5	0.540301	1.208936	0.231237	0.851651	1.000
82	REACTOME-UNBLOCKING-OF-NMDA-RECEPTORS-GLUTAMAT...	R-RNO-438066	12	0.399865	1.206617	0.262042	0.848212	1.000
83	GOBP-ACIDIC-AMINO-ACID-TRANSPORT	GO-0015800	5	0.540301	1.206126	0.241379	0.839595	1.000

Continuation of Table S7

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
84	GOBP-MONOCARBOXYLIC-ACID-TRANSPORT	5	0.540301	1.205875	0.239216	0.830418	1.000
85	GOBP-FOREBRAIN-DEVELOPMENT	10	0.431473	1.205413	0.237383	0.822064	1.000
86	GOBP-REGULATION-OF-PHOSPHOLIPASE-C-ACTIVITY	5	0.536025	1.203546	0.258449	0.818090	1.000
87	GOBP-CELLULAR-RESPONSE-TO-STARVATION	5	0.544106	1.202045	0.232902	0.813012	1.000
88	GOBP-REGULATION-OF-NEURONAL-SYNAPTIC-PLASTICITY	7	0.467012	1.194159	0.246602	0.826569	1.000
89	GOBP-REGULATION-OF-HORMONE-SECRETION	8	0.456692	1.189201	0.272556	0.831670	1.000
90	GOBP-PEPTIDYL-AMINO-ACID-MODIFICATION	22	0.337516	1.185001	0.246429	0.834955	1.000
91	GOBP-HEAD-DEVELOPMENT	23	0.333965	1.178692	0.265306	0.843617	1.000
92	GOBP-DENDRITE-MORPHOGENESIS	7	0.459567	1.174279	0.270059	0.847240	1.000
93	GOBP-NEUROTROPHIN-TRK-RECEPTOR-SIGNALING-PATHWAY	6	0.482493	1.163980	0.270270	0.867239	1.000
94	GOBP-GLIOGENESIS	12	0.385540	1.157432	0.282908	0.877059	1.000
95	REACTOME-OPIOID-SIGNALING	12	0.374912	1.152633	0.279383	0.882173	1.000
96	GOBP-MONOAMINE-TRANSPORT	5	0.522261	1.147676	0.306391	0.887151	1.000
97	GOBP-REGULATION-OF-MUSCLE-SYSTEM-PROCESS	8	0.432231	1.146412	0.283809	0.881638	1.000
98	GOBP-MUSCLE-ADAPTATION	5	0.502323	1.144917	0.288136	0.877039	1.000
99	GOBP-REGULATION-OF-ORGANELLE-ORGANIZATION	14	0.357174	1.140505	0.281536	0.880361	1.000
100	GOBP-NEUROTROPHIN-SIGNALING-PATHWAY	6	0.482493	1.136239	0.293878	0.884652	1.000
101	GOBP-CELL-MORPHOGENESIS-INVOLVED-IN-DIFFERENTI...	22	0.314961	1.130659	0.280443	0.892069	1.000
102	REACTOME-SIGNALING-BY-NTRK2-TRKB	6	0.475849	1.125405	0.317930	0.898172	1.000
103	GOBP-BIOLOGICAL-ADHESION	19	0.330123	1.121403	0.314885	0.900991	1.000
104	GOBP-REGULATION-OF-MUSCLE-ADAPTATION	5	0.502323	1.121282	0.321012	0.892711	1.000
105	GOBP-IONOTROPIC-GLUTAMATE-RECEPTOR-SIGNALING-P...	9	0.404500	1.113204	0.318182	0.907753	1.000
106	GOBP-REGULATION-OF-PHOSPHOLIPASE-ACTIVITY	6	0.451362	1.108617	0.332669	0.912161	1.000
107	GOBP-POSITIVE-REGULATION-OF-CELLULAR-COMPONENT...	9	0.402070	1.108345	0.337786	0.904541	1.000
108	GOBP-CELL-MORPHOGENESIS-INVOLVED-IN-NEURON-DIF...	22	0.314961	1.107255	0.323017	0.899540	1.000
109	GOBP-POSITIVE-REGULATION-OF-TRANSPORT	26	0.303492	1.107022	0.309055	0.891967	1.000
110	REACTOME-NERVOUS-SYSTEM-DEVELOPMENT	14	0.351735	1.104813	0.336614	0.890215	1.000
111	GOBP-REGULATION-OF-NEUROTRANSMITTER-RECEPTOR-A...	13	0.361988	1.101090	0.349515	0.892293	1.000
112	GOBP-REGULATION-OF-LIPASE-ACTIVITY	6	0.451362	1.098449	0.353430	0.891697	1.000
113	GOBP-NEURON-PROJECTION-ORGANIZATION	8	0.410714	1.095202	0.340741	0.892863	1.000
114	GOBP-CARBOHYDRATE-DERIVATIVE-BIOSYNTHETIC-PROCESS	5	0.488884	1.093777	0.352490	0.888770	1.000
115	GOBP-REGULATION-OF-ANION-TRANSPORT	20	0.311361	1.089931	0.363139	0.891604	1.000
116	GOBP-CELL-JUNCTION-ORGANIZATION	19	0.320351	1.080017	0.318761	0.886327	1.000
117	GOBP-CELLULAR-COMPONENT-MORPHOGENESIS	25	0.294572	1.087399	0.338374	0.883334	1.000
118	GOBP-LIPID-EXPORT-FROM-CELL	5	0.486862	1.087141	0.343874	0.876610	1.000
119	GOBP-REGULATION-OF-ANATOMICAL-STRUCTURE-MORPHO...	17	0.322232	1.085772	0.344828	0.872977	1.000
120	GOBP-PEPTIDYL-SERINE-MODIFICATION	12	0.356140	1.080782	0.356061	0.878651	1.000
121	GOBP-REGULATION-OF-CELLULAR-COMPONENT-BIOGENESIS	10	0.382421	1.071322	0.347092	0.896404	1.000
122	GOBP-CELL-MORPHOGENESIS	25	0.294572	1.068843	0.373002	0.895596	1.000
123	GOBP-REGULATION-OF-RESPONSE-TO-EXTERNAL-STIMULUS	15	0.3032101	1.061694	0.379648	0.907761	1.000
124	GOBP-RHYTHMIC-PROCESS	15	0.339938	1.059370	0.354167	0.907211	1.000
125	GOBP-REGULATION-OF-LONG-TERM-SYNAPTIC-POTENTIAL...	6	0.437012	1.057498	0.367387	0.905000	1.000
126	GOBP-NUCLEOBASE-CONTAINING-SMALL-MOLECULE-META...	7	0.419288	1.056727	0.384466	0.899863	1.000

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NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
127 REACTOME_LONG_TERM_POTENTIATION	R-HSA-9620244	10	0.368356	1.055905	0.390196	0.894971	1.000
128 GOBP_POSITIVE_REGULATION_OF_LOCOMOTION	GO:0040017	11	0.359513	1.055227	0.382524	0.889771	1.000
129 GOBP_REGULATION_OF_CELLULAR_COMPONENT_MOVEMENT	GO:0051270	15	0.330829	1.052534	0.387037	0.890358	1.000
130 GOBP_REGULATION_OF_TRANS_SYNAPTIC_SIGNALING	GO:0099177	40	0.261689	1.045476	0.392473	0.901945	1.000
131 GOBP_CELL_PART_MORPHOGENESIS	GO:0032990	25	0.295472	1.042650	0.415560	0.902186	1.000
132 GOBP_NEGATIVE_REGULATION_OF_CELLULAR_COMPONENT...	GO:0051129	11	0.353338	1.041928	0.428571	0.896953	1.000
133 GOBP_LONG_TERM_SYNAPTIC_POTENTIATION	GO:0060291	12	0.353374	1.038738	0.404494	0.898441	1.000
134 GOBP_POSITIVE_REGULATION_OF_PROTEIN_KINASE_ACT...	GO:0045860	18	0.303422	1.037906	0.426326	0.893967	1.000
135 REACTOME_EXTRACELLULAR_MATRIX_ORGANIZATION	R-RNO-1474244	5	0.465199	1.033787	0.419660	0.897985	1.000
136 GOBP_DNA_METABOLIC_PROCESS	GO:0060259	6	0.430250	1.032435	0.413255	0.895152	1.000
137 GOBP_CARBOXYLIC_ACID_TRANSPORT	GO:0046942	6	0.427394	1.030694	0.406910	0.893121	1.000
138 GOBP_AMINO_ACID_TRANSPORT	GO:0006865	6	0.427394	1.024442	0.403194	0.902651	1.000
139 GOBP_ORGANIC_ANION_TRANSPORT	GO:0015711	6	0.427394	1.024186	0.413442	0.896865	1.000
140 GOBP_AXON_DEVELOPMENT	GO:0061564	18	0.299339	1.020975	0.441860	0.898470	1.000
141 GOBP_PROTEIN_KINASE_B_SIGNALING	GO:0043491	6	0.426799	1.020850	0.421359	0.892488	1.000
142 GOBP_MUSCLE_SYSTEM_PROCESS	GO:0003012	9	0.363704	1.017603	0.431452	0.894329	1.000
143 GOBP_POSITIVE_REGULATION_OF_TRANSPERASE_ACTIVITY	GO:0051347	19	0.294287	1.017496	0.424408	0.888378	1.000
144 REACTOME_G_ALPHA_I_SIGNALING_EVENTS	R-RNO-118594	18	0.311993	1.016865	0.418079	0.883828	1.000
145 GOBP_SYNAPTIC_SIGNALING	GO:0099536	47	0.251308	1.016087	0.439153	0.879959	1.000
146 GOBP_MUSCLE_ORGAN_DEVELOPMENT	GO:0007517	9	0.364206	1.015718	0.425094	0.874785	1.000
147 GOBP_PURINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	GO:0007521	6	0.427055	1.012255	0.417457	0.877436	1.000
148 GOBP_CIRCADIAN_RHYTHM	GO:0007623	13	0.325966	1.010584	0.439338	0.875495	1.000
149 GOBP_GLIAL_CELL_DIFFERENTIATION	GO:0010001	10	0.350969	1.005991	0.431298	0.880504	1.000
150 GOBP_CENTRAL_NERVOUS_SYSTEM_DEVELOPMENT	GO:0007417	27	0.264750	0.995892	0.453382	0.899605	1.000
151 GOBP_CENTRAL_NERVOUS_SYSTEM_NEURON_DIFFERENTIA...	GO:0021953	5	0.442387	0.990993	0.443623	0.906285	1.000
152 GOBP_INTRACELLULAR_PROTEIN_TRANSPORT	GO:0006886	8	0.374951	0.987457	0.458647	0.909008	1.000
153 GOBP_DENDRITIC_SPINE_DEVELOPMENT	GO:0060996	6	0.407548	0.983436	0.479087	0.913247	1.000
154 GOBP_PROTEIN_PHOSPHORYLATION	GO:0006468	33	0.253179	0.982686	0.491228	0.909195	1.000
155 GOBP_REGULATION_OF_CELL_CELL_ADHESION	GO:0022407	9	0.358170	0.980487	0.482625	0.908682	1.000
156 GOBP_POSITIVE_REGULATION_OF_CELL_POPULATION_PR...	GO:0008284	21	0.279478	0.975358	0.509434	0.914859	1.000
157 GOBP_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION	GO:0045184	17	0.290231	0.965119	0.481188	0.934053	1.000
158 REACTOME_GPCR_LIGAND_BINDING	R-RNO-500792	8	0.362500	0.960461	0.465070	0.939485	1.000
159 GOBP_REGULATION_OF_SIGNALING_RECEPTOR_ACTIVITY	GO:0010469	14	0.305984	0.958621	0.493230	0.938103	1.000
160 GOBP_GAMETE_GENERATION	GO:0007276	9	0.346877	0.957874	0.487903	0.934140	1.000
161 GOBP_CELLULAR_MACROMOLECULE_CATABOLIC_PROCESS	GO:0044265	5	0.425713	0.956446	0.484112	0.932287	1.000
162 GOBP_REGULATION_OF_VASCULATURE_DEVELOPMENT	GO:1901342	5	0.415410	0.951749	0.506692	0.937684	1.000
163 GOBP_REGULATION_OF_CELL_ACTIVATION	GO:0050865	8	0.370634	0.949812	0.528155	0.936704	1.000
164 GOBP_TELENCEPHALON_DEVELOPMENT	GO:0021537	7	0.392458	0.945290	0.517304	0.941689	1.000
165 GOBP_SYNAPTIC_TRANSMISSION_GLUTAMATERGIC	GO:0035249	13	0.315167	0.943129	0.533582	0.941137	1.000
166 GOBP_PLATELET_ACTIVATION	GO:0030168	6	0.239458	0.941227	0.513627	0.940095	1.000
167 GOBP_NERVOUS_SYSTEM_PROCESS	GO:0050877	38	0.239492	0.940421	0.527103	0.936426	1.000
168 GOBP_REGULATION_OF_NEUROGENESIS	GO:0050767	14	0.302020	0.940375	0.508772	0.931008	1.000
169 GOBP_REGULATION_OF_CELL_DEVELOPMENT	GO:0060284	15	0.291492	0.939479	0.548638	0.927713	1.000

Continuation of Table S7

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
170 GOBP-POSITIVE-REGULATION_OF_PEPTIDASE-ACTIVITY	GO-0010952	7	0.372933	0.938042	0.533203	0.925641	1.000
171 GOBP-BEHAVIOR	GO-0007610	33	0.243044	0.936297	0.565455	0.924329	1.000
172 GOBP-MAINTENANCE-OF-LOCATION	GO-0051235	7	0.374341	0.932395	0.556886	0.928069	1.000
173 GOBP-POSITIVE-REGULATION_OF_CYS-TEINE-TYPE-ENDO...	GO-2001056	7	0.370391	0.930391	0.556797	0.927483	1.000
174 GOBP-NUCLEAR-TRANSPORT	GO-0051169	5	0.411925	0.923876	0.529297	0.937375	1.000
175 GOBP-REGULATION_OF_TRANSPORTER-ACTIVITY	GO-0032409	17	0.277075	0.923842	0.563601	0.932135	1.000
176 GOBP-REGULATION-OF-CELLULAR-RESPONSE-TO-STRESS	GO-0080135	9	0.337636	0.922644	0.540385	0.929685	1.000
177 GOBP-REGULATION-OF-PEPTIDYL-SERINE-PHOSPHORYLA...	GO-0033135	8	0.334193	0.920737	0.540741	0.928779	1.000
178 REACTOME-CLASS-C.3-METABOTROPIC-GLUTAMATE-PHER...	R-RNO-420499	7	0.358025	0.920452	0.547273	0.924190	1.000
179 GOBP-POSTSYNAPSE-ORGANIZATION	GO-0099173	10	0.328984	0.919403	0.560311	0.921404	1.000
180 GOBP-RESPONSE-TO-NERVE-GROWTH-FACTOR	GO-1990089	7	0.364561	0.918029	0.548255	0.919283	1.000
181 GOBP-COGNITION	GO-0050890	28	0.243820	0.916349	0.596330	0.918117	1.000
182 GOBP-SEXUAL-REPRODUCTION	GO-0019953	10	0.325728	0.915149	0.579848	0.915766	1.000
183 GOBP-LIPID-LOCALIZATION	GO-0010876	10	0.326341	0.914022	0.544031	0.913386	1.000
184 GOBP-CELL-CYCLE-PROCESS	GO-0022402	11	0.309162	0.913205	0.543925	0.910305	1.000
185 GOBP-CELLULAR-HOMEOSTASIS	GO-0019725	18	0.269594	0.905614	0.583181	0.921848	1.000
186 GOBP-NEURON-APOPTOTIC-PROCESS	GO-0051402	12	0.301217	0.904719	0.577821	0.919101	1.000
187 GOBP-CELLULAR-GLUCOSE-HOMEOSTASIS	GO-0001678	5	0.401787	0.903289	0.564797	0.917454	1.000
188 GOBP-NEGATIVE-REGULATION-OF-CELL-DEATH	GO-0060548	22	0.251391	0.900058	0.613553	0.919627	1.000
189 GOBP-PROTEIN-TETRAMERIZATION	GO-0051262	5	0.413626	0.898465	0.586694	0.918128	1.000
190 GOBP-POSITIVE-REGULATION-OF-PROTEIN-PHOSPHORYL...	GO-0001934	22	0.248824	0.896823	0.613553	0.916808	1.000
191 GOBP-POSITIVE-REGULATION-OF-PEPTIDYL-SERINE-PH...	GO-0033138	8	0.334193	0.886341	0.599222	0.934460	1.000
192 GOBP-POSITIVE-REGULATION-OF-PROTEIN-MODIFICATI...	GO-0031401	22	0.248824	0.884370	0.630713	0.933784	1.000
193 REACTOME-ONCOGENIC-MAPK-SIGNALING	R-HSA-6802957	5	0.393206	0.881970	0.592814	0.934243	1.000
194 GOBP-REGULATION-OF-TRANSFERASE-ACTIVITY	GO-0051338	21	0.252137	0.881283	0.639405	0.930875	1.000
195 GOBP-REGULATION-OF-HORMONE-LEVELS	GO-0010817	12	0.288500	0.879485	0.618774	0.929808	1.000
196 GOBP-PROTEIN-AUTOPHOSPHORYLATION	GO-0046777	5	0.396215	0.879459	0.571705	0.925129	1.000
197 GOBP-PATTERN-SPECIFICATION-PROCESS	GO-0007389	6	0.367403	0.877743	0.604478	0.924122	1.000
198 GOBP-EXOCYTOSIS	GO-0006887	11	0.298701	0.874911	0.606589	0.925410	1.000
199 GOBP-REGIONALIZATION	GO-0003002	6	0.367403	0.873721	0.613208	0.923244	1.000
200 GOBP-REGULATION-OF-CATION-TRANSMEMBRANE-TRANSPORT	GO-1904062	16	0.267303	0.872567	0.600000	0.921057	1.000
201 GOBP-REGULATION-OF-HYDROLASE-ACTIVITY	GO-0051336	22	0.243886	0.871070	0.638298	0.919432	1.000
202 REACTOME-CREB1-PHOSPHORYLATION-THROUGH-NMDA-RE...	R-RNO-442742	8	0.324068	0.868445	0.630058	0.920438	1.000
203 GOBP-REGULATION-OF-RESPONSE-TO-STRESS	GO-0080134	19	0.250805	0.868033	0.620112	0.916752	1.000
204 GOBP-POSITIVE-REGULATION-OF-SYNAPTIC-TRANSMISSION	GO-0050806	15	0.272247	0.867334	0.626894	0.913684	1.000
205 GOBP-REGULATION-OF-PROTEIN-KINASE-ACTIVITY	GO-0045859	21	0.252137	0.866160	0.655303	0.911538	1.000
206 GOBP-POSITIVE-REGULATION-OF-PROTEIN-SERINE-THR...	GO-0071902	9	0.311934	0.859442	0.631263	0.920460	1.000
207 GOBP-NERVE-DEVELOPMENT	GO-0021675	9	0.314140	0.855395	0.642857	0.923722	1.000
208 GOBP-POSITIVE-REGULATION-OF-PHOSPHORUS-METABOL...	GO-0010562	23	0.241394	0.853030	0.687956	0.924206	1.000
209 GOBP-PROTEIN-COMPLEX-OLIGOMERIZATION	GO-0051259	7	0.340791	0.847107	0.642578	0.931357	1.000
210 GOBP-REGULATION-OF-PROTEIN-STABILITY	GO-0031647	5	0.371534	0.843930	0.626016	0.933335	1.000
211 GOBP-REGULATION-OF-BODY-FLUID-LEVELS	GO-0050878	11	0.288916	0.838760	0.696296	0.939037	1.000
212 GOBP-MAPK-CASCADE	GO-0000165	18	0.250087	0.836738	0.696589	0.938760	1.000

Continuation of Table S7

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
213	GOBP-RESPONSE.TO.ETHANOL	5	0.367444	0.836215	0.657143	0.935451	1.000
214	GOBP-NEGATIVE-REGULATION.OF-PHOSPHORYLATION	7	0.330615	0.833684	0.627413	0.936264	1.000
215	REACTOME-INTEGRATION.OF-ENERGY-METABOLISM	5	0.374706	0.830532	0.685951	0.938164	1.000
216	GOBP-CIRCADIAN-REGULATION.OF-GENE-EXPRESSION	5	0.371419	0.826870	0.664032	0.940922	1.000
217	REACTOME-L1CAM-INTERACTIONS	5	0.365191	0.826149	0.938112	0.938112	1.000
218	GOBP-REGULATION.OF-INTRACELLULAR-SIGNAL-TRANSD...	21	0.235186	0.825809	0.692759	0.934416	1.000
219	GOBP-PROTEIN-CONTAINING-COMPLEX-SUBUNIT-ORGANL...	15	0.260947	0.825183	0.680154	0.931297	1.000
220	GOBP-FATTY-ACID-TRANSPORT	6	0.346687	0.824742	0.675048	0.927823	1.000
221	GOBP-AMYLOID-PRECURSOR-PROTEIN-METABOLIC-PROCESS	5	0.365158	0.823020	0.676768	0.926959	1.000
222	GOBP-POSITIVE-REGULATION.OF-RESPONSE.TO-EXTERN...	9	0.305171	0.822880	0.687379	0.923104	1.000
223	GOBP-POSITIVE-REGULATION.OF-SECRETION	6	0.341464	0.822208	0.672691	0.920092	1.000
224	GOBP-NEGATIVE-REGULATION.OF-NERVOUS-SYSTEM.DEV...	5	0.369760	0.821600	0.692022	0.917247	1.000
225	GOBP-WOUND-HEALING	13	0.265244	0.820774	0.686424	0.914767	1.000
226	GOBP-AMYLOID-PRECURSOR-PROTEIN-CATABOLIC-PROCESS	5	0.365158	0.820667	0.679842	0.910962	1.000
227	GOBP-AMYLOID-BETA-METABOLIC-PROCESS	5	0.365158	0.815890	0.662362	0.915814	1.000
228	GOBP-REGULATION.OF-CIRCADIAN-RHYTHM	7	0.323822	0.815228	0.695652	0.913084	1.000
229	GOBP-MITOTIC-CELL-CYCLE	10	0.283057	0.814593	0.705653	0.910174	1.000
230	GOBP-ORGANIC-HYDROXY-COMPOUND-TRANSPORT	6	0.324395	0.813897	0.683071	0.907495	1.000
231	REACTOME-RAS-ACTIVATION-UPON-CA2-INFLUX-THROUGH...	6	0.334698	0.809383	0.704415	0.911544	1.000
232	GOBP-MEMBRANE-ORGANIZATION	12	0.265516	0.803861	0.720532	0.917439	1.000
233	GOBP-DENDRITIC-SPINE-MORPHOGENESIS	5	0.356111	0.793899	0.714286	0.931159	1.000
234	GOBP-CELL-CELL-SIGNALING	56	0.198110	0.790801	0.802158	0.932513	1.000
235	REACTOME-SIGNALING-BY-NTRKS	18	0.235097	0.787114	0.781076	0.934896	1.000
236	GOBP-ADENYLATE-CYCLASE-INHIBITING-G-PROTEIN.CO...	5	0.349398	0.786204	0.760700	0.932513	1.000
237	GOBP-POSITIVE-REGULATION.OF-NEUROGENESIS	12	0.256342	0.782953	0.713755	0.934089	1.000
238	GOBP-POSITIVE-REGULATION.OF-NERVOUS-SYSTEM.DEV...	12	0.256342	0.782487	0.730916	0.930966	1.000
239	GOBP-NEURON-DEATH	18	0.233365	0.780036	0.766284	0.931243	1.000
240	GOBP-MULTICELLULAR-ORGANISM-REPRODUCTION	12	0.262573	0.779268	0.746032	0.928669	1.000
241	GOBP-ADENYLATE-CYCLASE-MODULATING-G-PROTEIN.CO...	11	0.263417	0.775778	0.759369	0.930842	1.000
242	GOBP-MEMORY	13	0.257184	0.775553	0.759358	0.927329	1.000
243	GOBP-REGULATION.OF-PROTEIN-PHOSPHORYLATION	25	0.207762	0.769296	0.809437	0.933750	1.000
244	GOBP-RESPONSE.TO-ACID-CHEMICAL	6	0.322092	0.765735	0.787004	0.935766	1.000
245	GOBP-RESPONSE.TO-NITROGEN-COMPOUND	35	0.195049	0.763210	0.793419	0.935845	1.000
246	GOBP-ACTIVATION.OF-MAPK-ACTIVITY	6	0.321361	0.762326	0.752621	0.933605	1.000
247	GOBP-POSITIVE-REGULATION.OF-CELL-DEVELOPMENT	12	0.256342	0.759465	0.753846	0.934435	1.000
248	GOBP-NEGATIVE-REGULATION.OF-CELL-DEVELOPMENT	6	0.317622	0.759359	0.763303	0.930862	1.000
249	GOBP-G-PROTEIN-COUPLED-RECEPTOR-SIGNALING-PATHWAY	18	0.222495	0.755584	0.805970	0.928319	1.000
250	GOBP-POSITIVE-REGULATION.OF-ION-TRANSPORT	17	0.204321	0.755754	0.789963	0.928925	1.000
251	GOBP-MALE-GAMETE-GENERATION	5	0.335701	0.755246	0.767442	0.925993	1.000
252	GOBP-POSITIVE-REGULATION.OF-MAP_KINASE-ACTIVITY	6	0.321361	0.754392	0.764591	0.923579	1.000
253	GOBP-CHROMATIN-ORGANIZATION	5	0.342757	0.754165	0.773513	0.920337	1.000
254	GOBP-COAGULATION	8	0.288796	0.746755	0.770245	0.927997	1.000
255	GOBP-REGULATION.OF-MAPK-CASCADE	13	0.246107	0.745048	0.788054	0.927042	1.000

Continuation of Table S7

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
256 REACTOME-SYNAPTIC-ADHESION-LIKE-MOLECULES	R-RNO-8849932	9	0.275180	0.741833	0.779661	0.927974	1.000
257 GOBP-REGULATION-OF-SYNAPTIC-TRANSMISSION-GLUTA...	GO-0051966	12	0.250000	0.739406	0.825095	0.927710	1.000
258 GOBP-REGULATION-OF-LIPID-LOCALIZATION	GO-1905952	5	0.329511	0.739249	0.798058	0.924372	1.000
259 GOBP-GLUTAMATE-RECEPTOR-SIGNALING-PATHWAY	GO-0007215	17	0.226199	0.735311	0.811069	0.926493	1.000
260 GOBP-POSITIVE-REGULATION-OF-CATALYTIC-ACTIVITY	GO-0043085	29	0.195329	0.731969	0.846863	0.927774	1.000
261 GOBP-PEPTIDYL-LYSINE-MODIFICATION	GO-0018205	5	0.323311	0.730193	0.830000	0.926902	1.000
262 GOBP-LONG-TERM-SYNAPTIC-DEPRESSION	GO-0060292	5	0.331897	0.722831	0.804040	0.933872	1.000
263 REACTOME-INTERFERON-SIGNALING	R-RNO-913531	6	0.305091	0.722232	0.804388	0.931079	1.000
264 GOBP-ORGANIC-ACID-TRANSPORT	GO-0015849	7	0.285378	0.721443	0.772201	0.928647	1.000
265 GOBP-CELLULAR-RESPONSE-TO-LIPID	GO-00071396	15	0.227292	0.716275	0.844037	0.932069	1.000
266 GOBP-SENSORY-PERCEPTION	GO-0007600	9	0.266628	0.715119	0.812627	0.930006	1.000
267 GOBP-NEGATIVE-REGULATION-OF-CELL-DIFFERENTIATION	GO-0045596	13	0.226667	0.711885	0.832335	0.930893	1.000
268 GOBP-MYOTUBE-DIFFERENTIATION	GO-0014902	5	0.317712	0.711491	0.852273	0.927980	1.000
269 GOBP-CELLULAR-RESPONSE-TO-NITROGEN-COMPOUND	GO-1901699	20	0.206874	0.710506	0.838420	0.925779	1.000
270 GOBP-NEGATIVE-REGULATION-OF-RESPONSE-TO-EXTERN...	GO-0032102	5	0.312866	0.697960	0.848980	0.938651	1.000
271 GOBP-ORGANOPHOSPHATE-METABOLIC-PROCESS	GO-0019637	8	0.266495	0.695321	0.833992	0.938551	1.000
272 GOBP-REGULATION-OF-PHOSPHORUS-METABOLIC-PROCESS	GO-0051174	26	0.186420	0.692740	0.867993	0.938315	1.000
273 GOBP-POSITIVE-REGULATION-OF-ESTABLISHMENT-OF-P...	GO-1904951	5	0.306104	0.691079	0.880240	0.936872	1.000
274 GOBP-NEGATIVE-REGULATION-OF-DEVELOPMENTAL-PROCESS	GO-0051093	13	0.226667	0.690446	0.858527	0.934257	1.000
275 GOBP-CHROMOSOME-ORGANIZATION	GO-0051276	6	0.293658	0.689974	0.859345	0.931466	1.000
276 GOBP-SENSORY-ORGAN-DEVELOPMENT	GO-0007423	8	0.266230	0.689264	0.829114	0.928990	1.000
277 GOBP-POSITIVE-REGULATION-OF-PROTEIN-METABOLIC...	GO-0051247	27	0.187329	0.687395	0.879121	0.927904	1.000
278 GOBP-NEGATIVE-REGULATION-OF-SYNAPTIC-TRANSMISSION	GO-0050805	6	0.289438	0.680039	0.851064	0.932858	1.000
279 GOBP-RESPONSE-TO-CALCIUM-ION	GO-0051592	6	0.279779	0.675474	0.867675	0.934761	1.000
280 REACTOME-SIGNALING-BY-GPCR	R-RNO-372790	22	0.189234	0.669443	0.891071	0.937887	1.000
281 GOBP-SKELETAL-MUSCLE-ORGAN-DEVELOPMENT	GO-0060538	5	0.302006	0.665249	0.846881	0.939023	1.000
282 GOBP-G-PROTEIN-COUPLED-GLUTAMATE-RECEPTOR-SIGN...	GO-0007216	8	0.250000	0.663957	0.882023	0.937046	1.000
283 GOBP-SMALL-MOLECULE-BIOSYNTHETIC-PROCESS	GO-0044283	5	0.292901	0.663176	0.901210	0.934713	1.000
284 GOBP-DEFENSE-RESPONSE-TO-OTHER-ORGANISM	GO-0098542	9	0.239715	0.652726	0.908549	0.942169	1.000
285 GOBP-CATION-TRANSPORT	GO-006812	25	0.182629	0.652561	0.925573	0.939061	1.000
286 GOBP-POSITIVE-REGULATION-OF-CATION-TRANSMEMBR...	GO-1904064	5	0.288685	0.632338	0.895050	0.954174	1.000
287 GOBP-REGULATION-OF-NEURON-DIFFERENTIATION	GO-0045664	5	0.282744	0.632942	0.906191	0.951125	1.000
288 GOBP-POSITIVE-REGULATION-OF-ANION-TRANSPORT	GO-1903793	9	0.229130	0.630228	0.916201	0.950156	1.000
289 GOBP-EPITHELIAL-CELL-PROLIFERATION	GO-0050673	12	0.204060	0.616150	0.933594	0.959030	1.000
290 GOBP-ADENYLATE-CYCLASE-INHIBITING-G-PROTEIN.CO...	GO-0007196	9	0.227848	0.608279	0.916058	0.961906	1.000
291 GOBP-REGULATION-OF-POSTSYNAPSE-ORGANIZATION	GO-0099175	6	0.245794	0.595094	0.940952	0.968330	1.000
292 GOBP-CELL-ACTIVATION	GO-0001775	22	0.167833	0.593614	0.937153	0.966003	1.000
293 GOBP-ERK1-AND-ERK2-CASCADE	GO-0070371	5	0.256109	0.569189	0.962887	0.978126	1.000
294 GOBP-VESICLE-MEDIATED-TRANSPORT-IN-SYNAPSE	GO-0099003	7	0.221735	0.562607	0.960452	0.978633	1.000
295 GOBP-REGULATION-OF-PROTEIN-LOCALIZATION	GO-0032880	18	0.193391	0.540815	0.973635	0.985748	1.000
296 GOBP-ORGANIC-HYDROXY-COMPOUND-METABOLIC-PROCESS	GO-1901615	8	0.196391	0.520707	0.976699	0.990253	1.000
297 REACTOME-G-ALPHA-Q-SIGNALING-EVENTS	R-RNO-416476	6	0.221354	0.516616	0.986166	0.988301	1.000
298 GOBP-NEUROINFLAMMATORY-RESPONSE	GO-0150076	5	0.228916	0.511031	0.994434	0.986752	1.000

Continuation of Table S7

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
299 GOBP-TEMPERATURE.HOMEOSTASIS	GO-0001659	5	0.228916	0.505619	0.980469	0.984958	1.000
300 REACTOME.ANTIINFLAMMATORY.RESPONSE.FAVOURING....	R-HSA-9662851	5	-0.228916	-0.507198	0.976331	0.984880	1.000
301 GOBP-CELL-CELL.SIGNALING.BY.WNT	GO-0198738	7	-0.197779	-0.510482	0.978947	0.986170	1.000
302 GOBP-CYTOKINE.PRODUCTION	GO-0001816	10	-0.179615	-0.527599	0.967532	0.982844	1.000
303 GOBP-REGULATION.OF.OSTEOCLAST.DIFFERENTIATION	GO-00045670	5	-0.246852	-0.545334	0.978088	0.978347	1.000
304 GOBP-SENSORY.PERCEPTION.OF.PAIN	GO-0019233	5	-0.240964	-0.546937	0.970833	0.979200	1.000
305 GOBP-EPHRAIN.RECEPTOR.SIGNALING.PATHWAY	GO-00048013	5	-0.253012	-0.568383	0.954918	0.970312	1.000
306 GOBP-REGULATION.OF.NERVOUS.SYSTEM.PROCESS	GO-00031644	8	-0.223237	-0.607216	0.933619	0.946897	1.000
307 REACTOME.EPHLEPHRAIN.SIGNALING	R-RNO-2682334	6	-0.256098	-0.620456	0.915289	0.939045	1.000
308 GOBP-EMBRYONIC.MORPHOGENESIS	GO-00045898	6	-0.258797	-0.626565	0.922764	0.936186	1.000
309 REACTOME.TRANSCRIPTIONAL.REGULATION.OF.WHITE.A...	R-RNO-381340	6	-0.261621	-0.627219	0.927835	0.937960	1.000
310 GOBP-RESPONSE.TO.MONOSACCHARIDE	GO-00034284	5	-0.278706	-0.631007	0.898925	0.936994	1.000
311 GOBP-RESPONSE.TO.CARBOHYDRATE	GO-0009743	5	-0.278706	-0.631744	0.906375	0.938600	1.000
312 GOBP-CELLULAR.MACROMOLECULE.LOCALIZATION	GO-00070727	20	-0.175390	-0.633743	0.937107	0.938994	1.000
313 GOBP-LONG-TERM.MEMORY	GO-0007616	6	-0.271592	-0.638189	0.904110	0.937157	1.000
314 GOBP-NEGATIVE.REGULATION.OF.CELL.POPULATION.PR...	GO-0008285	9	-0.232440	-0.638640	0.902490	0.939017	1.000
315 GOBP-POSITIVE.REGULATION.OF.APOPTOTIC.SIGNALIN...	GO-2001235	5	-0.285435	-0.638714	0.906582	0.941257	1.000
316 GOBP-REPRODUCTIVE.SYSTEM.DEVELOPMENT	GO-0061458	6	-0.271035	-0.641341	0.886905	0.941168	1.000
317 GOBP-HOMEOSTATIC.PROCESS	GO-00042592	31	-0.160737	-0.642270	0.918793	0.942579	1.000
318 GOBP-NEGATIVE.REGULATION.OF.TRANSPORT	GO-00051051	13	-0.201043	-0.645477	0.899782	0.941895	1.000
319 GOBP-REGULATION.OF.PEPTIDASE.ACTIVITY	GO-00052547	10	-0.228685	-0.653405	0.888438	0.936271	1.000
320 GOBP-REGULATION.OF.METAL.ION.TRANSPORT	GO-0010959	6	-0.277772	-0.653736	0.889130	0.938226	1.000
321 GOBP-INNATE.IMMUNE.RESPONSE	GO-00045087	7	-0.260760	-0.654917	0.866944	0.939337	1.000
322 GOBP-REGULATION.OF.MAP.KINASE.ACTIVITY	GO-00043405	9	-0.240464	-0.670469	0.837553	0.924839	1.000
323 GOBP-RESPONSE.TO.INTERLEUKIN.1	GO-00070555	5	-0.302904	-0.672631	0.832985	0.924760	1.000
324 GOBP-MULTICELLULAR.ORGANISMAL.HOMEOSTASIS	GO-00048871	12	-0.219280	-0.672693	0.870021	0.927020	1.000
325 GOBP-CELLULAR.RESPONSE.TO.DNA.DAMAGE.STIMULUS	GO-0006974	5	-0.305020	-0.676017	0.879142	0.925670	1.000
326 GOBP-ACTIVATION.OF.PROTEIN.KINASE.ACTIVITY	GO-00032147	10	-0.234035	-0.676804	0.865732	0.927011	1.000
327 REACTOME.NGF.STIMULATED.TRANSCRIPTION	R-RNO-9031628	9	-0.246881	-0.679442	0.866242	0.926420	1.000
328 REACTOME.NEGATIVE.REGULATION.OF.NMDA.RECEPTOR....	R-HSA-961732	8	-0.264214	-0.684021	0.875510	0.923613	1.000
329 GOBP-RESPONSE.TO.WOUNDING	GO-00096111	15	-0.216045	-0.688021	0.871681	0.921289	1.000
330 GOBP-CELLULAR.RESPONSE.TO.KETONE	GO-1901655	5	-0.312339	-0.688531	0.859155	0.923084	1.000
331 GOBP-REGULATION.OF.HEMOPOIESIS	GO-1903706	10	-0.241346	-0.690281	0.865385	0.923202	1.000
332 GOBP-INTRINSIC.APOPTOTIC.SIGNALING.PATHWAY	GO-0097193	5	-0.319499	-0.698322	0.861635	0.915427	1.000
333 GOBP-REGULATION.OF.GLIOGENESIS	GO-0014013	5	-0.316372	-0.705483	0.834016	0.908766	1.000
334 GOBP-CATION.TRANSMEMBRANE.TRANSPORT	GO-0098655	18	-0.204200	-0.706553	0.870968	0.909637	1.000
335 GOBP-CELL.JUNCTION.ASSEMBLY	GO-00034329	8	-0.261227	-0.708840	0.835443	0.909183	1.000
336 GOBP-NEGATIVE.REGULATION.OF.GENE.EXPRESSION	GO-0010629	11	-0.239767	-0.709817	0.824242	0.910340	1.000
337 GOBP-POSITIVE.REGULATION.OF.PROTEOLYSIS	GO-00045862	8	-0.261047	-0.711468	0.842767	0.910585	1.000
338 REACTOME.ASSEMBLY.AND.CELL.SURFACE.PRESENTATIO...	R-RNO-9609736	8	-0.264214	-0.712507	0.820988	0.911463	1.000
339 REACTOME.CELL.CYCLE.MITOTIC	GO-0006278	5	-0.322857	-0.712548	0.842324	0.913771	1.000
340 GOBP-POSITIVE.REGULATION.OF.GLIOGENESIS	GO-0014015	5	-0.316372	-0.716416	0.813008	0.910955	1.000
341 GOBP-POSITIVE.REGULATION.OF.EPITHELIAL.CELL.MI...	GO-0010634	5	-0.323887	-0.719243	0.805118	0.909375	1.000

Continuation of Table S7

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
342	REACTOME-CELL_CYCLE	R-RNO-1640170	6	-0.292499	-0.719399	0.840551	0.911584	1.000
343	GOBP-REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	GO-0045637	9	-0.257888	-0.719618	0.819328	0.913613	1.000
344	GOBP-RESPONSE_TO_ALCOHOL	GO-0097305	11	-0.246735	-0.720492	0.814815	0.914861	1.000
345	GOBP-CELLULAR_RESPONSE_TO_ORGANIC_CYCLIC_COMPOUND	GO-0071407	13	-0.229440	-0.721552	0.833333	0.915816	1.000
346	GOBP-POSITIVE_REGULATION_OF_CYTOKINE_PRODUCTION	GO-0001819	7	-0.278564	-0.722817	0.789264	0.916528	1.000
347	GOBP-REGULATION_OF_MITOTIC_CELL_CYCLE	GO-0007346	5	-0.322142	-0.724359	0.802419	0.916838	1.000
348	REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGG...	R-HSA-76002	7	-0.283210	-0.724800	0.798000	0.918615	1.000
349	GOBP-REGULATION_OF_MUSCLE_CELL_DIFFERENTIATION	GO-0051147	6	-0.303809	-0.725187	0.812775	0.920491	1.000
350	GOBP-REGULATION_OF_PROTEIN_MODIFICATION_PROCESS	GO-0031399	28	-0.261142	-0.733001	0.838636	0.912060	1.000
351	REACTOME_NEUREXINS_AND_NEUROLIGINS	R-RNO-6794361	9	-0.261142	-0.733115	0.809524	0.914344	1.000
352	GOBP-POSITIVE_REGULATION_OF_SIGNALING	GO-0023056	34	-0.182556	-0.735179	0.833333	0.913763	1.000
353	GOBP-LOCOMOTOR_BEHAVIOR	GO-0007626	8	-0.275000	-0.736751	0.804527	0.914065	1.000
354	GOBP-ENDOTHELIAL_CELL_PROLIFERATION	GO-0001935	8	-0.279074	-0.739076	0.795031	0.913033	1.000
355	GOBP-RESPONSE_TO_ALKALOID	GO-0043279	5	-0.337798	-0.740503	0.779070	0.913475	1.000
356	GOBP-TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THR...	GO-0007178	6	-0.312285	-0.741046	0.763043	0.915138	1.000
357	GOBP-LIPID_BIOSYNTHETIC_PROCESS	GO-0008610	6	-0.312603	-0.742144	0.774757	0.915978	1.000
358	GOBP-REGULATION_OF_LIPID_BIOSYNTHETIC_PROCESS	GO-0046890	6	-0.312603	-0.745215	0.803063	0.914160	1.000
359	GOBP-REGULATION_OF_PROTEOLYSIS	GO-0030162	12	-0.241193	-0.745667	0.783370	0.916085	1.000
360	GOBP-REGULATION_OF_CYSSTEINE_TYPE_ENDOPEPTIDASE...	GO-2000116	9	-0.269447	-0.747341	0.773019	0.916188	1.000
361	GOBP-DEFENSE_RESPONSE	GO-0006952	19	-0.213259	-0.751748	0.808190	0.912229	1.000
362	GOBP-NEGATIVE_REGULATION_OF_ION_TRANSPORT	GO-0043271	11	-0.246828	-0.752545	0.775000	0.913558	1.000
363	GOBP_MULTIORGANISM_PROCESS	GO-0051704	16	-0.228735	-0.754064	0.776573	0.913702	1.000
364	GOBP-CARBOHYDRATE_DERIVATIVE_METABOLIC_PROCESS	GO-1901135	8	-0.279235	-0.754475	0.764831	0.915685	1.000
365	REACTOME_MAPK_FAMILY_SIGNALING_CASCADES	R-RNO-5683057	12	-0.253182	-0.756055	0.787629	0.915858	1.000
366	GOBP-FAT_CELL_DIFFERENTIATION	GO-0045444	9	-0.272323	-0.761995	0.761616	0.909097	1.000
367	GOBP-POSITIVE_REGULATION_OF_ENDOTHELIAL_CELL_P...	GO-0001938	6	-0.322667	-0.763973	0.761506	0.908547	1.000
368	GOBP_LEUKOCYTE_MEDIATED_IMMUNITY	GO-0002443	8	-0.287500	-0.764228	0.751073	0.910698	1.000
369	GOBP-REGULATION_OF_LIPID_METABOLIC_PROCESS	GO-0019216	7	-0.300315	-0.765164	0.754678	0.911893	1.000
370	GOBP-REGULATION_OF_FAT_CELL_DIFFERENTIATION	GO-0045598	6	-0.315394	-0.766871	0.755061	0.911597	1.000
371	GOBP_METAL_ION_TRANSPORT	GO-0030001	11	-0.262125	-0.768832	0.742204	0.910973	1.000
372	REACTOME_NUCLEAR_EVENTS_KINASE_AND_TRANSCRIPTI...	R-RNO-198725	11	-0.259394	-0.774536	0.731006	0.904595	1.000
373	GOBP-RESPONSE_TO_TEMPERATURE_STIMULUS	GO-0009266	9	-0.279007	-0.774571	0.721519	0.907112	1.000
374	GOBP_APOPTOTIC_PROCESS	GO-0006915	35	-0.192045	-0.781123	0.815618	0.898614	1.000
375	GOBP-REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	GO-1902105	9	-0.284453	-0.781447	0.723493	0.900689	1.000
376	GOBP-POSITIVE_REGULATION_OF_EPITHELIAL_CELL_PR...	GO-0050679	7	-0.304020	-0.782213	0.740365	0.900515	1.000
377	GOBP-CALCIUM_ION_TRANSPORT	GO-0006816	11	-0.262125	-0.783848	0.701826	0.901949	1.000
378	GOBP-POSITIVE_REGULATION_OF_GENE_EXPRESSION	GO-0010628	16	-0.235251	-0.783966	0.744240	0.904309	1.000
379	REACTOME_HEMOSTASIS	R-RNO-109582	14	-0.250798	-0.791148	0.755940	0.894731	1.000
380	GOBP-REGULATION_OF_POSTSYNAPTIC_MEMBRANE_POTEN...	GO-0060078	14	-0.242890	-0.793276	0.722105	0.893882	1.000
381	GOBP-REGULATION_OF_NEURON_PROJECTION_DEVELOPMENT	GO-0010975	16	-0.235544	-0.793309	0.725055	0.896437	1.000
382	REACTOME_CIRCADIAN_CLOCK	R-HSA-400253	5	-0.354545	-0.795131	0.737705	0.895913	1.000
383	GOBP-ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO...	GO-0072594	5	-0.361555	-0.802688	0.706935	0.885710	1.000
384	GOBP-RESPONSE_TO_PEPTIDE	GO-1901652	18	-0.232673	-0.805931	0.737166	0.882776	1.000

Continuation of Table S7

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
385 REACTOME_PROTEIN_PROTEIN_INTERACTIONS_AT_SYNAPSES	R-RNO-6794362	12	-0.263158	-0.806973	0.714575	0.883612	1.000
386 GOBP_NEGATIVE_REGULATION_OF_LIPID_METABOLIC_PR...	GO-0045833	5	-0.359331	-0.809689	0.705882	0.881469	1.000
387 GOBP_NEGATIVE_REGULATION_OF_ANION_TRANSPORT	GO-1903792	8	-0.302382	-0.810514	0.686235	0.882675	1.000
388 GOBP_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENT...	GO-0002761	8	-0.302711	-0.813524	0.678350	0.879499	1.000
389 GOBP_REGULATION_OF_SYSTEM_PROCESS	GO-0044057	18	-0.238700	-0.813681	0.736739	0.881858	1.000
390 GOBP_POSITIVE_REGULATION_OF_DEFENSE_RESPONSE	GO-0031349	5	-0.358253	-0.814454	0.679513	0.883166	1.000
391 GOBP_PROTEIN_LOCALIZATION_TO_ORGANELLE	GO-0033365	8	-0.300993	-0.814635	0.704225	0.885508	1.000
392 GOBP_MUSCLE_TISSUE_DEVELOPMENT	GO-0060537	11	-0.281116	-0.818114	0.696842	0.882119	1.000
393 GOBP_RESPONSE_TO_OXYGEN_CONTAINING_COMPOUND	GO-1901700	39	-0.199484	-0.821008	0.736501	0.879639	1.000
394 GOBP_CELLULAR_RESPONSE_TO_ALCOHOL	GO-0097306	5	-0.361833	-0.822973	0.701903	0.878610	1.000
395 REACTOME_NEUTROPHIL_DEGRANULATION	R-RNO-6798695	6	-0.341463	-0.823651	0.660338	0.880154	1.000
396 GOBP_NEGATIVE_REGULATION_OF_MULTICELLULAR_ORGA...	GO-0051241	15	-0.250690	-0.824490	0.668860	0.881454	1.000
397 GOBP_REGULATION_OF_CELL_PROJECTION_ORGANIZATION	GO-0031344	20	-0.235060	-0.825317	0.692140	0.882725	1.000
398 GOBP_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY	GO-0002444	6	-0.341463	-0.827919	0.659919	0.880997	1.000
399 GOBP_DIVALENT_INORGANIC_CATION_HOMEOSTASIS	GO-0072507	13	-0.269552	-0.834821	0.692500	0.870895	1.000
400 GOBP_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	GO-0002263	6	-0.341463	-0.835395	0.655031	0.872581	1.000
401 GOBP_REGULATION_OF_CELL_DEATH	GO-0010941	34	-0.208777	-0.836920	0.731405	0.872578	1.000
402 GOBP_ENDOMEMBRANE_SYSTEM_ORGANIZATION	GO-0010256	6	-0.345614	-0.846190	0.639066	0.858012	1.000
403 GOBP_REGULATION_OF_CELLULAR_LOCALIZATION	GO-0060341	17	-0.245999	-0.848673	0.656613	0.855842	1.000
404 GOBP_REGULATION_OF_ENDOTHELIAL_CELL_MIGRATION	GO-0010594	5	-0.377361	-0.848914	0.652928	0.858065	1.000
405 GOBP_REGULATION_OF_CELLULAR_CATABOLIC_PROCESS	GO-0031329	10	-0.292255	-0.852262	0.642553	0.854766	1.000
406 GOBP_REGULATION_OF_CYTOSOLIC_CALCULUM_CONCE...	GO-0051480	13	-0.269552	-0.855593	0.641791	0.851355	1.000
407 GOBP_SECOND_MESSENGER_MEDIATED_SIGNALING	GO-0019932	16	-0.259088	-0.858059	0.638393	0.849343	1.000
408 GOBP_REGULATION_OF_CELL_DIFFERENTIATION	GO-0045595	36	-0.212871	-0.858170	0.664269	0.851756	1.000
409 GOBP_CELLULAR_RESPONSE_TO ABIOTIC_STIMULUS	GO-0071214	7	-0.341724	-0.859745	0.616601	0.851612	1.000
410 GOBP_POSITIVE_REGULATION_OF_CELL_PROJECTION_OR...	GO-0031346	10	-0.294934	-0.860325	0.639175	0.853199	1.000
411 GOBP_POSITIVE_REGULATION_OF_HYDROLASE_ACTIVITY	GO-0051345	16	-0.254525	-0.863409	0.640333	0.850267	1.000
412 GOBP_CALCULUM_MEDIATED_SIGNALING	GO-0019722	10	-0.301784	-0.867092	0.652977	0.845853	1.000
413 GOBP_MUSCLE_STRUCTURE_DEVELOPMENT	GO-0061061	16	-0.263450	-0.867893	0.633406	0.847142	1.000
414 GOBP_CIRCULATORY_SYSTEM_PROCESS	GO-0003013	5	-0.400419	-0.869143	0.613821	0.847502	1.000
415 GOBP_METAL_ION_HOMEOSTASIS	GO-0055065	14	-0.270270	-0.870285	0.610309	0.848077	1.000
416 GOBP_RESPONSE_TO PEPTIDE_HORMONE	GO-0043434	13	-0.274055	-0.870441	0.637097	0.850428	1.000
417 GOBP_CELLULAR_ION_HOMEOSTASIS	GO-0008873	14	-0.270270	-0.871187	0.627409	0.851754	1.000
418 GOBP_MYELOID_LEUKOCYTE_DIFFERENTIATION	GO-0002573	11	-0.292851	-0.875138	0.595618	0.846775	1.000
419 GOBP_POSITIVE_REGULATION_OF_MOLECULAR_FUNCTION	GO-0044093	37	-0.214430	-0.876418	0.651376	0.847137	1.000
420 GOBP_POSITIVE_REGULATION_OF_AXONOGENESIS	GO-0050772	5	-0.388118	-0.877223	0.594080	0.848456	1.000
421 REACTOME_ADAPTIVE_IMMUNE_SYSTEM	R-RNO-1280218	9	-0.317988	-0.878575	0.596194	0.848596	1.000
422 GOBP_REGULATION_OF_AXONOGENESIS	GO-0050770	7	-0.342160	-0.883526	0.603696	0.842097	1.000
423 GOBP_OSTEOCLAST_DIFFERENTIATION	GO-0030316	6	-0.367724	-0.883716	0.575630	0.844514	1.000
424 GOBP_RESPONSE_TO NICOTINE	GO-0035094	7	-0.345679	-0.885157	0.580499	0.844347	1.000
425 GOBP_REGULATION_OF_INFLAMMATORY_RESPONSE	GO-0050727	7	-0.353646	-0.887432	0.578000	0.842869	1.000
426 GOBP_RESPONSE_TO HEAT	GO-0009408	7	-0.347222	-0.892237	0.580392	0.836169	1.000
427 GOBP_ANIMAL_ORGAN_MORPHOGENESIS	GO-0009887	12	-0.293925	-0.896242	0.588727	0.831408	1.000

Continuation of Table S7

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
428	GOBP-EXCITATORY-CHEMICAL-SYNAPTIC-TRANSMISSION	5	-0.398286	-0.896846	0.565591	0.832856	1.000
429	GOBP-POSITIVE-REGULATION-OF-SMALL-MOLECULE-MET...	5	-0.403905	-0.900251	0.579710	0.829196	1.000
430	GOBP-REGULATION-OF-TRANSMEMBRANE-TRANSPORT	23	-0.243276	-0.900782	0.597458	0.830935	1.000
431	GOBP-REGULATION-OF-CELL-CYCLE-PROCESS	5	-0.4010583	-0.904073	0.556263	0.827612	1.000
432	GOBP-REGULATION-OF-DEFENSE-RESPONSE	7	-0.353646	-0.907198	0.565306	0.824377	1.000
433	GOBP-CHEMICAL-SYNAPTIC-TRANSMISSION-POSTSYNAPTIC	9	-0.325642	-0.907492	0.576344	0.826677	1.000
434	GOBP-NEGATIVE-REGULATION-OF-IMMUNE-SYSTEM-PROCESS	5	-0.405951	-0.910443	0.567901	0.823638	1.000
435	GOBP-LEUKOCYTE-DIFFERENTIATION	15	-0.281485	-0.911164	0.553061	0.825066	1.000
436	GOBP-REGULATION-OF-VASCULAR-ASSOCIATED-SMOOTH...	5	-0.404269	-0.911264	0.557203	0.827691	1.000
437	GOBP-CHEMICAL-HOMEOSTASIS	23	-0.240829	-0.913117	0.557447	0.826857	1.000
438	GOBP-CELL-POPULATION-PROLIFERATION	32	-0.230967	-0.917377	0.581292	0.821145	1.000
439	GOBP-PROTEOLYSIS	17	-0.273142	-0.917844	0.556769	0.823001	1.000
440	GOBP-ORGANONITROGEN-COMPOUND-BIOSYNTHETIC-PROCESS	13	-0.293081	-0.919931	0.567329	0.821940	1.000
441	GOBP-EMBRYO-DEVELOPMENT	14	-0.287247	-0.920467	0.540773	0.823744	1.000
442	GOBP-INTRACELLULAR-RECEPTOR-SIGNALING-PATHWAY	5	-0.412425	-0.922779	0.547619	0.821917	1.000
443	HALLMARK-KRAS-SIGNALING-UP	M5953	-0.384706	-0.924107	0.543611	0.822284	1.000
444	GOBP-REPRODUCTION	18	-0.265472	-0.925872	0.556745	0.821610	1.000
445	GOBP-ANATOMICAL-STRUCTURE-HOMEOSTASIS	7	-0.366772	-0.926661	0.548035	0.823007	1.000
446	GOBP-SMALL-GTPASE-MEDIATED-SIGNAL-TRANSDUCTION	8	-0.350114	-0.928278	0.520085	0.822898	1.000
447	REACTOME-INTRACELLULAR-SIGNALING-BY-SECOND-MES...	15	-0.277256	-0.929408	0.532225	0.823669	1.000
448	GOBP-CELL-SURFACE-RECEPTOR-SIGNALING-PATHWAY-I...	15	-0.282610	-0.930717	0.548729	0.824308	1.000
449	GOBP-ION-HOMEOSTASIS	16	-0.277778	-0.931811	0.528926	0.825120	1.000
450	GOBP-REGULATION-OF-EPITHELIAL-CELL-MIGRATION	6	-0.385622	-0.932442	0.548035	0.826958	1.000
451	GOBP-MYELOID-LEUKOCYTE-ACTIVATION	8	-0.350000	-0.932564	0.531697	0.829731	1.000
452	GOBP-REGULATION-OF-MEMBRANE-POTENTIAL	17	-0.276998	-0.933258	0.560000	0.831254	1.000
453	GOBP-DEVELOPMENTAL-PROCESS-INVOLVED-IN-REPRODU...	11	-0.322967	-0.935609	0.553377	0.829532	1.000
454	GOBP-CELLULAR-RESPONSE-TO-MOLECULE-OF-BACTERIA...	8	-0.359270	-0.943030	0.528184	0.817404	1.000
455	GOBP-CELLULAR-RESPONSE-TO-EXTRACELLULAR-STIMULUS	8	-0.349032	-0.943290	0.496774	0.815733	1.000
456	GOBP-RESPONSE-TO-ENDOGENOUS-STIMULUS	34	-0.233717	-0.945859	0.517986	0.817606	1.000
457	GOBP-CELLULAR-RESPONSE-TO-HORMONE-STIMULUS	11	-0.318423	-0.948209	0.520518	0.815549	1.000
458	GOBP-TRANSMEMBRANE-RECEPTOR-PROTEIN-TYROSINE-K...	19	-0.270459	-0.948857	0.514768	0.817212	1.000
459	GOBP-PHAGOCYTOSIS	5	-0.424990	-0.954268	0.495069	0.809423	1.000
460	REACTOME-DEVELOPMENTAL-BIOLOGY	R-RNO-1266738	-0.265255	-0.954517	0.517316	0.811991	1.000
461	GOBP-ERBB-SIGNALING-PATHWAY	GO-0038127	-0.428193	-0.958321	0.515924	0.807107	1.000
462	GOBP-CELLULAR-RESPONSE-TO-BIOTIC-STIMULUS	8	-0.359270	-0.959955	0.508097	0.806921	1.000
463	GOBP-POSITIVE-REGULATION-OF-MULTICELLULAR-ORGA...	32	-0.243568	-0.963246	0.516704	0.803043	1.000
464	GOBP-POSITIVE-REGULATION-OF-CELLULAR-PROTEIN-L...	7	-0.370922	-0.965362	0.477551	0.802094	1.000
465	GOBP-POSITIVE-REGULATION-OF-TRANSMEMBRANE-TRAN...	GO-1903829	-0.372886	-0.967529	0.459459	0.800604	1.000
466	GOBP-CELLULAR-RESPONSE-TO-OXYGEN-CONTAINING-CO...	GO-1901701	-0.247816	-0.969591	0.507463	0.799452	1.000
467	GOBP-PERIPHERAL-NERVOUS-SYSTEM-DEVELOPMENT	GO-0007422	-0.410127	-0.970162	0.467836	0.802346	1.000
468	GOBP-MONOCARBOXYLIC-ACID-METABOLIC-PROCESS	GO-0032787	-0.385791	-0.978392	0.491453	0.790244	1.000
469	GOBP-PROTEIN-MODIFICATION-BY-SMALL-PROTEIN-CON...	GO-0070647	-0.371359	-0.980746	0.481153	0.788432	1.000
470	GOBP-RESPONSE-TO-OXYGEN-LEVELS	GO-0070482					

Continuation of Table S7

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
471	GOBP-POSITIVE-REGULATION-OF-HEMOPOIESIS	GO-1903708	7	-0.390164	-0.982112	0.453280	0.788581	1.000
472	GOBP-INFLAMMATORY-RESPONSE	GO-0006954	12	-0.321055	-0.983722	0.447257	0.788435	1.000
473	GOBP-REGULATION-OF-MULTICELLULAR-ORGANISMAL-DE...	GO-2000026	31	-0.247448	-0.986242	0.494279	0.786297	1.000
474	GOBP-OSSIFICATION	GO-0001503	9	-0.355999	-0.987187	0.463938	0.787511	1.000
475	GOBP-REGULATION-OF-LYMPHOCYTE-ACTIVATION	GO-0051249	5	-0.447016	-0.994596	0.460581	0.774988	1.000
476	GOBP-CELLULAR-COMPONENT-DISASSEMBLY	GO-0022411	6	-0.412176	-0.997021	0.450397	0.773021	1.000
477	GOBP-POSITIVE-REGULATION-OF-MYELOID-LEUKOCYTE-...	GO-0002763	6	-0.415664	-0.997227	0.470833	0.775777	1.000
478	GOBP-PROTEIN-LOCALIZATION-TO-POSTSYNAPSE	GO-0062237	5	-0.449699	-0.998643	0.443320	0.776118	1.000
479	GOBP-SMALL-MOLECULE-METABOLIC-PROCESS	GO-0044281	16	-0.299032	-1.001057	0.433333	0.774084	1.000
480	GOBP-RESPONSE-TO-LIPID	GO-0033993	19	-0.289528	-1.001403	0.464368	0.776527	1.000
481	REACTOME-CELLULAR-RESPONSES-TO-EXTERNAL-STIMULI	R-RNO-8953897	11	-0.344597	-1.001478	0.435146	0.779584	1.000
482	GOBP-IMMUNE-SYSTEM-DEVELOPMENT	GO-0002520	17	-0.289842	-1.001718	0.474946	0.782287	1.000
483	GOBP-ASSOCIATIVE-LEARNING	GO-0008306	7	-0.396731	-1.003805	0.434426	0.780959	1.000
484	REACTOME-POST-TRANSLATIONAL-PROTEIN-MODIFICATION	R-RNO-597592	7	-0.392535	-1.004320	0.443750	0.783140	1.000
485	GOBP-POSITIVE-REGULATION-OF-DEVELOPMENTAL-PROCESS	GO-0051094	32	-0.247034	-1.005577	0.435268	0.783442	1.000
486	GOBP-LEARNING	GO-0007612	13	-0.332276	-1.013174	0.427293	0.770430	1.000
487	GOBP-REGULATION-OF-NERVOUS-SYSTEM-DEVELOPMENT	GO-0051960	15	-0.312689	-1.014100	0.420719	0.771742	1.000
488	GOBP-NEGATIVE-REGULATION-OF-SIGNALING	GO-0023057	21	-0.283387	-1.016667	0.422566	0.768912	1.000
489	GOBP-PROTEIN-LOCALIZATION-TO-SYNAPSE	GO-0035418	5	-0.449699	-1.018342	0.446721	0.768462	1.000
490	REACTOME-VESICLE-MEDIATED-TRANSPORT	R-RNO-5653656	5	-0.454482	-1.022191	0.430584	0.763599	1.000
491	GOBP-MYELOID-CELL-DIFFERENTIATION	GO-0030099	13	-0.325592	-1.023580	0.396146	0.763811	1.000
492	REACTOME-MEMBRANE-TRAFFICKING	R-RNO-199991	5	-0.454482	-1.024754	0.418919	0.764517	1.000
493	GOBP-EPITHELIAL-CELL-DIFFERENTIATION	GO-0030855	7	-0.396753	-1.026972	0.422833	0.762951	1.000
494	GOBP-REGULATION-OF-PROTEIN-SERINE-THREONINE-KI...	GO-0071900	12	-0.338359	-1.028841	0.401806	0.762259	1.000
495	GOBP-NEGATIVE-REGULATION-OF-CELL-CYCLE	GO-0045786	5	-0.464469	-1.032478	0.380435	0.757881	1.000
496	GOBP-AMEBOIDAL-TYPE-CELL-MIGRATION	GO-0001667	11	-0.345932	-1.032926	0.417323	0.760135	1.000
497	GOBP-RESPONSE-TO-KETONE	GO-1901654	7	-0.410843	-1.035647	0.393075	0.757547	1.000
498	GOBP-MUSCLE-CELL-DIFFERENTIATION	GO-0042692	10	-0.366490	-1.037740	0.390351	0.758434	1.000
499	GOBP-POSITIVE-REGULATION-OF-IMMUNE-RESPONSE	GO-0050778	9	-0.373772	-1.037740	0.410148	0.759642	1.000
500	GOBP-MUSCLE-CONTRACTION	GO-0006936	5	-0.465932	-1.037835	0.406639	0.762860	1.000
501	GOBP-ORGANIC-ACID-METABOLIC-PROCESS	GO-0006082	7	-0.408090	-1.038076	0.387295	0.765730	1.000
502	GOBP-TISSUE-HOMEOSTASIS	GO-0001894	5	-0.463968	-1.038352	0.413793	0.768513	1.000
503	GOBP-REGULATION-OF-IMMUNE-RESPONSE	GO-0050776	12	-0.340732	-1.039730	0.415556	0.768865	1.000
504	GOBP-CELLULAR-RESPONSE-TO-PEPTIDE	GO-1901653	13	-0.329145	-1.040098	0.378788	0.771418	1.000
505	GOBP-POSTTRANSCRIPTIONAL-REGULATION-OF-GENE-EX...	GO-0010608	8	-0.392071	-1.040296	0.377119	0.774486	1.000
506	GOBP-POSITIVE-REGULATION-OF-NUCLEOBASE-CONTAIN...	GO-0045935	28	-0.270192	-1.046896	0.395745	0.763597	1.000
507	GOBP-ENZYME-LINKED-RECEPTOR-PROTEIN-SIGNALING-...	GO-0007167	24	-0.273827	-1.047268	0.381395	0.766180	1.000
508	GOBP-RESPONSE-TO-HORMONE	GO-0009725	20	-0.291206	-1.047363	0.387029	0.769450	1.000
509	GOBP-CELLULAR-RESPONSE-TO-PEPTIDE-HORMONE-STIM...	GO-0071375	9	-0.374362	-1.047844	0.392070	0.771915	1.000
510	GOBP-NEGATIVE-REGULATION-OF-PROTEIN-CATABOLIC-...	GO-0042177	5	-0.471549	-1.051579	0.385396	0.766584	1.000
511	GOBP-PROTEIN-MODIFICATION-BY-SMALL-PROTEIN-CON...	GO-0032446	6	-0.435950	-1.053848	0.398374	0.765293	1.000
512	GOBP-LYMPHOCYTE-ACTIVATION	GO-0046649	10	-0.363932	-1.055417	0.363636	0.765435	1.000
513	REACTOME-SIGNALING-BY-RHO-GTPASES-MIRO-GTPASES...	R-RNO-9716542	9	-0.382580	-1.056650	0.366667	0.766464	1.000

Continuation of Table S7

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
514 GOBP-NEGATIVE-REGULATION-OF-KINASE-ACTIVITY	GO-0033673	5	-0.469344	-1.057049	0.388889	0.769239	1.000
515 REACTOME-TOLL-LIKE-RECEPTOR-TLR1-TLR2-CASCADE	R-RNO-168179	8	-0.404275	-1.057248	0.374494	0.772374	1.000
516 GOBP-INORGANIC-ION-TRANSMEMBRANE-TRANSPORT	GO-0098660	9	-0.392302	-1.058399	0.379913	0.773633	1.000
517 GOBP-CARBOHYDRATE-HOMEOSTASIS	GO-0033500	7	-0.420198	-1.059449	0.382845	0.774782	1.000
518 HALLMARK-ALLOGRAFT-REJECTION	M5950	7	-0.419098	-1.059857	0.398095	0.777519	1.000
519 REACTOME-TOLL-LIKE-RECEPTOR-CASCADES	R-RNO-168898	8	-0.404275	-1.061902	0.397119	0.776698	1.000
520 GOBP-NEGATIVE-REGULATION-OF-TRANSFERASE-ACTIVITY	GO-0051348	5	-0.469344	-1.064803	0.397059	0.774100	1.000
521 REACTOME-MYD88-INDEPENDENT-TLR4-CASCADE	R-RNO-166166	8	-0.404275	-1.065823	0.386364	0.775602	1.000
522 REACTOME-RHO-GTPASE-EFFECTORS	R-RNO-195258	9	-0.382580	-1.066570	0.379447	0.777547	1.000
523 REACTOME-INTERLEUKIN-17-SIGNALING	R-RNO-448424	6	-0.447398	-1.067316	0.374150	0.779940	1.000
524 GOBP-MUSCLE-CELL-DEVELOPMENT	GO-0055001	5	-0.471427	-1.069166	0.373757	0.779466	1.000
525 GOBP-CELLULAR-CARBOHYDRATE-METABOLIC-PROCESS	GO-0044262	5	-0.472915	-1.069227	0.346809	0.783131	1.000
526 GOBP-REGULATION-OF-SMALL-MOLECULE-METABOLIC-PR...	GO-0062012	9	-0.384896	-1.070763	0.344000	0.783572	1.000
527 REACTOME-RNA-POLYMERASE-II-TRANSCRIPTION	R-RNO-73857	20	-0.297121	-1.077177	0.332645	0.772374	1.000
528 GOBP-POSITIVE-REGULATION-OF-MYELOID-CELL-DIFFE...	GO-0045639	7	-0.426880	-1.089351	0.354379	0.748122	1.000
529 GOBP-ENDOTHELIAL-CELL-MIGRATION	GO-0043542	8	-0.413113	-1.093696	0.337278	0.742302	1.000
530 GOBP-POSITIVE-REGULATION-OF-BINDING	GO-0051099	6	-0.450264	-1.094518	0.346473	0.744404	1.000
531 REACTOME-SIGNALING-BY-RECEPTOR-TYROSINE-KINASES	R-RNO-9006934	26	-0.290839	-1.095382	0.326531	0.746264	1.000
532 GOBP-REGULATION-OF-CELL-ADHESION	GO-0030155	13	-0.352098	-1.096289	0.353319	0.747944	1.000
533 GOBP-POSITIVE-REGULATION-OF-CELL-DIFFERENTIATION	GO-0045597	27	-0.282151	-1.096442	0.326572	0.751471	1.000
534 REACTOME-INNATE-IMMUNE-SYSTEM	R-RNO-168249	16	-0.330559	-1.098612	0.331967	0.750533	1.000
535 REACTOME-TOLL-LIKE-RECEPTOR-9-TLR9-CASCADE	R-RNO-168138	8	-0.404275	-1.099496	0.330578	0.752523	1.000
536 GOBP-PROTEIN-DEPHOSPHORYLATION	GO-0006470	7	-0.443867	-1.102257	0.318182	0.750147	1.000
537 GOBP-POSITIVE-REGULATION-OF-BIOSYNTHETIC-PROCESS	GO-0009891	27	-0.282950	-1.102967	0.337963	0.752552	1.000
538 HALLMARK-UV-RESPONSE-UP	M5941	5	-0.493858	-1.104883	0.353783	0.752263	1.000
539 GOBP-REGULATION-OF-IMMUNE-SYSTEM-PROCESS	GO-0002682	21	-0.301268	-1.105639	0.300216	0.754703	1.000
540 GOBP-BLOOD-VESSEL-ENDOTHELIAL-CELL-MIGRATION	GO-0043534	8	-0.413113	-1.107592	0.325397	0.754224	1.000
541 GOBP-PROTEIN-LOCALIZATION-TO-MEMBRANE	GO-0072657	13	-0.357280	-1.111264	0.319743	0.749675	1.000
542 GOBP-CELLULAR-RESPONSE-TO-INORGANIC-SUBSTANCE	GO-0071241	11	-0.370174	-1.113550	0.331313	0.748361	1.000
543 GOBP-RESPONSE-TO-GROWTH-FACTOR	GO-0070848	18	-0.320566	-1.114251	0.313978	0.750833	1.000
544 GOBP-TISSUE-MORPHOGENESIS	GO-0048729	7	-0.448841	-1.115709	0.341202	0.751663	1.000
545 GOBP-TISSUE-MIGRATION	GO-0090130	9	-0.405878	-1.121775	0.314286	0.741900	1.000
546 REACTOME-INFECTIOUS-DISEASE	R-HSA-5663205	12	-0.359778	-1.12194	0.304255	0.745183	1.000
547 GOBP-DEPHOSPHORYLATION	GO-0016311	7	-0.443867	-1.128033	0.309237	0.736034	1.000
548 GOBP-MEMBRANE-PROTEIN-PROTEOLYSIS	GO-0033619	6	-0.479058	-1.129251	0.312227	0.737551	1.000
549 GOBP-NEGATIVE-REGULATION-OF-LOCOMOTION	GO-0040013	5	-0.496614	-1.130574	0.295833	0.738519	1.000
550 GOBP-RESPONSE-TO-LIGHT-STIMULUS	GO-0009416	11	-0.376255	-1.133790	0.317895	0.735093	1.000
551 GOBP-REGULATION-OF-CELLULAR-PROTEIN-LOCALIZATION	GO-1903827	12	-0.373706	-1.139122	0.293182	0.726784	1.000
552 GOBP-TRANSMEMBRANE-TRANSPORT	GO-0055085	27	-0.291497	-1.139126	0.289238	0.730977	1.000
553 GOBP-POSITIVE-REGULATION-OF-NEURON-DEATH	GO-1901216	5	-0.509087	-1.143212	0.314815	0.725663	1.000
554 GOBP-FC-EPSILON-RECEPTOR-SIGNALING-PATHWAY	GO-0038095	7	-0.457847	-1.145332	0.301518	0.724984	1.000
555 GOBP-NEGATIVE-REGULATION-OF-APOPTOTIC-SIGNALIN...	GO-2001234	7	-0.459021	-1.147099	0.292887	0.725161	1.000
556 GOBP-CARBOHYDRATE-METABOLIC-PROCESS	GO-0005975	9	-0.404643	-1.147320	0.299401	0.729039	1.000

Continuation of Table S7

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
557 GOBP-NEGATIVE-REGULATION-OF-PHOSPHORUS-METABOL...	GO-0010563	9	-0.402895	-1.147775	0.290456	0.732394	1.000
558 GOBP-RESPONSE-TO-BIOTIC-STIMULUS	GO-0009607	17	-0.330958	-1.148909	0.263636	0.734046	1.000
559 GOBP-RESPONSE-TO-INSULIN	GO-0032868	5	-0.512939	-1.150783	0.301969	0.734051	1.000
560 REACTOME-MAPK-TARGETS-NUCLEAR-EVENTS-MEDIATED...	R-HSA-450282	5	-0.517623	-1.153926	0.301010	0.731214	1.000
561 GOBP-VASCULATURE-DEVELOPMENT	GO-0001944	17	-0.336227	-1.155498	0.272917	0.732012	1.000
562 REACTOME-DISEASES-OF-SIGNAL-TRANSDUCTION-BY_GR...	R-HSA-5663202	12	-0.376227	-1.156413	0.269076	0.734648	1.000
563 GOBP-CELL-CELL-JUNCTION-ASSEMBLY	GO-0007043	5	-0.518789	-1.158427	0.289628	0.734235	1.000
564 GOBP-NEGATIVE-REGULATION-OF-RESPONSE-TO-STIMULUS	GO-0048585	16	-0.342970	-1.160829	0.261702	0.732601	1.000
565 GOBP-RESPONSE-TO-CYTOKINE	GO-0034097	23	-0.317811	-1.161548	0.273138	0.735465	1.000
566 GOBP-RESPONSE-TO-DRUG	GO-00042493	11	-0.394379	-1.162359	0.262821	0.738054	1.000
567 GOBP-PROTEIN-CATABOLIC-PROCESS	GO-0030163	8	-0.437013	-1.163100	0.286008	0.741101	1.000
568 GOBP-ORGANONITROGEN-COMPOUND-CATABOLIC-PROCESS	GO-1901565	10	-0.404112	-1.167916	0.278373	0.733660	1.000
569 HALLMARK-EPITHELIAL-MESENCHYMAL-TRANSITION	M5930	5	-0.530086	-1.169265	0.299413	0.734929	1.000
570 REACTOME-FC-EPSILON-RECEPTOR-FCER1-SIGNALING	R-RNO-2454202	7	-0.457847	-1.173043	0.260870	0.729951	1.000
571 GOBP-CYTOKINE-MEDIATED-SIGNALING-PATHWAY	GO-0019221	16	-0.350068	-1.177802	0.274678	0.722589	1.000
572 GOBP-REGULATION-OF-CARBOHYDRATE-METABOLIC-PROCESS	GO-0006109	5	-0.529298	-1.179125	0.295833	0.724295	1.000
573 GOBP-ANATOMICAL-STRUCTURE-FORMATION-INVOLVED_I...	GO-0048646	20	-0.331459	-1.181175	0.246888	0.723879	1.000
574 GOBP-OSTEOBLAST-DIFFERENTIATION	GO-0001649	5	-0.528953	-1.186429	0.288066	0.716058	1.000
575 GOBP-REGULATION-OF-CARBOHYDRATE-BIOSYNTHETIC_P...	GO-0043255	5	-0.529298	-1.188145	0.273453	0.716261	1.000
576 GOBP-POSITIVE-REGULATION-OF-DNA-BINDING-TRANSC...	GO-0051091	10	-0.417960	-1.190442	0.264192	0.715117	1.000
577 HALLMARK-HYPOXIA	M5891	5	-0.521764	-1.193107	0.268537	0.713096	1.000
578 GOBP-GROWTH	GO-0040007	14	-0.362667	-1.194045	0.217778	0.715498	1.000
579 GOBP-CARBOHYDRATE-BIOSYNTHETIC-PROCESS	GO-0016051	5	-0.529298	-1.194274	0.255274	0.719759	1.000
580 GOBP-T-CELL-ACTIVATION	GO-0042110	8	-0.439166	-1.194497	0.246781	0.724202	1.000
581 GOBP-BLOOD-VESSEL-MORPHOGENESIS	GO-0048514	14	-0.383743	-1.201805	0.228512	0.710959	1.000
582 GOBP-POSITIVE-REGULATION-OF-CELL-ADHESION	GO-0045785	7	-0.470971	-1.202342	0.230937	0.714346	1.000
583 GOBP-RESPONSE-TO-UV	GO-0009411	5	-0.524583	-1.203418	0.240938	0.716795	1.000
584 GOBP-CELL-CELL-JUNCTION-ORGANIZATION	GO-0045216	6	-0.503628	-1.204850	0.236253	0.718153	1.000
585 GOBP-RESPONSE-TO-TUMOR-NECROSIS-FACTOR	GO-0034612	7	-0.478162	-1.206102	0.253731	0.720159	1.000
586 GOBP-BIOLOGICAL-PROCESS-INVOLVED-IN-SYMBIOTIC....	GO-004440	10	-0.414804	-1.210546	0.233546	0.714001	1.000
587 GOBP-CALCIUM-ION-TRANSPORT-INTO-CYTOSOL	GO-0060402	7	-0.482775	-1.213035	0.253138	0.712839	1.000
588 GOBP-REGULATION-OF-DNA-BINDING-TRANSCRIPTION_F...	GO-0051090	16	-0.360993	-1.214691	0.236287	0.713508	1.000
589 GOBP-POSITIVE-REGULATION-OF-TRANSCRIPTION_BY_R...	GO-0045944	24	-0.324072	-1.217251	0.188437	0.711888	1.000
590 GOBP-GENERATION-OF-PRECURSOR-METABOLITES-AND-E...	GO-0006091	5	-0.540143	-1.218163	0.247401	0.714738	1.000
591 GOBP-NEGATIVE-REGULATION-OF-NUCLEOBASE-CONTAIN...	GO-0045934	13	-0.388176	-1.220782	0.214912	0.713221	1.000
592 REACTOME-CELLULAR-SENESCENCE	R-RNO-2559583	6	-0.520283	-1.224770	0.250000	0.708187	1.000
593 GOBP-SMOOTH-MUSCLE-CELL-PROLIFERATION	GO-0048659	6	-0.502625	-1.226034	0.234216	0.712949	1.000
594 GOBP-CARDIAC-MUSCLE-TISSUE-DEVELOPMENT	GO-0048738	6	-0.517251	-1.225409	0.247951	0.717445	1.000
595 GOBP-CIRCULATORY-SYSTEM-DEVELOPMENT	GO-0072359	21	-0.342821	-1.226122	0.204167	0.721104	1.000
596 GOBP-ANION-TRANSMEMBRANE-TRANSPORT	GO-0098656	7	-0.494550	-1.229908	0.216769	0.716618	1.000
597 GOBP-IMMUNE-EFFECTOR-PROCESS	GO-0002252	11	-0.409554	-1.230782	0.210989	0.719990	1.000
598 GOBP-REGULATION-OF-CELL-CYCLE	GO-0051726	13	-0.387077	-1.234892	0.210412	0.714926	1.000
599 GOBP-CALCIUM-ION-TRANSMEMBRANE-TRANSPORT	GO-0070588	7	-0.482775	-1.238704	0.223762	0.710275	1.000

Continuation of Table S7

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
600	GOBP-HEART_DEVELOPMENT	GO-0007507	6	-0.517251	-1.239939	0.209205	0.712925
601	REACTOME-SENESCENCE-ASSOCIATED-SECRETORY-PHENO...	R-RNO-2559582	6	-0.520283	-1.240168	0.210204	0.717999
602	GOBP-MORPHOGENESIS-OF-AN-EPITHELIUM	GO-0002009	6	-0.521096	-1.243535	0.223790	0.715126
603	GOBP-NEGATIVE-REGULATION-OF-PROTEOLYSIS	GO-0045861	8	-0.477530	-1.245738	0.213531	0.715072
604	GOBP-CYTOSOLIC-CALCIUM-ION-TRANSPORT	GO-0060401	7	-0.482775	-1.247522	0.210526	0.716020
605	GOBP-NEGATIVE-REGULATION-OF-HYDROLASE-ACTIVITY	GO-0051346	11	-0.420789	-1.248377	0.203947	0.719563
606	GOBP-LIPID-METABOLIC-PROCESS	GO-0006629	10	-0.441926	-1.249168	0.200855	0.723370
607	GOBP-REGULATION-OF-WNT-SIGNALING-PATHWAY	GO-0030111	5	-0.565248	-1.251328	0.226891	0.723427
608	REACTOME-LEISHMANIA-INFECTION	R-HSA-96558195	10	-0.427030	-1.251585	0.191176	0.728936
609	GOBP-MACROMOLECULE-CATABOLIC-PROCESS	GO-0009057	11	-0.425265	-1.253382	0.200413	0.730194
610	GOBP-FC-RECEPTOR-SIGNALING-PATHWAY	GO-0038093	8	-0.478834	-1.253430	0.185950	0.736469
611	GOBP-RESPONSE-TO-ORGANIC-CYCLIC-COMPOUND	GO-0014070	20	-0.353629	-1.254105	0.197368	0.740998
612	GOBP-CELLULAR-RESPONSE-TO-EXTERNAL-STIMULUS	GO-0071496	10	-0.442476	-1.256419	0.203285	0.740795
613	GOBP-MUSCLE-CELL-PROLIFERATION	GO-0033002	8	-0.484818	-1.261805	0.171843	0.731964
614	GOBP-POLYSACCHARIDE-METABOLIC-PROCESS	GO-0005976	5	-0.569708	-1.263789	0.185031	0.727453
615	GOBP-NEGATIVE-REGULATION-OF-PROTEIN-MODIFICATI...	GO-0031400	10	-0.449880	-1.281380	0.179654	0.690051
616	GOBP-REGULATION-OF-ANATOMICAL-STRUCTURE-SIZE	GO-0090066	10	-0.445457	-1.281516	0.190678	0.699836
617	GOBP-IMMUNE-RESPONSE-REGULATING-SIGNALING-PATHWAY	GO-000276	8	-0.478834	-1.282527	0.190377	0.701377
618	GOBP-RESPIRATORY-SYSTEM-DEVELOPMENT	GO-0060541	6	-0.53856	-1.284334	0.190476	0.703879
619	GOBP-CELL-CYCLE	GO-0007049	21	-0.349020	-1.286035	0.165198	0.709356
620	GOBP-PROTEIN-LOCALIZATION-TO-CELL-JUNCTION	GO-1902414	6	-0.539079	-1.286454	0.193548	0.709356
621	GOBP-RESPONSE-TO-ABIOTIC-STIMULUS	GO-0009628	27	-0.337552	-1.288025	0.142857	0.711664
622	GOBP-MONONUCLEAR-CELL-DIFFERENTIATION	GO-1903131	7	-0.491649	-1.295420	0.183299	0.697773
623	GOBP-EPIDERMIS-DEVELOPMENT	GO-0008544	5	-0.591297	-1.299997	0.172269	0.691564
624	REACTOME-DEATH-RECEPTOR-SIGNALING	R-RNO-73887	5	-0.570238	-1.301921	0.184000	0.692282
625	GOBP-POSITIVE-REGULATION-OF-IMMUNE-SYSTEM-PROCESS	GO-0002684	18	-0.370201	-1.310298	0.155844	0.676022
626	GOBP-REGULATION-OF-APOPTOTIC-SIGNALING-PATHWAY	GO-2001233	10	-0.448022	-1.311844	0.168085	0.678786
627	GOBP-RESPONSE-TO-MOLECULE-OF-BACTERIAL-ORIGIN	GO-0002237	13	-0.414004	-1.311908	0.141962	0.685612
628	GOBP-EMBRYO-DEVELOPMENT-ENDING-IN-BIRTH-OR-EGG...	GO-0009792	9	-0.486696	-1.314993	0.162698	0.684204
629	GOBP-APOPTOTIC-SIGNALING-PATHWAY	GO-0097190	15	-0.408208	-1.315730	0.138075	0.689218
630	GOBP-GLUCOSE-METABOLIC-PROCESS	GO-0006006	6	-0.551188	-1.322651	0.154661	0.678137
631	GOBP-NEGATIVE-REGULATION-OF-PROTEIN-METABOLIC-...	GO-0051248	20	-0.370325	-1.323908	0.127835	0.682022
632	GOBP-MONOSACCHARIDE-METABOLIC-PROCESS	GO-0005996	6	-0.551188	-1.331230	0.172211	0.668270
633	GOBP-REGULATION-OF-ORGAN-GROWTH	GO-0046620	5	-0.589085	-1.335141	0.159509	0.663790
634	GOBP-DEVELOPMENTAL-GROWTH	GO-0048589	10	-0.466972	-1.338962	0.158730	0.659872
635	GOBP-RESPONSE-TO-BACTERIUM	GO-0009617	13	-0.414004	-1.339566	0.136364	0.665467
636	GOBP-ORGAN-GROWTH	GO-0035265	5	-0.589085	-1.344123	0.136170	0.659775
637	GOBP-NEGATIVE-REGULATION-OF-CATALYTIC-ACTIVITY	GO-0043086	17	-0.397651	-1.344544	0.122318	0.665965
638	GOBP-STRIATED-MUSCLE-CELL-DIFFERENTIATION	GO-0051146	9	-0.490181	-1.345129	0.136268	0.672057
639	GOBP-EMBRYONIC-ORGAN-DEVELOPMENT	GO-0048458	7	-0.529455	-1.345221	0.139442	0.679514
640	GOBP-MITOCHONDRION-ORGANIZATION	GO-0007005	7	-0.538929	-1.346241	0.160000	0.684583
641	GOBP-ACTIVATION-OF-IMMUNE-RESPONSE	GO-0002253	5	-0.609398	-1.347338	0.140787	0.689059
642	GOBP-SKIN-DEVELOPMENT	GO-0043588	5	-0.608173	-1.350117	0.151394	0.680062

Continuation of Table S7

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
643 GOBP-NEGATIVE-REGULATION-OF-BIOSYNTHETIC-PROCESS	GO-0009890	13	-0.437255	-1.353876	0.125532	0.685923	1.000
644 GOBP-NEGATIVE-REGULATION-OF-CATABOLIC-PROCESS	GO-0009895	8	-0.510338	-1.355736	0.121535	0.688937	1.000
645 GOBP-REGULATION-OF-PROTEIN-CATABOLIC-PROCESS	GO-0042176	7	-0.526907	-1.357839	0.130802	0.691271	1.000
646 GOBP-REGULATION-OF-CATABOLIC-PROCESS	GO-0009894	13	-0.432226	-1.358588	0.127119	0.698141	1.000
647 GOBP-NEGATIVE-REGULATION-OF-INTRACELLULAR-SIGN...	GO-1902532	7	-0.533457	-1.363170	0.136264	0.692992	1.000
648 GOBP-APOPTOTIC-MITOCHONDRIAL-CHANGES	GO-0008637	6	-0.579419	-1.368273	0.152220	0.687266	1.000
649 GOBP-CELL-CELL-ADHESION	GO-0098609	14	-0.416022	-1.369775	0.111597	0.691535	1.000
650 GOBP-POSITIVE-REGULATION-OF-CELL-DEATH	GO-0010942	19	-0.385208	-1.369989	0.117914	0.700135	1.000
651 GOBP-RESPONSE-TO-METAL-ION	GO-0010038	15	-0.416804	-1.373779	0.111588	0.697334	1.000
652 HALMARK-TNFA-SIGNALING-VIA-NFKB	M5890	14	-0.438501	-1.376416	0.128151	0.698010	1.000
653 GOBP-RESPONSE-TO-CADMIUM-ION	GO-0046686	6	-0.573837	-1.379685	0.135628	0.698165	1.000
654 GOBP-LEUKOCYTE-CELL-CELL-ADHESION	GO-0007159	6	-0.580612	-1.381186	0.126253	0.703336	1.000
655 GOBP-RAS-PROTEIN-SIGNAL-TRANSDUCTION	GO-0007265	5	-0.617564	-1.384816	0.125000	0.700912	1.000
656 GOBP-REGULATION-OF-GROWTH	GO-0040008	13	-0.433207	-1.392815	0.106522	0.685317	1.000
657 GOBP-TUBE-DEVELOPMENT	GO-0035295	18	-0.390908	-1.393722	0.095745	0.692562	1.000
658 GOBP-EPITHELIUM-DEVELOPMENT	GO-0060429	15	-0.427629	-1.401216	0.097458	0.679332	1.000
659 GOBP-NEGATIVE-REGULATION-OF-PEPTIDASE-ACTIVITY	GO-0010466	6	-0.585469	-1.401791	0.112245	0.687830	1.000
660 GOBP-REGULATION-OF-PROTEIN-LOCALIZATION-TO-MEM...	GO-1905475	7	-0.547828	-1.401816	0.116935	0.698316	1.000
661 GOBP-RESPONSE-TO-INORGANIC-SUBSTANCE	GO-0010035	19	-0.399930	-1.403198	0.076253	0.704564	1.000
662 GOBP-REGULATION-OF-ANION-TRANSMEMBRANE-TRANSPORT	GO-0010035	5	-0.638373	-1.413985	0.115914	0.680861	1.000
663 HALMARK-P13K-AKT-MTOR-SIGNALING	GO-1903959	6	-0.595923	-1.417757	0.114053	0.680041	1.000
664 GOBP-DEVELOPMENTAL-CELL-GROWTH	M5923	5	-0.646082	-1.417794	0.095918	0.691151	1.000
665 GOBP-REGULATION-OF-CELLULAR-AMIDE-METABOLIC-PR...	GO-0034248	9	-0.500525	-1.417989	0.086498	0.701975	1.000
666 GOBP-RESPONSE-TO-RADIATION	GO-0009314	13	-0.441499	-1.419133	0.103926	0.710117	1.000
667 GOBP-NEGATIVE-REGULATION-OF-TRANSMEMBRANE-TRAN...	GO-0034763	6	-0.585290	-1.422206	0.104167	0.712038	1.000
668 GOBP-MATERNAL-PROCESS-INVOLVED-IN-FEMALE-PREGN...	GO-0060135	5	-0.630643	-1.422640	0.095041	0.723020	1.000
669 GOBP-NEGATIVE-REGULATION-OF-TRANSCRIPTION-BY-R...	GO-0000122	10	-0.486197	-1.422709	0.085339	0.735710	1.000
670 REACTOME-CYTOKINE-SIGNALING-IN-IMMUNE-SYSTEM	R-RNO-1280215	21	-0.390135	-1.427272	0.067391	0.733226	1.000
671 REACTOME-TRANSCRIPTIONAL-REGULATION-BY-TP53	R-RNO-3700989	6	-0.598846	-1.432778	0.113734	0.726744	1.000
672 REACTOME-ESTROGEN-DEPENDENT-NUCLEAR-EVENTS-DOW...	R-RNO-9634638	5	-0.646414	-1.437984	0.083658	0.719940	1.000
673 GOBP-NEGATIVE-REGULATION-OF-MOLECULAR-FUNCTION	GO-0044092	24	-0.383490	-1.438915	0.064103	0.729941	1.000
674 GOBP-RESPONSE-TO-OXIDATIVE-STRESS	GO-0006979	8	-0.537564	-1.448055	0.094456	0.711033	1.000
675 GOBP-RESPONSE-TO-REACTIVE-OXYGEN-SPECIES	GO-0000302	8	-0.537564	-1.452429	0.096311	0.709326	1.000
676 GOBP-POSITIVE-REGULATION-OF-DEVELOPMENTAL-GROWTH	GO-0048639	8	-0.547288	-1.453682	0.082474	0.719063	1.000
677 GOBP-CELL-GROWTH	GO-0016049	10	-0.495758	-1.460859	0.082136	0.707137	1.000
678 GOBP-POSITIVE-REGULATION-OF-GROWTH	GO-00445927	9	-0.536625	-1.463954	0.090909	0.711907	1.000
679 GOBP-CELLULAR-RESPONSE-TO-CADMIUM-ION	GO-0071276	5	-0.637243	-1.465920	0.078556	0.720059	1.000
680 GOBP-TUBE-MORPHOGENESIS	GO-0035239	15	-0.439513	-1.478317	0.063291	0.689578	1.000
681 GOBP-CELLULAR-LIPID-METABOLIC-PROCESS	GO-0044255	7	-0.580407	-1.489710	0.072835	0.664708	1.000
682 GOBP-CELLULAR-RESPONSE-TO-CHEMICAL-STRESS	GO-0062197	7	-0.587323	-1.504229	0.073996	0.631122	1.000
683 GOBP-NEGATIVE-REGULATION-OF-CYSTEINE-TYPE-ENDO...	GO-2000117	5	-0.662376	-1.504634	0.057940	0.644852	1.000
684 GOBP-CELLULAR-RESPONSE-TO-REACTIVE-OXYGEN-SPECIES	GO-0034614	7	-0.587323	-1.507702	0.069530	0.649586	1.000
685 GOBP-LEUKOCYTE-MIGRATION	GO-0050900	6	-0.631875	-1.510705	0.069388	0.654676	1.000

Continuation of Table S7

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
686	GOBP-NEGATIVE-REGULATION-OF-BINDING	6	-0.622556	-1.512076	0.066000	0.666636	1.000
687	GOBP-RESPONSE.TO.EXTRACELLULAR.STIMULUS	13	-0.467150	-1.519617	0.058065	0.656393	1.000
688	GOBP-PROTEIN.LOCALIZATION.TO.CELL.PERIPHERY	12	-0.496423	-1.520347	0.055666	0.671493	1.000
689	REACTOME-EXTRA.NUCLEAR.ESTROGEN-SIGNALING	7	-0.607930	-1.523406	0.062745	0.679231	1.000
690	GOBP-MULTI.MULTICELLULAR-ORGANISM-PROCESS	8	-0.557755	-1.525546	0.062366	0.690202	1.000
691	GOBP-HOMEOSTASIS-OF.NUMBER-OF.CELLS	5	-0.685487	-1.536664	0.058943	0.666886	1.000
692	GOBP-REGULATION-OF-CELLULAR-COMPONENT-SIZE	7	-0.603828	-1.545356	0.054167	0.654699	1.000
693	GOBP-PEPTIDE.BIOSYNTHETIC-PROCESS	6	-0.639139	-1.553564	0.047414	0.643668	1.000
694	GOBP-AMIDE.BIOSYNTHETIC-PROCESS	6	-0.639139	-1.554288	0.050201	0.661663	1.000
695	GOBP-GLAND.DEVELOPMENT	7	-0.625519	-1.561354	0.055985	0.656445	1.000
696	GOBP-IMPORT-INTO-CELL	6	-0.646326	-1.563310	0.048583	0.671175	1.000
697	GOBP-REGULATION-OF-PROTEIN.LOCALIZATION.TO.CEL...	6	-0.659548	-1.569864	0.051181	0.668626	1.000
698	GOBP-PROTEIN.LOCALIZATION.TO.PLASMA-MEMBRANE	7	-0.629465	-1.578859	0.036893	0.655763	1.000
699	GOBP-POSITIVE-REGULATION-OF-PRL-MIRNA-TRANSCRI...	7	-0.628178	-1.584943	0.041754	0.655981	1.000
700	GOBP-PEPTIDE-METABOLIC-PROCESS	11	-0.533437	-1.587809	0.033543	0.669259	1.000
701	GOBP-POSITIVE-REGULATION-OF-SMOOTH-MUSCLE-CELL...	5	-0.715656	-1.593259	0.039014	0.673200	1.000
702	GOBP-POSITIVE-REGULATION-OF-CELL-CELL-ADHESION	5	-0.717485	-1.601114	0.027837	0.670864	1.000
703	REACTOME-PTEN-REGULATION	5	-0.711920	-1.602902	0.036217	0.693613	1.000
704	GOBP-PRL-MIRNA-TRANSCRIPTION-BY-RNA-POLYMERASE-II	7	-0.628178	-1.608056	0.041841	0.702654	1.000
705	GOBP-RESPONSE.TO.NUTRIENT	5	-0.725790	-1.608398	0.036364	0.736059	1.000
706	GOBP-POSITIVE-REGULATION-OF-LEUKOCYTE-CELL-CEL...	5	-0.717485	-1.609459	0.028112	0.770410	1.000
707	GOBP-REGULATION-OF-PROTEIN-BINDING	7	-0.630009	-1.613016	0.032000	0.794032	1.000
708	GOBP-IN-UTERO-EMBRYONIC-DEVELOPMENT	8	-0.606849	-1.613797	0.034632	0.835592	1.000
709	GOBP-REGULATION-OF-DEVELOPMENTAL-GROWTH	9	-0.583251	-1.615060	0.037773	0.880631	1.000
710	HALLMARK-APOPTOSIS	6	-0.673505	-1.620250	0.030242	0.910137	1.000
711	GOBP-SPROUTING-ANGIOGENESIS	5	-0.719135	-1.623936	0.026804	0.955039	1.000
712	GOBP-REGULATION-OF-EXTRINSIC-APOPTOTIC-SIGNALI...	6	-0.686321	-1.624386	0.018557	1.000000	1.000
713	GOBP-AGING	13	-0.519766	-1.636957	0.028630	1.000000	1.000
714	REACTOME-SIGNALING-BY-INTERLEUKINS	15	-0.502410	-1.638089	0.035197	1.000000	1.000
715	GOBP-ENDOCRINE-SYSTEM-DEVELOPMENT	6	-0.699680	-1.661875	0.028513	1.000000	1.000
716	GOBP-REGULATION-OF-CELL-SIZE	5	-0.755216	-1.662006	0.026804	1.000000	1.000
717	GOBP-REGULATION-OF-BINDING	11	-0.559021	-1.662269	0.028986	1.000000	1.000
718	REACTOME-ESR-MEDIATED-SIGNALING	8	-0.644575	-1.694483	0.026477	1.000000	1.000
719	REACTOME-SIGNALING-BY-NUCLEAR-RECEPTORS	8	-0.644575	-1.723517	0.014403	1.000000	0.995
720	GOBP-EXTRINSIC-APOPTOTIC-SIGNALING-PATHWAY	7	-0.690277	-1.734438	0.014706	1.000000	0.989
721	GOBP-POSITIVE-REGULATION-OF-CELL-GROWTH	6	-0.755612	-1.774435	0.002049	1.000000	0.972
722	GOBP-CELLULAR-AMIDE-METABOLIC-PROCESS	12	-0.566680	-1.774934	0.006342	1.000000	0.972
723	REACTOME-INTERLEUKIN-4-AND-INTERLEUKIN-13-SIGN...	8	-0.687500	-1.818746	0.010121	1.000000	0.928
724	GOBP-RESPONSE.TO-MECHANICAL-STIMULUS	6	-0.773717	-1.850761	0.000000	1.000000	0.862

End of Table

Supplementary Table S8: SC cervical segment early profile (1 DPL peak) GSEA results.

Begin of Table S8									
	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val	
0	GOBP-RESPONSE.TO.LIGHT.STIMULUS	GO-0009416	11	0.731334	2.024651	0.000000	0.156407	0.142	
1	GOBP-PROTEIN.CONTAINING.COMPLEX.SUBUNIT.ORGANELLAR	GO-0043933	15	0.663449	1.974649	0.003026	0.160386	0.267	
2	GOBP-MEMORY	GO-0007613	13	0.673529	1.937396	0.000000	0.165605	0.381	
3	GOBP-REGULATION.OF.BINDING	GO-0051098	11	0.705199	1.920197	0.000000	0.158111	0.456	
4	GOBP-REGULATION.OF.PROTEIN.BINDING	GO-0043393	7	0.809960	1.910167	0.003284	0.141292	0.497	
5	GOBP-INFLAMMATORY-RESPONSE	GO-0006954	12	0.654238	1.886026	0.000000	0.152717	0.584	
6	GOBP-RESPONSE.TO.RADIATION	GO-0009314	13	0.639975	1.882968	0.001608	0.135849	0.595	
7	GOBP-RESPONSE.TO.NERVE.GROWTH.FACTOR	GO-1990089	7	0.776983	1.854240	0.003241	0.161113	0.692	
8	REACTOME.INTERLEUKIN-4.AND.INTERLEUKIN-13.SIGNALING	R-RNO-6785807	8	0.719360	1.810831	0.003236	0.221923	0.853	
9	GOBP-POSITIVE.REGULATION.OF.BINDING	GO-0051099	6	0.746774	1.714130	0.008264	0.504614	0.996	
10	GOBP-CYTOKINE-MEDIATED.SIGNALING.PATHWAY	GO-0019221	16	0.553707	1.702685	0.013235	0.507436	0.996	
11	GOBP-REGULATION.OF.NEURON.DIFFERENTIATION	GO-0045664	5	0.778648	1.693701	0.017974	0.499902	0.996	
12	GOBP-NEGATIVE.REGULATION.OF.PEPTIDASE-ACTIVITY	GO-0010466	6	0.718984	1.653030	0.017857	0.649190	0.999	
13	REACTOME.SIGNALING.BY.INTERLEUKINS	R-RNO-449147	15	0.546048	1.634720	0.020772	0.697544	0.999	
14	REACTOME.CYTOKINE.SIGNALING.IN.IMMUNE.SYSTEM	R-RNO-1280215	21	0.487838	1.625963	0.030726	0.698163	1.000	
15	GOBP-NEGATIVE.REGULATION.OF.MOLECULAR.FUNCTION	GO-0044092	24	0.481572	1.622320	0.025373	0.673187	1.000	
16	GOBP-EPITHELIAL-CELL.DIFFERENTIATION	GO-0030855	7	0.679012	1.620021	0.024958	0.645223	1.000	
17	GOBP-NEGATIVE.REGULATION.OF.BINDING	GO-0051100	6	0.709012	1.611042	0.021173	0.653762	1.000	
18	GOBP-CELLULAR.COMPONENT.DISASSEMBLY	GO-0022411	6	0.706912	1.608042	0.025000	0.632488	1.000	
19	GOBP-POSITIVE.REGULATION.OF.PEPTIDYL-SERINE.PHOSPHORYLATION	GO-0033138	8	0.639284	1.601790	0.030596	0.630937	1.000	
20	GOBP-REGULATION.OF.LIPID.METABOLIC.PROCESS	GO-0019216	7	0.661304	1.593920	0.025907	0.639143	1.000	
21	GOBP-REGULATION.OF.CELLULAR.COMPONENT.SIZE	GO-0032535	7	0.663806	1.593518	0.023659	0.612050	1.000	
22	GOBP-REGULATION.OF.OSTEOCLAST.DIFFERENTIATION	GO-0045670	5	0.734940	1.589716	0.027350	0.601488	1.000	
23	GOBP-RECEPTOR-MEDIATED.ENDOCYTOSIS	GO-0006898	6	0.686854	1.585166	0.026981	0.596329	1.000	
24	GOBP-REGULATION.OF.PROTEIN.LOCALIZATION.TO.MEMBRANE	GO-1905475	7	0.666355	1.584227	0.033708	0.576909	1.000	
25	GOBP-REGULATION.OF.PEPTIDYL-SERINE.PHOSPHORYLATION	GO-0033135	8	0.639284	1.573723	0.035439	0.597143	1.000	
26	GOBP-POSITIVE.REGULATION.OF.CELL.DEATH	GO-0010942	19	0.491058	1.568551	0.047407	0.597376	1.000	
27	GOBP-OSTEOCLAST.DIFFERENTIATION	GO-0030316	6	0.682927	1.561724	0.038898	0.605323	1.000	
28	GOBP.MULTICELLULAR.ORGANISM.PROCESS	GO-0044706	8	0.609696	1.553119	0.035256	0.622344	1.000	
29	GOBP-REGULATION.OF.PEPTIDASE-ACTIVITY	GO-0052547	10	0.573977	1.529107	0.034591	0.707040	1.000	
30	GOBP-RESPONSE.TO.UV	GO-0009411	5	0.696333	1.496278	0.035000	0.848450	1.000	
31	GOBP-RESPONSE.TO.METAL-ION	GO-0010038	15	0.493430	1.489503	0.060423	0.859173	1.000	
32	GOBP-PROTEIN.COMPLEX.OLIGOMERIZATION	GO-0051259	7	0.623111	1.488133	0.062500	0.840821	1.000	
33	GOBP-REGULATION.OF.PROTEIN.LOCALIZATION.TO.CELLULAR	GO-1904375	6	0.651848	1.485393	0.051282	0.830233	1.000	
34	GOBP-AGING	GO-0007568	13	0.509943	1.484576	0.046828	0.810366	1.000	
35	GOBP.LONG-TERM.SYNAPTIC.DEPRESSION	GO-0060292	5	0.690196	1.478621	0.041806	0.818449	1.000	
36	GOBP.INTRINSIC.APOPTOTIC.SIGNALING.PATHWAY	GO-0097193	5	0.695569	1.475786	0.048093	0.809136	1.000	
37	GOBP-REGULATION.OF.CELL.DEATH	GO-0010941	34	0.405518	1.475658	0.047757	0.788345	1.000	
38	GOBP-POSITIVE.REGULATION.OF.TRANSPORT	GO-0051050	26	0.432714	1.475257	0.060172	0.769975	1.000	
39	GOBP-NEGATIVE.REGULATION.OF.LIPID.METABOLIC.PROCESS	GO-0045833	5	0.680186	1.457372	0.056995	0.835328	1.000	
40	GOBP-NEGATIVE.REGULATION.OF.TRANSMEMBRANE-TRANSPORT	GO-0034763	6	0.644586	1.452012	0.064620	0.841271	1.000	

Continuation of Table S8

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
41 GOBP-DEFENSE.RESPONSE	GO-0006952	19	0.448065	1.440478	0.078669	0.877577	1.000
42 REACTOME.SIGNALING.BY.RECEPTOR.TYROSINE.KINASES	R-RNO-9006934	26	0.423263	1.432083	0.071756	0.898062	1.000
43 GOBP-CELLULAR.RESPONSE.TO.ABIOTIC.STIMULUS	GO-0071214	7	0.607824	1.424489	0.076800	0.915661	1.000
44 GOBP-LONG-TERM.MEMORY	GO-0007616	6	0.626814	1.417558	0.090150	0.931756	1.000
45 GOBP-NEGATIVE.REGULATION.OF.CYSTEINE.TYPE.ENDO...	GO-2000117	5	0.666466	1.414575	0.060504	0.927070	1.000
46 GOBP-RESPONSE.TO.INORGANIC.SUBSTANCE	GO-0010035	19	0.442936	1.413843	0.075893	0.910832	1.000
47 GOBP-RECEPTOR.METABOLIC.PROCESS	GO-0043112	5	0.649864	1.413676	0.087329	0.892677	1.000
48 GOBP-POSITIVE.REGULATION.OF.IMMUNE.SYSTEM.PROCESS	GO-0002684	18	0.443000	1.412332	0.097561	0.881013	1.000
49 GOBP-RECEPTOR.INTERNALIZATION	GO-0031623	5	0.649864	1.411213	0.081037	0.868797	1.000
50 GOBP-NEGATIVE.REGULATION.OF.CELL.DEATH	GO-0060548	22	0.420897	1.410717	0.081203	0.853872	1.000
51 GOBP-REGULATION.OF.FAT.CELL.DIFFERENTIATION	GO-0045598	6	0.616379	1.408797	0.109299	0.847150	1.000
52 GOBP-REGULATION.OF.CELL.SIZE	GO-0008361	5	0.658172	1.405710	0.096186	0.845925	1.000
53 GOBP-RESPONSE.TO.CYTOKINE	GO-0034097	23	0.425425	1.399292	0.076487	0.860231	1.000
54 GOBP-REGULATION.OF.RECEPTOR.MEDIATED.ENDOCYTOSIS	GO-0048259	5	0.654508	1.395425	0.086957	0.863283	1.000
55 GOBP-POSITIVE.REGULATION.OF.SMOOTH.MUSCLE.CELL...	GO-0048661	5	0.642403	1.392229	0.097403	0.858735	1.000
56 GOBP-REGULATION.OF.NEURON.PROJECTION.DEVELOPMENT	GO-0010975	16	0.449841	1.391981	0.078635	0.849382	1.000
57 GOBP-NEGATIVE.REGULATION.OF.LOCOMOTION	GO-0040013	5	0.651213	1.391131	0.098993	0.838860	1.000
58 GOBP-PROTEOLYSIS	GO-0006508	17	0.451662	1.390741	0.082840	0.826433	1.000
59 GOBP-COGNITION	GO-0050890	28	0.394444	1.384548	0.103499	0.839553	1.000
60 GOBP-ACTIVATION.OF.PROTEIN.KINASE.ACTIVITY	GO-0032147	10	0.514590	1.383987	0.107023	0.828201	1.000
61 REACTOME.POST.TRANSLATIONAL.PROTEIN.MODIFICATION	R-RNO-597592	7	0.580006	1.381619	0.095390	0.825779	1.000
62 GOBP-REGULATION.OF.ENDOCYTOSIS	GO-0002252	6	0.605406	1.379007	0.100993	0.824332	1.000
63 GOBP-REGULATION.OF.INFLAMMATORY.RESPONSE	GO-0050727	7	0.575485	1.374290	0.115192	0.833324	1.000
64 GOBP-IMMUNE.EFFECTOR.PROCESS	GO-0002391	11	0.483391	1.374238	0.116208	0.820729	1.000
65 GOBP-MYELOID.LEUKOCYTE.ACTIVATION	GO-0002274	8	0.550409	1.369653	0.116613	0.827405	1.000
66 GOBP-REGULATION.OF.IMMUNE.RESPONSE	GO-0050776	12	0.472895	1.367241	0.130094	0.824992	1.000
67 GOBP-LIPID.BIOSYNTHETIC.PROCESS	GO-0008610	6	0.594932	1.366774	0.125620	0.814742	1.000
68 GOBP-REGULATION.OF.DEFENSE.RESPONSE	GO-0031347	7	0.575485	1.362293	0.118314	0.822737	1.000
69 GOBP-NEGATIVE.REGULATION.OF.NEURON.DEATH	GO-1901215	11	0.487270	1.359693	0.110769	0.822197	1.000
70 GOBP-LIPID.METABOLIC.PROCESS	GO-0006629	10	0.503782	1.350586	0.131045	0.850484	1.000
71 GOBP-RESPONSE.TO.CADMIUM.ION	GO-0046686	6	0.587893	1.343796	0.113238	0.867106	1.000
72 GOBP-ACTIN.FILAMENT.BASED.PROCESS	GO-0030029	7	0.561922	1.341075	0.132787	0.866825	1.000
73 GOBP-POSITIVE.REGULATION.OF.ANION.TRANSPORT	GO-1903793	9	0.501529	1.339773	0.150000	0.860802	1.000
74 GOBP-REGULATION.OF.CELLULAR.CATABOLIC.PROCESS	GO-004031329	10	0.494057	1.334099	0.135350	0.873703	1.000
75 GOBP-REGULATION.OF.SMALL.MOLECULE.METABOLIC.PR...	GO-0062012	9	0.507014	1.333124	0.131833	0.866269	1.000
76 HALLMARK.ALLOGRAFT.REJECTION	M5950	7	0.555051	1.327995	0.122642	0.877645	1.000
77 GOBP-INOSITOL.LIPID.MEDIATED.SIGNALING	GO-0048017	8	0.537108	1.325488	0.138315	0.876894	1.000
78 GOBP-REGULATION.OF.LIPID.BIOSYNTHETIC.PROCESS	GO-0046890	6	0.594932	1.324216	0.141046	0.870868	1.000
79 GOBP-NEGATIVE.REGULATION.OF.SYNAPTIC.TRANSMISSION	GO-0050805	6	0.594143	1.323987	0.134021	0.860930	1.000
80 GOBP-NEGATIVE.REGULATION.OF.HYDROLASE.ACTIVITY	GO-0051346	11	0.475929	1.323606	0.159875	0.852291	1.000
81 GOBP-NEUROINFLAMMATORY.RESPONSE	GO-0150076	5	0.613684	1.323420	0.134775	0.842669	1.000
82 GOBP-RESPONSE.TO.NICOTINE	GO-0035094	7	0.546881	1.322992	0.162205	0.834242	1.000
83 GOBP-EXTRINSIC.APOPTOTIC.SIGNALING.PATHWAY	GO-0097191	7	0.544851	1.321975	0.159052	0.828229	1.000

Continuation of Table S8

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
84 GOBP-REGULATION-OF-CYSTEINE-TYPE-ENDOPEPTIDASE...	GO-2000116	9	0.500109	1.319724	0.141935	0.827449	1.000
85 GOBP-CELLULAR-RESPONSE-TO-INORGANIC-SUBSTANCE	GO-0071241	11	0.473490	1.316081	0.143951	0.831694	1.000
86 GOBP-CELLULAR-AMIDE-METABOLIC-PROCESS	GO-0043603	12	0.454528	1.313527	0.136508	0.832016	1.000
87 GOBP-RESPONSE-TO-ACID-CHEMICAL	GO-0001101	6	0.578391	1.309235	0.145614	0.839707	1.000
88 REACTOME-MEMBRANE-TRAFFICKING	R-RNO-199991	5	0.605869	1.305856	0.143836	0.843474	1.000
89 GOBP-NEGATIVE-REGULATION-OF-APOPTOTIC-SIGNALIN...	GO-2001234	7	0.548127	1.303325	0.158706	0.844108	1.000
90 REACTOME-EXTRA-NUCLEAR-ESTROGEN-SIGNALING	R-RNO-900939	7	0.538187	1.302169	0.155449	0.839367	1.000
91 GOBP-SMOOTH-MUSCLE-CELL-PROLIFERATION	GO-0048659	6	0.568056	1.300100	0.150820	0.838406	1.000
92 GOBP-POSITIVE-REGULATION-OF-CYTOKINE-PRODUCTION	GO-0001819	7	0.547419	1.299915	0.161840	0.830129	1.000
93 GOBP-REGULATION-OF-CELLULAR-COMPONENT-MOVEMENT	GO-0051270	15	0.424757	1.296439	0.159574	0.833624	1.000
94 GOBP-MONOSACCHARIDE-METABOLIC-PROCESS	GO-0005996	6	0.573451	1.295088	0.154093	0.830227	1.000
95 GOBP-GLUCOSE-METABOLIC-PROCESS	GO-0006006	6	0.573451	1.293002	0.170213	0.829205	1.000
96 GOBP-REGULATION-OF-HYDROLASE-ACTIVITY	GO-0051336	22	0.380764	1.290903	0.157353	0.828274	1.000
97 GOBP-REGULATION-OF-PROTEIN-LOCALIZATION	GO-0032880	18	0.409564	1.290876	0.152466	0.819921	1.000
98 GOBP-ASSOCIATIVE-LEARNING	GO-0008306	7	0.535321	1.290528	0.155116	0.812999	1.000
99 GOBP-NEURON-DEVELOPMENT	GO-0048666	34	0.357748	1.290232	0.147059	0.805755	1.000
100 GOBP-PERIPHERAL-NERVOUS-SYSTEM-DEVELOPMENT	GO-0007422	9	0.493287	1.288591	0.166667	0.803450	1.000
101 GOBP-OSTEOBLAST-DIFFERENTIATION	GO-0001649	5	0.601396	1.285479	0.164076	0.806703	1.000
102 GOBP-NEGATIVE-REGULATION-OF-CATABOLIC-PROCESS	GO-0009895	8	0.512299	1.284125	0.180952	0.804028	1.000
103 GOBP-NEGATIVE-REGULATION-OF-PROTEOLYSIS	GO-0045861	8	0.516302	1.283868	0.177711	0.797241	1.000
104 GOBP-CELL-PROJECTION-ORGANIZATION	GO-0030030	35	0.352332	1.282446	0.147937	0.795125	1.000
105 GOBP-NEGATIVE-REGULATION-OF-CATALYTIC-ACTIVITY	GO-0043086	17	0.413724	1.282438	0.171429	0.787633	1.000
106 GOBP-REGULATION-OF-LONG-TERM-SYNAPTIC-POTENTIAL...	GO-1900271	6	0.569506	1.280955	0.166392	0.785526	1.000
107 REACTOME-VESICLE-MEDIATED-TRANSPORT	R-RNO-5653656	5	0.605869	1.277447	0.167513	0.790898	1.000
108 GOBP-PEPTIDE-METABOLIC-PROCESS	GO-0005118	11	0.462628	1.273735	0.188768	0.796637	1.000
109 GOBP-LEUKOCYTE-MEDIATED-IMMUNITY	GO-0002443	8	0.505884	1.272230	0.181970	0.794709	1.000
110 GOBP-POSITIVE-REGULATION-OF-CELL-GROWTH	GO-0030307	6	0.575523	1.271877	0.168285	0.788739	1.000
111 GOBP-NEURON-DEATH	GO-0070997	18	0.401328	1.269323	0.177465	0.790942	1.000
112 GOBP-APOPTOTIC-PROCESS	GO-0006915	35	0.350878	1.268243	0.188652	0.787606	1.000
113 GOBP-IMPORT-INTO-CELL	GO-0098657	6	0.543017	1.267392	0.188103	0.783394	1.000
114 GOBP-POSITIVE-REGULATION-OF-GENE-EXPRESSION	GO-0010628	16	0.403644	1.254086	0.195455	0.822239	1.000
115 GOBP-PROTEIN-LOCALIZATION-TO-MEMBRANE	GO-0072657	13	0.433387	1.250538	0.201210	0.827483	1.000
116 GOBP-REGULATION-OF-PEPTIDE-HORMONE-SECRETION	GO-0090276	6	0.551877	1.250516	0.205255	0.820483	1.000
117 GOBP-LEUKOCYTE-MIGRATION	GO-0050900	6	0.548798	1.250033	0.212418	0.815028	1.000
118 GOBP-ENDOCYTOSIS	GO-0008597	8	0.502853	1.245864	0.206785	0.822112	1.000
119 REACTOME-EPH-EPHRIN-SIGNALING	R-RNO-268233	6	0.539735	1.244645	0.217600	0.819516	1.000
120 GOBP-REGULATION-OF-PEPTIDE-SECRETION	GO-0002791	7	0.516817	1.244606	0.214286	0.812935	1.000
121 GOBP-MULTICELLULAR-ORGANISMAL-HOMEOSTASIS	GO-0048871	12	0.441585	1.239758	0.231884	0.822510	1.000
122 GOBP-POSITIVE-REGULATION-OF-IMMUNE-RESPONSE	GO-0050778	9	0.471559	1.238038	0.221865	0.821737	1.000
123 GOBP-REGULATION-OF-HORMONE-LEVELS	GO-0010817	12	0.431505	1.233018	0.191063	0.832008	1.000
124 REACTOME-INNATE-IMMUNE-SYSTEM	R-RNO-168249	16	0.400564	1.232559	0.216301	0.826874	1.000
125 GOBP-CELLULAR-LIPID-METABOLIC-PROCESS	GO-0044255	7	0.519120	1.229210	0.226984	0.853554	1.000
126 GOBP-REGULATION-OF-PROTEOLYSIS	GO-0030162	12	0.425739	1.220094	0.227964	0.856463	1.000

Continuation of Table S8

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
127 GOBP_NERVOUS_SYSTEM_PROCESS	GO-0050877	38	0.336614	1.218500	0.218182	0.854986	1.000
128 GOBP_POSITIVE_REGULATION_OF_PHOSPHATIDYLINOSIT...	GO-0014068	5	0.568305	1.212722	0.227273	0.852496	1.000
129 REACTOME_SIGNALING_BY_NUCLEAR_RECEPTORS	R-RNO-9006931	8	0.481005	1.216913	0.231013	0.847074	1.000
130 GOBP_INSULIN_SECRETION	GO-0030073	7	0.510769	1.214703	0.223114	0.847977	1.000
131 GOBP_NEUROTROPIN_TK_R_RECEPTOR_SIGNALING_PATHWAY	GO-0048011	6	0.525482	1.214255	0.235489	0.843004	1.000
132 GOBP_REGULATION_OF_ANATOMICAL_STRUCTURE_SIZE	GO-0090066	10	0.462544	1.213797	0.232484	0.838243	1.000
133 GOBP_TEMPERATURE_HOMEOSTASIS	GO-0001659	5	0.555846	1.212463	0.233449	0.836545	1.000
134 GOBP_PROTEIN_LOCALIZATION_TO_PLASMA_MEMBRANE	GO-0072659	7	0.516984	1.211528	0.240196	0.833571	1.000
135 GOBP_REGULATION_OF_CARBOHYDRATE_BIOSYNTHETIC_P...	GO-0043255	5	0.563349	1.211510	0.233058	0.827503	1.000
136 GOBP_POSTSYNAPSE_ORGANIZATION	GO-0099173	10	0.459944	1.207936	0.230769	0.833425	1.000
137 GOBP_BEHAVIOR	GO-0007610	33	0.339927	1.206907	0.218571	0.830557	1.000
138 REACTOME_ESR_MEDIATED_SIGNALING	R-RNO-8939211	8	0.481005	1.206899	0.243200	0.824612	1.000
139 GOBP_POSITIVE_REGULATION_OF_LOCOMOTION	GO-0040017	11	0.434396	1.203674	0.234548	0.829002	1.000
140 GOBP_POSITIVE_REGULATION_OF_DEFENSE_RESPONSE	GO-0031349	5	0.562919	1.203225	0.243478	0.824646	1.000
141 GOBP_PEPTIDE_HORMONE_SECRETION	GO-0030072	7	0.510769	1.202905	0.256536	0.819926	1.000
142 GOBP_CARBOHYDRATE_BIOSYNTHETIC_PROCESS	GO-0016051	5	0.563349	1.202668	0.250853	0.815154	1.000
143 GOBP_REGULATION_OF_CATABOLIC_PROCESS	GO-0009894	13	0.417235	1.201575	0.240061	0.812810	1.000
144 GOBP_REGULATION_OF_CARBOHYDRATE_METABOLIC_PROCESS	GO-0006109	5	0.563349	1.199063	0.250000	0.814924	1.000
145 GOBP_CELLULAR_CARBOHYDRATE_METABOLIC_PROCESS	GO-0044262	5	0.545059	1.199572	0.245409	0.817851	1.000
146 GOBP_REGULATION_OF_CELL_PROJECTION_ORGANIZATION	GO-0031344	20	0.366652	1.194146	0.227273	0.820042	1.000
147 GOBP_REPRODUCTION	GO-0000003	18	0.373537	1.189810	0.243370	0.828380	1.000
148 GOBP_ENZYME_LINKED_RECEPTOR_PROTEIN_SIGNALING....	GO-0007167	24	0.351248	1.189558	0.248547	0.823564	1.000
149 HALLMARK_P13K_AKT_MTOR_SIGNALING	M5923	6	0.519843	1.185509	0.257240	0.830398	1.000
150 GOBP_NEUROTROPIN_SIGNALING_PATHWAY	GO-0038179	6	0.525482	1.183780	0.264559	0.830417	1.000
151 GOBP_NEURON_DIFFERENTIATION	GO-0030182	37	0.322061	1.182687	0.254446	0.828345	1.000
152 GOBP_REGULATION_OF_PROTEIN_SERINE_THREONINE_KI...	GO-0071900	12	0.413839	1.175638	0.253414	0.845425	1.000
153 GOBP_CELL_ACTIVATION	GO-0001775	22	0.354860	1.173056	0.265537	0.847939	1.000
154 GOBP_REGULATION_OF_PEPTIDE_TRANSPORT	GO-0090087	10	0.447898	1.168514	0.274845	0.856496	1.000
155 GOBP_EXOCYTOSIS	GO-0006887	11	0.415843	1.167485	0.268817	0.854262	1.000
156 GOBP_NEUROGENESIS	GO-0022008	41	0.318144	1.165592	0.255072	0.854924	1.000
157 GOBP_REGULATION_OF_HORMONE_SECRETION	GO-0046883	8	0.449184	1.162006	0.283388	0.860624	1.000
158 GOBP_OSSIFICATION	GO-0001503	9	0.441324	1.160569	0.250814	0.859754	1.000
159 GOBP_REGULATION_OF_POSTSYNAPSE_ORGANIZATION	GO-0099175	6	0.503139	1.160194	0.274062	0.855621	1.000
160 GOBP_POLYSACCHARIDE_METABOLIC_PROCESS	GO-0005976	5	0.545024	1.157751	0.294218	0.863447	1.000
161 GOBP_RESPONSE_TO_NUTRIENT	GO-0007584	5	0.542169	1.154661	0.285240	0.858999	1.000
162 GOBP_AMYLOID_PRECURSOR_PROTEIN_CATABOLIC_PROCESS	GO-0042987	5	0.533908	1.152009	0.284192	0.864240	1.000
163 GOBP_CARBOHYDRATE_DERIVATIVE_METABOLIC_PROCESS	GO-1901135	8	0.468011	1.151732	0.296296	0.859863	1.000
164 GOBP_POSITIVE_REGULATION_OF_GLIOGENESIS	GO-0014015	5	0.542169	1.151447	0.298658	0.855512	1.000
165 GOBP_AMYLOID_PRECURSOR_PROTEIN_METABOLIC_PROCESS	GO-0042982	5	0.533908	1.150729	0.270548	0.852576	1.000
166 GOBP_REGULATION_OF_GLIOGENESIS	GO-0014013	5	0.542169	1.150039	0.312715	0.849707	1.000
167 GOBP_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	GO-0002682	21	0.351613	1.146644	0.282318	0.855021	1.000
168 GOBP_POSITIVE_REGULATION_OF_SIGNALING	GO-0023056	34	0.317185	1.146341	0.281337	0.850756	1.000
169 GOBP_POSITIVE_REGULATION_OF_LIPASE_ACTIVITY	GO-0060193	5	0.526189	1.145270	0.316781	0.848899	1.000

Continuation of Table S8

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
170	REACTOME-EXTRACELLULAR_MATRIX_ORGANIZATION	R-RNO-1474244	5	0.532405	1.144847	0.302521	0.845091
171	GOBP-REGULATION_OF_RESPONSE_TO_STRESS	GO-0080134	19	0.360851	1.144728	0.291176	0.840556
172	GOBP-REGULATION_OF_PROTEIN_PHOSPHORYLATION	GO-0001932	25	0.339528	1.143798	0.285916	0.838443
173	GOBP-AMYLOID_BETA_METABOLIC_PROCESS	GO-0050435	5	0.533908	1.142297	0.336752	0.837789
174	REACTOME-ESTROGEN_DEPENDENT_NUCLEAR_EVENTS_DOW...	R-RNO-963463	5	0.523405	1.141606	0.305419	0.835188
175	GOBP-DENDRITE_MORPHOGENESIS	GO-0048813	7	0.470710	1.138868	0.306818	0.838435
176	REACTOME-SIGNALING_BY_NTRKS	R-RNO-166520	18	0.361961	1.136217	0.301994	0.841481
177	GOBP-NEGATIVE_REGULATION_OF_PROTEIN_METABOLIC...	GO-00051248	20	0.350078	1.134564	0.277698	0.841576
178	GOBP-CELLULAR_RESPONSE_TO_CADMIUM_ION	GO-0071276	5	0.515219	1.121235	0.345455	0.875689
179	REACTOME-INFECTIOUS_DISEASE	R-HSA-5663205	12	0.393573	1.121057	0.315866	0.871352
180	GOBP-REGULATION_OF_PHOSPHOLIPASE_C_ACTIVITY	GO-1900274	5	0.526189	1.116917	0.310051	0.878947
181	GOBP-NEGATIVE_REGULATION_OF_NEURON_APOPTOTIC_P...	GO-0043524	8	0.444330	1.116724	0.333858	0.874710
182	GOBP-CELL_MIGRATION	GO-0016477	22	0.333901	1.116014	0.303907	0.872159
183	GOBP-REGULATION_OF_EPITHELIAL_CELL_MIGRATION	GO-0010632	6	0.490485	1.111603	0.344123	0.879744
184	GOBP-MACROMOLECULE_CATABOLIC_PROCESS	GO-0009057	11	0.402012	1.109869	0.329835	0.879885
185	GOBP-CELL-CELL_JUNCTION_ORGANIZATION	GO-0045216	6	0.474992	1.108840	0.323680	0.878046
186	GOBP-POSITIVE_REGULATION_OF_CELLULAR_COMPONENT...	GO-0051130	24	0.328648	1.106696	0.327917	0.879389
187	GOBP-POSITIVE_REGULATION_OF_HYDROLASE_ACTIVITY	GO-0051345	16	0.364860	1.105460	0.317337	0.878308
188	GOBP-MONOCARBOXYLIC_ACID_METABOLIC_PROCESS	GO-0032787	6	0.494763	1.103949	0.349206	0.878078
189	GOBP-PROTEIN_KINASE_B_SIGNALING	GO-0043491	6	0.493972	1.103517	0.345719	0.874603
190	GOBP-NEGATIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	GO-0002683	5	0.507782	1.098553	0.341924	0.883987
191	GOBP-REGULATION_OF_PHOSPHORUS_METABOLIC_PROCESS	GO-0051174	26	0.321877	1.096215	0.328909	0.885936
192	GOBP-MEMBRANE_PROTEIN_PROTEOLYSIS	GO-0033619	6	0.479020	1.095820	0.352554	0.882529
193	GOBP-NEGATIVE_REGULATION_OF_ION_TRANSPORT	GO-0043271	11	0.403598	1.094968	0.345313	0.880552
194	GOBP-REGULATION_OF_CELLULAR_PROTEIN_LOCALIZATION	GO-1903827	12	0.376889	1.092240	0.349544	0.880917
195	GOBP-EPHRIIN_RECEPTOR_SIGNALING_PATHWAY	GO-0048013	5	0.510420	1.083570	0.377104	0.903329
196	GOBP-REGULATION_OF_CELL_DIFFERENTIATION	GO-0045595	36	0.302323	1.083207	0.347280	0.899732
197	GOBP-POSITIVE_REGULATION_OF_GROWTH	GO-0045927	9	0.418443	1.081892	0.376361	0.898933
198	GOBP-GENERATION_OF_PRECURSOR_METABOLITES_AND_E...	GO-0006091	5	0.506024	1.080559	0.386288	0.898319
199	GOBP-HORMONE_TRANSPORT	GO-0009914	9	0.423765	1.080050	0.371069	0.895341
200	GOBP-BIOLOGICAL_PROCESS_INVOLVED_IN_SYMBIOTIC...	GO-004440	10	0.404774	1.079636	0.341158	0.892087
201	GOBP-GLIOGENESIS	GO-0042063	12	0.379652	1.079543	0.368421	0.887909
202	GOBP-PROTEIN_PHOSPHORYLATION	GO-0006468	33	0.301978	1.077395	0.356742	0.889349
203	REACTOME-TRANSCRIPTIONAL_REGULATION_OF_WHITE_A...	R-RNO-381340	6	0.461663	1.069953	0.381877	0.905279
204	GOBP-POSITIVE_REGULATION_OF_ION_TRANSPORT	GO-0043270	17	0.346564	1.069327	0.379971	0.902581
205	GOBP-RESPONSE_TO_KETONE	GO-1901654	7	0.451195	1.068408	0.400000	0.900624
206	GOBP-APOPTOTIC_MITOCHONDRIAL_CHANGES	GO-0008637	6	0.473220	1.068247	0.382450	0.896725
207	GOBP-SECRETION	GO-0046903	24	0.318104	1.068228	0.361357	0.892465
208	GOBP-REGULATION_OF_TRANSFERASE_ACTIVITY	GO-0051338	21	0.322161	1.067402	0.365889	0.890366
209	GOBP-POSITIVE_REGULATION_OF_PROTEIN_MODIFICATI...	GO-0031401	22	0.320552	1.066035	0.359882	0.889894
210	GOBP-REGULATION_OF_PROTEIN_KINASE_ACTIVITY	GO-0045859	21	0.322161	1.064887	0.365926	0.888855
211	GOBP-REGULATION_OF_LIPASE_ACTIVITY	GO-0060191	6	0.456443	1.064859	0.390203	0.884750
212	GOBP-RESPONSE_TO_NITROGEN_COMPOUND	GO-1901698	35	0.298471	1.064434	0.380818	0.881945

Continuation of Table S8

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
213	REACTOME-TRANSCRIPTIONAL-REGULATION-BY_TP53	6	0.466900	1.063381	0.382504	0.880746	1.000
214	GOBP-PHOSPHATIDYLINOSITOL-3-KINASE-SIGNALING	7	0.445684	1.062397	0.396899	0.879243	1.000
215	GOBP-REGULATION-OF-VESICLE-MEDIATED-TRANSPORT	12	0.376180	1.061960	0.378336	0.876380	1.000
216	GOBP-CYTOSKELETON-ORGANIZATION	11	0.385993	1.058714	0.411498	0.881072	1.000
217	GOBP-CARBOHYDRATE-METABOLIC-PROCESS	9	0.409679	1.056483	0.404651	0.883010	1.000
218	GOBP-POSITIVE-REGULATION-OF-PROTEIN-PHOSPHORYL...	22	0.320552	1.054661	0.388809	0.883679	1.000
219	REACTOME-DEVELOPMENTAL-BIOLOGY	22	0.317886	1.054310	0.392012	0.880618	1.000
220	GOBP-REGULATION-OF-APOPTOTIC-SIGNALING-PATHWAY	10	0.382745	1.054163	0.389058	0.877053	1.000
221	GOBP-REGULATION-OF-PROTEIN-CATABOLIC-PROCESS	7	0.435116	1.053069	0.403846	0.876063	1.000
222	GOBP-CELLULAR-RESPONSE-TO-REACTIVE-OXYGEN-SPECIES	7	0.431659	1.052146	0.397351	0.874440	1.000
223	GOBP-POSITIVE-REGULATION-OF-PROTEOLYSIS	8	0.418493	1.050079	0.413183	0.875796	1.000
224	GOBP-ANATOMICAL-STRUCTURE-HOMEOSTASIS	7	0.438851	1.049167	0.399676	0.874237	1.000
225	GOBP-LOCOMOTION	31	0.298223	1.048894	0.397759	0.871042	1.000
226	GOBP-REGULATION-OF-PHOSPHOLIPASE-ACTIVITY	6	0.456443	1.048768	0.403330	0.867570	1.000
227	GOBP-MULTI-ORGANISM-PROCESS	16	0.346697	1.048652	0.400000	0.864015	1.000
228	GOBP-CELLULAR-RESPONSE-TO-CHEMICAL-STRESS	7	0.403946	1.048611	0.410774	0.860330	1.000
229	GOBP-REGULATION-OF-MYELOID-CELL-DIFFERENTIATION	9	0.403946	1.044423	0.401626	0.867293	1.000
230	GOBP-RESPONSE-TO-BACTERIUM	13	0.358196	1.033900	0.424427	0.890035	1.000
231	GOBP-REGULATION-OF-EXTRINSIC-APOPTOTIC-SIGNAL...	6	0.456893	1.031639	0.430213	0.891901	1.000
232	GOBP-TRANSMEMBRANE-RECEPTOR-PROTEIN-TYROSINE-K...	19	0.329555	1.028616	0.410795	0.895648	1.000
233	GOBP-PATTERN-SPECIFICATION-PROCESS	6	0.455501	1.028594	0.448445	0.891878	1.000
234	GOBP-PEPTIDE-SECRETION	9	0.399662	1.026116	0.429245	0.893993	1.000
235	GOBP-POSITIVE-REGULATION-OF-RESPONSE-TO-EXTERN...	9	0.400569	1.025470	0.436066	0.891625	1.000
236	GOBP-POSITIVE-REGULATION-OF-PROTEIN-SERINE-THR...	9	0.400686	1.024748	0.429936	0.889623	1.000
237	GOBP-TISSUE-HOMEOSTASIS	5	0.476300	1.021003	0.440735	0.895468	1.000
238	GOBP-REGULATION-OF-RESPONSE-TO-EXTERNAL-STIMULUS	15	0.338700	1.018327	0.440184	0.898385	1.000
239	GOBP-PROTEIN-TETRAMERIZATION	5	0.471601	1.017458	0.447712	0.896749	1.000
240	GOBP-PEPTIDYL-SERINE-MODIFICATION	12	0.358200	1.017098	0.436275	0.893858	1.000
241	GOBP-RESPONSE-TO-ABIOTIC-STIMULUS	27	0.290781	1.015575	0.452113	0.893915	1.000
242	GOBP-REGIONALIZATION	6	0.455501	1.013335	0.436306	0.898193	1.000
243	GOBP-POSITIVE-REGULATION-OF-PHOSPHORUS-METABOL...	23	0.305238	1.012302	0.446715	0.894581	1.000
244	GOBP-REGULATION-OF-VASCULAR-ASSOCIATED-SMOOTH...	5	0.473268	1.011766	0.474295	0.892266	1.000
245	GOBP-MYELOID-CELL-DIFFERENTIATION	13	0.355072	1.010661	0.436137	0.891178	1.000
246	GOBP-REGULATION-OF-ORGANELLE-ORGANIZATION	14	0.335259	1.010028	0.450663	0.889081	1.000
247	GOBP-RESPONSE-TO-MOLECULE-OF-BACTERIAL-ORIGIN	13	0.358196	1.008369	0.447368	0.889595	1.000
248	GOBP-PROTEIN-LOCALIZATION-TO-CELL-PERIPHERY	12	0.359051	1.007281	0.469630	0.888670	1.000
249	REACTOME-CIRCADIAN-CLOCK	5	0.475206	1.006488	0.479542	0.887025	1.000
250	GOBP-PROTEIN-CATABOLIC-PROCESS	8	0.402744	1.004216	0.460925	0.888738	1.000
251	GOBP-POSITIVE-REGULATION-OF-SYNAPTIC-TRANSMISSION	15	0.328667	0.998818	0.451219	0.897765	1.000
252	GOBP-POSITIVE-REGULATION-OF-MYELOID-LEUKOCYTE...	6	0.440364	0.997449	0.475712	0.897611	1.000
253	GOBP-CELLULAR-COMPONENT-MORPHOGENESIS	25	0.288621	0.996591	0.459538	0.896152	1.000
254	GOBP-NEGATIVE-REGULATION-OF-INTRACELLULAR-SIGN...	7	0.422870	0.991085	0.483037	0.905509	1.000
255	GOBP-GLAND-DEVELOPMENT	7	0.414551	0.988624	0.472222	0.907925	1.000

Continuation of Table S8

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
256 GOBP-REGULATION-OF-CELLULAR-LOCALIZATION	GO-0060341	17	0.310803	0.98251	0.457778	0.905324	1.000
257 GOBP-CELL-PART-MORPHOGENESIS	GO-0032990	25	0.288621	0.98560	0.480905	0.905831	1.000
258 GOBP-RESPONSE-TO-MECHANICAL-STIMULUS	GO-0009612	6	0.432266	0.985964	0.472178	0.903748	1.000
259 GOBP-APOPTOTIC-SIGNALING-PATHWAY	GO-0097190	15	0.325573	0.984426	0.491499	0.904095	1.000
260 GOBP-RESPONSE-TO-GROWTH-FACTOR	GO-0070488	18	0.312488	0.984261	0.476401	0.901109	1.000
261 GOBP-REGULATION-OF-ANION-TRANSPORT	GO-0040700	20	0.301751	0.983709	0.486291	0.898826	1.000
262 GOBP-REGULATION-OF-CELL-CYCLE-PROCESS	GO-0010564	5	0.461303	0.980566	0.507563	0.902841	1.000
263 GOBP-PROTEIN-PHOSPHORYLATION	GO-0006470	7	0.412974	0.979473	0.485981	0.901979	1.000
264 GOBP-DENDRITIC-SPINE-MORPHOGENESIS	GO-0060997	5	0.468992	0.976442	0.517065	0.905765	1.000
265 GOBP-NEGATIVE-REGULATION-OF-SIGNALING	GO-0002307	21	0.303422	0.975465	0.494186	0.904661	1.000
266 GOBP-POSITIVE-REGULATION-OF-LONG-TERM-SYNAPTIC...	GO-1900273	5	0.457866	0.975078	0.497400	0.902203	1.000
267 GOBP-CELL-MORPHOGENESIS	GO-0000902	25	0.288621	0.974976	0.503526	0.899055	1.000
268 GOBP-SMALL-MOLECULE-METABOLIC-PROCESS	GO-0044281	16	0.313622	0.973041	0.495495	0.900077	1.000
269 GOBP-MYELOID-LEUKOCYTE-DIFFERENTIATION	GO-0002573	11	0.346629	0.971778	0.507200	0.899526	1.000
270 GOBP-PHOSPHORYLATION	GO-0016311	7	0.412974	0.96836	0.521382	0.907452	1.000
271 GOBP-REGULATION-OF-NERVOUS-SYSTEM-DEVELOPMENT	GO-0051960	15	0.443648	0.964708	0.500000	0.904624	1.000
272 GOBP-REGULATION-OF-WNT-SIGNALING-PATHWAY	GO-0030111	5	0.372610	0.964204	0.510101	0.905655	1.000
273 GOBP-FAT-CELL-DIFFERENTIATION	GO-0045444	9	0.372610	0.964204	0.511774	0.903354	1.000
274 GOBP-MEMBRANE-ORGANIZATION	GO-0061024	12	0.329276	0.961667	0.521875	0.905806	1.000
275 GOBP-CARBOHYDRATE-HOMEOSTASIS	GO-0003350	7	0.397142	0.959953	0.491311	0.906341	1.000
276 GOBP-CELL-POPULATION-PROLIFERATION	GO-0008283	32	0.266205	0.959076	0.506456	0.904994	1.000
277 GOBP-RESPONSE-TO-ENDOGENOUS-STIMULUS	GO-0009719	34	0.263566	0.958047	0.513699	0.903952	1.000
278 GOBP-CELL-ACTIVATION-INVOLVED-IN-IMMUNE-RESPONSE	GO-0002263	6	0.414807	0.953358	0.520525	0.911605	1.000
279 GOBP-ESTABLISHMENT-OF-PROTEIN-LOCALIZATION-TO-...	GO-0072594	5	0.443663	0.951015	0.545455	0.913773	1.000
280 GOBP-RESPIRATORY-SYSTEM-DEVELOPMENT	GO-0060541	6	0.420268	0.950815	0.524181	0.910889	1.000
281 GOBP-SKELETAL-MUSCLE-ORGAN-DEVELOPMENT	GO-0060538	5	0.443771	0.950749	0.559567	0.907798	1.000
282 GOBP-DENDRITE-DEVELOPMENT	GO-0016358	10	0.359931	0.950358	0.545171	0.905315	1.000
283 GOBP-NEURON-PROJECTION-ORGANIZATION	GO-0106027	8	0.381665	0.950020	0.536667	0.902844	1.000
284 GOBP-RESPONSE-TO-OXIDATIVE-STRESS	GO-0006979	8	0.369099	0.949218	0.524721	0.901545	1.000
285 GOBP-REGULATION-OF-PROTEIN-MODIFICATION-PROCESS	GO-0031399	28	0.275739	0.948441	0.517493	0.900070	1.000
286 GOBP-POSITIVE-REGULATION-OF-PROTEIN-KINASE-ACT...	GO-0045860	18	0.299996	0.947939	0.509119	0.897908	1.000
287 GOBP-RESPONSE-TO-TUMOR-NECROSIS-FACTOR	GO-0034612	7	0.390819	0.947186	0.536050	0.896383	1.000
288 GOBP-GLIAL-CELL-DIFFERENTIATION	GO-0010001	10	0.348164	0.942545	0.534056	0.903336	1.000
289 REACTOME-NGF-STIMULATED-TRANSCRIPTION	R-RNO-9031628	9	0.353930	0.942122	0.521880	0.901241	1.000
290 GOBP-REGULATION-OF-CELLULAR-RESPONSE-TO-STRESS	GO-0080135	9	0.359889	0.941958	0.545455	0.898481	1.000
291 GOBP-MYELOID-LEUKOCYTE-MEDIATED-IMMUNITY	GO-0002444	6	0.414807	0.941251	0.546798	0.896902	1.000
292 GOBP-POSITIVE-REGULATION-OF-DEVELOPMENTAL-GROWTH	GO-0048639	8	0.381139	0.939303	0.546178	0.898086	1.000
293 GOBP-RESPONSE-TO-CALCIUM-ION	GO-0051592	6	0.412974	0.937279	0.543253	0.899311	1.000
294 GOBP-DEVELOPMENTAL-CELL-GROWTH	GO-0048588	5	0.430309	0.935343	0.539823	0.900355	1.000
295 GOBP-MALE-GAMETE-GENERATION	GO-0048232	5	0.428139	0.933271	0.545453	0.901903	1.000
296 GOBP-RESPONSE-TO-ALCOHOL	GO-0097305	11	0.342062	0.931378	0.552335	0.902965	1.000
297 GOBP-AMIDE-BIOSYNTHETIC-PROCESS	GO-0043604	6	0.407264	0.927346	0.550580	0.908628	1.000
298 REACTOME-NEUTROPHIL-DEGRANULATION	R-RNO-6798695	6	0.414807	0.926485	0.585324	0.907362	1.000

Continuation of Table S8

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
299	GOBP-PROTEIN_LOCALIZATION_TO_CELL_JUNCTION	6	0.397833	0.921168	0.575563	0.915602	1.000
300	GOBP-GAMETE_GENERATION	9	0.355826	0.920672	0.576983	0.913618	1.000
301	GOBP-POSITIVE_REGULATION_OF_MOLECULAR_FUNCTION	37	0.253866	0.919332	0.568966	0.913434	1.000
302	GOBP-RESPONSE_TO_REACTIVE_OXYGEN_SPECIES	8	0.369099	0.918985	0.571429	0.911168	1.000
303	GOBP-POSITIVE_REGULATION_OF_DNA_BINDING_TRANSC...	10	0.344294	0.918932	0.573718	0.908280	1.000
304	GOBP-SMALL_MOLECULE_BIOSYNTHETIC_PROCESS	5	0.431932	0.918490	0.591837	0.906158	1.000
305	GOBP-NEURON_APOPTOTIC_PROCESS	12	0.321733	0.908973	0.583882	0.923634	1.000
306	GOBP-PEPTIDE_BIOSYNTHETIC_PROCESS	6	0.407264	0.906961	0.594077	0.924892	1.000
307	GOBP-REGULATION_OF_ION_TRANSPORT	36	0.248988	0.906657	0.583902	0.922581	1.000
308	GOBP-ESTABLISHMENT_OF_PROTEIN_LOCALIZATION	17	0.290831	0.904299	0.599402	0.924406	1.000
309	GOBP-REGULATION_OF_DEVELOPMENTAL_GROWTH	9	0.352029	0.904064	0.571429	0.921993	1.000
310	GOBP-AMEBOIDAL_TYPE_CELL_MIGRATION	11	0.326439	0.903821	0.590980	0.919470	1.000
311	GOBP-REGULATION_OF_HEMOPOIESIS	10	0.336200	0.901923	0.594427	0.920550	1.000
312	GOBP-LEUKOCYTE_CELL_CELL_ADHESION	6	0.398548	0.899472	0.585209	0.922418	1.000
313	GOBP-MONOAMINE_TRANSPORT	5	0.422960	0.898652	0.612211	0.921107	1.000
314	GOBP-DENDRITIC_SPINE_DEVELOPMENT	6	0.397434	0.891762	0.609677	0.924132	1.000
315	GOBP-NEGATIVE_REGULATION_OF_ANION_TRANSPORT	8	0.352444	0.891762	0.602761	0.929284	1.000
316	REACTOME-ADAPTIVE_IMMUNE_SYSTEM	9	0.348963	0.890813	0.594340	0.928382	1.000
317	GOBP-RESPONSE_TO_BIOTIC_STIMULUS	17	0.288691	0.890720	0.604106	0.925672	1.000
318	GOBP-POSITIVE_REGULATION_OF_TRANSPERASE_ACTIVITY	19	0.279005	0.880034	0.626292	0.944098	1.000
319	REACTOME-MAPK_TARGETS_NUCLEAR_EVENTS_MEDIATED...	5	0.407757	0.877732	0.639594	0.945867	1.000
320	GOBP-POSITIVE_REGULATION_OF_ORGANELLE_ORGANIZA...	10	0.331060	0.877701	0.613354	0.942987	1.000
321	REACTOME_SIGNALING_BY_NTRK2_TRKB	6	0.385972	0.877293	0.610282	0.940881	1.000
322	GOBP-ORGANONITROGEN_COMPOUND_CATABOLIC_PROCESS	10	0.327478	0.876730	0.617886	0.939075	1.000
323	GOBP-CELL_CELL_JUNCTION_ASSEMBLY	5	0.407365	0.875615	0.613445	0.938195	1.000
324	GOBP-RESPONSE_TO_PEPITIDE_HORMONE	13	0.304436	0.873939	0.637747	0.938616	1.000
325	GOBP-POSITIVE_REGULATION_OF_NEURON_PROJECTION...	5	0.417717	0.873912	0.646667	0.935776	1.000
326	GOBP-REGULATION_OF_MITOTIC_CELL_CYCLE	5	0.405823	0.872542	0.635897	0.935650	1.000
327	GOBP-DEVELOPMENTAL_GROWTH	10	0.330048	0.872371	0.621875	0.933110	1.000
328	GOBP-REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENT...	8	0.349035	0.871666	0.610224	0.931570	1.000
329	GOBP-REGULATION_OF_CELLULAR_AMIDE_METABOLIC_PR...	9	0.334759	0.870242	0.630915	0.931515	1.000
330	GOBP-CARBOHYDRATE_DERIVATIVE_BIOSYNTHETIC_PROCESS	5	0.410411	0.865397	0.648557	0.938454	1.000
331	GOBP-REGULATION_OF_TRANSMEMBRANE_TRANSPORT	23	0.259338	0.864858	0.630952	0.936731	1.000
332	GOBP-REGULATION_OF_INTRACELLULAR_SIGNAL_TRANSD...	21	0.265874	0.864661	0.631420	0.934288	1.000
333	GOBP-MORPHOGENESIS_OF_AN_EPITHELIUM	6	0.382120	0.863905	0.659933	0.932876	1.000
334	GOBP-MITOCHONDRION_ORGANIZATION	7	0.363920	0.862446	0.661994	0.932936	1.000
335	GOBP-NEGATIVE_REGULATION_OF_RESPONSE_TO_EXTERN...	5	0.397421	0.862220	0.629948	0.930630	1.000
336	GOBP-MUSCLE_CELL_PROLIFERATION	8	0.344817	0.862010	0.623779	0.928261	1.000
337	GOBP-REGULATION_OF_ANION_TRANSMEMBRANE_TRANSPORT	5	0.404242	0.858347	0.649919	0.932419	1.000
338	HALLMARK_KRAS_SIGNALING_UP	6	0.375118	0.857722	0.657665	0.930820	1.000
339	GOBP-DEFENSE_RESPONSE_TO_OTHER_ORGANISM	9	0.330906	0.857605	0.653907	0.928176	1.000
340	GOBP-POSITIVE_REGULATION_OF_NEURON_DEATH	5	0.398006	0.856966	0.654762	0.926676	1.000
341	GOBP-POSITIVE_REGULATION_OF_LEUKOCYTE_CELL_CEL...	5	0.394961	0.855219	0.681818	0.927250	1.000

Continuation of Table S8

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
342	GOBP-POSITIVE-REGULATION_OF_SMALL-MOLECULE-MET...	GO-0062013	5	0.394061	0.851529	0.674576	0.931659	1.000
343	HALLMARK-APOPTOSIS	M5902	6	0.371032	0.850826	0.649241	0.930326	1.000
344	GOBP-CELL-GROWTH	GO-0016049	10	0.315533	0.848633	0.653784	0.931572	1.000
345	GOBP-POSITIVE-REGULATION_OF_CELL-CELL-ADHESION	GO-0022409	5	0.394961	0.845794	0.659933	0.934217	1.000
346	REACTOME-DISEASES-OF-SIGNAL-TRANSDUCTION-BY-GR...	R-HSA-5663202	12	0.298337	0.844743	0.668760	0.933562	1.000
347	GOBP-POSITIVE-REGULATION_OF_SECRETION	GO-0051047	6	0.379633	0.844214	0.671642	0.931761	1.000
348	GOBP-CYTOKINE-PRODUCTION	GO-0001816	10	0.319721	0.843242	0.670330	0.931033	1.000
349	GOBP-LEUKOCYTE-DIFFERENTIATION	GO-0002521	15	0.280259	0.842037	0.679412	0.930546	1.000
350	GOBP-POSITIVE-REGULATION_OF_EPITHELIAL-CELL-MI...	GO-0010634	5	0.399720	0.841966	0.676768	0.928000	1.000
351	GOBP-CELLULAR-RESPONSE-TO-HORMONE-STIMULUS	GO-0032870	11	0.301490	0.841537	0.663158	0.926197	1.000
352	GOBP-REGULATION-OF-LIPID-LOCALIZATION	GO-1905952	5	0.386854	0.837652	0.659649	0.930629	1.000
353	GOBP-POSITIVE-REGULATION_OF_TRANSMEMBRANE-TRAN...	GO-0034764	7	0.350120	0.837253	0.659677	0.928694	1.000
354	REACTOME-DEATH-RECEPTOR-SIGNALING	R-RNO-73887	5	0.394931	0.835480	0.683849	0.929264	1.000
355	GOBP-CIRCULATORY-SYSTEM-PROCESS	GO-0003013	5	0.393160	0.831678	0.708543	0.933569	1.000
356	GOBP-LOCOMOTORY-BEHAVIOR	GO-0007626	8	0.328581	0.831548	0.672727	0.931205	1.000
357	REACTOME-ANTI-INFLAMMATORY-RESPONSE-FAVOURING...	R-HSA-9662851	5	0.394997	0.830515	0.699357	0.930542	1.000
358	GOBP-NEGATIVE-REGULATION_OF_CELL-POPULATION-PR...	GO-0008285	9	0.322386	0.828292	0.697248	0.931860	1.000
359	GOBP-NEGATIVE-REGULATION_OF-PHOSPHORUS-METABOL...	GO-0010563	9	0.319854	0.828122	0.675241	0.929548	1.000
360	GOBP-REGULATION-OF-TRANS-SYNAPTIC-SIGNALING	GO-0099177	40	0.230950	0.826860	0.705882	0.929204	1.000
361	REACTOME-INTERLEUKIN-17-SIGNALING	R-RNO-448424	6	0.366655	0.824684	0.704620	0.930432	1.000
362	GOBP-BIOLOGICAL-ADHESION	GO-0022610	19	0.259896	0.823198	0.696581	0.930703	1.000
363	GOBP-REGULATION-OF-SYNAPTIC-TRANSMISSION-GLUTA...	GO-0051966	12	0.288064	0.821896	0.688207	0.930397	1.000
364	GOBP-POSITIVE-REGULATION_OF_CELL-PROJECTION-OR...	GO-0031346	10	0.307494	0.821359	0.690513	0.928841	1.000
365	GOBP-RESPONSE-TO-EXTRACELLULAR-STIMULUS	GO-0009991	13	0.284228	0.820526	0.705279	0.927756	1.000
366	GOBP-POSITIVE-REGULATION_OF_HEMOPOIESIS	GO-1903708	7	0.339236	0.819816	0.676033	0.926405	1.000
367	GOBP-CELLULAR-RESPONSE-TO-KETONE	GO-1901655	5	0.385603	0.818484	0.713299	0.926331	1.000
368	GOBP-RESPONSE-TO-DRUG	GO-0042493	11	0.299335	0.816898	0.685215	0.926489	1.000
369	GOBP-NEGATIVE-REGULATION_OF_NERVOUS-SYSTEM-DEV...	GO-0051961	5	0.381633	0.815470	0.734219	0.926507	1.000
370	GOBP-SYNAPSE-ORGANIZATION	GO-0050808	17	0.258545	0.813414	0.719530	0.927444	1.000
371	GOBP-CELLULAR-MACROMOLECULE-LOCALIZATION	GO-0070727	20	0.247342	0.808786	0.720117	0.933050	1.000
372	GOBP-NEGATIVE-REGULATION_OF_CELLULAR-COMPONENT...	GO-0051129	11	0.289179	0.807754	0.712934	0.932376	1.000
373	GOBP-ORGANIC-HYDROXY-COMPOUND-TRANSPORT	GO-0015850	6	0.354964	0.807369	0.701131	0.930581	1.000
374	GOBP-FOREBRAIN-DEVELOPMENT	GO-0030900	10	0.303420	0.806909	0.719937	0.928831	1.000
375	GOBP-SYNAPTIC-TRANSMISSION-GLUTAMATERGIC	GO-0035249	13	0.281601	0.806858	0.706314	0.926470	1.000
376	GOBP-ORGANIC-HYDROXY-COMPOUND-METABOLIC-PROCESS	GO-1901615	8	0.312500	0.803844	0.709729	0.929198	1.000
377	GOBP-REGULATION_OF-SYNAPSE-STRUCTURE-OR-ACTIVITY	GO-0050803	11	0.288568	0.800278	0.708006	0.932485	1.000
378	GOBP-NEGATIVE-REGULATION_OF-PROTEIN-MODIFICATI...	GO-0031400	10	0.300574	0.799051	0.732628	0.931987	1.000
379	GOBP-NEGATIVE-REGULATION_OF-BIOSYNTHETIC-PROCESS	GO-0008980	13	0.275581	0.790830	0.736999	0.931280	1.000
380	GOBP-POSITIVE-REGULATION_OF_CELLULAR-COMPONENT...	GO-0044089	9	0.304809	0.790528	0.725522	0.931269	1.000
381	GOBP-CATION-TRANSPORT	GO-0006812	25	0.232578	0.796186	0.755304	0.929377	1.000
382	GOBP-REGULATION_OF-MULTICELLULAR-ORGANISMAL-DE...	GO-2000026	31	0.225423	0.796149	0.760962	0.927011	1.000
383	GOBP-MUSCLE-STRUCTURE-DEVELOPMENT	GO-0061061	16	0.261437	0.795901	0.729771	0.924943	1.000
384	GOBP-REGULATION-OF-ENDOTHELIAL-CELL-MIGRATION	GO-0010594	5	0.371505	0.793322	0.718910	0.926977	1.000

Continuation of Table S8

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
385	GOBP-T-CELL-ACTIVATION	GO-0042110	8	0.311792	0.792435	0.714968	0.926005	1.000
386	GOBP-POSITIVE-REGULATION-OF-ESTABLISHMENT-OF-P...	GO-1904951	5	0.369980	0.792234	0.747856	0.923958	1.000
387	GOBP-LEARNING	GO-0007612	13	0.271170	0.792066	0.741486	0.921820	1.000
388	GOBP-CELLULAR-RESPONSE-TO-PEPTIDE-HORMONE-STIM...	GO-0071375	9	0.301261	0.790186	0.737785	0.922297	1.000
389	GOBP-NEGATIVE-REGULATION-OF-CELL-DEVELOPMENT	GO-0010721	6	0.349192	0.789736	0.739683	0.920643	1.000
390	GOBP-REGULATION-OF-GROWTH	GO-0040008	13	0.274262	0.789714	0.749221	0.918334	1.000
391	REACTOME-TOLL-LIKE-RECEPTOR-TLR1_TLR2-CASCADE	R-RNO-168179	8	0.310203	0.785535	0.754072	0.917797	1.000
392	GOBP-SEXUAL-REPRODUCTION	GO-0019953	10	0.300119	0.788021	0.755267	0.916332	1.000
393	GOBP-IN-UTERO-EMBRYONIC-DEVELOPMENT	GO-0001701	8	0.318600	0.786135	0.739550	0.917103	1.000
394	REACTOME-MYD88-INDEPENDENT-TLR4-CASCADE	R-RNO-166166	8	0.310203	0.786064	0.728896	0.914881	1.000
395	REACTOME-TOLL-LIKE-RECEPTOR-CASCADES	R-RNO-168898	8	0.310203	0.785346	0.735910	0.913672	1.000
396	REACTOME-TOLL-LIKE-RECEPTOR-9_TLR9-CASCADE	R-RNO-168138	8	0.310203	0.785136	0.736066	0.911697	1.000
397	GOBP-IMMUNE-SYSTEM-DEVELOPMENT	GO-0002520	17	0.250683	0.783089	0.770865	0.912517	1.000
398	GOBP-MUSCLE-ORGAN-DEVELOPMENT	GO-0007517	9	0.304404	0.782533	0.751926	0.911141	1.000
399	GOBP-CELLULAR-RESPONSE-TO-NITROGEN-COMPOUND	GO-1901699	20	0.242638	0.780204	0.762391	0.912438	1.000
400	GOBP-POSITIVE-REGULATION-OF-MAP-KINASE-ACTIVITY	GO-0043406	6	0.343175	0.778795	0.732323	0.912304	1.000
401	GOBP-NEGATIVE-REGULATION-OF-PROTEIN-CATABOLIC...	GO-0042177	5	0.359196	0.778208	0.744538	0.910943	1.000
402	GOBP-ACTIVATION-OF-MAPK-ACTIVITY	GO-0000187	6	0.343175	0.777692	0.743265	0.909440	1.000
403	GOBP-CELL-CELL-ADHESION	GO-0098609	14	0.267576	0.777395	0.774390	0.907578	1.000
404	GOBP-POSITIVE-REGULATION-OF-PEPTIDASE-ACTIVITY	GO-0010952	7	0.317311	0.773866	0.734177	0.910555	1.000
405	REACTOME-NUCLEAR-EVENTS-KINASE-AND-TRANSCRIPTI...	R-RNO-198725	11	0.277204	0.771880	0.732198	0.911372	1.000
406	GOBP-ENDOCRINE-SYSTEM-DEVELOPMENT	GO-0035270	6	0.340687	0.770364	0.757009	0.911445	1.000
407	GOBP-REGULATION-OF-PHOSPHATIDYLINOSITOL-3_KINA...	GO-0014066	6	0.335304	0.768954	0.750422	0.911330	1.000
408	GOBP-GROWTH	GO-0040007	14	0.258839	0.768222	0.751152	0.910227	1.000
409	GOBP-POSITIVE-REGULATION-OF-CYSTEINE-TYPE-ENDO...	GO-2001056	7	0.317311	0.762180	0.772655	0.916924	1.000
410	GOBP-RESPONSE-TO-LIPID	GO-0033993	19	0.233521	0.760477	0.787106	0.917257	1.000
411	GOBP-NEGATIVE-REGULATION-OF-RESPONSE-TO-STIMULUS	GO-0048585	16	0.247957	0.759614	0.765060	0.916298	1.000
412	GOBP-RESPONSE-TO-ALKALOID	GO-0043279	5	0.355800	0.759044	0.792208	0.914930	1.000
413	GOBP-CELLULAR-RESPONSE-TO-EXTERNAL-STIMULUS	GO-0071496	10	0.281551	0.756410	0.774351	0.916543	1.000
414	GOBP-NERVE-DEVELOPMENT	GO-0021675	9	0.292096	0.755192	0.788906	0.916172	1.000
415	GOBP-ORGANIC-ACID-METABOLIC-PROCESS	GO-0006082	7	0.312070	0.746952	0.780096	0.925727	1.000
416	GOBP-RESPONSE-TO-PEPTIDE	GO-1901652	18	0.231424	0.737830	0.818318	0.936087	1.000
417	GOBP-IMMUNE-RESPONSE-REGULATING-SIGNALING-PATHWAY	GO-000276	8	0.290419	0.735254	0.786859	0.937360	1.000
418	GOBP-POSITIVE-REGULATION-OF-AXONOGENESIS	GO-0050772	5	0.339464	0.732625	0.791946	0.938592	1.000
419	GOBP-RESPONSE-TO-OXYGEN-LEVELS	GO-0070482	8	0.293408	0.731985	0.801887	0.937252	1.000
420	GOBP-NEGATIVE-REGULATION-OF-NUCLEOBASE-CONTAIN...	GO-0045934	13	0.247796	0.730243	0.821981	0.937444	1.000
421	GOBP-LYMPHOCYTE-ACTIVATION	GO-0046649	10	0.267213	0.727710	0.815748	0.938572	1.000
422	GOBP-MAINTENANCE-OF-LOCATION	GO-0051235	7	0.302305	0.727826	0.798658	0.937597	1.000
423	GOBP-REGULATION-OF-VASCULATURE-DEVELOPMENT	GO-1901342	5	0.344698	0.726623	0.816225	0.935637	1.000
424	GOBP-REGULATION-OF-ANATOMICAL-STRUCTURE-MORPHO...	GO-0022603	17	0.233126	0.725730	0.817379	0.934705	1.000
425	GOBP-POSITIVE-REGULATION-OF-MYELOID-CELL-DIFFE...	GO-0045639	7	0.307659	0.722009	0.833608	0.937383	1.000
426	GOBP-REGULATION-OF-DNA-BINDING-TRANSCRIPTION-F...	GO-0051090	16	0.236485	0.721933	0.847534	0.935304	1.000
427	GOBP-HOMEOSTASIS-OF-NUMBER-OF-CELLS	GO-0048872	5	0.345987	0.721138	0.821429	0.934159	1.000

Continuation of Table S8

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
428	GOBP-REGULATION-OF-NEUROGENESIS	GO-0050767	14	0.242998	0.716996	0.816923	0.937268
429	GOBP-FC-RECEPTOR-SIGNALING-PATHWAY	GO-0038093	8	0.290419	0.715695	0.822531	0.936764
430	GOBP-ANION-TRANSMEMBRANE-TRANSPORT	GO-0098656	7	0.289420	0.713922	0.851097	0.936807
431	GOBP-CELL-CELL-SIGNALING-BY-WNT	GO-0198738	7	0.296278	0.713176	0.846278	0.935548
432	REACTOME-NERVOUS-SYSTEM-DEVELOPMENT	R-RNO-9675108	14	0.242413	0.711681	0.860075	0.935417
433	GOBP-POSITIVE-REGULATION-OF-MULTICELLULAR-ORGA...	GO-0051240	32	0.201189	0.710331	0.863448	0.934995
434	GOBP-CELL-JUNCTION-ASSEMBLY	GO-0034329	8	0.279590	0.710168	0.831818	0.933059
435	GOBP-MATERNAL-PROCESS-INVOLVED-IN-FEMALE-PREGN...	GO-0060135	5	0.335518	0.709035	0.829431	0.932337
436	GOBP-TRANSMEMBRANE-RECEPTOR-PROTEIN-SERINE-THR...	GO-0007178	6	0.315859	0.702517	0.836120	0.938281
437	GOBP-RESPONSE-TO-ETHANOL	GO-0045471	5	0.323430	0.700264	0.856900	0.938924
438	GOBP-REGULATION-OF-CYTOSKELETON-ORGANIZATION	GO-0051493	5	0.329569	0.699766	0.831918	0.937445
439	GOBP-VESICLE-MEDIATED-TRANSPORT-IN-SYNAPSE	GO-0099003	7	0.294535	0.694658	0.829431	0.941487
440	GOBP-POSITIVE-REGULATION-OF-CATION-TRANSMEMBRAN...	GO-1904064	5	0.320648	0.691599	0.873754	0.942878
441	GOBP-REGULATION-OF-CELL-DEVELOPMENT	GO-0060284	15	0.229648	0.690604	0.857143	0.941939
442	GOBP-CELLULAR-RESPONSE-TO-ORGANIC-CYCCLIC-COMPOUND	GO-0071407	13	0.234275	0.683445	0.855639	0.947886
443	GOBP-METAL-ION-HOMEOSTASIS	GO-0055065	14	0.226595	0.680277	0.875576	0.949360
444	GOBP-EMBRYONIC-ORGAN-DEVELOPMENT	GO-0048568	7	0.283612	0.679925	0.853081	0.947612
445	GOBP-INNATE-IMMUNE-RESPONSE	GO-0045087	7	0.283951	0.678606	0.859016	0.946985
446	GOBP-RESPONSE-TO-CARBOHYDRATE	GO-0009743	5	0.316124	0.678533	0.867450	0.944925
447	GOBP-REGULATION-OF-SIGNALING	GO-0010469	14	0.223878	0.673337	0.882261	0.948363
448	GOBP-RESPONSE-TO-MONOSACCHARIDE	GO-0034284	5	0.316124	0.672474	0.885615	0.947135
449	REACTOME-INTERFERON-SIGNALING	R-RNO-913531	6	0.302405	0.672344	0.880131	0.945167
450	GOBP-NEGATIVE-REGULATION-OF-TRANSCRIPTION-BY-R...	GO-0000122	10	0.248792	0.671990	0.865325	0.943408
451	GOBP-POSITIVE-REGULATION-OF-PEPTIDYL-TYROSINE...	GO-0050731	8	0.266278	0.670207	0.876161	0.943210
452	GOBP-REGULATION-OF-PEPTIDYL-TYROSINE-PHOSPHORY...	GO-0050730	9	0.255739	0.670059	0.888025	0.941313
453	GOBP-AXON-DEVELOPMENT	GO-0061564	18	0.215632	0.669048	0.870968	0.940311
454	GOBP-NEGATIVE-REGULATION-OF-KINASE-ACTIVITY	GO-0033673	5	0.299632	0.654671	0.900000	0.952772
455	GOBP-TRANSMEMBRANE-TRANSPORT	GO-0055085	27	0.188518	0.653054	0.905444	0.952259
456	GOBP-PRIMIRNA-TRANSCRIPTION-BY-RNA-POLYMERASE-II	GO-0061614	7	0.268801	0.647041	0.902973	0.956156
457	GOBP-NEGATIVE-REGULATION-OF-TRANSFERASE-ACTIVITY	GO-0051348	5	0.299632	0.643248	0.914634	0.957674
458	GOBP-POSITIVE-REGULATION-OF-PRIMIRNA-TRANSCRI...	GO-1902895	7	0.268801	0.640063	0.913540	0.958536
459	GOBP-REGULATION-OF-MAPK-CASCADE	GO-0043408	13	0.221274	0.639833	0.907353	0.956645
460	GOBP-CELLULAR-RESPONSE-TO-EXTRACELLULAR-STIMULUS	GO-0031668	8	0.249104	0.638959	0.900813	0.955340
461	REACTOME-LEISHMANIA-INFECTION	R-HSA-9658195	10	0.234170	0.638627	0.905956	0.953602
462	GOBP-CELL-MORPHOGENESIS-INVOLVED-IN-NEURON-DIF...	GO-0048667	22	0.194129	0.638581	0.912722	0.951583
463	GOBP-REGULATION-OF-CELLULAR-COMPONENT-BIOGENESIS	GO-0044087	10	0.237287	0.638313	0.926984	0.949765
464	GOBP-CELL-MORPHOGENESIS-INVOLVED-IN-DIFFERENTI...	GO-0000904	22	0.194129	0.633375	0.922401	0.952118
465	GOBP-POSITIVE-REGULATION-OF-NERVOUS-SYSTEM-DEV...	GO-0051962	12	0.219988	0.632319	0.902022	0.951022
466	GOBP-PROTEIN-MODIFICATION-BY-SMALL-PROTEIN-CON...	GO-0070647	7	0.267586	0.630601	0.929146	0.950468
467	HALLMARK-HYPOXIA	M5891	5	0.289757	0.628972	0.919672	0.949698
468	GOBP-POSITIVE-REGULATION-OF-CELL-DEVELOPMENT	GO-0010720	12	0.219988	0.627932	0.927100	0.948517
469	GOBP-POSITIVE-REGULATION-OF-NEUROGENESIS	GO-0050769	12	0.219988	0.625617	0.915873	0.948494
470	GOBP-REGULATION-OF-MAP-KINASE-ACTIVITY	GO-0043405	9	0.243214	0.621595	0.916129	0.949833

Continuation of Table S8

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
471	GOBP-REGULATION-OF-CIRCADIAN-RHYTHM	GO-0042752	7	0.253986	0.614443	0.911717	0.953731	1.000
472	GOBP-POSITIVE-REGULATION-OF-CELL-DIFFERENTIATION	GO-0045597	27	0.175149	0.607805	0.944915	0.956731	1.000
473	GOBP-POSITIVE-REGULATION-OF-INTRACELLULAR-SIGN...	GO-1902533	14	0.201074	0.599680	0.950617	0.960341	1.000
474	GOBP-RESPONSE-TO-INSULIN	GO-0032868	5	0.277108	0.593571	0.946218	0.962472	1.000
475	GOBP-G-PROTEIN-COUPLED-RECEPTOR-SIGNALING-PATHWAY	GO-0007186	18	0.186823	0.582440	0.942222	0.967754	1.000
476	GOBP-PURINE-CONTAINING-COMPOUND-METABOLIC-PROCESS	GO-0072521	6	0.255271	0.568945	0.956882	0.973543	1.000
477	HALLMARK-UV-RESPONSE-UP	M5941	5	0.269483	0.565472	0.948387	0.973326	1.000
478	GOBP-REGULATION-OF-AXONOGENESIS	GO-0050770	7	0.233223	0.557679	0.954248	0.975508	1.000
479	GOBP-MUSCLE-TISSUE-DEVELOPMENT	GO-0060537	11	0.201726	0.556529	0.965723	0.974073	1.000
480	GOBP-PROTEIN-LOCALIZATION-TO-POSTSYNAPSE	GO-0062237	5	0.252372	0.543229	0.971235	0.978316	1.000
481	GOBP-PROTEIN-LOCALIZATION-TO-SYNAPSE	GO-0035418	5	0.252372	0.529382	0.971901	0.982193	1.000
482	GOBP-CELL-SURFACE-RECEPTOR-SIGNALING-PATHWAY-I...	GO-1905114	15	0.164384	0.494930	0.978788	0.991200	1.000
483	GOBP-REGULATION-OF-GTPASE-ACTIVITY	GO-0043087	5	0.215819	0.465571	0.989667	0.995189	1.000
484	REACTOME-CELLULAR-RESPONSES-TO-EXTERNAL-STIMULI	R-RNO-8953897	11	0.167175	0.464879	0.995482	0.993217	1.000
485	REACTOME-RNA-POLYMERASE-II-TRANSCRIPTION	R-RNO-73857	20	-0.123186	-0.465799	1.000000	0.996698	1.000
486	GOBP-STRIATED-MUSCLE-CELL-DIFFERENTIATION	GO-0051146	9	-0.164557	-0.479524	0.994350	0.999266	1.000
487	REACTOME-TRANSCRIPTIONAL-REGULATION-BY-MECP2	R-RNO-8986944	7	-0.191591	-0.504664	0.997348	0.999203	1.000
488	GOBP-MUSCLE-CELL-DIFFERENTIATION	GO-0042692	10	-0.166667	-0.514977	0.982906	1.000000	1.000
489	REACTOME-SENESCENCE-ASSOCIATED-SECRETORY-PHENO...	R-RNO-2559582	6	-0.222271	-0.556103	0.967568	0.991866	1.000
490	REACTOME-CELLULAR-SENESCENCE	R-RNO-2559583	11	-0.222271	-0.569412	0.964557	0.989928	1.000
491	GOBP-ADENYLATE-CYCLASE-MODULATING-G-PROTEIN.CO...	GO-0007188	6	-0.186940	-0.587283	0.955556	0.984723	1.000
492	REACTOME-FC-EPSILON-RECEPTOR-FCER1-SIGNALING	R-RNO-2454202	7	-0.239276	-0.609136	0.923077	0.974938	1.000
493	GOBP-HEAD-DEVELOPMENT	GO-0060322	23	-0.160242	-0.614755	0.947712	0.974944	1.000
494	GOBP-ADENYLATE-CYCLASE-INHIBITING-G-PROTEIN.CO...	GO-0007193	9	-0.215190	-0.628394	0.924282	0.968275	1.000
495	GOBP-FC-EPSILON-RECEPTOR-SIGNALING-PATHWAY	GO-0038095	7	-0.239276	-0.635113	0.938667	0.966634	1.000
496	GOBP-CIRCADIAN-REGULATION-OF-GENE-EXPRESSION	GO-0032922	5	-0.276140	-0.646065	0.927273	0.960601	1.000
497	GOBP-RESPONSE-TO-STARVATION	GO-0042594	5	-0.283142	-0.650781	0.903704	0.960487	1.000
498	GOBP-RESPONSE-TO-INTERLEUKIN-1	GO-0070555	5	-0.284838	-0.653714	0.901809	0.961677	1.000
499	GOBP-REGULATION-OF-NEUROTRANSMITTER-RECEPTOR-A...	GO-0099601	13	-0.195481	-0.654521	0.898551	0.965121	1.000
500	GOBP-CELLULAR-RESPONSE-TO-STARVATION	GO-0009267	5	-0.283142	-0.658682	0.904040	0.965534	1.000
501	HALLMARK-TNFA-SIGNALING-VIA-NFKB	M5890	14	-0.200888	-0.661839	0.921630	0.966886	1.000
502	GOBP-CARDIAC-MUSCLE-TISSUE-DEVELOPMENT	GO-0048738	6	-0.269587	-0.670334	0.911616	0.961863	1.000
503	GOBP-HEART-DEVELOPMENT	GO-0007507	6	-0.269587	-0.670944	0.874372	0.965380	1.000
504	GOBP-CALCIUM-MEDIATED-SIGNALING	GO-0019728	10	-0.227258	-0.680030	0.889785	0.958847	1.000
505	REACTOME-LONG-TERM-POTENTIATION	R-HSA-9620244	10	-0.230769	-0.681744	0.857143	0.961359	1.000
506	GOBP-POSITIVE-REGULATION-OF-DEVELOPMENTAL-PROCESS	GO-0051094	32	-0.162931	-0.689288	0.910394	0.956818	1.000
507	REACTOME-INTEGRATION-OF-ENERGY-METABOLISM	R-RNO-163685	5	-0.301928	-0.695354	0.829146	0.953271	1.000
508	HALLMARK-EPITHELIAL-MESENCHYMAL-TRANSITION	M5930	5	-0.300634	-0.701377	0.851759	0.949871	1.000
509	GOBP-CELLULAR-GLUCOSE-HOMEOSTASIS	GO-0001678	5	-0.301575	-0.705709	0.853659	0.948157	1.000
510	GOBP-SMALL-GTPASE-MEDIATED-SIGNAL-TRANSDUCTION	GO-0007264	8	-0.255561	-0.707676	0.864000	0.949793	1.000
511	GOBP-ACTIVATION-OF-IMMUNE-RESPONSE	GO-0002253	5	-0.310665	-0.712578	0.815789	0.947851	1.000
512	GOBP-PROTEIN-MODIFICATION-BY-SMALL-PROTEIN-CON...	GO-0032446	6	-0.292821	-0.712630	0.798578	0.952225	1.000
513	GOBP-NEGATIVE-REGULATION-OF-MULTICELLULAR_ORGA...	GO-0051241	15	-0.206393	-0.717870	0.851312	0.949263	1.000

Continuation of Table S8

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
514 GOBP-REGULATION-OF-ORGAN-GROWTH	GO-0046620	5	-0.312659	-0.722558	0.816121	0.946963	1.000
515 GOBP-REGULATION-OF-PROTEIN-STABILITY	GO-0031647	5	-0.313842	-0.728050	0.802564	0.943638	1.000
516 GOBP-NUCLEAR-TRANSPORT	GO-0051169	5	-0.314507	-0.730524	0.823232	0.944683	1.000
517 GOBP-CENTRAL-NERVOUS-SYSTEM-DEVELOPMENT	GO-0007417	27	-0.179942	-0.731625	0.864780	0.947488	1.000
518 GOBP-ORGAN-GROWTH	GO-0035265	5	-0.312659	-0.738010	0.798077	0.941715	1.000
519 GOBP-CHEMICAL-SYNAPTIC-TRANSMISSION_POSTSYNAPTIC	GO-0099565	9	-0.252468	-0.739961	0.831551	0.943195	1.000
520 REACTOME-ONCOGENIC-MAPK-SIGNALING	R-HSA-6802957	5	-0.321002	-0.740085	0.805755	0.947628	1.000
521 REACTOME-PTEN-REGULATION	R-RNO-6807070	5	-0.318334	-0.741551	0.799032	0.949913	1.000
522 GOBP-CELLULAR-RESPONSE-TO-PEPTIDE	GO-1901653	13	-0.231209	-0.744935	0.817365	0.949101	1.000
523 GOBP-REGULATION-OF-MUSCLE-CELL-DIFFERENTIATION	GO-0051147	6	-0.292683	-0.747040	0.773196	0.950145	1.000
524 GOBP-PEPTIDYL-TYROSINE-MODIFICATION	GO-0018212	10	-0.252156	-0.756438	0.766017	0.939998	1.000
525 GOBP-IONOTROPIC-GLUTAMATE-RECEPTOR-SIGNALING_P...	GO-0035235	9	-0.260686	-0.757500	0.780899	0.943010	1.000
526 GOBP-MAPK-CASCADE	GO-0000165	18	-0.208081	-0.758138	0.804416	0.946671	1.000
527 GOBP-CELLULAR-RESPONSE-TO-ALCOHOL	GO-0097306	5	-0.320362	-0.761673	0.772947	0.945356	1.000
528 GOBP-NEGATIVE-REGULATION-OF-GENE-EXPRESSION	GO-0010629	11	-0.254639	-0.762293	0.763736	0.949217	1.000
529 GOBP-ADENYLATE-CYCLASE-INHIBITING-G-PROTEIN.CO...	GO-0007196	5	-0.319039	-0.762907	0.771290	0.952937	1.000
530 GOBP-CELLULAR-RESPONSE-TO-MOLECULE-OF-BACTERIA...	GO-0071219	8	-0.282041	-0.766307	0.744681	0.951783	1.000
531 GOBP-PROTEIN-AUTOPHOSPHORYLATION	GO-0046777	5	-0.333459	-0.771511	0.712737	0.947897	1.000
532 GOBP-LONG-TERM-SYNAPTIC-POTENTIATION	GO-0060291	12	-0.240740	-0.772275	0.752022	0.951451	1.000
533 REACTOME-DAG-AND-JP3-SIGNALING	R-RNO-1489509	8	-0.290713	-0.790385	0.737127	0.923639	1.000
534 GOBP-POSITIVE-REGULATION-OF-CELL-ADHESION	GO-0045785	7	-0.302610	-0.791134	0.694581	0.927062	1.000
535 GOBP-CELLULAR-RESPONSE-TO-BIOTIC-STIMULUS	GO-0071216	8	-0.282041	-0.800740	0.724311	0.914688	1.000
536 GOBP-NEGATIVE-REGULATION-OF-PHOSPHORYLATION	GO-0042326	7	-0.311726	-0.807121	0.682081	0.907340	1.000
537 GOBP-CELLULAR-RESPONSE-TO-LIPID	GO-0071396	15	-0.234555	-0.808222	0.741379	0.910224	1.000
538 REACTOME-GPCR-LIGAND-BINDING	R-RNO-500792	8	-0.288029	-0.808524	0.722222	0.914539	1.000
539 GOBP-MULTICELLULAR-ORGANISM-REPRODUCTION	GO-0032504	12	-0.258422	-0.808606	0.718391	0.919281	1.000
540 GOBP-CELL-CYCLE-PROCESS	GO-0022402	11	-0.257776	-0.811495	0.698864	0.918671	1.000
541 GOBP-CATION-TRANSMEMBRANE-TRANSPORT	GO-0098655	18	-0.218817	-0.816378	0.725490	0.914094	1.000
542 GOBP-POSITIVE-REGULATION-OF-MAPK-CASCADE	GO-0043410	9	-0.287201	-0.818418	0.705882	0.915203	1.000
543 GOBP-REGULATION-OF-CELL-CYCLE	GO-0051726	13	-0.245352	-0.818842	0.686813	0.919376	1.000
544 GOBP-RESPONSE-TO-WOUNDING	GO-0009611	15	-0.234839	-0.820998	0.708475	0.920329	1.000
545 GOBP-REGULATION-OF-CATION-TRANSMEMBRANE-TRANSPORT	GO-1904062	16	-0.232584	-0.827636	0.732558	0.912503	1.000
546 GOBP-CENTRAL-NERVOUS-SYSTEM-NEURON-DIFFERENTIA...	GO-0021953	5	-0.354529	-0.830699	0.669951	0.911536	1.000
547 GOBP-ORGANIC-ACID-TRANSPORT	GO-0015849	7	-0.312483	-0.831154	0.661247	0.915790	1.000
548 GOBP-SYNAPTIC-SIGNALING	GO-0099536	47	-0.189830	-0.831195	0.736111	0.920901	1.000
549 GOBP-REGULATION-OF-LEUKOCYTE-DIFFERENTIATION	GO-1902105	9	-0.287349	-0.834592	0.683924	0.919064	1.000
550 GOBP-INTRACELLULAR-RECEPTOR-SIGNALING-PATHWAY	GO-0030522	5	-0.361446	-0.835666	0.635697	0.922308	1.000
551 GOBP-DEVELOPMENTAL-PROCESS-INVOLVED-IN-REPRODU...	GO-0003006	11	-0.271677	-0.837441	0.678679	0.924002	1.000
552 GOBP-SENSORY_PERCEPTION-OF_PAIN	GO-0019233	5	-0.356824	-0.846704	0.647754	0.909909	1.000
553 REACTOME-L1CAM-INTERACTIONS	R-RNO-373760	5	-0.371938	-0.847899	0.641278	0.912885	1.000
554 GOBP-TELENCEPHALON-DEVELOPMENT	GO-0021537	7	-0.327266	-0.854563	0.620948	0.904387	1.000
555 GOBP-REGULATION-OF-NERVOUS-SYSTEM-PROCESS	GO-0031644	8	-0.315250	-0.854785	0.656250	0.909208	1.000
556 GOBP-RAS-PROTEIN-SIGNAL-TRANSDUCTION	GO-0007265	5	-0.369032	-0.861333	0.619403	0.900406	1.000

Continuation of Table S8

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
557 GOBP_ERBB_SIGNALING_PATHWAY	GO:0038127	5	-0.370318	-0.862676	0.600000	0.902787	1.000
558 GOBP_DEVELOPMENTAL_MATURATION	GO:0021700	5	-0.376095	-0.871410	0.606138	0.889387	1.000
559 GOBP_RESPONSE_TO_ORGANIC_CYCLIC_COMPOUND	GO:0014070	20	-0.232127	-0.871425	0.692568	0.894716	1.000
560 GOBP_PROTEIN_LOCALIZATION_TO_ORGANELLE	GO:0033365	8	-0.316730	-0.872468	0.643052	0.898238	1.000
561 GOBP_MONONUCLEAR_CELL_DIFFERENTIATION	GO:1903131	7	-0.337335	-0.876423	0.587786	0.895279	1.000
562 GOBP_WOUND_HEALING	GO:0042060	13	-0.266552	-0.878041	0.619048	0.897100	1.000
563 GOBP_ORGANOPHOSPHATE_METABOLIC_PROCESS	GO:0019637	8	-0.321259	-0.878735	0.605744	0.901120	1.000
564 GOBP_MITOTIC_CELL_CYCLE	GO:0000278	10	-0.295074	-0.884707	0.584856	0.893021	1.000
565 GOBP_CELL_CYCLE	GO:0007049	21	-0.232014	-0.884755	0.616822	0.898536	1.000
566 GOBP_DIVALENT_INORGANIC_CATION_HOMEOSTASIS	GO:0072507	13	-0.268182	-0.884754	0.605042	0.904078	1.000
567 GOBP_REGULATION_OF_CYTOSOLIC_CALCIIUM_IION_CONCE...	GO:0051480	13	-0.268182	-0.890004	0.606838	0.897193	1.000
568 GOBP_RESPONSE_TO_OXYGEN_CONTAINING_COMPOUND	GO:1901700	39	-0.207382	-0.896827	0.620301	0.887863	1.000
569 REACTOME_UNBLOCKING_OF_NMDA_RECEPTORS_GLUTAMAT...	R-RNO-438066	12	-0.272492	-0.899131	0.563050	0.888443	1.000
570 GOBP_REGULATION_OF_CELL_ADHESION	GO:0030155	13	-0.269920	-0.903591	0.570652	0.883910	1.000
571 GOBP_REGULATION_OF_NEURONAL_SYNAPTIC_PLASTICITY	GO:0048168	7	-0.347838	-0.903920	0.550532	0.888955	1.000
572 GOBP_REGULATION_OF_SYNAPTIC_PLASTICITY	GO:0048167	21	-0.239425	-0.911706	0.595819	0.876946	1.000
573 GOBP_TISSUE_MIGRATION	GO:0090130	9	-0.316349	-0.913044	0.563636	0.879695	1.000
574 GOBP_POSITIVE_REGULATION_OF_TRANSCRIPTION_BY_R...	GO:0045944	24	-0.235271	-0.914474	0.607029	0.882010	1.000
575 GOBP_NUCLEOBASE_CONTAINING_SMALL_MOLECULE_META...	GO:0055086	7	-0.352207	-0.918375	0.519231	0.878980	1.000
576 GOBP_SIGNAL_RELEASE	GO:0023061	14	-0.268200	-0.921973	0.573370	0.876616	1.000
577 GOBP_FATTY_ACID_TRANSPORT	GO:0015908	6	-0.361819	-0.926370	0.524155	0.872310	1.000
578 GOBP_REGULATION_OF_TRANSPORTER_ACTIVITY	GO:0032409	17	-0.266553	-0.928805	0.530547	0.872441	1.000
579 GOBP_CELLULAR_COMPONENT_MAINTENANCE	GO:0043954	5	-0.394519	-0.930372	0.509434	0.874593	1.000
580 GOBP_EMBRYO_DEVELOPMENT_ENDING_IN_BIRTH_OR_EGG...	GO:0009792	9	-0.324472	-0.937194	0.502645	0.864421	1.000
581 GOBP_EXCITATORY_CHEMICAL_SYNAPTIC_TRANSMISSION	GO:0098976	5	-0.409639	-0.937537	0.487245	0.869577	1.000
582 GOBP_REGULATION_OF_CATION_CHANNEL_ACTIVITY	GO:2001257	14	-0.279167	-0.939720	0.539157	0.870167	1.000
583 GOBP_REGULATION_OF_MEMBRANE_POTENTIAL	GO:0042391	17	-0.252523	-0.946615	0.529781	0.859462	1.000
584 GOBP_NEGATIVE_REGULATION_OF_TRANSPORT	GO:0051051	13	-0.288460	-0.947089	0.506631	0.864343	1.000
585 GOBP_INTRACELLULAR_TRANSPORT	GO:0046907	10	-0.316758	-0.947826	0.528875	0.868353	1.000
586 GOBP_TUBE_MORPHOGENESIS	GO:0035239	15	-0.279874	-0.948872	0.501520	0.872055	1.000
587 GOBP_REGULATION_OF_POSTSYNAPTIC_MEMBRANE_POTEN...	GO:0060078	14	-0.279329	-0.949256	0.488439	0.877298	1.000
588 GOBP_RESPONSE_TO_HORMONE	GO:0009725	20	-0.250457	-0.952379	0.524845	0.876172	1.000
589 GOBP_NEGATIVE_REGULATION_OF_CELL_PROJECTION_OR...	GO:0031345	5	-0.412094	-0.952807	0.497449	0.881728	1.000
590 GOBP_DNA_METABOLIC_PROCESS	GO:0066259	6	-0.389550	-0.964045	0.497561	0.860745	1.000
591 GOBP_REGULATION_OF_BODY_FLUID_LEVELS	GO:0050878	11	-0.313154	-0.969118	0.491071	0.855000	1.000
592 GOBP_CELLULAR_RESPONSE_TO_OXYGEN_CONTAINING_CO...	GO:1901701	29	-0.229191	-0.970686	0.501639	0.857879	1.000
593 GOBP_CELL_JUNCTION_ORGANIZATION	GO:0034330	19	-0.263086	-0.976853	0.512195	0.849215	1.000
594 GOBP_PEPITIDYL_LYSINE_MODIFICATION	GO:0018205	5	-0.421687	-0.978067	0.459135	0.852612	1.000
595 GOBP_POSTTRANSCRIPTIONAL_REGULATION_OF_GENE_EX...	GO:0010608	8	-0.355705	-0.982209	0.435530	0.846020	1.000
596 GOBP_CIRCADIEN_RHYTHM	GO:0007623	13	-0.301943	-0.986396	0.448179	0.844412	1.000
597 GOBP_NEGATIVE_REGULATION_OF_CELL_CYCLE	GO:0045786	5	-0.422990	-0.989018	0.439153	0.844602	1.000
598 GOBP_IION_HOMEOSTASIS	GO:0050801	16	-0.285720	-0.992548	0.498442	0.842587	1.000
599 GOBP_NUCLEOSIDE_PHOSPHATE_BIOSYNTHETIC_PROCESS	GO:1901293	5	-0.433867	-0.994340	0.402564	0.844711	1.000

Continuation of Table S8

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
600 GOBP-POSITIVE-REGULATION-OF-CELL-POPULATION.PR...	GO-0008284	21	-0.257296	-0.994828	0.454248	0.850271	1.000
601 REACTOME-ACTIVATION-OF-NMDA-RECEPTORS-AND-POST...	R-RNO-442755	16	-0.285815	-0.997261	0.449686	0.850728	1.000
602 GOBP-ORGANOPHOSPHATE-BIOSYNTHETIC-PROCESS	GO-0090407	5	-0.433867	-1.000910	0.405941	0.848062	1.000
603 GOBP-REGULATION-OF-LYMPHOCYTE-ACTIVATION	GO-0051249	5	-0.432380	-1.002407	0.426316	0.851182	1.000
604 GOBP-CELL-CELL-SIGNALING	GO-0007267	56	-0.228109	-1.011132	0.488722	0.835959	1.000
605 GOBP-SENSORY-ORGAN-DEVELOPMENT	GO-0007423	8	-0.372816	-1.015803	0.442815	0.831057	1.000
606 GOBP-CHROMATIN-ORGANIZATION	GO-0006325	5	-0.440684	-1.017015	0.417874	0.835256	1.000
607 REACTOME-SYNAPTIC-ADHESION-LIKE-MOLECULES	R-RNO-8849932	9	-0.347305	-1.020435	0.400576	0.833454	1.000
608 GOBP-NEUROTRANSMITTER-SECRETION	GO-0007269	6	-0.409184	-1.025063	0.410811	0.828958	1.000
609 GOBP-PEPTIDYL-AMINO-ACID-MODIFICATION	GO-0018193	22	-0.271854	-1.029677	0.386503	0.824282	1.000
610 REACTOME-OPIOID-SIGNALING	R-RNO-111885	12	-0.316767	-1.030936	0.371681	0.828131	1.000
611 REACTOME-G-ALPHA-I-SIGNALING-EVENTS	R-RNO-418594	18	-0.285294	-1.040324	0.395137	0.811748	1.000
612 GOBP-HOMEOSTATIC-PROCESS	GO-0042592	31	-0.246966	-1.042359	0.401274	0.814144	1.000
613 REACTOME-SIGNALING-BY-GPCR	R-RNO-372790	22	-0.270965	-1.046192	0.403786	0.811893	1.000
614 GOBP-EPIDERMIS-DEVELOPMENT	GO-0008544	5	-0.450774	-1.059160	0.340852	0.785794	1.000
615 GOBP-MUSCLE-CONTRACTION	GO-0006936	5	-0.469880	-1.065673	0.361179	0.776254	1.000
616 GOBP-REGULATION-OF-CELL-CELL-ADHESION	GO-0022407	9	-0.366146	-1.069118	0.362117	0.774713	1.000
617 GOBP-CIRCULATORY-SYSTEM-DEVELOPMENT	GO-00072359	21	-0.279545	-1.071580	0.366883	0.775759	1.000
618 GOBP-EMBRYO-DEVELOPMENT	GO-0009790	14	-0.313255	-1.077867	0.348571	0.767392	1.000
619 GOBP-REGULATION-OF-CELL-ACTIVATION	GO-00050865	8	-0.393407	-1.082446	0.331461	0.763416	1.000
620 GOBP-NEURON-MIGRATION	GO-0001764	5	-0.469880	-1.083499	0.332524	0.768072	1.000
621 GOBP-POSITIVE-REGULATION-OF-CELLULAR-PROTEIN-L...	GO-1903829	7	-0.400618	-1.084911	0.338462	0.771478	1.000
622 GOBP-CHEMICAL-HOMEOSTASIS	GO-0048878	23	-0.273175	-1.085782	0.331190	0.776773	1.000
623 REACTOME-HEMOSTASIS	R-RNO-109582	14	-0.320999	-1.086846	0.336449	0.781740	1.000
624 GOBP-REGULATION-OF-SYSTEM-PROCESS	GO-0044057	18	-0.302034	-1.090419	0.305556	0.780171	1.000
625 GOBP-BLOOD-VESSEL-ENDOTHELIAL-CELL-MIGRATION	GO-0043534	8	-0.390442	-1.092668	0.320113	0.782170	1.000
626 GOBP-REPRODUCTIVE-SYSTEM-DEVELOPMENT	GO-0061458	6	-0.450453	-1.095566	0.338624	0.782525	1.000
627 GOBP-ORGANONITROGEN-COMPOUND-BIOSYNTHETIC-PROCESS	GO-1901566	13	-0.324641	-1.096678	0.299145	0.787230	1.000
628 GOBP-PHAGOCYTOSIS	GO-0006909	5	-0.467382	-1.097065	0.316832	0.794352	1.000
629 REACTOME-G-ALPHA-Z-SIGNALING-EVENTS	R-RNO-418597	5	-0.471752	-1.099171	0.322251	0.797661	1.000
630 GOBP-ENDOTHELIAL-CELL-MIGRATION	GO-0043542	8	-0.390442	-1.100108	0.299728	0.803577	1.000
631 GOBP-POSITIVE-REGULATION-OF-APOPTOTIC-SIGNALIN...	GO-2001235	5	-0.468288	-1.100532	0.330864	0.810934	1.000
632 REACTOME-SIGNALING-BY-WNT	R-RNO-195721	7	-0.420337	-1.105882	0.290640	0.805106	1.000
633 GOBP-CALCIUM-ION-TRANSMEMBRANE-TRANSPORT	GO-0070588	7	-0.424147	-1.110710	0.280105	0.800752	1.000
634 GOBP-CALCIUM-ION-TRANSPORT-INTO-CYTOSOL	GO-0060402	7	-0.424147	-1.117466	0.304239	0.792073	1.000
635 GOBP-ENDOMEMBRANE-SYSTEM-ORGANIZATION	GO-0010256	6	-0.449637	-1.117554	0.293532	0.800688	1.000
636 GOBP-CYTOSOLIC-CALCIUM-ION-TRANSPORT	GO-0060401	7	-0.424147	-1.118174	0.289406	0.807864	1.000
637 GOBP-ERK1-AND-ERK2-CASCADE	GO-0070371	5	-0.48402	-1.121050	0.298969	0.808653	1.000
638 GOBP-BLOOD-VESSEL-MORPHOGENESIS	GO-0048514	14	-0.322893	-1.121898	0.268908	0.815701	1.000
639 GOBP-MUSCLE-CELL-DEVELOPMENT	GO-0055001	5	-0.469880	-1.125702	0.278772	0.814871	1.000
640 GOBP-SENSORY_PERCEPTION	GO-0007600	9	-0.387885	-1.130130	0.296296	0.811991	1.000
641 GOBP-GLUTAMATE-RECEPTOR-SIGNALING-PATHWAY	GO-0007215	17	-0.312382	-1.131526	0.258462	0.817675	1.000
642 GOBP-LIPID-LOCALIZATION	GO-0010876	10	-0.374061	-1.132740	0.260054	0.824113	1.000

Continuation of Table S8

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
643	GOBP-ANIMAL-ORGAN-MORPHOGENESIS	12	-0.350059	-1.133052	0.271084	0.833153	1.000
644	GOBP-INTRACELLULAR-PROTEIN-TRANSPORT	8	-0.411156	-1.133831	0.279070	0.840925	1.000
645	GOBP-POSITIVE-REGULATION-OF-PROTEIN-METABOLIC...	27	-0.270975	-1.139933	0.242902	0.832962	1.000
646	GOBP-REGULATION-OF-SECRETION	14	-0.339192	-1.141279	0.253731	0.839358	1.000
647	GOBP-EPITHELIUM-DEVELOPMENT	15	-0.329356	-1.147356	0.266254	0.833476	1.000
648	GOBP-POSITIVE-REGULATION-OF-BIOSYNTHETIC-PROCESS	27	-0.276951	-1.151029	0.224561	0.833618	1.000
649	REACTOME-NEUROTRANSMITTER-RECEPTORS-AND-POSTSY...	22	-0.305125	-1.156845	0.245342	0.827267	1.000
650	GOBP-CELLULAR-RESPONSE-TO-DNA-DAMAGE-STIMULUS	5	-0.492868	-1.157290	0.250000	0.836938	1.000
651	GOBP-REGULATION-OF-TRANSPORT	44	-0.264398	-1.157381	0.242308	0.847915	1.000
652	REACTOME-NEGATIVE-REGULATION-OF-NMDA-RECEPTOR-...	8	-0.425000	-1.165445	0.263587	0.835931	1.000
653	REACTOME-CELL-CYCLE-MITOTIC	5	-0.512472	-1.169057	0.270208	0.836588	1.000
654	REACTOME-G-PROTEIN-MEDIATED-EVENTS	9	-0.404509	-1.176073	0.247222	0.826860	1.000
655	REACTOME-CLASS-C.3-METABOTROPIC-GLUTAMATE-PHER...	7	-0.438878	-1.181698	0.273196	0.822243	1.000
656	GOBP-SECOND-MESSENGER-MEDIATED-SIGNALING	16	-0.335163	-1.181712	0.232416	0.834159	1.000
657	GOBP-RESPONSE-TO-HEAT	7	-0.454547	-1.186666	0.230137	0.832000	1.000
658	GOBP-INORGANIC-ION-TRANSMEMBRANE-TRANSPORT	9	-0.410062	-1.189560	0.220207	0.835034	1.000
659	GOBP-G-PROTEIN-COUPLED-GLUTAMATE-RECEPTOR-SIGN...	8	-0.426943	-1.189989	0.257895	0.846391	1.000
660	GOBP-CELLULAR-MACROMOLECULE-CATABOLIC-PROCESS	5	-0.528778	-1.194974	0.250000	0.844238	1.000
661	GOBP-REGULATION-OF-NMDA-RECEPTOR-ACTIVITY	10	-0.392088	-1.197114	0.238606	0.850653	1.000
662	REACTOME-INTRACELLULAR-SIGNALING-BY-SECOND-MES...	15	-0.354260	-1.198532	0.206395	0.860017	1.000
663	REACTOME-ASSEMBLY-AND-CELL-SURFACE-PRESENTATIO...	8	-0.425000	-1.200109	0.211082	0.868937	1.000
664	REACTOME-PLATELET-ACTIVATION-SIGNALING-AND-AGG...	7	-0.444800	-1.203356	0.240933	0.872798	1.000
665	GOBP-CELLULAR-ION-HOMEOSTASIS	14	-0.353332	-1.203588	0.213855	0.886603	1.000
666	GOBP-TUBE-DEVELOPMENT	18	-0.323425	-1.204573	0.223242	0.898713	1.000
667	REACTOME-CA-DEPENDENT-EVENTS	8	-0.443835	-1.208104	0.223684	0.902534	1.000
668	REACTOME-CREB1-PHOSPHORYLATION-THROUGH-NMDA-RE...	8	-0.441865	-1.213370	0.216285	0.901392	1.000
669	REACTOME-MAPK-FAMILY-SIGNALING-CASCADES	12	-0.368648	-1.216308	0.221239	0.907398	1.000
670	GOBP-RHYTHMIC-PROCESS	15	-0.352485	-1.218955	0.182109	0.915032	1.000
671	GOBP-MUSCLE-ADAPTATION	5	-0.530120	-1.223430	0.199482	0.916755	1.000
672	REACTOME-RHO-GTPASE-EFFECTORS	9	-0.427928	-1.227901	0.188482	0.918985	1.000
673	GOBP-POSITIVE-REGULATION-OF-CATALYTIC-ACTIVITY	29	-0.300557	-1.228735	0.189189	0.933457	1.000
674	GOBP-REGULATION-OF-METAL-ION-TRANSPORT	6	-0.487805	-1.228846	0.219451	0.951338	1.000
675	GOBP-COAGULATION	8	-0.435935	-1.230297	0.223404	0.964718	1.000
676	REACTOME-SIGNALING-BY-RHO-GTPASES-MIRO-GTPASES...	9	-0.427928	-1.231845	0.214076	0.979382	1.000
677	REACTOME-CELL-CYCLE	6	-0.503087	-1.235179	0.189744	0.987031	1.000
678	GOBP-NEGATIVE-REGULATION-OF-MUSCLE-ADAPTATION	5	-0.530120	-1.249901	0.206235	0.954187	1.000
679	GOBP-NEGATIVE-REGULATION-OF-DEVELOPMENTAL-PROCESS	13	-0.387444	-1.255958	0.180124	0.951670	1.000
680	REACTOME-TRAFFICKING-OF-GLUR2-CONTAINING-AMPA-...	8	-0.448863	-1.261993	0.169863	0.950040	1.000
681	REACTOME-TRAFFICKING-OF-AMPA-RECEPTORS	11	-0.407090	-1.273808	0.166227	0.930005	1.000
682	GOBP-TISSUE-MORPHOGENESIS	7	-0.483438	-1.276356	0.171795	0.941928	1.000
683	GOBP-REGULATION-OF-NEUROTRANSMITTER-TRANSPORT	6	-0.532052	-1.285005	0.157754	0.932300	1.000
684	GOBP-SKIN-DEVELOPMENT	5	-0.538375	-1.285045	0.180412	0.954883	1.000
685	GOBP-NEGATIVE-REGULATION-OF-CELL-DIFFERENTIATION	13	-0.387444	-1.291267	0.178082	0.955441	1.000

Continuation of Table S8

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
686 REACTOME_PROTEIN_PROTEIN_INTERACTIONS.AT_SYNAPSES	R-RNO-6794362	12	-0.401472	-1.294725	0.150142	0.965416	1.000
687 REACTOME_RAS_ACTIVATION.UPON_CA2_INFLUX_THROUGH...	R-HSA-442982	6	-0.524390	-1.296099	0.176623	0.986077	1.000
688 GOBP_VASCULATURE_DEVELOPMENT	GO-0001944	17	-0.347857	-1.301902	0.142395	0.989233	1.000
689 GOBP_REGULATION_OF_NEUROTRANSMITTER_LEVELS	GO-0001505	7	-0.500127	-1.309387	0.145553	0.988354	1.000
690 GOBP_RESPONSE_TO_TEMPERATURE_STIMULUS	GO-0009266	9	-0.453829	-1.309628	0.125000	1.000000	1.000
691 GOBP_MYOTUBE_DIFFERENTIATION	GO-0014902	5	-0.561243	-1.323961	0.145320	0.988590	1.000
692 GOBP_CELLULAR_HOMEOSTASIS	GO-0019725	18	-0.362388	-1.325645	0.116208	1.000000	1.000
693 REACTOME_TRANSMISSION_ACROSS_CHEMICAL_SYNAPSES	R-RNO-112315	23	-0.342572	-1.338900	0.106628	0.991694	1.000
694 GOBP_POSITIVE_REGULATION_OF_EPITHELIAL_CELL_PR...	GO-0050679	7	-0.509509	-1.340526	0.131054	1.000000	1.000
695 GOBP_ORGANIC_ANION_TRANSPORT	GO-0015711	6	-0.536585	-1.346933	0.134434	1.000000	1.000
696 GOBP_POSITIVE_REGULATION_OF_NUCLEOBASE_CONTAIN...	GO-0045935	28	-0.331436	-1.352039	0.095082	1.000000	1.000
697 REACTOME_BETA_CATENIN_INDEPENDENT_WNT_SIGNALING	R-RNO-3858494	5	-0.588614	-1.352726	0.165816	1.000000	1.000
698 GOBP_POSITIVE_REGULATION_OF_ENDOTHELIAL_CELL_P...	GO-0001938	6	-0.539942	-1.358840	0.118090	1.000000	1.000
699 GOBP_CARBOXYLIC_ACID_TRANSPORT	GO-0046942	6	-0.536585	-1.359162	0.121287	1.000000	1.000
700 GOBP_CALCIIUM_ION_TRANSPORT	GO-0006816	11	-0.441558	-1.361395	0.140162	1.000000	1.000
701 GOBP_NEUROTRANSMITTER_TRANSPORT	GO-0006836	7	-0.500127	-1.363157	0.118132	1.000000	1.000
702 GOBP_AMINO_ACID_TRANSPORT	GO-0006865	6	-0.536585	-1.369402	0.116580	1.000000	1.000
703 GOBP_METAL_ION_TRANSPORT	GO-0030001	11	-0.441558	-1.370622	0.123494	1.000000	1.000
704 GOBP_SPROUTING_ANGIOGENESIS	GO-0002040	5	-0.593774	-1.381245	0.105911	1.000000	1.000
705 GOBP_PLATELET_ACTIVATION	GO-0030168	6	-0.561841	-1.399578	0.101604	1.000000	1.000
706 GOBP_REGULATION_OF_MUSCLE_SYSTEM_PROCESS	GO-0090257	8	-0.487500	-1.399604	0.090659	1.000000	1.000
707 GOBP_CHROMOSOME_ORGANIZATION	GO-0051276	6	-0.565826	-1.412235	0.100756	1.000000	1.000
708 GOBP_TAXIS	GO-0042330	14	-0.427532	-1.434595	0.092308	1.000000	1.000
709 GOBP_NEURON_PROJECTION_GUIDANCE	GO-0097485	9	-0.498428	-1.448268	0.093093	1.000000	1.000
710 GOBP_MUSCLE_SYSTEM_PROCESS	GO-0003012	9	-0.493671	-1.448345	0.086592	1.000000	1.000
711 GOBP_ENDOTHELIAL_CELL_PROLIFERATION	GO-0001935	8	-0.520087	-1.450953	0.087324	1.000000	1.000
712 REACTOME_G_ALPHA_Q_SIGNALING_EVENTS	R-RNO-416476	6	-0.575778	-1.452381	0.097884	1.000000	1.000
713 GOBP_EPITHELIAL_CELL_PROLIFERATION	GO-0050673	12	-0.447118	-1.456253	0.078550	1.000000	1.000
714 REACTOME_NEURONAL_SYSTEM	R-RNO-112316	26	-0.372852	-1.458926	0.032468	1.000000	1.000
715 GOBP_MULTICELLULAR_ORGANISMAL_RESPONSE_TO_STRESS	GO-0033555	5	-0.629350	-1.469535	0.096774	1.000000	1.000
716 REACTOME_NEUREXINS_AND_NEUROLIGINS	R-RNO-6794361	9	-0.525013	-1.471839	0.086826	1.000000	1.000
717 GOBP_DICARBOXYLIC_ACID_TRANSPORT	GO-0006835	5	-0.650602	-1.490914	0.078385	1.000000	1.000
718 GOBP_REGULATION_OF_PROTEIN_TYROSINE_KINASE_ACT...	GO-0061097	5	-0.664016	-1.512291	0.083933	1.000000	1.000
719 GOBP_MONOCARBOXYLIC_ACID_TRANSPORT	GO-0015718	5	-0.650602	-1.521315	0.062331	1.000000	1.000
720 GOBP_ACIDIC_AMINO_ACID_TRANSPORT	GO-0015800	5	-0.650602	-1.528778	0.069767	1.000000	1.000
721 GOBP_POSITIVE_REGULATION_OF_PROTEIN_TYROSINE_K...	GO-0061098	5	-0.664016	-1.528883	0.058081	1.000000	1.000
722 GOBP_EMBRYONIC_MORPHOGENESIS	GO-0048598	6	-0.651750	-1.588475	0.056266	1.000000	1.000
723 GOBP_LIPID_EXPORT_FROM_CELL	GO-0140353	5	-0.732434	-1.707909	0.036765	1.000000	0.998
724 GOBP_ANATOMICAL_STRUCTURE_FORMATION_INVOLVED_I...	GO-0048646	20	-0.483673	-1.861030	0.010000	1.000000	0.903

End of Table

Supplementary Table S9: SC cervical segment early profile (8 DPL peak) GSEA results.

Begin of Table S9									
	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val	
0	REACTOME_INTERLEUKIN_4_AND_INTERLEUKIN_13_SIGNALING	R-RNO-6785807	8	0.767776	1.928067	0.003279	1.000000	0.626	
1	GOBP_REGULATION_OF_DEFENSE_RESPONSE	GO-0031347	7	0.708593	1.789521	0.019830	1.000000	0.951	
2	GOBP_EPITHELIAL_CELL_DIFFERENTIATION	GO-0030855	7	0.692776	1.758604	0.021538	1.000000	0.981	
3	GOBP_MULTICELLULAR_ORGANISM_PROCESS	GO-0044706	8	0.663654	1.750552	0.018576	1.000000	0.982	
4	GOBP_REGULATION_OF_INFLAMMATORY_RESPONSE	GO-0050727	7	0.708593	1.685824	0.036810	1.000000	0.997	
5	GOBP_INFLAMMATORY_RESPONSE	GO-0006954	12	0.558444	1.672846	0.010345	1.000000	0.999	
6	GOBP_OSTEOCLAST_DIFFERENTIATION	GO-0030316	6	0.731707	1.671057	0.022727	1.000000	0.999	
7	GOBP_GENERATION_OF_PRECURSOR_METABOLITES_AND_E...	GO-0006091	5	0.750803	1.661808	0.041436	1.000000	0.999	
8	GOBP_POLYSACCHARIDE_METABOLIC_PROCESS	GO-0005976	5	0.750910	1.635348	0.038567	1.000000	0.999	
9	REACTOME_SIGNALING_BY_INTERLEUKINS	R-RNO-449147	15	0.484726	1.621109	0.022059	1.000000	1.000	
10	GOBP_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	GO-0045670	5	0.722892	1.596826	0.057065	1.000000	1.000	
11	GOBP_OSTEOBLAST_DIFFERENTIATION	GO-0001649	5	0.734940	1.596129	0.056497	0.985193	1.000	
12	GOBP_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	GO-0097191	7	0.634945	1.590985	0.047059	0.933322	1.000	
13	GOBP_CYTOKINE_MEDIATED_SIGNALING_PATHWAY	GO-0019221	16	0.465831	1.569645	0.053232	0.960134	1.000	
14	GOBP_OSSIFICATION	GO-0001503	9	0.559035	1.526269	0.053628	1.000000	1.000	
15	GOBP_NEGATIVE_REGULATION_OF_PEPTIDASE_ACTIVITY	GO-0010466	6	0.653057	1.510690	0.076487	1.000000	1.000	
16	GOBP_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CEL...	GO-1904375	6	0.628164	1.497259	0.087324	1.000000	1.000	
17	GOBP_RESPONSE_TO_MECHANICAL_STIMULUS	GO-0009612	6	0.616665	1.495942	0.086455	1.000000	1.000	
18	GOBP_RESPONSE_TO_NUTRIENT	GO-0007584	5	0.667798	1.480369	0.120000	1.000000	1.000	
19	GOBP_RAS_PROTEIN_SIGNAL_TRANSDUCTION	GO-0007265	5	0.674900	1.465923	0.115068	1.000000	1.000	
20	GOBP_POSITIVE_REGULATION_OF_DEFENSE_RESPONSE	GO-0031349	5	0.658415	1.462696	0.089337	1.000000	1.000	
21	GOBP_POSITIVE_REGULATION_OF_CELL_GROWTH	GO-0030307	6	0.605973	1.452327	0.090643	1.000000	1.000	
22	GOBP_IN_UTERO_EMBRYONIC_DEVELOPMENT	GO-0001701	8	0.536433	1.440167	0.087948	1.000000	1.000	
23	GOBP_REPRODUCTION	GO-0000003	18	0.405538	1.409598	0.092105	1.000000	1.000	
24	GOBP_REGULATION_OF_BINDING	GO-0051098	11	0.484832	1.393095	0.097902	1.000000	1.000	
25	GOBP_PEPTIDE_METABOLIC_PROCESS	GO-0006518	11	0.475329	1.390729	0.082508	1.000000	1.000	
26	GOBP_LONG_TERM_SYNAPTIC_DEPRESSION	GO-0060292	5	0.632276	1.390187	0.139276	1.000000	1.000	
27	REACTOME_SIGNALING_BY_RECEPTOR_TYROSINE_KINASES	R-RNO-9006934	26	0.367065	1.378060	0.057692	1.000000	1.000	
28	GOBP_RESPONSE_TO_CYTOKINE	GO-0034097	23	0.372673	1.377423	0.069565	1.000000	1.000	
29	GOBP_SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCTION	GO-0007264	8	0.519251	1.348391	0.108696	1.000000	1.000	
30	GOBP_DEVELOPMENTAL_CELL_GROWTH	GO-0048588	5	0.619809	1.346352	0.156069	1.000000	1.000	
31	GOBP_REGULATION_OF_CARBOHYDRATE_BIOSYNTHETIC_P...	GO-0043255	5	0.594394	1.328837	0.168022	1.000000	1.000	
32	GOBP_GLUCOSE_METABOLIC_PROCESS	GO-0006006	6	0.548583	1.312218	0.157738	1.000000	1.000	
33	GOBP_CARBOHYDRATE_BIOSYNTHETIC_PROCESS	GO-0016051	5	0.594394	1.308581	0.200000	1.000000	1.000	
34	GOBP_POSITIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL...	GO-0048661	5	0.593711	1.304581	0.167614	1.000000	1.000	
35	GOBP_POSITIVE_REGULATION_OF_TRANSMEMBRANE_TRAN...	GO-0034764	7	0.513621	1.298830	0.136232	1.000000	1.000	
36	GOBP_MULTIORGANISM_PROCESS	GO-0051704	16	0.385276	1.296868	0.107807	1.000000	1.000	
37	GOBP_CARBOHYDRATE_METABOLIC_PROCESS	GO-0005975	9	0.477514	1.294860	0.157556	1.000000	1.000	
38	REACTOME_DEATH_RECEPTOR_SIGNALING	R-RNO-73887	5	0.592523	1.286264	0.195402	1.000000	1.000	
39	GOBP_CELLULAR_AMIDE_METABOLIC_PROCESS	GO-0043603	12	0.420567	1.286013	0.150538	1.000000	1.000	
40	GOBP_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNAL...	GO-2001236	6	0.544395	1.283536	0.178470	1.000000	1.000	

Continuation of Table S9

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
41	GOBP-REGULATION-OF-CARBOHYDRATE-METABOLIC-PROCESS	5	0.594394	1.282522	0.172414	1.000000	1.000
42	GOBP-MONOSACCHARIDE-METABOLIC-PROCESS	6	0.548583	1.282405	0.163793	1.000000	1.000
43	GOBP-POSITIVE-REGULATION-OF-GROWTH	9	0.464107	1.278091	0.174757	0.998510	1.000
44	GOBP-POSITIVE-REGULATION-OF-CELL-CELL-ADHESION	5	0.575633	1.276241	0.186667	0.983010	1.000
45	GOBP-NEGATIVE-REGULATION-OF-BINDING	6	0.546279	1.275935	0.173789	0.962643	1.000
46	GOBP-POSITIVE-REGULATION-OF-CYTOKINE-PRODUCTION	7	0.532139	1.271587	0.180473	0.956415	1.000
47	REACTOME_POST_TRANSLATIONAL-PROTEIN-MODIFICATION	7	0.509963	1.270654	0.176966	0.939635	1.000
48	REACTOME_TRANSCRIPTIONAL-REGULATION-OF-WHITE-A...	6	0.547506	1.267404	0.187683	0.931890	1.000
49	HALLMARK-KRAS-SIGNALING-UP	6	0.536219	1.262271	0.191950	0.930447	1.000
50	GOBP-MEMBRANE-PROTEIN-PROTEOLYSIS	6	0.534891	1.254472	0.221212	0.937499	1.000
51	GOBP-REGULATION-OF-CELLULAR-COMPONENT-SIZE	7	0.502345	1.252849	0.183544	0.925194	1.000
52	GOBP-PATTERN-SPECIFICATION-PROCESS	6	0.534629	1.242617	0.205797	0.941839	1.000
53	GOBP-REGIONALIZATION	6	0.534629	1.238482	0.183381	0.936612	1.000
54	GOBP-PROTEOLYSIS	17	0.368615	1.236575	0.175781	0.925322	1.000
55	REACTOME_NGF-STIMULATED-TRANSCRIPTION	9	0.441279	1.236553	0.196078	0.908865	1.000
56	GOBP-POSITIVE-REGULATION-OF-LEUKOCYTE-CELL-CEL...	5	0.575633	1.234217	0.223757	0.900205	1.000
57	GOBP-NEGATIVE-REGULATION-OF-CYSTEINE-TYPE-ENDO...	5	0.573224	1.229107	0.228986	0.900715	1.000
58	GOBP-DEFENSE-RESPONSE	19	0.361430	1.224563	0.155462	0.898626	1.000
59	HALLMARK-P13K-AKT-MTOR-SIGNALING	6	0.523310	1.214547	0.253687	0.914960	1.000
60	GOBP-TEMPERATURE-HOMEOSTASIS	21	0.564242	1.214039	0.221607	0.901204	1.000
61	REACTOME-CYTOKINE-SIGNALING-IN-IMMUNE-SYSTEM	5	0.356403	1.212873	0.199095	0.890125	1.000
62	GOBP-NEGATIVE-REGULATION-OF-MOLECULAR-FUNCTION	24	0.324624	1.206548	0.182266	0.894735	1.000
63	GOBP-NEGATIVE-REGULATION-OF-PROTEOLYSIS	8	0.464175	1.204284	0.236760	0.888220	1.000
64	GOBP-REGULATION-OF-PROTEIN-LOCALIZATION-TO-MEM...	7	0.487920	1.202228	0.240356	0.881018	1.000
65	GOBP-RESPONSE-TO-CADMIUM-ION	6	0.520517	1.202068	0.236025	0.868127	1.000
66	GOBP-REGULATION-OF-PROTEIN-BINDING	7	0.479152	1.201862	0.216463	0.855745	1.000
67	GOBP-LEUKOCYTE-CELL-CELL-ADHESION	6	0.507905	1.201333	0.230114	0.844824	1.000
68	GOBP-REGULATION-OF-CELL-DIFFERENTIATION	36	0.290006	1.179317	0.181347	0.900187	1.000
69	GOBP-CELLULAR-COMPONENT-DISASSEMBLY	6	0.498423	1.172343	0.259036	0.910011	1.000
70	GOBP-POSITIVE-REGULATION-OF-GENE-EXPRESSION	16	0.360265	1.169380	0.214022	0.906714	1.000
71	GOBP-RESPONSE-TO-LIGHT-STIMULUS	11	0.394086	1.163322	0.234043	0.897225	1.000
72	GOBP-CELLULAR-CARBOHYDRATE-METABOLIC-PROCESS	5	0.523302	1.159699	0.262599	0.911457	1.000
73	GOBP-REGULATION-OF-DEVELOPMENTAL-GROWTH	9	0.423354	1.150867	0.235880	0.907692	1.000
74	GOBP-EMBRYONIC-ORGAN-DEVELOPMENT	7	0.458922	1.153741	0.265244	0.904990	1.000
75	GOBP-POSITIVE-REGULATION-OF-DEVELOPMENTAL-GROWTH	8	0.439802	1.146351	0.248322	0.915290	1.000
76	REACTOME-ESTROGEN-DEPENDENT-NUCLEAR-EVENTS-DOW...	5	0.514740	1.139324	0.267516	0.923706	1.000
77	GOBP-POSITIVE-REGULATION-OF-IMMUNE-SYSTEM-PROCESS	18	0.330097	1.128884	0.273092	0.945679	1.000
78	GOBP-NEGATIVE-REGULATION-OF-SYNAPTIC-TRANSMISSION	6	0.463415	1.121776	0.262346	0.956663	1.000
79	GOBP-RESPONSE-TO-RADIATION	13	0.348463	1.120541	0.270073	0.948973	1.000
80	REACTOME-EXTRA-NUCLEAR-ESTROGEN-SIGNALING	7	0.444811	1.118851	0.352201	0.942883	1.000
81	GOBP-POSITIVE-REGULATION-OF-CELL-DIFFERENTIATION	27	0.296063	1.116553	0.288991	0.938608	1.000
82	GOBP-INOSITOL-LIPID-MEDIATED-SIGNALING	8	0.415065	1.114769	0.303797	0.932846	1.000
83	GOBP-REGULATION-OF-NEURON-PROJECTION-DEVELOPMENT	16	0.341137	1.110784	0.298387	0.933959	1.000

Continuation of Table S9

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
84	GOBP-ORGAN_GROWTH	5	0.500075	1.109664	0.287293	0.926466	1.000
85	GOBP-REGULATION_OF_CELL_DEVELOPMENT	15	0.351812	1.108910	0.319703	0.917965	1.000
86	GOBP-AMYLOID-PRECURSOR_PROTEIN_CATABOLIC_PROCESS	5	0.504594	1.107742	0.310924	0.910976	1.000
87	GOBP-AMYLOID-BETA-METABOLIC_PROCESS	5	0.504594	1.098848	0.321127	0.927831	1.000
88	HALLMARK-APOPTOSIS	6	0.470030	1.097675	0.275964	0.920801	1.000
89	GOBP-NEGATIVE-REGULATION_OF-PROTEIN-METABOLIC-...	20	0.309291	1.092760	0.296943	0.925408	1.000
90	GOBP-AMYLOID-PRECURSOR_PROTEIN-METABOLIC_PROCESS	5	0.504594	1.091440	0.331288	0.919090	1.000
91	GOBP-GLIAL-CELL-DIFFERENTIATION	10	0.381631	1.088551	0.302181	0.918071	1.000
92	GOBP-REGULATION_OF-NEURON-DIFFERENTIATION	5	0.502021	1.081772	0.339474	0.928593	1.000
93	GOBP-ENZYME-LINKED-RECEPTOR_PROTEIN-SIGNALING-...	24	0.294322	1.079026	0.357143	0.927382	1.000
94	GOBP-MATERNAL_PROCESS_INVOLVED_IN-FEMALE-PREGN...	5	0.493982	1.076724	0.324022	0.925090	1.000
95	GOBP-POSITIVE-REGULATION_OF-BINDING	6	0.462931	1.073787	0.355623	0.924552	1.000
96	GOBP-REGULATION_OF-ORGAN_GROWTH	5	0.500075	1.073762	0.345946	0.915146	1.000
97	GOBP-GLIOGENESIS	12	0.355263	1.070045	0.318033	0.917070	1.000
98	GOBP-MUSCLE-TISSUE-DEVELOPMENT	11	0.355426	1.061522	0.385382	0.932426	1.000
99	GOBP-RESPONSE-TO-NERVE-GROWTH-FACTOR	7	0.421744	1.057429	0.346749	0.935413	1.000
100	GOBP-POSITIVE-REGULATION_OF_PRL-MIRNA-TRANSCRIPT...	7	0.419753	1.052141	0.375723	0.942053	1.000
101	GOBP-PROTEIN_KINASE-B-SIGNALING	6	0.432191	1.049199	0.378698	0.941995	1.000
102	GOBP-PRL-MIRNA-TRANSCRIPTION_BY-RNA-POLYMERASE-II	7	0.419753	1.042930	0.378698	0.952045	1.000
103	GOBP-EMBRYO-DEVELOPMENT	14	0.330697	1.041867	0.402135	0.946044	1.000
104	GOBP-REGULATION_OF-NERVOUS-SYSTEM-DEVELOPMENT	15	0.322037	1.034656	0.389286	0.959105	1.000
105	GOBP-EMBRYO-DEVELOPMENT-ENDING_IN-BIRTH-OR-EGG...	9	0.386860	1.031723	0.385135	0.958757	1.000
106	GOBP-RESPONSE-TO-UV	5	0.484419	1.030987	0.395543	0.952226	1.000
107	GOBP-DEVELOPMENTAL-PROCESS_INVOLVED_IN-REPRODU...	11	0.353857	1.027703	0.411765	0.953442	1.000
108	GOBP-REGULATION_OF-ANION-TRANSMEMBRANE-TRANSPORT	5	0.464476	1.027488	0.372928	0.945357	1.000
109	GOBP-POSTSYNAPSE-ORGANIZATION	10	0.352042	1.027474	0.358108	0.936830	1.000
110	GOBP-DENDRITIC-SPINE-MORPHOGENESIS	5	0.460004	1.026925	0.381215	0.930023	1.000
111	GOBP-FC-RECEPTOR-SIGNALING-PATHWAY	8	0.383509	1.026480	0.410828	0.922961	1.000
112	GOBP-MULTICELLULAR-ORGANISM-REPRODUCTION	12	0.345784	1.026158	0.390728	0.915632	1.000
113	GOBP-MONOCARBOXYLIC-ACID-METABOLIC-PROCESS	6	0.430262	1.022932	0.389041	0.917172	1.000
114	GOBP-TRANSMEMBRANE-RECEPTOR_PROTEIN-TYROSINE-K...	19	0.302160	1.021616	0.397541	0.913085	1.000
115	GOBP-POSITIVE-REGULATION_OF-ION-TRANSPORT	17	0.303428	1.018016	0.430712	0.915224	1.000
116	GOBP-REGULATION_OF-CELLULAR-AMIDE-METABOLIC-PR...	9	0.380688	1.012514	0.381579	0.923090	1.000
117	GOBP-DENDRITIC-SPINE-DEVELOPMENT	6	0.437552	1.012193	0.408669	0.916264	1.000
118	GOBP-CELLULAR-RESPONSE-TO-CADMIUM-ION	5	0.458766	1.009430	0.397101	0.916537	1.000
119	GOBP-NEGATIVE-REGULATION_OF-LOCOMOTION	5	0.468553	1.007406	0.399417	0.914625	1.000
120	GOBP-NEGATIVE-REGULATION_OF-CELL-DEATH	22	0.279246	1.007133	0.452000	0.907908	1.000
121	REACTOME-SIGNALING-BY-NTRKS	18	0.300663	1.006880	0.429150	0.901166	1.000
122	GOBP-REGULATION_OF-CELL_CYCLE_PROCESS	5	0.464060	1.005042	0.406162	0.898734	1.000
123	GOBP-GLAND-DEVELOPMENT	7	0.392263	1.004778	0.436047	0.892251	1.000
124	GOBP-REGULATION_OF-POSTSYNAPSE-ORGANIZATION	6	0.414950	1.002934	0.426332	0.890159	1.000
125	REACTOME-NUCLEAR-EVENTS-KINASE-AND-TRANSCRIPTI...	11	0.336360	1.000049	0.441472	0.891347	1.000
126	GOBP-REGULATION_OF-CELL_CYCLE	13	0.324016	0.998656	0.441860	0.887933	1.000

Continuation of Table S9

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
127	GOBP-PERIPHERAL-NEUROUS-SYSTEM-DEVELOPMENT	GO-0007422	9	0.369745	0.995337	0.450658	0.890587	1.000
128	GOBP-APOPTOTIC-MITOCHONDRIAL-CHANGES	GO-0008637	6	0.417116	0.995061	0.426791	0.884472	1.000
129	GOBP-GAMETE-GENERATION	GO-0007276	9	0.353893	0.993465	0.457516	0.881802	1.000
130	REACTOME-EXTRACELLULAR-MATRIX-ORGANIZATION	R-RNO-1474244	5	0.449152	0.991652	0.428571	0.879964	1.000
131	GOBP-IMMUNE-RESPONSE-REGULATING-SIGNALING-PATHWAY	GO-000276	8	0.38509	0.989370	0.413907	0.879389	1.000
132	GOBP-HEART-DEVELOPMENT	GO-0007507	6	0.427288	0.986574	0.427245	0.879705	1.000
133	GOBP-REGULATION-OF-CELLULAR-CATABOLIC-PROCESS	GO-0031329	10	0.340760	0.977764	0.454545	0.895431	1.000
134	REACTOME-ESR-MEDIATED-SIGNALING	R-RNO-8939211	8	0.363962	0.977721	0.480519	0.888962	1.000
135	GOBP-CELL-MIGRATION	GO-0016477	22	0.265978	0.976290	0.489362	0.886158	1.000
136	GOBP-POSITIVE-REGULATION-OF-ANION-TRANSPORT	GO-1903793	9	0.354083	0.972301	0.438775	0.890388	1.000
137	GOBP-CARDIAC-MUSCLE-TISSUE-DEVELOPMENT	GO-0048738	6	0.427288	0.972158	0.454810	0.884296	1.000
138	REACTOME-SIGNALING-BY-NUCLEAR-RECEPTORS	R-RNO-9006931	8	0.363962	0.970168	0.462025	0.883506	1.000
139	GOBP-NEGATIVE-REGULATION-OF-RESPONSE-TO-EXTERN...	GO-0032102	5	0.440093	0.966406	0.449315	0.886825	1.000
140	GOBP-REGULATION-OF-GLIOGENESIS	GO-0014013	5	0.445783	0.965524	0.465116	0.882733	1.000
141	GOBP-RESPONSE-TO-ENDOGENOUS-STIMULUS	GO-0009719	34	0.248457	0.964608	0.550898	0.878647	1.000
142	GOBP-POSITIVE-REGULATION-OF-GLIOGENESIS	GO-0014015	5	0.445783	0.963776	0.469444	0.874774	1.000
143	GOBP-NEGATIVE-REGULATION-OF-MULTICELLULAR-ORGA...	GO-0051241	15	0.294671	0.962372	0.507634	0.872311	1.000
144	GOBP-NEGATIVE-REGULATION-OF-CATALYTIC-ACTIVITY	GO-0043086	17	0.277438	0.962310	0.500000	0.866442	1.000
145	GOBP-DEVELOPMENTAL-GROWTH	GO-0048589	10	0.344285	0.959631	0.531987	0.867501	1.000
146	GOBP-T-CELL-ACTIVATION	GO-0042110	8	0.374121	0.954632	0.495177	0.874260	1.000
147	GOBP-REGULATION-OF-INTRACELLULAR-SIGNAL-TRANSD...	GO-1902531	21	0.259226	0.943041	0.545852	0.896659	1.000
148	GOBP-NEGATIVE-REGULATION-OF-HYDROLASE-ACTIVITY	GO-0051346	11	0.318842	0.942035	0.526132	0.893067	1.000
149	GOBP-REGULATION-OF-CELL-SIZE	GO-0008361	5	0.440325	0.941803	0.492997	0.887749	1.000
150	GOBP-CARBOHYDRATE-DERIVATIVE-METABOLIC-PROCESS	GO-1901135	8	0.350714	0.931347	0.542587	0.909191	1.000
151	GOBP-REGULATION-OF-MULTICELLULAR-ORGANISMAL-DE...	GO-2000026	31	0.230075	0.922797	0.567416	0.925144	1.000
152	GOBP-RESPONSE-TO-NICOTINE	GO-0035094	7	0.370643	0.909068	0.545181	0.954898	1.000
153	GOBP-IMPORT-INTO-CELL	GO-0098657	6	0.379374	0.907303	0.532213	0.953187	1.000
154	GOBP-LOCOMOTION	GO-0040011	31	0.236258	0.906797	0.594872	0.948163	1.000
155	GOBP-ENDOCRINE-SYSTEM-DEVELOPMENT	GO-0035270	6	0.388898	0.902097	0.579288	0.954758	1.000
156	REACTOME-TOLL-LIKE-RECEPTOR-9-TLR9-CASCADE	R-RNO-168138	8	0.337500	0.896703	0.549689	0.962957	1.000
157	GOBP-POSITIVE-REGULATION-OF-INTRACELLULAR-SIGN...	GO-1902533	14	0.277580	0.891259	0.595420	0.970657	1.000
158	GOBP-POSITIVE-REGULATION-OF-NEUROUS-SYSTEM-DEV...	GO-0051962	12	0.291392	0.888685	0.615385	0.970968	1.000
159	GOBP-REGULATION-OF-LONG-TERM-SYNAPTIC-POTENTIAL...	GO-1900271	6	0.395831	0.887837	0.569697	0.967162	1.000
160	GOBP-POSITIVE-REGULATION-OF-CELL-DEVELOPMENT	GO-0010720	12	0.291392	0.887195	0.577358	0.962792	1.000
161	GOBP-MORPHOGENESIS-OF-AN-EPITHELIUM	GO-0002009	6	0.377364	0.885672	0.546828	0.960547	1.000
162	GOBP-REGULATION-OF-CELL-DEATH	GO-0010941	34	0.218658	0.885106	0.702857	0.956140	1.000
163	GOBP-CELL-CYCLE	GO-0007049	21	0.240702	0.876333	0.660944	0.972277	1.000
164	REACTOME-TOLL-LIKE-RECEPTOR-TLR1-TLR2-CASCADE	R-RNO-168179	8	0.337500	0.876317	0.604317	0.966671	1.000
165	REACTOME-TOLL-LIKE-RECEPTOR-CASCADES	R-RNO-168898	8	0.337500	0.874003	0.595469	0.966368	1.000
166	GOBP-ACTIVATION-OF-PROTEIN-KINASE-ACTIVITY	GO-0032147	10	0.302661	0.866458	0.660131	0.979557	1.000
167	GOBP-POSITIVE-REGULATION-OF-DEVELOPMENTAL-PROCESS	GO-0051094	32	0.219987	0.866439	0.677596	0.973791	1.000
168	GOBP-EPITHELIUM-DEVELOPMENT	GO-0060429	15	0.268780	0.864150	0.656604	0.973216	1.000
169	REACTOME-MYD88-INDEPENDENT-TLR4-CASCADE	R-RNO-166166	8	0.337500	0.860872	0.634375	0.975466	1.000

Continuation of Table S9

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
170 HALLMARK-UV-RESPONSE-UP	M5941	5	0.380834	0.857676	0.581538	0.977320	1.000
171 GOBP-REGULATION-OF-FAT-CELL-DIFFERENTIATION	GO-0045598	6	0.360765	0.857424	0.622590	0.972265	1.000
172 GOBP-POSITIVE-REGULATION-OF-NEUROGENESIS	GO-0050769	12	0.291392	0.857152	0.657895	0.967351	1.000
173 GOBP-REGULATION-OF-PEPTIDASE-ACTIVITY	GO-0052547	10	0.300129	0.856048	0.635783	0.964313	1.000
174 GOBP-REGULATION-OF-PROTEIN-LOCALIZATION	GO-0032880	18	0.241293	0.854419	0.687243	0.962496	1.000
175 GOBP-RESPONSE-TO-ACID-CHEMICAL	GO-0001101	6	0.353659	0.853122	0.615152	0.959845	1.000
176 GOBP-SMOOTH-MUSCLE-CELL-PROLIFERATION	GO-0048659	6	0.361882	0.849872	0.628895	0.962135	1.000
177 GOBP-CELL-GROWTH	GO-0016049	10	0.304418	0.844790	0.655063	0.968732	1.000
178 REACTOME-TRANSCRIPTIONAL-REGULATION-BY-TP53	R-RNO-3700989	6	0.362333	0.839633	0.634730	0.976080	1.000
179 GOBP-MUSCLE-ORGAN-DEVELOPMENT	GO-0007517	9	0.321487	0.837925	0.656463	0.974391	1.000
180 GOBP-REGULATION-OF-CELLULAR-PROTEIN-LOCALIZATION	GO-1903827	12	0.274621	0.835583	0.685512	0.974267	1.000
181 REACTOME-SENESCENCE-ASSOCIATED-SECRETORY-PHENO...	R-RNO-2559582	6	0.353990	0.830590	0.671429	0.980248	1.000
182 GOBP-REGULATION-OF-IMMUNE-SYSTEM-PROCESS	GO-0002682	21	0.236060	0.829946	0.733945	0.976614	1.000
183 GOBP-REGULATION-OF-NEUROGENESIS	GO-0050767	14	0.262496	0.828976	0.676976	0.973571	1.000
184 GOBP-AGING	GO-0007568	13	0.273130	0.828297	0.746032	0.969825	1.000
185 GOBP-ANION-TRANSMEMBRANE-TRANSPORT	GO-0098656	7	0.331314	0.827087	0.667598	0.967110	1.000
186 REACTOME-CELLULAR-SENESCENCE	R-RNO-2559583	6	0.353990	0.822443	0.696049	0.971927	1.000
187 GOBP-MUSCLE-CELL-DEVELOPMENT	GO-0055001	5	0.373862	0.818293	0.653959	0.976029	1.000
188 REACTOME-EPHLEPHRIN-SIGNALING	R-RNO-268233	6	0.344023	0.817183	0.664671	0.973255	1.000
189 GOBP-ACTIVATION-OF-IMMUNE-RESPONSE	GO-0002253	5	0.385484	0.816883	0.676471	0.968796	1.000
190 GOBP-REGULATION-OF-SMALL-MOLECULE-METABOLIC-PR...	GO-0062012	9	0.308172	0.814057	0.694245	0.969794	1.000
191 GOBP-NEGATIVE-REGULATION-OF-CELL-DEVELOPMENT	GO-0010721	6	0.343232	0.802302	0.676829	0.989877	1.000
192 GOBP-REGULATION-OF-PROTEIN-SERINE-THREONINE-KI...	GO-0071900	12	0.264284	0.798992	0.738182	0.991716	1.000
193 GOBP-LEUKOCYTE-MIGRATION	GO-0050900	6	0.334715	0.789060	0.725948	1.000000	1.000
194 GOBP-CELLULAR-RESPONSE-TO-ABIOTIC-STIMULUS	GO-0071214	7	0.318873	0.785546	0.737374	1.000000	1.000
195 GOBP-MEMORY	GO-0007613	13	0.256270	0.780718	0.776557	1.000000	1.000
196 GOBP-IMMUNE-EFFECTOR-PROCESS	GO-0002252	11	0.278438	0.780471	0.758278	1.000000	1.000
197 GOBP-RESPONSE-TO-CALCIUM-ION	GO-0051592	6	0.334890	0.778812	0.719547	1.000000	1.000
198 REACTOME-INTERLEUKIN-17-SIGNALING	R-RNO-448424	6	0.329268	0.778653	0.698225	1.000000	1.000
199 GOBP-CELL-CELL-JUNCTION-ORGANIZATION	GO-0045216	6	0.339838	0.774717	0.742857	1.000000	1.000
200 GOBP-POSITIVE-REGULATION-OF-CELL-DEATH	GO-0010942	19	0.225420	0.774498	0.814655	1.000000	1.000
201 GOBP-NEUTROPHIL-SIGNALING-PATHWAY	GO-0038179	6	0.322305	0.772804	0.743516	0.998424	1.000
202 GOBP-DENDRITE-MORPHOGENESIS	GO-0048813	7	0.306055	0.770433	0.765766	0.998015	1.000
203 GOBP-NEUTROPHIL-TRK-RECEPTOR-SIGNALING-PATHWAY	GO-0048011	6	0.322305	0.769894	0.761147	0.994084	1.000
204 GOBP-POSITIVE-REGULATION-OF-ESTABLISHMENT-OF-P...	GO-1904951	5	0.352768	0.764867	0.713018	0.999094	1.000
205 GOBP-ACTIN-FILAMENT-BASED-PROCESS	GO-0030029	7	0.312456	0.760639	0.776025	1.000000	1.000
206 REACTOME-VESICLE-MEDIATED-TRANSPORT	R-RNO-5653656	5	0.331088	0.758834	0.777473	1.000000	1.000
207 GOBP-RESPONSE-TO-OXIDATIVE-STRESS	GO-0006979	8	0.283711	0.757827	0.735385	0.997668	1.000
208 GOBP-REGULATION-OF-WNT-SIGNALING-PATHWAY	GO-0030111	5	0.337349	0.757000	0.783562	0.994470	1.000
209 GOBP-REGULATION-OF-PROTEOLYSIS	GO-0030162	12	0.253610	0.756228	0.819549	0.991016	1.000
210 GOBP-RESPONSE-TO-METAL-ION	GO-0010038	15	0.231584	0.751587	0.836957	0.994957	1.000
211 GOBP-CELLULAR-RESPONSE-TO-EXTERNAL-STIMULUS	GO-0071496	10	0.259668	0.749930	0.824324	0.992981	1.000
212 GOBP-RESPONSE-TO-NITROGEN-COMPOUND	GO-1901698	35	0.186702	0.743503	0.901099	0.990646	1.000

Continuation of Table S9

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
213	GOBP-RESPONSE.TO.REACTIVE.OXYGEN.SPECIES	8	0.282711	0.746249	0.809091	0.990023	1.000
214	GOBP-CELL-POPULATION-PROLIFERATION	32	0.196266	0.741401	0.896552	0.993756	1.000
215	GOBP-POSITIVE-REGULATION-OF.MULTICELLULAR.ORGANIZATION	32	0.184770	0.737359	0.887097	0.996138	1.000
216	GOBP-REGULATION-OF-IMMUNE-RESPONSE	12	0.244894	0.735095	0.851852	0.995413	1.000
217	GOBP-RESPONSE.TO.ABIOTIC.STIMULUS	27	0.182928	0.731664	0.897297	0.996344	1.000
218	GOBP-REGULATION-OF.LYMPHOCYTE-ACTIVATION	5	0.343593	0.731175	0.790831	0.992473	1.000
219	GOBP-REGULATION-OF.GROWTH	13	0.233882	0.728184	0.868526	0.992754	1.000
220	REACTOME.MEMBRANE-TRAFFICKING	5	0.331088	0.726834	0.767313	0.990679	1.000
221	REACTOME.PTEN-REGULATION	5	0.325301	0.724388	0.800539	0.990091	1.000
222	GOBP-ERK1-AND-ERK2-CASCADE	5	0.323153	0.723091	0.831522	0.987811	1.000
223	GOBP-REGULATION-OF.AXONOGENESIS	7	0.297853	0.719440	0.822430	0.989216	1.000
224	GOBP-PROTEIN-LOCALIZATION.TO.PLASMA.MEMBRANE	7	0.294941	0.718299	0.834375	0.986582	1.000
225	GOBP-TISSUE.HOMEOSTASIS	5	0.318826	0.717484	0.819945	0.983445	1.000
226	GOBP-REGULATION-OF.VASCULAR-ASSOCIATED.SMOOTH.MUSCLE-CONTRACTION	5	0.315843	0.715058	0.824713	0.982620	1.000
227	GOBP-NEURON-PROJECTION-ORGANIZATION	8	0.271581	0.714967	0.846645	0.978442	1.000
228	GOBP-CELLULAR-RESPONSE.TO.REACTIVE.OXYGEN.SPECIES	5	0.325301	0.713799	0.830946	0.975974	1.000
229	GOBP-PEPTIDE.BIOSYNTHETIC.PROCESS	6	0.293030	0.706216	0.842541	0.978914	1.000
230	REACTOME.MAPK-TARGETS.NUCLEAR.EVENTS.MEDIATED...BY.STRESS	5	0.325301	0.705175	0.854795	0.976224	1.000
231	GOBP-POSITIVE-REGULATION-OF-CELL-PROLIFERATION	5	0.329056	0.698898	0.806630	0.980674	1.000
232	GOBP-CELLULAR-RESPONSE.TO.CHEMICAL-STRESS	7	0.271651	0.698791	0.864687	0.976715	1.000
233	GOBP-LYMPHOCYTE-ACTIVATION	10	0.249493	0.697810	0.863192	0.969648	1.000
234	GOBP-AMIDE.BIOSYNTHETIC.PROCESS	6	0.293030	0.696169	0.865103	0.967746	1.000
235	GOBP-POSITIVE-REGULATION-OF-AXONOGENESIS	5	0.311193	0.686564	0.882522	0.970091	1.000
236	HALLMARK-TNFA-SIGNALING-VIA-NFkB	14	0.221946	0.683952	0.876471	0.971023	1.000
237	GOBP-INTRINSIC-APOPTOTIC-SIGNALING-PATHWAY	5	0.329056	0.682079	0.852410	0.961402	1.000
238	GOBP-MYELOID-LEUKOCYTE-ACTIVATION	8	0.263431	0.673795	0.901899	0.967876	1.000
239	GOBP-MITOCHONDRION-ORGANIZATION	7	0.270158	0.673448	0.859238	0.964376	1.000
240	REACTOME.DEVELOPMENTAL-BIOLOGY	22	0.182840	0.655850	0.972477	0.980329	1.000
241	GOBP-REGULATION-OF-PROTEIN-STABILITY	5	0.295000	0.652711	0.929203	0.979515	1.000
242	GOBP-POSITIVE-REGULATION-OF-TRANSPORT	26	0.173611	0.650317	0.945000	0.978124	1.000
243	GOBP-SKELETAL-MUSCLE-ORGAN.DEVELOPMENT	5	0.297959	0.640016	0.912698	0.983968	1.000
244	GOBP-POSITIVE-REGULATION-OF-CELL-ADHESION	7	0.261634	0.638870	0.921875	0.981153	1.000
245	GOBP-NEGATIVE-REGULATION-OF-TRANSMEMBRANE-TRANSPORT	6	0.262972	0.632197	0.909366	0.983306	1.000
246	GOBP-REGULATION-OF-LIPID-METABOLIC-PROCESS	7	0.242299	0.607653	0.961905	0.998616	1.000
247	GOBP-EPHRA-RECEPTOR-SIGNALING-PATHWAY	5	0.274744	0.605327	0.943662	0.996282	1.000
248	REACTOME-NEUTROPHIL-DEGRANULATION	6	0.247467	0.587872	0.948012	1.000000	1.000
249	GOBP-POSITIVE-REGULATION-OF-IMMUNE-RESPONSE	9	0.208628	0.583028	0.958955	1.000000	1.000
250	GOBP-CELL-ACTIVATION-INVOLVED-IN-IMMUNE-RESPONSE	6	0.247467	0.582866	0.975460	0.997674	1.000

Continuation of Table S9

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
256	GOBP-MYELOID-LEUKOCYTE-MEDIATED-IMMUNITY	GO-0002444	6	0.247407	0.580452	0.972299	0.995074
257	GOBP-LEUKOCYTE-MEDIATED-IMMUNITY	GO-0002443	8	0.222188	0.572327	0.980519	0.995039
258	GOBP-PROTEIN_COMPLEX-OLIGOMERIZATION	GO-0051259	7	0.222222	0.552016	0.978593	0.999383
259	GOBP-ANATOMICAL-STRUCTURE-HOMEOSTASIS	GO-0060249	7	0.226566	0.548169	0.991404	0.996942
260	GOBP-CELLULAR-RESPONSE-TO-EXTRACELLULAR-STIMULUS	GO-0031668	8	0.202274	0.543000	0.993289	0.994646
261	REACTOME-ONCOGENIC-MAPK-SIGNALING	R-HSA-6802957	5	0.248600	0.535473	0.994429	0.992668
262	GOBP-LIPID-METABOLIC-PROCESS	GO-0006629	10	0.166667	0.470092	1.000000	0.998360
263	GOBP-BIOLOGICAL-PROCESS-INVOLVED-IN-SYMBIOTIC-...	GO-0004440	10	-0.179329	-0.434554	0.997063	0.997894
264	REACTOME-DISEASES-OF-SIGNAL-TRANSDUCTION-BY-GR...	R-HSA-5663202	12	-0.178560	-0.448273	1.000000	0.999064
265	GOBP-POSITIVE-REGULATION-OF-NEURON-PROJECTION...	GO-0010976	5	-0.240354	-0.463801	0.990385	0.999698
266	REACTOME-INNATE-IMMUNE-SYSTEM	R-RNO-168249	16	-0.178249	-0.477495	0.993270	0.999902
267	REACTOME-CIRCADIAN-CLOCK	R-HSA-400253	5	-0.255756	-0.495929	0.983508	0.998695
268	GOBP-PROTEIN-CONTAINING-COMPLEX-SUBUNIT-ORGANI...	GO-00043933	15	-0.185927	-0.496951	0.988205	1.000000
269	GOBP-CIRCULATORY-SYSTEM-DEVELOPMENT	GO-0072359	21	-0.170903	-0.497220	0.992126	1.000000
270	GOBP-CELL-CELL-SIGNALING-BY-WNT	GO-0198738	7	-0.229118	-0.498419	0.989521	1.000000
271	GOBP-POSITIVE-REGULATION-OF-HEMOPOIESIS	GO-1903708	7	-0.229569	-0.500749	0.990881	1.000000
272	GOBP-NEGATIVE-REGULATION-OF-NEUROUS-SYSTEM.DEV...	GO-0051961	5	-0.255329	-0.501313	0.992320	1.000000
273	GOBP-RESPONSE-TO-TUMOR-NECROSIS-FACTOR	GO-0034612	7	-0.233210	-0.505677	0.991018	1.000000
274	REACTOME-INFECTIOUS-DISEASE	R-HSA-5663205	12	-0.203185	-0.510681	0.982736	1.000000
275	GOBP-NEGATIVE-REGULATION-OF-INTRACELLULAR-SIGN...	GO-1902532	7	-0.239241	-0.521006	0.984849	1.000000
276	GOBP-IMMUNE-SYSTEM-DEVELOPMENT	GO-0002520	17	-0.199439	-0.544372	0.971698	1.000000
277	GOBP-CELLULAR-LIPID-METABOLIC-PROCESS	GO-00404255	7	-0.250086	-0.544572	0.979167	1.000000
278	GOBP-RESPONSE-TO-INORGANIC-SUBSTANCE	GO-0010035	19	-0.195007	-0.551509	0.984416	1.000000
279	GOBP-ANIMAL-ORGAN-MORPHOGENESIS	GO-0009887	12	-0.221411	-0.553618	0.964132	1.000000
280	GOBP-APOPTOTIC-PROCESS	GO-0006915	35	-0.180580	-0.558051	0.977025	1.000000
281	REACTOME-CELLULAR-RESPONSES-TO-EXTERNAL-STIMULI	R-RNO-8953897	11	-0.227507	-0.558368	0.956091	1.000000
282	GOBP-LIPID-BIOSYNTHETIC-PROCESS	GO-0008610	6	-0.270764	-0.560922	0.960177	1.000000
283	GOBP-REGULATION-OF-DNA-BINDING-TRANSCRIPTION.F...	GO-0051090	16	-0.204344	-0.562120	0.962517	1.000000
284	GOBP-POSITIVE-REGULATION-OF-LOCOMOTION	GO-0040017	11	-0.232819	-0.563489	0.968706	1.000000
285	GOBP-REGULATION-OF-LIPID-BIOSYNTHETIC-PROCESS	GO-0046890	6	-0.270764	-0.564983	0.963127	1.000000
286	GOBP-CYTOSKELETON-ORGANIZATION	GO-0007010	11	-0.228390	-0.565010	0.964626	1.000000
287	GOBP-NEURON-MIGRATION	GO-0001764	5	-0.300690	-0.581807	0.952756	1.000000
288	GOBP-NUCLEAR-TRANSPORT	GO-0051169	5	-0.293542	-0.581813	0.960784	1.000000
289	GOBP-REGULATION-OF-PHOSPHATIDYLINOSITOL-3-KINA...	GO-0014066	6	-0.281220	-0.584534	0.954887	1.000000
290	GOBP-REGULATION-OF-PEPTIDE-TRANSPORT	GO-0090087	10	-0.243987	-0.585408	0.935714	1.000000
291	GOBP-REGULATION-OF-CYSTEINE-TYPE-ENDOPEPTIDASE...	GO-2000116	9	-0.250140	-0.586104	0.937053	1.000000
292	GOBP-RESPIRATORY-SYSTEM-DEVELOPMENT	GO-0060541	6	-0.283180	-0.589555	0.943164	1.000000
293	GOBP-MONONUCLEAR-CELL-DIFFERENTIATION	GO-1903131	7	-0.270395	-0.591864	0.956140	1.000000
294	GOBP-ORGANIC-HYDROXY-COMPOUND-METABOLIC-PROCESS	GO-1901615	8	-0.262872	-0.596172	0.953938	1.000000
295	GOBP-POSITIVE-REGULATION-OF-CELL-PROJECTION-OR...	GO-0031346	10	-0.247651	-0.596987	0.944915	1.000000
296	GOBP-NEGATIVE-REGULATION-OF-LIPID-METABOLIC-PR...	GO-0045833	5	-0.308315	-0.601860	0.937405	1.000000
297	REACTOME-NEUROUS-SYSTEM-DEVELOPMENT	R-RNO-9675108	14	-0.233211	-0.602211	0.956522	1.000000
298	GOBP-POSITIVE-REGULATION-OF-RESPONSE-TO-EXTERN...	GO-0032103	9	-0.261353	-0.603062	0.943503	1.000000

Continuation of Table S9

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
299	REACTOME_INTERFERON_SIGNALING	R-RNO-913531	6	-0.28557	-0.603072	1.000000	1.000
300	GOBP_TELENCEPHALON_DEVELOPMENT	GO-0021537	7	-0.275313	-0.603441	1.000000	1.000
301	GOBP_POSITIVE_REGULATION_OF_MYELOID_LEUKOCYTE....	GO-0002763	6	-0.287351	-0.605260	1.000000	1.000
302	GOBP_CIRCADIAN_REGULATION_OF_GENE_EXPRESSION	GO-0032922	5	-0.308461	-0.607590	1.000000	1.000
303	GOBP_NEGATIVE_REGULATION_OF_SIGNALING	GO-0023057	21	-0.215381	-0.608682	1.000000	1.000
304	GOBP_DEFENSE_RESPONSE_TO_OTHER_ORGANISM	GO-0098542	9	-0.260768	-0.609968	1.000000	1.000
305	GOBP_CELLULAR_RESPONSE_TO_MOLECULE_OF_BACTERIA...	GO-0071219	8	-0.270911	-0.610336	1.000000	1.000
306	REACTOME_LEISHMANIA_INFECTION	R-HSA-9658195	10	-0.257436	-0.611593	1.000000	1.000
307	GOBP_CELLULAR_RESPONSE_TO_BIOTIC_STIMULUS	GO-0071216	8	-0.270911	-0.611624	1.000000	1.000
308	GOBP_ERBB_SIGNALING_PATHWAY	GO-0038127	5	-0.319923	-0.621744	1.000000	1.000
309	GOBP_POSITIVE_REGULATION_OF_MAP_KINASE_ACTIVITY	GO-0043406	6	-0.306670	-0.625931	1.000000	1.000
310	GOBP_RESPONSE_TO_EXTRACELLULAR_STIMULUS	GO-0009991	13	-0.246978	-0.634605	1.000000	1.000
311	GOBP_NEURON_DEATH	GO-0070997	18	-0.227754	-0.635226	1.000000	1.000
312	GOBP_CELLULAR_RESPONSE_TO_NITROGEN_COMPOUND	GO-1901699	20	-0.224352	-0.635442	1.000000	1.000
313	GOBP_ACTIVATION_OF_MAPK_ACTIVITY	GO-0000187	6	-0.306670	-0.638037	1.000000	1.000
314	HALLMARK_HYPOXIA	M5891	5	-0.322070	-0.639832	1.000000	1.000
315	GOBP_POSITIVE_REGULATION_OF_CELLULAR_PROTEIN_L...	GO-1903829	7	-0.294354	-0.642755	1.000000	1.000
316	GOBP_POSITIVE_REGULATION_OF_CELL_POPULATION_PR...	GO-0006284	21	-0.226068	-0.645987	1.000000	1.000
317	GOBP_REGULATION_OF_PEPTIDE_SECRETION	GO-0002791	7	-0.294719	-0.646563	1.000000	1.000
318	GOBP_REGULATION_OF_CELLULAR_COMPONENT_MOVEMENT	GO-0051270	15	-0.243574	-0.647458	1.000000	1.000
319	GOBP_LEUKOCYTE_DIFFERENTIATION	GO-0002521	15	-0.244640	-0.647501	1.000000	1.000
320	GOBP_NEURON_APOPTOTIC_PROCESS	GO-0051402	12	-0.257323	-0.649058	1.000000	1.000
321	GOBP_RESPONSE_TO_INSULIN	GO-0032868	5	-0.334018	-0.649925	1.000000	1.000
322	GOBP_NEGATIVE_REGULATION_OF_TRANSCRIPTION_BY_R...	GO-0000122	10	-0.269231	-0.650027	1.000000	1.000
323	GOBP_MALE_GAMETE_GENERATION	GO-0048232	5	-0.335495	-0.650874	1.000000	1.000
324	GOBP_REGULATION_OF_PHOSPHOLIPASE_ACTIVITY	GO-0010517	6	-0.320280	-0.651386	1.000000	1.000
325	GOBP_REPRODUCTIVE_SYSTEM_DEVELOPMENT	GO-0061458	6	-0.308844	-0.651444	1.000000	1.000
326	GOBP_ENDOCYTOSIS	GO-0006897	8	-0.287483	-0.651584	1.000000	1.000
327	GOBP_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO...	GO-0072594	5	-0.331139	-0.652206	1.000000	1.000
328	GOBP_NEGATIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCE...	GO-0002683	5	-0.329963	-0.655059	1.000000	1.000
329	GOBP_REGULATION_OF_CELLULAR_LOCALIZATION	GO-0060341	17	-0.235582	-0.656158	1.000000	1.000
330	GOBP_LEARNING	GO-0007612	13	-0.258925	-0.658551	1.000000	1.000
331	REACTOME_FC_EPSILON_RECEPTOR_FCBRL_SIGNALING	R-RNO-2454202	7	-0.302159	-0.661043	1.000000	1.000
332	GOBP_NEGATIVE_REGULATION_OF_KINASE_ACTIVITY	GO-0033673	5	-0.337317	-0.661533	1.000000	1.000
333	GOBP_POSITIVE_REGULATION_OF_PROTEOLYSIS	GO-0045862	8	-0.293849	-0.664012	1.000000	1.000
334	GOBP_FC_EPSILON_RECEPTOR_SIGNALING_PATHWAY	GO-0038095	7	-0.302159	-0.665279	1.000000	1.000
335	GOBP_NEGATIVE_REGULATION_OF_TRANSFERASE_ACTIVITY	GO-0051348	5	-0.337317	-0.667390	1.000000	1.000
336	GOBP_REGULATION_OF_LIPASE_ACTIVITY	GO-0060191	6	-0.320280	-0.668285	1.000000	1.000
337	GOBP_GROWTH	GO-0040007	14	-0.259607	-0.680803	1.000000	1.000
338	GOBP_SENSORY_ORGAN_DEVELOPMENT	GO-0007423	8	-0.305097	-0.684877	1.000000	1.000
339	GOBP_REGULATION_OF_SYNAPSE_STRUCTURE_OR_ACTIVITY	GO-0050803	11	-0.275554	-0.684977	1.000000	1.000
340	GOBP_POSITIVE_REGULATION_OF_LIPASE_ACTIVITY	GO-0060193	5	-0.354080	-0.687315	1.000000	1.000
341	GOBP_CENTRAL_NERVOUS_SYSTEM_NEURON_DIFFERENTIA...	GO-0021953	5	-0.353947	-0.690241	1.000000	1.000

Continuation of Table S9

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
342	GOBP-REGULATION-OF-PHOSPHOLIPASE_C-ACTIVITY	GO-1900274	5	-0.354080	-0.691164	0.866261	1.000000	1.000
343	REACTOME-ADAPTIVE-IMMUNE-SYSTEM	R-RNO-1280218	9	-0.299815	-0.694748	0.858616	1.000000	1.000
344	GOBP-CYTOKINE-PRODUCTION	GO-0001816	10	-0.285218	-0.697272	0.845714	1.000000	1.000
345	GOBP-EPIDERMIS-DEVELOPMENT	GO-0005444	5	-0.357288	-0.698458	0.856925	1.000000	1.000
346	GOBP-NEGATIVE-REGULATION-OF-RESPONSE-TO-STIMULUS	GO-0048585	16	-0.259808	-0.702723	0.866667	1.000000	1.000
347	GOBP-DEPHOSPHORYLATION	GO-0016311	7	-0.327075	-0.703754	0.841390	1.000000	1.000
348	GOBP-PROTEIN-DEPHOSPHORYLATION	GO-0006470	7	-0.327075	-0.704532	0.861446	1.000000	1.000
349	GOBP-PROTEIN-LOCALIZATION-TO-ORGANELLE	GO-0033365	8	-0.313187	-0.711604	0.820090	1.000000	1.000
350	GOBP-HOMEOSTASIS-OF-NUMBER-OF-CELLS	GO-0048872	5	-0.363671	-0.713413	0.834375	1.000000	1.000
351	GOBP-NEGATIVE-REGULATION-OF-APOPTOTIC-SIGNALIN...	GO-2001234	7	-0.330524	-0.716275	0.837446	1.000000	1.000
352	GOBP-NEGATIVE-REGULATION-OF-BIOSYNTHETIC-PROCESS	GO-0009890	13	-0.280000	-0.719923	0.833559	1.000000	1.000
353	GOBP-APOPTOTIC-SIGNALING-PATHWAY	GO-0007190	15	-0.275763	-0.721857	0.836927	1.000000	1.000
354	GOBP-POSITIVE-REGULATION-OF-BIOSYNTHETIC-PROCESS	GO-0009891	27	-0.242064	-0.727331	0.844697	1.000000	1.000
355	GOBP-RESPONSE-TO-PEPTIDE	GO-1901652	18	-0.263232	-0.729296	0.837057	1.000000	1.000
356	GOBP-REGULATION-OF-PEPTIDYL-SERINE-PHOSPHORYLA...	GO-0033135	8	-0.331590	-0.730538	0.831871	1.000000	1.000
357	GOBP-REGULATION-OF-HEMOPOIESIS	GO-1903706	10	-0.303603	-0.732527	0.821429	1.000000	1.000
358	GOBP-REGULATION-OF-RECEPTOR-MEDIATED-ENDOCYTOSIS	GO-0048259	5	-0.375341	-0.732614	0.827640	1.000000	1.000
359	GOBP-REGULATION-OF-ENDOCYTOSIS	GO-0030100	6	-0.353210	-0.733751	0.808157	1.000000	1.000
360	GOBP-EPITHELIAL-CELL-PROLIFERATION	GO-0050673	12	-0.289440	-0.735470	0.804677	1.000000	1.000
361	GOBP-DEVELOPMENTAL-MATURATION	GO-0021700	5	-0.375720	-0.736934	0.819005	1.000000	1.000
362	GOBP-REGULATION-OF-CATABOLIC-PROCESS	GO-0009894	13	-0.286075	-0.737480	0.831276	1.000000	1.000
363	GOBP-SPROUTING-ANGIOGENESIS	GO-0002040	5	-0.374279	-0.738143	0.808847	1.000000	1.000
364	GOBP-RECEPTOR-MEDIATED-ENDOCYTOSIS	GO-0006898	6	-0.363201	-0.739924	0.804665	1.000000	1.000
365	GOBP-REGULATION-OF-CELL-PROJECTION-ORGANIZATION	GO-0031344	20	-0.255907	-0.740703	0.835092	1.000000	1.000
366	REACTOME-PLATELET-ACTIVATION-SIGNALING-AND-AGG...	R-HSA-76002	7	-0.347031	-0.742576	0.813711	1.000000	1.000
367	GOBP-NEGATIVE-REGULATION-OF-CATABOLIC-PROCESS	GO-0009895	8	-0.330968	-0.746305	0.795588	1.000000	1.000
368	GOBP-DNA-METABOLIC-PROCESS	GO-0006259	6	-0.353444	-0.748005	0.799694	1.000000	1.000
369	GOBP-CARBOHYDRATE-HOMEOSTASIS	GO-0033500	7	-0.348267	-0.750478	0.789669	1.000000	1.000
370	GOBP-AMEBOIDAL-TYPE-CELL-MIGRATION	GO-0001667	11	-0.311825	-0.751778	0.820208	1.000000	1.000
371	GOBP-POSITIVE-REGULATION-OF-PEPTIDYL-SERINE-PH...	GO-0033138	8	-0.331590	-0.753854	0.782107	1.000000	1.000
372	GOBP-RESPONSE-TO-GROWTH-FACTOR	GO-0070848	18	-0.272020	-0.754047	0.789688	1.000000	1.000
373	REACTOME-L1CAM-INTERACTIONS	R-RNO-373760	5	-0.389227	-0.754826	0.791069	1.000000	1.000
374	GOBP-REGULATION-OF-MITOTIC-CELL-CYCLE	GO-0007346	5	-0.381893	-0.756447	0.808777	1.000000	1.000
375	GOBP-MYELOID-CELL-DIFFERENTIATION	GO-0030099	13	-0.293053	-0.758075	0.790859	1.000000	1.000
376	GOBP-CELLULAR-RESPONSE-TO-STARVATION	GO-0009267	5	-0.394031	-0.759200	0.800000	1.000000	1.000
377	GOBP-RESPONSE-TO-STARVATION	GO-0042594	5	-0.394031	-0.760552	0.809524	1.000000	1.000
378	GOBP-BEHAVIOR	GO-0007610	33	-0.247835	-0.760574	0.817633	1.000000	1.000
379	GOBP-REGULATION-OF-MAP-KINASE-ACTIVITY	GO-0043405	9	-0.323107	-0.762156	0.767806	1.000000	1.000
380	GOBP-REGULATION-OF-PROTEIN-CATABOLIC-PROCESS	GO-0042176	7	-0.356153	-0.764681	0.787106	1.000000	1.000
381	GOBP-PROTEIN-TETRAMERIZATION	GO-0051262	5	-0.391983	-0.764966	0.779014	1.000000	1.000
382	GOBP-POSITIVE-REGULATION-OF-DNA-BINDING-TRANSC...	GO-0051091	10	-0.320704	-0.766860	0.762712	1.000000	1.000
383	GOBP-POSITIVE-REGULATION-OF-CELLULAR-COMPONENT...	GO-0051130	24	-0.264989	-0.772238	0.786885	1.000000	1.000
384	GOBP-CELL-PART-MORPHOGENESIS	GO-0032990	25	-0.263400	-0.773750	0.782383	1.000000	1.000

Continuation of Table S9

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
385	GOBP-FAT_CELL-DIFFERENTIATION	GO-0045444	9	-0.339851	-0.774667	0.783167	1.000000	1.000
386	GOBP-MUSCLE-STRUCTURE.DEVELOPMENT	GO-0061061	16	-0.289180	-0.775140	0.772606	1.000000	1.000
387	GOBP-REGULATION-OF-ORGANELLE-ORGANIZATION	GO-0033043	14	-0.298704	-0.777534	0.770805	1.000000	1.000
388	GOBP-CELL-MORPHOGENESIS	GO-0000902	25	-0.263400	-0.783049	0.786865	1.000000	1.000
389	REACTOME-CELL-CYCLE-MITOTIC	R-RNO-69278	5	-0.400386	-0.783532	0.766566	1.000000	1.000
390	GOBP-TUBE-MORPHOGENESIS	GO-0035239	15	-0.290677	-0.783915	0.748290	1.000000	1.000
391	GOBP-CELL-CELL-JUNCTION-ASSEMBLY	GO-0007043	5	-0.397898	-0.784814	0.754545	1.000000	1.000
392	GOBP-NEUROINFLAMMATORY-RESPONSE	GO-00150076	5	-0.399230	-0.785665	0.753012	1.000000	1.000
393	GOBP-CELLULAR-RESPONSE-TO-INORGANIC-SUBSTANCE	GO-0071241	11	-0.316262	-0.788489	0.759184	1.000000	1.000
394	GOBP-NEGATIVE-REGULATION-OF-CELL-POPULATION-PR...	GO-0008285	9	-0.340725	-0.791447	0.746398	1.000000	1.000
395	GOBP-CELLULAR-COMPONENT-MORPHOGENESIS	GO-0032989	25	-0.263400	-0.792434	0.769231	1.000000	1.000
396	GOBP-POSITIVE-REGULATION-OF-CATION-TRANSMEMBRAN...	GO-1904064	5	-0.404117	-0.795291	0.767255	1.000000	1.000
397	GOBP-TRANSMEMBRANE-RECEPTOR-PROTEIN-SERINE-THR...	GO-0007178	6	-0.379655	-0.796434	0.735795	1.000000	1.000
398	GOBP-RESPONSE-TO-TEMPERATURE-STIMULUS	GO-0009266	9	-0.336293	-0.797530	0.729323	1.000000	1.000
399	GOBP-PEPTIDYL-TYROSINE-MODIFICATION	GO-0018212	10	-0.333938	-0.802633	0.725989	1.000000	1.000
400	GOBP-MULTICELLULAR-ORGANISMAL-HOMEOSTASIS	GO-0048871	12	-0.325111	-0.803995	0.725784	1.000000	1.000
401	GOBP-INNATE-IMMUNE-RESPONSE	GO-0045087	7	-0.368286	-0.804406	0.721068	1.000000	1.000
402	GOBP-REGULATION-OF-LEUKOCYTE-DIFFERENTIATION	GO-1902105	9	-0.345681	-0.804544	0.731214	1.000000	1.000
403	GOBP-REGULATION-OF-PEPTIDYL-TYROSINE-PHOSPHORY...	GO-0050730	9	-0.343501	-0.805350	0.741007	1.000000	1.000
404	GOBP-RESPONSE-TO-BIOTIC-STIMULUS	GO-0009607	17	-0.297343	-0.808397	0.736983	1.000000	1.000
405	GOBP-REGULATION-OF-MYELOID-CELL-DIFFERENTIATION	GO-0045637	9	-0.349627	-0.809240	0.739007	1.000000	1.000
406	GOBP-RESPONSE-TO-BACTERIUM	GO-0009617	13	-0.313414	-0.809316	0.723577	1.000000	1.000
407	GOBP-POSITIVE-REGULATION-OF-PEPTIDYL-TYROSINE...	GO-0050731	8	-0.357239	-0.809377	0.729412	1.000000	1.000
408	GOBP-POSITIVE-REGULATION-OF-PEPTIDASE-ACTIVITY	GO-0010952	7	-0.383056	-0.811760	0.732475	1.000000	1.000
409	GOBP-NEGATIVE-REGULATION-OF-NEURON-APOPTOTIC-P...	GO-0043524	8	-0.364989	-0.812192	0.740371	1.000000	1.000
410	GOBP-RESPONSE-TO-MOLECULE-OF-BACTERIAL-ORIGIN	GO-0002237	13	-0.313414	-0.812485	0.722071	1.000000	1.000
411	GOBP-RESPONSE-TO-KETONE	GO-1901654	7	-0.371915	-0.812528	0.735649	1.000000	1.000
412	GOBP-POSITIVE-REGULATION-OF-EPITHELIAL-CELL-PR...	GO-0050679	7	-0.375596	-0.812759	0.723684	1.000000	1.000
413	GOBP-REGULATION-OF-TRANSMEMBRANE-TRANSPORT	GO-0034762	23	-0.279179	-0.812946	0.751948	1.000000	1.000
414	GOBP-MYELOID-LEUKOCYTE-DIFFERENTIATION	GO-0002573	11	-0.331706	-0.820860	0.716292	1.000000	1.000
415	GOBP-POSITIVE-REGULATION-OF-PROTEIN-SERINE-THR...	GO-0071902	9	-0.347650	-0.820937	0.686630	1.000000	1.000
416	GOBP-REGULATION-OF-APOPTOTIC-SIGNALING-PATHWAY	GO-2001233	10	-0.339242	-0.821410	0.713246	1.000000	1.000
417	GOBP-BIOLOGICAL-ADHESION	GO-0022610	19	-0.293850	-0.821840	0.709347	1.000000	1.000
418	GOBP-PHAGOCYTOSIS	GO-0006909	5	-0.412207	-0.822766	0.680000	1.000000	1.000
419	GOBP-NEGATIVE-REGULATION-OF-CELL-PROJECTION-OR...	GO-0031345	5	-0.425651	-0.824410	0.684533	1.000000	1.000
420	GOBP-POSITIVE-REGULATION-OF-ORGANELLE-ORGANIZA...	GO-0010638	10	-0.343888	-0.829104	0.704964	1.000000	1.000
421	GOBP-ORGANIC-ACID-METABOLIC-PROCESS	GO-0006082	7	-0.390387	-0.829716	0.728097	1.000000	1.000
422	GOBP-CELLULAR-RESPONSE-TO-OXYGEN-CONTAINING-CO...	GO-1901701	29	-0.276307	-0.829767	0.707347	1.000000	1.000
423	GOBP-POSITIVE-REGULATION-OF-CYSTEINE-TYPE-ENDO...	GO-2001056	7	-0.382056	-0.830499	0.699387	1.000000	1.000
424	GOBP-POSITIVE-REGULATION-OF-SMALL-MOLECULE-MET...	GO-0062013	5	-0.429502	-0.833493	0.687888	1.000000	1.000
425	GOBP-COGNITION	GO-0050890	28	-0.278408	-0.834299	0.711970	1.000000	1.000
426	GOBP-CELLULAR-RESPONSE-TO-ORGANIC-CYCLIC-COMPOUND	GO-0071407	13	-0.327560	-0.840052	0.687764	1.000000	1.000
427	GOBP-CELL-CYCLE-PROCESS	GO-0022402	11	-0.341129	-0.841574	0.684357	1.000000	1.000

Continuation of Table S9

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
428	GOBP-FOREBRAIN-DEVELOPMENT	GO-0030900	10	-0.353807	-0.843280	0.658640	1.000000	1.000
429	GOBP-VASCULATURE-DEVELOPMENT	GO-0001944	17	-0.313169	-0.846862	0.667092	1.000000	1.000
430	GOBP-LONG-TERM-MEMORY	GO-0007616	6	-0.418945	-0.848965	0.677321	1.000000	1.000
431	GOBP-SMALL-MOLECULE-METABOLIC-PROCESS	GO-0044281	16	-0.315272	-0.849990	0.672000	1.000000	1.000
432	GOBP-REGULATION-OF-EPITHELIAL-CELL-MIGRATION	GO-0010632	11	-0.412437	-0.850164	0.669219	1.000000	1.000
433	GOBP-NEGATIVE-REGULATION-OF-NEURON-DEATH	GO-1901215	11	-0.346541	-0.851593	0.666195	1.000000	1.000
434	GOBP-POSITIVE-REGULATION-OF-TRANSCRIPTION_BY_R...	GO-0045944	24	-0.288382	-0.854771	0.661125	1.000000	1.000
435	GOBP-SEXUAL-REPRODUCTION	GO-0019953	10	-0.361216	-0.855437	0.651982	1.000000	1.000
436	HALLMARK-ALLOGRAFT-REJECTION	M5950	7	-0.398766	-0.856491	0.672464	1.000000	1.000
437	GOBP-POSITIVE-REGULATION-OF-SECRETION	GO-0051047	6	-0.417540	-0.856519	0.658574	1.000000	1.000
438	GOBP-RESPONSE-TO-ORGANIC-CYCLIC-COMPOUND	GO-0014070	20	-0.303278	-0.858286	0.683463	1.000000	1.000
439	GOBP-AXON-DEVELOPMENT	GO-0061564	18	-0.311245	-0.859383	0.660027	1.000000	1.000
440	GOBP-EXOCYTOSIS	GO-0006887	11	-0.341889	-0.861158	0.644719	1.000000	1.000
441	GOBP-POSITIVE-REGULATION-OF-EPITHELIAL-CELL-MI...	GO-0010634	5	-0.438783	-0.864717	0.674961	1.000000	1.000
442	GOBP-CELL-ACTIVATION	GO-0001775	22	-0.301399	-0.866613	0.667529	1.000000	1.000
443	REACTOME-SIGNALING-BY-NTRK2-TRKB	R-RNO-9006115	6	-0.425140	-0.866803	0.650915	1.000000	1.000
444	GOBP-INTRACELLULAR-PROTEIN-TRANSPORT	GO-0006886	8	-0.390332	-0.867577	0.636914	1.000000	1.000
445	GOBP-NEURON-DEVELOPMENT	GO-0048666	34	-0.286932	-0.868466	0.685680	1.000000	1.000
446	GOBP-REGULATION-OF-CELL-ADHESION	GO-0030155	13	-0.335171	-0.869829	0.671683	1.000000	1.000
447	GOBP-RECEPTOR-INTERNALIZATION	GO-0031623	5	-0.445387	-0.872766	0.641509	1.000000	1.000
448	GOBP-INTRACELLULAR-TRANSPORT	GO-0046907	10	-0.359076	-0.873243	0.622669	1.000000	1.000
449	GOBP-CARBOHYDRATE-DERIVATIVE-BIOSYNTHETIC-PROCESS	GO-1901137	5	-0.449552	-0.874398	0.663987	1.000000	1.000
450	GOBP-REGULATION-OF-MAPK-CASCADE	GO-0043408	13	-0.337748	-0.875682	0.616690	1.000000	1.000
451	GOBP-NEGATIVE-REGULATION-OF-PHOSPHORUS-METABOL...	GO-0010563	9	-0.372811	-0.876602	0.641135	1.000000	1.000
452	GOBP-ORGANIC-ACID-TRANSPORT	GO-0015849	7	-0.406930	-0.876939	0.648286	1.000000	1.000
453	GOBP-NEGATIVE-REGULATION-OF-CELLULAR-COMPONENT...	GO-0051129	11	-0.355887	-0.878647	0.639437	1.000000	1.000
454	GOBP-RESPONSE-TO-OXYGEN-CONTAINING-COMPOUND	GO-1901700	39	-0.279630	-0.879353	0.676792	1.000000	1.000
455	GOBP-NEGATIVE-REGULATION-OF-NUCLEOBASE-CONTAIN...	GO-0045934	13	-0.345992	-0.881489	0.628809	1.000000	1.000
456	GOBP-POSTTRANSCRIPTIONAL-REGULATION-OF-GENE-EX...	GO-0010608	8	-0.390883	-0.881649	0.615611	1.000000	1.000
457	GOBP-FATTY-ACID-TRANSPORT	GO-0015908	6	-0.430345	-0.881809	0.665680	1.000000	1.000
458	GOBP-RECEPTOR-METABOLIC-PROCESS	GO-0043112	5	-0.445387	-0.881980	0.647239	1.000000	1.000
459	HALLMARK-EPITHELIAL-MESENCHYMAL-TRANSITION	M5930	5	-0.454682	-0.884296	0.629630	1.000000	1.000
460	GOBP-NEGATIVE-REGULATION-OF-DEVELOPMENTAL-PROCESS	GO-0051093	13	-0.349337	-0.887796	0.610169	1.000000	1.000
461	GOBP-NEGATIVE-REGULATION-OF-PROTEIN-CATABOLIC...	GO-0042177	5	-0.456622	-0.888480	0.630745	1.000000	1.000
462	GOBP-RESPONSE-TO-ALCOHOL	GO-0097305	11	-0.363933	-0.889245	0.638327	1.000000	1.000
463	GOBP-REGULATION-OF-PROTEIN-KINASE-ACTIVITY	GO-0045859	21	-0.318997	-0.893178	0.616883	1.000000	1.000
464	GOBP-TISSUE-MORPHOGENESIS	GO-0048729	7	-0.410229	-0.895797	0.595930	1.000000	1.000
465	GOBP-NEGATIVE-REGULATION-OF-PHOSPHORYLATION	GO-0042326	7	-0.420976	-0.896146	0.611963	1.000000	1.000
466	GOBP-PROTEIN-MODIFICATION-BY-SMALL-PROTEIN-CON...	GO-0070647	7	-0.416143	-0.896345	0.627422	1.000000	1.000
467	GOBP-CELL-MORPHOGENESIS-INVOLVED-IN-NEURON-DIF...	GO-0048667	22	-0.310800	-0.896685	0.604381	1.000000	1.000
468	GOBP-NERVE-DEVELOPMENT	GO-0021675	9	-0.382326	-0.899195	0.628040	1.000000	1.000
469	GOBP-NEGATIVE-REGULATION-OF-CELL-DIFFERENTIATION	GO-0045596	13	-0.349337	-0.900835	0.607789	1.000000	1.000
470	GOBP-CELL-PROJECTION-ORGANIZATION	GO-0030030	35	-0.291049	-0.902601	0.624526	1.000000	1.000

Continuation of Table S9

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
471	GOBP-CENTRAL-NERVOUS-SYSTEM-DEVELOPMENT	GO-0007417	27	-0.306093	-0.903294	0.630065	1.000000	1.000
472	GOBP-REGULATION-OF-GTPASE-ACTIVITY	GO-0043087	5	-0.468821	-0.903542	0.618380	1.000000	1.000
473	GOBP-REGULATION-OF-MYELOID-LEUKOCYTE-DIFFERENT...	GO-0002761	8	-0.402165	-0.903545	0.596439	1.000000	1.000
474	GOBP-CELL-MORPHOGENESIS-INVOLVED-IN-DIFFERENTI...	GO-0000904	22	-0.310800	-0.906143	0.599179	1.000000	1.000
475	GOBP-NEUROGENESIS	GO-0002208	41	-0.289017	-0.906875	0.605583	1.000000	1.000
476	GOBP-MEMBRANE-ORGANIZATION	GO-0061024	12	-0.357829	-0.906955	0.587671	1.000000	1.000
477	GOBP-REGULATION-OF-HYDROLASE-ACTIVITY	GO-0051336	22	-0.316071	-0.907069	0.590226	1.000000	1.000
478	GOBP-REGULATION-OF-SYNAPTIC-TRANSMISSION-GLUTA...	GO-0051966	12	-0.359162	-0.908388	0.576976	1.000000	1.000
479	GOBP-CELL-SURFACE-RECEPTOR-SIGNALING-PATHWAY-I...	GO-1905114	15	-0.340396	-0.913454	0.575472	1.000000	1.000
480	GOBP-REGULATION-OF-ENDOTHELIAL-CELL-MIGRATION	GO-0010594	5	-0.472437	-0.913488	0.595777	1.000000	1.000
481	GOBP-POSITIVE-REGULATION-OF-LONG-TERM-SYNAPTIC...	GO-1900273	5	-0.464470	-0.914546	0.582181	1.000000	1.000
482	GOBP-REGULATION-OF-TRANSPERASE-ACTIVITY	GO-0051338	21	-0.318997	-0.914913	0.590164	1.000000	1.000
483	GOBP-REGULATION-OF-ANATOMICAL-STRUCTURE-MORPHO...	GO-0022603	17	-0.336747	-0.916877	0.591588	1.000000	1.000
484	GOBP-NEURON-PROJECTION-GUIDANCE	GO-0097485	9	-0.398901	-0.918431	0.580370	1.000000	1.000
485	GOBP-TAXIS	GO-0042330	14	-0.350577	-0.919103	0.594558	1.000000	1.000
486	GOBP-POSITIVE-REGULATION-OF-APOPTOTIC-SIGNALIN...	GO-2001235	5	-0.467780	-0.919288	0.587253	1.000000	1.000
487	GOBP-TUBE-DEVELOPMENT	GO-0035295	18	-0.335675	-0.921567	0.579710	1.000000	1.000
488	GOBP-RESPONSE-TO-PEPTIDE-HORMONE	GO-0043434	13	-0.353696	-0.923220	0.570248	1.000000	1.000
489	GOBP-SMALL-MOLECULE-BIOSYNTHETIC-PROCESS	GO-0044283	5	-0.469987	-0.924224	0.599379	1.000000	1.000
490	REACTOME-CELL-CYCLE	R-RNO-1640170	6	-0.450964	-0.924601	0.594880	1.000000	1.000
491	GOBP-STRIATED-MUSCLE-CELL-DIFFERENTIATION	GO-0051146	9	-0.395422	-0.924678	0.561119	1.000000	1.000
492	GOBP-PROTEIN-LOCALIZATION-TO-CELL-PERIPHERY	GO-1990778	12	-0.369396	-0.927523	0.570827	1.000000	1.000
493	REACTOME-HEMOSTASIS	R-RNO-109582	14	-0.353735	-0.927999	0.539597	1.000000	1.000
494	GOBP-RESPONSE-TO-ETHANOL	GO-0045471	5	-0.485894	-0.934515	0.562998	1.000000	1.000
495	GOBP-MACROMOLECULE-CATABOLIC-PROCESS	GO-0009057	11	-0.373989	-0.934689	0.564246	1.000000	1.000
496	GOBP-TRANSMEMBRANE-TRANSPORT	GO-0055085	27	-0.314495	-0.934914	0.575604	1.000000	1.000
497	REACTOME-ANTI-INFLAMMATORY-RESPONSE-FAVOURING...	R-HSA-9662851	5	-0.479458	-0.939222	0.565831	1.000000	1.000
498	GOBP-POSITIVE-REGULATION-OF-MAPK-CASCADE	GO-0043410	9	-0.402317	-0.939257	0.558074	1.000000	1.000
499	GOBP-NEGATIVE-REGULATION-OF-GENE-EXPRESSION	GO-0010629	11	-0.385568	-0.940812	0.568182	1.000000	1.000
500	GOBP-POSITIVE-REGULATION-OF-SIGNALING	GO-0023056	34	-0.302186	-0.941259	0.555422	1.000000	1.000
501	GOBP-POSITIVE-REGULATION-OF-NUCLEOBASE-CONTAIN...	GO-0045935	28	-0.308099	-0.941843	0.532828	1.000000	1.000
502	GOBP-CELLULAR-MACROMOLECULE-LOCALIZATION	GO-0070727	20	-0.336918	-0.942973	0.562500	1.000000	1.000
503	GOBP-REGULATION-OF-RESPONSE-TO-STRESS	GO-0080134	19	-0.335504	-0.94213	0.533419	1.000000	1.000
504	GOBP-BLOOD-VESSEL-MORPHOGENESIS	GO-0048514	14	-0.358935	-0.946826	0.540184	1.000000	1.000
505	GOBP-POSITIVE-REGULATION-OF-HYDROLASE-ACTIVITY	GO-0051345	16	-0.340691	-0.947642	0.543742	1.000000	1.000
506	GOBP-REGULATION-OF-NERVOUS-SYSTEM-PROCESS	GO-0031644	8	-0.418656	-0.948201	0.534610	1.000000	1.000
507	GOBP-PROTEIN-CATABOLIC-PROCESS	GO-0030163	8	-0.422801	-0.949654	0.542692	1.000000	1.000
508	GOBP-WOUND-HEALING	GO-0042060	13	-0.377088	-0.952811	0.528671	1.000000	1.000
509	GOBP-POSITIVE-REGULATION-OF-MYELOID-CELL-DIFFE...	GO-0045639	7	-0.442972	-0.957806	0.533033	1.000000	1.000
510	GOBP-REGULATION-OF-SIGNALING-RECEPTOR-ACTIVITY	GO-0010469	14	-0.371588	-0.958910	0.541899	1.000000	1.000
511	GOBP-REGULATION-OF-TRANSPORTER-ACTIVITY	GO-0032409	17	-0.353068	-0.959125	0.543978	1.000000	1.000
512	GOBP-PROTEIN-LOCALIZATION-TO-CELL-JUNCTION	GO-1902414	6	-0.453162	-0.960169	0.519006	1.000000	1.000
513	GOBP-MONOAMINE-TRANSPORT	GO-0015844	5	-0.490798	-0.960898	0.528975	1.000000	1.000

Continuation of Table S9

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
514 GOBP-NEGATIVE-REGULATION-OF-CELL-CYCLE	GO-0045786	5	-0.497122	-0.962495	0.556982	1.000000	1.000
515 GOBP-RESPONSE-TO-MONOSACCHARIDE	GO-0034284	5	-0.490588	-0.964714	0.532813	1.000000	1.000
516 GOBP-CELL-JUNCTION-ASSEMBLY	GO-0034329	8	-0.425645	-0.966178	0.521355	1.000000	1.000
517 GOBP-LONG-TERM-SYNAPTIC-POTENTIATION	GO-0060291	12	-0.391069	-0.966525	0.521862	1.000000	1.000
518 GOBP-MYOTUBE-DIFFERENTIATION	GO-0014902	5	-0.504609	-0.967307	0.511664	1.000000	1.000
519 GOBP-MITOTIC-CELL-CYCLE	GO-0000278	10	-0.401660	-0.967775	0.503597	1.000000	1.000
520 GOBP-RESPONSE-TO-CARBOHYDRATE	GO-0009743	5	-0.490588	-0.970067	0.526398	1.000000	1.000
521 GOBP-PROTEIN-AUTOPHOSPHORYLATION	GO-0046777	5	-0.493727	-0.972767	0.526081	1.000000	1.000
522 GOBP-REGULATION-OF-VASCULATURE-DEVELOPMENT	GO-1901342	5	-0.502763	-0.972944	0.530735	1.000000	1.000
523 GOBP-CELLULAR-RESPONSE-TO-DNA-DAMAGE-STIMULUS	GO-0006974	5	-0.501008	-0.977080	0.504870	1.000000	1.000
524 GOBP-REGULATION-OF-MUSCLE-CELL-DIFFERENTIATION	GO-0051147	6	-0.462630	-0.978013	0.500732	1.000000	1.000
525 GOBP-NEURON-DIFFERENTIATION	GO-0030182	37	-0.317397	-0.984567	0.492665	1.000000	1.000
526 GOBP-DENDRITE-DEVELOPMENT	GO-0016358	10	-0.408862	-0.987919	0.482507	1.000000	1.000
527 GOBP-TISSUE-MIGRATION	GO-0090130	9	-0.428119	-0.990055	0.500697	1.000000	1.000
528 GOBP-REGULATION-OF-CELL-ACTIVATION	GO-0050865	8	-0.437033	-0.990954	0.483642	1.000000	1.000
529 GOBP-REGULATION-OF-RESPONSE-TO-EXTERNAL-STIMULUS	GO-0032101	15	-0.373453	-0.991244	0.487705	1.000000	1.000
530 GOBP-RESPONSE-TO-HEAT	GO-0009408	7	-0.453312	-0.994283	0.498503	1.000000	1.000
531 GOBP-REGULATION-OF-PEPTIDE-HORMONE-SECRETION	GO-0090276	6	-0.477434	-0.995865	0.465774	1.000000	1.000
532 GOBP-REGULATION-OF-NEUROTRANSMITTER-RECEPTOR-A...	GO-0099601	13	-0.391507	-0.998831	0.472185	1.000000	1.000
533 GOBP-PROTEIN-LOCALIZATION-TO-MEMBRANE	GO-0072657	13	-0.395401	-1.005983	0.470667	1.000000	1.000
534 GOBP-NEGATIVE-REGULATION-OF-PROTEIN-MODIFICATI...	GO-0031400	10	-0.419755	-1.006891	0.483501	1.000000	1.000
535 GOBP-POSITIVE-REGULATION-OF-PROTEIN-TYROSINE-K...	GO-0061098	5	-0.523198	-1.011460	0.493066	1.000000	1.000
536 GOBP-ORGANONITROGEN-COMPOUND-BIOSYNTHETIC-PROCESS	GO-1901566	13	-0.396977	-1.013550	0.466851	1.000000	1.000
537 GOBP-MAINTENANCE-OF-LOCATION	GO-0051235	7	-0.468402	-1.017832	0.442308	1.000000	1.000
538 GOBP-ESTABLISHMENT-OF-PROTEIN-LOCALIZATION	GO-0045184	17	-0.371833	-1.022337	0.441489	1.000000	1.000
539 GOBP-REGULATION-OF-PROTEIN-TYROSINE-KINASE-ACT...	GO-0061097	5	-0.523198	-1.023947	0.455259	1.000000	1.000
540 GOBP-SKIN-DEVELOPMENT	GO-0043588	5	-0.521690	-1.024713	0.472403	1.000000	1.000
541 GOBP-REGULATION-OF-ANATOMICAL-STRUCTURE-SIZE	GO-0090066	10	-0.435948	-1.026202	0.444142	1.000000	1.000
542 GOBP-REGULATION-OF-PHOSPHORUS-METABOLIC-PROCESS	GO-0051174	26	-0.343276	-1.027083	0.426938	1.000000	1.000
543 REACTOME-SIGNALING-BY-RHO-GTPASES-MIRO-GTPASES...	R-RNO-9716542	9	-0.441325	-1.028024	0.441727	1.000000	1.000
544 REACTOME-RHO-GTPASE-EFFECTORS	R-RNO-195258	9	-0.441325	-1.029454	0.437768	1.000000	1.000
545 GOBP-REGULATION-OF-MUSCLE-ADAPTATION	GO-0043502	5	-0.531995	-1.030072	0.450237	1.000000	1.000
546 GOBP-ENDOMEMBRANE-SYSTEM-ORGANIZATION	GO-0010256	6	-0.483640	-1.030834	0.430493	1.000000	1.000
547 GOBP-SYNAPTIC-TRANSMISSION-GLUTAMATERGIC	GO-0035249	13	-0.403943	-1.033428	0.428962	1.000000	1.000
548 GOBP-RESPONSE-TO-WOUNDING	GO-0009611	15	-0.393523	-1.038053	0.405442	1.000000	1.000
549 GOBP-MUSCLE-ADAPTATION	GO-0043500	5	-0.531995	-1.039975	0.436937	1.000000	1.000
550 GOBP-POSITIVE-REGULATION-OF-SYNAPTIC-TRANSMISSION	GO-0050806	15	-0.393039	-1.040106	0.408840	1.000000	1.000
551 GOBP-REGULATION-OF-PROTEIN-PHOSPHORYLATION	GO-0001932	25	-0.353239	-1.043536	0.420724	1.000000	1.000
552 GOBP-LOCOMOTORY-BEHAVIOR	GO-0007626	8	-0.464910	-1.045775	0.428157	1.000000	1.000
553 GOBP-CHEMICAL-SYNAPTIC-TRANSMISSION-POSTSYNAPTIC	GO-0099565	9	-0.445176	-1.053956	0.400875	1.000000	1.000
554 GOBP-REGULATION-OF-CELL-CELL-ADHESION	GO-0022407	9	-0.454900	-1.055344	0.391679	1.000000	1.000
555 GOBP-CELLULAR-RESPONSE-TO-KETONE	GO-1901655	5	-0.527455	-1.055367	0.408951	1.000000	1.000
556 GOBP-SYNAPSE-ORGANIZATION	GO-0050808	17	-0.386293	-1.058257	0.399225	1.000000	1.000

Continuation of Table S9

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
557 GOBP-POSITIVE-REGULATION_OF_TRANSPERASE-ACTIVITY	GO-0051347	19	-0.377536	-1.065566	0.371728	1.000000	1.000
558 GOBP-ENDOTHELIAL-CELL-MIGRATION	GO-0043542	8	-0.475854	-1.066189	0.385650	1.000000	1.000
559 GOBP-POSITIVE-REGULATION_OF_PROTEIN_KINASE-ACT...	GO-0045860	18	-0.384509	-1.068585	0.390564	1.000000	1.000
560 GOBP-ORGANIC-ANION-TRANSPORT	GO-0015711	6	-0.522709	-1.076434	0.411315	1.000000	1.000
561 GOBP-CELLULAR-RESPONSE-TO-PEPTIDE	GO-1901653	13	-0.417092	-1.078080	0.375848	1.000000	1.000
562 GOBP-REGULATION_OF_HORMONE-LEVELS	GO-0010817	12	-0.426909	-1.078515	0.367925	1.000000	1.000
563 GOBP-BLOOD-VESEL-ENDOTHELIAL-CELL-MIGRATION	GO-0043534	8	-0.475854	-1.079772	0.389855	1.000000	1.000
564 GOBP-CARBOXYLIC-ACID-TRANSPORT	GO-0046942	6	-0.522709	-1.080217	0.377953	1.000000	1.000
565 GOBP-AMINO-ACID-TRANSPORT	GO-0006865	6	-0.522709	-1.081939	0.368421	1.000000	1.000
566 GOBP-CIRCADIEN-RHYTHM	GO-0007623	13	-0.418095	-1.082361	0.366897	1.000000	1.000
567 GOBP-POSITIVE-REGULATION_OF_ENDOTHELIAL-CELL-P...	GO-0001938	6	-0.513757	-1.084172	0.365031	1.000000	1.000
568 GOBP-NERVOUS-SYSTEM-PROCESS	GO-0050877	38	-0.347938	-1.086358	0.342201	1.000000	1.000
569 GOBP-ACIDIC-AMINO-ACID-TRANSPORT	GO-0015800	5	-0.552591	-1.086464	0.366819	1.000000	1.000
570 GOBP-RESPONSE-TO-OXYGEN-LEVELS	GO-00070482	8	-0.473609	-1.087998	0.358900	1.000000	1.000
571 GOBP-REGULATION-OF-CATION-CHANNEL-ACTIVITY	GO-2001257	14	-0.419704	-1.088703	0.344491	1.000000	1.000
572 GOBP-POSITIVE-REGULATION_OF_MOLECULAR-FUNCTION	GO-0044093	37	-0.347159	-1.093316	0.340992	1.000000	1.000
573 GOBP-CELLULAR-GLUCOSE-HOMEOSTASIS	GO-0001678	5	-0.563699	-1.094113	0.361281	1.000000	1.000
574 GOBP-MONOCARBOXYLIC-ACID-TRANSPORT	GO-0015718	5	-0.552591	-1.094331	0.372274	1.000000	1.000
575 GOBP-DICARBOXYLIC-ACID-TRANSPORT	GO-0006835	5	-0.552591	-1.095316	0.369969	1.000000	1.000
576 GOBP-REGULATION-OF-ANION-TRANSPORT	GO-0044070	20	-0.386334	-1.095837	0.325641	1.000000	1.000
577 GOBP-RESPONSE-TO-DRUG	GO-0042493	11	-0.444759	-1.098961	0.326360	1.000000	1.000
578 GOBP-ENDOTHELIAL-CELL-PROLIFERATION	GO-0001935	8	-0.491416	-1.101823	0.320513	1.000000	1.000
579 GOBP-MUSCLE-CELL-DIFFERENTIATION	GO-0042692	10	-0.464815	-1.102901	0.373372	1.000000	1.000
580 GOBP-CELL-CELL-ADHESION	GO-0098609	14	-0.419438	-1.110284	0.318436	1.000000	1.000
581 GOBP-CALCIUM-MEDIATED-SIGNALING	GO-0019722	10	-0.465824	-1.113162	0.318182	1.000000	1.000
582 GOBP-RESPONSE-TO-INTERLEUKIN_1	GO-0070555	5	-0.564244	-1.116376	0.329670	1.000000	1.000
583 GOBP-PEPTIDE-SECRETION	GO-0002790	9	-0.485818	-1.119999	0.326590	1.000000	1.000
584 GOBP-REGULATION-OF-LIPID-LOCALIZATION	GO-1905952	5	-0.575748	-1.127522	0.315625	1.000000	1.000
585 GOBP-PEPTIDYL-AMINO-ACID-MODIFICATION	GO-0018193	22	-0.394009	-1.129270	0.282946	1.000000	1.000
586 GOBP-G-PROTEIN-COUPLED-RECEPTOR-SIGNALING-PATHWAY	GO-0007186	18	-0.408097	-1.134236	0.308201	1.000000	1.000
587 REACTOME-RNA-POLYMERASE-II-TRANSCRIPTION	R-RNO-73857	20	-0.397488	-1.134652	0.318471	1.000000	1.000
588 GOBP-REGULATION-OF-CELLULAR-RESPONSE-TO-STRESS	GO-0080135	9	-0.481712	-1.134963	0.309278	1.000000	1.000
589 GOBP-REGULATION-OF-NMDA-RECEPTOR-ACTIVITY	GO-2000310	10	-0.473536	-1.139352	0.309722	1.000000	1.000
590 GOBP-REGULATION-OF-PROTEIN-MODIFICATION-PROCESS	GO-0031399	28	-0.378627	-1.139712	0.286064	1.000000	1.000
591 GOBP-CHROMOSOME-ORGANIZATION	GO-0051276	6	-0.557842	-1.141265	0.311526	1.000000	1.000
592 GOBP-CELLULAR-RESPONSE-TO-ALCOHOL	GO-0097306	15	-0.596216	-1.142470	0.283969	1.000000	1.000
593 GOBP-RHYTHMIC-PROCESS	GO-0048511	15	-0.427663	-1.142810	0.299724	1.000000	1.000
594 GOBP-REGULATION-OF-CATION-TRANSMEMBRANE-TRANSPORT	GO-1904062	16	-0.424573	-1.144105	0.298343	1.000000	1.000
595 GOBP-POSITIVE-REGULATION-OF-CELLULAR-COMPONENT...	GO-0044089	9	-0.489456	-1.145159	0.312769	1.000000	1.000
596 GOBP-CELLULAR-COMPONENT-MAINTENANCE	GO-0043954	5	-0.577035	-1.145598	0.308442	1.000000	1.000
597 GOBP-RESPONSE-TO-HORMONE	GO-0009725	20	-0.400516	-1.151542	0.272490	1.000000	1.000
598 GOBP-ANATOMICAL-STRUCTURE-FORMATION-INVOLVED-I...	GO-0048646	20	-0.411032	-1.158368	0.271208	1.000000	1.000
599 GOBP-SECRETION	GO-0046903	24	-0.397534	-1.161727	0.270130	1.000000	1.000

Continuation of Table S9

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
600	GOBP-ORGANOPHOSPHATE-METABOLIC-PROCESS	GO-0019637	8	-0.511421	-1.161778	0.268012	1.000000	1.000
601	GOBP-POSITIVE-REGULATION-OF-PHOSPHORUS-METABOL...	GO-0010562	23	-0.402624	-1.164539	0.259446	1.000000	1.000
602	GOBP-POSITIVE-REGULATION-OF-PROTEIN-MODIFICATI...	GO-0031401	22	-0.409086	-1.173057	0.242967	0.998342	1.000
603	GOBP-ADENYLATE-CYCLASE-INHIBITING-G-PROTEIN.CO...	GO-0007196	5	-0.596236	-1.173152	0.261725	1.000000	1.000
604	GOBP-PROTEIN-PHOSPHORYLATION	GO-0006468	33	-0.381901	-1.173586	0.258724	1.000000	1.000
605	GOBP-MAPK-CASCADE	GO-0000165	18	-0.423257	-1.174522	0.242063	1.000000	1.000
606	GOBP-RESPONSE-TO-LIPID	GO-0033993	19	-0.424141	-1.174553	0.255629	1.000000	1.000
607	GOBP-NEGATIVE-REGULATION-OF-ION-TRANSPORT	GO-0043271	11	-0.473346	-1.176737	0.266943	1.000000	1.000
608	GOBP-CELLULAR-RESPONSE-TO-LIPID	GO-0071396	15	-0.451852	-1.178217	0.256831	1.000000	1.000
609	GOBP-ORGANONITROGEN-COMPOUND-CATABOLIC-PROCESS	GO-1901565	10	-0.493211	-1.179490	0.264069	1.000000	1.000
610	GOBP-CATION-TRANSPORT	GO-0006812	25	-0.405597	-1.181299	0.232617	1.000000	1.000
611	GOBP-REGULATION-OF-HORMONE-SECRETION	GO-0046883	8	-0.525095	-1.182016	0.266176	1.000000	1.000
612	GOBP-CIRCULATORY-SYSTEM-PROCESS	GO-0003013	5	-0.609112	-1.182520	0.233129	1.000000	1.000
613	GOBP-SENSORY-PERCEPTION-OF-PAIN	GO-0019233	5	-0.608226	-1.183996	0.242326	1.000000	1.000
614	GOBP-POSITIVE-REGULATION-OF-PROTEIN-PHOSPHORYL...	GO-0001934	22	-0.409086	-1.185452	0.256545	1.000000	1.000
615	GOBP-PROTEIN-MODIFICATION-BY-SMALL-PROTEIN-CON...	GO-0032446	6	-0.566924	-1.186729	0.263077	1.000000	1.000
616	GOBP-REGULATION-OF-ION-TRANSPORT	GO-0043269	36	-0.381749	-1.188255	0.223793	1.000000	1.000
617	GOBP-HEAD-DEVELOPMENT	GO-0060322	23	-0.415680	-1.192305	0.218629	1.000000	1.000
618	GOBP-RESPONSE-TO-ALKALOID	GO-0043279	5	-0.608198	-1.197047	0.265823	1.000000	1.000
619	REACTOME-MAPK-FAMILY-SIGNALING-CASCADES	R-RNO-5683057	12	-0.473506	-1.199269	0.240109	1.000000	1.000
620	GOBP-COAGULATION	GO-0050817	8	-0.537222	-1.201775	0.252252	1.000000	1.000
621	GOBP-CELL-JUNCTION-ORGANIZATION	GO-0034330	19	-0.433444	-1.202164	0.238095	1.000000	1.000
622	GOBP-LIPID-LOCALIZATION	GO-0010876	10	-0.496916	-1.210198	0.233658	1.000000	1.000
623	GOBP-CATION-TRANSMEMBRANE-TRANSPORT	GO-0098655	18	-0.441926	-1.215516	0.208820	1.000000	1.000
624	GOBP-NUCLEOBASE-CONTAINING-SMALL-MOLECULE-META...	GO-0055086	7	-0.566276	-1.216265	0.220264	1.000000	1.000
625	GOBP-CELLULAR-MACROMOLECULE-CATABOLIC-PROCESS	GO-0044265	5	-0.615464	-1.220344	0.218989	1.000000	1.000
626	GOBP-PEPTIDE-HORMONE-SECRETION	GO-0030072	7	-0.570427	-1.220394	0.209270	1.000000	1.000
627	GOBP-EMBRYONIC-MORPHOGENESIS	GO-0048598	6	-0.596193	-1.222666	0.227474	1.000000	1.000
628	GOBP-PEPTIDYL-SERINE-MODIFICATION	GO-0018209	12	-0.475743	-1.225924	0.206704	1.000000	1.000
629	GOBP-MULTICELLULAR-ORGANISMAL-RESPONSE-TO-STRESS	GO-0033555	5	-0.626071	-1.228291	0.225460	1.000000	1.000
630	REACTOME-INTEGRATION-OF-ENERGY-METABOLISM	R-RNO-163685	5	-0.627115	-1.233136	0.214734	0.994959	1.000
631	REACTOME-INTRACELLULAR-SIGNALING-BY-SECOND-MES...	R-RNO-9006925	15	-0.460083	-1.234268	0.216359	1.000000	1.000
632	GOBP-REGULATION-OF-SYNAPTIC-PLASTICITY	GO-0048167	21	-0.432408	-1.237526	0.193838	0.995584	1.000
633	GOBP-NEGATIVE-REGULATION-OF-ANION-TRANSPORT	GO-1903792	8	-0.547765	-1.240107	0.208999	0.994575	1.000
634	GOBP-ORGANIC-HYDROXY-COMPOUND-TRANSPORT	GO-0015850	6	-0.598071	-1.241865	0.214286	0.997390	1.000
635	GOBP-INSULIN-SECRETION	GO-0030073	7	-0.570427	-1.248338	0.220060	0.978718	1.000
636	GOBP-G-PROTEIN-COUPLED-GLUTAMATE-RECEPTOR-SIGN...	GO-0007216	8	-0.555863	-1.252400	0.206490	0.970793	1.000
637	GOBP-POSITIVE-REGULATION-OF-PROTEIN-METABOLIC...	GO-0051247	27	-0.423352	-1.253732	0.179975	0.975219	1.000
638	GOBP-PROTEIN-LOCALIZATION-TO-POSTSYNAPSE	GO-0062237	5	-0.643746	-1.257259	0.176744	0.969323	1.000
639	GOBP-LIPID-EXPORT-FROM-CELL	GO-0140353	5	-0.635321	-1.258486	0.181269	0.974921	1.000
640	GOBP-PROTEIN-LOCALIZATION-TO-SYNAPSE	GO-0035418	5	-0.643746	-1.259984	0.176378	0.979005	1.000
641	REACTOME-G-ALPHA-Q-SIGNALING-EVENTS	R-RNO-416476	6	-0.603556	-1.262308	0.178306	0.979645	1.000
642	REACTOME-GPCR-LIGAND-BINDING	R-RNO-500792	8	-0.565828	-1.262332	0.193922	0.991306	1.000

Continuation of Table S9

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
643 GOBP-REGULATION-OF-NEURONAL-SYNAPTIC-PLASTICITY	GO-0048168	7	-0.585449	-1.263048	0.197309	0.999959	1.000
644 GOBP-REGULATION-OF-SYSTEM-PROCESS	GO-0044057	18	-0.463942	-1.265682	0.186577	0.999555	1.000
645 GOBP-CHROMATIN-ORGANIZATION	GO-0006325	5	-0.654717	-1.266646	0.163666	1.000000	1.000
646 GOBP-ADENYLATE-CYCLASE-INHIBITING-G-PROTEIN.CO...	GO-0007193	9	-0.546766	-1.268443	0.180115	1.000000	1.000
647 GOBP-REGULATION-OF-MEMBRANE-POTENTIAL	GO-0042391	17	-0.461381	-1.273254	0.169935	0.999643	1.000
648 GOBP-VESICLE-MEDIATED-TRANSPORT-IN-SYNAPSE	GO-0099003	7	-0.591483	-1.273622	0.173333	1.000000	1.000
649 GOBP-EXCITATORY-CHEMICAL-SYNAPTIC-TRANSMISSION	GO-0098976	5	-0.662498	-1.278628	0.158805	0.999542	1.000
650 GOBP-REGULATION-OF-METAL-ION-TRANSPORT	GO-0010959	6	-0.619213	-1.284928	0.143279	0.980427	1.000
651 GOBP-CELLULAR-RESPONSE-TO-HORMONE-STIMULUS	GO-0032870	11	-0.525615	-1.291158	0.161517	0.962047	1.000
652 GOBP-POSITIVE-REGULATION-OF-CATALYTIC-ACTIVITY	GO-0043085	29	-0.423040	-1.295109	0.156627	0.955319	1.000
653 GOBP-REGULATION-OF-VESICLE-MEDIATED-TRANSPORT	GO-0060627	12	-0.504986	-1.296152	0.157447	0.963406	1.000
654 REACTOME-SIGNALING-BY-WNT	R-RNO-195721	7	-0.602468	-1.298483	0.152012	0.965032	1.000
655 GOBP-PLATELET-ACTIVATION	GO-0030168	6	-0.616553	-1.299624	0.172107	0.972347	1.000
656 GOBP-REGULATION-OF-TRANS-SYNAPTIC-SIGNALING	GO-0099177	40	-0.415125	-1.301278	0.135553	0.978024	1.000
657 GOBP-INTRACELLULAR-RECEPTOR-SIGNALING-PATHWAY	GO-0030522	5	-0.670527	-1.315061	0.137405	0.920358	1.000
658 REACTOME-OPIOID-SIGNALING	R-RNO-111885	12	-0.532007	-1.317205	0.126918	0.923636	1.000
659 REACTOME-RAS-ACTIVATION-UPON-CA2-INFLUX-THROUGH...	R-HSA-442982	6	-0.645104	-1.324186	0.131268	0.901819	1.000
660 GOBP-REGULATION-OF-POSTSYNAPTIC-MEMBRANE-POTEN...	GO-0060078	14	-0.507939	-1.327337	0.114325	0.899018	1.000
661 GOBP-CELLULAR-RESPONSE-TO-PEPTIDE-HORMONE-STIM...	GO-0071375	9	-0.579505	-1.338287	0.131657	0.856880	1.000
662 REACTOME-CREB1-PHOSPHORYLATION-THROUGH-NMDA-RE...	R-RNO-442742	8	-0.653605	-1.351515	0.104956	0.842773	1.000
663 GOBP-PURINE-CONTAINING-COMPOUND-METABOLIC-PROCESS	GO-0072521	6	-0.653605	-1.351515	0.122137	0.817701	1.000
664 REACTOME-TRAFFICKING-OF-GLUR2-CONTAINING-AMPA...	R-RNO-416993	8	-0.597618	-1.356767	0.120664	0.805597	1.000
665 GOBP-ADENYLATE-CYCLASE-MODULATING-G-PROTEIN.CO...	GO-0007188	11	-0.551606	-1.360440	0.111888	0.802109	1.000
666 GOBP-REGULATION-OF-CIRCADIAN-RHYTHM	GO-0042752	7	-0.632489	-1.364290	0.104046	0.796824	1.000
667 GOBP-ION-HOMEOSTASIS	GO-0050801	16	-0.509467	-1.365541	0.093878	0.804584	1.000
668 REACTOME-CLASS-C-3-METABOTROPIC-GLUTAMATE-PHER...	R-RNO-420499	7	-0.623198	-1.367355	0.110764	0.809659	1.000
669 GOBP-MUSCLE-CONTRACTION	GO-0006936	5	-0.702607	-1.368364	0.084375	0.819200	1.000
670 GOBP-REGULATION-OF-TRANSPORT	GO-0051049	44	-0.442158	-1.376852	0.075904	0.790028	1.000
671 GOBP-HORMONE-TRANSPORT	GO-0009914	9	-0.589728	-1.392303	0.094767	0.730630	1.000
672 GOBP-REGULATION-OF-CELLULAR-COMPONENT-BIOGENESIS	GO-0044087	10	-0.577488	-1.398875	0.098870	0.723042	1.000
673 GOBP-HOMEOSTATIC-PROCESS	GO-0042592	31	-0.452616	-1.399601	0.073885	0.722983	1.000
674 GOBP-REGULATION-OF-BODY-FLUID-LEVELS	GO-0050878	11	-0.576377	-1.403685	0.088359	0.716437	1.000
675 GOBP-SECOND-MESSENGER-MEDIATED-SIGNALING	GO-0019932	16	-0.532514	-1.407098	0.067024	0.714960	1.000
676 GOBP-NEUROTRANSMITTER-SECRETION	GO-0007269	6	-0.692969	-1.408347	0.061444	0.723541	1.000
677 GOBP-ORGANOPHOSPHATE-BIOSYNTHETIC-PROCESS	GO-0090407	5	-0.738159	-1.410495	0.061285	0.728433	1.000
678 GOBP-METAL-ION-HOMEOSTASIS	GO-0055065	14	-0.543855	-1.416322	0.078838	0.716275	1.000
679 GOBP-PEPTIDYL-LYSINE-MODIFICATION	GO-0018205	5	-0.718611	-1.425978	0.073244	0.684926	1.000
680 GOBP-IONOTROPIC-GLUTAMATE-RECEPTOR-SIGNALING_P...	GO-0035235	9	-0.615662	-1.428699	0.059002	0.687587	1.000
681 GOBP-CALCIUM-ION-TRANSPORT-INTO-CYTOSOL	GO-0060402	7	-0.654230	-1.429260	0.064897	0.701224	1.000
682 GOBP-CYTOSOLIC-CALCIUM-ION-TRANSPORT	GO-0060401	7	-0.654230	-1.432536	0.061285	0.701606	1.000
683 GOBP-MUSCLE-SYSTEM-PROCESS	GO-0003012	9	-0.598543	-1.433077	0.089021	0.715980	1.000
684 REACTOME-SYNAPTIC-ADHESION-LIKE-MOLECULES	R-RNO-8849932	9	-0.617106	-1.445398	0.066572	0.672724	1.000
685 GOBP-CALCIUM-ION-TRANSMEMBRANE-TRANSPORT	GO-0070588	7	-0.654230	-1.449090	0.077485	0.671131	1.000

Continuation of Table S9

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
686	GOBP-NUCLEOSIDE-PHOSPHATE-BIOSYNTHETIC-PROCESS	5	-0.738159	-1.454672	0.056162	0.661038	1.000
687	GOBP-NEGATIVE-REGULATION-OF-TRANSPORT	13	-0.571344	-1.456044	0.061141	0.672112	1.000
688	REACTOME-G-ALPHA-1-SIGNALING-EVENTS	18	-0.528796	-1.457380	0.055851	0.683992	1.000
689	GOBP-REGULATION-OF-MUSCLE-SYSTEM-PROCESS	8	-0.659383	-1.466323	0.049080	0.659484	1.000
690	REACTOME-ASSEMBLY-AND-CELL-SURFACE-PRESENTATION...	8	-0.653444	-1.470223	0.042773	0.658543	1.000
691	REACTOME-NEGATIVE-REGULATION-OF-NMDA-RECEPTOR...	8	-0.653444	-1.477888	0.054492	0.640059	1.000
692	REACTOME-TRANSCRIPTIONAL-REGULATION-BY-MBCP2	7	-0.688166	-1.488674	0.041667	0.605990	1.000
693	GOBP-INORGANIC-ION-TRANSMEMBRANE-TRANSPORT	9	-0.643190	-1.505724	0.050279	0.547194	1.000
694	REACTOME-SIGNALING-BY-GPCR	22	-0.524598	-1.525836	0.024516	0.480743	1.000
695	GOBP-SYNAPTIC-SIGNALING	47	-0.478985	-1.532798	0.028674	0.468244	1.000
696	REACTOME-G-PROTEIN-MEDIATED-EVENTS	9	-0.654350	-1.538890	0.036711	0.457880	1.000
697	GOBP-SENSORY-PERCEPTION	9	-0.667809	-1.547433	0.036550	0.441207	1.000
698	GOBP-REGULATION-OF-CYTOSOLIC-CALCIUM-ION-CONCE...	13	-0.602256	-1.554651	0.020690	0.430099	1.000
699	REACTOME-LONG-TERM-POTENTIATION	10	-0.648852	-1.556433	0.035813	0.439858	1.000
700	GOBP-DIVALENT-INORGANIC-CATION-HOMEOSTASIS	13	-0.602256	-1.557471	0.030997	0.453915	1.000
701	GOBP-NEUROTRANSMITTER-TRANSPORT	7	-0.722645	-1.560969	0.029586	0.458920	1.000
702	GOBP-REGULATION-OF-NEUROTRANSMITTER-LEVELS	10	-0.722645	-1.562921	0.025148	0.471327	1.000
703	REACTOME-TRAFICKING-OF-AMPA-RECEPTORS	11	-0.643234	-1.569108	0.027816	0.465570	1.000
704	GOBP-CHEMICAL-HOMEOSTASIS	23	-0.542770	-1.583397	0.017903	0.427749	1.000
705	REACTOME-CA-DEPENDENT-EVENTS	8	-0.699311	-1.586428	0.023460	0.435859	1.000
706	REACTOME-UNBLOCKING-OF-NMDA-RECEPTORS-GLUTAMAT...	12	-0.617424	-1.590209	0.024291	0.441943	1.000
707	GOBP-CELLULAR-ION-HOMEOSTASIS	14	-0.615715	-1.595216	0.018945	0.445566	1.000
708	REACTOME-NEUREXINS-AND-NEUROLIGINS	9	-0.683473	-1.599594	0.029155	0.452451	1.000
709	REACTOME-BETA-CATENIN-INDEPENDENT-WNT-SIGNALING	5	-0.807129	-1.608761	0.010654	0.441505	0.999
710	REACTOME-ACTIVATION-OF-NMDA-RECEPTORS-AND-POST...	16	-0.591208	-1.610997	0.017663	0.460898	0.999
711	REACTOME-DAG-AND-JP3-SIGNALING	8	-0.716803	-1.620917	0.012968	0.449983	0.998
712	GOBP-REGULATION-OF-SECRETION	14	-0.618539	-1.622892	0.024324	0.474336	0.997
713	GOBP-CELL-CELL-SIGNALING	56	-0.522178	-1.626755	0.007084	0.493022	0.997
714	GOBP-METAL-ION-TRANSPORT	11	-0.660112	-1.631975	0.020776	0.510406	0.997
715	REACTOME-PROTEIN-PROTEIN-INTERACTIONS-AT-SYNAPSES	12	-0.646596	-1.632099	0.009472	0.560541	0.997
716	GOBP-CALCIUM-ION-TRANSPORT	11	-0.660112	-1.644212	0.014045	0.550322	0.995
717	REACTOME-G-ALPHA-Z-SIGNALING-EVENTS	5	-0.845055	-1.661861	0.004710	0.514802	0.991
718	REACTOME-NEUROTRANSMITTER-RECEPTORS-AND-POSTSY...	22	-0.585312	-1.672455	0.009162	0.528034	0.984
719	GOBP-GLUTAMATE-RECEPTOR-SIGNALING-PATHWAY	17	-0.611666	-1.695879	0.014249	0.478738	0.960
720	GOBP-REGULATION-OF-NEUROTRANSMITTER-TRANSPORT	6	-0.825433	-1.708039	0.001490	0.506180	0.940
721	GOBP-CELLULAR-HOMEOSTASIS	18	-0.637441	-1.758646	0.003953	0.345479	0.772
722	REACTOME-TRANSMISSION-ACROSS-CHEMICAL-SYNAPSES	23	-0.608925	-1.767434	0.001342	0.412871	0.737
723	GOBP-SIGNAL-RELEASE	14	-0.677178	-1.799338	0.004065	0.417682	0.595
724	REACTOME-NEURONAL-SYSTEM	26	-0.634937	-1.884670	0.000000	0.252430	0.240

End of Table

Supplementary Table S10: SC cervical segment late profile Profile (45 DPL peak) GSEA results.

Begin of Table S10								
	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
0	REACTOME_G-PROTEIN-MEDIATED_EVENTS	R-RNO-112040	9	0.594937	2.096231	0.005464	0.321229	0.273
1	REACTOME_DAG-AND_IP3-SIGNALING	R-RNO-1489509	8	0.587500	2.038604	0.000000	0.240319	0.379
2	GOBP-NEUROINFLAMMATORY_RESPONSE	GO-0150076	5	0.746988	1.986881	0.000000	0.217888	0.478
3	REACTOME_CA-DEPENDENT_EVENTS	R-RNO-111996	8	0.587500	1.932299	0.005405	0.231253	0.603
4	GOBP_POSITIVE-REGULATION_OF_ESTABLISHMENT_OF_P...	GO-1904951	5	0.698795	1.873576	0.008032	0.253591	0.714
5	REACTOME_G_ALPHA_I-SIGNALING_EVENTS	R-RNO-418594	18	0.371429	1.802278	0.000000	0.308596	0.838
6	REACTOME_G_ALPHA_Z-SIGNALING_EVENTS	R-RNO-418597	5	0.590361	1.571350	0.027778	0.845724	0.998
7	REACTOME_ANTILINFLAMMATORY_RESPONSE_FAVOURING...	R-HSA-9662851	5	0.566265	1.558593	0.024691	0.788925	0.999
8	GOBP_VESICLE-MEDIATED_TRANSPORT_IN_SYNAPSE	GO-0099003	7	0.469136	1.483705	0.070270	0.980450	1.000
9	GOBP_ORGANOPHOSPHATE-BIOSYNTHETIC-PROCESS	GO-0090407	5	0.542169	1.436462	0.086066	1.000000	1.000
10	GOBP-REGULATION-OF-NEUROTRANSMITTER_TRANSPORT	GO-0051588	6	0.493152	1.423565	0.102326	1.000000	1.000
11	GOBP_NUCLEOSIDE-PHOSPHATE-BIOSYNTHETIC-PROCESS	GO-1901293	5	0.542169	1.423515	0.080645	0.945016	1.000
12	GOBP-REGULATION-OF-SECRETION	GO-0051046	14	0.324324	1.407917	0.083333	0.930927	1.000
13	REACTOME_OPIOID-SIGNALING	R-RNO-111885	12	0.342105	1.397053	0.130769	0.904115	1.000
14	GOBP-SIGNAL-RELEASE	GO-0023061	14	0.324324	1.351769	0.120567	1.000000	1.000
15	GOBP-RESPONSE-TO-HEAT	GO-0009408	7	0.425440	1.335581	0.124378	1.000000	1.000
16	REACTOME-TRAFFICKING-OF_AMPA-RECEPTORS	R-RNO-399719	11	0.345258	1.332677	0.123188	0.974669	1.000
17	GOBP-REGULATION-OF-CELLULAR-RESPONSE-TO-STRESS	GO-0080135	9	0.386593	1.329130	0.160221	0.933027	1.000
18	GOBP-RESPONSE-TO-TEMPERATURE-STIMULUS	GO-0009266	9	0.370397	1.327962	0.147929	0.887156	1.000
19	GOBP_POSITIVE-REGULATION-OF-SECRETION	GO-0051047	6	0.463415	1.304201	0.133028	0.927399	1.000
20	GOBP-REGULATION-OF-VESICLE-MEDIATED_TRANSPORT	GO-0060627	12	0.315789	1.275096	0.164179	0.989246	1.000
21	HALLMARK_ALLOGRAFT-REJECTION	M5950	7	0.399785	1.241317	0.169591	1.000000	1.000
22	GOBP_POSITIVE-REGULATION-OF_ORGANELLE-ORGANIZA...	GO-0010638	10	0.330788	1.233393	0.194805	1.000000	1.000
23	REACTOME_INTERFERON-SIGNALING	R-RNO-913531	6	0.419293	1.219348	0.171806	1.000000	1.000
24	GOBP_ORGANOPHOSPHATE-METABOLIC-PROCESS	GO-0019637	8	0.362500	1.212824	0.210811	1.000000	1.000
25	REACTOME_TRANSCRIPTIONAL-REGULATION_BY_MECP2	R-RNO-8986944	7	0.370370	1.166843	0.235577	1.000000	1.000
26	GOBP-REGULATION-OF-METAL-ION-TRANSPORT	GO-0010959	6	0.396546	1.164011	0.219298	1.000000	1.000
27	REACTOME_NEURONAL-SYSTEM	R-RNO-112316	26	0.225807	1.154877	0.212121	1.000000	1.000
28	GOBP-ADENYLATE-CYCLASE-MODULATING-G-PROTEIN_CO...	GO-0007188	11	0.303015	1.153771	0.245399	1.000000	1.000
29	REACTOME_ONCOGENIC_MAPK-SIGNALING	R-HSA-6802957	5	0.434005	1.145050	0.270161	1.000000	1.000
30	REACTOME_TRANSMISSION-ACROSS-CHEMICAL-SYNAPSES	R-RNO-112315	23	0.215385	1.14123	0.259740	1.000000	1.000
31	GOBP-REGULATION-OF-PEPTIDE-TRANSPORT	GO-0090087	10	0.307692	1.123151	0.290323	1.000000	1.000
32	GOBP-EXOCYTOSIS	GO-0006887	11	0.286390	1.120433	0.290541	1.000000	1.000
33	GOBP-NEUROTRANSMITTER_TRANSPORT	GO-0006836	7	0.345679	1.119814	0.301435	1.000000	1.000
34	REACTOME-NEUROTRANSMITTER-RECEPTORS-AND_POSTSY...	R-RNO-112314	22	0.212121	1.110935	0.319149	1.000000	1.000
35	GOBP-REGULATION-OF_ORGANELLE-ORGANIZATION	GO-0033043	14	0.250672	1.100765	0.290323	1.000000	1.000
36	GOBP-ESTABLISHMENT-OF-PROTEIN-LOCALIZATION	GO-0045184	17	0.229661	1.097540	0.299065	1.000000	1.000
37	GOBP_SECRETION	GO-0046903	24	0.206223	1.094243	0.300000	1.000000	1.000
38	GOBP_POSITIVE-REGULATION-OF_APOPTOTIC-SIGNALIN...	GO-2001235	5	0.421687	1.093242	0.291188	1.000000	1.000
39	GOBP_POSITIVE-REGULATION-OF-TRANSPORT	GO-0051050	26	0.209677	1.089743	0.370370	1.000000	1.000
40	GOBP-REGULATION-OF-NEURON-DIFFERENTIATION	GO-0045664	5	0.433735	1.089111	0.327189	1.000000	1.000

Continuation of Table S10

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
41	GOBP-REGULATION-OF-TRANS-SYNAPTIC-SIGNALING	40	0.171324	1.083724	0.291667	0.999037	1.000
42	GOBP-NUCLEOBASE-CONTAINING-SMALL-MOLECULE-META...	7	0.358025	1.082304	0.339207	0.980425	1.000
43	GOBP-HORMONE-TRANSPORT	9	0.303797	1.076570	0.318182	0.977801	1.000
44	GOBP-REGULATION-OF-NEUROTRANSMITTER-LEVELS	7	0.345679	1.056221	0.339806	1.000000	1.000
45	GOBP-POSITIVE-REGULATION-OF-PEPTIDYL-TYROSINE-...	8	0.316544	1.053905	0.378238	1.000000	1.000
46	GOBP-PEPTIDE-SECRETION	9	0.303797	1.036609	0.370166	1.000000	1.000
47	REACTOME-BETA-CATENIN-INDEPENDENT-WNT-SIGNALING	5	0.385542	1.036576	0.333333	1.000000	1.000
48	GOBP-PURINE-CONTAINING-COMPOUND-METABOLIC-PROCESS	6	0.353659	1.004120	0.393939	1.000000	1.000
49	GOBP-ENDOCYTOSIS	8	0.300000	0.998122	0.417526	1.000000	1.000
50	GOBP-MULTICELLULAR-ORGANISMAL-RESPONSE-TO-STRESS	5	0.385542	0.991290	0.460000	1.000000	1.000
51	GOBP-NEUROTRANSMITTER-SECRETION	6	0.341463	0.973863	0.480952	1.000000	1.000
52	GOBP-ENDOTHELIAL-CELL-PROLIFERATION	8	0.288864	0.961263	0.448649	1.000000	1.000
53	GOBP-REGULATION-OF-HORMONE-SECRETION	8	0.300000	0.955914	0.477273	1.000000	1.000
54	GOBP-REGULATION-OF-HEMOPOIESIS	10	0.256410	0.937107	0.486667	1.000000	1.000
55	GOBP-PEPTIDE-HORMONE-SECRETION	7	0.296296	0.933504	0.507614	1.000000	1.000
56	GOBP-INSULIN-SECRETION	7	0.296296	0.932732	0.547619	1.000000	1.000
57	REACTOME-PLATELET-ACTIVATION-SIGNALING-AND-AGG...	7	0.295410	0.932564	0.518518	1.000000	1.000
58	GOBP-CELL-CELL-SIGNALING	56	0.161374	0.929590	0.600000	1.000000	1.000
59	GOBP-REGULATION-OF-ION-TRANSPORT	36	0.161557	0.923654	0.531915	1.000000	1.000
60	GOBP-POSITIVE-REGULATION-OF-BINDING	6	0.317073	0.915520	0.539535	1.000000	1.000
61	GOBP-ADENYLATE-CYCLASE-INHIBITING-G-PROTEIN.CO...	5	0.337349	0.912058	0.583333	1.000000	1.000
62	REACTOME-GPCR-LIGAND-BINDING	8	0.275000	0.908907	0.497238	1.000000	1.000
63	GOBP-REGULATION-OF-PEPTIDE-SECRETION	7	0.296296	0.906814	0.511737	1.000000	1.000
64	GOBP-MEMORY	13	0.208661	0.887545	0.627586	1.000000	1.000
65	REACTOME-RAS-ACTIVATION-UPON-CA2-INFLUX-THROUG...	6	0.305898	0.885674	0.604348	1.000000	1.000
66	GOBP-EPITHELIAL-CELL-PROLIFERATION	12	0.219438	0.880116	0.609589	1.000000	1.000
67	GOBP-REGULATION-OF-PROTEIN-LOCALIZATION	18	0.185714	0.878188	0.616279	1.000000	1.000
68	REACTOME-ACTIVATION-OF-NMDA-RECEPTORS-AND-POST...	16	0.194444	0.872191	0.610000	1.000000	1.000
69	GOBP-REGULATION-OF-ENDOCYTOSIS	6	0.292683	0.871289	0.594203	1.000000	1.000
70	GOBP-ION-HOMEOSTASIS	16	0.194444	0.869180	0.685714	1.000000	1.000
71	GOBP-CELLULAR-RESPONSE-TO-ALCOHOL	5	0.318657	0.868549	0.617886	1.000000	1.000
72	GOBP-SYNAPTIC-TRANSMISSION-GLUTAMATERGIC	13	0.200000	0.866284	0.602941	1.000000	1.000
73	GOBP-REGULATION-OF-PEPTIDE-HORMONE-SECRETION	6	0.292683	0.865101	0.649038	1.000000	1.000
74	GOBP-RECEPTOR-MEDIATED-ENDOCYTOSIS	6	0.292683	0.856334	0.614679	1.000000	1.000
75	GOBP-REGULATION-OF-TRANSPORT	44	0.145711	0.855137	0.630435	1.000000	1.000
76	REACTOME-CLASS-C-3-METABOTROPIC-GLUTAMATE-PHER...	7	0.271605	0.853978	0.602151	1.000000	1.000
77	GOBP-DENDRITE-DEVELOPMENT	10	0.230769	0.847343	0.686391	1.000000	1.000
78	REACTOME-CREB1-PHOSPHORYLATION-THROUGH-NMDA.RE...	8	0.260203	0.841317	0.698413	1.000000	1.000
79	GOBP-ADENYLATE-CYCLASE-INHIBITING-G-PROTEIN.CO...	9	0.232374	0.834401	0.635870	1.000000	1.000
80	GOBP-SYNAPTIC-SIGNALING	47	0.141383	0.830334	0.660000	1.000000	1.000
81	GOBP-PHAGOCYTOSIS	5	0.316199	0.820870	0.655303	1.000000	1.000
82	GOBP-REGULATION-OF-VASCULAR-ASSOCIATED-SMOOTH...	5	0.313902	0.813714	0.712264	1.000000	1.000
83	REACTOME-INTEGRATION-OF-ENERGY-METABOLISM	5	0.313253	0.811089	0.710526	1.000000	1.000

Continuation of Table S10

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
84	GOBP-NEGATIVE-REGULATION-OF-CELL-DEVELOPMENT	6	0.276136	0.810615	0.695652	1.000000	1.000
85	GOBP-NERVE-DEVELOPMENT	9	0.227848	0.808345	0.751479	1.000000	1.000
86	GOBP-AMEBOIDAL-TYPE-CELL-MIGRATION	11	0.211167	0.799571	0.722222	1.000000	1.000
87	GOBP-REGULATION-OF-RECEPTOR-MEDIATED-ENDOCYTOSIS	5	0.289157	0.790245	0.761719	1.000000	1.000
88	GOBP-REGULATION-OF-SYNAPTIC-TRANSMISSION-GLUTA...	12	0.197366	0.788995	0.726619	1.000000	1.000
89	GOBP-REGULATION-OF-CYTOSKELETON-ORGANIZATION	5	0.289157	0.785252	0.736111	1.000000	1.000
90	GOBP-ACTIVATION-OF-MAPK-ACTIVITY	6	0.268293	0.780053	0.795652	1.000000	1.000
91	GOBP-POSITIVE-REGULATION-OF-EPITHELIAL-CELL-PR...	7	0.265510	0.779788	0.729282	1.000000	1.000
92	REACTOME-SIGNALING-BY-GPCR	22	0.152712	0.777521	0.736842	1.000000	1.000
93	GOBP-POSITIVE-REGULATION-OF-HEMOPOIESIS	7	0.246914	0.775330	0.799043	1.000000	1.000
94	GOBP-RECEPTOR-METABOLIC-PROCESS	5	0.289157	0.765591	0.735043	1.000000	1.000
95	GOBP-PEPTIDYL-SERINE-MODIFICATION	12	0.187444	0.764283	0.793333	1.000000	1.000
96	GOBP-RECEPTOR-INTERNALIZATION	5	0.289157	0.763128	0.765217	1.000000	1.000
97	GOBP-POSITIVE-REGULATION-OF-MAP-KINASE-ACTIVITY	6	0.268293	0.761989	0.772947	1.000000	1.000
98	GOBP-DEVELOPMENTAL-MATURATION	5	0.289157	0.749860	0.807843	1.000000	1.000
99	GOBP-REGULATION-OF-LONG-TERM-SYNAPTIC-POTENTIA...	6	0.255273	0.739757	0.815789	1.000000	1.000
100	GOBP-POSITIVE-REGULATION-OF-PHOSPHORUS-METABOL...	23	0.138461	0.738561	0.782051	1.000000	1.000
250	GOBP-CELL-PART-MORPHOGENESIS	25	-0.211248	-0.787343	0.734914	0.936496	1.000
251	GOBP-INFLAMMATORY-RESPONSE	12	-0.256564	-0.790906	0.756912	0.932674	1.000
252	GOBP-MYELOID-LEUKOCYTE-MEDIATED-IMMUNITY	6	-0.317299	-0.791671	0.734456	0.933406	1.000
253	GOBP-RESPIRATORY-SYSTEM-DEVELOPMENT	6	-0.314022	-0.795203	0.726343	0.929373	1.000
254	GOBP-REGULATION-OF-RESPONSE-TO-STRESS	19	-0.227322	-0.795848	0.726101	0.930325	1.000
255	GOBP-FOREBRAIN-DEVELOPMENT	10	-0.269207	-0.796760	0.719660	0.930763	1.000
256	GOBP-CELL-ACTIVATION-INVOLVED-IN-IMMUNE-RESPONSE	6	-0.317299	-0.798268	0.721716	0.930253	1.000
257	REACTOME-NEUTROPHIL-DEGRANULATION	6	-0.317299	-0.799810	0.715013	0.929658	1.000
258	GOBP-NEGATIVE-REGULATION-OF-APOPTOTIC-SIGNALIN...	7	-0.301710	-0.800805	0.706853	0.929969	1.000
259	GOBP-DENDRITE-MORPHOGENESIS	7	-0.300958	-0.804229	0.742749	0.926290	1.000
260	REACTOME-EXTRACELLULAR-MATRIX-ORGANIZATION	5	-0.347501	-0.813377	0.721536	0.913373	1.000
261	GOBP-CELL-CELL-JUNCTION-ASSEMBLY	5	-0.343091	-0.813501	0.669811	0.915160	1.000
262	GOBP-BIOLOGICAL-PROCESS-INVOLVED-IN-SYMBIOTIC....	10	-0.275517	-0.816560	0.697006	0.912089	1.000
263	GOBP-CELL-POPULATION-PROLIFERATION	32	-0.214072	-0.818989	0.698821	0.909805	1.000
264	GOBP-REGULATION-OF-CELLULAR-PROTEIN-LOCALIZATION	12	-0.265035	-0.820628	0.689157	0.908940	1.000
265	GOBP-REGULATION-OF-PROTEIN-PHOSPHORYLATION	25	-0.225885	-0.821403	0.704423	0.909624	1.000
266	GOBP-LOCOMOTORY-BEHAVIOR	8	-0.300000	-0.823014	0.696126	0.908631	1.000
267	GOBP-CELLULAR-LIPID-METABOLIC-PROCESS	7	-0.310454	-0.823059	0.711929	0.910545	1.000
268	GOBP-NEGATIVE-REGULATION-OF-NEURON-DEATH	11	-0.272538	-0.826276	0.684770	0.906912	1.000
269	GOBP-CHEMICAL-HOMEOSTASIS	23	-0.228217	-0.828217	0.687836	0.905475	1.000
270	GOBP-MORPHOGENESIS-OF-AN-EPITHELIUM	6	-0.332542	-0.829400	0.702945	0.905425	1.000
271	GOBP-NEGATIVE-REGULATION-OF-PROTEOLYSIS	8	-0.308854	-0.834784	0.702703	0.897880	1.000
272	GOBP-INTRACELLULAR-PROTEIN-TRANSPORT	8	-0.305823	-0.836534	0.684783	0.896815	1.000
273	GOBP-REGULATION-OF-OSTEOCLAST-DIFFERENTIATION	5	-0.355416	-0.836542	0.674839	0.898770	1.000
274	GOBP-LOCOMOTION	31	-0.222664	-0.843391	0.672359	0.887116	1.000
275	GOBP-ORGANONITROGEN-COMPOUND-BIOSYNTHETIC-PROCESS	13	-0.274732	-0.845775	0.657534	0.886729	1.000

Continuation of Table S10

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
276	GOBP-CHROMOSOME_ORGANIZATION	GO-0051276	6	-0.344368	-0.848940	0.675291	0.882959
277	GOBP-CELLULAR_RESPONSE_TO_PEP_TIDE_HORMONE_STIM...	GO-0071375	9	-0.303289	-0.851775	0.669565	0.879967
278	GOBP-SENSORY_PERCEPTION_OF_PAIN	GO-0019233	5	-0.359701	-0.852870	0.648294	0.879989
279	GOBP-ORGANIC_ACID_METABOLIC_PROCESS	GO-0006082	7	-0.315379	-0.853015	0.648546	0.881692
280	GOBP-RESPONSE_TO_ALCOHOL	GO-0097305	11	-0.277153	-0.853224	0.657647	0.883256
281	REACTOME-MEMBRANE_TRAFFICKING	R-RNO-199991	5	-0.356914	-0.856123	0.649077	0.879910
282	REACTOME-VESICLE_MEDIATED_TRANSPORT	R-RNO-5053656	5	-0.356914	-0.858032	0.643236	0.878430
283	REACTOME-RHO_GTPASE_EFFECTORS	R-RNO-195258	9	-0.305686	-0.858675	0.653382	0.879296
284	GOBP-PROTEIN_PHOSPHORYLATION	GO-0006468	33	-0.224879	-0.860153	0.672287	0.878637
285	GOBP-PERIPHERAL_NERVOUS_SYSTEM_DEVELOPMENT	GO-0007422	9	-0.302556	-0.862009	0.659731	0.877243
286	GOBP-TISSUE_MORPHOGENESIS	GO-0048729	7	-0.330144	-0.871102	0.635787	0.862795
287	GOBP-REGULATION_OF_PROTEIN_BINDING	GO-0043393	7	-0.329703	-0.872666	0.622307	0.861885
288	GOBP-PROTEIN_LOCALIZATION_TO_PLASMA_MEMBRANE	GO-0072659	7	-0.334640	-0.873147	0.612296	0.863007
289	GOBP-PROTEIN_COMPLEX_OLIGOMERIZATION	GO-0051259	7	-0.326575	-0.874530	0.620779	0.862387
290	GOBP-REGULATION_OF_PEP_TIDASE_ACTIVITY	GO-0052547	10	-0.297950	-0.875246	0.649939	0.862984
291	GOBP-PHOSPHATIDYLINOSITOL_3_KINASE_SIGNALING	GO-0014065	7	-0.334663	-0.875382	0.601258	0.864765
292	REACTOME-SIGNALING_BY_RHO_GTPASES_MIRO_GTPASES...	R-RNO-9716542	9	-0.305686	-0.875843	0.610849	0.865904
293	GOBP-REGULATION_OF_LIPID_LOCALIZATION	GO-1905952	5	-0.379489	-0.877565	0.609290	0.864694
294	GOBP-WOUND_HEALING	GO-0042060	13	-0.277601	-0.877816	0.625290	0.866209
295	GOBP-RESPONSE_TO_PEP_TIDE_HORMONE	GO-0043434	13	-0.277589	-0.877975	0.611561	0.867869
296	GOBP-CELL_ACTIVATION	GO-0001775	22	-0.244754	-0.878597	0.643703	0.868849
297	GOBP-RESPONSE_TO_HORMONE	GO-0009725	20	-0.251645	-0.878697	0.634173	0.870679
298	GOBP-POSITIVE_REGULATION_OF_CATALYTIC_ACTIVITY	GO-0043085	29	-0.236773	-0.879058	0.658405	0.872074
299	GOBP-EPITHELIAL_CELL_DIFFERENTIATION	GO-0030855	7	-0.327550	-0.880365	0.610619	0.871719
300	GOBP-TUBE_DEVELOPMENT	GO-0035295	18	-0.254102	-0.885621	0.614016	0.863885
301	GOBP-GLUCOSE_METABOLIC_PROCESS	GO-0006006	6	-0.353225	-0.886008	0.613184	0.865267
302	REACTOME-SIGNALING_BY_NUCLEAR_RECEPTORS	R-RNO-9006931	8	-0.321798	-0.886343	0.620823	0.866703
303	GOBP-POSITIVE_REGULATION_OF_PROTEIN_SERINE_THR...	GO-0071902	9	-0.312283	-0.886363	0.630824	0.868723
304	REACTOME-ESR-MEDIATED_SIGNALING	R-RNO-8939211	8	-0.321798	-0.886525	0.597070	0.870478
305	GOBP-SMALL_GTPASE-MEDIATED_SIGNAL_TRANSDUCTION	GO-0007264	8	-0.323232	-0.886584	0.618644	0.872443
306	GOBP-MONOCARBOXYLIC_ACID_METABOLIC_PROCESS	GO-0032787	6	-0.355194	-0.886618	0.601504	0.874458
307	GOBP-MONOSACCHARIDE_METABOLIC_PROCESS	GO-0005996	6	-0.353225	-0.886936	0.605469	0.875981
308	GOBP-MONOAMINE_TRANSPORT	GO-0015844	5	-0.377950	-0.889683	0.576503	0.872823
309	GOBP-POSITIVE_REGULATION_OF_MYELOID_LEUKOCYTE...	GO-0002763	6	-0.354979	-0.891500	0.607792	0.871390
310	GOBP-REGULATION_OF_SYNAPSE_STRUCTURE_OR_ACTIVITY	GO-0050803	11	-0.290626	-0.891631	0.595819	0.873204
311	REACTOME-SIGNALING_BY_NTRKS	R-RNO-166520	18	-0.258634	-0.894830	0.613611	0.869279
312	GOBP-SMALL_MOLECULE_METABOLIC_PROCESS	GO-0044281	16	-0.266292	-0.896214	0.590960	0.868646
313	GOBP-REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	GO-0045637	9	-0.308249	-0.897610	0.596698	0.867983
314	GOBP-ANION_TRANSMEMBRANE_TRANSPORT	GO-0098656	7	-0.340022	-0.898773	0.599499	0.867716
315	GOBP-PEPTIDE_BIOSYNTHETIC_PROCESS	GO-0043043	6	-0.362184	-0.905454	0.608966	0.856808
316	GOBP-AMIDE_BIOSYNTHETIC_PROCESS	GO-0043604	6	-0.362184	-0.906868	0.580769	0.856085
317	GOBP-INTRACELLULAR_TRANSPORT	GO-0046907	10	-0.309368	-0.906913	0.574316	0.858110
318	GOBP-POSITIVE_REGULATION_OF_ION_TRANSPORT	GO-0043270	17	-0.268282	-0.912266	0.587500	0.849900

Continuation of Table S10

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
319 GOBP.NERVOUS_SYSTEM.PROCESS	GO:0050877	38	-0.236307	-0.912821	0.577614	0.850850	1.000
320 GOBP.RAS.PROTEIN.SIGNAL.TRANSDUCTION	GO:0007265	5	-0.389252	-0.912947	0.588811	0.852673	1.000
321 GOBP.ORGANONITROGEN.COMPOUND.CATABOLIC.PROCESS	GO:1901565	10	-0.312859	-0.913405	0.556220	0.853854	1.000
322 GOBP.CELLULAR.HOMEOSTASIS	GO:0019725	18	-0.265920	-0.914289	0.570953	0.854267	1.000
323 GOBP.POSITIVE.REGULATION.OF.IMMUNE.SYSTEM.PROCESS	GO:0002684	18	-0.268208	-0.914390	0.574635	0.856182	1.000
324 GOBP.PROTEIN.KINASE.B.SIGNALING	GO:0043491	6	-0.371728	-0.915168	0.587071	0.856780	1.000
325 REACTOME.HEMOSTASIS	R-RNO-109582	14	-0.280338	-0.916834	0.546296	0.855469	1.000
326 GOBP.LONG.TERM.SYNAPTIC.POTENTIATION	GO:0060291	12	-0.293781	-0.919528	0.560414	0.852296	1.000
327 GOBP.CELLULAR.RESPONSE.TO.NITROGEN.COMPOUND	GO:1901699	20	-0.263656	-0.919554	0.575221	0.854382	1.000
328 GOBP.LEUKOCYTE.DIFFERENTIATION	GO:0002521	15	-0.284232	-0.920613	0.577227	0.854457	1.000
329 GOBP.CHROMATIN.ORGANIZATION	GO:0006325	5	-0.399327	-0.921961	0.568575	0.854036	1.000
330 GOBP.PROTEIN.CONTAINING.COMPLEX.SUBUNIT.ORGANIZATION	GO:0043933	15	-0.282135	-0.923272	0.572748	0.853597	1.000
331 GOBP.POSITIVE.REGULATION.OF.MYELOID.CELL.DIFFERENTIATION	GO:0045639	7	-0.347737	-0.925513	0.556544	0.851479	1.000
332 GOBP.PROTEIN.TETRAMERIZATION	GO:0051262	5	-0.405198	-0.930760	0.559367	0.842707	1.000
333 REACTOME.CELL.CYCLE.MITOTIC	R-RNO-69278	5	-0.396907	-0.932373	0.535533	0.841554	1.000
334 GOBP.POSTTRANSCRIPTIONAL.REGULATION.OF.GENE.EXPRESSION	GO:0010608	8	-0.337817	-0.933078	0.567436	0.842146	1.000
335 REACTOME.TRAFFICKING.OF.GLUR2.CONTAINING.AMPA.RECEPTOR	R-RNO-416993	8	-0.336724	-0.934288	0.545122	0.841766	1.000
336 GOBP.MUSCLE.SYSTEM.PROCESS	GO:0003012	9	-0.326958	-0.934652	0.545894	0.843078	1.000
337 GOBP.SMALL.MOLECULE.BIOSYNTHETIC.PROCESS	GO:0044283	5	-0.392995	-0.934734	0.545087	0.845052	1.000
338 GOBP.SYNAPSE.ORGANIZATION	GO:0050808	17	-0.273696	-0.934848	0.548206	0.846981	1.000
339 GOBP.PROTEIN.LOCALIZATION.TO.CELL.JUNCTION	GO:1902414	6	-0.373846	-0.935862	0.529948	0.847121	1.000
340 GOBP.POSITIVE.REGULATION.OF.SMOOTH.MUSCLE.CELL.CONTRACTILITY	GO:0048661	5	-0.393275	-0.938059	0.525266	0.844911	1.000
341 GOBP.REGULATION.OF.CATABOLIC.PROCESS	GO:0008894	13	-0.298883	-0.938481	0.549020	0.846274	1.000
342 GOBP.FATTY.ACID.TRANSPORT	GO:0015908	6	-0.376106	-0.938692	0.535668	0.848048	1.000
343 GOBP.POSITIVE.REGULATION.OF.SIGNALING	GO:0023056	34	-0.241549	-0.939576	0.579894	0.848355	1.000
344 GOBP.REGULATION.OF.LYMPHOCYTE.ACTIVATION	GO:0051249	5	-0.392239	-0.942049	0.519308	0.845318	1.000
345 GOBP.NEGATIVE.REGULATION.OF.TRANSPORT	GO:0051051	13	-0.296902	-0.950803	0.518182	0.829692	1.000
346 GOBP.CELL.MORPHOGENESIS.INVOLVED.IN.NEURON.DIFFERENTIATION	GO:0048667	22	-0.265740	-0.951242	0.528078	0.830967	1.000
347 GOBP.REGULATION.OF.AXONOGENESIS	GO:0050770	7	-0.357561	-0.951508	0.528061	0.832660	1.000
348 GOBP.PLATELET.ACTIVATION	GO:0030168	6	-0.376801	-0.954033	0.515789	0.829469	1.000
349 REACTOME.INFECTIOUS.DISEASE	R-HSA-5663205	12	-0.305608	-0.955767	0.518900	0.827979	1.000
350 GOBP.NEURON.DEATH	GO:0070997	18	-0.280448	-0.957834	0.524554	0.825968	1.000
351 GOBP.PROTEIN.LOCALIZATION.TO.CELL.PERIPHERY	GO:1990778	12	-0.314959	-0.957958	0.524684	0.827915	1.000
352 GOBP.MUSCLE.ORGAN.DEVELOPMENT	GO:0007517	9	-0.338417	-0.958220	0.519952	0.829616	1.000
353 GOBP.CELL.MORPHOGENESIS.INVOLVED.IN.DIFFERENTIATION	GO:0000904	22	-0.265740	-0.958284	0.527192	0.831730	1.000
354 HALLMARK.KRAS.SIGNALING.UP	M5953	6	-0.376214	-0.960802	0.506494	0.828613	1.000
355 GOBP.REGULATION.OF.PHOSPHORUS.METABOLIC.PROCESS	GO:0051174	26	-0.260514	-0.961582	0.527897	0.829218	1.000
356 GOBP.CELL.CELL.SIGNALING.BY.WNT	GO:0198738	7	-0.367762	-0.962011	0.505102	0.830594	1.000
357 GOBP.REGULATION.OF.CIRCADIAN.RHYTHM	GO:0042752	7	-0.362100	-0.963517	0.513043	0.829575	1.000
358 GOBP.CATION.TRANSPORT	GO:0006812	25	-0.264506	-0.964482	0.521413	0.829786	1.000
359 GOBP.METAL.ION.TRANSPORT	GO:0030001	11	-0.319596	-0.966319	0.504751	0.828161	1.000
360 GOBP.CALCIUM.ION.TRANSPORT	GO:0006816	11	-0.319596	-0.968776	0.508178	0.825217	1.000
361 GOBP.LIPID.LOCALIZATION	GO:0010876	10	-0.330697	-0.968894	0.508961	0.827196	1.000

Continuation of Table S10

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
362	GOBP-LEUKOCYTE-MIGRATION	GO-0050900	6	-0.385138	-0.969430	0.487990	0.828289	1.000
363	GOBP-RESPONSE.TO.DRUG	GO-0042493	11	-0.324968	-0.970119	0.505364	0.829115	1.000
364	GOBP-REGULATION.OF.FAT.CELL.DIFFERENTIATION	GO-0045598	6	-0.389155	-0.970252	0.494297	0.831079	1.000
365	GOBP-BEHAVIOR	GO-0007610	33	-0.255876	-0.971366	0.520256	0.830883	1.000
366	REACTOME-MAPK-TARGETS.NUCLEAR.EVENTS.MEDIATED....	R-HSA-450282	5	-0.420342	-0.971958	0.500652	0.831897	1.000
367	GOBP-REGULATION.OF.MUSCLE.SYSTEM.PROCESS	GO-0090257	8	-0.351782	-0.972163	0.484316	0.833827	1.000
368	GOBP-REGULATION.OF.CELL.SIZE	GO-0008361	5	-0.409639	-0.972250	0.484973	0.835983	1.000
369	GOBP-DEFENSE.RESPONSE	GO-0006952	19	-0.285875	-0.974380	0.512651	0.833542	1.000
370	GOBP-REGULATION.OF.CATION.CHANNEL.ACTIVITY	GO-2001257	14	-0.300767	-0.975014	0.501718	0.834455	1.000
371	GOBP-REGULATION.OF.NMDA.RECEPTOR.ACTIVITY	GO-2000310	10	-0.327141	-0.975625	0.498229	0.835486	1.000
372	GOBP-ORGANIC.HYDROXY.COMPOUND-TRANSPORT	GO-0015850	6	-0.386591	-0.975627	0.494297	0.837848	1.000
373	GOBP-NEGATIVE-REGULATION.OF.LIPID.METABOLIC.PR...	GO-0045833	5	-0.413736	-0.977581	0.456989	0.835975	1.000
374	REACTOME-CELLULAR.RESPONSES.TO.EXTERNAL.STIMULI	R-RNO-8953897	11	-0.320442	-0.977825	0.487945	0.837793	1.000
375	GOBP-AMINO-ACID-TRANSPORT	GO-0006865	6	-0.389695	-0.978924	0.493573	0.837872	1.000
376	GOBP-REGULATION.OF-TRANSMEMBRANE-TRANSPORT	GO-0034762	23	-0.274103	-0.980861	0.493003	0.830162	1.000
377	GOBP-RESPONSE.TO.WOUNDING	GO-0009611	15	-0.299312	-0.981384	0.499441	0.837509	1.000
378	GOBP-IMMUNE.SYSTEM.DEVELOPMENT	GO-0002520	17	-0.291260	-0.983641	0.479422	0.835024	1.000
379	GOBP-NEGATIVE-REGULATION.OF.LOCOMOTION	GO-0040013	5	-0.420013	-0.985637	0.473404	0.832823	1.000
380	GOBP-ORGANIC-ANION-TRANSPORT	GO-0015711	6	-0.389695	-0.985803	0.479896	0.834904	1.000
381	GOBP-CARBOXYLIC-ACID-TRANSPORT	GO-0046942	6	-0.389695	-0.990321	0.473548	0.827189	1.000
382	GOBP-REGULATION.OF-TRANSFERASE-ACTIVITY	GO-0051338	21	-0.283302	-0.990363	0.478735	0.829495	1.000
383	GOBP-RESPONSE.TO.NICOTINE	GO-0035094	7	-0.374343	-0.992663	0.467500	0.826919	1.000
384	GOBP-PROTEIN-LOCALIZATION.TO.MEMBRANE	GO-0072657	13	-0.306092	-0.992891	0.468499	0.828836	1.000
385	GOBP-NEGATIVE-REGULATION.OF.SIGNALING	GO-0023057	21	-0.276866	-0.992983	0.490545	0.831085	1.000
386	GOBP-SPROUTING-ANGIOGENESIS	GO-0002040	5	-0.421222	-0.994612	0.464332	0.830003	1.000
387	GOBP-REGULATION.OF-PROTEIN.KINASE-ACTIVITY	GO-0045859	21	-0.283302	-0.995622	0.472588	0.829999	1.000
388	GOBP-MUSCLE-STRUCTURE.DEVELOPMENT	GO-0061061	16	-0.294853	-0.996373	0.472222	0.830789	1.000
389	REACTOME-ESTROGEN-DEPENDENT.NUCLEAR.EVENTS.DOW...	R-RNO-963463	5	-0.423723	-0.997355	0.454784	0.830945	1.000
390	GOBP-REGULATION.OF-CELL.PROJECTION-ORGANIZATION	GO-0031344	20	-0.285703	-0.997825	0.468341	0.832361	1.000
391	REACTOME-POST-TRANSLATIONAL-PROTEIN-MODIFICATION	R-RNO-597592	7	-0.377869	-0.998508	0.490050	0.833302	1.000
392	GOBP-RESPONSE.TO.CADMIUM-ION	GO-0046686	6	-0.401690	-1.001733	0.473548	0.828313	1.000
393	GOBP-POSITIVE-REGULATION.OF-CELL-DEATH	GO-0010942	19	-0.289943	-1.001906	0.467778	0.830386	1.000
394	GOBP-POSITIVE-REGULATION.OF-MOLECULAR-FUNCTION	GO-0044093	37	-0.263296	-1.003181	0.453207	0.829905	1.000
395	GOBP-POSITIVE-REGULATION.OF-CELLULAR-COMPONENT...	GO-0044089	9	-0.358781	-1.004531	0.458937	0.829418	1.000
396	GOBP-NEGATIVE-REGULATION.OF-IMMUNE-SYSTEM-PROCESS	GO-0002683	5	-0.428853	-1.004846	0.451303	0.831201	1.000
397	GOBP-REGULATION.OF-CATION-TRANSMEMBRANE-TRANSPORT	GO-1904062	16	-0.302820	-1.005330	0.470990	0.832619	1.000
398	GOBP-RESPONSE.TO.UV	GO-0009411	5	-0.421474	-1.005371	0.454667	0.835070	1.000
399	GOBP-NEURON-MIGRATION	GO-0001764	5	-0.421617	-1.008002	0.442283	0.831338	1.000
400	REACTOME-RNA.POLYMERASE.II.TRANSCRIPTION	R-RNO-73857	20	-0.292694	-1.010033	0.463043	0.829555	1.000
401	GOBP-OSTEOCLAST-DIFFERENTIATION	GO-0030316	6	-0.400337	-1.010183	0.448635	0.831776	1.000
402	GOBP-ANATOMICAL-STRUCTURE-FORMATION-INVOLVED.I...	GO-0048646	20	-0.291298	-1.011654	0.463087	0.831140	1.000
403	GOBP-INORGANIC-ION-TRANSMEMBRANE-TRANSPORT	GO-0098600	9	-0.353803	-1.013285	0.430108	0.829812	1.000
404	GOBP-POSITIVE-REGULATION.OF-AXONOGENESIS	GO-0050772	5	-0.433603	-1.013886	0.441799	0.830928	1.000

Continuation of Table S10

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
405	GOBP-CIRCADIAN_RHYTHM	GO-0007623	13	-0.326391	-1.014513	0.457901	0.832087	1.000
406	REACTOME-SIGNALING_BY_RECEPTOR_TYROSINE_KINASES	R-RNO-9006934	26	-0.275990	-1.018421	0.448387	0.825379	1.000
407	GOBP-NEGATIVE-REGULATION_OF_ION_TRANSPORT	GO-0043271	11	-0.342893	-1.022542	0.426714	0.818137	1.000
408	GOBP-REGULATION_OF_PROTEOLYSIS	GO-0030162	12	-0.331043	-1.022584	0.443662	0.820629	1.000
409	REACTOME-G-ALPHA-Q-SIGNALING-EVENTS	R-RNO-416476	6	-0.411248	-1.023725	0.439735	0.820579	1.000
410	GOBP-ENDOMEMBRANE-SYSTEM-ORGANIZATION	GO-0010256	6	-0.410004	-1.025210	0.443850	0.819779	1.000
411	GOBP-MUSCLE-CELL-PROLIFERATION	GO-0033002	8	-0.374825	-1.025922	0.422794	0.820679	1.000
412	GOBP-REGULATION_OF_MYELOID_LEUKOCYTE-DIFFERENT...	GO-0002761	8	-0.370141	-1.027025	0.417800	0.820560	1.000
413	GOBP-LYMPHOCYTE-ACTIVATION	GO-0046649	10	-0.347701	-1.027032	0.447115	0.823187	1.000
414	GOBP-BIOLOGICAL-ADHESION	GO-0022610	19	-0.294813	-1.027039	0.423453	0.825820	1.000
415	GOBP-RESPONSE-TO-METAL-ION	GO-0010038	15	-0.313118	-1.027417	0.420814	0.827604	1.000
416	GOBP-REGULATION_OF_SYNAPTIC-PLASTICITY	GO-0048167	21	-0.287753	-1.028705	0.433880	0.827038	1.000
417	GOBP-POSITIVE-REGULATION_OF_CYSSTEINE-TYPE-ENDO...	GO-2001056	7	-0.391886	-1.028824	0.423750	0.829438	1.000
418	GOBP-REGULATION_OF_INFLAMMATORY-RESPONSE	GO-0050727	7	-0.321160	-1.031123	0.418114	0.826517	1.000
419	GOBP-POSITIVE-REGULATION_OF_CELL-POPULATION-PR...	GO-0008284	21	-0.292261	-1.031908	0.420530	0.827259	1.000
420	GOBP-MACROMOLECULE-CATABOLIC-PROCESS	GO-0009057	11	-0.342871	-1.033545	0.416568	0.825952	1.000
421	GOBP-CELL-JUNCTION-ORGANIZATION	GO-0034330	19	-0.302127	-1.034770	0.440176	0.825495	1.000
422	GOBP-CELLULAR-MACROMOLECULE-LOCALIZATION	GO-0070727	20	-0.291044	-1.036016	0.413755	0.825030	1.000
423	GOBP-NEGATIVE-REGULATION_OF_CELL-PROJECTION-OR...	GO-0031345	5	-0.440213	-1.036708	0.404700	0.826184	1.000
424	GOBP-AGING	GO-0007568	13	-0.327160	-1.038466	0.407070	0.824577	1.000
425	GOBP-MULTI-ORGANISM-PROCESS	GO-0051704	16	-0.311217	-1.038827	0.397536	0.826482	1.000
426	GOBP-NEGATIVE-REGULATION_OF_PROTEIN-CATABOLIC...	GO-0042177	5	-0.440124	-1.039431	0.399731	0.827774	1.000
427	GOBP-REGULATION_OF_CYSSTEINE-TYPE-ENDOPEPTIDASE...	GO-2000116	9	-0.364639	-1.039458	0.416766	0.830485	1.000
428	GOBP-MYELOID-CELL-DIFFERENTIATION	GO-0030099	13	-0.324685	-1.041287	0.413242	0.828708	1.000
429	GOBP-NEGATIVE-REGULATION_OF_CELL-CYCLE	GO-0045786	5	-0.441291	-1.043211	0.410188	0.826708	1.000
430	GOBP-REGULATION_OF_ANION-TRANSMEMBRANE-TRANSPORT	GO-1903959	5	-0.446068	-1.044960	0.412316	0.825186	1.000
431	GOBP-EPIDERMIS-DEVELOPMENT	GO-0008544	5	-0.440136	-1.045830	0.399464	0.825862	1.000
432	REACTOME-DEATH-RECEPTOR-SIGNALING	R-RNO-73887	5	-0.446982	-1.047353	0.398385	0.824791	1.000
433	GOBP-CARBOHYDRATE-DERIVATIVE-METABOLIC-PROCESS	GO-1901135	8	-0.379542	-1.047511	0.390511	0.827276	1.000
434	GOBP-CELLULAR-CARBOHYDRATE-METABOLIC-PROCESS	GO-0044262	5	-0.443114	-1.049487	0.397835	0.825011	1.000
435	GOBP-REGULATION_OF_DEFENSE-RESPONSE	GO-0031347	7	-0.395809	-1.049777	0.397727	0.827204	1.000
436	GOBP-REGULATION_OF_SMALL-MOLECULE-METABOLIC-PR...	GO-0062012	9	-0.367446	-1.051583	0.403423	0.825460	1.000
437	GOBP-CYTOKINE-PRODUCTION	GO-0001816	10	-0.358901	-1.052447	0.400984	0.826134	1.000
438	GOBP-RESPONSE-TO-ETHANOL	GO-0045471	5	-0.451259	-1.053275	0.384298	0.827046	1.000
439	GOBP-REGULATION_OF-CARBOHYDRATE-BIOSYNTHETIC-P...	GO-0043255	5	-0.447822	-1.053632	0.383798	0.828980	1.000
440	GOBP-CELLULAR-MACROMOLECULE-CATABOLIC-PROCESS	GO-0044265	5	-0.443521	-1.053650	0.370027	0.831833	1.000
441	GOBP-PROTEIN-CATABOLIC-PROCESS	GO-0030163	8	-0.383951	-1.054010	0.404674	0.833714	1.000
442	GOBP-REGULATION_OF-CARBOHYDRATE-METABOLIC-PROCESS	GO-0006109	5	-0.447822	-1.054522	0.382234	0.835360	1.000
443	GOBP-POSITIVE-REGULATION_OF_PEPTIDASE-ACTIVITY	GO-0010952	7	-0.391886	-1.055062	0.404551	0.836930	1.000
444	REACTOME-NGF-STIMULATED-TRANSCRIPTION	R-RNO-9031628	9	-0.373185	-1.057769	0.402895	0.833175	1.000
445	GOBP-POSITIVE-REGULATION_OF_CELL-GROWTH	GO-0030307	6	-0.413737	-1.058209	0.386305	0.835103	1.000
446	GOBP-REGULATION_OF-LIPASE-ACTIVITY	GO-0060191	6	-0.423051	-1.058339	0.374036	0.837746	1.000
447	GOBP-POSITIVE-REGULATION_OF_CELL-PROJECTION-OR...	GO-0031346	10	-0.357091	-1.063334	0.383353	0.827960	1.000

Continuation of Table S10

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
448	GOBP-RESPONSE.TO.NITROGEN.COMPOUND	35	-0.277884	-1.063930	0.397028	0.829442	1.000
449	GOBP-MYELOID-LEUKOCYTE-DIFFERENTIATION	11	-0.346319	-1.065109	0.389773	0.829400	1.000
450	GOBP-POSITIVE-REGULATION-OF-LEUKOCYTE-CELL-CEL...	5	-0.454164	-1.065268	0.378628	0.831966	1.000
451	GOBP-CARBOHYDRATE-BIOSYNTHETIC-PROCESS	5	-0.447822	-1.065283	0.366534	0.834969	1.000
452	GOBP-CALCIUM-MEDIATED-SIGNALING	10	-0.360061	-1.065963	0.365882	0.836185	1.000
453	GOBP-REGULATION-OF-EXTRINSIC-APOPTOTIC-SIGNALI...	6	-0.421645	-1.066739	0.376486	0.837302	1.000
454	GOBP-REGULATION-OF-IMMUNE-SYSTEM-PROCESS	21	-0.304706	-1.067738	0.384865	0.837741	1.000
455	GOBP-IMMUNE-EFFECTOR-PROCESS	11	-0.358006	-1.068809	0.386555	0.837981	1.000
456	GOBP-POSITIVE-REGULATION-OF-CELL-CELL-ADHESION	5	-0.454164	-1.069934	0.381770	0.838228	1.000
457	GOBP-POSITIVE-REGULATION-OF-IMMUNE-RESPONSE	9	-0.372555	-1.070215	0.397375	0.840773	1.000
458	GOBP-CENTRAL-NERVOUS-SYSTEM-NEURON-DIFFERENTIA...	5	-0.454860	-1.070765	0.362784	0.842428	1.000
459	GOBP-CELL-CELL-JUNCTION-ORGANIZATION	6	-0.421231	-1.070949	0.374836	0.845100	1.000
460	GOBP-REGULATION-OF-INTRACELLULAR-SIGNAL-TRANSD...	21	-0.301244	-1.072140	0.375965	0.844952	1.000
461	GOBP-HEAD-DEVELOPMENT	23	-0.295157	-1.077526	0.375679	0.833706	1.000
462	GOBP-RESPONSE-TO-LIPID	19	-0.308302	-1.077811	0.370130	0.836059	1.000
463	GOBP-LEUKOCYTE-CELL-CELL-ADHESION	6	-0.425514	-1.078188	0.368906	0.838178	1.000
464	GOBP-REGULATION-OF-MUSCLE-CELL-DIFFERENTIATION	6	-0.431095	-1.079195	0.343711	0.838850	1.000
465	GOBP-REGULATION-OF-PHOSPHOLIPASE-ACTIVITY	6	-0.423051	-1.083234	0.355128	0.831018	1.000
466	GOBP-TRANSMEMBRANE-RECEPTOR-PROTEIN-TYROSINE-K...	19	-0.313340	-1.083444	0.350593	0.833639	1.000
467	GOBP-REGULATION-OF-IMMUNE-RESPONSE	12	-0.347654	-1.083774	0.354143	0.835929	1.000
468	GOBP-NEGATIVE-REGULATION-OF-RESPONSE-TO-EXTERN...	5	-0.453184	-1.087272	0.371846	0.829648	1.000
469	GOBP-REGULATION-OF-CELLULAR-COMPONENT_SIZE	7	-0.419753	-1.087560	0.338481	0.832049	1.000
470	GOBP-TUBE-MORPHOGENESIS	15	-0.331361	-1.087687	0.371986	0.834947	1.000
471	GOBP-REGULATION-OF-NEURON-PROJECTION-DEVELOPMENT	16	-0.323705	-1.089146	0.362528	0.834554	1.000
472	GOBP-REGULATION-OF-BODY-FLUID-LEVELS	11	-0.363860	-1.089924	0.352381	0.835800	1.000
473	GOBP-REGULATION-OF-CELL-ADHESION	13	-0.343324	-1.091970	0.336406	0.833430	1.000
474	GOBP-CIRCADIAN-REGULATION-OF-GENE-EXPRESSION	5	-0.459417	-1.092222	0.348806	0.836075	1.000
475	GOBP-POSITIVE-REGULATION-OF-HYDROLASE-ACTIVITY	16	-0.327479	-1.092782	0.361820	0.837935	1.000
476	GOBP-RESPONSE-TO-CALCIUMION	6	-0.434908	-1.094373	0.354926	0.836920	1.000
477	GOBP-REGULATION-OF-WNT-SIGNALING-PATHWAY	5	-0.463976	-1.097482	0.339572	0.831580	1.000
478	GOBP-REGULATION-OF-CELLULAR-COMPONENT-BIOGENESIS	10	-0.370041	-1.099289	0.346062	0.829890	1.000
479	REACTOME-NERVOUS-SYSTEM-DEVELOPMENT	14	-0.348415	-1.099424	0.360505	0.832808	1.000
480	GOBP-EXTRINSIC-APOPTOTIC-SIGNALING-PATHWAY	7	-0.417851	-1.100332	0.354381	0.833868	1.000
481	GOBP-RHYTHMIC-PROCESS	15	-0.340945	-1.101998	0.350457	0.832794	1.000
482	GOBP-DEPHOSPHORYLATION	7	-0.417454	-1.103901	0.344870	0.830715	1.000
483	GOBP-RESPONSE-TO-INORGANIC-SUBSTANCE	19	-0.372502	-1.105189	0.332230	0.830651	1.000
484	REACTOME-LEISHMANIA-INFECTION	10	-0.372502	-1.105448	0.324096	0.833398	1.000
485	GOBP-REGULATION-OF-PROTEIN-MODIFICATION-PROCESS	28	-0.293170	-1.108197	0.334398	0.828956	1.000
486	GOBP-REGULATION-OF-ANATOMICAL-STRUCTURE_SIZE	10	-0.373628	-1.108788	0.324675	0.830747	1.000
487	HALLMARK-APOPTOSIS	6	-0.448852	-1.109981	0.332468	0.830973	1.000
488	REACTOME-INTERLEUKIN_4-AND-INTERLEUKIN_13-SIGN...	8	-0.411682	-1.115441	0.328377	0.819148	1.000
489	REACTOME-NUCLEAR-EVENTS-KINASE-AND-TRANSCRIPTI...	11	-0.362142	-1.115987	0.310545	0.821066	1.000
490	GOBP-POSITIVE-REGULATION-OF-DEVELOPMENTAL-PROCESS	32	-0.294911	-1.117229	0.325926	0.820882	1.000

Continuation of Table S10

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
491	GOBP-POSITIVE-REGULATION-OF-DEVELOPMENTAL-GROWTH	8	-0.402106	-1.121619	0.313119	0.811874	1.000
492	GOBP-PROTEIN-DEPHOSPHORYLATION	7	-0.417454	-1.122295	0.319753	0.813589	1.000
493	GOBP-REGULATION-OF-SIGNALING-RECEPTOR-ACTIVITY	14	-0.346317	-1.123498	0.323360	0.813942	1.000
494	GOBP-POSTSYNAPSE-ORGANIZATION	10	-0.380815	-1.128150	0.300358	0.804695	1.000
495	GOBP-GLUTAMATE-RECEPTOR-SIGNALING-PATHWAY	17	-0.302739	-1.131786	0.320542	0.798229	1.000
496	GOBP-POSITIVE-REGULATION-OF-RESPONSE-TO-EXTERN...	9	-0.394845	-1.132017	0.311869	0.801034	1.000
497	GOBP-NEURON-PROJECTION-ORGANIZATION	8	-0.405575	-1.134759	0.311111	0.796890	1.000
498	GOBP-NEGATIVE-REGULATION-OF-GENE-EXPRESSION	11	-0.374993	-1.135714	0.290023	0.797817	1.000
499	GOBP-CELLULAR-RESPONSE-TO-CADMIIUM-ION	5	-0.482215	-1.138282	0.313394	0.794154	1.000
500	GOBP-CELLULAR-RESPONSE-TO-CHEMICAL-STRESS	7	-0.435223	-1.139501	0.295311	0.793998	1.000
501	GOBP-NEGATIVE-REGULATION-OF-CATABOLIC-PROCESS	8	-0.417907	-1.142143	0.296020	0.790359	1.000
502	GOBP-CIRCULATORY-SYSTEM-PROCESS	5	-0.481928	-1.144898	0.284967	0.786259	1.000
503	REACTOME-CIRCADIAN-CLOCK	5	-0.481928	-1.145495	0.283784	0.788206	1.000
504	GOBP-REGULATION-OF-POSTSYNAPTIC-MEMBRANE-POTEN...	14	-0.354518	-1.147017	0.286517	0.787344	1.000
505	GOBP-CELLULAR-RESPONSE-TO-STARVATION	5	-0.493556	-1.147262	0.276299	0.790246	1.000
506	GOBP-POSITIVE-REGULATION-OF-GROWTH	9	-0.401078	-1.148445	0.293317	0.790565	1.000
507	GOBP-REGULATION-OF-LIPID-METABOLIC-PROCESS	7	-0.437311	-1.148642	0.288010	0.793736	1.000
508	GOBP-CELLULAR-RESPONSE-TO-OXYGEN-CONTAINING.CO...	29	-0.307794	-1.149442	0.292994	0.795135	1.000
509	GOBP-RESPONSE-TO-STARVATION	5	-0.493556	-1.149999	0.292414	0.797249	1.000
510	GOBP-NEGATIVE-REGULATION-OF-ANION-TRANSPORT	8	-0.420526	-1.153008	0.295261	0.792549	1.000
511	GOBP-RESPONSE-TO-ABIOTIC-STIMULUS	27	-0.310952	-1.153310	0.285093	0.795547	1.000
512	GOBP-HOMEOSTATIC-PROCESS	31	-0.307208	-1.153320	0.304162	0.799253	1.000
513	GOBP-FAT-CELL-DIFFERENTIATION	9	-0.403793	-1.154499	0.285542	0.799826	1.000
514	GOBP-OSISIFICATION	9	-0.409272	-1.156211	0.292121	0.798343	1.000
515	GOBP-CELLULAR-RESPONSE-TO-REACTIVE-OXYGEN-SPECIES	7	-0.435223	-1.156250	0.283019	0.802035	1.000
516	GOBP-TELENCEPHALON-DEVELOPMENT	7	-0.443837	-1.160992	0.291980	0.792124	1.000
517	GOBP-T-CELL-ACTIVATION	8	-0.435015	-1.166351	0.271122	0.780241	1.000
518	GOBP-REGULATION-OF-GROWTH	13	-0.362184	-1.167274	0.280138	0.781384	1.000
519	GOBP-MUSCLE-CELL-DIFFERENTIATION	10	-0.397286	-1.168011	0.272175	0.783061	1.000
520	GOBP-ASSOCIATIVE-LEARNING	7	-0.444444	-1.168120	0.263488	0.786570	1.000
521	GOBP-PEPTIDYL-LYSINE-MODIFICATION	5	-0.494318	-1.173760	0.265971	0.774111	1.000
522	GOBP-POSITIVE-REGULATION-OF-PROTEOLYSIS	8	-0.424733	-1.173811	0.251225	0.777776	1.000
523	GOBP-POSITIVE-REGULATION-OF-NEURON-PROJECTION...	5	-0.494436	-1.175628	0.253230	0.776401	1.000
524	GOBP-RESPONSE-TO-LIGHT-STIMULUS	11	-0.390823	-1.179917	0.243757	0.767660	1.000
525	GOBP-REGULATION-OF-BINDING	11	-0.389990	-1.182917	0.261176	0.763163	1.000
526	REACTOME-INTERLEUKIN-17-SIGNALING	6	-0.468932	-1.184224	0.242188	0.763462	1.000
527	REACTOME-SYNAPTIC-ADHESION-LIKE-MOLECULES	9	-0.414349	-1.186236	0.250000	0.761257	1.000
528	GOBP-CENTRAL-NERVOUS-SYSTEM-DEVELOPMENT	27	-0.323851	-1.191748	0.257895	0.749443	1.000
529	GOBP-TRANSMEMBRANE-TRANSPORT	27	-0.319713	-1.192429	0.239872	0.751462	1.000
530	GOBP-ORGANIC-ACID-TRANSPORT	7	-0.460695	-1.193345	0.250000	0.752860	1.000
531	GOBP-DEVELOPMENTAL-CELL-GROWTH	5	-0.501688	-1.194557	0.253989	0.753089	1.000
532	GOBP-CYTOSOLIC-CALCIUM-ION-TRANSPORT	7	-0.457551	-1.194649	0.252551	0.756768	1.000
533	GOBP-GROWTH	14	-0.372564	-1.198095	0.242563	0.750263	1.000

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NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
534	GOBP-CELL-GROWTH	GO-0016049	10	-0.415703	-1.198951	0.256691	0.751725
535	GOBP-TRANSMEMBRANE-RECEPTOR-PROTEIN-SERINE-THR...	GO-0007178	6	-0.475076	-1.198962	0.247706	0.755645
536	GOBP-CATION-TRANSMEMBRANE-TRANSPORT	GO-0098655	18	-0.352151	-1.199526	0.223451	0.758079
537	HALLMARK-HYPOXIA	M5891	5	-0.507555	-1.202818	0.232527	0.752501
538	GOBP-BLOOD-VESSEL-MORPHOGENESIS	GO-0048514	14	-0.376051	-1.205652	0.229807	0.748633
539	GOBP-GLIOGENESIS	GO-0042063	12	-0.398326	-1.206524	0.235916	0.750063
540	GOBP-CELL-JUNCTION-ASSEMBLY	GO-0034329	8	-0.435130	-1.206575	0.245169	0.753928
541	GOBP-CALCIUM-ION-TRANSMEMBRANE-TRANSPORT	GO-0070588	7	-0.457574	-1.208197	0.238095	0.753359
542	GOBP-REGULATION-OF-LIPID-BIOSYNTHETIC-PROCESS	GO-0046890	6	-0.488835	-1.209953	0.230971	0.752423
543	GOBP-REGULATION-OF-GTPASE-ACTIVITY	GO-0043087	5	-0.517147	-1.210823	0.237781	0.754081
544	GOBP-REGULATION-OF-NEUROTRANSMITTER-RECEPTOR-A...	GO-0099601	13	-0.391989	-1.217046	0.240319	0.739530
545	GOBP-LIPID-BIOSYNTHETIC-PROCESS	GO-0008610	6	-0.488835	-1.219674	0.221785	0.735834
546	GOBP-REGULATION-OF-SYSTEM-PROCESS	GO-0044057	18	-0.351110	-1.220016	0.232123	0.738880
547	GOBP-CALCIUM-ION-TRANSPORT-INTO-CYTOSOL	GO-0060402	7	-0.457574	-1.221395	0.214815	0.738616
548	GOBP-LIPID-METABOLIC-PROCESS	GO-0006629	10	-0.411482	-1.222056	0.195065	0.740835
549	GOBP-DNA-METABOLIC-PROCESS	GO-0006259	6	-0.486969	-1.224583	0.208440	0.737443
550	GOBP-GENERATION-OF-PRECURSOR-METABOLITES-AND-E...	GO-0006091	5	-0.518015	-1.227686	0.212435	0.732158
551	GOBP-CHEMICAL-SYNAPTIC-TRANSMISSION-POSTSYNAPTIC	GO-0099565	9	-0.434373	-1.229964	0.198565	0.729731
552	GOBP-REGULATION-OF-TRANSPORTER-ACTIVITY	GO-0032409	17	-0.360503	-1.233270	0.221477	0.724109
553	GOBP-REGULATION-OF-PROTEIN-CATABOLIC-PROCESS	GO-0042176	7	-0.472901	-1.233857	0.210263	0.726783
554	GOBP-POLYSACCHARIDE-METABOLIC-PROCESS	GO-0005976	5	-0.521907	-1.234258	0.206117	0.729835
555	GOBP-MULTICELLULAR-ORGANISM-PROCESS	GO-0044706	8	-0.445664	-1.235027	0.205845	0.731834
556	HALLMARK-P13K-AKT-MTOR-SIGNALING	M5923	6	-0.485913	-1.235116	0.207947	0.735857
557	GOBP-RESPONSE-TO-ALKALOID	GO-0043279	5	-0.524692	-1.235251	0.204216	0.739886
558	GOBP-REGULATION-OF-MEMBRANE-POTENTIAL	GO-0042391	17	-0.361744	-1.235976	0.210823	0.742088
559	GOBP-ENZYME-LINKED-RECEPTOR-PROTEIN-SIGNALING----	GO-0007167	24	-0.335142	-1.241271	0.203587	0.730496
560	GOBP-EPITHELIUM-DEVELOPMENT	GO-0060429	15	-0.377603	-1.242585	0.205069	0.731008
561	GOBP-NEGATIVE-REGULATION-OF-TRANSMEMBRANE-TRAN...	GO-0034763	6	-0.487645	-1.243878	0.213351	0.731537
562	GOBP-RESPONSE-TO-REACTIVE-OXYGEN-SPECIES	GO-0000302	8	-0.457126	-1.244465	0.195062	0.734155
563	GOBP-PEPTIDE-METABOLIC-PROCESS	GO-0006518	11	-0.419616	-1.248576	0.188679	0.726292
564	GOBP-POSITIVE-REGULATION-OF-DEFENSE-RESPONSE	GO-0031349	5	-0.529570	-1.248618	0.189225	0.730684
565	GOBP-MALE-GAMETE-GENERATION	GO-0048232	5	-0.524187	-1.250750	0.187761	0.728758
566	GOBP-CARBOHYDRATE-METABOLIC-PROCESS	GO-0005975	9	-0.444401	-1.251268	0.197026	0.731789
567	GOBP-RESPONSE-TO-OXIDATIVE-STRESS	GO-0006979	8	-0.457126	-1.251360	0.195787	0.736142
568	GOBP-RESPONSE-TO-CARBOHYDRATE	GO-0009743	5	-0.534035	-1.254285	0.186508	0.731575
569	GOBP-ANATOMICAL-STRUCTURE-RECEPTOR-SIGNALING-PATHWAY-I...	GO-0060249	7	-0.467912	-1.254322	0.191595	0.736149
570	GOBP-CELL-SURFACE-RECEPTOR-SIGNALING-PATHWAY-I...	GO-1905114	15	-0.389498	-1.255783	0.198228	0.736566
571	GOBP-OSTEOBLAST-DIFFERENTIATION	GO-0001649	15	-0.536696	-1.257891	0.181586	0.734822
572	GOBP-NEGATIVE-REGULATION-OF-MOLECULAR-FUNCTION	GO-0044092	24	-0.339132	-1.257925	0.200662	0.739501
573	GOBP-REGULATION-OF-RESPONSE-TO-EXTERNAL-STIMULUS	GO-0032101	15	-0.378443	-1.259602	0.186020	0.739071
574	REACTOME-MAPK-FAMILY-SIGNALING-CASCADES	R-RNO-5683057	12	-0.408721	-1.260498	0.183432	0.740967
575	GOBP-CELLULAR-RESPONSE-TO-LIPID	GO-0071396	15	-0.380553	-1.261367	0.197714	0.743066
576	GOBP-TEMPERATURE-HOMEOSTASIS	GO-0001659	5	-0.533074	-1.261925	0.183727	0.746142

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NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
577	GOBP-HOMEOSTASIS_OF_NUMBER_OF_CELLS	5	-0.529772	-1.264395	0.169168	0.743679	1.000
578	GOBP-CELLULAR_RESPONSE_TO ABIOTIC-STIMULUS	7	-0.475198	-1.265220	0.167949	0.746010	1.000
579	GOBP-POSITIVE REGULATION_OF_GLIOGENESIS	5	-0.531087	-1.266455	0.169786	0.747328	1.000
580	GOBP-LEARNING	13	-0.408207	-1.266534	0.175115	0.752185	1.000
581	REACTOME-NEUREXINS-AND-NEUROLIGINS	9	-0.450544	-1.267525	0.198529	0.754390	1.000
582	GOBP-POSITIVE REGULATION_OF DNA BINDING_TRANSC...	10	-0.421739	-1.267554	0.197115	0.759540	1.000
583	GOBP-REGULATION_OF_NERVOUS_SYSTEM_PROCESS	8	-0.464109	-1.269537	0.170581	0.758236	1.000
584	GOBP-EMBRYONIC MORPHOGENESIS	6	-0.498796	-1.269686	0.168659	0.763139	1.000
585	GOBP-DEVELOPMENTAL GROWTH	10	-0.423749	-1.270105	0.184431	0.767241	1.000
586	GOBP-REGULATION_OF_GLIOGENESIS	5	-0.531087	-1.271011	0.181217	0.769877	1.000
587	GOBP-RESPONSE_TO_OXYGEN LEVELS	8	-0.458119	-1.271251	0.199504	0.774609	1.000
588	GOBP-MEMBRANE PROTEIN PROTEOLYSIS	6	-0.507726	-1.278903	0.167500	0.755035	1.000
589	GOBP-NEGATIVE REGULATION_OF PHOSPHORYLATION	7	-0.484115	-1.280218	0.171795	0.756080	1.000
590	GOBP-RESPONSE_TO MONOSACCHARIDE	5	-0.534035	-1.284175	0.154248	0.748711	1.000
591	GOBP-REGULATION_OF PROTEIN LOCALIZATION_TO MEM...	7	-0.491644	-1.284911	0.169742	0.751987	1.000
592	GOBP-REPRODUCTIVE SYSTEM DEVELOPMENT	6	-0.507860	-1.290239	0.160622	0.740680	1.000
593	GOBP-CELL CYCLE	21	-0.361266	-1.294390	0.162338	0.732485	1.000
594	GOBP-POSITIVE REGULATION_OF CYTOKINE PRODUCTION	7	-0.492671	-1.295938	0.155303	0.733084	1.000
595	GOBP-NEGATIVE REGULATION_OF PHOSPHORUS METABOL...	9	-0.459155	-1.298443	0.159420	0.730495	1.000
596	GOBP-REGULATION_OF_CELL DEVELOPMENT	15	-0.395378	-1.305644	0.162870	0.712249	1.000
597	GOBP-DEFENSE RESPONSE_TO_OTHER ORGANISM	9	-0.458029	-1.306437	0.168246	0.715316	1.000
598	GOBP-STRATIATED MUSCLE CELL DIFFERENTIATION	9	-0.457695	-1.310346	0.138012	0.707658	1.000
599	GOBP-POSITIVE REGULATION_OF NEURON DEATH	5	-0.558999	-1.313916	0.123684	0.701518	1.000
600	GOBP-SEXUAL REPRODUCTION	10	-0.443052	-1.318118	0.141119	0.693240	1.000
601	GOBP-REGULATION_OF MAPK CASCADE	13	-0.417588	-1.321482	0.144330	0.688323	1.000
602	REACTOME-PROTEIN-PROTEIN INTERACTIONS AT SYNAPSES	12	-0.426543	-1.322381	0.142191	0.691091	1.000
603	GOBP-POSITIVE REGULATION_OF NEUROGENESIS	12	-0.435647	-1.325748	0.156398	0.686159	1.000
604	GOBP-REGULATION_OF DNA BINDING_TRANSCRIPTION F...	16	-0.400618	-1.331179	0.146893	0.674755	1.000
605	GOBP-CELLULAR COMPONENT MAINTENANCE	5	-0.554217	-1.332403	0.127688	0.676482	1.000
606	GOBP-REGULATION_OF MAP_KINASE ACTIVITY	9	-0.466486	-1.335335	0.123609	0.673049	1.000
607	GOBP-TISSUE HOMEOSTASIS	5	-0.569047	-1.336046	0.118170	0.676356	1.000
608	GOBP-EXCITATORY CHEMICAL SYNAPTIC TRANSMISSION	5	-0.566265	-1.338878	0.127027	0.672802	1.000
609	GOBP-PROTEOLYSIS	17	-0.400677	-1.343693	0.132353	0.662858	1.000
610	GOBP-CELLULAR AMIDE METABOLIC PROCESS	12	-0.440920	-1.345630	0.118624	0.662289	1.000
611	GOBP-POSITIVE REGULATION_OF NERVOUS SYSTEM DEV...	12	-0.435647	-1.347126	0.126874	0.663629	1.000
612	GOBP-POSITIVE REGULATION_OF_CELL DEVELOPMENT	12	-0.435647	-1.348094	0.119266	0.666504	1.000
613	GOBP-NEGATIVE REGULATION_OF TRANSFERASE ACTIVITY	5	-0.567320	-1.348916	0.107374	0.669835	1.000
614	GOBP-RESPONSE_TO ACID-CHEMICAL	6	-0.540298	-1.350641	0.128827	0.670002	1.000
615	GOBP-NEGATIVE REGULATION_OF KINASE ACTIVITY	5	-0.567320	-1.352262	0.130319	0.671002	1.000
616	GOBP-ENDOCRINE SYSTEM DEVELOPMENT	6	-0.544967	-1.353699	0.121019	0.672398	1.000
617	REACTOME-ADAPTIVE IMMUNE SYSTEM	9	-0.479020	-1.354940	0.125604	0.674344	1.000
618	GOBP-REGULATION_OF_CELL DIFFERENTIATION	36	-0.354908	-1.357724	0.109589	0.671399	1.000
619	GOBP-RESPONSE_TO MOLECULE OF BACTERIAL ORIGIN	13	-0.426628	-1.359718	0.124717	0.671509	1.000

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	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
620	GOBP-MUSCLE-CELL-DEVELOPMENT	GO-0055001	5	-0.575080	-1.360765	0.124021	0.674221	1.000
621	GOBP-MAINTENANCE-OF-LOCATION	GO-0051235	7	-0.518681	-1.363608	0.118987	0.671265	1.000
622	GOBP-EPHRIN-RECEPTOR-SIGNALING-PATHWAY	GO-0048013	5	-0.579619	-1.363899	0.106860	0.676852	1.000
623	GOBP-RESPONSE-TO-RADIATION	GO-0009314	13	-0.425259	-1.364248	0.114155	0.682350	1.000
624	GOBP-REGULATION-OF-CELL-CYCLE	GO-0051726	13	-0.431755	-1.364761	0.105324	0.687555	1.000
625	GOBP-NUCLEAR-TRANSPORT	GO-0051169	5	-0.579672	-1.365935	0.112299	0.690582	1.000
626	GOBP-NEGATIVE-REGULATION-OF-MULTICELLULAR-ORGA...	GO-0051241	15	-0.419828	-1.368762	0.108945	0.688183	1.000
627	GOBP-GLAND-DEVELOPMENT	GO-0048732	7	-0.516818	-1.369349	0.116688	0.693296	1.000
628	GOBP-RESPONSE-TO-INSULIN	GO-0032868	5	-0.580450	-1.370812	0.105882	0.695571	1.000
629	GOBP-CELLULAR-RESPONSE-TO-ORGANIC-CYCLIC-COMPOUND	GO-0071407	13	-0.429510	-1.374165	0.112903	0.691322	1.000
630	GOBP-AMYLOID-PRECURSOR-PROTEIN-METABOLIC-PROCESS	GO-0042982	5	-0.591906	-1.374238	0.115735	0.698307	1.000
631	GOBP-REGULATION-OF-NEUROGENESIS	GO-0050767	14	-0.427392	-1.374314	0.099429	0.705545	1.000
632	GOBP-NEGATIVE-REGULATION-OF-BINDING	GO-0051100	6	-0.553052	-1.377020	0.102302	0.704180	1.000
633	REACTOME-TRANSCRIPTIONAL-REGULATION-BY-TP53	R-RNO-3700989	6	-0.551622	-1.377981	0.105882	0.701299	1.000
634	REACTOME-TRANSCRIPTIONAL-REGULATION-OF-WHITE-A...	R-RNO-381340	6	-0.550990	-1.385444	0.100000	0.689177	1.000
635	GOBP-RESPONSE-TO-BACTERIUM	GO-0009617	13	-0.426628	-1.386959	0.098751	0.691787	1.000
636	GOBP-AMYLOID-BETA-METABOLIC-PROCESS	GO-0050435	5	-0.591906	-1.389481	0.085979	0.690987	1.000
637	GOBP-RESPONSE-TO-METABOLIC-STIMULUS	GO-0009612	6	-0.549972	-1.390586	0.100128	0.694990	1.000
638	GOBP-POSITIVE-REGULATION-OF-TRANSCRIPTION-BY-R...	GO-0045944	24	-0.379912	-1.391704	0.090513	0.699176	1.000
639	GOBP-MULTICELLULAR-ORGANISMAL-HOMEOSTASIS	GO-0048871	12	-0.446302	-1.395349	0.111507	0.694320	1.000
640	GOBP-RESPONSE-TO-BIOTIC-STIMULUS	GO-0009607	17	-0.418454	-1.396798	0.094655	0.697301	1.000
641	GOBP-INTRACELLULAR-RECEPTOR-SIGNALING-PATHWAY	GO-0030522	5	-0.587159	-1.399064	0.104698	0.697198	1.000
642	GOBP-PRL-MIRNA-TRANSCRIPTION-BY-RNA-POLYMERASE-II	GO-0061614	7	-0.539743	-1.402169	0.086101	0.693956	1.000
643	GOBP-NEGATIVE-REGULATION-OF-RESPONSE-TO-STIMULUS	GO-0045853	16	-0.422233	-1.403473	0.096591	0.697519	1.000
644	REACTOME-INNATE-IMMUNE-SYSTEM	R-RNO-168249	16	-0.417786	-1.404493	0.093541	0.702132	1.000
645	GOBP-AMYLOID-PRECURSOR-PROTEIN-CATABOLIC-PROCESS	GO-0042987	5	-0.591906	-1.404896	0.098404	0.709548	1.000
646	GOBP-NEGATIVE-REGULATION-OF-NUCLEOBASE-CONTAIN...	GO-0045934	13	-0.445136	-1.418345	0.094907	0.669908	1.000
647	REACTOME-L1CAM-INTERACTIONS	R-RNO-373760	5	-0.594714	-1.419588	0.085752	0.674160	1.000
648	GOBP-REGULATION-OF-DEVELOPMENTAL-GROWTH	GO-0048638	9	-0.489745	-1.421006	0.082339	0.678127	1.000
649	GOBP-POSITIVE-REGULATION-OF-PRL-MIRNA-TRANSCRI...	GO-1902895	7	-0.539743	-1.429396	0.075738	0.657644	1.000
650	GOBP-IONOTROPIC-GLUTAMATE-RECEPTOR-SIGNALING-P...	GO-0035235	9	-0.504775	-1.438119	0.083233	0.636544	1.000
651	GOBP-PROTEIN-MODIFICATION-BY-SMALL-PROTEIN-CON...	GO-0032446	6	-0.575895	-1.438750	0.073491	0.643001	1.000
652	GOBP-GAMETE-GENERATION	GO-0007276	9	-0.513086	-1.438868	0.086480	0.651357	1.000
653	GOBP-CELLULAR-RESPONSE-TO-EXTRACELLULAR-STIMULUS	GO-0031668	8	-0.536060	-1.442127	0.088378	0.648002	1.000
654	GOBP-REGULATION-OF-PROTEIN-SERINE-THREONINE-KI...	GO-0071900	12	-0.467172	-1.443003	0.082654	0.654186	1.000
655	GOBP-REGULATION-OF-CELLULAR-AMIDE-METABOLIC-PR...	GO-0034248	9	-0.507164	-1.445152	0.078883	0.655805	1.000
656	GOBP-REGULATION-OF-MULTICELLULAR-ORGANISMAL-DE...	GO-2000026	31	-0.379564	-1.447050	0.069189	0.658550	1.000
657	GOBP-NEGATIVE-REGULATION-OF-INTRACELLULAR-SIGN...	GO-1902532	7	-0.548625	-1.448399	0.084054	0.663723	1.000
658	GOBP-IMPORT-INTO-CELL	GO-0098657	6	-0.584713	-1.451937	0.058278	0.660618	1.000
659	GOBP-POSITIVE-REGULATION-OF-CELL-DIFFERENTIATION	GO-0034597	27	-0.392753	-1.452230	0.069767	0.669521	1.000
660	GOBP-RESPONSE-TO-TUMOR-NECROSIS-FACTOR	GO-0034612	7	-0.555600	-1.463283	0.072822	0.638260	1.000
661	REACTOME-FC-EPSILON-RECEPTOR-FCER1-SIGNALING	R-RNO-2454202	7	-0.563379	-1.466777	0.073698	0.635173	1.000
662	GOBP-COAGULATION	GO-0050817	8	-0.538641	-1.468227	0.072319	0.640218	1.000

Continuation of Table S10

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
663	GOBP-RESPONSE.TO.INTERLEUKIN.1	GO-0070555	5	-0.610610	-1.470030	0.067974	0.643565	1.000
664	GOBP-NEGATIVE-REGULATION-OF-PROTEIN-METABOLIC-...	GO-0051248	20	-0.413824	-1.470491	0.057175	0.652406	1.000
665	HALLMARK-TNFA-SIGNALING-VIA-NFKB	M5890	14	-0.461190	-1.475459	0.066069	0.644694	1.000
666	GOBP-MONONUCLEAR-CELL-DIFFERENTIATION	GO-1903131	7	-0.580466	-1.476975	0.086903	0.650004	1.000
667	GOBP-REPRODUCTION	GO-0000003	18	-0.430579	-1.481878	0.053333	0.642502	1.000
668	GOBP-RESPONSE.TO.OXYGEN-CONTAINING-COMPOUND	GO-1901700	39	-0.385835	-1.482274	0.056114	0.652491	1.000
669	GOBP-REGULATION-OF-NERVOUS-SYSTEM-DEVELOPMENT	GO-0051960	15	-0.452406	-1.485541	0.057303	0.651253	1.000
670	REACTOME-TOLL-LIKE-RECEPTOR-TLR1-TLR2-CASCADE	R-RNO-168179	8	-0.548139	-1.487205	0.060991	0.657311	1.000
671	GOBP-MUSCLE-CONTRACTION	GO-0006936	5	-0.634728	-1.494381	0.064603	0.642431	1.000
672	GOBP-FC-EPSILON-RECEPTOR-SIGNALING-PATHWAY	GO-0038095	7	-0.563379	-1.498453	0.039390	0.639404	1.000
673	GOBP-SENSORY-ORGAN-DEVELOPMENT	GO-0007423	8	-0.549151	-1.503507	0.049689	0.633504	1.000
674	GOBP-NEGATIVE-REGULATION-OF-PROTEIN-MODIFICATION...	GO-0031400	10	-0.504088	-1.503823	0.057075	0.644809	1.000
675	REACTOME-MYD88-INDEPENDENT-TLR4-CASCADE	R-RNO-166166	8	-0.548139	-1.505562	0.043956	0.651107	1.000
676	REACTOME-SIGNALING-BY-INTERLEUKINS	R-RNO-449147	15	-0.460942	-1.512339	0.060364	0.638254	1.000
677	GOBP-PROTEIN-AUTOPHOSPHORYLATION	GO-0040777	5	-0.651508	-1.512554	0.038513	0.650658	1.000
678	REACTOME-TOLL-LIKE-RECEPTOR-CASCADES	R-RNO-168898	8	-0.548139	-1.515488	0.058531	0.652903	1.000
679	REACTOME-TOLL-LIKE-RECEPTOR-9-TLR9-CASCADE	R-RNO-168138	8	-0.548139	-1.517552	0.056180	0.658529	1.000
680	GOBP-REGULATION-OF-PROTEIN-LOCALIZATION.TO.CEL...	GO-1904375	6	-0.589519	-1.520005	0.041184	0.663322	1.000
681	REACTOME-DEVELOPMENTAL-BIOLOGY	R-RNO-1266738	22	-0.431203	-1.527839	0.051780	0.648015	1.000
682	GOBP-VASCULATURE-DEVELOPMENT	GO-0001944	17	-0.454094	-1.544242	0.038889	0.601383	1.000
683	REACTOME-CYTOKINE-SIGNALING-IN-IMMUNE-SYSTEM	R-RNO-1280215	21	-0.445101	-1.544747	0.027233	0.613704	1.000
684	REACTOME-EPH-EPHRIN-SIGNALING	R-RNO-268233	6	-0.605914	-1.545544	0.051680	0.625601	1.000
685	GOBP-CELLULAR-RESPONSE.TO-MOLECULE-OF-BACTERIA...	GO-0071219	8	-0.564782	-1.546037	0.042787	0.639417	1.000
686	GOBP-POSITIVE-REGULATION-OF-MULTICELLULAR_ORGA...	GO-0051240	32	-0.402424	-1.551042	0.037473	0.635967	1.000
687	GOBP-RESPONSE.TO-CYTOKINE	GO-0034097	23	-0.427778	-1.552018	0.044565	0.648442	1.000
688	GOBP-POSITIVE-REGULATION-OF-NUCLEOBASE-CONTAIN...	GO-0045935	28	-0.417179	-1.555679	0.032258	0.650075	1.000
689	GOBP-CELLULAR-RESPONSE.TO-BIOTIC-STIMULUS	GO-0071216	8	-0.564782	-1.560310	0.035409	0.649493	1.000
690	GOBP-GLIAL-CELL-DIFFERENTIATION	GO-0010001	10	-0.533520	-1.560560	0.041225	0.666713	1.000
691	GOBP-POSITIVE-REGULATION-OF-GENE-EXPRESSION	GO-0010628	16	-0.466790	-1.564181	0.039282	0.671026	1.000
692	GOBP-INNATE-IMMUNE-RESPONSE	GO-0045087	7	-0.587317	-1.565076	0.033088	0.686940	1.000
693	GOBP-POSITIVE-REGULATION-OF-BIOSYNTHETIC-PROCESS	GO-0009891	27	-0.422646	-1.567580	0.034079	0.697514	1.000
694	GOBP-PROTEIN-MODIFICATION-BY-SMALL-PROTEIN-CON...	GO-0070647	7	-0.610735	-1.571455	0.020779	0.702460	1.000
695	GOBP-ANIMAL-ORGAN-MORPHOGENESIS	GO-0009887	12	-0.512549	-1.584745	0.034118	0.670030	1.000
696	GOBP-RESPONSE.TO-ORGANIC-CYCLIC-COMPOUND	GO-0014070	20	-0.450509	-1.591954	0.029412	0.662038	1.000
697	GOBP-RESPONSE.TO-NUTRIENT	GO-0007584	5	-0.685809	-1.592299	0.036096	0.683969	1.000
698	GOBP-SKELETAL-MUSCLE-ORGAN-DEVELOPMENT	GO-0060538	5	-0.662651	-1.592826	0.031496	0.707263	1.000
699	REACTOME-CELLULAR-SENESCENCE	R-RNO-2559583	6	-0.635771	-1.597409	0.029793	0.711672	1.000
700	GOBP-NEGATIVE-REGULATION-OF-BIOSYNTHETIC-PROCESS	GO-0009890	13	-0.501403	-1.597435	0.022910	0.740058	1.000
701	REACTOME-SENESCENCE-ASSOCIATED-SECRETORY-PHENO...	R-RNO-2559582	6	-0.635771	-1.604546	0.030303	0.734571	1.000
702	GOBP-FC-RECEPTOR-SIGNALING-PATHWAY	GO-0038093	8	-0.585707	-1.611141	0.024722	0.732085	1.000
703	GOBP-IMMUNE-RESPONSE-REGULATING-SIGNALING-PATHWAY	GO-000276	8	-0.585707	-1.615680	0.035714	0.743025	1.000
704	GOBP-MAPK-CASCADE	GO-0000165	18	-0.472144	-1.619633	0.031710	0.757535	1.000
705	GOBP-ACTIVATION-OF-IMMUNE-RESPONSE	GO-0002253	5	-0.686490	-1.622097	0.021136	0.782588	1.000

Continuation of Table S10							
NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
706 GOBP-CELLULAR-RESPONSE-TO-EXTERNAL-STIMULUS	GO-0071496	10	-0.560067	-1.623904	0.023143	0.813685	1.000
707 GOBP-EMBRYO-DEVELOPMENT-ENDING-IN-BIRTH-OR-EGG...	GO-0009792	9	-0.575492	-1.633763	0.020408	0.803747	1.000
708 GOBP-CYTOKINE-MEDIATED-SIGNALING-PATHWAY	GO-0019221	16	-0.491688	-1.636183	0.022198	0.836990	1.000
709 GOBP-MUSCLE-TISSUE-DEVELOPMENT	GO-0060537	11	-0.541374	-1.639085	0.026590	0.873023	1.000
710 GOBP-NEGATIVE-REGULATION-OF-TRANSCRIPTION-BY-R...	GO-0000122	10	-0.564503	-1.639437	0.025362	0.929092	1.000
711 GOBP-DEVELOPMENTAL-PROCESS-INVOLVED-IN-REPRODU...	GO-0003006	11	-0.547095	-1.653222	0.019653	0.902553	1.000
712 GOBP-MATERNAL-PROCESS-INVOLVED-IN-FEMALE-PREGN...	GO-0060135	5	-0.710804	-1.665547	0.018692	0.892859	0.999
713 GOBP-SKIN-DEVELOPMENT	GO-0043588	5	-0.702984	-1.689212	0.015027	0.812773	0.998
714 GOBP-CIRCULATORY-SYSTEM-DEVELOPMENT	GO-0072359	21	-0.482465	-1.694184	0.015284	0.855002	0.998
715 GOBP-IN-UTERO-EMBRYONIC-DEVELOPMENT	GO-0001701	8	-0.618549	-1.697652	0.017566	0.916660	0.998
289 REACTOME-NGF-STIMULATED-TRANSCRIPTION	R-RNO-9031628	9	0.353930	0.942122	0.521880	0.901241	1.000
716 GOBP-RESPONSE-TO-EXTRACELLULAR-STIMULUS	GO-0009991	13	-0.531490	-1.703521	0.017281	0.976334	0.998
717 GOBP-REGULATION-OF-ORGAN-GROWTH	GO-0046620	5	-0.724434	-1.712719	0.009044	1.000000	0.996
718 GOBP-EMBRYONIC-ORGAN-DEVELOPMENT	GO-0048568	7	-0.659482	-1.715278	0.020000	1.000000	0.996
719 GOBP-ORGAN-GROWTH	GO-0035265	5	-0.724434	-1.718715	0.015424	1.000000	0.996
720 GOBP-EMBRYO-DEVELOPMENT	GO-0009790	14	-0.536858	-1.741192	0.021542	1.000000	0.996
721 GOBP-HEART-DEVELOPMENT	GO-0007507	6	-0.695437	-1.741786	0.010178	1.000000	0.996
722 GOBP-CARDIAC-MUSCLE-TISSUE-DEVELOPMENT	GO-0048738	6	-0.695437	-1.746402	0.010390	1.000000	0.996
723 GOBP-MULTICELLULAR-ORGANISM-REPRODUCTION	GO-0032504	12	-0.569524	-1.764001	0.014068	1.000000	0.992
724 REACTOME-P-TEN-REGULATION	R-RNO-6807070	5	-0.754674	-1.777577	0.006402	1.000000	0.990
End of Table							

Supplementary Table S11: CTX-M early profile (1 DPL peak) GSEA results.

Begin of Table S11									
	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val	
0	GOBP-REGULATION-OF-NEURONAL-SYNAPTIC-PLASTICITY	GO-0048168	7	0.781099	1.916008	0.000000	0.512575	0.545	
1	REACTOME-NEGATIVE-REGULATION-OF-NMDA-RECEPTOR-...	R-HSA-9617324	8	0.740255	1.915856	0.005226	0.257571	0.546	
2	REACTOME-UNBLOCKING-OF-NMDA-RECEPTORS-GLUTAMAT...	R-RNO-438066	12	0.643641	1.885993	0.005367	0.231565	0.663	
3	REACTOME-ASSEMBLY-AND-CELL-SURFACE-PRESENTATIO...	R-RNO-9609736	8	0.740255	1.870816	0.001812	0.201931	0.719	
4	REACTOME-SYNAPTIC-ADHESION-LIKE-MOLECULES	R-RNO-8849932	9	0.652410	1.695269	0.013889	0.793753	1.000	
5	REACTOME-RAS-ACTIVATION-UPON-CA2-INFLUX-THROUGH...	R-HSA-442982	6	0.718701	1.666102	0.018416	0.828941	1.000	
6	GOBP-CELL-SURFACE-RECEPTOR-SIGNALING-PATHWAY_I...	GO-1905114	15	0.526334	1.651526	0.024561	0.795491	1.000	
7	REACTOME-LONG-TERM-POTENTIATION	R-HSA-9620244	10	0.591587	1.630903	0.031414	0.805733	1.000	
8	REACTOME-TRANSMISSION-ACROSS-CHEMICAL-SYNAPSES	R-RNO-112315	23	0.468524	1.628466	0.026891	0.728449	1.000	
9	REACTOME-ACTIVATION-OF-NMDA-RECEPTORS-AND-POST...	R-RNO-442755	16	0.513227	1.573137	0.028053	0.961150	1.000	
10	GOBP-POSTSYNAPSE-ORGANIZATION	GO-0099173	10	0.566282	1.569294	0.043478	0.895008	1.000	
11	REACTOME-NEURONAL-SYSTEM	R-RNO-112316	26	0.446338	1.561307	0.028862	0.866438	1.000	
12	GOBP-RESPONSE-TO-ALCOHOL	GO-0097305	11	0.545978	1.559732	0.033748	0.806638	1.000	
13	GOBP-REGULATION-OF-SYNAPTIC-PLASTICITY	GO-0048167	21	0.460294	1.558922	0.030822	0.753051	1.000	
14	GOBP-RESPONSE-TO-ETHANOL	GO-0045471	5	0.718747	1.553164	0.033028	0.729094	1.000	
15	REACTOME-MAPK-FAMILY-SIGNALING-CASCADES	R-RNO-5683057	12	0.526082	1.525754	0.049296	0.814406	1.000	
16	GOBP-EXCITATORY-CHEMICAL-SYNAPTIC-TRANSMISSION	GO-0098976	5	0.703966	1.522089	0.049360	0.785421	1.000	
17	REACTOME-NEUROTRANSMITTER-RECEPTORS-AND-POSTSY...	R-RNO-112314	22	0.438207	1.497067	0.043253	0.866216	1.000	
18	REACTOME-PROTEIN-PROTEIN-INTERACTIONS-AT-SYNAPSES	R-RNO-6794362	12	0.523716	1.493978	0.066087	0.835384	1.000	
19	GOBP-IONOTROPIC-GLUTAMATE-RECEPTOR-SIGNALING_P...	GO-0035235	9	0.556691	1.48562	0.084359	0.819220	1.000	
20	GOBP-PROTEIN-LOCALIZATION-TO-CELL-JUNCTION	GO-1902414	6	0.646341	1.468410	0.068783	0.872393	1.000	
21	GOBP-INORGANIC-ION-TRANSMEMBRANE-TRANSPORT	GO-0098660	9	0.550990	1.465765	0.069324	0.844717	1.000	
22	REACTOME-ONCOGENIC-MAPK-SIGNALING	R-HSA-6802957	5	0.667239	1.454165	0.071813	0.862716	1.000	
23	GOBP-REGULATION-OF-CELLULAR-COMPONENT-SIZE	GO-0032535	7	0.596441	1.441923	0.100000	0.883021	1.000	
24	GOBP-REGULATION-OF-NMDA-RECEPTOR-ACTIVITY	GO-2000310	10	0.521728	1.434390	0.086799	0.882025	1.000	
25	GOBP-PROTEIN-CONTAINING-COMPLEX-SUBUNIT-ORGANI...	GO-0043933	14	0.459858	1.409104	0.108202	0.971007	1.000	
26	GOBP-LEARNING	GO-0007612	13	0.470597	1.401058	0.104167	0.972712	1.000	
27	REACTOME-NEUREXINS-AND-NEUROLIGINS	R-RNO-6794361	9	0.532515	1.388430	0.125912	0.999461	1.000	
28	GOBP-PROTEIN-COMPLEX-OLIGOMERIZATION	GO-0051259	6	0.590112	1.384438	0.110912	0.984565	1.000	
29	GOBP-PROTEIN-LOCALIZATION-TO-CELL-PERIPHERY	GO-1990778	12	0.481015	1.382953	0.106618	0.958746	1.000	
30	GOBP-PROTEIN-LOCALIZATION-TO-POSTSYNAPSE	GO-0062237	5	0.638554	1.380786	0.121528	0.937810	1.000	
31	GOBP-PROTEIN-LOCALIZATION-TO-MEMBRANE	GO-0072657	14	0.451927	1.372858	0.116402	0.943251	1.000	
32	GOBP-PROTEIN-LOCALIZATION-TO-SYNAPSE	GO-0035418	5	0.638554	1.368986	0.121324	0.931889	1.000	
33	GOBP-CELLULAR-COMPONENT-MAINTENANCE	GO-0043954	5	0.626506	1.367283	0.128521	0.911429	1.000	
34	GOBP-REGULATION-OF-POSTSYNAPTIC-MEMBRANE-POTEN...	GO-0060078	14	0.446026	1.359635	0.093379	0.918392	1.000	
35	GOBP-REGULATION-OF-NEUROTRANSMITTER-RECEPTOR_A...	GO-0099601	13	0.453801	1.358894	0.108153	0.896114	1.000	
36	GOBP-MONOAMINE-TRANSPORT	GO-0015844	5	0.615020	1.337279	0.155867	0.963628	1.000	
37	GOBP-ASSOCIATIVE-LEARNING	GO-0008306	7	0.559081	1.327215	0.165517	0.982683	1.000	
38	GOBP-CATION-TRANSPORT	GO-0006812	25	0.379935	1.326090	0.138514	0.962526	1.000	
39	REACTOME-CREB1-PHOSPHORYLATION-THROUGH-NMDA_RE...	R-RNO-442742	8	0.520260	1.325481	0.149281	0.941185	1.000	
40	GOBP-NEURON-PROJECTION-ORGANIZATION	GO-0106027	8	0.512422	1.322168	0.141869	0.932008	1.000	

Continuation of Table S11

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
41	GOBP-GENERATION-OF-PRECURSOR-METABOLITES-AND-E...	5	0.608986	1.311754	0.157143	0.953841	1.000
42	GOBP-HOMEOSTASIS-OF-NUMBER-OF-CELLS	5	0.594912	1.307946	0.160940	0.947470	1.000
43	GOBP-INNATE-IMMUNE-RESPONSE	7	0.526377	1.283827	0.186125	1.000000	1.000
44	GOBP-GLUTAMATE-RECEPTOR-SIGNALING-PATHWAY	17	0.399607	1.266181	0.174576	1.000000	1.000
45	REACTOME-CELLULAR-RESPONSES-TO-EXTERNAL-STIMULI	12	0.438862	1.252634	0.203327	1.000000	1.000
46	GOBP-RESPONSE-TO-NUTRIENT	5	0.567904	1.247074	0.221223	1.000000	1.000
47	HALLMARK-P3K-AKT-MTOR-SIGNALING	6	0.522204	1.227863	0.203936	1.000000	1.000
48	GOBP-RESPONSE-TO-ABIOTIC-STIMULUS	27	0.336080	1.224115	0.190557	1.000000	1.000
49	GOBP-REGULATION-OF-ANATOMICAL-STRUCTURE-SIZE	10	0.437734	1.207463	0.219684	1.000000	1.000
50	GOBP-REGULATION-OF-WNT-SIGNALING-PATHWAY	5	0.548305	1.203603	0.254000	1.000000	1.000
51	GOBP-MALE-GAMETE-GENERATION	5	0.548145	1.197118	0.248201	1.000000	1.000
52	GOBP-REGULATION-OF-POSTSYNAPSE-ORGANIZATION	6	0.504298	1.181934	0.273205	1.000000	1.000
53	GOBP-REGULATION-OF-MEMBRANE-POTENTIAL	17	0.363453	1.172667	0.249158	1.000000	1.000
54	GOBP-REGULATION-OF-METAL-ION-TRANSPORT	6	0.511707	1.169342	0.274194	1.000000	1.000
55	GOBP-MEMBRANE-ORGANIZATION	12	0.410460	1.167651	0.282098	1.000000	1.000
56	GOBP-NEUROTRANSMITTER-SECRETION	6	0.502626	1.154663	0.288396	1.000000	1.000
57	GOBP-CATION-TRANSMEMBRANE-TRANSPORT	18	0.354188	1.153508	0.273684	1.000000	1.000
58	GOBP-G-PROTEIN-COUPLED-RECEPTOR-SIGNALING-PATHWAY	18	0.346863	1.151636	0.263934	1.000000	1.000
59	REACTOME-POST-TRANSLATIONAL-PROTEIN-MODIFICATION	7	0.471931	1.147994	0.294872	1.000000	1.000
60	GOBP-DENDRITIC-SPINE-DEVELOPMENT	6	0.511171	1.146298	0.329609	1.000000	1.000
61	REACTOME-INTERFERON-SIGNALING	6	0.497862	1.141704	0.291367	1.000000	1.000
62	GOBP-DEVELOPMENTAL-MATURATION	5	0.530720	1.131630	0.344178	1.000000	1.000
63	GOBP-REGULATION-OF-TRANSPORTER-ACTIVITY	17	0.354141	1.131436	0.314721	1.000000	1.000
64	GOBP-ORGANIC-HYDROXY-COMPOUND-TRANSPORT	6	0.495429	1.128347	0.326376	1.000000	1.000
65	GOBP-CHEMICAL-SYNAPTIC-TRANSMISSION-POSTSYNAPTIC	9	0.430212	1.120542	0.306644	1.000000	1.000
66	REACTOME-MEMBRANE-TRAFFICKING	5	0.516645	1.121580	0.341284	1.000000	1.000
67	GOBP-REGULATION-OF-CYTOSOLIC-CALCIUM-ION-CONCE...	13	0.376914	1.118450	0.313406	1.000000	1.000
68	GOBP-REGULATION-OF-ION-TRANSPORT	36	0.296374	1.116070	0.332149	1.000000	1.000
69	GOBP-DIVALENT-INORGANIC-CATION-HOMEOSTASIS	13	0.376914	1.108401	0.326050	1.000000	1.000
70	GOBP-HEAD-DEVELOPMENT	22	0.322022	1.107567	0.312187	1.000000	1.000
71	GOBP-CALCIUM-ION-TRANSPORT-INTO-CYTOSOL	7	0.447161	1.107132	0.336237	1.000000	1.000
72	GOBP-METAL-ION-TRANSPORT	11	0.380502	1.096673	0.332740	1.000000	1.000
73	GOBP-REGULATION-OF-SIGNALING-RECEPTOR-ACTIVITY	14	0.365134	1.091687	0.351304	1.000000	1.000
74	REACTOME-TRANSCRIPTIONAL-REGULATION-BY-MECP2	7	0.449566	1.089911	0.353680	1.000000	1.000
75	REACTOME-INFECTIOUS-DISEASE	13	0.365399	1.088924	0.353041	1.000000	1.000
76	GOBP-CYTOSOLIC-CALCIUM-ION-TRANSPORT	7	0.447161	1.087455	0.388785	1.000000	1.000
77	REACTOME-VESICLE-MEDIATED-TRANSPORT	5	0.516645	1.085773	0.372881	1.000000	1.000
78	GOBP-PROTEIN-LOCALIZATION-TO-PLASMA-MEMBRANE	7	0.440613	1.084246	0.355240	1.000000	1.000
79	REACTOME-TRAFFICKING-OF-AMPA-RECEPTORS	11	0.385754	1.084218	0.339789	1.000000	1.000
80	GOBP-RESPONSE-TO-DRUG	11	0.379930	1.082146	0.361552	1.000000	1.000
81	GOBP-PEPTIDE-BIOSYNTHETIC-PROCESS	7	0.440217	1.082037	0.350442	1.000000	1.000
82	GOBP-RESPIRATORY-SYSTEM-DEVELOPMENT	6	0.460410	1.072992	0.379747	1.000000	1.000
83	GOBP-DEVELOPMENTAL-CELL-GROWTH	5	0.499393	1.072022	0.386809	1.000000	1.000

Continuation of Table S11

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
84	GOBP-CALCIUM-ION-TRANSPORT	11	0.380502	1.071964	0.364791	1.000000	1.000
85	GOBP-SEXUAL-REPRODUCTION	10	0.388175	1.070595	0.352740	1.000000	1.000
86	GOBP-LONG-TERM-SYNAPTIC-DEPRESSION	5	0.496568	1.067658	0.385714	1.000000	1.000
87	GOBP-CALCIUM-ION-TRANSMEMBRANE-TRANSPORT	7	0.447161	1.066191	0.366972	1.000000	1.000
88	GOBP-AMIDE-BIOSYNTHETIC-PROCESS	7	0.440217	1.066106	0.403478	1.000000	1.000
89	REACTOME-DISEASES-OF-SIGNAL-TRANSDUCTION-BY_GR...	12	0.367294	1.066026	0.381944	1.000000	1.000
90	GOBP-NEGATIVE-REGULATION-OF-BINDING	6	0.459380	1.061192	0.381125	1.000000	1.000
91	REACTOME-CIRCADIAN-CLOCK	5	0.483531	1.058528	0.382784	1.000000	1.000
92	GOBP-ANION-TRANSMEMBRANE-TRANSPORT	7	0.424702	1.053892	0.381282	1.000000	1.000
93	GOBP-REGULATION-OF_CELL-PROJECTION-ORGANIZATION	20	0.320443	1.052005	0.384880	1.000000	1.000
94	GOBP-CELL-CELL-SIGNALING-BY-WNT	7	0.432237	1.050591	0.418944	1.000000	1.000
95	GOBP-REGULATION-OF_CATION-TRANSMEMBRANE-TRANSPORT	16	0.334915	1.044905	0.409241	1.000000	1.000
96	GOBP-NEGATIVE-REGULATION-OF_SYNAPTIC-TRANSMISSION	6	0.442020	1.039826	0.433526	1.000000	1.000
97	GOBP-POSITIVE-REGULATION-OF_CELL-PROJECTION_OR...	10	0.381644	1.033391	0.425225	1.000000	1.000
98	GOBP-REGULATION-OF-NEUROTRANSMITTER-LEVELS	7	0.422952	1.031098	0.415301	1.000000	1.000
99	GOBP-REGULATION-OF_TRANSPORT	44	0.267789	1.028635	0.411664	1.000000	1.000
100	GOBP-METAL-ION-HOMEOSTASIS	14	0.344780	1.027953	0.427877	1.000000	1.000
101	GOBP-REGULATION-OF_CELL-SIZE	5	0.481054	1.027845	0.433824	1.000000	1.000
102	GOBP-NEURON-DEVELOPMENT	33	0.280429	1.026671	0.427336	1.000000	1.000
103	GOBP-NEUROTRANSMITTER-TRANSPORT	7	0.422952	1.022985	0.428829	1.000000	1.000
104	GOBP-REGULATION-OF-NEUROTRANSMITTER-TRANSPORT	6	0.441118	1.019756	0.440741	1.000000	1.000
105	GOBP-SENSORY-PERCEPTION	9	0.380311	1.017152	0.441331	1.000000	1.000
106	GOBP-NEUROGENESIS	40	0.267049	1.012745	0.444631	1.000000	1.000
107	GOBP-RESPONSE-TO-OXYGEN-LEVELS	8	0.398507	1.004018	0.432916	1.000000	1.000
108	GOBP-CENTRAL-NERVOUS-SYSTEM-DEVELOPMENT	26	0.279412	0.991034	0.466667	1.000000	1.000
109	GOBP-TRANSMEMBRANE-TRANSPORT	27	0.276427	0.984567	0.480607	1.000000	1.000
110	GOBP-REGULATION-OF-PROTEIN-BINDING	7	0.400157	0.979250	0.487455	1.000000	1.000
111	REACTOME-L1CAM-INTERACTIONS	5	0.446396	0.977406	0.475564	1.000000	1.000
112	GOBP-IMPORT-INTO-CELL	6	0.421627	0.973758	0.497345	1.000000	1.000
113	GOBP-DEFENSE-RESPONSE-TO-OTHER-ORGANISM	9	0.352219	0.972414	0.470270	1.000000	1.000
114	GOBP-RESPONSE-TO-MECHANICAL-STIMULUS	6	0.412262	0.968258	0.494624	1.000000	1.000
115	GOBP-CELLULAR-RESPONSE-TO-HORMONE-STIMULUS	11	0.342638	0.965464	0.510714	1.000000	1.000
116	GOBP-EPHRIN-RECEPTOR-SIGNALING-PATHWAY	5	0.440017	0.958411	0.491773	1.000000	1.000
117	GOBP-ADENYLATE-CYCLASE-INHIBITING-G-PROTEIN_CO...	9	0.353721	0.957431	0.488496	1.000000	1.000
118	GOBP-NEURON-DIFFERENTIATION	36	0.256198	0.953390	0.553366	1.000000	1.000
119	GOBP-NEGATIVE-REGULATION-OF-MOLECULAR-FUNCTION	24	0.281609	0.950693	0.527919	1.000000	1.000
120	GOBP-CELLULAR-RESPONSE-TO-PEPTIDE-HORMONE-STIM...	9	0.351531	0.950209	0.521515	1.000000	1.000
121	GOBP-MORPHOGENESIS-OF-AN-EPITHELIUM	6	0.407845	0.949197	0.501742	1.000000	1.000
122	GOBP-ORGANONITROGEN-COMPOUND-BIOSYNTHETIC-PROCESS	13	0.312304	0.944903	0.540587	1.000000	1.000
123	GOBP-VESICLE-MEDIATED-TRANSPORT-IN-SYNAPSE	7	0.387115	0.934607	0.530797	1.000000	1.000
124	REACTOME-SIGNALING-BY-GPCR	22	0.269010	0.919776	0.548231	1.000000	1.000
125	GOBP-REGULATION-OF-PROTEIN-LOCALIZATION-TO_CEL...	6	0.397394	0.916372	0.553571	1.000000	1.000
126	GOBP-POSITIVE-REGULATION-OF_CELL-DEATH	19	0.275996	0.911815	0.585366	1.000000	1.000

Continuation of Table S11

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
127 GOBP-REGULATION-OF-CATION-CHANNEL-ACTIVITY	GO-2001257	14	0.306712	0.910644	0.568873	1.000000	1.000
128 GOBP-MULTICELLULAR-ORGANISMAL-HOMEOSTASIS	GO-0048871	12	0.317023	0.910180	0.575916	1.000000	1.000
129 GOBP-PEPTIDE-METABOLIC-PROCESS	GO-0006518	12	0.310859	0.903648	0.583190	1.000000	1.000
130 GOBP-TISSUE-HOMEOSTASIS	GO-0001894	5	0.423233	0.902167	0.578947	1.000000	1.000
131 GOBP-CELLULAR-ION-HOMEOSTASIS	GO-0006873	14	0.293939	0.901647	0.595745	1.000000	1.000
132 GOBP-RESPONSE-TO-MONOSACCHARIDE	GO-0034284	5	0.412327	0.900519	0.604736	1.000000	1.000
133 GOBP-CELL-PROJECTION-ORGANIZATION	GO-0030030	34	0.240126	0.893037	0.636852	1.000000	1.000
134 REACTOME-EPH-EPHRIN-SIGNALING	R-RNO-2682334	6	0.383213	0.886275	0.597450	1.000000	1.000
135 GOBP-RESPONSE-TO-CARBOHYDRATE	GO-0009743	5	0.412327	0.884967	0.610811	1.000000	1.000
136 GOBP-GAMETE-GENERATION	GO-0007276	9	0.332485	0.883397	0.607509	1.000000	1.000
137 GOBP-ENDOCRINE-SYSTEM-DEVELOPMENT	GO-0035270	6	0.384554	0.882929	0.629964	1.000000	1.000
138 GOBP-CELLULAR-AMIDE-METABOLIC-PROCESS	GO-0043603	13	0.295258	0.878717	0.612628	1.000000	1.000
139 GOBP-CARBOHYDRATE-METABOLIC-PROCESS	GO-0005975	9	0.334131	0.877108	0.614498	1.000000	1.000
140 GOBP-CELLULAR-RESPONSE-TO-ALCOHOL	GO-00097306	5	0.414001	0.875581	0.624329	1.000000	1.000
141 GOBP-LOCOMOTORY-BEHAVIOR	GO-0007626	7	0.360912	0.868117	0.625688	1.000000	1.000
142 GOBP-REGULATION-OF-ANION-TRANSMEMBRANE-TRANSPORT	GO-1903959	5	0.402034	0.862474	0.642322	1.000000	1.000
143 GOBP-TELENCEPHALON-DEVELOPMENT	GO-0021537	6	0.369488	0.856174	0.629565	1.000000	1.000
144 GOBP-POSITIVE-REGULATION-OF-PEPTIDASE-ACTIVITY	GO-0010952	7	0.344226	0.845646	0.646739	1.000000	1.000
145 GOBP-MONONUCLEAR-CELL-DIFFERENTIATION	GO-1903131	7	0.347866	0.844114	0.625862	1.000000	1.000
146 GOBP-TISSUE-MORPHOGENESIS	GO-0048729	7	0.344560	0.842446	0.642606	1.000000	1.000
147 GOBP-RESPONSE-TO-PEPTIDE-HORMONE	GO-0043434	13	0.280000	0.842190	0.662752	1.000000	1.000
148 GOBP-PROTEIN-MODIFICATION-BY-SMALL-PROTEIN-CON...	GO-0070647	7	0.345390	0.840351	0.661080	1.000000	1.000
149 GOBP-REGULATION-OF-LONG-TERM-SYNAPTIC-POTENTIAL...	GO-1900271	6	0.365854	0.838525	0.646956	1.000000	1.000
150 GOBP-CELL-GROWTH	GO-0016049	10	0.300048	0.837426	0.689119	1.000000	1.000
151 GOBP-POSITIVE-REGULATION-OF-CYSTEINE-TYPE-ENDO...	GO-2001056	7	0.344226	0.835953	0.686238	1.000000	1.000
152 REACTOME-DEVELOPMENTAL-BIOLOGY	R-RNO-1266738	23	0.245577	0.833641	0.701493	1.000000	1.000
153 REACTOME-ANTI-INFLAMMATORY-RESPONSE-FAVOURING...	R-HSA-9662851	5	0.385542	0.826516	0.678571	1.000000	1.000
154 GOBP-HOMEOSTATIC-PROCESS	GO-0042592	31	0.228752	0.825424	0.720588	1.000000	1.000
155 REACTOME-TRANSCRIPTIONAL-REGULATION-OF-WHITE-A...	R-RNO-381340	6	0.357542	0.822755	0.687713	1.000000	1.000
156 GOBP-REGULATION-OF-TRANSMEMBRANE-TRANSPORT	GO-0034762	23	0.238610	0.820490	0.722615	1.000000	1.000
157 GOBP-POLYSACCHARIDE-METABOLIC-PROCESS	GO-0005976	5	0.378159	0.813496	0.680702	1.000000	1.000
158 GOBP-POSITIVE-REGULATION-OF-PROTEOLYSIS	GO-0045862	8	0.315445	0.807562	0.705776	1.000000	1.000
159 GOBP-REGULATION-OF-HORMONE-LEVELS	GO-0010817	12	0.276045	0.805861	0.719595	1.000000	1.000
160 GOBP-CELLULAR-MACROMOLECULE-LOCALIZATION	GO-0070727	21	0.241402	0.805852	0.718519	1.000000	1.000
161 GOBP-CELLULAR-RESPONSE-TO-KETONE	GO-1901655	5	0.373494	0.800468	0.697133	1.000000	1.000
162 GOBP-DENDRITIC-SPINE-MORPHOGENESIS	GO-0060997	5	0.374724	0.800062	0.703704	1.000000	1.000
163 GOBP-MONOCARBOXYLIC-ACID-METABOLIC-PROCESS	GO-0032787	6	0.347766	0.796355	0.725314	1.000000	1.000
164 GOBP-PROTEOLYSIS	GO-0006508	17	0.249834	0.795647	0.730570	1.000000	1.000
165 REACTOME-NGF-STIMULATED-TRANSCRIPTION	R-RNO-9031628	9	0.303798	0.795264	0.717813	1.000000	1.000
166 GOBP-POSITIVE-REGULATION-OF-SECRETION	GO-0051047	6	0.342337	0.792974	0.719643	1.000000	1.000
167 GOBP-CELL-JUNCTION-ORGANIZATION	GO-0034330	19	0.237372	0.786197	0.767327	1.000000	1.000
168 GOBP-REGULATION-OF-TRANS-SYNAPTIC-SIGNALING	GO-0099177	40	0.205484	0.784573	0.801639	1.000000	1.000
169 GOBP-CELL-CELL-JUNCTION-ASSEMBLY	GO-0007043	5	0.365342	0.784135	0.723133	1.000000	1.000

Continuation of Table S11

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
170 GOBP-CALCIUM-MEDIATED-SIGNALING	GO-0019722	10	0.279283	0.779990	0.737881	1.000000	1.000
171 GOBP-POSITIVE-REGULATION-OF-LONG-TERM-SYNAPTIC...	GO-1900273	5	0.361446	0.777931	0.726433	1.000000	1.000
172 GOBP-LIPID-EXPORT-FROM-CELL	GO-0140353	5	0.356493	0.772829	0.710383	1.000000	1.000
173 GOBP-SYNAPSE-ORGANIZATION	GO-0050808	17	0.239357	0.766052	0.786078	1.000000	1.000
174 GOBP-NEGATIVE-REGULATION-OF-KINASE-ACTIVITY	GO-0033673	5	0.345566	0.764877	0.732394	1.000000	1.000
175 GOBP-ACTIVATION-OF-IMMUNE-RESPONSE	GO-0002253	5	0.348574	0.759090	0.750439	1.000000	1.000
176 GOBP-IMMUNE-EFFECTOR-PROCESS	GO-0002252	10	0.274678	0.758344	0.756554	1.000000	1.000
177 GOBP-NEGATIVE-REGULATION-OF-TRANSFERASE-ACTIVITY	GO-0051348	5	0.345566	0.757384	0.769088	1.000000	1.000
178 GOBP-EPITHELIAL-DEVELOPMENT	GO-0060429	15	0.245003	0.757081	0.799325	1.000000	1.000
179 GOBP-CIRCADIEN-REGULATION-OF-GENE-EXPRESSION	GO-0032922	5	0.345256	0.754532	0.771325	1.000000	1.000
180 GOBP-ION-HOMEOSTASIS	GO-0050801	16	0.236438	0.749590	0.816949	1.000000	1.000
181 REACTOME-DAG-AND-IP3-SIGNALING	R-RNO-1489509	8	0.297147	0.749121	0.772487	1.000000	1.000
182 GOBP-CHROMATIN-ORGANIZATION	GO-0006325	5	0.351723	0.748818	0.794118	1.000000	1.000
183 GOBP-ORGANIC-ANION-TRANSPORT	GO-0015711	6	0.316344	0.732696	0.774194	1.000000	1.000
184 GOBP-EXTRINSIC-APOPTOTIC-SIGNALING-PATHWAY	GO-0097191	7	0.300851	0.731105	0.789931	1.000000	1.000
185 GOBP-ORGANIC-ACID-TRANSPORT	GO-0015849	7	0.297027	0.729627	0.798932	1.000000	1.000
186 GOBP-CARBOXYLIC-ACID-TRANSPORT	GO-0046942	6	0.316344	0.729463	0.819421	1.000000	1.000
187 GOBP-REGULATION-OF-NEURON-PROJECTION-DEVELOPMENT	GO-0010975	16	0.232202	0.729073	0.805604	1.000000	1.000
188 GOBP-DEFENSE-RESPONSE	GO-0006952	19	0.223639	0.727821	0.818182	1.000000	1.000
189 REACTOME-LEISHMANIA-INFECTION	R-HSA-9658195	10	0.257005	0.721314	0.812174	1.000000	1.000
190 GOBP-REGULATION-OF-RECEPTOR-MEDIATED-ENDOCYTOSIS	GO-0048259	5	0.327154	0.720272	0.807760	1.000000	1.000
191 GOBP-AMINO-ACID-TRANSPORT	GO-0006865	6	0.316344	0.719928	0.797891	1.000000	1.000
192 GOBP-REGULATION-OF-BINDING	GO-0051098	11	0.261227	0.717951	0.826087	1.000000	1.000
193 GOBP-REGULATION-OF-NERVOUS-SYSTEM-PROCESS	GO-0031644	8	0.277634	0.717705	0.802768	1.000000	1.000
194 GOBP-REGULATION-OF-MUSCLE-CELL-DIFFERENTIATION	GO-0051147	6	0.308707	0.717231	0.828671	1.000000	1.000
195 GOBP-AXON-DEVELOPMENT	GO-0061564	18	0.222157	0.715808	0.813067	1.000000	1.000
196 GOBP-REGULATION-OF-PROTEIN-TYROSINE-KINASE-ACT...	GO-0061097	5	0.331277	0.712493	0.815838	1.000000	1.000
197 GOBP-CELLULAR-HOMEOSTASIS	GO-0019725	18	0.212137	0.707958	0.855670	1.000000	1.000
198 GOBP-CELLULAR-CARBOHYDRATE-METABOLIC-PROCESS	GO-0044262	5	0.331203	0.705829	0.818182	1.000000	1.000
199 GOBP-POSITIVE-REGULATION-OF-PROTEIN-TYROSINE-K...	GO-0061098	5	0.331277	0.705551	0.825137	1.000000	1.000
200 GOBP-CELL-CELL-SIGNALING	GO-0007267	56	0.178555	0.705300	0.881034	1.000000	1.000
201 GOBP-POSITIVE-REGULATION-OF-DNA-BINDING-TRANSC...	GO-0051091	10	0.257131	0.699441	0.843310	1.000000	1.000
202 GOBP-RESPONSE-TO-LIGHT-STIMULUS	GO-0009416	11	0.246059	0.698442	0.842105	1.000000	1.000
203 GOBP-CELL-MORPHOGENESIS-INVOLVED-IN-NEURON-DIF...	GO-0048667	21	0.204781	0.688575	0.880471	1.000000	1.000
204 GOBP-CELL-MORPHOGENESIS-INVOLVED-IN-DIFFERENTI...	GO-0009094	21	0.204781	0.688382	0.899174	1.000000	1.000
205 GOBP-POSITIVE-REGULATION-OF-HYDROLASE-ACTIVITY	GO-0051345	16	0.218988	0.688054	0.893103	1.000000	1.000
206 GOBP-CELL-CELL-JUNCTION-ORGANIZATION	GO-0045216	6	0.300433	0.683021	0.849732	1.000000	1.000
207 GOBP-NEUROUS-SYSTEM-PROCESS	GO-0050877	38	0.177821	0.679960	0.915398	1.000000	1.000
208 GOBP-ORGANIC-ACID-METABOLIC-PROCESS	GO-0006082	7	0.271215	0.664879	0.862917	1.000000	1.000
209 GOBP-CHEMICAL-HOMEOSTASIS	GO-0048878	23	0.192896	0.659706	0.917763	1.000000	1.000
210 REACTOME-DEATH-RECEPTOR-SIGNALING	R-RNO-73887	5	0.302565	0.655314	0.878049	1.000000	1.000
211 GOBP-POSITIVE-REGULATION-OF-CELL-GROWTH	GO-0030307	6	0.286138	0.654587	0.881119	1.000000	1.000
212 GOBP-REGULATION-OF-CARBOHYDRATE-METABOLIC-PROCESS	GO-0006109	5	0.303491	0.653217	0.888889	1.000000	1.000

Continuation of Table S11

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
213	GOBP-RECEPTOR-INTERNALIZATION	5	0.298956	0.652523	0.902256	1.000000	1.000
214	GOBP-REGULATION-OF-CARBOHYDRATE-BIOSYNTHETIC.P...	5	0.303491	0.651037	0.876977	1.000000	1.000
215	GOBP-CARBOHYDRATE-BIOSYNTHETIC-PROCESS	5	0.303491	0.649120	0.893382	1.000000	1.000
216	GOBP-ORGANIC-HYDROXY-COMPOUND-METABOLIC-PROCESS	7	0.260367	0.640437	0.904425	1.000000	1.000
217	GOBP-RESPONSE-TO-ORGANIC-CYCLOC-COMPOUND	20	0.188783	0.640182	0.934319	1.000000	1.000
218	GOBP-RECEPTOR-METABOLIC-PROCESS	5	0.298956	0.639929	0.908425	1.000000	1.000
219	GOBP-PURINE-CONTAINING-COMPOUND-METABOLIC-PROCESS	5	0.296816	0.636404	0.903108	1.000000	1.000
220	GOBP-REGULATION-OF-AXONOGENESIS	7	0.262879	0.631115	0.916667	1.000000	1.000
221	GOBP-RESPONSE-TO-HORMONE	20	0.187325	0.625584	0.928934	1.000000	1.000
222	HALLMARK-EPITHELIAL-MESENCHYMAL-TRANSITION	5	0.292480	0.625527	0.904315	1.000000	1.000
223	GOBP-COGNITION	28	0.176986	0.624492	0.939597	1.000000	1.000
224	GOBP-CARBOHYDRATE-DERIVATIVE-METABOLIC-PROCESS	7	0.254496	0.622185	0.933333	1.000000	1.000
225	GOBP-ADENYLATE-CYCLASE-MODULATING-G-PROTEIN.CO...	11	0.220115	0.619251	0.908475	1.000000	1.000
226	GOBP-REGULATION-OF-PROTEIN-LOCALIZATION.TO.MEM...	7	0.255202	0.617966	0.938849	1.000000	1.000
227	GOBP-LONG-TERM-MEMORY	6	0.268293	0.616842	0.907749	1.000000	1.000
228	GOBP-MUSCLE-CONTRACTION	5	0.274263	0.603266	0.932331	1.000000	1.000
229	GOBP-POSITIVE-REGULATION-OF-IMMUNE-RESPONSE	9	0.224443	0.602341	0.941712	1.000000	1.000
230	GOBP-G-PROTEIN-COUPLED-GLUTAMATE-RECEPTOR.SIGN...	8	0.233191	0.593848	0.961739	1.000000	1.000
231	HALLMARK-KRAS-SIGNALING-UP	6	0.256678	0.590334	0.950368	1.000000	1.000
232	GOBP-REGULATION-OF-CYSTEINE-TYPE-ENDOPEPTIDASE...	9	0.222544	0.580748	0.942761	1.000000	1.000
233	GOBP-CELLULAR-RESPONSE-TO-PEPTIDE	13	0.184918	0.563296	0.955556	1.000000	1.000
234	REACTOME-TOLL-LIKE-RECEPTOR-CASCADES	8	0.214829	0.561910	0.965950	1.000000	1.000
235	REACTOME-TOLL-LIKE-RECEPTOR-TLR1-TLR2-CASCADE	8	0.214829	0.560567	0.959664	1.000000	1.000
236	GOBP-REGULATION-OF-LIPID-LOCALIZATION	5	0.262895	0.557740	0.958042	1.000000	1.000
237	GOBP-CYTOKINE-MEDIATED-SIGNALING-PATHWAY	16	0.179934	0.555415	0.956294	1.000000	1.000
238	REACTOME-MYD88-INDEPENDENT-TLR4-CASCADE	8	0.214829	0.554786	0.957895	1.000000	1.000
239	GOBP-REGULATION-OF-PEPTIDASE-ACTIVITY	10	0.201975	0.553361	0.954466	1.000000	1.000
240	REACTOME-CYTOKINE-SIGNALING-IN-IMMUNE-SYSTEM	21	0.164324	0.549787	0.974705	1.000000	1.000
241	REACTOME-GPCR-LIGAND-BINDING	8	0.214718	0.549163	0.968921	1.000000	1.000
242	REACTOME-TOLL-LIKE-RECEPTOR-9-TLR9-CASCADE	8	0.214829	0.548355	0.974271	1.000000	1.000
243	HALLMARK-UV-RESPONSE-UP	5	0.253012	0.546216	0.964413	1.000000	1.000
244	REACTOME-RNA-POLYMERASE-II-TRANSCRIPTION	20	0.164587	0.545866	0.978477	1.000000	1.000
245	GOBP-SYNAPTIC-SIGNALING	47	0.143227	0.540769	0.978477	1.000000	1.000
246	GOBP-RESPONSE-TO-RADIATION	13	0.178188	0.535104	0.968366	1.000000	1.000
247	REACTOME-CLASS-C-3-METABOTROPIC-GLUTAMATE-PHER...	7	0.220433	0.534279	0.976991	1.000000	1.000
248	GOBP-REGULATION-OF-SYNAPTIC-TRANSMISSION-GLUTA...	12	0.182611	0.529528	0.978078	1.000000	1.000
249	GOBP-SYNAPTIC-TRANSMISSION-GLUTAMATERGIC	13	0.173333	0.520766	0.986014	1.000000	1.000
250	GOBP-RECEPTOR-MEDIATED-ENDOCYTOSIS	6	0.227034	0.519119	0.983842	1.000000	1.000
251	GOBP-BEHAVIOR	32	0.140793	0.518516	0.986820	1.000000	1.000
252	GOBP-MEMORY	13	0.167040	0.497877	0.986755	1.000000	1.000
253	GOBP-POSITIVE-REGULATION-OF-APOPTOTIC-SIGNALIN...	5	0.224829	0.492571	0.988743	1.000000	1.000
254	GOBP-CELLULAR-RESPONSE-TO-ORGANIC-CYCLOC-COMPOUND	13	0.162668	0.484457	0.986159	1.000000	1.000
255	GOBP-NEGATIVE-REGULATION-OF-INTRACELLULAR-SIGN...	7	0.194301	0.476022	0.990942	1.000000	1.000

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NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
256	GOBP-BIOLOGICAL_PROCESS_INVOLVED_IN_SYMBIOTIC....	11	0.162939	0.465491	0.991119	0.998179	1.000
257	GOBP-NEGATIVE-REGULATION-OF-CELL_CYCLE	5	0.211429	0.458665	0.996344	0.995238	1.000
258	GOBP-NEGATIVE-REGULATION-OF-PHOSPHORYLATION	7	-0.173870	-0.437660	1.000000	0.998710	1.000
259	GOBP-MAINTENANCE-OF-LOCATION	7	-0.180946	-0.463343	1.000000	0.998949	1.000
260	GOBP-MULTICELLULAR-ORGANISM-REPRODUCTION	12	-0.156481	-0.480749	0.995283	0.999093	1.000
261	GOBP-REPRODUCTION	18	-0.155263	-0.535406	0.987469	0.988415	1.000
262	GOBP-SKIN-DEVELOPMENT	5	-0.254108	-0.581444	0.962306	0.969275	1.000
263	GOBP-NEGATIVE-REGULATION-OF-LIPID_METABOLIC_PR...	5	-0.253012	-0.582144	0.952703	0.971020	1.000
264	REACTOME-TRAFFICKING-OF-GLUR2-CONTAINING_AMP_A...	8	-0.215549	-0.585660	0.938636	0.971191	1.000
265	GOBP-REGULATION-OF-CELL_CYCLE	13	-0.184345	-0.587451	0.957143	0.972236	1.000
266	GOBP-TEMPERATURE-HOMEOSTASIS	5	-0.254099	-0.591173	0.942350	0.971958	1.000
267	GOBP-RESPONSE-TO-INORGANIC-SUBSTANCE	13	-0.191088	-0.607055	0.939675	0.964928	1.000
268	GOBP-REGULATION-OF-GROWTH	13	-0.191088	-0.607055	0.939675	0.964928	1.000
269	GOBP-POSITIVE-REGULATION-OF-GLIOGENESIS	5	-0.269114	-0.609859	0.926339	0.967185	1.000
270	GOBP-REGULATION-OF-GLIOGENESIS	6	-0.256098	-0.611202	0.921839	0.968196	1.000
271	GOBP-LIPID-BIOSYNTHETIC-PROCESS	5	-0.269493	-0.612292	0.944444	0.969623	1.000
272	GOBP-POSITIVE-REGULATION-OF-DEFENSE-RESPONSE	23	-0.166121	-0.620586	0.950980	0.965125	1.000
273	GOBP-RESPONSE-TO-CYTOKINE	6	-0.256098	-0.623806	0.943182	0.964544	1.000
274	GOBP-REGULATION-OF-LIPID-BIOSYNTHETIC-PROCESS	10	-0.217944	-0.631622	0.932432	0.959707	1.000
275	GOBP-LIPID-LOCALIZATION	6	-0.256098	-0.633327	0.913979	0.960213	1.000
276	GOBP-MEMBRANE-PROTEIN-PROTEOLYSIS	5	-0.284848	-0.643041	0.881944	0.952922	1.000
277	GOBP-REGULATION-OF-NEURON-DIFFERENTIATION	11	-0.215800	-0.649973	0.912621	0.947936	1.000
278	GOBP-DEVELOPMENTAL-PROCESS_INVOLVED_IN_REPRODU...	10	-0.226968	-0.655576	0.882793	0.944404	1.000
279	GOBP-NEGATIVE-REGULATION-OF-TRANSCRIPTION_BY_R...	12	-0.208271	-0.657235	0.916667	0.944770	1.000
280	GOBP-REGULATION-OF-PROTEOLYSIS	6	-0.269659	-0.660083	0.867882	0.944001	1.000
281	GOBP-MYELOID-LEUKOCYTE-MEDIATED-IMMUNITY	7	-0.259259	-0.665538	0.885906	0.940047	1.000
282	GOBP-POSITIVE-REGULATION-OF-CYTOKINE-PRODUCTION	6	-0.269659	-0.667967	0.873239	0.939627	1.000
283	GOBP-CELL-ACTIVATION_INVOLVED_IN-IMMUNE-RESPONSE	6	-0.269659	-0.668550	0.895455	0.941036	1.000
284	REACTOME-NEUTROPHIL-DEGRANULATION	8	-0.247295	-0.671180	0.877996	0.940182	1.000
285	GOBP-SENSORY-ORGAN-DEVELOPMENT	12	-0.215408	-0.675545	0.890215	0.937450	1.000
286	GOBP-MACROMOLECULE-CATABOLIC-PROCESS	8	-0.256322	-0.677363	0.866051	0.937491	1.000
287	GOBP-PROTEIN-CATABOLIC-PROCESS	7	-0.259259	-0.677878	0.841014	0.938894	1.000
288	GOBP-REGULATION-OF-LIPID_METABOLIC_PROCESS	15	-0.204562	-0.681852	0.871122	0.936345	1.000
289	REACTOME-NERVOUS-SYSTEM-DEVELOPMENT	6	-0.283584	-0.684116	0.848233	0.935664	1.000
290	GOBP-FATTY-ACID-TRANSPORT	16	-0.203320	-0.688312	0.880488	0.932763	1.000
291	GOBP-REGULATION-OF-DNA-BINDING-TRANSCRIPTION_F...	5	-0.301205	-0.688983	0.856818	0.934121	1.000
292	GOBP-REGULATION-OF-LYMPHOCYTE-ACTIVATION	18	-0.204443	-0.690701	0.903890	0.934360	1.000
293	GOBP-RESPONSE-TO-PEPTIDE	17	-0.204443	-0.692723	0.866828	0.934012	1.000
294	GOBP-RESPONSE-TO-BIOTIC-STIMULUS	5	-0.301205	-0.694311	0.842105	0.934121	1.000
295	GOBP-NEGATIVE-REGULATION-OF-IMMUNE-SYSTEM-PROCESS	5	-0.308902	-0.695608	0.851598	0.934644	1.000
296	GOBP-MONOCARBOXYLIC-ACID-TRANSPORT	5	-0.307242	-0.695624	0.832589	0.936830	1.000
297	GOBP-RESPONSE-TO-INTERLEUKIN_1	6	-0.293253	-0.698087	0.828947	0.935812	1.000
298	GOBP-GLUCOSE-METABOLIC-PROCESS	6	-0.293253	-0.698087	0.828947	0.935812	1.000

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	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	PWER.p.val
299	GOBP-ACIDIC-AMINO-ACID-TRANSPORT	GO-0015800	5	-0.308902	-0.701007	0.813901	0.934403	1.000
300	REACTOME-INNATE-IMMUNE-SYSTEM	R-RNO-168249	16	-0.204625	-0.702432	0.873418	0.934737	1.000
301	GOBP-DICARBOXYLIC-ACID-TRANSPORT	GO-0006835	5	-0.308902	-0.703640	0.827887	0.935347	1.000
302	GOBP-ANATOMICAL-STRUCTURE-HOMEOSTASIS	GO-0060249	7	-0.279928	-0.707145	0.836559	0.932640	1.000
303	GOBP-REGULATION-OF-EXTRINSIC-APOPTOTIC-SIGNAL...	GO-2001236	6	-0.294985	-0.712982	0.794702	0.927117	1.000
304	GOBP-MONOSACCHARIDE-METABOLIC-PROCESS	GO-0005996	6	-0.293253	-0.723077	0.816742	0.914954	1.000
305	REACTOME-INTERLEUKIN_17-SIGNALING	R-RNO-448424	6	-0.298419	-0.726614	0.811927	0.912056	1.000
306	GOBP-MUSCLE-CELL-DEVELOPMENT	GO-0055001	5	-0.320854	-0.728444	0.809313	0.911832	1.000
307	GOBP-LYMPHOCYTE-ACTIVATION	GO-0046649	9	-0.250399	-0.728843	0.814480	0.913422	1.000
308	GOBP-SMALL-MOLECULE-METABOLIC-PROCESS	GO-0044281	15	-0.224832	-0.731900	0.827586	0.911452	1.000
309	GOBP-SPROUTING-ANGIOGENESIS	GO-0002040	5	-0.317531	-0.734660	0.780911	0.909667	1.000
310	GOBP-FOREBRAIN-DEVELOPMENT	GO-0030900	9	-0.263111	-0.736853	0.808756	0.908416	1.000
311	GOBP-ADENYLATE-CYCLASE-INHIBITING-G-PROTEIN_CO...	GO-0007196	5	-0.325301	-0.737170	0.773365	0.910209	1.000
312	GOBP-FAT-CELL-DIFFERENTIATION	GO-0045444	9	-0.265600	-0.739438	0.801782	0.908874	1.000
313	GOBP-NEGATIVE-REGULATION-OF-MULTICELLULAR_ORGA...	GO-0051241	15	-0.222144	-0.740049	0.840095	0.910257	1.000
314	GOBP-LONG-TERM-SYNAPTIC-POTENTIATION	GO-0060291	12	-0.239148	-0.741261	0.821101	0.910670	1.000
315	GOBP-POSITIVE-REGULATION-OF-NEURON-DEATH	GO-1901216	5	-0.320817	-0.742290	0.791111	0.911553	1.000
316	GOBP-TRANSMEMBRANE-RECEPTOR-PROTEIN-SERINE_THR...	GO-0007178	6	-0.304878	-0.745276	0.765700	0.909174	1.000
317	GOBP-CELLULAR-RESPONSE-TO-ABIOTIC-STIMULUS	GO-0071214	7	-0.295278	-0.745740	0.772727	0.910701	1.000
318	REACTOME-PTEN-REGULATION	R-RNO-6807070	5	-0.323984	-0.746391	0.776190	0.911881	1.000
319	REACTOME-ESTROGEN-DEPENDENT-NUCLEAR-EVENTS-DOW...	R-RNO-9634638	5	-0.331505	-0.747471	0.774194	0.912348	1.000
320	HALLMARK-HYPOXIA	M5891	5	-0.325574	-0.749039	0.778539	0.912065	1.000
321	GOBP-NEGATIVE-REGULATION-OF-PROTEIN-CATABOLIC...	GO-0042177	5	-0.326477	-0.749072	0.765086	0.914293	1.000
322	GOBP-POSITIVE-REGULATION-OF-SYNAPTIC-TRANSMISSION	GO-0050806	15	-0.220952	-0.749122	0.810127	0.916499	1.000
323	GOBP-EPITHELIAL-CELL-DIFFERENTIATION	GO-0030855	7	-0.288901	-0.755181	0.783550	0.909189	1.000
324	GOBP-ENDOTHELIAL-CELL-MIGRATION	GO-0043542	8	-0.283127	-0.757845	0.772627	0.907374	1.000
325	GOBP-CYTOKINE-PRODUCTION	GO-0001816	10	-0.269231	-0.758496	0.777778	0.908540	1.000
326	GOBP-RESPONSE-TO-ENDOGENOUS-STIMULUS	GO-0009719	34	-0.190516	-0.759401	0.806701	0.909379	1.000
327	GOBP-LIPID-METABOLIC-PROCESS	GO-0006629	10	-0.262501	-0.762689	0.749431	0.906802	1.000
328	GOBP-RAS-PROTEIN-SIGNAL-TRANSDUCTION	GO-0007265	5	-0.332501	-0.762930	0.745182	0.908649	1.000
329	GOBP-REPRODUCTIVE-SYSTEM-DEVELOPMENT	GO-0061458	6	-0.315536	-0.763075	0.749436	0.910766	1.000
330	GOBP-CELLULAR-RESPONSE-TO-EXTERNAL-STIMULUS	GO-0071496	10	-0.267887	-0.766684	0.763855	0.907215	1.000
331	GOBP-BLOOD-VESSEL-ENDOTHELIAL-CELL-MIGRATION	GO-0043534	8	-0.283127	-0.769042	0.774038	0.905680	1.000
332	GOBP-CELLULAR-RESPONSE-TO-INORGANIC-SUBSTANCE	GO-0071241	11	-0.259288	-0.773824	0.755294	0.900322	1.000
333	REACTOME-INTEGRATION-OF-ENERGY-METABOLISM	R-RNO-163685	5	-0.349398	-0.775081	0.707944	0.900636	1.000
334	GOBP-CELLULAR-GLUCOSE-HOMEOSTASIS	GO-0001678	5	-0.346620	-0.780082	0.736170	0.894328	1.000
335	GOBP-POSITIVE-REGULATION-OF-AXONOGENESIS	GO-0050772	5	-0.351033	-0.781171	0.704289	0.894677	1.000
336	REACTOME-TRANSCRIPTIONAL-REGULATION-BY_TP53	R-RNO-3700989	6	-0.324536	-0.782046	0.723595	0.895581	1.000
337	GOBP-REGULATION-OF-PROTEIN-CATABOLIC-PROCESS	GO-0042176	7	-0.307750	-0.784342	0.716312	0.894014	1.000
338	GOBP-NEGATIVE-REGULATION-OF-PHOSPHORUS-METABOL...	GO-0010563	9	-0.281844	-0.787856	0.744240	0.890415	1.000
339	GOBP-CELL-CYCLE	GO-0007049	21	-0.228462	-0.791204	0.729798	0.887067	1.000
340	GOBP-MUSCLE-CELL-DIFFERENTIATION	GO-0042692	10	-0.275592	-0.795760	0.725962	0.881622	1.000
341	GOBP-NEGATIVE-REGULATION-OF_CELL_PROJECTION_OR...	GO-0031345	5	-0.348812	-0.797818	0.718681	0.880271	1.000

Continuation of Table S11

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
342	GOBP-REGIONALIZATION	GO-0003002	6	-0.334450	-0.801745	0.651316	0.876002	1.000
343	GOBP-TUBE.MORPHOGENESIS	GO-0035239	15	-0.242575	-0.804184	0.717540	0.874035	1.000
344	REACTOME-SENESCENCE-ASSOCIATED-SECRETORY-PHENO...	R-RNO-2559582	6	-0.335032	-0.804710	0.706897	0.875521	1.000
345	GOBP-NEGATIVE-REGULATION-OF-CELLULAR-COMPONENT...	GO-0051129	11	-0.268916	-0.805780	0.712941	0.876019	1.000
346	GOBP-RESPONSE-TO-HEAT	GO-0009408	7	-0.319900	-0.807277	0.702280	0.875623	1.000
347	GOBP-RESPONSE-TO-TUMOR-NECROSIS-FACTOR	GO-0034612	7	-0.311517	-0.807476	0.659722	0.877682	1.000
348	GOBP-PATTERN-SPECIFICATION-PROCESS	GO-0007389	6	-0.334450	-0.808249	0.699152	0.878653	1.000
349	GOBP-REGULATION-OF-SMALL-MOLECULE-METABOLIC-PR...	GO-0062012	9	-0.286530	-0.811637	0.725664	0.874773	1.000
350	GOBP-AMEBOIDAL-TYPE-CELL-MIGRATION	GO-0001667	11	-0.264891	-0.812548	0.704225	0.875468	1.000
351	GOBP-NEGATIVE-REGULATION-OF-CATABOLIC-PROCESS	GO-0009895	8	-0.304186	-0.815049	0.699580	0.873390	1.000
352	HALLMARK-TNFA-SIGNALING-VIA-NFKB	M5890	14	-0.256757	-0.818429	0.705736	0.869578	1.000
353	GOBP-LEUKOCYTE-MEDIATED-IMMUNITY	GO-0002443	7	-0.326653	-0.819113	0.690171	0.870697	1.000
354	GOBP-POSITIVE-REGULATION-OF-CATALYTIC-ACTIVITY	GO-0043085	30	-0.206873	-0.819280	0.734211	0.872781	1.000
355	GOBP-NEGATIVE-REGULATION-OF-CATALYTIC-ACTIVITY	GO-0043086	17	-0.233521	-0.821300	0.696833	0.871339	1.000
356	GOBP-CELL-CYCLE-PROCESS	GO-0022402	11	-0.271568	-0.826031	0.694915	0.864647	1.000
357	REACTOME-CELLULAR-SENESCENCE	R-RNO-2559583	6	-0.335032	-0.828571	0.663462	0.862387	1.000
358	REACTOME-INTRACELLULAR-SIGNALING-BY-SECOND-MES...	R-RNO-9006925	15	-0.252302	-0.830639	0.703529	0.860774	1.000
359	GOBP-POSITIVE-REGULATION-OF-NEURON-PROJECTION...	GO-0010976	5	-0.372420	-0.832378	0.668919	0.860023	1.000
360	GOBP-REGULATION-OF-CELLULAR-RESPONSE-TO-STRESS	GO-0080135	9	-0.304897	-0.832561	0.660173	0.862113	1.000
361	GOBP-NEURON-MIGRATION	GO-0001764	5	-0.367985	-0.832772	0.647186	0.864229	1.000
362	GOBP-NEGATIVE-REGULATION-OF-HYDROLASE-ACTIVITY	GO-0051346	11	-0.285178	-0.837472	0.667513	0.858269	1.000
363	GOBP-SIGNAL-RELEASE	GO-0023061	14	-0.258677	-0.837683	0.702765	0.860287	1.000
364	GOBP-TUBE-DEVELOPMENT	GO-0035295	18	-0.241712	-0.839918	0.694789	0.858677	1.000
365	GOBP-CARBOHYDRATE-HOMEOSTASIS	GO-0033500	7	-0.324111	-0.843211	0.638767	0.854445	1.000
366	GOBP-NEGATIVE-REGULATION-OF-BIOSYNTHETIC-PROCESS	GO-0009890	13	-0.269100	-0.843599	0.642298	0.856217	1.000
367	GOBP-MATERNAL-PROCESS-INVOLVED-IN-FEMALE-PREGN...	GO-0060135	5	-0.378671	-0.849495	0.612245	0.846914	1.000
368	GOBP-T-CELL-ACTIVATION	GO-0042110	8	-0.313698	-0.851963	0.619450	0.844440	1.000
369	GOBP-REGULATION-OF-IMMUNE-RESPONSE	GO-0050776	12	-0.269079	-0.856588	0.646789	0.838087	1.000
370	GOBP-RESPONSE-TO-METAL-ION	GO-0010038	15	-0.259735	-0.856653	0.639798	0.840387	1.000
371	GOBP-RESPONSE-TO-TEMPERATURE-STIMULUS	GO-0009266	9	-0.306770	-0.857408	0.622768	0.841448	1.000
372	GOBP-POSITIVE-REGULATION-OF-NERVOUS-SYSTEM-DEV...	GO-0051962	12	-0.282567	-0.859499	0.630137	0.840010	1.000
373	GOBP-SECOND-MESSENGER-MEDIATED-SIGNALING	GO-0019932	16	-0.258510	-0.859891	0.641509	0.841717	1.000
374	GOBP-CELL-PART-MORPHOGENESIS	GO-0032990	24	-0.233945	-0.860018	0.668317	0.843864	1.000
375	GOBP-POSITIVE-REGULATION-OF-MOLECULAR-FUNCTION	GO-0044093	38	-0.208895	-0.861152	0.708543	0.844159	1.000
376	GOBP-SMALL-GTPASE-MEDIATED-SIGNAL-TRANSDUCTION	GO-0007264	8	-0.320989	-0.863386	0.598639	0.842199	1.000
377	GOBP-PROTEIN-DEPHOSPHORYLATION	GO-0006470	7	-0.364037	-0.864037	0.613839	0.843434	1.000
378	GOBP-POSITIVE-REGULATION-OF-CELL-DEVELOPMENT	GO-0010720	12	-0.282567	-0.864345	0.634091	0.845369	1.000
379	GOBP-MUSCLE-STRUCTURE-DEVELOPMENT	GO-0061061	16	-0.263372	-0.864734	0.631336	0.847185	1.000
380	GOBP-MYELOID-LEUKOCYTE-ACTIVATION	GO-0002274	8	-0.323697	-0.871687	0.583732	0.836091	1.000
381	GOBP-STRIATED-MUSCLE-CELL-DIFFERENTIATION	GO-0051146	9	-0.310895	-0.871731	0.615044	0.838494	1.000
382	GOBP-DEPHOSPHORYLATION	GO-0016311	7	-0.341408	-0.872111	0.606593	0.840197	1.000
383	GOBP-CELL-MORPHOGENESIS	GO-0000902	24	-0.233945	-0.878377	0.633417	0.830476	1.000
384	GOBP-CELLULAR-COMPONENT-MORPHOGENESIS	GO-0032989	24	-0.233945	-0.879280	0.618421	0.831209	1.000

Continuation of Table S11

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
385	GOBP-REGULATION-OF-TRANSFERASE-ACTIVITY	GO-0051338	22	-0.242689	-0.879610	0.629108	0.833170	1.000
386	GOBP-POSITIVE-REGULATION-OF-NEUROGENESIS	GO-0050769	12	-0.282567	-0.880404	0.600000	0.834143	1.000
387	GOBP-RESPONSE-TO-REACTIVE-OXYGEN-SPECIES	GO-0000302	8	-0.328910	-0.880405	0.598684	0.836655	1.000
388	GOBP-AGING	GO-0007568	13	-0.274918	-0.881289	0.632850	0.837252	1.000
389	GOBP-REGULATION-OF-PROTEIN-KINASE-ACTIVITY	GO-0045859	22	-0.242689	-0.884060	0.629268	0.834164	1.000
390	REACTOME-SIGNALING-BY-INTERLEUKINS	R-RNO-449147	15	-0.275931	-0.886121	0.588372	0.832399	1.000
391	GOBP-IN-UTERO-EMBRYONIC-DEVELOPMENT	GO-0001701	8	-0.326012	-0.887219	0.578947	0.832700	1.000
392	GOBP-RESPONSE-TO-OXIDATIVE-STRESS	GO-0006979	8	-0.328910	-0.888782	0.612832	0.832228	1.000
393	GOBP-GROWTH	GO-0040007	14	-0.274933	-0.890512	0.589681	0.831507	1.000
394	GOBP-POSITIVE-REGULATION-OF-BINDING	GO-0051099	6	-0.375421	-0.902941	0.576200	0.809259	1.000
395	GOBP-NEGATIVE-REGULATION-OF-GENE-EXPRESSION	GO-0010629	12	-0.294195	-0.910059	0.580866	0.797277	1.000
396	GOBP-CELLULAR-RESPONSE-TO-LIPID	GO-00071396	15	-0.267680	-0.910147	0.544776	0.799546	1.000
397	GOBP-NEGATIVE-REGULATION-OF-CELL-POPULATION-PR...	GO-0008285	9	-0.327903	-0.910835	0.571101	0.800834	1.000
398	GOBP-DENDRITE-MORPHOGENESIS	GO-0048813	6	-0.376298	-0.911757	0.577273	0.801541	1.000
399	GOBP-REGULATION-OF-DEVELOPMENTAL-GROWTH	GO-0048638	9	-0.323231	-0.915726	0.561905	0.796034	1.000
400	GOBP-NEGATIVE-REGULATION-OF-ANION-TRANSPORT	GO-1903792	8	-0.337424	-0.918697	0.518779	0.792587	1.000
401	GOBP-RESPONSE-TO-KETONE	GO-1901654	7	-0.358025	-0.924728	0.509091	0.783122	1.000
402	GOBP-REGULATION-OF-CELL-CYCLE-PROCESS	GO-0010564	5	-0.409639	-0.925832	0.508584	0.783162	1.000
403	GOBP-CELLULAR-RESPONSE-TO-EXTRACELLULAR-STIMULUS	GO-0031668	8	-0.346803	-0.929313	0.538462	0.778878	1.000
404	GOBP-POSITIVE-REGULATION-OF-PRL-MIRNA-TRANSCRI...	GO-1902895	7	-0.357373	-0.929771	0.512987	0.780376	1.000
405	GOBP-GLIOGENESIS	GO-0042063	12	-0.308196	-0.932110	0.507576	0.777902	1.000
406	GOBP-REGULATION-OF-VASCULATURE-DEVELOPMENT	GO-1901342	5	-0.409639	-0.932877	0.527964	0.778805	1.000
407	GOBP-ORGANONITROGEN-COMPOUND-CATABOLIC-PROCESS	GO-1901565	9	-0.335179	-0.933142	0.529817	0.780749	1.000
408	GOBP-REGULATION-OF-CELL-DEATH	GO-0010941	34	-0.230783	-0.933885	0.593516	0.781664	1.000
409	GOBP-RESPONSE-TO-OXYGEN-CONTAINING-COMPOUND	GO-1901700	39	-0.223029	-0.938172	0.538265	0.775290	1.000
410	GOBP-CELL-JUNCTION-ASSEMBLY	GO-0034329	8	-0.347106	-0.940314	0.529284	0.773229	1.000
411	GOBP-PRL-MIRNA-TRANSCRIPTION-BY-RNA-POLYMERASE-II	GO-0061614	7	-0.357373	-0.940976	0.535354	0.774328	1.000
412	GOBP-POSITIVE-REGULATION-OF-SIGNALING	GO-0023056	34	-0.233395	-0.943714	0.540540	0.770991	1.000
413	GOBP-RESPONSE-TO-NICOTINE	GO-0035094	7	-0.372282	-0.945054	0.500000	0.770783	1.000
414	GOBP-REGULATION-OF-ANATOMICAL-STRUCTURE-MORPHO...	GO-0022603	17	-0.270747	-0.945691	0.513761	0.772012	1.000
415	GOBP-PEPTIDYL-LYSINE-MODIFICATION	GO-0018205	5	-0.421687	-0.947734	0.463636	0.770260	1.000
416	GOBP-MULTI-ORGANISM-PROCESS	GO-0051704	16	-0.268408	-0.947898	0.516908	0.772471	1.000
417	GOBP-NEGATIVE-REGULATION-OF-LOCOMOTION	GO-0040013	5	-0.411548	-0.950942	0.486486	0.769095	1.000
418	GOBP-RESPONSE-TO-CALCIUM-ION	GO-0051592	6	-0.397419	-0.952814	0.512472	0.767958	1.000
419	GOBP-RESPONSE-TO-INSULIN	GO-0032868	5	-0.421687	-0.954913	0.460385	0.766197	1.000
420	GOBP-RHYTHMIC-PROCESS	GO-0048511	15	-0.289539	-0.960088	0.502193	0.758422	1.000
421	GOBP-CARDIAC-MUSCLE-TISSUE-DEVELOPMENT	GO-0048738	6	-0.399005	-0.961195	0.473804	0.758543	1.000
422	GOBP-RESPONSE-TO-UV	GO-0009411	5	-0.421687	-0.962103	0.460215	0.759130	1.000
423	GOBP-HEART-DEVELOPMENT	GO-0007507	6	-0.399005	-0.966126	0.513825	0.753252	1.000
424	GOBP-INTRACELLULAR-RECEPTOR-SIGNALING-PATHWAY	GO-0030522	5	-0.421687	-0.974270	0.446390	0.738748	1.000
425	GOBP-REGULATION-OF-CATABOLIC-PROCESS	GO-0009894	13	-0.304496	-0.974811	0.479167	0.740086	1.000
426	HALLMARK-APOPTOSIS	M5902	6	-0.402439	-0.976512	0.442890	0.738801	1.000
427	GOBP-ORGANOPHOSPHATE-METABOLIC-PROCESS	GO-0019637	7	-0.383814	-0.976890	0.444196	0.740538	1.000

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	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
428	GOBP.EPIDERMIS_DEVELOPMENT	GO-0008544	5	-0.429430	-0.981328	0.453901	0.733757	1.000
429	GOBP.RESPONSE.TO.NITROGEN.COMPOUND	GO-1901698	34	-0.242459	-0.984378	0.489189	0.729904	1.000
430	GOBP.FC.RECEPTOR_SIGNALING.PATHWAY	GO-0038093	8	-0.367628	-0.985707	0.466488	0.729748	1.000
431	GOBP.GLIAL.CELL.DIFFERENTIATION	GO-0010001	10	-0.328888	-0.986562	0.439636	0.730557	1.000
432	REACTOME_SIGNALING_BY_RHO_GTPASES_MIRO_GTPASES...	R-RNO-9716542	10	-0.358318	-0.987619	0.441704	0.730941	1.000
433	GOBP.NEGATIVE.REGULATION.OF.SIGNALING	GO-0023057	21	-0.271482	-0.991009	0.476886	0.726425	1.000
434	REACTOME_G_ALPHA_I_SIGNALING_EVENTS	R-RNO-118594	18	-0.291099	-0.991084	0.469586	0.728795	1.000
435	GOBP.POSITIVE.REGULATION.OF.DEVELOPMENTAL_PROCESS	GO-0051094	32	-0.249293	-0.994182	0.467934	0.725033	1.000
436	GOBP.CIRCULATORY_SYSTEM_PROCESS	GO-0003013	5	-0.439660	-0.995168	0.439583	0.725659	1.000
437	GOBP.MITOCHONDRION.ORGANIZATION	GO-0007005	7	-0.392524	-0.998847	0.439462	0.720145	1.000
438	GOBP.POSITIVE.REGULATION.OF.GROWTH	GO-0045927	9	-0.362039	-1.000936	0.457275	0.718351	1.000
439	GOBP.IMMUNE.RESPONSE.REGULATING_SIGNALING_PATHWAY	GO-0002764	8	-0.367628	-1.002030	0.431718	0.718566	1.000
440	GOBP.POSITIVE.REGULATION.OF.ION.TRANSPORT	GO-0043270	17	-0.294705	-1.004698	0.452607	0.715351	1.000
441	GOBP.POSITIVE.REGULATION.OF.TRANSCRIPTION_BY_R...	GO-0045944	24	-0.267564	-1.005569	0.448276	0.715883	1.000
442	GOBP.RESPONSE.TOLLIPID	GO-0033993	19	-0.291581	-1.005700	0.431981	0.718279	1.000
443	GOBP.REGULATION.OF.ENDOCYTOSIS	GO-0030100	6	-0.393889	-1.007133	0.396963	0.717957	1.000
444	GOBP.NEGATIVE.REGULATION.OF.PEPTIDASE_ACTIVITY	GO-0010466	6	-0.403001	-1.008248	0.408791	0.718233	1.000
445	GOBP.REGULATION.OF.SYNAPSE_STRUCTURE_OR_ACTIVITY	GO-0050803	11	-0.344835	-1.008382	0.434053	0.720594	1.000
446	GOBP.NEGATIVE.REGULATION.OF.NEURON.DEATH	GO-1901215	11	-0.335921	-1.012184	0.419431	0.715298	1.000
447	GOBP.BLOOD.VESSEL.MORPHOGENESIS	GO-0048514	14	-0.314399	-1.012474	0.422604	0.717344	1.000
448	GOBP.HORMONE.TRANSPORT	GO-0009914	9	-0.367314	-1.013092	0.454746	0.718774	1.000
449	GOBP.REGULATION.OF_PHOSPHOLIPASE_ACTIVITY	GO-0010517	6	-0.421805	-1.013275	0.433260	0.721144	1.000
450	GOBP.POSITIVE.REGULATION.OF_TRANSPORT	GO-0051050	26	-0.260782	-1.013471	0.418421	0.723443	1.000
451	GOBP.EMBRYONIC.ORGAN.DEVELOPMENT	GO-0048568	7	-0.402272	-1.014816	0.407767	0.723365	1.000
452	GOBP.REGULATION.OF.NERVOUS.SYSTEM.DEVELOPMENT	GO-0051960	15	-0.308777	-1.020681	0.399072	0.713300	1.000
453	REACTOME_RHO_GTPASE_EFFECTORS	R-RNO-195258	9	-0.358318	-1.022186	0.400911	0.712687	1.000
454	GOBP.SKELETAL.MUSCLE.ORGAN.DEVELOPMENT	GO-0060538	5	-0.453676	-1.022777	0.414847	0.714123	1.000
455	GOBP.POSITIVE.REGULATION.OF.CATION.TRANSMEMBR...	GO-1904064	5	-0.457831	-1.023281	0.405702	0.715794	1.000
456	GOBP.MULTICELLULAR.ORGANISM.PROCESS	GO-0044706	8	-0.380294	-1.031012	0.392202	0.702392	1.000
457	REACTOME_ESR_MEDIATED_SIGNALING	R-RNO-8939211	8	-0.381377	-1.031156	0.417411	0.704776	1.000
458	REACTOME_SIGNALING_BY_NUCLEAR_RECEPTORS	R-RNO-9006931	8	-0.381377	-1.034182	0.402685	0.701087	1.000
459	GOBP.POSITIVE.REGULATION.OF_ENDOTHELIAL_CELL_P...	GO-0001938	6	-0.426829	-1.035582	0.397727	0.701009	1.000
460	GOBP.REGULATION.OF_FAT_CELL_DIFFERENTIATION	GO-0045598	6	-0.426829	-1.043922	0.413721	0.686487	1.000
461	GOBP.CELLULAR.MACROMOLECULE.CATABOLIC_PROCESS	GO-0044265	6	-0.434427	-1.044203	0.395034	0.688561	1.000
462	GOBP.DENDRITE.DEVELOPMENT	GO-0016358	9	-0.370671	-1.044955	0.377622	0.689636	1.000
463	GOBP.REGULATION.OF_LIPASE_ACTIVITY	GO-0060191	6	-0.421805	-1.045516	0.410314	0.691084	1.000
464	REACTOME_NUCLEAR_EVENTS_KINASE_AND_TRANSCRIPTI...	R-RNO-198725	11	-0.346103	-1.048037	0.387097	0.688389	1.000
465	GOBP.RESPONSE.TO.ACID.CHEMICAL	GO-0001101	6	-0.429247	-1.054035	0.362385	0.678548	1.000
466	GOBP.TISSUE.MIGRATION	GO-0090130	9	-0.375095	-1.056320	0.369412	0.676626	1.000
467	REACTOME_EXTRA_NUCLEAR_ESTROGEN_SIGNALING	R-RNO-9009391	7	-0.409420	-1.056554	0.375000	0.678885	1.000
468	GOBP.INFLAMMATORY_RESPONSE	GO-0006954	12	-0.340398	-1.057100	0.366162	0.680461	1.000
469	GOBP.NERVE.DEVELOPMENT	GO-0021675	9	-0.375723	-1.057863	0.380952	0.681604	1.000
470	GOBP.CELLULAR.COMPONENT_DISASSEMBLY	GO-0022411	6	-0.437583	-1.060260	0.353201	0.679334	1.000

Continuation of Table S11

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
471	GOBP-REGULATION-OF-NEUROGENESIS	GO-0050767	14	-0.325453	-1.060387	0.376417	0.681794	1.000
472	GOBP-REGULATION-OF-CELLULAR-AMIDE-METABOLIC-PR...	GO-0034248	9	-0.390062	-1.060565	0.373550	0.684027	1.000
473	REACTOME-SIGNALING-BY-RECEPTOR-TYROSINE-KINASES	R-RNO-9006934	26	-0.280017	-1.062107	0.354460	0.683678	1.000
474	GOBP-ENDOMEMBRANE-SYSTEM-ORGANIZATION	GO-0010256	6	-0.430845	-1.069021	0.368664	0.671895	1.000
475	GOBP-GLAND-DEVELOPMENT	GO-0048732	7	-0.402467	-1.069662	0.362637	0.673228	1.000
476	GOBP-NUCLEOBASE-CONTAINING-SMALL-MOLECULE-META...	GO-0055086	6	-0.428977	-1.075120	0.352442	0.664571	1.000
477	REACTOME-INTERLEUKIN-4-AND-INTERLEUKIN-13-SIGN...	R-RNO-6785807	8	-0.404856	-1.077324	0.346491	0.663043	1.000
478	GOBP-NEGATIVE-REGULATION-OF-CYSTEINE-TYPE-ENDO...	GO-2000117	5	-0.468326	-1.078380	0.338144	0.663618	1.000
479	GOBP-RESPONSE-TO-NERVE-GROWTH-FACTOR	GO-1990089	7	-0.423809	-1.081504	0.356659	0.660073	1.000
480	GOBP-CIRCADIEN-RHYTHM	GO-0007623	13	-0.336001	-1.083242	0.346983	0.659120	1.000
481	GOBP-CELLULAR-LIPID-METABOLIC-PROCESS	GO-0044255	7	-0.432099	-1.085232	0.337995	0.657629	1.000
482	GOBP-REGULATION-OF-MUSCLE-ADAPTATION	GO-0043502	5	-0.485028	-1.085627	0.330377	0.659557	1.000
483	GOBP-POSITIVE-REGULATION-OF-CELL-DIFFERENTIATION	GO-0044597	27	-0.286857	-1.088229	0.328395	0.657100	1.000
484	GOBP-MUSCLE-ADAPTATION	GO-0043500	5	-0.485028	-1.090867	0.342553	0.654380	1.000
485	REACTOME-ADAPTIVE-IMMUNE-SYSTEM	R-RNO-1280218	9	-0.396149	-1.090980	0.334831	0.656990	1.000
486	GOBP-REGULATION-OF-ENDOTHELIAL-CELL-MIGRATION	GO-0010594	5	-0.469218	-1.092217	0.339956	0.657177	1.000
487	GOBP-MUSCLE-TISSUE-DEVELOPMENT	GO-0060537	11	-0.364630	-1.093953	0.310185	0.650247	1.000
488	GOBP-REGULATION-OF-SYSTEM-PROCESS	GO-0044057	18	-0.312299	-1.095575	0.315534	0.655949	1.000
489	GOBP-LEUKOCYTE-DIFFERENTIATION	GO-0002521	15	-0.332221	-1.096322	0.327059	0.657234	1.000
490	GOBP-CELL-CELL-ADHESION	GO-0098609	14	-0.336362	-1.097380	0.328090	0.657673	1.000
491	REACTOME-G-ALPHA-Q-SIGNALING-EVENTS	R-RNO-116476	6	-0.441481	-1.097480	0.295872	0.660292	1.000
492	GOBP-ACTIN-FILAMENT-BASED-PROCESS	GO-0030029	7	-0.434950	-1.099979	0.324885	0.657698	1.000
493	GOBP-RESPONSE-TO-EXTRACELLULAR-STIMULUS	GO-0009991	13	-0.354342	-1.102728	0.314088	0.654722	1.000
494	GOBP-PROTEIN-MODIFICATION-BY-SMALL-PROTEIN-CON...	GO-0032446	6	-0.451260	-1.103399	0.322072	0.656258	1.000
495	GOBP-CHROMOSOME-ORGANIZATION	GO-0051276	6	-0.456582	-1.103499	0.332558	0.658982	1.000
496	GOBP-CELLULAR-RESPONSE-TO-NITROGEN-COMPOUND	GO-1901699	20	-0.304568	-1.105511	0.314496	0.657665	1.000
497	GOBP-CELLULAR-RESPONSE-TO-MOLECULE-OF-BACTERIA...	GO-0071219	8	-0.414255	-1.107187	0.338983	0.656965	1.000
498	GOBP-CELLULAR-RESPONSE-TO-BIOTIC-STIMULUS	GO-0071216	8	-0.414255	-1.108849	0.341743	0.656435	1.000
499	GOBP-VASCULATURE-DEVELOPMENT	GO-0001944	17	-0.329129	-1.109046	0.307107	0.658942	1.000
500	GOBP-NEGATIVE-REGULATION-OF-RESPONSE-TO-STIMULUS	GO-0048585	16	-0.329406	-1.110165	0.311778	0.659424	1.000
501	GOBP-POSTTRANSCRIPTIONAL-REGULATION-OF-GENE-EX...	GO-0010608	8	-0.413927	-1.110962	0.338747	0.660639	1.000
502	GOBP-POSITIVE-REGULATION-OF-EPITHELIAL-CELL-PR...	GO-0050679	7	-0.439593	-1.111480	0.312217	0.662666	1.000
503	GOBP-REGULATION-OF-PROTEIN-PHOSPHORYLATION	GO-0001932	26	-0.293559	-1.111877	0.312039	0.664775	1.000
504	REACTOME-G-PROTEIN-MEDIATED-EVENTS	R-RNO-112040	9	-0.405331	-1.113472	0.312896	0.664544	1.000
505	GOBP-RESPONSE-TO-BACTERIUM	GO-0009617	13	-0.358277	-1.114412	0.299766	0.665713	1.000
506	GOBP-ENZYME-LINKED-RECEPTOR-PROTEIN-SIGNALING-...	GO-0007167	24	-0.298400	-1.114720	0.280952	0.668198	1.000
507	GOBP-EXOCYTOSIS	GO-0006887	11	-0.373088	-1.118984	0.303738	0.662121	1.000
508	GOBP-REGULATION-OF-CELLULAR-LOCALIZATION	GO-0060341	17	-0.327939	-1.120243	0.276543	0.662469	1.000
509	GOBP-REGULATION-OF-HYDROLASE-ACTIVITY	GO-0051336	22	-0.304948	-1.120986	0.305000	0.664010	1.000
510	GOBP-REGULATION-OF-SECRETION	GO-0051046	14	-0.340877	-1.123877	0.288636	0.660600	1.000
511	GOBP-RESPONSE-TO-MOLECULE-OF-BACTERIAL-ORIGIN	GO-0002237	13	-0.358277	-1.126364	0.304850	0.658412	1.000
512	GOBP-PROTEIN-AUTOPHOSPHORYLATION	GO-0046777	5	-0.497262	-1.126946	0.299776	0.660240	1.000
513	GOBP-POSITIVE-REGULATION-OF-DEVELOPMENTAL-GROWTH	GO-0048639	8	-0.416174	-1.128899	0.291566	0.658917	1.000

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NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
514	GOBP-NEGATIVE-REGULATION-OF-NEURON-APOPTOTIC.P...	8	-0.414987	-1.130412	0.309051	0.658857	1.000
515	GOBP-PHAGOCYTOSIS	5	-0.509836	-1.143983	0.313559	0.632695	1.000
516	REACTOME-CA-DEPENDENT-EVENTS	8	-0.422217	-1.144941	0.280702	0.633807	1.000
517	GOBP-RESPONSE-TO-CADMIUM-ION	6	-0.475866	-1.148759	0.287016	0.628795	1.000
518	GOBP-REGULATION-OF-CELLULAR-PROTEIN-LOCALIZATION	12	-0.379526	-1.150157	0.275463	0.629160	1.000
519	GOBP-POSITIVE-REGULATION-OF-TRANSFERASE-ACTIVITY	20	-0.322847	-1.153459	0.251908	0.625623	1.000
520	GOBP-POSITIVE-REGULATION-OF-BIOSYNTHETIC-PROCESS	27	-0.300146	-1.153824	0.248101	0.628072	1.000
521	GOBP-DNA-METABOLIC-PROCESS	6	-0.479290	-1.154001	0.262115	0.630914	1.000
522	GOBP-POSITIVE-REGULATION-OF-GENE-EXPRESSION	16	-0.338283	-1.154576	0.258929	0.632854	1.000
523	GOBP-MUSCLE-ORGAN-DEVELOPMENT	9	-0.405063	-1.157730	0.270455	0.629164	1.000
524	REACTOME-SIGNALING-BY-NTRKS	18	-0.338492	-1.157962	0.263279	0.631988	1.000
525	GOBP-NEGATIVE-REGULATION-OF-PROTEOLYSIS	8	-0.429925	-1.161640	0.260465	0.627181	1.000
526	GOBP-DEVELOPMENTAL-GROWTH	10	-0.407473	-1.166236	0.265823	0.620987	1.000
527	REACTOME-SIGNALING-BY-NTRK2-TRKB	6	-0.470358	-1.169336	0.252252	0.622740	1.000
528	GOBP-INTRINSIC-APOPTOTIC-SIGNALING-PATHWAY	5	-0.511537	-1.168036	0.265589	0.623889	1.000
529	GOBP-MYELOID-CELL-DIFFERENTIATION	13	-0.374590	-1.171992	0.241218	0.624357	1.000
530	GOBP-ORGAN-GROWTH	5	-0.520901	-1.171992	0.257143	0.621830	1.000
531	GOBP-REGULATION-OF-CELLULAR-COMPONENT-BIOGENESIS	10	-0.407796	-1.172532	0.245033	0.623716	1.000
532	GOBP-ENDOCYTOSIS	8	-0.451996	-1.174935	0.270089	0.621673	1.000
533	HALLMARK-ALLOGRAFT-REJECTION	7	-0.451705	-1.175717	0.242206	0.623391	1.000
534	GOBP-PEPTIDE-SECRETION	9	-0.419296	-1.176778	0.269136	0.624595	1.000
535	GOBP-REGULATION-OF-HEMOPOIESIS	10	-0.401519	-1.178265	0.226164	0.625035	1.000
536	GOBP-REGULATION-OF-ORGAN-GROWTH	5	-0.520901	-1.178843	0.264192	0.627318	1.000
537	GOBP-ANIMAL-ORGAN-MORPHOGENESIS	12	-0.384453	-1.179949	0.250608	0.628334	1.000
538	GOBP-PEPTIDE-HORMONE-SECRETION	7	-0.462657	-1.180585	0.227373	0.630647	1.000
539	GOBP-NEGATIVE-REGULATION-OF-TRANSPORT	13	-0.374087	-1.181478	0.245700	0.632317	1.000
540	GOBP-POSITIVE-REGULATION-OF-PROTEIN-KINASE-ACT...	19	-0.329468	-1.182284	0.219388	0.634086	1.000
541	GOBP-NEURON-DEATH	18	-0.332965	-1.182483	0.224344	0.637134	1.000
542	GOBP-POSITIVE-REGULATION-OF-PROTEIN-METABOLIC...	28	-0.305819	-1.185579	0.219277	0.633776	1.000
543	GOBP-POSITIVE-REGULATION-OF-EPITHELIAL-CELL-MI...	5	-0.522545	-1.187202	0.257143	0.633882	1.000
544	GOBP-MITOTIC-CELL-CYCLE	10	-0.408735	-1.196900	0.238095	0.616369	1.000
545	GOBP-REGULATION-OF-ANION-TRANSPORT	20	-0.333087	-1.200152	0.199531	0.613302	1.000
546	GOBP-POSITIVE-REGULATION-OF-IMMUNE-SYSTEM-PROCESS	18	-0.343170	-1.201359	0.231144	0.614200	1.000
547	REACTOME-MAPK-TARGETS-NUCLEAR-EVENTS-MEDIATED...	5	-0.531873	-1.202588	0.259794	0.615350	1.000
548	GOBP-REGULATION-OF-CELLULAR-CATABOLIC-PROCESS	10	-0.417480	-1.206441	0.235033	0.610388	1.000
549	GOBP-PERIPHERAL-NERVOUS-SYSTEM-DEVELOPMENT	9	-0.432363	-1.209099	0.224622	0.608281	1.000
550	GOBP-INSULIN-SECRETION	7	-0.462657	-1.214204	0.220297	0.600374	1.000
551	GOBP-RESPONSE-TO-STARVATION	5	-0.534429	-1.215167	0.233100	0.601724	1.000
552	GOBP-REGULATION-OF-MYELOID-CELL-DIFFERENTIATION	9	-0.428584	-1.215325	0.185268	0.604938	1.000
553	GOBP-POSITIVE-REGULATION-OF-TRANSMEMBRANE_TRAN...	7	-0.469136	-1.224432	0.209135	0.589792	1.000
554	GOBP-ESTABLISHMENT-OF-PROTEIN-LOCALIZATION	18	-0.352385	-1.225421	0.185542	0.591255	1.000
555	GOBP-REGULATION-OF-CIRCADIAN-RHYTHM	7	-0.485904	-1.229740	0.230769	0.585873	1.000
556	REACTOME-EXTRACELLULAR-MATRIX-ORGANIZATION	5	-0.528771	-1.232212	0.189655	0.583885	1.000

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NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
557 GOBP-BIOLOGICAL-ADHESION	GO-0022610	19	-0.344879	-1.232526	0.179612	0.586803	1.000
558 GOBP-REGULATION-OF-APOPTOTIC-SIGNALING-PATHWAY	GO-2001233	10	-0.419575	-1.233713	0.209821	0.588060	1.000
559 GOBP-NEGATIVE-REGULATION-OF-RESPONSE-TO-EXTERN...	GO-0032102	5	-0.528865	-1.234965	0.216518	0.588902	1.000
560 GOBP-APOPTOTIC-MITOCHONDRIAL-CHANGES	GO-0008637	6	-0.523316	-1.237878	0.219457	0.586277	1.000
561 GOBP-INTRACELLULAR-TRANSPORT	GO-0046907	11	-0.407199	-1.238383	0.208738	0.588858	1.000
562 GOBP-CELLULAR-RESPONSE-TO-STARVATION	GO-0009267	5	-0.534429	-1.238448	0.211207	0.592492	1.000
563 GOBP-SENSORY-PERCEPTION-OF-PAIN	GO-0019233	5	-0.556438	-1.242430	0.225882	0.587266	1.000
564 REACTOME-OPIOID-SIGNALING	R-RNO-111885	12	-0.405099	-1.246191	0.182898	0.583488	1.000
565 GOBP-NEGATIVE-REGULATION-OF-PROTEIN-METABOLIC...	GO-0051248	20	-0.349207	-1.249851	0.180974	0.579234	1.000
566 GOBP-MULTICELLULAR-ORGANISMAL-RESPONSE-TO-STRESS	GO-0033555	5	-0.551579	-1.251002	0.212903	0.580755	1.000
567 GOBP-PROTEIN-LOCALIZATION-TO-ORGANELLE	GO-0033365	9	-0.459187	-1.257994	0.211905	0.569801	1.000
568 GOBP-CELLULAR-RESPONSE-TO-CHEMICAL-STRESS	GO-0062197	7	-0.493212	-1.259794	0.180365	0.569875	1.000
569 GOBP-EMBRYO-DEVELOPMENT-ENDING-IN-BIRTH-OR-EGG...	GO-0009792	9	-0.448569	-1.260423	0.206972	0.572279	1.000
570 GOBP-REGULATION-OF-CELL-DEVELOPMENT	GO-0060284	15	-0.382197	-1.264667	0.188073	0.566753	1.000
571 GOBP-CELLULAR-RESPONSE-TO-REACTIVE-OXYGEN-SPECIES	GO-0034614	7	-0.493212	-1.266365	0.179426	0.567096	1.000
572 GOBP-MUSCLE-SYSTEM-PROCESS	GO-0003012	9	-0.447964	-1.269166	0.170115	0.565017	1.000
573 GOBP-REGULATION-OF-PHOSPHORUS-METABOLIC-PROCESS	GO-0051174	27	-0.329132	-1.271459	0.154047	0.564183	1.000
574 GOBP-CELLULAR-RESPONSE-TO-OXYGEN-CONTAINING.CO...	GO-1901701	29	-0.322270	-1.272893	0.161376	0.565130	1.000
575 GOBP-CIRCULATORY-SYSTEM-DEVELOPMENT	GO-0072359	21	-0.346169	-1.279052	0.152542	0.556300	1.000
576 REACTOME-FC-EPSILON-RECEPTOR-FCER1-SIGNALING	R-RNO-2454202	7	-0.501189	-1.280601	0.167421	0.557180	1.000
577 GOBP-REGULATION-OF-VESICLE-MEDIATED-TRANSPORT	GO-0060627	12	-0.414013	-1.282753	0.154964	0.556506	1.000
578 GOBP-INTRACELLULAR-PROTEIN-TRANSPORT	GO-0006886	9	-0.453770	-1.284977	0.155660	0.555683	1.000
579 GOBP-REGULATION-OF-HORMONE-SECRETION	GO-0046883	8	-0.477997	-1.285158	0.190588	0.559274	1.000
580 GOBP-PROTEIN-PHOSPHORYLATION	GO-0006468	34	-0.319813	-1.285706	0.120643	0.562099	1.000
581 GOBP-NEUROTROPHIN-TRK-RECEPTOR-SIGNALING-PATHWAY	GO-0048011	6	-0.536785	-1.288560	0.179487	0.559957	1.000
582 GOBP-EMBRYONIC-MORPHOGENESIS	GO-0048598	6	-0.534977	-1.289572	0.171296	0.561904	1.000
583 GOBP-POSITIVE-REGULATION-OF-MULTICELLULAR-ORGA...	GO-0051240	32	-0.329443	-1.292199	0.132353	0.560299	1.000
584 GOBP-PEPTIDYL-TYROSINE-MODIFICATION	GO-0018212	10	-0.453646	-1.304735	0.136771	0.538046	1.000
585 GOBP-NEGATIVE-REGULATION-OF-PROTEIN-MODIFICATI...	GO-0031400	10	-0.451818	-1.306018	0.150685	0.539412	1.000
586 GOBP-SECRETION	GO-0046903	24	-0.350144	-1.308687	0.112782	0.537767	1.000
587 GOBP-POSITIVE-REGULATION-OF-NUCLEOBASE-CONTAIN...	GO-0045935	28	-0.340671	-1.314828	0.124352	0.529026	1.000
588 GOBP-NEGATIVE-REGULATION-OF-NEUROUS-SYSTEM.DEV...	GO-0051961	5	-0.578964	-1.315364	0.167800	0.531792	1.000
589 GOBP-ENDOTHELIAL-CELL-PROLIFERATION	GO-0001935	8	-0.478698	-1.316020	0.162291	0.534343	1.000
590 GOBP-NEUROTROPHIN-SIGNALING-PATHWAY	GO-0038179	6	-0.536785	-1.318328	0.177778	0.533873	1.000
591 GOBP-RESPONSE-TO-ALKALOID	GO-0043279	5	-0.588934	-1.318452	0.176734	0.537787	1.000
592 GOBP-REGULATION-OF-IMMUNE-SYSTEM-PROCESS	GO-0002682	21	-0.365909	-1.321638	0.125000	0.535601	1.000
593 GOBP-NEGATIVE-REGULATION-OF-TRANSMEMBRANE-TRAN...	GO-0034763	6	-0.542706	-1.321895	0.167442	0.539277	1.000
594 GOBP-FC-EPSILON-RECEPTOR-SIGNALING-PATHWAY	GO-0038095	7	-0.501189	-1.323492	0.166292	0.539976	1.000
595 GOBP-CYTOSKELETON-ORGANIZATION	GO-0007010	11	-0.439665	-1.324858	0.141026	0.541338	1.000
596 GOBP-REGULATION-OF-MUSCLE-SYSTEM-PROCESS	GO-0090257	8	-0.494203	-1.333279	0.138952	0.527858	1.000
597 GOBP-REGULATION-OF-LEUKOCYTE-DIFFERENTIATION	GO-1902105	9	-0.476719	-1.334808	0.128395	0.528801	1.000
598 GOBP-REGULATION-OF-PROTEIN-SERINE-THREONINE-KI...	GO-0071900	12	-0.434254	-1.340059	0.167920	0.521623	1.000
599 GOBP-APOPTOTIC-PROCESS	GO-0006915	35	-0.334089	-1.342518	0.105943	0.520980	1.000

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NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
600	GOBP-REGULATION-OF-PEPTIDYL-TYROSINE-PHOSPHORY...	9	-0.465386	-1.343222	0.150562	0.523966	1.000
601	GOBP-POSITIVE-REGULATION-OF-PEPTIDYL-TYROSINE...	8	-0.499029	-1.350519	0.127359	0.513184	1.000
602	GOBP-TRANSMEMBRANE-RECEPTOR-PROTEIN-TYROSINE-K...	19	-0.375799	-1.353577	0.101990	0.511299	1.000
603	GOBP-EMBRYO-DEVELOPMENT	14	-0.416274	-1.356255	0.103704	0.510021	1.000
604	GOBP-NEGATIVE-REGULATION-OF-NUCLEOBASE-CONTAIN...	13	-0.427517	-1.357015	0.127359	0.512921	1.000
605	GOBP-POSITIVE-REGULATION-OF-PROTEIN-PHOSPHORYL...	23	-0.370149	-1.362873	0.109865	0.505537	1.000
606	REACTOME-G-ALPHA-Z-SIGNALING-EVENTS	5	-0.601370	-1.364935	0.161702	0.505954	1.000
607	GOBP-CELLULAR-RESPONSE-TO-CADMIUM-ION	5	-0.614021	-1.365182	0.140426	0.509935	1.000
608	GOBP-MAPK-CASCADE	18	-0.404724	-1.384270	0.081081	0.475607	1.000
609	GOBP-LEUKOCYTE-MIGRATION	6	-0.572415	-1.386692	0.127962	0.475008	1.000
610	GOBP-REGULATION-OF-OSTEOCLAST-DIFFERENTIATION	5	-0.608122	-1.388514	0.128261	0.475292	1.000
611	GOBP-POSITIVE-REGULATION-OF-PROTEIN-MODIFICATI...	23	-0.370149	-1.397436	0.086634	0.460417	1.000
612	GOBP-REGULATION-OF-MYELOID-LEUKOCYTE-DIFFERENT...	8	-0.510990	-1.401103	0.126728	0.457852	1.000
613	GOBP-REGULATION-OF-PHOSPHOLIPASE-C-ACTIVITY	5	-0.626951	-1.403147	0.131519	0.458186	1.000
614	GOBP-POSITIVE-REGULATION-OF-PHOSPHORUS-METABOL...	24	-0.364279	-1.406203	0.084788	0.450868	1.000
615	GOBP-REGULATION-OF-EPITHELIAL-CELL-MIGRATION	6	-0.572718	-1.408643	0.116331	0.456568	1.000
616	GOBP-POSITIVE-REGULATION-OF-MYELOID-CELL-DIFFE...	7	-0.538151	-1.415053	0.110619	0.447727	1.000
617	GOBP-LEUKOCYTE-CELL-CELL-ADHESION	6	-0.573299	-1.416138	0.113379	0.450191	1.000
618	GOBP-OSTEOCLAST-DIFFERENTIATION	6	-0.585457	-1.417361	0.113586	0.452130	1.000
619	GOBP-POSITIVE-REGULATION-OF-LIPASE-ACTIVITY	5	-0.626951	-1.419689	0.127155	0.452289	1.000
620	GOBP-POSITIVE-REGULATION-OF-5SMALL-MOLECULE-MET...	5	-0.617940	-1.420272	0.114486	0.455667	1.000
621	GOBP-COAGULATION	8	-0.534606	-1.420283	0.108040	0.460287	1.000
622	GOBP-NEURON-APOPTOTIC-PROCESS	12	-0.461134	-1.420525	0.109785	0.464664	1.000
623	GOBP-APOPTOTIC-SIGNALING-PATHWAY	15	-0.434984	-1.425114	0.079646	0.459807	1.000
624	GOBP-PROTEIN-KINASE-B-SIGNALING	6	-0.567364	-1.428146	0.106335	0.458683	1.000
625	GOBP-POSITIVE-REGULATION-OF-ANION-TRANSPORT	9	-0.504673	-1.431539	0.097950	0.456758	1.000
626	GOBP-LOCOMOTION	31	-0.364744	-1.435691	0.061008	0.453196	1.000
627	GOBP-OSTEOBLAST-DIFFERENTIATION	5	-0.629492	-1.436988	0.116173	0.455562	1.000
628	GOBP-REGULATION-OF-BODY-FLUID-LEVELS	11	-0.465844	-1.438244	0.087379	0.458236	1.000
629	GOBP-REGULATION-OF-MITOTIC-CELL-CYCLE	5	-0.645340	-1.441063	0.101053	0.457130	1.000
630	GOBP-POSITIVE-REGULATION-OF-CELLULAR-COMPONENT...	9	-0.514756	-1.443105	0.077626	0.458254	1.000
631	GOBP-REGULATION-OF-GTPASE-ACTIVITY	5	-0.628153	-1.443191	0.097674	0.463328	1.000
632	GOBP-RESPONSE-TO-WOUNDING	15	-0.440615	-1.444487	0.067757	0.465771	1.000
633	GOBP-REGULATION-OF-DEFENSE-RESPONSE	7	-0.568663	-1.444987	0.095794	0.470247	1.000
634	GOBP-ACTIVATION-OF-PROTEIN-KINASE-ACTIVITY	11	-0.482024	-1.446256	0.067470	0.473086	1.000
635	GOBP-PLATELET-ACTIVATION	6	-0.597364	-1.448538	0.106195	0.474467	1.000
636	GOBP-REGULATION-OF-PROTEIN-MODIFICATION-PROCESS	29	-0.370814	-1.459878	0.048593	0.457843	1.000
637	GOBP-REGULATION-OF-PROTEIN-STABILITY	5	-0.640537	-1.460026	0.084862	0.463138	1.000
638	GOBP-POSITIVE-REGULATION-OF-CELL-CELL-ADHESION	5	-0.647452	-1.462526	0.084112	0.463652	1.000
639	GOBP-REGULATION-OF-CELL-DIFFERENTIATION	36	-0.360082	-1.470044	0.034392	0.453617	1.000
640	GOBP-REGULATION-OF-INFLAMMATORY-RESPONSE	7	-0.568653	-1.471006	0.085253	0.457322	1.000
641	GOBP-NEGATIVE-REGULATION-OF-ION-TRANSPORT	11	-0.486188	-1.479829	0.064815	0.445835	1.000
642	GOBP-REGULATION-OF-PEPTIDE-HORMONE-SECRETION	6	-0.620792	-1.481370	0.068966	0.448876	1.000

Continuation of Table S11

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
643	GOBP-NEUROINFLAMMATORY_RESPONSE	GO-0150076	5	-0.641995	-1.484543	0.082005	0.448162	1.000
644	GOBP-IMMUNE-SYSTEM-DEVELOPMENT	GO-0002520	17	-0.422402	-1.487282	0.060976	0.448288	1.000
645	GOBP-REGULATION-OF-PEPTIDYL-SERINE-PHOSPHORYLA...	GO-00033135	8	-0.560988	-1.488460	0.073563	0.451582	1.000
646	GOBP-POSITIVE-REGULATION-OF-LEUKOCYTE-CELL-CEL...	GO-1903039	5	-0.647452	-1.489033	0.082774	0.456418	1.000
647	GOBP-POSITIVE-REGULATION-OF-PEPTIDYL-SERINE-PH...	GO-00033138	8	-0.560988	-1.494309	0.075472	0.451005	1.000
648	REACTOME-HEMOSTASIS	R-RNO-109582	14	-0.457796	-1.498634	0.060533	0.447438	1.000
649	GOBP-CELLULAR-RESPONSE-TO-DNA-DAMAGE-STIMULUS	GO-0006974	5	-0.664264	-1.505843	0.080610	0.438424	1.000
650	GOBP-REGULATION-OF-CELL-ACTIVATION	GO-0050865	8	-0.564424	-1.507741	0.047414	0.440705	1.000
651	GOBP-MYOTUBE-DIFFERENTIATION	GO-0014902	5	-0.674591	-1.509458	0.080000	0.443495	1.000
652	GOBP-CELL-ACTIVATION	GO-0001775	21	-0.421811	-1.513681	0.058974	0.440404	1.000
653	GOBP-EPITHELIAL-CELL-PROLIFERATION	GO-0050673	12	-0.492856	-1.515965	0.059102	0.442164	1.000
654	GOBP-AMYLOID-BETA-METABOLIC-PROCESS	GO-0050435	5	-0.682707	-1.525907	0.059671	0.427671	1.000
655	GOBP-NEGATIVE-REGULATION-OF-DEVELOPMENTAL-PROCESS	GO-0051093	13	-0.484403	-1.528867	0.055556	0.428761	1.000
656	GOBP-PEPTIDYL-AMINO-ACID-MODIFICATION	GO-0018193	22	-0.419766	-1.532452	0.037879	0.427877	1.000
657	GOBP-AMYLOID-LEUKOCYTE-DIFFERENTIATION	GO-0002573	11	-0.509890	-1.541709	0.064516	0.416116	1.000
658	GOBP-REGULATION-OF-CYTOSKELETON-ORGANIZATION	GO-0051493	5	-0.672583	-1.548426	0.050439	0.407886	1.000
659	GOBP-NEGATIVE-REGULATION-OF-CELL-DIFFERENTIATION	GO-0044596	13	-0.484403	-1.548510	0.056931	0.414387	1.000
660	GOBP-REGULATION-OF-MULTICELLULAR-ORGANISMAL-DE...	GO-2000026	31	-0.394403	-1.554820	0.025510	0.408844	1.000
661	REACTOME-CELL-CYCLE-MITOTIC	R-RNO-69278	5	-0.674765	-1.559186	0.063781	0.406821	1.000
662	GOBP-NEGATIVE-REGULATION-OF-CELL-DEVELOPMENT	GO-0010721	6	-0.633310	-1.568572	0.052521	0.394476	1.000
663	GOBP-AMYLOID-PRECURSOR-PROTEIN-CATABOLIC-PROCESS	GO-0042987	5	-0.682707	-1.583778	0.075055	0.369826	1.000
664	GOBP-POSITIVE-REGULATION-OF-HEMOPOIESIS	GO-1903708	7	-0.624195	-1.589717	0.055046	0.364446	1.000
665	GOBP-AMYLOID-PRECURSOR-PROTEIN-METABOLIC-PROCESS	GO-0042982	5	-0.682707	-1.597760	0.054374	0.354896	1.000
666	GOBP-POSITIVE-REGULATION-OF-RESPONSE-TO-EXTERN...	GO-0032103	9	-0.571632	-1.600836	0.042654	0.354805	1.000
667	REACTOME-BETA-CATENIN-INDEPENDENT-WNT-SIGNALING	R-RNO-3858494	5	-0.713583	-1.603333	0.046771	0.356887	1.000
668	GOBP-REGULATION-OF-RESPONSE-TO-STRESS	GO-0080134	19	-0.460005	-1.611166	0.035800	0.349061	1.000
669	GOBP-NEURON-PROJECTION-GUIDANCE	GO-0097485	9	-0.581613	-1.625345	0.039352	0.329714	1.000
670	GOBP-REGULATION-OF-PROTEIN-LOCALIZATION	GO-0032880	18	-0.472000	-1.633561	0.041667	0.322134	1.000
671	GOBP-CELL-POPULATION-PROLIFERATION	GO-0008283	31	-0.418403	-1.641530	0.017032	0.313427	1.000
672	GOBP-POSITIVE-REGULATION-OF-SMOOTH-MUSCLE-CELL...	GO-0048661	5	-0.718896	-1.641695	0.040632	0.319717	1.000
673	GOBP-NEGATIVE-REGULATION-OF-APOPTOTIC-SIGNALIN...	GO-2001234	7	-0.632371	-1.644545	0.034169	0.320978	1.000
674	GOBP-ESTABLISHMENT-OF-PROTEIN-LOCALIZATION-TO-...	GO-0072594	6	-0.691121	-1.649947	0.033860	0.319172	1.000
675	GOBP-ERBB-SIGNALING-PATHWAY	GO-0038127	5	-0.728548	-1.656747	0.049661	0.313216	1.000
676	GOBP-WOUND-HEALING	GO-0042060	13	-0.519775	-1.665462	0.019231	0.303139	1.000
677	GOBP-REGULATION-OF-INTRACELLULAR-SIGNAL-TRANSD...	GO-1902531	21	-0.463694	-1.666739	0.011933	0.308253	1.000
678	GOBP-POSITIVE-REGULATION-OF-MYELOID-LEUKOCYTE-...	GO-0002763	6	-0.675452	-1.671388	0.030501	0.306890	1.000
679	GOBP-RESPONSE-TO-GROWTH-FACTOR	GO-0070848	18	-0.481308	-1.681438	0.017370	0.294907	1.000
680	GOBP-TAXIS	GO-0042330	14	-0.515160	-1.683985	0.027335	0.298163	1.000
681	GOBP-POSITIVE-REGULATION-OF-PHOSPHATIDYLINOSIT...	GO-0014068	5	-0.749227	-1.684059	0.026906	0.305932	1.000
682	REACTOME-SIGNALING-BY-WNT	R-RNO-195721	7	-0.643566	-1.688209	0.029345	0.306713	1.000
683	GOBP-INOSITOL-LIPID-MEDIATED-SIGNALING	GO-0048017	8	-0.614242	-1.692759	0.026570	0.306614	1.000
684	GOBP-REGULATION-OF-MAP-KINASE-ACTIVITY	GO-0043405	9	-0.616295	-1.701887	0.013667	0.296605	0.999
685	GOBP-REGULATION-OF-PEPTIDE-SECRETION	GO-0002791	7	-0.674308	-1.708127	0.027842	0.292878	0.999

Continuation of Table S11

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
686 GOBP-POSITIVE-REGULATION_OF_CELLULAR-PROTEIN_L...	GO-1903829	7	-0.677764	-1.721510	0.015625	0.278120	0.998
687 GOBP-ANATOMICAL-STRUCTURE-FORMATION-INVOLVED_I...	GO-0048646	20	-0.481020	-1.750632	0.009804	0.239676	0.994
688 GOBP-NEGATIVE-REGULATION-OF-CELL-DEATH	GO-0060548	22	-0.470940	-1.752907	0.014286	0.243146	0.994
689 GOBP-POSITIVE-REGULATION-OF-INTRACELLULAR-SIGN...	GO-1902533	14	-0.542037	-1.759478	0.008791	0.240231	0.993
690 GOBP-REGULATION-OF-ORGANELLE-ORGANIZATION	GO-0033043	14	-0.564031	-1.767300	0.006928	0.235417	0.991
691 GOBP-CELL-MIGRATION	GO-0016477	22	-0.486011	-1.784100	0.004975	0.218312	0.985
692 REACTOME-CELL-CYCLE	R-RNO-1640170	6	-0.754056	-1.798801	0.010438	0.203691	0.978
693 GOBP-PEPTIDYL-SERINE-MODIFICATION	GO-0018209	12	-0.586349	-1.806308	0.018561	0.200268	0.973
694 GOBP-NUCLEAR-TRANSPORT	GO-0051169	5	-0.792643	-1.824440	0.006608	0.180546	0.957
695 GOBP-SMOOTH-MUSCLE-CELL-PROLIFERATION	GO-0048659	6	-0.766386	-1.824954	0.011338	0.187454	0.957
696 GOBP-REGULATION-OF-VASCULAR-ASSOCIATED-SMOOTH...	GO-1904705	5	-0.817806	-1.829163	0.008529	0.188675	0.953
697 GOBP-REGULATION-OF-CELLULAR-COMPONENT-MOVEMENT	GO-0051270	15	-0.566820	-1.834603	0.005076	0.189225	0.939
698 GOBP-POSITIVE-REGULATION-OF-CELLULAR-COMPONENT...	GO-0051130	24	-0.493686	-1.856780	0.004988	0.166144	0.911
699 GOBP-POSITIVE-REGULATION-OF-PROTEIN-SERINE-THR...	GO-0071902	9	-0.664176	-1.886095	0.004762	0.138093	0.852
700 GOBP-REGULATION-OF-CELL-ADHESION	GO-0030155	13	-0.598240	-1.886961	0.014151	0.144055	0.851
701 GOBP-ERK1-AND-ERK2-CASCADE	GO-0070371	5	-0.841075	-1.891822	0.004338	0.145961	0.836
702 REACTOME-PLATELET-ACTIVATION-SIGNALING-AND-AGG...	R-HSA-76002	7	-0.725904	-1.901326	0.004484	0.141143	0.815
703 GOBP-PHOSPHATIDYLINOSITOL-3-KINASE-SIGNALING	GO-0014065	7	-0.745647	-1.911279	0.006849	0.137642	0.777
704 GOBP-POSITIVE-REGULATION-OF-ESTABLISHMENT-OF-P...	GO-1904951	5	-0.856813	-1.935586	0.004535	0.116525	0.692
705 GOBP-REGULATION-OF-MAPK-CASCADE	GO-0043408	13	-0.609137	-1.948559	0.002481	0.111934	0.650
706 GOBP-REGULATION-OF-PHOSPHATIDYLINOSITOL-3-KINA...	GO-0014066	6	-0.783878	-1.963295	0.004237	0.102936	0.599
707 GOBP-POSITIVE-REGULATION-OF-CELL-ADHESION	GO-0045785	7	-0.752015	-1.973063	0.004695	0.101850	0.566
708 GOBP-POSITIVE-REGULATION-OF-CELL-POPULATION-PR...	GO-0008284	21	-0.557474	-2.015513	0.000000	0.074913	0.441
709 GOBP-ACTIVATION-OF-MAPK-ACTIVITY	GO-0000187	6	-0.838398	-2.018368	0.000000	0.080351	0.431
710 GOBP-REGULATION-OF-CELL-CELL-ADHESION	GO-0022407	9	-0.756126	-2.065082	0.004202	0.055305	0.294
711 GOBP-POSITIVE-REGULATION-OF-LOCOMOTION	GO-0040017	11	-0.707142	-2.087959	0.000000	0.049878	0.249
712 GOBP-POSITIVE-REGULATION-OF-MAP-KINASE-ACTIVITY	GO-0043406	6	-0.838398	-2.089277	0.000000	0.056779	0.248
713 GOBP-OSSIFICATION	GO-0001503	9	-0.771636	-2.111545	0.000000	0.050400	0.192
714 GOBP-POSITIVE-REGULATION-OF-MAPK-CASCADE	GO-0043410	9	-0.768611	-2.153635	0.000000	0.039986	0.130
715 GOBP-POSITIVE-REGULATION-OF-ORGANELLE-ORGANIZA...	GO-0010638	10	-0.747409	-2.157120	0.002299	0.047046	0.122
716 GOBP-REGULATION-OF-PEPTIDE-TRANSPORT	GO-0090087	10	-0.738994	-2.159328	0.000000	0.060828	0.118
717 GOBP-MUSCLE-CELL-PROLIFERATION	GO-0033002	8	-0.792860	-2.163419	0.000000	0.089101	0.115
718 GOBP-REGULATION-OF-RESPONSE-TO-EXTERNAL-STIMULUS	GO-0032101	15	-0.686656	-2.283672	0.000000	0.037286	0.025

End of Table

Supplementary Table S12: CTX-M early profile (8 DPL peak) GSEA results.

Begin of Table S12									
	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val	
0	REACTOME_UNBLOCKING_OF_NMDA_RECEPTORS_GUTAMAT...	R-RNO-438066	12	0.599549	1.767262	0.007737	1.000000	0.986	
1	REACTOME_NEURONAL_SYSTEM	R-RNO-112316	26	0.481141	1.766692	0.009091	1.000000	0.987	
2	REACTOME_TRANSMISSION_ACROSS_CHEMICAL_SYNAPSES	R-RNO-112315	23	0.489211	1.753888	0.005576	1.000000	0.992	
3	GOBP_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY	GO-0007186	18	0.520962	1.715385	0.024299	1.000000	0.998	
4	REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATION	R-RNO-597592	7	0.670988	1.667953	0.015625	1.000000	1.000	
5	GOBP_PROTEIN_LOCALIZATION_TO_CELL_PERIPHERY	GO-1990778	12	0.571855	1.664676	0.019891	1.000000	1.000	
6	REACTOME_NEGATIVE_REGULATION_OF_NMDA_RECEPTOR....	R-HSA-961732	8	0.625000	1.654605	0.025180	1.000000	1.000	
7	REACTOME_NEUROTRANSMITTER_RECEPTORS_AND_POSTSY...	R-RNO-112314	22	0.467556	1.650605	0.016981	1.000000	1.000	
8	GOBP_CELLULAR_RESPONSE_TO_ALCOHOL	GO-0097306	5	0.733359	1.646519	0.015534	0.958915	1.000	
9	REACTOME_ASSEMBLY_AND_CELL_SURFACE_PRESENTATIO...	R-RNO-9609736	8	0.625000	1.639665	0.036663	0.921557	1.000	
10	REACTOME_ACTIVATION_OF_NMDA_RECEPTORS_AND_POST...	R-RNO-442755	16	0.499603	1.635245	0.039106	0.850281	1.000	
11	GOBP_PROTEIN_LOCALIZATION_TO_CELL_JUNCTION	GO-1902414	6	0.682927	1.614915	0.025145	0.895684	1.000	
12	GOBP_CELLULAR_RESPONSE_TO_KETONE	GO-1901655	5	0.746988	1.600881	0.037951	0.904788	1.000	
13	GOBP_GLUTAMATE_RECEPTOR_SIGNALING_PATHWAY	GO-0007215	17	0.479191	1.584430	0.038610	0.931415	1.000	
14	REACTOME_LONG_TERM_POTENTIATION	R-HSA-9620244	10	0.565748	1.570278	0.047714	0.945878	1.000	
15	GOBP_ADENYLATE_CYCLASE_INHIBITING_G_PROTEIN.CO...	GO-0007193	9	0.566426	1.544682	0.062147	1.000000	1.000	
16	GOBP_PROTEIN_LOCALIZATION_TO_MEMBRANE	GO-00072657	14	0.497549	1.540480	0.049702	0.995066	1.000	
17	REACTOME_SYNAPTIC_ADHESION_LIKE_MOLECULES	R-RNO-8849932	9	0.558248	1.538382	0.062030	0.951029	1.000	
18	GOBP_ORGANIC_HYDROXY_COMPOUND_TRANSPORT	GO-0015850	6	0.649641	1.522391	0.077821	0.990228	1.000	
19	HALLMARK_P13K_AKT_MTOR_SIGNALING	M5923	6	0.638770	1.513777	0.073705	0.987905	1.000	
20	GOBP_POSITIVE_REGULATION_OF_CELL_DEATH	GO-0010942	19	0.447558	1.512260	0.047348	0.948185	1.000	
21	GOBP_REGULATION_OF_NMDA_RECEPTOR_ACTIVITY	GO-2000310	10	0.531271	1.505432	0.068053	0.940561	1.000	
22	GOBP_POSITIVE_REGULATION_OF_IMMUNE_RESPONSE	GO-0050778	9	0.554897	1.502780	0.056075	0.912790	1.000	
23	GOBP_PROTEIN_LOCALIZATION_TO_POSTSYNAPSE	GO-0062237	5	0.674699	1.501587	0.059730	0.880402	1.000	
24	GOBP_PROTEIN_LOCALIZATION_TO_SYNAPSE	GO-0035418	5	0.674699	1.493818	0.069388	0.881773	1.000	
25	GOBP_IONOTROPIC_GLUTAMATE_RECEPTOR_SIGNALING_P...	GO-0035235	9	0.556379	1.486816	0.063116	0.882940	1.000	
26	GOBP_SMALL_MOLECULE_METABOLIC_PROCESS	GO-0044281	15	0.450474	1.467918	0.072937	0.938840	1.000	
27	REACTOME_PROTEIN_PROTEIN_INTERACTIONS_AT_SYNAPSES	R-RNO-6794362	12	0.501960	1.467711	0.062264	0.906280	1.000	
28	GOBP_CARBOHYDRATE_METABOLIC_PROCESS	GO-0005975	9	0.526143	1.443969	0.098456	0.987862	1.000	
29	GOBP_CELL_SURFACE_RECEPTOR_SIGNALING_PATHWAY_I...	GO-1905114	15	0.466804	1.443516	0.077799	0.957145	1.000	
30	REACTOME_RAS_ACTIVATION_UPON_CA2_INFLUX_THROUGH...	R-HSA-442982	6	0.609756	1.441100	0.103448	0.937064	1.000	
31	GOBP_ACTIVATION_OF_IMMUNE_RESPONSE	GO-0002253	5	0.649649	1.440250	0.108499	0.911991	1.000	
32	GOBP_MAINTENANCE_OF_LOCATION	GO-0051235	7	0.572121	1.417574	0.095506	0.989674	1.000	
33	REACTOME_LEISHMANIA_INFECTION	R-HSA-9658195	10	0.500275	1.416263	0.096045	0.966601	1.000	
34	GOBP_REGULATION_OF_POSTSYNAPTIC_MEMBRANE_POTEN...	GO-0060078	14	0.442009	1.402884	0.098113	1.000000	1.000	
35	GOBP_IMMUNE_EFFECTOR_PROCESS	GO-0002252	10	0.497732	1.398479	0.105364	0.996011	1.000	
36	REACTOME_ANTIINFLAMMATORY_RESPONSE_FAVOURING...	R-HSA-9662851	5	0.622568	1.393101	0.127953	0.993792	1.000	
37	GOBP_VESICLE_MEDIATED_TRANSPORT_IN_SYNAPSE	GO-0099003	7	0.555577	1.391908	0.122000	0.973296	1.000	
38	GOBP_NEGATIVE_REGULATION_OF_MOLECULAR_FUNCTION	GO-0044092	24	0.392892	1.389408	0.087657	0.959330	1.000	
39	GOBP_CATION_TRANSPORT	GO-0006812	25	0.385385	1.387241	0.103774	0.944523	1.000	
40	REACTOME_CIRCADIAN_CLOCK	R-HSA-400253	5	0.618496	1.386783	0.122841	0.923209	1.000	

Continuation of Table S12

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
41	GOBP-POSTSYNAPSE.ORGANIZATION	GO-0009173	10	0.480596	1.386317	0.124521	0.903493	1.000
42	GOBP-PROTEOLYSIS	GO-0006508	17	0.424658	1.385751	0.112132	0.885159	1.000
43	GOBP-RESPONSE.TO.ALCOHOL	GO-00097305	11	0.471336	1.369583	0.119565	0.930747	1.000
44	GOBP-SEXUAL.REPRODUCTION	GO-0019953	10	0.483559	1.369220	0.130515	0.911607	1.000
45	GOBP-CELLULAR.RESPONSE.TO.PEPTIDE.HORMONE.STIM...	GO-0071375	9	0.505884	1.362149	0.110887	0.920825	1.000
46	REACTOME-NEUREXINS.AND-NEUROLIGINS	R-RNO-6794361	9	0.503978	1.360998	0.122807	0.905795	1.000
47	REACTOME-INFECTIOUS.DISEASE	R-HSA-5663205	13	0.441916	1.359202	0.113949	0.894054	1.000
48	GOBP-CIRCADIAN.REGULATION.OF.GENE.EXPRESSION	GO-0032922	5	0.609411	1.353397	0.164284	0.890780	1.000
49	GOBP-MEMBRANE.PROTEIN.PROTEOLYSIS	GO-0033619	6	0.570490	1.342228	0.120459	0.924599	1.000
50	GOBP-REGULATION.OF.CARBOHYDRATE.METABOLIC.PROCESS	GO-0006109	5	0.600490	1.338495	0.163306	0.920831	1.000
51	GOBP-REGULATION.OF.CARBOHYDRATE.BIOSYNTHETIC.P...	GO-00043255	5	0.600490	1.328573	0.166667	0.941821	1.000
52	GOBP-CELLULAR.COMPONENT.MAINTENANCE	GO-00043954	5	0.581473	1.328249	0.156701	0.925489	1.000
53	GOBP-INORGANIC.ION.TRANSMEMBRANE.TRANSPORT	GO-0009860	9	0.490646	1.328124	0.153696	0.908666	1.000
54	GOBP-CARBOHYDRATE.BIOSYNTHETIC.PROCESS	GO-0016051	5	0.600490	1.324532	0.180233	0.905341	1.000
55	GOBP-EXCITATORY.CHEMICAL.SYNAPTIC.TRANSMISSION	GO-0009876	5	0.602410	1.319737	0.164329	0.907662	1.000
56	GOBP-RESPONSE.TO.DRUG	GO-00042493	11	0.457964	1.316027	0.160517	0.905523	1.000
57	GOBP-ORGANIC.HYDROXY.COMPOUND.METABOLIC.PROCESS	GO-1901615	7	0.534261	1.314287	0.156190	0.896015	1.000
58	GOBP-PROTEIN.LOCALIZATION.TO.PLASMA.MEMBRANE	GO-0072659	7	0.530609	1.302524	0.169524	0.925840	1.000
59	REACTOME-INNATE.IMMUNE.SYSTEM	R-RNO-108249	16	0.397738	1.291572	0.165049	0.951549	1.000
60	GOBP-EXOCYTOSIS	GO-0006887	11	0.447674	1.290058	0.160305	0.941658	1.000
61	GOBP-CELL-ACTIVATION.INVOLVED.IN.IMMUNE.RESPONSE	GO-0002263	6	0.534412	1.287372	0.186992	0.935826	1.000
62	GOBP-CELL-CELL-SIGNALING.BY.WNT	GO-0198738	7	0.504783	1.282608	0.186792	0.938801	1.000
63	GOBP-MYELOID-LEUKOCYTE-MEDIATED-IMMUNITY	GO-0002444	6	0.534412	1.273605	0.201887	0.958142	1.000
64	GOBP-REGULATION.OF.ION.TRANSPORT	GO-0043269	36	0.332705	1.270922	0.154696	0.952589	1.000
65	REACTOME-EPHLEPHRIN.SIGNALING	R-RNO-2682334	6	0.536661	1.269958	0.219608	0.941435	1.000
66	GOBP-REGULATION.OF.WNT.SIGNALING.PATHWAY	GO-0030111	5	0.579201	1.267367	0.201550	0.936521	1.000
67	GOBP-MALE.GAMETE.GENERATION	GO-0048232	5	0.582629	1.258748	0.227898	0.954460	1.000
68	GOBP-CATION.TRANSMEMBRANE.TRANSPORT	GO-00098655	18	0.375694	1.251294	0.176692	0.967766	1.000
69	REACTOME-NEUTROPHIL-DEGRANULATION	R-RNO-6798695	6	0.534412	1.247381	0.210821	0.967722	1.000
70	GOBP-NEGATIVE.REGULATION.OF.KINASE.ACTIVITY	GO-0033673	5	0.556317	1.243092	0.215190	0.970109	1.000
71	GOBP-RESPONSE.TO.KETONE	GO-1901654	7	0.495849	1.23282	0.204771	0.981859	1.000
72	GOBP-CARBOHYDRATE.DERIVATIVE.METABOLIC.PROCESS	GO-1901135	7	0.491393	1.234215	0.220561	0.976181	1.000
73	GOBP-POSITIVE.REGULATION.OF.APOPTOTIC.SIGNALIN...	GO-2001235	5	0.552899	1.227370	0.229167	0.987272	1.000
74	GOBP-NEGATIVE.REGULATION.OF.TRANSFERASE.ACTIVITY	GO-0051348	5	0.556317	1.225645	0.258189	0.980182	1.000
75	GOBP-DIVALENT.INORGANIC.CATION.HOMEOSTASIS	GO-0072507	13	0.396348	1.221757	0.223529	0.980908	1.000
76	GOBP-CELLULAR.RESPONSE.TO.PEPTIDE	GO-1901653	13	0.402694	1.221236	0.214552	0.969922	1.000
77	GOBP-METAL-ION.HOMEOSTASIS	GO-0055065	14	0.382044	1.217116	0.217472	0.972269	1.000
78	GOBP-REGULATION.OF.CYTOSOLIC.CALCIUM-ION.CONCE...	GO-0051480	13	0.396348	1.215116	0.209016	0.966724	1.000
79	REACTOME-SIGNALING.BY.GPCR	R-RNO-372790	22	0.344419	1.212778	0.212406	0.963190	1.000
80	GOBP-RESPONSE.TO.ETHANOL	GO-0045471	5	0.560562	1.212334	0.248555	0.952796	1.000
81	REACTOME-DAG-AND-IP3-SIGNALING	R-RNO-1489509	8	0.460017	1.202414	0.219282	0.974958	1.000
82	REACTOME-TRAFFICKING.OF-AMPA-RECEPTORS	R-RNO-399719	11	0.412893	1.198867	0.248148	0.975097	1.000
83	GOBP-GAMETE.GENERATION	GO-0007276	9	0.437644	1.198554	0.227687	0.964709	1.000

Continuation of Table S12

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
84	GOBP-REGULATION-OF-PROTEIN-BINDING	7	0.467713	1.197843	0.249035	0.955764	1.000
85	GOBP-CELLULAR-RESPONSE-TO-HORMONE-STIMULUS	11	0.414508	1.194315	0.250454	0.956450	1.000
86	GOBP-ADENYLATE-CYCLASE-MODULATING-G-PROTEIN.CO...	11	0.404822	1.188431	0.258964	0.964689	1.000
87	GOBP-CELL-GROWTH	10	0.418957	1.187323	0.243446	0.957192	1.000
88	GOBP-RESPONSE-TO-PEPTIDE-HORMONE	13	0.382065	1.179166	0.258491	0.972906	1.000
89	GOBP-POLYSACCHARIDE-METABOLIC-PROCESS	5	0.538759	1.174383	0.302804	0.977399	1.000
90	GOBP-GENERATION-OF-PRECURSOR-METABOLITES-AND-E...	5	0.531151	1.174191	0.261364	0.967326	1.000
91	GOBP-REGULATION-OF-TRANSPORT	44	0.297782	1.173940	0.246454	0.957650	1.000
92	GOBP-RESPONSE-TO-TUMOR-NECROSIS-FACTOR	7	0.468438	1.170961	0.264325	0.956953	1.000
93	REACTOME-ONCOGENIC-MAPK-SIGNALING	5	0.525484	1.167804	0.291913	0.957541	1.000
94	REACTOME-TOLL-LIKE-RECEPTOR-CASCADES	8	0.443908	1.167086	0.257692	0.949763	1.000
95	GOBP-NEUROTRANSMITTER-SECRETION	6	0.495026	1.166082	0.257194	0.942995	1.000
96	REACTOME-TOLL-LIKE-RECEPTOR-9-TLR9-CASCADE	8	0.443908	1.164425	0.264815	0.938456	1.000
97	GOBP-ORGANONITROGEN-COMPOUND-BIOSYNTHETIC-PROCESS	13	0.376284	1.155559	0.291045	0.957207	1.000
98	REACTOME-MYD88-INDEPENDENT-TLR4-CASCADE	8	0.443908	1.152916	0.299228	0.955563	1.000
99	GOBP-REGULATION-OF-IMMUNE-RESPONSE	12	0.388875	1.152083	0.285981	0.948296	1.000
100	GOBP-HOMEOSTASIS-OF-NUMBER-OF-CELLS	5	0.516576	1.151661	0.297619	0.940228	1.000
101	GOBP-REGULATION-OF-VASCULATURE-DEVELOPMENT	5	0.521127	1.145698	0.310277	0.949348	1.000
102	GOBP-NEURON-DEVELOPMENT	33	0.301410	1.144035	0.295956	0.945291	1.000
103	GOBP-REGULATION-OF-CATION-TRANSMEMBRANE-TRANSPORT	16	0.350693	1.137787	0.304991	0.955541	1.000
104	REACTOME-TOLL-LIKE-RECEPTOR-TLR1-TLR2-CASCADE	8	0.443908	1.135608	0.312871	0.953069	1.000
105	GOBP-CELL-PART-MORPHOGENESIS	24	0.307266	1.121845	0.293333	0.987063	1.000
106	GOBP-CHEMICAL-HOMEOSTASIS	23	0.314824	1.120183	0.317739	0.982921	1.000
107	GOBP-CHEMICAL-SYNAPTIC-TRANSMISSION-POSTSYNAPTIC	9	0.416186	1.117581	0.312500	0.981564	1.000
108	GOBP-REGULATION-OF-CELL-CYCLE-PROCESS	5	0.504774	1.114742	0.315582	0.981262	1.000
109	GOBP-CELLULAR-COMPOONENT-MORPHOGENESIS	24	0.307266	1.112686	0.300000	0.978967	1.000
110	GOBP-CELL-MORPHOGENESIS	24	0.307266	1.104890	0.308571	0.993441	1.000
111	GOBP-POSITIVE-REGULATION-OF-PROTEOLYSIS	8	0.417302	1.100775	0.316479	0.997177	1.000
112	GOBP-SENSORY-PERCEPTION	9	0.409659	1.100690	0.343396	0.988610	1.000
113	GOBP-AXON-DEVELOPMENT	18	0.326472	1.100681	0.340909	0.980000	1.000
114	REACTOME-ADAPTIVE-IMMUNE-SYSTEM	9	0.409772	1.096708	0.345865	0.983661	1.000
115	GOBP-REGULATION-OF-NEUROTRANSMITTER-RECEPTOR-A...	13	0.353560	1.094960	0.312977	0.980572	1.000
116	GOBP-ORGANOPHOSPHATE-METABOLIC-PROCESS	7	0.434539	1.090255	0.362173	0.985966	1.000
117	GOBP-RESPONSE-TO-ORGANIC-CYCLIC-COMPOUND	20	0.314935	1.089081	0.324428	0.981338	1.000
118	GOBP-REGULATION-OF-CELLULAR-COMPOONENT-SIZE	7	0.435292	1.087705	0.350294	0.977140	1.000
119	GOBP-REGULATION-OF-NEUROTRANSMITTER-TRANSPORT	6	0.459410	1.085058	0.354709	0.976954	1.000
120	GOBP-REGULATION-OF-ANATOMICAL-STRUCTURE-MORPHO...	17	0.325554	1.080761	0.369231	0.981494	1.000
121	GOBP-CELL-MORPHOGENESIS-INVOLVED-IN-DIFFERENTI...	21	0.307997	1.078785	0.360687	0.979547	1.000
122	GOBP-DENDRITIC-SPINE-DEVELOPMENT	6	0.458716	1.077025	0.360000	0.976507	1.000
123	GOBP-CALCIUM-ION-TRANSMEMBRANE-TRANSPORT	7	0.407058	1.074369	0.366279	0.976179	1.000
124	GOBP-REGULATION-OF-PROTEIN-LOCALIZATION-TO-CEL...	6	0.459751	1.068439	0.383364	0.985589	1.000
125	GOBP-CELLULAR-RESPONSE-TO-ABIOTIC-STIMULUS	7	0.424712	1.068338	0.379747	0.978040	1.000
126	GOBP-REGULATION-OF-LIPID-LOCALIZATION	5	0.471522	1.062273	0.355809	0.987476	1.000

Continuation of Table S12

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
127 GOBP-NEURON-DIFFERENTIATION	GO-0030182	36	0.270440	1.061561	0.376426	0.981945	1.000
128 GOBP-TISSUE-MORPHOGENESIS	GO-0048729	7	0.433176	1.057567	0.389299	0.986120	1.000
129 REACTOME-MAPK-FAMILY-SIGNALING-CASCADES	R-RNO-5683057	12	0.363356	1.057383	0.360000	0.979067	1.000
130 GOBP-CELLULAR-CARBOHYDRATE-METABOLIC-PROCESS	GO-0044262	5	0.479705	1.055874	0.394286	0.975939	1.000
131 REACTOME-INTERFERON-SIGNALING	R-RNO-913531	6	0.462584	1.054918	0.388031	0.971249	1.000
132 GOBP-NEGATIVE-REGULATION-OF-CATALYTIC-ACTIVITY	GO-0043086	17	0.321296	1.054675	0.394636	0.964675	1.000
133 GOBP-MEMBRANE-ORGANIZATION	GO-0061024	12	0.348778	1.054186	0.394052	0.958887	1.000
134 GOBP-REGULATION-OF-CELL-DEATH	GO-0010941	34	0.271458	1.050272	0.382716	0.962473	1.000
135 GOBP-INNATE-IMMUNE-RESPONSE	GO-0045087	7	0.416964	1.046135	0.389925	0.967067	1.000
136 GOBP-CELL-MORPHOGENESIS-INVOLVED-IN-NEURON-DIF...	GO-0048667	21	0.307997	1.044866	0.400000	0.963384	1.000
137 GOBP-CALCIUM-ION-TRANSPORT-INTO-CYTOSOL	GO-0060402	7	0.419594	1.044473	0.393881	0.957474	1.000
138 GOBP-ION-HOMEOSTASIS	GO-0050801	16	0.323956	1.043940	0.391386	0.951886	1.000
139 GOBP-NEGATIVE-REGULATION-OF-BINDING	GO-0051100	6	0.450813	1.042911	0.399209	0.947883	1.000
140 GOBP-CELLULAR-RESPONSE-TO-ORGANIC-CYCLIC-COMPOUND	GO-0071407	13	0.339044	1.042247	0.375234	0.943052	1.000
141 GOBP-REGULATION-OF-CIRCADIAN-RHYTHM	GO-0042752	7	0.424438	1.040647	0.389210	0.940827	1.000
142 GOBP-CYTOSOLIC-CALCIUM-ION-TRANSPORT	GO-0060401	7	0.419594	1.039804	0.397032	0.936633	1.000
143 GOBP-BIOLOGICAL-PROCESS-INVOLVED-IN-SYMBIOTIC....	GO-0044440	11	0.355021	1.039016	0.407045	0.932487	1.000
144 GOBP-RESPONSE-TO-ABIOTIC-STIMULUS	GO-0009628	27	0.283635	1.037845	0.395221	0.929101	1.000
145 REACTOME-DISEASES-OF-SIGNAL-TRANSDUCTION-BY-GR...	R-HSA-5663202	12	0.343512	1.037206	0.387879	0.924519	1.000
146 GOBP-NEURON-PROJECTION-ORGANIZATION	GO-0106027	8	0.388486	1.033247	0.400756	0.928633	1.000
147 GOBP-REGULATION-OF-DNA-BINDING-TRANSCRIPTION.F...	GO-0051090	16	0.323758	1.033039	0.419729	0.922774	1.000
148 GOBP-IMMUNE-RESPONSE-REGULATING-SIGNALING-PATHWAY	GO-000276	8	0.392711	1.029455	0.404990	0.925761	1.000
149 GOBP-REGULATION-OF-MEMBRANE-POTENTIAL	GO-0042391	17	0.307845	1.029203	0.414313	0.920301	1.000
150 GOBP-CELLULAR-MACROMOLECULE-LOCALIZATION	GO-0070727	21	0.291373	1.028264	0.415385	0.916554	1.000
151 GOBP-NEGATIVE-REGULATION-OF-INTRACELLULAR-SIGN...	GO-1902532	7	0.407904	1.028053	0.408318	0.911033	1.000
152 GOBP-PURINE-CONTAINING-COMPOUND-METABOLIC-PROCESS	GO-0072521	5	0.457319	1.027097	0.413793	0.907393	1.000
153 GOBP-NEGATIVE-REGULATION-OF-HYDROLASE-ACTIVITY	GO-0051346	11	0.348570	1.024390	0.425182	0.908427	1.000
154 GOBP-FC-RECEPTOR-SIGNALING-PATHWAY	GO-0038093	8	0.392711	1.024169	0.420233	0.903077	1.000
155 GOBP-REGULATION-OF-SYNAPTIC-PLASTICITY	GO-0048167	21	0.289887	1.022758	0.427798	0.900573	1.000
156 GOBP-NEGATIVE-REGULATION-OF-LIPID-METABOLIC-PR...	GO-0045833	5	0.467277	1.022428	0.430528	0.895637	1.000
157 GOBP-MORPHOGENESIS-OF-AN-EPITHELIUM	GO-0002009	6	0.434657	1.014973	0.419776	0.908418	1.000
158 GOBP-POSITIVE-REGULATION-OF-LONG-TERM-SYNAPTIC...	GO-0022411	5	0.419650	1.006000	0.435845	0.923892	1.000
159 GOBP-CELLULAR-COMPOONENT-DISASSEMBLY	GO-1900273	20	0.299109	1.005229	0.440454	0.915517	1.000
160 GOBP-CELLULAR-RESPONSE-TO-NITROGEN-COMPOUND	GO-001699	20	0.370471	1.000882	0.422311	0.920492	1.000
161 GOBP-LIPID-METABOLIC-PROCESS	GO-0006629	10	0.317513	0.999257	0.474806	0.918982	1.000
162 GOBP-PROTEIN-CONTAINING-COMPLEX-SUBUNIT-ORGANI...	GO-0043933	14	0.384669	0.996918	0.433712	0.919149	1.000
163 GOBP-MYELOID-LEUKOCYTE-ACTIVATION	GO-0002274	8	0.414724	0.996597	0.450943	0.914387	1.000
164 GOBP-REGULATION-OF-POSTSYNAPSE-ORGANIZATION	GO-0099175	6	0.396953	0.996004	0.450192	0.910261	1.000
165 GOBP-LEUKOCYTE-MEDIATED-IMMUNITY	GO-0002443	7	0.414994	0.995828	0.471664	0.905301	1.000
166 GOBP-MONOCARBOXYLIC-ACID-METABOLIC-PROCESS	GO-0032787	6	0.312188	0.995270	0.479705	0.901291	1.000
167 GOBP-CELLULAR-RESPONSE-TO-LIPID	GO-0071396	15	0.332749	0.991903	0.457249	0.904456	1.000
168 GOBP-METAL-ION-TRANSPORT	GO-0030001	11	0.332749	0.991903	0.457249	0.904456	1.000
169 GOBP-REGULATION-OF-METAL-ION-TRANSPORT	GO-0010959	6	0.418273	0.984740	0.457594	0.916178	1.000

Continuation of Table S12

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
170	GOBP-REGULATION-OF-PEPTIDASE-ACTIVITY	10	0.347059	0.984723	0.465160	0.910851	1.000
171	GOBP-NEUROGENESIS	40	0.250693	0.982420	0.466179	0.911267	1.000
172	GOBP-REGULATION-OF-CYSTEINE-TYPE-ENDOPEPTIDASE...	9	0.357373	0.981355	0.485714	0.908361	1.000
173	GOBP-NEUROTRANSMITTER-TRANSPORT	7	0.390018	0.979530	0.495088	0.907485	1.000
174	GOBP-CELLULAR-ION-HOMEOSTASIS	14	0.312609	0.979095	0.479769	0.903351	1.000
175	GOBP-RESPONSE-TO-INORGANIC-SUBSTANCE	19	0.283453	0.977421	0.488189	0.902277	1.000
176	GOBP-REGULATION-OF-CELL-PROJECTION-ORGANIZATION	20	0.282854	0.975901	0.454714	0.900691	1.000
177	REACTOME-DEATH-RECEPTOR-SIGNALING	5	0.443503	0.974998	0.474187	0.897617	1.000
178	GOBP-POSITIVE-REGULATION-OF-PEPTIDASE-ACTIVITY	7	0.382506	0.973969	0.486486	0.895059	1.000
179	GOBP-CELL-PROJECTION-ORGANIZATION	34	0.247858	0.973406	0.498127	0.891501	1.000
180	GOBP-MONOAMINE-TRANSPORT	5	0.436190	0.972685	0.470588	0.888112	1.000
181	REACTOME-CLASS-C-3-METABOTROPIC-GLUTAMATE-PHER...	7	0.388363	0.970466	0.489066	0.885528	1.000
182	GOBP-CELL-CELL-SIGNALING	56	0.246844	0.970390	0.516729	0.883836	1.000
183	GOBP-CELLULAR-RESPONSE-TO-BIOTIC-STIMULUS	8	0.372045	0.968683	0.446565	0.882977	1.000
184	GOBP-REGULATION-OF-NEUROTRANSMITTER-LEVELS	7	0.390018	0.963483	0.492000	0.889946	1.000
185	GOBP-REGULATION-OF-SMALL-MOLECULE-METABOLIC-PR...	9	0.352176	0.962927	0.497186	0.886396	1.000
186	GOBP-RESPONSE-TO-PEPTIDE	18	0.290173	0.962011	0.504817	0.883828	1.000
187	GOBP-POSITIVE-REGULATION-OF-DNA-BINDING-TRANSC...	10	0.342296	0.961944	0.491651	0.879249	1.000
188	GOBP-CALCIUM-ION-TRANSPORT	11	0.332734	0.957760	0.501010	0.883825	1.000
189	GOBP-CELL-CELL-JUNCTION-ORGANIZATION	6	0.402150	0.954384	0.485149	0.886741	1.000
190	GOBP-NUCLEOBASE-CONTAINING-SMALL-MOLECULE-META...	6	0.390479	0.951806	0.497248	0.887984	1.000
191	GOBP-POSITIVE-REGULATION-OF-CYSTEINE-TYPE-ENDO...	7	0.382506	0.949186	0.504836	0.889052	1.000
192	GOBP-CELLULAR-RESPONSE-TO-MOLECULE-OF-BACTERIA...	8	0.372045	0.946386	0.512195	0.890450	1.000
193	GOBP-REGULATION-OF-CELLULAR-RESPONSE-TO-STRESS	9	0.347656	0.942644	0.478846	0.893936	1.000
194	GOBP-RESPONSE-TO-HORMONE	20	0.269218	0.941289	0.533203	0.892206	1.000
195	GOBP-G-PROTEIN-COUPLED-GLUTAMATE-RECEPTOR-SIGN...	8	0.355481	0.937343	0.504854	0.896167	1.000
196	GOBP-AMIDE-BIOSYNTHETIC-PROCESS	7	0.370359	0.925960	0.520599	0.917174	1.000
197	REACTOME-TRANSCRIPTIONAL-REGULATION-BY-MECP2	7	0.367854	0.923250	0.558608	0.918499	1.000
198	GOBP-POSITIVE-REGULATION-OF-EPITHELIAL-CELL-MI...	5	0.411448	0.922268	0.532673	0.916225	1.000
199	GOBP-PEPTIDE-BIOSYNTHETIC-PROCESS	7	0.370359	0.919648	0.545977	0.917395	1.000
200	GOBP-RESPONSE-TO-LUV	5	0.418289	0.919499	0.544304	0.913182	1.000
201	REACTOME-TRAFFICKING-OF-GLUR2-CONTAINING-AMPA...	8	0.356793	0.916066	0.574510	0.916193	1.000
202	GOBP-NEGATIVE-REGULATION-OF-PHOSPHORYLATION	7	0.358529	0.914931	0.565619	0.914247	1.000
203	GOBP-REGULATION-OF-NEURONAL-SYNAPTIC-PLASTICITY	7	0.368752	0.912572	0.581262	0.914885	1.000
204	GOBP-CHROMATIN-ORGANIZATION	5	0.412014	0.911626	0.558767	0.912375	1.000
205	GOBP-LIPID-LOCALIZATION	10	0.321276	0.904167	0.568932	0.924083	1.000
206	REACTOME-GPCR-LIGAND-BINDING	8	0.350766	0.903521	0.565056	0.921107	1.000
207	GOBP-REGULATION-OF-PROTEIN-LOCALIZATION-TO-MEM...	7	0.350512	0.899644	0.544423	0.925018	1.000
208	GOBP-DENDRITE-DEVELOPMENT	9	0.337296	0.899244	0.590164	0.921416	1.000
209	GOBP-REGULATION-OF-TRANSPORTER-ACTIVITY	17	0.269605	0.897677	0.588583	0.920326	1.000
210	GOBP-TRANSMEMBRANE-TRANSPORT	27	0.239632	0.895454	0.608133	0.920583	1.000
211	GOBP-PEPTIDE-METABOLIC-PROCESS	12	0.291689	0.893916	0.579737	0.919553	1.000
212	GOBP-ORGANIC-ACID-TRANSPORT	7	0.357413	0.891554	0.586207	0.920520	1.000

Continuation of Table S12

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
213 REACTOME-INTEGRATION_OF_ENERGY_METABOLISM	R-RNO-163685	5	0.396270	0.88936	0.583658	0.921664	1.000
214 GOBP-DEFENSE-RESPONSE	GO-0006952	19	0.260661	0.883292	0.617375	0.929224	1.000
215 REACTOME-OPIOID-SIGNALING	R-RNO-111885	12	0.292389	0.877554	0.619329	0.936954	1.000
216 GOBP-POSITIVE-REGULATION_OF_HYDROLASE-ACTIVITY	GO-0051345	16	0.268775	0.876779	0.609524	0.934229	1.000
217 REACTOME-G-PROTEIN-MEDIATED-EVENTS	R-RNO-112040	9	0.321144	0.874675	0.609195	0.934320	1.000
218 GOBP-CELLULAR-LIPID-METABOLIC-PROCESS	GO-0044255	7	0.348862	0.874139	0.606403	0.931096	1.000
219 GOBP-POSITIVE-REGULATION_OF_CELL-PROJECTION_OR...	GO-0031346	10	0.312916	0.871929	0.598425	0.931311	1.000
220 REACTOME-G-ALPHA1-SIGNALING-EVENTS	R-RNO-418594	18	0.259510	0.865754	0.654611	0.940146	1.000
221 GOBP-CIRCADIAN-RHYTHM	GO-0007623	13	0.287040	0.865731	0.642293	0.935966	1.000
222 GOBP-RESPONSE-TO-LIGHT-STIMULUS	GO-0009416	11	0.302633	0.865727	0.635659	0.931781	1.000
223 GOBP-ADENYLATE-CYCLASE-INHIBITING-G-PROTEIN_CO...	GO-0007196	5	0.380858	0.863708	0.603622	0.927653	1.000
224 GOBP-ORGANIC-ACID-METABOLIC-PROCESS	GO-0006082	7	0.337435	0.861323	0.651515	0.932241	1.000
225 GOBP-CARBOHYDRATE-HOMEOSTASIS	GO-0033500	7	0.340805	0.853592	0.611321	0.943670	1.000
226 GOBP-RESPONSE-TO-LIPID	GO-0033993	19	0.245778	0.850103	0.686567	0.946427	1.000
227 GOBP-REGULATION_OF_NEURON-PROJECTION-DEVELOPMENT	GO-0010975	16	0.256981	0.847185	0.640884	0.947871	1.000
228 GOBP-CELL-CYCLE-PROCESS	GO-0022402	11	0.289247	0.844740	0.644841	0.948574	1.000
229 GOBP-REGULATION_OF_PROTEIN-KINASE-ACTIVITY	GO-0045859	22	0.238338	0.843939	0.680529	0.945904	1.000
230 REACTOME-MEMBRANE-TRAFFICKING	R-RNO-199991	5	0.378263	0.841714	0.626667	0.946037	1.000
231 GOBP-DENDRITIC-SPINE-MORPHOGENESIS	GO-0060997	5	0.383785	0.840892	0.615830	0.943584	1.000
232 REACTOME-VESICLE-MEDIATED-TRANSPORT	R-RNO-5653656	5	0.378263	0.840365	0.605210	0.940561	1.000
233 REACTOME-CELLULAR-RESPONSES-TO-EXTERNAL-STIMULI	R-RNO-8953897	12	0.282566	0.837989	0.660952	0.941259	1.000
234 GOBP-REGULATION_OF_CELLULAR-LOCALIZATION	GO-0060341	17	0.253392	0.836788	0.683919	0.939613	1.000
235 GOBP-REGULATION_OF_CATION-CHANNEL-ACTIVITY	GO-2001257	14	0.271212	0.836063	0.687140	0.937045	1.000
236 GOBP-REGULATION_OF-TRANSFERASE-ACTIVITY	GO-0051338	22	0.238338	0.832550	0.675325	0.939704	1.000
237 GOBP-REGULATION_OF-TRANSMISSION-GLUTA...	GO-0051966	12	0.277533	0.831553	0.662942	0.937683	1.000
238 GOBP-RESPONSE-TO-MECHANICAL-STIMULUS	GO-0009612	6	0.343800	0.830438	0.663620	0.935989	1.000
239 GOBP-REGULATION_OF-LIPID-BIOSYNTHETIC-PROCESS	GO-0046890	6	0.348824	0.828937	0.631179	0.934991	1.000
240 GOBP-EPHRIIN-RECEPTOR-SIGNALING-PATHWAY	GO-0048013	5	0.373630	0.827878	0.667276	0.933158	1.000
241 GOBP-REGULATION_OF-LIPID-METABOLIC-PROCESS	GO-0019216	7	0.334597	0.825843	0.680970	0.933070	1.000
242 GOBP-REGULATION_OF-BINDING	GO-0051098	11	0.283300	0.825405	0.677485	0.930081	1.000
243 GOBP-DEVELOPMENTAL-MATURATION	GO-0021700	5	0.371699	0.824958	0.689788	0.927111	1.000
244 GOBP-CELLULAR-AMIDE-METABOLIC-PROCESS	GO-0043603	13	0.271337	0.822135	0.669903	0.928731	1.000
245 REACTOME-EXTRACELLULAR-MATRIX-ORGANIZATION	R-RNO-1474244	5	0.373111	0.813596	0.674374	0.940641	1.000
246 REACTOME-CREB1-PHOSPHORYLATION_THROUGH-NMDA-RE...	R-RNO-442742	8	0.317774	0.812689	0.706865	0.938528	1.000
247 GOBP-RESPONSE-TO-OXYGEN-LEVELS	GO-0070482	8	0.308629	0.810585	0.686992	0.938419	1.000
248 GOBP-CELLULAR-HOMEOSTASIS	GO-0019725	18	0.241028	0.807897	0.719536	0.939391	1.000
249 GOBP-LIPID-BIOSYNTHETIC-PROCESS	GO-0008610	6	0.348824	0.807835	0.699422	0.935790	1.000
250 HALLMARK-KRAS-SIGNALING-UP	M5953	6	0.353659	0.806476	0.695327	0.934730	1.000
251 REACTOME_CA-DEPENDENT-EVENTS	R-RNO-111996	8	0.312355	0.806235	0.706320	0.931387	1.000
252 GOBP-CELLULAR-GLUCOSE-HOMEOSTASIS	GO-0001678	5	0.367711	0.804152	0.706667	0.931676	1.000
253 GOBP-REGULATION_OF-TRANS-SYNAPTIC-SIGNALING	GO-0099177	40	0.206981	0.801417	0.777365	0.933142	1.000
254 GOBP-HOMEOSTATIC-PROCESS	GO-0042592	31	0.207882	0.794460	0.780669	0.942172	1.000
255 GOBP-SYNAPTIC-SIGNALING	GO-0099536	47	0.199763	0.792993	0.768482	0.941205	1.000

Continuation of Table S12

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
256 GOBP-RESPONSE.TO.OXIDATIVE-STRESS	GO-0006979	8	0.293935	0.791877	0.707865	0.939705	1.000
257 REACTOME-DEVELOPMENTAL-BIOLOGY	R-RNO-1266738	23	0.213141	0.788358	0.751402	0.942282	1.000
258 GOBP-POSITIVE-REGULATION-OF-DEFENSE-RESPONSE	GO-0031349	5	0.354899	0.782766	0.714008	0.948455	1.000
259 GOBP-REGULATION-OF-LONG-TERM-SYNAPTIC-POTENTIAL...	GO-1900271	6	0.322412	0.781691	0.721190	0.946756	1.000
260 GOBP-SYNAPTIC-TRANSMISSION-GLUTAMATERGIC	GO-0035249	13	0.251809	0.779644	0.729242	0.946475	1.000
261 GOBP-LEUKOCYTE-MIGRATION	GO-0050900	6	0.324711	0.775101	0.728846	0.950337	1.000
262 REACTOME-NERVOUS-SYSTEM-DEVELOPMENT	R-RNO-9675108	15	0.239258	0.773632	0.774067	0.949345	1.000
263 GOBP-POSITIVE-REGULATION-OF-CELL-GROWTH	GO-0030307	6	0.328895	0.772978	0.718310	0.946797	1.000
264 GOBP-CHROMOSOME-ORGANIZATION	GO-0051276	6	0.330331	0.771235	0.743396	0.946142	1.000
265 GOBP-REGULATION-OF-MUSCLE-CELL-DIFFERENTIATION	GO-0051147	6	0.327717	0.767821	0.738140	0.948031	1.000
266 GOBP-NEGATIVE-REGULATION-OF-SYNAPTIC-TRANSMISSION	GO-0050805	6	0.319437	0.767107	0.744639	0.945664	1.000
267 GOBP-TISSUE-HOMEOSTASIS	GO-0001894	5	0.346281	0.763209	0.765799	0.948525	1.000
268 GOBP-REGULATION-OF-SIGNALING-RECEPTOR-ACTIVITY	GO-0010469	14	0.243745	0.755460	0.788151	0.957130	1.000
269 GOBP-PHAGOCYTOSIS	GO-0006909	5	0.343375	0.754432	0.777164	0.955363	1.000
270 GOBP-REGULATION-OF-ENDOTHELIAL-CELL-MIGRATION	GO-0010594	5	0.337736	0.752240	0.741445	0.955273	1.000
271 GOBP-RESPONSE.TO-REACTIVE-OXYGEN-SPECIES	GO-0000302	8	0.293935	0.748928	0.793103	0.956977	1.000
272 REACTOME-G-ALPHA-Z-SIGNALING-EVENTS	R-RNO-418597	5	0.330284	0.746144	0.779026	0.957829	1.000
273 GOBP-REGULATION-OF-ANATOMICAL-STRUCTURE-SIZE	GO-0090066	10	0.264047	0.742440	0.778672	0.960302	1.000
274 GOBP-RESPONSE.TO-HEAT	GO-0009408	7	0.295050	0.741020	0.749012	0.958969	1.000
275 GOBP-IMPORT-INTO-CELL	GO-0098657	6	0.307442	0.736290	0.788497	0.962602	1.000
276 GOBP-POSITIVE-REGULATION-OF-CATALYTIC-ACTIVITY	GO-0043085	30	0.197456	0.735547	0.841418	0.960231	1.000
277 GOBP-RESPONSE.TO-NICOTINE	GO-0035094	7	0.291804	0.733417	0.777778	0.959910	1.000
278 GOBP-PROTEIN-MODIFICATION-BY-SMALL-PROTEIN.CON...	GO-0070647	7	0.296117	0.731456	0.789077	0.959198	1.000
279 GOBP-REGULATION-OF-PROTEOLYSIS	GO-0030162	12	0.247674	0.731135	0.822857	0.956246	1.000
280 GOBP-POSITIVE-REGULATION-OF-MOLECULAR-FUNCTION	GO-0044093	38	0.185061	0.727425	0.870270	0.958267	1.000
281 GOBP-CARBOXYLIC-ACID-TRANSPORT	GO-0046942	6	0.301914	0.721422	0.813462	0.963427	1.000
282 GOBP-MACROMOLECULE-CATABOLIC-PROCESS	GO-0009057	12	0.242237	0.719259	0.828846	0.962974	1.000
283 GOBP-FATTY-ACID-TRANSPORT	GO-0015908	6	0.297320	0.715959	0.875000	0.964024	1.000
284 GOBP-AMINO-ACID-TRANSPORT	GO-0006865	6	0.301914	0.715152	0.808300	0.961654	1.000
285 REACTOME-CYTOKINE-SIGNALING-IN-IMMUNE-SYSTEM	R-RNO-1280215	21	0.208564	0.714243	0.853229	0.959638	1.000
286 GOBP-MEMORY	GO-0007613	13	0.23206	0.712980	0.862934	0.958073	1.000
287 GOBP-REGULATION-OF-HYDROLASE-ACTIVITY	GO-0051336	22	0.193388	0.703611	0.867993	0.967384	1.000
288 GOBP-SYNAPSE-ORGANIZATION	GO-0050808	17	0.211608	0.702442	0.838951	0.965781	1.000
289 GOBP-REGULATION-OF-EPITHELIAL-CELL-MIGRATION	GO-0010632	6	0.300762	0.700556	0.819066	0.964929	1.000
290 GOBP-ORGANIC-ANION-TRANSPORT	GO-0015711	6	0.301914	0.700302	0.843100	0.961976	1.000
291 REACTOME-INTERLEUKIN-17-SIGNALING	R-RNO-448424	6	0.295063	0.693681	0.854685	0.967384	1.000
292 GOBP-REGULATION-OF-CELL-SIZE	GO-0008361	5	0.313253	0.689142	0.839695	0.970118	1.000
293 REACTOME-L1CAM-INTERACTIONS	R-RNO-373760	5	0.309009	0.687405	0.833333	0.968941	1.000
294 GOBP-POSITIVE-REGULATION-OF-SECRETION	GO-0051047	6	0.290187	0.686810	0.834368	0.966388	1.000
295 HALLMARK-EPITHELIAL-MESENCHYMAL-TRANSITION	M5930	5	0.313253	0.686411	0.856631	0.963662	1.000
296 GOBP-SIGNAL-RELEASE	GO-0023061	14	0.218155	0.686170	0.861272	0.960739	1.000
297 GOBP-MULTICELLULAR-ORGANISMAL-HOMEOSTASIS	GO-0048871	12	0.231059	0.684004	0.859922	0.960114	1.000
298 REACTOME-INTRACELLULAR-SIGNALING-BY-SECOND-MES...	R-RNO-9006925	15	0.215209	0.680585	0.875000	0.960998	1.000

Continuation of Table S12

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
299	GOBP-LONG-TERM-MEMORY	6	0.293141	0.680347	0.856016	0.958036	1.000
300	GOBP-REGULATION-OF-GROWTH	13	0.220873	0.679830	0.884990	0.955506	1.000
301	GOBP-REGULATION-OF-AXONOGENESIS	7	0.275751	0.679046	0.850860	0.953338	1.000
302	GOBP-DEFENSE-RESPONSE-TO-OTHER-ORGANISM	9	0.242620	0.669537	0.868668	0.961543	1.000
303	GOBP-PROTEIN-COMPLEX-OLIGOMERIZATION	6	0.280488	0.660281	0.898467	0.968989	1.000
304	GOBP-PROTEIN-CATABOLIC-PROCESS	8	0.252928	0.652824	0.863281	0.973925	1.000
305	GOBP-REGULATION-OF-CELLULAR-PROTEIN-LOCALIZATION	12	0.216407	0.641644	0.899431	0.982249	1.000
306	GOBP-MULTICELLULAR-ORGANISM-REPRODUCTION	12	0.215359	0.635015	0.915851	0.985680	1.000
307	GOBP-RESPONSE-TO-MONOSACCHARIDE	5	0.285028	0.634057	0.889439	0.983380	1.000
308	GOBP-RESPONSE-TO-CARBOHYDRATE	5	0.285028	0.633948	0.920849	0.980312	1.000
309	GOBP-POSITIVE-REGULATION-OF-SIGNALING	34	0.162188	0.629597	0.933573	0.981168	1.000
310	GOBP-LIPID-EXPORT-FROM-CELL	5	0.286001	0.629435	0.886100	0.978110	1.000
311	GOBP-RESPONSE-TO-RADIATION	13	0.199795	0.614111	0.924797	0.988360	1.000
312	GOBP-NEGATIVE-REGULATION-OF-PROTEIN-CATABOLIC-...	5	0.283785	0.608440	0.902622	0.990070	1.000
313	GOBP-DENDRITE-MORPHOGENESIS	6	0.246336	0.594799	0.938462	0.996975	1.000
314	GOBP-LONG-TERM-SYNAPTIC-DEPRESSION	5	0.277108	0.594548	0.953488	0.993990	1.000
315	GOBP-DEVELOPMENTAL-PROCESS-INVOLVED-IN-REPRODU...	11	0.207086	0.585594	0.948718	0.997271	1.000
316	GOBP-LONG-TERM-SYNAPTIC-POTENTIATION	12	0.185252	0.559760	0.959770	1.000000	1.000
317	GOBP-RESPIRATORY-SYSTEM-DEVELOPMENT	6	0.233123	0.557378	0.968064	1.000000	1.000
318	GOBP-EPITHELIAL-DEVELOPMENT	15	0.175139	0.555795	0.979284	1.000000	1.000
319	GOBP-RESPONSE-TO-METAL-ION	5	0.176868	0.553491	0.966403	1.000000	1.000
320	GOBP-RESPONSE-TO-ALKALOID	5	0.253012	0.552635	0.971429	1.000000	1.000
321	GOBP-NEGATIVE-REGULATION-OF-PROTEIN-METABOLIC-...	20	0.154904	0.541200	0.975096	1.000000	1.000
322	GOBP-LOCOMOTORY-BEHAVIOR	7	0.209876	0.534543	0.972167	1.000000	1.000
323	GOBP-REGULATION-OF-PROTEIN-TYROSINE-KINASE-ACT...	5	0.226692	0.513598	0.990892	1.000000	1.000
324	GOBP-POSITIVE-REGULATION-OF-PROTEIN-TYROSINE-K...	5	0.226692	0.494297	0.990272	1.000000	1.000
325	GOBP-CELLULAR-MACROMOLECULE-CATABOLIC-PROCESS	6	0.205525	0.492125	0.988000	1.000000	1.000
326	GOBP-MONOCARBOXYLIC-ACID-TRANSPORT	5	0.221969	0.490913	0.990138	1.000000	1.000
327	GOBP-DICARBOXYLIC-ACID-TRANSPORT	5	0.221969	0.488723	0.983806	1.000000	1.000
328	GOBP-ACIDIC-AMINO-ACID-TRANSPORT	5	0.221969	0.488624	0.990758	0.999477	1.000
329	GOBP-POSITIVE-REGULATION-OF-CATION-TRANSMEMBR...	5	0.216867	0.483912	0.984526	0.997421	1.000
330	GOBP-ENDOCRINE-SYSTEM-DEVELOPMENT	6	0.195122	0.459736	0.998073	0.998173	1.000
331	GOBP-POSITIVE-REGULATION-OF-SYNAPTIC-TRANSMISSION	15	0.123646	0.387066	1.000000	0.999577	1.000
332	GOBP-ASSOCIATIVE-LEARNING	7	-0.172840	-0.437457	0.997925	0.997725	1.000
333	GOBP-LEARNING	13	-0.160000	-0.509510	0.989407	0.988764	1.000
334	GOBP-DEVELOPMENTAL-CELL-GROWTH	5	-0.231032	-0.511076	0.984704	0.990831	1.000
335	GOBP-SENSORY-PERCEPTION-OF-PAIN	5	-0.228916	-0.511214	0.988327	0.993362	1.000
336	GOBP-POSITIVE-REGULATION-OF-AXONOGENESIS	5	-0.228072	-0.515626	0.985972	0.994722	1.000
337	GOBP-INTRINSIC-APOPTOTIC-SIGNALING-PATHWAY	5	-0.238854	-0.536096	0.979798	0.990148	1.000
338	GOBP-TELECEPHALON-DEVELOPMENT	6	-0.225076	-0.538504	0.968685	0.991723	1.000
339	GOBP-ORGANONITROGEN-COMPOUND-CATABOLIC-PROCESS	9	-0.196260	-0.542240	0.976143	0.992776	1.000
340	GOBP-CELLULAR-RESPONSE-TO-CHEMICAL-STRESS	7	-0.213626	-0.543730	0.966457	0.994763	1.000
341	GOBP-NEGATIVE-REGULATION-OF-PROTEIN-MODIFICATI...	10	-0.192595	-0.545186	0.969290	0.995445	1.000

Continuation of Table S12

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
342	GOBP-CELLULAR-RESPONSE-TO-REACTIVE-OXYGEN-SPECIES	GO-0034614	7	-0.213626	-0.556955	0.958606	0.993755	1.000
343	GOBP-NEGATIVE-REGULATION-OF-PHOSPHORUS-METABOL...	GO-0010563	9	-0.209941	-0.578375	0.962882	0.984608	1.000
344	GOBP-RESPONSE-TO-INSULIN	GO-0032868	5	-0.258670	-0.582876	0.963855	0.984424	1.000
345	GOBP-NEGATIVE-REGULATION-OF-PROTEOLYSIS	GO-0045861	8	-0.221846	-0.594173	0.954048	0.979692	1.000
346	GOBP-MUSCLE-CELL-DIFFERENTIATION	GO-0042692	10	-0.206411	-0.597244	0.928279	0.980259	1.000
347	REACTOME-G-ALPHA-Q-SIGNALING-EVENTS	R-RNO-416476	6	-0.250671	-0.602232	0.943633	0.979159	1.000
348	GOBP-NEGATIVE-REGULATION-OF-SIGNALING	GO-0023057	21	-0.168192	-0.603420	0.951965	0.980816	1.000
349	GOBP-CELLULAR-RESPONSE-TO-INORGANIC-SUBSTANCE	GO-0071241	11	-0.207337	-0.608424	0.936403	0.979745	1.000
350	GOBP-REGULATION-OF-PROTEIN-CATABOLIC-PROCESS	GO-0042176	7	-0.234568	-0.611932	0.926829	0.979685	1.000
351	GOBP-POSITIVE-REGULATION-OF-NEURON-PROJECTION...	GO-0010976	5	-0.277108	-0.612155	0.933472	0.982158	1.000
352	REACTOME-RNA-POLYMERASE-II-TRANSCRIPTION	R-RNO-73857	20	-0.174087	-0.612674	0.931818	0.984429	1.000
353	GOBP-RESPONSE-TO-STARVATION	GO-0042594	5	-0.279034	-0.620718	0.919840	0.980280	1.000
354	GOBP-ENDOMEMBRANE-SYSTEM-ORGANIZATION	GO-0010256	6	-0.264239	-0.623202	0.929936	0.980791	1.000
355	GOBP-NEGATIVE-REGULATION-OF-CATABOLIC-PROCESS	GO-0009895	8	-0.237500	-0.625109	0.880478	0.981720	1.000
356	GOBP-CELLULAR-RESPONSE-TO-STARVATION	GO-0009267	5	-0.279034	-0.626345	0.910256	0.983227	1.000
357	GOBP-ERBB-SIGNALING-PATHWAY	GO-0038127	5	-0.282080	-0.645640	0.904471	0.967977	1.000
358	GOBP-POSITIVE-REGULATION-OF-TRANSMEMBRANE-TRAN...	GO-0034764	7	-0.252738	-0.649519	0.909474	0.966782	1.000
359	GOBP-IN-UTERO-EMBRYONIC-DEVELOPMENT	GO-0001701	8	-0.245971	-0.650473	0.897796	0.968449	1.000
360	GOBP-POSITIVE-REGULATION-OF-BINDING	GO-0051099	6	-0.269324	-0.654575	0.884368	0.966870	1.000
361	GOBP-AGING	GO-0007568	13	-0.208250	-0.654924	0.887202	0.969244	1.000
362	GOBP-MATERNAL-PROCESS-INVOLVED-IN-FEMALE-PREGN...	GO-0060135	5	-0.199408	-0.658233	0.888000	0.968572	1.000
363	GOBP-REPRODUCTION	GO-0000003	18	-0.192079	-0.660973	0.902954	0.968215	1.000
364	REACTOME-SENESCENCE-ASSOCIATED-SECRETORY-PHENO...	R-RNO-2559582	6	-0.285057	-0.672682	0.854911	0.957863	1.000
365	REACTOME-CELLULAR-SENESCENCE	R-RNO-2559583	6	-0.285057	-0.679519	0.858012	0.952438	1.000
366	GOBP-NEGATIVE-REGULATION-OF-CYSTEINE-TYPE-ENDO...	GO-2000117	38	-0.168442	-0.682399	0.884536	0.951614	1.000
367	GOBP-NERVOUS-SYSTEM-PROCESS	GO-0050877	38	-0.168442	-0.682399	0.900222	0.947851	1.000
368	GOBP-REGULATION-OF-BODY-FLUID-LEVELS	GO-0050878	11	-0.232167	-0.692414	0.855422	0.944853	1.000
369	GOBP-REPRODUCTIVE-SYSTEM-DEVELOPMENT	GO-0061458	6	-0.297362	-0.702570	0.836401	0.934618	1.000
370	GOBP-NEGATIVE-REGULATION-OF-PEPTIDASE-ACTIVITY	GO-0010466	6	-0.294806	-0.702609	0.845188	0.937247	1.000
371	GOBP-POSITIVE-REGULATION-OF-TRANSPORT	GO-0051050	26	-0.189778	-0.705069	0.877419	0.936640	1.000
372	GOBP-REGULATION-OF-RECEPTOR-MEDIATED-ENDOCYTOSIS	GO-0048259	5	-0.313253	-0.706368	0.845098	0.937608	1.000
373	GOBP-POSITIVE-REGULATION-OF-PROTEIN-METABOLIC...	GO-0051247	28	-0.188501	-0.706767	0.856566	0.939750	1.000
374	GOBP-MULTI-ORGANISM-PROCESS	GO-0051704	16	-0.212949	-0.709658	0.810526	0.938615	1.000
375	GOBP-RECEPTOR-INTERNALIZATION	GO-0031623	5	-0.313253	-0.710046	0.816284	0.940840	1.000
376	GOBP-CELL-JUNCTION-ORGANIZATION	GO-0034330	19	-0.202071	-0.711488	0.853763	0.941722	1.000
377	GOBP-RAS-PROTEIN-SIGNAL-TRANSDUCTION	GO-0007265	5	-0.321382	-0.711882	0.820866	0.943860	1.000
378	GOBP-NEGATIVE-REGULATION-OF-TRANSCRIPTION-BY-R...	GO-0000122	10	-0.245314	-0.711927	0.841365	0.946566	1.000
379	GOBP-SECRETION	GO-0046903	24	-0.245314	-0.717904	0.871397	0.941127	1.000
380	GOBP-RECEPTOR-METABOLIC-PROCESS	GO-0043112	5	-0.313253	-0.720599	0.817814	0.940374	1.000
381	GOBP-REGULATION-OF-PHOSPHORUS-METABOLIC-PROCESS	GO-0005174	27	-0.189590	-0.721419	0.852083	0.941932	1.000
382	GOBP-RESPONSE-TO-INTERLEUKIN-1	GO-0070555	5	-0.324362	-0.722393	0.820202	0.943300	1.000
383	GOBP-REGULATION-OF-PROTEIN-MODIFICATION-PROCESS	GO-0031399	29	-0.184554	-0.723281	0.838565	0.944847	1.000
384	REACTOME-TRANSCRIPTIONAL-REGULATION-OF-WHITE-A...	R-RNO-381340	6	-0.301403	-0.724765	0.819473	0.945415	1.000

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NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
385	GOBP-NEGATIVE-REGULATION-OF-ANION-TRANSPORT	8	-0.270102	-0.734156	0.797040	0.934775	1.000
386	GOBP-DNA-METABOLIC-PROCESS	6	-0.301284	-0.734569	0.831622	0.936849	1.000
387	GOBP-CYTOKINE-MEDIATED-SIGNALING-PATHWAY	16	-0.229538	-0.742451	0.807440	0.927766	1.000
388	GOBP-POSITIVE-REGULATION-OF-ION-TRANSPORT	17	-0.216652	-0.742717	0.801282	0.930198	1.000
389	GOBP-POSITIVE-REGULATION-OF-TRANSPERASE-ACTIVITY	20	-0.208386	-0.743377	0.829374	0.931964	1.000
390	GOBP-POSITIVE-REGULATION-OF-PROTEIN-KINASE-ACT...	19	-0.216495	-0.744362	0.812641	0.933228	1.000
391	GOBP-PROTEIN-MODIFICATION-BY-SMALL-PROTEIN-CON...	6	-0.308346	-0.750415	0.746362	0.926497	1.000
392	GOBP-REGULATION-OF-PROTEIN-PHOSPHORYLATION	26	-0.198132	-0.751383	0.806981	0.927796	1.000
393	GOBP-REGULATION-OF-CATABOLIC-PROCESS	13	-0.236574	-0.754200	0.790456	0.926377	1.000
394	GOBP-REGULATION-OF-SYNAPSE-STRUCTURE-OR-ACTIVITY	11	-0.258287	-0.755567	0.781457	0.927117	1.000
395	GOBP-RECEPTOR-MEDIATED-ENDOCYTOSIS	6	-0.317073	-0.757030	0.755144	0.927644	1.000
396	GOBP-EPITHELIAL-CELL-DIFFERENTIATION	7	-0.293164	-0.757752	0.746753	0.929292	1.000
397	GOBP-TRANSMEMBRANE-RECEPTOR-PROTEIN-TYROSINE-K...	19	-0.220571	-0.767063	0.804721	0.917088	1.000
398	GOBP-SENSORY-ORGAN-DEVELOPMENT	8	-0.285768	-0.772060	0.762575	0.911530	1.000
399	GOBP-POSITIVE-REGULATION-OF-GROWTH	9	-0.285464	-0.780914	0.758763	0.899665	1.000
400	GOBP-STRIATED-MUSCLE-CELL-DIFFERENTIATION	9	-0.283263	-0.781312	0.730435	0.901885	1.000
401	GOBP-REGULATION-OF-APOPTOTIC-SIGNALING-PATHWAY	10	-0.270555	-0.785243	0.726115	0.898120	1.000
402	GOBP-REGULATION-OF-HORMONE-LEVELS	12	-0.259475	-0.786651	0.750552	0.898658	1.000
403	GOBP-FC-EPSILON-RECEPTOR-SIGNALING-PATHWAY	7	-0.308626	-0.787454	0.734440	0.900117	1.000
404	GOBP-ACTIVATION-OF-PROTEIN-KINASE-ACTIVITY	11	-0.268280	-0.788453	0.725051	0.901213	1.000
405	REACTOME-FC-EPSILON-RECEPTOR-FCERL-SIGNALING	R-RNO-2454202	-0.308626	-0.793560	0.700405	0.895308	1.000
406	GOBP-GLUCOSE-METABOLIC-PROCESS	6	-0.335856	-0.795741	0.710145	0.894369	1.000
407	GOBP-GROWTH	14	-0.246004	-0.797152	0.737705	0.894606	1.000
408	GOBP-MONOSACCHARIDE-METABOLIC-PROCESS	6	-0.335856	-0.799464	0.696703	0.893437	1.000
409	GOBP-ANATOMICAL-STRUCTURE-HOMEOSTASIS	7	-0.314748	-0.805320	0.706114	0.886145	1.000
410	GOBP-CELL-CELL-JUNCTION-ASSEMBLY	5	-0.358965	-0.816731	0.688985	0.869493	1.000
411	GOBP-RESPONSE-TO-CYTOKINE	23	-0.225677	-0.817631	0.723077	0.870743	1.000
412	GOBP-CYTOKINE-PRODUCTION	10	-0.291006	-0.821314	0.683406	0.867254	1.000
413	GOBP-RESPONSE-TO-CALCIUMION	6	-0.345653	-0.821789	0.671610	0.869237	1.000
414	GOBP-PROTEIN-PHOSPHORYLATION	34	-0.205306	-0.823090	0.728051	0.869606	1.000
415	GOBP-EMBRYO-DEVELOPMENT-ENDING-IN-BIRTH-OR-EGG...	9	-0.304509	-0.827766	0.654167	0.864222	1.000
416	GOBP-PROTEIN-LOCALIZATION-TO-ORGANELLE	9	-0.300453	-0.828968	0.678005	0.864973	1.000
417	GOBP-ANION-TRANSMEMBRANE-TRANSPORT	7	-0.324898	-0.829963	0.677485	0.866037	1.000
418	REACTOME-SIGNALING-BY-INTERLEUKINS	R-RNO-449147	-0.264002	-0.831652	0.687631	0.865939	1.000
419	GOBP-NEGATIVE-REGULATION-OF-RESPONSE_TO_STIMULUS	16	-0.255234	-0.833663	0.681917	0.865198	1.000
420	GOBP-INFLAMMATORY-RESPONSE	12	-0.270697	-0.835236	0.665975	0.865216	1.000
421	GOBP-REGULATION-OF-PROTEIN-SERINE-THREONINE-KI...	12	-0.270946	-0.836699	0.658281	0.865487	1.000
422	GOBP-RESPONSE-TO-NUTRIENT	5	-0.369227	-0.839967	0.615385	0.862237	1.000
423	GOBP-POSITIVE-REGULATION-OF-CYTOKINE-PRODUCTION	7	-0.337379	-0.843292	0.630522	0.858849	1.000
424	GOBP-CELLULAR-RESPONSE-TO-DNA-DAMAGE-STIMULUS	5	-0.381317	-0.844896	0.634888	0.858719	1.000
425	GOBP-REGULATION-OF-TRANSMEMBRANE-TRANSPORT	23	-0.229275	-0.848327	0.688000	0.855293	1.000
426	GOBP-CIRCULATORY-SYSTEM-PROCESS	5	-0.378825	-0.856179	0.640177	0.843392	1.000
427	REACTOME-EXTRA_NUCLEAR_ESTROGEN-SIGNALING	R-RNO-9009391	-0.327997	-0.856661	0.637500	0.845514	1.000

Continuation of Table S12

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
428	GOBP-RESPONSE.TO.EXTRACELLULAR-STIMULUS	GO-0009991	13	-0.270838	-0.85729	0.657143	0.844451	1.000
429	GOBP-MITOCHONDRION-ORGANIZATION	GO-0007005	7	-0.341089	-0.861891	0.590717	0.841679	1.000
430	GOBP-HEAD-DEVELOPMENT	GO-0060322	22	-0.240355	-0.864015	0.665948	0.840813	1.000
431	GOBP-REGULATION.OF.NEURON-DIFFERENTIATION	GO-0045664	5	-0.388307	-0.872358	0.587992	0.828038	1.000
432	REACTOME-ESR-MEDIATED-SIGNALING	R-RNO-8939211	8	-0.338501	-0.872965	0.610638	0.829632	1.000
433	GOBP-REGULATION.OF.PHOSPHOLIPASE-ACTIVITY	GO-0010517	6	-0.366609	-0.875161	0.589011	0.828298	1.000
434	GOBP-TRANSMEMBRANE-RECEPTOR-PROTEIN-SERINE-THR...	GO-0007178	6	-0.366676	-0.880524	0.573171	0.821016	1.000
435	GOBP-REGULATION.OF-ANION-TRANSPORT	GO-0044070	20	-0.250368	-0.881046	0.614583	0.822922	1.000
436	GOBP-NEUROINFLAMMATORY-RESPONSE	GO-0150076	5	-0.406765	-0.885663	0.592593	0.817032	1.000
437	GOBP-BEHAVIOR	GO-0007610	32	-0.228647	-0.888361	0.649462	0.814760	1.000
438	GOBP-NEGATIVE-REGULATION.OF-BIOSYNTHETIC-PROCESS	GO-0009890	13	-0.288633	-0.889027	0.616667	0.816342	1.000
439	GOBP-REGULATION.OF-RESPONSE.TO-STRESS	GO-0080134	19	-0.254154	-0.889199	0.621444	0.818915	1.000
440	REACTOME-PTEN-REGULATION	R-RNO-6807070	5	-0.394737	-0.891453	0.573441	0.817562	1.000
441	GOBP-REGULATION.OF-LIPASE-ACTIVITY	GO-0060191	6	-0.366609	-0.892741	0.602851	0.818033	1.000
442	GOBP-EXTRINSIC-APOPTOTIC-SIGNALING-PATHWAY	GO-0097191	7	-0.349639	-0.896040	0.576763	0.814410	1.000
443	GOBP-POSITIVE-REGULATION.OF-PHOSPHORUS-METABOL...	GO-0010562	24	-0.245896	-0.903667	0.599129	0.802835	1.000
444	GOBP-EMBRYO-DEVELOPMENT	GO-0009790	14	-0.282021	-0.904685	0.588595	0.803546	1.000
445	REACTOME-SIGNALING-BY-NUCLEAR-RECEPTORS	R-RNO-9006931	8	-0.338501	-0.904953	0.548902	0.806065	1.000
446	GOBP-NEGATIVE-REGULATION.OF-NEURON-DEATH	GO-1901215	11	-0.311375	-0.909173	0.559748	0.800613	1.000
447	GOBP-NEURON-PROJECTION-GUIDANCE	GO-0097485	9	-0.330302	-0.910156	0.561122	0.801634	1.000
448	GOBP-REGULATION.OF-INFLAMMATORY-RESPONSE	GO-0050727	7	-0.363485	-0.913370	0.532328	0.798312	1.000
449	GOBP-REGULATION.OF-INTRACELLULAR-SIGNAL-TRANSD...	GO-1902531	21	-0.254182	-0.914834	0.591880	0.798571	1.000
450	GOBP-REGULATION.OF-DEVELOPMENTAL-GROWTH	GO-0048638	9	-0.333629	-0.919956	0.552521	0.791288	1.000
451	GOBP-REGULATION.OF-CELLULAR-CATABOLIC-PROCESS	GO-0031329	10	-0.323984	-0.920713	0.537500	0.792908	1.000
452	GOBP-RESPONSE.TO-TEMPERATURE-STIMULUS	GO-0009266	9	-0.329560	-0.922647	0.560729	0.791843	1.000
453	GOBP-SECOND-MESSENGER-MEDIATED-SIGNALING	GO-0019932	16	-0.283695	-0.923255	0.570281	0.793607	1.000
454	GOBP-NEGATIVE-REGULATION.OF-APOPTOTIC-SIGNALIN...	GO-2001234	7	-0.355149	-0.923526	0.544330	0.796167	1.000
455	GOBP-RESPONSE.TO-BIOTIC-STIMULUS	GO-0009607	17	-0.269934	-0.923730	0.553015	0.798786	1.000
456	GOBP-CELLULAR-RESPONSE.TO-EXTERNAL-STIMULUS	GO-0071496	10	-0.321061	-0.926882	0.527668	0.795473	1.000
457	GOBP-POSITIVE-REGULATION.OF-PROTEIN-PHOSPHORYL...	GO-0001934	23	-0.254269	-0.929932	0.547672	0.792449	1.000
458	GOBP-POSITIVE-REGULATION.OF-ENDOTHELIAL-CELL-P...	GO-0001938	6	-0.392052	-0.932804	0.536481	0.789779	1.000
459	GOBP-POSITIVE-REGULATION.OF-RESPONSE.TO-EXTERN...	GO-0032103	9	-0.340538	-0.934166	0.517103	0.790093	1.000
460	GOBP-REGULATION.OF-DEFENSE-RESPONSE	GO-0031347	7	-0.363485	-0.934217	0.518518	0.793053	1.000
461	GOBP-POSITIVE-REGULATION.OF-PROTEIN-MODIFICATI...	GO-0031401	23	-0.254269	-0.935823	0.545249	0.793057	1.000
462	GOBP-REGULATION.OF-SECRETION	GO-0051046	14	-0.290654	-0.937945	0.515789	0.792118	1.000
463	REACTOME-ESTROGEN-DEPENDENT-NUCLEAR-EVENTS-DOW...	R-RNO-9634638	5	-0.422580	-0.940690	0.501976	0.789525	1.000
464	GOBP-PROTEIN-AUTOPHOSPHORYLATION	GO-0046777	5	-0.427721	-0.942062	0.516807	0.789606	1.000
465	GOBP-POSITIVE-REGULATION.OF-ANION-TRANSPORT	GO-1903793	9	-0.339402	-0.943960	0.506383	0.788921	1.000
466	GOBP-REGULATION.OF-ANION-TRANSMEMBRANE-TRANSPORT	GO-1903959	5	-0.433974	-0.944357	0.494759	0.791342	1.000
467	GOBP-NEGATIVE-REGULATION.OF-IMMUNE-SYSTEM-PROCESS	GO-0002683	5	-0.416878	-0.944591	0.510000	0.794030	1.000
468	GOBP-MULTICELLULAR-ORGANISMAL-RESPONSE.TO-STRESS	GO-0033555	5	-0.418725	-0.948150	0.490196	0.790156	1.000
469	GOBP-MULTICELLULAR-ORGANISM-PROCESS	GO-0044706	8	-0.356735	-0.950113	0.519669	0.789266	1.000
470	REACTOME-SIGNALING-BY-NTRK2-TRKB	R-RNO-9006115	6	-0.397650	-0.953251	0.480851	0.781583	1.000

Continuation of Table S12

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
471	GOBP-RESPONSE-TO-BACTERIUM	GO-0009617	13	-0.305742	-0.956488	0.468619	0.782260	1.000
472	GOBP-TUBE-DEVELOPMENT	GO-0035295	18	-0.288885	-0.957790	0.537209	0.782733	1.000
473	GOBP-APOPTOTIC-SIGNALING-PATHWAY	GO-0097190	15	-0.295560	-0.961525	0.480885	0.778411	1.000
474	GOBP-REGULATION-OF-NERVOUS-SYSTEM-PROCESS	GO-0031644	8	-0.362500	-0.964128	0.515030	0.776098	1.000
475	GOBP-RESPONSE-TO-MOLECULE-OF-BACTERIAL-ORIGIN	GO-0002237	13	-0.305742	-0.964169	0.492569	0.779182	1.000
476	GOBP-DEPHOSPHORYLATION	GO-0016311	7	-0.386051	-0.965168	0.494071	0.780208	1.000
477	GOBP-NEGATIVE-REGULATION-OF-GENE-EXPRESSION	GO-0010629	12	-0.318014	-0.965273	0.491262	0.783182	1.000
478	GOBP-RESPONSE-TO-NITROGEN-COMPOUND	GO-1901698	34	-0.238680	-0.965556	0.515528	0.785829	1.000
479	GOBP-NEGATIVE-REGULATION-OF-TRANSPORT	GO-0051051	13	-0.305741	-0.966728	0.508097	0.786711	1.000
480	GOBP-PROTEIN-DEPHOSPHORYLATION	GO-0006470	7	-0.386051	-0.974787	0.483193	0.772767	1.000
481	GOBP-CALCIUM-MEDIATED-SIGNALING	GO-0019722	10	-0.339575	-0.975222	0.461009	0.775091	1.000
482	GOBP-POSITIVE-REGULATION-OF-SMALL-MOLECULE-MET...	GO-0062013	5	-0.442234	-0.979207	0.460922	0.769641	1.000
483	GOBP-REGULATION-OF-CELLULAR-AMIDE-METABOLIC-PR...	GO-0034248	9	-0.349749	-0.982392	0.482546	0.766080	1.000
484	GOBP-PEPTIDYL-LYSINE-MODIFICATION	GO-0018205	5	-0.437258	-0.984175	0.457023	0.765644	1.000
485	GOBP-NEURON-MIGRATION	GO-0001764	5	-0.446074	-0.984552	0.458599	0.768061	1.000
486	REACTOME-SIGNALING-BY-RHO-GTPASES-MIRO-GTPASES...	R-RNO-9716542	9	-0.361939	-0.984646	0.462185	0.771139	1.000
487	GOBP-POSITIVE-REGULATION-OF-NERVOUS-SYSTEM-DEV...	GO-0051962	12	-0.327832	-0.985401	0.471338	0.772930	1.000
488	GOBP-REGULATION-OF-CELL-CYCLE	GO-0051726	13	-0.314983	-0.990465	0.472917	0.765862	1.000
489	GOBP-NERVE-DEVELOPMENT	GO-0021675	9	-0.357722	-0.990604	0.469828	0.768935	1.000
490	GOBP-MUSCLE-CONTRACTION	GO-0006936	5	-0.443507	-0.990908	0.432203	0.771607	1.000
491	GOBP-CENTRAL-NERVOUS-SYSTEM-DEVELOPMENT	GO-0007417	26	-0.262922	-0.995004	0.452915	0.766192	1.000
492	REACTOME-RHO-GTPASE-EFFECTORS	R-RNO-195258	9	-0.361939	-0.995536	0.466258	0.768398	1.000
493	GOBP-FOREBRAIN-DEVELOPMENT	GO-0030900	9	-0.360003	-0.995656	0.442797	0.771578	1.000
494	GOBP-NEGATIVE-REGULATION-OF-ION-TRANSPORT	GO-0043271	11	-0.332248	-1.003890	0.448578	0.757417	1.000
495	GOBP-APOPTOTIC-MITOCHONDRIAL-CHANGES	GO-0008637	6	-0.418457	-1.004043	0.448413	0.760487	1.000
496	GOBP-POSITIVE-REGULATION-OF-CELL-DEVELOPMENT	GO-0010720	12	-0.327832	-1.004247	0.427686	0.763535	1.000
497	GOBP-POSITIVE-REGULATION-OF-NEUROGENESIS	GO-0050769	12	-0.327832	-1.008814	0.463675	0.757201	1.000
498	GOBP-REGULATION-OF-FAT-CELL-DIFFERENTIATION	GO-0045598	6	-0.422965	-1.009266	0.433684	0.759644	1.000
499	GOBP-GLAND-DEVELOPMENT	GO-0048732	7	-0.410313	-1.013658	0.441118	0.753776	1.000
500	GOBP-REGULATION-OF-PROTEIN-LOCALIZATION	GO-0032880	18	-0.294564	-1.015817	0.434599	0.752548	1.000
501	GOBP-TUBE-MORPHOGENESIS	GO-0035239	15	-0.319601	-1.018500	0.417391	0.750149	1.000
502	GOBP-POSTTRANSCRIPTIONAL-REGULATION-OF-GENE-EX...	GO-0010608	8	-0.377077	-1.023671	0.431250	0.742483	1.000
503	GOBP-REGULATION-OF-PHOSPHOLIPASE-C-ACTIVITY	GO-1900274	5	-0.469837	-1.024230	0.405010	0.744666	1.000
504	GOBP-NEGATIVE-REGULATION-OF-CELL-PROJECTION-OR...	GO-0031345	5	-0.459349	-1.027290	0.415800	0.741512	1.000
505	GOBP-ENZYME-LINKED-RECEPTOR-PROTEIN-SIGNALING-...	GO-0007167	24	-0.282056	-1.033670	0.405738	0.731122	1.000
506	GOBP-POSITIVE-REGULATION-OF-LIPASE-ACTIVITY	GO-0060193	5	-0.469837	-1.034701	0.418327	0.732352	1.000
507	GOBP-GLIOGENESIS	GO-0042063	12	-0.344391	-1.038106	0.404711	0.728380	1.000
508	GOBP-REGULATION-OF-ENDOCYTOSIS	GO-0030100	6	-0.432507	-1.042375	0.390756	0.722614	1.000
509	GOBP-CELL-JUNCTION-ASSEMBLY	GO-0034329	8	-0.393436	-1.045495	0.382883	0.719494	1.000
510	GOBP-RHYTHMIC-PROCESS	GO-0048511	15	-0.325814	-1.051108	0.371795	0.710839	1.000
511	GOBP-REGULATION-OF-EXTRINSIC-APOPTOTIC-SIGNALI...	GO-2001236	6	-0.440920	-1.060859	0.367220	0.694258	1.000
512	GOBP-AMEBOIDAL-TYPE-CELL-MIGRATION	GO-0001667	11	-0.358920	-1.070693	0.332645	0.677125	1.000
513	GOBP-CELL-CELL-ADHESION	GO-0098609	14	-0.333064	-1.072490	0.352818	0.676714	1.000

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	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
514	REACTOME_HEMOSTASIS	R-RNO-109582	14	-0.340238	-1.072648	0.341253	0.679734	1.000
515	GOBP_CELLULAR_RESPONSE_TO_CADMIUM_ION	GO-0071276	5	-0.476646	-1.073487	0.341948	0.681347	1.000
516	GOBP_COGNITION	GO-0050890	28	-0.277684	-1.074058	0.369803	0.683485	1.000
517	GOBP_RESPONSE_TO_NERVE_GROWTH_FACTOR	GO-1990089	7	-0.416604	-1.074307	0.351410	0.686446	1.000
518	GOBP_POSITIVE_REGULATION_OF_DEVELOPMENTAL_GROWTH	GO-0048639	8	-0.405376	-1.075322	0.349398	0.687802	1.000
519	REACTOME_CELL_CYCLE_MITOTIC	R-RNO-69278	5	-0.481637	-1.080460	0.354077	0.680278	1.000
520	HALLMARK_ALLOGRAFT_REJECTION	M5950	7	-0.420106	-1.081981	0.354701	0.680350	1.000
521	GOBP_BIOLOGICAL_ADHESION	GO-0022610	19	-0.308902	-1.082776	0.334719	0.682193	1.000
522	GOBP_MAPK_CASCADE	GO-0000165	18	-0.319594	-1.097376	0.336000	0.654962	1.000
523	GOBP_NEUROTROPHIN_TRK_RECEPTOR_SIGNALING_PATHWAY	GO-0048011	6	-0.469326	-1.098035	0.348837	0.656868	1.000
524	GOBP_CELL_CYCLE	GO-0007049	21	-0.313180	-1.101047	0.334021	0.653889	1.000
525	GOBP_RESPONSE_TO_CADMIUM_ION	GO-0046686	6	-0.451277	-1.102935	0.324544	0.653196	1.000
526	GOBP_NEUROTROPHIN_SIGNALING_PATHWAY	GO-0038179	6	-0.469326	-1.105882	0.319920	0.650732	1.000
527	GOBP_INTRACELLULAR_PROTEIN_TRANSPORT	GO-0006886	9	-0.401980	-1.106531	0.304979	0.652766	1.000
528	GOBP_INTRACELLULAR_TRANSPORT	GO-0046907	11	-0.370596	-1.109246	0.314465	0.650503	1.000
529	GOBP_POSITIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	GO-0002684	18	-0.319970	-1.114180	0.329140	0.643943	1.000
530	GOBP_SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCTION	GO-0007264	8	-0.419915	-1.117525	0.311850	0.640153	1.000
531	GOBP_REGULATION_OF_VESICLE_MEDIATED_TRANSPORT	GO-0060627	12	-0.368537	-1.120440	0.313853	0.637676	1.000
532	GOBP_GLIAL_CELL_DIFFERENTIATION	GO-0010001	10	-0.384941	-1.123095	0.295359	0.635543	1.000
533	GOBP_POSITIVE_REGULATION_OF_GENE_EXPRESSION	GO-0010628	16	-0.335354	-1.127036	0.304255	0.630940	1.000
534	GOBP_DEVELOPMENTAL_GROWTH	GO-0048589	10	-0.393514	-1.128503	0.308642	0.631287	1.000
535	GOBP_APOPTOTIC_PROCESS	GO-0006915	35	-0.283163	-1.133320	0.282328	0.624915	1.000
536	GOBP_NEGATIVE_REGULATION_OF_DEVELOPMENTAL_PROCESS	GO-0051093	13	-0.368151	-1.143135	0.268344	0.607482	1.000
537	GOBP_TISSUE_MIGRATION	GO-0090130	9	-0.419638	-1.145282	0.296460	0.606683	1.000
538	GOBP_REGULATION_OF_PROTEIN_STABILITY	GO-0031647	5	-0.498605	-1.148561	0.276210	0.603212	1.000
539	GOBP_POSITIVE_REGULATION_OF_PROTEIN_SERINE_THR...	GO-0071902	9	-0.408232	-1.152179	0.273834	0.599364	1.000
540	GOBP_NEGATIVE_REGULATION_OF_NEURON_APOPTOTIC_P...	GO-0043524	8	-0.447016	-1.153905	0.275154	0.598805	1.000
541	GOBP_COAGULATION	GO-0050817	8	-0.455158	-1.160078	0.265351	0.590287	1.000
542	GOBP_CYTOSKELETON_ORGANIZATION	GO-0007010	11	-0.396997	-1.160675	0.274059	0.592441	1.000
543	GOBP_NEGATIVE_REGULATION_OF_CELL_DIFFERENTIATION	GO-0045596	13	-0.368151	-1.161903	0.252796	0.593427	1.000
544	REACTOME_SIGNALING_BY_WNT	R-RNO-195721	7	-0.455899	-1.167902	0.259958	0.585046	1.000
545	GOBP_NEGATIVE_REGULATION_OF_CELLULAR_COMPONENT...	GO-0051129	11	-0.392823	-1.168719	0.260128	0.586714	1.000
546	GOBP_REGULATION_OF_NERVOUS_SYSTEM_DEVELOPMENT	GO-0051960	15	-0.360378	-1.171842	0.262821	0.583974	1.000
547	REACTOME_TRANSCRIPTIONAL_REGULATION_BY_TP53	R-RNO-3700989	6	-0.496894	-1.174781	0.279116	0.581606	1.000
548	GOBP_ENDOCYTOSIS	GO-0006897	8	-0.445022	-1.175419	0.269311	0.583694	1.000
549	GOBP_SPROUTING_ANGIOGENESIS	GO-0002040	5	-0.533935	-1.176640	0.281720	0.584706	1.000
550	GOBP_POSITIVE_REGULATION_OF_EPITHELIAL_CELL_PR...	GO-0050679	7	-0.474771	-1.178516	0.267241	0.584150	1.000
551	GOBP_BLOOD_VESSEL_MORPHOGENESIS	GO-0048514	14	-0.370220	-1.180105	0.235294	0.584479	1.000
552	GOBP_FAT_CELL_DIFFERENTIATION	GO-0045444	9	-0.427304	-1.180434	0.239837	0.587250	1.000
553	GOBP_NEGATIVE_REGULATION_OF_TRANSMEMBRANE_TRAN...	GO-0034763	6	-0.491642	-1.183266	0.251037	0.584939	1.000
554	GOBP_ORGAN_GROWTH	GO-0035265	5	-0.546573	-1.188716	0.272366	0.577403	1.000
555	GOBP_PROTEIN_KINASE_B_SIGNALING	GO-0043491	6	-0.495492	-1.191238	0.254620	0.576117	1.000
556	GOBP_REGULATION_OF_LYMPHOCYTE_ACTIVATION	GO-0051249	5	-0.544297	-1.197027	0.247917	0.568054	1.000

Continuation of Table S12

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
557 GOBP-PLATELET-ACTIVATION	GO-0030168	6	-0.504833	-1.197210	0.245726	0.571165	1.000
558 GOBP-INSULIN-SECRETION	GO-0030073	7	-0.475066	-1.199055	0.235294	0.571310	1.000
559 GOBP-NEGATIVE-REGULATION-OF-NUCLEOBASE-CONTAIN...	GO-0045934	13	-0.382797	-1.202841	0.210526	0.566992	1.000
560 GOBP-EMBRYONIC-MORPHOGENESIS	GO-0048598	6	-0.491263	-1.207787	0.239754	0.560649	1.000
561 GOBP-HORMONE-TRANSPORT	GO-0009914	9	-0.424347	-1.210269	0.217822	0.559266	1.000
562 GOBP-BLOOD-VESSEL-ENDOTHELIAL-CELL-MIGRATION	GO-0043534	8	-0.453042	-1.213456	0.245690	0.556420	1.000
563 GOBP-REGULATION-OF-PEPTIDYL-TYROSINE-PHOSPHORY...	GO-0050730	9	-0.439054	-1.215781	0.239175	0.555681	1.000
564 GOBP-PEPTIDYL-TYROSINE-MODIFICATION	GO-0018212	10	-0.419442	-1.216641	0.204124	0.557402	1.000
565 GOBP-ENDOTHELIAL-CELL-MIGRATION	GO-0043542	8	-0.453042	-1.217064	0.220044	0.560197	1.000
566 GOBP-REGULATION-OF-MITOTIC-CELL-CYCLE	GO-0007346	5	-0.539917	-1.218885	0.237903	0.559966	1.000
567 GOBP-INTRACELLULAR-RECEPTOR-SIGNALING-PATHWAY	GO-0030522	5	-0.552522	-1.222920	0.239919	0.555663	1.000
568 GOBP-EMBRYONIC-ORGAN-DEVELOPMENT	GO-0048568	7	-0.493073	-1.227143	0.225610	0.551115	1.000
569 GOBP-RESPONSE-TO-ACID-CHEMICAL	GO-0001101	6	-0.505889	-1.232070	0.210421	0.544766	1.000
570 GOBP-HEART-DEVELOPMENT	GO-0007507	6	-0.520285	-1.232219	0.224101	0.548187	1.000
571 REACTOME-MAPK-TARGETS-NUCLEAR-EVENTS-MEDIATED...	R-HSA-450282	5	-0.561187	-1.233441	0.231092	0.549400	1.000
572 GOBP-SKIN-DEVELOPMENT	GO-0043588	5	-0.542083	-1.238939	0.223195	0.542384	1.000
573 GOBP-POSITIVE-REGULATION-OF-LOCOMOTION	GO-0040017	11	-0.428609	-1.239449	0.197959	0.545164	1.000
574 GOBP-REGULATION-OF-IMMUNE-SYSTEM-PROCESS	GO-0002682	21	-0.344463	-1.240053	0.169133	0.547757	1.000
575 GOBP-REGULATION-OF-SYSTEM-PROCESS	GO-0044057	18	-0.365548	-1.240926	0.200846	0.549736	1.000
576 GOBP-REGULATION-OF-CYTOSKELETON-ORGANIZATION	GO-0051493	5	-0.554605	-1.240950	0.217391	0.553548	1.000
577 GOBP-CARDIAC-MUSCLE-TISSUE-DEVELOPMENT	GO-0048738	6	-0.520285	-1.243663	0.200418	0.551720	1.000
578 GOBP-POSITIVE-REGULATION-OF-PEPTIDYL-TYROSINE...	GO-0050731	8	-0.468586	-1.246005	0.197034	0.550952	1.000
579 GOBP-AMYLOID-PRECURSOR-PROTEIN-METABOLIC-PROCESS	GO-0042982	5	-0.569151	-1.247118	0.212058	0.552460	1.000
580 GOBP-LEUKOCYTE-CELL-CELL-ADHESION	GO-0007159	6	-0.534680	-1.247267	0.198783	0.556044	1.000
581 GOBP-REGULATION-OF-ORGAN-GROWTH	GO-0046620	5	-0.546573	-1.248735	0.200820	0.557220	1.000
582 GOBP-POSITIVE-REGULATION-OF-SMOOTH-MUSCLE-CELL...	GO-0048661	5	-0.550295	-1.251361	0.220859	0.556179	1.000
583 GOBP-PEPTIDE-HORMONE-SECRETION	GO-0030072	7	-0.475066	-1.252879	0.212982	0.557599	1.000
584 GOBP-RESPONSE-TO-ENDOGENOUS-STIMULUS	GO-0009719	34	-0.321686	-1.253451	0.167391	0.560453	1.000
585 GOBP-PERIPHERAL-NERVOUS-SYSTEM-DEVELOPMENT	GO-0007422	9	-0.453690	-1.254995	0.209016	0.561007	1.000
586 GOBP-RESPONSE-TO-OXYGEN-CONTAINING-COMPOUND	GO-1901700	39	-0.314459	-1.256246	0.169772	0.562651	1.000
587 GOBP-ENDOTHELIAL-CELL-PROLIFERATION	GO-0001935	8	-0.467869	-1.256616	0.198381	0.566195	1.000
588 GOBP-ESTABLISHMENT-OF-PROTEIN-LOCALIZATION-TO...	GO-0072594	6	-0.522297	-1.262512	0.193416	0.557938	1.000
589 GOBP-CELLULAR-RESPONSE-TO-EXTRACELLULAR-STIMULUS	GO-0031668	8	-0.473513	-1.264480	0.179959	0.558265	1.000
590 GOBP-AMYLOID-PRECURSOR-PROTEIN-CATABOLIC-PROCESS	GO-0042987	5	-0.569151	-1.266016	0.212724	0.559536	1.000
591 GOBP-POSITIVE-REGULATION-OF-CELLULAR-PROTEIN L...	GO-1903829	7	-0.494507	-1.271144	0.170732	0.553254	1.000
592 GOBP-ESTABLISHMENT-OF-PROTEIN-LOCALIZATION	GO-0045184	18	-0.372201	-1.275383	0.168399	0.548454	1.000
593 GOBP-MITOTIC-CELL-CYCLE	GO-0002278	10	-0.436571	-1.275402	0.190476	0.552771	1.000
594 HALLMARK-HYPOXIA	M5891	5	-0.564267	-1.277061	0.182203	0.553482	1.000
595 GOBP-POSITIVE-REGULATION-OF-INTRACELLULAR-SIGN...	GO-1902533	14	-0.397074	-1.279130	0.169197	0.553648	1.000
596 GOBP-NEGATIVE-REGULATION-OF-CELL-DEATH	GO-0060548	22	-0.361069	-1.287355	0.183932	0.540643	1.000
597 HALLMARK-APOPTOSIS	M5902	6	-0.544245	-1.287596	0.198198	0.544585	1.000
598 GOBP-REGULATION-OF-NEUROGENESIS	GO-0050767	14	-0.404806	-1.294264	0.148559	0.535449	1.000
599 GOBP-INOSITOL-LIPID-MEDIATED-SIGNALING	GO-0048017	8	-0.495881	-1.294940	0.168399	0.538567	1.000

Continuation of Table S12

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
600 HALLMARK-UV-RESPONSE-UP	M5941	5	-0.572518	-1.295872	0.186441	0.541404	1.000
601 GOBP-MUSCLE-CELL-DEVELOPMENT	GO-0055001	5	-0.575117	-1.297733	0.179435	0.541769	1.000
602 GOBP-AMYLOID-BETA-METABOLIC-PROCESS	GO-0050435	5	-0.569151	-1.300247	0.178357	0.540693	1.000
603 GOBP-VASCULATURE-DEVELOPMENT	GO-0001944	17	-0.384114	-1.302199	0.159915	0.541130	1.000
604 GOBP-REGIONALIZATION	GO-0003002	6	-0.550943	-1.302645	0.154506	0.544892	1.000
605 GOBP-POSITIVE-REGULATION-OF-DEVELOPMENTAL-PROCESS	GO-0051094	32	-0.325929	-1.312977	0.121277	0.528227	1.000
606 GOBP-NEGATIVE-REGULATION-OF-CELL-POPULATION-PR...	GO-0008285	9	-0.480222	-1.315295	0.146751	0.527680	1.000
607 REACTOME-PLATELET-ACTIVATION-SIGNALING-AND-AGG...	R-HSA-76002	7	-0.519365	-1.315499	0.134956	0.531967	1.000
608 GOBP-REGULATION-OF-HORMONE-SECRETION	GO-0046883	8	-0.495165	-1.319630	0.154959	0.527597	1.000
609 GOBP-EPIDERMIS-DEVELOPMENT	GO-0008544	5	-0.579498	-1.320089	0.169422	0.531184	1.000
610 GOBP-NEGATIVE-REGULATION-OF-CELL-CYCLE	GO-0045786	5	-0.585152	-1.324033	0.142276	0.527542	1.000
611 GOBP-PATTERN-SPECIFICATION-PROCESS	GO-0007389	6	-0.550943	-1.329192	0.160083	0.521782	1.000
612 GOBP-REGULATION-OF-PEPTIDE-HORMONE-SECRETION	GO-0090276	6	-0.559672	-1.330337	0.148374	0.524241	1.000
613 GOBP-CELLULAR-RESPONSE-TO-OXYGEN-CONTAINING.CO...	GO-1901701	29	-0.349899	-1.334255	0.114407	0.520829	1.000
614 GOBP-PEPTIDE-SECRETION	GO-0002790	9	-0.475666	-1.338868	0.131915	0.515499	1.000
615 GOBP-REGULATION-OF-PEPTIDYL-SERINE-PHOSPHORYLA...	GO-0033135	8	-0.503369	-1.339895	0.140725	0.518143	1.000
616 GOBP-REGULATION-OF-MUSCLE-ADAPTATION	GO-0043502	5	-0.591301	-1.342875	0.150091	0.516677	1.000
617 REACTOME-BETA-CATENIN-INDEPENDENT-WNT-SIGNALING	R-RNO-3858494	5	-0.586736	-1.345371	0.150826	0.516470	1.000
618 GOBP-CELL-ACTIVATION	GO-0001775	21	-0.378232	-1.345901	0.124197	0.520503	1.000
619 GOBP-POSITIVE-REGULATION-OF-PEPTIDYL-SERINE-PH...	GO-0033138	8	-0.503369	-1.348521	0.132383	0.520212	1.000
620 GOBP-REGULATION-OF-ORGANELLE-ORGANIZATION	GO-0033043	14	-0.425096	-1.361664	0.124731	0.497228	1.000
621 GOBP-TAXIS	GO-0042330	14	-0.420183	-1.363002	0.117391	0.499503	1.000
622 GOBP-REGULATION-OF-CELLULAR-COMPONENT-MOVEMENT	GO-0051270	15	-0.416302	-1.364720	0.123318	0.500953	1.000
623 GOBP-REGULATION-OF-GTPASE-ACTIVITY	GO-0043087	5	-0.594421	-1.367121	0.150101	0.501364	1.000
624 GOBP-MUSCLE-ADAPTATION	GO-0043500	5	-0.591301	-1.369894	0.131631	0.500891	1.000
625 GOBP-PRLMIRNA-TRANSCRIPTION-BY-RNA-POLYMERASE.II	GO-0061614	7	-0.540994	-1.376152	0.128514	0.492995	1.000
626 GOBP-POSITIVE-REGULATION-OF-PRLMIRNA-TRANSCRI...	GO-1902895	7	-0.540994	-1.377712	0.130081	0.495068	1.000
627 GOBP-MONONUCLEAR-CELL-DIFFERENTIATION	GO-1903131	7	-0.531582	-1.377879	0.121399	0.499973	1.000
628 GOBP-REGULATION-OF-MAP-KINASE-ACTIVITY	GO-0043405	9	-0.490243	-1.378515	0.129103	0.503858	1.000
629 GOBP-POSITIVE-REGULATION-OF-NEURON-DEATH	GO-1901216	5	-0.610837	-1.383073	0.107071	0.500295	1.000
630 GOBP-TEMPERATURE-HOMEOSTASIS	GO-0001659	5	-0.610729	-1.387734	0.144269	0.496130	1.000
631 GOBP-POSITIVE-REGULATION-OF-LEUKOCYTE-CELL-CEL...	GO-1903039	5	-0.625227	-1.389115	0.119748	0.498816	1.000
632 GOBP-ACTIN-FILAMENT-BASED-PROCESS	GO-0030029	7	-0.547046	-1.390985	0.120582	0.500557	1.000
633 GOBP-OSTEOBLAST-DIFFERENTIATION	GO-0001649	5	-0.602279	-1.396642	0.128205	0.494447	1.000
634 GOBP-POSITIVE-REGULATION-OF-GLIOGENESIS	GO-0014015	5	-0.615425	-1.397355	0.117886	0.498841	1.000
635 GOBP-RESPONSE-TO-WOUNDING	GO-0009611	15	-0.431944	-1.398397	0.108051	0.502279	1.000
636 GOBP-REGULATION-OF-RESPONSE-TO-EXTERNAL-STIMULUS	GO-0032101	15	-0.425832	-1.399342	0.076923	0.505897	1.000
637 GOBP-REGULATION-OF-GLIOGENESIS	GO-0014013	5	-0.615425	-1.399512	0.124473	0.511528	1.000
638 GOBP-NEURON-DEATH	GO-0070997	18	-0.414330	-1.403058	0.094595	0.509347	1.000
639 GOBP-POSITIVE-REGULATION-OF-CELL-CELL-ADHESION	GO-0022409	5	-0.625227	-1.421438	0.117886	0.475040	1.000
640 GOBP-REGULATION-OF-CELLULAR-COMPONENT-BIOGENESIS	GO-0044087	10	-0.501060	-1.430004	0.069721	0.443309	1.000
641 GOBP-POSITIVE-REGULATION-OF-CELLULAR-COMPONENT...	GO-0051130	24	-0.386394	-1.439997	0.088421	0.447206	1.000
642 REACTOME-CELL-CYCLE	R-RNO-1640170	6	-0.589117	-1.440993	0.110647	0.451208	1.000

Continuation of Table S12

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
643	GOBP-POSITIVE-REGULATION_OF_PHOSPHATIDYLINOSIT...	5	-0.640037	-1.441014	0.113636	0.457072	1.000
644	GOBP-NUCLEAR-TRANSPORT	5	-0.648141	-1.444187	0.106996	0.456106	1.000
645	REACTOME-INTERLEUKIN_4-AND-INTERLEUKIN_13-SIGN...	8	-0.542144	-1.450218	0.096579	0.449526	1.000
646	GOBP-NEGATIVE-REGULATION_OF_RESPONSE_TO_EXTERN...	5	-0.649576	-1.450960	0.104895	0.453997	1.000
647	GOBP-RESPONSE-TO-GROWTH-FACTOR	18	-0.439938	-1.473195	0.074786	0.413154	1.000
648	GOBP-PHOSPHATIDYLINOSITOL_3_KINASE-SIGNALING	7	-0.591342	-1.474078	0.082803	0.417188	1.000
649	GOBP-NEURON-APOPTOTIC-PROCESS	12	-0.478088	-1.474587	0.086242	0.422006	1.000
650	GOBP-REGULATION_OF_MAPK-CASCADE	13	-0.478367	-1.476210	0.057377	0.424326	1.000
651	GOBP-NEGATIVE-REGULATION_OF_LOCOMOTION	5	-0.674416	-1.490691	0.086316	0.400576	1.000
652	GOBP-EPITHELIAL-CELL-PROLIFERATION	12	-0.482710	-1.492066	0.072435	0.403646	1.000
653	GOBP-T-CELL-ACTIVATION	8	-0.569826	-1.501333	0.081933	0.391856	1.000
654	GOBP-LOCOMOTION	31	-0.378983	-1.510029	0.046256	0.379981	1.000
655	GOBP-PEPTIDYL-AMINO-ACID-MODIFICATION	22	-0.418669	-1.510622	0.036017	0.384932	1.000
656	GOBP-POSITIVE-REGULATION_OF_CELL-DIFFERENTIATION	27	-0.397351	-1.514642	0.043912	0.382852	1.000
657	GOBP-POSITIVE-REGULATION_OF_ESTABLISHMENT_OF_P...	5	-0.677115	-1.518990	0.072495	0.380272	1.000
658	GOBP-MUSCLE-SYSTEM-PROCESS	8	-0.584220	-1.519516	0.047826	0.385371	1.000
659	GOBP-REGULATION_OF_MUSCLE-SYSTEM-PROCESS	8	-0.584220	-1.52674	0.045652	0.385200	1.000
660	GOBP-MYOTUBE-DIFFERENTIATION	5	-0.683719	-1.529059	0.060345	0.379134	1.000
661	GOBP-CIRCULATORY-SYSTEM-DEVELOPMENT	21	-0.425040	-1.531168	0.052747	0.381561	1.000
662	GOBP-MUSCLE-STRUCTURE-DEVELOPMENT	16	-0.469936	-1.536619	0.040632	0.377089	1.000
663	GOBP-ANIMAL-ORGAN-MORPHOGENESIS	12	-0.503698	-1.539273	0.044625	0.378050	1.000
664	GOBP-REGULATION_OF_CELL-DEVELOPMENT	15	-0.472826	-1.544749	0.037657	0.373583	1.000
665	GOBP-SMOOTH-MUSCLE-CELL-PROLIFERATION	6	-0.659402	-1.565843	0.055066	0.337845	1.000
666	GOBP-REGULATION_OF_CELL-ADHESION	13	-0.506298	-1.573046	0.038055	0.329712	1.000
667	GOBP-LYMPHOCYTE-ACTIVATION	9	-0.565885	-1.589436	0.054167	0.306512	1.000
668	GOBP-PEPTIDYL-SERINE-MODIFICATION	12	-0.515823	-1.596325	0.037895	0.299959	1.000
669	GOBP-ACTIVATION_OF_MAPK-ACTIVITY	6	-0.677561	-1.609641	0.024145	0.281506	1.000
670	GOBP-POSITIVE-REGULATION_OF_MAP_KINASE-ACTIVITY	6	-0.677561	-1.610984	0.032990	0.284697	1.000
671	GOBP-MYELOID-CELL-DIFFERENTIATION	13	-0.511716	-1.618745	0.030501	0.277068	1.000
672	GOBP-WOUND-HEALING	13	-0.523043	-1.619145	0.036559	0.282313	1.000
673	GOBP-REGULATION_OF_PHOSPHATIDYLINOSITOL_3_KINA...	6	-0.668211	-1.620133	0.029528	0.286553	1.000
674	GOBP-POSITIVE-REGULATION_OF_CELLULAR-COMPONENT...	9	-0.581902	-1.621444	0.047131	0.290513	1.000
675	GOBP-NEGATIVE-REGULATION_OF_MULTICELLULAR_ORGA...	15	-0.498699	-1.625225	0.030905	0.289950	1.000
676	GOBP-REGULATION_OF_PEPTIDE-SECRETION	7	-0.631246	-1.635431	0.033058	0.277872	1.000
677	REACTOME-SIGNALING-BY-RECEPTOR-TYROSINE-KINASES	26	-0.437481	-1.644474	0.027197	0.267731	1.000
678	GOBP-CELL-MIGRATION	22	-0.458771	-1.651563	0.013158	0.262281	1.000
679	GOBP-REGULATION_OF_MULTICELLULAR-ORGANISMAL.DE...	31	-0.423982	-1.652043	0.010917	0.268200	1.000
680	GOBP-REGULATION_OF_OSTEOCLAST-DIFFERENTIATION	5	-0.722892	-1.652381	0.032922	0.274207	1.000
681	GOBP-REGULATION_OF_CELL-ACTIVATION	8	-0.619836	-1.658298	0.041580	0.270636	1.000
682	GOBP-MYELOID-LEUKOCYTE-DIFFERENTIATION	11	-0.509032	-1.674263	0.024283	0.250379	1.000
683	GOBP-NEGATIVE-REGULATION_OF_NERVOUS-SYSTEM.DEV...	5	-0.758339	-1.680847	0.015054	0.231535	0.999
684	GOBP-POSITIVE-REGULATION_OF_MYELOID-LEUKOCYTE...	6	-0.720262	-1.691009	0.025478	0.236108	0.999
685	GOBP-MUSCLE-ORGAN-DEVELOPMENT	9	-0.618178	-1.697899	0.041580	0.231359	0.999

Continuation of Table S12

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
686	GOBP-REGULATION-OF-PEPTIDE-TRANSPORT	10	-0.595757	-1.717912	0.020450	0.205472	0.997
687	GOBP-REGULATION-OF-VASCULAR-ASSOCIATED-SMOOTH...	5	-0.763553	-1.724440	0.012793	0.201777	0.996
688	GOBP-MUSCLE-CELL-PROLIFERATION	8	-0.648073	-1.731200	0.016563	0.198255	0.994
689	GOBP-POSITIVE-REGULATION-OF-MULTICELLULAR-ORGA...	32	-0.443673	-1.737259	0.008197	0.196567	0.994
690	GOBP-POSITIVE-REGULATION-OF-MAPK-CASCADE	9	-0.632339	-1.748022	0.015217	0.188448	0.991
691	GOBP-REGULATION-OF-CELL-ADHESION	9	-0.642770	-1.755669	0.019190	0.184707	0.990
692	GOBP-REGULATION-OF-CELL-DIFFERENTIATION	36	-0.431519	-1.766512	0.008715	0.177398	0.985
693	GOBP-POSITIVE-REGULATION-OF-ORGANELLE-ORGANIZA...	10	-0.619184	-1.778978	0.014644	0.167682	0.978
694	HALLMARK-TNFA-SIGNALING-VIA-NFKB	14	-0.562234	-1.783902	0.010142	0.167690	0.975
695	GOBP-OSTEOCLAST-DIFFERENTIATION	6	-0.731707	-1.787862	0.017893	0.168708	0.970
696	GOBP-OSSIFICATION	9	-0.637738	-1.790477	0.010142	0.172434	0.969
697	GOBP-ERK1-AND-ERK2-CASCADE	5	-0.793286	-1.797290	0.008299	0.171282	0.958
698	GOBP-POSITIVE-REGULATION-OF-MYELOID-CELL-DIFFE...	7	-0.717991	-1.799217	0.006237	0.176799	0.957
699	GOBP-LEUKOCYTE-DIFFERENTIATION	15	-0.562342	-1.802932	0.013100	0.180780	0.955
700	GOBP-SKELETAL-MUSCLE-ORGAN-DEVELOPMENT	5	-0.793857	-1.827798	0.012685	0.156117	0.929
701	GOBP-REGULATION-OF-MYELOID-CELL-DIFFERENTIATION	9	-0.667040	-1.841018	0.004132	0.147869	0.905
702	GOBP-REGULATION-OF-MYELOID-LEUKOCYTE-DIFFERENT...	8	-0.686563	-1.842793	0.010460	0.154857	0.903
703	GOBP-POSITIVE-REGULATION-OF-CELL-ADHESION	7	-0.727441	-1.876811	0.008032	0.122151	0.825
704	GOBP-REGULATION-OF-LEUKOCYTE-DIFFERENTIATION	9	-0.695397	-1.895522	0.012712	0.109228	0.765
705	GOBP-POSITIVE-REGULATION-OF-TRANSCRIPTION-BY-R...	24	-0.518103	-1.897927	0.002105	0.114690	0.757
706	GOBP-ANATOMICAL-STRUCTURE-FORMATION-INVOLVED-I...	20	-0.534976	-1.904357	0.002070	0.116432	0.729
707	GOBP-POSITIVE-REGULATION-OF-HEMOPOIESIS	7	-0.745360	-1.909096	0.003953	0.120339	0.717
708	REACTOME-SIGNALING-BY-NTRKS	18	-0.562111	-1.922023	0.004283	0.115332	0.658
709	GOBP-NEGATIVE-REGULATION-OF-CELL-DEVELOPMENT	10	-0.678086	-1.926710	0.004090	0.121362	0.643
710	REACTOME-NGF-STIMULATED-TRANSCRIPTION	6	-0.815338	-1.940928	0.002096	0.117181	0.591
711	GOBP-CELL-POPULATION-PROLIFERATION	31	-0.496633	-1.970494	0.000000	0.108387	0.476
712	REACTOME-NUCLEAR-EVENTS-KINASE-AND-TRANSCRIPTI...	11	-0.679255	-1.990635	0.002179	0.103686	0.427
713	GOBP-MUSCLE-TISSUE-DEVELOPMENT	11	-0.674644	-2.018202	0.002304	0.091098	0.334
714	GOBP-POSITIVE-REGULATION-OF-CELL-POPULATION-PR...	21	-0.571767	-2.033686	0.000000	0.096320	0.289
715	GOBP-POSITIVE-REGULATION-OF-BIOSYNTHETIC-PROCESS	27	-0.535520	-2.059733	0.002088	0.099952	0.235
716	GOBP-POSITIVE-REGULATION-OF-NUCLEOBASE-CONTAIN...	28	-0.545353	-2.087747	0.000000	0.116790	0.185
717	GOBP-IMMUNE-SYSTEM-DEVELOPMENT	17	-0.608753	-2.088167	0.002212	0.233580	0.185

End of Table

Supplementary Table S13: CTX-M late profile (45 DPL peak) GSEA results.

Begin of Table S13									
	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val	
0	GOBP-TEMPERATURE.HOMEOSTASIS	GO-0001659	5	0.814246	1.904456	0.003205	1.000000		0.724
1	GOBP-LONG-TERM.MEMORY	GO-0007616	6	0.692177	1.737028	0.034843	1.000000		0.976
2	GOBP-NEGATIVE-REGULATION-OF-LIPID-METABOLIC.PR...	GO-00045833	5	0.724414	1.727147	0.046053	1.000000		0.978
3	GOBP-REGULATION-OF-LIPID-METABOLIC.PROCESS	GO-0019216	7	0.624385	1.719359	0.010753	1.000000		0.979
4	GOBP-CELLULAR-RESPONSE-TO-ORGANIC_CYCLIC-COMPOUND	GO-0071407	13	0.480000	1.695269	0.021552	1.000000		0.987
5	GOBP-CARBOHYDRATE.HOMEOSTASIS	GO-0003500	7	0.608837	1.655799	0.025735	1.000000		0.994
6	GOBP-REGULATION-OF_SMALL-MOLECULE.METABOLIC.PR...	GO-0006212	9	0.528680	1.650303	0.029167	1.000000		0.995
7	GOBP-MULTICELLULAR-ORGANISMAL.HOMEOSTASIS	GO-00048871	12	0.471564	1.632236	0.043269	1.000000		0.997
8	GOBP-MORPHOGENESIS-OF-AN-EPITHELIUM	GO-0002009	6	0.621951	1.594586	0.050955	1.000000		0.999
9	GOBP-CELLULAR-RESPONSE-TO-KETONE	GO-1901655	5	0.612336	1.432981	0.078261	1.000000		1.000
10	GOBP-ENDOTHELIAL-CELL-PROLIFERATION	GO-0001935	8	0.492299	1.411948	0.098540	1.000000		1.000
11	GOBP-NEGATIVE-REGULATION-OF-CATALYTIC-ACTIVITY	GO-00043086	17	0.363209	1.404382	0.091398	1.000000		1.000
12	GOBP-POSITIVE-REGULATION-OF-APOPTOTIC-SIGNALIN...	GO-2001235	5	0.579000	1.402481	0.108280	1.000000		1.000
13	GOBP-REGULATION-OF-VASCULATURE.DEVELOPMENT	GO-1901342	5	0.571971	1.393704	0.116208	1.000000		1.000
14	GOBP-SMALL-MOLECULE.METABOLIC.PROCESS	GO-00044281	15	0.391764	1.390275	0.055814	1.000000		1.000
15	GOBP-MALE.GAMETE-GENERATION	GO-00048232	5	0.577344	1.387334	0.110063	1.000000		1.000
16	GOBP-RESPONSE-TO-CARBOHYDRATE	GO-00009743	5	0.580980	1.380092	0.130000	1.000000		1.000
17	GOBP-MYELOID-LEUKOCYTE-ACTIVATION	GO-0002274	8	0.475974	1.375632	0.108949	1.000000		1.000
18	GOBP-NEGATIVE-REGULATION-OF-IMMUNE-SYSTEM.PROCESS	GO-00002683	5	0.568080	1.368483	0.109756	1.000000		1.000
19	GOBP-LIPID-METABOLIC.PROCESS	GO-0006629	10	0.438158	1.357959	0.120370	1.000000		1.000
20	GOBP-ESTABLISHMENT-OF-PROTEIN-LOCALIZATION-TO-...	GO-00072594	6	0.524390	1.340301	0.115152	1.000000		1.000
21	GOBP-CELLULAR-RESPONSE-TO-DNA-DAMAGE-STIMULUS	GO-0006974	5	0.568726	1.338634	0.138554	1.000000		1.000
22	GOBP-LEUKOCYTE-MIGRATION	GO-00050900	6	0.524390	1.335666	0.119205	1.000000		1.000
23	GOBP-POSITIVE-REGULATION-OF-LOCOMOTION	GO-0004017	11	0.428572	1.334863	0.130952	1.000000		1.000
24	GOBP-EPITHELIAL-CELL-PROLIFERATION	GO-00050673	12	0.381579	1.322804	0.103960	1.000000		1.000
25	GOBP-RESPONSE-TO-MONOSACCHARIDE	GO-00034284	5	0.580980	1.321477	0.128125	1.000000		1.000
26	GOBP-BLOOD_VESSEL-ENDOTHELIAL-CELL-MIGRATION	GO-00043534	8	0.444610	1.317215	0.142857	1.000000		1.000
27	GOBP-REGULATION-OF-ENDOTHELIAL-CELL-MIGRATION	GO-00010594	5	0.565265	1.314722	0.166667	1.000000		1.000
28	GOBP-REGULATION-OF-EPITHELIAL-CELL-MIGRATION	GO-00010632	6	0.507243	1.312504	0.151515	1.000000		1.000
29	GOBP-REGULATION-OF-LIPID-BIOSYNTHETIC.PROCESS	GO-00046890	6	0.515207	1.297160	0.153846	1.000000		1.000
30	GOBP-ENDOTHELIAL-CELL-MIGRATION	GO-00043542	8	0.444610	1.292866	0.153846	1.000000		1.000
31	GOBP-POSITIVE-REGULATION-OF-IMMUNE-RESPONSE	GO-00050778	9	0.421582	1.278661	0.181818	1.000000		1.000
32	GOBP-LIPID-BIOSYNTHETIC.PROCESS	GO-0008610	6	0.515207	1.277405	0.155709	1.000000		1.000
33	GOBP-CELLULAR-GLUCOSE-HOMEOSTASIS	GO-00016678	5	0.554217	1.270988	0.166163	1.000000		1.000
34	GOBP-RESPONSE-TO-ORGANIC_CYCLIC-COMPOUND	GO-0014070	20	0.314057	1.260219	0.128655	1.000000		1.000
35	GOBP-CELL-ACTIVATION	GO-0001775	21	0.298530	1.251973	0.154696	1.000000		1.000
36	GOBP-PHAGOCYTOSIS	GO-0006909	5	0.518072	1.250350	0.170732	1.000000		1.000
37	GOBP-CELLULAR-LIPID-METABOLIC.PROCESS	GO-00044255	7	0.471653	1.248008	0.194946	1.000000		1.000
38	GOBP-PATTERN-SPECIFICATION.PROCESS	GO-0007389	6	0.476510	1.246578	0.170492	1.000000		1.000
39	GOBP-NEGATIVE-REGULATION-OF-GENE-EXPRESSION	GO-00010629	12	0.368421	1.240564	0.188285	1.000000		1.000
40	GOBP-RESPONSE-TO-NITROGEN-COMPOUND	GO-1901698	34	0.264033	1.238171	0.116279	1.000000		1.000

Continuation of Table S13

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
41	GOBP-PEPTIDE-BIOSYNTHETIC-PROCESS	7	0.444321	1.238102	0.184906	1.000000	1.000
42	GOBP-POSITIVE-REGULATION-OF-ANION-TRANSPORT	9	0.417721	1.232201	0.199134	1.000000	1.000
43	GOBP-INTRINSIC-APOPTOTIC-SIGNALING-PATHWAY	5	0.503992	1.223392	0.199357	1.000000	1.000
44	GOBP-CELLULAR-RESPONSE-TO-NITROGEN-COMPOUND	20	0.302673	1.223322	0.193939	1.000000	1.000
45	GOBP-TISSUE-MORPHOGENESIS	7	0.444444	1.211666	0.189189	1.000000	1.000
46	GOBP-MEMORY	13	0.348991	1.210904	0.181395	1.000000	1.000
47	GOBP-REGULATION-OF-CELLULAR-CATABOLIC-PROCESS	10	0.375560	1.207050	0.195833	1.000000	1.000
48	GOBP-CELL-CYCLE-PROCESS	11	0.363636	1.200359	0.194805	1.000000	1.000
49	GOBP-REGIONALIZATION	6	0.475610	1.196240	0.231317	1.000000	1.000
50	GOBP-AMIDE-BIOSYNTHETIC-PROCESS	7	0.444321	1.188910	0.246269	1.000000	1.000
51	GOBP-REGULATION-OF-PEPTIDE-HORMONE-SECRETION	6	0.457240	1.187195	0.228374	1.000000	1.000
52	GOBP-PLATELET-ACTIVATION	6	0.451219	1.179721	0.228669	1.000000	1.000
53	GOBP-TISSUE-MIGRATION	9	0.408387	1.178161	0.240506	1.000000	1.000
54	GOBP-NEGATIVE-REGULATION-OF-CELL-CYCLE	5	0.492080	1.160302	0.259016	1.000000	1.000
55	GOBP-POSITIVE-REGULATION-OF-DEFENSE-RESPONSE	5	0.474561	1.148284	0.249147	1.000000	1.000
56	GOBP-FAT-CELL-DIFFERENTIATION	9	0.367277	1.133323	0.248062	1.000000	1.000
57	GOBP-NEGATIVE-REGULATION-OF-MOLECULAR-FUNCTION	24	0.263408	1.127556	0.262069	1.000000	1.000
58	GOBP-DEVELOPMENTAL-PROCESS-INVOLVED-IN-REPRODUCTION	11	0.337662	1.122976	0.244898	1.000000	1.000
59	GOBP-CARBOHYDRATE-DERIVATIVE-METABOLIC-PROCESS	7	0.407407	1.117982	0.285714	1.000000	1.000
60	GOBP-MITOTIC-CELL-CYCLE	10	0.358974	1.117073	0.296943	1.000000	1.000
61	GOBP-PHOSPHATIDYLINOSITOL-3-KINASE-SIGNALING	7	0.407407	1.114405	0.283088	1.000000	1.000
62	GOBP-NEGATIVE-REGULATION-OF-HYDROLASE-ACTIVITY	11	0.341251	1.104337	0.287500	1.000000	1.000
63	GOBP-ANATOMICAL-STRUCTURE-HOMEOSTASIS	7	0.395092	1.091505	0.309859	1.000000	1.000
64	GOBP-LYMPHOCYTE-ACTIVATION	9	0.367089	1.089079	0.324786	1.000000	1.000
65	REACTOME-MEMBRANE-TRAFFICKING	5	0.454434	1.084972	0.299094	1.000000	1.000
66	REACTOME-G-ALPHA-Z-SIGNALING-EVENTS	5	0.445783	1.073439	0.346479	1.000000	1.000
67	REACTOME-VESICLE-MEDIATED-TRANSPORT	5	0.454434	1.066071	0.345794	1.000000	1.000
68	GOBP-RESPONSE-TO-NUTRIENT	5	0.453874	1.064207	0.361635	1.000000	1.000
69	GOBP-REGULATION-OF-IMMUNE-RESPONSE	12	0.305695	1.060285	0.355769	1.000000	1.000
70	GOBP-NEGATIVE-REGULATION-OF-PHOSPHORUS-METABOLISM	9	0.348214	1.058991	0.371429	1.000000	1.000
71	GOBP-REGULATION-OF-INFLAMMATORY-RESPONSE	7	0.384692	1.057949	0.328720	1.000000	1.000
72	GOBP-REGULATION-OF-DEFENSE-RESPONSE	7	0.384692	1.056955	0.340000	1.000000	1.000
73	GOBP-REGULATION-OF-CELL-ACTIVATION	8	0.362500	1.055096	0.368231	1.000000	1.000
74	GOBP-MONOCARBOXYLIC-ACID-METABOLIC-PROCESS	6	0.408672	1.054570	0.378571	1.000000	1.000
75	GOBP-POSITIVE-REGULATION-OF-EPITHELIAL-CELL-MIGRATION	5	0.445783	1.054308	0.369637	1.000000	1.000
76	GOBP-REGULATION-OF-HORMONE-LEVELS	12	0.304942	1.054018	0.393443	1.000000	1.000
77	GOBP-EPIDERMIS-DEVELOPMENT	5	0.431328	1.044782	0.403614	1.000000	1.000
78	GOBP-LEUKOCYTE-MEDIATED-IMMUNITY	7	0.382716	1.042437	0.349265	1.000000	1.000
79	GOBP-T-CELL-ACTIVATION	8	0.362500	1.041906	0.378788	1.000000	1.000
80	GOBP-OSSIFICATION	9	0.341772	1.041450	0.389830	1.000000	1.000
81	GOBP-ERBB-SIGNALING-PATHWAY	5	0.445783	1.039690	0.374150	1.000000	1.000
82	REACTOME-BETA-CATENIN-INDEPENDENT-WNT-SIGNALING	5	0.445783	1.037556	0.372014	1.000000	1.000
83	GOBP-REGULATION-OF-PEPTIDE-SECRETION	7	0.390455	1.035456	0.394366	1.000000	1.000

Continuation of Table S13

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val	
84	GOBP-PROTEIN_KINASE_B-SIGNALING	6	0.406964	1.032593	0.381119	1.000000	1.000	
85	GOBP-REGULATION_OF_PHOSPHATIDYLINOSITOL-3.KINA...	6	0.402439	1.030972	0.391304	1.000000	1.000	
86	GOBP-CYTOSKELETON_ORGANIZATION	11	0.308775	1.021986	0.383966	1.000000	1.000	
87	GOBP-EMBRYO-DEVELOPMENT_ENDING_IN_BIRTH_OR_EGG...	9	0.341772	1.020099	0.403101	1.000000	1.000	
88	GOBP-CIRCADIAN_REGULATION_OF_GENE_EXPRESSION	5	0.420377	1.019278	0.396875	1.000000	1.000	
89	GOBP-CELLULAR_RESPONSE_TO_ALCOHOL	5	0.433735	1.016363	0.372483	1.000000	1.000	
90	GOBP-NEGATIVE_REGULATION_OF_BIOSYNTHETIC_PROCESS	13	0.279729	1.011303	0.403361	1.000000	1.000	
91	GOBP-NEGATIVE_REGULATION_OF_SYNAPTIC_TRANSMISSION	6	0.398952	1.009713	0.438538	1.000000	1.000	
92	GOBP-NEGATIVE_REGULATION_OF_ANION_TRANSPORT	8	0.348817	1.007726	0.453061	1.000000	1.000	
93	GOBP-ORGANIC_HYDROXY_COMPOUND_TRANSPORT	6	0.378203	1.000933	0.425087	1.000000	1.000	
94	GOBP-REGULATION_OF_PEPTIDE_TRANSPORT	10	0.313833	0.999715	0.457831	1.000000	1.000	
95	GOBP-NEGATIVE_REGULATION_OF_RESPONSE_TO_EXTERN...	5	0.418326	0.999598	0.421569	1.000000	1.000	
96	GOBP-REGULATION_OF_PHOSPHORUS_METABOLIC_PROCESS	27	0.228089	0.994008	0.475862	1.000000	1.000	
97	GOBP-CIRCULATORY_SYSTEM_PROCESS	5	0.426402	0.993006	0.405844	1.000000	1.000	
98	GOBP-INSULIN_SECRETION	7	0.365790	0.989077	0.417476	1.000000	1.000	
99	REACTOME-NEUTROPHIL_DEGRANULATION	R-RNO-6798695	6	0.378049	0.988374	0.451389	1.000000	1.000
100	GOBP-POSITIVE_REGULATION_OF_EPITHELIAL_CELL_PR...	7	0.358025	0.985677	0.407692	1.000000	1.000	
101	GOBP-PEPTIDE_HORMONE_SECRETION	7	0.365790	0.984920	0.444840	1.000000	1.000	
102	GOBP-REGULATION_OF_CELL_CYCLE_PROCESS	5	0.399378	0.983288	0.448276	1.000000	1.000	
103	GOBP-MULTICELLULAR_ORGANISM_REPRODUCTION	12	0.285784	0.980875	0.468402	1.000000	1.000	
104	GOBP-NEGATIVE_REGULATION_OF_TRANSCRIPTION_BY_R...	10	0.326612	0.976803	0.456522	1.000000	1.000	
105	GOBP-RESPONSE_TO_NICOTINE	7	0.361004	0.976342	0.469751	1.000000	1.000	
106	GOBP-REGULATION_OF_NEUROTRANSMITTER_TRANSPORT	6	0.381196	0.976023	0.480000	1.000000	1.000	
107	GOBP-POSITIVE_REGULATION_OF_RESPONSE_TO_EXTERN...	9	0.327050	0.975590	0.444915	1.000000	1.000	
108	GOBP-PROTEIN_AUTOPHOSPHORYLATION	5	0.409639	0.973133	0.453642	1.000000	1.000	
109	GOBP-CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	6	0.378049	0.972605	0.490260	1.000000	1.000	
110	GOBP-NEURON_MIGRATION	5	0.409639	0.969626	0.437700	1.000000	1.000	
111	GOBP-MYELOID_LEUKOCYTE-MEDIATED IMMUNITY	6	0.378049	0.968809	0.489286	1.000000	1.000	
112	GOBP-NEGATIVE_REGULATION_OF_PROTEIN_MODIFICATI...	10	0.304006	0.964258	0.496154	1.000000	1.000	
113	GOBP-NEGATIVE_REGULATION_OF_SIGNALING	21	0.240151	0.961587	0.509554	1.000000	1.000	
114	GOBP-MATERNAL_PROCESS_INVOLVED_IN_FEMALE_PREGN...	5	0.408584	0.960171	0.470968	1.000000	1.000	
115	GOBP-REGULATION_OF_ORGAN_GROWTH	5	0.397590	0.957730	0.478395	1.000000	1.000	
116	GOBP-IN-UTERO-EMBRYONIC_DEVELOPMENT	8	0.337500	0.957276	0.505618	1.000000	1.000	
117	GOBP-MAINTENANCE_OF_LOCATION	7	0.351857	0.954443	0.510949	1.000000	1.000	
118	GOBP-REGULATION_OF-CARBOHYDRATE_BIOSYNTHETIC_P...	5	0.397590	0.952087	0.467320	1.000000	1.000	
119	REACTOME-SIGNALING_BY_WNT	R-RNO-195721	7	0.345679	0.946157	0.503521	1.000000	1.000
120	GOBP-REGULATION_OF_MITOTIC_CELL_CYCLE	5	0.398390	0.942650	0.500000	1.000000	1.000	
121	GOBP-REGULATION_OF-CARBOHYDRATE_METABOLIC_PROCESS	5	0.397590	0.941609	0.507886	1.000000	1.000	
122	GOBP-POSITIVE_REGULATION_OF_ESTABLISHMENT_OF_P...	5	0.397590	0.936090	0.512739	1.000000	1.000	
123	GOBP-NEUROINFLAMMATORY_RESPONSE	5	0.397590	0.931265	0.529231	1.000000	1.000	
124	GOBP-CELLULAR_RESPONSE_TO_OXYGEN-CONTAINING_CO...	29	0.206252	0.930143	0.559055	1.000000	1.000	
125	GOBP-ORGANONITROGEN_COMPOUND_BIOSYNTHETIC_PROCESS	GO-1901701	13	0.266667	0.927968	0.566667	1.000000	1.000
126	GOBP-POSITIVE_REGULATION_OF_PHOSPHATIDYLINOSIT...	GO-0014068	5	0.397590	0.927255	0.520767	1.000000	1.000

Continuation of Table S13

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
127 GOBP-ORGAN_GROWTH	GO-0035265	5	0.397590	0.917706	0.539855	1.000000	1.000
128 GOBP-MUSCLE-CELL-DEVELOPMENT	GO-0055001	5	0.385542	0.916988	0.545150	1.000000	1.000
129 GOBP-LONG-TERM-SYNAPTIC-DEPRESSION	GO-0060292	5	0.385556	0.915172	0.510972	1.000000	1.000
130 GOBP-PROTEIN-MODIFICATION-BY-SMALL-PROTEIN-CON...	GO-0032446	6	0.360075	0.913811	0.571885	1.000000	1.000
131 GOBP-PROTEIN-MODIFICATION-BY-SMALL-PROTEIN-CON...	GO-0070647	7	0.332776	0.913194	0.588235	1.000000	1.000
132 GOBP-SPROUTING-ANGIOGENESIS	GO-0002040	5	0.394763	0.911516	0.535503	1.000000	1.000
133 GOBP-REGULATION-OF-PROTEIN-MODIFICATION-PROCESS	GO-0031399	29	0.209465	0.910855	0.605839	1.000000	1.000
134 GOBP-REGULATION-OF-CELLULAR-COMPONENT-MOVEMENT	GO-0051270	15	0.245556	0.909407	0.630769	1.000000	1.000
135 GOBP-PRL-MIRNA-TRANSCRIPTION-BY-RNA-POLYMERASE-II	GO-0061614	7	0.323428	0.906663	0.581132	1.000000	1.000
136 GOBP-GLUCOSE-METABOLIC-PROCESS	GO-0006006	6	0.351847	0.902609	0.600000	1.000000	1.000
137 GOBP-TISSUE-HOMEOSTASIS	GO-0001894	5	0.385542	0.902144	0.574074	1.000000	1.000
138 GOBP-CARBOHYDRATE-BIOSYNTHETIC-PROCESS	GO-0016051	5	0.397590	0.899090	0.571031	1.000000	1.000
139 GOBP-REGULATION-OF-HORMONE-SECRETION	GO-0046883	8	0.321656	0.898972	0.575758	1.000000	1.000
140 GOBP-POSITIVE-REGULATION-OF-PRL-MIRNA-TRANSCRI...	GO-1902895	7	0.323428	0.894710	0.562044	1.000000	1.000
141 GOBP-POSITIVE-REGULATION-OF-ENDOTHELIAL-CELL-P...	GO-0001938	6	0.353658	0.893448	0.605960	1.000000	1.000
142 GOBP-SKELETAL-MUSCLE-ORGAN-DEVELOPMENT	GO-0060538	5	0.385542	0.892829	0.575949	1.000000	1.000
143 GOBP-NEUROTRANSMITTER-SECRETION	GO-0007269	6	0.351443	0.890271	0.612245	1.000000	1.000
144 GOBP-CYTOKINE-PRODUCTION	GO-0001816	10	0.275555	0.884713	0.608696	1.000000	1.000
145 GOBP-MONOSACCHARIDE-METABOLIC-PROCESS	GO-0005996	6	0.351847	0.882583	0.565693	1.000000	1.000
146 GOBP-POSITIVE-REGULATION-OF-CYTOKINE-PRODUCTION	GO-0001819	7	0.318705	0.882047	0.580882	1.000000	1.000
147 GOBP-NEGATIVE-REGULATION-OF-RESPONSE-TO-STIMULUS	GO-0048585	16	0.226430	0.880522	0.646707	1.000000	1.000
148 GOBP-CELLULAR-MACROMOLECULE-CATABOLIC-PROCESS	GO-0044265	6	0.341463	0.874619	0.559871	1.000000	1.000
149 GOBP-RESPONSE-TO-BIOTIC-STIMULUS	GO-0009607	17	0.228605	0.874089	0.650538	1.000000	1.000
150 GOBP-NEGATIVE-REGULATION-OF-NUCLEOBASE-CONTAIN...	GO-0045934	13	0.254257	0.871554	0.654545	1.000000	1.000
151 GOBP-RESPONSE-TO-INSULIN	GO-0032868	5	0.368194	0.870799	0.589595	1.000000	1.000
152 GOBP-RESPONSE-TO-ALKALOID	GO-0043279	5	0.368372	0.870473	0.608434	1.000000	1.000
153 GOBP-REGULATION-OF-CELLULAR-RESPONSE-TO-STRESS	GO-0080135	9	0.286117	0.869576	0.660517	1.000000	1.000
154 GOBP-PROTEIN-DEPHOSPHORYLATION	GO-0006470	7	0.315974	0.869000	0.642857	1.000000	1.000
155 GOBP-PEPTIDE-SECRETION	GO-0002790	9	0.281645	0.866491	0.628352	1.000000	1.000
156 GOBP-POSITIVE-REGULATION-OF-PROTEIN-PHOSPHORYL...	GO-0001934	23	0.201080	0.862527	0.720000	1.000000	1.000
157 GOBP-POSITIVE-REGULATION-OF-NEURON-DEATH	GO-1901216	5	0.362233	0.862181	0.588757	1.000000	1.000
158 GOBP-REGULATION-OF-VESICLE-MEDIATED-TRANSPORT	GO-0060627	12	0.255489	0.860303	0.699074	1.000000	1.000
159 GOBP-RESPONSE-TO-CALCIUM-ION	GO-0051592	6	0.329268	0.859991	0.653430	1.000000	1.000
160 GOBP-ORGANIC-ACID-METABOLIC-PROCESS	GO-0006082	7	0.313544	0.857757	0.648855	1.000000	1.000
161 GOBP-LEUKOCYTE-DIFFERENTIATION	GO-0002521	15	0.226083	0.855127	0.664865	1.000000	1.000
162 REACTOME-OPIOID-SIGNALING	R-RNO-111885	12	0.250000	0.848256	0.652381	1.000000	1.000
163 GOBP-REGULATION-OF-PHOSPHOLIPASE-ACTIVITY	GO-0010517	6	0.320891	0.847567	0.651007	1.000000	1.000
164 GOBP-REGULATION-OF-FAT-CELL-DIFFERENTIATION	GO-0045598	6	0.326866	0.847358	0.645270	1.000000	1.000
165 GOBP-ORGANOPHOSPHATE-METABOLIC-PROCESS	GO-0019637	7	0.308642	0.839576	0.642857	1.000000	1.000
166 GOBP-DEPHOSPHORYLATION	GO-0016311	7	0.315974	0.837657	0.656489	1.000000	1.000
167 GOBP-REGULATION-OF-LIPASE-ACTIVITY	GO-0060191	6	0.320891	0.834725	0.694545	1.000000	1.000
168 GOBP-POSITIVE-REGULATION-OF-SMALL-MOLECULE-MET...	GO-0062013	5	0.353934	0.833634	0.672956	1.000000	1.000
169 GOBP-REPRODUCTIVE-SYSTEM-DEVELOPMENT	GO-0061458	6	0.329268	0.828429	0.667797	1.000000	1.000

Continuation of Table S13

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
170 GOBP-POSITIVE-REGULATION_OF_PROTEIN-MODIFICATION...	GO-0031401	23	0.201080	0.826885	0.711656	1.000000	1.000
171 GOBP-REGULATION_OF_LIPID-LOCALIZATION	GO-1905952	5	0.342119	0.826247	0.706485	1.000000	1.000
172 REACTOME_NUCLEAR-EVENTS.KINASE-AND-TRANSCRIPTI...	R-RNO-198725	11	0.246753	0.818523	0.786290	1.000000	1.000
173 GOBP-RESPONSE_TO_TEMPERATURE-STIMULUS	GO-0009266	9	0.265823	0.815903	0.732000	1.000000	1.000
174 GOBP-POSITIVE-REGULATION_OF_NEURON-PROJECTION...	GO-0010976	5	0.340959	0.815362	0.669670	1.000000	1.000
175 GOBP-REGULATION_OF_RESPONSE_TO-STRESS	GO-0080134	19	0.202853	0.815264	0.758242	1.000000	1.000
176 GOBP-POSITIVE-REGULATION_OF_CELLULAR-PROTEIN-L...	GO-1903829	7	0.299543	0.810529	0.688172	1.000000	1.000
177 GOBP-MUSCLE-TISSUE-DEVELOPMENT	GO-0060537	11	0.246753	0.808128	0.758475	1.000000	1.000
178 GOBP-HORMONE-TRANSPORT	GO-0009914	9	0.269563	0.806984	0.722846	1.000000	1.000
179 GOBP-HOMEOSTATIC-PROCESS	GO-0042592	31	0.181896	0.806767	0.762712	1.000000	1.000
180 GOBP-PEPTIDYL-SERINE-MODIFICATION	GO-0018209	12	0.236842	0.804434	0.754167	1.000000	1.000
181 GOBP-DEFENSE-RESPONSE	GO-0006952	19	0.204479	0.802198	0.805031	1.000000	1.000
182 GOBP-RESPONSE_TO_TUMOR-NECROSIS-FACTOR	GO-0034612	7	0.293054	0.801823	0.763441	1.000000	1.000
183 GOBP-IMMUNE-SYSTEM-DEVELOPMENT	GO-0002520	17	0.211268	0.799547	0.754717	1.000000	1.000
184 GOBP-ORGANIC-HYDROXY-COMPOUND-METABOLIC-PROCESS	GO-1901615	7	0.293523	0.797391	0.738351	1.000000	1.000
185 GOBP-NEGATIVE-REGULATION_OF_CYSTEINE-TYPE-ENDO...	GO-2000117	5	0.333518	0.794337	0.710884	1.000000	1.000
186 GOBP-VASCULATURE-DEVELOPMENT	GO-0001944	7	0.201569	0.792881	0.789744	1.000000	1.000
187 GOBP-POSITIVE-REGULATION_OF_IMMUNE-SYSTEM-PROCESS	GO-0002684	18	0.195830	0.789344	0.801242	1.000000	1.000
188 REACTOME-INTEGRATION_OF_ENERGY-METABOLISM	R-RNO-163685	5	0.337349	0.787045	0.699690	1.000000	1.000
189 GOBP-NEGATIVE-REGULATION_OF_CELL-POPULATION_PR...	GO-0008285	9	0.259077	0.786441	0.782443	1.000000	1.000
190 GOBP-VESICLE-MEDIATED-TRANSPORT_IN-SYNAPSE	GO-0099003	7	0.280546	0.782036	0.740072	1.000000	1.000
191 GOBP-IMPORT_INTO-CELL	GO-0098657	6	0.304878	0.776063	0.786408	1.000000	1.000
192 GOBP-REGULATION_OF_CELL-CYCLE	GO-0051726	13	0.219995	0.774998	0.798030	1.000000	1.000
193 GOBP-INFLAMMATORY-RESPONSE	GO-0006954	12	0.231622	0.774764	0.764940	1.000000	1.000
194 GOBP-CELLULAR-RESPONSE_TO-ABIOTIC-STIMULUS	GO-0071214	7	0.289581	0.774728	0.756944	1.000000	1.000
195 GOBP-REGULATION_OF_NEUROTRANSMITTER-LEVELS	GO-0001505	7	0.283994	0.774473	0.762542	1.000000	1.000
196 GOBP-CELL-MIGRATION	GO-0016477	22	0.186293	0.771530	0.788889	1.000000	1.000
197 GOBP-REGULATION_OF_PROTEIN-BINDING	GO-0043393	7	0.283951	0.769649	0.742537	1.000000	1.000
198 GOBP-ESTABLISHMENT_OF_PROTEIN-LOCALIZATION	GO-0045184	18	0.186380	0.767593	0.848485	1.000000	1.000
199 GOBP-GAMETE-GENERATION	GO-0007276	9	0.256660	0.766181	0.717949	1.000000	1.000
200 GOBP-RESPONSE_TO_LIPID	GO-0033993	19	0.189719	0.763951	0.787356	1.000000	1.000
201 GOBP-OSTEOBLAST-DIFFERENTIATION	GO-0001649	5	0.325301	0.761783	0.764706	1.000000	1.000
202 GOBP-REGULATION_OF_DNA-BINDING-TRANSCRIPTION_F...	GO-0051090	16	0.205669	0.757254	0.837696	1.000000	1.000
203 GOBP-PROTEIN-LOCALIZATION_TO-ORGANELLE	GO-0033365	9	0.252003	0.757238	0.815574	1.000000	1.000
204 REACTOME-INTRACELLULAR-SIGNALING_BY-SECOND-MES...	R-RNO-9006925	15	0.205479	0.756747	0.839024	1.000000	1.000
205 GOBP-EXOCYTOSIS	GO-0006887	11	0.230617	0.754101	0.798246	1.000000	1.000
206 GOBP-NEUROTRANSMITTER-TRANSPORT	GO-0006836	7	0.283994	0.750662	0.818182	1.000000	1.000
207 GOBP-CIRCULATORY-SYSTEM-DEVELOPMENT	GO-0072359	21	0.180914	0.747816	0.840491	1.000000	1.000
208 GOBP-POSITIVE-REGULATION_OF_PEPTIDYL-SERINE_PH...	GO-0033138	8	0.262348	0.745399	0.799228	1.000000	1.000
209 GOBP-REGULATION_OF_PEPTIDYL-SERINE-PHOSPHORYLA...	GO-0033135	8	0.262348	0.744444	0.832714	1.000000	1.000
210 GOBP-RESPONSE_TO-PEPTIDE	GO-1901652	18	0.192842	0.737911	0.856322	1.000000	1.000
211 GOBP-POSITIVE-REGULATION_OF_SECRETION	GO-0051047	6	0.285577	0.735848	0.844884	1.000000	1.000
212 GOBP-PEPTIDYL-LYSINE-MODIFICATION	GO-0018205	5	0.306102	0.734276	0.818182	1.000000	1.000

Continuation of Table S13

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
213	GOBP-MULTI-MULTICELLULAR-ORGANISM-PROCESS	8	0.254816	0.734001	0.797753	1.000000	1.000
214	GOBP-POSTTRANSCRIPTIONAL-REGULATION-OF_GENE.EX...	8	0.262097	0.732178	0.836957	1.000000	1.000
215	GOBP-RESPONSE-TO-BACTERIUM	13	0.208473	0.731638	0.841346	1.000000	1.000
216	GOBP-REGULATION-OF_OSTEOCLAST-DIFFERENTIATION	5	0.316704	0.731299	0.819079	1.000000	1.000
217	GOBP-REGULATION-OF_RESPONSE-TO-EXTERNAL-STIMULUS	15	0.198920	0.729445	0.888350	1.000000	1.000
218	GOBP-MONOAMINE-TRANSPORT	5	0.309087	0.727351	0.796178	1.000000	1.000
219	GOBP-ANATOMICAL-STRUCTURE-FORMATION-INVOLVED_I...	20	0.182319	0.726442	0.883333	1.000000	1.000
220	REACTOME-NGF-STIMULATED-TRANSCRIPTION	9	0.240506	0.725770	0.841202	1.000000	1.000
221	GOBP-RESPONSE-TO-MOLECULE-OF_BACTERIAL-ORIGIN	13	0.208473	0.721411	0.861472	1.000000	1.000
222	REACTOME-ANTI-INFLAMMATORY-RESPONSE-FAVOURING...	5	0.295695	0.720439	0.864112	1.000000	1.000
223	GOBP-MUSCLE-ORGAN-DEVELOPMENT	9	0.240506	0.717366	0.835878	1.000000	1.000
224	GOBP-MYELOID-CELL-DIFFERENTIATION	13	0.200000	0.716302	0.868020	1.000000	1.000
225	GOBP-POSITIVE-REGULATION-OF_ION-TRANSPORT	17	0.184707	0.713772	0.835979	1.000000	1.000
226	REACTOME-G-PROTEIN-MEDIATED-EVENTS	9	0.240506	0.712580	0.851711	1.000000	1.000
227	GOBP-CELLULAR-RESPONSE-TO-LIPID	15	0.196834	0.711133	0.867299	1.000000	1.000
228	GOBP-RESPONSE-TO-HORMONE	20	0.178921	0.710022	0.875598	1.000000	1.000
229	GOBP-PURINE-CONTAINING-COMPOUND-METABOLIC-PROCESS	5	0.301205	0.709762	0.823529	1.000000	1.000
230	GOBP-POSITIVE-REGULATION-OF_NUCLEOBASE-CONTAIN...	28	0.156521	0.708527	0.928571	1.000000	1.000
231	GOBP-INTRACELLULAR-TRANSPORT	11	0.205048	0.700831	0.896396	1.000000	1.000
232	GOBP-REGULATION-OF_IMMUNE-SYSTEM-PROCESS	21	0.002682	0.691734	0.926471	1.000000	1.000
233	REACTOME-PTEN-REGULATION	5	0.292803	0.688775	0.849315	1.000000	1.000
234	GOBP-POSITIVE-REGULATION-OF_DNA-BINDING-TRANSC...	10	0.220355	0.685448	0.902542	1.000000	1.000
235	GOBP-ENDOCYTOSIS	8	0.238350	0.684700	0.84615	1.000000	1.000
236	GOBP-SEXUAL-REPRODUCTION	10	0.216397	0.682760	0.911017	1.000000	1.000
237	GOBP-RESPONSE-TO-ENDOGENOUS-STIMULUS	34	0.148491	0.682056	0.923077	1.000000	1.000
238	GOBP-RESPONSE-TO-HEAT	7	0.259259	0.681657	0.855634	1.000000	1.000
239	GOBP-REGULATION-OF-ANION-TRANSMEMBRANE-TRANSPORT	5	0.277308	0.678854	0.888217	1.000000	1.000
240	GOBP-REGULATION-OF_PHOSPHOLIPASE_C-ACTIVITY	5	0.277108	0.672640	0.910891	1.000000	1.000
241	GOBP-POSITIVE-REGULATION-OF_BIOSYNTHETIC-PROCESS	27	0.152424	0.670750	0.937500	1.000000	1.000
242	GOBP-POSITIVE-REGULATION-OF_LIPASE-ACTIVITY	5	0.277108	0.661533	0.892857	1.000000	1.000
243	GOBP-RESPONSE-TO-KETONE	7	0.246020	0.660559	0.930909	1.000000	1.000
244	GOBP-ACTIN-FILAMENT-BASED-PROCESS	7	0.233478	0.655700	0.936090	1.000000	1.000
245	REACTOME-EXTRA-NUCLEAR-ESTROGEN-SIGNALING	7	0.234568	0.652697	0.922535	1.000000	1.000
246	GOBP-ANION-TRANSMEMBRANE-TRANSPORT	7	0.246914	0.650432	0.913534	1.000000	1.000
247	GOBP-INOSITOL-LIPID-MEDIATED-SIGNALING	8	0.225000	0.650068	0.937743	1.000000	1.000
248	GOBP-RESPONSE-TO-OXYGEN-CONTAINING-COMPOUND	39	0.138749	0.649540	0.973684	1.000000	1.000
249	GOBP-TRANSMEMBRANE-RECEPTOR-PROTEIN-SERINE-THR...	6	0.246771	0.646403	0.922819	1.000000	1.000
250	GOBP-SKIN-DEVELOPMENT	5	0.261893	0.643392	0.946844	1.000000	1.000
251	HALLMARK-TNFA-SIGNALING-VIA-NFKB	14	0.175742	0.614026	0.938967	1.000000	1.000
252	GOBP-RESPIRATORY-SYSTEM-DEVELOPMENT	6	0.231707	0.606982	0.949833	1.000000	1.000
253	GOBP-OSTEOCLAST-DIFFERENTIATION	6	0.235081	0.595391	0.966777	1.000000	1.000
254	GOBP-REGULATION-OF_APOPTOTIC-SIGNALING-PATHWAY	10	0.189368	0.587928	0.972763	1.000000	1.000
255	GOBP-NEGATIVE-REGULATION-OF_CELL-DIFFERENTIATION	13	0.165930	0.586558	0.986607	1.000000	1.000

Continuation of Table S13

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
256	GOBP-CELL-CYCLE	GO-0007049	21	0.145012	0.586369	0.994253	1.000000
257	GOBP-CELL-CELL-SIGNALING-BY-WNT	GO-0198738	7	0.208614	0.583451	0.982456	1.000000
258	GOBP-NEGATIVE-REGULATION-OF-DEVELOPMENTAL-PROCESS	GO-0051093	13	0.165930	0.583417	0.995305	1.000000
259	GOBP-POSITIVE-REGULATION-OF-TRANSCRIPTION-BY-R...	GO-0045944	24	0.140625	0.578241	1.000000	1.000000
260	GOBP-NEGATIVE-REGULATION-OF-APOPTOTIC-SIGNALIN...	GO-2001234	7	0.220223	0.577453	0.961538	1.000000
261	GOBP-REGULATION-OF-VASCULAR-ASSOCIATED-SMOOTH...	GO-1904705	5	0.239620	0.573663	0.983051	1.000000
262	HALLMARK-P13K-AKT-MTOR-SIGNALING	M5923	6	0.219512	0.559363	0.983819	1.000000
263	GOBP-MUSCLE-CELL-PROLIFERATION	GO-0033002	8	0.187500	0.557557	0.975207	1.000000
264	GOBP-LIPID-LOCALIZATION	GO-0010876	10	0.175669	0.550018	0.996032	1.000000
265	GOBP-POSITIVE-REGULATION-OF-ORGANELLE-ORGANIZA...	GO-0010638	10	0.173917	0.548175	0.982759	1.000000
266	GOBP-REGULATION-OF-WNT-SIGNALING-PATHWAY	GO-0030111	5	0.228027	0.546103	0.996678	1.000000
267	GOBP-SMOOTH-MUSCLE-CELL-PROLIFERATION	GO-0048659	6	0.209084	0.545528	0.980328	1.000000
268	GOBP-REGULATION-OF-ANION-TRANSPORT	GO-0044070	20	0.136901	0.544324	0.994048	1.000000
269	GOBP-POSITIVE-REGULATION-OF-SMOOTH-MUSCLE-CELL...	GO-0048661	5	0.223978	0.535401	0.993671	0.997532
270	GOBP-ACTIVATION-OF-PROTEIN-KINASE-ACTIVITY	GO-0032147	11	0.155590	0.516693	1.000000	0.997329
271	GOBP-INTRACELLULAR-PROTEIN-TRANSPORT	GO-0006886	9	0.164557	0.498538	0.988550	0.996400
272	GOBP-IMMUNE-EFFECTOR-PROCESS	GO-0002252	10	-0.134766	-0.345584	1.000000	0.999880
273	GOBP-CELLULAR-RESPONSE-TO-HORMONE-STIMULUS	GO-0032870	11	-0.150731	-0.392427	1.000000	1.000000
274	GOBP-REGULATION-OF-EXTRINSIC-APOPTOTIC-SIGNAL...	GO-2001236	6	-0.186094	-0.403957	0.998613	1.000000
275	REACTOME-TRANSCRIPTIONAL-REGULATION-OF-WHITE-A...	R-RNO-381340	6	-0.212786	-0.462341	0.997097	1.000000
276	GOBP-REGULATION-OF-CELLULAR-AMIDE-METABOLIC-PR...	GO-0034248	9	-0.189715	-0.467366	0.992147	1.000000
277	GOBP-REGULATION-OF-ORGANELLE-ORGANIZATION	GO-0033043	14	-0.168282	-0.467599	0.995000	1.000000
278	GOBP-CELLULAR-RESPONSE-TO-BIOTIC-STIMULUS	GO-0071216	8	-0.198581	-0.468590	0.993216	1.000000
279	REACTOME-ADAPTIVE-IMMUNE-SYSTEM	R-RNO-1280218	9	-0.191698	-0.471214	0.989348	1.000000
280	GOBP-RESPONSE-TO-INTERLEUKIN-1	GO-0070555	5	-0.229479	-0.473619	0.994444	1.000000
281	GOBP-CELLULAR-RESPONSE-TO-MOLECULE-OF-BACTERIA...	GO-0071219	8	-0.198581	-0.474250	0.990305	1.000000
282	GOBP-PEPTIDE-METABOLIC-PROCESS	GO-0006518	12	-0.183110	-0.486386	0.978205	1.000000
283	GOBP-REGULATION-OF-PROTEIN-LOCALIZATION	GO-0032880	18	-0.167688	-0.489118	0.983503	1.000000
284	GOBP-POSITIVE-REGULATION-OF-PROTEIN-SERINE-THR...	GO-0071902	9	-0.201980	-0.498164	0.985155	1.000000
285	GOBP-MONONUCLEAR-CELL-DIFFERENTIATION	GO-1903131	7	-0.224790	-0.503386	0.976257	1.000000
286	REACTOME-INTERLEUKIN-4-AND-INTERLEUKIN-13-SIGN...	R-RNO-6785807	8	-0.214935	-0.510316	0.983095	1.000000
287	GOBP-REGULATION-OF-PROTEIN-STABILITY	GO-0031647	5	-0.255184	-0.519954	0.990085	1.000000
288	GOBP-DNA-METABOLIC-PROCESS	GO-0008259	6	-0.239383	-0.526487	0.990028	1.000000
289	GOBP-CELL-CELL-JUNCTION-ASSEMBLY	GO-0007043	5	-0.256930	-0.526981	0.994092	1.000000
290	GOBP-CELLULAR-RESPONSE-TO-PEPTIDE	GO-1901653	13	-0.196494	-0.529136	0.975124	1.000000
291	GOBP-CARDIAC-MUSCLE-TISSUE-DEVELOPMENT	GO-0048738	6	-0.242804	-0.530971	0.982906	1.000000
292	GOBP-REGULATION-OF-NEURON-DIFFERENTIATION	GO-0045664	5	-0.251916	-0.532045	0.990085	1.000000
293	GOBP-CELL-CELL-JUNCTION-ORGANIZATION	GO-0045216	6	-0.233707	-0.533305	0.977077	1.000000
294	GOBP-HEART-DEVELOPMENT	GO-0007507	6	-0.242804	-0.535297	0.988506	1.000000
295	GOBP-REGULATION-OF-PROTEIN-SERINE-THREONINE-KI...	GO-0071900	12	-0.203842	-0.544512	0.959688	1.000000
296	GOBP-POSITIVE-REGULATION-OF-MULTICELLULAR-ORGA...	GO-0051240	32	-0.169276	-0.545413	0.965792	1.000000
297	GOBP-LEUKOCYTE-CELL-CELL-ADHESION	GO-0007159	6	-0.255921	-0.546946	0.974648	1.000000
298	REACTOME-RHO-GTPASE-EFFECTORS	R-RNO-195258	9	-0.222492	-0.548346	0.959239	1.000000

Continuation of Table S13

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
299	GOBP-NEUROTROPHIN_SIGNALING_PATHWAY	6	-0.252671	-0.552026	0.965116	1.000000	1.000
300	GOBP-NEUROTROPHIN_TRK_RECEPTOR_SIGNALING_PATHWAY	6	-0.252671	-0.552258	0.965418	1.000000	1.000
301	REACTOME_SIGNALING_BY_RHO_GTPASES_MIRO_GTPASES...	9	-0.222492	-0.552469	0.967213	1.000000	1.000
302	GOBP-POSITIVE_REGULATION_OF_MYELOID_LEUKOCYTE_...	6	-0.253089	-0.552531	0.964789	1.000000	1.000
303	GOBP-EMBRYO_DEVELOPMENT	14	-0.203764	-0.557204	0.965736	1.000000	1.000
304	GOBP-REPRODUCTION	18	-0.195183	-0.561298	0.949559	1.000000	1.000
305	GOBP-POSITIVE_REGULATION_OF_CELL_POPULATION_PR...	21	-0.188474	-0.568377	0.957473	1.000000	1.000
306	GOBP-RESPONSE_TO_PEPTIDE_HORMONE	13	-0.213034	-0.577342	0.947301	1.000000	1.000
307	GOBP-REGULATION_OF_CELLULAR_PROTEIN_LOCALIZATION	12	-0.222388	-0.580566	0.945806	1.000000	1.000
308	REACTOME_SIGNALING_BY_NTRK2_TRKB	6	-0.269203	-0.581761	0.956091	1.000000	1.000
309	GOBP-EPITHELIAL_DEVELOPMENT	15	-0.210201	-0.582500	0.950980	1.000000	1.000
310	GOBP-APOPTOTIC_MITOCHONDRIAL_CHANGES	6	-0.268293	-0.583587	0.942623	1.000000	1.000
311	GOBP-CELLULAR_RESPONSE_TO_PEPTIDE_HORMONE_STIM...	9	-0.235502	-0.584194	0.953020	1.000000	1.000
312	GOBP-CARBOHYDRATE_METABOLIC_PROCESS	9	-0.231172	-0.584253	0.947226	1.000000	1.000
313	GOBP-CELLULAR_RESPONSE_TO_CADMIUM_ION	5	-0.282311	-0.584815	0.959762	1.000000	1.000
314	GOBP-ORGANIC_ACID_TRANSPORT	7	-0.258741	-0.586746	0.954930	1.000000	1.000
315	GOBP-REGULATION_OF_PROTEIN_PHOSPHORYLATION	26	-0.190821	-0.588820	0.946449	1.000000	1.000
316	GOBP-RESPONSE_TO_ALCOHOL	11	-0.228698	-0.590459	0.951031	1.000000	1.000
317	GOBP-TUBE_MORPHOGENESIS	15	-0.212796	-0.594081	0.942118	1.000000	1.000
318	GOBP-MUSCLE_STRUCTURE_DEVELOPMENT	16	-0.231337	-0.594303	0.931336	1.000000	1.000
319	GOBP-AMEBOIDAL_TYPE_CELL_MIGRATION	11	-0.231325	-0.594378	0.924084	1.000000	1.000
320	GOBP-REGULATION_OF_CELL_CELL_ADHESION	9	-0.242315	-0.599360	0.933333	1.000000	1.000
321	GOBP-POSITIVE_REGULATION_OF_MYELOID_CELL_DIFFE...	7	-0.266941	-0.599893	0.942008	1.000000	1.000
322	GOBP-RESPONSE_TO_GROWTH_FACTOR	18	-0.205535	-0.600109	0.944030	1.000000	1.000
323	GOBP-RESPONSE_TO_CADMIUM_ION	6	-0.268293	-0.600749	0.951591	1.000000	1.000
324	GOBP-REGULATION_OF_BODY_FLUID_LEVELS	11	-0.233867	-0.602086	0.916991	1.000000	1.000
325	GOBP-RECEPTOR-MEDIATED_ENDOCYTOSIS	6	-0.273939	-0.602892	0.930736	1.000000	1.000
326	GOBP-RESPONSE_TO_INORGANIC_SUBSTANCE	19	-0.208591	-0.606924	0.926380	1.000000	1.000
327	GOBP-POSITIVE_REGULATION_OF_CELL_PROJECTION_OR...	10	-0.242937	-0.607580	0.912698	1.000000	1.000
328	GOBP-POSITIVE_REGULATION_OF_CELL_CELL_ADHESION	5	-0.296853	-0.608212	0.943396	1.000000	1.000
329	REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGG...	7	-0.269794	-0.609963	0.926491	1.000000	1.000
330	GOBP-POSITIVE_REGULATION_OF_LEUKOCYTE_CELL_CELL...	5	-0.296853	-0.612453	0.931983	1.000000	1.000
331	GOBP-REGULATION_OF_CELL_ADHESION	13	-0.269794	-0.613021	0.930719	1.000000	1.000
332	GOBP-RECEPTOR_METABOLIC_PROCESS	5	-0.301951	-0.614015	0.928994	1.000000	1.000
333	GOBP-CELLULAR_AMIDE_METABOLIC_PROCESS	13	-0.227821	-0.617642	0.938383	1.000000	1.000
334	GOBP-RECEPTOR_INTERNALIZATION	5	-0.301951	-0.620130	0.933921	1.000000	1.000
335	REACTOME_ESTROGEN_DEPENDENT_NUCLEAR_EVENTS_DOW...	5	-0.306896	-0.620840	0.940388	1.000000	1.000
336	GOBP-REGULATION_OF_SECRETION	14	-0.226643	-0.622799	0.910112	1.000000	1.000
337	GOBP-REGULATION_OF_CYTOSKELETON_ORGANIZATION	5	-0.304652	-0.624357	0.937213	1.000000	1.000
338	GOBP-APOPTOTIC_PROCESS	35	-0.191656	-0.624722	0.929465	1.000000	1.000
339	GOBP-POSITIVE_REGULATION_OF_CELL_ADHESION	7	-0.273998	-0.626934	0.916667	1.000000	1.000
340	GOBP-NEGATIVE_REGULATION_OF_BINDING	6	-0.283967	-0.625287	0.925287	1.000000	1.000
341	REACTOME_DAG_AND_IP3_SIGNALING	8	-0.264178	-0.629021	0.908108	1.000000	1.000

Continuation of Table S13

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
342	GOBP-POSITIVE-REGULATION-OF-HEMOPOIESIS	GO-1903708	7	-0.274618	-0.629421	0.933803	1.000000	1.000
343	GOBP-POSITIVE-REGULATION-OF-TRANSPORT	GO-0051050	26	-0.201958	-0.629931	0.924617	1.000000	1.000
344	GOBP-NEGATIVE-REGULATION-OF-PHOSPHORYLATION	GO-0042326	7	-0.269673	-0.630261	0.918056	1.000000	1.000
345	GOBP-REGULATION-OF-PROTEIN-KINASE-ACTIVITY	GO-0045859	22	-0.210358	-0.630322	0.924821	1.000000	1.000
346	GOBP-SENSORY-ORGAN-DEVELOPMENT	GO-0007423	8	-0.261451	-0.630941	0.910448	1.000000	1.000
347	GOBP-MYELOID-LEUKOCYTE-DIFFERENTIATION	GO-0002573	11	-0.240745	-0.633576	0.899619	1.000000	1.000
348	GOBP-REGULATION-OF-MYELOID-CELL-DIFFERENTIATION	GO-0045637	9	-0.260595	-0.634610	0.893793	1.000000	1.000
349	GOBP-RHYTHMIC-PROCESS	GO-0048511	15	-0.223861	-0.635339	0.909091	1.000000	1.000
350	GOBP-REGULATION-OF-TRANSFERASE-ACTIVITY	GO-0051338	22	-0.210358	-0.636603	0.92944	1.000000	1.000
351	REACTOME-INFECTIOUS-DISEASE	R-HSA-5663205	13	-0.233286	-0.637487	0.910141	1.000000	1.000
352	GOBP-GLAND-DEVELOPMENT	GO-0048732	7	-0.273537	-0.637524	0.904564	1.000000	1.000
353	GOBP-EMBRYONIC-ORGAN-DEVELOPMENT	GO-0048568	7	-0.278018	-0.637648	0.916782	1.000000	1.000
354	GOBP-EXTRINSIC-APOPTOTIC-SIGNALING-PATHWAY	GO-0097191	7	-0.275159	-0.639215	0.924016	1.000000	1.000
355	GOBP-CARBOXYLIC-ACID-TRANSPORT	GO-0046942	6	-0.297865	-0.640700	0.911444	1.000000	1.000
356	GOBP-AMYLOID-PRECURSOR-PROTEIN-CATABOLIC-PROCESS	GO-0042987	5	-0.313635	-0.641880	0.911047	1.000000	1.000
357	GOBP-APOPTOTIC-SIGNALING-PATHWAY	GO-0097190	15	-0.219418	-0.642542	0.895466	1.000000	1.000
358	GOBP-POSITIVE-REGULATION-OF-PROTEIN-KINASE-ACT...	GO-00045860	19	-0.230736	-0.642381	0.915357	1.000000	1.000
359	GOBP-MUSCLE-CONTRACTION	GO-0006936	5	-0.303538	-0.642748	0.931034	1.000000	1.000
360	GOBP-NEGATIVE-REGULATION-OF-PROTEOLYSIS	GO-0045861	8	-0.273370	-0.645770	0.900415	1.000000	1.000
361	GOBP-CELLULAR-RESPONSE-TO-EXTERNAL-STIMULUS	GO-0071496	10	-0.258692	-0.645791	0.904110	1.000000	1.000
362	GOBP-AMYLOID-BETA-METABOLIC-PROCESS	GO-0050435	5	-0.313635	-0.646333	0.926901	1.000000	1.000
363	REACTOME-HEMOSTASIS	R-RNO-109582	14	-0.239259	-0.646844	0.897277	1.000000	1.000
364	GOBP-ORGANIC-ANION-TRANSPORT	GO-0015711	6	-0.297865	-0.647119	0.906340	1.000000	1.000
365	GOBP-SIGNAL-RELEASE	GO-0023061	14	-0.234367	-0.648667	0.887626	1.000000	1.000
366	GOBP-ACTIVATION-OF-MAPK-ACTIVITY	GO-0000187	6	-0.298718	-0.648827	0.887784	1.000000	1.000
367	GOBP-POSITIVE-REGULATION-OF-MAP-KINASE-ACTIVITY	GO-0043406	6	-0.298718	-0.652095	0.890625	1.000000	1.000
368	GOBP-ERK1-AND-ERK2-CASCADE	GO-0070371	5	-0.315006	-0.652474	0.902299	1.000000	1.000
369	GOBP-AMYLOID-PRECURSOR-PROTEIN-METABOLIC-PROCESS	GO-0042982	5	-0.313635	-0.654672	0.919762	1.000000	1.000
370	REACTOME-SIGNALING-BY-RECEPTOR-TYROSINE-KINASES	R-RNO-9006934	26	-0.208386	-0.655216	0.913753	1.000000	1.000
371	GOBP-AMINO-ACID-TRANSPORT	GO-0006865	6	-0.297865	-0.656011	0.882192	1.000000	1.000
372	GOBP-NEGATIVE-REGULATION-OF-TRANSPORT	GO-0051051	13	-0.243735	-0.658247	0.891551	1.000000	1.000
373	GOBP-CELLULAR-COMPONENT-DISASSEMBLY	GO-0022411	6	-0.304863	-0.659169	0.897210	1.000000	1.000
374	HALLMARK-ALLOGRAFT-REJECTION	M950	7	-0.287153	-0.662770	0.866571	1.000000	1.000
375	GOBP-INTRACELLULAR-RECEPTOR-SIGNALING-PATHWAY	GO-0030522	5	-0.319670	-0.663450	0.907378	1.000000	1.000
376	REACTOME-TRANSCRIPTIONAL-REGULATION-BY_TP53	R-RNO-3700989	6	-0.305988	-0.665919	0.889685	1.000000	1.000
377	GOBP-CIRCADIEN-RHYTHM	GO-0007623	13	-0.242158	-0.669401	0.883605	1.000000	1.000
378	GOBP-BLOOD-VESSEL-MORPHOGENESIS	GO-0048514	14	-0.242010	-0.672604	0.875792	1.000000	1.000
379	GOBP-MULTI-ORGANISM-PROCESS	GO-0051704	16	-0.238143	-0.676448	0.885856	1.000000	1.000
380	GOBP-EPITHELIAL-CELL-DIFFERENTIATION	GO-0030855	7	-0.294644	-0.676880	0.867332	1.000000	1.000
381	REACTOME-G-ALPHA-J-SIGNALING-EVENTS	R-RNO-418594	18	-0.241829	-0.681996	0.867629	1.000000	1.000
382	GOBP-POSITIVE-REGULATION-OF-GENE-EXPRESSION	GO-0010628	16	-0.241829	-0.684043	0.875940	1.000000	1.000
383	GOBP-CHROMOSOME-ORGANIZATION	GO-0051276	6	-0.310535	-0.686257	0.882857	1.000000	1.000
384	GOBP-DEFENSE-RESPONSE-TO-OTHER-ORGANISM	GO-0098542	9	-0.282711	-0.689018	0.848728	1.000000	1.000

Continuation of Table S13

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
385	REACTOME_INTERFERON_SIGNALING	R-RNO-913531	6	-0.316956	-0.694171	0.862937	1.000000	1.000
386	GOBP_LOCOMOTORY_BEHAVIOR	GO-0007626	7	-0.313139	-0.695674	0.856738	1.000000	1.000
387	GOBP_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENT...	GO-0002761	8	-0.297615	-0.699103	0.840382	1.000000	1.000
388	REACTOME_SIGNALING_BY_NUCLEAR_RECEPTORS	R-RNO-9006931	8	-0.296105	-0.700032	0.847645	1.000000	1.000
389	REACTOME_ESR_MEDIATED_SIGNALING	R-RNO-8939211	8	-0.296105	-0.703331	0.850283	1.000000	1.000
390	REACTOME_SIGNALING_BY_GPCR	R-RNO-372790	22	-0.233039	-0.705576	0.849169	1.000000	1.000
391	GOBP_POSITIVE_REGULATION_OF_TRANSMEMBRANE_TRAN...	GO-0034764	7	-0.305749	-0.705832	0.833563	1.000000	1.000
392	GOBP_HOMEOSTASIS_OF_NUMBER_OF_CELLS	GO-0048872	5	-0.346055	-0.706306	0.882436	1.000000	1.000
393	GOBP_POSITIVE_REGULATION_OF_CELL_DEATH	GO-0010942	19	-0.237071	-0.706332	0.828125	1.000000	1.000
394	GOBP_FATTY_ACID_TRANSPORT	GO-0015908	6	-0.322993	-0.710433	0.835425	1.000000	1.000
395	GOBP_CELL_POPULATION_PROLIFERATION	GO-0008283	31	-0.217964	-0.710488	0.834313	1.000000	1.000
396	GOBP_POSITIVE_REGULATION_OF_CATION_TRANSMEMBRAN...	GO-1904064	5	-0.345956	-0.710602	0.853727	1.000000	1.000
397	GOBP_NUCLEOBASE_CONTAINING_SMALL_MOLECULE_META...	GO-0055086	6	-0.327393	-0.714940	0.829167	1.000000	1.000
398	GOBP_POSITIVE_REGULATION_OF_PHOSPHORUS_METABOL...	GO-0010562	24	-0.231216	-0.716746	0.849882	1.000000	1.000
399	GOBP_REGULATION_OF_MUSCLE_CELL_DIFFERENTIATION	GO-0051147	6	-0.333756	-0.717497	0.842486	1.000000	1.000
400	GOBP_NEGATIVE_REGULATION_OF_CELL_DEVELOPMENT	GO-0010721	6	-0.330506	-0.719270	0.835674	1.000000	1.000
401	GOBP_REGULATION_OF_MULTICELLULAR_ORGANISMAL_DE...	GO-2000026	31	-0.227293	-0.722435	0.830080	1.000000	1.000
402	GOBP_POSITIVE_REGULATION_OF_HYDROLASE_ACTIVITY	GO-0051345	16	-0.255473	-0.724038	0.820859	1.000000	1.000
403	GOBP_CHROMATIN_ORGANIZATION	GO-0006325	5	-0.353719	-0.725093	0.815138	1.000000	1.000
404	GOBP_GROWTH	GO-0040007	14	-0.259608	-0.726812	0.822194	1.000000	1.000
405	GOBP_CELL_CELL_ADHESION	GO-0098609	14	-0.263346	-0.730242	0.824691	1.000000	1.000
406	GOBP_POSITIVE_REGULATION_OF_CELLULAR_COMPONENT...	GO-0051130	24	-0.238189	-0.730897	0.817647	1.000000	1.000
407	GOBP_REGULATION_OF_GTPASE_ACTIVITY	GO-0043087	5	-0.348025	-0.731125	0.839763	1.000000	1.000
408	GOBP_RESPONSE_TO_CYTOKINE	GO-0034097	23	-0.239776	-0.731706	0.825581	1.000000	1.000
409	GOBP_NEGATIVE_REGULATION_OF_TRANSFERASE_ACTIVITY	GO-0051348	5	-0.361759	-0.733221	0.833581	1.000000	1.000
410	GOBP_ACTIVATION_OF_IMMUNE_RESPONSE	GO-0002253	5	-0.354224	-0.733408	0.819648	1.000000	1.000
411	GOBP_NEGATIVE_REGULATION_OF_PEPTIDASE_ACTIVITY	GO-0010466	6	-0.340694	-0.734390	0.833568	1.000000	1.000
412	REACTOME_SIGNALING_BY_NTRKS	R-RNO-166520	18	-0.248057	-0.739366	0.813107	1.000000	1.000
413	GOBP_SECRETION	GO-0046903	24	-0.243405	-0.742188	0.820574	1.000000	1.000
414	GOBP_NEGATIVE_REGULATION_OF_MULTICELLULAR_ORGA...	GO-0051241	15	-0.268702	-0.747280	0.808132	1.000000	1.000
415	GOBP_NEGATIVE_REGULATION_OF_KINASE_ACTIVITY	GO-0033673	5	-0.361759	-0.749036	0.812772	1.000000	1.000
416	REACTOME_DEATH_RECEPTOR_SIGNALING	R-RNO-73887	5	-0.359991	-0.750335	0.823034	1.000000	1.000
417	GOBP_LOCOMOTION	GO-0040011	31	-0.234846	-0.751881	0.796275	1.000000	1.000
418	GOBP_RESPONSE_TO_OXYGEN_LEVELS	GO-0070482	8	-0.314410	-0.754234	0.766074	1.000000	1.000
419	GOBP_POSITIVE_REGULATION_OF_MOLECULAR_FUNCTION	GO-0044093	38	-0.231138	-0.754824	0.828442	1.000000	1.000
420	GOBP_REGULATION_OF_HEMOPOIESIS	GO-1903706	10	-0.298894	-0.755286	0.783290	1.000000	1.000
421	GOBP_MUSCLE_ADAPTATION	GO-0043500	5	-0.368963	-0.755514	0.810198	1.000000	1.000
422	GOBP_DEVELOPMENTAL_GROWTH	GO-0048589	10	-0.300573	-0.756066	0.773263	1.000000	1.000
423	GOBP_NEGATIVE_REGULATION_OF_TRANSMEMBRANE_TRAN...	GO-0034763	6	-0.349388	-0.759644	0.776824	1.000000	1.000
424	GOBP_RESPONSE_TO_NERVE_GROWTH_FACTOR	GO-1990089	7	-0.329110	-0.760620	0.778976	1.000000	1.000
425	GOBP_REGULATION_OF_GROWTH	GO-0040008	13	-0.276903	-0.761201	0.789541	1.000000	1.000
426	GOBP_NEGATIVE_REGULATION_OF_NEURON_DEATH	GO-1901215	11	-0.295422	-0.763768	0.804491	1.000000	1.000
427	GOBP_REGULATION_OF_MUSCLE_ADAPTATION	GO-0043502	5	-0.368963	-0.764256	0.793353	1.000000	1.000

Continuation of Table S13

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
428 GOBP-TUBE-DEVELOPMENT	GO-0035295	18	-0.254150	-0.765548	0.774074	1.000000	1.000
429 GOBP-POSITIVE-REGULATION-OF-TRANSFERASE-ACTIVITY	GO-0051347	20	-0.255747	-0.765790	0.796569	1.000000	1.000
430 GOBP-PROTEIN-PHOSPHORYLATION	GO-0006468	34	-0.237587	-0.767455	0.782066	1.000000	1.000
431 GOBP-REGULATION-OF-CELL-DEATH	GO-0010941	34	-0.232024	-0.767660	0.783784	1.000000	1.000
432 GOBP-CYTOKINE-MEDIATED-SIGNALING-PATHWAY	GO-0019221	16	-0.267389	-0.772549	0.771887	1.000000	1.000
433 GOBP-MITOCHONDRION-ORGANIZATION	GO-0007005	7	-0.340541	-0.774785	0.769126	1.000000	1.000
434 GOBP-NEGATIVE-REGULATION-OF-LOCOMOTION	GO-0040013	5	-0.388531	-0.775937	0.777937	1.000000	1.000
435 GOBP-REGULATION-OF-NEURON-PROJECTION-DEVELOPMENT	GO-0010975	16	-0.273408	-0.776840	0.781595	1.000000	1.000
436 GOBP-REGULATION-OF-HYDROLASE-ACTIVITY	GO-0051336	22	-0.259044	-0.779545	0.760241	1.000000	1.000
437 REACTOME-CA-DEPENDENT-EVENTS	R-RNO-111996	8	-0.328887	-0.7782301	0.761714	1.000000	1.000
438 GOBP-REGULATION-OF-PROTEIN-LOCALIZATION-TO-CELL...	GO-1904375	6	-0.357154	-0.783576	0.736990	1.000000	1.000
439 GOBP-NEGATIVE-REGULATION-OF-CELL-DEATH	GO-0060548	22	-0.259547	-0.784844	0.774818	1.000000	1.000
440 GOBP-G-PROTEIN-COUPLED-RECEPTOR-SIGNALING-PATHWAY	GO-0007186	18	-0.272829	-0.787235	0.746377	1.000000	1.000
441 GOBP-CELL-GROWTH	GO-0016049	10	-0.303582	-0.788422	0.735799	1.000000	1.000
442 GOBP-TRANSMEMBRANE-RECEPTOR-PROTEIN-TYROSINE-K...	GO-0007169	19	-0.268968	-0.790665	0.745476	1.000000	1.000
443 GOBP-CELLULAR-RESPONSE-TO-EXTRACELLULAR-STIMULUS	GO-0031668	8	-0.333081	-0.791764	0.721622	1.000000	1.000
444 GOBP-NEGATIVE-REGULATION-OF-ION-TRANSPORT	GO-0043271	11	-0.306981	-0.794594	0.728232	1.000000	1.000
445 GOBP-RESPONSE-TO-EXTRACELLULAR-STIMULUS	GO-0009991	13	-0.295187	-0.799165	0.750000	1.000000	1.000
446 GOBP-CHEMICAL-HOMEOSTASIS	GO-0048878	23	-0.259722	-0.799658	0.736780	1.000000	1.000
447 GOBP-REGULATION-OF-LONG-TERM-SYNAPTIC-POTENTIAL...	GO-1900271	6	-0.365355	-0.801993	0.727532	1.000000	1.000
448 GOBP-PROTEIN-CONTAINING-COMPLEX-SUBUNIT-ORGANIL...	GO-0043933	14	-0.295101	-0.802851	0.742058	1.000000	1.000
449 GOBP-REGULATION-OF-MAP-KINASE-ACTIVITY	GO-0043405	9	-0.321961	-0.806139	0.719321	1.000000	1.000
450 GOBP-REGULATION-OF-ANATOMICAL-STRUCTURE-MORPHO...	GO-0022603	17	-0.285184	-0.808593	0.720960	1.000000	1.000
451 GOBP-RESPONSE-TO-METAL-ION	GO-0010038	15	-0.290037	-0.808813	0.724816	1.000000	1.000
452 GOBP-REGULATION-OF-DEVELOPMENTAL-GROWTH	GO-0048638	9	-0.321767	-0.809462	0.722444	1.000000	1.000
453 REACTOME-DISEASES-OF-SIGNAL-TRANSDUCTION-BY-GR...	R-HSA-5663202	12	-0.306526	-0.810784	0.738095	1.000000	1.000
454 GOBP-RESPONSE-TO-ETHANOL	GO-0045471	5	-0.393956	-0.811577	0.737991	1.000000	1.000
455 REACTOME-CELL-CYCLE	R-RNO-1640170	6	-0.369360	-0.812255	0.723435	1.000000	1.000
456 GOBP-SENSORY-PERCEPTION-OF-PAIN	GO-0019233	5	-0.397003	-0.812557	0.746627	1.000000	1.000
457 GOBP-CELLULAR-CARBOHYDRATE-METABOLIC-PROCESS	GO-0044262	5	-0.397722	-0.814037	0.734421	1.000000	1.000
458 GOBP-PERIPHERAL-NERVOUS-SYSTEM-DEVELOPMENT	GO-0007422	9	-0.325904	-0.816645	0.704453	1.000000	1.000
459 GOBP-PROTEIN-COMPLEX-OLIGOMERIZATION	GO-0051259	6	-0.377942	-0.818744	0.729844	1.000000	1.000
460 GOBP-RESPONSE-TO-ACID-CHEMICAL	GO-0001101	6	-0.379902	-0.820568	0.719149	1.000000	1.000
461 GOBP-CELLULAR-RESPONSE-TO-INORGANIC-SUBSTANCE	GO-0071241	11	-0.321863	-0.820611	0.727632	1.000000	1.000
462 GOBP-NEURON-APOPTOTIC-PROCESS	GO-0051402	12	-0.311935	-0.828918	0.684685	1.000000	1.000
463 GOBP-REGULATION-OF-LEUKOCYTE-DIFFERENTIATION	GO-1902105	9	-0.334481	-0.830614	0.679947	1.000000	1.000
464 GOBP-ANIMAL-ORGAN-MORPHOGENESIS	GO-0009887	12	-0.314526	-0.831447	0.701665	1.000000	1.000
465 GOBP-REGULATION-OF-MUSCLE-SYSTEM-PROCESS	GO-0090257	8	-0.356456	-0.837017	0.714479	1.000000	1.000
466 HALLMARK_UV_RESPONSE_UP	M5941	5	-0.403116	-0.837776	0.705968	1.000000	1.000
467 GOBP-DICARBOXYLIC-ACID-TRANSPORT	GO-0006835	5	-0.410381	-0.839722	0.680973	1.000000	1.000
468 GOBP-DENDRITE-DEVELOPMENT	GO-0016358	9	-0.337469	-0.842253	0.688568	1.000000	1.000
469 GOBP-ACIDIC-AMINO-ACID-TRANSPORT	GO-0015800	5	-0.410381	-0.846052	0.677892	1.000000	1.000
470 GOBP-NEGATIVE-REGULATION-OF-NERVOUS-SYSTEM-DEV...	GO-0051961	5	-0.408714	-0.847596	0.693114	1.000000	1.000

Continuation of Table S13

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
471	HALLMARK_KRAS_SIGNALING_UP	M5953	6	-0.395184	-0.852253	0.669916	1.000000	1.000
472	GOBP_ADENYLATE_CYCLASE_MODULATING_G_PROTEIN_CO...	GO-0007188	11	-0.328870	-0.853764	0.667110	1.000000	1.000
473	GOBP_REGULATION_OF_INTRACELLULAR_SIGNAL_TRANSD...	GO-1902531	21	-0.285087	-0.853801	0.659498	1.000000	1.000
474	GOBP_ENZYME_LINKED_RECEPTOR_PROTEIN_SIGNALING...	GO-0007167	24	-0.275870	-0.859539	0.659880	1.000000	1.000
475	GOBP_WOUND_HEALING	GO-0042060	13	-0.315768	-0.861277	0.630295	1.000000	1.000
476	GOBP_NEURON_DEATH	GO-0070997	18	-0.297878	-0.861295	0.665874	1.000000	1.000
477	REACTOME_CELL_CYCLE_MITOTIC	R-RNO-69278	5	-0.416731	-0.861429	0.672059	1.000000	1.000
478	GOBP_MONOCARBOXYLIC_ACID_TRANSPORT	GO-0015718	5	-0.410381	-0.861549	0.660287	1.000000	1.000
479	GOBP_POLYSACCHARIDE_METABOLIC_PROCESS	GO-0005976	5	-0.421869	-0.862686	0.689655	1.000000	1.000
480	GOBP_NEURON_DEVELOPMENT	GO-0048666	33	-0.261170	-0.864704	0.661346	1.000000	1.000
481	REACTOME_LEISHMANIA_INFECTION	R-HSA-9658195	10	-0.342506	-0.865841	0.643709	1.000000	1.000
482	GOBP_REGULATION_OF_ION_TRANSPORT	GO-0043269	36	-0.375941	-0.869786	0.652174	1.000000	1.000
483	GOBP_PROTEIN_LOCALIZATION_TO_PLASMA_MEMBRANE	GO-0072659	7	-0.375941	-0.871323	0.645658	1.000000	1.000
484	GOBP_PEPTIDYL_AMINO_ACID_MODIFICATION	GO-0018193	22	-0.289376	-0.871391	0.654126	1.000000	1.000
485	GOBP_CELLULAR_RESPONSE_TO_REACTIVE_OXYGEN_SPECIES	GO-0034614	7	-0.376777	-0.872004	0.650815	1.000000	1.000
486	GOBP_POSITIVE_REGULATION_OF_LONG_TERM_SYNAPTIC...	GO-1900273	5	-0.431655	-0.873566	0.654179	1.000000	1.000
487	GOBP_AXON_DEVELOPMENT	GO-0061564	18	-0.291397	-0.874527	0.642363	1.000000	1.000
488	GOBP_CELL_JUNCTION_ASSEMBLY	GO-0034329	8	-0.372319	-0.875121	0.642663	1.000000	1.000
489	REACTOME_G_ALPHA_Q_SIGNALING_EVENTS	R-RNO-416476	6	-0.404208	-0.877174	0.654232	1.000000	1.000
490	GOBP_REGULATION_OF_CATABOLIC_PROCESS	GO-0009894	13	-0.321200	-0.878636	0.622930	1.000000	1.000
491	GOBP_COAGULATION	GO-0050817	8	-0.370974	-0.879443	0.629921	1.000000	1.000
492	GOBP_IMMUNE_RESPONSE_REGULATING_SIGNALING_PATHWAY	GO-000276	8	-0.372319	-0.881626	0.646492	1.000000	1.000
493	GOBP_CELLULAR_RESPONSE_TO_CHEMICAL_STRESS	GO-0062197	7	-0.376777	-0.882384	0.635117	1.000000	1.000
494	GOBP_NEGATIVE_REGULATION_OF_PROTEIN_METABOLIC...	GO-0051248	20	-0.297064	-0.882813	0.649940	1.000000	1.000
495	GOBP_NEGATIVE_REGULATION_OF_NEURON_APOPTOTIC_P...	GO-0043524	8	-0.367909	-0.884537	0.636115	1.000000	1.000
496	GOBP_RESPONSE_TO_OXIDATIVE_STRESS	GO-0006979	8	-0.372121	-0.885925	0.620548	1.000000	1.000
497	GOBP_REGULATION_OF_LYMPHOCYTE_ACTIVATION	GO-0051249	5	-0.431955	-0.891683	0.660322	1.000000	1.000
498	GOBP_FC_RECEPTOR_SIGNALING_PATHWAY	GO-0038093	8	-0.372394	-0.892107	0.596974	1.000000	1.000
499	GOBP_RESPONSE_TO_REACTIVE_OXYGEN_SPECIES	GO-0000302	8	-0.372121	-0.895040	0.599469	1.000000	1.000
500	REACTOME_CELLULAR_RESPONSES_TO_EXTERNAL_STIMULI	R-RNO-8953897	12	-0.344571	-0.896131	0.618090	1.000000	1.000
501	REACTOME_SIGNALING_BY_INTERLEUKINS	R-RNO-449147	15	-0.315050	-0.897001	0.606516	1.000000	1.000
502	HALLMARK_HYPOXIA	M5891	5	-0.437716	-0.897564	0.624460	1.000000	1.000
503	REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM	R-RNO-1280215	21	-0.296233	-0.898123	0.595849	1.000000	1.000
504	GOBP_REGULATION_OF_SYNAPTIC_TRANSMISSION_GLUTA...	GO-0051966	12	-0.338009	-0.900185	0.600249	1.000000	1.000
505	GOBP_CELL_PROJECTION_ORGANIZATION	GO-0030030	34	-0.275215	-0.904872	0.610660	1.000000	1.000
506	GOBP_POSITIVE_REGULATION_OF_GROWTH	GO-0045927	9	-0.369929	-0.906332	0.603518	1.000000	1.000
507	GOBP_POSITIVE_REGULATION_OF_PROTEIN_METABOLIC...	GO-0051247	28	-0.285922	-0.909707	0.603995	1.000000	1.000
508	GOBP_MEMBRANE_ORGANIZATION	GO-0061024	12	-0.324015	-0.912819	0.583867	1.000000	1.000
509	GOBP_MUSCLE_CELL_DIFFERENTIATION	GO-0042692	10	-0.359719	-0.914700	0.580563	1.000000	1.000
510	REACTOME_INNATE_IMMUNE_SYSTEM	R-RNO-168249	16	-0.340150	-0.916022	0.588235	1.000000	1.000
511	GOBP_CELLULAR_RESPONSE_TO_STARVATION	GO-0009267	5	-0.445614	-0.917221	0.606607	1.000000	1.000
512	GOBP_POSITIVE_REGULATION_OF_AXONOGENESIS	GO-0050772	5	-0.442360	-0.918098	0.589080	1.000000	1.000
513	GOBP_FC_EPSILON_RECEPTOR_SIGNALING_PATHWAY	GO-0038095	7	-0.404406	-0.919451	0.610335	1.000000	1.000

Continuation of Table S13

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
514	GOBP-RESPONSE_TO_STARVATION	5	-0.445614	-0.920998	0.588674	1.000000	1.000
515	GOBP-POSITIVE-REGULATION_OF_CATALYTIC_ACTIVITY	30	-0.288219	-0.921532	0.581158	1.000000	1.000
516	GOBP-REGULATION_OF_CELLULAR_LOCALIZATION	17	-0.319435	-0.922197	0.585784	1.000000	1.000
517	REACTOME_FC_EPSILON_RECEPTOR_FCHRL_SIGNALING	7	-0.404406	-0.923777	0.576056	1.000000	1.000
518	GOBP-BIOLOGICAL-PROCESS_INVOLVED_IN_SYMBIOTIC....	11	-0.358994	-0.928067	0.572005	1.000000	1.000
519	GOBP-DEVELOPMENTAL_CELL_GROWTH	5	-0.449049	-0.930773	0.568513	1.000000	1.000
520	GOBP-REGULATION_OF_CELL_DIFFERENTIATION	36	-0.287615	-0.932209	0.588432	1.000000	1.000
521	GOBP-REGULATION_OF_CYSSTEINE_TYPE_ENDOPEPTIDASE...	9	-0.376841	-0.932613	0.548139	1.000000	1.000
522	GOBP-POSITIVE-REGULATION_OF_DEVELOPMENTAL_GROWTH	8	-0.394318	-0.932422	0.572414	1.000000	1.000
523	GOBP-REGULATION_OF_ENDOCYTOSIS	6	-0.431767	-0.941092	0.541787	1.000000	1.000
524	REACTOME_GPCR_LIGAND_BINDING	8	-0.398844	-0.943625	0.549724	1.000000	1.000
525	GOBP-REGULATION_OF_RECEPTOR_MEDIATED_ENDOCYTOSIS	5	-0.457062	-0.943758	0.562942	1.000000	1.000
526	GOBP-NERVE_DEVELOPMENT	9	-0.383326	-0.944485	0.549587	1.000000	1.000
527	GOBP-ENDOMEMBRANE_SYSTEM_ORGANIZATION	6	-0.433298	-0.945618	0.565460	1.000000	1.000
528	GOBP-REGULATION_OF_CELL_DEVELOPMENT	15	-0.332473	-0.947404	0.543532	1.000000	1.000
529	GOBP-MACROMOLECULE_CATABOLIC_PROCESS	12	-0.359068	-0.949170	0.539052	1.000000	1.000
530	GOBP-POSITIVE-REGULATION_OF_CELL_GROWTH	6	-0.443117	-0.954214	0.532578	1.000000	1.000
531	GOBP-REGULATION_OF_CIRCADIAN_RHYTHM	7	-0.422127	-0.954991	0.546593	1.000000	1.000
532	GOBP-GLIAL-CELL_DIFFERENTIATION	10	-0.379435	-0.955364	0.541724	1.000000	1.000
533	GOBP-BIOLOGICAL_ADHESION	19	-0.322720	-0.956929	0.519573	1.000000	1.000
534	GOBP-POSITIVE-REGULATION_OF_PROTEOLYSIS	8	-0.400377	-0.960244	0.512855	1.000000	1.000
535	GOBP-RESPONSE_TO_WOUNDING	15	-0.347811	-0.963425	0.517767	1.000000	1.000
536	GOBP-CELLULAR_MACROMOLECULE_LOCALIZATION	21	-0.318958	-0.963815	0.523077	1.000000	1.000
537	GOBP-REGULATION_OF_BINDING	11	-0.375072	-0.970026	0.501323	1.000000	1.000
538	GOBP-NEURON_PROJECTION_GUIDANCE	9	-0.394243	-0.970742	0.529491	1.000000	1.000
539	GOBP-REGULATION_OF_SYNAPSE_STRUCTURE_OR_ACTIVITY	11	-0.375352	-0.972750	0.504551	1.000000	1.000
540	GOBP-NEGATIVE-REGULATION_OF_INTRACELLULAR_SIGN...	7	-0.422518	-0.974353	0.504132	1.000000	1.000
541	GOBP-REGULATION_OF_MAPK_CASCADE	13	-0.360615	-0.975328	0.492366	1.000000	1.000
542	GOBP-REGULATION_OF_NERVOUS_SYSTEM_DEVELOPMENT	15	-0.347593	-0.976842	0.508642	1.000000	1.000
543	GOBP-INNATE_IMMUNE_RESPONSE	7	-0.430172	-0.977855	0.509642	1.000000	1.000
544	GOBP-NEURON_DIFFERENTIATION	36	-0.296160	-0.978842	0.516968	1.000000	1.000
545	GOBP-POSITIVE-REGULATION_OF_MAPK_CASCADE	9	-0.400377	-0.980287	0.503285	1.000000	1.000
546	GOBP-GENERATION_OF_PRECURSOR_METABOLITES_AND_E...	5	-0.478377	-0.984062	0.509299	1.000000	1.000
547	GOBP-REGULATION_OF_CELL_PROJECTION_ORGANIZATION	20	-0.335810	-0.989216	0.497549	1.000000	1.000
548	GOBP-MULTICELLULAR_ORGANISMAL_RESPONSE_TO_STRESS	5	-0.484750	-0.992234	0.469208	1.000000	1.000
549	GOBP-TAXIS	14	-0.359202	-0.995285	0.477387	1.000000	1.000
550	GOBP-LIPID_EXPORT_FROM_CELL	5	-0.488924	-1.002163	0.482014	1.000000	1.000
551	GOBP-CELLULAR_COMPONENT_MORPHOGENESIS	24	-0.321972	-1.003070	0.464576	1.000000	1.000
552	GOBP-CELL_PART_MORPHOGENESIS	24	-0.321972	-1.005885	0.468160	1.000000	1.000
553	GOBP-MUSCLE_SYSTEM_PROCESS	9	-0.395253	-1.007126	0.457143	1.000000	1.000
554	REACTOME_CIRCADIAN_CLOCK	5	-0.492923	-1.007630	0.476401	1.000000	1.000
555	GOBP-POSITIVE-REGULATION_OF_CYSSTEINE_TYPE_ENDO...	7	-0.439456	-1.009106	0.492517	1.000000	1.000
556	GOBP-CELL_MORPHOGENESIS	24	-0.321972	-1.010261	0.465476	1.000000	1.000

Continuation of Table S13

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
557	GOBP-EMBRYONIC-MORPHOGENESIS	GO-0048598	6	-0.455930	-1.010781	0.452211	1.000000	1.000
558	HALLMARK-APOPTOSIS	M5902	6	-0.467373	-1.011378	0.464849	1.000000	1.000
559	GOBP-REGULATION-OF-TRANSPORT	GO-0051049	44	-0.308809	-1.016790	0.448889	1.000000	1.000
560	GOBP-REGULATION-OF-POSTSYNAPSE-ORGANIZATION	GO-0099175	6	-0.460119	-1.017007	0.456311	1.000000	1.000
561	GOBP-SMALL-GTPASE-MEDIATED-SIGNAL-TRANSDUCTION	GO-0007264	8	-0.436041	-1.018066	0.469880	1.000000	1.000
562	GOBP-REGULATION-OF-NEUROGENESIS	GO-0050767	14	-0.373634	-1.020277	0.443742	1.000000	1.000
563	GOBP-DENDRITIC-SPINE-MORPHOGENESIS	GO-0060997	5	-0.497036	-1.021181	0.453102	1.000000	1.000
564	GOBP-CELL-MORPHOGENESIS-INVOLVED-IN-DIFFERENTI...	GO-0000904	21	-0.346012	-1.024785	0.452607	1.000000	1.000
565	REACTOME-TRAFFICKING-OF-GLUR2-CONTAINING-AMPA...	R-RNO-416993	8	-0.429855	-1.025037	0.470509	1.000000	1.000
566	GOBP-COGNITION	GO-0050890	28	-0.322019	-1.025425	0.438279	1.000000	1.000
567	GOBP-POSITIVE-REGULATION-OF-PEPTIDASE-ACTIVITY	GO-0010952	7	-0.439456	-1.025468	0.449376	1.000000	1.000
568	GOBP-CELL-MORPHOGENESIS-INVOLVED-IN-NEURON-DIF...	GO-0048667	21	-0.346012	-1.025485	0.438107	1.000000	1.000
569	GOBP-DENDRITIC-SPINE-DEVELOPMENT	GO-0060996	6	-0.469296	-1.028298	0.422438	1.000000	1.000
570	GOBP-DENDRITE-MORPHOGENESIS	GO-0048813	6	-0.470610	-1.029367	0.443526	1.000000	1.000
571	GOBP-CELLULAR-HOMEOSTASIS	GO-0019725	18	-0.357835	-1.029437	0.438788	1.000000	1.000
572	GOBP-NEUROGENESIS	GO-0022008	40	-0.313680	-1.036672	0.415919	1.000000	1.000
573	GOBP-REGULATION-OF-PROTEOLYSIS	GO-0030162	12	-0.391617	-1.037270	0.443456	1.000000	1.000
574	GOBP-REGULATION-OF-PROTEIN-LOCALIZATION-TO-MEM...	GO-1905475	7	-0.446443	-1.039867	0.428571	1.000000	1.000
575	GOBP-POSITIVE-REGULATION-OF-PEPTIDYL-TYROSINE...	GO-0050731	8	-0.439800	-1.041256	0.409029	1.000000	1.000
576	GOBP-MEMBRANE-PROTEIN-PROTEOLYSIS	GO-0033619	6	-0.472809	-1.041374	0.425626	1.000000	1.000
577	GOBP-PROTEOLYSIS	GO-0006508	17	-0.357102	-1.046264	0.415648	1.000000	1.000
578	GOBP-REGULATION-OF-TRANSMEMBRANE-TRANSPORT	GO-0034762	23	-0.340909	-1.051141	0.413998	1.000000	1.000
579	GOBP-BEHAVIOR	GO-0007610	32	-0.328696	-1.053493	0.420118	1.000000	1.000
580	GOBP-POSITIVE-REGULATION-OF-NERVOUS-SYSTEM-DEV...	GO-0051962	12	-0.406712	-1.056167	0.404732	1.000000	1.000
581	GOBP-G-PROTEIN-COUPLED-GLUTAMATE-RECEPTOR-SIGN...	GO-0007216	8	-0.454723	-1.060345	0.395561	1.000000	1.000
582	REACTOME-ONCOGENIC-MAPK-SIGNALING	R-HSA-6802967	5	-0.515237	-1.063095	0.400281	1.000000	1.000
583	GOBP-STRIATED-MUSCLE-CELL-DIFFERENTIATION	GO-0051146	9	-0.439544	-1.063622	0.378729	1.000000	1.000
584	GOBP-ENDOCRINE-SYSTEM-DEVELOPMENT	GO-0035270	6	-0.483186	-1.064178	0.406685	1.000000	1.000
585	GOBP-REGULATION-OF-NEURONAL-SYNAPTIC-PLASTICITY	GO-0048168	7	-0.477437	-1.072065	0.391365	1.000000	1.000
586	GOBP-NUCLEAR-TRANSPORT	GO-0051169	5	-0.512201	-1.073673	0.387697	1.000000	1.000
587	GOBP-POSITIVE-REGULATION-OF-NEUROGENESIS	GO-0050769	12	-0.406712	-1.074596	0.375979	1.000000	1.000
588	GOBP-CELLULAR-COMPONENT-MAINTENANCE	GO-0043954	5	-0.522502	-1.080046	0.374456	1.000000	1.000
589	GOBP-POSITIVE-REGULATION-OF-CELL-DEVELOPMENT	GO-0010720	12	-0.406712	-1.080283	0.371681	1.000000	1.000
590	GOBP-NEGATIVE-REGULATION-OF-CELLULAR-COMPONENT...	GO-0051129	11	-0.411096	-1.082345	0.374194	1.000000	1.000
591	GOBP-POSITIVE-REGULATION-OF-CELLULAR-COMPONENT...	GO-0044089	9	-0.436868	-1.083633	0.386179	1.000000	1.000
592	REACTOME-MAPK-TARGETS-NUCLEAR-EVENTS-MEDIATED...	R-HSA-450282	5	-0.530120	-1.084974	0.364943	1.000000	1.000
593	GOBP-AGING	GO-0007568	13	-0.403173	-1.087372	0.368758	1.000000	1.000
594	GOBP-POSITIVE-REGULATION-OF-INTRACELLULAR-SIGN...	GO-1902533	14	-0.395490	-1.095511	0.340452	1.000000	1.000
595	GOBP-REGULATION-OF-PEPTIDASE-ACTIVITY	GO-0052547	10	-0.441739	-1.101688	0.356307	1.000000	1.000
596	GOBP-SENSORY-PERCEPTION	GO-0007600	9	-0.452981	-1.111169	0.349933	1.000000	1.000
597	GOBP-ION-HOMEOSTASIS	GO-0050801	16	-0.390991	-1.112541	0.341404	1.000000	1.000
598	GOBP-SYNAPTIC-TRANSMISSION-GLUTAMATERGIC	GO-0035249	13	-0.410925	-1.112704	0.341837	1.000000	1.000
599	GOBP-REGULATION-OF-PEPTIDYL-TYROSINE-PHOSPHORY...	GO-0050730	9	-0.462756	-1.122932	0.316778	1.000000	1.000

Continuation of Table S13

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
600	REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATION	R-RNO-597592	7	-0.496854	-1.123051	0.334752	1.000000
601	GOBP_ADENYLATE_CYCLASE_INHIBITING_G_PROTEIN_CO...	GO-0007193	9	-0.453729	-1.126028	0.335142	1.000000
602	GOBP_REGULATION_OF_SIGNALING_RECEPTOR_ACTIVITY	GO-0010469	14	-0.416229	-1.126545	0.320203	1.000000
603	GOBP_CENTRAL_NERVOUS_SYSTEM_DEVELOPMENT	GO-0007417	26	-0.361100	-1.127087	0.304551	1.000000
604	GOBP_POSITIVE_REGULATION_OF_GLIOGENESIS	GO-0014015	5	-0.552516	-1.127870	0.306428	1.000000
605	GOBP_REGULATION_OF_METAL_ION_TRANSPORT	GO-0010959	6	-0.511182	-1.129126	0.315049	1.000000
606	GOBP_SECOND_MESSENGER_MEDIATED_SIGNALING	GO-0007196	16	-0.401719	-1.132291	0.327500	1.000000
607	REACTOME_NERVOUS_SYSTEM_DEVELOPMENT	R-RNO-9675108	15	-0.401931	-1.138058	0.299007	1.000000
608	GOBP_POSITIVE_REGULATION_OF_BINDING	GO-0051099	6	-0.515832	-1.138606	0.314706	1.000000
609	REACTOME_CELLULAR_SENESCENCE	R-RNO-2559583	6	-0.524390	-1.139635	0.333809	1.000000
610	GOBP_REGULATION_OF_GLIOGENESIS	GO-0014013	5	-0.552516	-1.144229	0.285075	1.000000
611	REACTOME_SENESCENCE_ASSOCIATED_SECRETORY_PHENO...	R-RNO-2559582	6	-0.524390	-1.146157	0.281831	1.000000
612	GOBP_NEGATIVE_REGULATION_OF_CATABOLIC_PROCESS	GO-0009895	8	-0.481073	-1.149288	0.306383	1.000000
613	REACTOME_TRAFFICKING_OF_AMPA_RECEPTORS	R-RNO-399719	11	-0.451166	-1.149474	0.295699	1.000000
614	REACTOME_INTERLEUKIN_17_SIGNALING	R-RNO-448424	6	-0.524390	-1.152525	0.290323	1.000000
615	GOBP_GLIOGENESIS	GO-0042063	12	-0.446941	-1.160225	0.269821	1.000000
616	GOBP_REGULATION_OF_CELLULAR_COMPONENT_BIOGENESIS	GO-0044087	10	-0.459190	-1.161174	0.296296	1.000000
617	GOBP_DEVELOPMENTAL_MATURATION	GO-0021700	5	-0.578313	-1.170570	0.284875	1.000000
618	GOBP_RAS_PROTEIN_SIGNAL_TRANSDUCTION	GO-0007265	5	-0.568525	-1.174403	0.265625	1.000000
619	GOBP_FOREBRAIN_DEVELOPMENT	GO-0030900	9	-0.478198	-1.175461	0.277778	1.000000
620	GOBP_REGULATION_OF_SYSTEM_PROCESS	GO-0044057	18	-0.414025	-1.176605	0.273515	1.000000
621	REACTOME_CLASS_C_3_METABOTROPIC_GLUTAMATE_PHER...	R-RNO-420499	7	-0.527205	-1.181464	0.258250	1.000000
622	GOBP_ORGANONITROGEN_COMPOUND_CATABOLIC_PROCESS	GO-1901565	9	-0.484991	-1.188145	0.265823	1.000000
623	GOBP_REGULATION_OF_PROTEIN_TYROSINE_KINASE_ACT...	GO-0061097	5	-0.578313	-1.191033	0.244666	1.000000
624	REACTOME_MYD88_INDEPENDENT_TLR4_CASCADE	R-RNO-166166	8	-0.500000	-1.193399	0.251001	1.000000
625	GOBP_POSITIVE_REGULATION_OF_PROTEIN_TYROSINE_K...	GO-0061098	5	-0.578313	-1.193493	0.228814	1.000000
626	GOBP_PROTEIN_LOCALIZATION_TO_CELL_PERIPHERY	GO-1990778	12	-0.454596	-1.197825	0.246173	1.000000
627	REACTOME_DEVELOPMENTAL_BIOLOGY	R-RNO-1266738	23	-0.392781	-1.199451	0.243013	1.000000
628	REACTOME_TOLL_LIKE_RECEPTOR_9_TLR9_CASCADE	R-RNO-168138	8	-0.500000	-1.199451	0.242991	1.000000
629	GOBP_METAL_ION_HOMEOSTASIS	GO-0055065	14	-0.438007	-1.200006	0.241730	1.000000
630	GOBP_CELLULAR_ION_HOMEOSTASIS	GO-0006873	14	-0.430252	-1.200130	0.234414	1.000000
631	REACTOME_TOLL_LIKE_RECEPTOR_CASCADES	R-RNO-168898	8	-0.500000	-1.201143	0.261224	1.000000
632	GOBP_POSITIVE_REGULATION_OF_CELL_DIFFERENTIATION	GO-0045597	27	-0.383984	-1.201938	0.238754	1.000000
633	GOBP_TELENCEPHALON_DEVELOPMENT	GO-0021537	6	-0.547686	-1.202760	0.232295	1.000000
634	REACTOME_TOLL_LIKE_RECEPTOR_TLR1_TLR2_CASCADE	R-RNO-168179	8	-0.500000	-1.206976	0.209809	1.000000
635	GOBP_DIVALENT_INORGANIC_CATION_HOMEOSTASIS	GO-0072507	13	-0.454779	-1.210221	0.230089	1.000000
636	GOBP_REGULATION_OF_NERVOUS_SYSTEM_PROCESS	GO-0031644	8	-0.525000	-1.217776	0.216714	1.000000
637	GOBP_REGULATION_OF_CYTOSOLIC_CALCIIUM_ION_CONCE...	GO-0051480	13	-0.454779	-1.218932	0.224439	1.000000
638	GOBP_MYOTUBE_DIFFERENTIATION	GO-0014902	5	-0.600574	-1.220344	0.191176	1.000000
639	GOBP_ASSOCIATIVE_LEARNING	GO-0006306	7	-0.534403	-1.222552	0.209538	1.000000
640	GOBP_RESPONSE_TO_ABiotic_STIMULUS	GO-0009628	27	-0.390779	-1.223687	0.220554	1.000000
641	GOBP_RESPONSE_TO_UV	GO-0009411	5	-0.593740	-1.232479	0.194074	1.000000
642	GOBP_POSITIVE_REGULATION_OF_SIGNALING	GO-0023056	34	-0.381787	-1.237294	0.201835	1.000000

Continuation of Table S13

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
643	GOBP-POSITIVE-REGULATION_OF_SYNAPTIC-TRANSMISSION	GO-0050806	15	-0.446310	-1.243693	0.197270	1.000000	1.000
644	GOBP-REGULATION_OF_NEUROTRANSMITTER-RECEPTOR-A...	GO-0099601	13	-0.464089	-1.244266	0.198980	1.000000	1.000
645	GOBP-NERVOUS-SYSTEM-PROCESS	GO-0050877	38	-0.383299	-1.246184	0.170843	1.000000	1.000
646	GOBP-REGULATION_OF_CELL-SIZE	GO-0008361	5	-0.616342	-1.249027	0.193303	1.000000	1.000
647	GOBP-RESPONSE-TO-DRUG	GO-0042493	11	-0.483898	-1.254085	0.183448	1.000000	1.000
648	GOBP-PEPTIDYL-TYROSINE-MODIFICATION	GO-0018212	10	-0.491220	-1.260758	0.195187	1.000000	1.000
649	GOBP-CATION-TRANSPORT	GO-0006812	25	-0.405444	-1.262656	0.174323	1.000000	1.000
650	GOBP-POSITIVE-REGULATION_OF_DEVELOPMENTAL-PROCESS	GO-0051094	32	-0.390252	-1.269152	0.186421	1.000000	1.000
651	REACTOME-EPHLEPHRIN-SIGNALING	R-RNO-2682334	6	-0.594419	-1.278423	0.161572	1.000000	1.000
652	GOBP-REGULATION_OF_TRANS-SYNAPTIC-SIGNALING	GO-0099177	40	-0.391732	-1.280379	0.162556	1.000000	1.000
653	GOBP-PROTEIN-LOCALIZATION_TO-CELL-JUNCTION	GO-1902414	6	-0.592862	-1.283175	0.165242	1.000000	1.000
654	GOBP-REGULATION_OF_CATION-TRANSMEMBRANE-TRANSPORT	GO-1904062	16	-0.445148	-1.284100	0.167920	1.000000	1.000
655	GOBP-EPHRLIN-RECEPTOR-SIGNALING-PATHWAY	GO-0048013	5	-0.625294	-1.284540	0.142433	1.000000	1.000
656	GOBP-RESPONSE-TO-MECHANICAL-STIMULUS	GO-0009612	6	-0.598820	-1.286244	0.154728	1.000000	1.000
657	GOBP-CALCIUM-MEDIATED-SIGNALING	GO-0019722	10	-0.513248	-1.289832	0.170077	1.000000	1.000
658	GOBP-REGULATION_OF_AXONOGENESIS	GO-0050770	7	-0.551931	-1.291324	0.155705	1.000000	1.000
659	GOBP-CELL-SURFACE-RECEPTOR-SIGNALING-PATHWAY_I...	GO-1905114	15	-0.461716	-1.291678	0.141800	1.000000	1.000
660	GOBP-REGULATION_OF_MEMBRANE-POTENTIAL	GO-0042391	17	-0.452883	-1.296827	0.168130	1.000000	1.000
661	GOBP-SYNAPSE-ORGANIZATION	GO-0050808	17	-0.453899	-1.298745	0.161491	1.000000	1.000
662	GOBP-REGULATION_OF_ANATOMICAL-STRUCTURE-SIZE	GO-0090066	10	-0.509417	-1.301084	0.156836	1.000000	1.000
663	GOBP-PROTEIN-LOCALIZATION_TO-MEMBRANE	GO-0072657	14	-0.478424	-1.314003	0.129111	1.000000	1.000
664	GOBP-PROTEIN-CATABOLIC-PROCESS	GO-0030163	8	-0.554964	-1.324773	0.151070	1.000000	1.000
665	GOBP-MAPK-CASCADE	GO-0000165	18	-0.449601	-1.325786	0.135135	1.000000	1.000
666	GOBP-NEURON-PROJECTION-ORGANIZATION	GO-0106027	8	-0.558306	-1.327725	0.139785	1.000000	1.000
667	GOBP-CELL-JUNCTION-ORGANIZATION	GO-0034330	19	-0.444941	-1.330638	0.133333	1.000000	1.000
668	GOBP-ADENYLATE-CYCLASE-INHIBITING-G-PROTEIN_CO...	GO-0007193	5	-0.646547	-1.334125	0.113128	1.000000	1.000
669	GOBP-PROTEIN-LOCALIZATION_TO-POSTSYNAPSE	GO-0062237	5	-0.644871	-1.338003	0.110951	1.000000	1.000
670	GOBP-TRANSMEMBRANE-TRANSPORT	GO-0055085	27	-0.423912	-1.346033	0.116359	1.000000	1.000
671	GOBP-PROTEIN-LOCALIZATION_TO-SYNAPSE	GO-0035418	5	-0.644871	-1.347787	0.104634	1.000000	1.000
672	GOBP-REGULATION_OF_CELLULAR-COMPONENT-SIZE	GO-0032535	7	-0.591471	-1.351600	0.114168	1.000000	1.000
673	GOBP-RESPONSE-TO-RADIATION	GO-0009314	13	-0.497857	-1.353789	0.116751	1.000000	1.000
674	HALLMARK-EPITHELIAL-MESENCHYMAL-TRANSITION	M5930	5	-0.644960	-1.357589	0.098240	1.000000	1.000
675	GOBP-REGULATION_OF_SYNAPTIC-PLASTICITY	GO-0048167	21	-0.457507	-1.362874	0.110843	1.000000	1.000
676	GOBP-HEAD-DEVELOPMENT	GO-0060322	22	-0.452719	-1.367406	0.091667	1.000000	1.000
677	GOBP-REGULATION_OF_CATION-CHANNEL-ACTIVITY	GO-2001257	14	-0.500998	-1.371778	0.115854	1.000000	1.000
678	REACTOME-L1CAM-INTERACTIONS	R-RNO-373760	5	-0.621936	-1.394307	0.071736	0.940606	1.000
679	GOBP-REGULATION_OF_PROTEIN-CATABOLIC-PROCESS	GO-0042176	7	-0.621936	-1.407330	0.067511	0.886952	1.000
680	REACTOME-RNA-POLYMERASE-II-TRANSCRIPTION	R-RNO-73857	20	-0.473125	-1.408702	0.083933	0.902358	1.000
681	GOBP-CELL-CELL-SIGNALING	GO-0007267	56	-0.425812	-1.412175	0.081839	0.904939	1.000
682	REACTOME-EXTRACELLULAR-MATRIX-ORGANIZATION	R-RNO-1474244	5	-0.690200	-1.419354	0.070100	0.887782	1.000
683	GOBP-REGULATION_OF-TRANSPORTER-ACTIVITY	GO-0032409	17	-0.497362	-1.421711	0.073983	0.898037	1.000
684	GOBP-RESPONSE-TO-LIGHT-STIMULUS	GO-0009416	11	-0.541968	-1.425348	0.083979	0.902774	1.000
685	GOBP-NEGATIVE-REGULATION_OF_CELL-PROJECTION_OR...	GO-0031345	5	-0.691376	-1.430457	0.057863	0.897435	1.000

Continuation of Table S13

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
686	GOBP-REGULATION-OF-POSTSYNAPTIC-MEMBRANE-POTEN...	14	-0.530373	-1.442613	0.058752	0.849494	1.000
687	GOBP-LONG-TERM-SYNAPTIC-POTENTIATION	12	-0.543404	-1.448000	0.067639	0.846073	1.000
688	GOBP-CATION-TRANSMEMBRANE-TRANSPORT	18	-0.511180	-1.448633	0.063246	0.869335	1.000
689	GOBP-POSTSYNAPSE-ORGANIZATION	10	-0.585837	-1.474440	0.049096	0.747872	1.000
690	GOBP-REGULATION-OF-NMDA-RECEPTOR-ACTIVITY	10	-0.584558	-1.492679	0.040682	0.679055	1.000
691	REACTOME-PROTEIN-PROTEIN-INTERACTIONS-AT-SYNAPSES	12	-0.563934	-1.502185	0.038911	0.655744	1.000
692	GOBP-CHEMICAL-SYNAPTIC-TRANSMISSION-POSTSYNAPTIC	9	-0.627280	-1.508233	0.034993	0.647702	1.000
693	GOBP-SYNAPTIC-SIGNALING	47	-0.464335	-1.525744	0.041989	0.586923	1.000
694	REACTOME-SYNAPTIC-ADHESION-LIKE-MOLECULES	9	-0.628279	-1.530006	0.038564	0.589731	1.000
695	GOBP-CALCIUM-ION-TRANSPORT	11	-0.602221	-1.551766	0.019815	0.516079	1.000
696	GOBP-IONOTROPIC-GLUTAMATE-RECEPTOR-SIGNALING-P...	9	-0.632724	-1.552929	0.021769	0.534304	1.000
697	GOBP-CALCIUM-ION-TRANSMEMBRANE-TRANSPORT	7	-0.694495	-1.568769	0.022191	0.487994	1.000
698	GOBP-EXCITATORY-CHEMICAL-SYNAPTIC-TRANSMISSION	5	-0.759036	-1.569967	0.013043	0.506471	1.000
699	GOBP-METAL-ION-TRANSPORT	11	-0.602221	-1.570468	0.025572	0.529265	1.000
700	REACTOME-NEUREXINS-AND-NEUROLIGINS	9	-0.650585	-1.572629	0.019417	0.547126	1.000
701	REACTOME-TRANSMISSION-ACROSS-CHEMICAL-SYNAPSES	23	-0.523620	-1.576184	0.024882	0.560184	1.000
702	GOBP-CALCIUM-ION-TRANSPORT-INTO-CYTOSOL	7	-0.694495	-1.577596	0.016925	0.584850	1.000
703	GOBP-CYTOSOLIC-CALCIUM-ION-TRANSPORT	7	-0.694495	-1.582640	0.021614	0.596277	1.000
704	GOBP-LEARNING	13	-0.578894	-1.593336	0.026515	0.579069	1.000
705	REACTOME-RAS-ACTIVATION-UPON-CA2-INFLUX-THROUG...	6	-0.732040	-1.609258	0.012676	0.536089	1.000
706	REACTOME-CREB1-PHOSPHORYLATION-THROUGH-NMDA-RE...	8	-0.686836	-1.613974	0.011189	0.554203	1.000
707	REACTOME-LONG-TERM-POTENTIATION	10	-0.643855	-1.640353	0.018494	0.468409	1.000
708	REACTOME-NEURONAL-SYSTEM	26	-0.525283	-1.645742	0.016336	0.484998	0.997
709	GOBP-GLUTAMATE-RECEPTOR-SIGNALING-PATHWAY	17	-0.758617	-1.668039	0.010000	0.428699	0.995
710	REACTOME-NEUROTRANSMITTER-RECEPTORS-AND-POSTSY...	22	-0.554506	-1.686760	0.006002	0.394026	0.981
711	REACTOME-TRANSCRIPTIONAL-REGULATION-BY-MECP2	7	-0.758617	-1.706046	0.009749	0.356542	0.960
712	REACTOME-ACTIVATION-OF-NMDA-RECEPTORS-AND-POST...	16	-0.605770	-1.712185	0.008883	0.382714	0.953
713	GOBP-NEGATIVE-REGULATION-OF-PROTEIN-CATABOLIC-...	5	-0.832030	-1.712568	0.005848	0.444565	0.952
714	REACTOME-MAPK-FAMILY-SIGNALING-CASCADES	12	-0.666907	-1.760786	0.005141	0.306394	0.839
715	REACTOME-ASSEMBLY-AND-CELL-SURFACE-PRESENTATIO...	8	-0.758077	-1.772551	0.001376	0.335735	0.798
716	REACTOME-UNBLOCKING-OF-NMDA-RECEPTORS-GLUTAMAT...	12	-0.664723	-1.772840	0.003916	0.444888	0.797
717	GOBP-INORGANIC-ION-TRANSMEMBRANE-TRANSPORT	9	-0.726479	-1.794163	0.000000	0.520146	0.716
718	REACTOME-NEGATIVE-REGULATION-OF-NMDA-RECEPTOR-...	8	-0.758077	-1.820415	0.005420	0.749830	0.596

End of Table

Supplementary Table S14: BG early profile (1 DPL peak) GSEA results.

Begin of Table S14								
	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
0	GOBP-REGIONALIZATION	GO-0003002	6	0.795552	2.033180	0.000000	0.374573	0.380
1	GOBP-PATTERN-SPECIFICATION_PROCESS	GO-0007389	6	0.795552	1.997639	0.000000	0.254615	0.471
2	GOBP-REGULATION_OF_NEUROTRANSMITTER_RECEPTOR_A...	GO-0009601	13	0.556547	1.873164	0.000000	0.476056	0.826
3	GOBP-MEMORY	GO-0007613	13	0.560787	1.822978	0.006780	0.505561	0.916
4	GOBP_POSITIVE_REGULATION_OF_NEURON_PROJECTION...	GO-0010976	5	0.776988	1.820985	0.014793	0.410562	0.923
5	REACTOME-SIGNALING-BY_NTRK2-TRKB	R-RNO-9006115	6	0.697617	1.806138	0.017391	0.381213	0.945
6	GOBP_CATION_TRANSPORT	GO-0006812	25	0.440951	1.797742	0.004425	0.343217	0.952
7	GOBP-REGULATION_OF_CATION_CHANNEL_ACTIVITY	GO-2001257	14	0.517522	1.784610	0.003546	0.327694	0.965
8	GOBP-REGULATION_OF_CATION_TRANSMEMBRANE_TRANSPORT	GO-1904062	16	0.493500	1.756228	0.007117	0.353100	0.985
9	GOBP-REGULATION_OF_NMDA_RECEPTOR_ACTIVITY	GO-2000310	10	0.567724	1.740969	0.009901	0.347295	0.990
10	GOBP-LONG-TERM-MEMORY	GO-0007616	6	0.650395	1.617003	0.056548	0.625724	1.000
11	GOBP-REGULATION_OF_SIGNALING_RECEPTOR_ACTIVITY	GO-0010469	14	0.472601	1.602173	0.045752	0.618898	1.000
12	GOBP-RESPONSE_TO_NERVE_GROWTH_FACTOR	GO-1990089	7	0.589754	1.595750	0.050746	0.589619	1.000
13	GOBP_CATION_TRANSMEMBRANE_TRANSPORT	GO-0008655	18	0.446054	1.588654	0.034188	0.566391	1.000
14	GOBP-REGULATION_OF_CELL_PROJECTION_ORGANIZATION	GO-0031344	20	0.418111	1.583646	0.022901	0.541412	1.000
15	GOBP-DEVELOPMENTAL-CELL-GROWTH	GO-0048588	5	0.683493	1.551274	0.060150	0.588788	1.000
16	GOBP-REGULATION_OF_PHOSPHOLIPASE_ACTIVITY	GO-0010517	6	0.609756	1.549827	0.051672	0.558037	1.000
17	GOBP-REGULATION_OF_MEMBRANE_POTENTIAL	GO-0042391	17	0.436748	1.549519	0.011450	0.527735	1.000
18	GOBP_POSITIVE_REGULATION_OF_CELL_PROJECTION_OR...	GO-0031346	10	0.509386	1.535480	0.055363	0.533615	1.000
19	GOBP-REGULATION_OF_POSTSYNAPTIC_MEMBRANE_POTEN...	GO-0060078	14	0.453953	1.516340	0.062044	0.554028	1.000
20	GOBP-NEGATIVE-REGULATION_OF_NEURON_APOPTOTIC_P...	GO-0043524	8	0.522920	1.497864	0.082822	0.572828	1.000
21	GOBP-REGULATION_OF_LIPASE_ACTIVITY	GO-0060191	6	0.609756	1.495094	0.072674	0.553403	1.000
22	REACTOME-UNBLOCKING_OF_NMDA_RECEPTORS-GLUTAMAT...	R-RNO-438066	12	0.464444	1.490851	0.063694	0.539180	1.000
23	REACTOME-PROTEIN-PROTEIN-INTERACTIONS-AT_SYNAPSES	R-RNO-6794362	12	0.459785	1.480677	0.078231	0.539346	1.000
24	GOBP-BEHAVIOR	GO-0007610	32	0.335125	1.448239	0.042857	0.595613	1.000
25	GOBP-REGULATION_OF_PHOSPHOLIPASE_C_ACTIVITY	GO-1900274	5	0.617969	1.423842	0.118980	0.634326	1.000
26	GOBP_POSITIVE_REGULATION_OF_LIPASE_ACTIVITY	GO-0060193	5	0.617969	1.423718	0.119444	0.611125	1.000
27	GOBP-IONOTROPIC-GLUTAMATE-RECEPTOR-SIGNALING_P...	GO-0035235	9	0.474758	1.412292	0.085366	0.617777	1.000
28	GOBP_PERIPHERAL_NERVOUS_SYSTEM_DEVELOPMENT	GO-0007422	9	0.495494	1.396987	0.102719	0.634366	1.000
29	GOBP-NEURON_PROJECTION_ORGANIZATION	GO-0106027	8	0.492915	1.389429	0.103030	0.632393	1.000
30	GOBP-REGULATION_OF_TRANSPORTER_ACTIVITY	GO-0032409	17	0.382473	1.386217	0.064777	0.619928	1.000
31	REACTOME_SYNAPTIC_ADHESION-LIKE-MOLECULES	R-RNO-8849932	9	0.480187	1.384744	0.119632	0.604215	1.000
32	GOBP-NEUROTROPHIN-SIGNALING-PATHWAY	GO-0038179	6	0.538930	1.380173	0.116071	0.596165	1.000
33	GOBP-RECEPTOR-METABOLIC-PROCESS	GO-0043112	5	0.595182	1.379532	0.126582	0.580186	1.000
34	GOBP_POSITIVE_REGULATION_OF_PROTEIN-TYROSINE_K...	GO-0061098	5	0.578313	1.368779	0.117493	0.590172	1.000
35	GOBP-REGULATION_OF_SYNAPSE_STRUCTURE_OR_ACTIVITY	GO-0050803	11	0.435506	1.367590	0.134948	0.576764	1.000
36	GOBP-RECEPTOR-INTERNALIZATION	GO-0031623	5	0.593162	1.367022	0.111979	0.562235	1.000
37	GOBP-REGULATION_OF_PEPITIDYL-SERINE-PHOSPHORYLA...	GO-0033135	8	0.485175	1.366892	0.089286	0.547740	1.000
38	GOBP-SENSORY_PERCEPTION_OF_PAIN	GO-0019233	5	0.573679	1.339308	0.137755	0.597092	1.000
39	GOBP-REGULATION_OF_NEURON_PROJECTION-DEVELOPMENT	GO-0010975	16	0.370848	1.337354	0.116981	0.586709	1.000
40	GOBP-SENSORY_PERCEPTION	GO-0007606	9	0.455696	1.333043	0.128028	0.581937	1.000

Continuation of Table S14

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
41 GOBP-REGULATION-OF-NEURON-DIFFERENTIATION	GO-0045664	5	0.580022	1.330974	0.151596	0.572494	1.000
42 REACTOME-ACTIVATION-OF-NMDA-RECEPTORS-AND-POST...	R-RNO-442755	16	0.365657	1.330818	0.122744	0.559507	1.000
43 GOBP-REGULATION-OF-PROTEIN-TYROSINEKINASE-ACT...	GO-0061097	5	0.578313	1.328704	0.122016	0.551767	1.000
44 GOBP-LOCOMOTORY-BEHAVIOR	GO-0007626	7	0.494400	1.323526	0.146199	0.550826	1.000
45 GOBP-LONG-TERM-SYNAPTIC-DEPRESSION	GO-0060292	5	0.563514	1.320130	0.142857	0.546482	1.000
46 GOBP-NEUROTROPHIN-TRK-RECEPTOR-SIGNALING-PATHWAY	GO-0048011	6	0.538930	1.319499	0.126471	0.536203	1.000
47 GOBP-REGULATION-OF-POSTSYNAPSE-ORGANIZATION	GO-0009175	6	0.545098	1.317964	0.144847	0.528018	1.000
48 GOBP-NUCLEAR-TRANSPORT	GO-0051169	5	0.554217	1.313552	0.144022	0.525729	1.000
49 GOBP-POSITIVE-REGULATION-OF-PEPTIDYL-SERINE-PH...	GO-00033138	8	0.485175	1.307605	0.151057	0.526956	1.000
50 REACTOME-LONG-TERM-POTENTIATION	R-HSA-9620244	10	0.426928	1.295503	0.141892	0.542745	1.000
51 REACTOME-SIGNALING-BY-NTRKS	R-RNO-166520	18	0.336214	1.273990	0.140288	0.577693	1.000
52 GOBP-RESPONSE-TO-ETHANOL	GO-0045471	5	0.538866	1.272913	0.182306	0.569154	1.000
53 GOBP-COGNITION	GO-00050890	28	0.307498	1.256976	0.123348	0.593327	1.000
54 GOBP-DIVALENT-INORGANIC-CATION-HOMEOSTASIS	GO-00072507	13	0.360895	1.247641	0.153846	0.604446	1.000
55 GOBP-CELLULAR-ION-HOMEOSTASIS	GO-0006873	14	0.355879	1.232970	0.163121	0.628052	1.000
56 GOBP-MUSCLE-CELL-DEVELOPMENT	GO-0055001	5	0.542169	1.224567	0.192612	0.637110	1.000
57 GOBP-DEVELOPMENTAL-MATURATION	GO-0021700	5	0.518072	1.205502	0.241935	0.673235	1.000
58 GOBP-NERVOUS-SYSTEM-PROCESS	GO-00050877	38	0.270208	1.204162	0.211957	0.664721	1.000
59 GOBP-REGULATION-OF-TRANS-SYNAPTIC-SIGNALING	GO-0009177	40	0.264572	1.199557	0.196532	0.665228	1.000
60 GOBP-POSITIVE-REGULATION-OF-CELL-GROWTH	GO-00030307	6	0.487905	1.197148	0.238095	0.660755	1.000
61 GOBP-REGULATION-OF-CYTOSOLIC-CALCIUM-ION-CONCE...	GO-0051480	13	0.360895	1.193457	0.240678	0.659144	1.000
62 GOBP-REGULATION-OF-CELL-SIZE	GO-0008361	5	0.512112	1.183697	0.248021	0.672083	1.000
63 GOBP-ORGANIC-ACID-TRANSPORT	GO-0015849	7	0.444444	1.173247	0.236923	0.686786	1.000
64 REACTOME-RAS-ACTIVATION-UPON-CA2-INFLUX-THROUGH...	R-HSA-442982	6	0.477844	1.172527	0.224377	0.677850	1.000
65 GOBP-POSITIVE-REGULATION-OF-HYDROLASE-ACTIVITY	GO-0051345	16	0.327144	1.167971	0.217082	0.679120	1.000
66 GOBP-GLUTAMATE-RECEPTOR-SIGNALING-PATHWAY	GO-0007215	17	0.315300	1.164302	0.195572	0.678056	1.000
67 GOBP-SYNAPTIC-SIGNALING	GO-0009536	47	0.255185	1.150386	0.262032	0.703371	1.000
68 GOBP-POSITIVE-REGULATION-OF-SYNAPTIC-TRANSMISSION	GO-0050806	15	0.329092	1.138220	0.278985	0.724065	1.000
69 GOBP-REGULATION-OF-DEVELOPMENTAL-GROWTH	GO-0048638	9	0.384908	1.132101	0.293919	0.729817	1.000
70 GOBP-ORGANIC-ANION-TRANSPORT	GO-0015711	6	0.439024	1.102555	0.308333	0.797133	1.000
71 GOBP-AMINO-ACID-TRANSPORT	GO-0006865	6	0.439024	1.101150	0.305476	0.789939	1.000
72 GOBP-CELL-PROJECTION-ORGANIZATION	GO-0030030	34	0.253033	1.097412	0.305000	0.789395	1.000
73 GOBP-REGULATION-OF-NEURONAL-SYNAPTIC-PLASTICITY	GO-0048168	7	0.407407	1.096331	0.293255	0.781742	1.000
74 HALMARK-KRAS-SIGNALING-UP	M5953	6	0.440225	1.094307	0.327635	0.776511	1.000
75 GOBP-CARBOXYLIC-ACID-TRANSPORT	GO-0046942	6	0.439024	1.090292	0.336158	0.777030	1.000
76 GOBP-DEVELOPMENTAL-GROWTH	GO-0048589	10	0.359641	1.086984	0.326797	0.774748	1.000
77 REACTOME-CREB1-PHOSPHORYLATION-THROUGH-NMDA-RE...	R-RNO-442742	8	0.385350	1.080723	0.354232	0.780394	1.000
78 GOBP-FATTY-ACID-TRANSPORT	GO-0015908	6	0.430383	1.076296	0.314103	0.780704	1.000
79 GOBP-NEGATIVE-REGULATION-OF-SYNAPTIC-TRANSMISSION	GO-0050805	6	0.430383	1.076296	0.356948	0.771920	1.000
80 REACTOME-TRANSCRIPTIONAL-REGULATION-BY-MECP2	R-RNO-8986944	7	0.415662	1.074945	0.342342	0.765758	1.000
81 GOBP-POSITIVE-REGULATION-OF-DEVELOPMENTAL-GROWTH	GO-0048639	8	0.391848	1.074624	0.345345	0.757375	1.000
82 GOBP-NEGATIVE-REGULATION-OF-NEURON-DEATH	GO-1901215	11	0.350828	1.071086	0.335526	0.757026	1.000
83 GOBP-REGULATION-OF-ION-TRANSPORT	GO-0043269	36	0.241413	1.069443	0.376190	0.751694	1.000

Continuation of Table S14

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
84	GOBP-METAL-ION-HOMEOSTASIS	14	0.311357	1.069291	0.342373	0.743143	1.000
85	GOBP-CHEMICAL-SYNAPTIC-TRANSMISSION_POSTSYNAPTIC	9	0.368604	1.069141	0.344322	0.734907	1.000
86	GOBP-REGULATION-OF-NERVOUS-SYSTEM-PROCESS	8	0.370539	1.065195	0.364458	0.735540	1.000
87	GOBP-CALCIUM-ION-TRANSPORT	11	0.326203	1.057797	0.363636	0.744813	1.000
88	GOBP-REGULATION-OF-TRANSMEMBRANE-TRANSPORT	23	0.272029	1.055202	0.404255	0.742345	1.000
89	GOBP-ION-HOMEOSTASIS	16	0.291622	1.040765	0.412451	0.768703	1.000
90	GOBP-NERVE-DEVELOPMENT	9	0.360256	1.038763	0.366154	0.764999	1.000
91	GOBP-LONG-TERM-SYNAPTIC-POTENTIATION	12	0.316767	1.038123	0.382550	0.758268	1.000
92	GOBP-TRANSMEMBRANE-TRANSPORT	27	0.255763	1.037034	0.401914	0.752712	1.000
93	GOBP-CELL-CELL-SIGNALING	56	0.228038	1.032624	0.461538	0.755162	1.000
94	GOBP-MONOCARBOXYLIC-ACID-TRANSPORT	5	0.433735	1.023149	0.398844	0.769170	1.000
95	GOBP-REGULATION-OF-SYNAPTIC-PLASTICITY	21	0.259426	1.006589	0.420863	0.801096	1.000
96	GOBP-CELLULAR-COMPONENT-MAINTENANCE	5	0.432154	1.005735	0.398396	0.795378	1.000
97	GOBP-DICARBOXYLIC-ACID-TRANSPORT	5	0.433735	1.005512	0.422977	0.787825	1.000
98	GOBP-ACIDIC-AMINO-ACID-TRANSPORT	5	0.433735	1.005445	0.427778	0.780020	1.000
99	GOBP-METAL-ION-TRANSPORT	11	0.326203	0.996820	0.425532	0.792439	1.000
100	GOBP-SYNAPSE-ORGANIZATION	17	0.276010	0.990800	0.460076	0.801108	1.000
101	GOBP-STRIATED-MUSCLE-CELL-DIFFERENTIATION	9	0.341772	0.989157	0.428571	0.795412	1.000
102	GOBP-RESPONSE-TO-MONOSACCHARIDE	5	0.409639	0.973442	0.441096	0.824746	1.000
103	GOBP-POSITIVE-REGULATION-OF-TRANSMEMBRANE-TRAN...	7	0.364674	0.973000	0.429429	0.817939	1.000
104	GOBP-POSITIVE-REGULATION-OF-AXONOGENESIS	5	0.421498	0.963786	0.497175	0.832291	1.000
105	GOBP-REGULATION-OF-CELLULAR-COMPONENT-SIZE	7	0.361878	0.960598	0.461538	0.832096	1.000
106	REACTOME-NEGATIVE-REGULATION-OF-NMDA-RECEPTOR-...	8	0.340328	0.959167	0.486567	0.827729	1.000
107	GOBP-POSITIVE-REGULATION-OF-GROWTH	9	0.317078	0.958318	0.485981	0.822102	1.000
108	REACTOME-NEURONAL-SYSTEM	26	0.237341	0.958216	0.515021	0.814918	1.000
109	HALLMARK-P13K-AKT-MTOR-SIGNALING	6	0.376224	0.953599	0.497297	0.818473	1.000
110	GOBP-POSITIVE-REGULATION-OF-TRANSFERASE-ACTIVITY	20	0.250000	0.951431	0.514925	0.816169	1.000
111	REACTOME-ASSEMBLY-AND-CELL-SURFACE-PRESENTATIO-...	8	0.340328	0.941593	0.530675	0.830928	1.000
112	GOBP-RESPONSE-TO-CARBOHYDRATE	5	0.409639	0.940428	0.464986	0.826241	1.000
113	GOBP-POSITIVE-REGULATION-OF-PROTEIN-KINASE-ACT-...	19	0.246377	0.937982	0.569853	0.824475	1.000
114	GOBP-POSITIVE-REGULATION-OF-BINDING	6	0.381388	0.935662	0.510204	0.822769	1.000
115	GOBP-POSITIVE-REGULATION-OF_PHOSPHORUS-METABOL-...	24	0.234375	0.933318	0.549783	0.816495	1.000
116	REACTOME-TRAFFICKING-OF-AMPA-RECEPTORS	11	0.302856	0.934727	0.529032	0.810934	1.000
117	GOBP-PEPTIDYL-SERINE-MODIFICATION	12	0.289577	0.927907	0.539519	0.819104	1.000
118	GOBP-POSITIVE-REGULATION-OF-CATALYTIC-ACTIVITY	30	0.216781	0.915958	0.561947	0.840105	1.000
119	GOBP-MATERNAL-PROCESS-INVOLVED-IN-FEMALE-PREGN-...	5	0.394862	0.908630	0.530120	0.849826	1.000
120	GOBP-POSITIVE-REGULATION-OF-PROTEIN_PHOSPHORYL-...	23	0.230769	0.904863	0.584746	0.851065	1.000
121	GOBP-POSTSYNAPSE-ORGANIZATION	10	0.301895	0.904744	0.590476	0.844335	1.000
122	GOBP-RECEPTOR-MEDIATED-ENDOCYTOSIS	6	0.362353	0.904330	0.582386	0.838338	1.000
123	GOBP-POSITIVE-REGULATION-OF-PROTEIN-MODIFICATI-...	23	0.230769	0.903878	0.597744	0.832607	1.000
124	GOBP-REGULATION-OF-HORMONE-LEVELS	12	0.280914	0.902472	0.586441	0.829060	1.000
125	GOBP-CARBOHYDRATE-DERIVATIVE-METABOLIC-PROCESS	7	0.345679	0.901310	0.542773	0.825067	1.000
126	GOBP-CELLULAR-HOMEOSTASIS	18	0.248577	0.896771	0.564854	0.828038	1.000

Continuation of Table S14

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
127	GOBP-POSITIVE-REGULATION_OF_CATION_TRANSMEMBRAN...	5	0.388807	0.896107	0.580381	0.822969	1.000
128	GOBP-INOSITOL_LIPID-MEDIATED-SIGNALING	8	0.316281	0.893039	0.585443	0.822919	1.000
129	GOBP-ORGANOPHOSPHATE-METABOLIC-PROCESS	7	0.333333	0.891909	0.549206	0.818998	1.000
130	GOBP-REGULATION_OF_ORGAN-GROWTH	5	0.373494	0.890604	0.586301	0.815375	1.000
131	GOBP-ENDOCYTOSIS	8	0.321347	0.883073	0.585586	0.825358	1.000
132	GOBP-ORGAN-GROWTH	5	0.373494	0.867635	0.620596	0.851432	1.000
133	GOBP-CHEMICAL-HOMEOSTASIS	23	0.217691	0.866808	0.692982	0.846693	1.000
134	GOBP-REGULATION_OF_AXONOGENESIS	7	0.323434	0.866770	0.587692	0.840499	1.000
135	GOBP-REGULATION_OF_TRANSPORT	44	0.187517	0.861945	0.700535	0.843909	1.000
136	GOBP-NEURON-DEVELOPMENT	33	0.197215	0.840987	0.730594	0.881311	1.000
137	GOBP-POSITIVE-REGULATION_OF_PEPTIDYL-TYROSINE...	8	0.296511	0.813904	0.685294	0.928365	1.000
138	GOBP-CELL_JUNCTION-ORGANIZATION	19	0.217074	0.807625	0.755102	0.934495	1.000
139	GOBP-POSITIVE-REGULATION_OF_NEUROGENESIS	12	0.248249	0.798608	0.731707	0.946356	1.000
140	GOBP-REGULATION_OF_CYTOSKELETON-ORGANIZATION	5	0.349398	0.798413	0.728022	0.940125	1.000
141	GOBP-POLYSACCHARIDE-METABOLIC-PROCESS	5	0.339283	0.793756	0.731507	0.942519	1.000
142	GOBP-POSITIVE-REGULATION_OF_NERVOUS-SYSTEM.DEV...	12	0.248249	0.793264	0.761745	0.936779	1.000
143	GOBP-POSITIVE-REGULATION_OF_CELL-DEVELOPMENT	12	0.248249	0.792632	0.781351	0.931519	1.000
144	GOBP-MYOTUBE-DIFFERENTIATION	5	0.325301	0.746720	0.809659	1.000000	1.000
145	GOBP-NEURON-DIFFERENTIATION	36	0.167530	0.740298	0.897059	1.000000	1.000
146	GOBP-SENSORY-ORGAN-DEVELOPMENT	8	0.259238	0.733515	0.780186	1.000000	1.000
147	GOBP-DENDRITIC-MORPHOGENESIS	6	0.292683	0.727726	0.820581	1.000000	1.000
148	GOBP-DENDRITIC-SPINE-DEVELOPMENT	6	0.292683	0.727455	0.788162	1.000000	1.000
149	GOBP-REGULATION_OF_DEFENSE-RESPONSE	7	0.271769	0.727136	0.835694	1.000000	1.000
150	GOBP-GENERATION_OF_PRECURSOR-METABOLITES-AND.E...	5	0.313253	0.725343	0.835227	1.000000	1.000
151	GOBP-MUSCLE-CELL-DIFFERENTIATION	10	0.243590	0.723570	0.848765	0.998903	1.000
152	GOBP-INSULIN-SECRETION	7	0.272025	0.722257	0.809231	0.994467	1.000
153	GOBP-DENDRITIC-SPINE-MORPHOGENESIS	5	0.315435	0.721876	0.846821	0.988669	1.000
154	GOBP-REGULATION_OF_PROTEIN-PHOSPHORYLATION	26	0.179999	0.721078	0.848485	0.983493	1.000
155	GOBP-GLIOGENESIS	12	0.223684	0.716417	0.845614	0.984438	1.000
156	GOBP-REGULATION_OF_INFLAMMATORY-RESPONSE	7	0.271769	0.714030	0.842105	0.981635	1.000
157	GOBP-PEPTIDE-SECRETION	9	0.245444	0.713969	0.810056	0.975498	1.000
158	GOBP-CELL-SURFACE-RECEPTOR-SIGNALING-PATHWAY_I...	15	0.197042	0.705349	0.888136	0.981056	1.000
159	GOBP-POSITIVE-REGULATION_OF_MOLECULAR-FUNCTION	38	0.163384	0.701977	0.911765	0.979315	1.000
160	GOBP-POSITIVE-REGULATION_OF_DEFENSE-RESPONSE	5	0.295127	0.691171	0.872396	0.987825	1.000
161	GOBP-REGULATION_OF_LONG-TERM-SYNAPTIC-POTENTIA...	6	0.280488	0.688337	0.861963	0.985042	1.000
162	GOBP-ACTIVATION_OF_PROTEIN-KINASE-ACTIVITY	11	0.225829	0.685366	0.858025	0.982414	1.000
163	GOBP-PEPTIDE-HORMONE-SECRETION	7	0.272025	0.677376	0.888889	0.986013	1.000
164	GOBP-EMBRYO-DEVELOPMENT-ENDING-IN-BIRTH-OR-EGG...	9	0.227848	0.664860	0.860759	0.994652	1.000
165	GOBP-REGULATION_OF_SYNAPTIC-TRANSMISSION-GLUTA...	12	0.199810	0.657028	0.936842	0.997048	1.000
166	GOBP-PEPTIDYL-TYROSINE-MODIFICATION	10	0.217949	0.652299	0.905363	0.995832	1.000
167	GOBP-GLIAL-CELL-DIFFERENTIATION	10	0.217949	0.648116	0.915825	0.993686	1.000
168	GOBP-REGULATION_OF_PEPTIDYL-TYROSINE-PHOSPHORY...	9	0.215190	0.642636	0.914191	0.992961	1.000
169	GOBP-POSITIVE-REGULATION_OF_LONG-TERM-SYNAPTIC...	5	0.277109	0.642364	0.901370	0.987418	1.000

Continuation of Table S14

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
170	GOBP-POSITIVE-REGULATION_OF_DNA-BINDING..TRANSC...	10	0.217949	0.637609	0.909091	0.985752	1.000
171	GOBP-EMBRYONIC.MORPHOGENESIS	6	0.251273	0.621357	0.943953	0.993251	1.000
172	GOBP-CELLULAR-RESPONSE.TO-ABIOTIC-STIMULUS	7	0.234568	0.612392	0.945289	0.994035	1.000
173	GOBP-SYNAPTIC.TRANSMISSION.GLUTAMATERGIC	13	0.186968	0.610930	0.963415	0.989322	1.000
174	GOBP-TEMPERATURE.HOMEOSTASIS	5	0.264083	0.603791	0.935484	0.988146	1.000
175	GOBP-NEUROGENESIS	40	0.135842	0.598825	0.985849	0.985561	1.000
176	GOBP-NEGATIVE-REGULATION_OF-ANION-TRANSPORT	8	0.212500	0.593632	0.969419	0.983221	1.000
177	GOBP-RESPONSE.TO-NUTRIENT	5	0.240964	0.557474	0.975000	0.994878	1.000
178	GOBP-REGULATION_OF-METAL-ION..TRANSPORT	6	0.222248	0.555794	0.972678	0.989955	1.000
179	GOBP-ANION..TRANSMEMBRANE..TRANSPORT	7	0.209877	0.538815	0.982609	0.990215	1.000
180	GOBP-TELECEPHALON.DEVELOPMENT	6	0.200215	0.513294	1.000000	0.991088	1.000
181	GOBP-DENDRITE.DEVELOPMENT	9	-0.169825	-0.421612	0.995792	0.997950	1.000
182	REACTOME-GPCR.LIGAND-BINDING	8	-0.191630	-0.456364	0.993865	0.996325	1.000
183	GOBP-REGULATION_OF-PROTEIN.KINASE..ACTIVITY	22	-0.152553	-0.476431	0.992042	0.995066	1.000
184	GOBP-REGULATION_OF-TRANSFERASE..ACTIVITY	22	-0.152553	-0.480209	0.997358	0.999202	1.000
185	REACTOME-INTERFERON-SIGNALING	6	-0.249880	-0.546301	0.979782	0.977704	1.000
186	GOBP-NEURON-MIGRATION	5	-0.258937	-0.547467	0.968504	0.979031	1.000
187	GOBP-MUSCLE..TISSUE.DEVELOPMENT	11	-0.212192	-0.554019	0.962910	0.977843	1.000
188	GOBP-G-PROTEIN.COUPLED-GLUTAMATE-RECEPTOR.SIGN...	8	-0.231319	-0.558337	0.962853	0.977504	1.000
189	GOBP-NEGATIVE-REGULATION_OF-ION-TRANSPORT	11	-0.216081	-0.566890	0.948468	0.975020	1.000
190	GOBP-LIPID.EXPORT.FROM-CELL	5	-0.271597	-0.569057	0.959016	0.975739	1.000
191	GOBP-T-CELL-ACTIVATION	8	-0.242287	-0.585993	0.940666	0.967468	1.000
192	GOBP-POSITIVE-REGULATION_OF-SECRETION	6	-0.271901	-0.586346	0.944954	0.969097	1.000
193	GOBP-G-PROTEIN.COUPLED-RECEPTOR-SIGNALING..PATHWAY	18	-0.200370	-0.594394	0.934051	0.965623	1.000
194	GOBP-INFLAMMATORY-RESPONSE	12	-0.231952	-0.616344	0.922554	0.952071	1.000
195	GOBP-POSITIVE-REGULATION_OF-CELLULAR-COMPONENT...	24	-0.203035	-0.636922	0.908740	0.937042	1.000
196	GOBP-PEPTIDYL-AMINO-ACID-MODIFICATION	22	-0.206343	-0.652997	0.898123	0.924371	1.000
197	GOBP-REGULATION_OF-ENDOCYTOSIS	6	-0.300046	-0.661145	0.894009	0.918418	1.000
198	GOBP-REGULATION_OF-CELL-DEVELOPMENT	15	-0.230942	-0.666005	0.889675	0.915462	1.000
199	GOBP-REGULATION_OF-NERVOUS-SYSTEM.DEVELOPMENT	15	-0.235938	-0.672473	0.875342	0.910643	1.000
200	GOBP-SKELETAL-MUSCLE-ORGAN.DEVELOPMENT	5	-0.334096	-0.679968	0.896147	0.904833	1.000
201	GOBP-TAXIS	14	-0.243338	-0.681463	0.876902	0.905071	1.000
202	GOBP-RESPONSE.TO-HEAT	7	-0.290321	-0.682955	0.859873	0.905257	1.000
203	GOBP-INNATE-IMMUNE-RESPONSE	7	-0.298775	-0.685053	0.869894	0.904760	1.000
204	REACTOME-POST-TRANSLATIONAL-PROTEIN-MODIFICATION	7	-0.302892	-0.687271	0.870207	0.904123	1.000
205	GOBP-CELLULAR-COMPONENT-MORPHOGENESIS	24	-0.220795	-0.688067	0.853137	0.904996	1.000
206	GOBP-DEFENSE-RESPONSE	19	-0.225312	-0.689072	0.859395	0.905689	1.000
207	GOBP-REGULATION_OF-NEUROGENESIS	14	-0.241124	-0.690108	0.863388	0.906352	1.000
208	GOBP-CIRCULATORY-SYSTEM-PROCESS	5	-0.328266	-0.690497	0.867200	0.907709	1.000
209	GOBP-RESPONSE.TO-ALKALOID	5	-0.333665	-0.692290	0.874433	0.907645	1.000
210	GOBP-REGULATION_OF-ANATOMICAL-STRUCTURE-MORPHO...	17	-0.232867	-0.695752	0.860027	0.905634	1.000
211	GOBP-CELL-MORPHOGENESIS	24	-0.220795	-0.698983	0.863937	0.903715	1.000
212	GOBP-CELL-PART-MORPHOGENESIS	24	-0.220795	-0.700919	0.853529	0.903406	1.000

Continuation of Table S14

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
213	GOBP-MUSCLE.CONTRACTION	5	-0.336882	-0.703906	0.882258	0.901710	1.000
214	GOBP-REGULATION.OF.RECEPTOR.MEDIATED.ENDOCYTOSIS	5	-0.348446	-0.713329	0.851974	0.892453	1.000
215	GOBP-MONOCARBOXYLIC.ACID.METABOLIC.PROCESS	6	-0.322380	-0.715135	0.848159	0.892147	1.000
216	GOBP-PEPTIDE.METABOLIC.PROCESS	12	-0.266934	-0.724419	0.811403	0.882653	1.000
217	GOBP-POSITIVE.REGULATION.OF.INTRACELLULAR.SIGN...	14	-0.262033	-0.731756	0.850214	0.875542	1.000
218	GOBP-NEGATIVE.REGULATION.OF.PEPTIDASE.ACTIVITY	6	-0.335684	-0.735434	0.818040	0.872770	1.000
219	GOBP-ACTIVATION.OF.MAPK-ACTIVITY	6	-0.336967	-0.740621	0.801562	0.867809	1.000
220	GOBP-IN.UTERO.EMBRYONIC.DEVELOPMENT	8	-0.305708	-0.740752	0.800298	0.869386	1.000
221	GOBP-VESICLE.MEDIATED.TRANSPORT.IN.SYNAPSE	7	-0.320928	-0.740795	0.781818	0.871075	1.000
222	GOBP-POSITIVE.REGULATION.OF.MAP.KINASE.ACTIVITY	6	-0.336967	-0.743018	0.810345	0.869985	1.000
223	GOBP-NEGATIVE.REGULATION.OF.LIPID.METABOLIC.PR...	5	-0.359910	-0.744028	0.811232	0.870377	1.000
224	GOBP-POSITIVE.REGULATION.OF.PROTEIN.METABOLIC...	28	-0.226118	-0.746772	0.801556	0.868671	1.000
225	GOBP-REGULATION.OF.PHOSPHORUS.METABOLIC.PROCESS	27	-0.226993	-0.748995	0.810323	0.867606	1.000
226	GOBP-REGULATION.OF.INTRACELLULAR.SIGNAL.TRANS...	21	-0.236480	-0.749125	0.816406	0.869188	1.000
227	REACTOME-TRANSCRIPTIONAL.REGULATION.OF.WHITE-A...	6	-0.340009	-0.753964	0.786482	0.864581	1.000
228	GOBP-CARBOHYDRATE.HOMEOSTASIS	7	-0.327619	-0.755096	0.786237	0.864889	1.000
229	GOBP-POSITIVE.REGULATION.OF.GLIOGENESIS	5	-0.367355	-0.756854	0.794913	0.864336	1.000
230	GOBP-REGULATION.OF.LYMPHOCYTE-ACTIVATION	5	-0.363501	-0.759099	0.797030	0.863120	1.000
231	GOBP-MULTICELLULAR-ORGANISMAL.RESPONSE.TO.STRESS	5	-0.368926	-0.763752	0.768852	0.858766	1.000
232	GOBP-DEFENSE.RESPONSE.TO.OTHER-ORGANISM	9	-0.306646	-0.763813	0.777299	0.860439	1.000
233	GOBP-ORGANIC-HYDROXY-COMPOUND.METABOLIC.PROCESS	7	-0.329471	-0.768195	0.767516	0.856178	1.000
234	GOBP-REGULATION.OF.GLIOGENESIS	5	-0.367355	-0.769565	0.771160	0.856067	1.000
235	GOBP-HEART.DEVELOPMENT	6	-0.347948	-0.775517	0.751903	0.849694	1.000
236	GOBP-CARDIAC.MUSCLE.TISSUE.DEVELOPMENT	6	-0.347948	-0.778112	0.762557	0.847880	1.000
237	GOBP-ORGANIC-HYDROXY-COMPOUND-TRANSPORT	6	-0.357129	-0.781629	0.725637	0.844799	1.000
238	GOBP-MAPK.CASCADE	18	-0.262669	-0.782731	0.777933	0.845085	1.000
239	GOBP-REGULATION.OF.MAP-KINASE-ACTIVITY	9	-0.310818	-0.782838	0.726172	0.846683	1.000
240	GOBP-REGULATION.OF.ANATOMICAL-STRUCTURE-SIZE	10	-0.299178	-0.782893	0.745714	0.848366	1.000
241	GOBP-CELLULAR-CARBOHYDRATE.METABOLIC.PROCESS	5	-0.375523	-0.785391	0.773148	0.846500	1.000
242	GOBP-REGULATION.OF.MUSCLE-CELL-DIFFERENTIATION	6	-0.355428	-0.785527	0.743511	0.848105	1.000
243	GOBP-NEGATIVE.REGULATION.OF-TRANSPORT	13	-0.286187	-0.785537	0.734551	0.849859	1.000
244	GOBP-EXOCYTOSIS	11	-0.300909	-0.790332	0.742938	0.844853	1.000
245	GOBP-MULTICELLULAR-ORGANISMAL.PROCESS	8	-0.325989	-0.790866	0.742560	0.845854	1.000
246	GOBP-REGULATION.OF-PEPTIDE-HORMONE-SECRETION	6	-0.363780	-0.793880	0.748068	0.843151	1.000
247	GOBP-REGULATION.OF-PEPTIDE-SECRETION	7	-0.343115	-0.803564	0.745038	0.830685	1.000
248	GOBP-INORGANIC-ION-TRANSMEMBRANE-TRANSPORT	9	-0.322544	-0.803706	0.715774	0.832272	1.000
249	GOBP-PROTEIN-CONTAINING-COMPLEX-SUBUNIT-ORGANI...	14	-0.289326	-0.806501	0.701513	0.829799	1.000
250	GOBP-REGULATION.OF-SYSTEM-PROCESS	18	-0.271833	-0.809292	0.730028	0.827443	1.000
251	GOBP-ADENYLATE-CYCLASE-INHIBITING-G-PROTEIN.CO...	5	-0.386404	-0.809356	0.734158	0.829136	1.000
252	REACTOME-NEUREXINS-AND-NEUROLIGINS	9	-0.324146	-0.809974	0.726471	0.830048	1.000
253	GOBP-POSITIVE.REGULATION.OF-SIGNALING	34	-0.237600	-0.813645	0.738966	0.826352	1.000
254	GOBP-EMBRYO.DEVELOPMENT	14	-0.288469	-0.825061	0.682652	0.811049	1.000
255	REACTOME-CLASS-C_3-METABOTROPIC-GLUTAMATE-PHER...	7	-0.349545	-0.825956	0.676737	0.811449	1.000

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NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
256 GOBP-PROTEIN_PHOSPHORYLATION	GO-0006468	34	-0.244965	-0.826224	0.701149	0.812819	1.000
257 GOBP-RESPONSE_TO_ALCOHOL	GO-0097305	11	-0.312598	-0.830026	0.688218	0.808631	1.000
258 GOBP-ORGANIC_ACID_METABOLIC_PROCESS	GO-0006082	7	-0.361574	-0.830306	0.710879	0.809981	1.000
259 GOBP-RESPONSE_TO_CALCIUM_ION	GO-0051592	6	-0.380301	-0.832963	0.689708	0.807619	1.000
260 GOBP-CELLULAR_RESPONSE_TO_NITROGEN_COMPOUND	GO-1901699	20	-0.277458	-0.837828	0.690958	0.802128	1.000
261 GOBP-MONOAMINE_TRANSPORT	GO-0015844	5	-0.396070	-0.838617	0.677083	0.802647	1.000
262 GOBP-NEGATIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	GO-0002683	5	-0.403248	-0.840231	0.722311	0.802037	1.000
263 GOBP-PEPTIDE_BIOSYNTHETIC_PROCESS	GO-0043043	7	-0.368201	-0.842160	0.676971	0.800936	1.000
264 GOBP-NEUROTRANSMITTER_SECRETION	GO-0007269	6	-0.387671	-0.842863	0.662461	0.801633	1.000
265 REACTOME_TRANSMISSION_ACROSS_CHEMICAL_SYNAPSES	R-RNO-112315	23	-0.265954	-0.845244	0.685601	0.799709	1.000
266 REACTOME_ONCOGENIC_MAPK_SIGNALING	R-HSA-6802957	5	-0.411024	-0.845937	0.675719	0.800374	1.000
267 GOBP-AMIDE_BIOSYNTHETIC_PROCESS	GO-0043604	7	-0.381977	-0.850134	0.685759	0.801679	1.000
268 GOBP-REGULATION_OF_NEUROTRANSMITTER_TRANSPORT	GO-0051588	6	-0.381977	-0.850134	0.685759	0.801679	1.000
269 REACTOME_NEUROTRANSMITTER_RECEPTORS_AND_POSTSYNAPTIC_TRANSMISSION	R-RNO-112314	22	-0.271442	-0.851369	0.666229	0.797441	1.000
270 REACTOME_EXTRACELLULAR_MATRIX_ORGANIZATION	R-RNO-1474244	5	-0.414832	-0.854713	0.678627	0.793887	1.000
271 GOBP-RESPONSE_TO_GROWTH_FACTOR	GO-0070848	18	-0.285305	-0.857323	0.648322	0.791391	1.000
272 GOBP-CALCIUM_ION_TRANSPORT_INTO_CYTOSOL	GO-0060402	7	-0.375595	-0.857672	0.666170	0.792570	1.000
273 GOBP-CELL_MORPHOGENESIS_INVOLVED_IN_NEURON_DIFFERENTIATION	GO-0048667	21	-0.276004	-0.857895	0.648074	0.793975	1.000
274 GOBP-MYELOID_LEUKOCYTE_ACTIVATION	GO-0002274	8	-0.359600	-0.860698	0.630277	0.791256	1.000
275 GOBP-CELL_MORPHOGENESIS_INVOLVED_IN_NEURON_DIFFERENTIATION	GO-0000904	21	-0.276004	-0.862922	0.673307	0.789473	1.000
276 GOBP-AXON_DEVELOPMENT	GO-0061564	18	-0.289943	-0.863928	0.655827	0.789675	1.000
277 REACTOME_DEATH_RECEPTOR_SIGNALING	R-RNO-73887	5	-0.419493	-0.865334	0.670017	0.789222	1.000
278 GOBP-MUSCLE_SYSTEM_PROCESS	GO-0003012	9	-0.350214	-0.867375	0.643895	0.787891	1.000
279 GOBP-CYTOSOLIC_CALCIUM_ION_TRANSPORT	GO-0060401	7	-0.375595	-0.868712	0.635693	0.787531	1.000
280 GOBP-REGULATION_OF_VESICLE_MEDIATED_TRANSPORT	GO-0060627	12	-0.315591	-0.869931	0.620934	0.787388	1.000
281 GOBP-PROTEIN_COMPLEX_OLIGOMERIZATION	GO-0051259	6	-0.397790	-0.874762	0.635258	0.781468	1.000
282 GOBP-RESPONSE_TO_PEPTIDE	GO-1901652	18	-0.292727	-0.877093	0.627717	0.779537	1.000
283 GOBP-CALCIUM_ION_TRANSMEMBRANE_TRANSPORT	GO-0070588	7	-0.375595	-0.877148	0.628788	0.781237	1.000
284 GOBP-ADENYLATE_CYCLASE_MODULATING_G_PROTEIN_COUPLED_RECEPTOR_ACTIVATION	GO-0007188	11	-0.335552	-0.879306	0.595652	0.779339	1.000
285 GOBP-NEGATIVE_REGULATION_OF_CYSSTEINE_TYPE_ENDOPLASMIC_RETICULUM_FUNCTION	GO-2000117	5	-0.425797	-0.880236	0.641654	0.779557	1.000
286 GOBP-MUSCLE_ORGAN_DEVELOPMENT	GO-0007517	9	-0.355412	-0.880239	0.603976	0.781350	1.000
287 GOBP-CARBOHYDRATE_BIOSYNTHETIC_PROCESS	GO-0016051	5	-0.430286	-0.883736	0.650382	0.777398	1.000
288 GOBP-CALCIUM_MEDIATED_SIGNALING	GO-0019722	10	-0.344400	-0.884372	0.616783	0.778263	1.000
289 GOBP-NEGATIVE_REGULATION_OF_CATALYTIC_ACTIVITY	GO-0043086	17	-0.299231	-0.888683	0.623790	0.772936	1.000
290 REACTOME_DISEASES_OF_SIGNAL_TRANSDUCTION_BY_G_PROTEIN_COUPLING	R-HSA-5663202	12	-0.328506	-0.890767	0.600559	0.771091	1.000
291 GOBP-RESPONSE_TO_PEPTIDE_HORMONE	GO-0043434	13	-0.320200	-0.891461	0.603878	0.771743	1.000
292 GOBP-HORMONE_TRANSPORT	GO-0009914	9	-0.357943	-0.893159	0.601783	0.770589	1.000
293 GOBP-POSITIVE_REGULATION_OF_RESPONSE_TO_EXTERNAL_STIMULUS	GO-0032103	9	-0.357943	-0.893159	0.601783	0.770589	1.000
294 GOBP-LIPID_LOCALIZATION	GO-0010876	10	-0.349426	-0.898180	0.584962	0.765836	1.000
295 GOBP-NUCLEOBASE_CONTAINING_SMALL_MOLECULE_METABOLISM	GO-0055086	6	-0.409846	-0.903127	0.597201	0.759328	1.000
296 GOBP-ANIMAL_ORGAN_MORPHOGENESIS	GO-0009887	12	-0.333184	-0.903343	0.572028	0.760775	1.000
297 GOBP-REGULATION_OF_CARBOHYDRATE_BIOSYNTHETIC_PROCESS	GO-0043255	5	-0.430286	-0.903514	0.608108	0.762280	1.000
298 GOBP-REGULATION_OF_SMALL_MOLECULE_METABOLIC_PROCESS	GO-0062012	9	-0.370130	-0.904961	0.608889	0.761663	1.000

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NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
299	REACTOME-TRAFFICKING_OF_GLR2-CONTAINING-AMPA....	R-RNO-416993	8	-0.375613	-0.905719	0.578550	0.762253
300	GOBP-REGULATION_OF_LIPID-METABOLIC_PROCESS	GO-0019216	7	-0.386184	-0.908596	0.583072	0.759201
301	GOBP-REGULATION_OF-CARBOHYDRATE-METABOLIC-PROCESS	GO-0006109	5	-0.430286	-0.910658	0.595506	0.757263
302	GOBP-CELLULAR-AMIDE-METABOLIC_PROCESS	GO-0043603	13	-0.327409	-0.910707	0.575676	0.759000
303	GOBP-PURINE-CONTAINING-COMPOUND-METABOLIC-PROCESS	GO-0072521	5	-0.440350	-0.915421	0.572123	0.753035
304	GOBP-NEGATIVE-REGULATION_OF-CELL-PROJECTION_OR...	GO-0031345	5	-0.445133	-0.917350	0.607085	0.751543
305	GOBP-INTRACELLULAR-TRANSPORT	GO-0046907	11	-0.348456	-0.918302	0.574409	0.751681
306	GOBP-LYMPHOCYTE-ACTIVATION	GO-0046649	9	-0.365535	-0.918410	0.560761	0.753320
307	GOBP-OSSIFICATION	GO-0001503	9	-0.379966	-0.920649	0.547724	0.751289
308	GOBP-REGULATION_OF-PEPTIDASE-ACTIVITY	GO-0052547	10	-0.363103	-0.923294	0.574405	0.748487
309	GOBP-NEGATIVE-REGULATION_OF-CELL-DEATH	GO-0060548	22	-0.298039	-0.924676	0.568493	0.747958
310	GOBP-DEPHOSPHORYLATION	GO-0016311	7	-0.405771	-0.928483	0.572755	0.742973
311	GOBP-CELL-GROWTH	GO-0016049	10	-0.357757	-0.930615	0.564470	0.741130
312	GOBP-NEURON-APOPTOTIC-PROCESS	GO-0051402	12	-0.340113	-0.932211	0.556309	0.740223
313	GOBP-REGULATION_OF-CELL-DIFFERENTIATION	GO-0045595	36	-0.270246	-0.934746	0.545918	0.737302
314	GOBP-POSITIVE-REGULATION_OF-EPITHELIAL-CELL-PR...	GO-0050679	7	-0.409642	-0.938258	0.541667	0.733102
315	GOBP-REGULATION_OF-ANION-TRANSMEMBRANE-TRANSPORT	GO-1903959	5	-0.448869	-0.938745	0.582400	0.734056
316	GOBP-REGULATION_OF-LIPID-LOCALIZATION	GO-1905952	5	-0.450405	-0.939823	0.551672	0.734068
317	GOBP-CELL-CELL-SIGNALING-BY-WNT	GO-0198738	7	-0.408384	-0.940435	0.542042	0.734786
318	GOBP-RESPONSE-TO-ENDOGENOUS-STIMULUS	GO-0009719	34	-0.275295	-0.940452	0.528809	0.736565
319	GOBP-CELL-MIGRATION	GO-0016477	22	-0.295742	-0.940588	0.537333	0.738165
320	GOBP-MUSCLE-ADAPTATION	GO-0043500	5	-0.454840	-0.941714	0.567901	0.738049
321	GOBP-PROTEIN-LOCALIZATION_TO-SYNAPSE	GO-0035418	5	-0.451705	-0.942334	0.576531	0.738776
322	GOBP-GROWTH	GO-0040007	14	-0.329649	-0.946533	0.535211	0.732944
323	GOBP-PROTEIN-LOCALIZATION_TO-PLASMA-MEMBRANE	GO-0072659	7	-0.406902	-0.946864	0.557576	0.734171
324	REACTOME-CELL-CYCLE-MITOTIC	R-RNO-69278	5	-0.450702	-0.949090	0.541085	0.732129
325	GOBP-PROTEIN-LOCALIZATION_TO-POSTSYNAPSE	GO-0062237	5	-0.451705	-0.949144	0.554662	0.733893
326	GOBP-SMALL-MOLECULE-METABOLIC-PROCESS	GO-0042281	15	-0.332213	-0.949978	0.527817	0.734314
327	GOBP-POSITIVE-REGULATION_OF-TRANSPORT	GO-0051050	26	-0.291410	-0.952397	0.530105	0.731819
328	GOBP-PROTEIN-DEPHOSPHORYLATION	GO-0006470	7	-0.405771	-0.952424	0.510284	0.733648
329	GOBP-REGULATION_OF-MUSCLE-ADAPTATION	GO-0043502	5	-0.454840	-0.954144	0.543131	0.732505
330	GOBP-REGULATION_OF-WNT-SIGNALING_PATHWAY	GO-0030111	5	-0.463355	-0.954902	0.559271	0.733030
331	GOBP-EXTRINSIC-APOPTOTIC-SIGNALING_PATHWAY	GO-0097191	7	-0.420125	-0.955076	0.524088	0.734636
332	GOBP-EPITHELIAL-CELL-DIFFERENTIATION	GO-0030855	7	-0.409356	-0.955216	0.524024	0.736281
333	GOBP-EMBRYONIC-ORGAN-DEVELOPMENT	GO-0048568	7	-0.412491	-0.955405	0.540458	0.737877
334	GOBP-SECRETION	GO-0046903	24	-0.299420	-0.959709	0.542969	0.731860
335	GOBP-ENDOCRINE-SYSTEM-DEVELOPMENT	GO-0035270	6	-0.435930	-0.960273	0.503852	0.732717
336	GOBP-RESPONSE-TO-NITROGEN-COMPOUND	GO-1901698	34	-0.286851	-0.963127	0.526510	0.729262
337	REACTOME-MAPK-FAMILY-SIGNALING-CASCADES	R-RNO-5683057	12	-0.349705	-0.964209	0.504348	0.729165
338	GOBP-POSITIVE-REGULATION_OF_PHOSPHATIDYLINOSIT...	GO-0014068	5	-0.472075	-0.965485	0.638392	0.728790
339	REACTOME-CELLULAR-RESPONSES_TO-EXTERNAL-STIMULI	R-RNO-8053897	12	-0.350516	-0.965697	0.510086	0.730313
340	HALLMARK-EPITHELIAL-MESENCHYMAL-TRANSITION	M5930	5	-0.464885	-0.966558	0.532925	0.730588
341	REACTOME_NERVOUS_SYSTEM-DEVELOPMENT	R-RNO-9675108	15	-0.337498	-0.968958	0.504881	0.728042

Continuation of Table S14

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
342	REACTOME_NEUTROPHIL_DEGRANULATION	R-RNO-6798695	6	-0.440796	-0.969933	0.511905	0.728158	1.000
343	GOBP_SPROUTING_ANGIOGENESIS	GO-0002040	5	-0.477801	-0.971365	0.515823	0.727496	1.000
344	GOBP_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	GO-0002263	6	-0.440796	-0.973448	0.512938	0.725539	1.000
345	GOBP_NEUROTRANSMITTER_TRANSPORT	GO-0006836	7	-0.428602	-0.976511	0.499232	0.721888	1.000
346	GOBP_REGULATION_OF_NEUROTRANSMITTER_LEVELS	GO-0001505	7	-0.428602	-0.978564	0.496229	0.719929	1.000
347	GOBP_POSITIVE_REGULATION_OF_CYSSTEINE_TYPE_ENDO...	GO-2001056	7	-0.422371	-0.979975	0.494012	0.719123	1.000
348	GOBP_EXCITATORY_CHEMICAL_SYNAPTIC_TRANSMISSION	GO-0009876	5	-0.472269	-0.980034	0.494506	0.720956	1.000
349	GOBP_FOREBRAIN_DEVELOPMENT	GO-0030900	9	-0.398592	-0.980358	0.490674	0.722309	1.000
350	GOBP_POSITIVE_REGULATION_OF_PEPTIDASE_ACTIVITY	GO-0010952	7	-0.422371	-0.980670	0.495342	0.723748	1.000
351	GOBP_LEUKOCYTE_CELL_CELL_ADHESION	GO-0007159	6	-0.443084	-0.980710	0.514821	0.725644	1.000
352	GOBP_POSITIVE_REGULATION_OF_ENDOTHELIAL_CELL_P...	GO-0001938	6	-0.450245	-0.983842	0.484472	0.721678	1.000
353	GOBP_ADENYLATE_CYCLASE_INHIBITING_G_PROTEIN_CO...	GO-0007196	9	-0.384718	-0.983851	0.485714	0.723635	1.000
354	REACTOME_SIGNALING_BY_RECEPTOR_TYROSINE_KINASES	R-RNO-9006934	26	-0.303992	-0.984868	0.469309	0.723837	1.000
355	HALLMARK_UV_RESPONSE_UP	M5941	5	-0.482279	-0.986752	0.506536	0.722246	1.000
356	GOBP_NEUROINFLAMMATORY_RESPONSE	GO-0150076	5	-0.475460	-0.987031	0.483819	0.723670	1.000
357	GOBP_RESPONSE_TO_INTERLEUKIN_1	GO-0070555	5	-0.469547	-0.987733	0.501538	0.724349	1.000
358	GOBP_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY	GO-0002444	6	-0.440796	-0.988536	0.489764	0.724887	1.000
359	GOBP_MALE_GAMETE_GENERATION	GO-0048232	5	-0.407030	-0.988875	0.489130	0.726218	1.000
360	GOBP_NEGATIVE_REGULATION_OF_HYDROLASE_ACTIVITY	GO-0051346	11	-0.370726	-0.990923	0.473609	0.724406	1.000
361	GOBP_REGULATION_OF_GROWTH	GO-0040008	13	-0.358004	-0.992030	0.473397	0.724205	1.000
362	REACTOME_G_ALPHA_Q_SIGNALING_EVENTS	R-RNO-416476	6	-0.446040	-0.994336	0.483821	0.721409	1.000
363	GOBP_AMEBOIDAL_TYPE_CELL_MIGRATION	GO-0001667	11	-0.371903	-0.995528	0.461201	0.721094	1.000
364	GOBP_REGULATION_OF_CELLULAR_COMPONENT_BIOGENESIS	GO-0044087	10	-0.387436	-0.997655	0.484050	0.719261	1.000
365	GOBP_REGULATION_OF_MUSCLE_SYSTEM_PROCESS	GO-0090257	8	-0.413910	-0.998384	0.468702	0.719752	1.000
366	GOBP_POSITIVE_REGULATION_OF_MULTICELLULAR_ORGA...	GO-0051240	32	-0.295986	-0.998781	0.467949	0.721042	1.000
367	REACTOME_ANTIINFLAMMATORY_RESPONSE_FAVORING...	R-HSA-9662851	5	-0.478060	-0.999069	0.462366	0.722576	1.000
368	GOBP_PHOSPHATIDYLINOSITOL_3_KINASE_SIGNALING	GO-0014065	7	-0.438727	-1.002825	0.468606	0.717320	1.000
369	GOBP_CARBOHYDRATE_METABOLIC_PROCESS	GO-0005975	9	-0.396140	-1.004090	0.466851	0.716757	1.000
370	GOBP_POSITIVE_REGULATION_OF_PROTEOLYSIS	GO-0045862	8	-0.416338	-1.004554	0.467391	0.717921	1.000
371	GOBP_CELLULAR_RESPONSE_TO_STARVATION	GO-0009267	5	-0.493329	-1.004799	0.490015	0.719528	1.000
372	GOBP_MULTICELLULAR_ORGANISMAL_HOMEOSTASIS	GO-0048871	12	-0.376595	-1.005207	0.470109	0.720827	1.000
373	GOBP_FAT_CELL_DIFFERENTIATION	GO-0045444	9	-0.404516	-1.005938	0.478582	0.721497	1.000
374	GOBP_REGULATION_OF_PHOSPHATIDYLINOSITOL_3_KINA...	GO-0014066	6	-0.450967	-1.006929	0.481651	0.721637	1.000
375	REACTOME_EPH_EPHRIN_SIGNALING	R-RNO-2682334	6	-0.459712	-1.008983	0.469419	0.719632	1.000
376	REACTOME_DAG_AND_IP3_SIGNALING	R-RNO-1489509	8	-0.416769	-1.010299	0.467262	0.719058	1.000
377	GOBP_REGULATION_OF_HYDROLASE_ACTIVITY	GO-0051336	22	-0.325901	-1.012859	0.443857	0.716150	1.000
378	GOBP_CELLULAR_RESPONSE_TO_PEPTIDE_HORMONE_STIM...	GO-0071375	9	-0.406157	-1.015340	0.449405	0.713284	1.000
379	GOBP_REGULATION_OF_PROTEIN_MODIFICATION_PROCESS	GO-0031399	29	-0.306673	-1.019740	0.428756	0.706491	1.000
380	GOBP_HOMEOSTATIC_PROCESS	GO-0042592	31	-0.307377	-1.022093	0.444159	0.703629	1.000
381	GOBP_REGULATION_OF_MAPK_CASCADE	GO-0043408	13	-0.367007	-1.024035	0.436700	0.701903	1.000
382	GOBP_NEGATIVE_REGULATION_OF_KINASE_ACTIVITY	GO-0033673	5	-0.495056	-1.026687	0.451078	0.698963	1.000
383	GOBP_CELLULAR_RESPONSE_TO_EXTERNAL_STIMULUS	GO-0071496	10	-0.400279	-1.027209	0.419214	0.699968	1.000
384	GOBP_NEGATIVE_REGULATION_OF_TRANSFERASE_ACTIVITY	GO-0051348	5	-0.495056	-1.027819	0.441130	0.700780	1.000

Continuation of Table S14

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
385	GOBP-RESPONSE-TO-UV	5	-0.503461	-1.028990	0.445652	0.700442	1.000
386	GOBP-RESPONSE-TO-STARVATION	5	-0.493329	-1.029565	0.437908	0.701271	1.000
387	GOBP-NEGATIVE-REGULATION-OF-PHOSPHORYLATION	7	-0.441962	-1.029846	0.431008	0.702814	1.000
388	GOBP-REGULATION-OF-SECRETION	14	-0.366493	-1.034277	0.422652	0.695971	1.000
389	GOBP-REGULATION-OF-CYSTEINE-TYPE-ENDOPEPTIDASE...	9	-0.413344	-1.043637	0.402077	0.678820	1.000
390	REACTOME-DEVELOPMENTAL-BIOLOGY	23	-0.328959	-1.044384	0.412550	0.679374	1.000
391	GOBP-NEGATIVE-REGULATION-OF-SIGNALING	21	-0.336964	-1.048748	0.402850	0.672597	1.000
392	GOBP-RAS-PROTEIN-SIGNAL-TRANSDUCTION	5	-0.517023	-1.055691	0.405864	0.660812	1.000
393	GOBP-ORGANONITROGEN-COMPOUND-BIOSYNTHETIC-PROCESS	13	-0.382275	-1.057446	0.395184	0.659325	1.000
394	GOBP-POSITIVE-REGULATION-OF-ION-TRANSPORT	17	-0.358662	-1.057859	0.390647	0.660433	1.000
395	GOBP-REGULATION-OF-ANION-TRANSPORT	20	-0.349890	-1.059001	0.380886	0.660163	1.000
396	GOBP-NEGATIVE-REGULATION-OF-LOCOMOTION	5	-0.502628	-1.060607	0.386435	0.659060	1.000
397	GOBP-POSITIVE-REGULATION-OF-MAPK-CASCADE	9	-0.412827	-1.061161	0.384389	0.660041	1.000
398	GOBP-POSITIVE-REGULATION-OF-CELLULAR-COMPONENT...	9	-0.423034	-1.061309	0.406755	0.661829	1.000
399	GOBP-ESTABLISHMENT-OF-PROTEIN-LOCALIZATION	18	-0.359840	-1.061989	0.396783	0.662564	1.000
400	GOBP-SIGNAL-RELEASE	14	-0.377679	-1.062816	0.374302	0.662972	1.000
401	GOBP-ASSOCIATIVE-LEARNING	7	-0.460200	-1.064057	0.406480	0.662524	1.000
402	REACTOME-RNA-POLYMERASE-II-TRANSCRIPTION	20	-0.351475	-1.066125	0.374507	0.660340	1.000
403	GOBP-CELLULAR-GLUCOSE-HOMEOSTASIS	5	-0.512427	-1.068103	0.395210	0.658267	1.000
404	GOBP-CELLULAR-RESPONSE-TO-PEPTIDE	13	-0.382318	-1.069068	0.395862	0.658262	1.000
405	GOBP-CIRCADIAN-REGULATION-OF-GENE-EXPRESSION	5	-0.515160	-1.069613	0.384498	0.659201	1.000
406	REACTOME-INTERLEUKIN-4-AND-INTERLEUKIN-13-SIGN...	8	-0.449741	-1.071826	0.398571	0.656595	1.000
407	GOBP-SEXUAL-REPRODUCTION	10	-0.416722	-1.072864	0.365682	0.656649	1.000
408	GOBP-REGULATION-OF-CELLULAR-COMPONENT-MOVEMENT	15	-0.373971	-1.073419	0.374294	0.657593	1.000
409	GOBP-REGULATION-OF-OSTEOCLAST-DIFFERENTIATION	5	-0.513404	-1.073717	0.382848	0.659065	1.000
410	GOBP-REGULATION-OF-CELL-DEATH	34	-0.322989	-1.084159	0.343150	0.638977	1.000
411	GOBP-REGULATION-OF-HORMONE-SECRETION	8	-0.446121	-1.084608	0.373494	0.640138	1.000
412	REACTOME-CA-DEPENDENT-EVENTS	8	-0.440478	-1.085465	0.333333	0.640376	1.000
413	GOBP-ENDOTHELIAL-CELL-MIGRATION	8	-0.461052	-1.086193	0.372635	0.640887	1.000
414	GOBP-ACTIVATION-OF-IMMUNE-RESPONSE	5	-0.521884	-1.088918	0.354267	0.637460	1.000
415	GOBP-REGULATION-OF-CELL-ACTIVATION	8	-0.459134	-1.099515	0.342342	0.617923	1.000
416	GOBP-RESPONSE-TO-NICOTINE	7	-0.475707	-1.103661	0.358548	0.611465	1.000
417	GOBP-NEURON-PROJECTION-GUIDANCE	9	-0.442951	-1.105987	0.343612	0.608811	1.000
418	GOBP-NEGATIVE-REGULATION-OF-CELLULAR-COMPONENT...	11	-0.418384	-1.108764	0.338912	0.605050	1.000
419	GOBP-RESPONSE-TO-TEMPERATURE-STIMULUS	9	-0.441108	-1.112314	0.324168	0.599623	1.000
420	GOBP-GAMETE-GENERATION	9	-0.445456	-1.112449	0.329078	0.601329	1.000
421	GOBP-PROTEIN-KINASE-B-SIGNALING	6	-0.507879	-1.113993	0.335866	0.600006	1.000
422	GOBP-REGULATION-OF-CELLULAR-CATABOLIC-PROCESS	10	-0.4303129	-1.114546	0.331420	0.600801	1.000
423	GOBP-LEARNING	13	-0.400810	-1.115254	0.325352	0.601471	1.000
424	GOBP-BLOOD-VESSEL-ENDOTHELIAL-CELL-MIGRATION	7	-0.461052	-1.116691	0.319749	0.600587	1.000
425	GOBP-CELLULAR-LIPID-METABOLIC-PROCESS	8	-0.481714	-1.117480	0.327300	0.601067	1.000
426	GOBP-RESPONSE-TO-EXTRACELLULAR-STIMULUS	13	-0.413583	-1.118410	0.324750	0.601075	1.000
427	REACTOME-SIGNALING-BY-GPCR	22	-0.354932	-1.120183	0.302865	0.599164	1.000
	R-RNO-372790						

Continuation of Table S14

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
428	REACTOME_L1CAM_INTERACTIONS	R-RNO-373760	5	-0.546893	-1.120938	0.325914	0.599627
429	GOBP_POSITIVE_REGULATION_OF_NEURON_DEATH	GO-1901216	5	-0.541925	-1.122610	0.326923	0.598241
430	GOBP_RESPONSE_TO_OXYGEN_LEVELS	GO-0070482	8	-0.464156	-1.123583	0.311047	0.598175
431	REACTOME_INTRACELLULAR_SIGNALING_BY_SECOND_MES...	R-RNO-9006925	15	-0.388713	-1.123719	0.311522	0.599949
432	GOBP_TRANSMEMBRANE_RECEPTOR_PROTEIN_TYROSINE_K...	GO-0007169	19	-0.369271	-1.126988	0.315364	0.595051
433	GOBP_CYTOKINE_MEDIATED_SIGNALING_PATHWAY	GO-0019221	16	-0.385985	-1.127792	0.297260	0.595450
434	GOBP_POSITIVE_REGULATION_OF_CELL_DEATH	GO-0010942	19	-0.372147	-1.131475	0.311634	0.589656
435	GOBP_NEURON_DEATH	GO-0070997	18	-0.376074	-1.133688	0.301061	0.587087
436	GOBP_POSITIVE_REGULATION_OF_PROTEIN_SERINE_THR...	GO-0071902	9	-0.446523	-1.135837	0.298682	0.584469
437	GOBP_POSITIVE_REGULATION_OF_DEVELOPMENTAL_PROCE...	GO-0051094	32	-0.338772	-1.139227	0.293520	0.579437
438	GOBP_MORPHOGENESIS_OF_AN_EPITHELIUM	GO-0002009	6	-0.509450	-1.139361	0.314815	0.581188
439	GOBP_PROTEIN_AUTOPHOSPHORYLATION	GO-0046777	5	-0.553332	-1.140026	0.314425	0.581823
440	GOBP_MUSCLE_STRUCTURE_DEVELOPMENT	GO-0061061	16	-0.396315	-1.142965	0.306849	0.577695
441	GOBP_NEGATIVE_REGULATION_OF_PROTEOLYSIS	GO-0045861	8	-0.469777	-1.145393	0.288084	0.574484
442	GOBP_REGULATION_OF_CELL_CELL_ADHESION	GO-0022407	9	-0.459300	-1.145529	0.292467	0.570294
443	REACTOME_G_ALPHA_I_SIGNALING_EVENTS	R-RNO-418594	18	-0.379797	-1.148312	0.280822	0.572578
444	GOBP_NEGATIVE_REGULATION_OF_CELL_CYCLE	GO-0045786	5	-0.554217	-1.148394	0.297078	0.574417
445	GOBP_CELLULAR_RESPONSE_TO_KETONE	GO-1901655	5	-0.552973	-1.149409	0.293461	0.574417
446	GOBP_POSITIVE_REGULATION_OF_CELL_DIFFERENTIATION	GO-0045597	27	-0.344946	-1.150488	0.284967	0.574196
447	GOBP_REGULATION_OF_PROTEIN_STABILITY	GO-0031647	5	-0.566259	-1.150598	0.293564	0.576102
448	GOBP_TISSUE_MIGRATION	GO-0090130	9	-0.457598	-1.154792	0.279104	0.569072
449	GOBP_CELLULAR_RESPONSE_TO_ALCOHOL	GO-0097306	5	-0.557662	-1.154854	0.278135	0.571038
450	REACTOME_ESTROGEN_DEPENDENT_NUCLEAR_EVENTS_DOW...	R-RNO-9634638	5	-0.557976	-1.155832	0.285943	0.571301
451	GOBP_RESPIRATORY_SYSTEM_DEVELOPMENT	GO-0060541	6	-0.521203	-1.158269	0.283742	0.568111
452	GOBP_REGULATION_OF_CELLULAR_AMIDE_METABOLIC_PR...	GO-0034248	9	-0.467688	-1.159762	0.282421	0.566966
453	GOBP_EPIDERMIS_DEVELOPMENT	GO-0008544	5	-0.561536	-1.159794	0.278207	0.569021
454	GOBP_EPHRIN_RECEPTOR_SIGNALING_PATHWAY	GO-0048013	5	-0.561362	-1.164966	0.277512	0.560548
455	GOBP_POSITIVE_REGULATION_OF_CELL_CELL_ADHESION	GO-0022409	5	-0.570060	-1.168124	0.293185	0.555695
456	GOBP_REGULATION_OF_PEPTIDE_TRANSPORT	GO-0090087	10	-0.442469	-1.169897	0.278499	0.553887
457	GOBP_ANATOMICAL_STRUCTURE_FORMATION_INVOLVED_I...	GO-0048646	20	-0.385197	-1.171160	0.259591	0.553202
458	GOBP_IMPORT_INTO_CELL	GO-0098657	6	-0.531559	-1.174518	0.275969	0.548020
459	GOBP_REGULATION_OF_BINDING	GO-0051098	11	-0.452476	-1.174642	0.265335	0.549847
460	GOBP_HOMEOSTASIS_OF_NUMBER_OF_CELLS	GO-0048872	5	-0.554608	-1.176729	0.266254	0.547597
461	GOBP_INTRACELLULAR_RECEPTOR_SIGNALING_PATHWAY	GO-0030522	5	-0.562297	-1.177173	0.248788	0.548710
462	GOBP_REGULATION_OF_CELL_ADHESION	GO-0030155	13	-0.427447	-1.177257	0.264828	0.550667
463	GOBP_MEMBRANE_ORGANIZATION	GO-0061024	12	-0.406104	-1.177556	0.267525	0.551749
464	GOBP_SECOND_MESSENGER_MEDIATED_SIGNALING	GO-0019932	16	-0.402811	-1.179236	0.267983	0.550574
465	GOBP_GLAND_DEVELOPMENT	GO-0048732	7	-0.509580	-1.179953	0.264122	0.551194
466	GOBP_POSITIVE_REGULATION_OF_ORGANELLE_ORGANIZA...	GO-0010638	10	-0.455895	-1.180425	0.263533	0.552337
467	GOBP_REGULATION_OF_FAT_CELL_DIFFERENTIATION	GO-0045598	6	-0.542297	-1.180577	0.257576	0.554212
468	REACTOME_G_PROTEIN_MEDIATED_EVENTS	R-RNO-112040	9	-0.468667	-1.181526	0.248889	0.554314
469	GOBP_LOCOMOTION	GO-0040011	31	-0.354203	-1.182814	0.253827	0.553695
470	GOBP_LIPID_METABOLIC_PROCESS	GO-0006629	10	-0.453245	-1.183579	0.249288	0.554258

Continuation of Table S14

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
471	GOBP-MEMBRANE-PROTEIN-PROTEOLYSIS	GO-0033619	6	-0.534829	-1.183702	0.272586	0.556206	1.000
472	GOBP-POSITIVE-REGULATION-OF-GENE-EXPRESSION	GO-0010628	16	-0.404110	-1.184729	0.248032	0.556217	1.000
473	GOBP-SMALL-GTPASE-MEDIATED-SIGNAL-TRANSDUCTION	GO-0007264	8	-0.493019	-1.185563	0.261516	0.556509	1.000
474	GOBP-POSITIVE-REGULATION-OF-LEUKOCYTE-CELL-CEL...	GO-1903039	5	-0.570060	-1.185918	0.230887	0.558019	1.000
475	GOBP-CELLULAR-RESPONSE-TO-EXTRACELLULAR-STIMULUS	GO-0031668	8	-0.497305	-1.186036	0.279001	0.560033	1.000
476	GOBP-OSTEOBLAST-DIFFERENTIATION	GO-0001649	5	-0.566061	-1.190067	0.242376	0.553522	1.000
477	GOBP-REGULATION-OF-CIRCADIAN-RHYTHM	GO-0042752	7	-0.514972	-1.192325	0.260212	0.551068	1.000
478	REACTOME-CIRCADIAN-CLOCK	R-HSA-400253	5	-0.573930	-1.195935	0.244019	0.545312	1.000
479	GOBP-REGULATION-OF-MULTICELLULAR-ORGANISMAL-DE...	GO-2000026	31	-0.362303	-1.205084	0.236709	0.527647	1.000
480	HALLMARK-APOPTOSIS	M5902	6	-0.550328	-1.209423	0.215873	0.520616	1.000
481	GOBP-BIOLOGICAL-ADHESION	GO-0022610	19	-0.394708	-1.210534	0.226519	0.520402	1.000
482	GOBP-LEUKOCYTE-MIGRATION	GO-0050900	6	-0.544886	-1.213434	0.214391	0.516189	1.000
483	REACTOME-CELLULAR-SENESCENCE	GO-2559583	6	-0.559810	-1.218086	0.222910	0.508285	1.000
484	REACTOME-EXTRA-NUCLEAR-ESTROGEN-SIGNALING	R-RNO-9009391	7	-0.528607	-1.220095	0.223077	0.506211	1.000
485	GOBP-CYTOSKELETON-ORGANIZATION	GO-0007010	11	-0.474431	-1.220989	0.231760	0.506650	1.000
486	REACTOME-PTEN-REGULATION	R-RNO-6807070	5	-0.594614	-1.221061	0.226415	0.508713	1.000
487	REACTOME-SENESCENCE-ASSOCIATED-SECRETORY-PHENO...	R-RNO-2559582	6	-0.559810	-1.227801	0.200000	0.496446	1.000
488	GOBP-RESPONSE-TO-ABIOTIC-STIMULUS	GO-0009628	27	-0.381607	-1.230990	0.198925	0.491983	1.000
489	GOBP-LEUKOCYTE-MEDIATED-IMMUNITY	GO-0002443	7	-0.526107	-1.233912	0.214176	0.488042	1.000
490	GOBP-OSTEOCLAST-DIFFERENTIATION	GO-0030316	6	-0.569164	-1.234265	0.206731	0.489500	1.000
491	GOBP-POSTTRANSCRIPTIONAL-REGULATION-OF-GENE-EX...	GO-0010608	8	-0.509474	-1.234846	0.217066	0.490295	1.000
492	GOBP-NEGATIVE-REGULATION-OF-CATABOLIC-PROCESS	GO-0009895	8	-0.509810	-1.237152	0.202050	0.487432	1.000
493	GOBP-RESPONSE-TO-MECHANICAL-STIMULUS	GO-0009612	6	-0.559612	-1.238363	0.210687	0.487117	1.000
494	GOBP-REGULATION-OF-LIPID-BIOSYNTHETIC-PROCESS	GO-0046890	6	-0.571877	-1.238642	0.216718	0.488716	1.000
495	GOBP-POSITIVE-REGULATION-OF-CELL-ADHESION	GO-0045785	7	-0.539602	-1.239507	0.209199	0.489233	1.000
496	GOBP-REGULATION-OF-RESPONSE-TO-STRESS	GO-0080134	19	-0.410329	-1.239849	0.202514	0.490625	1.000
497	GOBP-INTRINSIC-APOPTOTIC-SIGNALING-PATHWAY	GO-0097193	5	-0.595652	-1.240722	0.183359	0.490984	1.000
498	REACTOME-INTEGRATION-OF-ENERGY-METABOLISM	R-RNO-163685	5	-0.612785	-1.243963	0.197390	0.485938	1.000
499	GOBP-CELL-JUNCTION-ASSEMBLY	GO-0034329	8	-0.519218	-1.244396	0.200295	0.487276	1.000
500	GOBP-NEGATIVE-REGULATION-OF-PROTEIN-CATABOLIC...	GO-0042177	5	-0.603428	-1.245600	0.193199	0.486963	1.000
501	GOBP-REGULATION-OF-PROTEIN-SERINE-THREONINE-KI...	GO-0071900	12	-0.461404	-1.247432	0.204769	0.485419	1.000
502	GOBP-RESPONSE-TO-OXYGEN-CONTAINING-COMPOUND	GO-1901700	39	-0.359915	-1.248847	0.188045	0.484644	1.000
503	GOBP-DEVELOPMENTAL-PROCESS-INVOLVED-IN-REPRODU...	GO-0003006	11	-0.482261	-1.249592	0.202899	0.485306	1.000
504	REACTOME-FC-EPSILON-RECEPTOR-FCER1-SIGNALING	R-RNO-2454202	7	-0.537202	-1.250647	0.191063	0.485288	1.000
505	GOBP-FC-EPSILON-RECEPTOR-SIGNALING-PATHWAY	GO-0038095	7	-0.537202	-1.250977	0.189024	0.486745	1.000
506	GOBP-PROTEIN-LOCALIZATION-TO-ORGANELLE	GO-0033365	9	-0.510995	-1.251775	0.183381	0.487145	1.000
507	GOBP-REGULATION-OF-PROTEOLYSIS	GO-0030162	12	-0.455525	-1.253173	0.195225	0.486534	1.000
508	GOBP-MAINTENANCE-OF-LOCATION	GO-0051235	7	-0.540365	-1.253625	0.207143	0.487841	1.000
509	GOBP-RESPONSE-TO-BIOTIC-STIMULUS	GO-0009607	17	-0.426189	-1.255092	0.199158	0.486850	1.000
510	GOBP-PEPTIDYL-LYSINE-MODIFICATION	GO-0018205	5	-0.601123	-1.255610	0.186520	0.488046	1.000
511	GOBP-REPRODUCTION	GO-0000003	18	-0.422724	-1.258602	0.163265	0.483948	1.000
512	GOBP-ERK1-AND-ERK2-CASCADE	GO-0070371	5	-0.602525	-1.259114	0.175115	0.485174	1.000
513	GOBP-REGULATION-OF-CELL-CYCLE-PROCESS	GO-0010564	5	-0.605539	-1.261307	0.173313	0.482861	1.000

Continuation of Table S14

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
514 GOBP-REGULATION-OF-ORGANELLE-ORGANIZATION	GO-0033043	14	-0.440816	-1.261566	0.195122	0.484709	1.000
515 GOBP-LIPID-BIOSYNTHETIC-PROCESS	GO-0008610	6	-0.571877	-1.263558	0.176563	0.482898	1.000
516 GOBP-NEGATIVE-REGULATION-OF-RESPONSE-TO-EXTERN...	GO-0032102	5	-0.610088	-1.264972	0.181126	0.482005	1.000
517 GOBP-REGULATION-OF-DNA-BINDING-TRANSCRIPTION.F...	GO-0051090	16	-0.432672	-1.269080	0.176144	0.474919	1.000
518 GOBP-PROTEIN-LOCALIZATION-TO-MEMBRANE	GO-0072657	14	-0.454465	-1.270282	0.178121	0.474634	1.000
519 GOBP-CELLULAR-COMPONENT-DISASSEMBLY	GO-0022411	6	-0.582656	-1.275201	0.156105	0.465813	1.000
520 GOBP-ESTABLISHMENT-OF-PROTEIN-LOCALIZATION-TO...	GO-0072594	6	-0.572273	-1.278013	0.165635	0.461857	1.000
521 GOBP-MULTICELLULAR-ORGANISM-REPRODUCTION	GO-0032504	12	-0.473916	-1.280665	0.169188	0.458971	1.000
522 GOBP-REGULATION-OF-CELLULAR-RESPONSE-TO-STRESS	GO-0080135	9	-0.510234	-1.281282	0.176558	0.460050	1.000
523 GOBP-RESPONSE-TO-INSULIN	GO-0032868	5	-0.621597	-1.282353	0.159420	0.460180	1.000
524 GOBP-ANATOMICAL-STRUCTURE-HOMEOSTASIS	GO-0060249	7	-0.552246	-1.282803	0.174528	0.461561	1.000
525 REACTOME-G-ALPHA-Z-SIGNALING-EVENTS	R-RNO-418597	5	-0.623425	-1.284219	0.172414	0.461037	1.000
526 GOBP-POSITIVE-REGULATION-OF-CYTOKINE-PRODUCTION	GO-0001819	7	-0.556004	-1.285835	0.175150	0.459874	1.000
527 GOBP-POSITIVE-REGULATION-OF-LOCOMOTION	GO-0040017	11	-0.478343	-1.286289	0.173104	0.461199	1.000
528 GOBP-PROTEIN-LOCALIZATION-TO-CELL-PERIPHERY	GO-1990778	12	-0.475630	-1.286669	0.171388	0.462808	1.000
529 GOBP-MONONUCLEAR-CELL-DIFFERENTIATION	GO-1903131	7	-0.553067	-1.288037	0.182371	0.462345	1.000
530 GOBP-APOPTOTIC-PROCESS	GO-0006915	35	-0.381447	-1.289892	0.153186	0.460708	1.000
531 GOBP-ACTIN-FILAMENT-BASED-PROCESS	GO-0030029	7	-0.549885	-1.290410	0.159940	0.462110	1.000
532 GOBP-CELLULAR-RESPONSE-TO-HORMONE-STIMULUS	GO-0032870	11	-0.489732	-1.292907	0.165975	0.458502	1.000
533 GOBP-HEAD-DEVELOPMENT	GO-0060322	22	-0.414989	-1.294014	0.167726	0.458470	1.000
534 GOBP-CELL-CELL-ADHESION	GO-0098609	14	-0.456416	-1.297615	0.170765	0.453007	1.000
535 REACTOME-MEMBRANE-TRAFFICKING	R-RNO-199991	5	-0.627173	-1.300739	0.158654	0.448624	1.000
536 GOBP-AGING	GO-0007568	13	-0.469088	-1.303006	0.171788	0.446118	1.000
537 GOBP-NEGATIVE-REGULATION-OF-CELL-POPULATION-PR...	GO-0008285	9	-0.522323	-1.303332	0.151825	0.447952	1.000
538 GOBP-TISSUE-MORPHOGENESIS	GO-0048729	7	-0.550675	-1.304957	0.156923	0.447002	1.000
539 GOBP-AMYLOID-BETA-METABOLIC-PROCESS	GO-0050435	5	-0.633039	-1.306881	0.125786	0.444996	1.000
540 GOBP-REGULATION-OF-PROTEIN-LOCALIZATION-TO-CEL...	GO-1904375	6	-0.587960	-1.306930	0.145062	0.447421	1.000
541 GOBP-POSITIVE-REGULATION-OF-ESTABLISHMENT-OF-P...	GO-1904951	5	-0.631771	-1.312334	0.147673	0.437844	1.000
542 GOBP-CELLULAR-MACROMOLECULE-LOCALIZATION	GO-0070727	21	-0.425897	-1.312821	0.134349	0.439223	1.000
543 GOBP-POSITIVE-REGULATION-OF-CELL-POPULATION-PR...	GO-0008284	21	-0.421622	-1.312956	0.138441	0.441427	1.000
544 GOBP-PROTEOLYSIS	GO-0006508	17	-0.450445	-1.312972	0.128065	0.443932	1.000
545 GOBP-NEGATIVE-REGULATION-OF-INTRACELLULAR-SIGN...	GO-1902532	7	-0.559033	-1.312992	0.139466	0.446414	1.000
546 GOBP-CELL-CELL-JUNCTION-ASSEMBLY	GO-0007043	5	-0.628631	-1.314178	0.127055	0.446192	1.000
547 REACTOME-INFECTIOUS-DISEASE	R-HSA-5663205	13	-0.477951	-1.315433	0.144044	0.445762	1.000
548 GOBP-POSITIVE-REGULATION-OF-SMALL-MOLECULE-MET...	GO-0062013	5	-0.635402	-1.318008	0.122417	0.442287	1.000
549 REACTOME-NGF-STIMULATED-TRANSCRIPTION	R-RNO-9031628	9	-0.524113	-1.322209	0.145115	0.435186	1.000
550 GOBP-PROTEIN-LOCALIZATION-TO-CELL-JUNCTION	GO-1902414	6	-0.609480	-1.322591	0.144216	0.436764	1.000
551 GOBP-AMYLOID-PRECURSOR-PROTEIN-METABOLIC-PROCESS	GO-0042982	5	-0.630309	-1.324007	0.124595	0.436316	1.000
552 REACTOME-VESICLE-MEDIATED-TRANSPORT	R-RNO-5653656	5	-0.627173	-1.324319	0.137600	0.438319	1.000
553 GOBP-AMYLOID-PRECURSOR-PROTEIN-CATABOLIC-PROCESS	GO-0042987	5	-0.630309	-1.326422	0.127451	0.435923	1.000
554 REACTOME-CELL-CYCLE	R-RNO-1640170	6	-0.590729	-1.328338	0.135542	0.434269	1.000
555 REACTOME-OPIOID-SIGNALING	R-RNO-111885	12	-0.489571	-1.333008	0.122963	0.426280	1.000
556 GOBP-REGULATION-OF-RESPONSE-TO-EXTERNAL-STIMULUS	GO-0032101	15	-0.469180	-1.335375	0.122253	0.423528	1.000

Continuation of Table S14

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
557 REACTOME-CYTOKINE.SIGNALING.IN.IMMUNE.SYSTEM	R-RNO-1280215	21	-0.438737	-1.336157	0.136126	0.424438	1.000
558 HALLMARK-HYPOXIA	M5891	5	-0.640660	-1.341054	0.124807	0.416019	1.000
559 GOBP-REGULATION-OF-PROTEIN.LOCALIZATION	GO-0032880	18	-0.439813	-1.341594	0.120805	0.417429	1.000
560 GOBP-POSITIVE.REGULATION-OF-CELLULAR-PROTEIN.L...	GO-1903829	7	-0.575381	-1.341643	0.125000	0.419883	1.000
561 GOBP-EPITHELIIUM.DEVELOPMENT	GO-0060429	15	-0.466605	-1.344429	0.125176	0.416549	1.000
562 GOBP-INTRACELLULAR-PROTEIN-TRANSPORT	GO-0006886	9	-0.534929	-1.346239	0.120715	0.414884	1.000
563 HALLMARK-TNFA.SIGNALING.VIA-NFKB	M5890	14	-0.475107	-1.353748	0.116901	0.400574	1.000
564 REACTOME-INTERLEUKIN-17-SIGNALING	R-RNO-448424	6	-0.617888	-1.362088	0.119335	0.385255	1.000
565 GOBP-RESPONSE-TO-HORMONE	GO-0009725	20	-0.436937	-1.364745	0.123835	0.381856	1.000
566 GOBP-POSITIVE.REGULATION-OF-EPITHELIAL-CELL.MI...	GO-0010634	5	-0.661651	-1.365557	0.092332	0.382734	1.000
567 GOBP-ENDOMEMBRANE-SYSTEM-ORGANIZATION	GO-0010256	6	-0.615238	-1.368580	0.109940	0.378576	1.000
568 GOBP-REGULATION-OF-GTPASE-ACTIVITY	GO-0043087	5	-0.656120	-1.372505	0.106725	0.372952	1.000
569 GOBP-REGULATION-OF-CATABOLIC-PROCESS	GO-0009894	13	-0.494918	-1.373650	0.105644	0.372994	1.000
570 GOBP-NEGATIVE.REGULATION-OF-NEUROUS.SYSTEM.DEV...	GO-0051961	5	-0.663511	-1.373919	0.075710	0.374979	1.000
571 GOBP-RESPONSE-TO-INORGANIC-SUBSTANCE	GO-0010035	19	-0.457066	-1.373941	0.116248	0.377476	1.000
572 GOBP-NEGATIVE.REGULATION-OF-MULTICELLULAR-ORGA...	GO-0051241	15	-0.473331	-1.374968	0.106534	0.377747	1.000
573 GOBP-CELL-CYCLE-PROCESS	GO-0022402	11	-0.522879	-1.380349	0.101156	0.368932	1.000
574 GOBP-POSITIVE.REGULATION-OF-HEMOPOIESIS	GO-1903708	7	-0.604938	-1.382346	0.103048	0.367235	1.000
575 GOBP-CELLULAR-RESPONSE-TO-ORGANIC-CYCLIC-COMPOUND	GO-0071407	13	-0.495187	-1.383210	0.103550	0.367858	1.000
576 REACTOME-TRANSCRIPTIONAL.REGULATION-BY-TP53	R-RNO-3700989	6	-0.630828	-1.385165	0.087500	0.366304	1.000
577 REACTOME-SIGNALING-BY-NUCLEAR-RECEPTORS	R-RNO-9006931	8	-0.578316	-1.386378	0.102453	0.366225	1.000
578 GOBP-CELLULAR-MACROMOLECULE-CATABOLIC-PROCESS	GO-0044265	6	-0.630397	-1.388491	0.089292	0.363972	1.000
579 GOBP-RESPONSE-TO-ACID-CHEMICAL	GO-0001101	6	-0.630962	-1.389425	0.085139	0.364565	1.000
580 GOBP-RESPONSE-TO-CYTOKINE	GO-0034097	23	-0.444123	-1.391782	0.095872	0.361911	1.000
581 GOBP-NEGATIVE.REGULATION-OF-PROTEIN-METABOLIC-...	GO-0051248	20	-0.460963	-1.399774	0.083799	0.348249	1.000
582 GOBP-NEGATIVE.REGULATION-OF-TRANSMEMBRANE-TRAN...	GO-0034763	6	-0.632308	-1.399997	0.088550	0.350289	1.000
583 GOBP-CELL-CELL-JUNCTION-ORGANIZATION	GO-0045216	6	-0.629966	-1.400035	0.094595	0.352784	1.000
584 GOBP-NEGATIVE.REGULATION-OF-MOLECULAR-FUNCTION	GO-0044092	24	-0.445276	-1.400230	0.084918	0.354855	1.000
585 GOBP-NEGATIVE.REGULATION-OF-CELL-DEVELOPMENT	GO-0010721	6	-0.632957	-1.400496	0.089202	0.357000	1.000
586 GOBP-REPRODUCTIVE-SYSTEM-DEVELOPMENT	GO-0061458	6	-0.641572	-1.401005	0.082792	0.358474	1.000
587 GOBP-RESPONSE-TO-TUMOR-NECROSIS-FACTOR	GO-0034612	7	-0.607462	-1.403199	0.094815	0.356791	1.000
588 REACTOME-NUCLEAR-EVENTS-KINASE-AND-TRANSCRIPTI...	R-RNO-198725	11	-0.533065	-1.403523	0.093484	0.358863	1.000
589 GOBP-NEGATIVE.REGULATION-OF-PHOSPHORUS-METABOL...	GO-0010563	9	-0.560604	-1.406121	0.089419	0.355892	1.000
590 REACTOME-ESR-MEDIATED-SIGNALING	R-RNO-8939211	8	-0.578316	-1.406476	0.083458	0.357889	1.000
591 GOBP-REGULATION-OF-PROTEIN-LOCALIZATION-TO-MEM...	GO-1905475	7	-0.604870	-1.406846	0.080871	0.359883	1.000
592 GOBP-RESPONSE-TO-LIGHT-STIMULUS	GO-0009416	11	-0.523387	-1.410242	0.095729	0.355214	1.000
593 GOBP-REGULATION-OF-VASCULATURE-DEVELOPMENT	GO-1901342	5	-0.686454	-1.413411	0.073600	0.351240	1.000
594 REACTOME-SIGNALING-BY-WNT	R-RNO-195721	7	-0.611373	-1.414512	0.085139	0.351682	1.000
595 REACTOME-LEISHMANIA-INFECTION	R-HSA-9658195	10	-0.539120	-1.415090	0.091298	0.353179	1.000
596 GOBP-NEGATIVE.REGULATION-OF-TRANSCRIPTION-BY-R...	GO-0000122	10	-0.545247	-1.417694	0.087770	0.350286	1.000
597 GOBP-RESPONSE-TO-KETONE	GO-1901654	7	-0.621300	-1.418721	0.102832	0.350822	1.000
598 GOBP-POSITIVE.REGULATION-OF-IMMUNE-RESPONSE	GO-0050778	9	-0.553220	-1.419267	0.093220	0.352513	1.000
599 GOBP-RESPONSE-TO-ORGANIC-CYCLIC-COMPOUND	GO-0014070	20	-0.460948	-1.423189	0.074728	0.347424	1.000

Continuation of Table S14

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
600 GOBP-CENTRAL-NERVOUS-SYSTEM-DEVELOPMENT	GO-0007417	26	-0.446402	-1.423451	0.081117	0.349762	1.000
601 REACTOME-PLATELET-ACTIVATION-SIGNALING-AND-AGG...	R-HSA-76002	7	-0.601663	-1.434621	0.082831	0.329465	1.000
602 GOBP-CELL-ACTIVATION	GO-0001775	21	-0.469663	-1.436794	0.074667	0.327892	1.000
603 GOBP-ENDOTHELIAL-CELL-PROLIFERATION	GO-0001935	8	-0.579062	-1.437413	0.077160	0.329297	1.000
604 GOBP-TISSUE-HOMEOSTASIS	GO-0001894	5	-0.695341	-1.442242	0.068182	0.322665	1.000
605 GOBP-MULTI-ORGANISM-PROCESS	GO-0051704	16	-0.495280	-1.443253	0.080711	0.323192	1.000
606 GOBP-IMMUNE-RESPONSE-REGULATING-SIGNALING-PATHWAY	GO-000276	8	-0.608852	-1.445589	0.076358	0.321128	1.000
607 REACTOME-ADAPTIVE-IMMUNE-SYSTEM	R-RNO-1280218	9	-0.570356	-1.455088	0.073906	0.304840	1.000
608 GOBP-VASCULATURE-DEVELOPMENT	GO-0001944	17	-0.499892	-1.458490	0.065826	0.301290	1.000
609 GOBP-GLUCOSE-METABOLIC-PROCESS	GO-0006006	6	-0.673422	-1.466457	0.053042	0.288099	1.000
610 GOBP-NEGATIVE-REGULATION-OF-GENE-EXPRESSION	GO-0010629	12	-0.545970	-1.467629	0.065248	0.288487	1.000
611 GOBP-CELL-POPULATION-PROLIFERATION	GO-0008283	31	-0.439369	-1.469941	0.051572	0.286800	1.000
612 GOBP-FC-RECEPTOR-SIGNALING-PATHWAY	GO-0038093	8	-0.608852	-1.470034	0.074242	0.289307	1.000
613 GOBP-BLOOD-VESSEL-MORPHOGENESIS	GO-0048514	14	-0.524079	-1.471157	0.064156	0.289922	1.000
614 GOBP-CELLULAR-RESPONSE-TO-BIOTIC-STIMULUS	GO-0071216	8	-0.604991	-1.471758	0.061605	0.291454	1.000
615 GOBP-DNA-METABOLIC-PROCESS	GO-0006259	6	-0.673749	-1.478918	0.044961	0.280553	1.000
616 GOBP-REGULATION-OF-LEUKOCYTE-DIFFERENTIATION	GO-1902105	9	-0.587632	-1.479242	0.063470	0.282481	1.000
617 GOBP-CELLULAR-RESPONSE-TO-MOLECULE-OF-BACTERIA...	GO-0071219	8	-0.604991	-1.481979	0.061728	0.280022	1.000
618 GOBP-ORGANONITROGEN-COMPOUND-CATABOLIC-PROCESS	GO-1901565	9	-0.604426	-1.482138	0.051750	0.282513	1.000
619 GOBP-REGULATION-OF-EXTRINSIC-APOPTOTIC-SIGNALI...	GO-2001236	6	-0.672396	-1.482403	0.046948	0.284975	1.000
620 GOBP-TUBE-DEVELOPMENT	GO-0035295	18	-0.510793	-1.484679	0.052561	0.283516	1.000
621 GOBP-MUSCLE-CELL-PROLIFERATION	GO-0033002	8	-0.612194	-1.484760	0.043541	0.286353	1.000
622 GOBP-REGULATION-OF-PROTEIN-CATABOLIC-PROCESS	GO-0042176	7	-0.637297	-1.485548	0.056923	0.282305	1.000
623 GOBP-ERBB-SIGNALING-PATHWAY	GO-0038127	5	-0.722630	-1.489523	0.034215	0.283106	1.000
624 GOBP-CHROMATIN-ORGANIZATION	GO-0006325	5	-0.722892	-1.490524	0.036866	0.284118	1.000
626 GOBP-MONOSACCHARIDE-METABOLIC-PROCESS	GO-0005996	6	-0.673422	-1.491129	0.051128	0.289027	1.000
627 GOBP-EPITHELIAL-CELL-PROLIFERATION	GO-0050673	12	-0.550209	-1.491385	0.069672	0.291564	1.000
628 GOBP-POSITIVE-REGULATION-OF-APOPTOTIC-SIGNALIN...	GO-2001235	5	-0.734940	-1.493987	0.043339	0.289385	1.000
629 GOBP-IMMUNE-EFFECTOR-PROCESS	GO-0002252	10	-0.583485	-1.494707	0.048780	0.291249	1.000
630 GOBP-TUBE-MORPHOGENESIS	GO-0035239	15	-0.522309	-1.505098	0.053908	0.273409	1.000
631 GOBP-PROTEIN-MODIFICATION-BY-SMALL-PROTEIN-CON...	GO-0032446	6	-0.691855	-1.508328	0.033233	0.270355	1.000
632 GOBP-POSITIVE-REGULATION-OF-SMOOTH-MUSCLE-CELL...	GO-0048661	5	-0.732086	-1.509184	0.037736	0.271924	1.000
633 GOBP-RESPONSE-TO-BACTERIUM	GO-0009617	13	-0.559844	-1.510477	0.042877	0.272539	1.000
634 GOBP-NEGATIVE-REGULATION-OF-PROTEIN-MODIFICATI...	GO-0031400	10	-0.600181	-1.514599	0.044863	0.268169	1.000
635 GOBP-POSITIVE-REGULATION-OF-MYELOID-LEUKOCYTE...	GO-0002763	6	-0.686842	-1.515990	0.048465	0.268528	1.000
636 REACTOME-BETA-CATENIN-INDEPENDENT-WNT-SIGNALING	R-RNO-3858494	5	-0.740174	-1.519006	0.022013	0.265945	1.000
637 GOBP-CIRCADIEN-RHYTHM	GO-0007623	13	-0.545876	-1.519849	0.043185	0.267258	1.000
638 GOBP-MITOTIC-CELL-CYCLE	GO-0000278	10	-0.590661	-1.519872	0.042336	0.270544	1.000
639 GOBP-RESPONSE-TO-RADIATION	GO-0009314	13	-0.551247	-1.523121	0.049226	0.266780	1.000
640 GOBP-NEGATIVE-REGULATION-OF-BINDING	GO-0051100	6	-0.678112	-1.523159	0.046225	0.270076	1.000
641 GOBP-REGULATION-OF-CELLULAR-LOCALIZATION	GO-0060341	17	-0.522519	-1.524919	0.031464	0.270129	1.000
642 REACTOME-MAPK-TARGETS-NUCLEAR-EVENTS-MEDIATED....	R-HSA-450282	5	-0.715967	-1.526846	0.035427	0.270064	1.000

Continuation of Table S14

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
643 GOBP-BIOLOGICAL-PROCESS-INVOLVED-IN-SYMBIOTIC....	GO-004440	11	-0.574124	-1.527849	0.046784	0.271718	1.000
644 GOBP-ENZYME-LINKED-RECEPTOR-PROTEIN-SIGNALING....	GO-0007167	24	-0.478180	-1.538891	0.034076	0.255122	1.000
645 GOBP-CHROMOSOME-ORGANIZATION	GO-0051276	6	-0.705104	-1.540686	0.027287	0.255059	1.000
646 GOBP-REGULATION-OF-MITOTIC-CELL-CYCLE	GO-0007346	5	-0.742239	-1.540790	0.033333	0.258328	1.000
647 GOBP-SKIN-DEVELOPMENT	GO-0043588	5	-0.730149	-1.541176	0.040310	0.261079	1.000
648 GOBP-MITOCHONDRION-ORGANIZATION	GO-0007005	7	-0.675904	-1.548931	0.036220	0.250316	1.000
649 GOBP-RESPONSE-TO-REACTIVE-OXYGEN-SPECIES	GO-0000302	8	-0.647348	-1.550406	0.031019	0.251207	1.000
650 REACTOME-HEMOSTASIS	R-RNO-109582	14	-0.554022	-1.551307	0.031989	0.253327	1.000
651 GOBP-PHAGOCYTOSIS	GO-0006909	5	-0.739949	-1.551887	0.024316	0.256039	1.000
652 GOBP-RHYTHMIC-PROCESS	GO-0048511	15	-0.549462	-1.555519	0.028302	0.252716	1.000
653 GOBP-NEGATIVE-REGULATION-OF-NUCLEOBASE-CONTAIN...	GO-0045934	13	-0.561585	-1.557017	0.036212	0.253808	1.000
654 REACTOME-SIGNALING-BY-INTERLEUKINS	R-RNO-449147	15	-0.540274	-1.558723	0.036932	0.253987	1.000
655 GOBP-RESPONSE-TO-MOLECULE-OF-BACTERIAL-ORIGIN	GO-0002237	13	-0.559844	-1.562099	0.028050	0.251192	1.000
656 GOBP-REGULATION-OF-EPITHELIAL-CELL-MIGRATION	GO-0010632	6	-0.705708	-1.565336	0.018293	0.249027	1.000
657 GOBP-RESPONSE-TO-OXIDATIVE-STRESS	GO-0006979	8	-0.647348	-1.566597	0.031157	0.250695	1.000
658 GOBP-NEGATIVE-REGULATION-OF-APOPTOTIC-SIGNALIN...	GO-2001234	7	-0.674534	-1.569100	0.028860	0.249839	1.000
659 GOBP-REGULATION-OF-PROTEIN-BINDING	GO-0043393	7	-0.673716	-1.570443	0.033537	0.253602	1.000
660 GOBP-REGULATION-OF-BODY-FLUID-LEVELS	GO-0050878	11	-0.597467	-1.570443	0.024965	0.255950	1.000
661 GOBP-REGULATION-OF-HEMOPOIESIS	GO-1903706	10	-0.619904	-1.572032	0.031884	0.257611	1.000
662 GOBP-POSITIVE-REGULATION-OF-ANION-TRANSPORT	GO-1903793	9	-0.632214	-1.573492	0.027616	0.259134	1.000
663 GOBP-CELLULAR-HEALING	GO-0071241	13	-0.573044	-1.582571	0.028610	0.244817	1.000
664 GOBP-CELLULAR-RESPONSE-TO-INORGANIC-SUBSTANCE	GO-0042060	11	-0.605947	-1.582897	0.021645	0.248496	1.000
665 GOBP-CELLULAR-RESPONSE-TO-DNA-DAMAGE-STIMULUS	GO-0006974	5	-0.761192	-1.584056	0.016975	0.250800	1.000
666 GOBP-REGULATION-OF-MYELOID-LEUKOCYTE-DIFFERENT...	GO-0002761	8	-0.655406	-1.584343	0.025875	0.254975	1.000
667 GOBP-APOPTOTIC-MITOCHONDRIAL-CHANGES	GO-0008637	6	-0.724333	-1.585737	0.014354	0.256772	1.000
668 GOBP-CYTOKINE-PRODUCTION	GO-0001816	10	-0.612547	-1.586598	0.028571	0.260261	1.000
669 GOBP-NEGATIVE-REGULATION-OF-RESPONSE-TO-STIMULUS	GO-0048585	16	-0.531339	-1.586816	0.037657	0.264960	1.000
670 GOBP-NEGATIVE-REGULATION-OF-BIOSYNTHETIC-PROCESS	GO-0009890	13	-0.577697	-1.591550	0.019417	0.260685	1.000
671 REACTOME-TOLL-LIKE-RECEPTOR-TLR1-TLR2-CASCADE	R-RNO-168179	8	-0.670845	-1.592570	0.029806	0.264088	1.000
672 GOBP-RESPONSE-TO-METAL-ION	GO-0010038	15	-0.543059	-1.598558	0.015850	0.256662	1.000
673 REACTOME-TOLL-LIKE-RECEPTOR-CASCADES	R-RNO-168898	8	-0.670845	-1.599909	0.020313	0.259409	1.000
674 GOBP-REGULATION-OF-VASCULAR-ASSOCIATED-SMOOTH...	GO-1904705	5	-0.778860	-1.602224	0.014331	0.260437	1.000
675 REACTOME-TOLL-LIKE-RECEPTOR-9-TLR9-CASCADE	R-RNO-168138	8	-0.670845	-1.607773	0.033528	0.254186	1.000
676 GOBP-NEGATIVE-REGULATION-OF-CELL-DIFFERENTIATION	GO-0045596	13	-0.588441	-1.609863	0.012894	0.255832	1.000
677 GOBP-REGULATION-OF-CELLULAR-PROTEIN-LOCALIZATION	GO-1903827	12	-0.597250	-1.609962	0.024148	0.261616	1.000
678 GOBP-CIRCULATORY-SYSTEM-DEVELOPMENT	GO-0072359	21	-0.514645	-1.612949	0.030749	0.260931	1.000
679 GOBP-PROTEIN-CATABOLIC-PROCESS	GO-0030163	8	-0.669457	-1.617114	0.022189	0.258427	1.000
680 HALLMARK-ALLOGRAFT-REJECTION	M5950	7	-0.702358	-1.625750	0.016743	0.247502	1.000
681 REACTOME-MYD88-INDEPENDENT-TLR4-CASCADE	R-RNO-166166	8	-0.670845	-1.626224	0.024206	0.253095	1.000
682 GOBP-TRANSMEMBRANE-RECEPTOR-PROTEIN-SERINE-THR...	GO-0007178	6	-0.750179	-1.626701	0.016248	0.258933	1.000
683 GOBP-POSITIVE-REGULATION-OF-MYELOID-CELL-DIFFE...	GO-0045639	7	-0.708362	-1.635383	0.020000	0.246571	1.000
684 REACTOME-SIGNALING-BY-RHO-GTPASES-MIRO-GTPASES...	R-RNO-9716542	9	-0.660284	-1.636720	0.010219	0.250339	1.000
685 GOBP-CELLULAR-RESPONSE-TO-LIPID	GO-0071396	15	-0.578584	-1.646026	0.013793	0.237044	1.000

Continuation of Table S14

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
686 GOBP-CELLULAR-RESPONSE-TO-OXYGEN-CONTAINING.CO...	GO-1901701	29	-0.493290	-1.646801	0.019330	0.242403	1.000
687 GOBP-APOPTOTIC-SIGNALING-PATHWAY	GO-0097190	15	-0.582939	-1.654206	0.017833	0.233949	0.999
688 GOBP-NEGATIVE-REGULATION-OF-DEVELOPMENTAL-PROCESS	GO-0051093	13	-0.58441	-1.660823	0.017143	0.226673	0.999
689 GOBP-REGULATION-OF-IMMUNE-RESPONSE	GO-0050776	12	-0.613339	-1.665371	0.015471	0.224716	0.999
690 GOBP-PROTEIN-MODIFICATION-BY-SMALL-PROTEIN.CON...	GO-0070647	7	-0.727459	-1.669098	0.014948	0.225311	0.999
691 GOBP-POSITIVE-REGULATION-OF-TRANSCRIPTION-BY-R...	GO-0045944	24	-0.520024	-1.670979	0.019048	0.229584	0.999
692 GOBP-POSITIVE-REGULATION-OF-BIOSYNTHETIC-PROCESS	GO-0008981	27	-0.526428	-1.675706	0.011827	0.228155	0.999
693 GOBP-MACROMOLECULE-CATABOLIC-PROCESS	GO-0009057	12	-0.616347	-1.675857	0.015737	0.236765	0.999
694 GOBP-RESPONSE-TO-WOUNDING	GO-0009611	15	-0.593490	-1.679823	0.009790	0.236967	0.998
695 GOBP-POSITIVE-REGULATION-OF-PRL-MIRNA-TRANSCRI...	GO-1902895	7	-0.737014	-1.686360	0.011994	0.231239	0.996
696 GOBP-COAGULATION	GO-0050817	8	-0.695155	-1.687644	0.014948	0.238675	0.996
697 GOBP-CELL-CYCLE	GO-0007049	21	-0.543600	-1.689326	0.014825	0.245422	0.995
698 REACTOME-RHO-GTPASE-EFFECTORS	R-RNO-195258	9	-0.660284	-1.692465	0.011628	0.249449	0.994
699 GOBP-REGULATION-OF-MYELOID-CELL-DIFFERENTIATION	GO-0045637	9	-0.680721	-1.693223	0.008511	0.259851	0.994
700 GOBP-CELLULAR-RESPONSE-TO-CADMIIUM-ION	GO-0071276	5	-0.817470	-1.699882	0.001577	0.256770	0.988
701 GOBP-SMOOTH-MUSCLE-CELL-PROLIFERATION	GO-0048659	6	-0.765608	-1.704261	0.004615	0.260477	0.987
702 GOBP-PRL-MIRNA-TRANSCRIPTION-BY-RNA-POLYMERASE-II	GO-0061614	7	-0.737014	-1.712164	0.003035	0.257147	0.983
703 GOBP-IMMUNE-SYSTEM-DEVELOPMENT	GO-0002520	17	-0.577877	-1.712215	0.008392	0.273084	0.983
704 GOBP-REGULATION-OF-CELL-CYCLE	GO-0051726	13	-0.622145	-1.717631	0.011817	0.277643	0.978
705 GOBP-RESPONSE-TO-DRUG	GO-0042493	11	-0.659907	-1.719809	0.010309	0.291391	0.978
706 GOBP-POSITIVE-REGULATION-OF-IMMUNE-SYSTEM-PROCESS	GO-0002684	18	-0.567760	-1.720327	0.006748	0.312281	0.978
707 GOBP-REGULATION-OF-IMMUNE-SYSTEM-PROCESS	GO-0002682	21	-0.554817	-1.721168	0.005479	0.335933	0.978
708 GOBP-RESPONSE-TO-LIPID	GO-0033993	19	-0.572650	-1.725202	0.011111	0.351913	0.975
709 GOBP-CELLULAR-RESPONSE-TO-CHEMICAL-STRESS	GO-0062197	7	-0.761052	-1.753678	0.001536	0.285094	0.938
710 GOBP-REGULATION-OF-APOPTOTIC-SIGNALING-PATHWAY	GO-2001233	10	-0.678609	-1.761606	0.004392	0.289781	0.911
711 GOBP-CELLULAR-RESPONSE-TO-REACTIVE-OXYGEN-SPECIES	GO-0034614	7	-0.761052	-1.780140	0.007452	0.265944	0.864
712 GOBP-LEUKOCYTE-DIFFERENTIATION	GO-0002521	15	-0.630362	-1.813362	0.002721	0.204134	0.724
713 GOBP-RESPONSE-TO-CADMIIUM-ION	GO-0046686	6	-0.843411	-1.826616	0.000000	0.206032	0.673
714 GOBP-POSITIVE-REGULATION-OF-NUCLEOBASE-CONTAIN...	GO-0045935	28	-0.551661	-1.838182	0.003861	0.209858	0.614
715 GOBP-MYELOID-LEUKOCYTE-DIFFERENTIATION	GO-0002573	11	-0.696257	-1.846048	0.001406	0.237667	0.583
716 GOBP-MYELOID-CELL-DIFFERENTIATION	GO-0030099	13	-0.689421	-1.893598	0.001379	0.180309	0.396
717 REACTOME-INNATE-IMMUNE-SYSTEM	R-RNO-168249	16	-0.639921	-1.899566	0.001372	0.253494	0.376
718 GOBP-PLATELET-ACTIVATION	GO-0030168	6	-0.862601	-1.917365	0.000000	0.399732	0.305

End of Table

Supplementary Table S15: BG early profile (8 DPL peak) GSEA results.

Begin of Table S15								
	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
0	GOBP-MEMORY	GO:0007613	13	0.586962	2.102377	0.000000	0.625162	0.373
1	GOBP-CATION-TRANSPORT	GO:0008112	25	0.421588	1.803097	0.007067	1.000000	0.973
2	GOBP-NERVE-DEVELOPMENT	GO:0021675	9	0.565701	1.733075	0.014925	1.000000	0.993
3	REACTOME-SIGNALING-BY-NTRK2-TRKB	R-RNO-9006115	6	0.662655	1.713326	0.037037	1.000000	0.996
4	GOBP_POSITIVE-REGULATION-OF-LIPASE-ACTIVITY	GO:0060193	5	0.698339	1.702445	0.029326	1.000000	0.998
5	GOBP-NEGATIVE-REGULATION-OF-NEURON-APOPTOTIC-P...	GO:0043524	8	0.565633	1.682155	0.031447	1.000000	0.999
6	GOBP-REGULATION-OF-PHOSPHOLIPASE-C-ACTIVITY	GO:1900274	5	0.698339	1.677069	0.027778	1.000000	0.999
7	GOBP-SYNAPTIC-SIGNALING	GO:0099536	47	0.337414	1.628808	0.020101	1.000000	1.000
8	GOBP-BEHAVIOR	GO:0007610	32	0.353545	1.625855	0.013636	1.000000	1.000
9	GOBP-REGULATION-OF-NEURON-PROJECTION-DEVELOPMENT	GO:0010975	16	0.431813	1.603620	0.042105	1.000000	1.000
10	GOBP-REGULATION-OF-PHOSPHOLIPASE-ACTIVITY	GO:0010517	6	0.613173	1.591696	0.040984	1.000000	1.000
11	GOBP-RESPONSE-TO-NERVE-GROWTH-FACTOR	GO:1990089	7	0.592249	1.590288	0.050000	1.000000	1.000
12	GOBP-REGULATION-OF-LIPASE-ACTIVITY	GO:0060191	6	0.613173	1.582726	0.063768	1.000000	1.000
13	GOBP-NEUROTROPHIN-SIGNALING-PATHWAY	GO:0038179	6	0.594194	1.574801	0.048991	1.000000	1.000
14	GOBP-NEURON-DEVELOPMENT	GO:0048666	33	0.339039	1.563936	0.026217	1.000000	1.000
15	GOBP-CELL-CELL-SIGNALING	GO:0007267	56	0.331361	1.553680	0.009174	1.000000	1.000
16	GOBP-NEUROTROPHIN-TRK-RECEPTOR-SIGNALING-PATHWAY	GO:0048011	6	0.594194	1.553286	0.055556	0.946455	1.000
17	GOBP-REGULATION-OF-TRANS-SYNAPTIC-SIGNALING	GO:0099177	40	0.327914	1.544139	0.021186	0.929174	1.000
18	GOBP-NERVOUS-SYSTEM-PROCESS	GO:0050877	38	0.317309	1.542059	0.013216	0.887685	1.000
19	GOBP-REGULATION-OF-PEPTIDYL-SERINE-PHOSPHORYLA...	GO:0033135	8	0.519312	1.541639	0.072555	0.844781	1.000
20	GOBP-REGULATION-OF-NMDA-RECEPTOR-ACTIVITY	GO:2000310	10	0.475723	1.522818	0.057692	0.874604	1.000
21	GOBP-LONG-TERM-MEMORY	GO:0007616	6	0.564900	1.520606	0.065903	0.841472	1.000
22	GOBP_POSITIVE-REGULATION-OF-PEPTIDYL-SERINE_PH...	GO:0033138	8	0.519312	1.519085	0.095238	0.809561	1.000
23	GOBP-REGULATION-OF-NEURON-DIFFERENTIATION	GO:0045664	5	0.626381	1.508076	0.077957	0.814428	1.000
24	GOBP-NEURON-DIFFERENTIATION	GO:0030182	36	0.324184	1.501531	0.048673	0.802127	1.000
25	GOBP_POSITIVE-REGULATION-OF-LONG-TERM-SYNAPTIC...	GO:1900273	5	0.631234	1.500513	0.082888	0.775103	1.000
26	GOBP-NEGATIVE-REGULATION-OF-NEURON-DEATH	GO:1901215	11	0.450046	1.496745	0.049342	0.758595	1.000
27	GOBP-REGULATION-OF-SYNAPSE-STRUCTURE-OR-ACTIVITY	GO:0050803	11	0.454545	1.488265	0.055728	0.760855	1.000
28	GOBP-REGULATION-OF-ION-TRANSPORT	GO:0043269	36	0.313378	1.475224	0.049020	0.778360	1.000
29	GOBP_POSITIVE-REGULATION-OF-TRANSPORT	GO:0010562	24	0.342758	1.469525	0.044715	0.770544	1.000
30	GOBP_COGNITION	GO:0050890	28	0.328435	1.443552	0.047101	0.836379	1.000
31	HALLMARK_KRAS-SIGNALING_UP	M5953	6	0.530501	1.436866	0.075581	0.834213	1.000
32	GOBP_POSITIVE-REGULATION-OF-TRANSMEMBRANE_TRAN...	GO:0034764	7	0.515390	1.435338	0.089385	0.814059	1.000
33	GOBP-REGULATION-OF-TRANSPORT	GO:0051049	44	0.293922	1.413607	0.053922	0.867050	1.000
34	GOBP-REGULATION-OF-CATION-TRANSMEMBRANE_TRANSP...	GO:1904062	16	0.376954	1.395064	0.111511	0.910023	1.000
35	GOBP_POSITIVE-REGULATION-OF-NEURON_PROJECTION...	GO:0010976	5	0.573435	1.394029	0.107817	0.888373	1.000
36	GOBP-REGULATION-OF-CELL_PROJECTION-ORGANIZATION	GO:0031344	20	0.350048	1.393083	0.082353	0.868397	1.000
37	GOBP-REGULATION-OF-PROTEIN-PHOSPHORYLATION	GO:0001932	26	0.308394	1.381989	0.084677	0.887928	1.000
38	GOBP-TRANSMEMBRANE-RECEPTOR-PROTEIN-TYROSINE_K...	GO:0007169	19	0.336086	1.365265	0.091549	0.927280	1.000
39	GOBP_POSITIVE-REGULATION-OF-PEPTIDYL-TYROSINE...	GO:0050731	8	0.462500	1.363957	0.133127	0.908630	1.000
40	GOBP-NEGATIVE-REGULATION-OF-CATALYTIC-ACTIVITY	GO:0043086	17	0.336174	1.349111	0.107807	0.943980	1.000

Continuation of Table S15

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
41	GOBP-REGULATION-OF-LONG-TERM-SYNAPTIC-POTENTIAL...	6	0.526804	1.345409	0.151335	0.935476	1.000
42	GOBP-POSITIVE-REGULATION-OF-TRANSFERASE-ACTIVITY	20	0.320449	1.317525	0.124481	1.000000	1.000
43	GOBP-POSITIVE-REGULATION-OF-SYNAPTIC-TRANSMISSION	15	0.346662	1.315701	0.138047	1.000000	1.000
44	GOBP-CELL-PROJECTION-ORGANIZATION	34	0.288777	1.313954	0.097778	0.994272	1.000
45	REACTOME-ACTIVATION-OF-NMDA-RECEPTORS-AND-POST...	16	0.344284	1.307321	0.108696	0.998971	1.000
46	GOBP-POSITIVE-REGULATION-OF-HYDROLASE-ACTIVITY	16	0.343225	1.306930	0.131034	0.978962	1.000
47	GOBP-NEGATIVE-REGULATION-OF-PEPTIDASE-ACTIVITY	6	0.502978	1.299203	0.158358	0.988251	1.000
48	GOBP-POSITIVE-REGULATION-OF-CATALYTIC-ACTIVITY	30	0.283846	1.295197	0.116183	0.982978	1.000
49	GOBP-NEUROGENESIS	40	0.276123	1.287505	0.106481	0.990969	1.000
50	HALLMARK-P13K-AKT-MTOR-SIGNALING	6	0.490942	1.280965	0.184438	0.996258	1.000
51	GOBP-CATION-TRANSMEMBRANE-TRANSPORT	18	0.331029	1.279110	0.162630	0.984469	1.000
52	GOBP-REGULATION-OF-CATION-CHANNEL-ACTIVITY	14	0.353197	1.270461	0.175862	0.998630	1.000
53	GOBP-PERIPHERAL-NERVOUS-SYSTEM-DEVELOPMENT	9	0.411433	1.264759	0.170213	1.000000	1.000
54	GOBP-NEGATIVE-REGULATION-OF-CYSTEINE-TYPE-ENDO...	5	0.513106	1.261071	0.165746	0.998356	1.000
55	GOBP-POSITIVE-REGULATION-OF-CELL-PROJECTION-OR...	10	0.398549	1.260058	0.179710	0.984178	1.000
56	GOBP-REGULATION-OF-NEUROTRANSMITTER-RECEPTOR-A...	13	0.356768	1.255446	0.160839	0.983494	1.000
57	GOBP-POSITIVE-REGULATION-OF-PROTEIN-MODIFICATI...	23	0.298172	1.254352	0.167347	0.970161	1.000
58	GOBP-SYNAPSE-ORGANIZATION	17	0.323054	1.251861	0.185714	0.963410	1.000
59	GOBP-REGULATION-OF-HORMONE-LEVELS	12	0.358843	1.241763	0.188679	0.985164	1.000
60	REACTOME-UNBLOCKING-OF-NMDA-RECEPTORS-GLUTAMAT...	12	0.348542	1.235293	0.192308	0.993437	1.000
61	GOBP-DEFENSE-RESPONSE	19	0.507890	1.23504	0.179931	0.984065	1.000
62	GOBP-POSITIVE-REGULATION-OF-CATION-TRANSMEMBR...	5	0.323054	1.227369	0.184282	0.991750	1.000
63	REACTOME-LONG-TERM-POTENTIATION	10	0.384855	1.226857	0.195783	0.978042	1.000
64	GOBP-AXON-DEVELOPMENT	18	0.313077	1.225383	0.184502	0.967772	1.000
65	GOBP-REGULATION-OF-PHOSPHORUS-METABOLIC-PROCESS	27	0.285357	1.223307	0.185520	0.953309	1.000
66	GOBP-POSITIVE-REGULATION-OF-PROTEIN-PHOSPHORYL...	23	0.298172	1.221312	0.205761	0.953216	1.000
67	GOBP-REGULATION-OF-MEMBRANE-POTENTIAL	17	0.318722	1.216002	0.219231	0.956842	1.000
68	GOBP-PEPTIDYL-TYROSINE-MODIFICATION	10	0.385097	1.214244	0.210031	0.949391	1.000
69	GOBP-RECEPTOR-METABOLIC-PROCESS	5	0.482779	1.204479	0.190981	0.968869	1.000
70	GOBP-SENSORY-PERCEPTION	9	0.397368	1.204000	0.216617	0.969000	1.000
71	GOBP-SMALL-GTPASE-MEDIATED-SIGNAL-TRANSDUCTION	8	0.398566	1.192449	0.234568	0.985311	1.000
72	GOBP-REGULATION-OF-TRANSFERASE-ACTIVITY	22	0.278565	1.189361	0.210970	0.982882	1.000
73	REACTOME-TRANSCRIPTIONAL-REGULATION-BY-MECP2	7	0.422698	1.188313	0.255014	0.973254	1.000
74	GOBP-REGULATION-OF-SIGNALING-RECEPTOR-ACTIVITY	14	0.323774	1.188187	0.243506	0.960856	1.000
75	GOBP-REGULATION-OF-POSTSYNAPTIC-MEMBRANE-POTEN...	14	0.332216	1.185434	0.227891	0.958073	1.000
76	GOBP-ION-HOMEOSTASIS	16	0.319886	1.183774	0.250784	0.951084	1.000
77	GOBP-INSULIN-SECRETION	7	0.430593	1.180256	0.267606	0.951314	1.000
78	GOBP-PROTEIN-PHOSPHORYLATION	34	0.251425	1.179764	0.239669	0.940795	1.000
79	GOBP-PEPTIDE-HORMONE-SECRETION	7	0.430593	1.178769	0.271053	0.932536	1.000
80	GOBP-REGULATION-OF-INTRACELLULAR-SIGNAL-TRANSD...	21	0.1902531	1.176046	0.219331	0.930137	1.000
81	GOBP-NEURON-PROJECTION-ORGANIZATION	8	0.387500	1.173090	0.254777	0.927808	1.000
82	GOBP-ACTIVATION-OF-PROTEIN-KINASE-ACTIVITY	11	0.345323	1.166073	0.264407	0.939484	1.000
83	GOBP-ORGANOPHOSPHATE-METABOLIC-PROCESS	7	0.414705	1.165045	0.279279	0.931595	1.000

Continuation of Table S15

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
84	GOBP-NEUROINFLAMMATORY_RESPONSE	5	0.479492	1.164680	0.275660	0.921762	1.000
85	GOBP-REGULATION_OF_PROTEIN_KINASE_ACTIVITY	22	0.275655	1.158781	0.260700	0.931319	1.000
86	GOBP-TRANSMEMBRANE_TRANSPORT	27	0.263346	1.158768	0.250000	0.920647	1.000
87	GOBP-INOSITOL_LIPID_MEDIATED_SIGNALING	8	0.398535	1.157872	0.264797	0.912807	1.000
88	GOBP-REGULATION_OF_ANION_TRANSMEMBRANE_TRANSPORT	5	0.457831	1.156713	0.255495	0.906300	1.000
89	GOBP-RECEPTOR_INTERNALIZATION	5	0.482779	1.154286	0.253561	0.904133	1.000
90	GOBP-POSITIVE_REGULATION_OF_CELL_GROWTH	6	0.443102	1.147331	0.270195	0.917229	1.000
91	GOBP-LEUKOCYTE_MIGRATION	6	0.439024	1.143018	0.287390	0.921876	1.000
92	GOBP-REGULATION_OF_TRANSMEMBRANE_TRANSPORT	23	0.270006	1.142541	0.256098	0.913708	1.000
93	GOBP-CARBOHYDRATE_DERIVATIVE_METABOLIC_PROCESS	7	0.416946	1.136472	0.275281	0.923102	1.000
94	GOBP-ERBB_SIGNALING_PATHWAY	5	0.464265	1.133795	0.277922	0.921966	1.000
95	GOBP-PEPTIDE_SECRETION	9	0.371115	1.131023	0.265244	0.921237	1.000
96	GOBP-DENDRITE_MORPHOGENESIS	6	0.426829	1.130645	0.273481	0.912858	1.000
97	REACTOME-ONCOGENIC_MAPK_SIGNALING	5	0.471383	1.124776	0.291444	0.922290	1.000
98	GOBP-INFLAMMATORY_RESPONSE	12	0.331357	1.122780	0.283077	0.919544	1.000
99	GOBP-REGULATION_OF_CYTOSOLIC_CALCIIUM_IION_CONCE...	13	0.318126	1.115304	0.306931	0.934062	1.000
100	GOBP-SYNAPTIC_TRANSMISSION_GLUTAMATERGIC	13	0.311801	1.113933	0.305031	0.929455	1.000
101	GOBP-CELLULAR_MACROMOLECULE_LOCALIZATION	21	0.266577	1.107370	0.324042	0.941316	1.000
102	GOBP-DIVALENT_INORGANIC_CATION_HOMEOSTASIS	13	0.318126	1.102203	0.300353	0.948280	1.000
103	GOBP-REGULATION_OF_POSTSYNAPSE_ORGANIZATION	6	0.426829	1.101668	0.315493	0.941231	1.000
104	GOBP-PEPTIDYL_SERINE_MODIFICATION	12	0.321562	1.095198	0.328720	0.953425	1.000
105	GOBP-CELL_MORPHOGENESIS	24	0.252174	1.095061	0.321970	0.944877	1.000
106	GOBP-CELLULAR_RESPONSE_TO_KETONE	5	0.450174	1.094522	0.332454	0.937640	1.000
107	GOBP-REGULATION_OF_PROTEIN_TYROSINE_KINASE_ACT...	5	0.445783	1.092863	0.309524	0.934014	1.000
108	GOBP-CELLULAR_COMPONENT_MORPHOGENESIS	24	0.252174	1.091624	0.318519	0.929815	1.000
109	GOBP-REGULATION_OF_AXONOGENESIS	7	0.395062	1.085877	0.331429	0.938819	1.000
110	GOBP-REGULATION_OF_PROTEIN_MODIFICATION_PROCESS	29	0.244284	1.085133	0.331967	0.932642	1.000
111	GOBP-POSITIVE_REGULATION_OF_TRANSPORT	26	0.245082	1.084306	0.323144	0.926742	1.000
112	GOBP-CELLULAR_IION_HOMEOSTASIS	14	0.302520	1.083749	0.335463	0.920401	1.000
113	GOBP-DENDRITIC_SPINE_DEVELOPMENT	6	0.426829	1.081383	0.352025	0.919669	1.000
114	GOBP-REGULATION_OF_SYNAPTIC_TRANSMISSION_GLUTA...	12	0.313965	1.079286	0.343653	0.917671	1.000
115	GOBP-POSITIVE_REGULATION_OF_SIGNALING	34	0.227816	1.078752	0.337719	0.911041	1.000
116	REACTOME-ANTIINFLAMMATORY_RESPONSE_FAVOURING...	5	0.442468	1.078693	0.371274	0.903369	1.000
117	GOBP-POSITIVE_REGULATION_OF_MOLECULAR_FUNCTION	38	0.227800	1.077548	0.384977	0.899165	1.000
118	GOBP-CELL_PART_MORPHOGENESIS	24	0.252174	1.076980	0.347985	0.893424	1.000
119	GOBP-LONG_TERM_SYNAPTIC_POTENTIATION	12	0.315452	1.076076	0.316993	0.889058	1.000
120	GOBP-DENDRITIC_SPINE_MORPHOGENESIS	5	0.442226	1.069899	0.344444	0.899395	1.000
121	GOBP-POSITIVE_REGULATION_OF_PROTEIN_TYROSINE_K...	5	0.445783	1.068143	0.352770	0.896931	1.000
122	GOBP-G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY	18	0.267645	1.066953	0.361940	0.892892	1.000
123	GOBP-POSITIVE_REGULATION_OF_PROTEIN_KINASE_ACT...	19	0.269296	1.066930	0.309701	0.885755	1.000
124	GOBP-CHEMICAL_HOMEOSTASIS	23	0.254702	1.064461	0.348276	0.885741	1.000
125	GOBP-NEURON_APOPTOTIC_PROCESS	12	0.314215	1.063549	0.338762	0.881176	1.000
126	GOBP-NEGATIVE_REGULATION_OF_TRANSMEMBRANE_TRAN...	6	0.415659	1.062069	0.371274	0.878158	1.000

Continuation of Table S15

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
127 GOBP-REGULATION-OF-HYDROLASE-ACTIVITY	GO-0051336	22	0.254058	1.057424	0.364662	0.885089	1.000
128 GOBP-SENSORY-ORGAN-DEVELOPMENT	GO-0007423	8	0.352899	1.052645	0.386997	0.892513	1.000
129 GOBP-REGULATION-OF-RESPONSE-TO-STRESS	GO-0080134	19	0.264390	1.046480	0.385185	0.902969	1.000
130 GOBP-CELLULAR-RESPONSE-TO-ALCOHOL	GO-0097306	5	0.450355	1.045421	0.373595	0.899036	1.000
131 GOBP-REGULATION-OF-CELL-SIZE	GO-0008361	5	0.433987	1.045017	0.346253	0.893491	1.000
132 GOBP-PEPTIDYL-AMINO-ACID-MODIFICATION	GO-0018193	22	0.252041	1.042614	0.418605	0.893309	1.000
133 GOBP-PROTEIN-LOCALIZATION-TO-ORGANELLE	GO-0033365	9	0.341772	1.036763	0.380645	0.903611	1.000
134 GOBP-CARBOHYDRATE-HOMEOSTASIS	GO-0033500	7	0.375534	1.033026	0.400000	0.907923	1.000
135 GOBP-NEURON-PROJECTION-GUIDANCE	GO-0097485	9	0.338754	1.031171	0.381098	0.906215	1.000
136 GOBP-RAS-PROTEIN-SIGNAL-TRANSDUCTION	GO-0007265	5	0.423330	1.030746	0.394256	0.900849	1.000
137 GOBP-POSITIVE-REGULATION-OF-CELLULAR-COMPONENT...	GO-0051130	24	0.240645	1.028609	0.406716	0.900403	1.000
138 GOBP-RESPONSE-TO-HEAT	GO-0009408	7	0.359033	1.018019	0.406332	0.923290	1.000
139 GOBP-POSITIVE-REGULATION-OF-DEVELOPMENTAL-GROWTH	GO-0048639	8	0.340391	1.008511	0.414474	0.943312	1.000
140 GOBP-POSITIVE-REGULATION-OF-CELLULAR-PROTEIN-L...	GO-1903829	7	0.358025	0.999044	0.428962	0.964263	1.000
141 GOBP-NEGATIVE-REGULATION-OF-ION-TRANSPORT	GO-0043271	11	0.303419	0.994393	0.442953	0.970867	1.000
142 GOBP-METAL-ION-HOMEOSTASIS	GO-0055065	14	0.269796	0.987987	0.467320	0.982499	1.000
143 REACTOME-VESICLE-MEDIATED-TRANSPORT	R-RNO-5053656	5	0.407940	0.985816	0.428177	0.981701	1.000
144 GOBP-POSITIVE-REGULATION-OF-DNA-BINDING-TRANSC...	GO-0051091	10	0.308924	0.984774	0.440972	0.978320	1.000
145 GOBP-POSITIVE-REGULATION-OF-PROTEIN-METABOLIC...	GO-0051247	28	0.220289	0.982415	0.466667	0.978120	1.000
146 GOBP-POSITIVE-REGULATION-OF-ION-TRANSPORT	GO-0043607	17	0.256037	0.978768	0.454545	0.982328	1.000
147 GOBP-NEGATIVE-REGULATION-OF-SYNAPTIC-TRANSMISSION	GO-0050805	6	0.378630	0.977581	0.444759	0.978852	1.000
148 REACTOME-TRANSMISSION-ACROSS-CHEMICAL-SYNAPSES	R-RNO-112315	23	0.231832	0.974077	0.513410	0.982237	1.000
149 GOBP-DEVELOPMENTAL-CELL-GROWTH	GO-0048588	5	0.410743	0.973896	0.451351	0.976205	1.000
150 GOBP-POSITIVE-REGULATION-OF-SECRETION	GO-0051047	6	0.370498	0.973735	0.498623	0.970138	1.000
151 GOBP-POLYSACCHARIDE-METABOLIC-PROCESS	GO-0005976	5	0.410612	0.972679	0.500000	0.966567	1.000
152 GOBP-SENSORY-PERCEPTION-OF-PAIN	GO-0019233	5	0.404815	0.971314	0.452778	0.964141	1.000
153 GOBP-NEGATIVE-REGULATION-OF-CELL-DEATH	GO-0060548	22	0.235332	0.970019	0.452632	0.961146	1.000
154 GOBP-REGULATION-OF-TRANSPORTER-ACTIVITY	GO-0032409	17	0.254705	0.969205	0.506211	0.957279	1.000
155 GOBP-TELENCEPHALON-DEVELOPMENT	GO-0021537	6	0.373313	0.968221	0.460177	0.953511	1.000
156 GOBP-ORGAN-GROWTH	GO-0035265	5	0.397590	0.964999	0.488372	0.956633	1.000
157 REACTOME-MEMBRANE-TRAFFICKING	R-RNO-199991	5	0.407940	0.964058	0.479564	0.953360	1.000
158 GOBP-RECEPTOR-MEDIATED-ENDOCYTOSIS	GO-0006898	6	0.365437	0.961877	0.513889	0.953675	1.000
159 GOBP-HORMONE-TRANSPORT	GO-0009914	9	0.304349	0.961550	0.469697	0.948517	1.000
160 GOBP-NEGATIVE-REGULATION-OF-PHOSPHORYLATION	GO-0042326	7	0.335472	0.955856	0.511299	0.957641	1.000
161 GOBP-REGULATION-OF-NEURONAL-SYNAPTIC-PLASTICITY	GO-0048168	7	0.345679	0.955195	0.488372	0.953786	1.000
162 GOBP-REGULATION-OF-ORGAN-GROWTH	GO-0046620	5	0.397590	0.952337	0.510870	0.955254	1.000
163 GOBP-REGULATION-OF-PEPTIDYL-TYROSINE-PHOSPHORY...	GO-0050730	9	0.307995	0.948712	0.506536	0.959750	1.000
164 GOBP-ADENYLATE-CYCLASE-MODULATING-G-PROTEIN-CO...	GO-0007188	11	0.281481	0.948564	0.503425	0.954287	1.000
165 GOBP-GENERATION-OF-PRECURSOR-METABOLITES-AND-E...	GO-0006091	5	0.396848	0.947667	0.491979	0.950660	1.000
166 GOBP-POSITIVE-REGULATION-OF-AXONOGENESIS	GO-0050772	5	0.385542	0.945480	0.492837	0.950859	1.000
167 GOBP-REGULATION-OF-DEVELOPMENTAL-GROWTH	GO-0048638	9	0.297021	0.938085	0.521173	0.964712	1.000
168 GOBP-MITOCHONDRION-ORGANIZATION	GO-0007005	7	0.339085	0.937404	0.497024	0.960953	1.000
169 GOBP-CELL-JUNCTION-ORGANIZATION	GO-0034330	19	0.234019	0.934708	0.547101	0.962515	1.000

Continuation of Table S15

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
170	GOBP-NEGATIVE-REGULATION-OF-LIPID-METABOLIC-PR...	5	0.394411	0.934026	0.518841	0.958576	1.000
171	GOBP-POSITIVE-REGULATION-OF BINDING	6	0.355724	0.935076	0.507246	0.955281	1.000
172	GOBP-POSITIVE-REGULATION-OF LOCOMOTION	11	0.285560	0.932979	0.527687	0.950026	1.000
173	GOBP-SMALL-MOLECULE-METABOLIC-PROCESS	15	0.255727	0.932883	0.546358	0.944808	1.000
174	GOBP-AMIDE-BIOSYNTHETIC-PROCESS	7	0.333333	0.932368	0.543103	0.940606	1.000
175	GOBP-PEPTIDE-BIOSYNTHETIC-PROCESS	7	0.333333	0.926905	0.498599	0.949502	1.000
176	GOBP-REGULATION-OF-SYNAPTIC-PLASTICITY	21	0.218710	0.925628	0.616279	0.947459	1.000
177	GOBP-LONG-TERM-SYNAPTIC-DEPRESSION	5	0.395899	0.924260	0.541114	0.945615	1.000
178	GOBP-MUSCLE-CELL-DEVELOPMENT	5	0.385542	0.915145	0.531856	0.961820	1.000
179	GOBP-RESPONSE-TO-CARBOHYDRATE	5	0.385542	0.913011	0.542936	0.961964	1.000
180	GOBP-DEVELOPMENTAL-MATURATION	5	0.373494	0.908876	0.564033	0.967152	1.000
181	GOBP-REGULATION-OF-CYTOSKELETON-ORGANIZATION	5	0.373494	0.907331	0.557692	0.965531	1.000
182	GOBP-RESPONSE-TO-MONOSACCHARIDE	5	0.385542	0.905847	0.536458	0.963827	1.000
183	GOBP-APOPTOTIC-PROCESS	35	0.193760	0.903012	0.636752	0.965401	1.000
184	GOBP-CELLULAR-RESPONSE-TO-ORGANIC-CYCLIC-COMPOUND	13	0.253333	0.902028	0.573333	0.962511	1.000
185	GOBP-MATERNAL-PROCESS-INVOLVED-IN-FEMALE-PREGN...	5	0.360141	0.899742	0.568783	0.963086	1.000
186	GOBP-POSITIVE-REGULATION-OF-CELL-DEVELOPMENT	12	0.259269	0.899731	0.557522	0.957958	1.000
187	GOBP-POSITIVE-REGULATION-OF-NEUROGENESIS	12	0.259269	0.899265	0.590361	0.953830	1.000
188	GOBP-POSITIVE-REGULATION-OF-NERVOUS-SYSTEM-DEV...	12	0.259269	0.898636	0.615132	0.950226	1.000
189	GOBP-REGULATION-OF-NERVOUS-SYSTEM-DEVELOPMENT	15	0.241474	0.898195	0.590580	0.946213	1.000
190	GOBP-LOCOMOTORY-BEHAVIOR	7	0.318211	0.895599	0.605341	0.947725	1.000
191	GOBP-ENDOCYTOSIS	8	0.311423	0.890978	0.579251	0.954650	1.000
192	GOBP-RESPONSE-TO-ALKALOID	5	0.367966	0.890768	0.578947	0.950124	1.000
193	GOBP-NEGATIVE-REGULATION-OF-SIGNALING	21	0.216297	0.887056	0.641975	0.953204	1.000
194	GOBP-REGIONALIZATION	6	0.347957	0.885320	0.555556	0.952450	1.000
195	GOBP-CELLULAR-LIPID-METABOLIC-PROCESS	7	0.315690	0.882531	0.586826	0.954271	1.000
196	REACTOME-RAS-ACTIVATION-UPON-CA2-INFLUX-THROUG...	6	0.338946	0.880258	0.603352	0.954814	1.000
197	GOBP-POSITIVE-REGULATION-OF-EPITHELIAL-CELL-MI...	5	0.365226	0.877313	0.592208	0.957150	1.000
198	REACTOME-TRAFFICKING-OF-AMPA-RECEPTORS	11	0.266731	0.874100	0.604027	0.959434	1.000
199	GOBP-TAXIS	14	0.236919	0.873412	0.649123	0.956033	1.000
200	GOBP-POSITIVE-REGULATION-OF-ESTABLISHMENT-OF-P...	5	0.349398	0.862803	0.634006	0.975384	1.000
201	GOBP-NEGATIVE-REGULATION-OF-IMMUNE-SYSTEM-PROCESS	5	0.361673	0.858712	0.601626	0.979823	1.000
202	GOBP-EXOCYTOSIS	11	0.257296	0.858165	0.665493	0.976274	1.000
203	GOBP-CELL-GROWTH	10	0.269231	0.857107	0.663664	0.974019	1.000
204	GOBP-PATTERN-SPECIFICATION-PROCESS	6	0.347957	0.855514	0.587896	0.973106	1.000
205	GOBP-MONOCARBOXYLIC-ACID-METABOLIC-PROCESS	6	0.318527	0.854511	0.625000	0.970685	1.000
206	REACTOME-NEUROTRANSMITTER-RECEPTORS-AND-POSTSY...	22	0.207947	0.850462	0.752852	0.975242	1.000
207	REACTOME-G-ALPHA1-SIGNALING-EVENTS	18	0.221461	0.850117	0.684397	0.971298	1.000
208	GOBP-MYELOID-LEUKOCYTE-ACTIVATION	8	0.286177	0.846631	0.662614	0.974352	1.000
209	GOBP-SEXUAL-REPRODUCTION	10	0.269231	0.843937	0.670554	0.975632	1.000
210	GOBP-MULTICELLULAR-ORGANISMAL-RESPONSE-TO-STRESS	5	0.350514	0.842098	0.645946	0.975001	1.000
211	GOBP-REGULATION-OF-PROTEIN-LOCALIZATION	18	0.212244	0.838529	0.687747	0.978205	1.000
212	GOBP-RESPONSE-TO-ALCOHOL	11	0.252925	0.835988	0.677419	0.978964	1.000

Continuation of Table S15

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
213	GOBP-POSITIVE-REGULATION-OF-GROWTH	GO-0045927	9	0.270808	0.835707	0.683386	0.974867	1.000
214	GOBP-ESTABLISHMENT-OF-PROTEIN-LOCALIZATION_TO...	GO-0072594	6	0.329268	0.835500	0.660969	0.970988	1.000
215	GOBP-REGULATION-OF-CELLULAR-PROTEIN-LOCALIZATION	GO-1903827	12	0.250000	0.83545	0.688136	0.972744	1.000
216	GOBP-DEVELOPMENTAL-GROWTH	GO-004589	10	0.258477	0.832207	0.723810	0.968875	1.000
217	GOBP-CELL-CELL-SIGNALING-BY-WNT	GO-0198738	7	0.296296	0.823581	0.656151	0.981719	1.000
218	GOBP-NEGATIVE-REGULATION-OF-TRANSPORT	GO-0051051	13	0.233166	0.822824	0.692053	0.978871	1.000
219	GOBP-CARBOHYDRATE-METABOLIC-PROCESS	GO-0005975	9	0.265823	0.822407	0.669697	0.975404	1.000
220	GOBP-EMBRYONIC-MORPHOGENESIS	GO-0045898	6	0.305481	0.821845	0.647383	0.972196	1.000
221	GOBP-PROTEIN-LOCALIZATION_TO-CELL-PERIPHERY	GO-1990778	12	0.230842	0.814754	0.720000	0.983078	1.000
222	GOBP-NUCLEAR-TRANSPORT	GO-0051169	5	0.337349	0.813810	0.685792	0.980459	1.000
223	GOBP-IONOTROPIC-GLUTAMATE-RECEPTOR-SIGNALING_P...	GO-0035235	9	0.267109	0.807978	0.730897	0.988804	1.000
224	GOBP-REGULATION-OF-ANATOMICAL-STRUCTURE-MORPHO...	GO-0022603	17	0.209805	0.807023	0.719425	0.986574	1.000
225	GOBP-REGULATION-OF-PEPTIDE-HORMONE-SECRETION	GO-0090276	6	0.308128	0.802247	0.701705	0.991283	1.000
226	GOBP-GAMETE-GENERATION	GO-0007276	9	0.265823	0.801765	0.718310	0.987654	1.000
227	GOBP-CELLULAR-HOMEOSTASIS	GO-0019725	18	0.204987	0.800822	0.756554	0.985030	1.000
228	GOBP-REGULATION-OF-CELLULAR-RESPONSE_TO-STRESS	GO-0080135	9	0.260908	0.800268	0.758730	0.981711	1.000
229	GOBP-PHOSPHATIDYLINOSITOL-3-KINASE-SIGNALING	GO-0014065	7	0.291107	0.799913	0.715100	0.978006	1.000
230	GOBP-NEGATIVE-REGULATION-OF-PROTEOLYSIS	GO-0045861	8	0.271355	0.793693	0.699088	0.985918	1.000
231	GOBP-REGULATION-OF-PEPTIDE-SECRETION	GO-0002791	7	0.284243	0.792518	0.698925	0.984037	1.000
232	GOBP-REGULATION-OF-CELLULAR-LOCALIZATION	GO-0060341	17	0.205774	0.791055	0.773381	0.982720	1.000
233	GOBP-REGULATION-OF-MUSCLE-ADAPTATION	GO-0043502	5	0.330002	0.790020	0.730245	0.980536	1.000
234	GOBP-RESPONSE_TO-ETHANOL	GO-0045471	5	0.333807	0.786552	0.716180	0.983302	1.000
235	GOBP-REGULATION-OF-CYSTEINE-TYPE-ENDOPEPTIDASE...	GO-2000116	9	0.248969	0.781194	0.766355	0.989686	1.000
236	REACTOME-INTERFERON-SIGNALING	R-RNO-913531	6	0.304565	0.780894	0.692308	0.986150	1.000
237	REACTOME-ASSEMBLY-AND-CELL-SURFACE-PRESENTATIO...	R-RNO-9609736	8	0.262346	0.780622	0.715493	0.982460	1.000
238	GOBP-INTRACELLULAR-TRANSPORT	GO-0046907	11	0.233766	0.778058	0.781759	0.983076	1.000
239	GOBP-NUCLEOBASE-CONTAINING-SMALL-MOLECULE-META...	GO-0055086	6	0.307594	0.776835	0.732733	0.981080	1.000
240	GOBP-REGULATION-OF-EPITHELIAL-CELL-MIGRATION	GO-0010632	6	0.295882	0.774116	0.736559	0.982007	1.000
241	GOBP-ESTABLISHMENT-OF-PROTEIN-LOCALIZATION	GO-0045184	18	0.195018	0.772842	0.816254	0.980412	1.000
242	GOBP-NEGATIVE-REGULATION-OF-MOLECULAR-FUNCTION	GO-0044092	24	0.181228	0.772735	0.789272	0.976602	1.000
243	REACTOME-NEGATIVE-REGULATION-OF-NMDA-RECEPTOR...	R-HSA-961732	8	0.262346	0.771380	0.791277	0.974756	1.000
244	GOBP-REGULATION-OF-CELLULAR-COMPONENT_SIZE	GO-0032535	7	0.280910	0.770440	0.749235	0.972834	1.000
245	GOBP-MUSCLE-ADAPTATION	GO-0043500	5	0.330002	0.769423	0.735135	0.970818	1.000
246	GOBP-REGULATION-OF-PEPTIDASE-ACTIVITY	GO-0052547	10	0.244091	0.769163	0.784257	0.967374	1.000
247	GOBP-REGULATION-OF-NEUROGENESIS	GO-0050767	14	0.209302	0.762407	0.795775	0.975525	1.000
248	GOBP-TEMPERATURE-HOMEOSTASIS	GO-0001659	5	0.313253	0.757283	0.752187	0.979907	1.000
249	GOBP-POSITIVE-REGULATION-OF-CELL-DEATH	GO-0010942	19	0.185679	0.743625	0.851406	0.999491	1.000
250	GOBP-REGULATION-OF-DEFENSE-RESPONSE	GO-0031347	7	0.262837	0.741803	0.821429	0.998800	1.000
251	GOBP-ORGANIC-HYDROXY-COMPOUND-METABOLIC-PROCESS	GO-1901615	7	0.252259	0.739034	0.771015	0.999180	1.000
252	GOBP-POSITIVE-REGULATION-OF-ANION-TRANSPORT	GO-1903793	9	0.240506	0.735512	0.844720	1.000000	1.000
253	GOBP-POSTSYNAPSE-ORGANIZATION	GO-0099173	10	0.243590	0.735128	0.803125	0.997910	1.000
254	GOBP-REGULATION-OF-VESICLE-MEDIATED_TRANSPORT	GO-0060627	12	0.209818	0.727286	0.846875	1.000000	1.000
255	GOBP-REGULATION-OF-CELL-DEVELOPMENT	GO-0060284	15	0.201262	0.726365	0.862295	1.000000	1.000

Continuation of Table S15

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
256	GOBP-EMBRYO-DEVELOPMENT	14	0.204587	0.725824	0.830935	1.000000	1.000
257	GOBP-CELL-MORPHOGENESIS INVOLVED IN NEURON DIFF...	21	0.175457	0.720842	0.888430	1.000000	1.000
258	GOBP-REGULATION-OF-CELLULAR-COMPONENT-MOVEMENT	15	0.191562	0.715050	0.848592	1.000000	1.000
259	GOBP-APOPTOTIC-MITOCHONDRIAL-CHANGES	6	0.273523	0.714223	0.849003	1.000000	1.000
260	GOBP-REGULATION-OF-INFLAMMATORY-RESPONSE	7	0.262837	0.713966	0.785124	1.000000	1.000
261	GOBP-CELL-MORPHOGENESIS INVOLVED IN DIFFERENTI...	21	0.175457	0.713868	0.846715	1.000000	1.000
262	GOBP-NEGATIVE-REGULATION-OF-KINASE-ACTIVITY	5	0.289044	0.709549	0.861878	1.000000	1.000
263	GOBP-PROTEIN-LOCALIZATION-TO-PLASMA-MEMBRANE	7	0.257121	0.707852	0.871166	1.000000	1.000
264	GOBP-NEGATIVE-REGULATION-OF-INTRACELLULAR-SIGN...	7	0.261763	0.704334	0.835294	1.000000	1.000
265	GOBP-DENDRITE-DEVELOPMENT	9	0.223438	0.699453	0.870432	1.000000	1.000
266	GOBP-NEGATIVE-REGULATION-OF-TRANSFERASE-ACTIVITY	5	0.289044	0.694647	0.844327	1.000000	1.000
267	GOBP-REGULATION-OF-ORGANELLE-ORGANIZATION	14	0.200978	0.693270	0.903448	1.000000	1.000
268	GOBP-MEMBRANE-ORGANIZATION	12	0.200978	0.692565	0.871473	1.000000	1.000
269	REACTOME-DEATH-RECEPTOR-SIGNALING	5	0.293522	0.690907	0.845960	1.000000	1.000
270	GOBP-ADENYLATE-CYCLASE-INHIBITING-G-PROTEIN.CO...	9	0.222140	0.684025	0.890282	1.000000	1.000
271	GOBP-PROTEIN-KINASE-B-SIGNALING	6	0.257489	0.681750	0.876081	1.000000	1.000
272	GOBP-FATTY-ACID-TRANSPORT	6	0.268396	0.681750	0.853521	1.000000	1.000
273	GOBP-REGULATION-OF-MAP-KINASE-ACTIVITY	9	0.214761	0.676153	0.906832	1.000000	1.000
274	GOBP-REGULATION-OF-PHOSPHATIDYLINOSITOL-3-KINA...	6	0.256098	0.675583	0.881720	1.000000	1.000
275	GOBP-CELL-SURFACE-RECEPTOR-SIGNALING-PATHWAY.I...	15	0.177210	0.675576	0.924460	1.000000	1.000
276	GOBP-NEGATIVE-REGULATION-OF-APOPTOTIC-SIGNALIN...	7	0.235976	0.670109	0.887240	1.000000	1.000
277	GOBP-ANION-TRANSMEMBRANE-TRANSPORT	7	0.240082	0.663266	0.911504	1.000000	1.000
278	GOBP-REGULATION-OF-MUSCLE-CELL-DIFFERENTIATION	6	0.256098	0.662156	0.888889	1.000000	1.000
279	GOBP-REGULATION-OF-PROTEIN-LOCALIZATION-TO-CEL...	6	0.265603	0.662001	0.898072	1.000000	1.000
280	GOBP-INTRINSIC-APOPTOTIC-SIGNALING-PATHWAY	5	0.266292	0.659204	0.887671	1.000000	1.000
281	GOBP-PEPTIDE-METABOLIC-PROCESS	12	0.193260	0.653903	0.914754	1.000000	1.000
282	REACTOME-DISEASES-OF-SIGNAL-TRANSDUCTION-BY-GR...	12	0.190461	0.653163	0.906832	1.000000	1.000
283	REACTOME-SYNAPTIC-ADHESION-LIKE-MOLECULES	9	0.216571	0.649236	0.900000	1.000000	1.000
284	GOBP-ORGANIC-ACID-TRANSPORT	7	0.229544	0.646966	0.913947	1.000000	1.000
285	GOBP-MALE-GAMETE-GENERATION	5	0.258920	0.637455	0.910053	1.000000	1.000
286	GOBP-REGULATION-OF-PROTEIN-LOCALIZATION-TO-MEM...	7	0.234568	0.632121	0.915989	1.000000	1.000
287	GOBP-REGULATION-OF-PEPTIDE-TRANSPORT	10	0.192271	0.627037	0.948718	1.000000	1.000
288	GOBP-REGULATION-OF-LIPID-METABOLIC-PROCESS	7	0.224911	0.624483	0.933908	1.000000	1.000
289	GOBP-POSITIVE-REGULATION-OF-PHOSPHATIDYLINOSIT...	5	0.253012	0.624423	0.951031	1.000000	1.000
290	GOBP-REGULATION-OF-CELL-CYCLE-PROCESS	5	0.253012	0.616766	0.936464	1.000000	1.000
291	GOBP-POSITIVE-REGULATION-OF-SMOOTH-MUSCLE-CELL...	5	0.249521	0.613950	0.931579	1.000000	1.000
292	GOBP-CELLULAR-GLUCOSE-HOMEOSTASIS	5	0.253012	0.610753	0.943978	1.000000	1.000
293	GOBP-CHEMICAL-SYNAPTIC-TRANSMISSION-POSTSYNAPTIC	9	0.198286	0.608456	0.962428	1.000000	1.000
294	GOBP-CELLULAR-CARBOHYDRATE-METABOLIC-PROCESS	5	0.253012	0.599794	0.939726	1.000000	1.000
295	GOBP-PROTEIN-DEPHOSPHORYLATION	7	0.214328	0.593257	0.965714	1.000000	1.000
296	GOBP-NEGATIVE-REGULATION-OF-HYDROLASE-ACTIVITY	11	0.179643	0.586794	0.938710	1.000000	1.000
297	GOBP-DEPHOSPHORYLATION	7	0.214328	0.583958	0.946429	1.000000	1.000
298	GOBP-EMBRYO-DEVELOPMENT-ENDING-IN-BIRTH-OR-EGG...	9	0.186571	0.576436	0.964602	1.000000	1.000

Continuation of Table S15

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
299	GOBP-EMBRYONIC-ORGAN-DEVELOPMENT	GO-0048568	7	0.203897	0.573003	0.985955	1.000000	1.000
300	GOBP-NEGATIVE-REGULATION-OF-ANION-TRANSPORT	GO-1903792	8	0.195135	0.572101	0.977654	1.000000	1.000
301	GOBP-IN-UTERO-EMBRYONIC-DEVELOPMENT	GO-0001701	8	0.196000	0.570899	0.959877	1.000000	1.000
302	GOBP-NEURON-MIGRATION	GO-0001764	5	0.232317	0.558362	0.983146	1.000000	1.000
303	REACTOME-L1CAM-INTERACTIONS	R-RNO-373760	5	0.228916	0.555463	0.975207	1.000000	1.000
304	GOBP-ORGANONITROGEN-COMPOUND-BIOSYNTHETIC-PROCESS	GO-1901566	13	0.160000	0.550076	0.980645	0.999474	1.000
305	GOBP-POSITIVE-REGULATION-OF-PROTEOLYSIS	GO-0045862	8	0.188316	0.545840	0.982301	0.997882	1.000
306	GOBP-OSSIFICATION	GO-0001503	9	0.173241	0.539555	0.985673	0.996778	1.000
307	GOBP-EXTRINSIC-APOPTOTIC-SIGNALING-PATHWAY	GO-0097191	7	0.192200	0.527174	0.981651	0.997181	1.000
308	GOBP-STRIPATED-MUSCLE-CELL-DIFFERENTIATION	GO-0051146	9	0.167890	0.520091	0.984849	0.995529	1.000
309	GOBP-EPITHELIAL-CELL-DIFFERENTIATION	GO-0030855	7	0.172840	0.479206	0.993711	0.999106	1.000
310	GOBP-REGULATION-OF-SMALL-MOLECULE-METABOLIC-PR...	GO-0062012	9	0.161147	0.475423	0.990683	0.996274	1.000
311	GOBP-CALCIUM-MEDIATED-SIGNALING	GO-0019722	10	-0.141026	-0.383831	1.000000	0.999366	1.000
312	GOBP-MUSCLE-CELL-DIFFERENTIATION	GO-0042692	10	-0.153846	-0.422492	0.997054	1.000000	1.000
313	GOBP-NEGATIVE-REGULATION-OF-DEVELOPMENTAL-PROCESS	GO-0051093	13	-0.155610	-0.454574	0.993026	0.999088	1.000
314	GOBP-NEGATIVE-REGULATION-OF-CELL-DIFFERENTIATION	GO-0045596	13	-0.155610	-0.455983	0.985975	1.000000	1.000
315	REACTOME-PROTEIN-PROTEIN-INTERACTIONS-AT-SYNAPSES	R-RNO-6794362	12	-0.163838	-0.473252	0.988795	1.000000	1.000
316	GOBP-NEGATIVE-REGULATION-OF-CELLULAR-COMPONENT...	GO-0051129	11	-0.170382	-0.479859	0.982353	1.000000	1.000
317	GOBP-LIPID-EXPORT-FROM-CELL	GO-0140353	5	-0.225316	-0.484504	0.984472	1.000000	1.000
318	GOBP-MAINTENANCE-OF-LOCATION	GO-0051235	7	-0.207377	-0.500630	0.970326	1.000000	1.000
319	GOBP-RESPONSE-TO-PEPTIDE	GO-1901652	18	-0.158643	-0.507489	0.984148	1.000000	1.000
320	GOBP-REGULATION-OF-ANION-TRANSPORT	GO-0044070	20	-0.154479	-0.508653	0.983193	1.000000	1.000
321	REACTOME-EPHLEPHRIN-SIGNALING	R-RNO-2682334	6	-0.220944	-0.515362	0.979719	1.000000	1.000
322	GOBP-REGULATION-OF-CELLULAR-AMIDE-METABOLIC-PR...	GO-0034248	9	-0.199357	-0.517716	0.976574	1.000000	1.000
323	GOBP-NEGATIVE-REGULATION-OF-CELL-DEVELOPMENT	GO-0010721	6	-0.227567	-0.525068	0.982732	1.000000	1.000
324	GOBP-NEGATIVE-REGULATION-OF-NERVOUS-SYSTEM.DEV...	GO-0051961	5	-0.249492	-0.538065	0.981337	1.000000	1.000
325	GOBP-CELLULAR-RESPONSE-TO-NITROGEN-COMPOUND	GO-1901699	20	-0.161836	-0.538748	0.960396	1.000000	1.000
326	GOBP-REGULATION-OF-CARBOHYDRATE-BIOSYNTHETIC-P...	GO-0043255	5	-0.255061	-0.545114	0.972561	1.000000	1.000
327	GOBP-REGULATION-OF-CARBOHYDRATE-METABOLIC-PROCESS	GO-0006109	5	-0.255061	-0.549076	0.970874	1.000000	1.000
328	REACTOME-PTEN-REGULATION	R-RNO-6807070	5	-0.252572	-0.550394	0.979133	1.000000	1.000
329	GOBP-REGULATION-OF-RECEPTOR-MEDIATED-ENDOCYTOSIS	GO-0048259	5	-0.254355	-0.552087	0.976708	1.000000	1.000
330	GOBP-CARBOHYDRATE-BIOSYNTHETIC-PROCESS	GO-0016051	5	-0.255061	-0.553159	0.958194	1.000000	1.000
331	GOBP-VESICLE-MEDIATED-TRANSPORT-IN-SYNAPSE	GO-0099003	7	-0.227890	-0.554455	0.961821	1.000000	1.000
332	GOBP-CALCIUM-ION-TRANSPORT	GO-0006816	11	-0.198673	-0.555909	0.953587	1.000000	1.000
333	GOBP-METAL-ION-TRANSPORT	GO-0030001	11	-0.198673	-0.556515	0.960584	1.000000	1.000
334	REACTOME-POST-TRANSLATIONAL-PROTEIN-MODIFICATION	R-RNO-597592	7	-0.232667	-0.560671	0.957227	1.000000	1.000
335	GOBP-MULTICELLULAR-ORGANISM-REPRODUCTION	GO-0032504	12	-0.195390	-0.563693	0.954802	1.000000	1.000
336	GOBP-REGULATION-OF-HORMONE-SECRETION	GO-0046883	8	-0.219294	-0.570924	0.958841	1.000000	1.000
337	GOBP-POSITIVE-REGULATION-OF-PEPTIDASE-ACTIVITY	GO-0010952	7	-0.234846	-0.571187	0.957252	1.000000	1.000
338	GOBP-CELLULAR-COMPONENT-MAINTENANCE	GO-0043954	5	-0.261672	-0.573965	0.958730	1.000000	1.000
339	REACTOME-NERVOUS-SYSTEM-DEVELOPMENT	R-RNO-9675108	15	-0.187591	-0.575109	0.963432	1.000000	1.000
340	GOBP-POSITIVE-REGULATION-OF-CYSTEINE-TYPE-ENDO...	GO-2001056	7	-0.234846	-0.577513	0.945227	1.000000	1.000
341	GOBP-AMINO-ACID-TRANSPORT	GO-0008685	6	-0.251394	-0.577904	0.957317	1.000000	1.000

Continuation of Table S15

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
342	GOBP-CARBOXYLIC-ACID-TRANSPORT	GO-0046942	6	-0.251394	-0.580232	0.940092	1.000000	1.000
343	GOBP-GROWTH	GO-0040007	14	-0.192353	-0.580407	0.960469	1.000000	1.000
344	GOBP-MAPK-CASCADE	GO-0000165	18	-0.181914	-0.580996	0.954240	1.000000	1.000
345	GOBP-ORGANIC-ANION-TRANSPORT	GO-0015711	6	-0.251394	-0.590596	0.946792	1.000000	1.000
346	GOBP-CELLULAR-RESPONSE-TO-ABIOTIC-STIMULUS	GO-0071214	7	-0.245403	-0.591865	0.946237	1.000000	1.000
347	GOBP-REGULATION-OF-ENDOTHELIAL-CELL-MIGRATION	GO-0010594	5	-0.269864	-0.594629	0.949765	1.000000	1.000
348	GOBP-LEUKOCYTE-MEDIATED-IMMUNITY	GO-0002443	7	-0.239585	-0.596431	0.940549	1.000000	1.000
349	GOBP-POSTTRANSCRIPTIONAL-REGULATION-OF_GENE.EX...	GO-0010608	8	-0.238569	-0.600247	0.937879	1.000000	1.000
350	GOBP-LIPID-METABOLIC-PROCESS	GO-0006629	10	-0.219572	-0.602721	0.925501	1.000000	1.000
351	GOBP-REGULATION-OF-ENDOCYTOSIS	GO-0030100	6	-0.260772	-0.604509	0.934959	1.000000	1.000
352	GOBP-MONOAMINE-TRANSPORT	GO-0015844	5	-0.279081	-0.609293	0.921753	1.000000	1.000
353	GOBP-MYOTUBE-DIFFERENTIATION	GO-0014902	5	-0.278270	-0.609567	0.928105	1.000000	1.000
354	GOBP-NEGATIVE-REGULATION-OF-CELL-PROJECTION.OR...	GO-0031345	5	-0.272993	-0.610160	0.948136	1.000000	1.000
355	GOBP-PURINE-CONTAINING-COMPOUND-METABOLIC-PROCESS	GO-0072521	5	-0.282557	-0.614695	0.918712	1.000000	1.000
356	GOBP-NEGATIVE-REGULATION-OF-CATABOLIC-PROCESS	GO-0009895	8	-0.245632	-0.620396	0.906793	1.000000	1.000
357	GOBP-NEGATIVE-REGULATION-OF-PHOSPHORUS-METABOL...	GO-0010563	9	-0.236030	-0.624501	0.922628	1.000000	1.000
358	GOBP-REGULATION-OF-BINDING	GO-0051098	11	-0.222590	-0.624824	0.896652	1.000000	1.000
359	GOBP-RESPONSE-TO-NUTRIENT	GO-0007584	5	-0.293930	-0.627922	0.924194	1.000000	1.000
360	REACTOME-DEVELOPMENTAL-BIOLOGY	R-RNO-1266738	23	-0.186103	-0.631221	0.924528	1.000000	1.000
361	GOBP-RESPONSE-TO-TEMPERATURE-STIMULUS	GO-0009266	9	-0.241522	-0.632063	0.891655	1.000000	1.000
362	GOBP-CELLULAR-AMIDE-METABOLIC-PROCESS	GO-0043603	13	-0.214767	-0.632609	0.914454	1.000000	1.000
363	GOBP-REGULATION-OF-NERVOUS-SYSTEM-PROCESS	GO-0031644	8	-0.242875	-0.632875	0.905488	1.000000	1.000
364	GOBP-PROTEIN-AUTOPHOSPHORYLATION	GO-0046777	5	-0.293641	-0.641719	0.908082	1.000000	1.000
365	GOBP-CELLULAR-RESPONSE-TO-DNA-DAMAGE-STIMULUS	GO-0006974	5	-0.299925	-0.643431	0.914242	1.000000	1.000
366	GOBP-HOMEOSTATIC-PROCESS	GO-0042592	31	-0.177620	-0.643605	0.916880	1.000000	1.000
367	GOBP-EPHRIIN-RECEPTOR-SIGNALING-PATHWAY	GO-0048013	5	-0.299163	-0.645748	0.894737	1.000000	1.000
368	GOBP-REGULATION-OF-MAPK-CASCADE	GO-0043408	13	-0.220998	-0.652356	0.899713	1.000000	1.000
369	GOBP-POSITIVE-REGULATION-OF-ORGANELLE-ORGANIZA...	GO-0010638	10	-0.239262	-0.652751	0.893275	1.000000	1.000
370	GOBP-DICARBOXYLIC-ACID-TRANSPORT	GO-0006835	5	-0.301410	-0.654380	0.895223	1.000000	1.000
371	GOBP-MONOCARBOXYLIC-ACID-TRANSPORT	GO-0015718	5	-0.301410	-0.655807	0.887439	1.000000	1.000
372	GOBP-ACIDIC-AMINO-ACID-TRANSPORT	GO-0015800	5	-0.301410	-0.656609	0.906396	1.000000	1.000
373	GOBP-REGULATION-OF-GROWTH	GO-0040008	13	-0.228395	-0.659025	0.877874	1.000000	1.000
374	GOBP-POSITIVE-REGULATION-OF_SMALL-MOLECULE-MET...	GO-0062013	5	-0.304800	-0.661614	0.879365	1.000000	1.000
375	GOBP-T-CELL-ACTIVATION	GO-0042110	8	-0.260073	-0.666083	0.870343	1.000000	1.000
376	GOBP-DEVELOPMENTAL-PROCESS-INVOLVED-IN-REPRODU...	GO-0003006	11	-0.236683	-0.667634	0.869048	1.000000	1.000
377	GOBP-OSTEOBLAST-DIFFERENTIATION	GO-0001649	5	-0.308052	-0.668621	0.882927	1.000000	1.000
378	GOBP-POSITIVE-REGULATION-OF_GENE-EXPRESSION	GO-0010628	16	-0.212132	-0.669254	0.889037	1.000000	1.000
379	GOBP-CELL-MIGRATION	GO-0016477	22	-0.202540	-0.678299	0.878415	1.000000	1.000
380	GOBP-CELL-ACTIVATION-INVOLVED-IN-IMMUNE-RESPONSE	GO-0002263	6	-0.296951	-0.682961	0.873846	1.000000	1.000
381	GOBP-REGULATION-OF-MITOTIC-CELL-CYCLE	GO-0007346	5	-0.318508	-0.683943	0.872441	1.000000	1.000
382	GOBP-MULTICELLULAR-ORGANISMAL-HOMEOSTASIS	GO-0048871	12	-0.231107	-0.684411	0.861386	1.000000	1.000
383	GOBP-REPRODUCTION	GO-0000003	18	-0.213401	-0.686385	0.878492	1.000000	1.000
384	GOBP-SECRETION	GO-0046903	24	-0.200204	-0.688006	0.841379	1.000000	1.000

Continuation of Table S15

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
385	REACTOME_NEUTROPHIL_DEGRANULATION	R-RNO-6798695	6	-0.296951	-0.688892	0.842788	1.000000	1.000
386	GOBP_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY	GO-0002444	6	-0.296951	-0.688918	0.840874	1.000000	1.000
387	GOBP_NEGATIVE_REGULATION_OF_PROTEIN_METABOLIC...	GO-0051248	20	-0.206313	-0.689445	0.860846	1.000000	1.000
388	GOBP_INORGANIC_ION_TRANSMEMBRANE_TRANSPORT	GO-0098660	9	-0.259364	-0.694213	0.848440	1.000000	1.000
389	GOBP_PROTEIN_CONTAINING_COMPLEX_SUBUNIT_ORGANI...	GO-0043933	14	-0.237787	-0.696493	0.852113	1.000000	1.000
390	REACTOME_CELL_CYCLE_MITOTIC	R-RNO-69278	5	-0.321875	-0.697897	0.825954	1.000000	1.000
391	GOBP_ACTIVATION_OF_MAPK_ACTIVITY	GO-0000187	6	-0.304350	-0.700099	0.847962	1.000000	1.000
392	GOBP_PHAGOCYTOSIS	GO-0006909	5	-0.319697	-0.701582	0.835404	1.000000	1.000
393	REACTOME_MAPK_FAMILY_SIGNALING_CASCADES	R-RNO-5983057	12	-0.241086	-0.702155	0.848617	1.000000	1.000
394	GOBP_NEGATIVE_REGULATION_OF_RESPONSE_TO_STIMULUS	GO-0048585	16	-0.226152	-0.702886	0.858921	1.000000	1.000
395	REACTOME_NEURONAL_SYSTEM	R-RNO-112316	26	-0.197839	-0.706650	0.853175	1.000000	1.000
396	GOBP_POSITIVE_REGULATION_OF_MAP_KINASE_ACTIVITY	GO-0043406	6	-0.304350	-0.710201	0.829630	1.000000	1.000
397	GOBP_POSITIVE_REGULATION_OF_DEFENSE_RESPONSE	GO-0031349	5	-0.322895	-0.711115	0.844828	1.000000	1.000
398	GOBP_CELL_JUNCTION_ASSEMBLY	GO-0034329	8	-0.283964	-0.712001	0.828006	1.000000	1.000
399	GOBP_REGULATION_OF_PROTEOLYSIS	GO-0030162	12	-0.249696	-0.715038	0.839763	1.000000	1.000
400	REACTOME_SIGNALING_BY_NTRKS	R-RNO-166520	18	-0.223378	-0.715060	0.820690	1.000000	1.000
401	GOBP_REGULATION_OF_LIPID_BIOSYNTHETIC_PROCESS	GO-0046890	6	-0.315189	-0.715415	0.828869	1.000000	1.000
402	GOBP_GLIAL_CELL_DIFFERENTIATION	GO-0010001	10	-0.258211	-0.715725	0.857576	1.000000	1.000
403	GOBP_POSITIVE_REGULATION_OF_MULTICELLULAR_ORGA...	GO-0051240	32	-0.198697	-0.717295	0.844208	1.000000	1.000
404	REACTOME_OPIOID_SIGNALING	R-RNO-111885	17	-0.253079	-0.719531	0.829662	1.000000	1.000
405	GOBP_GLAND_DEVELOPMENT	GO-0048732	7	-0.297555	-0.727632	0.796043	1.000000	1.000
406	GOBP_REGULATION_OF_LIPID_LOCALIZATION	GO-1905952	5	-0.332818	-0.728137	0.830745	1.000000	1.000
407	REACTOME_CREB1_PHOSPHORYLATION_THROUGH_NMDA_RE...	R-RNO-442742	8	-0.284086	-0.730558	0.823976	1.000000	1.000
408	GOBP_ADENYLATE_CYCLASE_INHIBITING_G_PROTEIN_CO...	GO-0007196	5	-0.332218	-0.730829	0.816746	1.000000	1.000
409	GOBP_LIPID_BIOSYNTHETIC_PROCESS	GO-0008610	6	-0.315189	-0.731892	0.818325	1.000000	1.000
410	GOBP_ORGANIC_ACID_METABOLIC_PROCESS	GO-0006082	7	-0.297588	-0.732509	0.796712	1.000000	1.000
411	GOBP_CARDIAC_MUSCLE_TISSUE_DEVELOPMENT	GO-0048738	6	-0.321305	-0.734381	0.777778	1.000000	1.000
412	GOBP_GLUTAMATE_RECEPTOR_SIGNALING_PATHWAY	GO-0007215	17	-0.230791	-0.735311	0.797844	1.000000	1.000
413	GOBP_NEGATIVE_REGULATION_OF_LOCOMOTION	GO-0040013	5	-0.334751	-0.735552	0.796825	1.000000	1.000
414	GOBP_ERK1_AND_ERK2_CASCADE	GO-0070371	5	-0.337477	-0.736978	0.799051	1.000000	1.000
415	GOBP_ENDOCRINE_SYSTEM_DEVELOPMENT	GO-0035270	6	-0.316227	-0.737751	0.801964	1.000000	1.000
416	GOBP_HEART_DEVELOPMENT	GO-0007507	6	-0.321305	-0.738306	0.794643	1.000000	1.000
417	GOBP_ANIMAL_ORGAN_MORPHOGENESIS	GO-0009887	12	-0.254598	-0.738699	0.802038	1.000000	1.000
418	GOBP_REGULATION_OF_LYMPHOCYTE_ACTIVATION	GO-0051249	5	-0.346482	-0.742661	0.797488	1.000000	1.000
419	REACTOME_CELL_CYCLE	R-RNO-1640170	6	-0.324282	-0.747242	0.789147	1.000000	1.000
420	GOBP_NEURON_DEATH	GO-0070997	18	-0.230725	-0.748150	0.816804	1.000000	1.000
421	GOBP_SIGNAL_RELEASE	GO-0023061	14	-0.248176	-0.754013	0.801688	1.000000	1.000
422	GOBP_GLIOGENESIS	GO-0042063	12	-0.261970	-0.756692	0.775298	1.000000	1.000
423	GOBP_REGULATION_OF_APOPTOTIC_SIGNALING_PATHWAY	GO-2001233	10	-0.275270	-0.758591	0.777941	1.000000	1.000
424	GOBP_LIPID_LOCALIZATION	GO-0010876	10	-0.279097	-0.762122	0.754491	1.000000	1.000
425	GOBP_REGULATION_OF_PROTEIN_SERINE_THREONINE_KI...	GO-0071900	12	-0.267358	-0.762288	0.767544	1.000000	1.000
426	GOBP_LYMPHOCYTE_ACTIVATION	GO-0046649	9	-0.293889	-0.764905	0.761905	1.000000	1.000
427	GOBP_GLUCOSE_METABOLIC_PROCESS	GO-0006006	6	-0.335603	-0.765267	0.755385	1.000000	1.000

Continuation of Table S15

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
428 REACTOME-GPCR-LIGAND-BINDING	R-RNO-500792	8	-0.300888	-0.770134	0.769120	1.000000	1.000
429 REACTOME-SIGNALING-BY_GPCR	R-RNO-372790	22	-0.225838	-0.772090	0.782967	1.000000	1.000
430 GOBP-MONOSACCHARIDE-METABOLIC-PROCESS	GO-0005996	6	-0.335603	-0.772918	0.725962	1.000000	1.000
431 GOBP-REGULATION_OF_DNA-BINDING_TRANSCRIPTION.F...	GO-0051090	16	-0.250585	-0.775492	0.762500	1.000000	1.000
432 GOBP-CIRCULATORY_SYSTEM-PROCESS	GO-0003013	5	-0.356138	-0.780847	0.775157	1.000000	1.000
433 GOBP-REGULATION_OF_CELL-DEATH	GO-0010941	34	-0.213025	-0.784339	0.760052	1.000000	1.000
434 GOBP-REGULATION_OF_FAT-CELL-DIFFERENTIATION	GO-0045598	6	-0.339784	-0.785009	0.752252	1.000000	1.000
435 GOBP-RESPONSE_TO_TUMOR-NECROSIS-FACTOR	GO-0034612	7	-0.324557	-0.785861	0.754123	1.000000	1.000
436 REACTOME-EXTRA_NUCLEAR-ESTROGEN-SIGNALING	R-RNO-9009391	7	-0.318658	-0.786100	0.748126	1.000000	1.000
437 REACTOME-EXTRA-CELLULAR-MATRIX-ORGANIZATION	R-RNO-1474244	5	-0.363523	-0.790234	0.755556	1.000000	1.000
438 GOBP-REGULATION_OF-PROTEIN-BINDING	GO-0043393	7	-0.329582	-0.790254	0.734158	1.000000	1.000
439 GOBP-RESPONSE_TO_NITROGEN-COMPOUND	GO-1901698	34	-0.216616	-0.790364	0.750639	1.000000	1.000
440 REACTOME-INTEGRATION_OF-ENERGY-METABOLISM	R-RNO-163685	5	-0.366499	-0.791501	0.730645	1.000000	1.000
441 GOBP-RESPONSE_TO_UV	GO-0009411	5	-0.363129	-0.792886	0.741486	1.000000	1.000
442 GOBP-RESPONSE_TO-ENDOGENOUS-STIMULUS	GO-0009719	34	-0.217058	-0.799391	0.735369	1.000000	1.000
443 GOBP-REGULATION_OF_CELL-DIFFERENTIATION	GO-0045595	36	-0.219299	-0.800329	0.747736	1.000000	1.000
444 GOBP-REGULATION_OF-EXTRINSIC-APOPTOTIC-SIGNAL...	GO-2001236	6	-0.351206	-0.805878	0.738583	1.000000	1.000
445 GOBP-REGULATION_OF-CELLULAR-CATABOLIC-PROCESS	GO-0031329	10	-0.290981	-0.808215	0.724812	1.000000	1.000
446 GOBP-REGULATION_OF-SYSTEM-PROCESS	GO-0044057	18	-0.245200	-0.808749	0.704708	1.000000	1.000
447 GOBP-POSITIVE-REGULATION_OF-PROTEIN-SERINE-THR...	GO-0071902	9	-0.304207	-0.810455	0.732169	1.000000	1.000
448 GOBP-REGULATION_OF-SECRETION	GO-0051046	14	-0.265804	-0.810918	0.701556	1.000000	1.000
449 GOBP-PROTEIN-LOCALIZATION_TO-MEMBRANE	GO-0071667	14	-0.264422	-0.812529	0.709632	1.000000	1.000
450 GOBP-REGULATION_OF-METAL-ION-TRANSPORT	GO-0010959	6	-0.347358	-0.812577	0.701219	1.000000	1.000
451 GOBP-AMEBOIDAL-TYPE-CELL-MIGRATION	GO-0001667	11	-0.292051	-0.816310	0.679831	1.000000	1.000
452 GOBP-MUSCLE-CELL-PROLIFERATION	GO-0033002	8	-0.326586	-0.817419	0.702128	1.000000	1.000
453 GOBP-IMMUNE-EFFECTOR-PROCESS	GO-0002252	10	-0.299667	-0.819964	0.708029	1.000000	1.000
454 GOBP-TISSUE-MIGRATION	GO-0090130	9	-0.315495	-0.822786	0.700752	1.000000	1.000
455 GOBP-FORBRAIN-DEVELOPMENT	GO-0030900	9	-0.312941	-0.825249	0.710526	1.000000	1.000
456 GOBP-LEUKOCYTE-CELL-CELL-ADHESION	GO-0007159	6	-0.360315	-0.829140	0.689441	1.000000	1.000
457 GOBP-CIRCADIAN-REGULATION_OF-GENE-EXPRESSION	GO-0032922	5	-0.377575	-0.834692	0.672000	1.000000	1.000
458 GOBP-RESPONSE_TO-INSULIN	GO-0032868	5	-0.387578	-0.834944	0.713141	1.000000	1.000
459 GOBP-EPIDERMIS-DEVELOPMENT	GO-0008544	5	-0.375858	-0.835332	0.698113	1.000000	1.000
460 GOBP-REGULATION_OF-WNT-SIGNALING-PATHWAY	GO-0030111	5	-0.389317	-0.836626	0.697205	1.000000	1.000
461 GOBP-REGULATION_OF-NEUROTRANSMITTER-TRANSPORT	GO-0051588	6	-0.370947	-0.846788	0.677019	1.000000	1.000
462 GOBP-REGULATION_OF-ANATOMICAL-STRUCTURE-SIZE	GO-0090066	10	-0.307604	-0.847605	0.668175	1.000000	1.000
463 REACTOME-SIGNALING-BY-RECEPTOR-TYROSINE-KINASES	R-RNO-9006934	26	-0.243280	-0.848284	0.682561	1.000000	1.000
464 GOBP-APOPTOTIC-SIGNALING-PATHWAY	GO-0097190	15	-0.277939	-0.853598	0.662393	1.000000	1.000
465 GOBP-RESPIRATORY-SYSTEM-DEVELOPMENT	GO-0060541	6	-0.371669	-0.858307	0.655763	1.000000	1.000
466 GOBP-POSITIVE-REGULATION_OF-INTRACELLULAR-SIGN...	GO-1902533	14	-0.287822	-0.860357	0.643994	1.000000	1.000
467 GOBP-HOMEOSTASIS-OF-NUMBER_OF-CELLS	GO-0048872	5	-0.394862	-0.860543	0.649612	1.000000	1.000
468 GOBP-LOCOMOTION	GO-0040011	31	-0.243054	-0.863587	0.671018	1.000000	1.000
469 GOBP-REGULATION_OF-VASCULATURE-DEVELOPMENT	GO-1901342	5	-0.396738	-0.864099	0.662903	1.000000	1.000
470 GOBP-NEGATIVE-REGULATION_OF-PROTEIN-MODIFICATI...	GO-0031400	10	-0.320006	-0.865652	0.645926	1.000000	1.000

Continuation of Table S15

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
471	GOBP-PROTEOLYSIS	GO-0006508	17	-0.277090	-0.873182	0.609929	1.000000	1.000
472	GOBP-CELLULAR_RESPONSE.TO.PEPTIDE	GO-1901653	13	-0.295253	-0.874776	0.617111	1.000000	1.000
473	GOBP-NEGATIVE-REGULATION-OF-CELL-POPULATION.PR...	GO-0008285	9	-0.333921	-0.875372	0.622419	1.000000	1.000
474	GOBP-MULTI-ORGANISM-PROCESS	GO-0051704	16	-0.284382	-0.877456	0.629477	1.000000	1.000
475	REACTOME-TRAFFICKING-OF-GLUR2-CONTAINING-AMPA-...	R-RNO-416993	8	-0.341685	-0.879027	0.628866	1.000000	1.000
476	GOBP-POSITIVE-REGULATION-OF-CELL-CELL-ADHESION	GO-0022409	5	-0.406004	-0.879239	0.654664	1.000000	1.000
477	HALLMARK-ALLOGRAFT-REJECTION	M5950	7	-0.360129	-0.879627	0.627871	1.000000	1.000
478	GOBP-REGULATION-OF-CELLULAR-COMPONENT-BIOGENESIS	GO-0044087	10	-0.315922	-0.879857	0.611026	1.000000	1.000
479	GOBP-POSITIVE-REGULATION-OF-LEUKOCYTE-CELL-CEL...	GO-1903039	5	-0.406004	-0.884296	0.618012	1.000000	1.000
480	GOBP-NEUROTRANSMITTER-SECRETION	GO-0007269	6	-0.381670	-0.885794	0.634969	1.000000	1.000
481	GOBP-POSITIVE-REGULATION-OF-MAPK-CASCADE	GO-00043410	9	-0.338713	-0.896571	0.589260	1.000000	1.000
482	GOBP-LEARNING	GO-0007612	13	-0.313048	-0.901216	0.585366	1.000000	1.000
483	GOBP-RESPONSE-TO-OXYGEN-CONTAINING-COMPOUND	GO-1901700	39	-0.236732	-0.901216	0.590377	1.000000	1.000
484	GOBP-CELL-ACTIVATION	GO-0001775	21	-0.273791	-0.906303	0.586486	1.000000	1.000
485	REACTOME-ESTROGEN-DEPENDENT-NUCLEAR-EVENTS.DOW...	R-RNO-9634638	5	-0.413713	-0.906913	0.601926	1.000000	1.000
486	GOBP-CELLULAR-RESPONSE-TO-LIPID	GO-0071396	15	-0.291263	-0.910595	0.587021	1.000000	1.000
487	GOBP-SECOND-MESSENGER-MEDIATED-SIGNALING	GO-0019932	16	-0.287964	-0.910788	0.559441	1.000000	1.000
488	GOBP-MUSCLE-STRUCTURE-DEVELOPMENT	GO-0061061	16	-0.296298	-0.915626	0.558533	1.000000	1.000
489	GOBP-MITOTIC-CELL-CYCLE	GO-0000278	10	-0.338358	-0.918131	0.589443	1.000000	1.000
490	REACTOME-DAG-AND-JP3-SIGNALING	R-RNO-1489509	8	-0.375960	-0.918524	0.570370	1.000000	1.000
491	GOBP-POSITIVE-REGULATION-OF-RESPONSE-TO-EXTERN...	GO-0032103	9	-0.344439	-0.927152	0.545727	1.000000	1.000
492	GOBP-HEAD-DEVELOPMENT	GO-0060322	22	-0.277441	-0.927152	0.539095	1.000000	1.000
493	GOBP-DEFENSE-RESPONSE-TO-OTHER-ORGANISM	GO-0098542	9	-0.350618	-0.930056	0.582335	1.000000	1.000
494	GOBP-CELLULAR-COMPONENT-DISASSEMBLY	GO-0023411	6	-0.402313	-0.937126	0.551669	0.997346	1.000
495	GOBP-POSITIVE-REGULATION-OF-IMMUNE-RESPONSE	GO-0050778	9	-0.357252	-0.938338	0.558209	0.998924	1.000
496	GOBP-ANATOMICAL-STRUCTURE-HOMEOSTASIS	GO-0060249	7	-0.380477	-0.939679	0.549467	1.000000	1.000
497	GOBP-MULTI-MULTICELLULAR-ORGANISM-PROCESS	GO-0044706	8	-0.370361	-0.940234	0.517804	1.000000	1.000
498	GOBP-REGULATION-OF-MULTICELLULAR-ORGANISMAL-DE...	GO-2000026	31	-0.264240	-0.941307	0.540365	1.000000	1.000
499	GOBP-ORGANIC-HYDROXY-COMPOUND-TRANSPORT	GO-0015850	6	-0.400176	-0.941840	0.543307	1.000000	1.000
500	REACTOME-INTERLEUKIN-4-AND-INTERLEUKIN-13-SIGN...	R-RNO-6785807	8	-0.378643	-0.944547	0.533626	1.000000	1.000
501	GOBP-PROTEIN-COMPLEX-OLIGOMERIZATION	GO-0051259	6	-0.407538	-0.945818	0.556904	1.000000	1.000
502	GOBP-REGULATION-OF-PROTEIN-CATABOLIC-PROCESS	GO-0042176	7	-0.381075	-0.945906	0.519637	1.000000	1.000
503	GOBP-ENDOTHELIAL-CELL-PROLIFERATION	GO-0001935	8	-0.376708	-0.946219	0.524540	1.000000	1.000
504	GOBP-RESPONSE-TO-PEPTIDE-HORMONE	GO-0043434	13	-0.317643	-0.946855	0.533898	1.000000	1.000
505	GOBP-ACTIVATION-OF-IMMUNE-RESPONSE	GO-0002253	5	-0.428592	-0.948476	0.541411	1.000000	1.000
506	GOBP-FAT-CELL-DIFFERENTIATION	GO-0045444	9	-0.362500	-0.949317	0.563798	1.000000	1.000
507	GOBP-REGULATION-OF-GTPASE-ACTIVITY	GO-0043087	5	-0.436050	-0.950546	0.540582	1.000000	1.000
508	GOBP-IMPORT-INTO-CELL	GO-0098657	6	-0.420317	-0.950650	0.565149	1.000000	1.000
509	GOBP-ENDOTHELIAL-CELL-MIGRATION	GO-0043542	8	-0.377033	-0.952699	0.523006	1.000000	1.000
510	GOBP-ENDOMEMBRANE-SYSTEM-ORGANIZATION	GO-0010256	6	-0.403745	-0.953531	0.541213	1.000000	1.000
511	GOBP-REGULATION-OF-PROTEIN-STABILITY	GO-0031647	5	-0.437451	-0.953783	0.545598	1.000000	1.000
512	GOBP-BLOOD-VESSEL-ENDOTHELIAL-CELL-MIGRATION	GO-0043534	8	-0.377053	-0.958857	0.532012	1.000000	1.000
513	GOBP-SKELETAL-MUSCLE-ORGAN-DEVELOPMENT	GO-0060538	5	-0.439272	-0.967618	0.510870	1.000000	1.000

Continuation of Table S15

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
514	GOBP-NEGATIVE-REGULATION-OF-GENE-EXPRESSION	GO-0010629	12	-0.339042	-0.971567	0.489362	1.000000	1.000
515	REACTOME-CLASS-C.3-METABOTROPIC-GLUTAMATE-PHER...	R-RNO-420499	7	-0.407264	-0.973462	0.510736	1.000000	1.000
516	GOBP-RESPONSE-TO-ABIOTIC-STIMULUS	GO-0009628	27	-0.274885	-0.975755	0.503320	1.000000	1.000
517	GOBP-POSITIVE-REGULATION-OF-CELLULAR-COMPONENT...	GO-0044089	9	-0.370638	-0.976899	0.489943	1.000000	1.000
518	REACTOME-INTRACELLULAR-SIGNALING-BY-SECOND-MES...	R-RNO-9006925	15	-0.323305	-0.979541	0.485836	1.000000	1.000
519	GOBP-ACTIN-FILAMENT-BASED-PROCESS	GO-0030029	7	-0.402114	-0.979852	0.513514	1.000000	1.000
520	GOBP-PROTEIN-LOCALIZATION-TO-SYNAPSE	GO-0035418	5	-0.457618	-0.980945	0.529687	1.000000	1.000
521	GOBP-POSITIVE-REGULATION-OF-CELL-POPULATION-PR...	GO-0008284	21	-0.290149	-0.982022	0.491252	1.000000	1.000
522	HALLMARK-EPITHELIAL-MESENCHYMAL-TRANSITION	M5930	5	-0.454135	-0.984350	0.477707	1.000000	1.000
523	GOBP-SMOOTH-MUSCLE-CELL-PROLIFERATION	GO-0048659	6	-0.419735	-0.985087	0.507042	1.000000	1.000
524	GOBP-SPROUTING-ANGIOGENESIS	GO-0002040	5	-0.457282	-0.986906	0.505017	1.000000	1.000
525	GOBP-CELLULAR-RESPONSE-TO-OXYGEN-CONTAINING-CO...	GO-1901701	29	-0.274257	-0.987229	0.471910	1.000000	1.000
526	GOBP-RESPONSE-TO-WOUNDING	GO-0009611	15	-0.333577	-0.992935	0.484286	1.000000	1.000
527	GOBP-PROTEIN-LOCALIZATION-TO-POSTSYNAPSE	GO-0062237	5	-0.457618	-0.994452	0.477419	1.000000	1.000
528	GOBP-CENTRAL-NERVOUS-SYSTEM-DEVELOPMENT	GO-0007417	26	-0.281200	-0.997138	0.454301	1.000000	1.000
529	GOBP-REGULATION-OF-CELL-ACTIVATION	GO-0050865	8	-0.396144	-1.001272	0.465569	1.000000	1.000
530	GOBP-BIOLOGICAL-ADHESION	GO-0022610	19	-0.308483	-1.002934	0.464088	1.000000	1.000
531	GOBP-REGULATION-OF-GLIOGENESIS	GO-0014013	5	-0.459194	-1.003377	0.474441	1.000000	1.000
532	GOBP-CALCIUM-ION-TRANSMEMBRANE-TRANSPORT	GO-0070588	7	-0.413700	-1.003565	0.471842	1.000000	1.000
533	GOBP-MUSCLE-TISSUE-DEVELOPMENT	GO-0060537	11	-0.354671	-1.004038	0.450581	1.000000	1.000
534	REACTOME-G-PROTEIN-MEDIATED-EVENTS	R-RNO-112040	9	-0.380591	-1.005494	0.485673	1.000000	1.000
535	REACTOME-NEUREXINS-AND-NEUROLIGINS	R-RNO-6794361	9	-0.383585	-1.006864	0.453102	1.000000	1.000
536	GOBP-POSITIVE-REGULATION-OF-GLIOGENESIS	GO-0014015	5	-0.459194	-1.007796	0.455975	1.000000	1.000
537	REACTOME-TRANSCRIPTIONAL-REGULATION-OF-WHITE-A...	R-RNO-381340	6	-0.426829	-1.008355	0.451163	1.000000	1.000
538	GOBP-CALCIUM-ION-TRANSPORT-INTO-CYTOSOL	GO-0060402	7	-0.413700	-1.009157	0.455752	1.000000	1.000
539	G...	GO-0007216	8	-0.390362	-1.009738	0.457143	1.000000	1.000
540	GOBP-CYTOSOLIC-CALCIUM-ION-TRANSPORT	GO-0060401	7	-0.413700	-1.010712	0.470229	1.000000	1.000
541	REACTOME-CA-DEPENDENT-EVENTS	R-RNO-111996	8	-0.394839	-1.013624	0.445802	1.000000	1.000
542	GOBP-REGULATION-OF-MUSCLE-SYSTEM-PROCESS	GO-0090257	8	-0.398763	-1.016763	0.482655	1.000000	1.000
543	GOBP-MUSCLE-SYSTEM-PROCESS	GO-0003012	9	-0.386318	-1.019082	0.448680	1.000000	1.000
544	GOBP-REPRODUCTIVE-SYSTEM-DEVELOPMENT	GO-0061458	6	-0.445970	-1.019978	0.440367	1.000000	1.000
545	GOBP-CELL-CYCLE-PROCESS	GO-0022402	11	-0.365200	-1.022490	0.429178	1.000000	1.000
546	GOBP-RESPONSE-TO-STARVATION	GO-0042594	5	-0.475357	-1.033415	0.419558	1.000000	1.000
547	GOBP-INNATE-IMMUNE-RESPONSE	GO-0045087	7	-0.427049	-1.035124	0.431517	1.000000	1.000
548	GOBP-EPITHELIAL-CELL-PROLIFERATION	GO-0050673	12	-0.359808	-1.039745	0.424965	1.000000	1.000
549	GOBP-CELLULAR-RESPONSE-TO-STARVATION	GO-0009267	5	-0.473537	-1.042028	0.406400	1.000000	1.000
550	GOBP-MUSCLE-CONTRACTION	GO-0006936	5	-0.497188	-1.048822	0.402174	1.000000	1.000
551	GOBP-DNA-METABOLIC-PROCESS	GO-0006259	6	-0.452777	-1.050817	0.417533	0.986631	1.000
552	GOBP-NEGATIVE-REGULATION-OF-BINDING	GO-0051100	6	-0.447037	-1.053793	0.441221	0.983605	1.000
553	GOBP-RESPONSE-TO-OXYGEN-LEVELS	GO-0070482	8	-0.414000	-1.059415	0.409836	0.972756	1.000
554	GOBP-AMYLOID-PRECURSOR-PROTEIN-METABOLIC-PROCESS	GO-0042982	5	-0.492010	-1.060547	0.388060	0.975387	1.000
555	GOBP-REGULATION-OF-OSTEOCLAST-DIFFERENTIATION	GO-0045670	5	-0.492541	-1.063147	0.404025	0.973855	1.000
556	GOBP-RESPONSE-TO-ORGANIC-CYCLIC-COMPOUND	GO-0014070	20	-0.319441	-1.064552	0.392351	0.975593	1.000

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NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
557 GOBP-AMYLOID-BETA-METABOLIC-PROCESS	GO-0050435	5	-0.492010	-1.064621	0.415000	0.981502	1.000
558 GOBP-PROTEIN-MODIFICATION-BY-SMALL-PROTEIN-CON...	GO-0032446	6	-0.456732	-1.069884	0.383915	0.971669	1.000
559 GOBP-AMYLOID-PRECURSOR-PROTEIN-CATABOLIC-PROCESS	GO-0042987	5	-0.492010	-1.070152	0.396923	0.977022	1.000
560 REACTOME-ESR-MEDIATED-SIGNALING	R-RNO-8939211	8	-0.426994	-1.072066	0.376190	0.977608	1.000
561 GOBP-CELL-CELL-ADHESION	GO-0098609	14	-0.363485	-1.074994	0.379404	0.974460	1.000
562 GOBP-INTRACELLULAR-PROTEIN-TRANSPORT	GO-0006886	9	-0.399135	-1.075824	0.380466	0.978055	1.000
563 GOBP-EXCITATORY-CHEMICAL-SYNAPTIC-TRANSMISSION	GO-0098976	5	-0.491521	-1.077748	0.395899	0.978250	1.000
564 GOBP-REGULATION-OF-RESPONSE-TO-EXTERNAL-STIMULUS	GO-0032101	15	-0.356463	-1.085414	0.370739	0.960645	1.000
565 GOBP-PROTEIN-LOCALIZATION-TO-CELL-JUNCTION	GO-1902414	6	-0.474984	-1.088023	0.355385	0.958550	1.000
566 GOBP-RESPONSE-TO-NICOTINE	GO-0035094	7	-0.456882	-1.089531	0.366771	0.960144	1.000
567 GOBP-VASCULATURE-DEVELOPMENT	GO-0001944	17	-0.343906	-1.089783	0.347709	0.965642	1.000
568 GOBP-RESPONSE-TO-KETONE	GO-1901654	7	-0.454154	-1.089983	0.368343	0.971484	1.000
569 REACTOME-PLATELET-ACTIVATION-SIGNALING-AND-AGG...	R-HSA-76002	7	-0.450459	-1.100777	0.348367	0.944502	1.000
570 GOBP-REGULATION-OF-CATABOLIC-PROCESS	GO-0009894	13	-0.372462	-1.100988	0.349138	0.950167	1.000
571 REACTOME-SIGNALING-BY-NUCLEAR-RECEPTORS	R-RNO-9006931	8	-0.426994	-1.104251	0.365152	0.946103	1.000
572 GOBP-ASSOCIATIVE-LEARNING	GO-0008306	7	-0.454096	-1.110026	0.340062	0.934589	1.000
573 GOBP-WOUND-HEALING	GO-0042060	13	-0.381623	-1.114408	0.319502	0.927445	1.000
574 GOBP-RESPONSE-TO-GROWTH-FACTOR	GO-0070848	18	-0.338391	-1.115007	0.330111	0.931911	1.000
575 GOBP-POSITIVE-REGULATION-OF-CELL-ADHESION	GO-0045785	7	-0.459129	-1.123231	0.322239	0.912577	1.000
576 GOBP-CYTOSKELETON-ORGANIZATION	GO-0007010	11	-0.394125	-1.124160	0.315407	0.916161	1.000
577 GOBP-RESPONSE-TO-HORMONE	GO-0009725	20	-0.342029	-1.126390	0.308921	0.915289	1.000
578 GOBP-ENZYME-LINKED-RECEPTOR-PROTEIN-SIGNALING....	GO-0007167	24	-0.320712	-1.127490	0.323529	0.918189	1.000
579 GOBP-EPIHELIAL-DEVELOPMENT	GO-0060429	15	-0.365037	-1.130119	0.304721	0.916337	1.000
580 GOBP-NEGATIVE-REGULATION-OF-MULTICELLULAR-ORGA...	GO-0051241	15	-0.370502	-1.132096	0.310830	0.916429	1.000
581 GOBP-PROTEIN-CATABOLIC-PROCESS	GO-0030163	8	-0.444902	-1.132385	0.327354	0.922130	1.000
582 GOBP-POSITIVE-REGULATION-OF-DEVELOPMENTAL-PROCESS	GO-0051094	32	-0.314084	-1.134654	0.297789	0.921511	1.000
583 REACTOME-CYTOKINE-SIGNALING-IN-IMMUNE-SYSTEM	R-RNO-1280215	21	-0.335608	-1.135350	0.309917	0.926036	1.000
584 GOBP-REGULATION-OF-CELL-ADHESION	GO-0030155	13	-0.388785	-1.138985	0.326180	0.920555	1.000
585 GOBP-CELL-CELL-JUNCTION-ASSEMBLY	GO-0007043	5	-0.524304	-1.140321	0.314103	0.923106	1.000
586 GOBP-CIRCULATORY-SYSTEM-DEVELOPMENT	GO-0072359	21	-0.344811	-1.140686	0.294430	0.928942	1.000
587 GOBP-NEGATIVE-REGULATION-OF-TRANSCRIPTION-BY-R...	GO-0000122	10	-0.425685	-1.140895	0.298422	0.935235	1.000
588 REACTOME-G-ALPHA-Z-SIGNALING-EVENTS	R-RNO-418597	5	-0.518144	-1.142769	0.281834	0.935980	1.000
589 GOBP-REGULATION-OF-VASCULAR-ASSOCIATED-SMOOTH...	GO-1904705	5	-0.510798	-1.143030	0.304478	0.942366	1.000
590 GOBP-CELLULAR-RESPONSE-TO-CADMIUM-ION	GO-0071276	5	-0.515070	-1.143813	0.309562	0.946963	1.000
591 GOBP-POSITIVE-REGULATION-OF-NEURON-DEATH	GO-1901216	5	-0.523392	-1.145828	0.301858	0.947563	1.000
592 GOBP-BLOOD-VESSEL-MORPHOGENESIS	GO-0048514	14	-0.386338	-1.152489	0.278184	0.932296	1.000
593 GOBP-RESPONSE-TO-METAL-ION	GO-0010038	15	-0.378169	-1.152804	0.292887	0.938324	1.000
594 GOBP-CELLULAR-RESPONSE-TO-PEPTIDE-HORMONE-STIM...	GO-0071375	9	-0.437952	-1.160068	0.306092	0.920952	1.000
595 GOBP-CELLULAR-RESPONSE-TO-MOLECULE-OF-BACTERIA...	GO-0071219	8	-0.457646	-1.167378	0.274032	0.903951	1.000
596 GOBP-POSITIVE-REGULATION-OF-CELL-DIFFERENTIATION	GO-0045597	27	-0.331392	-1.171701	0.237838	0.896409	1.000
597 REACTOME-ADAPTIVE-IMMUNE-SYSTEM	R-RNO-1280218	9	-0.448359	-1.171790	0.253776	0.903447	1.000
598 GOBP-RESPONSE-TO-INORGANIC-SUBSTANCE	GO-0010035	19	-0.359472	-1.175542	0.267956	0.898297	1.000
599 GOBP-POSITIVE-REGULATION-OF-EPITHELIAL-CELL-PR...	GO-0050679	7	-0.477754	-1.176447	0.272162	0.902646	1.000

Continuation of Table S15

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
600	GOBP-CELLULAR-RESPONSE-TO-BIOTIC-STIMULUS	8	-0.457646	-1.182256	0.282090	0.890172	1.000
601	GOBP-RESPONSE-TO-EXTRACELLULAR-STIMULUS	13	-0.401407	-1.182627	0.255618	0.896368	1.000
602	GOBP-NEUROTRANSMITTER-TRANSPORT	7	-0.487949	-1.184139	0.266667	0.898454	1.000
603	REACTOME-INFECTIOUS-DISEASE	13	-0.402949	-1.186614	0.262272	0.897612	1.000
604	GOBP-REGULATION-OF-CIRCADIAN-RHYTHM	7	-0.485345	-1.187146	0.267584	0.903607	1.000
605	GOBP-ANATOMICAL-STRUCTURE-FORMATION-INVOLVED.I...	20	-0.356987	-1.189714	0.251058	0.901997	1.000
606	GOBP-CYTOTKINE-MEDIATED-SIGNALING-PATHWAY	16	-0.382404	-1.195623	0.247326	0.889620	1.000
607	GOBP-POSITIVE-REGULATION-OF-ENDOTHELIAL-CELL-P...	6	-0.518302	-1.198118	0.239940	0.888312	1.000
608	REACTOME-CIRCADIAN-CLOCK	5	-0.558157	-1.198494	0.230047	0.895175	1.000
609	GOBP-REGULATION-OF-NEUROTRANSMITTER-LEVELS	7	-0.487949	-1.207694	0.241641	0.871023	1.000
610	GOBP-CELLULAR-RESPONSE-TO-EXTERNAL-STIMULUS	10	-0.438739	-1.209200	0.233859	0.873588	1.000
611	REACTOME-LEISHMANIA-INFECTION	10	-0.444701	-1.211175	0.244868	0.874624	1.000
612	GOBP-PROTEIN-MODIFICATION-BY-SMALL-PROTEIN-CON...	7	-0.502210	-1.212991	0.242613	0.875561	1.000
613	HALLMARK-UV-RESPONSE-UP	5	-0.555993	-1.213373	0.218354	0.883537	1.000
614	GOBP-MONONUCLEAR-CELL-DIFFERENTIATION	7	-0.504386	-1.217453	0.230089	0.877573	1.000
615	REACTOME-SIGNALING-BY-INTERLEUKINS	15	-0.394507	-1.225899	0.220630	0.855973	1.000
616	GOBP-RESPONSE-TO-ACID-CHEMICAL	6	-0.523940	-1.228774	0.205970	0.854344	1.000
617	GOBP-RESPONSE-TO-LIGHT-STIMULUS	11	-0.445851	-1.231855	0.206442	0.851560	1.000
618	REACTOME-RHO-GTPASE-EFFECTORS	9	-0.467014	-1.233821	0.204748	0.852782	1.000
619	GOBP-CELLULAR-RESPONSE-TO-CHEMICAL-STRESS	7	-0.517462	-1.235686	0.229970	0.854351	1.000
620	GOBP-TUBE-DEVELOPMENT	18	-0.376918	-1.236840	0.208564	0.858781	1.000
621	GOBP-MEMBRANE-PROTEIN-PROTEOLYSIS	6	-0.532106	-1.237013	0.200603	0.866961	1.000
622	REACTOME-SIGNALING-BY-RHO-GTPASES-MIRO-GTPASES...	9	-0.467014	-1.237437	0.228614	0.874390	1.000
623	GOBP-CELL-CELL-JUNCTION-ORGANIZATION	6	-0.539751	-1.244711	0.224060	0.855990	1.000
624	REACTOME-SIGNALING-BY-WNT	7	-0.490777	-1.245724	0.202808	0.861006	1.000
625	GOBP-TUBE-MORPHOGENESIS	15	-0.407913	-1.248990	0.203081	0.857874	1.000
626	GOBP-RESPONSE-TO-CALCIUM-ION	6	-0.550809	-1.249243	0.196172	0.866307	1.000
627	GOBP-PEPTIDYL-LYSINE-MODIFICATION	5	-0.577399	-1.256788	0.195618	0.847889	1.000
628	GOBP-RESPONSE-TO-LIPID	19	-0.387268	-1.258514	0.188782	0.850135	1.000
629	GOBP-CELL-POPULATION-PROLIFERATION	31	-0.349394	-1.259985	0.189857	0.854376	1.000
630	GOBP-AGING	13	-0.434099	-1.269062	0.172943	0.830071	1.000
631	GOBP-RESPONSE-TO-OXIDATIVE-STRESS	8	-0.503877	-1.273106	0.175150	0.824349	1.000
632	GOBP-MUSCLE-ORGAN-DEVELOPMENT	9	-0.476076	-1.276722	0.189349	0.820506	1.000
633	GOBP-RESPONSE-TO-REACTIVE-OXYGEN-SPECIES	8	-0.503877	-1.280173	0.185759	0.817224	1.000
634	GOBP-NEGATIVE-REGULATION-OF-RESPONSE-TO-EXTERN...	5	-0.594458	-1.282683	0.143082	0.817937	1.000
635	GOBP-CELLULAR-RESPONSE-TO-REACTIVE-OXYGEN-SPECIES	7	-0.517462	-1.284035	0.176901	0.822688	1.000
636	GOBP-NEGATIVE-REGULATION-OF-CELL-CYCLE	5	-0.590361	-1.293442	0.153094	0.798017	1.000
637	GOBP-SKIN-DEVELOPMENT	5	-0.590361	-1.296129	0.162939	0.797520	1.000
638	GOBP-PRL-MIRNA-TRANSCRIPTION-BY-RNA-POLYMERASE-II	7	-0.543210	-1.301003	0.155172	0.789622	1.000
639	GOBP-NEGATIVE-REGULATION-OF-BIOSYNTHETIC-PROCESS	13	-0.441104	-1.301772	0.145049	0.796712	1.000
640	GOBP-REGULATION-OF-IMMUNE-RESPONSE	12	-0.445444	-1.303244	0.156338	0.801388	1.000
641	GOBP-POSITIVE-REGULATION-OF-APOPTOTIC-SIGNALIN...	5	-0.590361	-1.303845	0.153846	0.809322	1.000
642	GOBP-NEGATIVE-REGULATION-OF-NUCLEOBASE-CONTAIN...	13	-0.441144	-1.305200	0.154381	0.814562	1.000

Continuation of Table S15

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
643 GOBP-POSITIVE-REGULATION_OF_PRL-MIRNA-TRANSCRI...	GO-1902895	7	-0.543210	-1.308474	0.147761	0.812417	1.000
644 GOBP-BIOLOGICAL-PROCESS-INVOLVED-IN-SYMBIOTIC....	GO-004440	11	-0.468308	-1.313195	0.130564	0.804651	1.000
645 GOBP-POSITIVE-REGULATION_OF_CYTOKINE-PRODUCTION	GO-0001819	7	-0.529457	-1.315668	0.137558	0.806027	1.000
646 GOBP-TISSUE-HOMEOSTASIS	GO-0001894	5	-0.617752	-1.316657	0.154446	0.812683	1.000
647 REACTOME-TRANSCRIPTIONAL-REGULATION_BY_TP53	R-RNO-3700989	6	-0.568724	-1.320485	0.140060	0.808267	1.000
648 GOBP-MORPHOGENESIS-OF-AN-EPITHELIUM	GO-0002009	6	-0.564938	-1.320495	0.121396	0.819616	1.000
649 GOBP-RESPONSE-TO-CYTOKINE	GO-0034097	23	-0.384359	-1.321209	0.121751	0.828558	1.000
650 GOBP-RESPONSE-TO-RADIATION	GO-0009314	13	-0.453353	-1.324540	0.135135	0.826742	1.000
651 GOBP-RESPONSE-TO-BIOTIC-STIMULUS	GO-0009607	17	-0.420353	-1.324562	0.125683	0.838863	1.000
652 GOBP-ORGANONITROGEN-COMPOUND-CATABOLIC-PROCESS	GO-1901565	9	-0.499458	-1.328261	0.141384	0.836013	1.000
653 GOBP-CELL-CYCLE	GO-0007049	21	-0.402671	-1.334929	0.128137	0.821869	1.000
654 GOBP-OSTEOCLAST-DIFFERENTIATION	GO-0030316	6	-0.589089	-1.354193	0.121951	0.755060	1.000
655 GOBP-FC-RECEPTOR-SIGNALING-PATHWAY	GO-0038093	8	-0.533909	-1.357554	0.105797	0.753613	1.000
656 GOBP-IMMUNE-RESPONSE-REGULATING-SIGNALING-PATHWAY	GO-000276	8	-0.533909	-1.358258	0.126506	0.762686	1.000
657 GOBP-CIRCADIAN-RHYTHM	GO-0007623	13	-0.468835	-1.358722	0.122628	0.773043	1.000
658 REACTOME-RNA-POLYMERASE-III-TRANSCRIPTION	R-RNO-73857	20	-0.420654	-1.380226	0.098202	0.702127	1.000
659 REACTOME-G-ALPHA-Q-SIGNALING-EVENTS	R-RNO-416476	2	-0.595291	-1.380667	0.117363	0.711960	1.000
660 REACTOME-CELLULAR-RESPONSES-TO-EXTERNAL-STIMULI	R-RNO-8953897	12	-0.491161	-1.392040	0.102817	0.681195	1.000
661 GOBP-CELLULAR-MACROMOLECULE-CATABOLIC-PROCESS	GO-0044265	6	-0.594837	-1.396994	0.096519	0.673791	1.000
662 GOBP-CYTOKINE-PRODUCTION	GO-0001816	10	-0.500590	-1.397545	0.098257	0.683218	1.000
663 GOBP-INTRACELLULAR-RECEPTOR-SIGNALING-PATHWAY	GO-0030522	5	-0.650602	-1.401082	0.076443	0.682430	1.000
664 GOBP-CELLULAR-RESPONSE-TO-EXTRACELLULAR-STIMULUS	GO-0031668	8	-0.552303	-1.404357	0.089419	0.682470	1.000
665 GOBP-COAGULATION	GO-0050817	8	-0.546685	-1.406119	0.104012	0.688634	1.000
666 REACTOME-INNATE-IMMUNE-SYSTEM	R-RNO-168249	16	-0.448105	-1.406603	0.111898	0.699762	1.000
667 GOBP-TISSUE-MORPHOGENESIS	GO-0048729	7	-0.576078	-1.420323	0.090484	0.659447	1.000
668 GOBP-PLATELET-ACTIVATION	GO-0030168	6	-0.612069	-1.423467	0.078025	0.660328	1.000
669 GOBP-REGULATION-OF-BODY-FLUID-LEVELS	GO-0050878	11	-0.504163	-1.428257	0.088496	0.655637	1.000
670 GOBP-CELLULAR-RESPONSE-TO-INORGANIC-SUBSTANCE	GO-0071241	11	-0.513412	-1.429643	0.089574	0.663382	1.000
671 GOBP-NEGATIVE-REGULATION-OF-PROTEIN-CATABOLIC....	GO-0042177	5	-0.660691	-1.429925	0.082298	0.676168	1.000
672 GOBP-RESPONSE-TO-CADMIUM-ION	GO-0046686	6	-0.619537	-1.434778	0.056146	0.671078	1.000
673 REACTOME-HEMOSTASIS	R-RNO-109582	14	-0.467906	-1.442918	0.086131	0.655561	1.000
674 GOBP-REGULATION-OF-CELL-CELL-ADHESION	GO-0022407	9	-0.536418	-1.446826	0.076700	0.654301	1.000
675 GOBP-CELLULAR-RESPONSE-TO-HORMONE-STIMULUS	GO-0032870	11	-0.531242	-1.475629	0.063328	0.563856	1.000
676 REACTOME-MAPK-TARGETS-NUCLEAR-EVENTS-MEDIATED....	R-HSA-450282	5	-0.676909	-1.478375	0.057692	0.567292	1.000
677 HALLMARK-TNFA-SIGNALING-VIA-NFKB	M5890	14	-0.499837	-1.492754	0.056277	0.532340	1.000
678 GOBP-REGULATION-OF-CELL-CYCLE	GO-0051726	13	-0.510416	-1.500639	0.052709	0.519832	1.000
679 REACTOME-BETA-CATENIN-INDEPENDENT-WNT-SIGNALING	R-RNO-3858494	5	-0.691304	-1.501532	0.046774	0.529601	1.000
680 GOBP-FC-EPSILON-RECEPTOR-SIGNALING-PATHWAY	GO-0038095	7	-0.622534	-1.509061	0.047041	0.517593	1.000
681 GOBP-REGULATION-OF-IMMUNE-SYSTEM-PROCESS	GO-0002682	21	-0.460122	-1.509232	0.049731	0.530836	1.000
682 GOBP-MACROMOLECULE-CATABOLIC-PROCESS	GO-0009057	12	-0.528122	-1.509751	0.056548	0.543332	1.000
683 REACTOME-MYD88-INDEPENDENT-TLR4-CASCADE	R-RNO-166166	8	-0.595824	-1.510770	0.049347	0.554601	1.000
684 REACTOME-INTERLEUKIN-17-SIGNALING	R-RNO-448424	6	-0.656629	-1.515415	0.041475	0.554572	1.000
685 GOBP-REGULATION-OF-MYELOID-LEUKOCYTE-DIFFERENT...	GO-0002761	8	-0.591163	-1.515754	0.067485	0.569509	1.000

Continuation of Table S15

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
686	REACTOME-TOLL-LIKE-RECEPTOR-CASCADES	R-RNO-168898	8	-0.595824	-1.521964	0.047913	0.564319
687	REACTOME-TOLL-LIKE-RECEPTOR-9_TLR9-CASCADE	R-RNO-168138	8	-0.595824	-1.527133	0.040000	0.562309
688	REACTOME-FC-EPSILON-RECEPTOR-FCER1-SIGNALING	R-RNO-2454202	7	-0.622534	-1.530240	0.042105	0.567781
689	GOBP-RHYTHMIC-PROCESS	GO-0048511	15	-0.507901	-1.547678	0.038516	0.522763
690	REACTOME-TOLL-LIKE-RECEPTOR-TLR1_TLR2-CASCADE	R-RNO-168179	8	-0.595824	-1.557066	0.039394	0.506852
691	REACTOME-NGF-STIMULATED-TRANSCRIPTION	R-RNO-9031628	9	-0.573671	-1.564125	0.038348	0.497564
692	GOBP-POSITIVE-REGULATION-OF-IMMUNE-SYSTEM-PROCESS	GO-0002684	18	-0.481099	-1.572991	0.027510	0.485703
693	GOBP-RESPONSE-TO-INTERLEUKIN-1	GO-0070555	5	-0.699716	-1.575267	0.028892	0.496384
694	GOBP-POSITIVE-REGULATION-OF-MYELOID-CELL-DIFFE...	GO-0045639	7	-0.634592	-1.575442	0.039809	0.515600
695	REACTOME-NUCLEAR-EVENTS-KINASE-AND-TRANSCRIPTI...	R-RNO-198725	11	-0.558055	-1.589192	0.031161	0.486285
696	GOBP-IMMUNE-SYSTEM-DEVELOPMENT	GO-0002520	17	-0.505115	-1.592543	0.026426	0.495009
697	GOBP-POSITIVE-REGULATION-OF-MYELOID-LEUKOCYTE-...	GO-0002763	6	-0.698977	-1.609914	0.019118	0.455885
698	GOBP-RESPONSE-TO-BACTERIUM	GO-0009617	13	-0.551643	-1.614482	0.031474	0.461098
699	GOBP-POSITIVE-REGULATION-OF-BIOSYNTHETIC-PROCESS	GO-0009891	27	-0.460307	-1.616333	0.030914	0.477278
700	GOBP-TRANSMEMBRANE-RECEPTOR-PROTEIN-SERINE-THR...	GO-0007178	6	-0.684808	-1.618317	0.012480	0.494704
701	GOBP-RESPONSE-TO-MOLECULE-OF-BACTERIAL-ORIGIN	GO-0002237	13	-0.551643	-1.619766	0.031609	0.516284
702	HALLMARK-HYPOXIA	M5891	5	-0.747985	-1.623891	0.021104	0.529960
703	HALLMARK-APOPTOSIS	M5902	6	-0.715914	-1.643744	0.014218	0.483331
704	GOBP-REGULATION-OF-LEUKOCYTE-DIFFERENTIATION	GO-1902105	9	-0.625920	-1.666078	0.011799	0.433024
705	GOBP-REGULATION-OF-MYELOID-CELL-DIFFERENTIATION	GO-0045637	9	-0.627973	-1.667471	0.018547	0.459465
706	GOBP-MYELOID-LEUKOCYTE-DIFFERENTIATION	GO-0002573	11	-0.594605	-1.667495	0.017518	0.494679
707	GOBP-MYELOID-CELL-DIFFERENTIATION	GO-0030099	13	-0.573203	-1.675075	0.018651	0.503931
708	GOBP-CHROMOSOME-ORGANIZATION	GO-0051276	6	-0.735472	-1.679460	0.020093	0.528623
709	GOBP-POSITIVE-REGULATION-OF-NUCLEOBASE-CONTAIN...	GO-0045935	28	-0.482639	-1.682217	0.019894	0.569421
710	GOBP-RESPONSE-TO-MECHANICAL-STIMULUS	GO-0009612	6	-0.720544	-1.687154	0.008157	0.611013
711	GOBP-CHROMATIN-ORGANIZATION	GO-0006325	5	-0.795181	-1.713097	0.007899	0.562914
712	REACTOME-SENESCENCE-ASSOCIATED-SECRETORY-PHENO...	R-RNO-2559582	6	-0.767245	-1.745132	0.003150	0.481880
713	GOBP-POSITIVE-REGULATION-OF-TRANSCRIPTION-BY-R...	GO-0045944	24	-0.509287	-1.748578	0.020747	0.545625
714	REACTOME-CELLULAR-SENESCENCE	R-RNO-2559583	6	-0.767245	-1.780211	0.003175	0.492311
715	GOBP-LEUKOCYTE-DIFFERENTIATION	GO-0002521	15	-0.566125	-1.785010	0.008287	0.590950
716	GOBP-POSITIVE-REGULATION-OF-HEMOPOIESIS	GO-1903708	7	-0.724212	-1.787789	0.001582	0.768016
717	GOBP-REGULATION-OF-HEMOPOIESIS	GO-1903706	10	-0.656561	-1.814804	0.010606	0.887978
718	GOBP-RESPONSE-TO-DRUG	GO-0042493	11	-0.670402	-1.898578	0.004373	0.731224

End of Table

Supplementary Table S16: BG late profile (45 DPL peak) GSEA results.

Begin of Table S16									
	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val	
0	GOBP-CELL-CYCLE	GO:0007049	21	0.688508	2.187956	0.000000	0.008712	0.007	
1	GOBP-NEGATIVE-REGULATION_OF_GENE-EXPRESSION	GO:0010629	12	0.747671	2.080675	0.000000	0.027282	0.043	
2	GOBP-POSTTRANSCRIPTIONAL-REGULATION_OF_GENE-EX...	GO:0010608	8	0.837801	2.059416	0.000000	0.022322	0.052	
3	GOBP-CELLULAR-AMIDE-METABOLIC-PROCESS	GO:0043603	13	0.704689	2.000565	0.000000	0.042499	0.130	
4	GOBP-GROWTH	GO:0040007	14	0.678726	1.941892	0.000000	0.075044	0.264	
5	GOBP-GAMETE-GENERATION	GO:0007276	9	0.749268	1.908591	0.000000	0.091444	0.364	
6	GOBP-PEPTIDE-METABOLIC-PROCESS	GO:0006518	12	0.689573	1.903534	0.001361	0.082782	0.383	
7	GOBP-REGULATION_OF_CELLULAR-AMIDE-METABOLIC-PR...	GO:0034248	9	0.734005	1.870772	0.001397	0.112932	0.529	
8	GOBP-MULTICELLULAR-ORGANISM-REPRODUCTION	GO:0032504	12	0.666189	1.852039	0.005369	0.127062	0.607	
9	GOBP-ORGANONITROGEN-COMPOUND-BIOSYNTHETIC-PROCESS	GO:1901566	13	0.654682	1.849304	0.000000	0.117583	0.615	
10	GOBP-NEGATIVE-REGULATION_OF_MULTICELLULAR-ORGA...	GO:0051241	15	0.627710	1.826315	0.005236	0.140529	0.730	
11	GOBP-REGULATION-OF-GROWTH	GO:0040008	13	0.651571	1.811658	0.002714	0.150821	0.774	
12	GOBP-POSITIVE-REGULATION_OF_MAP_KINASE-ACTIVITY	GO:0043406	6	0.798853	1.810989	0.004373	0.140642	0.779	
13	GOBP-REGULATION-OF-MAP-KINASE-ACTIVITY	GO:0043405	9	0.701610	1.800464	0.002837	0.146364	0.812	
14	GOBP-SEXUAL-REPRODUCTION	GO:0019953	10	0.690190	1.799481	0.002878	0.138514	0.815	
15	GOBP-POSITIVE-REGULATION_OF_PROTEIN-SERINE-THR...	GO:0071902	6	0.686880	1.784689	0.008475	0.151177	0.861	
16	GOBP-ACTIVATION_OF_MAPK-ACTIVITY	GO:0000187	6	0.798853	1.784683	0.001427	0.142284	0.861	
17	GOBP-POSITIVE-REGULATION_OF_CELL-POPULATION-PR...	GO:0008284	21	0.565608	1.784369	0.005249	0.134584	0.861	
18	GOBP-POSITIVE-REGULATION_OF_ESTABLISHMENT_OF_P...	GO:1904951	5	0.843560	1.766732	0.000000	0.154477	0.900	
19	GOBP-REGULATION_OF_PROTEIN-SERINE-THREONINE-KI...	GO:0071900	12	0.639657	1.766392	0.001395	0.146994	0.900	
20	GOBP-ERK1-AND-ERK2-CASCADE	GO:0070371	5	0.827784	1.765826	0.002981	0.140700	0.901	
21	GOBP-MITOTIC-CELL-CYCLE	GO:0000278	10	0.676616	1.763109	0.008523	0.138416	0.906	
22	GOBP-MUSCLE-ADAPTATION	GO:0043500	5	0.823221	1.760237	0.001618	0.137139	0.909	
23	GOBP-MONOSACCHARIDE-METABOLIC-PROCESS	GO:0005996	6	0.775158	1.755633	0.003012	0.137359	0.922	
24	GOBP-GLUCOSE-METABOLIC-PROCESS	GO:0006006	6	0.775158	1.750625	0.001484	0.138716	0.933	
25	GOBP-POSITIVE-REGULATION_OF_CELL-ADHESION	GO:0045785	7	0.729700	1.743435	0.004348	0.143252	0.948	
26	GOBP-CELL-GROWTH	GO:0016049	10	0.650283	1.734641	0.005772	0.149353	0.959	
27	GOBP-REGULATION_OF_DNA-BINDING-TRANSCRIPTION_F...	GO:0051090	16	0.575079	1.725752	0.003937	0.156378	0.974	
28	GOBP-REGULATION_OF_ANION-TRANSMEMBRANE-TRANSPORT	GO:1903959	5	0.801351	1.724875	0.009174	0.152392	0.975	
29	GOBP-REGULATION_OF_CELLULAR-COMPONENT_MOVEMENT	GO:0051270	15	0.585625	1.718063	0.010430	0.158724	0.979	
30	GOBP-AMIDE-BIOSYNTHETIC-PROCESS	GO:0043604	7	0.712430	1.710088	0.012640	0.166351	0.986	
31	GOBP-DEVELOPMENTAL-PROCESS_INVOLVED_IN_REPRODU...	GO:0003006	11	0.631560	1.708764	0.014205	0.163182	0.987	
32	GOBP-NEGATIVE-REGULATION_OF_MOLECULAR-FUNCTION	GO:0044092	24	0.527897	1.705909	0.008816	0.162268	0.987	
33	GOBP-PROTEIN-DEPHOSPHORYLATION	GO:0006470	7	0.719714	1.705505	0.007267	0.157965	0.987	
34	GOBP-ORGAN-GROWTH	GO:0035265	5	0.801419	1.705058	0.006192	0.153948	0.988	
35	GOBP-PEPTIDE-BIOSYNTHETIC-PROCESS	GO:0043043	7	0.712430	1.702800	0.008451	0.152984	0.988	
36	GOBP-CARBOHYDRATE-METABOLIC-PROCESS	GO:0005975	9	0.666849	1.700850	0.016997	0.151199	0.989	
37	GOBP-REGULATION_OF_MUSCLE-ADAPTATION	GO:0043502	5	0.823221	1.693276	0.001563	0.158753	0.993	
38	GOBP-DEPHOSPHORYLATION	GO:0016311	7	0.719714	1.688806	0.010057	0.161593	0.994	
39	GOBP-MULTI-ORGANISM-PROCESS	GO:0051704	16	0.572056	1.688659	0.014925	0.157862	0.994	
40	GOBP-POSITIVE-REGULATION_OF_LOCOMOTION	GO:0040017	11	0.630808	1.683650	0.012766	0.161349	0.994	

Continuation of Table S16

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
41	GOBP-REGULATION-OF-ORGAN-GROWTH	GO-0046620	5	0.801419	1.680083	0.013255	0.162600	0.996
42	GOBP-REGULATION-OF-PEPTIDE-SECRETION	GO-0002791	7	0.701645	1.661094	0.013699	0.188761	0.999
43	GOBP-NEGATIVE-REGULATION-OF-CELL-DIFFERENTIATION	GO-0045596	13	0.595946	1.658601	0.016086	0.188547	0.999
44	GOBP-NEGATIVE-REGULATION-OF-DEVELOPMENTAL-PROCESS	GO-0051093	13	0.595946	1.655921	0.017380	0.188221	0.999
45	GOBP-REGULATION-OF-PEPTIDE-TRANSPORT	GO-0090087	10	0.631603	1.655710	0.016506	0.184481	0.999
46	GOBP-NEGATIVE-REGULATION-OF-CELLULAR-COMPONENT...	GO-0051129	11	0.617579	1.655543	0.025352	0.180818	0.999
47	GOBP-RESPONSE-TO-TUMOR-NECROSIS-FACTOR	GO-0034612	7	0.707604	1.651983	0.012987	0.182869	0.999
48	GOBP-CELL-CYCLE-PROCESS	GO-0022402	11	0.599334	1.650543	0.019310	0.181391	0.999
49	GOBP-POSITIVE-REGULATION-OF-APOPTOTIC-SIGNALIN...	GO-2001235	5	0.783133	1.646733	0.010870	0.184106	1.000
50	GOBP-REGULATION-OF-ANION-TRANSPORT	GO-0044070	20	0.526105	1.645768	0.015645	0.182027	1.000
51	GOBP-EXTRINSIC-APOPTOTIC-SIGNALING-PATHWAY	GO-0097191	7	0.691442	1.638405	0.011799	0.189770	1.000
52	GOBP-REGULATION-OF-MULTICELLULAR-ORGANISMAL-DE...	GO-2000026	31	0.477615	1.632374	0.013514	0.195428	1.000
53	GOBP-MEMBRANE-PROTEIN-PROTEOLYSIS	GO-0038619	6	0.721138	1.631770	0.010903	0.193118	1.000
54	GOBP-MALE-GAMETE-GENERATION	GO-0048232	5	0.764139	1.620189	0.010989	0.209931	1.000
55	GOBP-CIRCULATORY-SYSTEM-DEVELOPMENT	GO-0072359	21	0.499822	1.617551	0.022078	0.210402	1.000
56	GOBP-CELLULAR-CARBOHYDRATE-METABOLIC-PROCESS	GO-0044262	5	0.749962	1.608577	0.018663	0.223117	1.000
57	GOBP-CELLULAR-RESPONSE-TO-EXTERNAL-STIMULUS	GO-0071496	10	0.614118	1.604973	0.021739	0.226382	1.000
58	GOBP-MUSCLE-CELL-PROLIFERATION	GO-0033002	8	0.656806	1.602217	0.011494	0.227589	1.000
59	GOBP-REGULATION-OF-CELLULAR-CATABOLIC-PROCESS	GO-0031329	10	0.612452	1.596786	0.022378	0.233894	1.000
60	GOBP-CELLULAR-GLUCOSE-HOMEOSTASIS	GO-0001678	5	0.739652	1.592208	0.019727	0.238339	1.000
61	GOBP-CELL-POPULATION-PROLIFERATION	GO-0008283	31	0.469021	1.590572	0.013189	0.237552	1.000
62	GOBP-REGULATION-OF-EXTRINSIC-APOPTOTIC-SIGNALI...	GO-2001236	6	0.704620	1.580704	0.023881	0.253528	1.000
63	GOBP-CELLULAR-RESPONSE-TO-OXYGEN-CONTAINING-CO...	GO-1901701	29	0.463302	1.580182	0.021303	0.250319	1.000
64	GOBP-ANION-TRANSMEMBRANE-TRANSPORT	GO-0098656	7	0.668632	1.579817	0.026826	0.247288	1.000
65	GOBP-REPRODUCTION	GO-0000003	18	0.510132	1.564785	0.032425	0.274049	1.000
66	GOBP-SKIN-DEVELOPMENT	GO-0043588	5	0.727062	1.555852	0.027950	0.288245	1.000
67	GOBP-CELLULAR-RESPONSE-TO-LIPID	GO-0071396	15	0.523995	1.548531	0.038889	0.300991	1.000
68	GOBP-CELLULAR-RESPONSE-TO-EXTRACELLULAR-STIMULUS	GO-0031668	8	0.632456	1.547673	0.026462	0.298607	1.000
69	GOBP-AMYLOID-BETA-METABOLIC-PROCESS	GO-0050435	5	0.722308	1.545967	0.015576	0.297773	1.000
70	GOBP-CELLULAR-COMPONENT-DISASSEMBLY	GO-0022411	6	0.694200	1.540547	0.025335	0.305784	1.000
71	GOBP-AMYLOID-PRECURSOR-PROTEIN-METABOLIC-PROCESS	GO-0042982	5	0.722308	1.539824	0.024206	0.303123	1.000
72	GOBP-AMYLOID-PRECURSOR-PROTEIN-CATABOLIC-PROCESS	GO-0042987	5	0.722308	1.534315	0.025797	0.311598	1.000
73	GOBP-REGULATION-OF-CARBOHYDRATE-METABOLIC-PROCESS	GO-0006109	5	0.711265	1.528994	0.027650	0.318735	1.000
74	GOBP-CELL-MIGRATION	GO-0016477	22	0.472978	1.526626	0.047739	0.320484	1.000
75	GOBP-PROTEIN-PHOSPHORYLATION	GO-0006468	34	0.446659	1.522357	0.035496	0.326567	1.000
76	GOBP-POSITIVE-REGULATION-OF-MAPK-CASCADE	GO-0043410	9	0.600959	1.520716	0.050992	0.325895	1.000
77	GOBP-ESTABLISHMENT-OF-PROTEIN-LOCALIZATION	GO-0045184	18	0.502325	1.517711	0.040682	0.329100	1.000
78	GOBP-PEPTIDE-SECRETION	GO-0002790	9	0.595202	1.516385	0.038028	0.327883	1.000
79	GOBP-LIPID-METABOLIC-PROCESS	GO-0006629	10	0.564921	1.516164	0.043988	0.324205	1.000
80	GOBP-HEART-DEVELOPMENT	GO-0007507	6	0.682015	1.515066	0.030257	0.322826	1.000
81	GOBP-NUCLEAR-TRANSPORT	GO-0051169	5	0.719320	1.511851	0.041481	0.326353	1.000
82	GOBP-POSITIVE-REGULATION-OF-MULTICELLULAR-ORGA...	GO-0051240	32	0.444260	1.511406	0.040964	0.323502	1.000
83	GOBP-PEPTIDE-HORMONE-SECRETION	GO-0030072	7	0.635005	1.511232	0.035211	0.319931	1.000

Continuation of Table S16

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
84	GOBP-NEGATIVE-REGULATION-OF-PROTEIN-METABOLIC...	20	0.493293	1.511107	0.049682	0.316400	1.000
85	GOBP-CARDIAC-MUSCLE-TISSUE-DEVELOPMENT	6	0.682015	1.507559	0.042587	0.320904	1.000
86	GOBP-POLYSACCHARIDE-METABOLIC-PROCESS	5	0.712255	1.506432	0.034429	0.319805	1.000
87	GOBP-NEGATIVE-REGULATION-OF-SIGNALING	21	0.023057	1.505065	0.046572	0.318868	1.000
88	GOBP-PROTEIN-LOCALIZATION-TO-ORGANELLE	9	0.590261	1.504442	0.038905	0.316575	1.000
89	GOBP-NEGATIVE-REGULATION-OF-CATALYTIC-ACTIVITY	17	0.499422	1.502805	0.044595	0.316882	1.000
90	GOBP-MUSCLE-TISSUE-DEVELOPMENT	11	0.552588	1.501256	0.047026	0.316783	1.000
91	GOBP-CARBOHYDRATE-BIOSYNTHETIC-PROCESS	5	0.711265	1.500809	0.042122	0.314355	1.000
92	GOBP-REGULATION-OF-MITOTIC-CELL-CYCLE	5	0.699075	1.499104	0.029687	0.314417	1.000
93	REACTOME-CELL-CYCLE-MITOTIC	5	0.708654	1.497430	0.035008	0.315158	1.000
94	GOBP-INSULIN-SECRETION	7	0.635005	1.494897	0.046784	0.317424	1.000
95	GOBP-REGULATION-OF-MAPK-CASCADE	13	0.0043408	1.492548	0.049333	0.319076	1.000
96	GOBP-REGULATION-OF-CARBOHYDRATE-BIOSYNTHETIC-P...	5	0.711265	1.491633	0.036641	0.317667	1.000
97	GOBP-REGULATION-OF-PHOSPHATIDYLINOSITOL-3-KINA...	6	0.664193	1.488207	0.039514	0.322096	1.000
98	GOBP-REGULATION-OF-HORMONE-LEVELS	12	0.539114	1.487776	0.062927	0.319780	1.000
99	GOBP-REGULATION-OF-MUSCLE-SYSTEM-PROCESS	8	0.593085	1.487711	0.049635	0.316706	1.000
100	REACTOME-SIGNALING-BY-RHO-GTPASES-MIRO-GTPASES...	9	0.586295	1.486456	0.048951	0.316065	1.000
101	GOBP-SECRETION	24	0.455603	1.483955	0.063452	0.318480	1.000
102	REACTOME-RHO-GTPASE-EFFECTORS	9	0.586295	1.483700	0.050776	0.315982	1.000
103	GOBP-MUSCLE-CELL-DEVELOPMENT	5	0.702409	1.483187	0.053731	0.314149	1.000
104	GOBP-CELLULAR-RESPONSE-TO-DNA-DAMAGE-STIMULUS	5	0.700093	1.482426	0.041359	0.312940	1.000
105	REACTOME-SIGNALING-BY-GPCR	22	0.459041	1.481280	0.051414	0.312404	1.000
106	GOBP-POSITIVE-REGULATION-OF-CELLULAR-COMPONENT...	24	0.449022	1.474650	0.051546	0.323955	1.000
107	GOBP-DEVELOPMENTAL-GROWTH	10	0.559522	1.473146	0.059219	0.324163	1.000
108	GOBP-REGULATION-OF-PROTEIN-STABILITY	5	0.701171	1.470555	0.048632	0.326888	1.000
109	REACTOME-CELL-CYCLE	6	0.650876	1.467244	0.046407	0.331125	1.000
110	GOBP-REGULATION-OF-PEPTIDE-HORMONE-SECRETION	6	0.658570	1.466014	0.049275	0.330835	1.000
111	GOBP-REGULATION-OF-PROTEIN-KINASE-ACTIVITY	22	0.449097	1.463482	0.063325	0.333354	1.000
112	REACTOME-CIRCADIAN-CLOCK	5	0.691443	1.461657	0.046656	0.334293	1.000
113	GOBP-ACTIVATION-OF-PROTEIN-KINASE-ACTIVITY	11	0.535297	1.457646	0.067227	0.340153	1.000
114	GOBP-MACROMOLECULE-CATABOLIC-PROCESS	12	0.52189	1.457064	0.077562	0.338406	1.000
115	GOBP-INOSITOL-LIPID-MEDIATED-SIGNALING	8	0.587361	1.453691	0.079096	0.342817	1.000
116	REACTOME-DEATH-RECEPTOR-SIGNALING	5	0.682140	1.452914	0.049401	0.341342	1.000
117	REACTOME-G-ALPHA-Q-SIGNALING-EVENTS	6	0.645659	1.449127	0.078550	0.347137	1.000
118	GOBP-PHOSPHATIDYLINOSITOL-3-KINASE-SIGNALING	7	0.599973	1.448985	0.078148	0.344482	1.000
119	GOBP-REGULATION-OF-TRANSFERASE-ACTIVITY	22	0.449097	1.444248	0.082051	0.352067	1.000
120	GOBP-INTRACELLULAR-TRANSPORT	11	0.532943	1.440905	0.083562	0.356632	1.000
121	GOBP-INTRACELLULAR-RECEPTOR-SIGNALING-PATHWAY	5	0.682014	1.439067	0.079755	0.357722	1.000
122	REACTOME-DISEASES-OF-SIGNAL-TRANSDUCTION-BY-GR...	12	0.515641	1.438080	0.096454	0.357144	1.000
123	GOBP-REGULATION-OF-PHOSPHORUS-METABOLIC-PROCESS	27	0.427554	1.437162	0.062344	0.356425	1.000
124	GOBP-REGULATION-OF-SMALL-MOLECULE-METABOLIC-PR...	9	0.555652	1.434624	0.073171	0.359152	1.000
125	GOBP-NEGATIVE-REGULATION-OF-PHOSPHORYLATION	7	0.602882	1.432820	0.064140	0.360320	1.000
126	GOBP-REGULATION-OF-PROTEIN-LOCALIZATION	18	0.467655	1.431893	0.086050	0.359342	1.000

Continuation of Table S16

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
127 GOBP-POSITIVE-REGULATION_OF_PROTEIN_PHOSPHORYL...	GO-0001934	23	0.442270	1.428026	0.091837	0.365005	1.000
128 GOBP-REGULATION_OF_APOPTOTIC-SIGNALING.PATHWAY	GO-2001233	10	0.545515	1.426399	0.070126	0.365903	1.000
129 GOBP-REGULATION_OF_VASCULATURE.DEVELOPMENT	GO-1901342	5	0.670521	1.424845	0.065282	0.366506	1.000
130 GOBP-POSITIVE-REGULATION_OF_ORGANELLE-ORGANIZA...	GO-0010638	10	0.535680	1.424758	0.077465	0.363830	1.000
131 GOBP-REGULATION_OF_CELL-DIFFERENTIATION	GO-0045595	36	0.412612	1.423751	0.075243	0.363213	1.000
132 GOBP-REGULATION_OF_PROTEIN_PHOSPHORYLATION	GO-0001932	26	0.432652	1.422958	0.075031	0.362126	1.000
133 GOBP-POSITIVE-REGULATION_OF_NUCLEOBASE-CONTAIN...	GO-0045935	28	0.420682	1.421636	0.075871	0.362526	1.000
134 GOBP-INTRACELLULAR-PROTEIN-TRANSPORT	GO-0006886	9	0.565899	1.420945	0.093931	0.361380	1.000
135 GOBP-REGULATION_OF_HORMONE-SECRETION	GO-0046883	8	0.581110	1.419628	0.085554	0.361742	1.000
136 REACTOME-PLATELET_ACTIVATION-SIGNALING-AND-AGG...	R-HSA-76002	7	0.602485	1.417533	0.071839	0.363887	1.000
137 GOBP-POSITIVE-REGULATION_OF_PROTEIN-MODIFICATI...	GO-0031401	23	0.442270	1.416368	0.082687	0.363833	1.000
138 GOBP-TISSUE-MORPHOGENESIS	GO-0048729	7	0.611578	1.415876	0.066474	0.362201	1.000
139 GOBP-DNA-METABOLIC-PROCESS	GO-0009259	6	0.624629	1.411682	0.096070	0.368744	1.000
140 GOBP-NEGATIVE-REGULATION_OF_PHOSPHORUS-METABOL...	GO-0010563	9	0.561169	1.411395	0.089655	0.366827	1.000
141 GOBP-HORMONE-TRANSPORT	GO-0009914	9	0.565425	1.410075	0.092287	0.367036	1.000
142 GOBP-POSITIVE-REGULATION_OF_GROWTH	GO-0045927	9	0.554940	1.408940	0.084626	0.366708	1.000
143 GOBP-CARBOHYDRATE-HOMEOSTASIS	GO-0033500	7	0.591453	1.408855	0.085014	0.364359	1.000
144 REACTOME-INNATE-IMMUNE-SYSTEM	R-RNO-168249	16	0.470422	1.408168	0.091146	0.363221	1.000
145 GOBP-POSITIVE-REGULATION_OF_BIOSYNTHETIC-PROCESS	GO-0009891	27	0.428590	1.406929	0.085242	0.363299	1.000
146 GOBP-EMBRYO-DEVELOPMENT	GO-0009790	14	0.479642	1.402893	0.090066	0.370051	1.000
147 GOBP-NEGATIVE-REGULATION_OF_HYDROLASE-ACTIVITY	GO-0051346	11	0.512405	1.402540	0.076596	0.368365	1.000
148 REACTOME-OPIOID-SIGNALING	R-RNO-111885	12	0.505661	1.401353	0.106648	0.368777	1.000
149 GOBP-REGULATION_OF_CELL-CYCLE-PROCESS	GO-0010564	5	0.659436	1.400113	0.081325	0.369255	1.000
150 REACTOME-SIGNALING_BY_INTERLEUKINS	R-RNO-449147	15	0.475314	1.396138	0.088591	0.375485	1.000
151 GOBP-REGULATION_OF_INTRACELLULAR-SIGNAL-TRANSD...	GO-1902531	21	0.443092	1.390477	0.101430	0.385886	1.000
152 GOBP-WOUND-HEALING	GO-0042060	13	0.484829	1.389330	0.087379	0.385880	1.000
153 GOBP-POSITIVE-REGULATION_OF_PROTEIN-KINASE-ACT...	GO-0045860	19	0.451097	1.386529	0.093298	0.389640	1.000
154 GOBP-LEUKOCYTE-MIGRATION	GO-0050900	6	0.623666	1.386375	0.074405	0.387382	1.000
155 GOBP-NEGATIVE-REGULATION_OF_CELL-CYCLE	GO-0045786	5	0.650330	1.383859	0.090016	0.390544	1.000
156 GOBP-POSITIVE-REGULATION_OF_PPTIDYL-TYROSINE...	GO-0050731	8	0.558929	1.379317	0.109705	0.398812	1.000
157 GOBP-POSITIVE-REGULATION_OF_LEUKOCYTE-CELL-CEL...	GO-1903039	5	0.659362	1.375481	0.080425	0.405416	1.000
158 GOBP-REGULATION_OF_PPTIDYL-TYROSINE-PHOSPHORY...	GO-0050730	9	0.537944	1.375472	0.117898	0.402897	1.000
159 GOBP-POSITIVE-REGULATION_OF_CELL-CELL-ADHESION	GO-0022409	5	0.659362	1.372807	0.099248	0.406428	1.000
160 GOBP-SMALL-MOLECULE-METABOLIC-PROCESS	GO-0044281	15	0.464769	1.372731	0.097497	0.404128	1.000
161 GOBP-POSITIVE-REGULATION_OF_MOLECULAR-FUNCTION	GO-0044093	38	0.391160	1.372464	0.099515	0.402239	1.000
162 GOBP-REGULATION_OF_CELL-ADHESION	GO-0030155	13	0.485208	1.372309	0.113855	0.400022	1.000
163 GOBP-REGULATION_OF_CATABOLIC-PROCESS	GO-0009894	13	0.485129	1.370629	0.103356	0.401187	1.000
164 GOBP-CYTOKINE-PRODUCTION	GO-0001816	10	0.515139	1.368169	0.111111	0.404171	1.000
165 GOBP-REGULATION_OF-ANATOMICAL-STRUCTURE-MORPHO...	GO-0022603	17	0.456246	1.367727	0.103811	0.402754	1.000
166 GOBP-NEGATIVE-REGULATION_OF-TRANSPORT	GO-0051051	13	0.487307	1.366904	0.095890	0.402385	1.000
167 GOBP-REGULATION_OF_PROTEIN-MODIFICATION-PROCESS	GO-0031399	29	0.404457	1.366818	0.101759	0.400154	1.000
168 GOBP-POSITIVE-REGULATION_OF_PHOSPHORUS-METABOL...	GO-0010562	24	0.420828	1.366376	0.094645	0.398889	1.000
169 GOBP-RHYTHMIC-PROCESS	GO-0048511	15	0.466049	1.364993	0.104497	0.399738	1.000

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NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
170	GOBP-POSITIVE-REGULATION_OF_INTRACELLULAR_SIGN...	14	0.482014	1.362877	0.114911	0.402024	1.000
171	REACTOME_TOLL LIKE RECEPTOR_TLR1_TLR2_CASCADE	8	0.548196	1.361252	0.119829	0.403425	1.000
172	GOBP-RESPONSE_TO_LIPID	19	0.440622	1.359410	0.102394	0.405305	1.000
173	REACTOME_SIGNALING_BY_RECEPTOR_TYROSINE_KINASES	26	0.411548	1.357700	0.105721	0.406869	1.000
174	GOBP-POSITIVE-REGULATION_OF_TRANSPERASE_ACTIVITY	20	0.426411	1.357673	0.110115	0.404586	1.000
175	REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM	21	0.418228	1.357347	0.095541	0.402929	1.000
176	GOBP-REGULATION_OF_SYSTEM_PROCESS	18	0.445123	1.355734	0.107527	0.404441	1.000
177	GOBP-BIOLOGICAL_ADHESION	19	0.431715	1.355368	0.114213	0.403013	1.000
178	REACTOME_TOLL LIKE RECEPTOR_9_TLR9_CASCADE	8	0.548196	1.354986	0.118477	0.401524	1.000
179	GOBP-REGULATION_OF_IMMUNE_SYSTEM_PROCESS	21	0.425941	1.354439	0.122581	0.400468	1.000
180	GOBP-CELL_ACTIVATION	21	0.423276	1.350968	0.115183	0.405431	1.000
181	GOBP-MUSCLE_SYSTEM_PROCESS	9	0.535406	1.346895	0.127168	0.411836	1.000
182	REACTOME_TOLL LIKE RECEPTOR_CASCADES	8	0.548196	1.345482	0.123769	0.412702	1.000
183	GOBP-CELLULAR_RESPONSE_TO_ORGANIC_CYCLIC_COMPOUND	13	0.483889	1.345478	0.119522	0.410459	1.000
184	GOBP-CELLULAR_LIPID_METABOLIC_PROCESS	7	0.567552	1.343670	0.132267	0.412495	1.000
185	GOBP-ANIMAL_ORGAN_MORPHOGENESIS	12	0.523845	1.339686	0.127717	0.413986	1.000
186	GOBP-POSITIVE-REGULATION_OF_ANION_TRANSPORT	9	0.485941	1.342009	0.124128	0.417229	1.000
187	GOBP-DENDRITE_MORPHOGENESIS	6	0.609136	1.339594	0.116864	0.415200	1.000
188	GOBP-NEGATIVE-REGULATION_OF_CELL_DEVELOPMENT	6	0.597567	1.338643	0.142857	0.415158	1.000
189	GOBP-AGING	13	0.478849	1.338337	0.098886	0.413548	1.000
190	GOBP-POSITIVE-REGULATION_OF_SMALL_MOLECULE_MET...	5	0.626517	1.337757	0.117647	0.412663	1.000
191	GOBP-POSITIVE-REGULATION_OF_PHOSPHATIDYLINOSIT...	5	0.640491	1.335813	0.106481	0.414744	1.000
192	GOBP-REGULATION_OF_CELL_DEVELOPMENT	15	0.457587	1.330442	0.124332	0.418799	1.000
193	GOBP-POSITIVE-REGULATION_OF_GENE_EXPRESSION	16	0.449029	1.328050	0.131613	0.427672	1.000
194	GOBP-PEPTIDYL_TYROSINE_MODIFICATION	10	0.505245	1.327831	0.139535	0.426020	1.000
195	REACTOME_MYD88_INDEPENDENT_TLR4_CASCADE	8	0.548196	1.326410	0.127479	0.427070	1.000
196	GOBP-CELL_CELL_JUNCTION_ORGANIZATION	6	0.578863	1.326052	0.140741	0.425630	1.000
197	GOBP-CYTOSKELETON_ORGANIZATION	11	0.486544	1.325712	0.139860	0.424272	1.000
198	GOBP-CIRCADIAN_REGULATION_OF_GENE_EXPRESSION	5	0.638993	1.325358	0.125387	0.426849	1.000
199	GOBP-NEGATIVE-REGULATION_OF_PEPTIDASE_ACTIVITY	6	0.583218	1.322887	0.135878	0.426422	1.000
200	GOBP-REGULATION_OF_DEVELOPMENTAL_GROWTH	9	0.512722	1.317824	0.154596	0.436173	1.000
201	GOBP-REGULATION_OF_CELL_CYCLE	13	0.466994	1.317583	0.153215	0.434634	1.000
202	GOBP-REGULATION_OF_VESICLE_MEDIATED_TRANSPORT	12	0.472274	1.317058	0.144847	0.433619	1.000
203	REACTOME_NUCLEAR_EVENTS_KINASE_AND_TRANSCRIPTI...	11	0.490012	1.316712	0.160443	0.432249	1.000
204	GOBP-IMMUNE_EFFECTOR_PROCESS	10	0.491873	1.313193	0.153619	0.437955	1.000
205	GOBP-PEPTIDYL_AMINO_ACID_MODIFICATION	22	0.405121	1.311419	0.150524	0.439718	1.000
206	GOBP-NEGATIVE-REGULATION_OF_ANION_TRANSPORT	8	0.531564	1.308292	0.145533	0.444595	1.000
207	GOBP-NEGATIVE-REGULATION_OF_KINASE_ACTIVITY	5	0.616901	1.307733	0.142410	0.443731	1.000
208	GOBP-POSITIVE-REGULATION_OF_RESPONSE_TO_EXTERN...	9	0.509486	1.305695	0.130682	0.446492	1.000
209	GOBP_FC_EPSILON_RECEPTOR_SIGNALING_PATHWAY	7	0.546725	1.304911	0.150585	0.446127	1.000
210	GOBP-RESPONSE_TO ABIOTIC STIMULUS	27	0.391948	1.303733	0.150127	0.446530	1.000
211	GOBP-CIRCADIAN_RHYTHM	13	0.467047	1.302695	0.151099	0.446720	1.000
212	GOBP-POSITIVE-REGULATION_OF_DEVELOPMENTAL_PROCESS	32	0.378183	1.301815	0.144623	0.446595	1.000

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NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
213	GOBP-AMERBODAL-TYPE-CELL-MIGRATION	GO-0001667	11	0.479249	1.301809	0.155492	0.444520
214	GOBP-CELLULAR-RESPONSE-TO-BIOTIC-STIMULUS	GO-0071216	8	0.528909	1.300663	0.155340	0.445004
215	GOBP-RESPONSE-TO-METAL-ION	GO-0010038	15	0.438684	1.300163	0.146405	0.444211
216	GOBP-MAPK-CASCADE	GO-0000165	18	0.427742	1.296140	0.150633	0.451464
217	GOBP-MAINTENANCE-OF-LOCATION	GO-0051235	7	0.549026	1.295737	0.182891	0.450090
218	GOBP-REGULATION-OF-EPITHELIAL-CELL-MIGRATION	GO-0010632	6	0.572369	1.292844	0.151376	0.454628
219	GOBP-MORPHOGENESIS-OF-AN-EPITHELIUM	GO-0002009	6	0.568842	1.290065	0.156923	0.458745
220	GOBP-CELLULAR-RESPONSE-TO-MOLECULE-OF-BACTERIA...	GO-0071219	8	0.528909	1.287259	0.159884	0.462789
221	REACTOME-FC-EPSILON-RECEPTOR-FCERL-SIGNALING	R-RNO-2454202	7	0.546725	1.285485	0.175809	0.465018
222	HALLMARK-P13K-AKT-MTOR-SIGNALING	M5923	6	0.584171	1.284133	0.162003	0.466143
223	GOBP-NEGATIVE-REGULATION-OF-TRANSFERASE-ACTIVITY	GO-0051348	5	0.616901	1.279802	0.155146	0.474391
224	GOBP-NEGATIVE-REGULATION-OF-LIPID-METABOLIC-PR...	GO-0045833	5	0.596416	1.277023	0.151033	0.478635
225	GOBP-LEUKOCYTE-MEDIATED-IMMUNITY	GO-0002443	7	0.544984	1.276300	0.186289	0.478114
226	GOBP-BIOLOGICAL-PROCESS-INVOLVED-IN-SYMBIOTIC-...	GO-004440	11	0.468690	1.276127	0.187151	0.476431
227	GOBP-NEGATIVE-REGULATION-OF-PROTEIN-MODIFICATI...	GO-0031400	10	0.488954	1.275801	0.167147	0.475111
228	GOBP-RESPIRATORY-SYSTEM-DEVELOPMENT	GO-0060541	6	0.562539	1.275423	0.155750	0.473829
229	GOBP-REGULATION-OF-RESPONSE-TO-EXTERNAL-STIMULUS	GO-0032101	15	0.440306	1.274191	0.166223	0.474702
230	GOBP-PHAGOCYTOSIS	GO-0006909	5	0.596194	1.272247	0.178102	0.477093
231	GOBP-REGULATION-OF-IMMUNE-RESPONSE	GO-0050776	12	0.463542	1.269733	0.178025	0.480603
232	GOBP-CELLULAR-MACROMOLECULE-CATABOLIC-PROCESS	GO-0044265	6	0.565084	1.266547	0.186930	0.485381
233	GOBP-POSITIVE-REGULATION-OF-IMMUNE-RESPONSE	GO-0050778	9	0.494630	1.265115	0.183616	0.486473
234	GOBP-IMMUNE-SYSTEM-DEVELOPMENT	GO-0002520	17	0.421271	1.261054	0.198693	0.493671
235	GOBP-RESPONSE-TO-OXYGEN-CONTAINING-COMPOUND	GO-1901700	39	0.363294	1.259069	0.182578	0.496209
236	GOBP-EPIDERMIS-DEVELOPMENT	GO-0008544	5	0.592191	1.255675	0.186414	0.501873
237	GOBP-RESPONSE-TO-STARVATION	GO-0042594	5	0.599538	1.255592	0.167428	0.499952
238	REACTOME-ONCOGENIC-MAPK-SIGNALING	R-HSA-6802957	5	0.579567	1.255411	0.160247	0.498307
239	GOBP-REGULATION-OF-SECRETION	GO-0051046	14	0.440896	1.254781	0.198639	0.497608
240	GOBP-REGULATION-OF-PROTEIN-LOCALIZATION-TO-CEL...	GO-1904375	6	0.556410	1.252942	0.175150	0.499745
241	GOBP-PROTEIN-KINASE-B-SIGNALING	GO-0043491	6	0.553920	1.249983	0.198519	0.504670
242	GOBP-LIPID-BIOSYNTHETIC-PROCESS	GO-0008610	6	0.551339	1.248703	0.177273	0.505417
243	GOBP-GENERATION-OF-PRECURSOR-METABOLITES-AND-E...	GO-0006091	5	0.591884	1.247717	0.175655	0.505510
244	GOBP-EXOCYTOSIS	GO-0006887	11	0.467386	1.247404	0.194602	0.504197
245	GOBP-SYNAPTIC-TRANSMISSION-GLUTAMATERGIC	GO-0035249	13	0.443172	1.245997	0.199450	0.505260
246	GOBP-CELL-CELL-SIGNALING-BY-WNT	GO-0198738	7	0.532574	1.245715	0.199702	0.503792
247	GOBP-TISSUE-MIGRATION	GO-0090130	9	0.492764	1.245689	0.192253	0.501841
248	GOBP-CELLULAR-RESPONSE-TO-STARVATION	GO-0009267	5	0.599538	1.245307	0.197550	0.500686
249	HALLMARK-ALLOGRAFT-REJECTION	M5950	7	0.523029	1.244982	0.190407	0.499321
250	GOBP-RESPONSE-TO-NICOTINE	GO-0035094	7	0.520972	1.244914	0.196221	0.497497
251	GOBP-RESPONSE-TO-HEAT	GO-0009408	7	0.526650	1.244487	0.207101	0.496383
252	GOBP-REGULATION-OF-LIPID-BIOSYNTHETIC-PROCESS	GO-0046890	6	0.551339	1.240934	0.206186	0.502223
253	GOBP-NUCLEOBASE-CONTAINING-SMALL-MOLECULE-META...	GO-0055086	6	0.562170	1.240793	0.171303	0.500524
254	GOBP-DENDRITE-DEVELOPMENT	GO-0016358	9	0.485690	1.239314	0.200577	0.501961
255	GOBP-NEGATIVE-REGULATION-OF-PROTEOLYSIS	GO-0045861	8	0.498687	1.238821	0.198839	0.501059

Continuation of Table S16

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
256	GOBP-REGULATION-OF-MUSCLE-CELL-DIFFERENTIATION	6	0.546523	1.237255	0.196839	0.502591	1.000
257	GOBP-RESPONSE-TO-TEMPERATURE-STIMULUS	9	0.491301	1.235251	0.219686	0.505296	1.000
258	GOBP-RESPONSE-TO-WOUNDING	15	0.419366	1.232915	0.213406	0.508311	1.000
259	GOBP-SENSORY-ORGAN-DEVELOPMENT	8	0.497150	1.231893	0.208824	0.508529	1.000
260	HALLMARK-UV-RESPONSE-UP	5	0.582492	1.231775	0.184664	0.506828	1.000
261	GOBP-REGULATION-OF-LIPID-LOCALIZATION	5	0.585014	1.230809	0.209302	0.507033	1.000
262	GOBP-CELLULAR-HOMEOSTASIS	18	0.399758	1.230119	0.207124	0.506487	1.000
263	GOBP-CALCIUM-MEDIATED-SIGNALING	10	0.472657	1.229017	0.231760	0.507055	1.000
264	GOBP-GLIOGENESIS	12	0.443824	1.226090	0.215924	0.511621	1.000
265	GOBP-MUSCLE-CELL-DIFFERENTIATION	10	0.467184	1.225729	0.216939	0.510547	1.000
266	GOBP-NEGATIVE-REGULATION-OF-NUCLEOBASE-CONTAIN...	13	0.432858	1.222027	0.236209	0.516921	1.000
267	GOBP-EPITHELIAL-DEVELOPMENT	15	0.411775	1.221909	0.215405	0.515219	1.000
268	GOBP-NEGATIVE-REGULATION-OF-BINDING	6	0.53769	1.220617	0.219178	0.516132	1.000
269	GOBP-NEGATIVE-REGULATION-OF-CELL-DEATH	22	0.382921	1.220571	0.209476	0.514344	1.000
270	GOBP-ENDOCYTOSIS	8	0.485744	1.219781	0.245763	0.514211	1.000
271	REACTOME-CREB1-PHOSPHORYLATION-THROUGH-NMDA-RE...	8	0.492374	1.218431	0.221264	0.515310	1.000
272	GOBP-MYELOID-LEUKOCYTE-ACTIVATION	8	0.498349	1.217270	0.229885	0.515757	1.000
273	GOBP-POSITIVE-REGULATION-OF-GLIOGENESIS	5	0.581865	1.216961	0.208889	0.514500	1.000
274	GOBP-REGULATION-OF-GLIOGENESIS	5	0.581865	1.216936	0.210031	0.512683	1.000
275	GOBP-VASCULATURE-DEVELOPMENT	17	0.403699	1.214326	0.218016	0.516391	1.000
276	GOBP-REGULATION-OF-CIRCADIAN-RHYTHM	7	0.515882	1.212905	0.229607	0.517650	1.000
277	GOBP-PROTEIN-CONTAINING-COMPLEX-SUBUNIT-ORGANI...	14	0.422913	1.211492	0.206199	0.518871	1.000
278	GOBP-IMMUNE-RESPONSE-REGULATING-SIGNALING-PATHWAY	8	0.486627	1.209947	0.232353	0.520420	1.000
279	GOBP-NEGATIVE-REGULATION-OF-TRANSCRIPTION-BY-R...	10	0.453957	1.208252	0.224688	0.522156	1.000
280	GOBP-FC-RECEPTOR-SIGNALING-PATHWAY	8	0.486627	1.205783	0.235123	0.526148	1.000
281	GOBP-CELL-CELL-ADHESION	14	0.415307	1.204427	0.242991	0.527179	1.000
282	GOBP-NEUROINFLAMMATORY-RESPONSE	5	0.573692	1.203893	0.228482	0.526408	1.000
283	REACTOME-G-ALPHA-I-SIGNALING-EVENTS	18	0.389164	1.203531	0.228000	0.525298	1.000
284	GOBP-POSITIVE-REGULATION-OF-IMMUNE-SYSTEM-PROCESS	18	0.391003	1.203228	0.245235	0.524112	1.000
285	GOBP-POSITIVE-REGULATION-OF-PROTEIN-METABOLIC...	28	0.361105	1.201013	0.245211	0.527087	1.000
286	GOBP-REGULATION-OF-TRANSPORT	44	0.341687	1.200031	0.233129	0.527383	1.000
287	GOBP-NEGATIVE-REGULATION-OF-RESPONSE-TO-STIMULUS	16	0.403143	1.196681	0.252964	0.532740	1.000
288	GOBP-NEGATIVE-REGULATION-OF-BIOSYNTHETIC-PROCESS	13	0.427791	1.196112	0.240163	0.532252	1.000
289	GOBP-REGULATION-OF-CELLULAR-RESPONSE-TO-STRESS	9	0.464100	1.195211	0.243243	0.532273	1.000
290	GOBP-RESPONSE-TO-EXTRACELLULAR-STIMULUS	13	0.415206	1.194894	0.252604	0.531049	1.000
291	GOBP-REGULATION-OF-PROTEIN-LOCALIZATION-TO-MEM...	7	0.500774	1.194333	0.247344	0.530510	1.000
292	REACTOME-ADAPTIVE-IMMUNE-SYSTEM	9	0.471049	1.192328	0.250350	0.532769	1.000
293	REACTOME-INTERLEUKIN-17-SIGNALING	6	0.529888	1.188046	0.240713	0.540449	1.000
294	GOBP-ANATOMICAL-STRUCTURE-FORMATION-INVOLVED-I...	20	0.376960	1.187418	0.251664	0.539973	1.000
295	GOBP-REGULATION-OF-NEUROGENESIS	14	0.413505	1.186522	0.236559	0.540083	1.000
296	GOBP-REGULATION-OF-ENDOCYTOSIS	6	0.529622	1.186454	0.256757	0.538483	1.000
297	GOBP-NEGATIVE-REGULATION-OF-RESPONSE-TO-EXTERN...	5	0.550816	1.186100	0.243865	0.537413	1.000
298	GOBP-REGULATION-OF-WNT-SIGNALING-PATHWAY	5	0.542501	1.183165	0.259601	0.541996	1.000

Continuation of Table S16

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
299 GOBP-NEGATIVE-REGULATION-OF-INTRACELLULAR-SIGN...	GO:1902532	7	0.492611	1.180187	0.253201	0.546695	1.000
300 GOBP-OSSIFICATION	GO:0001503	9	0.455032	1.179942	0.266003	0.545307	1.000
301 GOBP-RESPONSE-TO-CYTOKINE	GO:0034097	23	0.359814	1.177830	0.272050	0.547783	1.000
302 GOBP-APOPTOTIC-SIGNALING-PATHWAY	GO:0097190	15	0.403423	1.176062	0.248340	0.549870	1.000
303 GOBP-CELL-SURFACE-RECEPTOR-SIGNALING-PATHWAY.I...	GO:1905114	15	0.396832	1.174149	0.253012	0.551920	1.000
304 GOBP-APOPTOTIC-PROCESS	GO:0006915	35	0.339034	1.173946	0.268382	0.550526	1.000
305 GOBP-IN-UTERO-EMBRYONIC-DEVELOPMENT	GO:0001701	8	0.476621	1.171853	0.279346	0.553468	1.000
306 GOBP-CELLULAR-MACROMOLECULE-LOCALIZATION	GO:0070727	21	0.367995	1.169685	0.260638	0.556296	1.000
307 GOBP-GLIAL-CELL-DIFFERENTIATION	GO:0010001	10	0.447063	1.167633	0.301653	0.563125	1.000
308 GOBP-POSITIVE-REGULATION-OF-DEVELOPMENTAL-GROWTH	GO:0048639	8	0.474140	1.165329	0.288160	0.562248	1.000
309 GOBP-MYELOID-LEUKOCYTE-MEDIATED-IMMUNITY	GO:0002444	6	0.519028	1.164971	0.282511	0.561272	1.000
310 GOBP-TUBE-MORPHOGENESIS	GO:0035239	15	0.401487	1.164474	0.294355	0.560555	1.000
311 GOBP-CELLULAR-RESPONSE-TO-ABIOTIC-STIMULUS	GO:0071214	7	0.499442	1.164237	0.277126	0.559294	1.000
312 GOBP-CELL-ACTIVATION-INVOLVED-IN-IMMUNE-RESPONSE	GO:0002263	6	0.519028	1.163116	0.275510	0.559941	1.000
313 GOBP-POSITIVE-REGULATION-OF-CELL-DIFFERENTIATION	GO:0045597	27	0.348091	1.156402	0.286076	0.572871	1.000
314 GOBP-MYOTUBE-DIFFERENTIATION	GO:0014902	5	0.549092	1.155885	0.280063	0.572102	1.000
315 GOBP-FAT-CELL-DIFFERENTIATION	GO:0045444	9	0.453397	1.15280	0.279137	0.571640	1.000
316 GOBP-SECOND-MESSENGER-MEDIATED-SIGNALING	GO:0019932	16	0.393316	1.154762	0.289438	0.570992	1.000
317 GOBP-POSITIVE-REGULATION-OF-SMOOTH-MUSCLE-CELL...	GO:0048661	5	0.548366	1.154630	0.276074	0.569493	1.000
318 GOBP-DEVELOPMENTAL-MATURATION	GO:0021700	5	0.550425	1.153933	0.267296	0.569121	1.000
319 GOBP-NEGATIVE-REGULATION-OF-CYSTEINE-TYPE-ENDO...	GO:2000117	5	0.547560	1.153016	0.271772	0.569349	1.000
320 GOBP-TUBE-DEVELOPMENT	GO:0035295	18	0.357352	1.152265	0.294584	0.569122	1.000
321 GOBP-TRANSMEMBRANE-RECEPTOR-PROTEIN-SERINE-THR...	GO:0007178	6	0.503166	1.147195	0.294210	0.578417	1.000
322 GOBP-REGULATION-OF-ORGANELLE-ORGANIZATION	GO:0033043	14	0.401040	1.145773	0.302778	0.579823	1.000
323 GOBP-REGULATION-OF-VASCULAR-ASSOCIATED-SMOOTH...	GO:1904705	5	0.548016	1.144649	0.284211	0.580348	1.000
324 GOBP-REGULATION-OF-LIPID-METABOLIC-PROCESS	GO:0019216	7	0.491135	1.144137	0.309838	0.579666	1.000
325 GOBP-DEVELOPMENTAL-CELL-GROWTH	GO:0048588	5	0.534123	1.143479	0.296703	0.579301	1.000
326 GOBP-POSITIVE-REGULATION-OF-NEUROGENESIS	GO:0050769	12	0.415343	1.141462	0.300135	0.581749	1.000
327 GOBP-POSITIVE-REGULATION-OF-TRANSPORT	GO:0051050	26	0.340548	1.139583	0.312339	0.584002	1.000
328 GOBP-POSITIVE-REGULATION-OF-NERVOUS-SYSTEM.DEV...	GO:0051962	12	0.415343	1.138847	0.310014	0.583898	1.000
329 GOBP-ORGANOPHOSPHATE-METABOLIC-PROCESS	GO:0019637	7	0.477045	1.137561	0.293605	0.588831	1.000
330 REACTOME-NEUTROPHIL-DEGRANULATION	R-RNO-6798695	6	0.519028	1.132963	0.316788	0.593051	1.000
331 GOBP-POSITIVE-REGULATION-OF-TRANSCRIPTION-BY-R...	GO:0045944	24	0.344203	1.128876	0.334180	0.600161	1.000
332 GOBP-POSITIVE-REGULATION-OF-CELL-DEVELOPMENT	GO:0010720	12	0.415343	1.128726	0.312329	0.598649	1.000
333 GOBP-LEUKOCYTE-CELL-CELL-ADHESION	GO:0007159	6	0.505302	1.128426	0.308908	0.597555	1.000
334 GOBP-REGULATION-OF-ENDOTHELIAL-CELL-MIGRATION	GO:0010594	5	0.538282	1.128186	0.310811	0.596252	1.000
335 GOBP-ENDOTHELIAL-CELL-MIGRATION	GO:0043542	8	0.453348	1.125762	0.318248	0.599534	1.000
336 GOBP-EPITHELIAL-CELL-PROLIFERATION	GO:0050673	12	0.397316	1.122931	0.318560	0.603601	1.000
337 GOBP-POSITIVE-REGULATION-OF-PRIMI-NA-TRANSCRI...	GO:1902895	7	0.465476	1.122829	0.317578	0.602025	1.000
338 GOBP-ESTABLISHMENT-OF-PROTEIN-LOCALIZATION-TO...	GO:0072594	6	0.508250	1.122642	0.330838	0.600648	1.000
339 GOBP-REGULATION-OF-NERVOUS-SYSTEM-DEVELOPMENT	GO:0051960	15	0.382404	1.122603	0.321990	0.598947	1.000
340 GOBP-LIPID-LOCALIZATION	GO:0010876	10	0.423531	1.122448	0.337589	0.597504	1.000
341 GOBP-ENDOTHELIAL-CELL-PROLIFERATION	GO:0001935	8	0.452199	1.122329	0.305233	0.596061	1.000

Continuation of Table S16

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
342	GOBP-ACTIVATION_OF_IMMUNE_RESPONSE	5	0.527031	1.119666	0.318797	0.599965	1.000
343	GOBP-RESPONSE_TO_PEPTIDE	18	0.364172	1.114022	0.318003	0.610077	1.000
344	GOBP-CELLULAR_RESPONSE_TO_PEPTIDE	13	0.388033	1.112072	0.346829	0.612526	1.000
345	GOBP-POSITIVE_REGULATION_OF_DNA_BINDING_TRANSC...	10	0.431486	1.112050	0.351801	0.610813	1.000
346	GOBP-REGULATION_OF_BINDING	11	0.407816	1.111845	0.338889	0.609479	1.000
347	GOBP-BLOOD_VESSEL_ENDOTHELIAL_CELL_MIGRATION	8	0.453348	1.111832	0.334290	0.607756	1.000
348	GOBP-CHROMOSOME_ORGANIZATION	6	0.498133	1.111392	0.323881	0.607034	1.000
349	GOBP-ENZYMELINKED-RECEPTOR_PROTEIN-SIGNALING...	24	0.344563	1.111224	0.319588	0.605622	1.000
350	GOBP-POSITIVE_REGULATION_OF_EPITHELIAL_CELL_M...	5	0.522837	1.110860	0.347894	0.604663	1.000
351	GOBP-MUSCLE_ORGAN_DEVELOPMENT	9	0.430380	1.107472	0.336606	0.610093	1.000
352	REACTOME_HEMOSTASIS	14	0.381172	1.106388	0.326693	0.610564	1.000
353	GOBP-ERBB-SIGNALING_PATHWAY	5	0.533063	1.106259	0.336350	0.609103	1.000
354	GOBP-NEGATIVE_REGULATION_OF_NERVOUS_SYSTEM_DEV...	5	0.522341	1.103815	0.336907	0.612493	1.000
355	REACTOME_NGF_STIMULATED_TRANSCRIPTION	9	0.430380	1.103376	0.342291	0.611719	1.000
356	GOBP-EMBRYO_DEVELOPMENT_ENDING_IN_BIRTH_OR_EGG...	9	0.431500	1.100904	0.354749	0.615180	1.000
357	GOBP-NEGATIVE_REGULATION_OF_LOCOMOTION	5	0.518707	1.09563	0.356391	0.616141	1.000
358	GOBP-SMOOTH_MUSCLE_CELL_PROLIFERATION	6	0.489239	1.098565	0.349558	0.616509	1.000
359	GOBP-PROTEOLYSIS	17	0.357695	1.097549	0.343791	0.616739	1.000
360	GOBP-SIGNAL_RELEASE	14	0.385764	1.097515	0.335655	0.615123	1.000
361	GOBP-RESPONSE_TO_RADIATION	13	0.386176	1.095649	0.356383	0.617285	1.000
362	GOBP-MUSCLE_STRUCTURE_DEVELOPMENT	16	0.367559	1.095438	0.341623	0.616122	1.000
363	GOBP-RESPONSE_TO_INORGANIC_SUBSTANCE	19	0.348756	1.088134	0.337317	0.629541	1.000
364	GOBP-POSITIVE_REGULATION_OF_SIGNALING	34	0.312732	1.087711	0.367470	0.628748	1.000
365	GOBP-POSITIVE_REGULATION_OF_CELLULAR_PROTEIN_L...	10	0.416232	1.086685	0.396501	0.629095	1.000
366	GOBP-POSITIVE_REGULATION_OF_CATALYTIC_ACTIVITY	30	0.313789	1.081676	0.357500	0.637711	1.000
367	GOBP-POSITIVE_REGULATION_OF_CELL_PROJECTION_OR...	7	0.466446	1.086685	0.396501	0.639317	1.000
368	GOBP-RESPONSE_TO_LIGHT_STIMULUS	11	0.400435	1.078758	0.349933	0.640086	1.000
369	GOBP-REGULATION_OF_TRANSMEMBRANE_TRANSPORT	23	0.336479	1.077926	0.359335	0.640068	1.000
370	GOBP-PRLMIRNA_TRANSCRIPTION_BY_RNA_POLYMERASE_II	7	0.465476	1.077596	0.384844	0.638940	1.000
371	GOBP-EMBRYONIC_MORPHOGENESIS	6	0.481537	1.077177	0.364329	0.638069	1.000
372	GOBP-MULTICELLULAR_ORGANISM_PROCESS	8	0.440811	1.073254	0.385475	0.644691	1.000
373	GOBP-LOCOMOTORY_BEHAVIOR	7	0.445776	1.072978	0.389630	0.643446	1.000
374	GOBP-MONOCARBOXYLIC_ACID_METABOLIC_PROCESS	6	0.475344	1.072290	0.370753	0.643122	1.000
375	GOBP-ACTIN_FILAMENT_BASED_PROCESS	7	0.452026	1.064971	0.400000	0.656219	1.000
376	GOBP-RESPONSE_TO_UV	5	0.508481	1.064011	0.373846	0.656435	1.000
377	GOBP-DENDRITIC_SPINE_DEVELOPMENT	6	0.469681	1.062871	0.408511	0.657092	1.000
378	GOBP-LOCOMOTION	31	0.314593	1.062725	0.387137	0.655611	1.000
379	GOBP-REGULATION_OF_RECEPTOR_MEDIATED_ENDOCYTOSIS	5	0.4048259	1.060962	0.396947	0.657474	1.000
380	GOBP-ENDOCRINE_SYSTEM_DEVELOPMENT	6	0.462989	1.060483	0.402108	0.656745	1.000
381	GOBP-POSITIVE_REGULATION_OF_CELL_GROWTH	6	0.473943	1.059006	0.389985	0.658255	1.000
382	GOBP-CYTOKINE_MEDIATED_SIGNALING_PATHWAY	16	0.357563	1.058510	0.408488	0.657512	1.000
383	REACTOME_NERVOUS_SYSTEM_DEVELOPMENT	15	0.366370	1.058065	0.400804	0.656659	1.000
384	GOBP-DENDRITIC_SPINE_MORPHOGENESIS	5	0.504773	1.055511	0.407108	0.659997	1.000

Continuation of Table S16

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
385	GOBP-REGULATION-OF-CELLULAR-PROTEIN-LOCALIZATION	12	0.386367	1.054114	0.424791	0.661222	1.000
386	REACTOME.MAPK.FAMILY.SIGNALING.CASCADES	12	0.376086	1.053462	0.385773	0.660904	1.000
387	GOBP-NEGATIVE-REGULATION-OF-ION-TRANSPORT	11	0.394235	1.051641	0.395512	0.662787	1.000
388	REACTOME.BETA.CATENIN.INDEPENDENT.WNT.SIGNALING	5	0.487389	1.050013	0.387334	0.664455	1.000
389	GOBP-LEUKOCYTE-DIFFERENTIATION	15	0.358574	1.049430	0.400273	0.664020	1.000
390	GOBP-REGULATION-OF-CYTOSKELETON-ORGANIZATION	5	0.492740	1.048578	0.411326	0.663915	1.000
391	GOBP-STRIATED.MUSCLE-CELL-DIFFERENTIATION	9	0.410926	1.047798	0.422190	0.663912	1.000
392	GOBP-REGULATION-OF-INFLAMMATORY-RESPONSE	7	0.443346	1.047142	0.394074	0.663428	1.000
393	GOBP-REGULATION-OF-RESPONSE-TO-STRESS	19	0.341173	1.047023	0.410923	0.662021	1.000
394	GOBP-ANATOMICAL-STRUCTURE.HOMEOSTASIS	7	0.451283	1.045383	0.433681	0.663678	1.000
395	GOBP-MATERNAL-PROCESS-INVOLVED-IN-FEMALE-PREGN...	5	0.504715	1.045235	0.424806	0.662300	1.000
396	GOBP-MYELOID-CELL-DIFFERENTIATION	13	0.366349	1.043979	0.401628	0.663160	1.000
397	GOBP-OSTEOBLAST-DIFFERENTIATION	5	0.498963	1.042697	0.416413	0.664087	1.000
398	GOBP-RAS-PROTEIN-SIGNAL-TRANSDUCTION	5	0.492870	1.042666	0.402496	0.662497	1.000
399	GOBP-PLATELET-ACTIVATION	6	0.468289	1.041768	0.430250	0.662638	1.000
400	GOBP-CELL-CELL-JUNCTION-ASSEMBLY	5	0.485091	1.040883	0.429217	0.662671	1.000
401	GOBP-TRANSMEMBRANE-RECEPTOR-PROTEIN-TYROSINE.K...	19	0.332104	1.037489	0.404066	0.667992	1.000
402	GOBP-LYMPHOCYTE-ACTIVATION	9	0.401397	1.037332	0.430727	0.666633	1.000
403	GOBP-PROTEIN-AUTOPHOSPHORYLATION	5	0.496904	1.037102	0.427300	0.665426	1.000
404	GOBP-REGULATION-OF-DEPENDENCE-RESPONSE	7	0.443346	1.034927	0.429608	0.668034	1.000
405	REACTOME.EXTRA-NUCLEAR-ESTROGEN-SIGNALING	7	0.441011	1.033165	0.437500	0.669833	1.000
406	GOBP-CELLULAR-RESPONSE-TO-NITROGEN-COMPOUND	20	0.331766	1.030252	0.439024	0.674103	1.000
407	GOBP-HOMEOSTATIC-PROCESS	31	0.304893	1.029128	0.442260	0.674585	1.000
408	REACTOME.SIGNALING-BY-NTRKS	18	0.331083	1.027240	0.450382	0.676653	1.000
409	REACTOME.MAPK-TARGETS.NUCLEAR-EVENTS-MEDIATED-...	5	0.494016	1.023955	0.441221	0.681471	1.000
410	GOBP-REGULATION-OF-NERVOUS-SYSTEM-PROCESS	8	0.410960	1.021646	0.436496	0.684285	1.000
411	REACTOME.INTERLEUKIN-4-AND-INTERLEUKIN-13-SIGN...	8	0.416372	1.020253	0.439706	0.685488	1.000
412	GOBP-RESPONSE-TO-ORGANIC-CYCLIC-COMPOUND	20	0.325243	1.016115	0.443734	0.692034	1.000
413	REACTOME.INTRACELLULAR-SIGNALING-BY-SECOND.MES...	15	0.344252	1.015788	0.453939	0.690962	1.000
414	GOBP-BLOOD-VESSEL-MORPHOGENESIS	14	0.352240	1.014332	0.451436	0.692131	1.000
415	GOBP-CELLULAR-RESPONSE-TO-REACTIVE-OXYGEN-SPECIES	7	0.426616	1.011869	0.478261	0.695409	1.000
416	GOBP-PROTEIN-LOCALIZATION-TO-MEMBRANE	14	0.351339	1.008080	0.469003	0.701420	1.000
417	GOBP-NEGATIVE-REGULATION-OF-APOPTOTIC-SIGNALIN...	7	0.427422	1.007577	0.456973	0.700713	1.000
418	GOBP-TISSUE-HOMEOSTASIS	5	0.464039	1.004884	0.465544	0.704206	1.000
419	GOBP-REGULATION-OF-PEPTIDASE-ACTIVITY	10	0.384852	1.004185	0.470027	0.703931	1.000
420	GOBP-POSITIVE-REGULATION-OF-EPITHELIAL-CELL-PR...	7	0.427957	1.003570	0.466476	0.703414	1.000
421	REACTOME-CELLULAR-RESPONSES-TO-EXTERNAL-STIMULI	12	0.356991	1.001096	0.455540	0.706588	1.000
422	REACTOME-RAS-ACTIVATION-UPON-CA2-INFLUX-THROUG...	6	0.443347	0.998714	0.474926	0.709540	1.000
423	GOBP-CELLULAR-RESPONSE-TO-INORGANIC-SUBSTANCE	11	0.367213	0.997991	0.471467	0.709387	1.000
424	GOBP-REPRODUCTIVE-SYSTEM-DEVELOPMENT	6	0.449761	0.995980	0.511799	0.711593	1.000
425	GOBP-ORGANIC-ACID-METABOLIC-PROCESS	7	0.422551	0.992550	0.482759	0.716673	1.000
426	GOBP-NEURON-PROJECTION-ORGANIZATION	8	0.401315	0.992347	0.494876	0.715365	1.000
427	GOBP-REGULATION-OF-FAT-CELL-DIFFERENTIATION	6	0.444888	0.992321	0.477134	0.713743	1.000

Continuation of Table S16

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
428	REACTOME-SIGNALING-BY-WNT	7	0.422309	0.991450	0.485163	0.713639	1.000
429	GOBP-POSITIVE-REGULATION-OF-CELL-DEATH	19	0.323513	0.991026	0.487646	0.712826	1.000
430	GOBP-INFLAMMATORY-RESPONSE	12	0.353663	0.988831	0.488340	0.715356	1.000
431	GOBP-CELLULAR-RESPONSE-TO-CHEMICAL-STRESS	7	0.426616	0.988541	0.496296	0.714223	1.000
432	GOBP-REGULATION-OF-SYNAPTIC-TRANSMISSION-GLUTA...	12	0.360982	0.986172	0.494006	0.716996	1.000
433	GOBP-POSITIVE-REGULATION-OF-ION-TRANSPORT	17	0.332098	0.984433	0.498694	0.718805	1.000
434	GOBP-POSITIVE-REGULATION-OF-CYTOKINE-PRODUCTION	7	0.409537	0.983649	0.488987	0.718721	1.000
435	GOBP-REGULATION-OF-PROTEOLYSIS	12	0.350844	0.980225	0.504155	0.723611	1.000
436	GOBP-CARBOHYDRATE-DERIVATIVE-METABOLIC-PROCESS	7	0.411593	0.979137	0.505344	0.721437	1.000
437	GOBP-REGULATION-OF-CELL-PROJECTION-ORGANIZATION	20	0.311545	0.977057	0.493438	0.726396	1.000
438	GOBP-CENTRAL-NERVOUS-SYSTEM-DEVELOPMENT	26	0.298163	0.973574	0.508035	0.731471	1.000
439	GOBP-PROTEIN-CATABOLIC-PROCESS	8	0.400432	0.973231	0.510294	0.730471	1.000
440	REACTOME-ESTROGEN-DEPENDENT-NUCLEAR-EVENTS-DOW...	5	0.464124	0.970563	0.515432	0.733706	1.000
441	REACTOME-L1CAM-INTERACTIONS	5	0.459885	0.968841	0.520129	0.735343	1.000
442	GOBP-REGULATION-OF-CELL-CELL-ADHESION	9	0.370863	0.965184	0.521739	0.740525	1.000
443	GOBP-SPROUTING-ANGIOGENESIS	5	0.445783	0.964818	0.526287	0.739547	1.000
444	GOBP-REGULATION-OF-ION-TRANSPORT	36	0.281308	0.962357	0.504717	0.741861	1.000
445	HALLMARK-KRAS-SIGNALING-UP	6	0.427254	0.962357	0.511144	0.740738	1.000
446	GOBP-FORBRAIN-DEVELOPMENT	9	0.368201	0.959535	0.523605	0.744157	1.000
447	GOBP-RESPONSE-TO-HORMONE	20	0.303155	0.958693	0.498094	0.744002	1.000
448	REACTOME-ESR-MEDIATED-SIGNALING	8	0.390477	0.952048	0.52941	0.754856	1.000
449	GOBP-RESPONSE-TO-MOLECULE-OF-BACTERIAL-ORIGIN	13	0.341481	0.948940	0.533512	0.759038	1.000
450	GOBP-REGULATION-OF-SYNAPTIC-PLASTICITY	21	0.301222	0.948194	0.530612	0.758826	1.000
451	GOBP-REGULATION-OF-NEURON-PROJECTION-DEVELOPMENT	16	0.321198	0.947812	0.539267	0.757873	1.000
452	GOBP-NEGATIVE-REGULATION-OF-CELL-POPULATION-PR...	9	0.375509	0.946639	0.538889	0.758281	1.000
453	GOBP-NEGATIVE-REGULATION-OF-TRANSMEMBRANE-TRAN...	6	0.425084	0.945885	0.547511	0.757964	1.000
454	GOBP-RESPONSE-TO-BACTERIUM	13	0.341481	0.943250	0.522161	0.761138	1.000
455	GOBP-TRANSMEMBRANE-TRANSPORT	27	0.281659	0.939829	0.551151	0.766197	1.000
456	REACTOME-PTEN-REGULATION	5	0.438356	0.939664	0.543344	0.764852	1.000
457	REACTOME-SIGNALING-BY-NUCLEAR-RECEPTORS	8	0.390477	0.939314	0.551429	0.763744	1.000
458	GOBP-REGULATION-OF-NEURONAL-SYNAPTIC-PLASTICITY	7	0.397562	0.934431	0.579942	0.770800	1.000
459	GOBP-REGULATION-OF-CELL-DEATH	34	0.269086	0.934338	0.558458	0.769342	1.000
460	GOBP-POSITIVE-REGULATION-OF-ENDOTHELIAL-CELL-P...	6	0.415427	0.932238	0.566717	0.771359	1.000
461	GOBP-POSITIVE-REGULATION-OF-CELLULAR-COMPONENT...	9	0.358511	0.929561	0.546610	0.774723	1.000
462	REACTOME-CA-DEPENDENT-EVENTS	8	0.376383	0.927259	0.554412	0.777243	1.000
463	GOBP-PROTEIN-MODIFICATION-BY-SMALL-PROTEIN-CON...	7	0.382716	0.926243	0.548246	0.777492	1.000
464	REACTOME-CLASS-C-3-METABOTROPIC-GLUTAMATE-PHER...	7	0.391143	0.926022	0.575284	0.776209	1.000
465	GOBP-SYNAPSE-ORGANIZATION	17	0.304132	0.922526	0.578947	0.781022	1.000
466	GOBP-CHEMICAL-HOMEOSTASIS	23	0.287481	0.921428	0.563975	0.781299	1.000
467	GOBP-PROTEIN-LOCALIZATION-TO-SYNAPSE	5	0.435596	0.921200	0.574400	0.780051	1.000
468	GOBP-CELL-CELL-SIGNALING	56	0.267935	0.917385	0.605882	0.785098	1.000
469	GOBP-REGULATION-OF-ANATOMICAL-STRUCTURE-SIZE	10	0.351096	0.916205	0.583215	0.785377	1.000
470	REACTOME-INFECTIOUS-DISEASE	13	0.322038	0.911119	0.572238	0.792527	1.000

Continuation of Table S16

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
471	GOBP-ORGANONITROGEN_COMPOUND_CATABOLIC_PROCESS	9	0.352892	0.909317	0.589563	0.794082	1.000
472	GOBP-ORGANIC_HYDROXY_COMPOUND_METABOLIC_PROCESS	7	0.378620	0.906487	0.587706	0.797436	1.000
473	GOBP-RESPONSE_TO_NITROGEN_COMPOUND	34	0.264833	0.906443	0.589461	0.795827	1.000
474	GOBP-PROTEIN_LOCALIZATION_TO_POSTSYNAPSE	5	0.435596	0.903073	0.608696	0.800167	1.000
475	GOBP-LEARNING	13	0.323243	0.902751	0.576407	0.799033	1.000
476	GOBP-NEURON_MIGRATION	5	0.426890	0.898373	0.625373	0.805023	1.000
477	GOBP-POSTSYNAPSE_ORGANIZATION	10	0.341655	0.896550	0.594142	0.806755	1.000
478	GOBP-CELLULAR_RESPONSE_TO_HORMONE_STIMULUS	11	0.328024	0.895276	0.623580	0.807270	1.000
479	GOBP-CELL_JUNCTION_ORGANIZATION	19	0.285241	0.894956	0.600519	0.806116	1.000
480	GOBP-SMALL_GTPASE-MEDIATED_SIGNAL_TRANSDUCTION	8	0.362990	0.892702	0.610719	0.808371	1.000
481	GOBP-PROTEIN_LOCALIZATION_TO_CELL_PERIPHERY	12	0.325203	0.889001	0.603001	0.813071	1.000
482	GOBP-ENDOMEMBRANE_SYSTEM_ORGANIZATION	6	0.386855	0.886390	0.630792	0.815749	1.000
483	GOBP-NEGATIVE_REGULATION_OF_CELL_PROJECTION_OR...	5	0.423335	0.885512	0.632504	0.815587	1.000
484	GOBP-REGULATION_OF_CYSSTEINE_TYPE_ENDOPEPTIDASE...	9	0.341495	0.885374	0.619392	0.814149	1.000
485	GOBP-POSITIVE_REGULATION_OF_BINDING	6	0.396872	0.881922	0.632308	0.818334	1.000
486	REACTOME-GPCR_LIGAND_BINDING	8	0.356439	0.881907	0.615385	0.816674	1.000
487	GOBP-RESPONSE_TO_ACID_CHEMICAL	6	0.397203	0.881807	0.626973	0.815166	1.000
488	GOBP-POSITIVE_REGULATION_OF_AXONOGENESIS	5	0.420261	0.880661	0.658462	0.815480	1.000
489	GOBP-SKELETAL_MUSCLE_ORGAN_DEVELOPMENT	5	0.409639	0.879974	0.625564	0.815026	1.000
490	REACTOME-G_PROTEIN-MEDIATED_EVENTS	9	0.346721	0.879284	0.627424	0.814445	1.000
491	GOBP-CELLULAR_RESPONSE_TO_CADMIUM_ION	5	0.416524	0.876469	0.640000	0.817565	1.000
492	GOBP-GLAND_DEVELOPMENT	7	0.370188	0.876077	0.654572	0.816530	1.000
493	GOBP-REGULATION_OF_CELLULAR_LOCALIZATION	17	0.294597	0.874694	0.649551	0.817175	1.000
494	GOBP-T-CELL_ACTIVATION	8	0.361342	0.874094	0.625869	0.816503	1.000
495	REACTOME-DEVELOPMENTAL_BIOLOGY	23	0.270858	0.870693	0.650773	0.820653	1.000
496	GOBP-CELLULAR_COMPONENT_MAINTENANCE	5	0.416096	0.869140	0.650078	0.821553	1.000
497	REACTOME-EPH_EPHRIN_SIGNALING	6	0.381367	0.866242	0.660633	0.824697	1.000
498	GOBP-HOMEOSTASIS_OF_NUMBER_OF_CELLS	5	0.408684	0.862973	0.630468	0.828557	1.000
499	GOBP-RESPONSE_TO_CADMIUM_ION	6	0.382837	0.861826	0.665726	0.828908	1.000
500	GOBP-PROTEIN_LOCALIZATION_TO_CELL_JUNCTION	6	0.386283	0.861748	0.647416	0.827358	1.000
501	REACTOME-EXTRACELLULAR_MATRIX_ORGANIZATION	5	0.402740	0.859492	0.673252	0.829330	1.000
502	GOBP-G_PROTEIN_COUPLED_GLUTAMATE_RECEPTOR_SIGN...	8	0.348932	0.856184	0.655882	0.833119	1.000
503	GOBP-PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_CON...	6	0.378049	0.851239	0.665685	0.839549	1.000
504	GOBP-CELLULAR_RESPONSE_TO_PEPITIDE_HORMONE_STIM...	9	0.328738	0.850864	0.666207	0.838610	1.000
505	GOBP-TELENCEPHALON_DEVELOPMENT	6	0.377617	0.848078	0.676602	0.841544	1.000
506	GOBP-EMBRYONIC_ORGAN_DEVELOPMENT	7	0.364950	0.846729	0.688478	0.842041	1.000
507	GOBP-REGULATION_OF_CELLULAR_COMPONENT_SIZE	7	0.354772	0.845475	0.672439	0.842496	1.000
508	REACTOME-LEISHMANIA_INFECTION	10	0.316437	0.844331	0.652463	0.842573	1.000
509	GOBP-REGULATION_OF_PROTEIN_TYROSINE_KINASE_ACT...	5	0.399069	0.841215	0.693098	0.845928	1.000
510	GOBP-RESPONSE_TO_CALCMIUM_ION	6	0.376664	0.840017	0.685714	0.846329	1.000
511	GOBP-POSITIVE_REGULATION_OF_MYELOID_CELL_DIFFE...	7	0.352811	0.838458	0.693908	0.847360	1.000
512	GOBP-RESPONSE_TO_INSULIN	5	0.397599	0.835759	0.712782	0.850035	1.000
513	GOBP-POSITIVE_REGULATION_OF_PROTEIN_TYROSINE_K...	5	0.399069	0.833736	0.718110	0.851572	1.000

Continuation of Table S16

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
514 GOBP-PURINE-CONTAINING-COMPOUND-METABOLIC-PROCESS	GO-0072521	5	0.392307	0.832345	0.722741	0.852079	1.000
515 GOBP-POSITIVE-REGULATION-OF-SECRETION	GO-0051047	6	0.372137	0.830466	0.696319	0.853451	1.000
516 GOBP-MYELOID-LEUKOCYTE-DIFFERENTIATION	GO-0002573	11	0.304565	0.829793	0.687943	0.852964	1.000
517 GOBP-INTRINSIC-APOPTOTIC-SIGNALING-PATHWAY	GO-0097193	5	0.387377	0.829400	0.694228	0.851870	1.000
518 GOBP-CELL-PROJECTION-ORGANIZATION	GO-0030030	34	0.238263	0.828379	0.708892	0.851821	1.000
519 GOBP-RECEPTOR-MEDIATED-ENDOCYTOSIS	GO-0006898	6	0.365151	0.828134	0.713056	0.850616	1.000
520 GOBP-CELL-MORPHOGENESIS-INVOLVED-IN-NEURON-DIF...	GO-0048667	21	0.258517	0.827948	0.716837	0.849258	1.000
521 GOBP-RESPONSE-TO-PEPTIDE-HORMONE	GO-0043434	13	0.293289	0.825155	0.712912	0.852002	1.000
522 GOBP-CELL-MORPHOGENESIS-INVOLVED-IN-DIFFERENTI...	GO-0000904	21	0.258517	0.824600	0.692695	0.851306	1.000
523 HALLMARK-APOPTOSIS	M5902	6	0.361849	0.817405	0.694084	0.860792	1.000
524 GOBP-POSITIVE-REGULATION-OF-CYSTEINE-TYPE-ENDO...	GO-2001056	7	0.344234	0.816348	0.715152	0.860803	1.000
525 GOBP-POSITIVE-REGULATION-OF-NEURON-DEATH	GO-1901216	5	0.389248	0.815837	0.718894	0.859933	1.000
526 GOBP-PEPTIDYL-SERINE-MODIFICATION	GO-0018209	12	0.293566	0.814723	0.707483	0.859935	1.000
527 GOBP-POSITIVE-REGULATION-OF-PEPTIDASE-ACTIVITY	GO-0010952	7	0.344234	0.814641	0.705185	0.858420	1.000
528 GOBP-APOPTOTIC-MITOCHONDRIAL-CHANGES	GO-0008637	6	0.361234	0.814500	0.714495	0.857025	1.000
529 GOBP-MULTICELLULAR-ORGANISMAL-RESPONSE-TO-STRESS	GO-0033555	5	0.380015	0.813928	0.746154	0.856258	1.000
530 GOBP-REGULATION-OF-HYDROLASE-ACTIVITY	GO-0051336	22	0.254768	0.811522	0.713342	0.858315	1.000
531 REACTOME-CELLULAR-SENESCENCE	R-RNO-2559583	6	0.358464	0.810048	0.743161	0.858980	1.000
532 GOBP-SYNAPTIC-SIGNALING	GO-0099536	47	0.227103	0.808653	0.742690	0.859521	1.000
533 REACTOME-SENESCENCE-ASSOCIATED-SECRETORY-PHENO...	R-RNO-2559582	6	0.358464	0.807668	0.704918	0.859329	1.000
534 GOBP-POSITIVE-REGULATION-OF-SYNAPTIC-TRANSMISSION	GO-0050806	15	0.278566	0.805956	0.732713	0.860339	1.000
535 GOBP-COGNITION	GO-0050890	28	0.239326	0.804769	0.720497	0.860569	1.000
536 GOBP-NEGATIVE-REGULATION-OF-IMMUNE-SYSTEM-PROCESS	GO-0002683	5	0.373534	0.804194	0.739968	0.859799	1.000
537 GOBP-REGULATION-OF-LYMPHOCYTE-ACTIVATION	GO-0051249	5	0.386456	0.802546	0.753776	0.860670	1.000
538 GOBP-RESPONSE-TO-ENDOGENOUS-STIMULUS	GO-0009719	34	0.23127	0.800723	0.734055	0.861736	1.000
539 GOBP-RESPONSE-TO-OXYGEN-LEVELS	GO-0070482	8	0.320802	0.800698	0.733612	0.860177	1.000
540 GOBP-MUSCLE-CONTRACTION	GO-0006936	5	0.378086	0.794110	0.757079	0.868107	1.000
541 GOBP-CHEMICAL-SYNAPTIC-TRANSMISSION-POSTSYNAPTIC	GO-0099565	9	0.308284	0.793965	0.733894	0.866716	1.000
542 GOBP-POSITIVE-REGULATION-OF-DEFENSE-RESPONSE	GO-0031349	5	0.374790	0.792777	0.753870	0.866856	1.000
543 GOBP-RECEPTOR-INTERNALIZATION	GO-0031623	5	0.368751	0.785952	0.783489	0.874925	1.000
544 GOBP-RECEPTOR-METABOLIC-PROCESS	GO-0043112	5	0.368751	0.779191	0.792109	0.883164	1.000
545 GOBP-REGULATION-OF-CELLULAR-COMPONENT-BIOGENESIS	GO-0044087	10	0.294901	0.778720	0.742075	0.882233	1.000
546 GOBP-POSITIVE-REGULATION-OF-TRANSMEMBRANE-TRAN...	GO-0034764	7	0.331291	0.776100	0.764368	0.884304	1.000
547 REACTOME-INTEGRATION-OF-ENERGY-METABOLISM	R-RNO-163685	5	0.355879	0.775341	0.782071	0.883763	1.000
548 GOBP-REGULATION-OF-PROTEIN-BINDING	GO-0043393	7	0.328518	0.772513	0.752907	0.885987	1.000
549 GOBP-REGULATION-OF-TRANS-SYNAPTIC-SIGNALING	GO-0099177	40	0.223399	0.765029	0.798788	0.894640	1.000
550 GOBP-RESPONSE-TO-GROWTH-FACTOR	GO-0070848	18	0.250419	0.764327	0.782956	0.893940	1.000
551 GOBP-REGULATION-OF-PROTEIN-CATABOLIC-PROCESS	GO-0042176	7	0.320324	0.759465	0.765832	0.898977	1.000
552 GOBP-HEAD-DEVELOPMENT	GO-0060322	22	0.236883	0.751412	0.816195	0.908441	1.000
553 GOBP-LONG-TERM-SYNAPTIC-DEPRESSION	GO-0060292	5	0.352008	0.748006	0.819165	0.911247	1.000
554 GOBP-CELLULAR-ION-HOMEOSTASIS	GO-0008873	14	0.263148	0.746604	0.794078	0.911592	1.000
555 GOBP-MITOCHONDRION-ORGANIZATION	GO-0007005	7	0.310399	0.742492	0.806967	0.915269	1.000
556 GOBP-NEURON-DEVELOPMENT	GO-0048666	33	0.209590	0.735766	0.809002	0.922335	1.000

Continuation of Table S16

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
557 GOBP-NEURON-DIFFERENTIATION	GO-0030182	36	0.213715	0.726414	0.828916	0.932489	1.000
558 GOBP-COAGULATION	GO-0050817	8	0.297789	0.725442	0.826761	0.932029	1.000
559 GOBP-EPITHELIAL-CELL-DIFFERENTIATION	GO-0030855	7	0.311233	0.725118	0.821429	0.930727	1.000
560 GOBP-REGULATION-OF-POSTSYNAPSE-ORGANIZATION	GO-0099175	6	0.326741	0.723270	0.824806	0.931485	1.000
561 GOBP-POSITIVE-REGULATION-OF-PROTEOLYSIS	GO-0045862	8	0.291015	0.722199	0.820550	0.931140	1.000
562 GOBP-REGULATION-OF-GTPASE-ACTIVITY	GO-0043087	5	0.342363	0.718798	0.855118	0.933698	1.000
563 GOBP-RESPONSE-TO-NUTRIENT	GO-0007584	5	0.335713	0.713776	0.852146	0.938057	1.000
564 GOBP-NEUROGENESIS	GO-0022008	40	0.201882	0.713425	0.837545	0.936812	1.000
565 REACTOME-TRANSCRIPTIONAL-REGULATION-BY-TP53	R-RNO-3700989	6	0.321822	0.713096	0.847458	0.935600	1.000
566 GOBP-POSITIVE-REGULATION-OF-MYELOID-LEUKOCYTE----	GO-0002763	6	0.314213	0.708836	0.858824	0.939093	1.000
567 GOBP-ORGANIC-HYDROXY-COMPOUND-TRANSPORT	GO-0015850	6	0.315467	0.707041	0.826023	0.939513	1.000
568 GOBP-NEGATIVE-REGULATION-OF-CATABOLIC-PROCESS	GO-0009895	6	0.281105	0.703266	0.834734	0.942368	1.000
569 HALLMARK-HYPOXIA	M5891	5	0.332456	0.702769	0.839637	0.941340	1.000
570 REACTOME-TRANSCRIPTIONAL-REGULATION-OF-WHITE-A---	R-RNO-381340	6	0.313055	0.702469	0.846847	0.940026	1.000
571 GOBP-REGULATION-OF-CELL-ACTIVATION	GO-0050865	8	0.278881	0.692941	0.861386	0.949342	1.000
572 GOBP-NERVOUS-SYSTEM-PROCESS	GO-0050877	38	0.201346	0.690816	0.854897	0.949999	1.000
573 GOBP-MEMBRANE-ORGANIZATION	GO-0061024	12	0.247880	0.682772	0.862797	0.957545	1.000
574 GOBP-RESPONSE-TO-OXIDATIVE-STRESS	GO-0006979	8	0.274812	0.682431	0.865248	0.956217	1.000
575 GOBP-RESPONSE-TO-REACTIVE-OXYGEN-SPECIES	GO-0000302	8	0.274812	0.680847	0.856330	0.956232	1.000
576 GOBP-NEGATIVE-REGULATION-OF-SYNAPTIC-TRANSMISSION	GO-0050805	5	0.302797	0.677124	0.895833	0.958410	1.000
577 GOBP-RESPONSE-TO-MONOSACCHARIDE	GO-0034284	6	0.319893	0.677009	0.874433	0.956879	1.000
578 GOBP-POSITIVE-REGULATION-OF-HYDROLASE-ACTIVITY	GO-0051345	16	0.227822	0.676636	0.878113	0.955644	1.000
579 GOBP-REGULATION-OF-AXOGENESIS	GO-0050770	7	0.288068	0.676066	0.868644	0.954620	1.000
580 GOBP-G-PROTEIN-COUPLED-RECEPTOR-SIGNALING-PATHWAY	GO-0007186	18	0.223313	0.676056	0.878828	0.952994	1.000
581 GOBP-RESPONSE-TO-CARBOHYDRATE	GO-1903131	7	0.291129	0.674017	0.887240	0.953485	1.000
582 GOBP-RESPONSE-TO-CARBOHYDRATE	GO-0009743	5	0.319893	0.671858	0.909375	0.954195	1.000
583 GOBP-ION-HOMEOSTASIS	GO-0050801	16	0.226014	0.667336	0.878378	0.957281	1.000
584 GOBP-CELL-PART-MORPHOGENESIS	GO-0032990	24	0.204069	0.664174	0.905897	0.958852	1.000
585 GOBP-CELLULAR-COMPONENT-MORPHOGENESIS	GO-0032989	24	0.204069	0.663606	0.894147	0.957788	1.000
586 GOBP-CELL-MORPHOGENESIS	GO-0000902	24	0.204069	0.659993	0.902378	0.959807	1.000
587 GOBP-MULTICELLULAR-ORGANISMAL-HOMEOSTASIS	GO-0048871	12	0.240227	0.659317	0.887671	0.958837	1.000
588 GOBP-REGULATION-OF-SYNAPSE-STRUCTURE-OR-ACTIVITY	GO-0050803	11	0.248887	0.657875	0.894366	0.958703	1.000
589 GOBP-CELL-JUNCTION-ASSEMBLY	GO-0034329	8	0.266507	0.653921	0.901288	0.960963	1.000
590 GOBP-POSITIVE-REGULATION-OF-HEMOPOIESIS	GO-1903708	7	0.275255	0.652232	0.904192	0.960964	1.000
591 GOBP-REGULATION-OF-PHOSPHOLIPASE-ACTIVITY	GO-0010517	6	0.284849	0.640894	0.917647	0.969926	1.000
592 GOBP-CHROMATIN-ORGANIZATION	GO-0006325	5	0.299886	0.638827	0.929003	0.970120	1.000
593 GOBP-TEMPERATURE-HOMEOSTASIS	GO-0001659	5	0.303063	0.638534	0.918836	0.968740	1.000
594 GOBP-REGULATION-OF-BODY-FLUID-LEVELS	GO-0050878	11	0.231723	0.637373	0.888738	0.968126	1.000
595 GOBP-REGULATION-OF-LIPASE-ACTIVITY	GO-0060191	6	0.284849	0.635814	0.910470	0.967887	1.000
596 GOBP-DEFENSE-RESPONSE	GO-0006952	19	0.198859	0.628519	0.922380	0.972454	1.000
597 GOBP-TAXIS	GO-0042330	14	0.217005	0.620908	0.910714	0.977097	1.000
598 GOBP-REGULATION-OF-MYELOID-CELL-DIFFERENTIATION	GO-0045637	9	0.241323	0.620662	0.907143	0.975657	1.000
599 GOBP-LONG-TERM-SYNAPTIC-POTENTIATION	GO-0060291	12	0.220013	0.619716	0.923611	0.974821	1.000

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NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
600 REACTOME_NEUREXINS_AND_NEUROLIGINS	R-RNO-6794361	9	0.242981	0.616868	0.926491	0.975482	1.000
601 GOBP_IMPORT_INTO_CELL	GO-0098657	6	0.270001	0.614051	0.916176	0.976052	1.000
602 GOBP_PROTEIN_LOCALIZATION_TO_PLASMA_MEMBRANE	GO-0072659	7	0.264032	0.612996	0.918759	0.975287	1.000
603 GOBP_BEHAVIOR	GO-0007610	32	0.180228	0.609970	0.945679	0.975952	1.000
604 GOBP_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENT...	GO-0002761	8	0.242378	0.604517	0.917012	0.978470	1.000
605 GOBP_RESPONSE_TO_BIOTIC_STIMULUS	GO-0009607	17	0.197730	0.603226	0.946738	0.977794	1.000
606 REACTOME_LONG_TERM_POTENTIATION	R-HSA-9620244	10	0.225161	0.594295	0.945302	0.982453	1.000
607 GOBP_ASSOCIATIVE_LEARNING	GO-0008306	7	0.255620	0.592860	0.935484	0.981834	1.000
608 GOBP_METAL_ION_TRANSPORT	GO-0030001	11	0.215412	0.587824	0.935441	0.983504	1.000
609 GOBP_LIPID_EXPORT_FROM_CELL	GO-0140353	5	0.275638	0.584391	0.945312	0.984160	1.000
610 HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	M5930	5	0.268031	0.583003	0.952160	0.983478	1.000
611 GOBP_CALCIIUM_ION_TRANSPORT	GO-0006816	11	0.215412	0.577884	0.941909	0.985009	1.000
612 REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION	R-RNO-73857	20	0.176889	0.561027	0.953905	0.992801	1.000
613 GOBP_CELLULAR_RESPONSE_TO_KETONE	GO-1901655	5	0.259139	0.550715	0.975904	0.996523	1.000
614 GOBP_RESPONSE_TO_MECHANICAL_STIMULUS	GO-0009612	6	0.243902	0.550654	0.973479	0.994921	1.000
615 REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATION	R-RNO-597592	7	0.234188	0.550396	0.969914	0.993431	1.000
616 GOBP_PEPITIDYL_LYSINE_MODIFICATION	GO-0018205	5	0.256173	0.549842	0.981482	0.992080	1.000
617 GOBP_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	GO-1902105	9	0.212615	0.540235	0.969609	0.994837	1.000
618 GOBP_CIRCULATORY_SYSTEM_PROCESS	GO-0003013	5	0.254032	0.539799	0.980798	0.993428	1.000
619 GOBP_METAL_ION_HOMEOSTASIS	GO-0005065	14	0.183963	0.535566	0.971698	0.993513	1.000
620 GOBP_AMINO_ACID_TRANSPORT	GO-0006865	6	0.237175	0.534135	0.981846	0.992465	1.000
621 GOBP_REGULATION_OF_HEMOPOIESIS	GO-1903706	10	0.201782	0.534026	0.967742	0.990893	1.000
622 GOBP_CARBOXYLIC_ACID_TRANSPORT	GO-0046942	6	0.237175	0.533323	0.971976	0.989580	1.000
623 GOBP_REGULATION_OF_CYTOSOLIC_CALCIIUM_ION_CONCE...	GO-0051480	13	0.186371	0.532482	0.970549	0.988294	1.000
624 GOBP_ORGANIC_ANION_TRANSPORT	GO-0015711	6	0.237175	0.532296	0.980031	0.986794	1.000
625 GOBP_DIVALENT_INORGANIC_CATION_HOMEOSTASIS	GO-0072507	13	0.163751	0.522581	0.972490	0.988855	1.000
626 GOBP_CELLULAR_RESPONSE_TO_ALCOHOL	GO-0097306	5	0.246986	0.511750	0.987988	0.990736	1.000
627 HALLMARK_TNFA_SIGNALING_VIA_NFKB	M5890	14	0.164738	0.473874	0.989390	0.997981	1.000
628 GOBP_POSITIVE_REGULATION_OF_NEURON_PROJECTION...	GO-0010976	5	0.213312	0.450531	0.998466	0.999848	1.000
629 GOBP_ORGANIC_ACID_TRANSPORT	GO-0015849	7	0.175111	0.420216	1.000000	1.000000	1.000
630 GOBP_POSITIVE_REGULATION_OF_PEPITIDYL_SERINE_PH...	GO-0033138	8	0.160609	0.413800	0.995726	0.999859	1.000
631 GOBP_REGULATION_OF_PEPITIDYL_SERINE_PHOSPHORYLA...	GO-0033135	8	0.160609	0.407824	1.000000	0.998574	1.000
632 GOBP_MONOAMINE_TRANSPORT	GO-0015844	5	-0.234939	-0.539969	0.983389	0.986805	1.000
633 GOBP_OSTEOCLAST_DIFFERENTIATION	GO-0030316	6	-0.215261	-0.551849	0.976676	0.994314	1.000
634 GOBP_RESPONSE_TO_KETONE	GO-1901654	7	-0.209877	-0.557894	0.980892	1.000000	1.000
635 GOBP_RESPONSE_TO_INTERLEUKIN_1	GO-0070555	5	-0.241161	-0.568188	0.985549	1.000000	1.000
636 GOBP_NEURON_DEATH	GO-0070997	18	-0.151896	-0.580561	0.958678	1.000000	1.000
637 GOBP_REGULATION_OF_CELL_SIZE	GO-0008361	5	-0.253012	-0.605023	0.964770	1.000000	1.000
638 GOBP_INORGANIC_ION_TRANSMEMBRANE_TRANSPORT	GO-0098660	9	-0.214062	-0.641498	0.927336	1.000000	1.000
639 GOBP_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	GO-0045670	5	-0.271720	-0.644746	0.929179	1.000000	1.000
640 GOBP_REGIONALIZATION	GO-0003002	6	-0.256098	-0.661413	0.928144	1.000000	1.000
641 GOBP_PATTERN_SPECIFICATION_PROCESS	GO-0007389	6	-0.256098	-0.664408	0.915584	1.000000	1.000
642 GOBP_AXON_DEVELOPMENT	GO-0061564	18	-0.168375	-0.665138	0.944186	1.000000	1.000

Continuation of Table S16

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	PWER.p.val
643	GOBP.INNATE.IMMUNE.RESPONSE	GO-0045087	7	-0.246914	-0.669381	0.867069	1.000000	1.000
644	GOBP.NEUTROPHIN.SIGNALING.PATHWAY	GO-0038179	6	-0.268293	-0.685256	0.880126	1.000000	1.000
645	GOBP.NEUTROPHIN_TTK.RECEPTOR.SIGNALING.PATHWAY	GO-0048011	6	-0.268293	-0.694379	0.877976	1.000000	1.000
646	GOBP.LONG.TERM.MEMORY	GO-0007616	6	-0.256098	-0.694480	0.891374	1.000000	1.000
647	REACTOME.ASSEMBLY.AND.CELL.SURFACE.PRESENTATIO...	R-RNO-9609736	8	-0.249903	-0.714602	0.852941	1.000000	1.000
648	REACTOME.NEGATIVE.REGULATION.OF.NMDA.RECEPTOR...	R-HSA-9617324	8	-0.243903	-0.732055	0.843949	1.000000	1.000
649	GOBP.RESPONSE.TO.ALCOHOL	GO-0097305	11	-0.221654	-0.742545	0.812950	1.000000	1.000
650	GOBP.DEFENSE.RESPONSE.TO.OTHER.ORGANISM	GO-0098542	9	-0.244763	-0.763849	0.775578	0.994076	1.000
651	GOBP.REGULATION.OF.PHOSPHOLIPASE.C.ACTIVITY	GO-1900274	5	-0.325301	-0.765502	0.789174	1.000000	1.000
652	GOBP.POSITIVE.REGULATION.OF.LIPASE.ACTIVITY	GO-0060193	5	-0.325301	-0.772834	0.753086	1.000000	1.000
653	GOBP.REGULATION.OF.MEMBRANE.POTENTIAL	GO-0042391	17	-0.205273	-0.774434	0.793860	1.000000	1.000
654	GOBP.CALCIUM.ION.TRANSMEMBRANE.TRANSPORT	GO-0070588	7	-0.283951	-0.777547	0.744548	1.000000	1.000
655	GOBP.CYTOSOLIC.CALCIUM.ION.TRANSPORT	GO-0060401	7	-0.283951	-0.779044	0.738853	1.000000	1.000
656	GOBP.NEURON.PROJECTION.GUIDANCE	GO-0097485	9	-0.261453	-0.785441	0.746875	1.000000	1.000
657	GOBP.CALCIUM.ION.TRANSPORT.INTO.CYTOSOL	GO-0060402	7	-0.283951	-0.788305	0.765060	1.000000	1.000
658	GOBP.EPHRIN.RECEPTOR.SIGNALING.PATHWAY	GO-0048013	5	-0.337349	-0.795211	0.719888	1.000000	1.000
659	REACTOME.ANTI.INFLAMMATORY.RESPONSE.FAVOURING...	R-HSA-9662851	5	-0.349398	-0.811318	0.699717	1.000000	1.000
660	GOBP.ADENYLATE.CYCLASE.MODULATING.G.PROTEIN.CO...	GO-0007188	11	-0.253295	-0.835694	0.668990	1.000000	1.000
661	REACTOME.SIGNALING.BY.NTRK2.TRK2	R-RNO-9006115	6	-0.329268	-0.837158	0.658147	1.000000	1.000
662	GOBP.POSITIVE.REGULATION.OF.CATION.TRANSMEMBRA...	GO-1904064	5	-0.349398	-0.847774	0.675439	1.000000	1.000
663	GOBP.CATION.TRANSPORT	GO-0006812	25	-0.200800	-0.854463	0.697561	1.000000	1.000
664	GOBP.EXCITATORY.CHEMICAL.SYNAPTIC.TRANSMISSION	GO-0098976	5	-0.368844	-0.866533	0.63846	0.996438	1.000
665	GOBP.FATTY.ACID.TRANSPORT	GO-0015908	6	-0.329268	-0.870402	0.591429	1.000000	1.000
666	GOBP.RESPONSE.TO.ETHANOL	GO-0045471	5	-0.367185	-0.874586	0.601173	1.000000	1.000
667	GOBP.RESPONSE.TO.DRUG	GO-0042493	11	-0.268354	-0.883165	0.641221	1.000000	1.000
668	GOBP.SENSORY.PERCEPTION.OF.PAIN	GO-0019233	5	-0.367579	-0.887802	0.531609	1.000000	1.000
669	GOBP.RESPONSE.TO.NERVE.GROWTH.FACTOR	GO-1990089	7	-0.333333	-0.889620	0.557276	1.000000	1.000
670	GOBP.ADENYLATE.CYCLASE.INHIBITING.G.PROTEIN.CO...	GO-0007193	9	-0.297020	-0.890131	0.593333	1.000000	1.000
671	REACTOME.INTERFERON.SIGNALING	R-RNO-913531	6	-0.353659	-0.898999	0.571429	1.000000	1.000
672	GOBP.REGULATION.OF.METAL.ION.TRANSPORT	GO-0010959	6	-0.353659	-0.907339	0.563798	1.000000	1.000
673	GOBP.REGULATION.OF.POSTSYNAPTIC.MEMBRANE.POTEN...	GO-0060078	14	-0.249274	-0.909562	0.581590	1.000000	1.000
674	GOBP.DICARBOXYLIC.ACID.TRANSPORT	GO-0006835	5	-0.396002	-0.925038	0.508065	1.000000	1.000
675	GOBP.NERVE.DEVELOPMENT	GO-0021675	9	-0.311409	-0.932972	0.517915	1.000000	1.000
676	GOBP.POSITIVE.REGULATION.OF.LONG.TERM.SYNAPTIC...	GO-1900273	5	-0.397590	-0.941043	0.462908	1.000000	1.000
677	GOBP.NEGATIVE.REGULATION.OF.PROTEIN.CATABOLIC...	GO-0042177	5	-0.404920	-0.946734	0.501577	1.000000	1.000
678	GOBP.ACIDIC.AMINO.ACID.TRANSPORT	GO-0015800	5	-0.396002	-0.951964	0.462567	1.000000	1.000
679	GOBP.MONOCARBOXYLIC.ACID.TRANSPORT	GO-0015718	5	-0.396002	-0.953832	0.510324	1.000000	1.000
680	GOBP.NEURON.APOPTOTIC.PROCESS	GO-0051402	12	-0.285176	-0.969210	0.488722	1.000000	1.000
681	GOBP.PROTEIN.COMPLEX.OLIGOMERIZATION	GO-0051259	6	-0.390244	-0.984699	0.444444	1.000000	1.000
682	GOBP.NEGATIVE.REGULATION.OF.NEURON.DEATH	GO-1901215	11	-0.296922	-0.993928	0.460993	1.000000	1.000
683	GOBP.REGULATION.OF.NEURON.DIFFERENTIATION	GO-0045664	5	-0.421687	-0.995958	0.404624	1.000000	1.000
684	GOBP.ADENYLATE.CYCLASE.INHIBITING.G.PROTEIN.CO...	GO-0007196	5	-0.424679	-1.019082	0.368732	1.000000	1.000
685	GOBP.REGULATION.OF.LONG.TERM.SYNAPTIC.POTENTIA...	GO-1900271	6	-0.402439	-1.025188	0.393082	1.000000	1.000

Continuation of Table S16

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
686 GOBP-CATION-TRANSMEMBRANE-TRANSPORT	GO-0098655	18	-0.259978	-1.025837	0.378855	1.000000	1.000
687 GOBP-REGULATION-OF-TRANSPORTER-ACTIVITY	GO-0032409	17	-0.270550	-1.027270	0.386555	1.000000	1.000
688 REACTOME-NEURONAL-SYSTEM	R-RNO-112316	26	-0.240174	-1.029561	0.390110	1.000000	1.000
689 REACTOME-TRAFFICKING-OF-AMPA-RECEPTORS	R-RNO-399719	11	-0.326846	-1.044494	0.355072	1.000000	1.000
690 REACTOME-DAG-AND-IP3-SIGNALING	R-RNO-1489509	8	-0.362500	-1.054230	0.368601	1.000000	1.000
691 GOBP-PERIPHERAL-NEUROUS-SYSTEM-DEVELOPMENT	GO-0007422	9	-0.341772	-1.072286	0.341297	1.000000	1.000
692 REACTOME-NEUROTRANSMITTER-RECEPTORS-AND-POSTSY...	R-RNO-112314	22	-0.264780	-1.074473	0.324074	1.000000	1.000
693 GOBP-REGULATION-OF-CATION-TRANSMEMBRANE-TRANSPORT	GO-1904062	16	-0.290334	-1.111868	0.321429	1.000000	1.000
694 REACTOME-ACTIVATION-OF-NMDA-RECEPTORS-AND-POST...	R-RNO-442755	16	-0.303180	-1.115232	0.330709	1.000000	1.000
695 GOBP-REGULATION-OF-SIGNALING-RECEPTOR-ACTIVITY	GO-0010469	14	-0.308697	-1.115484	0.270270	1.000000	1.000
696 REACTOME-TRANSCRIPTIONAL-REGULATION-BY-MECP2	R-RNO-8986944	7	-0.400512	-1.118382	0.273927	1.000000	1.000
697 REACTOME-TRANSMISSION-ACROSS-CHEMICAL-SYNAPSES	R-RNO-112315	23	-0.287669	-1.194233	0.216667	0.879095	1.000
698 GOBP-REGULATION-OF-NEUROTRANSMITTER-RECEPTOR-A...	GO-0099601	13	-0.343780	-1.197952	0.253012	0.908238	1.000
699 REACTOME-VESICLE-MEDIATED-TRANSPORT	R-RNO-5653656	5	-0.518072	-1.218409	0.198347	0.880527	1.000
700 REACTOME-MEMBRANE-TRAFFICKING	R-RNO-199991	5	-0.518072	-1.226903	0.201149	0.895837	1.000
701 GOBP-RESPONSE-TO-ALKALOID	GO-0043279	5	-0.530120	-1.242053	0.184358	0.892776	1.000
702 GOBP-REGULATION-OF-CATION-CHANNEL-ACTIVITY	GO-2001257	14	-0.344012	-1.242065	0.188679	0.945244	1.000
703 GOBP-REGULATION-OF-NEUROTRANSMITTER-TRANSPORT	GO-0051588	6	-0.487805	-1.248661	0.193651	0.978972	1.000
704 GOBP-VESICLE-MEDIATED-TRANSPORT-IN-SYNAPSE	GO-0099003	7	-0.456790	-1.250071	0.201220	1.000000	1.000
705 GOBP-NEUROTRANSMITTER-SECRETION	GO-0007269	6	-0.487805	-1.257625	0.179331	1.000000	1.000
706 REACTOME-UNBLOCKING-OF-NMDA-RECEPTORS-GLUTAMAT...	R-RNO-438066	12	-0.385784	-1.301319	0.125000	0.976863	1.000
707 REACTOME-PROTEIN-PROTEIN-INTERACTIONS-AT-SYNAPSES	R-RNO-6794362	12	-0.380925	-1.314834	0.132353	1.000000	1.000
708 REACTOME-TRAFFICKING-OF-GLUR2-CONTAINING-AMPA-...	R-RNO-416993	8	-0.468963	-1.343074	0.132492	0.972490	1.000
709 GOBP-NEUROTRANSMITTER-TRANSPORT	GO-0006836	7	-0.493827	-1.352076	0.149123	1.000000	1.000
710 GOBP-REGULATION-OF-NEUROTRANSMITTER-LEVELS	GO-0001505	7	-0.493827	-1.356853	0.103896	1.000000	1.000
711 GOBP-REGULATION-OF-NMDA-RECEPTOR-ACTIVITY	GO-2000310	10	-0.435820	-1.373401	0.104918	1.000000	1.000
712 GOBP-MEMORY	GO-0007613	13	-0.402633	-1.382369	0.108787	1.000000	1.000
713 REACTOME-SYNAPTIC-ADHESION-LIKE-MOLECULES	R-RNO-8849932	9	-0.475681	-1.442328	0.064286	1.000000	1.000
714 GOBP-GLUTAMATE-RECEPTOR-SIGNALING-PATHWAY	GO-0007215	17	-0.392060	-1.442749	0.074074	1.000000	1.000
715 GOBP-IONOTROPIC-GLUTAMATE-RECEPTOR-SIGNALING-P...	GO-0035235	9	-0.474252	-1.448275	0.088328	1.000000	1.000
716 GOBP-NEGATIVE-REGULATION-OF-NEURON-APOPTOTIC-P...	GO-0043524	8	-0.499217	-1.468829	0.057239	1.000000	1.000
717 GOBP-SENSORY-PERCEPTION	GO-0007600	9	-0.478823	-1.484719	0.071429	1.000000	1.000
718 REACTOME-G-ALPHA-Z-SIGNALING-EVENTS	R-RNO-418597	5	-0.674699	-1.613486	0.043353	1.000000	0.999

End of Table

Continuation of Table S17

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
41	GOBP-SYNAPSE_ORGANIZATION	17	0.367498	1.206755	0.193995	1.000000	1.000
42	GOBP-ANION_TRANSMEMBRANE_TRANSPORT	7	0.484816	1.202431	0.245119	1.000000	1.000
43	GOBP-POSITIVE_REGULATION_OF_CELL_CELL_ADHESION	5	0.566699	1.199950	0.258621	1.000000	1.000
44	GOBP-POSITIVE_REGULATION_OF_INTRACELLULAR_SIGN...	14	0.375734	1.193349	0.252294	1.000000	1.000
45	GOBP-POSITIVE_REGULATION_OF_CELL_PROJECTION_OR...	10	0.427649	1.184902	0.231626	1.000000	1.000
46	GOBP-RESPONSE_TO_ETHANOL	5	0.542169	1.183501	0.296460	1.000000	1.000
47	HALLMARK-APOPTOSIS	6	0.510464	1.178983	0.266385	1.000000	1.000
48	GOBP-POSITIVE_REGULATION_OF_CELLULAR_COMPONENT...	9	0.434788	1.169869	0.261641	1.000000	1.000
49	GOBP-REGULATION_OF_CELL_DEVELOPMENT	15	0.370353	1.157085	0.290179	1.000000	1.000
50	GOBP-POSITIVE_REGULATION_OF_MYELOID_LEUKOCYTE...	6	0.503249	1.156960	0.303226	1.000000	1.000
51	GOBP-SYNAPTIC_TRANSMISSION_GUTAMATERGIC	13	0.384734	1.156334	0.260090	1.000000	1.000
52	GOBP-REGULATION_OF_CELLULAR_CATABOLIC_PROCESS	10	0.416026	1.156097	0.261574	1.000000	1.000
53	GOBP-POSITIVE_REGULATION_OF_PHOSPHATIDYLINOSIT...	5	0.538615	1.152584	0.316929	1.000000	1.000
54	GOBP-POSITIVE_REGULATION_OF_CELL_DEVELOPMENT	12	0.379869	1.150691	0.272517	1.000000	1.000
55	GOBP-POSITIVE_REGULATION_OF_SYNAPTIC_TRANSMISSION	15	0.365869	1.148001	0.274882	1.000000	1.000
56	GOBP-REGULATION_OF_SYNAPTIC_TRANSMISSION_GLUTA...	12	0.390195	1.145650	0.281250	1.000000	1.000
57	GOBP-POSITIVE_REGULATION_OF_PROTEIN_KINASE_ACT...	19	0.379022	1.141511	0.274827	1.000000	1.000
58	GOBP-REGULATION_OF_POSTSYNAPSE_ORGANIZATION	6	0.498165	1.137474	0.307036	1.000000	1.000
59	GOBP-POSITIVE_REGULATION_OF_LONG_TERM_SYNAPTIC...	5	0.526397	1.134293	0.326489	1.000000	1.000
60	GOBP-POSITIVE_REGULATION_OF_CELL_GROWTH	6	0.477160	1.131145	0.321962	1.000000	1.000
61	GOBP-REGULATION_OF_CATION_CHANNEL_ACTIVITY	14	0.360711	1.129517	0.286667	1.000000	1.000
62	REACTOME-ASSEMBLY_AND_CELL_SURFACE_PRESENTATIO...	8	0.438776	1.128746	0.292411	1.000000	1.000
63	GOBP-POSITIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL...	5	0.518698	1.128432	0.347107	1.000000	1.000
64	GOBP-POSITIVE_REGULATION_OF_TRANSFERASE_ACTIVITY	20	0.329227	1.125665	0.286976	1.000000	1.000
65	GOBP-MEMBRANE_PROTEIN_PROTEOLYSIS	6	0.485537	1.122872	0.318275	1.000000	1.000
66	GOBP-REGULATION_OF_INTRACELLULAR_SIGNAL_TRANSD...	21	0.325240	1.121250	0.291866	1.000000	1.000
67	REACTOME-NEGATIVE_REGULATION_OF_NMDA_RECEPTOR...	8	0.437876	1.115430	0.317181	1.000000	1.000
68	GOBP-POSITIVE_REGULATION_OF_NEUROGENESIS	12	0.379869	1.113779	0.310421	1.000000	1.000
69	REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM	21	0.323308	1.109734	0.294664	1.000000	1.000
70	GOBP-REGIONALIZATION	6	0.471138	1.108806	0.321962	1.000000	1.000
71	GOBP-NEUROINFLAMMATORY_RESPONSE	5	0.505053	1.107442	0.344262	1.000000	1.000
72	GOBP-RECEPTOR_INTERNALIZATION	5	0.504324	1.107137	0.343313	1.000000	1.000
73	GOBP-POSITIVE_REGULATION_OF_NERVOUS_SYSTEM_DEV...	12	0.379869	1.099315	0.350000	1.000000	1.000
74	GOBP-PATTERN_SPECIFICATION_PROCESS	6	0.471138	1.096640	0.330595	1.000000	1.000
75	GOBP-CALCIUM-MEDIATED_SIGNALING	10	0.400984	1.095929	0.334047	1.000000	1.000
76	GOBP-POSITIVE_REGULATION_OF_DNA_BINDING_TRANSC...	10	0.398091	1.095271	0.327434	1.000000	1.000
77	GOBP-CHEMICAL_SYNAPTIC_TRANSMISSION_POSTSYNAPTIC	9	0.406591	1.088896	0.361419	1.000000	1.000
78	GOBP-REGULATION_OF_CATABOLIC_PROCESS	13	0.358236	1.086171	0.345416	1.000000	1.000
79	GOBP-RECEPTOR_METABOLIC_PROCESS	5	0.504324	1.082956	0.364017	1.000000	1.000
80	REACTOME-DEVELOPMENTAL_BIOLOGY	23	0.311160	1.081602	0.340090	1.000000	1.000
81	REACTOME_LONG_TERM_POTENTIATION	10	0.393010	1.081486	0.359140	1.000000	1.000
82	REACTOME_SYNAPTIC_ADHESION_LIKE_MOLECULES	9	0.402539	1.079910	0.350731	1.000000	1.000
83	GOBP-NEGATIVE_REGULATION_OF_CATABOLIC_PROCESS	8	0.416918	1.070067	0.354626	1.000000	1.000

Continuation of Table S17

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
84 GOBP-NEGATIVE-REGULATION-OF-PEPTIDASE-ACTIVITY	GO-0010466	6	0.471463	1.077746	0.371179	1.000000	1.000
85 GOBP-BIOLOGICAL-PROCESS-INVOLVED-IN-SYMBIOTIC....	GO-004440	11	0.381215	1.077044	0.371495	1.000000	1.000
86 GOBP-REGULATION-OF-PROTEIN-CATABOLIC-PROCESS	GO-0042176	7	0.434353	1.076275	0.362869	1.000000	1.000
87 REACTOME-ACTIVATION-OF-NMDA-RECEPTORS-AND-POST...	R-RNO-442755	16	0.337730	1.075855	0.350515	1.000000	1.000
88 GOBP-DEVELOPMENTAL-MATURATION	GO-0021700	5	0.501132	1.075507	0.395299	1.000000	1.000
89 GOBP-LEARNING	GO-0007612	13	0.355124	1.075018	0.343750	1.000000	1.000
90 GOBP-NEGATIVE-REGULATION-OF-LOCOMOTION	GO-0040013	5	0.490676	1.070620	0.403614	1.000000	1.000
91 GOBP-SMALL-GTPASE-MEDIATED-SIGNAL-TRANSDUCTION	GO-0007264	8	0.407477	1.066816	0.364583	1.000000	1.000
92 GOBP-AMEBOIDAL-TYPE-CELL-MIGRATION	GO-0001667	11	0.371425	1.061049	0.374449	1.000000	1.000
93 GOBP-POSITIVE-REGULATION-OF-PROTEIN-TYROSINE-K...	GO-0061098	5	0.489330	1.059815	0.388664	1.000000	1.000
94 GOBP-REGULATION-OF-VASCULATURE-DEVELOPMENT	GO-1901342	5	0.494091	1.059164	0.397727	1.000000	1.000
95 GOBP-REGULATION-OF-MEMBRANE-POTENTIAL	GO-0042391	17	0.325084	1.058898	0.383178	1.000000	1.000
96 GOBP-GLIAL-CELL-DIFFERENTIATION	GO-0010001	10	0.386239	1.058745	0.344754	1.000000	1.000
97 GOBP-CELL-MIGRATION	GO-0016477	22	0.299695	1.058637	0.373239	1.000000	1.000
98 GOBP-MAINTENANCE-OF-LOCATION	GO-0051235	7	0.445555	1.058433	0.375271	1.000000	1.000
99 GOBP-REGULATION-OF-PROTEIN-TYROSINE-KINASE-ACT...	GO-0061097	5	0.489330	1.055188	0.407834	1.000000	1.000
100 GOBP-REGULATION-OF-PEPTIDE-SECRETION	GO-0002791	7	0.418152	1.049450	0.406393	1.000000	1.000
101 GOBP-OSTEOBLAST-DIFFERENTIATION	GO-0001649	5	0.476929	1.045568	0.405063	1.000000	1.000
102 GOBP-POSITIVE-REGULATION-OF-ION-TRANSPORT	GO-0043270	17	0.310992	1.044829	0.378076	1.000000	1.000
103 GOBP-REGULATION-OF-ENDOTHELIAL-CELL-MIGRATION	GO-0010594	5	0.416726	1.044273	0.411628	1.000000	1.000
104 GOBP-ASSOCIATIVE-LEARNING	GO-0008306	7	0.418025	1.041709	0.405579	1.000000	1.000
105 GOBP-REGULATION-OF-MAP-KINASE-ACTIVITY	GO-0024111	6	0.451399	1.039386	0.405830	1.000000	1.000
106 GOBP-CELLULAR-COMPONENT-DISASSEMBLY	GO-0043406	6	0.437450	1.038454	0.412903	1.000000	1.000
107 GOBP-POSITIVE-REGULATION-OF-MAP-KINASE-ACTIVITY	GO-0006954	12	0.359969	1.037183	0.396514	1.000000	1.000
108 GOBP-INFLAMMATORY-RESPONSE	GO-0006006	6	0.442840	1.032139	0.415778	1.000000	1.000
109 GOBP-GLUCOSE-METABOLIC-PROCESS	GO-0009057	12	0.349866	1.031642	0.404922	1.000000	1.000
110 GOBP-MACROMOLECULE-CATABOLIC-PROCESS	GO-0045859	22	0.293744	1.028128	0.401478	1.000000	1.000
111 GOBP-REGULATION-OF-PROTEIN-KINASE-ACTIVITY	GO-0005996	6	0.442840	1.026317	0.422078	1.000000	1.000
112 GOBP-MONOSACCHARIDE-METABOLIC-PROCESS	GO-0043085	30	0.272058	1.026071	0.427184	1.000000	1.000
113 GOBP-POSITIVE-REGULATION-OF-CATALYTIC-ACTIVITY	GO-0051270	15	0.327632	1.024178	0.433036	1.000000	1.000
114 GOBP-REGULATION-OF-CELLULAR-COMPONENT-MOVEMENT	GO-0050900	6	0.439851	1.016347	0.451745	1.000000	1.000
115 GOBP-LEUKOCYTE-MIGRATION	GO-0043933	14	0.323505	1.012129	0.432314	1.000000	1.000
116 GOBP-PROTEIN-CONTAINING-COMPLEX-SUBUNIT-ORGANI...	GO-0034330	19	0.303180	1.012069	0.422062	1.000000	1.000
117 GOBP-CELL-JUNCTION-ORGANIZATION	GO-0051338	22	0.293744	1.009808	0.415423	1.000000	1.000
118 GOBP-REGULATION-OF-TRANSFERASE-ACTIVITY	R-RNO-9675108	15	0.321819	1.008948	0.463470	1.000000	1.000
119 REACTOME-NERVOUS-SYSTEM-DEVELOPMENT	GO-1903708	7	0.420502	1.002097	0.445148	1.000000	1.000
120 GOBP-POSITIVE-REGULATION-OF-HEMOPOIESIS	GO-0006518	12	0.338941	0.995506	0.436242	1.000000	1.000
121 GOBP-PEPTIDE-METABOLIC-PROCESS	GO-000187	6	0.437450	0.991307	0.470982	1.000000	1.000
122 GOBP-ACTIVATION-OF-MAPK-ACTIVITY	GO-0097191	7	0.407963	0.989224	0.441176	1.000000	1.000
123 GOBP-EXTRINSIC-APOPTOTIC-SIGNALING-PATHWAY	GO-0060292	5	0.448846	0.987093	0.477974	1.000000	1.000
124 GOBP-LONG-TERM-SYNAPTIC-DEPRESSION	GO-0008361	5	0.455062	0.986457	0.465217	1.000000	1.000
125 GOBP-REGULATION-OF-CELL-SIZE	GO-0060078	14	0.322480	0.983107	0.475059	1.000000	1.000
126 GOBP-REGULATION-OF-POSTSYNAPTIC-MEMBRANE-POTEN...							

Continuation of Table S17

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
127	GOBP-REGULATION-OF_GLIOGENESIS	5	0.450503	0.977214	0.484009	1.000000	1.000
128	GOBP-RESPONSE-TO_NERVE_GROWTH_FACTOR	7	0.407407	0.972910	0.474012	1.000000	1.000
129	GOBP-CELLULAR-AMIDE-METABOLIC-PROCESS	13	0.324687	0.969786	0.484234	1.000000	1.000
130	GOBP-REGULATION-OF_EXTRINSIC_APOPTOTIC_SIGNALING...	6	0.417758	0.967784	0.511677	1.000000	1.000
131	GOBP-MULTICELLULAR-ORGANISMAL-RESPONSE-TO_STRESS	5	0.445724	0.966886	0.479570	1.000000	1.000
132	GOBP-REGULATION-OF_DEVELOPMENTAL_GROWTH	9	0.364100	0.965483	0.516269	1.000000	1.000
133	GOBP-POSITIVE-REGULATION-OF_BINDING	6	0.413650	0.963924	0.484979	1.000000	1.000
134	GOBP-POSITIVE-REGULATION-OF_GLIOGENESIS	5	0.450503	0.963718	0.495868	1.000000	1.000
135	GOBP-REGULATION-OF_CELL_PROJECTION_ORGANIZATION	20	0.283550	0.957109	0.502222	1.000000	1.000
136	HALLMARK-EPITHELIAL-MESENCHYMAL-TRANSITION	5	0.438653	0.955454	0.524590	1.000000	1.000
137	GOBP-DENDRITE-DEVELOPMENT	9	0.364871	0.953309	0.531959	1.000000	1.000
138	GOBP-NEGATIVE-REGULATION-OF_APOPTOTIC_SIGNALING...	7	0.387210	0.947575	0.505643	1.000000	1.000
139	GOBP-LEUKOCYTE-CELL-CELL-ADHESION	6	0.415721	0.946043	0.516340	1.000000	1.000
140	GOBP-LIPID-METABOLIC-PROCESS	10	0.351092	0.945994	0.489177	1.000000	1.000
141	GOBP-REGULATION-OF-OSTEOCLAST-DIFFERENTIATION	5	0.443696	0.944510	0.548387	1.000000	1.000
142	GOBP-REGULATION-OF-EPITHELIAL-CELL-MIGRATION	6	0.402629	0.939678	0.521839	1.000000	1.000
143	GOBP-NEGATIVE-REGULATION-OF_CELL-DEVELOPMENT	6	0.398058	0.937006	0.520971	1.000000	1.000
144	GOBP-POSITIVE-REGULATION-OF-PEPTIDYL-SERINE-PH...	8	0.365276	0.936772	0.534216	1.000000	1.000
145	GOBP-POSITIVE-REGULATION-OF_MYELOID-CELL_DIFFER...	7	0.371227	0.935273	0.557576	1.000000	1.000
146	GOBP-POSITIVE-REGULATION-OF_DEVELOPMENTAL-PROCESS	32	0.249967	0.934314	0.563380	1.000000	1.000
147	REACTOME-INFECTIOUS-DISEASE	13	0.303754	0.932967	0.498824	1.000000	1.000
148	GOBP-CELL-SURFACE-RECEPTOR-SIGNALING-PATHWAY-I...	15	0.298042	0.927256	0.544643	1.000000	1.000
149	GOBP-POSITIVE-REGULATION-OF_CELL-ADHESION	7	0.382311	0.928428	0.551148	1.000000	1.000
150	GOBP-POSITIVE-REGULATION-OF_LOCOMOTION	11	0.328671	0.927256	0.548753	1.000000	1.000
151	GOBP-POSITIVE-REGULATION-OF_HYDROLASE-ACTIVITY	16	0.282051	0.925516	0.557920	1.000000	1.000
152	GOBP-REGULATION-OF-PEPTIDYL-SERINE-PHOSPHORYLA...	8	0.365276	0.922288	0.520607	1.000000	1.000
153	GOBP-REGULATION-OF-NEUROGENESIS	14	0.304957	0.921722	0.562637	1.000000	1.000
154	GOBP-POSITIVE-REGULATION-OF_SMALL-MOLECULE-MET...	5	0.431685	0.917948	0.566160	1.000000	1.000
155	GOBP-LONG-TERM-MEMORY	6	0.403833	0.916711	0.556769	1.000000	1.000
156	GOBP-DICARBOXYLIC-ACID-TRANSPORT	5	0.425305	0.914108	0.551579	1.000000	1.000
157	GOBP-PROTEOLYSIS	17	0.277918	0.911478	0.580645	1.000000	1.000
158	GOBP-ACIDIC-AMINO-ACID-TRANSPORT	5	0.425305	0.909964	0.567194	1.000000	1.000
159	GOBP-MONOCARBOXYLIC-ACID-TRANSPORT	5	0.425305	0.906268	0.567265	1.000000	1.000
160	GOBP-PHAGOCYTOSIS	5	0.425305	0.905543	0.590810	1.000000	1.000
161	GOBP-REGULATION-OF_NERVOUS_SYSTEM_DEVELOPMENT	15	0.283040	0.902900	0.584245	1.000000	1.000
162	GOBP-REGULATION-OF_NERVOUS_SYSTEM_PROCESS	8	0.360080	0.902207	0.548246	1.000000	1.000
163	GOBP-PROTEIN_CATABOLIC-PROCESS	8	0.356101	0.896435	0.588636	1.000000	1.000
164	GOBP-OSTEOCLAST-DIFFERENTIATION	6	0.393031	0.896094	0.577825	1.000000	1.000
165	GOBP-DEFENSE-RESPONSE	19	0.267423	0.894638	0.623810	1.000000	1.000
166	GOBP-REGULATION-OF_BINDING	11	0.306993	0.889018	0.598699	1.000000	1.000
167	GOBP-DEVELOPMENTAL-GROWTH	10	0.327520	0.887204	0.594714	1.000000	1.000
168	GOBP-FATTY-ACID-TRANSPORT	6	0.384886	0.884425	0.614256	1.000000	1.000
169	REACTOME-CREB1-PHOSPHORYLATION-THROUGH_NMDA_RE...	8	0.357587	0.883979	0.609244	1.000000	1.000

Continuation of Table S17

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
170	GOBP-GLIOGENESIS	12	0.294140	0.876877	0.619835	1.000000	1.000
171	GOBP-IGNOTROPIC-GLUTAMATE-RECEPTOR-SIGNALING.P...	9	0.325609	0.874038	0.633640	1.000000	1.000
172	GOBP-CARBOHYDRATE-DERIVATIVE-METABOLIC-PROCESS	7	0.358171	0.868516	0.614512	1.000000	1.000
173	GOBP-REGULATION-OF-ANION-TRANSMEMBRANE-TRANSPORT	5	0.396508	0.861733	0.640000	1.000000	1.000
174	GOBP-REGULATION-OF-MITOTIC-CELL-CYCLE	5	0.398101	0.856412	0.605603	1.000000	1.000
175	GOBP-REGULATION-OF-RECEPTOR-MEDIATED-ENDOCYTOSIS	5	0.389182	0.856377	0.642105	1.000000	1.000
176	HALLMARK-P13K-AKT-MTOR-SIGNALING	6	0.379046	0.856030	0.623950	1.000000	1.000
177	GOBP-REGULATION-OF-DEFENSE-RESPONSE	7	0.344986	0.855838	0.621681	1.000000	1.000
178	GOBP-REGULATION-OF-PHOSPHATIDYLINOSITOL-3-KINA...	6	0.365162	0.853868	0.645570	1.000000	1.000
179	GOBP-POSITIVE-REGULATION-OF-IMMUNE-SYSTEM-PROCESS	18	0.259599	0.853585	0.695175	1.000000	1.000
180	GOBP-RESPONSE-TO-ACID-CHEMICAL	6	0.356119	0.849036	0.612159	1.000000	1.000
181	GOBP-CATION-TRANSPORT	25	0.239421	0.847218	0.696471	1.000000	1.000
182	GOBP-NEURON-PROJECTION-GUIDANCE	9	0.315733	0.846694	0.646018	1.000000	1.000
183	GOBP-ORGANONITROGEN-COMPOUND-CATABOLIC-PROCESS	9	0.314072	0.845971	0.654945	1.000000	1.000
184	GOBP-REGULATION-OF-CELLULAR-COMPONENT-BIOGENESIS	10	0.311204	0.845318	0.634146	1.000000	1.000
185	GOBP-REGULATION-OF-INFLAMMATORY-RESPONSE	7	0.344986	0.844846	0.639013	1.000000	1.000
186	GOBP-OSSIFICATION	9	0.321536	0.843701	0.673709	1.000000	1.000
187	GOBP-NEGATIVE-REGULATION-OF-CATALYTIC-ACTIVITY	17	0.265127	0.843126	0.688940	1.000000	1.000
188	GOBP-INOSITOL-LIPID-MEDIATED-SIGNALING	8	0.325680	0.840450	0.664516	1.000000	1.000
189	GOBP-REGULATION-OF-METAL-ION-TRANSPORT	6	0.366070	0.839500	0.649378	1.000000	1.000
190	GOBP-BLOOD-VESSEL-ENDOTHELIAL-CELL-MIGRATION	8	0.324666	0.839001	0.629956	1.000000	1.000
191	GOBP-EMBRYO-DEVELOPMENT	14	0.271175	0.838341	0.697674	1.000000	1.000
192	GOBP-NEGATIVE-REGULATION-OF-PROTEOLYSIS	8	0.329330	0.838054	0.672234	1.000000	1.000
193	GOBP-ORGANIC-ANION-TRANSPORT	6	0.359263	0.837877	0.612903	1.000000	1.000
194	REACTOME-ANTI-INFLAMMATORY-RESPONSE-FAVOURING...	5	0.392749	0.837121	0.676349	1.000000	1.000
195	GOBP-ENDOTHELIAL-CELL-MIGRATION	8	0.324666	0.836888	0.658174	1.000000	1.000
196	GOBP-AMINO-ACID-TRANSPORT	6	0.359263	0.837728	0.651163	1.000000	1.000
197	GOBP-REGULATION-OF-TRANSPORTER-ACTIVITY	17	0.257673	0.833500	0.704104	1.000000	1.000
198	GOBP-POSITIVE-REGULATION-OF-CELLULAR-COMPONENT...	24	0.228588	0.830867	0.719626	1.000000	1.000
199	GOBP-ORGANOPHOSPHATE-METABOLIC-PROCESS	7	0.335993	0.829930	0.659836	1.000000	1.000
200	REACTOME-TOLL-LIKE-RECEPTOR-TLR1-TLR2-CASCADE	8	0.318183	0.828919	0.639130	1.000000	1.000
201	GOBP-NEGATIVE-REGULATION-OF-MULTICELLULAR-ORGA...	15	0.263888	0.825812	0.722222	1.000000	1.000
202	GOBP-ERK1-AND-ERK2-CASCADE	5	0.380414	0.824145	0.696099	1.000000	1.000
203	GOBP-POSITIVE-REGULATION-OF-MOLECULAR-FUNCTION	38	0.212001	0.823991	0.741206	1.000000	1.000
204	REACTOME-TOLL-LIKE-RECEPTOR-CASCADES	8	0.318183	0.822216	0.686147	1.000000	1.000
205	GOBP-POSITIVE-REGULATION-OF-DEVELOPMENTAL-GROWTH	7	0.322491	0.821554	0.699317	1.000000	1.000
206	GOBP-PHOSPHATIDYLINOSITOL-3-KINASE-SIGNALING	8	0.332870	0.820578	0.653445	1.000000	1.000
207	GOBP-NEGATIVE-REGULATION-OF-GENE-EXPRESSION	12	0.281832	0.820019	0.672414	1.000000	1.000
208	GOBP-ION-HOMEOSTASIS	16	0.260396	0.814869	0.709800	1.000000	1.000
209	GOBP-CARBOXYLIC-ACID-TRANSPORT	6	0.359263	0.811294	0.675676	1.000000	1.000
210	GOBP-MYOTUBE-DIFFERENTIATION	5	0.371388	0.810892	0.697425	1.000000	1.000
211	GOBP-REGULATION-OF-MUSCLE-CELL-DIFFERENTIATION	6	0.354563	0.810393	0.699789	1.000000	1.000
212	GOBP-HEART-DEVELOPMENT	6	0.347103	0.809820	0.704782	1.000000	1.000

Continuation of Table S17

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
213	GOBP-ORGANIC-ACID-TRANSPORT	GO-0015849	7	0.329990	0.808744	0.664336	1.000000	1.000
214	GOBP-ADENYLATE-CYCLASE-INHIBITING-G-PROTEIN.CO...	GO-0007193	5	0.367498	0.805808	0.684322	1.000000	1.000
215	REACTOME-TOLL-LIKE-RECEPTOR-9-TLR9-CASCADE	R-RNO-168138	8	0.318183	0.805366	0.695279	1.000000	1.000
216	GOBP-IN-UTERO-EMBRYONIC-DEVELOPMENT	GO-0001701	8	0.317241	0.803982	0.709607	1.000000	1.000
217	GOBP-RESPONSE-TO-NUTRIENT	GO-0007584	5	0.373494	0.803456	0.706383	1.000000	1.000
218	GOBP-MUSCLE-CELL-DEVELOPMENT	GO-0005001	5	0.380880	0.802668	0.712153	1.000000	1.000
219	REACTOME-MYD88-INDEPENDENT-TLR4-CASCADE	R-RNO-166166	8	0.318183	0.801749	0.700214	1.000000	1.000
220	GOBP-RECEPTOR-MEDIATED-ENDOCYTOSIS	GO-0006898	6	0.349180	0.800684	0.692771	1.000000	1.000
221	GOBP-REGULATION-OF-PEPTIDASE-ACTIVITY	GO-00052547	10	0.292289	0.796440	0.712389	1.000000	1.000
222	GOBP-CARDIAC-MUSCLE-TISSUE-DEVELOPMENT	GO-00048738	6	0.347103	0.795046	0.702643	1.000000	1.000
223	GOBP-INORGANIC-ION-TRANSMEMBRANE-TRANSPORT	GO-00098660	9	0.302462	0.789109	0.737443	1.000000	1.000
224	GOBP-REGULATION-OF-ENDOCYTOSIS	GO-00030100	6	0.337786	0.783627	0.740506	1.000000	1.000
225	GOBP-POSITIVE-REGULATION-OF-MAPK-CASCADE	GO-00043410	9	0.290787	0.781524	0.746204	1.000000	1.000
226	GOBP-REGULATION-OF-PROTEIN-LOCALIZATION-TO-CEL...	GO-1904375	6	0.343577	0.780996	0.723577	1.000000	1.000
227	REACTOME-EXTRACELLULAR-MATRIX-ORGANIZATION	R-RNO-1474244	5	0.355376	0.780906	0.754132	1.000000	1.000
228	GOBP-RAS-PROTEIN-SIGNAL-TRANSDUCTION	GO-0007265	5	0.354766	0.778564	0.719123	1.000000	1.000
229	GOBP-MAPK-CASCADE	GO-0000165	18	0.237574	0.778521	0.791011	1.000000	1.000
230	GOBP-POSITIVE-REGULATION-OF-GROWTH	GO-00045927	9	0.296827	0.777671	0.740000	1.000000	1.000
231	GOBP-IMPORT-INTO-CELL	GO-00098657	6	0.347569	0.777326	0.753275	1.000000	1.000
232	GOBP-GENERATION-OF-PRECURSOR-METABOLITES-AND-E...	GO-0006091	5	0.358021	0.773973	0.758621	1.000000	1.000
233	GOBP-REGULATION-OF-MUSCLE-ADAPTATION	GO-00043502	5	0.355997	0.770206	0.752083	1.000000	1.000
234	GOBP-NEGATIVE-REGULATION-OF-RESPONSE-TO-EXTERN...	GO-0032102	5	0.357464	0.768025	0.752119	1.000000	1.000
235	GOBP-CALCIUM-ION-TRANSPORT	GO-0000816	11	0.259740	0.767802	0.783158	1.000000	1.000
236	GOBP-CELL-GROWTH	GO-0016049	10	0.273934	0.764706	0.776824	1.000000	1.000
237	GOBP-TELECEPHALON-DEVELOPMENT	GO-0021537	6	0.329295	0.763871	0.776000	1.000000	1.000
238	REACTOME-MAPK-FAMILY-SIGNALING-CASCADES	R-RNO-5683057	12	0.259837	0.760389	0.804989	1.000000	1.000
239	GOBP-REGULATION-OF-VASCULAR-ASSOCIATED-SMOOTH...	GO-1904705	5	0.360374	0.760343	0.742739	1.000000	1.000
240	REACTOME-POST-TRANSLATIONAL-PROTEIN-MODIFICATION	R-RNO-597592	7	0.305997	0.757408	0.772727	1.000000	1.000
241	GOBP-EMBRYO-DEVELOPMENT-ENDING-IN-BIRTH-OR-EGG...	GO-0009792	9	0.282313	0.751503	0.780702	1.000000	1.000
242	GOBP-SMOOTH-MUSCLE-CELL-PROLIFERATION	GO-00048659	6	0.322037	0.749119	0.790948	1.000000	1.000
243	GOBP-CELL-MORPHOGENESIS-INVOLVED-IN-DIFFERENTI...	GO-0000904	21	0.215358	0.748977	0.803097	1.000000	1.000
244	GOBP-CYTOSOLIC-CALCIUM-ION-TRANSPORT	GO-00060401	7	0.310150	0.745409	0.761388	1.000000	1.000
245	GOBP-ACTIVATION-OF-IMMUNE-RESPONSE	GO-0002253	5	0.343390	0.744703	0.766004	1.000000	1.000
246	GOBP-CALCIUM-ION-TRANSPORT-INTO-CYTOSOL	GO-00060402	7	0.310150	0.744586	0.773389	1.000000	1.000
247	GOBP-METAL-ION-TRANSPORT	GO-00030001	11	0.259740	0.740979	0.781116	1.000000	1.000
248	GOBP-MUSCLE-ADAPTATION	GO-00043500	5	0.355997	0.740367	0.808791	1.000000	1.000
249	GOBP-CALCIUM-ION-TRANSMEMBRANE-TRANSPORT	GO-00070588	7	0.310150	0.739938	0.780172	1.000000	1.000
250	GOBP-REGULATION-OF-IMMUNE-RESPONSE	GO-00050776	12	0.249068	0.738205	0.820000	1.000000	1.000
251	GOBP-PURINE-CONTAINING-COMPOUND-METABOLIC-PROCESS	GO-00072521	5	0.349788	0.737375	0.792123	1.000000	1.000
252	GOBP-CARBOHYDRATE-METABOLIC-PROCESS	GO-00059575	9	0.274287	0.735193	0.812095	1.000000	1.000
253	REACTOME-TRANSCRIPTIONAL-REGULATION-BY_TP53	R-RNO-3700989	6	0.319635	0.734475	0.797040	1.000000	1.000
254	GOBP-STRIPATED-MUSCLE-CELL-DIFFERENTIATION	GO-00051146	9	0.276853	0.734353	0.803738	1.000000	1.000
255	GOBP-CELL-MORPHOGENESIS-INVOLVED-IN-NEURON-DIF...	GO-00048667	21	0.215358	0.734223	0.849462	1.000000	1.000

Continuation of Table S17

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
256	GOBP-LONG-TERM-SYNAPTIC-POTENTIATION	12	0.247401	0.731094	0.805621	1.000000	1.000
257	GOBP-RESPONSE-TO-UV	5	0.337143	0.725460	0.792812	1.000000	1.000
258	GOBP-NEGATIVE-REGULATION-OF-PROTEIN-CATABOLIC...	5	0.337883	0.725332	0.808102	1.000000	1.000
259	GOBP-POSITIVE-REGULATION-OF-PROTEIN-SERINE-THR...	9	0.272946	0.722368	0.813901	1.000000	1.000
260	GOBP-REGULATION-OF-NEURON-PROJECTION-DEVELOPMENT	16	0.223822	0.722330	0.827354	1.000000	1.000
261	GOBP-EPITHELIAL-CELL-DIFFERENTIATION	7	0.300703	0.719321	0.794372	1.000000	1.000
262	GOBP-PEPTIDE-SECRETION	9	0.268923	0.718667	0.823529	1.000000	1.000
263	GOBP-BIOLOGICAL-ADHESION	19	0.211763	0.715531	0.853881	1.000000	1.000
264	GOBP-PERIPHERAL-NERVOUS-SYSTEM-DEVELOPMENT	9	0.265823	0.712362	0.815287	1.000000	1.000
265	GOBP-SMALL-MOLECULE-METABOLIC-PROCESS	15	0.225565	0.710981	0.852495	1.000000	1.000
266	GOBP-POSITIVE-REGULATION-OF-NEURON-DEATH	5	0.326391	0.708261	0.819302	1.000000	1.000
267	GOBP-MORPHOGENESIS-OF-AN-EPITHELIUM	6	0.296444	0.703586	0.804671	1.000000	1.000
268	GOBP-PROTEIN-LOCALIZATION-TO-MEMBRANE	14	0.223389	0.701269	0.855011	1.000000	1.000
269	GOBP-CELL-JUNCTION-ASSEMBLY	8	0.268824	0.700649	0.843096	1.000000	1.000
270	GOBP-REGULATION-OF-PROTEIN-SERINE-THREONINE-KI...	12	0.241542	0.700541	0.866667	1.000000	1.000
271	GOBP-SECOND-MESSENGER-MEDIATED-SIGNALING	16	0.217178	0.697857	0.874419	1.000000	1.000
272	GOBP-SYNAPTIC-SIGNALING	47	0.177273	0.696971	0.919668	1.000000	1.000
273	REACTOME-MAPK-TARGETS-NUCLEAR-EVENTS-MEDIATED...	5	0.320955	0.695698	0.859756	1.000000	1.000
274	REACTOME-TRANSCRIPTIONAL-REGULATION-OF-WHITE-A...	6	0.298753	0.694437	0.852174	1.000000	1.000
275	GOBP-MONOCARBOXYLIC-ACID-METABOLIC-PROCESS	6	0.301281	0.693398	0.853002	1.000000	1.000
276	GOBP-NEGATIVE-REGULATION-OF-MOLECULAR-FUNCTION	24	0.194352	0.693343	0.891473	1.000000	1.000
277	GOBP-CELL-PART-MORPHOGENESIS	24	0.192448	0.690071	0.895981	1.000000	1.000
278	GOBP-MEMORY	13	0.233218	0.686438	0.854031	1.000000	1.000
279	GOBP-CELLULAR-COMPONENT-MORPHOGENESIS	24	0.192448	0.685958	0.907767	1.000000	1.000
280	GOBP-PROTEIN-COMPLEX-OLIGOMERIZATION	6	0.291032	0.683836	0.860927	1.000000	1.000
281	GOBP-REGULATION-OF-PEPTIDE-HORMONE-SECRETION	6	0.296185	0.679374	0.876380	1.000000	1.000
282	GOBP-CELL-MORPHOGENESIS	24	0.192448	0.678776	0.898058	1.000000	1.000
283	REACTOME-SIGNALING-BY-NTRKS	18	0.211639	0.678661	0.899772	1.000000	1.000
284	GOBP-CELL-CELL-JUNCTION-ASSEMBLY	5	0.308489	0.674775	0.847390	1.000000	1.000
285	REACTOME-SIGNALING-BY-RECEPTOR-TYROSINE-KINASES	26	0.184079	0.672300	0.923645	1.000000	1.000
286	REACTOME-NEUROTRANSMITTER-RECEPTORS-AND-POSTSY...	22	0.190123	0.664551	0.923991	1.000000	1.000
287	GOBP-NEGATIVE-REGULATION-OF-CELLULAR-COMPONENT...	11	0.233055	0.663433	0.899533	1.000000	1.000
288	GOBP-REGULATION-OF-DNA-BINDING-TRANSCRIPTION-F...	16	0.211128	0.662605	0.901149	1.000000	1.000
289	GOBP-REGULATION-OF-CIRCADIAN-RHYTHM	7	0.280875	0.662429	0.874715	1.000000	1.000
290	GOBP-CELL-CELL-JUNCTION-ORGANIZATION	6	0.285936	0.657428	0.875789	1.000000	1.000
291	GOBP-REGULATION-OF-MAPK-CASCADE	13	0.220571	0.656707	0.897092	0.999632	1.000
292	GOBP-ADENYLATE-CYCLASE-INHIBITING-G-PROTEIN-CO...	9	0.242444	0.649845	0.903930	1.000000	1.000
293	GOBP-FC-EPSILON-RECEPTOR-SIGNALING-PATHWAY	7	0.0038095	0.648375	0.907757	1.000000	1.000
294	REACTOME-INTERFERON-SIGNALING	6	0.286098	0.644584	0.899782	1.000000	1.000
295	GOBP-PROTEIN-LOCALIZATION-TO-CELL-JUNCTION	6	0.280488	0.639035	0.900212	1.000000	1.000
296	REACTOME-ADAPTIVE-IMMUNE-SYSTEM	9	0.246677	0.637809	0.902335	1.000000	1.000
297	GOBP-IMMUNE-RESPONSE-REGULATING-SIGNALING-PATHWAY	8	0.244512	0.630564	0.924211	1.000000	1.000
298	REACTOME-FC-EPSILON-RECEPTOR-FCER1-SIGNALING	7	0.260042	0.625683	0.920705	1.000000	1.000

Continuation of Table S17

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
299	GOBP.FC.RECEPTOR.SIGNALING.PATHWAY	8	0.244512	0.623948	0.920705	1.000000	1.000
300	GOBP.PROTEIN.LOCALIZATION.TO.PLASMA.MEMBRANE	7	0.245205	0.621636	0.935982	1.000000	1.000
301	GOBP.PROTEIN.LOCALIZATION.TO.POSTSYNAPSE	5	0.277108	0.612834	0.927536	1.000000	1.000
302	GOBP.INSULIN.SECRETION	7	0.247778	0.611511	0.920091	1.000000	1.000
303	GOBP.PEPTIDE.HORMONE.SECRETION	7	0.247778	0.608272	0.942350	1.000000	1.000
304	GOBP.EXCITATORY.CHEMICAL.SYNAPTIC.TRANSMISSION	5	0.277108	0.595552	0.934599	1.000000	1.000
305	REACTOME.DAG.AND.IP3.SIGNALING	8	0.234189	0.598181	0.946467	1.000000	1.000
306	GOBP.PROTEIN.LOCALIZATION.TO.SYNAPSE	5	0.277108	0.594815	0.926882	1.000000	1.000
307	GOBP.REGULATION.OF.LIPID.LOCALIZATION	5	0.266685	0.568277	0.941685	1.000000	1.000
308	GOBP.POSITIVE.REGULATION.OF.SIGNALING	34	0.145338	0.563750	0.988263	1.000000	1.000
309	GOBP.REGULATION.OF.PROTEIN.BINDING	7	0.229171	0.562036	0.956236	1.000000	1.000
310	GOBP.NEGATIVE.REGULATION.OF.ANION.TRANSPORT	8	0.225000	0.557854	0.966316	1.000000	1.000
311	GOBP.NEGATIVE.REGULATION.OF.SYNAPTIC.TRANSMISSION	6	0.231707	0.548428	0.981777	1.000000	1.000
312	GOBP.COGNITION	28	0.146929	0.545219	0.990453	1.000000	1.000
313	REACTOME.LEISHMANIA.INFECTION	10	0.195544	0.537774	0.974359	1.000000	1.000
314	GOBP.NEGATIVE.REGULATION.OF.BINDING	6	0.227526	0.529328	0.986900	1.000000	1.000
315	GOBP.DIVALENT.INORGANIC.CATION.HOMEOSTASIS	13	0.175471	0.525989	0.974194	1.000000	1.000
316	GOBP.REGULATION.OF.CYTOSOLIC.CALCIUM.ION.CONCE...	13	0.175471	0.524212	0.982456	1.000000	1.000
317	GOBP.RESPONSE.TO.MECHANICAL.STIMULUS	6	0.219512	0.500502	0.993377	1.000000	1.000
318	REACTOME.PROTEIN.PROTEIN.INTERACTIONS.AT.SYNAPSES	12	0.167516	0.494912	0.988426	1.000000	1.000
319	GOBP.MUSCLE.CELL.DIFFERENTIATION	10	0.179487	0.487547	0.989107	1.000000	1.000
320	GOBP.NEGATIVE.REGULATION.OF.KINASE.ACTIVITY	5	0.223847	0.481315	0.991091	1.000000	1.000
321	GOBP.METAL.ION.HOMEOSTASIS	14	0.157335	0.478386	0.993228	1.000000	1.000
322	GOBP.NEGATIVE.REGULATION.OF.TRANSFERASE.ACTIVITY	5	0.223847	0.465631	0.993711	1.000000	1.000
323	GOBP.ORGANIC.ACID.METABOLIC.PROCESS	7	0.187750	0.454007	0.995283	1.000000	1.000
324	GOBP.REGULATION.OF.NEURON.DIFFERENTIATION	5	0.204819	0.433908	1.000000	1.000000	1.000
325	GOBP.PROTEIN.LOCALIZATION.TO.CELL.PERIPHERY	12	0.139492	0.411755	1.000000	0.999098	1.000
326	GOBP.MALE.GAMETE.GENERATION	5	-0.240964	-0.510617	0.992095	0.984988	1.000
327	GOBP.NEURON.DEVELOPMENT	33	-0.145683	-0.515500	0.986087	0.986139	1.000
328	GOBP.CELL.PROJECTION.ORGANIZATION	34	-0.143257	-0.519058	0.987784	0.987463	1.000
329	GOBP.POLYSACCHARIDE.METABOLIC.PROCESS	5	-0.256169	-0.542382	0.969981	0.981309	1.000
330	HALLMARK.HYPOXIA	5	-0.257328	-0.545221	0.974903	0.982559	1.000
331	GOBP.RESPONSE.TO.LIGHT.STIMULUS	11	-0.196439	-0.545893	0.970480	0.984803	1.000
332	GOBP.MULTICELLULAR.ORGANISM.PROCESS	8	-0.221115	-0.548046	0.967308	0.986452	1.000
333	GOBP.REGULATION.OF.SYSTEM.PROCESS	18	-0.174105	-0.548478	0.962393	0.988816	1.000
334	GOBP.REGULATION.OF.AXONOGENESIS	7	-0.227215	-0.550781	0.965116	0.990367	1.000
335	GOBP.ENDOCYTOSIS	8	-0.223243	-0.552687	0.968045	0.992057	1.000
336	HALLMARK.UV.RESPONSE.UP	5	-0.267794	-0.562542	0.960073	0.988595	1.000
337	REACTOME.NEUREXINS.AND.NEURLIGINS	9	-0.219053	-0.567618	0.954710	0.989538	1.000
338	GOBP.EPHRIN.RECEPTOR.SIGNALING.PATHWAY	5	-0.265060	-0.570726	0.955473	0.990339	1.000
339	GOBP.NUCLEOBASE.CONTAINING.SMALL.MOLECULE.META...	6	-0.254952	-0.573318	0.966797	0.991559	1.000
340	GOBP.RESPONSE.TO.METAL.ION	15	-0.191781	-0.574399	0.939068	0.993505	1.000
341	GOBP.GAMETE.GENERATION	9	-0.217731	-0.575077	0.939068	0.995754	1.000

Continuation of Table S17

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
342	GOBP-REGULATION-OF-CARBOHYDRATE-BIOSYNTHETIC.P...	5	-0.275296	-0.575165	0.948718	0.998348	1.000
343	GOBP-HORMONE-TRANSPORT	9	-0.224620	-0.578500	0.957295	0.999134	1.000
344	GOBP-ADENYLATE-CYCLASE-MODULATING-G-PROTEIN.CO...	11	-0.214345	-0.581683	0.945355	0.999870	1.000
345	GOBP-POSITIVE-REGULATION-OF-PROTEOLYSIS	8	-0.234908	-0.587582	0.940972	0.998535	1.000
346	GOBP-CARBOHYDRATE-BIOSYNTHETIC-PROCESS	5	-0.275296	-0.589868	0.960967	0.999773	1.000
347	GOBP-REGULATION-OF-CARBOHYDRATE-METABOLIC-PROCESS	5	-0.275296	-0.590619	0.945055	1.000000	1.000
348	GOBP-REGULATION-OF-PROTEIN-LOCALIZATION.TO.MEM...	7	-0.246606	-0.604782	0.927619	0.995013	1.000
349	GOBP-CELLULAR-RESPONSE.TO.INORGANIC-SUBSTANCE	11	-0.220897	-0.604914	0.940270	0.997609	1.000
350	REACTOME-TRAFFICKING-OF-AMPA-RECEPTORS	11	-0.222052	-0.607773	0.927239	0.998209	1.000
351	GOBP-APOPTOTIC-MITOCHONDRIAL-CHANGES	6	-0.272970	-0.609014	0.942272	0.999959	1.000
352	GOBP-CELL-CELL-SIGNALING	56	-0.167222	-0.615451	0.950931	0.997605	1.000
353	GOBP-ENDOCRINE-SYSTEM-DEVELOPMENT	6	-0.273646	-0.615759	0.932961	1.000000	1.000
354	REACTOME-EPHLEPHRIN-SIGNALING	6	-0.268293	-0.616092	0.939394	1.000000	1.000
355	GOBP-NEGATIVE-REGULATION-OF-LIPID-METABOLIC.PR...	5	-0.291155	-0.620533	0.907197	1.000000	1.000
356	REACTOME-INTERLEUKIN-17-SIGNALING	6	-0.275947	-0.623455	0.913556	1.000000	1.000
357	GOBP-CELL-CELL-ADHESION	14	-0.210742	-0.629030	0.931699	0.999636	1.000
358	GOBP-POSITIVE-REGULATION-OF-CYSTEINE-TYPE-ENDO...	7	-0.266783	-0.630817	0.918330	1.000000	1.000
359	GOBP-G-PROTEIN-COUPLED-RECEPTOR-SIGNALING-PATHWAY	18	-0.200818	-0.638090	0.924028	0.997283	1.000
360	GOBP-REGULATION-OF-CELL-CYCLE-PROCESS	5	-0.303711	-0.638338	0.936210	0.999801	1.000
361	GOBP-REGULATION-OF-ANATOMICAL-STRUCTURE-SIZE	10	-0.244465	-0.640823	0.897727	1.000000	1.000
362	GOBP-POSITIVE-REGULATION-OF-PEPTIDASE-ACTIVITY	7	-0.266783	-0.644383	0.902574	0.999815	1.000
363	GOBP-MUSCLE-STRUCTURE-DEVELOPMENT	16	-0.216015	-0.648015	0.911032	0.999087	1.000
364	GOBP-NEGATIVE-REGULATION-OF-TRANSMEMBRANE-TRAN...	6	-0.285851	-0.649824	0.903808	1.000000	1.000
365	GOBP-CHEMICAL-HOMEOSTASIS	23	-0.198177	-0.652738	0.922414	0.999773	1.000
366	GOBP-RESPONSE.TO.DRUG	11	-0.233766	-0.652795	0.906643	1.000000	1.000
367	GOBP-RESPONSE.TO.INORGANIC-SUBSTANCE	19	-0.202899	-0.653263	0.908612	1.000000	1.000
368	REACTOME-TRANSMISSION-ACROSS-CHEMICAL-SYNAPSES	23	-0.193982	-0.653524	0.922242	1.000000	1.000
369	GOBP-CELL-CELL-SIGNALING-BY.WNT	7	-0.271004	-0.656767	0.904936	1.000000	1.000
370	GOBP-REGULATION-OF-HORMONE-SECRETION	8	-0.264162	-0.658798	0.893657	1.000000	1.000
371	GOBP-PROTEIN-DEPHOSPHORYLATION	7	-0.279892	-0.665068	0.878277	1.000000	1.000
372	GOBP-BEHAVIOR	32	-0.188070	-0.667340	0.911519	1.000000	1.000
373	REACTOME-DISEASES-OF-SIGNAL-TRANSDUCTION-BY-GR...	12	-0.241488	-0.669008	0.882662	1.000000	1.000
374	GOBP-DEPHOSPHORYLATION	7	-0.279892	-0.678107	0.869403	0.997637	1.000
375	GOBP-POSITIVE-REGULATION-OF-DEFENSE-RESPONSE	5	-0.323706	-0.679219	0.890411	0.999183	1.000
376	GOBP-REGULATION-OF-TRANS-SYNAPTIC-SIGNALING	40	-0.187856	-0.680931	0.925203	0.999987	1.000
377	GOBP-NEGATIVE-REGULATION-OF-INTRACELLULAR-SIGN...	7	-0.283354	-0.684168	0.856884	0.999094	1.000
378	GOBP-REGULATION-OF-FAT-CELL-DIFFERENTIATION	6	-0.307407	-0.694871	0.860735	0.988479	1.000
379	REACTOME-CELLULAR-RESPONSES-TO-EXTERNAL-STIMULI	12	-0.244948	-0.699014	0.864865	0.985939	1.000
380	GOBP-CELLULAR-CARBOHYDRATE-METABOLIC-PROCESS	5	-0.330969	-0.699395	0.852612	0.985299	1.000
381	REACTOME-INTEGRATION-OF-ENERGY-METABOLISM	5	-0.328368	-0.704236	0.835644	0.984873	1.000
382	GOBP-CELLULAR-RESPONSE-TO-EXTRACELLULAR-STIMULUS	8	-0.285972	-0.704882	0.850000	0.986901	1.000
383	GOBP-GROWTH	14	-0.245664	-0.708034	0.840951	0.985658	1.000
384	GOBP-POSITIVE-REGULATION-OF-AXONOGENESIS	5	-0.335168	-0.712317	0.825832	0.982795	1.000

Continuation of Table S17

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
385	GOBP-ORGAN_GROWTH	GO-0035265	5	-0.335429	-0.715125	0.859073	0.981899	1.000
386	GOBP-CELLULAR-MACROMOLECULE-LOCALIZATION	GO-0070727	21	-0.224746	-0.720497	0.846939	0.977051	1.000
387	GOBP-NEGATIVE-REGULATION-OF-NERVOUS-SYSTEM.DEV...	GO-0051961	5	-0.329935	-0.721797	0.834601	0.978258	1.000
388	GOBP-NEUROTROPHIN-TRK-RECEPTOR-SIGNALING-PATHWAY	GO-0048011	6	-0.319117	-0.728551	0.843212	0.971647	1.000
389	GOBP-NEUROTROPHIN-SIGNALING-PATHWAY	GO-0038179	6	-0.319117	-0.728908	0.833984	0.974096	1.000
390	GOBP-REGULATION-OF-CELL-ADHESION	GO-0030155	13	-0.249013	-0.731353	0.829907	0.973608	1.000
391	REACTOME-CIRCADIAN-CLOCK	R-HSA-400253	5	-0.337444	-0.736192	0.796610	0.969516	1.000
392	GOBP-REGULATION-OF-ORGAN-GROWTH	GO-0046620	5	-0.335429	-0.736608	0.805714	0.971860	1.000
393	GOBP-REGULATION-OF-PROTEIN-PHOSPHORYLATION	GO-0001932	26	-0.217357	-0.739541	0.819700	0.970385	1.000
394	GOBP-REGULATION-OF-LEUKOCYTE-DIFFERENTIATION	GO-1902105	9	-0.286388	-0.741212	0.789773	0.970786	1.000
395	GOBP-NEGATIVE-REGULATION-OF-SIGNALING	GO-0023057	21	-0.228914	-0.741306	0.808970	0.973633	1.000
396	GOBP-ACTIN-FILAMENT-BASED-PROCESS	GO-0030029	7	-0.307528	-0.743940	0.790566	0.972400	1.000
397	GOBP-POSITIVE-REGULATION-OF-CELL-DEATH	GO-0010942	19	-0.237814	-0.744352	0.799648	0.974813	1.000
398	GOBP-NEUROGENESIS	GO-0022008	40	-0.201593	-0.745815	0.848185	0.975510	1.000
399	GOBP-TUBE-MORPHOGENESIS	GO-0035239	15	-0.250059	-0.749656	0.781818	0.972355	1.000
400	GOBP-NERVOUS-SYSTEM-PROCESS	GO-0050877	38	-0.204811	-0.752788	0.831034	0.970425	1.000
401	GOBP-CELLULAR-ION-HOMEOSTASIS	GO-0006873	14	-0.255505	-0.753119	0.809074	0.972966	1.000
402	REACTOME-DEATH-RECEPTOR-SIGNALING	R-RNO-73887	5	-0.350561	-0.753531	0.774436	0.975423	1.000
403	GOBP-CELLULAR-RESPONSE-TO-EXTERNAL-STIMULUS	GO-0071496	10	-0.284928	-0.755885	0.766727	0.974839	1.000
404	GOBP-MITOTIC-CELL-CYCLE	GO-0000278	5	-0.283106	-0.757317	0.779130	0.975492	1.000
405	GOBP-REGULATION-OF-WNT-SIGNALING-PATHWAY	GO-0030111	10	-0.355168	-0.757418	0.756007	0.978465	1.000
406	GOBP-LOCOMOTION	GO-0040011	31	-0.214758	-0.758474	0.810858	0.979906	1.000
407	GOBP-POSITIVE-REGULATION-OF-CELL-DIFFERENTIATION	GO-0045597	27	-0.218191	-0.758597	0.812825	0.982837	1.000
408	GOBP-REGULATION-OF-GROWTH	GO-0040008	13	-0.263334	-0.758766	0.788194	0.985694	1.000
409	GOBP-RESPONSE-TO-ALCOHOL	GO-0097305	11	-0.272727	-0.759184	0.763251	0.988147	1.000
410	GOBP-CYTOKINE-MEDIATED-SIGNALING-PATHWAY	GO-0019221	16	-0.250105	-0.766793	0.769674	0.978708	1.000
411	GOBP-GLUTAMATE-RECEPTOR-SIGNALING-PATHWAY	GO-0007215	17	-0.249207	-0.766885	0.801038	0.981711	1.000
412	GOBP-NEGATIVE-REGULATION-OF-SIGNALING-PATHWAY	GO-2000117	5	-0.353347	-0.767754	0.760536	0.983480	1.000
413	GOBP-TISSUE-MORPHOGENESIS	GO-0048729	7	-0.316556	-0.768656	0.802607	0.985115	1.000
414	GOBP-ORGANONITROGEN-COMPOUND-BIOSYNTHETIC-PROCESS	GO-1901566	13	-0.270174	-0.768825	0.779751	0.988051	1.000
415	GOBP-CELL-CYCLE-PROCESS	GO-0022402	11	-0.285995	-0.769204	0.756708	0.990583	1.000
416	REACTOME-ESTROGEN-DEPENDENT-NUCLEAR-EVENTS.DOW...	R-RNO-9634638	5	-0.367007	-0.769814	0.754128	0.992726	1.000
417	GOBP-REGULATION-OF-SYNAPTIC-PLASTICITY	GO-0048167	21	-0.235194	-0.772035	0.754685	0.992286	1.000
418	GOBP-REGULATION-OF-MYELOID-LEUKOCYTE-DIFFERENT...	GO-0002761	8	-0.302660	-0.775109	0.759013	0.990186	1.000
419	GOBP-RESPONSE-TO-RADIATION	GO-0009314	13	-0.272304	-0.777141	0.740143	0.989798	1.000
420	GOBP-REGULATION-OF-CYTOSKELETON-ORGANIZATION	GO-0051493	5	-0.366054	-0.777897	0.749035	0.991889	1.000
421	GOBP-REGULATION-OF-CYSTEINE-TYPE-ENDOPEPTIDASE...	GO-2000116	9	-0.301265	-0.781742	0.757634	0.988311	1.000
422	GOBP-REGULATION-OF-MUSCLE-SYSTEM-PROCESS	GO-0090257	8	-0.316917	-0.787403	0.714795	0.981270	1.000
423	GOBP-NERVE-DEVELOPMENT	GO-0021675	9	-0.305370	-0.791670	0.724907	0.976929	1.000
424	GOBP-BLOOD-VESSEL-MORPHOGENESIS	GO-0048514	14	-0.272567	-0.792021	0.739895	0.979529	1.000
425	GOBP-REGULATION-OF-PROTEIN-LOCALIZATION	GO-0032880	18	-0.251046	-0.792461	0.732472	0.982133	1.000
426	GOBP-RESPONSE-TO-STARVATION	GO-0042594	5	-0.377560	-0.794471	0.736842	0.981754	1.000
427	GOBP-POSITIVE-REGULATION-OF-PRL-MI-RNA-TRANSCRI...	GO-1902895	7	-0.344199	-0.796278	0.705996	0.981868	1.000

Continuation of Table S17

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
428	GOBP-TEMPERATURE.HOMEOSTASIS	GO-0001659	5	-0.381414	-0.797433	0.706204	0.983237	1.000
429	GOBP-CENTRAL.NERVOUS.SYSTEM.DEVELOPMENT	GO-0007417	26	-0.235665	-0.797927	0.746219	0.985702	1.000
430	HALLMARK-KRAS.SIGNALING.UP	M5953	6	-0.351981	-0.799536	0.729679	0.986129	1.000
431	GOBP-GLAND.DEVELOPMENT	GO-0048732	7	-0.334184	-0.805072	0.684615	0.979153	1.000
432	GOBP-REGULATION.OF.PROTEOLYSIS	GO-0030162	12	-0.283622	-0.806262	0.740608	0.980184	1.000
433	GOBP-RESPONSE.TO.CALCIUM.ION	GO-0051592	6	-0.365854	-0.806709	0.667300	0.982781	1.000
434	GOBP-FAT.CELL.DIFFERENTIATION	GO-0045444	9	-0.317881	-0.810416	0.705882	0.979299	1.000
435	GOBP-RESPONSE.TO.HEAT	GO-0009408	7	-0.344344	-0.810717	0.696798	0.982136	1.000
436	GOBP-POSITIVE.REGULATION.OF.TRANSPORT	GO-0051050	26	-0.239038	-0.811073	0.747826	0.984882	1.000
437	GOBP-REGULATION.OF.CELL.DEATH	GO-0010941	34	-0.226950	-0.811999	0.752212	0.986512	1.000
438	GOBP-NEGATIVE.REGULATION.OF.CELL.CYCLE	GO-0045786	5	-0.381268	-0.819739	0.669246	0.975192	1.000
439	GOBP-REGULATION.OF.CELLULAR.LOCALIZATION	GO-0060341	17	-0.266993	-0.820239	0.719852	0.977604	1.000
440	GOBP-NEGATIVE.REGULATION.OF.PHOSPHORYLATION	GO-0042326	7	-0.342878	-0.821338	0.659615	0.978906	1.000
441	GOBP-POSITIVE.REGULATION.OF.PROTEIN.MODIFICATI...	GO-0031401	23	-0.251991	-0.821441	0.746317	0.982211	1.000
442	GOBP-POSITIVE.REGULATION.OF.PHOSPHORUS.METABOL...	GO-0010562	24	-0.244858	-0.821718	0.731922	0.985244	1.000
443	GOBP-PRLMIRNA.TRANSCRIPTION.BY.RNA.POLYMERASE.II	GO-0061614	7	-0.344199	-0.822491	0.661654	0.987379	1.000
444	GOBP-AXON.DEVELOPMENT	GO-0061564	18	-0.259866	-0.822546	0.737030	0.990842	1.000
445	GOBP-REGULATION.OF.MYELOID.CELL.DIFFERENTIATION	GO-0045637	9	-0.318119	-0.826042	0.675373	0.987472	1.000
446	GOBP-CELLULAR.RESPONSE.TO.STARVATION	GO-0009267	5	-0.377560	-0.826344	0.670565	0.990525	1.000
447	GOBP-NEGATIVE.REGULATION.OF.ION.TRANSPORT	GO-0043271	11	-0.298889	-0.828319	0.703846	0.990259	1.000
448	GOBP-NEURON.APOPTOTIC.PROCESS	GO-0051402	12	-0.296602	-0.829549	0.680851	0.991302	1.000
449	GOBP-CELLULAR.RESPONSE.TO.KETONE	GO-1901655	5	-0.393422	-0.833599	0.656075	0.986883	1.000
450	REACTOME.G.ALPHA.I.SIGNALING.EVENTS	R-RNO-418594	18	-0.266325	-0.837792	0.696270	0.990121	1.000
451	GOBP-REGULATION.OF.SMALL.MOLECULE.METABOLIC.PR...	GO-0062012	9	-0.326279	-0.834213	0.681481	0.993030	1.000
452	REACTOME.NEURONAL.SYSTEM	R-RNO-112316	26	-0.246910	-0.834586	0.700717	0.996046	1.000
453	GOBP-AMIDE.BIOSYNTHETIC.PROCESS	GO-0043604	7	-0.359650	-0.836378	0.651837	0.996060	1.000
454	GOBP-POSITIVE.REGULATION.OF.EPITHELIAL.CELL.PR...	GO-0050679	7	-0.351124	-0.837435	0.657356	0.997702	1.000
455	REACTOME.INNATE.IMMUNE.SYSTEM	R-RNO-168249	16	-0.282102	-0.839177	0.661202	0.997616	1.000
456	GOBP-NEGATIVE.REGULATION.OF.TRANSCRIPTION.BY.R...	GO-0000122	10	-0.323154	-0.850224	0.677596	0.978910	1.000
457	GOBP-REGULATION.OF.CELL.CYCLE	GO-0051726	13	-0.295029	-0.852917	0.648746	0.976855	1.000
458	GOBP-POSITIVE.REGULATION.OF.PROTEIN.PHOSPHORYL...	GO-0001934	23	-0.251991	-0.852972	0.678261	0.980478	1.000
459	GOBP-REGULATION.OF.PEPTIDE.TRANSPORT	GO-0090087	10	-0.321012	-0.856704	0.625709	0.976337	1.000
460	GOBP-REGULATION.OF.CELL.CELL-ADHESION	GO-0022407	9	-0.335140	-0.862699	0.622430	0.967519	1.000
461	GOBP-CELLULAR.HOMEOSTASIS	GO-0019725	18	-0.268978	-0.863256	0.642218	0.970059	1.000
462	GOBP-REGULATION.OF.CELLULAR.PROTEIN.LOCALIZATION	GO-1903827	12	-0.303139	-0.864231	0.631776	0.971709	1.000
463	GOBP-PEPTIDE.BIOSYNTHETIC.PROCESS	GO-0043043	7	-0.359650	-0.866282	0.632114	0.971149	1.000
464	REACTOME.SIGNALING.BY.NUCLEAR.RECEPTORS	R-RNO-9006931	8	-0.354072	-0.869335	0.626894	0.968392	1.000
465	GOBP-NEURON.MIGRATION	GO-0001764	5	-0.410807	-0.871054	0.614943	0.968471	1.000
466	GOBP-CELLULAR.RESPONSE.TO.PEPTIDE.HORMONE.STIM...	GO-0071375	9	-0.338317	-0.871283	0.627737	0.971786	1.000
467	GOBP-HEAD.DEVELOPMENT	GO-0060322	22	-0.268655	-0.872931	0.641667	0.971999	1.000
468	GOBP-POSITIVE.REGULATION.OF.PROTEIN.METABOLIC...	GO-0051247	28	-0.250585	-0.873654	0.650602	0.974098	1.000
469	GOBP-RESPONSE.TO.NICOTINE	GO-0035094	7	-0.365317	-0.875416	0.629496	0.974039	1.000
470	GOBP-PROTEIN.PHOSPHORYLATION	GO-0006468	34	-0.248383	-0.876064	0.666667	0.976588	1.000

Continuation of Table S17

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
471 REACTOME_ESR-MEDIATED-SIGNALING	R-RNO-8939211	8	-0.354072	-0.870575	0.631485	0.979360	1.000
472 GOBP-NEGATIVE-REGULATION-OF-NEURON-APOPTOTIC.P...	GO-0043524	8	-0.351938	-0.877826	0.637383	0.980623	1.000
473 GOBP-EMBRYONIC-ORGAN-DEVELOPMENT	GO-0048568	7	-0.365075	-0.877952	0.618147	0.984399	1.000
474 GOBP-CYTOSKELETON-ORGANIZATION	GO-0007010	11	-0.317989	-0.878412	0.634409	0.987372	1.000
475 GOBP-RESPONSE-TO-KETONE	GO-1901670	7	-0.370370	-0.879927	0.605948	0.988111	1.000
476 GOBP-TRANSMEMBRANE-RECEPTOR-PROTEIN-TYROSINE.K...	GO-0007169	19	-0.270578	-0.880858	0.626736	0.990137	1.000
477 GOBP-REGULATION-OF-HYDROLASE-ACTIVITY	GO-0051336	22	-0.265347	-0.881264	0.639860	0.993278	1.000
478 GOBP-MATERNAL-PROCESS-INVOLVED-IN-FEMALE-PREGN...	GO-0060135	5	-0.408336	-0.881512	0.608949	0.996902	1.000
479 GOBP-CELLULAR-RESPONSE-TO-ALCOHOL	GO-0097306	5	-0.412911	-0.881996	0.605948	1.000000	1.000
480 REACTOME_L1CAM-INTERACTIONS	R-RNO-373760	5	-0.419935	-0.882346	0.609037	1.000000	1.000
481 GOBP-MUSCLE-SYSTEM-PROCESS	GO-0003012	9	-0.333340	-0.882634	0.592593	1.000000	1.000
482 GOBP-FOREBRAIN-DEVELOPMENT	GO-0030900	9	-0.348172	-0.882935	0.603571	1.000000	1.000
483 GOBP-NEGATIVE-REGULATION-OF-IMMUNE-SYSTEM-PROCESS	GO-0002683	5	-0.418955	-0.883651	0.634387	1.000000	1.000
484 GOBP-LIPID-LOCALIZATION	GO-0010876	10	-0.332354	-0.888362	0.608939	1.000000	1.000
485 GOBP-LIPID-BIOSYNTHETIC-PROCESS	GO-0008610	6	-0.388824	-0.889669	0.585687	1.000000	1.000
486 REACTOME-OPIOID-SIGNALING	R-RNO-111885	12	-0.316882	-0.890202	0.615809	1.000000	1.000
487 GOBP-REGULATION-OF-LIPID-BIOSYNTHETIC-PROCESS	GO-0046890	6	-0.388824	-0.891199	0.608696	1.000000	1.000
488 GOBP-REGULATION-OF-LIPID-METABOLIC-PROCESS	GO-0019216	7	-0.366724	-0.891576	0.606589	1.000000	1.000
489 GOBP-RESPONSE-TO-EXTRACELLULAR-STIMULUS	GO-0009991	13	-0.308974	-0.899458	0.571691	1.000000	1.000
490 GOBP-POSITIVE-REGULATION-OF-IMMUNE-RESPONSE	GO-0050778	9	-0.351577	-0.899844	0.578067	1.000000	1.000
491 GOBP-REGULATION-OF-APOPTOTIC-SIGNALING-PATHWAY	GO-2001233	10	-0.334615	-0.901610	0.589416	1.000000	1.000
492 GOBP-REGULATION-OF-PROTEIN-STABILITY	GO-0031647	5	-0.418211	-0.902545	0.574040	1.000000	1.000
493 GOBP-REGULATION-OF-MULTICELLULAR-ORGANISMAL.DE...	GO-2000026	31	-0.257397	-0.906882	0.599343	1.000000	1.000
494 GOBP-REGULATION-OF-CELL-DIFFERENTIATION	GO-0045595	36	-0.251371	-0.906986	0.611667	1.000000	1.000
495 GOBP-REGULATION-OF-ION-TRANSPORT	GO-0043269	36	-0.256301	-0.911642	0.585586	0.999507	1.000
496 GOBP-CIRCULATORY-SYSTEM-PROCESS	GO-0003013	5	-0.434575	-0.912002	0.579048	1.000000	1.000
497 REACTOME-RNA-POLYMERASE-II-TRANSCRIPTION	R-RNO-73857	20	-0.281754	-0.912620	0.588441	1.000000	1.000
498 GOBP-HOMEOSTASIS-OF-NUMBER-OF-CELLS	GO-0048872	5	-0.441927	-0.912791	0.541267	1.000000	1.000
499 GOBP-RESPONSE-TO-OXYGEN-LEVELS	GO-0070482	8	-0.359091	-0.913025	0.593284	1.000000	1.000
500 GOBP-NEGATIVE-REGULATION-OF-NEURON-DEATH	GO-1901215	11	-0.333774	-0.913181	0.566794	1.000000	1.000
501 GOBP-REGULATION-OF-HEMOPOIESIS	GO-1903706	10	-0.336589	-0.913780	0.573386	1.000000	1.000
502 GOBP-MEMBRANE-ORGANIZATION	GO-0061024	12	-0.328512	-0.916532	0.559322	1.000000	1.000
503 GOBP-AGING	GO-0007568	13	-0.314324	-0.917559	0.572183	1.000000	1.000
504 GOBP-REGULATION-OF-IMMUNE-SYSTEM-PROCESS	GO-0002682	21	-0.281532	-0.918504	0.568995	1.000000	1.000
505 GOBP-MUSCLE-CELL-PROLIFERATION	GO-0033002	8	-0.360822	-0.919022	0.530055	1.000000	1.000
506 GOBP-CELL-CYCLE	GO-0007049	21	-0.287419	-0.923409	0.592721	1.000000	1.000
507 GOBP-SEXUAL-REPRODUCTION	GO-0019953	10	-0.343185	-0.923677	0.549719	1.000000	1.000
508 GOBP-NEGATIVE-REGULATION-OF-CELL-PROJECTION.OR...	GO-0031345	5	-0.429033	-0.926137	0.536680	1.000000	1.000
509 GOBP-NEGATIVE-REGULATION-OF-TRANSPORT	GO-0051051	13	-0.319679	-0.926790	0.555957	1.000000	1.000
510 GOBP-TAXIS	GO-0042330	14	-0.313669	-0.930418	0.528029	1.000000	1.000
511 GOBP-NEGATIVE-REGULATION-OF-PROTEIN-METABOLIC...	GO-0051248	20	-0.292818	-0.932154	0.570690	1.000000	1.000
512 GOBP-REGULATION-OF-LYMPHOCYTE-ACTIVATION	GO-0051249	5	-0.443989	-0.933993	0.523232	1.000000	1.000
513 GOBP-TISSUE-MIGRATION	GO-0090130	9	-0.368271	-0.938072	0.529740	1.000000	1.000

Continuation of Table S17

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
514	GOBP-NEGATIVE-REGULATION-OF-BIOSYNTHETIC-PROCESS	13	-0.324287	-0.938104	0.522769	1.000000	1.000
515	GOBP-REGULATION-OF-CELLULAR-AMIDE-METABOLIC-PR...	9	-0.356078	-0.939209	0.539823	1.000000	1.000
516	GOBP-NEURON-DIFFERENTIATION	36	-0.260207	-0.941202	0.553691	1.000000	1.000
517	GOBP-MULTICELLULAR-ORGANISMAL-HOMEOSTASIS	12	-0.328087	-0.945827	0.526882	1.000000	1.000
518	GOBP-CELLULAR-RESPONSE-TO-CADMIIUM	15	-0.439672	-0.946908	0.525714	1.000000	1.000
519	GOBP-MITOCHONDRIUM-ORGANIZATION	7	-0.400982	-0.947426	0.493433	1.000000	1.000
520	GOBP-ESTABLISHMENT-OF-PROTEIN-LOCALIZATION	18	-0.302140	-0.949733	0.520761	1.000000	1.000
521	REACTOME-HEMOSTASIS	14	-0.319070	-0.953966	0.509338	1.000000	1.000
522	GOBP-REGULATION-OF-NEURONAL-SYNAPTIC-PLASTICITY	7	-0.396569	-0.955004	0.491651	1.000000	1.000
523	REACTOME-SIGNALING-BY-GPCR	22	-0.293603	-0.959340	0.514580	1.000000	1.000
524	GOBP-PEPTIDYL-SERINE-MODIFICATION	12	-0.343046	-0.960068	0.477860	1.000000	1.000
525	GOBP-RESPONSE-TO-ABIOTIC-STIMULUS	27	-0.279535	-0.962076	0.505357	1.000000	1.000
526	GOBP-POSITIVE-REGULATION-OF-ESTABLISHMENT-OF-P...	5	-0.459867	-0.965862	0.500000	1.000000	1.000
527	GOBP-RESPONSE-TO-ALKALOID	5	-0.461792	-0.966374	0.501859	1.000000	1.000
528	GOBP-POSITIVE-REGULATION-OF-EPITHELIAL-CELL-M...	5	-0.444285	-0.969285	0.482176	1.000000	1.000
529	GOBP-REGULATION-OF-PHOSPHORUS-METABOLIC-PROCESS	27	-0.280212	-0.969288	0.494585	1.000000	1.000
530	GOBP-RESPIRATORY-SYSTEM-DEVELOPMENT	6	-0.425602	-0.970452	0.480151	1.000000	1.000
531	REACTOME-TRAFFICKING-OF-GLUR2-CONTAINING-AMPA-...	8	-0.389211	-0.970595	0.503846	1.000000	1.000
532	GOBP-RESPONSE-TO-TUMOR-NECROSIS-FACTOR	7	-0.416594	-0.971300	0.485437	1.000000	1.000
533	GOBP-MUSCLE-TISSUE-DEVELOPMENT	11	-0.349242	-0.971709	0.488055	1.000000	1.000
534	GOBP-REGULATION-OF-HORMONE-LEVELS	12	-0.344315	-0.971828	0.486289	1.000000	1.000
535	HALLMARK-ALLOGRAFT-REJECTION	7	-0.408881	-0.972166	0.495238	1.000000	1.000
536	GOBP-CELLULAR-COMPONENT-MAINTENANCE	5	-0.450586	-0.973630	0.486339	1.000000	1.000
537	GOBP-MONAMINE-TRANSPORT	5	-0.455045	-0.976931	0.490458	1.000000	1.000
538	GOBP-REGULATION-OF-VESICLE-MEDIATED-TRANSPORT	12	-0.343768	-0.978932	0.489484	1.000000	1.000
539	GOBP-NEGATIVE-REGULATION-OF-PHOSPHORUS-METABOL...	9	-0.378151	-0.983265	0.450835	1.000000	1.000
540	GOBP-ESTABLISHMENT-OF-PROTEIN-LOCALIZATION-TO-...	6	-0.424945	-0.983634	0.445087	1.000000	1.000
541	GOBP-NEGATIVE-REGULATION-OF-CELL-DEATH	22	-0.293635	-0.984654	0.498246	1.000000	1.000
542	GOBP-SKIN-DEVELOPMENT	5	-0.455807	-0.985693	0.464627	1.000000	1.000
543	GOBP-INTRINSIC-APOPTOTIC-SIGNALING-PATHWAY	5	-0.474233	-0.986493	0.480151	1.000000	1.000
544	GOBP-NEGATIVE-REGULATION-OF-HYDROLASE-ACTIVITY	11	-0.353201	-0.986570	0.468806	1.000000	1.000
545	GOBP-REGULATION-OF-SECRETION	14	-0.332096	-0.987147	0.473776	1.000000	1.000
546	GOBP-POSITIVE-REGULATION-OF-SECRETION	6	-0.437681	-0.988090	0.462121	1.000000	1.000
547	GOBP-PROTEIN-AUTOPHOSPHORYLATION	5	-0.466222	-0.988456	0.459259	1.000000	1.000
548	GOBP-LIPID-EXPORT-FROM-CELL	5	-0.455096	-0.989409	0.452865	1.000000	1.000
549	GOBP-NEGATIVE-REGULATION-OF-NUCLEOBASE-CONTAIN...	13	-0.340262	-0.989511	0.448276	1.000000	1.000
550	GOBP-PROTEIN-LOCALIZATION-TO-ORGANELLE	9	-0.378395	-0.990193	0.449458	1.000000	1.000
551	GOBP-NEGATIVE-REGULATION-OF-PROTEIN-MODIFICATI...	10	-0.373822	-0.990643	0.480874	1.000000	1.000
552	REACTOME-ONCOGENIC-MAPK-SIGNALING	5	-0.465631	-1.000876	0.457295	1.000000	1.000
553	GOBP-EPITHELIAL-DEVELOPMENT	15	-0.334743	-1.001599	0.456637	1.000000	1.000
554	REACTOME-PLATELET-ACTIVATION-SIGNALING-AND-AGG...	7	-0.420169	-1.002076	0.448399	1.000000	1.000
555	GOBP-ERBB-SIGNALING-PATHWAY	5	-0.472232	-1.003205	0.453668	1.000000	1.000
556	GOBP-CELLULAR-MACROMOLECULE-CATABOLIC-PROCESS	6	-0.440747	-1.003959	0.434109	1.000000	1.000

Continuation of Table S17

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
557	GOBP-MUSCLE-CONTRACTION	5	-0.483260	-1.010656	0.444444	1.000000	1.000
558	GOBP-REGULATION.OF.GTPASE.ACTIVITY	5	-0.466401	-1.012724	0.432971	1.000000	1.000
559	GOBP-NEGATIVE-REGULATION.OF.RESPONSE.TO.STIMULUS	16	-0.340426	-1.015809	0.436330	1.000000	1.000
560	GOBP-SECRETION	24	-0.304797	-1.016794	0.442341	1.000000	1.000
561	GOBP-RESPONSE.TO.OXIDATIVE-STRESS	8	-0.411000	-1.017841	0.436090	1.000000	1.000
562	GOBP-ENDOTHELIAL-CELL-PROLIFERATION	8	-0.404972	-1.020263	0.408318	1.000000	1.000
563	GOBP-NEURON-DEATH	18	-0.321066	-1.020649	0.408273	1.000000	1.000
564	GOBP-POSITIVE-REGULATION.OF.ORGANELLE-ORGANIZA...	10	-0.375709	-1.021307	0.425243	1.000000	1.000
565	GOBP-EPIDERMIS-DEVELOPMENT	5	-0.479728	-1.022036	0.448718	1.000000	1.000
566	GOBP-MYELOID-LEUKOCYTE-DIFFERENTIATION	11	-0.376473	-1.023769	0.428846	1.000000	1.000
567	GOBP-RESPONSE.TO.MONOSACCHARIDE	5	-0.481747	-1.024687	0.410646	1.000000	1.000
568	GOBP-RESPONSE.TO.CARBOHYDRATE	5	-0.481747	-1.024895	0.425612	1.000000	1.000
569	GOBP-CELLULAR-RESPONSE.TO.PEPTIDE	13	-0.362164	-1.030840	0.425725	1.000000	1.000
570	GOBP-RESPONSE.TO.PEPTIDE.HORMONE	13	-0.373743	-1.032592	0.434028	1.000000	1.000
571	GOBP-RESPONSE.TO.TEMPERATURE.STIMULUS	9	-0.399247	-1.032598	0.392336	1.000000	1.000
572	GOBP-RESPONSE.TO.REACTIVE.OXYGEN-SPECIES	8	-0.411000	-1.039949	0.395872	1.000000	1.000
573	REACTOME-EXTRA_NUCLEAR-ESTROGEN-SIGNALING	7	-0.450473	-1.044871	0.395221	1.000000	1.000
574	GOBP-CIRCULATORY-SYSTEM-DEVELOPMENT	21	-0.320841	-1.046599	0.382143	1.000000	1.000
575	GOBP-POSITIVE-REGULATION.OF.ENDOTHELIAL-CELL.P...	6	-0.458149	-1.047039	0.403013	1.000000	1.000
576	GOBP-POSTTRANSCRIPTIONAL-REGULATION.OF.GENE.EX...	8	-0.415152	-1.047486	0.395307	1.000000	1.000
577	GOBP-CELLULAR-RESPONSE.TO.MOLECULE.OF.BACTERIA...	8	-0.421684	-1.050226	0.403704	1.000000	1.000
578	REACTOME-NGF-STIMULATED-TRANSCRIPTION	9	-0.413370	-1.053783	0.397790	1.000000	1.000
579	GOBP-HOMEOSTATIC-PROCESS	31	-0.294474	-1.054194	0.364407	1.000000	1.000
580	GOBP-CARBOHYDRATE-HOMEOSTASIS	7	-0.441105	-1.054769	0.381982	1.000000	1.000
581	GOBP-PEPTIDYL-AMINO-ACID-MODIFICATION	22	-0.321413	-1.055029	0.403571	1.000000	1.000
582	GOBP-CELLULAR-RESPONSE.TO.BIOTIC-STIMULUS	8	-0.421684	-1.055460	0.361624	1.000000	1.000
583	GOBP-G-PROTEIN-COUPLED-GLUTAMATE-RECEPTOR-SIGN...	8	-0.432013	-1.055966	0.387097	1.000000	1.000
584	GOBP-POSITIVE-REGULATION.OF.MULTICELLULAR.ORGAN...	32	-0.302216	-1.057806	0.376491	1.000000	1.000
585	GOBP-CELLULAR-RESPONSE.TO.HORMONE-STIMULUS	11	-0.382360	-1.058641	0.377163	1.000000	1.000
586	GOBP-POSITIVE-REGULATION.OF.APOPTOTIC-SIGNALIN...	5	-0.508850	-1.069576	0.364662	1.000000	1.000
587	REACTOME_NUCLEAR-EVENTS-KINASE-AND-TRANSCRIPTI...	11	-0.399388	-1.082255	0.373473	1.000000	1.000
588	REACTOME-INTRACELLULAR-SIGNALING_BY_SECOND_MES...	15	-0.363970	-1.082823	0.343525	1.000000	1.000
589	GOBP-SENSORY_PERCEPTION_OF_PAIN	5	-0.514541	-1.097756	0.337864	1.000000	1.000
590	GOBP-VESICLE-MEDIATED-TRANSPORT-IN-SYNAPSE	7	-0.457735	-1.099625	0.335849	1.000000	1.000
591	GOBP-ENZYME-LINKED-RECEPTOR-PROTEIN-SIGNALING....	24	-0.329189	-1.103545	0.340619	1.000000	1.000
592	GOBP-RESPONSE.TO.MOLECULE.OF.BACTERIAL-ORIGIN	13	-0.381479	-1.108690	0.310219	1.000000	1.000
593	GOBP-REGULATION.OF.PROTEIN-MODIFICATION_PROCESS	29	-0.321889	-1.111505	0.362500	1.000000	1.000
594	GOBP-SIGNAL-RELEASE	14	-0.364823	-1.112872	0.325000	1.000000	1.000
595	REACTOME-CLASS_C_3-METABOTROPIC-GLUTAMATE-PHER...	7	-0.467421	-1.113107	0.323917	1.000000	1.000
596	GOBP-RESPONSE.TO.BACTERIUM	13	-0.381479	-1.114098	0.300725	1.000000	1.000
597	GOBP-DEFENSE-RESPONSE.TO.OTHER-ORGANISM	9	-0.424023	-1.116243	0.317940	1.000000	1.000
598	GOBP-T-CELL-ACTIVATION	8	-0.440402	-1.116846	0.311808	1.000000	1.000
599	GOBP-IMMUNE-EFFECTOR-PROCESS	10	-0.421477	-1.118004	0.319312	1.000000	1.000

Continuation of Table S17

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
600	GOBP-POSITIVE-REGULATION_OF_CYTOKINE-PRODUCTION	GO-0001819	7	-0.473974	-1.122191	0.323793	1.000000	1.000
601	GOBP-MYELOID-CELL-DIFFERENTIATION	GO-0030099	13	-0.394082	-1.124852	0.323636	1.000000	1.000
602	GOBP-INTRACELLULAR-PROTEIN-TRANSPORT	GO-0006886	9	-0.434450	-1.125901	0.304348	1.000000	1.000
603	GOBP-REGULATION_OF_CELLULAR-RESPONSE_TO_STRESS	GO-0080135	9	-0.436322	-1.133599	0.282908	1.000000	1.000
604	GOBP-CIRCADIAN-RHYTHM	GO-0007623	13	-0.398569	-1.135474	0.289617	1.000000	1.000
605	GOBP-RESPONSE_TO_CADMIUM_ION	GO-0046686	6	-0.497680	-1.135741	0.298279	1.000000	1.000
606	GOBP-NEGATIVE-REGULATION_OF_DEVELOPMENTAL-PROCESS	GO-0051093	13	-0.401756	-1.136608	0.284710	1.000000	1.000
607	REACTOME-GPCR-LIGAND-BINDING	R-RNO-500792	8	-0.450624	-1.137968	0.302632	1.000000	1.000
608	GOBP-TISSUE-HOMEOSTASIS	GO-0001894	5	-0.551256	-1.138624	0.306358	1.000000	1.000
609	GOBP-TRANSMEMBRANE-RECEPTOR-PROTEIN-SERINE-THR...	GO-0007178	6	-0.508179	-1.140026	0.322097	1.000000	1.000
610	REACTOME-PTEN-REGULATION	R-RNO-6807070	5	-0.536815	-1.140867	0.321839	1.000000	1.000
611	GOBP-MUSCLE-ORGAN-DEVELOPMENT	GO-0007517	9	-0.443124	-1.141710	0.296429	1.000000	1.000
612	GOBP-RESPONSE_TO_CYTOKINE	GO-0034097	23	-0.341815	-1.147188	0.290844	1.000000	1.000
613	REACTOME-G-PROTEIN-MEDIATED-EVENTS	GO-0007423	9	-0.443302	-1.148263	0.292776	1.000000	1.000
614	HALLMARK-TNFA-SIGNALING-VIA-NFKB	M5890	14	-0.388945	-1.149273	0.281250	1.000000	1.000
615	GOBP-CELLULAR-RESPONSE_TO_CHEMICAL-STRESS	GO-0062197	7	-0.478848	-1.152781	0.312741	1.000000	1.000
616	GOBP-CELLULAR-RESPONSE_TO_REACTIVE-OXYGEN-SPECIES	GO-0034614	7	-0.478848	-1.157208	0.282477	1.000000	1.000
617	GOBP-SENSORY-ORGAN-DEVELOPMENT	GO-0007423	8	-0.459658	-1.157982	0.275605	1.000000	1.000
618	GOBP-RESPONSE_TO_NITROGEN-COMPOUND	GO-1901698	34	-0.324602	-1.158801	0.260274	1.000000	1.000
619	GOBP-TUBE-DEVELOPMENT	GO-0035295	18	-0.367834	-1.159369	0.270945	1.000000	1.000
620	GOBP-RESPONSE_TO_BIOTIC-STIMULUS	GO-0009607	17	-0.379776	-1.161181	0.275000	1.000000	1.000
621	GOBP-REGULATION_OF-NEUROTRANSMITTER-LEVELS	GO-0001505	7	-0.487229	-1.165854	0.258589	1.000000	1.000
622	GOBP-INTRACELLULAR-TRANSPORT	GO-0046907	11	-0.427955	-1.168588	0.284895	1.000000	1.000
623	GOBP-MULTI-ORGANISM-PROCESS	GO-0051704	16	-0.385973	-1.169561	0.252951	1.000000	1.000
624	GOBP-INTRACELLULAR-RECEPTOR-SIGNALING-PATHWAY	GO-0030522	5	-0.547279	-1.171722	0.279029	1.000000	1.000
625	GOBP-DEVELOPMENTAL-PROCESS-INVOLVED-IN-REPRODU...	GO-0003006	11	-0.428170	-1.172364	0.273874	1.000000	1.000
626	GOBP-RESPONSE_TO-GROWTH-FACTOR	GO-0070848	18	-0.373102	-1.172486	0.270650	1.000000	1.000
627	REACTOME-CA-DEPENDENT-EVENTS	R-RNO-111996	8	-0.467645	-1.173623	0.262570	1.000000	1.000
628	GOBP-RESPONSE_TO-WOUNDING	GO-0009611	15	-0.394074	-1.174360	0.239604	1.000000	1.000
629	GOBP-REGULATION_OF-TRANSPORT	GO-0051049	44	-0.320616	-1.174566	0.230118	1.000000	1.000
630	GOBP-INNATE-IMMUNE-RESPONSE	GO-0045087	7	-0.498767	-1.176941	0.246094	1.000000	1.000
631	GOBP-CELLULAR-RESPONSE_TO-DNA-DAMAGE-STIMULUS	GO-0006974	5	-0.553815	-1.179150	0.274336	1.000000	1.000
632	GOBP-NEUROTRANSMITTER-TRANSPORT	GO-0006836	7	-0.487229	-1.179804	0.255083	1.000000	1.000
633	GOBP-CELLULAR-RESPONSE_TO-ABIOTIC-STIMULUS	GO-0071214	7	-0.489387	-1.184321	0.254335	1.000000	1.000
634	GOBP-NEGATIVE-REGULATION_OF-CELL-DIFFERENTIATION	GO-0045596	13	-0.401756	-1.184588	0.237660	1.000000	1.000
635	GOBP-POSITIVE-REGULATION_OF-ANION-TRANSPORT	GO-1903793	9	-0.459818	-1.185317	0.264815	1.000000	1.000
636	GOBP-APOPTOTIC-PROCESS	GO-0006915	35	-0.330345	-1.187828	0.229730	1.000000	1.000
637	GOBP-REGULATION_OF-NEUROTRANSMITTER-TRANSPORT	GO-0051588	6	-0.523714	-1.204312	0.240076	1.000000	1.000
638	GOBP-RESPONSE_TO-ENDOGENOUS-STIMULUS	GO-0009719	34	-0.336124	-1.209688	0.186047	1.000000	1.000
639	GOBP-MULTICELLULAR-ORGANISM-REPRODUCTION	GO-0032504	12	-0.418760	-1.210626	0.223636	1.000000	1.000
640	GOBP-RESPONSE_TO-OXYGEN-CONTAINING-COMPOUND	GO-1901700	39	-0.330835	-1.210829	0.198413	1.000000	1.000
641	GOBP-CELLULAR-GLUCOSE-HOMEOSTASIS	GO-0001678	5	-0.579450	-1.224206	0.224206	1.000000	1.000
642	GOBP-POSITIVE-REGULATION_OF-CELLULAR-PROTEIN-L...	GO-1903829	7	-0.519609	-1.222117	0.210630	1.000000	1.000

Continuation of Table S17

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
643 REACTOME-CELLULAR_SENESCENCE	R-RNO-2559583	6	-0.539751	-1.231341	0.213611	1.000000	1.000
644 GOBP-RESPONSE.TO.HORMONE	GO-0009725	20	-0.385429	-1.234662	0.175347	1.000000	1.000
645 REACTOME_SENESCENCE-ASSOCIATED-SECRETORY_PHENO...	R-RNO-2559582	6	-0.539751	-1.237579	0.227778	1.000000	1.000
646 GOBP-POSITIVE-REGULATION-OF-TRANSCRIPTION-BY-R...	GO-0045944	24	-0.373162	-1.238477	0.179115	1.000000	1.000
647 GOBP-NUCLEAR-TRANSPORT	GO-0051169	5	-0.571574	-1.239763	0.208647	1.000000	1.000
648 GOBP-WOUND-HEALING	GO-0042060	13	-0.437100	-1.240211	0.209220	1.000000	1.000
649 GOBP-ENDOMEMBRANE-SYSTEM-ORGANIZATION	GO-0010256	6	-0.542079	-1.241413	0.216822	1.000000	1.000
650 GOBP-RESPONSE.TO.LIPID	GO-0033993	19	-0.394147	-1.247149	0.195164	1.000000	1.000
651 GOBP-POSITIVE-REGULATION-OF-RESPONSE.TO-EXTERN...	GO-0032103	9	-0.483751	-1.254024	0.199275	1.000000	1.000
652 GOBP-POSITIVE-REGULATION-OF-CELL-POPULATION-PR...	GO-0008284	21	-0.390006	-1.254825	0.169611	1.000000	1.000
653 GOBP-SPROUTING-ANGIOGENESIS	GO-0002040	5	-0.587800	-1.255246	0.217143	1.000000	1.000
654 GOBP-REGULATION-OF-ORGANELLE-ORGANIZATION	GO-0033043	14	-0.423197	-1.255777	0.177331	1.000000	1.000
655 REACTOME-CELL-CYCLE-MITOTIC	R-RNO-69278	5	-0.594870	-1.262422	0.215534	1.000000	1.000
656 REACTOME-SIGNALING-BY-WNT	R-RNO-195721	7	-0.539098	-1.268229	0.215470	1.000000	1.000
657 GOBP-POSITIVE-REGULATION-OF-GENE-EXPRESSION	GO-0010628	16	-0.413721	-1.273607	0.174863	1.000000	1.000
658 GOBP-RESPONSE.TO.PEPTIDE	GO-1901652	18	-0.409999	-1.276927	0.149228	1.000000	1.000
659 GOBP-POSITIVE-REGULATION-OF-BIOSYNTHETIC-PROCESS	GO-0009891	27	-0.370181	-1.280812	0.142373	1.000000	1.000
660 GOBP-ANATOMICAL-STRUCTURE-HOMEOSTASIS	GO-0060249	7	-0.551538	-1.293833	0.180113	1.000000	1.000
661 GOBP-NEUROTRANSMITTER-SECRETION	GO-0007269	6	-0.571402	-1.298017	0.167293	1.000000	1.000
662 GOBP-REPRODUCTION	GO-0000003	18	-0.415411	-1.309239	0.139746	1.000000	1.000
663 GOBP-RESPONSE.TO-INSULIN	GO-0032868	5	-0.611207	-1.309444	0.177449	1.000000	1.000
664 GOBP-LEUKOCYTE-DIFFERENTIATION	GO-0002521	15	-0.436468	-1.311407	0.144366	1.000000	1.000
665 GOBP-LYMPHOCYTE-ACTIVATION	GO-0046649	9	-0.505247	-1.312335	0.168880	1.000000	1.000
666 GOBP-VASCULATURE-DEVELOPMENT	GO-0001944	17	-0.412708	-1.314231	0.134513	1.000000	1.000
667 REACTOME-G-ALPHA-Z-SIGNALING-EVENTS	R-RNO-418597	5	-0.599928	-1.314658	0.153846	1.000000	1.000
668 GOBP-DNA-METABOLIC-PROCESS	GO-0006259	6	-0.590536	-1.316252	0.146947	1.000000	1.000
669 REACTOME-G-ALPHA-Q-SIGNALING-EVENTS	R-RNO-416476	6	-0.574715	-1.324297	0.145422	1.000000	1.000
670 GOBP-EPITHELIAL-CELL-PROLIFERATION	GO-0050673	12	-0.482462	-1.332953	0.123574	1.000000	1.000
671 GOBP-NEGATIVE-REGULATION-OF-CELL-POPULATION-PR...	GO-0008285	9	-0.526182	-1.336109	0.164021	1.000000	1.000
672 GOBP-EXOCYTOSIS	GO-0006887	11	-0.491934	-1.338361	0.134752	1.000000	1.000
673 GOBP-CHROMATIN-ORGANIZATION	GO-0006325	5	-0.634096	-1.350145	0.144665	1.000000	1.000
674 GOBP-CYTOKINE-PRODUCTION	GO-0001816	10	-0.500136	-1.355593	0.123616	1.000000	1.000
675 GOBP-CELLULAR-RESPONSE.TO.LIPID	GO-0071396	15	-0.451310	-1.356311	0.128521	1.000000	1.000
676 GOBP-EMBRYONIC-MORPHOGENESIS	GO-0048598	6	-0.598975	-1.369116	0.123260	1.000000	1.000
677 GOBP-POSITIVE-REGULATION-OF-NUCLEOBASE-CONTAIN...	GO-0045935	28	-0.404568	-1.369721	0.093537	1.000000	1.000
678 GOBP-RHYTHMIC-PROCESS	GO-0048511	15	-0.460344	-1.369945	0.123862	1.000000	1.000
679 GOBP-CELLULAR-RESPONSE.TO-NITROGEN-COMPOUND	GO-1901699	20	-0.432242	-1.375963	0.094033	1.000000	1.000
680 GOBP-REGULATION-OF-CELL-ACTIVATION	GO-0050865	8	-0.562184	-1.391066	0.088448	1.000000	1.000
681 GOBP-APOPTOTIC-SIGNALING-PATHWAY	GO-0097190	15	-0.468701	-1.395557	0.104452	1.000000	1.000
682 REACTOME-MEMBRANE-TRAFFICKING	R-RNO-199991	5	-0.666381	-1.422593	0.118421	0.967296	1.000
683 GOBP-SENSORY_PERCEPTION	GO-0007600	9	-0.559274	-1.426705	0.100569	0.973322	1.000
684 GOBP-PROTEIN-MODIFICATION-BY-SMALL-PROTEIN-CON...	GO-0070647	7	-0.603033	-1.427123	0.095149	0.998888	1.000
685 GOBP-MYELOID-LEUKOCYTE-ACTIVATION	GO-0002274	8	-0.581523	-1.428807	0.087199	1.000000	1.000

Continuation of Table S17

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
686 REACTOME-VESICLE-MEDIATED-TRANSPORT	R-RNO-5653656	5	-0.666381	-1.432497	0.104046	1.000000	1.000
687 GOBP-LEUKOCYTE-MEDIATED-IMMUNITY	GO-0002443	7	-0.606019	-1.450108	0.084149	0.965792	1.000
688 GOBP-LOCOMOTORY-BEHAVIOR	GO-0007626	7	-0.593397	-1.450393	0.090559	0.995552	1.000
689 GOBP-RESPONSE-TO-ORGANIC-CYCLIC-COMPOUND	GO-0014070	20	-0.450526	-1.458316	0.051002	0.983416	1.000
690 GOBP-REGULATION-OF-ANION-TRANSPORT	GO-0044070	20	-0.444602	-1.459106	0.066318	1.000000	1.000
691 GOBP-ANIMAL-ORGAN-MORPHOGENESIS	GO-0009887	12	-0.521575	-1.460099	0.073741	1.000000	1.000
692 GOBP-IMMUNE-SYSTEM-DEVELOPMENT	GO-0002520	17	-0.478511	-1.461233	0.066038	1.000000	1.000
693 GOBP-REGULATION-OF-RESPONSE-TO-STRESS	GO-0080134	19	-0.462979	-1.467809	0.066308	1.000000	1.000
694 GOBP-REGULATION-OF-BODY-FLUID-LEVELS	GO-0050878	11	-0.528423	-1.475043	0.086556	1.000000	1.000
695 REACTOME-CELL-CYCLE	R-RNO-1640170	6	-0.662755	-1.476919	0.055856	1.000000	1.000
696 GOBP-SKELETAL-MUSCLE-ORGAN-DEVELOPMENT	GO-0060538	5	-0.686747	-1.479346	0.055118	1.000000	1.000
697 GOBP-PROTEIN-MODIFICATION-BY-SMALL-PROTEIN-CON...	GO-0032446	6	-0.659361	-1.491438	0.069943	1.000000	1.000
698 REACTOME-BETA-CATENIN-INDEPENDENT-WNT-SIGNALING	R-RNO-3858494	5	-0.699678	-1.493149	0.058712	1.000000	1.000
699 GOBP-ANATOMICAL-STRUCTURE-FORMATION-INVOLVED-I...	GO-0048646	20	-0.454745	-1.495917	0.052158	1.000000	1.000
700 GOBP-REGULATION-OF-RESPONSE-TO-EXTERNAL-STIMULUS	GO-0032101	15	-0.511835	-1.507414	0.042403	1.000000	1.000
701 GOBP-MONONUCLEAR-CELL-DIFFERENTIATION	GO-1903131	7	-0.629639	-1.525069	0.064912	1.000000	1.000
702 GOBP-ORGANIC-HYDROXY-COMPOUND-TRANSPORT	GO-0015850	6	-0.674419	-1.528868	0.054820	1.000000	1.000
703 REACTOME-RHO-GTPASE-EFFECTORS	R-RNO-195258	9	-0.604415	-1.539969	0.054206	1.000000	1.000
704 GOBP-PEPTIDYL-LYSINE-MODIFICATION	GO-0018205	5	-0.729186	-1.545917	0.047445	1.000000	1.000
705 GOBP-CHROMOSOME-ORGANIZATION	GO-0051276	6	-0.688163	-1.585605	0.025440	0.963933	1.000
706 GOBP-CELLULAR-RESPONSE-TO-OXYGEN-CONTAINING-CO...	GO-1901701	29	-0.458270	-1.586052	0.020443	1.000000	1.000
707 GOBP-CIRCADIAN-REGULATION-OF-GENE-EXPRESSION	GO-0032922	5	-0.751861	-1.587849	0.027290	1.000000	1.000
708 REACTOME-SIGNALING-BY-RHO-GTPASES-MIRO-GTPASES...	R-RNO-9716542	9	-0.604415	-1.588145	0.038168	1.000000	1.000
709 GOBP-CELL-POPULATION-PROLIFERATION	GO-0008283	31	-0.447355	-1.599630	0.022034	1.000000	1.000
710 GOBP-CELLULAR-RESPONSE-TO-ORGANIC-CYCLIC-COMPOUND	GO-0071407	13	-0.560914	-1.630957	0.026502	1.000000	1.000
711 GOBP-REPRODUCTIVE-SYSTEM-DEVELOPMENT	GO-0061458	6	-0.729849	-1.661377	0.009174	0.965187	1.000
712 GOBP-RESPONSE-TO-INTERLEUKIN-1	GO-0070555	5	-0.781354	-1.682932	0.017208	0.940891	1.000
713 GOBP-COAGULATION	GO-0050817	8	-0.676126	-1.709760	0.020794	0.878536	0.995
714 GOBP-PLATELET-ACTIVATION	GO-0030168	6	-0.777872	-1.756444	0.007692	0.706238	0.974
715 REACTOME-NEUTROPHIL-DEGRANULATION	R-RNO-6798695	6	-0.789539	-1.767587	0.003466	0.807992	0.964
716 GOBP-MYELOID-LEUKOCYTE-MEDIATED-IMMUNITY	GO-0002444	6	-0.789539	-1.787366	0.003906	0.897560	0.935
717 GOBP-CELL-ACTIVATION-INVOLVED-IN-IMMUNE-RESPONSE	GO-0002263	6	-0.789539	-1.810870	0.005386	1.000000	0.892
718 GOBP-CELL-ACTIVATION	GO-0001775	21	-0.566059	-1.827684	0.003503	1.000000	0.844

End of Table

Supplementary Table S18: CB early profile (8 DPL peak) GSEA results.

Begin of Table S18									
	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val	
0	GOBP-POSITIVE-REGULATION_OF_TRANSMEMBRANE_TRAN...	GO-0034764	7	0.634079	1.681567	0.018100	1.000000	0.949	
1	GOBP-POSITIVE-REGULATION_OF_CATION_TRANSMEMBR...	GO-1904064	5	0.685165	1.601183	0.050000	1.000000	0.989	
2	HALLMARK-P13K-AKT-MTOR-SIGNALING	M5923	6	0.595609	1.559698	0.052209	1.000000	0.994	
3	GOBP-MAINTENANCE-OF-LOCATION	GO-0051235	7	0.548383	1.487546	0.053812	1.000000	1.000	
4	GOBP-POSITIVE-REGULATION_OF_SMOOTH_MUSCLE_CELL...	GO-0048661	5	0.626506	1.450866	0.073913	1.000000	1.000	
5	GOBP-MULTICELLULAR_ORGANISMAL_RESPONSE_TO_STRESS	GO-0033555	5	0.590239	1.400324	0.090909	1.000000	1.000	
6	GOBP-REGULATION_OF_CELL_SIZE	GO-0008361	5	0.602410	1.398462	0.099617	1.000000	1.000	
7	GOBP-DEVELOPMENTAL_CELL-GROWTH	GO-0048588	5	0.578313	1.350037	0.105660	1.000000	1.000	
8	GOBP-REGULATION_OF_CELLULAR_COMPONENT_SIZE	GO-0032535	7	0.481481	1.291670	0.116279	1.000000	1.000	
9	HALLMARK-EPITHELIAL_MESENCHYMAL_TRANSITION	M5930	5	0.542169	1.279244	0.150376	1.000000	1.000	
10	GOBP-POSITIVE-REGULATION_OF_CELL-GROWTH	GO-0044255	6	0.500000	1.255753	0.162879	1.000000	1.000	
11	GOBP-CELLULAR_LIPID_METABOLIC_PROCESS	GO-0004255	7	0.463166	1.249504	0.181373	1.000000	1.000	
12	GOBP-IMPORT-INTO-CELL	GO-0098657	6	0.487805	1.239003	0.163180	1.000000	1.000	
13	GOBP-RESPONSE-TO-ETHANOL	GO-0045471	5	0.530120	1.235441	0.189003	1.000000	1.000	
14	GOBP-LEUKOCYTE-MIGRATION	GO-0050900	6	0.473379	1.183697	0.247826	1.000000	1.000	
15	GOBP-NEUROTRANSMITTER_TRANSPORT	GO-0006836	7	0.419753	1.175854	0.240000	1.000000	1.000	
16	GOBP-NEUROINFLAMMATORY_RESPONSE	GO-0150076	5	0.506024	1.175312	0.216867	1.000000	1.000	
17	GOBP-REGULATION_OF_PPTIDYL_TYROSINE_PHOSPHORY...	GO-0050730	9	0.379754	1.169050	0.251337	1.000000	1.000	
18	GOBP-PURINE-CONTAINING-COMPOUND_METABOLIC_PROCESS	GO-0072521	5	0.506024	1.158525	0.248120	1.000000	1.000	
19	GOBP-REGULATION_OF_CIRCADIAN_RHYTHM	GO-0042752	7	0.419753	1.141470	0.231405	1.000000	1.000	
20	REACTOME-ADAPTIVE-IMMUNE-SYSTEM	R-RNO-1280218	9	0.376899	1.124814	0.238806	1.000000	1.000	
21	GOBP-CALCIUM-MEDIATED-SIGNALING	GO-0019722	10	0.344439	1.124603	0.255556	1.000000	1.000	
22	GOBP-REGULATION_OF_NEUROTRANSMITTER_LEVELS	GO-0001505	7	0.419753	1.120681	0.261044	1.000000	1.000	
23	GOBP-POSITIVE-REGULATION_OF_DNA-BINDING_TRANSC...	GO-0051091	10	0.355452	1.098615	0.320442	1.000000	1.000	
24	GOBP-PHAGOCYTOSIS	GO-0006909	5	0.474411	1.097960	0.307407	1.000000	1.000	
25	GOBP-SYNAPTIC-SIGNALING	GO-0099536	47	0.213272	1.085643	0.319149	1.000000	1.000	
26	GOBP-POSITIVE-REGULATION_OF_PPTIDYL_TYROSINE...	GO-0050731	8	0.387488	1.074784	0.347222	1.000000	1.000	
27	GOBP-POSITIVE-REGULATION_OF_SECRETION	GO-0051047	6	0.426829	1.074168	0.329218	1.000000	1.000	
28	GOBP-REGULATION_OF_NEUROTRANSMITTER_TRANSPORT	GO-0051588	6	0.414634	1.070534	0.334677	1.000000	1.000	
29	GOBP-REGULATION_OF_METAL-ION_TRANSPORT	GO-0010959	6	0.418551	1.069529	0.330645	1.000000	1.000	
30	GOBP-ANION_TRANSMEMBRANE_TRANSPORT	GO-0098656	7	0.380083	1.061942	0.352423	1.000000	1.000	
31	GOBP-NEUROTRANSMITTER-SECRETION	GO-0007269	6	0.414634	1.054983	0.356364	1.000000	1.000	
32	GOBP-LONG-TERM-SYNAPTIC-DEPRESSION	GO-0060292	5	0.445783	1.053680	0.371901	1.000000	1.000	
33	GOBP-GENERATION_OF_PRECURSOR_METABOLITES-AND-E...	GO-0006091	5	0.457831	1.052033	0.335766	1.000000	1.000	
34	GOBP-REGULATION_OF_CATION_TRANSMEMBRANE_TRANSPORT	GO-1904062	16	0.276959	1.049990	0.356164	1.000000	1.000	
35	GOBP-NEGATIVE-REGULATION_OF_PPTIDASE-ACTIVITY	GO-0010466	6	0.413066	1.045760	0.354086	1.000000	1.000	
36	GOBP-EXTRINSIC-APOPTOTIC-SIGNALING_PATHWAY	GO-0097191	7	0.382716	1.045181	0.392405	1.000000	1.000	
37	GOBP-REGULATION_OF_SYNAPTIC_TRANSMISSION-GLUTA...	GO-0051966	12	0.312473	1.040453	0.383648	1.000000	1.000	
38	GOBP-REGULATION_OF_TRANSMEMBRANE_TRANSPORT	GO-0034762	23	0.253381	1.036645	0.390805	1.000000	1.000	
39	GOBP-ORGANIC-HYDROXY-COMPOUND_METABOLIC_PROCESS	GO-1901615	7	0.376333	1.033767	0.400000	1.000000	1.000	
40	GOBP-REGULATION_OF_SYNAPSE-STRUCTURE-OR-ACTIVITY	GO-0050803	11	0.315907	1.031784	0.366013	1.000000	1.000	

Continuation of Table S18

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
41	REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATION	R-RNO-597592	7	0.382716	1.029434	0.403509	1.000000
42	GOBP_NEGATIVE_REGULATION_OF_LOCOMOTION	GO-0040013	5	0.437111	1.027291	0.364341	1.000000
43	GOBP_PEPIDYL_TYROSINE_MODIFICATION	GO-0018212	10	0.323728	1.026020	0.421875	1.000000
44	GOBP_MONOAMINE_TRANSPORT	GO-0015844	5	0.421678	0.995500	0.422481	1.000000
45	GOBP_PROTEIN_KINASE_B_SIGNALING	GO-0043491	6	0.386692	0.990706	0.437247	1.000000
46	GOBP_TRANSMEMBRANE_TRANSPORT	GO-0055085	27	0.226163	0.988514	0.500000	1.000000
47	GOBP_DEVELOPMENTAL_MATURATION	GO-0021700	5	0.424817	0.975783	0.447876	1.000000
48	GOBP_SYNAPTIC_TRANSMISSION_GLUTAMATERGIC	GO-0035249	13	0.281411	0.971804	0.522988	1.000000
49	GOBP_DENDRITIC_SPINE_DEVELOPMENT	GO-0060996	6	0.388227	0.964698	0.500000	1.000000
50	GOBP_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING...	GO-2001236	6	0.378049	0.947307	0.504202	1.000000
51	GOBP_DENDRITE_MORPHOGENESIS	GO-0048813	6	0.374035	0.941670	0.523810	1.000000
52	GOBP_DENDRITIC_SPINE_MORPHOGENESIS	GO-0060997	5	0.403918	0.925754	0.516605	1.000000
53	GOBP_REGULATION_OF_MEMBRANE_POTENTIAL	GO-0042391	17	0.239437	0.916956	0.571429	1.000000
54	GOBP_PATERN_SPECIFICATION_PROCESS	GO-0007389	6	0.361926	0.909083	0.537778	1.000000
55	GOBP_INORGANIC_ION_TRANSMEMBRANE_TRANSPORT	GO-0098660	9	0.291581	0.904032	0.601010	1.000000
56	REACTOME_ANTINFLAMMATORY_RESPONSE_FAVOURING...	R-HSA-9662851	5	0.383721	0.897969	0.608163	1.000000
57	GOBP_MORPHOGENESIS_OF_AN_EPITHELIUM	GO-0002009	6	0.348872	0.896994	0.628459	1.000000
58	GOBP_REGIONALIZATION	GO-0003002	6	0.361926	0.895205	0.560484	1.000000
59	GOBP_CATION_TRANSMEMBRANE_TRANSPORT	GO-0098655	18	0.224483	0.893480	0.661157	1.000000
60	GOBP_REGULATION_OF_NMDA_RECEPTOR_ACTIVITY	GO-2000310	10	0.282051	0.888327	0.632979	1.000000
61	GOBP_REGULATION_OF_LONG_TERM_SYNAPTIC_POTENTIAL...	GO-1900271	6	0.351370	0.879746	0.597561	1.000000
62	GOBP_POSITIVE_REGULATION_OF_GLIOGENESIS	GO-0014015	5	0.373494	0.872370	0.637631	1.000000
63	GOBP_REGULATION_OF_GLIOGENESIS	GO-0014013	5	0.373494	0.868551	0.607930	1.000000
64	GOBP_CALCIIUM_ION_TRANSMEMBRANE_TRANSPORT	GO-0070588	7	0.311632	0.865025	0.653509	1.000000
65	GOBP_TISSUE_MORPHOGENESIS	GO-0048729	7	0.315186	0.864055	0.646091	1.000000
66	GOBP_REGULATION_OF_SIGNALING_RECEPTOR_ACTIVITY	GO-0010469	14	0.243939	0.862282	0.680000	1.000000
67	HALLMARK_ALLOGRAFT_REJECTION	M950	7	0.315448	0.854894	0.621005	1.000000
68	GOBP_CYTOSOLIC_CALCIIUM_ION_TRANSPORT	GO-0060401	7	0.311632	0.849554	0.656652	1.000000
69	GOBP_GLIAL_CELL_DIFFERENTIATION	GO-0010001	10	0.264346	0.841469	0.668639	1.000000
70	GOBP_SMOOTH_MUSCLE_CELL_PROLIFERATION	GO-0048659	6	0.326512	0.834000	0.693023	1.000000
71	GOBP_CALCIIUM_ION_TRANSPORT_INTO_CYTOSOL	GO-0060402	7	0.311632	0.830171	0.652000	1.000000
72	REACTOME_RAS_ACTIVATION_UPON_CA2_INFLUX_THROUGH...	R-HSA-442982	6	0.317073	0.825116	0.681034	1.000000
73	GOBP_PROTEIN_LOCALIZATION_TO_PLASMA_MEMBRANE	GO-0072659	7	0.308642	0.825014	0.709544	1.000000
74	GOBP_EMBRYO_DEVELOPMENT	GO-0009790	14	0.228986	0.824119	0.762431	1.000000
75	GOBP_POSITIVE_REGULATION_OF_NERVOUS_SYSTEM_DEV...	GO-0051962	12	0.239554	0.824112	0.718563	1.000000
76	GOBP_REGULATION_OF_VASCULAR_ASSOCIATED_SMOOTH...	GO-1904705	5	0.347794	0.821874	0.705454	1.000000
77	GOBP_POSITIVE_REGULATION_OF_LONG_TERM_SYNAPTIC...	GO-1900273	5	0.359789	0.814904	0.689139	1.000000
78	GOBP_GLIOGENESIS	GO-0042063	12	0.235990	0.802063	0.760234	1.000000
79	GOBP_REGULATION_OF_POSTSYNAPTIC_MEMBRANE_POTEN...	GO-0060078	14	0.229730	0.801394	0.760479	1.000000
80	GOBP_POSITIVE_REGULATION_OF_NEUROGENESIS	GO-0050769	12	0.239546	0.800818	0.722628	1.000000
81	GOBP_EPITHELIAL_CELL_DIFFERENTIATION	GO-0030855	7	0.298946	0.799980	0.746835	1.000000
82	GOBP_POSITIVE_REGULATION_OF_CELL_DEVELOPMENT	GO-0010720	12	0.239554	0.799867	0.737143	1.000000
83	GOBP_REGULATION_OF_ANION_TRANSMEMBRANE_TRANSPORT	GO-1903959	5	0.337733	0.799748	0.759398	1.000000

Continuation of Table S18

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
84	GOBP-POSITIVE-REGULATION_OF_NEURON-PROJECTION...	5	0.348753	0.794252	0.796296	1.000000	1.000
85	GOBP-POSITIVE-REGULATION_OF_LEUKOCYTE-CELL-CEL...	5	0.337349	0.784630	0.805447	1.000000	1.000
86	GOBP-POSITIVE-REGULATION_OF_CELL-CELL-ADHESION	5	0.337349	0.784565	0.810606	1.000000	1.000
87	GOBP-REGULATION_OF_PROTEIN-CATABOLIC-PROCESS	7	0.281888	0.782932	0.778261	1.000000	1.000
88	GOBP-SIGNAL-RELEASE	14	0.212320	0.775929	0.848485	1.000000	1.000
89	GOBP-REGULATION_OF_POSTSYNAPSE-ORGANIZATION	6	0.297679	0.775893	0.838057	1.000000	1.000
90	GOBP-DIVALENT-INORGANIC-CATION-HOMEOSTASIS	13	0.226667	0.765988	0.764706	1.000000	1.000
91	GOBP-REGULATION_OF_CYTOSOLIC-CALCIUM-ION-CONCE...	13	0.226667	0.764472	0.826667	1.000000	1.000
92	REACTOME-EPHLEPHRIN-SIGNALING	6	0.304878	0.763666	0.828947	1.000000	1.000
93	GOBP-REGULATION_OF_PHOSPHOLIPASE-ACTIVITY	6	0.291749	0.761602	0.832618	1.000000	1.000
94	REACTOME-SIGNALING-BY-NTRK2-TRKB	6	0.301961	0.760647	0.797571	1.000000	1.000
95	GOBP-SYNAPSE-ORGANIZATION	17	0.204680	0.756041	0.842520	1.000000	1.000
96	GOBP-METAL-ION-TRANSPORT	11	0.222583	0.755444	0.808989	1.000000	1.000
97	GOBP-REGULATION_OF_PHOSPHOLIPASE-C-ACTIVITY	5	0.318083	0.754633	0.829545	1.000000	1.000
98	GOBP-POSITIVE-REGULATION_OF_LIPASE-ACTIVITY	5	0.318083	0.752016	0.809160	1.000000	1.000
99	GOBP-CATION-TRANSPORT	25	0.169638	0.746098	0.855422	1.000000	1.000
100	GOBP-REGULATION_OF_PROTEIN-TYROSINE-KINASE-ACT...	5	0.316145	0.739822	0.830777	1.000000	1.000
101	GOBP-TELENCEPHALON-DEVELOPMENT	6	0.292683	0.737821	0.836134	1.000000	1.000
102	GOBP-CALCIUM-ION-TRANSPORT	11	0.222583	0.733632	0.852041	1.000000	1.000
103	HALLMARK-KRAS-SIGNALING-UP	6	0.292720	0.729363	0.825726	1.000000	1.000
104	GOBP-REGULATION_OF_LIPASE-ACTIVITY	6	0.291749	0.726278	0.859575	1.000000	1.000
105	GOBP-POSITIVE-REGULATION_OF_PROTEIN-TYROSINE-K...	5	0.316145	0.717369	0.877863	1.000000	1.000
106	GOBP-REGULATION_OF-ANATOMICAL-STRUCTURE-SIZE	10	0.230769	0.716076	0.865285	1.000000	1.000
107	GOBP-CHEMICAL-SYNAPTIC-TRANSMISSION_POSTSYNAPTIC	9	0.240506	0.715221	0.861386	1.000000	1.000
108	HALLMARK-APOPTOSIS	6	0.287659	0.713471	0.861905	1.000000	1.000
109	GOBP-NEGATIVE-REGULATION_OF-CATABOLIC-PROCESS	8	0.248459	0.701080	0.873096	1.000000	1.000
110	GOBP-NEURON-MIGRATION	5	0.298133	0.699933	0.875000	1.000000	1.000
111	GOBP-AMYLOID-BETA-METABOLIC-PROCESS	5	0.289157	0.693705	0.902985	1.000000	1.000
112	GOBP-ORGANIC-ACID-TRANSPORT	7	0.259259	0.693472	0.918803	1.000000	1.000
113	GOBP-EPHRIN-RECEPTOR-SIGNALING-PATHWAY	5	0.301205	0.692274	0.870722	1.000000	1.000
114	GOBP-NEGATIVE-REGULATION_OF-IMMUNE-SYSTEM-PROCESS	5	0.292511	0.686598	0.910156	1.000000	1.000
115	GOBP-AMYLOID-PRECURSOR-PROTEIN-CATABOLIC-PROCESS	5	0.289157	0.674389	0.921162	1.000000	1.000
116	GOBP-AMYLOID-PRECURSOR-PROTEIN-METABOLIC-PROCESS	5	0.289157	0.671919	0.912281	1.000000	1.000
117	GOBP-REGULATION_OF-NEUROTRANSMITTER-RECEPTOR-A...	13	0.186667	0.670323	0.946746	1.000000	1.000
118	GOBP-REGULATION_OF-CATION-CHANNEL-ACTIVITY	14	0.189189	0.662374	0.935065	1.000000	1.000
119	GOBP-AMINO-ACID-TRANSPORT	6	0.256098	0.648466	0.946154	1.000000	1.000
120	GOBP-CARBOXYLIC-ACID-TRANSPORT	6	0.256098	0.635214	0.956863	1.000000	1.000
121	GOBP-NEURON-PROJECTION-ORGANIZATION	8	0.210602	0.634519	0.965812	1.000000	1.000
122	GOBP-BIOLOGICAL-ADHESION	19	0.166682	0.627984	0.982301	1.000000	1.000
123	GOBP-ORGANIC-ANION-TRANSPORT	6	0.260698	0.617411	0.968000	1.000000	1.000
124	GOBP-ACTIN-FILAMENT-BASED-PROCESS	7	0.222222	0.612260	0.942478	1.000000	1.000
125	GOBP-POSTSYNAPSE-ORGANIZATION	10	0.191677	0.603822	0.972527	1.000000	1.000
126	GOBP-REGULATION_OF_NERVOUS-SYSTEM-PROCESS	8	0.201793	0.577702	0.985222	0.999113	1.000

Continuation of Table S18

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
127	GOBP-REGULATION-OF-PROTEIN-LOCALIZATION-TO-CEL...	6	0.222314	0.552862	0.991803	0.998223	1.000
128	GOBP-REGULATION-OF-PROTEIN-LOCALIZATION-TO-MEM...	7	0.198703	0.531375	0.995745	0.994638	1.000
129	GOBP-STRIATED-MUSCLE-CELL-DIFFERENTIATION	9	-0.193886	-0.450544	0.993703	0.996086	1.000
130	GOBP-REGULATION-OF-SYSTEM-PROCESS	18	-0.172399	-0.467421	0.991842	0.995836	1.000
131	GOBP-CELL-JUNCTION-ORGANIZATION	19	-0.174643	-0.476901	0.982778	0.996045	1.000
132	GOBP-REGULATION-OF-SECRETION	14	-0.197071	-0.507269	0.980347	0.991733	1.000
133	GOBP-NEGATIVE-REGULATION-OF-TRANSMEMBRANE-TRAN...	6	-0.247119	-0.508387	0.985526	0.993150	1.000
134	GOBP-NEGATIVE-REGULATION-OF-ANION-TRANSPORT	8	-0.229170	-0.516100	0.982301	0.992868	1.000
135	GOBP-NEUROGENESIS	40	-0.172650	-0.525990	0.969116	0.991707	1.000
136	GOBP-POSITIVE-REGULATION-OF-CELL-PROJECTION_OR...	10	-0.223183	-0.532551	0.974201	0.991232	1.000
137	GOBP-LIPID-EXPORT-FROM-CELL	5	-0.277850	-0.543986	0.991946	0.988855	1.000
138	GOBP-REGULATION-OF-NERVOUS-SYSTEM-DEVELOPMENT	15	-0.203369	-0.555603	0.954076	0.985927	1.000
139	GOBP-REGULATION-OF-CELL-DEVELOPMENT	15	-0.210868	-0.556547	0.963006	0.987243	1.000
140	GOBP-ORGANONITROGEN-COMPOUND-CATABOLIC-PROCESS	9	-0.240705	-0.557480	0.974328	0.985560	1.000
141	GOBP-CELLULAR-AMIDE-METABOLIC-PROCESS	13	-0.219976	-0.561018	0.949701	0.987799	1.000
142	GOBP-PROTEIN-PHOSPHORYLATION	7	-0.259362	-0.561054	0.971286	0.990497	1.000
143	GOBP-DEPHOSPHORYLATION	7	-0.259362	-0.566792	0.967363	0.989674	1.000
144	GOBP-ION-HOMEOSTASIS	16	-0.220759	-0.578842	0.949425	0.985556	1.000
145	GOBP-PEPTIDE-METABOLIC-PROCESS	12	-0.228444	-0.579699	0.945783	0.986823	1.000
146	GOBP-REGULATION-OF-NEUROGENESIS	14	-0.225653	-0.581275	0.950178	0.987651	1.000
147	GOBP-POSITIVE-REGULATION-OF-HYDROLASE-ACTIVITY	16	-0.220654	-0.581678	0.957176	0.989182	1.000
148	GOBP-CIRCULATORY-SYSTEM-PROCESS	5	-0.293884	-0.586455	0.961379	0.988360	1.000
149	GOBP-ADENYLATE-CYCLASE-INHIBITING-G-PROTEIN_CO...	5	-0.296749	-0.586690	0.975477	0.989960	1.000
150	GOBP-FATTY-ACID-TRANSPORT	6	-0.286086	-0.588928	0.953333	0.990332	1.000
151	GOBP-DENDRITE-DEVELOPMENT	9	-0.253643	-0.590114	0.948466	0.991353	1.000
152	GOBP-REGULATION-OF-CELLULAR-COMPONENT-BIOGENESIS	10	-0.254006	-0.593447	0.941919	0.991163	1.000
153	REACTOME-TRANSCRIPTIONAL-REGULATION-BY-MECP2	7	-0.271605	-0.596366	0.951838	0.991160	1.000
154	GOBP-SKIN-DEVELOPMENT	5	-0.306130	-0.599186	0.965326	0.991159	1.000
155	GOBP-CELL-CELL-SIGNALING	56	-0.200858	-0.605848	0.929240	0.988675	1.000
156	GOBP-PROTEIN-CATABOLIC-PROCESS	8	-0.265234	-0.607355	0.944374	0.989458	1.000
157	GOBP-ASSOCIATIVE-LEARNING	7	-0.282554	-0.611691	0.958442	0.988355	1.000
158	GOBP-SECOND-MESSENGER-MEDIATED-SIGNALING	16	-0.230918	-0.613348	0.931634	0.989010	1.000
159	GOBP-MITOCHONDRION-ORGANIZATION	7	-0.283342	-0.614331	0.954068	0.990113	1.000
160	GOBP-PROTEIN-CONTAINING-COMPLEX-SUBUNIT_ORGANI...	14	-0.237607	-0.620384	0.928489	0.987466	1.000
161	GOBP-DICARBOXYLIC-ACID-TRANSPORT	5	-0.320166	-0.622395	0.931081	0.987843	1.000
162	GOBP-MONOCARBOXYLIC-ACID-TRANSPORT	5	-0.320166	-0.628881	0.952957	0.984885	1.000
163	GOBP-PEPTIDE-SECRETION	9	-0.268755	-0.629794	0.916250	0.985992	1.000
164	GOBP-RESPONSE-TO-ACID-CHEMICAL	6	-0.301644	-0.632268	0.918314	0.986058	1.000
165	GOBP-ADENYLATE-CYCLASE-INHIBITING-G-PROTEIN_CO...	9	-0.275620	-0.636440	0.915276	0.984598	1.000
166	GOBP-ACIDIC-AMINO-ACID-TRANSPORT	5	-0.320166	-0.637038	0.940781	0.985917	1.000
167	GOBP-POSITIVE-REGULATION-OF-SYNAPTIC-TRANSMISSION	15	-0.244579	-0.640077	0.914520	0.985308	1.000
168	GOBP-REGULATION-OF-TRANSPORTER-ACTIVITY	17	-0.239102	-0.642434	0.905512	0.985183	1.000
169	GOBP-CARBOHYDRATE-DERIVATIVE-METABOLIC-PROCESS	7	-0.298604	-0.644311	0.924552	0.985458	1.000

Continuation of Table S18

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
170 REACTOME_INTERLEUKIN_4_AND_INTERLEUKIN_13_SIGNALING...	R-RNO-6785807	8	-0.283977	-0.645245	0.922597	0.986452	1.000
171 GOBP_METAL_ION_HOMEOSTASIS	GO-0055065	14	-0.250432	-0.646316	0.902074	0.987338	1.000
172 GOBP_POSITIVE_REGULATION_OF_CELLULAR_COMPONENT...	GO-0044089	9	-0.280358	-0.650148	0.911250	0.985935	1.000
173 GOBP_REGULATION_OF_HYDROLASE_ACTIVITY	GO-0051336	22	-0.229194	-0.651949	0.885301	0.986164	1.000
174 GOBP_REGULATION_OF_PEPIDYL_SERINE_PHOSPHORYLA...	GO-0033135	8	-0.289440	-0.655576	0.912769	0.984907	1.000
175 GOBP_POSITIVE_REGULATION_OF_PEPIDYL_SERINE_PH...	GO-0033138	8	-0.289440	-0.655576	0.912769	0.984907	1.000
176 GOBP_REGULATION_OF_NEURON_PROJECTION_DEVELOPMENT	GO-0010975	16	-0.249055	-0.663219	0.892236	0.981600	1.000
177 GOBP_HORMONE_TRANSPORT	GO-0009914	9	-0.286605	-0.665599	0.878079	0.981199	1.000
178 REACTOME_DAG_AND_IP3_SIGNALING	R-RNO-1489509	8	-0.295281	-0.665896	0.908755	0.982772	1.000
179 GOBP_CELLULAR_ION_HOMEOSTASIS	GO-0006873	14	-0.257362	-0.665943	0.878394	0.984546	1.000
180 GOBP_NEURON_DIFFERENTIATION	GO-0030182	36	-0.225736	-0.666950	0.905782	0.985438	1.000
181 GOBP_NEURON_DEVELOPMENT	GO-0048666	33	-0.225949	-0.670011	0.896368	0.984431	1.000
182 GOBP_LEUKOCYTE_CELL_ADHESION	GO-0007159	6	-0.319552	-0.675286	0.911023	0.981105	1.000
183 GOBP_NEGATIVE_REGULATION_OF_PROTEIN_CATABOLIC...	GO-0042177	5	-0.340745	-0.675607	0.909934	0.982634	1.000
184 GOBP_POSITIVE_REGULATION_OF_CELL_ADHESION	GO-0045785	7	-0.313810	-0.677726	0.902622	0.982364	1.000
185 REACTOME_ASSEMBLY_AND_CELL_SURFACE_PRESENTATIO...	R-RNO-9609736	8	-0.306355	-0.679803	0.883895	0.982143	1.000
186 GOBP_REGULATION_OF_HORMONE_SECRETION	GO-0046883	8	-0.297974	-0.681255	0.886650	0.982428	1.000
187 GOBP_PROTEIN_LOCALIZATION_TO_MEMBRANE	GO-0072657	14	-0.260992	-0.683930	0.867731	0.981563	1.000
188 GOBP_INSULIN_SECRETION	GO-0030073	7	-0.319996	-0.688753	0.866841	0.978463	1.000
189 GOBP_REGULATION_OF_PEPIDE_HORMONE_SECRETION	GO-0090276	6	-0.333844	-0.690467	0.865591	0.978424	1.000
190 GOBP_MUSCLE_CELL_PROLIFERATION	GO-0033002	8	-0.307317	-0.691654	0.861935	0.979046	1.000
191 GOBP_LIPID_LOCALIZATION	GO-0010876	10	-0.293993	-0.691669	0.869148	0.980880	1.000
192 GOBP_CELL_JUNCTION_ASSEMBLY	GO-0034329	8	-0.309910	-0.692878	0.888889	0.981458	1.000
193 GOBP_CELLULAR_RESPONSE_TO_ALCOHOL	GO-0097306	5	-0.355466	-0.694041	0.889972	0.982078	1.000
194 REACTOME_NEGATIVE_REGULATION_OF_NMDA_RECEPTOR...	R-HSA-961732	8	-0.306355	-0.694702	0.875312	0.983265	1.000
195 GOBP_CELL_CELL_ADHESION	GO-0098609	14	-0.271572	-0.695653	0.861111	0.984088	1.000
196 GOBP_REGULATION_OF_TRANS_SYNAPTIC_SIGNALING	GO-0099177	40	-0.228364	-0.698575	0.864693	0.982972	1.000
197 GOBP_REGULATION_OF_MAP_KINASE_ACTIVITY	GO-0043405	9	-0.294355	-0.699447	0.851485	0.983886	1.000
198 REACTOME_SYNAPTIC_ADHESION LIKE MOLECULES	R-RNO-8849932	9	-0.309940	-0.704381	0.864030	0.980168	1.000
199 GOBP_EPIDERMIS_DEVELOPMENT	GO-0008544	5	-0.357499	-0.705539	0.878146	0.980728	1.000
200 GOBP_PEPIDE_HORMONE_SECRETION	GO-0030072	7	-0.319996	-0.706593	0.865359	0.981415	1.000
201 GOBP_MUSCLE_CELL_DEVELOPMENT	GO-0055001	5	-0.358724	-0.707120	0.872801	0.982723	1.000
202 GOBP_REGULATION_OF_PEPIDE_SECRETION	GO-0002791	7	-0.322934	-0.710476	0.868594	0.980845	1.000
203 REACTOME_DEVELOPMENTAL BIOLOGY	R-RNO-1266738	23	-0.248339	-0.711282	0.846847	0.981836	1.000
204 GOBP_REGULATION_OF_CELL_ADHESION	GO-0030155	13	-0.281693	-0.715923	0.861575	0.978361	1.000
205 GOBP_CELL_SURFACE_RECEPTOR_SIGNALING_PATHWAY_I...	GO-1905114	15	-0.280164	-0.716640	0.842410	0.979387	1.000
206 GOBP_PROTEIN_LOCALIZATION_TO_CELL_PERIPHERY	GO-1990778	12	-0.287609	-0.717736	0.817073	0.979912	1.000
207 GOBP_ACTIVATION_OF_PROTEIN_KINASE_ACTIVITY	GO-0032147	11	-0.292900	-0.721006	0.819036	0.978002	1.000
208 GOBP_NEGATIVE_REGULATION_OF_PROTEOLYSIS	GO-0045861	8	-0.319944	-0.721914	0.841495	0.978841	1.000
209 REACTOME_ACTIVATION_OF_NMDA_RECEPTORS_AND_POST...	R-RNO-442755	16	-0.277294	-0.728393	0.819840	0.973131	1.000
210 REACTOME_CLASS_C_3_METABOTROPIC_GLUTAMATE_PHER...	R-RNO-420499	7	-0.335924	-0.729184	0.856579	0.974083	1.000
211 GOBP_CELL_PROJECTION_ORGANIZATION	GO-0030030	34	-0.245045	-0.730975	0.841202	0.973709	1.000
212 GOBP_REGULATION_OF_TRANSPORT	GO-0051049	44	-0.243744	-0.732220	0.834547	0.974001	1.000

Continuation of Table S18

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
213	GOBP-NEGATIVE-REGULATION-OF-APOPTOTIC-SIGNALIN...	7	-0.336986	-0.735430	0.849333	0.971962	1.000
214	GOBP-CELL-CELL-JUNCTION-ORGANIZATION	6	-0.353998	-0.739752	0.856369	0.968332	1.000
215	GOBP-CELLULAR-COMPONENT-DISASSEMBLY	6	-0.358087	-0.740828	0.822517	0.968903	1.000
216	REACTOME-LONG-TERM-POTENTIATION	10	-0.308754	-0.741850	0.817848	0.969468	1.000
217	GOBP-NEGATIVE-REGULATION-OF-CELL-CYCLE	5	-0.371225	-0.746387	0.843490	0.965306	1.000
218	GOBP-NEGATIVE-REGULATION-OF-TRANSPORT	13	-0.299604	-0.755241	0.831982	0.955444	1.000
219	GOBP-COGNITION	28	-0.257377	-0.755861	0.797400	0.956504	1.000
220	REACTOME-GPCR-LIGAND-BINDING	8	-0.335623	-0.756539	0.807789	0.957473	1.000
221	GOBP-LONG-TERM-MEMORY	6	-0.367677	-0.756970	0.831117	0.958827	1.000
222	GOBP-MEMBRANE-PROTEIN-PROTEOLYSIS	6	-0.370276	-0.757663	0.822997	0.959841	1.000
223	GOBP-AMIDE-BIOSYNTHETIC-PROCESS	7	-0.351409	-0.760924	0.809403	0.957247	1.000
224	REACTOME-MAPK-FAMILY-SIGNALING-CASCADES	12	-0.274160	-0.766607	0.789354	0.953140	1.000
225	GOBP-REGULATION-OF-CELL-PROJECTION-ORGANIZATION	20	-0.357044	-0.767682	0.803364	0.953624	1.000
226	GOBP-ORGANOPHOSPHATE-METABOLIC-PROCESS	7	-0.357044	-0.767682	0.803364	0.953624	1.000
227	REACTOME-UNBLOCKING-OF-NMDA-RECEPTORS-GLUTAMAT...	12	-0.312925	-0.767774	0.801921	0.954432	1.000
228	GOBP-PEPTIDE-BIOSYNTHETIC-PROCESS	7	-0.351409	-0.775069	0.794308	0.946976	1.000
229	GOBP-SECRETION	24	-0.271511	-0.776448	0.790466	0.946980	1.000
230	GOBP-REGULATION-OF-CELLULAR-AMIDE-METABOLIC-PR...	9	-0.335781	-0.780293	0.790932	0.943343	1.000
231	REACTOME-NERVOUS-SYSTEM-DEVELOPMENT	15	-0.301423	-0.782444	0.796296	0.941063	1.000
232	GOBP-EXCITATORY-CHEMICAL-SYNAPTIC-TRANSMISSION	5	-0.390909	-0.783407	0.790368	0.942759	1.000
233	GOBP-CELL-MORPHOGENESIS	24	-0.277341	-0.785549	0.789130	0.941600	1.000
234	GOBP-REGULATION-OF-SYNAPTIC-PLASTICITY	21	-0.276833	-0.786668	0.771271	0.941844	1.000
235	GOBP-MEMORY	13	-0.308508	-0.786725	0.750296	0.943711	1.000
236	GOBP-REGULATION-OF-INFLAMMATORY-RESPONSE	7	-0.365516	-0.789266	0.755442	0.941935	1.000
237	GOBP-REGULATION-OF-PROTEIN-MODIFICATION-PROCESS	29	-0.266413	-0.789312	0.760087	0.943819	1.000
238	GOBP-SMALL-GTPASE-MEDIATED-SIGNAL-TRANSDUCTION	8	-0.350595	-0.789430	0.772953	0.945597	1.000
239	GOBP-GAMETE-GENERATION	9	-0.339026	-0.790113	0.764115	0.946562	1.000
240	GOBP-CELL-PART-MORPHOGENESIS	24	-0.277341	-0.790308	0.766703	0.948243	1.000
241	GOBP-CELLULAR-COMPONENT-MORPHOGENESIS	24	-0.277341	-0.791355	0.783814	0.948707	1.000
242	GOBP-REGULATION-OF-DEFENSE-RESPONSE	7	-0.365516	-0.792119	0.761528	0.949491	1.000
243	GOBP-REGULATION-OF-CATABOLIC-PROCESS	13	-0.308806	-0.792138	0.751790	0.951452	1.000
244	GOBP-LEARNING	13	-0.315778	-0.793315	0.757757	0.951690	1.000
245	GOBP-REGULATION-OF-VESICLE-MEDIATED-TRANSPORT	12	-0.317547	-0.795673	0.755924	0.949953	1.000
246	REACTOME-TRANSCRIPTIONAL-REGULATION-OF-WHITE-A...	6	-0.379745	-0.796041	0.764398	0.951452	1.000
247	GOBP-POSITIVE-REGULATION-OF-DEFENSE-RESPONSE	5	-0.401263	-0.798473	0.799180	0.949814	1.000
248	GOBP-POSITIVE-REGULATION-OF-PHOSPHATIDYLINOSIT...	5	-0.404513	-0.799418	0.769022	0.950426	1.000
249	REACTOME-SIGNALING-BY-INTERLEUKINS	15	-0.308748	-0.801534	0.762791	0.949333	1.000
250	GOBP-POSITIVE-REGULATION-OF-MAP-KINASE-ACTIVITY	6	-0.389175	-0.802827	0.768246	0.949300	1.000
251	GOBP-PROTEIN-LOCALIZATION-TO-CELL-JUNCTION	6	-0.384957	-0.803630	0.764554	0.950121	1.000
252	GOBP-POLYSACCHARIDE-METABOLIC-PROCESS	5	-0.407891	-0.804296	0.759891	0.951130	1.000
253	GOBP-PROTEOLYSIS	17	-0.296938	-0.805342	0.739380	0.951605	1.000
254	GOBP-CELL-CELL-JUNCTION-ASSEMBLY	5	-0.411711	-0.805352	0.763305	0.953634	1.000
255	GOBP-ACTIVATION-OF-MAPK-ACTIVITY	6	-0.389175	-0.807223	0.751989	0.952631	1.000

Continuation of Table S18

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
256	GOBP-REGULATION-OF-PROTEIN-PHOSPHORYLATION	26	-0.278752	-0.812441	0.740331	0.946535	1.000
257	GOBP-REGULATION-OF-INTRACELLULAR-SIGNAL-TRANSD...	21	-0.293087	-0.817928	0.728285	0.939690	1.000
258	GOBP-NEGATIVE-REGULATION-OF-ION-TRANSPORT	11	-0.335574	-0.819094	0.709070	0.939871	1.000
259	GOBP-MACROMOLECULE-CATABOLIC-PROCESS	12	-0.323257	-0.823257	0.719812	0.935144	1.000
260	GOBP-ORGANONITROGEN-COMPOUND-BIOSYNTHETIC-PROCESS	13	-0.323550	-0.826726	0.713951	0.931513	1.000
261	GOBP-RESPIRATORY-SYSTEM-DEVELOPMENT	6	-0.393648	-0.827205	0.752604	0.932752	1.000
262	GOBP-CELL-MORPHOGENESIS-INVOLVED-IN-NEURON-DIF...	21	-0.295704	-0.827959	0.709030	0.933445	1.000
263	GOBP-POSITIVE-REGULATION-OF-CATALYTIC-ACTIVITY	30	-0.285548	-0.831598	0.726681	0.929525	1.000
264	GOBP-FOREBRAIN-DEVELOPMENT	9	-0.357521	-0.832151	0.706897	0.930642	1.000
265	GOBP-SEXUAL-REPRODUCTION	10	-0.352724	-0.834845	0.713759	0.928004	1.000
266	GOBP-RESPONSE-TO-ALCOHOL	11	-0.347850	-0.838036	0.715651	0.924741	1.000
267	GOBP-POSITIVE-REGULATION-OF-MOLECULAR-FUNCTION	38	-0.279474	-0.839183	0.722103	0.924795	1.000
268	GOBP-GLUCOSE-METABOLIC-PROCESS	6	-0.402487	-0.840461	0.730924	0.924688	1.000
269	GOBP-CELL-MORPHOGENESIS-INVOLVED-IN-DIFFERENTI...	21	-0.295704	-0.841079	0.713969	0.925803	1.000
270	GOBP-POSITIVE-REGULATION-OF-SIGNALING	34	-0.285893	-0.843108	0.714133	0.924295	1.000
271	GOBP-MAPK-CASCADE	18	-0.312752	-0.843483	0.701814	0.925699	1.000
272	GOBP-MONOSACCHARIDE-METABOLIC-PROCESS	6	-0.402487	-0.843875	0.713731	0.927048	1.000
273	GOBP-POSITIVE-REGULATION-OF-PHOSPHORUS-METABOL...	24	-0.297093	-0.844084	0.727273	0.928755	1.000
274	REACTOME-EXTRACELLULAR-MATRIX-ORGANIZATION	5	-0.416565	-0.845655	0.700269	0.927979	1.000
275	GOBP-REGULATION-OF-CELLULAR-LOCALIZATION	17	-0.316613	-0.846091	0.703072	0.929297	1.000
276	GOBP-REGULATION-OF-ANATOMICAL-STRUCTURE-MORPHO...	17	-0.314426	-0.846493	0.696552	0.930758	1.000
277	REACTOME-SIGNALING-BY-GPCR	22	-0.301464	-0.847945	0.698009	0.930243	1.000
278	GOBP-ADENYLATE-CYCLASE-MODULATING-G-PROTEIN.CO...	11	-0.340793	-0.848593	0.655422	0.931207	1.000
279	GOBP-CELLULAR-HOMEOSTASIS	18	-0.312006	-0.848644	0.686164	0.933219	1.000
280	GOBP-AXON-DEVELOPMENT	18	-0.307699	-0.848666	0.690722	0.935322	1.000
281	GOBP-CENTRAL-NERVOUS-SYSTEM-DEVELOPMENT	26	-0.297615	-0.852865	0.691548	0.929815	1.000
282	GOBP-NEGATIVE-REGULATION-OF-PHOSPHORUS-METABOL...	9	-0.367892	-0.855815	0.680798	0.926597	1.000
283	GOBP-VESICLE-MEDIATED-TRANSPORT-IN-SYNAPSE	7	-0.397977	-0.857149	0.704427	0.926325	1.000
284	GOBP-IMMUNE-EFFECTOR-PROCESS	10	-0.362676	-0.857198	0.678441	0.928356	1.000
285	GOBP-G-PROTEIN-COUPLED-RECEPTOR-SIGNALING-PATHWAY	18	-0.315908	-0.858409	0.678330	0.928190	1.000
286	GOBP-MALE-GAMETE-GENERATION	5	-0.433735	-0.859674	0.660403	0.927937	1.000
287	GOBP-NEURON-APOPTOTIC-PROCESS	12	-0.344081	-0.862356	0.658019	0.925077	1.000
288	GOBP-ACTIVATION-OF-IMMUNE-RESPONSE	5	-0.435676	-0.867597	0.684931	0.917538	1.000
289	GOBP-NEGATIVE-REGULATION-OF-CYSTEINE-TYPE-ENDO...	5	-0.438609	-0.874406	0.682256	0.906974	1.000
290	REACTOME-VESICLE-MEDIATED-TRANSPORT	5	-0.443327	-0.874984	0.678238	0.907972	1.000
291	REACTOME-G-ALPHA1-SIGNALING-EVENTS	18	-0.317548	-0.875680	0.649718	0.908745	1.000
292	GOBP-CELL-GROWTH	10	-0.367305	-0.876308	0.655340	0.909546	1.000
293	GOBP-NEGATIVE-REGULATION-OF-SYNAPTIC-TRANSMISSION	6	-0.415980	-0.877388	0.646597	0.909204	1.000
294	GOBP-GLAND-DEVELOPMENT	7	-0.408347	-0.878649	0.648825	0.909678	1.000
295	GOBP-REGULATION-OF-BINDING	11	-0.359697	-0.879989	0.644150	0.909223	1.000
296	GOBP-POSITIVE-REGULATION-OF-PROTEIN-MODIFICATI...	23	-0.313212	-0.880207	0.656319	0.910960	1.000
297	GOBP-RESPONSE-TO-NUTRIENT	5	-0.445784	-0.881715	0.665757	0.910143	1.000
298	GOBP-EMBRYO-DEVELOPMENT-ENDING-IN-BIRTH-OR-EGG...	9	-0.382137	-0.884617	0.657500	0.906398	1.000

Continuation of Table S18

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
299	GOBP-CARBOHYDRATE-METABOLIC-PROCESS	9	-0.380630	-0.884891	0.647131	0.908019	1.000
300	GOBP-IONOTROPIC-GLUTAMATE-RECEPTOR-SIGNALING.P...	9	-0.376037	-0.885641	0.656289	0.908661	1.000
301	REACTOME-MEMBRANE-TRAFFICKING	5	-0.443327	-0.886122	0.659459	0.909926	1.000
302	GOBP-REGULATION-OF-PHOSPHORUS-METABOLIC-PROCESS	27	-0.304471	-0.886521	0.660870	0.911319	1.000
303	GOBP-RESPONSE-TO-UV	5	-0.442483	-0.886539	0.661517	0.913488	1.000
304	GOBP-OSTEOBLAST-DIFFERENTIATION	5	-0.454240	-0.888900	0.657754	0.911010	1.000
305	GOBP-APOPTOTIC-MITOCHONDRIAL-CHANGES	6	-0.425430	-0.891543	0.656417	0.908019	1.000
306	GOBP-REGULATION-OF-TRANSFERASE-ACTIVITY	22	-0.319744	-0.892851	0.634938	0.907729	1.000
307	GOBP-EMBRYONIC-MORPHOGENESIS	6	-0.427338	-0.893156	0.650190	0.909242	1.000
308	GOBP-MYOTUBE-DIFFERENTIATION	5	-0.452618	-0.894736	0.633609	0.908288	1.000
309	GOBP-POSITIVE-REGULATION-OF-TRANSPORT	26	-0.311186	-0.895129	0.648291	0.909733	1.000
310	GOBP-POSITIVE-REGULATION-OF-SMALL-MOLECULE-MET...	5	-0.454852	-0.898450	0.620321	0.905173	1.000
311	GOBP-NEGATIVE-REGULATION-OF-SIGNALING	12	-0.363630	-0.899305	0.626478	0.905751	1.000
312	GOBP-PROTEIN-PHOSPHORYLATION	21	-0.324175	-0.900817	0.622047	0.904842	1.000
313	GOBP-PROTEIN-PHOSPHORYLATION	34	-0.299829	-0.901227	0.620022	0.906226	1.000
314	GOBP-POSITIVE-REGULATION-OF-PROTEIN-KINASE-ACTIVITY	23	-0.313212	-0.903069	0.615128	0.904766	1.000
315	GOBP-REGULATION-OF-PROTEIN-KINASE-ACTIVITY	22	-0.319744	-0.906602	0.607821	0.899690	1.000
316	GOBP-HOMEOSTASIS-OF-NUMBER-OF-CELLS	5	-0.457813	-0.907640	0.617766	0.899772	1.000
317	GOBP-PROTEIN-LOCALIZATION-TO-POSTSYNAPSE	5	-0.462052	-0.909168	0.604336	0.898876	1.000
318	GOBP-CELLULAR-MACROMOLECULE-LOCALIZATION	21	-0.320447	-0.909519	0.600660	0.900366	1.000
319	GOBP-NERVOUS-SYSTEM-PROCESS	38	-0.303719	-0.910068	0.605042	0.901471	1.000
320	GOBP-REGULATION-OF-LYMPHOCYTE-ACTIVATION	5	-0.456349	-0.910253	0.613636	0.903377	1.000
321	GOBP-REGULATION-OF-FAT-CELL-DIFFERENTIATION	6	-0.438605	-0.912003	0.613423	0.901912	1.000
322	GOBP-REGULATION-OF-MAPK-CASCADE	13	-0.361865	-0.912646	0.598566	0.902844	1.000
323	GOBP-RESPONSE-TO-DRUG	11	-0.370977	-0.913092	0.583738	0.904112	1.000
324	GOBP-INFLAMMATORY-RESPONSE	12	-0.365702	-0.913767	0.616505	0.904903	1.000
325	GOBP-PROTEIN-LOCALIZATION-TO-SYNAPSE	5	-0.462052	-0.917417	0.587169	0.899595	1.000
326	GOBP-EPITHELIUM-DEVELOPMENT	15	-0.351674	-0.919425	0.586247	0.897721	1.000
327	GOBP-WOUND-HEALING	13	-0.365414	-0.921845	0.586729	0.894894	1.000
328	GOBP-HEAD-DEVELOPMENT	22	-0.324855	-0.926472	0.583058	0.887190	1.000
329	GOBP-REGULATION-OF-VASCULATURE-DEVELOPMENT	5	-0.471428	-0.926616	0.560876	0.889206	1.000
330	GOBP-POSITIVE-REGULATION-OF-TRANSFERASE-ACTIVITY	20	-0.336846	-0.928507	0.570304	0.887589	1.000
331	GOBP-REGULATION-OF-ENDOCYTOSIS	6	-0.441263	-0.929737	0.600522	0.887242	1.000
332	GOBP-REGULATION-OF-DNA-BINDING-TRANSCRIPTION.F...	16	-0.349400	-0.931666	0.582367	0.885333	1.000
333	GOBP-LOCOMOTION	31	-0.316732	-0.934462	0.589071	0.881361	1.000
334	GOBP-BEHAVIOR	32	-0.313088	-0.935927	0.567308	0.880217	1.000
335	GOBP-REGULATION-OF-PROTEOLYSIS	12	-0.371230	-0.940270	0.552311	0.872786	1.000
336	GOBP-TEMPERATURE-HOMEOSTASIS	5	-0.475103	-0.941418	0.575305	0.872600	1.000
337	GOBP-REGULATION-OF-CELL-CELL-ADHESION	9	-0.406290	-0.941579	0.556391	0.874613	1.000
338	GOBP-POSITIVE-REGULATION-OF-ESTABLISHMENT-OF_P...	5	-0.479214	-0.942112	0.557952	0.875715	1.000
339	REACTOME-CIRCADIAN-CLOCK	5	-0.487314	-0.943023	0.570442	0.862342	1.000
340	GOBP-RESPONSE-TO-LIGHT-STIMULUS	11	-0.389385	-0.949427	0.539683	0.863704	1.000
341	GOBP-RESPONSE-TO-WOUNDING	15	-0.365622	-0.950174	0.546620	0.864447	1.000

Continuation of Table S18

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
342	GOBP-POSITIVE-REGULATION-OF-GROWTH	GO-0045927	9	-0.404314	-0.950258	0.559343	0.866564	1.000
343	GOBP-ESTABLISHMENT-OF-PROTEIN-LOCALIZATION	GO-0045184	18	-0.349232	-0.951107	0.553022	0.867128	1.000
344	GOBP-DEVELOPMENTAL-GROWTH	GO-0048589	10	-0.401727	-0.951248	0.567308	0.869177	1.000
345	GOBP-REGULATION-OF-GTPASE-ACTIVITY	GO-0043087	5	-0.480972	-0.951959	0.557123	0.869931	1.000
346	REACTOME-LEISHMANIA-INFECTIO	R-HSA-9658195	10	-0.395238	-0.952150	0.563659	0.871791	1.000
347	GOBP-IN-UTERO-EMBRYONIC-DEVELOPMENT	GO-0001701	8	-0.425529	-0.952958	0.568702	0.872337	1.000
348	GOBP-NEGATIVE-REGULATION-OF-PROTEIN-MODIFICATION	GO-0031400	10	-0.406245	-0.954104	0.539855	0.872071	1.000
349	REACTOME-DEATH-RECEPTOR-SIGNALING	R-RNO-73887	5	-0.486466	-0.955720	0.544952	0.870727	1.000
350	GOBP-NEGATIVE-REGULATION-OF-INTRACELLULAR-SIGNALING	GO-1902532	7	-0.437106	-0.958242	0.554140	0.867389	1.000
351	GOBP-RECEPTOR-INTERNALIZATION	GO-0031623	5	-0.494890	-0.958871	0.546961	0.868421	1.000
352	GOBP-G-PROTEIN-COUPLED-GLUTAMATE-RECEPTOR-SIGNALING	GO-0007216	8	-0.422644	-0.959570	0.538657	0.869213	1.000
353	GOBP-ORGANIC-ACID-METABOLIC-PROCESS	GO-0006082	7	-0.433558	-0.960023	0.529936	0.870558	1.000
354	GOBP-REGULATION-OF-MUSCLE-CELL-DIFFERENTIATION	GO-0051147	6	-0.465580	-0.961155	0.520750	0.870326	1.000
355	GOBP-GLUTAMATE-RECEPTOR-SIGNALING-PATHWAY	GO-0007215	17	-0.362039	-0.964349	0.534025	0.865538	1.000
356	REACTOME-NEUROTRANSMITTER-RECEPTORS-AND-POSTSYNAPTIC	R-RNO-112314	22	-0.343138	-0.965251	0.540000	0.865637	1.000
357	GOBP-REGULATION-OF-MUSCLE-SYSTEM-PROCESS	GO-00090257	8	-0.438128	-0.965628	0.540676	0.867176	1.000
358	GOBP-POSITIVE-REGULATION-OF-PROTEIN-METABOLIC-PROCESS	GO-0051247	28	-0.332455	-0.965983	0.544858	0.868812	1.000
359	GOBP-REGULATION-OF-DEVELOPMENTAL-GROWTH	GO-0048638	9	-0.422696	-0.967731	0.543226	0.867259	1.000
360	REACTOME-PROTEIN-PROTEIN-INTERACTIONS-AT-SYNAPSES	R-RNO-6794362	12	-0.394165	-0.970692	0.506634	0.862815	1.000
361	GOBP-HEART-DEVELOPMENT	GO-0007507	6	-0.467978	-0.970929	0.529032	0.864687	1.000
362	REACTOME-CYTOKINE-SIGNALING-IN-IMMUNE-SYSTEM	R-RNO-1280215	21	-0.349148	-0.971337	0.547778	0.866156	1.000
363	GOBP-MEMBRANE-ORGANIZATION	GO-0061024	12	-0.392707	-0.971816	0.523298	0.867394	1.000
364	GOBP-SENSORY-ORGAN-DEVELOPMENT	GO-0007423	8	-0.427625	-0.972444	0.508728	0.868306	1.000
365	GOBP-SENSORY-PERCEPTION	GO-0007600	9	-0.409585	-0.972546	0.522670	0.870523	1.000
366	GOBP-POSITIVE-REGULATION-OF-CELLULAR-COMPONENT-TRANSPORT	GO-0051130	24	-0.337240	-0.973445	0.524698	0.870984	1.000
367	GOBP-POSITIVE-REGULATION-OF-HEMOPOIESIS	GO-1903708	7	-0.450708	-0.974867	0.538847	0.870171	1.000
368	GOBP-REGULATION-OF-PROTEIN-SERINE-THREONINE-KINASE-ACTIVITY	GO-0071900	12	-0.386944	-0.977065	0.512315	0.867286	1.000
369	GOBP-NEGATIVE-REGULATION-OF-PHOSPHORYLATION	GO-0042326	7	-0.445823	-0.977728	0.512041	0.868159	1.000
370	GOBP-NEGATIVE-REGULATION-OF-TRANSFERASE-ACTIVITY	GO-0051348	5	-0.504454	-0.981067	0.516438	0.862534	1.000
371	GOBP-CARDIAC-MUSCLE-TISSUE-DEVELOPMENT	GO-0048738	6	-0.467978	-0.982297	0.492848	0.862042	1.000
372	GOBP-POSITIVE-REGULATION-OF-PROTEIN-KINASE-ACTIVITY	GO-0045860	19	-0.363393	-0.982850	0.521691	0.863090	1.000
373	GOBP-MONOCARBOXYLIC-ACID-METABOLIC-PROCESS	GO-0032787	6	-0.464644	-0.983229	0.499331	0.864703	1.000
374	GOBP-RECEPTOR-METABOLIC-PROCESS	GO-0043112	5	-0.494890	-0.984874	0.503448	0.863198	1.000
375	GOBP-REGULATION-OF-ION-TRANSPORT	GO-0043269	36	-0.328275	-0.987730	0.494612	0.859025	1.000
376	GOBP-NUCLEAR-TRANSPORT	GO-0051169	5	-0.503324	-0.988208	0.503383	0.860423	1.000
377	REACTOME-INNATE-IMMUNE-SYSTEM	R-RNO-168249	16	-0.370581	-0.989422	0.515789	0.859854	1.000
378	GOBP-CELL-MIGRATION	GO-0016477	22	-0.349300	-0.990111	0.488294	0.860717	1.000
379	GOBP-MUSCLE-CELL-DIFFERENTIATION	GO-0042692	10	-0.409796	-0.991929	0.523694	0.858847	1.000
380	GOBP-NEGATIVE-REGULATION-OF-BINDING	GO-0051100	6	-0.477434	-0.992192	0.494148	0.860729	1.000
381	GOBP-MUSCLE-CONTRACTION	GO-0006936	5	-0.506732	-0.992936	0.487110	0.861403	1.000
382	GOBP-REGULATION-OF-OSTEOCLAST-DIFFERENTIATION	GO-0045670	5	-0.502493	-0.993573	0.487738	0.862413	1.000
383	GOBP-SENSORY-PERCEPTION-OF-PAIN	GO-0019233	5	-0.493976	-0.995700	0.494595	0.859704	1.000
384	GOBP-REGULATION-OF-CELL-DEATH	GO-0010941	34	-0.336609	-0.995738	0.492600	0.862166	1.000

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	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
385	GOBP-REGULATION-OF-ENDOTHELIAL-CELL-MIGRATION	GO-0010594	5	-0.505829	-0.995910	0.496011	0.864317	1.000
386	REACTOME-DISEASES-OF-SIGNAL-TRANSDUCTION-BY_GR...	R-HSA-5663202	12	-0.397706	-0.996564	0.505455	0.865259	1.000
387	GOBP-NEGATIVE-REGULATION-OF-KINASE-ACTIVITY	GO-0033673	5	-0.504454	-0.997571	0.480170	0.865427	1.000
388	GOBP-NEGATIVE-REGULATION-OF-LIPID-METABOLIC-PR...	GO-0045833	5	-0.514950	-0.998249	0.467940	0.866417	1.000
389	GOBP-NEGATIVE-REGULATION-OF-MOLECULAR-FUNCTION	GO-0044092	24	-0.345614	-0.999845	0.481195	0.864976	1.000
390	GOBP-REGULATION-OF-RECEPTOR-MEDIATED-ENDOCYTOSIS	GO-0048259	5	-0.510252	-1.003910	0.487614	0.857114	1.000
391	GOBP-PROTEIN-AUTOPHOSPHORYLATION	GO-0046777	5	-0.513834	-1.005372	0.467480	0.855944	1.000
392	GOBP-RESPONSE-TO-CARBOHYDRATE	GO-0009743	5	-0.512255	-1.007988	0.483266	0.851775	1.000
393	GOBP-PEPTIDYL-SERINE-MODIFICATION	GO-0018209	12	-0.411258	-1.010005	0.460890	0.849207	1.000
394	GOBP-NEGATIVE-REGULATION-OF-CELL-DEVELOPMENT	GO-0010721	6	-0.488130	-1.013867	0.452349	0.841992	1.000
395	GOBP-NEGATIVE-REGULATION-OF-NERVOUS-SYSTEM-DEV...	GO-0051961	5	-0.504016	-1.014013	0.462500	0.844197	1.000
396	GOBP-CHEMICAL-HOMEOSTASIS	GO-0048878	23	-0.352719	-1.014069	0.468397	0.846634	1.000
397	GOBP-RESPONSE-TO-MONOSACCHARIDE	GO-0034284	5	-0.512255	-1.015044	0.466572	0.846628	1.000
398	GOBP-CELLULAR-COMPONENT-MAINTENANCE	GO-0043453	5	-0.513453	-1.017411	0.451268	0.843086	1.000
399	GOBP-NEURON-PROJECTION-GUIDANCE	GO-0097485	9	-0.439338	-1.018113	0.453184	0.843989	1.000
400	GOBP-REGULATION-OF-CELLULAR-CATABOLIC-PROCESS	GO-0031329	10	-0.424600	-1.019401	0.470096	0.843123	1.000
401	REACTOME-INTERFERON-SIGNALING	R-RNO-913531	6	-0.485531	-1.019997	0.451268	0.844221	1.000
402	GOBP-RESPONSE-TO-ALKALOID	GO-0043279	5	-0.518072	-1.022121	0.435247	0.841342	1.000
403	GOBP-REGULATION-OF-EPITHELIAL-CELL-MIGRATION	GO-0010632	6	-0.488591	-1.022388	0.428016	0.843257	1.000
404	GOBP-REGULATION-OF-CELLULAR-COMPONENT-MOVEMENT	GO-0051270	15	-0.392554	-1.022894	0.464692	0.844514	1.000
405	GOBP-POSITIVE-REGULATION-OF-CELL-DIFFERENTIATION	GO-0045597	27	-0.359060	-1.023380	0.454345	0.845900	1.000
406	GOBP-BIOLOGICAL-PROCESS-INVOLVED-IN-SYMBIOTIC-...	GO-004440	11	-0.417840	-1.025857	0.436019	0.841956	1.000
407	GOBP-REGULATION-OF-PHOSPHATIDYLINOSITOL-3-KINA...	GO-0014066	6	-0.491266	-1.026606	0.453595	0.842593	1.000
408	REACTOME-SIGNALING-BY-WNT	R-RNO-195721	7	-0.477680	-1.027590	0.450392	0.842767	1.000
409	GOBP-POSITIVE-REGULATION-OF-ION-TRANSPORT	GO-0043270	17	-0.384523	-1.028080	0.444319	0.844098	1.000
410	GOBP-NEGATIVE-REGULATION-OF-NEURON-APOPTOTIC_P...	GO-0043524	8	-0.460376	-1.029150	0.441890	0.844021	1.000
411	REACTOME-TRANSMISSION-ACROSS-CHEMICAL-SYNAPSES	R-RNO-112315	23	-0.359738	-1.029511	0.448430	0.845740	1.000
412	GOBP-OSSIFICATION	GO-0001503	9	-0.439058	-1.030010	0.434080	0.847156	1.000
413	GOBP-REGULATION-OF-AXONOGENESIS	GO-0050770	7	-0.480227	-1.030538	0.412739	0.848520	1.000
414	GOBP-POSITIVE-REGULATION-OF-MAPK-CASCADE	GO-0043410	9	-0.442603	-1.030539	0.431181	0.851302	1.000
415	REACTOME-CREB1-PHOSPHORYLATION-THROUGH-NMDA-RE...	R-RNO-442742	8	-0.464570	-1.034443	0.424051	0.843484	1.000
416	GOBP-REGULATION-OF-PROTEIN-BINDING	GO-0043393	7	-0.476756	-1.038274	0.439791	0.835977	1.000
417	GOBP-NEGATIVE-REGULATION-OF-MULTICELLULAR_ORGA...	GO-0051241	15	-0.401193	-1.038663	0.422170	0.837663	1.000
418	GOBP-REGULATION-OF-ORGAN-GROWTH	GO-0046620	5	-0.529944	-1.039577	0.425474	0.838028	1.000
419	GOBP-POSITIVE-REGULATION-OF-AXONOGENESIS	GO-0050772	5	-0.522941	-1.040028	0.430556	0.839466	1.000
420	REACTOME-G-ALPHA-Z-SIGNALING-EVENTS	R-RNO-418597	5	-0.521000	-1.040966	0.423611	0.839653	1.000
421	GOBP-MUSCLE-STRUCTURE-DEVELOPMENT	GO-0061061	16	-0.393444	-1.041659	0.451835	0.840629	1.000
422	GOBP-REGULATION-OF-LIPID-LOCALIZATION	GO-1905952	5	-0.465508	-1.041910	0.423868	0.842783	1.000
423	GOBP-POSITIVE-REGULATION-OF-DEVELOPMENTAL-GROWTH	GO-0048639	8	-0.465508	-1.043629	0.422879	0.841062	1.000
424	GOBP-PHOSPHATIDYLINOSITOL-3-KINASE-SIGNALING	GO-0014065	7	-0.477351	-1.045551	0.417344	0.838712	1.000
425	GOBP-LIPID-METABOLIC-PROCESS	GO-0006629	10	-0.437588	-1.046918	0.436518	0.837895	1.000
426	REACTOME-NEUREXINS-AND-NEUROLIGINS	R-RNO-6794361	9	-0.449711	-1.047289	0.440594	0.839715	1.000
427	GOBP-RESPONSE-TO-MECHANICAL-STIMULUS	GO-0009612	6	-0.509930	-1.049657	0.397117	0.835702	1.000

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NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
428	GOBP-POSITIVE-REGULATION-OF-INTRACELLULAR-SIGN...	14	-0.410030	-1.054073	0.418033	0.826174	1.000
429	GOBP-INTRACELLULAR-PROTEIN-TRANSPORT	9	-0.459869	-1.056107	0.413580	0.823356	1.000
430	GOBP-CYTOSKELETON-ORGANIZATION	11	-0.439503	-1.057694	0.409976	0.822015	1.000
431	GOBP-INOSITOL-LIPID-MEDIATED-SIGNALING	8	-0.475753	-1.058219	0.409439	0.823317	1.000
432	GOBP-CELLULAR-CARBOHYDRATE-METABOLIC-PROCESS	5	-0.533794	-1.059430	0.398929	0.822864	1.000
433	GOBP-EMBRYONIC-ORGAN-DEVELOPMENT	7	-0.483291	-1.059645	0.385101	0.825207	1.000
434	GOBP-ORGAN-GROWTH	5	-0.529944	-1.059876	0.404167	0.827399	1.000
435	REACTOME-BETA-CATENIN-INDEPENDENT-WNT-SIGNALING	5	-0.531400	-1.063301	0.370421	0.820622	1.000
436	GOBP-NEGATIVE-REGULATION-OF-CATALYTIC-ACTIVITY	17	-0.401790	-1.065959	0.405780	0.815934	1.000
437	GOBP-REGULATION-OF-PEPTIDE-TRANSPORT	10	-0.451905	-1.066714	0.390036	0.816556	1.000
438	GOBP-APOPTOTIC-PROCESS	35	-0.353009	-1.067269	0.404482	0.817778	1.000
439	GOBP-REGULATION-OF-APOPTOTIC-SIGNALING-PATHWAY	10	-0.447476	-1.067539	0.397546	0.819883	1.000
440	REACTOME-LIGAND-INTERACTIONS	5	-0.544527	-1.067551	0.399171	0.822785	1.000
441	GOBP-POSITIVE-REGULATION-OF-ORGANELLE-ORGANIZA...	10	-0.451521	-1.067589	0.394673	0.825649	1.000
442	GOBP-REGULATION-OF-MULTICELLULAR-ORGANISMAL-DE...	31	-0.357134	-1.075588	0.380851	0.805237	1.000
443	GOBP-REGULATION-OF-CYTOSKELETON-ORGANIZATION	5	-0.540803	-1.075615	0.349933	0.808092	1.000
444	GOBP-RESPONSE-TO-NERVE-GROWTH-FACTOR	7	-0.491605	-1.076152	0.372215	0.809546	1.000
445	GOBP-NERVE-DEVELOPMENT	9	-0.463842	-1.076488	0.401741	0.811619	1.000
446	GOBP-RHYTHMIC-PROCESS	15	-0.415136	-1.080386	0.377598	0.803425	1.000
447	GOBP-ENDOCRINE-SYSTEM-DEVELOPMENT	6	-0.517580	-1.080770	0.356784	0.805173	1.000
448	GOBP-RESPONSE-TO-EXTRACELLULAR-STIMULUS	13	-0.423274	-1.081271	0.371328	0.806764	1.000
449	GOBP-POSITIVE-REGULATION-OF-MYELOID-CELL-DIFFE...	7	-0.505257	-1.081700	0.374359	0.808540	1.000
450	GOBP-FAT-CELL-DIFFERENTIATION	9	-0.461689	-1.086858	0.354061	0.796433	1.000
451	GOBP-NEGATIVE-REGULATION-OF-RESPONSE-TO-EXTERN...	5	-0.552747	-1.092012	0.363874	0.784385	1.000
452	GOBP-REGULATION-OF-PEPTIDASE-ACTIVITY	10	-0.461979	-1.092486	0.366748	0.785910	1.000
453	GOBP-INTRINSIC-APOPTOTIC-SIGNALING-PATHWAY	5	-0.546028	-1.092903	0.337802	0.787705	1.000
454	GOBP-NUCLEOBASE-CONTAINING-SMALL-MOLECULE-META...	6	-0.522361	-1.093808	0.342704	0.787886	1.000
455	GOBP-MATERNAL-PROCESS-INVOLVED-IN-FEMALE-PREGN...	5	-0.547650	-1.094254	0.360811	0.789575	1.000
456	GOBP-RECEPTOR-MEDIATED-ENDOCYTOSIS	6	-0.524928	-1.094730	0.341927	0.791123	1.000
457	GOBP-EXOCYTOSIS	11	-0.445940	-1.097064	0.361474	0.787356	1.000
458	GOBP-REGULATION-OF-LEUKOCYTE-DIFFERENTIATION	9	-0.473565	-1.098939	0.354321	0.784823	1.000
459	GOBP-AMEBOIDAL-TYPE-CELL-MIGRATION	11	-0.462080	-1.102169	0.352246	0.778427	1.000
460	GOBP-OSTEOCLAST-DIFFERENTIATION	6	-0.532135	-1.102181	0.347712	0.781394	1.000
461	GOBP-RAS-PROTEIN-SIGNAL-TRANSDUCTION	5	-0.551180	-1.103545	0.343324	0.780224	1.000
462	REACTOME-HEMOSTASIS	14	-0.434580	-1.105133	0.349112	0.778446	1.000
463	GOBP-POSTTRANSCRIPTIONAL-REGULATION-OF-GENE-EX...	8	-0.494436	-1.105477	0.341740	0.780452	1.000
464	GOBP-IMMUNE-RESPONSE-REGULATING-SIGNALING-PATHWAY	8	-0.492427	-1.107423	0.338832	0.777720	1.000
465	REACTOME-TOLL-LIKE-RECEPTOR-9-TLR9-CASCADE	8	-0.494573	-1.108818	0.336683	0.776540	1.000
466	REACTOME-MYD88-INDEPENDENT-TLR4-CASCADE	8	-0.494573	-1.109328	0.341371	0.778194	1.000
467	GOBP-TAXIS	14	-0.428495	-1.110798	0.326744	0.776863	1.000
468	GOBP-MYELOID-LEUKOCYTE-ACTIVATION	8	-0.490411	-1.111388	0.319481	0.778058	1.000
469	GOBP-TUBE-MORPHOGENESIS	15	-0.425619	-1.112571	0.340278	0.777468	1.000
470	GOBP-REGULATION-OF-HORMONE-LEVELS	12	-0.453927	-1.113239	0.328622	0.778494	1.000

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	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
471	GOBP-NEGATIVE-REGULATION-OF-NEURON-DEATH	GO-1901215	11	-0.452437	-1.114802	0.333741	0.776651	1.000
472	REACTOME_TOLL-LIKE-RECEPTOR-CASCADES	R-RNO-168898	8	-0.494573	-1.116775	0.317781	0.774171	1.000
473	REACTOME_TOLL-LIKE-RECEPTOR-TLR1-TLR2-CASCADE	R-RNO-168179	8	-0.494573	-1.118786	0.335045	0.771512	1.000
474	GOBP-ORGANIC-HYDROXY-COMPOUND-TRANSPORT	GO-0015850	6	-0.533197	-1.121222	0.320051	0.767263	1.000
475	GOBP-FC-RECEPTOR-SIGNALING-PATHWAY	GO-0038093	8	-0.492427	-1.121832	0.302564	0.768629	1.000
476	GOBP-REGULATION-OF-ORGANELLE-ORGANIZATION	GO-0033043	14	-0.434467	-1.124089	0.336105	0.764993	1.000
477	GOBP-FC-EPSILON-RECEPTOR-SIGNALING-PATHWAY	GO-0038095	7	-0.513467	-1.127053	0.312581	0.759210	1.000
478	GOBP-POSITIVE-REGULATION-OF-MYELOID-LEUKOCYTE....	GO-0002763	6	-0.538832	-1.130451	0.288512	0.752033	1.000
479	REACTOME_FC-EPSILON-RECEPTOR-FCERL-SIGNALING	R-RNO-2454202	7	-0.513467	-1.132265	0.305520	0.749660	1.000
480	GOBP-GROWTH	GO-0040007	14	-0.447146	-1.135248	0.313860	0.744224	1.000
481	GOBP-BLOOD-VESSEL-MORPHOGENESIS	GO-0048514	14	-0.441572	-1.136421	0.309327	0.743980	1.000
482	GOBP-REGULATION-OF-CELL-ACTIVATION	GO-0050865	8	-0.504492	-1.137817	0.321429	0.742810	1.000
483	GOBP-REGULATION-OF-NEURONAL-SYNAPTIC-PLASTICITY	GO-0048168	7	-0.528319	-1.139618	0.325611	0.740528	1.000
484	GOBP-REGULATION-OF-BODY-FLUID-LEVELS	GO-0050878	11	-0.466218	-1.140047	0.299031	0.742402	1.000
485	GOBP-POSITIVE-REGULATION-OF-PROTEIN-SERINE-THR....	GO-0071902	9	-0.493555	-1.141359	0.296798	0.741461	1.000
486	GOBP-SMALL-MOLECULE-METABOLIC-PROCESS	GO-0044281	15	-0.442990	-1.141393	0.310983	0.744539	1.000
487	REACTOME-INFECTIOUS-DISEASE	R-HSA-5663205	13	-0.448255	-1.143323	0.314079	0.741997	1.000
488	GOBP-ENDOCYTOSIS	GO-0068897	8	-0.502546	-1.144852	0.288804	0.740235	1.000
489	GOBP-POSITIVE-REGULATION-OF-NEURON-DEATH	GO-1901216	5	-0.580665	-1.147928	0.293478	0.734172	1.000
490	GOBP-POSITIVE-REGULATION-OF-DEVELOPMENTAL-PROCESS	GO-0051094	32	-0.390242	-1.148293	0.280553	0.736120	1.000
491	GOBP-PROTEIN-COMPLEX-OLIGOMERIZATION	GO-0051259	6	-0.549081	-1.149312	0.280000	0.736151	1.000
492	GOBP-CELLULAR-RESPONSE-TO-MOLECULE-OF-BACTERIA...	GO-0071219	8	-0.519658	-1.151403	0.265789	0.732997	1.000
493	GOBP-RESPONSE-TO-NICOTINE	GO-0035094	7	-0.530603	-1.151682	0.272152	0.735404	1.000
494	GOBP-REGULATION-OF-GROWTH	GO-0040008	13	-0.463149	-1.154998	0.286047	0.728615	1.000
495	GOBP-PROTEIN-MODIFICATION-BY-SMALL-PROTEIN-CON...	GO-0070647	7	-0.535659	-1.157397	0.278859	0.724745	1.000
496	GOBP-LOCOMOTORY-BEHAVIOR	GO-0007626	19	-0.533040	-1.158419	0.253947	0.724770	1.000
497	GOBP-CIRCADIAN-RHYTHM	GO-0007623	13	-0.462430	-1.161839	0.270463	0.717091	1.000
498	GOBP-DEFENSE-RESPONSE	GO-0006952	19	-0.426618	-1.164526	0.260771	0.711494	1.000
499	HALLMARK-HYPOXIA	M5891	5	-0.597419	-1.167531	0.266297	0.705531	1.000
500	REACTOME-ONCOGENIC-MAPK-SIGNALING	R-HSA-6802957	5	-0.595493	-1.167960	0.257576	0.707449	1.000
501	GOBP-LEUKOCYTE-MEDIATED-IMMUNITY	GO-0002443	7	-0.534614	-1.169171	0.259843	0.706984	1.000
502	GOBP-CELLULAR-RESPONSE-TO-BIOTIC-STIMULUS	GO-0071216	8	-0.519658	-1.170445	0.248724	0.706499	1.000
503	GOBP-NEGATIVE-REGULATION-OF-GENE-EXPRESSION	GO-0010629	12	-0.467989	-1.171800	0.271166	0.705439	1.000
504	GOBP-INTRACELLULAR-RECEPTOR-SIGNALING-PATHWAY	GO-0030522	5	-0.598187	-1.171837	0.237964	0.708621	1.000
505	GOBP-REGULATION-OF-PROTEIN-LOCALIZATION	GO-0032880	18	-0.435204	-1.176950	0.258701	0.695876	1.000
506	GOBP-CELLULAR-RESPONSE-TO-DNA-DAMAGE-STIMULUS	GO-0006974	5	-0.593801	-1.177345	0.240766	0.697846	1.000
507	GOBP-MULTI-MULTICELLULAR-ORGANISM-PROCESS	GO-0044706	8	-0.525535	-1.180214	0.256281	0.692455	1.000
508	GOBP-BLOOD-VESSEL-ENDOTHELIAL-CELL-MIGRATION	GO-0043534	8	-0.527351	-1.180496	0.250318	0.694796	1.000
509	GOBP-POSITIVE-REGULATION-OF-IMMUNE-RESPONSE	GO-0050778	9	-0.505468	-1.180894	0.263094	0.696809	1.000
510	GOBP-ENDOTHELIAL-CELL-MIGRATION	GO-0043542	8	-0.527351	-1.183422	0.227895	0.691892	1.000
511	GOBP-INTRACELLULAR-TRANSPORT	GO-0046907	11	-0.490728	-1.183502	0.256442	0.694954	1.000
512	GOBP-NEURON-DEATH	GO-0070997	18	-0.433687	-1.186376	0.258427	0.689069	1.000
513	REACTOME-NEURONAL-SYSTEM	R-RNO-112316	26	-0.415133	-1.186667	0.232533	0.691378	1.000

Continuation of Table S18

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
514 GOBP-REGULATION-OF-CELLULAR-PROTEIN-LOCALIZATION	GO-1903827	12	-0.475343	-1.186710	0.257414	0.694621	1.000
515 GOBP-POSITIVE-REGULATION-OF-EPITHELIAL-CELL-MI...	GO-0010634	5	-0.601667	-1.189394	0.227901	0.689628	1.000
516 GOBP-POSITIVE-REGULATION-OF-LOCOMOTION	GO-0040017	11	-0.488367	-1.189772	0.262470	0.691892	1.000
517 REACTOME-TRAFFICKING-OF-AMPA-RECEPTORS	R-RNO-399719	11	-0.484541	-1.190284	0.245466	0.693518	1.000
518 GOBP-POSITIVE-REGULATION-OF-APOPTOTIC-SIGNALIN...	GO-2001235	5	-0.607085	-1.193152	0.219945	0.687550	1.000
519 GOBP-RESPONSE-TO-TUMOR-NECROSIS-FACTOR	GO-0034612	7	-0.540302	-1.193449	0.221790	0.690117	1.000
520 GOBP-POSITIVE-REGULATION-OF-RESPONSE-TO-EXTERN...	GO-0032103	9	-0.510972	-1.195092	0.250000	0.688196	1.000
521 GOBP-REGULATION-OF-NEURON-DIFFERENTIATION	GO-0045664	5	-0.611769	-1.196472	0.209524	0.687116	1.000
522 GOBP-POSITIVE-REGULATION-OF-PROTEOLYSIS	GO-0045862	8	-0.536159	-1.196725	0.237726	0.689679	1.000
523 GOBP-NEGATIVE-REGULATION-OF-CELL-DEATH	GO-0060548	22	-0.424765	-1.200169	0.239824	0.682420	1.000
524 GOBP-ANATOMICAL-STRUCTURE-FORMATION-INVOLVED-I...	GO-0048646	20	-0.428956	-1.201419	0.223799	0.681931	1.000
525 GOBP-POSITIVE-REGULATION-OF-CELL-DEATH	GO-0010942	19	-0.438592	-1.203814	0.236486	0.677882	1.000
526 GOBP-PLATELET-ACTIVATION	GO-0030168	6	-0.580264	-1.204079	0.206675	0.680490	1.000
527 GOBP-HOMEOSTATIC-PROCESS	GO-0042592	31	-0.405974	-1.204617	0.214208	0.682204	1.000
528 GOBP-POSITIVE-REGULATION-OF-PEPTIDASE-ACTIVITY	GO-0010952	7	-0.555656	-1.205996	0.197659	0.681377	1.000
529 GOBP-PROTEIN-MODIFICATION-BY-SMALL-PROTEIN-CON...	GO-0032446	6	-0.580344	-1.208274	0.204515	0.677691	1.000
530 GOBP-TISSUE-MIGRATION	GO-0090130	9	-0.515267	-1.208624	0.224335	0.680283	1.000
531 GOBP-NEGATIVE-REGULATION-OF-CELL-POPULATION-PR...	GO-0008285	9	-0.528002	-1.212078	0.219603	0.672566	1.000
532 GOBP-REGULATION-OF-CYSTEINE-TYPE-ENDOPEPTIDASE...	GO-2000116	9	-0.514813	-1.212329	0.213936	0.675292	1.000
533 GOBP-ANIMAL-ORGAN-MORPHOGENESIS	GO-0009887	12	-0.488471	-1.213169	0.210094	0.676180	1.000
534 GOBP-CELLULAR-RESPONSE-TO-KETONE	GO-1901655	5	-0.614852	-1.213389	0.202740	0.679147	1.000
535 GOBP-ERK1-AND-ERK2-CASCADE	GO-0070371	5	-0.596592	-1.214516	0.201058	0.678838	1.000
536 GOBP-MUSCLE-SYSTEM-PROCESS	GO-0003012	9	-0.526770	-1.215073	0.223844	0.680489	1.000
537 GOBP-PEPTIDYL-AMINO-ACID-MODIFICATION	GO-0018193	22	-0.426557	-1.218703	0.215664	0.672063	1.000
538 GOBP-REGULATION-OF-MUSCLE-ADAPTATION	GO-0043502	5	-0.617149	-1.220319	0.191257	0.670538	1.000
539 GOBP-NEGATIVE-REGULATION-OF-CELL-PROJECTION-OR...	GO-0031345	5	-0.620292	-1.223452	0.195973	0.663858	1.000
540 REACTOME-INTEGRATION-OF-ENERGY-METABOLISM	R-RNO-163685	5	-0.628517	-1.223640	0.195739	0.666816	1.000
541 GOBP-POSITIVE-REGULATION-OF-CYSTEINE-TYPE-ENDO...	GO-2001056	7	-0.555656	-1.225671	0.190039	0.663673	1.000
542 GOBP-MUSCLE-ADAPTATION	GO-0043500	5	-0.617149	-1.228946	0.171034	0.656684	1.000
543 REACTOME-TRANSCRIPTIONAL-REGULATION-BY-TP53	R-RNO-3700989	6	-0.585918	-1.229184	0.205298	0.659622	1.000
544 GOBP-REGULATION-OF-MYELOID-LEUKOCYTE-DIFFERENT...	GO-0002761	8	-0.549896	-1.229196	0.200260	0.663368	1.000
545 GOBP-REGULATION-OF-RESPONSE-TO-EXTERNAL-STIMULUS	GO-0032101	15	-0.477336	-1.231059	0.194866	0.660977	1.000
546 GOBP-ERBB-SIGNALING-PATHWAY	GO-0038127	5	-0.630523	-1.232083	0.181579	0.661175	1.000
547 REACTOME-TRAFFICKING-OF-GLUR2-CONTAINING-AMPA-...	R-RNO-416993	8	-0.549668	-1.234836	0.188535	0.656042	1.000
548 GOBP-NEGATIVE-REGULATION-OF-PROTEIN-METABOLIC-...	GO-0051248	20	-0.445174	-1.235514	0.198864	0.657596	1.000
549 GOBP-REGULATION-OF-CELL-DIFFERENTIATION	GO-0045595	36	-0.414412	-1.245504	0.173220	0.628594	1.000
550 REACTOME-SIGNALING-BY-NTRK5	R-RNO-166520	18	-0.463043	-1.246975	0.189655	0.627649	1.000
551 GOBP-RESPONSE-TO-RADIATION	GO-0009314	13	-0.490165	-1.251703	0.193357	0.616164	1.000
552 GOBP-PERIPHERAL-NERVOUS-SYSTEM-DEVELOPMENT	GO-0007422	9	-0.537156	-1.251859	0.190898	0.619397	1.000
553 GOBP-NEGATIVE-REGULATION-OF-RESPONSE-TO-STIMULUS	GO-0048585	16	-0.475600	-1.253112	0.178322	0.619324	1.000
554 GOBP-POSITIVE-REGULATION-OF-BINDING	GO-0051099	6	-0.607606	-1.253645	0.163073	0.621480	1.000
555 REACTOME-G-ALPHA-Q-SIGNALING-EVENTS	R-RNO-416476	6	-0.607757	-1.254597	0.171123	0.621983	1.000
556 GOBP-TUBE-DEVELOPMENT	GO-0035295	18	-0.463594	-1.256568	0.164948	0.619430	1.000

Continuation of Table S18

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
557 REACTOME_OPIOID_SIGNALLING	R-RNO-111885	12	-0.512486	-1.256768	0.163070	0.622511	1.000
558 GOBP_SPROUTING_ANGIOGENESIS	GO-0002040	5	-0.644819	-1.258721	0.154891	0.619889	1.000
559 GOBP_POSITIVE_REGULATION_OF_PRL_MIRNA_TRANSCRIPTION...	GO-1902895	7	-0.578642	-1.259399	0.178893	0.621653	1.000
560 GOBP_PRL_MIRNA_TRANSCRIPTION_BY_RNA_POLYMERASE_II	GO-0061614	7	-0.578642	-1.259705	0.163636	0.624529	1.000
561 GOBP_PEPTIDYL_LYSINE_MODIFICATION	GO-0018205	5	-0.631805	-1.260173	0.151915	0.626985	1.000
562 REACTOME_SIGNALING_BY_RECEPTOR_TYROSINE_KINASES	R-RNO-9006934	26	-0.436353	-1.260465	0.177560	0.630053	1.000
563 GOBP_RESPONSE_TO_INSULIN	GO-0032868	5	-0.635883	-1.261164	0.154263	0.631720	1.000
564 GOBP_REGULATION_OF_CELL_CYCLE_PROCESS	GO-0010564	5	-0.634288	-1.261231	0.166893	0.635565	1.000
565 GOBP_CELL_CYCLE	GO-0007049	21	-0.449087	-1.267321	0.149490	0.619114	1.000
566 GOBP_REGULATION_OF_RESPONSE_TO_STRESS	GO-0080134	19	-0.462761	-1.271287	0.164798	0.609774	1.000
567 GOBP_NEGATIVE_REGULATION_OF_CELLULAR_COMPONENT...	GO-0051129	11	-0.516756	-1.271363	0.167651	0.613599	1.000
568 GOBP_CELL_ACTIVATION	GO-0001775	21	-0.450516	-1.274195	0.162042	0.608086	1.000
569 GOBP_RESPONSE_TO ABIOTIC STIMULUS	GO-0009628	27	-0.436302	-1.278149	0.145394	0.598101	1.000
570 GOBP_RESPONSE_TO_KETONE	GO-1901654	7	-0.586229	-1.278803	0.160804	0.599806	1.000
571 GOBP_CARBOHYDRATE_HOMEOSTASIS	GO-0033500	7	-0.583299	-1.281675	0.141772	0.594322	1.000
572 GOBP_RESPONSE_TO_CALCIIUM_ION	GO-0051592	6	-0.616889	-1.282772	0.146405	0.594890	1.000
573 GOBP_MULTIORGANISM_PROCESS	GO-0051704	16	-0.476899	-1.283422	0.154913	0.596759	1.000
574 GOBP_COAGULATION	GO-0050817	8	-0.572784	-1.287836	0.143392	0.585801	1.000
575 GOBP_POSITIVE_REGULATION_OF_CELLULAR_PROTEIN...	GO-1903829	7	-0.600093	-1.290053	0.136483	0.582333	1.000
576 GOBP_RESPONSE_TO_ENDOGENOUS_STIMULUS	GO-0009719	34	-0.428934	-1.290251	0.136752	0.585741	1.000
577 REACTOME_NGF_STIMULATED_TRANSCRIPTION	R-RNO-9031628	9	-0.554841	-1.291909	0.137717	0.584166	1.000
578 GOBP_MUSCLE_TISSUE_DEVELOPMENT	GO-0060537	11	-0.538445	-1.297069	0.118873	0.570823	1.000
579 GOBP_DEVELOPMENTAL_PROCESS_INVOLVED_IN_REPRODU...	GO-0003006	11	-0.537393	-1.299761	0.132616	0.566497	1.000
580 GOBP_DEFENSE_RESPONSE_TO_OTHER_ORGANISM	GO-0098542	9	-0.558386	-1.301892	0.118812	0.563558	1.000
581 GOBP_REGULATION_OF_SMALL_MOLECULE_METABOLIC_PR...	GO-0062012	9	-0.561030	-1.302998	0.118306	0.563899	1.000
582 GOBP_REGULATION_OF_LIPID_METABOLIC_PROCESS	GO-0019216	7	-0.600028	-1.304611	0.124679	0.562481	1.000
583 GOBP_MONONUCLEAR_CELL_DIFFERENTIATION	GO-1903131	7	-0.598281	-1.304773	0.149874	0.565999	1.000
584 GOBP_INNATE_IMMUNE_RESPONSE	GO-0045087	7	-0.607080	-1.312189	0.129887	0.546105	1.000
585 GOBP_REGULATION_OF_MITOTIC_CELL_CYCLE	GO-0007346	5	-0.663435	-1.313064	0.125000	0.547133	1.000
586 GOBP_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO...	GO-0072594	6	-0.624114	-1.313382	0.106289	0.550329	1.000
587 GOBP_MITOTIC_CELL_CYCLE	GO-0000278	10	-0.554408	-1.314412	0.114673	0.551153	1.000
588 GOBP_MULTICELLULAR_ORGANISM_REPRODUCTION	GO-0032504	12	-0.519882	-1.315770	0.148681	0.550967	1.000
589 GOBP_NEUROTROPHIN_SIGNALING_PATHWAY	GO-0038179	6	-0.633634	-1.317171	0.111111	0.550374	1.000
590 GOBP_REGULATION_OF_HEMOPOIESIS	GO-1903706	10	-0.551038	-1.320645	0.135802	0.543056	1.000
591 GOBP_TRANSMEMBRANE_RECEPTOR_PROTEIN_TYROSINE_K...	GO-0007169	19	-0.485845	-1.322687	0.144495	0.540418	1.000
592 GOBP_CYTOKINE_MEDIATED_SIGNALING_PATHWAY	GO-0019221	16	-0.493639	-1.322800	0.119590	0.544288	1.000
593 GOBP_LYMPHOCYTE_ACTIVATION	GO-0046649	9	-0.571244	-1.323303	0.138650	0.546848	1.000
594 GOBP_REGULATION_OF_IMMUNE_RESPONSE	GO-0050776	12	-0.536988	-1.323476	0.124088	0.550627	1.000
595 GOBP_NEUROTROPHIN_TRK_RECEPTOR_SIGNALING_PATHWAY	GO-0048011	6	-0.633634	-1.323949	0.115538	0.553294	1.000
596 REACTOME_G_PROTEIN_MEDIATED_EVENTS	R-RNO-112040	9	-0.571028	-1.324025	0.120988	0.557562	1.000
597 GOBP_NEGATIVE_REGULATION_OF_TRANSCRIPTION_BY_R...	GO-0000122	10	-0.546933	-1.325030	0.125945	0.558490	1.000
598 GOBP_POSITIVE_REGULATION_OF_ENDOTHELIAL_CELL_P...	GO-0001938	6	-0.637985	-1.326998	0.130890	0.556233	1.000
599 GOBP_POSITIVE_REGULATION_OF_GENE_EXPRESSION	GO-0010628	16	-0.499931	-1.329373	0.124857	0.552649	1.000

Continuation of Table S18

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
600	GOBP-REGULATION-OF-CELLULAR-RESPONSE-TO-STRESS	GO-0080135	9	-0.579178	-1.333126	0.120585	0.544455	1.000
601	GOBP-RESPONSE-TO-OXYGEN-LEVELS	GO-0070482	8	-0.591888	-1.335357	0.114103	0.541322	1.000
602	HALLMARK-TNFA-SIGNALING-VIA-NFKB	M590	14	-0.513846	-1.335793	0.122970	0.544412	1.000
603	GOBP-NEGATIVE-REGULATION-OF-HYDROLASE-ACTIVITY	GO-0051346	11	-0.542857	-1.339425	0.108935	0.536785	1.000
604	GOBP-SKELETAL-MUSCLE-ORGAN-DEVELOPMENT	GO-0060538	5	-0.685491	-1.340974	0.094415	0.536130	1.000
605	GOBP-POSITIVE-REGULATION-OF-IMMUNE-SYSTEM-PROCESS	GO-0002684	18	-0.505520	-1.346063	0.090498	0.523633	1.000
606	GOBP-REGULATION-OF-WNT-SIGNALING-PATHWAY	GO-0030111	5	-0.688480	-1.346639	0.085754	0.526443	1.000
607	GOBP-CELLULAR-RESPONSE-TO-PEPTIDE-HORMONE-STIM...	GO-0071375	9	-0.586567	-1.347261	0.103362	0.529159	1.000
608	GOBP-CELL-ACTIVATION-INVOLVED-IN-IMMUNE-RESPONSE	GO-0002263	6	-0.654873	-1.347995	0.087075	0.531460	1.000
609	GOBP-CELLULAR-RESPONSE-TO-LIPID	GO-0071396	15	-0.509074	-1.349005	0.104953	0.533025	1.000
610	GOBP-NEGATIVE-REGULATION-OF-NUCLEOBASE-CONTAIN...	GO-0045934	13	-0.545054	-1.349650	0.109027	0.535637	1.000
611	REACTOME-NEUTROPHIL-DEGRANULATION	R-RNO-6798695	6	-0.654873	-1.349777	0.098667	0.540153	1.000
612	GOBP-CELLULAR-GLUCOSE-HOMEOSTASIS	GO-0001678	5	-0.685186	-1.350977	0.084337	0.540837	1.000
613	GOBP-POSITIVE-REGULATION-OF-MULTICELLULAR-ORGA...	GO-0051240	32	-0.458485	-1.351387	0.114754	0.544371	1.000
614	GOBP-REGULATION-OF-CELL-CYCLE	GO-0051726	13	-0.535257	-1.351941	0.109606	0.547388	1.000
615	GOBP-LIPID-BIOSYNTHETIC-PROCESS	GO-0008610	6	-0.659353	-1.353785	0.083879	0.545991	1.000
616	GOBP-CELL-CELL-SIGNALING-BY-WNT	GO-0198738	7	-0.624074	-1.356213	0.090561	0.542985	1.000
617	GOBP-NEGATIVE-REGULATION-OF-BIOSYNTHETIC-PROCESS	GO-0009890	13	-0.533960	-1.357306	0.093859	0.544293	1.000
618	GOBP-CELLULAR-RESPONSE-TO-EXTRACELLULAR-STIMULUS	GO-0031668	8	-0.602057	-1.361504	0.091925	0.534450	1.000
619	GOBP-T-CELL-ACTIVATION	GO-0042110	8	-0.605059	-1.361838	0.094697	0.538744	1.000
620	GOBP-CELLULAR-RESPONSE-TO-STARVATION	GO-0009267	5	-0.698734	-1.363189	0.076398	0.539616	1.000
621	GOBP-REGULATION-OF-LIPID-BIOSYNTHETIC-PROCESS	GO-0046890	6	-0.659353	-1.364065	0.093176	0.541956	1.000
622	GOBP-MULTICELLULAR-ORGANISMAL-HOMEOSTASIS	GO-0048871	12	-0.547096	-1.365463	0.098321	0.542740	1.000
623	GOBP-POSITIVE-REGULATION-OF-CYTOKINE-PRODUCTION	GO-0001819	7	-0.632302	-1.365757	0.097345	0.547173	1.000
624	GOBP-REPRODUCTION	GO-0000003	18	-0.503871	-1.366529	0.091954	0.550180	1.000
625	GOBP-ENDOTHELIAL-CELL-PROLIFERATION	GO-0001935	8	-0.613882	-1.366962	0.093710	0.554124	1.000
626	GOBP-AGING	GO-0007568	13	-0.537121	-1.367624	0.098301	0.557470	1.000
627	REACTOME-CA-DEPENDENT-EVENTS	R-RNO-111996	8	-0.613456	-1.367630	0.077419	0.563507	1.000
628	GOBP-MYELOID-LEUKOCYTE-MEDIATED-IMMUNITY	GO-0002444	6	-0.654873	-1.368569	0.095816	0.566194	1.000
629	GOBP-CELL-CYCLE-PROCESS	GO-0022402	11	-0.565366	-1.369923	0.094645	0.566818	1.000
630	GOBP-CELLULAR-MACROMOLECULE-CATABOLIC-PROCESS	GO-0044265	6	-0.665301	-1.373403	0.099355	0.560339	1.000
631	REACTOME-PLATELET-ACTIVATION-SIGNALING-AND-AGG...	R-HSA-76002	7	-0.625394	-1.373762	0.096306	0.565522	1.000
632	GOBP-CELL-POPULATION-PROLIFERATION	GO-0008283	31	-0.468222	-1.381003	0.088267	0.544315	1.000
633	GOBP-REGULATION-OF-ANION-TRANSPORT	GO-0044070	20	-0.489206	-1.382665	0.085106	0.544417	1.000
634	GOBP-CIRCULATORY-SYSTEM-DEVELOPMENT	GO-0072359	21	-0.498398	-1.384517	0.084081	0.544142	1.000
635	GOBP-POSITIVE-REGULATION-OF-EPITHELIAL-CELL-PR...	GO-0050679	7	-0.625349	-1.386790	0.079324	0.542269	1.000
636	GOBP-CHROMATIN-ORGANIZATION	GO-0006325	5	-0.695507	-1.387774	0.055935	0.545083	1.000
637	GOBP-POSITIVE-REGULATION-OF-CELL-POPULATION-PR...	GO-0008284	21	-0.498657	-1.389268	0.075028	0.546130	1.000
638	GOBP-PROTEIN-LOCALIZATION-TO-ORGANELLE	GO-0033365	9	-0.605475	-1.390180	0.070263	0.549206	1.000
639	GOBP-MUSCLE-ORGAN-DEVELOPMENT	GO-0007517	9	-0.602148	-1.390990	0.073658	0.553119	1.000
640	GOBP-ENZYMELINKED-RECEPTOR-PROTEIN-SIGNALING....	GO-0007167	24	-0.489849	-1.398259	0.064978	0.531454	1.000
641	GOBP-POSITIVE-REGULATION-OF-ANION-TRANSPORT	GO-1903793	9	-0.602035	-1.398876	0.087763	0.535511	1.000
642	GOBP-RESPONSE-TO-STARVATION	GO-0042594	5	-0.698734	-1.405055	0.064171	0.519721	1.000

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NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
643 GOBP-REGULATION-OF-PROTEIN-STABILITY	GO-0031647	5	-0.704817	-1.411878	0.068966	0.502191	1.000
644 GOBP-RESPONSE-TO-OXYGEN-CONTAINING-COMPOUND	GO-1901700	39	-0.467609	-1.426152	0.051447	0.457789	1.000
645 GOBP-RESPONSE-TO-LIPID	GO-0033993	19	-0.514598	-1.429730	0.061017	0.451814	1.000
646 GOBP-CELLULAR-RESPONSE-TO-ABIOTIC-STIMULUS	GO-0071214	7	-0.656175	-1.434210	0.059627	0.442607	1.000
647 GOBP-CELLULAR-RESPONSE-TO-PEPTIDE	GO-1901653	13	-0.567004	-1.434478	0.051435	0.447567	1.000
648 GOBP-MYELOID-LEUKOCYTE-DIFFERENTIATION	GO-0002573	11	-0.591863	-1.435353	0.056931	0.451116	1.000
649 GOBP-REGULATION-OF-MYELOID-CELL-DIFFERENTIATION	GO-0045637	9	-0.620915	-1.436069	0.065854	0.455236	1.000
650 REACTOME-ESTROGEN-DEPENDENT-NUCLEAR-EVENTS-DOW...	R-RNO-9634638	5	-0.731514	-1.437364	0.042553	0.457334	1.000
651 GOBP-RESPONSE-TO-INORGANIC-SUBSTANCE	GO-0010035	19	-0.515211	-1.438111	0.057175	0.461411	1.000
652 GOBP-RESPONSE-TO-NITROGEN-COMPOUND	GO-1901698	34	-0.481730	-1.438718	0.048077	0.466002	1.000
653 GOBP-VASCULATURE-DEVELOPMENT	GO-0001944	17	-0.541411	-1.447895	0.052692	0.441139	1.000
654 GOBP-REGULATION-OF-IMMUNE-SYSTEM-PROCESS	GO-0002682	21	-0.517109	-1.448162	0.060502	0.446920	1.000
655 GOBP-TISSUE-HOMEOSTASIS	GO-0001894	5	-0.730595	-1.449404	0.034483	0.449333	1.000
656 GOBP-CARBOHYDRATE-BIOSYNTHETIC-PROCESS	GO-0016051	5	-0.735446	-1.450579	0.046703	0.452508	1.000
657 GOBP-CELLULAR-RESPONSE-TO-INORGANIC-SUBSTANCE	GO-0071241	11	-0.595297	-1.452256	0.038694	0.449702	1.000
658 GOBP-REGULATION-OF-CARBOHYDRATE-METABOLIC-PROCESS	GO-0006109	5	-0.735446	-1.455973	0.037241	0.447052	1.000
659 GOBP-CELLULAR-RESPONSE-TO-EXTERNAL-STIMULUS	GO-0071496	10	-0.613285	-1.456497	0.041262	0.452565	1.000
660 GOBP-RESPONSE-TO-MOLECULE-OF-BACTERIAL-ORIGIN	GO-0002237	13	-0.573657	-1.457839	0.049763	0.455531	1.000
661 GOBP-APOPTOTIC-SIGNALING-PATHWAY	GO-0097190	15	-0.557619	-1.458684	0.039261	0.459883	1.000
662 GOBP-REGULATION-OF-CARBOHYDRATE-BIOSYNTHETIC-P...	GO-0043255	5	-0.735446	-1.459505	0.047490	0.464199	1.000
663 HALLMARK-UV-RESPONSE-UP	M5941	5	-0.733690	-1.464476	0.037344	0.454873	1.000
664 REACTOME-ESR-MEDIATED-SIGNALING	R-RNO-8939211	8	-0.652815	-1.469482	0.049869	0.445088	1.000
665 REACTOME-CELL-CYCLE	R-RNO-1640170	6	-0.703607	-1.470180	0.042553	0.451373	1.000
666 GOBP-RESPONSE-TO-OXIDATIVE-STRESS	GO-0006979	8	-0.658290	-1.471982	0.051414	0.453490	1.000
667 REACTOME-SIGNALING-BY-NUCLEAR-RECEPTORS	R-RNO-9006931	8	-0.652815	-1.473035	0.048969	0.457839	1.000
668 REACTOME-NUCLEAR-EVENTS-KINASE-AND-TRANSCRIPTI...	R-RNO-198725	11	-0.605835	-1.475356	0.042908	0.458328	1.000
669 GOBP-RESPONSE-TO-BACTERIUM	GO-0009617	13	-0.572657	-1.480237	0.035294	0.448426	1.000
670 GOBP-DNA-METABOLIC-PROCESS	GO-0006259	6	-0.704260	-1.483121	0.036896	0.446954	1.000
671 GOBP-NEGATIVE-REGULATION-OF-CELL-DIFFERENTIATION	GO-0045596	13	-0.596055	-1.485279	0.042503	0.448219	1.000
672 GOBP-CELLULAR-RESPONSE-TO-CADMIUM-ION	GO-0071276	5	-0.753648	-1.486642	0.036697	0.452443	1.000
673 GOBP-RESPONSE-TO-GROWTH-FACTOR	GO-0070848	18	-0.545097	-1.487974	0.038117	0.456843	1.000
674 GOBP-RESPONSE-TO-REACTIVE-OXYGEN-SPECIES	GO-0000302	8	-0.658290	-1.488636	0.049808	0.464979	1.000
675 GOBP-CELLULAR-RESPONSE-TO-NITROGEN-COMPOUND	GO-1901699	20	-0.545764	-1.502901	0.030067	0.420395	1.000
676 GOBP-NEGATIVE-REGULATION-OF-DEVELOPMENTAL-PROCESS	GO-0051093	13	-0.596055	-1.505536	0.027187	0.419574	1.000
677 GOBP-CELLULAR-RESPONSE-TO-HORMONE-STIMULUS	GO-0032870	11	-0.625261	-1.505621	0.028916	0.429250	1.000
678 GOBP-ENDOMEMBRANE-SYSTEM-ORGANIZATION	GO-0010256	6	-0.729473	-1.507025	0.028461	0.434377	1.000
679 REACTOME-MAPK-TARGETS-NUCLEAR-EVENTS-MEDIATED-...	R-HSA-450282	5	-0.761795	-1.511425	0.023448	0.427747	1.000
680 GOBP-POSITIVE-REGULATION-OF-NUCLEOBASE-CONTAIN...	GO-0045935	28	-0.519870	-1.513458	0.029001	0.430795	1.000
681 GOBP-CELLULAR-RESPONSE-TO-REACTIVE-OXYGEN-SPECIES	GO-0034614	7	-0.705586	-1.517514	0.029040	0.426558	1.000
682 REACTOME-EXTRA-NUCLEAR-ESTROGEN-SIGNALING	R-RNO-9009391	7	-0.697905	-1.518169	0.025990	0.435436	1.000
683 GOBP-RESPONSE-TO-PEPTIDE-HORMONE	GO-0043434	13	-0.587908	-1.524988	0.027091	0.421098	1.000
684 GOBP-RESPONSE-TO-PEPTIDE	GO-1901652	18	-0.562621	-1.528581	0.018931	0.419428	1.000
685 GOBP-MYELOID-CELL-DIFFERENTIATION	GO-0030099	13	-0.607730	-1.529383	0.023952	0.428292	1.000

Continuation of Table S18

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
686 GOBP-ANATOMICAL-STRUCTURE-HOMEOSTASIS	GO-0060249	7	-0.706786	-1.536390	0.028169	0.414164	1.000
687 GOBP-RESPONSE.TO.ORGANIC-CYCLIC-COMPOUND	GO-0014070	20	-0.551466	-1.538216	0.019473	0.420615	1.000
688 REACTOME-SENESCENCE-ASSOCIATED-SECRETORY-PHENO...	R-RNO-2559582	6	-0.743931	-1.544775	0.022457	0.408269	1.000
689 GOBP-RESPONSE.TO.BIOTIC-STIMULUS	GO-0009607	17	-0.575603	-1.548995	0.022599	0.406303	1.000
690 GOBP-RESPONSE.TO.HORMONE	GO-0009725	20	-0.563460	-1.551259	0.015730	0.412053	1.000
691 GOBP-POSITIVE-REGULATION.OF.BIOSYNTHETIC-PROCESS	GO-0009891	27	-0.537777	-1.551505	0.022801	0.425528	1.000
692 GOBP-RESPONSE.TO.METAL-ION	GO-0010038	15	-0.586003	-1.552706	0.022353	0.436035	1.000
693 REACTOME-CELLULAR-SENESCENCE	R-RNO-2559583	6	-0.743931	-1.555659	0.018494	0.440793	1.000
694 REACTOME-CELL-CYCLE-MITOTIC	R-RNO-69278	5	-0.777316	-1.560863	0.014865	0.435689	1.000
695 GOBP-CYTOKINE-PRODUCTION	GO-0001816	10	-0.653944	-1.564655	0.023002	0.436099	1.000
696 GOBP-LEUKOCYTE-DIFFERENTIATION	GO-0002521	15	-0.601688	-1.565265	0.026775	0.453241	1.000
697 GOBP-CELLULAR-RESPONSE.TO.CHEMICAL-STRESS	GO-0062197	7	-0.705586	-1.568984	0.022930	0.457875	1.000
698 REACTOME-RHO-GTPASE-EFFECTORS	R-RNO-195258	9	-0.683420	-1.572556	0.018916	0.462620	1.000
699 REACTOME-INTRACELLULAR-SIGNALING-BY-SECOND-MES...	R-RNO-9006925	15	-0.597985	-1.573132	0.015012	0.482392	1.000
700 REACTOME-SIGNALING-BY-RHO-GTPASES-MIRO-GTPASES...	R-RNO-9716542	9	-0.683420	-1.573596	0.019876	0.504761	1.000
701 REACTOME-PTEN-REGULATION	R-RNO-6807070	5	-0.795312	-1.574377	0.017287	0.528511	1.000
702 GOBP-CIRCADIAN-REGULATION.OF.GENE-EXPRESSION	GO-0032922	5	-0.810652	-1.582998	0.009615	0.511561	1.000
703 GOBP-RESPONSE.TO.CYTOKINE	GO-0034097	23	-0.561041	-1.590455	0.012182	0.503463	1.000
704 GOBP-RESPONSE.TO.INTERLEUKIN-1	GO-0070555	5	-0.788071	-1.592308	0.011080	0.527145	1.000
705 GOBP-CELLULAR-RESPONSE.TO.ORGANIC-CYCLIC-COMPOUND	GO-0071407	13	-0.628618	-1.605673	0.017815	0.492604	0.999
706 GOBP-CHROMOSOME-ORGANIZATION	GO-0051276	6	-0.779348	-1.616309	0.011749	0.474459	0.998
707 GOBP-IMMUNE-SYSTEM-DEVELOPMENT	GO-0002520	17	-0.602560	-1.621369	0.005855	0.484531	0.997
708 REACTOME-INTERLEUKIN-17-SIGNALING	R-RNO-448424	6	-0.779880	-1.624243	0.010540	0.511357	0.997
709 REACTOME-CELLULAR-RESPONSES.TO.EXTERNAL-STIMULI	R-RNO-8953897	12	-0.659393	-1.624315	0.003563	0.561680	0.997
710 GOBP-REPRODUCTIVE-SYSTEM-DEVELOPMENT	GO-0061458	6	-0.768679	-1.630165	0.004098	0.580990	0.995
711 GOBP-CELLULAR-RESPONSE.TO.OXYGEN-CONTAINING.CO...	GO-1901701	29	-0.556350	-1.633406	0.007503	0.630095	0.995
712 GOBP-POSITIVE-REGULATION.OF-TRANSCRIPTION-BY-R...	GO-0045944	24	-0.562724	-1.634757	0.005525	0.709635	0.995
713 GOBP-TRANSMEMBRANE-RECEPTOR-PROTEIN-SERINE.THR...	GO-0007178	6	-0.793485	-1.642650	0.009272	0.760634	0.992
714 GOBP-RESPONSE.TO.CADMIUM-ION	GO-0046686	6	-0.811818	-1.668194	0.005249	0.687236	0.959
715 REACTOME-RNA-POLYMERASE-II-TRANSCRIPTION	R-RNO-73857	20	-0.603682	-1.670752	0.006787	0.833580	0.954
716 GOBP-RESPONSE.TO.HEAT	GO-0009408	7	-0.770551	-1.697763	0.005141	0.786915	0.885
717 GOBP-EPITHELIAL-CELL-PROLIFERATION	GO-0050673	12	-0.676235	-1.702127	0.003550	1.000000	0.876
718 GOBP-RESPONSE.TO-TEMPERATURE-STIMULUS	GO-0009266	9	-0.835824	-1.940079	0.000000	0.059114	0.056

End of Table

Supplementary Table S19: CB late profile (45 DPL peak) GSEA results.

Begin of Table S19									
	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val	
0	GOBP_NERVE_DEVELOPMENT	GO:0021675	9	0.716460	2.134525	0.000000	0.229673	0.297	
1	GOBP_NEUROTROPHIN_TRK_RECEPTOR_SIGNALING_PATHWAY	GO:0048011	6	0.756005	2.012518	0.000000	0.294539	0.603	
2	GOBP_NEUROTROPHIN_SIGNALING_PATHWAY	GO:0038179	6	0.756005	1.964451	0.005666	0.274723	0.720	
3	GOBP_NEGATIVE_REGULATION_OF_NEURON_APOPTOTIC_P...	GO:0043524	8	0.644055	1.874099	0.014085	0.364420	0.896	
4	GOBP_MULTICELLULAR_ORGANISMAL_RESPONSE_TO_STRESS	GO:0033555	5	0.747005	1.776908	0.032432	0.498949	0.973	
5	GOBP_NUCLEAR_TRANSPORT	GO:0051169	5	0.728041	1.751098	0.021390	0.476310	0.986	
6	GOBP_SKELETAL_MUSCLE_ORGAN_DEVELOPMENT	GO:0060538	5	0.732227	1.74755	0.022059	0.416709	0.986	
7	GOBP_REGULATION_OF_NEUROGENESIS	GO:0050767	14	0.468034	1.694843	0.018462	0.478156	0.997	
8	GOBP_POSITIVE_REGULATION_OF_BINDING	GO:0051099	6	0.631168	1.659829	0.028490	0.507211	0.998	
9	GOBP_REGULATION_OF_CELL_DEVELOPMENT	GO:0060284	15	0.457693	1.647894	0.038095	0.483624	0.998	
10	GOBP_REGULATION_OF_CELL_DIFFERENTIATION	GO:0045595	36	0.330436	1.616250	0.013575	0.514549	1.000	
11	GOBP_REGULATION_OF_NERVOUS_SYSTEM_DEVELOPMENT	GO:0051960	15	0.417206	1.588721	0.055738	0.540900	1.000	
12	GOBP_REGULATION_OF_PHOSPHOLIPASE_ACTIVITY	GO:0010517	6	0.597561	1.579981	0.057221	0.521679	1.000	
13	GOBP_PEPTIDYL_AMINO_ACID_MODIFICATION	GO:0018193	22	0.363230	1.538866	0.047619	0.592602	1.000	
14	GOBP_REGULATION_OF_LIPASE_ACTIVITY	GO:0060191	6	0.597561	1.533080	0.086705	0.568456	1.000	
15	GOBP_INTRACELLULAR_TRANSPORT	GO:0046907	11	0.452115	1.530977	0.057927	0.538756	1.000	
16	GOBP_REGULATION_OF_NEURON_DIFFERENTIATION	GO:0045664	5	0.617818	1.514529	0.068493	0.547635	1.000	
17	GOBP_POSITIVE_REGULATION_OF_CELL_DEVELOPMENT	GO:0010720	12	0.432380	1.514442	0.062706	0.517392	1.000	
18	GOBP_NEGATIVE_REGULATION_OF_CELL_DIFFERENTIATION	GO:0045596	13	0.411971	1.484162	0.070513	0.565311	1.000	
19	GOBP_NEGATIVE_REGULATION_OF_DEVELOPMENTAL_PROCESS	GO:0051093	13	0.411971	1.481328	0.083871	0.543793	1.000	
20	GOBP_POSITIVE_REGULATION_OF_NEUROGENESIS	GO:0050769	12	0.432380	1.480072	0.072131	0.520629	1.000	
21	GOBP_POSITIVE_REGULATION_OF_NERVOUS_SYSTEM_DEV...	GO:0051962	12	0.432380	1.475271	0.084416	0.507155	1.000	
22	GOBP_NEURON_APOPTOTIC_PROCESS	GO:0051402	12	0.425131	1.462701	0.070968	0.515005	1.000	
23	GOBP_PERIPHERAL_NERVOUS_SYSTEM_DEVELOPMENT	GO:0007422	9	0.457535	1.455716	0.080357	0.509114	1.000	
24	GOBP_REGULATION_OF_PHOSPHOLIPASE_C_ACTIVITY	GO:1900274	5	0.590361	1.441845	0.114362	0.520327	1.000	
25	GOBP_REGULATION_OF_MULTICELLULAR_ORGANISMAL_DE...	GO:2000026	31	0.306068	1.431152	0.047619	0.524655	1.000	
26	GOBP_POSITIVE_REGULATION_OF_LIPASE_ACTIVITY	GO:0060193	5	0.590361	1.424417	0.085873	0.520287	1.000	
27	GOBP_RESPONSE_TO_STARVATION	GO:0042594	5	0.575313	1.423891	0.083102	0.502754	1.000	
28	GOBP_CELLULAR_RESPONSE_TO_STARVATION	GO:0009267	5	0.575313	1.413315	0.108992	0.508393	1.000	
29	GOBP_REGULATION_OF_GTPASE_ACTIVITY	GO:0043087	5	0.575313	1.375816	0.133880	0.577743	1.000	
30	GOBP_FC_EPSILON_RECEPTOR_SIGNALING_PATHWAY	GO:0038095	7	0.481482	1.369556	0.111782	0.572921	1.000	
31	GOBP_NEGATIVE_REGULATION_OF_PROTEIN_METABOLIC...	GO:0051248	20	0.332383	1.354928	0.111913	0.589906	1.000	
32	GOBP_NEGATIVE_REGULATION_OF_PROTEOLYSIS	GO:0045861	8	0.456930	1.341875	0.133333	0.604494	1.000	
33	GOBP_NEGATIVE_REGULATION_OF_NEURON_DEATH	GO:1901215	11	0.400801	1.335697	0.141538	0.602383	1.000	
34	GOBP_POSITIVE_REGULATION_OF_GLOIOGENESIS	GO:0014015	5	0.546907	1.332623	0.136816	0.592521	1.000	
35	GOBP_POSITIVE_REGULATION_OF_LOCOMOTION	GO:0040017	11	0.395448	1.332378	0.133779	0.576815	1.000	
36	GOBP_SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCTION	GO:0007264	8	0.453414	1.332291	0.153425	0.561364	1.000	
37	REACTOME_FC_EPSILON_RECEPTOR_FCRH_SIGNALING	R-RNO-2454202	7	0.481481	1.329276	0.150000	0.553650	1.000	
38	GOBP_REGULATION_OF_GLOIOGENESIS	GO:0014013	5	0.546907	1.324237	0.135977	0.550937	1.000	
39	GOBP_MUSCLE_ORGAN_DEVELOPMENT	GO:0007517	9	0.429393	1.323356	0.150769	0.539286	1.000	
40	GOBP_INTRACELLULAR_PROTEIN_TRANSPORT	GO:0006886	9	0.423097	1.318148	0.132743	0.537549	1.000	

Continuation of Table S19

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
41	REACTOME.BETA_CATENIN_INDEPENDENT_WNT_SIGNALING	R-RNO-3858494	5	0.527452	1.309498	0.156522	0.543938	1.000
42	GOBP.MYOTUBE_DIFFERENTIATION	GO-0014902	5	0.542169	1.304991	0.170455	0.540888	1.000
43	GOBP.RHYTHMIC_PROCESS	GO-0048511	15	0.341645	1.283914	0.138047	0.572486	1.000
44	GOBP.REGULATION_OF_BINDING	GO-0051098	11	0.381002	1.278581	0.179878	0.572397	1.000
45	REACTOME.SIGNALING_BY_WNT	R-RNO-195721	7	0.440998	1.267772	0.173410	0.583030	1.000
46	GOBP.MUSCLE_TISSUE_DEVELOPMENT	GO-0060537	11	0.355989	1.234762	0.205607	0.647616	1.000
47	REACTOME.CELLULAR_SENESCENCE	R-RNO-2559583	6	0.463415	1.229137	0.202740	0.647220	1.000
48	REACTOME.SIGNALING_BY_NTRKS	R-RNO-166520	18	0.309306	1.225833	0.179856	0.641921	1.000
49	REACTOME.SENESCENCE_ASSOCIATED_SECRETORY_PHENO...	R-RNO-2559582	6	0.463415	1.221107	0.218289	0.639940	1.000
50	HALLMARK_KRAS_SIGNALING_UP	M5953	6	0.469763	1.220152	0.217514	0.629797	1.000
51	GOBP.PEPTIDYL_LYSINE_MODIFICATION	GO-0018205	5	0.481928	1.215751	0.220472	0.628005	1.000
52	REACTOME.CELL_CYCLE_MITOTIC	R-RNO-69278	5	0.493718	1.205332	0.248603	0.641023	1.000
53	GOBP.REGULATION_OF_PEPTIDYL_TYROSINE_PHOSPHORYL...	GO-0050730	9	0.383853	1.201798	0.224377	0.638281	1.000
54	GOBP.NEGATIVE_REGULATION_OF_PEPTIDASE_ACTIVITY	GO-0010466	6	0.451545	1.200791	0.209945	0.629241	1.000
55	GOBP.CIRCADIAN_REGULATION_OF_GENE_EXPRESSION	GO-0032922	5	0.486814	1.193968	0.240113	0.633790	1.000
56	REACTOME.MYD88_INDEPENDENT_TLR4_CASCADE	R-RNO-166166	8	0.387500	1.184682	0.219020	0.643827	1.000
57	GOBP.NEGATIVE_REGULATION_OF_CYSSTEINE_TYPE_ENDO...	GO-2000117	5	0.489926	1.180252	0.230769	0.642828	1.000
58	REACTOME.TOLL LIKE RECEPTOR_TLR1_TLR2_CASCADE	R-RNO-168179	8	0.387500	1.178623	0.250765	0.635857	1.000
59	GOBP.DEPHOSPHORYLATION	GO-0016311	7	0.409268	1.169015	0.278515	0.647711	1.000
60	REACTOME.TOLL LIKE RECEPTOR_CASCADES	R-RNO-168898	8	0.387500	1.155161	0.249275	0.670074	1.000
61	GOBP.RESPONSE_TO_NERVE_GROWTH_FACTOR	GO-1990089	7	0.413277	1.147483	0.285714	0.677009	1.000
62	GOBP.PROTEIN_DEPHOSPHORYLATION	GO-0006470	7	0.409268	1.144085	0.298851	0.674264	1.000
63	GOBP.NEURON_PROJECTION_GUIDANCE	GO-0097485	9	0.363208	1.120672	0.303681	0.719431	1.000
64	GOBP.RESPONSE_TO_INTERLEUKIN_1	GO-0070555	5	0.457831	1.116054	0.293814	0.719585	1.000
65	REACTOME.TOLL LIKE RECEPTOR_9_TLR9_CASCADE	R-RNO-168138	5	0.387500	1.113771	0.280347	0.714299	1.000
66	GOBP.REGULATION_OF_MUSCLE_ADAPTATION	GO-0043502	5	0.452378	1.104137	0.301047	0.726482	1.000
67	GOBP.INOSITOL_LIPID_MEDIATED_SIGNALING	GO-0048017	8	0.377988	1.103656	0.318885	0.716931	1.000
68	GOBP.RAS_PROTEIN_SIGNAL_TRANSDUCTION	GO-0007265	5	0.455482	1.093220	0.321244	0.732153	1.000
69	GOBP.POSITIVE_REGULATION_OF_PEPTIDYL_SERINE_PH...	GO-0033138	8	0.359703	1.084723	0.361979	0.743248	1.000
70	GOBP.POSITIVE_REGULATION_OF_MULTICELLULAR_ORGA...	GO-0051240	32	0.240193	1.084691	0.327465	0.732898	1.000
71	REACTOME.CELL_CYCLE	R-RNO-1640170	6	0.415120	1.083348	0.352632	0.725709	1.000
72	GOBP.POSITIVE_REGULATION_OF_AXONOGENESIS	GO-0050772	5	0.438849	1.078785	0.334239	0.726323	1.000
73	GOBP.MUSCLE_ADAPTATION	GO-0043500	5	0.452378	1.077121	0.330275	0.720460	1.000
74	GOBP.REGULATION_OF_PEPTIDYL_SERINE_PHOSPHORYLA...	GO-0033135	8	0.359703	1.076031	0.335329	0.713469	1.000
75	GOBP.NEGATIVE_REGULATION_OF_CELL_DEATH	GO-0060548	22	0.268185	1.068055	0.332090	0.722301	1.000
76	GOBP.DEVELOPMENTAL_GROWTH	GO-0048589	10	0.333508	1.045291	0.373771	0.768877	1.000
77	GOBP.PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_CON...	GO-0032446	6	0.388088	1.041826	0.388406	0.766668	1.000
78	GOBP.NEURON_DEATH	GO-0070997	18	0.263215	1.032896	0.410256	0.777486	1.000
79	REACTOME.SIGNALING_BY_RECEPTOR_TYROSINE_KINASES	R-RNO-9006934	26	0.229652	1.024655	0.429688	0.788181	1.000
80	GOBP.POSITIVE_REGULATION_OF_CELLULAR_COMPONENT...	GO-0051130	24	0.238158	1.023835	0.423611	0.780463	1.000
81	GOBP.CELLULAR_COMPONENT_MORPHOGENESIS	GO-0032989	24	0.235420	1.022987	0.444444	0.772778	1.000
82	GOBP.CELL_MORPHOGENESIS	GO-0000902	24	0.235420	1.019011	0.422053	0.772606	1.000
83	GOBP.REGULATION_OF_ENDOCYTOSIS	GO-0030100	6	0.389262	1.015818	0.437888	0.770661	1.000

Continuation of Table S19

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
84	GOBP-NEGATIVE-REGULATION-OF-CELL-POPULATION.PR...	9	0.329339	1.014069	0.428144	0.765887	1.000
85	GOBP-CELL-MORPHOGENESIS-INVOLVED-IN-DIFFERENTI...	21	0.241925	1.014042	0.455830	0.757020	1.000
86	GOBP-PEPTIDYL-TYROSINE-MODIFICATION	10	0.309895	1.013318	0.419753	0.749825	1.000
87	GOBP-CELL-PART-MORPHOGENESIS	24	0.235420	1.006619	0.415094	0.756027	1.000
88	GOBP-TRANSMEMBRANE-RECEPTOR-PROTEIN-SERINE-THR...	6	0.378049	1.005526	0.389535	0.750183	1.000
89	GOBP-CELL-MORPHOGENESIS-INVOLVED-IN-NEURON-DIF...	21	0.241925	0.998708	0.448630	0.757084	1.000
90	GOBP-REGULATION-OF-PROTEOLYSIS	12	0.288387	0.990185	0.448276	0.768204	1.000
91	GOBP-REGULATION-OF-INTRACELLULAR-SIGNAL-TRANSD...	21	0.233492	0.985595	0.487719	0.763245	1.000
92	REACTOME-INTERLEUKIN_17-SIGNALING	6	0.378049	0.987267	0.475138	0.758124	1.000
93	GOBP-REGULATION-OF-PHOSPHATIDYLINOSITOL-3-KINA...	6	0.378035	0.986633	0.431267	0.751468	1.000
94	GOBP-GROWTH	14	0.262635	0.983833	0.468227	0.749883	1.000
95	GOBP-NEGATIVE-REGULATION-OF-MULTICELLULAR-ORGA...	15	0.264120	0.975911	0.450658	0.758765	1.000
96	GOBP-POSITIVE-REGULATION-OF-CELL-POPULATION.PR...	21	0.232286	0.975493	0.473186	0.751821	1.000
97	GOBP-TRANSMEMBRANE-RECEPTOR-PROTEIN-TYROSINE.K...	19	0.234887	0.960266	0.531773	0.776809	1.000
98	GOBP-POSITIVE-REGULATION-OF-INTRACELLULAR-SIGN...	14	0.258148	0.944790	0.535928	0.802576	1.000
99	GOBP-POSITIVE-REGULATION-OF-PHOSPHATIDYLINOSIT...	5	0.378161	0.934229	0.522310	0.817339	1.000
100	REACTOME-MAPK-TARGETS-NUCLEAR-EVENTS-MEDIATED...	5	0.373494	0.929190	0.524638	0.820399	1.000
101	GOBP-ENDOCYTOSIS	8	0.317761	0.926144	0.546828	0.818990	1.000
102	GOBP-RESPONSE-TO-GROWTH-FACTOR	18	0.235347	0.924477	0.568690	0.814326	1.000
103	GOBP-POSITIVE-REGULATION-OF-EPITHELIAL-CELL.MI...	5	0.375650	0.918646	0.522078	0.819024	1.000
104	GOBP-MUSCLE-CELL-DEVELOPMENT	5	0.372794	0.915466	0.562857	0.818056	1.000
105	GOBP-CIRCADIAN-RHYTHM	13	0.256841	0.909546	0.560137	0.822730	1.000
106	GOBP-POSITIVE-REGULATION-OF-PEPTIDYL-TYROSINE...	8	0.305413	0.907952	0.557103	0.818416	1.000
107	GOBP-CELLULAR-MACROMOLECULE-CATABOLIC-PROCESS	6	0.340300	0.901461	0.576819	0.824088	1.000
108	GOBP-OSSIFICATION	9	0.292325	0.897862	0.587349	0.823741	1.000
109	GOBP-DEVELOPMENTAL-CELL-GROWTH	5	0.363172	0.893180	0.569892	0.826537	1.000
110	REACTOME-ADAPTIVE-IMMUNE-SYSTEM	9	0.295496	0.889328	0.573529	0.826876	1.000
111	GOBP-REGULATION-OF-VESICLE-MEDIATED-TRANSPORT	12	0.251160	0.889098	0.593443	0.820013	1.000
112	GOBP-NEGATIVE-REGULATION-OF-CELL-PROJECTION.OR...	5	0.368189	0.885217	0.598425	0.820328	1.000
113	GOBP-POSITIVE-REGULATION-OF-ORGANELLE-ORGANIZA...	10	0.275196	0.883026	0.612613	0.817529	1.000
114	GOBP-CELL-POPULATION-PROLIFERATION	31	0.194700	0.882057	0.637860	0.812175	1.000
115	GOBP-NEGATIVE-REGULATION-OF-PROTEIN-MODIFICATI...	10	0.272593	0.876698	0.629179	0.815539	1.000
116	GOBP-GLIOGENESIS	12	0.256193	0.874804	0.638978	0.812294	1.000
117	GOBP-NEGATIVE-REGULATION-OF-CELL-DEVELOPMENT	6	0.327420	0.872096	0.610959	0.810770	1.000
118	REACTOME-INNATE-IMMUNE-SYSTEM	16	0.223922	0.864512	0.638095	0.818424	1.000
119	GOBP-RESPONSE-TO-PEPTIDE	18	0.225209	0.863760	0.621053	0.813164	1.000
120	REACTOME-DEATH-RECEPTOR-SIGNALING	5	0.356092	0.850111	0.635389	0.832587	1.000
121	GOBP-NEGATIVE-REGULATION-OF-NERVOUS-SYSTEM.DEV...	5	0.348451	0.847495	0.655353	0.830251	1.000
122	GOBP-POSITIVE-REGULATION-OF-CELL-DIFFERENTIATION	27	0.196802	0.839909	0.694444	0.837437	1.000
123	GOBP-NEGATIVE-REGULATION-OF-PHOSPHORYLATION	7	0.301912	0.839595	0.652709	0.831210	1.000
124	GOBP-REGULATION-OF-CIRCADIAN-RHYTHM	7	0.304121	0.836531	0.663044	0.830127	1.000
125	GOBP-POSITIVE-REGULATION-OF-DEVELOPMENTAL-PROCESS	32	0.176184	0.832391	0.740458	0.831071	1.000
126	GOBP-TAXIS	14	0.231693	0.832133	0.674267	0.825044	1.000

Continuation of Table S19

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
127 GOBP-CELLULAR-GLUCOSE-HOMEOSTASIS	GO-0001678	5	0.346271	0.829617	0.650273	0.823230	1.000
128 GOBP-ENZYME-LINKED-RECEPTOR-PROTEIN-SIGNALING....	GO-0007167	24	0.187124	0.820410	0.715867	0.833635	1.000
129 REACTOME-SIGNALING-BY-NTRK2-TRKB	R-RNO-9006115	6	0.304272	0.799453	0.712329	0.863987	1.000
130 GOBP-REGULATION-OF-VASCULAR-ASSOCIATED-SMOOTH...	GO-1904705	5	0.323702	0.791959	0.724868	0.870263	1.000
131 GOBP-POSITIVE-REGULATION-OF-PROTEIN-TYROSINE-K...	GO-00061098	5	0.323331	0.784913	0.731904	0.875942	1.000
132 GOBP-RESPONSE-TO-INSULIN	GO-0032868	5	0.326827	0.781643	0.735897	0.874723	1.000
133 GOBP-REGULATION-OF-PROTEIN-TYROSINE-KINASE-ACT...	GO-0061097	5	0.323331	0.779706	0.740053	0.871251	1.000
134 GOBP-FC-RECEPTOR-SIGNALING-PATHWAY	GO-0038093	8	0.258225	0.766793	0.807580	0.886239	1.000
135 GOBP-REGULATION-OF-AXONOGENESIS	GO-0050770	7	0.267458	0.761439	0.755043	0.888616	1.000
136 GOBP-ESTABLISHMENT-OF-PROTEIN-LOCALIZATION-TO...	GO-0072594	6	0.290600	0.759529	0.744565	0.885148	1.000
137 GOBP-IMMUNE-RESPONSE-REGULATING-SIGNALING-PATHWAY	GO-0002764	8	0.258225	0.759285	0.735736	0.879044	1.000
138 GOBP-NEGATIVE-REGULATION-OF-INTRACELLULAR-SIGN...	GO-1902532	7	0.264403	0.749274	0.750000	0.887674	1.000
139 GOBP-RESPONSE-TO-CALCIUM-ION	GO-0051592	6	0.279673	0.737742	0.810959	0.899069	1.000
140 GOBP-MYELOID-LEUKOCYTE-DIFFERENTIATION	GO-0002573	11	0.218297	0.717416	0.853035	0.922017	1.000
141 REACTOME-EXTRACELLULAR-MATRIX-ORGANIZATION	R-RNO-1474244	5	0.279941	0.710499	0.818182	0.925219	1.000
142 REACTOME-TRANSCRIPTIONAL-REGULATION-BY-TP53	R-RNO-3700989	6	0.269051	0.708610	0.835165	0.921394	1.000
143 GOBP-REGULATION-OF-RESPONSE-TO-EXTERNAL-STIMULUS	GO-0032101	15	0.191644	0.699205	0.875000	0.927876	1.000
144 REACTOME-CIRCADIAN-CLOCK	R-HSA-400253	5	0.273243	0.671574	0.890710	0.954912	1.000
145 GOBP-CELLULAR-COMPONENT-MAINTENANCE	GO-0043954	5	0.277108	0.653934	0.899244	0.967523	1.000
146 GOBP-REPRODUCTION	GO-0000003	18	0.160220	0.653657	0.908127	0.961271	1.000
147 REACTOME-G-ALPHA-Q-SIGNALING-EVENTS	R-RNO-416476	6	0.243902	0.649381	0.924471	0.958618	1.000
148 GOBP-MYELOID-LEUKOCYTE-MEDIATED-IMMUNITY	GO-0002444	6	0.230647	0.628173	0.945409	0.971514	1.000
149 REACTOME-NEUTROPHIL-DEGRANULATION	R-RNO-6798695	6	0.230647	0.621796	0.942779	0.970507	1.000
150 GOBP-CELL-ACTIVATION-INVOLVED-IN-IMMUNE-RESPONSE	GO-0002263	6	0.230647	0.608382	0.958904	0.974498	1.000
151 GOBP-NEGATIVE-REGULATION-OF-RESPONSE-TO-STIMULUS	GO-0048585	16	0.154738	0.588399	0.957929	0.980415	1.000
152 GOBP-REGULATION-OF-CYTOSKELETON-ORGANIZATION	GO-0051493	5	0.224575	0.554040	0.984127	0.990694	1.000
153 GOBP-DEVELOPMENTAL-MATURATION	GO-0021700	5	0.218154	0.551313	0.972900	0.985373	1.000
154 GOBP-REGULATION-OF-RECEPTOR-MEDIATED-ENDOCYTOSIS	GO-0048259	5	0.216867	0.538108	0.977143	0.983573	1.000
155 GOBP-NEGATIVE-REGULATION-OF-PROTEIN-CATABOLIC...	GO-0042177	5	-0.216810	-0.478337	0.988449	0.989492	1.000
156 GOBP-RESPONSE-TO-OXIDATIVE-STRESS	GO-0006979	8	-0.193124	-0.492650	0.983824	0.987941	1.000
157 GOBP-RESPONSE-TO-REACTIVE-OXYGEN-SPECIES	GO-0000302	8	-0.193124	-0.494061	0.992296	0.989300	1.000
158 GOBP-POSITIVE-REGULATION-OF-MYELOID-LEUKOCYTE...	GO-0002763	6	-0.221299	-0.514193	0.984102	0.984878	1.000
159 GOBP-REGULATION-OF-MYELOID-LEUKOCYTE-DIFFERENT...	GO-0002761	8	-0.203522	-0.523400	0.974852	0.983415	1.000
160 GOBP-POSITIVE-REGULATION-OF-MYELOID-CELL-DIFFE...	GO-0045639	7	-0.217987	-0.524860	0.969088	0.984618	1.000
161 GOBP-CELLULAR-RESPONSE-TO-ABIOTIC-STIMULUS	GO-0071214	7	-0.215440	-0.545773	0.964451	0.977746	1.000
162 HALLMARK-TNFA-SIGNALING-VIA-NFKB	M5890	14	-0.180369	-0.550461	0.970845	0.977218	1.000
163 GOBP-RECEPTOR-MEDIATED-ENDOCYTOSIS	GO-0008698	6	-0.243525	-0.565002	0.959055	0.971348	1.000
164 GOBP-G-PROTEIN-COUPLED-GLUTAMATE-RECEPTOR-SIGN...	GO-0007216	8	-0.219274	-0.569855	0.950151	0.970416	1.000
165 GOBP-LEUKOCYTE-MEDIATED-IMMUNITY	GO-0002443	7	-0.231359	-0.571788	0.957878	0.971020	1.000
166 GOBP-MYELOID-CELL-DIFFERENTIATION	GO-0030099	13	-0.194897	-0.573897	0.944776	0.971565	1.000
167 GOBP-CELLULAR-RESPONSE-TO-CHEMICAL-STRESS	GO-0062197	7	-0.241171	-0.593668	0.925117	0.960420	1.000
168 GOBP-NEGATIVE-REGULATION-OF-SIGNALING	GO-0023057	21	-0.173317	-0.596654	0.931507	0.960159	1.000
169 GOBP-CELLULAR-RESPONSE-TO-REACTIVE-OXYGEN-SPECIES	GO-0034614	7	-0.241171	-0.601966	0.937042	0.958073	1.000

Continuation of Table S19

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
170	REACTOME_NUCLEAR_EVENTS_KINASE_AND_TRANSCRIPTI...	R-RNO-198725	11	-0.213670	-0.606468	0.928465	0.956486
171	GOBP_REGULATION_OF_ORGANELLE_ORGANIZATION	GO-00303043	14	-0.203183	-0.607879	0.924638	0.957175
172	GOBP_NEGATIVE_REGULATION_OF_NUCLEOBASE_CONTAIN...	GO-0045934	13	-0.203541	-0.617184	0.906021	0.951579
173	GOBP_RESPONSE_TO_UV	GO-0009411	5	-0.280211	-0.621026	0.935430	0.950225
174	GOBP_CELLULAR_RESPONSE_TO_EXTRACELLULAR_STIMULUS	GO-0031668	8	-0.238400	-0.622128	0.904687	0.951089
175	REACTOME_TRAFFICKING_OF_GLR2_CONTAINING_AMPA...	R-RNO-416993	8	-0.244391	-0.628898	0.917933	0.947131
176	GOBP_REGULATION_OF_WNT_SIGNALING_PATHWAY	GO-0030111	5	-0.283753	-0.631496	0.932496	0.946580
177	GOBP_CELL_CELL_SIGNALING_BY_WNT	GO-0198738	7	-0.261444	-0.642730	0.905054	0.937927
178	GOBP_RESPONSE_TO_CADMIUM_ION	GO-0046686	6	-0.276102	-0.647506	0.905132	0.935300
179	GOBP_GLIAL_CELL_DIFFERENTIATION	GO-0010001	10	-0.234361	-0.650355	0.896296	0.934345
180	GOBP_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	GO-0045637	9	-0.237986	-0.651613	0.889222	0.934854
181	GOBP_POSITIVE_REGULATION_OF_NUCLEOBASE_CONTAIN...	GO-0045935	28	-0.178292	-0.655201	0.884097	0.933197
182	REACTOME_CLASS_C_3_METABOTROPIC_GLUTAMATE_PHER...	R-RNO-420499	7	-0.270473	-0.665859	0.862442	0.924447
183	GOBP_INTRACELLULAR_RECEPTOR_SIGNALING_PATHWAY	GO-0030522	5	-0.311048	-0.670695	0.889984	0.921375
184	GOBP_POSITIVE_REGULATION_OF_CATION_TRANSMEMBR...	GO-1904064	5	-0.302928	-0.672107	0.889688	0.921559
185	GOBP_APOPTOTIC_SIGNALING_PATHWAY	GO-0097190	15	-0.218418	-0.674857	0.880597	0.920520
186	GOBP_MEMBRANE_PROTEIN_PROTEOLYSIS	GO-0033619	6	-0.294101	-0.681947	0.870253	0.914634
187	GOBP_EXOCYTOSIS	GO-0006887	11	-0.236962	-0.685883	0.854197	0.912216
188	GOBP_MULTIORGANISM_PROCESS	GO-0051704	16	-0.212412	-0.686118	0.860465	0.913661
189	GOBP_EPIDERMIS_DEVELOPMENT	GO-0008544	5	-0.312094	-0.695811	0.862237	0.904629
190	GOBP_NEGATIVE_REGULATION_OF_RESPONSE_TO_EXTERN...	GO-0032142	5	-0.312990	-0.695979	0.857820	0.906159
191	REACTOME_SIGNALING_BY_INTERLEUKINS	R-RNO-419147	15	-0.218451	-0.696064	0.833557	0.907777
192	GOBP_RESPONSE_TO_INORGANIC_SUBSTANCE	GO-0010035	19	-0.208576	-0.698735	0.841160	0.906495
193	GOBP_EPITHELIAL_CELL_DIFFERENTIATION	GO-0030855	7	-0.289977	-0.700842	0.838473	0.905845
194	REACTOME_INTERLEUKIN_4_AND_INTERLEUKIN_13_SIGN...	R-RNO-6785807	8	-0.271211	-0.705093	0.845921	0.902560
195	GOBP_POSITIVE_REGULATION_OF_BIOSYNTHETIC_PROCESS	GO-0009891	27	-0.195950	-0.705130	0.855014	0.904228
196	GOBP_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	GO-0045670	5	-0.318916	-0.711721	0.824121	0.897970
197	GOBP_RECEPTOR_METABOLIC_PROCESS	GO-0043112	5	-0.324880	-0.711824	0.849693	0.899572
198	GOBP_RECEPTOR_INTERNALIZATION	GO-0031623	5	-0.324880	-0.712408	0.854200	0.900732
199	GOBP_ADENYLATE_CYCLASE_INHIBITING_G_PROTEIN_CO...	GO-0007196	5	-0.323373	-0.716630	0.834356	0.897477
200	GOBP_REGULATION_OF_ANATOMICAL_STRUCTURE_MORPHO...	GO-0022603	17	-0.218761	-0.720172	0.812325	0.894997
201	REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGG...	R-HSA-76002	7	-0.289228	-0.721285	0.824534	0.895440
202	GOBP_RESPONSE_TO_ALKALOID	GO-0043279	5	-0.326817	-0.724384	0.827974	0.893429
203	GOBP_FAT_CELL_DIFFERENTIATION	GO-0045444	9	-0.267182	-0.724990	0.802711	0.894405
204	GOBP_NEGATIVE_REGULATION_OF_GENE_EXPRESSION	GO-0010629	12	-0.249044	-0.725765	0.818689	0.895138
205	GOBP_PROTEIN_LOCALIZATION_TO_ORGANELLE	GO-0033365	9	-0.268830	-0.727100	0.813846	0.895210
206	GOBP_CELLULAR_RESPONSE_TO_CADMIUM_ION	GO-0071276	5	-0.334615	-0.729147	0.843849	0.894329
207	GOBP_ENDOMEMBRANE_SYSTEM_ORGANIZATION	GO-0010256	6	-0.312383	-0.730533	0.797468	0.894425
208	REACTOME_TRANSCRIPTIONAL_REGULATION_OF_WHITE_A...	R-RNO-381340	6	-0.315745	-0.730972	0.819149	0.895643
209	GOBP_IMMUNE_SYSTEM_DEVELOPMENT	GO-0002520	17	-0.228782	-0.749271	0.771709	0.874415
210	GOBP_POSITIVE_REGULATION_OF_CELL_PROJECTION_OR...	GO-0031346	10	-0.267422	-0.750112	0.773529	0.875089
211	GOBP_CELL_CYCLE_PROCESS	GO-0022402	11	-0.262715	-0.751268	0.796160	0.875304
212	GOBP_RESPONSE_TO_CARBOHYDRATE	GO-0009743	5	-0.349136	-0.759058	0.775244	0.866819

Continuation of Table S19

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
213	REACTOME_NGF_STIMULATED_TRANSCRIPTION	R-RNO-9031628	9	-0.277320	-0.759388	0.797317	0.868114
214	GOBP_RESPONSE_TO_MONOSACCHARIDE	GO-0034284	5	-0.349136	-0.763212	0.794992	0.864620
215	GOBP_NEGATIVE_REGULATION_OF_TRANSFERASE_ACTIVITY	GO-0051348	5	-0.352325	-0.764850	0.801262	0.864059
216	GOBP_POSITIVE_REGULATION_OF_GENE_EXPRESSION	GO-0010628	16	-0.240542	-0.766466	0.739766	0.863703
217	GOBP_REGULATION_OF_HEMOPOIESIS	GO-1903706	10	-0.281720	-0.766568	0.777280	0.865292
218	GOBP_NEGATIVE_REGULATION_OF_KINASE_ACTIVITY	GO-0033673	5	-0.352325	-0.770150	0.778365	0.862024
219	GOBP_RESPONSE_TO_METAL_ION	GO-0010038	15	-0.245883	-0.770387	0.737752	0.863382
220	HALLMARK_HYPOXIA	M5891	5	-0.350418	-0.772066	0.802817	0.862738
221	GOBP_DNA_METABOLIC_PROCESS	GO-0006259	6	-0.329523	-0.772090	0.752280	0.864452
222	GOBP_REGULATION_OF_MUSCLE_CELL_DIFFERENTIATION	GO-0051147	6	-0.334677	-0.774887	0.754977	0.862413
223	GOBP_OSTEOCLAST_DIFFERENTIATION	GO-0030316	6	-0.329268	-0.780695	0.770291	0.855920
224	GOBP_SYNAPTIC_TRANSMISSION_GLUTAMATERGIC	GO-0035249	13	-0.262932	-0.784731	0.756637	0.851929
225	GOBP_REGULATION_OF_PROTEIN_STABILITY	GO-0031647	5	-0.360329	-0.785335	0.764706	0.852799
226	GOBP_REGULATION_OF_GROWTH	GO-0040008	13	-0.259519	-0.785883	0.742358	0.853817
227	GOBP_REGULATION_OF_DEFENSE_RESPONSE	GO-0031347	7	-0.316721	-0.785921	0.735669	0.855502
228	GOBP_NEGATIVE_REGULATION_OF_PHOSPHORUS_METABOLISM	GO-0010563	9	-0.299500	-0.788221	0.724458	0.854087
229	GOBP_POSITIVE_REGULATION_OF_TRANSCRIPTION_BY_RNA	GO-0045944	24	-0.224299	-0.788419	0.737748	0.855545
230	GOBP_REGULATION_OF_INFLAMMATORY_RESPONSE	GO-0050727	7	-0.316721	-0.790661	0.714286	0.854050
231	GOBP_AXON_DEVELOPMENT	GO-0061564	18	-0.239499	-0.795630	0.737796	0.848623
232	GOBP_LIPID_EXPORT_FROM_CELL	GO-0140353	5	-0.361199	-0.796504	0.770000	0.849207
233	GOBP_POSITIVE_REGULATION_OF_NEURON_PROJECTION	GO-0010976	5	-0.362405	-0.807342	0.717156	0.835262
234	GOBP_IMMUNE_EFFECTOR_PROCESS	GO-0002252	10	-0.290836	-0.810351	0.723781	0.832654
235	REACTOME_CELLULAR_RESPONSES_TO_EXTERNAL_STIMULI	R-RNO-8953897	12	-0.272210	-0.815441	0.705185	0.826919
236	GOBP_NEGATIVE_REGULATION_OF_TRANSCRIPTION_BY_RNA	GO-0000122	10	-0.294302	-0.819400	0.695586	0.822517
237	GOBP_NEGATIVE_REGULATION_OF_ION_TRANSPORT	GO-0043271	11	-0.284096	-0.819880	0.706408	0.823522
238	GOBP_POSITIVE_REGULATION_OF_HYDROLASE_ACTIVITY	GO-0051345	16	-0.257597	-0.820083	0.686630	0.824902
239	GOBP_REGULATION_OF_HYDROLASE_ACTIVITY	GO-0051336	22	-0.231034	-0.822310	0.690608	0.823318
240	GOBP_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	GO-1902105	9	-0.312046	-0.827982	0.688550	0.816727
241	REACTOME_G_ALPHA_Z_SIGNALLING_EVENTS	R-RNO-418597	5	-0.377357	-0.828000	0.725240	0.815406
242	GOBP_MUSCLE_CELL_PROLIFERATION	GO-0033002	8	-0.319296	-0.832926	0.677130	0.812693
243	GOBP_MUSCLE_CONTRACTION	GO-0006936	5	-0.377676	-0.833988	0.678333	0.812861
244	GOBP_REGULATION_OF_NEURONAL_SYNAPTIC_PLASTICITY	GO-0048168	7	-0.338107	-0.834045	0.682109	0.814505
245	GOBP_REGULATION_OF_SYNAPTIC_TRANSMISSION_GLUTAMATERGIC	GO-0051966	12	-0.287141	-0.836542	0.682558	0.812395
246	REACTOME_INTEGRATION_OF_ENERGY_METABOLISM	R-RNO-163685	5	-0.382286	-0.844165	0.682770	0.802633
247	GOBP_ERBB_SIGNALING_PATHWAY	GO-0038127	5	-0.387135	-0.845756	0.683465	0.801862
248	REACTOME_PTEN_REGULATION	R-RNO-6807070	5	-0.392361	-0.847346	0.688119	0.800929
249	GOBP_REGULATION_OF_PEPTIDE_TRANSPORT	GO-0090087	10	-0.306555	-0.848186	0.655275	0.801412
250	GOBP_REPRODUCTIVE_SYSTEM_DEVELOPMENT	GO-0061458	6	-0.366397	-0.849486	0.663974	0.801059
251	REACTOME_HEMOSTASIS	R-RNO-109582	14	-0.270109	-0.853170	0.638849	0.796822
252	GOBP_POSITIVE_REGULATION_OF_CELLULAR_PROTEIN_LIPID_METABOLISM	GO-1903829	7	-0.344320	-0.853286	0.663522	0.798319
253	GOBP_LEUKOCYTE_DIFFERENTIATION	GO-0002521	15	-0.269955	-0.858602	0.660511	0.791633
254	HALLMARK_UV_RESPONSE_UP	M5941	5	-0.386158	-0.866742	0.644817	0.780346
255	REACTOME_NERVOUS_SYSTEM_DEVELOPMENT	R-RNO-9675108	15	-0.276845	-0.868774	0.649783	0.778747

Continuation of Table S19

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
256 GOBP-AMINO-ACID-TRANSPORT	GO-0006865	6	-0.377787	-0.869132	0.643518	0.779782	1.000
257 GOBP-GENERATION-OF-PRECURSOR-METABOLITES-AND-E...	GO-0006091	5	-0.391059	-0.869932	0.660626	0.780172	1.000
258 HALLMARK-EPITHELIAL-MESENCHYMAL-TRANSITION	M5930	5	-0.399774	-0.872622	0.641694	0.777565	1.000
259 GOBP-ACIDIC-AMINO-ACID-TRANSPORT	GO-0015800	5	-0.400030	-0.874559	0.640063	0.776048	1.000
260 GOBP-FOREBRAIN-DEVELOPMENT	GO-0030900	9	-0.327152	-0.876378	0.620214	0.774754	1.000
261 GOBP-MONOCARBOXYLIC-ACID-TRANSPORT	GO-0015718	5	-0.400030	-0.877846	0.647152	0.773952	1.000
262 GOBP-NEURON-DIFFERENTIATION	GO-0030182	36	-0.230265	-0.878739	0.625806	0.774156	1.000
263 REACTOME-CYTOKINE-SIGNALING-IN-IMMUNE-SYSTEM	R-RNO-1280215	21	-0.253180	-0.880151	0.616848	0.773503	1.000
264 GOBP-NEGATIVE-REGULATION-OF-APOPTOTIC-SIGNALIN...	GO-2001234	7	-0.358084	-0.883371	0.612598	0.769735	1.000
265 GOBP-CELL-GROWTH	GO-0016049	10	-0.320079	-0.884379	0.620061	0.769689	1.000
266 GOBP-SECOND-MESSENGER-MEDIATED-SIGNALING	GO-0019932	16	-0.275405	-0.884474	0.602837	0.771188	1.000
267 GOBP-POLYSACCHARIDE-METABOLIC-PROCESS	GO-0005976	5	-0.404792	-0.884751	0.626959	0.772424	1.000
268 GOBP-RESPONSE-TO-RADIATION	GO-0009314	13	-0.296204	-0.886404	0.608069	0.771471	1.000
269 HALLMARK-ALLOGRAFT-REJECTION	M5950	7	-0.350936	-0.889334	0.594679	0.768374	1.000
270 GOBP-NEGATIVE-REGULATION-OF-TRANSMEMBRANE-TRAN...	GO-0034763	6	-0.384651	-0.889589	0.623211	0.769641	1.000
271 GOBP-DICARBOXYLIC-ACID-TRANSPORT	GO-0006835	5	-0.400030	-0.889811	0.617323	0.770939	1.000
272 GOBP-REGULATION-OF-ANION-TRANSPORT	GO-0044070	20	-0.267697	-0.891794	0.593620	0.769456	1.000
273 GOBP-MYELOID-LEUKOCYTE-ACTIVATION	GO-0002274	8	-0.346707	-0.892671	0.609984	0.769696	1.000
274 GOBP-MUSCLE-CELL-DIFFERENTIATION	GO-0042692	10	-0.322350	-0.894323	0.602446	0.768631	1.000
275 GOBP-CARBOXYLIC-ACID-TRANSPORT	GO-0046942	6	-0.377787	-0.894904	0.599686	0.769262	1.000
276 GOBP-ORGANIC-ANION-TRANSPORT	GO-0015711	6	-0.377787	-0.894918	0.624801	0.770978	1.000
277 GOBP-REGULATION-OF-HORMONE-LEVELS	GO-0010817	12	-0.304395	-0.898904	0.603107	0.764228	1.000
278 GOBP-REGULATION-OF-DEVELOPMENTAL-GROWTH	GO-0048638	9	-0.333877	-0.900555	0.600299	0.764750	1.000
279 GOBP-POSITIVE-REGULATION-OF-DEVELOPMENTAL-GROWTH	GO-0048639	8	-0.348332	-0.902195	0.600000	0.763601	1.000
280 GOBP-CELLULAR-AMIDE-METABOLIC-PROCESS	GO-0043603	13	-0.298001	-0.902775	0.567208	0.764326	1.000
281 GOBP-REGULATION-OF-NEURON-PROJECTION-DEVELOPMENT	GO-0010975	16	-0.286580	-0.906522	0.556369	0.759731	1.000
282 GOBP-LOCOMOTION	GO-0040011	31	-0.245498	-0.908095	0.574324	0.758782	1.000
283 GOBP-RESPONSE-TO-WOUNDING	GO-0009611	15	-0.290837	-0.908517	0.570213	0.759803	1.000
284 REACTOME-GPCR-LIGAND-BINDING	R-RNO-500792	8	-0.351378	-0.911322	0.585404	0.756749	1.000
285 GOBP-POSITIVE-REGULATION-OF-PEPTIDASE-ACTIVITY	GO-0010952	7	-0.370545	-0.911348	0.598425	0.758431	1.000
286 GOBP-NEGATIVE-REGULATION-OF-BIOSYNTHETIC-PROCESS	GO-0009890	13	-0.302366	-0.913161	0.585477	0.757014	1.000
287 GOBP-ORGANONITROGEN-COMPOUND-CATABOLIC-PROCESS	GO-1901565	9	-0.334709	-0.913310	0.569925	0.758465	1.000
288 GOBP-ORGANIC-HYDROXY-COMPOUND-METABOLIC-PROCESS	GO-1901615	7	-0.371510	-0.913924	0.571865	0.759191	1.000
289 GOBP-CELLULAR-RESPONSE-TO-PEPTIDE	GO-1901653	13	-0.297408	-0.916727	0.549708	0.756209	1.000
290 GOBP-NEUROGENESIS	GO-0022008	40	-0.236953	-0.916868	0.568063	0.757728	1.000
291 GOBP-POSITIVE-REGULATION-OF-NEURON-DEATH	GO-1901216	5	-0.425528	-0.919531	0.574713	0.754904	1.000
292 GOBP-DENDRITE-MORPHOGENESIS	GO-0048813	6	-0.389871	-0.922603	0.579200	0.751296	1.000
293 GOBP-CELL-PROJECTION-ORGANIZATION	GO-0030030	34	-0.245138	-0.927658	0.576000	0.744303	1.000
294 GOBP-PROTEOLYSIS	GO-0006508	17	-0.286877	-0.928002	0.555862	0.745388	1.000
295 GOBP-NEGATIVE-REGULATION-OF-CATALYTIC-ACTIVITY	GO-0043086	17	-0.324458	-0.928426	0.545455	0.746474	1.000
296 GOBP-REGULATION-OF-PEPTIDASE-ACTIVITY	GO-0052547	10	-0.332497	-0.930334	0.564829	0.744843	1.000
297 GOBP-POSITIVE-REGULATION-OF-CYSTEINE-TYPE-ENDO...	GO-2001056	7	-0.370545	-0.930947	0.546154	0.745555	1.000
298 GOBP-CELLULAR-RESPONSE-TO-INORGANIC-SUBSTANCE	GO-0071241	11	-0.315615	-0.932828	0.526786	0.744035	1.000

Continuation of Table S19

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
299	GOBP-SMOOTH_MUSCLE_CELL_PROLIFERATION	6	-0.398447	-0.934553	0.576299	0.742700	1.000
300	GOBP-STRIATED_MUSCLE_CELL_DIFFERENTIATION	9	-0.341317	-0.937127	0.564897	0.739773	1.000
301	GOBP-NEGATIVE_REGULATION_OF_CELLULAR_COMPONENT...	11	-0.325939	-0.938715	0.547865	0.738658	1.000
302	GOBP-ACTIVATION_OF_IMMUNE_RESPONSE	5	-0.428702	-0.941001	0.565284	0.736407	1.000
303	GOBP-PROTEIN_CATABOLIC_PROCESS	8	-0.364916	-0.941266	0.526946	0.737698	1.000
304	GOBP-RESPONSE_TO_LIGHT_STIMULUS	11	-0.331621	-0.942911	0.542522	0.736741	1.000
305	GOBP-RESPONSE_TO_EXTRACELLULAR_STIMULUS	13	-0.319965	-0.943742	0.546742	0.736956	1.000
306	GOBP-ADENYLATE_CYCLASE_INHIBITING_G_PROTEIN_CO...	9	-0.339965	-0.945407	0.537178	0.735814	1.000
307	GOBP-MUSCLE_SYSTEM_PROCESS	9	-0.345063	-0.946457	0.531531	0.735615	1.000
308	GOBP-POSITIVE_REGULATION_OF_PROTEIN_MODIFICATI...	23	-0.268879	-0.946773	0.540136	0.736772	1.000
309	GOBP-AGING	13	-0.309497	-0.948457	0.546529	0.735278	1.000
310	GOBP-POSITIVE_REGULATION_OF_HEMOPOIESIS	7	-0.384439	-0.949407	0.543413	0.735218	1.000
311	GOBP-WOUND_HEALING	13	-0.314736	-0.950013	0.532394	0.735951	1.000
312	GOBP-REGULATION_OF_PROTEIN_MODIFICATION_PROCESS	29	-0.255617	-0.950032	0.535763	0.737736	1.000
313	GOBP-INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	5	-0.428605	-0.950756	0.541735	0.738263	1.000
314	GOBP-POSITIVE_REGULATION_OF_PROTEIN_PHOSPHORYL...	23	-0.354468	-0.951544	0.537271	0.738719	1.000
315	GOBP-REGULATION_OF_CYSSTEINE_TYPE_ENDOPEPTIDASE...	9	-0.354468	-0.952869	0.531758	0.738182	1.000
316	GOBP-REGULATION_OF_HORMONE_SECRETION	8	-0.369613	-0.954904	0.510355	0.736154	1.000
317	GOBP-ANION_TRANSMEMBRANE_TRANSPORT	7	-0.388139	-0.959733	0.529595	0.729021	1.000
318	GOBP-CELLULAR_RESPONSE_TO_EXTERNAL_STIMULUS	10	-0.345361	-0.960914	0.517291	0.728628	1.000
319	REACTOME_ESR-MEDIATED_SIGNALING	8	-0.373438	-0.962693	0.503771	0.727455	1.000
320	GOBP-RESPONSE_TO_MECHANICAL_STIMULUS	6	-0.412773	-0.962693	0.512618	0.728910	1.000
321	GOBP-POSITIVE_REGULATION_OF_PHOSPHORUS_METABOL...	24	-0.278428	-0.964034	0.533145	0.728296	1.000
322	REACTOME_SIGNALING_BY_NUCLEAR_RECEPTORS	8	-0.373438	-0.964499	0.504532	0.729301	1.000
323	GOBP-CELLULAR_MACROMOLECULE_LOCALIZATION	21	-0.278806	-0.968014	0.476124	0.724269	1.000
324	GOBP-APOPTOTIC_PROCESS	35	-0.257820	-0.968184	0.516689	0.725827	1.000
325	GOBP-REGULATION_OF_ANATOMICAL_STRUCTURE_SIZE	10	-0.345788	-0.968624	0.485755	0.726905	1.000
326	GOBP-NEURON_DEVELOPMENT	33	-0.253922	-0.970567	0.506089	0.725102	1.000
327	GOBP-VESICLE-MEDIATED_TRANSPORT_IN_SYNAPSE	7	-0.398980	-0.972332	0.503077	0.723649	1.000
328	GOBP-CARBOHYDRATE_METABOLIC_PROCESS	9	-0.359253	-0.973079	0.506647	0.724113	1.000
329	GOBP-RESPONSE_TO_PEPTIDE_HORMONE	13	-0.320752	-0.973571	0.486956	0.725045	1.000
330	GOBP-REGULATION_OF_NERVOUS_SYSTEM_PROCESS	8	-0.373448	-0.974197	0.525926	0.725663	1.000
331	GOBP-REGULATION_OF_CELL_SIZE	5	-0.446919	-0.976029	0.512945	0.724062	1.000
332	HALMARK_APOPTOSIS	6	-0.426829	-0.979121	0.497653	0.719819	1.000
333	GOBP-REGULATION_OF_CELL_CYCLE_PROCESS	5	-0.449546	-0.980811	0.487220	0.718478	1.000
334	GOBP-CELLULAR_CARBOHYDRATE_METABOLIC_PROCESS	5	-0.451188	-0.981542	0.484520	0.719017	1.000
335	GOBP-CELLULAR_RESPONSE_TO_OXYGEN-CONTAINING_CO...	29	-0.265757	-0.982574	0.485830	0.718942	1.000
336	REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION	20	-0.290317	-0.982988	0.495105	0.720062	1.000
337	GOBP-POSITIVE_REGULATION_OF_TRANSMEMBRANE_TRAN...	7	-0.393066	-0.984528	0.493865	0.718955	1.000
338	GOBP-POSITIVE_REGULATION_OF_TRANSPORT	26	-0.276812	-0.985001	0.497997	0.720000	1.000
339	GOBP-NEGATIVE_REGULATION_OF_TRANSPORT	13	-0.331129	-0.986447	0.475714	0.718978	1.000
340	GOBP-POSITIVE_REGULATION_OF_GROWTH	9	-0.367439	-0.986500	0.483434	0.720763	1.000
341	GOBP-PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_CON...	7	-0.401263	-0.986768	0.481833	0.722124	1.000

Continuation of Table S19

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
342 REACTOME-SIGNALING-BY-RHO-GTPASES-MIRO-GTPASES...	R-RNO-9716542	9	-0.365638	-0.988068	0.488954	0.721460	1.000
343 GOBP-NEGATIVE-REGULATION-OF-HYDROLASE-ACTIVITY	GO-0051346	11	-0.342233	-0.988672	0.466872	0.722172	1.000
344 GOBP-REGULATION-OF-PROTEIN-CATABOLIC-PROCESS	GO-0042176	7	-0.400422	-0.989379	0.490712	0.722715	1.000
345 GOBP-POSITIVE-REGULATION-OF-RESPONSE-TO-EXTERN...	GO-0032103	9	-0.367555	-0.989817	0.483871	0.723755	1.000
346 GOBP-ESTABLISHMENT-OF-PROTEIN-LOCALIZATION	GO-0045184	18	-0.299860	-0.991287	0.473118	0.722888	1.000
347 REACTOME-RHO-GTPASE-EFFECTORS	R-RNO-195258	9	-0.365638	-0.994973	0.473354	0.717316	1.000
348 GOBP-RESPONSE-TO-NITROGEN-COMPOUND	GO-1901698	34	-0.266885	-0.996718	0.472703	0.715862	1.000
349 GOBP-REGULATION-OF-POSTSYNAPSE-ORGANIZATION	GO-0099175	6	-0.425630	-0.997498	0.487692	0.716241	1.000
350 GOBP-POSITIVE-REGULATION-OF-PRL-MIRNA-TRANSCRIP...	GO-1902895	7	-0.409414	-0.998037	0.485732	0.717158	1.000
351 GOBP-MULTIMULTICELLULAR-ORGANISM-PROCESS	GO-0044706	8	-0.381563	-0.999175	0.482707	0.716811	1.000
352 GOBP-DENDRITE-DEVELOPMENT	GO-0016358	9	-0.378092	-1.001311	0.478807	0.714550	1.000
353 GOBP-REGULATION-OF-IMMUNE-RESPONSE	GO-0050776	12	-0.342849	-1.005521	0.462304	0.708107	1.000
354 GOBP-MUSCLE-STRUCTURE-DEVELOPMENT	GO-0061061	16	-0.318472	-1.005947	0.454810	0.709117	1.000
355 GOBP-REGULATION-OF-CELL-DEATH	GO-0010941	34	-0.267575	-1.009335	0.450875	0.704441	1.000
356 GOBP-RESPONSE-TO-ENDOGENOUS-STIMULUS	GO-0009719	34	-0.263912	-1.010844	0.442257	0.703465	1.000
357 GOBP-DEVELOPMENTAL-PROCESS-INVOLVED-IN-REPRODU...	GO-0003006	11	-0.354516	-1.015562	0.431884	0.695824	1.000
358 GOBP-REGULATION-OF-RESPONSE-TO-STRESS	GO-0080134	19	-0.305656	-1.016273	0.432815	0.696386	1.000
359 GOBP-MALE-GAMETE-GENERATION	GO-0048232	5	-0.457950	-1.016966	0.431008	0.697009	1.000
360 GOBP-CYTOKINE-PRODUCTION	GO-0001816	10	-0.366651	-1.017102	0.440184	0.698654	1.000
361 GOBP-ORGANOPHOSPHATE-METABOLIC-PROCESS	GO-0019637	7	-0.410218	-1.019518	0.443932	0.695785	1.000
362 GOBP-REGULATION-OF-MUSCLE-SYSTEM-PROCESS	GO-0090257	8	-0.390017	-1.021426	0.436252	0.693852	1.000
363 GOBP-PRL-MIRNA-TRANSCRIPTION-BY-RNA-POLYMERASE.II	GO-0061614	7	-0.409414	-1.023804	0.435858	0.691031	1.000
364 GOBP-MACROMOLECULE-CATABOLIC-PROCESS	GO-0009057	12	-0.345243	-1.024631	0.421439	0.691285	1.000
365 GOBP-POSITIVE-REGULATION-OF-SMOOTH-MUSCLE-CELL...	GO-0048661	5	-0.468740	-1.024964	0.451664	0.692561	1.000
366 GOBP-PEPTIDE-METABOLIC-PROCESS	GO-0006518	12	-0.346609	-1.025600	0.433333	0.693190	1.000
367 GOBP-LIPID-BIOSYNTHETIC-PROCESS	GO-0008610	6	-0.451636	-1.026332	0.454839	0.693733	1.000
368 GOBP-REGULATION-OF-APOPTOTIC-SIGNALING-PATHWAY	GO-2001233	10	-0.373453	-1.030180	0.437117	0.687802	1.000
369 GOBP-NEGATIVE-REGULATION-OF-MOLECULAR-FUNCTION	GO-0044092	24	-0.293879	-1.036402	0.414734	0.677503	1.000
370 REACTOME-POST-TRANSLATIONAL-PROTEIN-MODIFICATION	R-RNO-597592	7	-0.424254	-1.038582	0.413961	0.675090	1.000
371 GOBP-CHROMOSOME-ORGANIZATION	GO-0051276	6	-0.455757	-1.040464	0.432000	0.673184	1.000
372 GOBP-CELL-CYCLE	GO-0007049	21	-0.298989	-1.041823	0.408392	0.672266	1.000
373 GOBP-CHROMATIN-ORGANIZATION	GO-0006325	5	-0.477464	-1.042114	0.429892	0.673624	1.000
374 GOBP-BIOLOGICAL-PROCESS-INVOLVED-IN-SYMBIOTIC....	GO-004440	11	-0.358102	-1.043259	0.389706	0.673307	1.000
375 REACTOME-EXTRA-NUCLEAR-ESTROGEN-SIGNALING	R-RNO-9009391	7	-0.412535	-1.043692	0.392638	0.674439	1.000
376 GOBP-REGULATION-OF-MAP-KINASE-ACTIVITY	GO-0043405	9	-0.396884	-1.049881	0.399390	0.663867	1.000
377 GOBP-NEGATIVE-REGULATION-OF-ANION-TRANSPORT	GO-1903792	8	-0.413731	-1.050368	0.425373	0.664755	1.000
378 GOBP-REGULATION-OF-LIPID-BIOSYNTHETIC-PROCESS	GO-0046890	6	-0.451636	-1.050932	0.413399	0.665590	1.000
379 GOBP-CELL-MIGRATION	GO-0016477	22	-0.299230	-1.053247	0.391365	0.662799	1.000
380 GOBP-POSITIVE-REGULATION-OF-PROTEIN-METABOLIC-...	GO-0051247	28	-0.290077	-1.053387	0.383064	0.664460	1.000
381 GOBP-ORGANIC-ACID-METABOLIC-PROCESS	GO-0006082	7	-0.423125	-1.054399	0.418429	0.664417	1.000
382 GOBP-REGIONALIZATION	GO-0003002	6	-0.457696	-1.061866	0.388802	0.651247	1.000
383 GOBP-MULTICELLULAR-ORGANISM-REPRODUCTION	GO-0032504	12	-0.354333	-1.061933	0.391176	0.653073	1.000
384 GOBP-MONOCARBOXYLIC-ACID-METABOLIC-PROCESS	GO-0032787	6	-0.467408	-1.065208	0.407407	0.648238	1.000

Continuation of Table S19

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
385	GOBP-TEMPERATURE.HOMEOSTASIS	5	-0.483173	-1.065225	0.393365	0.650154	1.000
386	GOBP-REGULATION.OF.CELLULAR.COMPONENT.SIZE	7	-0.430674	-1.065392	0.382540	0.651744	1.000
387	GOBP-POSITIVE.REGULATION.OF.MOLECULAR.FUNCTION	38	-0.281602	-1.066679	0.374339	0.651023	1.000
388	GOBP-MITOCHONDRION.ORGANIZATION	7	-0.424789	-1.070054	0.379786	0.646119	1.000
389	GOBP-REGULATION.OF.LIPID.LOCALIZATION	5	-0.487070	-1.070534	0.372287	0.647149	1.000
390	GOBP-INORGANIC.ION.TRANSMEMBRANE.TRANSPORT	9	-0.398262	-1.071592	0.373874	0.646927	1.000
391	GOBP-MONONUCLEAR.CELL.DIFFERENTIATION	7	-0.440983	-1.073382	0.381395	0.645323	1.000
392	GOBP-REGULATION.OF.PEPTIDE-SECRETION	7	-0.435257	-1.074379	0.396605	0.645276	1.000
393	GOBP-BEHAVIOR	32	-0.287017	-1.074908	0.363995	0.646104	1.000
394	GOBP-RESPONSE.TO.DRUG	11	-0.382544	-1.075417	0.383459	0.646951	1.000
395	GOBP-PATTERN.SPECIFICATION.PROCESS	6	-0.457696	-1.077303	0.367852	0.645178	1.000
396	HALEMARK.PI3K-AKT-MTOR-SIGNALING	6	-0.457696	-1.077303	0.367852	0.645178	1.000
397	GOBP-COAGULATION	8	-0.412018	-1.078993	0.355039	0.645687	1.000
398	GOBP-POSITIVE.REGULATION.OF.CELL.GROWTH	6	-0.457696	-1.081262	0.371560	0.642900	1.000
399	GOBP-APOPTOTIC.MITOCHONDRIAL.CHANGES	6	-0.457707	-1.083253	0.373089	0.640820	1.000
400	GOBP-PEPTIDYL-SERINE.MODIFICATION	12	-0.369179	-1.083884	0.359352	0.641730	1.000
401	GOBP-PURINE.CONTAINING.COMPOUND.METABOLIC.PROCESS	5	-0.504696	-1.087283	0.379147	0.637014	1.000
402	GOBP-NEGATIVE.REGULATION.OF.CELL-CYCLE	5	-0.489833	-1.088109	0.352025	0.637399	1.000
403	GOBP-REGULATION.OF.PEPTIDE.HORMONE-SECRETION	6	-0.462238	-1.090499	0.348800	0.634457	1.000
404	GOBP-REGULATION.OF.PROTEIN.BINDING	7	-0.446570	-1.091029	0.359014	0.635339	1.000
405	GOBP-RESPONSE.TO.OXYGEN.LEVELS	8	-0.417329	-1.093067	0.361801	0.633135	1.000
406	GOBP-POSITIVE.REGULATION.OF.MAPK-CASCADE	9	-0.401725	-1.097210	0.355725	0.626592	1.000
407	GOBP-CYTOKINE-MEDIATED-SIGNALING.PATHWAY	16	-0.344914	-1.103342	0.350852	0.615894	1.000
408	GOBP-ORGANIC-ACID-TRANSPORT	7	-0.442124	-1.104464	0.344186	0.615520	1.000
409	GOBP-REGULATION.OF.CELL.PROJECTION.ORGANIZATION	20	-0.320244	-1.104696	0.345481	0.616962	1.000
410	GOBP-REGULATION.OF.CELLULAR.COMPONENT.MOVEMENT	15	-0.355715	-1.106169	0.330893	0.615865	1.000
411	GOBP-REGULATION.OF-PHOSPHORUS.METABOLIC.PROCESS	27	-0.304770	-1.106267	0.318783	0.617643	1.000
412	GOBP-NUCLEOBASE-CONTAINING.SMALL-MOLECULE.META...	6	-0.469581	-1.111326	0.310680	0.609554	1.000
413	GOBP-ADENYLATE-CYCLASE.MODULATING-G.PROTEIN.CO...	11	-0.392753	-1.113992	0.321888	0.606260	1.000
414	GOBP-POSITIVE.REGULATION.OF.PROTEIN-KINASE-ACT...	19	-0.334578	-1.115983	0.330544	0.604244	1.000
415	GOBP-REGULATION.OF-EPITHELIAL-CELL-MIGRATION	6	-0.474950	-1.116804	0.328051	0.604596	1.000
416	GOBP-OSTEOBLAST-DIFFERENTIATION	5	-0.505072	-1.119887	0.325434	0.600151	1.000
417	GOBP-MEMORY	13	-0.366294	-1.121579	0.318314	0.598368	1.000
418	GOBP-AMYLOID-PRECURSOR-PROTEIN.METABOLIC.PROCESS	5	-0.513831	-1.122059	0.323102	0.599330	1.000
419	GOBP-ENDOCRINE.SYSTEM.DEVELOPMENT	6	-0.477092	-1.123713	0.304085	0.598122	1.000
420	GOBP-CELLULAR.COMPONENT.DISASSEMBLY	6	-0.492541	-1.123913	0.328125	0.599714	1.000
421	GOBP-COGNITION	28	-0.306297	-1.124522	0.297151	0.600522	1.000
422	GOBP-LIPID.METABOLIC.PROCESS	10	-0.401989	-1.126219	0.302766	0.599110	1.000
423	REACTOME.OPIOID-SIGNALING	12	-0.384285	-1.128213	0.302147	0.597167	1.000
424	GOBP-REGULATION.OF-SECRETION	14	-0.369306	-1.130722	0.306452	0.593834	1.000
425	GOBP-REGULATION.OF-PROTEIN-PHOSPHORYLATION	26	-0.316306	-1.131548	0.319559	0.594035	1.000
426	GOBP-AMYLOID-PRECURSOR-PROTEIN.CATABOLIC.PROCESS	5	-0.513831	-1.131756	0.312893	0.595621	1.000
427	GOBP-HEAD.DEVELOPMENT	22	-0.325822	-1.132129	0.294444	0.596817	1.000

Continuation of Table S19

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
428 GOBP-RESPONSE.TO.KETONE	GO-1901654	7	-0.460814	-1.132589	0.321212	0.597937	1.000
429 GOBP-RESPONSE.TO.OXYGEN.CONTAINING.COMPOUND	GO-1901700	39	-0.292916	-1.133877	0.307798	0.597428	1.000
430 GOBP-REGULATION.OF.CELLULAR.LOCALIZATION	GO-0060341	17	-0.356823	-1.134481	0.296719	0.598225	1.000
431 GOBP-TELENCEPHALON.DEVELOPMENT	GO-0021537	6	-0.489302	-1.136469	0.306154	0.596305	1.000
432 GOBP-REGULATION.OF.PROTEIN.LOCALIZATION	GO-0032880	18	-0.342539	-1.136729	0.299572	0.597847	1.000
433 GOBP-POSITIVE.REGULATION.OF.ESTABLISHMENT.OF.P...	GO-1904951	5	-0.531465	-1.136807	0.292994	0.599756	1.000
434 GOBP-REGULATION.OF.CATION.TRANSMEMBRANE.TRANSPORT	GO-1904062	16	-0.350513	-1.136874	0.300429	0.601767	1.000
435 GOBP-POSITIVE.REGULATION.OF.SECRETION	GO-0051047	6	-0.483004	-1.137199	0.307573	0.603158	1.000
436 GOBP-RESPONSE.TO.BACTERIUM	GO-0009617	13	-0.376744	-1.139488	0.303892	0.600476	1.000
437 GOBP-LIPID.LOCALIZATION	GO-0010876	10	-0.413902	-1.139589	0.291982	0.602350	1.000
438 GOBP-SKIN.DEVELOPMENT	GO-0043588	5	-0.520756	-1.139811	0.300161	0.604112	1.000
439 GOBP-CALCIUM.MEDIATED.SIGNALING	GO-0019722	10	-0.410246	-1.140862	0.298682	0.603952	1.000
440 REACTOME-TRAFFICKING.OF.AMPA.RECEPTORS	R-RNO-399719	11	-0.398962	-1.140884	0.318043	0.606067	1.000
441 GOBP-RESPONSE.TO.TUMOR.NECROSIS.FACTOR	GO-0034612	7	-0.464982	-1.141812	0.323752	0.606015	1.000
442 GOBP-RESPONSE.TO.MOLECULE.OF.BACTERIAL.ORIGIN	GO-0002237	13	-0.376744	-1.142116	0.278393	0.607536	1.000
443 GOBP-HEART.DEVELOPMENT	GO-0007507	6	-0.483281	-1.142589	0.305556	0.608743	1.000
444 GOBP-ACTIVATION.OF.MAPK-ACTIVITY	GO-0000187	6	-0.491622	-1.143003	0.297420	0.610011	1.000
445 GOBP-CARDIAC.MUSCLE.TISSUE.DEVELOPMENT	GO-0048738	6	-0.483281	-1.144317	0.292259	0.609397	1.000
446 GOBP-AMYLOID.BETA.METABOLIC.PROCESS	GO-0050435	5	-0.513831	-1.146426	0.301092	0.607154	1.000
447 GOBP-CYTOSKELETON.ORGANIZATION	GO-0007010	11	-0.398312	-1.147816	0.280802	0.606504	1.000
448 GOBP-POSITIVE.REGULATION.OF.PROTEOLYSIS	GO-0045862	8	-0.441417	-1.156338	0.284639	0.590180	1.000
449 GOBP-FATTY.ACID.TRANSPORT	GO-0015908	6	-0.488282	-1.156757	0.282012	0.591446	1.000
450 GOBP-NEGATIVE.REGULATION.OF.BINDING	GO-0051100	6	-0.500753	-1.158003	0.302652	0.590846	1.000
451 GOBP-RESPONSE.TO.HORMONE	GO-0009725	20	-0.349848	-1.160979	0.276243	0.586734	1.000
452 GOBP-REGULATION.OF.CARBOHYDRATE.METABOLIC.PROCESS	GO-0006109	5	-0.538005	-1.161470	0.269663	0.587870	1.000
453 GOBP-REGULATION.OF.SYSTEM.PROCESS	GO-0044057	18	-0.349048	-1.161691	0.270156	0.589577	1.000
454 GOBP-POSITIVE.REGULATION.OF.LONG-TERM.SYNAPTIC...	GO-1900273	5	-0.528088	-1.162740	0.265244	0.589441	1.000
455 GOBP-POSITIVE.REGULATION.OF.TRANSFERASE-ACTIVITY	GO-0051347	20	-0.345124	-1.162971	0.277008	0.591233	1.000
456 GOBP-REGULATION.OF.ANION.TRANSMEMBRANE.TRANSPORT	GO-1903959	5	-0.543331	-1.166724	0.273322	0.585584	1.000
457 GOBP-REGULATION.OF.MAPK.CASCADE	GO-0043408	13	-0.383372	-1.167423	0.272597	0.586178	1.000
458 GOBP-REGULATION.OF.IMMUNE.SYSTEM.PROCESS	GO-0002682	21	-0.337135	-1.167719	0.262319	0.587701	1.000
459 GOBP-LEUKOCYTE.MIGRATION	GO-0050900	6	-0.512104	-1.169182	0.278317	0.586481	1.000
460 GOBP-NEUROINFLAMMATORY.RESPONSE	GO-0150076	5	-0.541722	-1.169645	0.270313	0.587819	1.000
461 GOBP-POSITIVE.REGULATION.OF.MAP_KINASE-ACTIVITY	GO-0043406	6	-0.491622	-1.169869	0.267188	0.589556	1.000
462 GOBP-POSTTRANSCRIPTIONAL.REGULATION.OF.GENE.EX...	GO-0010608	8	-0.453214	-1.172598	0.272152	0.585820	1.000
463 GOBP-CENTRAL.NERVOUS.SYSTEM.DEVELOPMENT	GO-0007417	26	-0.327907	-1.172702	0.271093	0.587926	1.000
464 GOBP-SEXUAL.REPRODUCTION	GO-0019953	10	-0.418138	-1.172721	0.264012	0.590185	1.000
465 GOBP-POSITIVE.REGULATION.OF.PROTEIN.SERINE.THR...	GO-0071902	9	-0.434921	-1.177397	0.256966	0.581964	1.000
466 GOBP-CARBOHYDRATE.BIOSYNTHETIC.PROCESS	GO-0016051	5	-0.538005	-1.178939	0.276295	0.580951	1.000
467 GOBP-MITOTIC.CELL.CYCLE	GO-0000278	10	-0.418891	-1.181548	0.246246	0.577580	1.000
468 GOBP-POSITIVE.REGULATION.OF.APOPTOTIC.SIGNALIN...	GO-2001235	5	-0.538350	-1.184676	0.242378	0.573012	1.000
469 GOBP-CELLULAR.RESPONSE.TO.NITROGEN.COMPOUND	GO-1901699	20	-0.344172	-1.184750	0.259722	0.575144	1.000
470 GOBP-PHOSPHATIDYLINOSITOL.3.KINASE.SIGNALING	GO-0014065	7	-0.488598	-1.193283	0.243750	0.558675	1.000

Continuation of Table S19

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
471	GOBP-T-CELL-ACTIVATION	GO-0042110	8	-0.455090	-1.195040	0.255887	0.557188	1.000
472	GOBP-REGULATION-OF-CARBOHYDRATE-BIOSYNTHETIC-P...	GO-0043255	5	-0.538005	-1.199603	0.233385	0.549619	1.000
473	GOBP-IN-UTERO-EMBRYONIC-DEVELOPMENT	GO-0001701	8	-0.459415	-1.199870	0.229358	0.551284	1.000
474	GOBP-MAINTENANCE-OF-LOCATION	GO-0051235	7	-0.489072	-1.203225	0.241379	0.546513	1.000
475	GOBP-EPHRIN-RECEPTOR-SIGNALING-PATHWAY	GO-0048013	5	-0.546727	-1.204412	0.234921	0.546165	1.000
476	GOBP-REGULATION-OF-ORGAN-GROWTH	GO-0046620	5	-0.546824	-1.204461	0.234528	0.548326	1.000
477	GOBP-ORGANIC-HYDROXY-COMPOUND-TRANSPORT	GO-0015850	6	-0.508624	-1.204714	0.237421	0.550031	1.000
478	GOBP-REGULATION-OF-CELL-CYCLE	GO-0051726	13	-0.391102	-1.204743	0.240469	0.552240	1.000
479	GOBP-CARBOHYDRATE-HOMEOSTASIS	GO-0033500	7	-0.499021	-1.204775	0.236392	0.554472	1.000
480	GOBP-EPITHELIAL-CELL-PROLIFERATION	GO-0050673	12	-0.410303	-1.204933	0.249645	0.556434	1.000
481	REACTOME-ANTI-INFLAMMATORY-RESPONSE-FAVOURING...	R-HSA-9662851	5	-0.545676	-1.205220	0.226006	0.557963	1.000
482	GOBP-ORGAN-GROWTH	GO-0035265	5	-0.545676	-1.205220	0.232372	0.556468	1.000
483	GOBP-PROTEIN-COMPLEX-OLIGOMERIZATION	GO-0051259	6	-0.512195	-1.207555	0.233282	0.557508	1.000
484	GOBP-NEURON-PROJECTION-ORGANIZATION	GO-0106027	8	-0.474623	-1.209028	0.234472	0.556660	1.000
485	GOBP-REGULATION-OF-CATION-CHANNEL-ACTIVITY	GO-2001257	14	-0.393446	-1.211686	0.236575	0.552824	1.000
486	GOBP-ANATOMICAL-STRUCTURE-FORMATION-INVOLVED-I...	GO-0048646	20	-0.361323	-1.212468	0.234890	0.553507	1.000
487	GOBP-G-PROTEIN-COUPLED-RECEPTOR-SIGNALING-PATHWAY	GO-0007186	18	-0.370194	-1.212754	0.222069	0.555236	1.000
488	GOBP-INNATE-IMMUNE-RESPONSE	GO-0045087	7	-0.492671	-1.213076	0.223054	0.556841	1.000
489	GOBP-CELLULAR-RESPONSE-TO-DNA-DAMAGE-STIMULUS	GO-0006974	5	-0.549407	-1.213623	0.217391	0.557993	1.000
490	GOBP-EMBRYONIC-MORPHOGENESIS	GO-0048598	6	-0.515498	-1.213743	0.224490	0.560115	1.000
491	GOBP-HORMONE-TRANSPORT	GO-0009914	9	-0.453956	-1.214581	0.220521	0.560711	1.000
492	REACTOME-LEISHMANIA-INFECTION	R-HSA-9658195	10	-0.437418	-1.217557	0.218182	0.556523	1.000
493	GOBP-RESPONSE-TO-NICOTINE	GO-0035094	7	-0.492001	-1.217577	0.223765	0.558949	1.000
494	GOBP-REGULATION-OF-TRANSPORT	GO-0051049	44	-0.313415	-1.218465	0.203974	0.559528	1.000
495	GOBP-POSITIVE-REGULATION-OF-CELL-DEATH	GO-0010942	19	-0.368148	-1.219931	0.213353	0.558773	1.000
496	GOBP-REGULATION-OF-POSTSYNAPTIC-MEMBRANE-POTEN...	GO-0060078	14	-0.398170	-1.220125	0.248521	0.560843	1.000
497	GOBP-RESPONSE-TO-ABIOTIC-STIMULUS	GO-0009628	27	-0.332079	-1.221049	0.216552	0.561226	1.000
498	GOBP-REGULATION-OF-CELLULAR-COMPONENT-BIOGENESIS	GO-0044087	10	-0.436790	-1.221276	0.236232	0.563217	1.000
499	GOBP-NEGATIVE-REGULATION-OF-SYNAPTIC-TRANSMISSION	GO-0050805	6	-0.527455	-1.221517	0.216906	0.565200	1.000
500	GOBP-GAMETE-GENERATION	GO-0007276	9	-0.458359	-1.222527	0.239819	0.565570	1.000
501	GOBP-LYMPHOCYTE-ACTIVATION	GO-0046649	9	-0.452148	-1.222930	0.224961	0.567174	1.000
502	REACTOME-INTERFERON-SIGNALING	R-RNO-913531	6	-0.513568	-1.225899	0.199690	0.562677	1.000
503	GOBP-POSITIVE-REGULATION-OF-CYTOKINE-PRODUCTION	GO-0001819	7	-0.490150	-1.226258	0.229904	0.564623	1.000
504	REACTOME-L1CAM-INTERACTIONS	R-RNO-373760	5	-0.569629	-1.226452	0.185304	0.566697	1.000
505	GOBP-REGULATION-OF-FAT-CELL-DIFFERENTIATION	GO-0045598	6	-0.519832	-1.226634	0.215071	0.568850	1.000
506	REACTOME-MEMBRANE-TRAFFICKING	R-RNO-199991	5	-0.567644	-1.231422	0.199336	0.559949	1.000
507	REACTOME-VESICLE-MEDIATED-TRANSPORT	R-RNO-5653656	5	-0.567644	-1.234194	0.207120	0.556313	1.000
508	GOBP-RESPONSE-TO-NUTRIENT	GO-0007584	5	-0.566265	-1.235051	0.206557	0.553570	1.000
509	GOBP-EXTRINSIC-APOPTOTIC-SIGNALING-PATHWAY	GO-0097191	7	-0.499437	-1.237725	0.218009	0.553337	1.000
510	GOBP-POSITIVE-REGULATION-OF-DEFENSE-RESPONSE	GO-0031349	5	-0.332754	-1.240009	0.205329	0.550652	1.000
511	GOBP-POSITIVE-REGULATION-OF-CATALYTIC-ACTIVITY	GO-0043085	30	-0.332754	-1.241417	0.190728	0.550066	1.000
512	GOBP-NEGATIVE-REGULATION-OF-CATABOLIC-PROCESS	GO-0009895	8	-0.474679	-1.243397	0.213961	0.548192	1.000
513	REACTOME-DEVELOPMENTAL-BIOLOGY	R-RNO-1266738	23	-0.351760	-1.243875	0.191781	0.549716	1.000

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NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
514	GOBP-REGULATION-OF-VASCULATURE-DEVELOPMENT	5	-0.570549	-1.246922	0.196694	0.545302	1.000
515	GOBP-ASSOCIATIVE-LEARNING	7	-0.509752	-1.249283	0.197869	0.542141	1.000
516	GOBP-RESPONSE-TO-CYTOKINE	23	-0.361301	-1.249424	0.188105	0.544495	1.000
517	GOBP-VASCULATURE-DEVELOPMENT	17	-0.382477	-1.250226	0.174785	0.545221	1.000
518	GOBP-ANIMAL-ORGAN-MORPHOGENESIS	12	-0.419316	-1.256274	0.210604	0.533583	1.000
519	REACTOME-SIGNALING-BY-GPCR	22	-0.365841	-1.256903	0.206327	0.534907	1.000
520	GOBP-PHAGOCYTOSIS	5	-0.572634	-1.258110	0.179650	0.534639	1.000
521	REACTOME-G-ALPHA-L-SIGNALING-EVENTS	18	-0.384200	-1.260236	0.175714	0.532272	1.000
522	GOBP-PROTEIN-AUTOPHOSPHORYLATION	5	-0.569624	-1.260647	0.176287	0.534069	1.000
523	GOBP-POSITIVE-REGULATION-OF-CELL-ADHESION	7	-0.504424	-1.261099	0.204082	0.535748	1.000
524	GOBP-ERK1-AND-ERK2-CASCADE	5	-0.571016	-1.263284	0.189189	0.533315	1.000
525	GOBP-SENSORY-PERCEPTION	9	-0.474957	-1.264574	0.183486	0.533108	1.000
526	REACTOME-INTRACELLULAR-SIGNALING-BY-SECOND-MES...	15	-0.396819	-1.264710	0.184319	0.535607	1.000
527	GOBP-RESPONSE-TO-ORGANIC-CYCLIC-COMPOUND	20	-0.377711	-1.264952	0.178218	0.537722	1.000
528	GOBP-INFLAMMATORY-RESPONSE	12	-0.427786	-1.270050	0.186047	0.528770	1.000
529	REACTOME-G-PROTEIN-MEDIATED-EVENTS	9	-0.470248	-1.272588	0.188707	0.525519	1.000
530	GOBP-CIRCULATORY-SYSTEM-DEVELOPMENT	21	-0.373626	-1.279667	0.189373	0.511963	1.000
531	REACTOME-TRANSCRIPTIONAL-REGULATION-BY-MECP2	7	-0.523311	-1.281195	0.161481	0.511060	1.000
532	GOBP-POSITIVE-REGULATION-OF-CELLULAR-COMPONENT...	9	-0.483154	-1.281937	0.167656	0.512010	1.000
533	GOBP-LONG-TERM-SYNAPTIC-DEPRESSION	5	-0.588178	-1.282561	0.161695	0.513440	1.000
534	GOBP-CIRCULATORY-SYSTEM-PROCESS	5	-0.584403	-1.283104	0.154560	0.514891	1.000
535	GOBP-BLOOD-VESSEL-MORPHOGENESIS	14	-0.419025	-1.284355	0.168103	0.514604	1.000
536	GOBP-CELLULAR-RESPONSE-TO-KETONE	5	-0.593023	-1.288191	0.164110	0.508849	1.000
537	GOBP-CELLULAR-RESPONSE-TO-MOLECULE-OF-BACTERIA...	8	-0.501819	-1.289122	0.165615	0.509438	1.000
538	GOBP-REGULATION-OF-CELLULAR-PROTEIN-LOCALIZATION	12	-0.433045	-1.293586	0.150972	0.501685	1.000
539	GOBP-PEPTIDE-SECRETION	9	-0.481040	-1.295741	0.186364	0.499634	1.000
540	GOBP-SECRETION	24	-0.365882	-1.299166	0.157025	0.494901	1.000
541	GOBP-EMBRYO-DEVELOPMENT	14	-0.421062	-1.301056	0.164575	0.493515	1.000
542	GOBP-CELLULAR-RESPONSE-TO-BIOTIC-STIMULUS	8	-0.501819	-1.301787	0.162003	0.494651	1.000
543	GOBP-MONAMINE-TRANSPORT	5	-0.598248	-1.307422	0.144026	0.484616	1.000
544	GOBP-REGULATION-OF-TRANSPORTER-ACTIVITY	17	-0.393676	-1.309685	0.166667	0.482440	1.000
545	GOBP-CELLULAR-RESPONSE-TO-HORMONE-STIMULUS	11	-0.454816	-1.310839	0.146747	0.482734	1.000
546	GOBP-DENDRITIC-SPINE-MORPHOGENESIS	5	-0.599045	-1.311494	0.159869	0.484130	1.000
547	GOBP-POSITIVE-REGULATION-OF-IMMUNE-RESPONSE	9	-0.487429	-1.311855	0.148710	0.486172	1.000
548	GOBP-REGULATION-OF-CATABOLIC-PROCESS	13	-0.432216	-1.313775	0.163324	0.484715	1.000
549	GOBP-REGULATION-OF-PROTEIN-KINASE-ACTIVITY	22	-0.380570	-1.319553	0.143875	0.474411	1.000
550	GOBP-MEMBRANE-ORGANIZATION	12	-0.440024	-1.321384	0.157083	0.473365	1.000
551	GOBP-REGULATION-OF-TRANSFERASE-ACTIVITY	22	-0.380570	-1.323464	0.142857	0.472733	1.000
552	GOBP-INSULIN-SECRETION	7	-0.540570	-1.323464	0.158400	0.474060	1.000
553	GOBP-REGULATION-OF-MEMBRANE-POTENTIAL	17	-0.401530	-1.323477	0.149931	0.476888	1.000
554	GOBP-REGULATION-OF-LONG-TERM-SYNAPTIC-POTENTIAL...	6	-0.558430	-1.326098	0.147152	0.473977	1.000
555	GOBP-CELLULAR-RESPONSE-TO-PEPTIDE-HORMONE-STIM...	9	-0.494963	-1.326667	0.149701	0.475469	1.000
556	GOBP-REGULATION-OF-BODY-FLUID-LEVELS	11	-0.460312	-1.326765	0.130631	0.478170	1.000

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NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
557 GOBP-EMBRYONIC-ORGAN-DEVELOPMENT	GO-0048568	7	-0.53119	-1.328820	0.135671	0.476362	1.000
558 GOBP-RESPONSE-TO-ACID-CHEMICAL	GO-0001101	6	-0.560792	-1.329695	0.142420	0.477103	1.000
559 REACTOME-DISEASES-OF-SIGNAL-TRANSDUCTION-BY-GR...	R-HSA-5663202	12	-0.450596	-1.331092	0.133523	0.476550	1.000
560 GOBP-CATION-TRANSMEMBRANE-TRANSPORT	GO-0098655	18	-0.401962	-1.332976	0.146067	0.475067	1.000
561 GOBP-GLUTAMATE-RECEPTOR-SIGNALING-PATHWAY	GO-0007215	17	-0.409920	-1.332294	0.136691	0.472916	1.000
562 GOBP-REGULATION-OF-LYMPHOCYTE-ACTIVATION	GO-0051249	5	-0.609746	-1.337698	0.115445	0.470481	1.000
563 GOBP-PEPTIDE-BIOSYNTHETIC-PROCESS	GO-0043043	7	-0.550471	-1.338581	0.114062	0.471559	1.000
564 GOBP-PROTEIN-KINASE-B-SIGNALING	GO-0043491	6	-0.571452	-1.340615	0.117371	0.469880	1.000
565 GOBP-NERVOUS-SYSTEM-PROCESS	GO-0050877	38	-0.353650	-1.343867	0.131649	0.465254	1.000
566 GOBP-REGULATION-OF-NEUROTRANSMITTER-TRANSPORT	GO-0051588	6	-0.571740	-1.345454	0.130631	0.464630	1.000
567 GOBP-REGULATION-OF-ION-TRANSPORT	GO-0043269	36	-0.355551	-1.345570	0.128415	0.467416	1.000
568 REACTOME-INFECTIOUS-DISEASE	R-HSA-5663205	13	-0.449653	-1.346975	0.147710	0.467423	1.000
569 REACTOME-MAPK-FAMILY-SIGNALING-CASCADES	R-RNO-5683057	12	-0.459249	-1.347573	0.135258	0.469139	1.000
570 GOBP-PEPTIDE-HORMONE-SECRETION	GO-0030072	7	-0.540570	-1.349861	0.125758	0.467347	1.000
571 GOBP-MATERNAL-PROCESS-INVOLVED-IN-FEMALE-PREGN...	GO-0060135	5	-0.616936	-1.350344	0.115016	0.469452	1.000
572 GOBP-LEARNING	GO-0007612	13	-0.446031	-1.351147	0.119708	0.470804	1.000
573 GOBP-REGULATION-OF-DNA-BINDING-TRANSCRIPTION.F...	GO-0051090	16	-0.422064	-1.353097	0.131653	0.469540	1.000
574 GOBP-TUBE-DEVELOPMENT	GO-0035295	18	-0.404631	-1.353511	0.120433	0.471772	1.000
575 GOBP-REGULATION-OF-CELLULAR-AMIDE-METABOLIC.PR...	GO-0034248	9	-0.504229	-1.353689	0.120611	0.474597	1.000
576 GOBP-METAL-ION-TRANSPORT	GO-0030001	11	-0.474680	-1.354806	0.123907	0.475138	1.000
577 GOBP-POSITIVE-REGULATION-OF-IMMUNE-SYSTEM-PROCESS	GO-0002684	18	-0.412335	-1.355853	0.131728	0.476100	1.000
578 GOBP-HOMEOSTASIS-OF-NUMBER-OF-CELLS	GO-0048872	5	-0.600912	-1.356267	0.118859	0.478422	1.000
579 GOBP-MAPK-CASCADE	GO-0000165	18	-0.408262	-1.360107	0.130560	0.472406	1.000
580 GOBP-GLAND-DEVELOPMENT	GO-0048732	7	-0.545173	-1.364767	0.087500	0.465332	1.000
581 GOBP-REGULATION-OF-LIPID-METABOLIC-PROCESS	GO-0019216	7	-0.554776	-1.369639	0.111614	0.456912	1.000
582 GOBP-SENSORY-ORGAN-DEVELOPMENT	GO-0007423	8	-0.528165	-1.373030	0.126657	0.452446	1.000
583 GOBP-POSITIVE-REGULATION-OF-SMALL-MOLECULE-MET...	GO-0062013	5	-0.629364	-1.375097	0.098592	0.450887	1.000
584 GOBP-NEURON-MIGRATION	GO-0001764	5	-0.628224	-1.375136	0.109635	0.454174	1.000
585 GOBP-CALCIUM-ION-TRANSPORT	GO-0006816	11	-0.474680	-1.376588	0.121037	0.454185	1.000
586 REACTOME-EPH-EPHRIN-SIGNALING	R-RNO-2682334	6	-0.589306	-1.378982	0.111111	0.452091	1.000
587 GOBP-LEUKOCYTE-CELL-CELL-ADHESION	GO-0007159	6	-0.589032	-1.380513	0.093991	0.452025	1.000
588 GOBP-AMIDE-BIOSYNTHETIC-PROCESS	GO-0043604	7	-0.550471	-1.382719	0.109063	0.450463	1.000
589 GOBP-REGULATION-OF-CELL-ADHESION	GO-0030155	13	-0.461229	-1.382864	0.107143	0.453542	1.000
590 GOBP-ACTIN-FILAMENT-BASED-PROCESS	GO-0030029	7	-0.567215	-1.386808	0.104651	0.447770	1.000
591 GOBP-CARBOHYDRATE-DERIVATIVE-METABOLIC-PROCESS	GO-1901135	7	-0.544695	-1.387697	0.107765	0.449276	1.000
592 GOBP-ACTIVATION-OF-PROTEIN-KINASE-ACTIVITY	GO-0032147	11	-0.477842	-1.387876	0.110795	0.452460	1.000
593 GOBP-CELL-SURFACE-RECEPTOR-SIGNALING-PATHWAY.I...	GO-1905114	15	-0.448187	-1.388299	0.104499	0.454937	1.000
594 GOBP-RESPONSE-TO-LIPID	GO-0033993	19	-0.421497	-1.389190	0.110169	0.456226	1.000
595 GOBP-PLATELET-ACTIVATION	GO-0030168	6	-0.585410	-1.390205	0.100154	0.457457	1.000
596 GOBP-LOCOMOTORY-BEHAVIOR	GO-0007626	7	-0.573009	-1.391185	0.082803	0.458931	1.000
597 GOBP-DEFENSE-RESPONSE-TO-OTHER-ORGANISM	GO-0098542	9	-0.512433	-1.391623	0.089706	0.461525	1.000
598 GOBP-CELLULAR-LIPID-METABOLIC-PROCESS	GO-0044255	7	-0.552009	-1.392030	0.099071	0.464183	1.000
599 GOBP-CELL-ACTIVATION	GO-0001775	21	-0.402232	-1.394754	0.102703	0.461494	1.000

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NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
600 REACTOME-DAG-AND-IP3-SIGNALING	R-RNO-1489509	8	-0.532998	-1.395594	0.091757	0.463483	1.000
601 REACTOME-ESTROGEN-DEPENDENT-NUCLEAR-EVENTS.DOW...	R-RNO-9634638	5	-0.644819	-1.398937	0.092800	0.458940	1.000
602 GOBP-REGULATION-OF-SYNAPSE-STRUCTURE-OR-ACTIVITY	GO-0050803	11	-0.493107	-1.399041	0.100149	0.462513	1.000
603 GOBP-REGULATION-OF-TRANSMEMBRANE-TRANSPORT	GO-0034762	23	-0.395083	-1.399124	0.108635	0.466299	1.000
604 GOBP-IMPORT-INTO-CELL	GO-0098657	6	-0.608864	-1.416063	0.083462	0.429288	1.000
605 GOBP-DEFENSE-RESPONSE	GO-0006952	19	-0.423416	-1.416133	0.093750	0.432970	1.000
606 GOBP-POSITIVE-REGULATION-OF-EPITHELIAL-CELL-PR...	GO-0050679	7	-0.578217	-1.417640	0.096367	0.433237	1.000
607 GOBP-POSTSYNAPSE-ORGANIZATION	GO-0099173	10	-0.497259	-1.420517	0.109774	0.429686	1.000
608 GOBP-REGULATION-OF-PROTEIN-SERINE-THREONINE-KI...	GO-0071900	12	-0.488818	-1.422382	0.105030	0.428992	1.000
609 GOBP-CELLULAR-RESPONSE-TO-ALCOHOL	GO-0097306	5	-0.651170	-1.425066	0.068643	0.426362	1.000
610 REACTOME-CA-DEPENDENT-EVENTS	R-RNO-111996	8	-0.547443	-1.428880	0.079193	0.421109	1.000
611 GOBP-REGULATION-OF-METAL-ION-TRANSPORT	GO-0010959	6	-0.614436	-1.432021	0.091054	0.417668	1.000
612 GOBP-CHEMICAL-SYNAPTIC-TRANSMISSION-POSTSYNAPTIC	GO-0099565	9	-0.528614	-1.432541	0.094453	0.420176	1.000
613 GOBP-TISSUE-HOMEOSTASIS	GO-0001894	5	-0.657539	-1.433148	0.064516	0.422534	1.000
614 GOBP-POSITIVE-REGULATION-OF-ENDOTHELIAL-CELL-P...	GO-0001938	6	-0.624595	-1.442753	0.072231	0.404969	1.000
615 GOBP-AMEBOIDAL-TYPE-CELL-MIGRATION	GO-0001667	11	-0.512086	-1.444559	0.083333	0.404701	1.000
616 GOBP-ORGANONITROGEN-COMPOUND-BIOSYNTHETIC-PROCESS	GO-1901566	13	-0.486044	-1.444572	0.071953	0.408585	1.000
617 GOBP-POSITIVE-REGULATION-OF-ION-TRANSPORT	GO-0043270	17	-0.446042	-1.451748	0.071625	0.396230	1.000
618 GOBP-TUBE-MORPHOGENESIS	GO-0035239	15	-0.469390	-1.454345	0.064378	0.394332	1.000
619 GOBP-EMBRYO-DEVELOPMENT-ENDING-IN-BIRTH-OR-EGG...	GO-0009792	9	-0.541175	-1.455118	0.071964	0.396393	1.000
620 GOBP-PROTEIN-LOCALIZATION-TO-PLASMA-MEMBRANE	GO-0072659	7	-0.585726	-1.466549	0.069291	0.395854	1.000
621 GOBP-SYNAPSE-ORGANIZATION	GO-0050808	17	-0.454425	-1.466549	0.067659	0.378477	1.000
622 GOBP-PROTEIN-PHOSPHORYLATION	GO-0006468	34	-0.386669	-1.467295	0.071332	0.380543	1.000
623 GOBP-PROTEIN-LOCALIZATION-TO-POSTSYNAPSE	GO-0062237	5	-0.672227	-1.470965	0.060897	0.376563	1.000
624 GOBP-POSITIVE-REGULATION-OF-ANION-TRANSPORT	GO-1903793	9	-0.553478	-1.477057	0.066566	0.367605	1.000
625 GOBP-REGULATION-OF-CELLULAR-CATABOLIC-PROCESS	GO-0031329	10	-0.537397	-1.479244	0.051593	0.366640	1.000
626 GOBP-RESPIRATORY-SYSTEM-DEVELOPMENT	GO-0060541	6	-0.626841	-1.482244	0.056782	0.364355	1.000
627 GOBP-CYTOSOLIC-CALCIUM-ION-TRANSPORT	GO-0060401	7	-0.609325	-1.482586	0.061947	0.367604	1.000
628 GOBP-PROTEIN-LOCALIZATION-TO-SYNAPSE	GO-0035418	5	-0.672227	-1.483414	0.047468	0.369518	1.000
629 GOBP-CELL-JUNCTION-ASSEMBLY	GO-0034329	8	-0.576809	-1.484034	0.066874	0.372058	1.000
630 REACTOME-ONCOGENIC-MAPK-SIGNALING	R-HSA-6802957	5	-0.676784	-1.489062	0.041401	0.364767	1.000
631 GOBP-ENDOTHELIAL-CELL-PROLIFERATION	GO-0001935	8	-0.578586	-1.490484	0.056662	0.365591	1.000
632 GOBP-DENDRITIC-SPINE-DEVELOPMENT	GO-0060996	6	-0.637936	-1.495950	0.049844	0.358155	1.000
633 GOBP-CALCIUM-ION-TRANSPORT-INTO-CYTOSOL	GO-0060402	7	-0.609325	-1.497642	0.059724	0.358664	1.000
634 GOBP-CELLULAR-HOMEOSTASIS	GO-0019725	18	-0.464489	-1.499157	0.055398	0.359548	1.000
635 GOBP-REGULATION-OF-ENDOTHELIAL-CELL-MIGRATION	GO-0010594	5	-0.687709	-1.506538	0.044481	0.347189	1.000
636 GOBP-RESPONSE-TO-ETHANOL	GO-0045471	5	-0.701938	-1.513302	0.032915	0.338450	1.000
637 GOBP-REGULATION-OF-CELL-ACTIVATION	GO-0050865	8	-0.587446	-1.514668	0.054773	0.339581	1.000
638 GOBP-NEGATIVE-REGULATION-OF-LIPID-METABOLIC-PR...	GO-0045833	5	-0.692033	-1.514924	0.036050	0.343250	1.000
639 GOBP-SPROUTING-ANGIOGENESIS	GO-0002040	5	-0.694896	-1.523025	0.042879	0.329679	1.000
640 GOBP-CATION-TRANSPORT	GO-0006812	25	-0.430202	-1.523611	0.045330	0.332702	1.000
641 REACTOME-NEUREXINS-AND-NEUROLIGINS	R-RNO-6794361	9	-0.566586	-1.524936	0.044709	0.334261	1.000
642 GOBP-POSITIVE-REGULATION-OF-DNA-BINDING-TRANSC...	GO-0051091	10	-0.543097	-1.527402	0.043091	0.333168	1.000

Continuation of Table S19

	NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
643	GOBP-RESPONSE.TO.TEMPERATURE.STIMULUS	GO-0009266	9	-0.581502	-1.527997	0.026393	0.336107	1.000
644	GOBP-HOMEOSTATIC.PROCESS	GO-0042592	31	-0.416435	-1.528865	0.038822	0.338393	1.000
645	GOBP-EPITHELIAL.DEVELOPMENT	GO-0060429	15	-0.483532	-1.533457	0.053672	0.333036	1.000
646	GOBP-MONOSACCHARIDE.METABOLIC.PROCESS	GO-0005996	6	-0.648945	-1.535324	0.046584	0.333685	1.000
647	GOBP-POSITIVE.REGULATION.OF.LEUKOCYTE.CELL.CEL...	GO-1903039	5	-0.704221	-1.536566	0.038400	0.335698	1.000
648	GOBP-REGULATION.OF.PROTEIN.LOCALIZATION.TO.MEM...	GO-1906475	7	-0.614175	-1.536597	0.039002	0.340377	1.000
649	GOBP-REGULATION.OF.MITOTIC.CELL.CYCLE	GO-0007346	5	-0.702046	-1.537972	0.036107	0.342601	1.000
650	GOBP-REGULATION.OF.TRANS.SYNAPTIC.SIGNALING	GO-0009177	40	-0.399298	-1.540052	0.034574	0.342755	1.000
651	GOBP-BIOLOGICAL.ADHESION	GO-0022610	19	-0.463707	-1.542025	0.042936	0.343676	1.000
652	REACTOME-PROTEIN.PROTEIN.INTERACTIONS.AT.SYNAPSES	R-RNO-6794362	12	-0.533407	-1.543097	0.046899	0.346338	1.000
653	GOBP-RESPONSE.TO.BIOTIC.STIMULUS	GO-0009607	17	-0.481567	-1.545354	0.043228	0.346602	1.000
654	GOBP-POSITIVE.REGULATION.OF.SIGNALING	GO-0023056	34	-0.408622	-1.547248	0.035480	0.347697	1.000
655	GOBP-CALCIUM-ION.TRANSMEMBRANE.TRANSPORT	GO-0070588	7	-0.609325	-1.548876	0.036741	0.349279	1.000
656	GOBP-GLUCOSE.METABOLIC.PROCESS	GO-0006006	6	-0.648945	-1.551068	0.043614	0.349803	1.000
657	GOBP-REGULATION.OF.PROTEIN.LOCALIZATION.TO.CEL...	GO-1904375	6	-0.660698	-1.558760	0.035484	0.338178	1.000
658	GOBP-CHEMICAL.HOMEOSTASIS	GO-0048878	23	-0.440941	-1.566298	0.045961	0.327065	1.000
659	GOBP-POSITIVE.REGULATION.OF.CELL.CELL.ADHESION	GO-0022409	5	-0.704221	-1.569203	0.020833	0.326644	1.000
660	GOBP-CELL.CELL.JUNCTION.ASSEMBLY	GO-0007043	5	-0.731175	-1.574314	0.020701	0.321685	1.000
661	GOBP-CELLULAR.RESPONSE.TO.ORGANIC.CYCLIC.COMPOUND	GO-0071407	13	-0.520332	-1.584871	0.044978	0.304318	1.000
662	GOBP-SMALL.MOLECULE.METABOLIC.PROCESS	GO-0044281	15	-0.506576	-1.585161	0.031343	0.308917	1.000
663	GOBP-REGULATION.OF-NEUROTRANSMITTER.RECEPTOR.A...	GO-0099601	9	-0.535129	-1.585931	0.027818	0.313133	1.000
664	GOBP-REGULATION.OF.CELL.CELL.ADHESION	GO-0022407	13	-0.595247	-1.587014	0.032305	0.316746	1.000
665	GOBP-ION.HOMEOSTASIS	GO-0050801	16	-0.502610	-1.587008	0.023876	0.322501	1.000
666	GOBP-PROTEIN.LOCALIZATION.TO.CELL.JUNCTION	GO-1902414	6	-0.693762	-1.591490	0.014241	0.319366	1.000
667	GOBP-CELL.JUNCTION.ORGANIZATION	GO-0034330	19	-0.480441	-1.593919	0.031073	0.320600	1.000
668	GOBP-REGULATION.OF-NMDA.RECEPTOR.ACTIVITY	GO-2000310	10	-0.560693	-1.594472	0.025037	0.325689	1.000
669	GOBP-NEGATIVE.REGULATION.OF.LOCOMOTION	GO-0040013	5	-0.712905	-1.597060	0.030945	0.326241	1.000
670	GOBP-NEUROTRANSMITTER.TRANSPORT	GO-0006836	7	-0.650850	-1.607798	0.033846	0.307398	1.000
671	GOBP-LONG-TERM.MEMORY	GO-0007616	6	-0.701639	-1.610295	0.017134	0.307980	1.000
672	GOBP-TRANSMEMBRANE.TRANSPORT	GO-0072657	27	-0.449229	-1.610499	0.019894	0.313933	1.000
673	GOBP-PROTEIN.LOCALIZATION.TO.MEMBRANE	GO-0072657	14	-0.518001	-1.619715	0.032164	0.300818	1.000
674	GOBP-REGULATION.OF.EXTRINSIC.APOPTOTIC.SIGNALI...	GO-2001236	6	-0.686812	-1.622524	0.019449	0.300929	1.000
675	GOBP-CELL.CELL.JUNCTION.ORGANIZATION	GO-0045216	6	-0.679886	-1.622891	0.018349	0.306918	1.000
676	REACTOME-NEURONAL.SYSTEM	R-RNO-112316	26	-0.449025	-1.625147	0.025210	0.308451	1.000
677	GOBP-REGULATION.OF.CELLULAR.RESPONSE.TO.STRESS	GO-0080135	9	-0.607338	-1.626709	0.024818	0.312643	1.000
678	GOBP-NEUROTRANSMITTER.SECRETION	GO-0007269	5	-0.699857	-1.629409	0.021309	0.313798	1.000
679	GOBP-EXCITATORY.CHEMICAL.SYNAPTIC.TRANSMISSION	GO-0098976	5	-0.734940	-1.629608	0.014516	0.321232	1.000
680	GOBP-PROTEIN-CONTAINING.COMPLEX.SUBUNIT.ORGANI...	GO-0043933	14	-0.531547	-1.632389	0.021930	0.323768	1.000
681	GOBP-CELLULAR.RESPONSE.TO.LIPID	GO-0071396	15	-0.514470	-1.634339	0.024390	0.327604	1.000
682	GOBP-ANATOMICAL.STRUCTURE.HOMEOSTASIS	GO-0060249	7	-0.670165	-1.634582	0.013333	0.335888	1.000
683	GOBP-REGULATION.OF-NEUROTRANSMITTER.LEVELS	GO-0001505	7	-0.650850	-1.646717	0.017799	0.315420	1.000
684	GOBP-NEGATIVE.REGULATION.OF-IMMUNE.SYSTEM.PROCESS	GO-0002683	5	-0.747473	-1.654530	0.013932	0.305515	1.000
685	GOBP-MULTICELLULAR.ORGANISMAL.HOMEOSTASIS	GO-0048871	12	-0.572448	-1.669085	0.023529	0.281698	1.000

Continuation of Table S19

NAME	ID	SIZE	ES	NES	NOM.p.val	FDR.q.val	FWER.p.val
686 GOBP-TISSUE-MIGRATION	GO-0090130	9	-0.620679	-1.675839	0.015576	0.276290	1.000
687 GOBP-SENSORY_PERCEPTION_OF_PAIN	GO-0019233	5	-0.762718	-1.684219	0.013997	0.267451	1.000
688 GOBP-REGULATION_OF_SMALL-MOLECULE-METABOLIC-PR...	GO-0062012	9	-0.627242	-1.685356	0.010370	0.273429	1.000
689 GOBP-SYNAPTIC-SIGNALING	GO-0099536	47	-0.427485	-1.689640	0.012870	0.272643	1.000
690 GOBP-SIGNAL-RELEASE	GO-0023061	14	-0.543418	-1.698342	0.012931	0.263249	1.000
691 GOBP-IONOTROPIC-GLUTAMATE-RECEPTOR-SIGNALING-P...	GO-0035235	9	-0.632911	-1.710785	0.017161	0.249509	0.998
692 GOBP-REGULATION-OF-SIGNALING-RECEPTOR-ACTIVITY	GO-0010469	14	-0.553057	-1.724086	0.011869	0.231932	0.997
693 REACTOME-TRANSMISSION-ACROSS-CHEMICAL-SYNAPSES	R-RNO-112315	23	-0.503234	-1.734796	0.005517	0.220369	0.996
694 REACTOME-CREB1-PHOSPHORYLATION_THROUGH-NMDA-RE...	R-RNO-442742	8	-0.668566	-1.735813	0.009119	0.226884	0.995
695 GOBP-METAL-ION-HOMEOSTASIS	GO-0055065	14	-0.561354	-1.742089	0.011445	0.223768	0.989
696 GOBP-REGULATION-OF-SYNAPTIC-PLASTICITY	GO-0048167	21	-0.515871	-1.746472	0.016484	0.224581	0.988
697 GOBP-CELL-CELL-SIGNALING	GO-0007267	56	-0.459364	-1.765695	0.003886	0.200745	0.983
698 GOBP-RESPONSE-TO-HEAT	GO-0009408	7	-0.721531	-1.772382	0.004651	0.199109	0.979
699 GOBP-LONG-TERM-SYNAPTIC-POTENTIATION	GO-0060291	12	-0.617680	-1.776981	0.005780	0.201518	0.976
700 GOBP-PROTEIN-LOCALIZATION-TO-CELL-PERIPHERY	GO-1990778	12	-0.607005	-1.784797	0.004451	0.197299	0.968
701 REACTOME-SYNAPTIC-ADHESION-LIKE-MOLECULES	R-RNO-884932	9	-0.670886	-1.792105	0.006107	0.194969	0.961
702 GOBP-DIVALENT-INORGANIC-CATION-HOMEOSTASIS	GO-0072507	13	-0.607158	-1.815839	0.009777	0.167554	0.923
703 GOBP-CELLULAR-ION-HOMEOSTASIS	GO-0006873	14	-0.593443	-1.816342	0.011817	0.177216	0.921
704 REACTOME-NEUROTRANSMITTER-RECEPTORS-AND-POSTSY...	R-RNO-112314	22	-0.524333	-1.818207	0.001377	0.186140	0.917
705 REACTOME-RAS-ACTIVATION-UPON-CA2-INFLUX-THROUG...	R-HSA-442982	6	-0.780488	-1.823158	0.006483	0.191050	0.901
706 GOBP-RESPONSE-TO-ALCOHOL	GO-0097305	11	-0.634361	-1.825040	0.004405	0.203475	0.899
707 GOBP-REGULATION-OF-CYTOSOLIC-CALCIUM-ION-CONCE...	GO-0051480	13	-0.607158	-1.830605	0.005857	0.206569	0.883
708 REACTOME-LONG-TERM-POTENTIATION	R-HSA-9620244	10	-0.667578	-1.834206	0.007321	0.217874	0.876
709 GOBP-CELL-CELL-ADHESION	GO-0098609	14	-0.618002	-1.904023	0.004219	0.117604	0.624
710 GOBP-MORPHOGENESIS-OF-AN-EPITHELIUM	GO-0002009	6	-0.809941	-1.907440	0.001605	0.126101	0.611
711 REACTOME-UNBLOCKING-OF-NMDA-RECEPTORS-GLUTAMAT...	R-RNO-438066	12	-0.657895	-1.949656	0.004431	0.091273	0.444
712 REACTOME-NEGATIVE-REGULATION-OF-NMDA-RECEPTOR-...	R-HSA-9617324	8	-0.762500	-1.955284	0.003063	0.097942	0.429
713 GOBP-ENDOTHELIAL-CELL-MIGRATION	GO-0043542	8	-0.764257	-1.963357	0.000000	0.104155	0.401
714 REACTOME-ASSEMBLY-AND-CELL-SURFACE-PRESENTATIO...	R-RNO-9609736	8	-0.762500	-1.964867	0.000000	0.123102	0.396
715 GOBP-TISSUE-MORPHOGENESIS	GO-0048729	7	-0.806186	-1.988465	0.001515	0.116012	0.326
716 GOBP-BLOOD-VESEL-ENDOTHELIAL-CELL-MIGRATION	GO-0043534	8	-0.764257	-1.989083	0.000000	0.154295	0.325
717 GOBP-POSITIVE-REGULATION-OF-SYNAPTIC-TRANSMISSION	GO-0050806	15	-0.666694	-2.062194	0.000000	0.088657	0.138
718 REACTOME-ACTIVATION-OF-NMDA-RECEPTORS-AND-POST...	R-RNO-442755	16	-0.671154	-2.150442	0.000000	0.044580	0.035

End of Table

2 Supplementary Figures

2.1 Pearson Correlation Plots

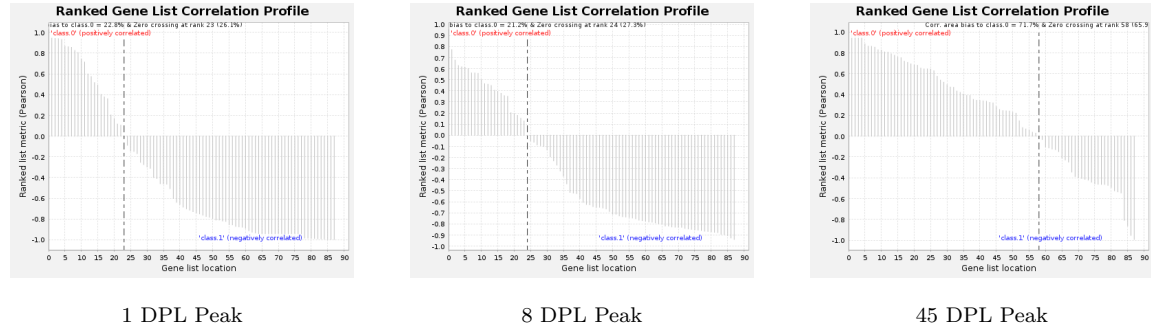


Figure S1: Bar plots of SC rostral segment 1, 8 and 45 DPL, Ranked Gene List Pearson Correlation Profile.

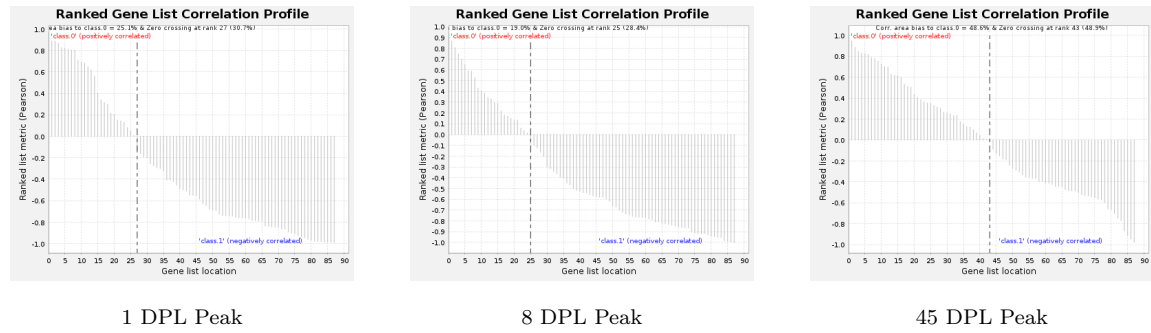


Figure S2: Bar plots of SC caudal segment 1, 8 and 45 DPL, Ranked Gene List Pearson Correlation Profile.

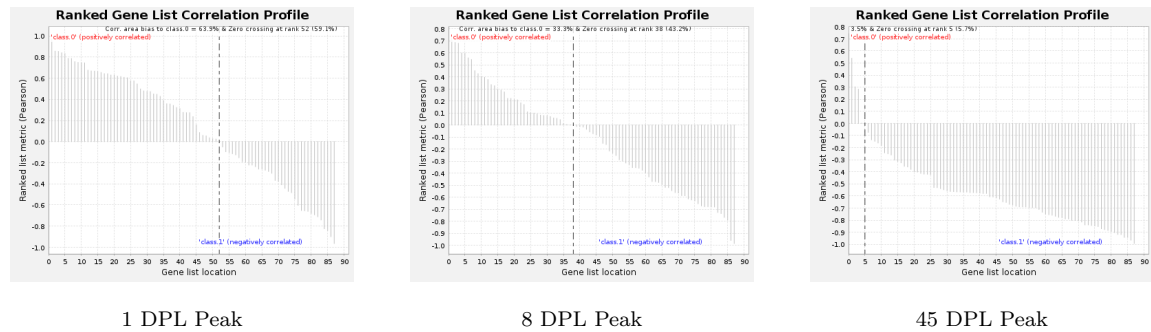
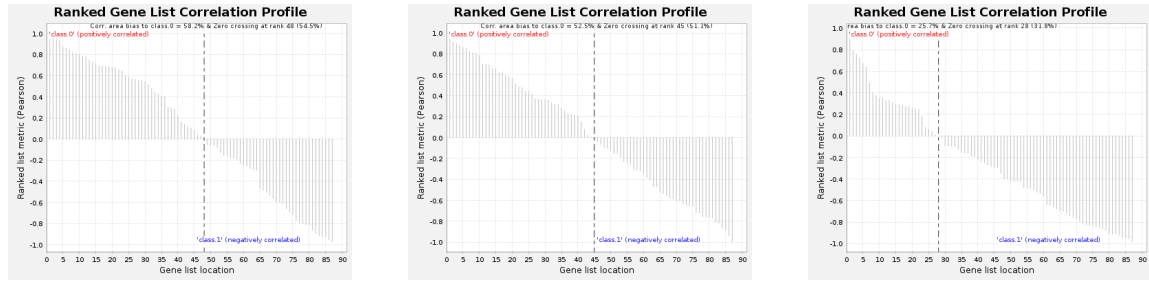


Figure S3: Bar plots of SC cervical segment 1, 8 and 45 DPL, Ranked Gene List Pearson Correlation Profile.

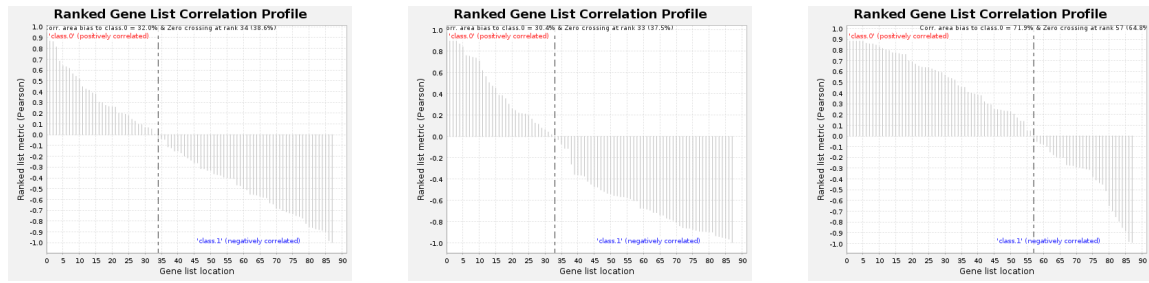


1 DPL Peak

8 DPL Peak

45 DPL Peak

Figure S4: Bar plots of CTX-M 1, 8 and 45 DPL, Ranked Gene List Pearson Correlation Profile.

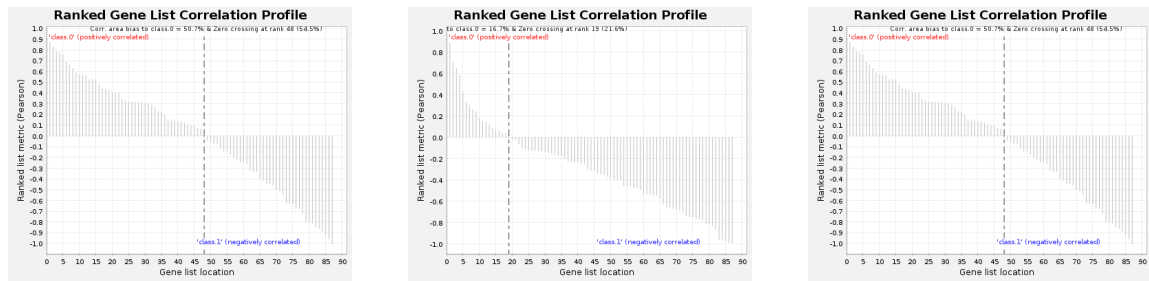


1 DPL Peak

8 DPL Peak

45 DPL Peak

Figure S5: Bar plots of BG 1, 8 and 45 DPL, Ranked Gene List Pearson Correlation Profile.



1 DPL Peak

8 DPL Peak

45 DPL Peak

Figure S6: Bar plots of CB 1, 8 and 45 DPL, Ranked Gene List Pearson Correlation Profile.

2.2 NES vs Significance Plots

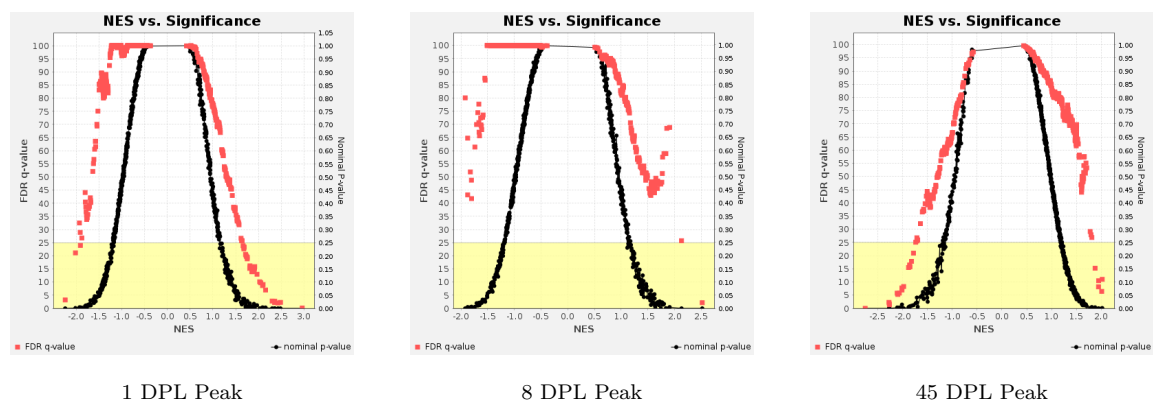


Figure S7: Plots of the distribution of SC rostral segment 1, 8 and 45 DPL, NES values. Significant pathways, $FDR \leq 0.25$, are highlighted in yellow.

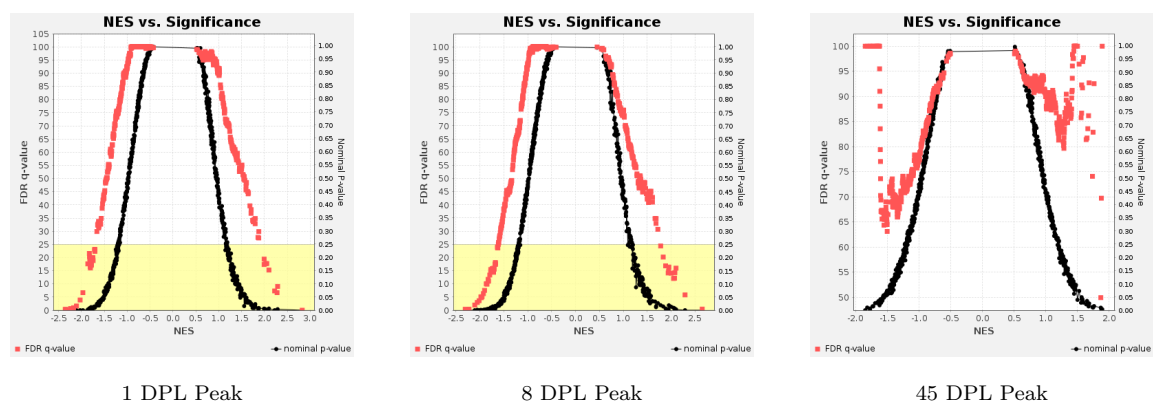


Figure S8: Plots of the distributions of SC caudal section's 1, 8 and 45 DPL, NES values. Significant pathways, $FDR \leq 0.25$, are highlighted in yellow.

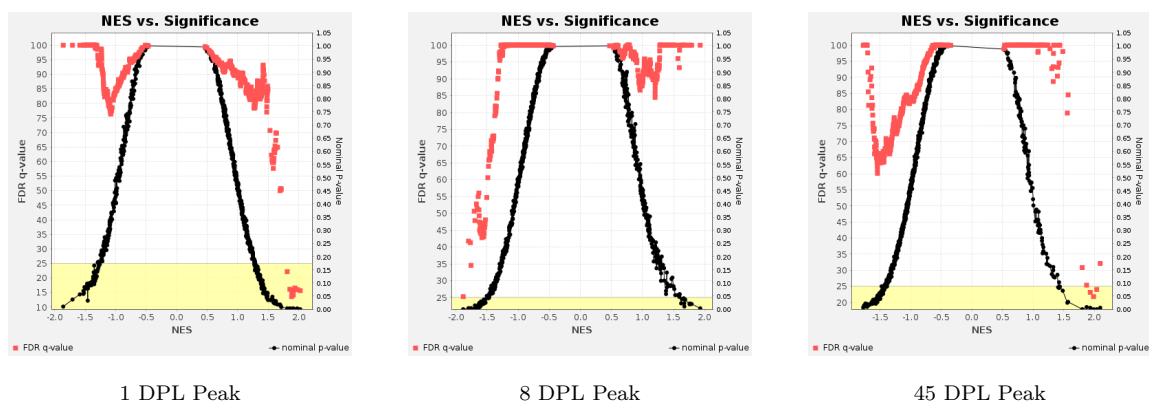


Figure S9: Plots of the distributions of SC cervical section's 1, 8 and 45 DPL, NES values. Significant pathways, $FDR \leq 0.25$, are highlighted in yellow.

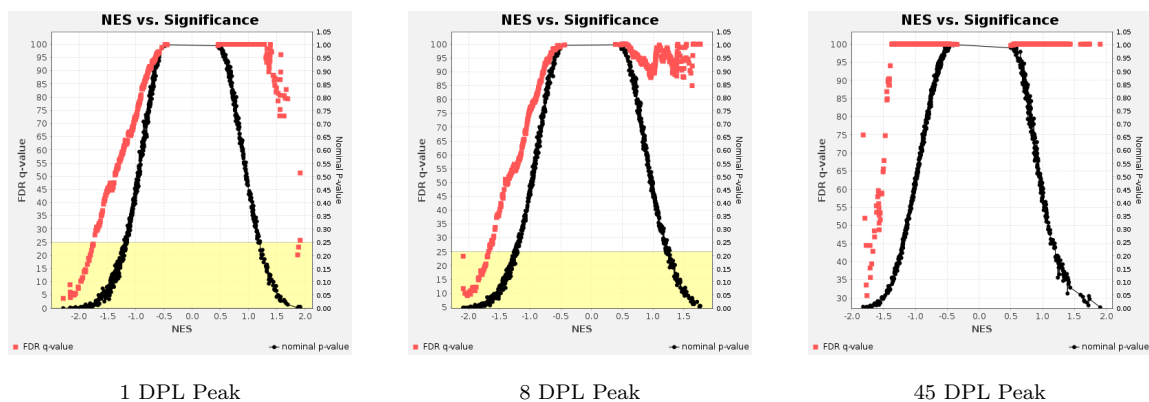


Figure S10: Plots of the distributions of CTX-M 1, 8 and 45 DPL, NES values. Significant pathways, $FDR \leq 0.25$, are highlighted in yellow.

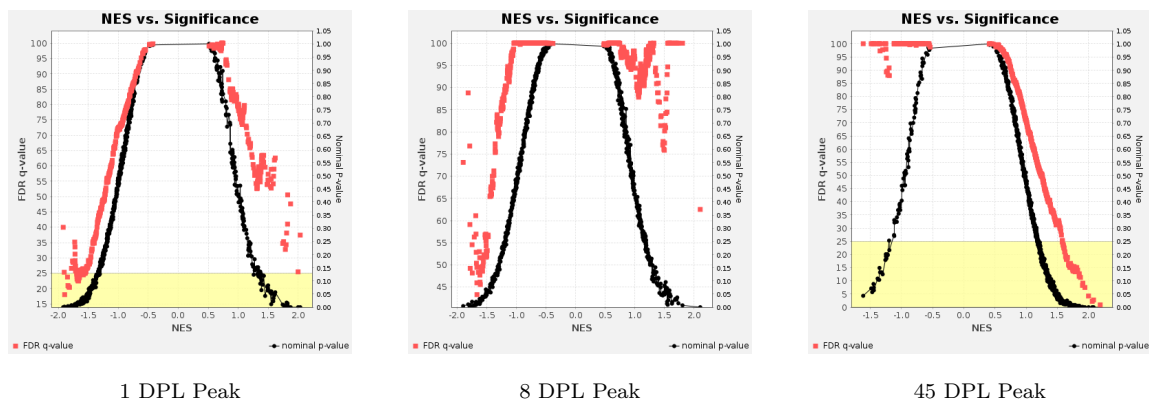


Figure S11: Plots of the distributions of BG 1, 8 and 45 DPL, NES values. Significant pathways, $FDR \leq 0.25$, are highlighted in yellow.

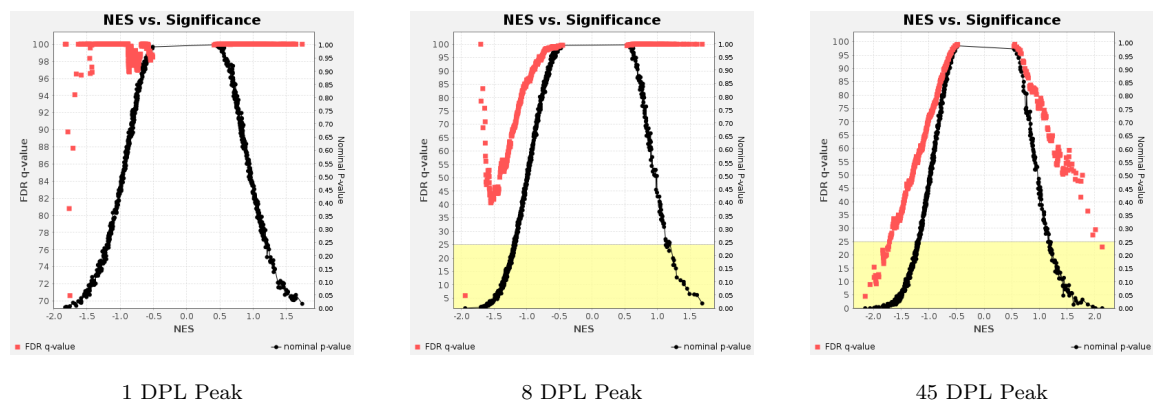


Figure S12: Plots of the distributions of CB 1, 8 and 45 DPL, NES values. Significant pathways, $FDR \leq 0.25$, are highlighted in yellow.

2.3 Leading Edge Analysis

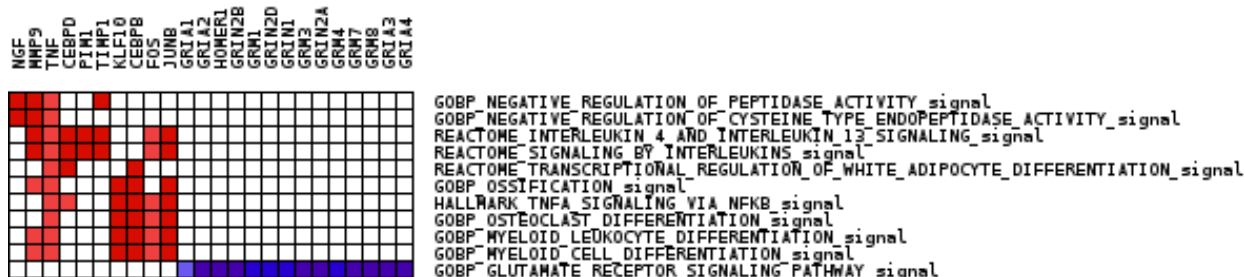


Figure S13: SC rostral 1 DPL Leading Edge Analysis results

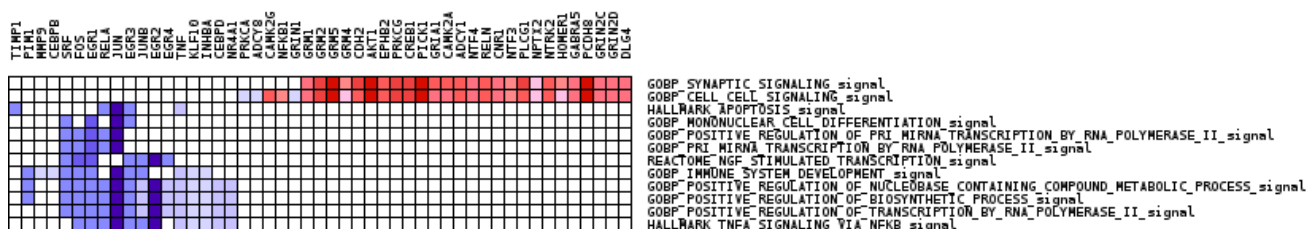


Figure S14: SC rostral 45 DPL Leading Edge Analysis results

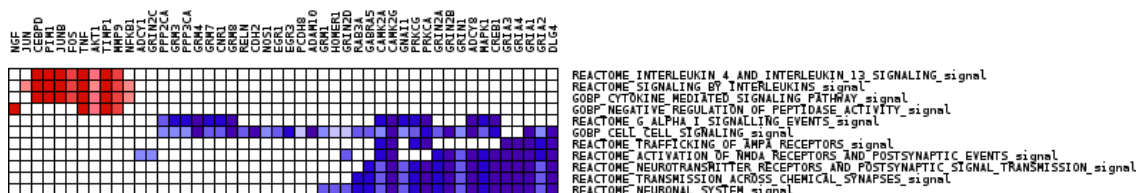


Figure S15: SC caudal 1 DPL Leading Edge Analysis results

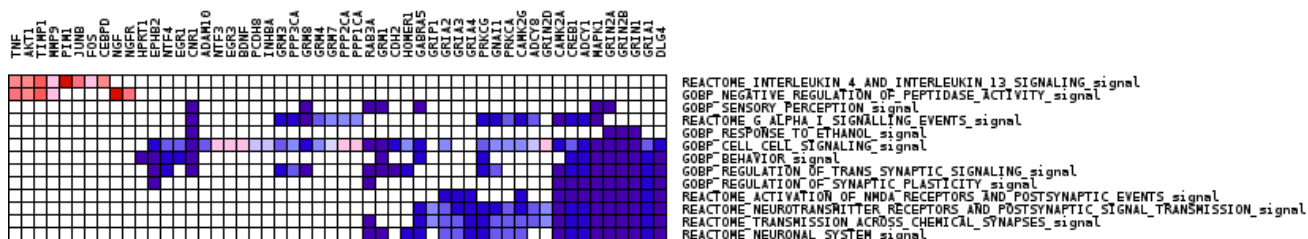
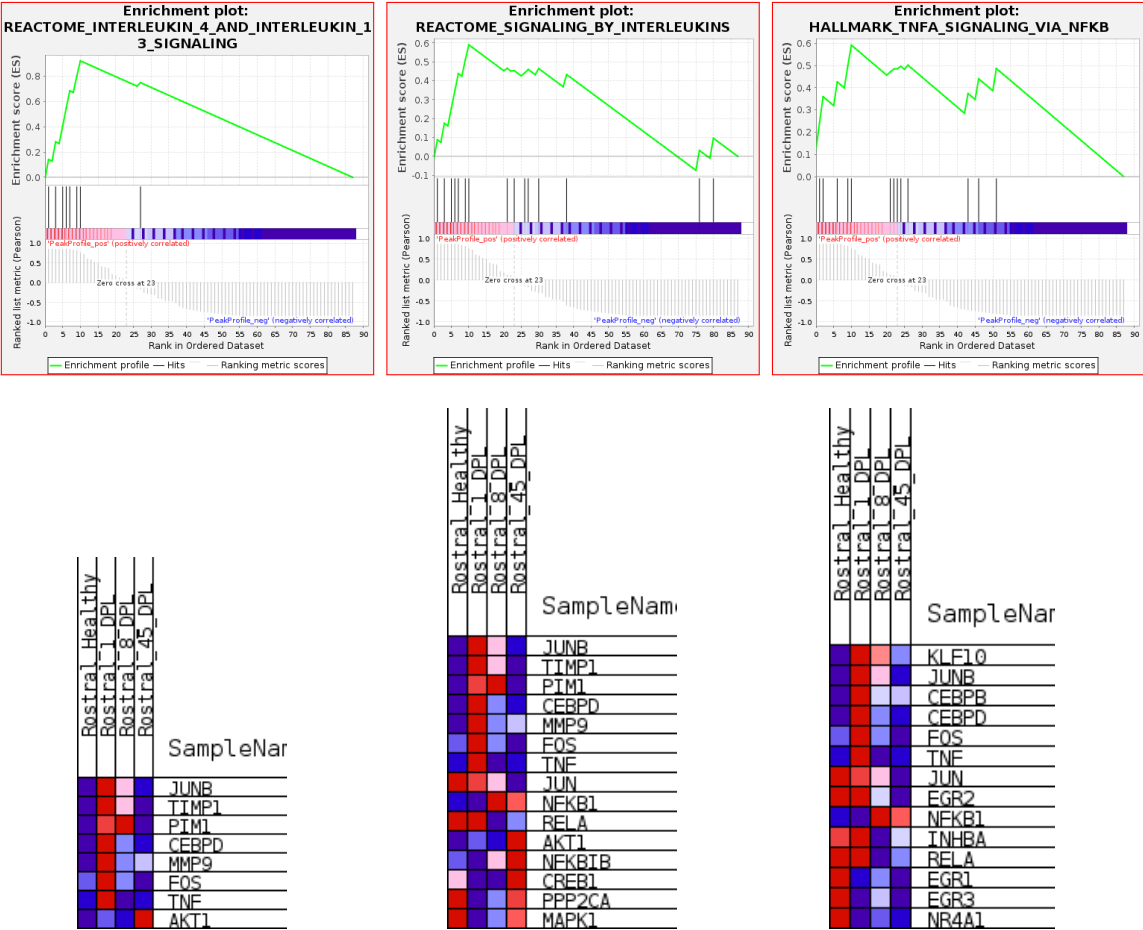
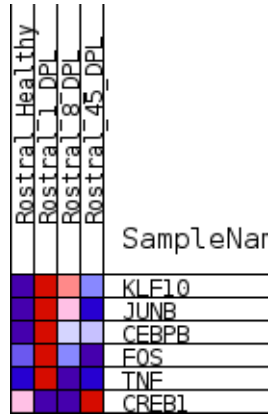
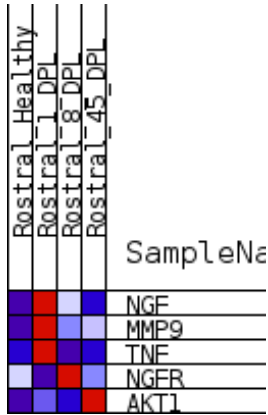
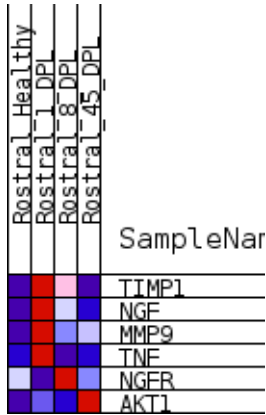
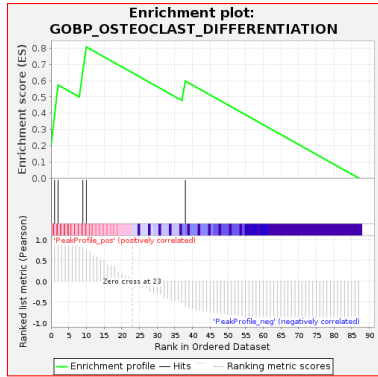
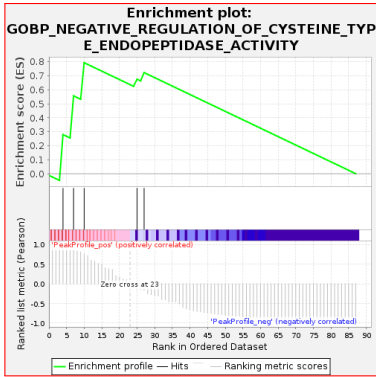
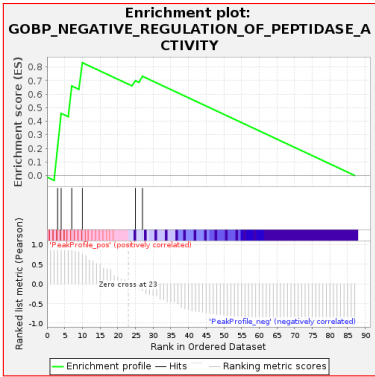


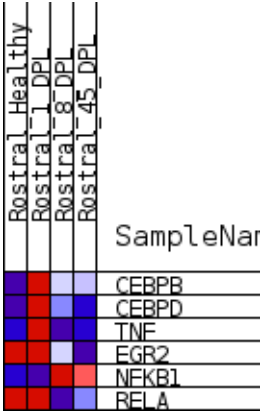
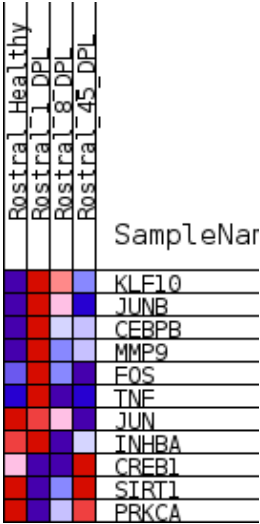
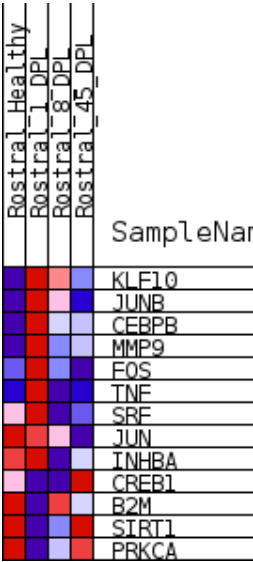
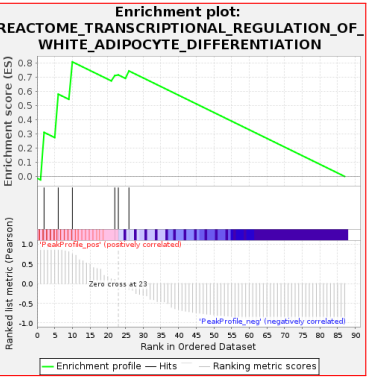
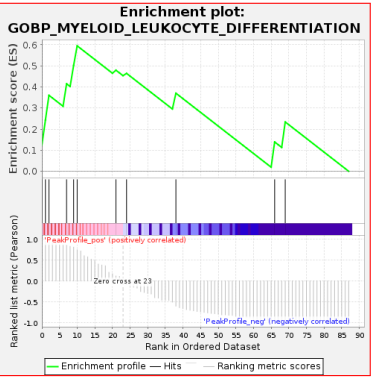
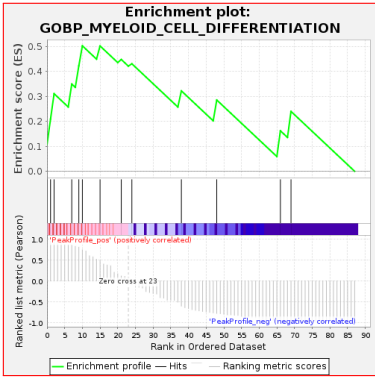
Figure S16: SC caudal 8 DPL Leading Edge Analysis results

2.4 Deregulated Pathways EN Plots and Heatmaps

2.4.1 SC rostral 1 DPL Peak Pathways







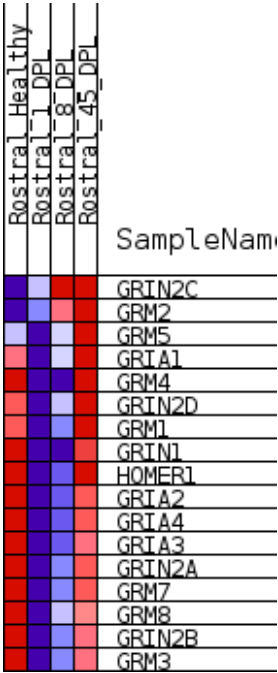
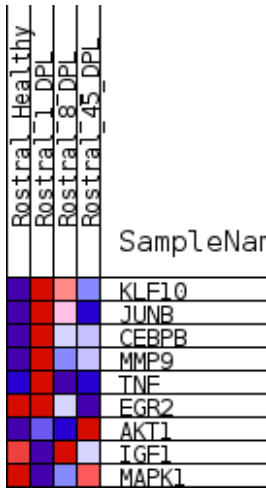
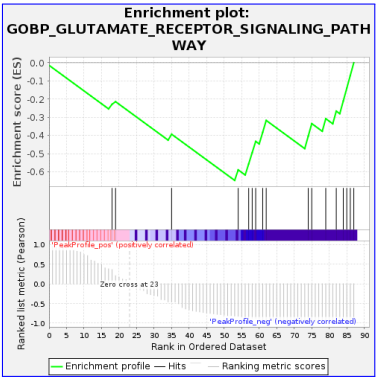
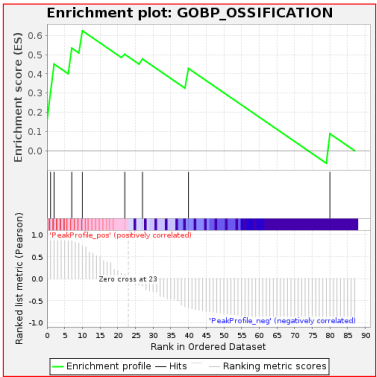


Figure S21: Enrichment plots (upper) and corresponding gene set Heatmaps (lower) of SC rostral 1 DPL peak deregulated pathways ($FDR \leq 0.1$). Up-regulated pathways are framed in red, down-regulated in blue.

2.4.2 SC rostral 8 DPL Peak Pathways

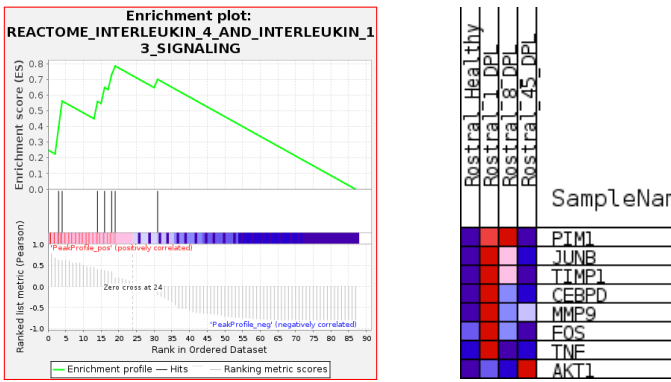
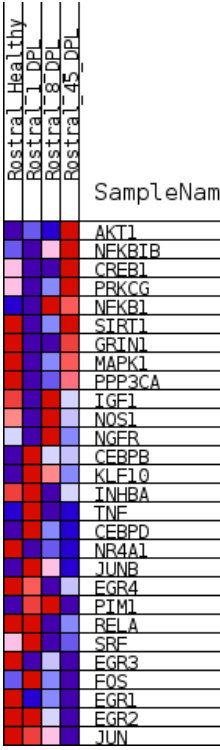
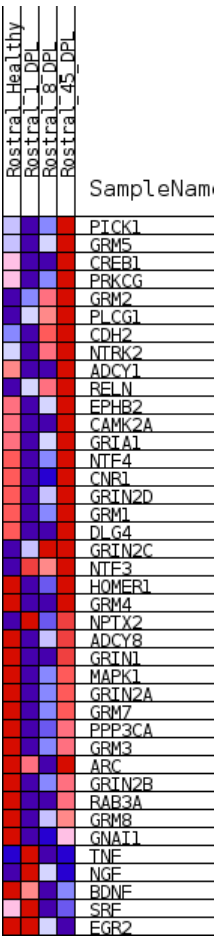
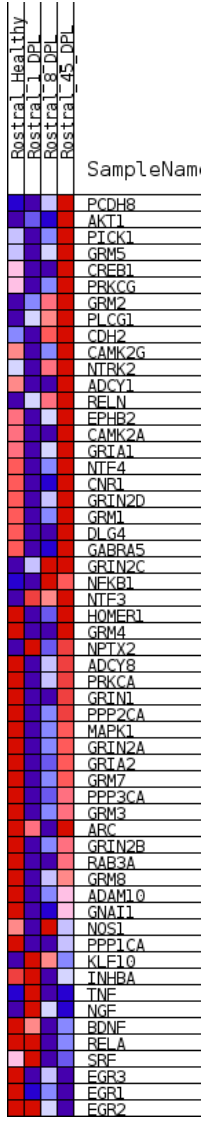
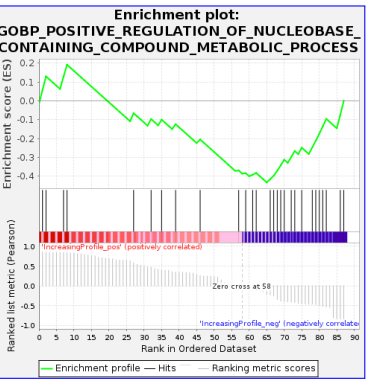
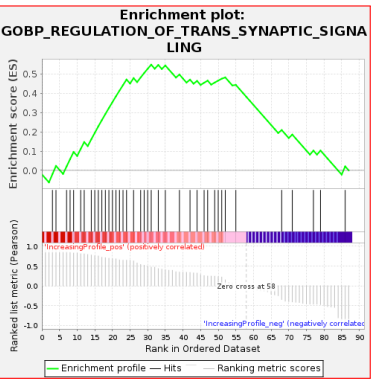
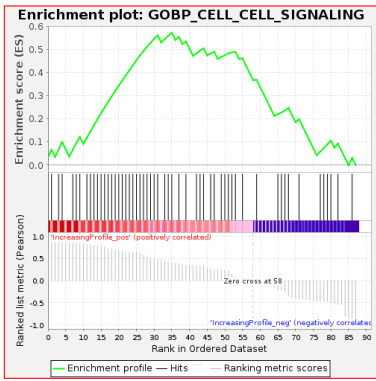
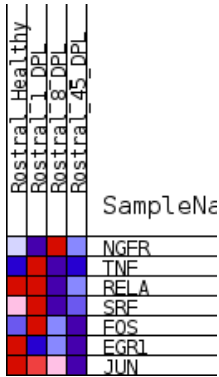
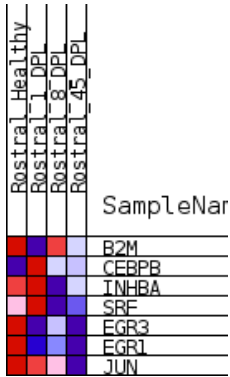
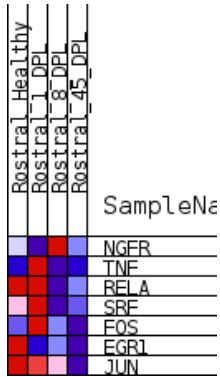
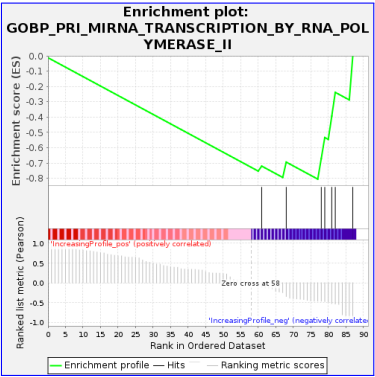
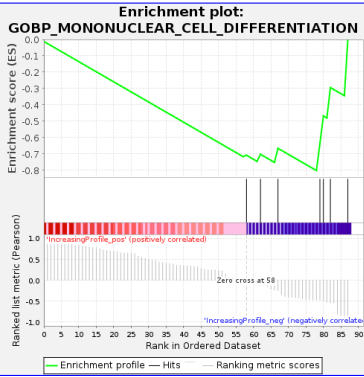
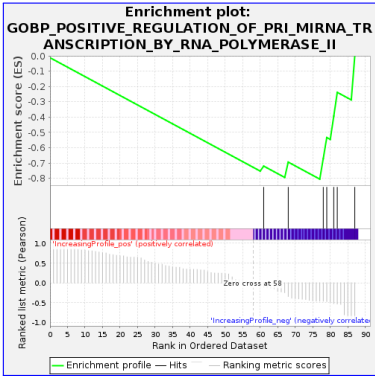


Figure S22: Enrichment plots (upper) and corresponding gene set Heatmaps (lower) of SC rostral 8 DPL peak deregulated pathways ($FDR \leq 0.1$). Up-regulated pathways are framed in red, down-regulated in blue.

2.4.3 SC rostral 45 DPL Peak Pathways





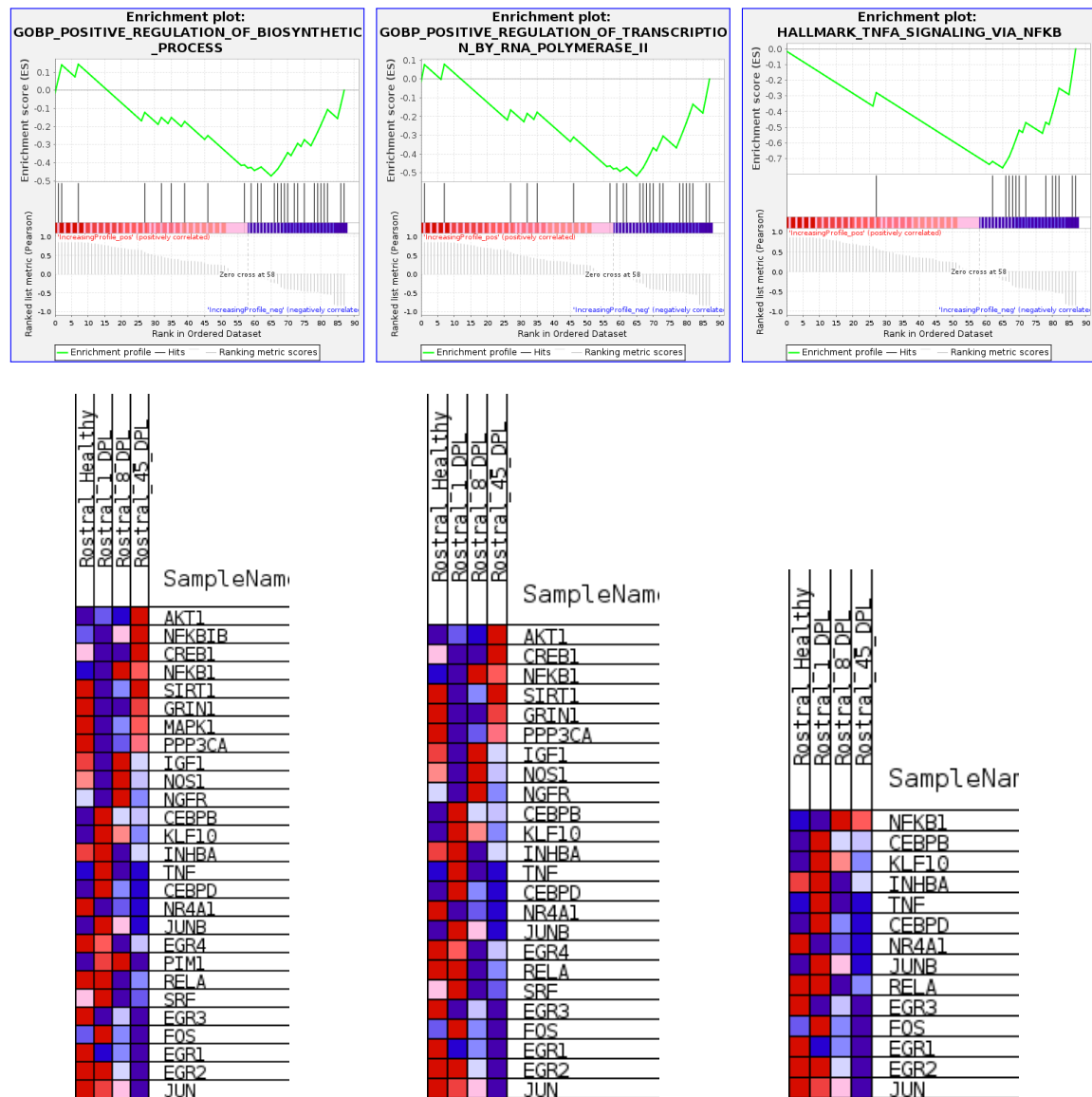
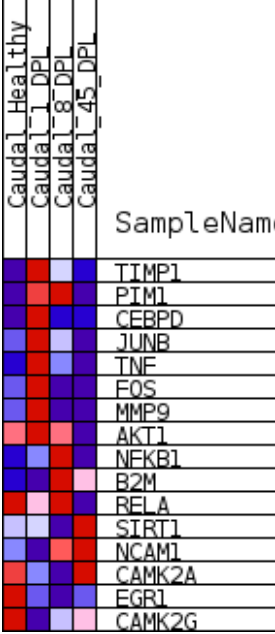
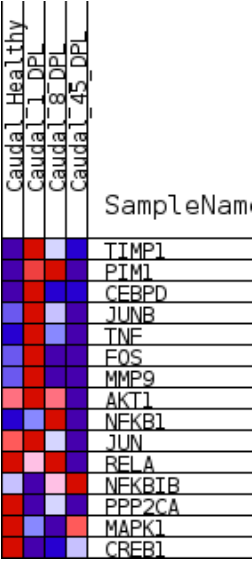
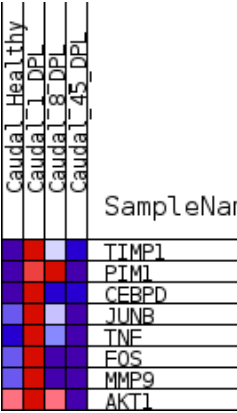
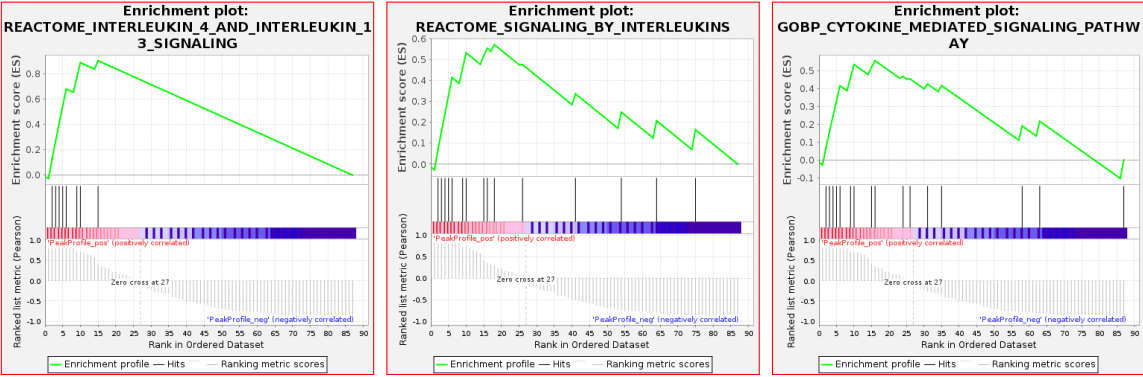
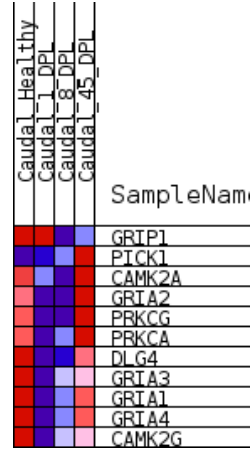
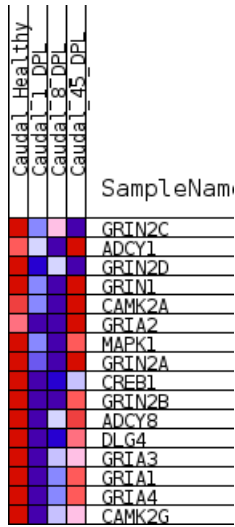
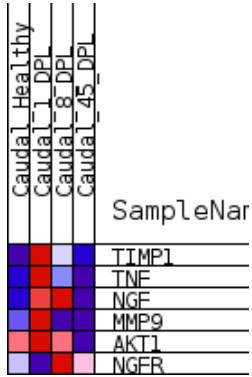
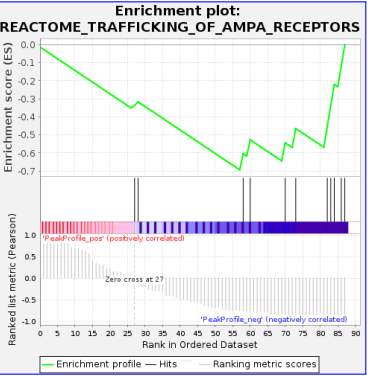
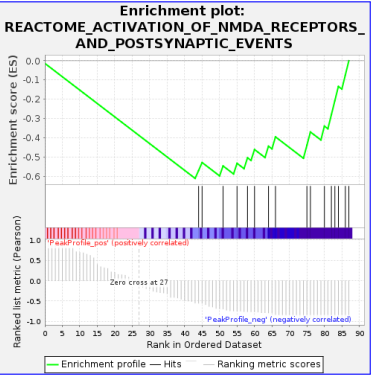
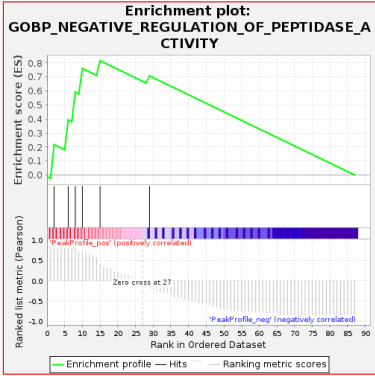
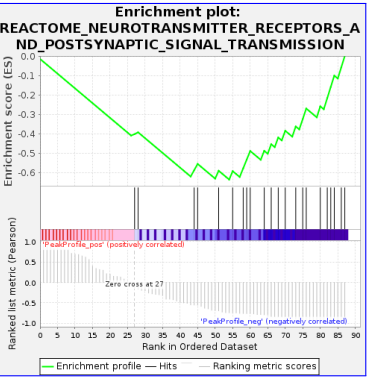
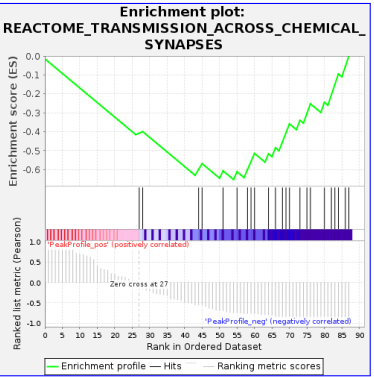
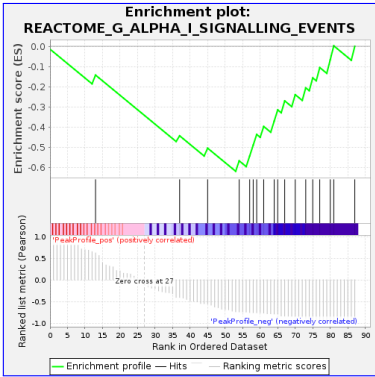


Figure S23: Enrichment plots (upper) and corresponding gene set Heatmaps (lower) of SC rostral 45 DPL peak deregulated pathways ($FDR \leq 0.1$). Up-regulated pathways are framed in red, down-regulated in blue.

2.4.4 SC caudal 1 DPL Peak Pathways







Caudal_Healthy	Caudal_1_DPL	Caudal_8_DPL	Caudal_45_DPL	SampleName
				GRM2
				PPP1CA
				ADCY1
				PPP2CA
				GRM3
				CAMK2A
				GNAI1
				PPP3CA
				MAPK1
				CNR1
				GRM7
				PRKCG
				PRKCA
				CREB1
				GRM4
				ADCY8
				GRM8
				CAMK2G

Caudal_Healthy	Caudal_1_DPL	Caudal_8_DPL	Caudal_45_DPL	SampleName
				GRIP1
				PICK1
				GRIN2C
				ADCY1
				GRIN2D
				GRIN1
				CAMK2A
				GNAI1
				GRIA2
				MAPK1
				GRIN2A
				GABRA5
				RAB3A
				PRKCG
				PRKCA
				CREB1
				GRIN2B
				ADCY8
				DLG4
				GRIA3
				GRIA1
				GRIA4
				CAMK2G

Caudal_Healthy	Caudal_1_DPL	Caudal_8_DPL	Caudal_45_DPL	SampleName
				GRIP1
				PICK1
				GRIN2C
				ADCY1
				GRIN2D
				GRIN1
				CAMK2A
				GNAI1
				GRIA2
				MAPK1
				GRIN2A
				GABRA5
				PRKCG
				PRKCA
				CREB1
				GRIN2B
				ADCY8
				DLG4
				GRIA3
				GRIA1
				GRIA4
				CAMK2G

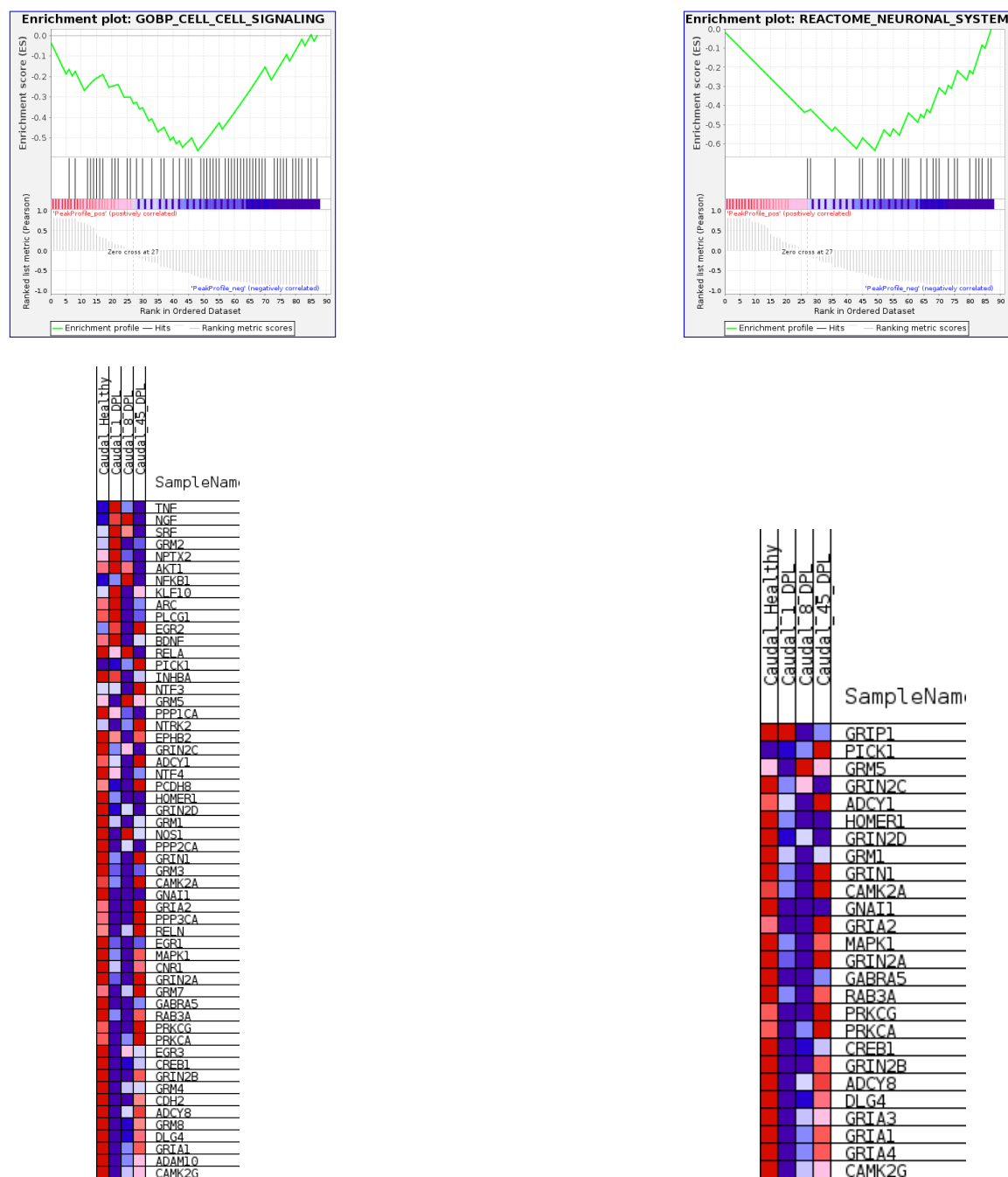
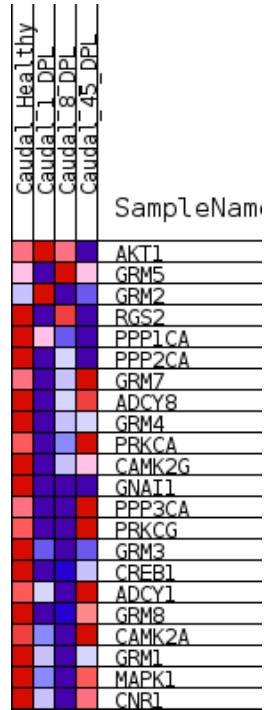
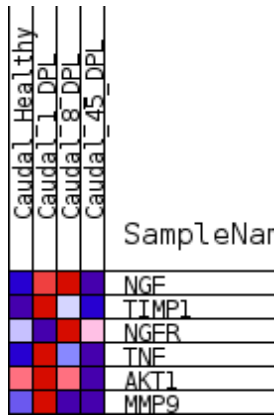
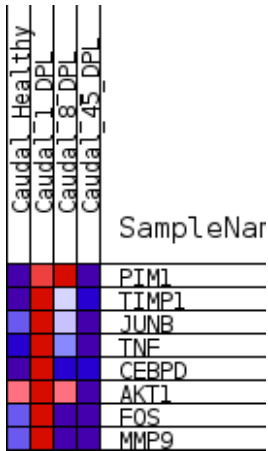
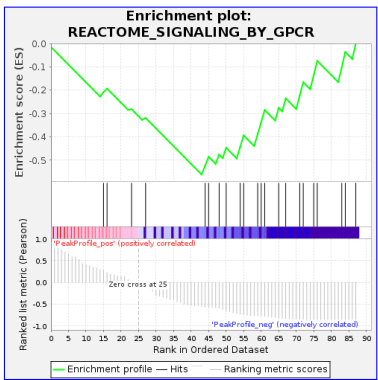
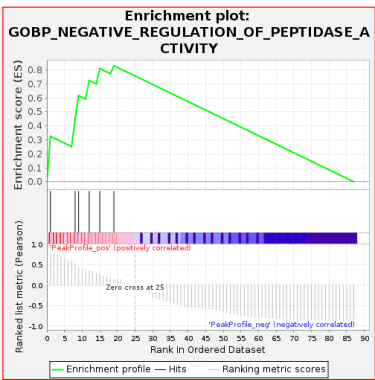
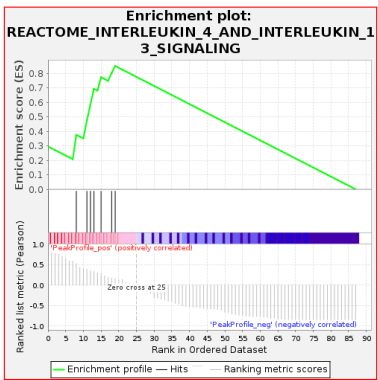
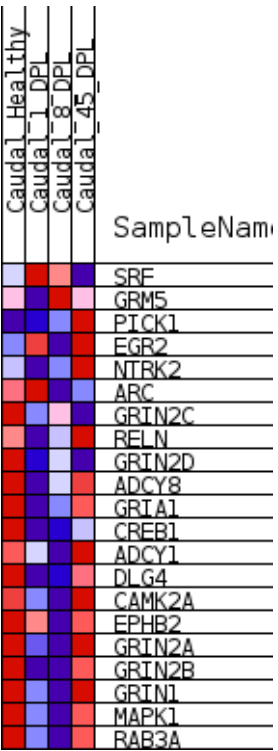
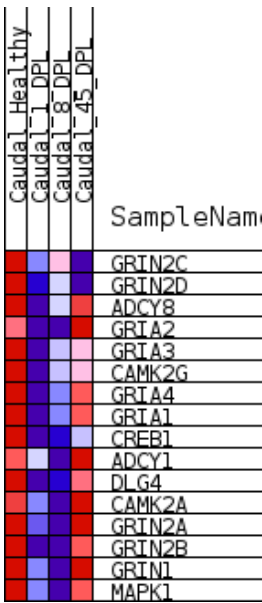
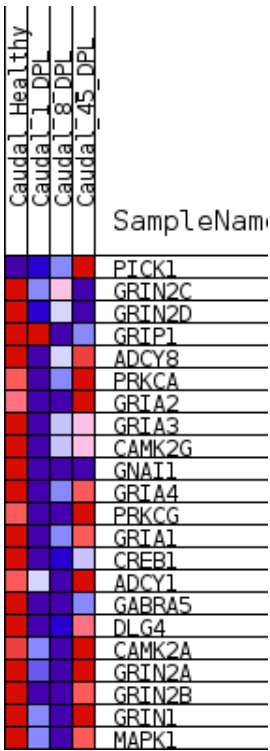
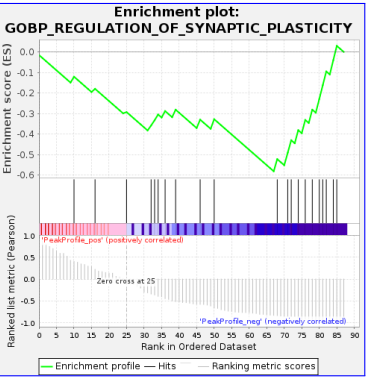
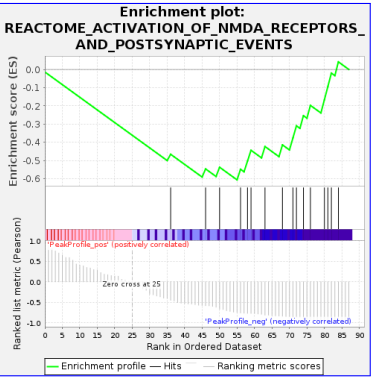
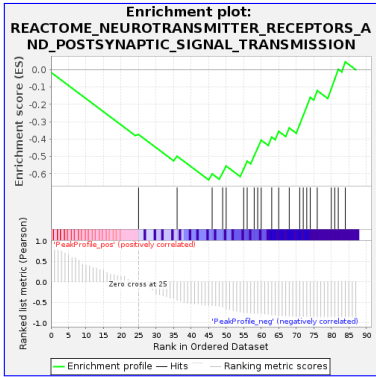
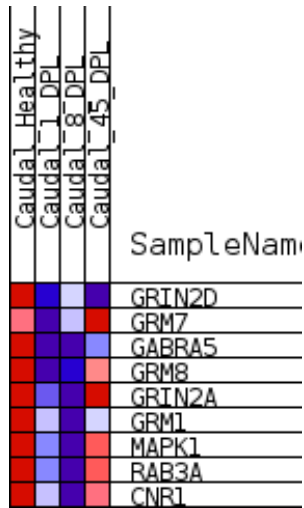
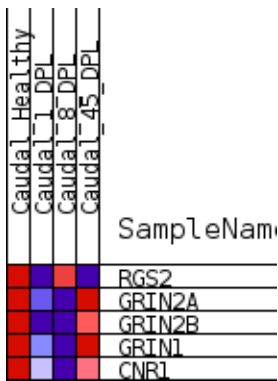
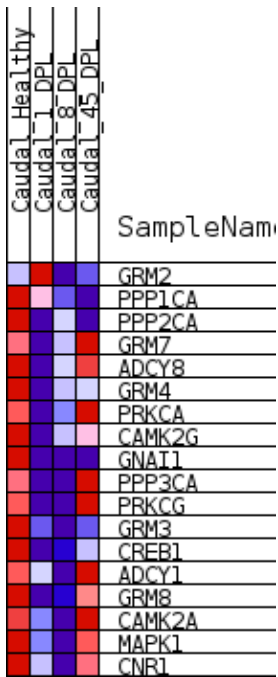
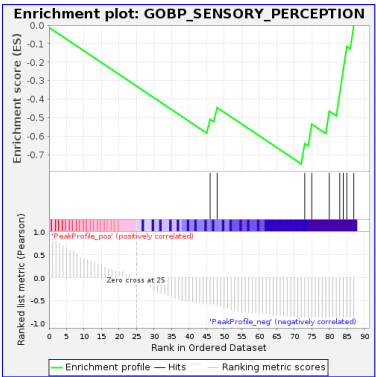
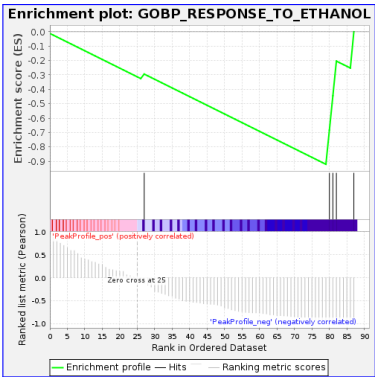
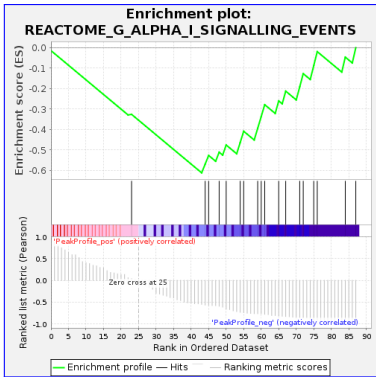


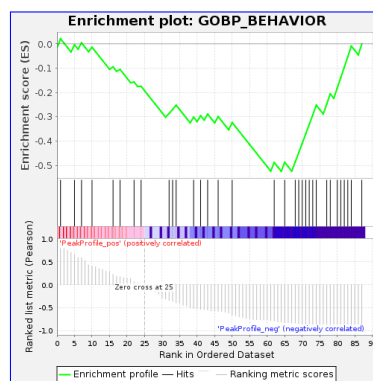
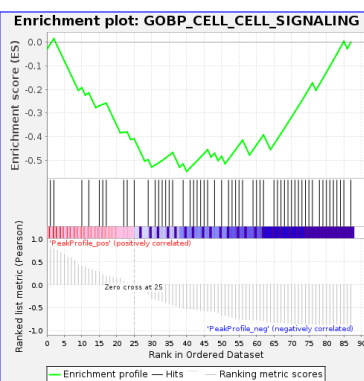
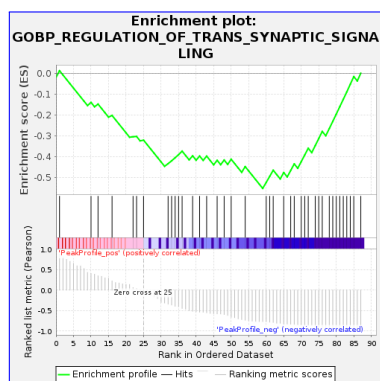
Figure S24: Enrichment plots (upper) and corresponding gene set Heatmaps (lower) of SC caudal 1 DPL peak deregulated pathways ($FDR \leq 0.1$). Up-regulated pathways are framed in red, down-regulated in blue.

2.4.5 SC caudal 8 DPL Peak Pathways









Caudal_Healthy	Caudal_1_DPL	Caudal_8_DPL	Caudal_45_DPL	SampleName
				NGF
				SRF
				TNF
				GRM5
				NPTX2
				GRM2
				PICK1
				EGR2
				NTRK2
				ARC
				PLCG1
				GRIN2C
				RELN
				NTF3
				BDNF
				GRIN2D
				GRM7
				ADCY8
				GRM4
				GNAI1
				PPP3CA
				HOMER1
				PRKCG
				GRM3
				GRIA1
				NTF4
				CREB1
				ADCY1
				DLG4
				GRM8
				CAMK2A
				EPHB2
				CDH2
				GRIN2A
				GRIN2B
				GRIN1
				GRM1
				MAPK1
				RAB3A
				CNR1

Caudal_Healthy	Caudal_1_DPL	Caudal_8_DPL	Caudal_45_DPL	SampleName
				NGF
				NFKB1
				SRF
				TNF
				AKT1
				GRM5
				RELA
				NPTX2
				GRM2
				PICK1
				NOS1
				KLF10
				EGR2
				NTRK2
				ARC
				PLCG1
				GRIN2C
				RELN
				NTF3
				EGR3
				BDNF
				PPP1CA
				PPP2CA
				GRIN2D
				GRM7
				ADCY8
				INHBA
				PCDH8
				GRM4
				PRKCA
				GRIA2
				CAMK2G
				GNAI1
				PPP3CA
				HOMER1
				PRKCG
				ADAM10
				GRM3
				GRIA1
				EGR1
				NTF4
				CREB1
				ADCY1
				GABRA5
				DLG4
				GRM8
				CAMK2A
				EPHB2
				CDH2
				GRIN2A
				GRIN2B
				GRIN1
				GRM1
				MAPK1
				RAB3A
				CNR1

Caudal_Healthy	Caudal_1_DPL	Caudal_8_DPL	Caudal_45_DPL	SampleName
				NGF
				B2M
				CEBPB
				SRF
				GRM5
				FOS
				NPTX2
				JUN
				EGR2
				NTRK2
				ARC
				RELN
				NTF3
				BDNF
				GRIN2D
				ADCY8
				HOMER1
				PRKCG
				GRIA1
				EGR1
				NTF4
				CREB1
				ADCY1
				GABRA5
				DLG4
				HPRT1
				EPHB2
				GRIN2A
				GRIN2B
				GRIN1
				GRM1
				MAPK1
				CNR1

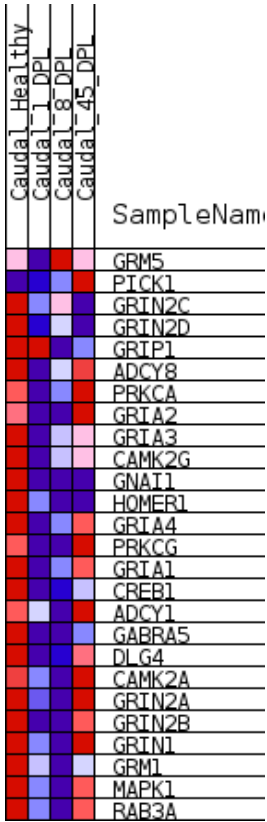
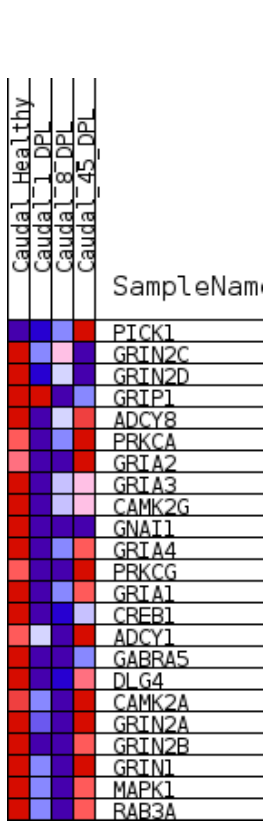
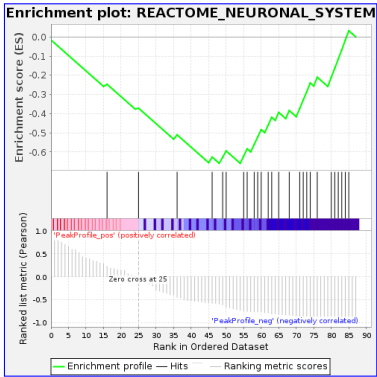
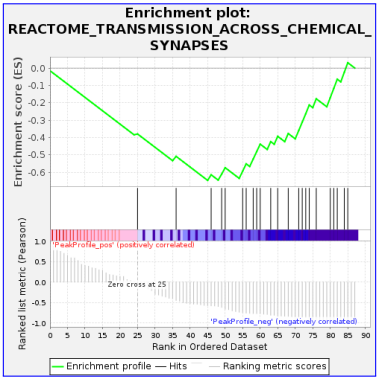
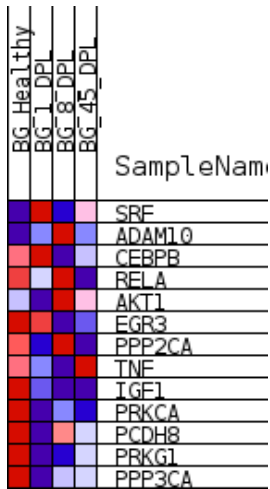
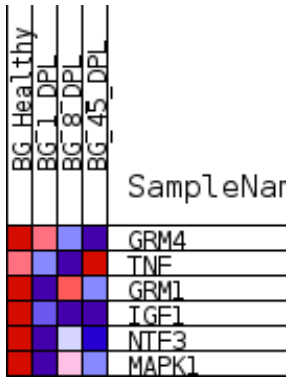
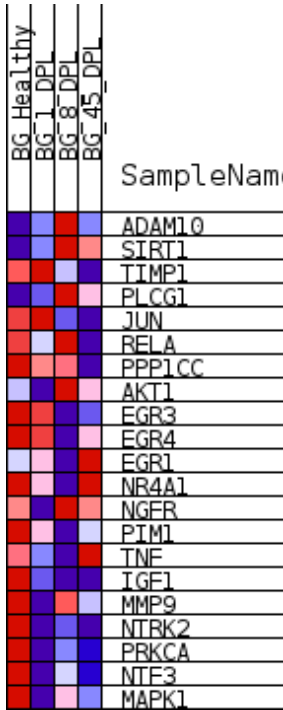
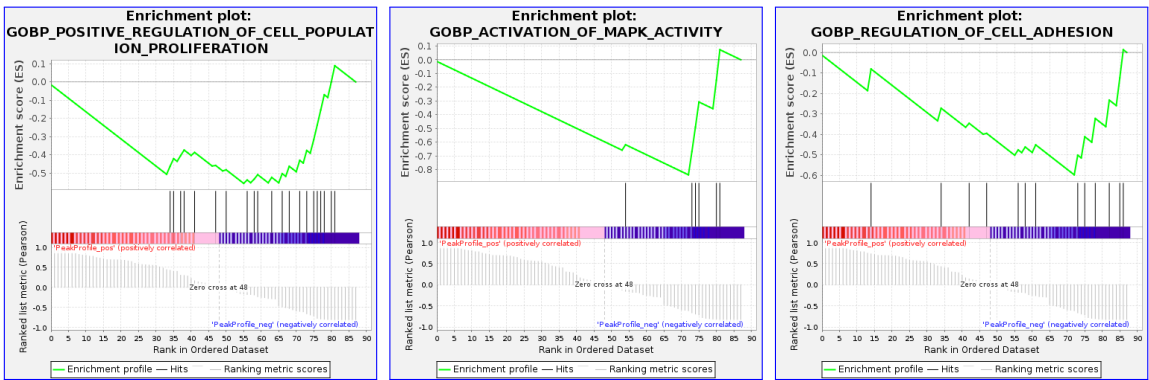
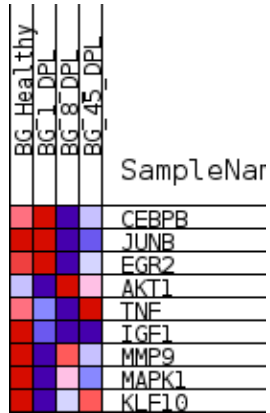
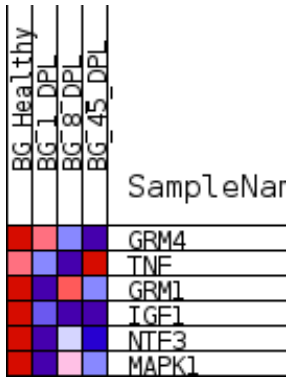
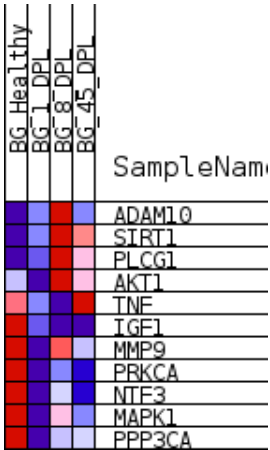
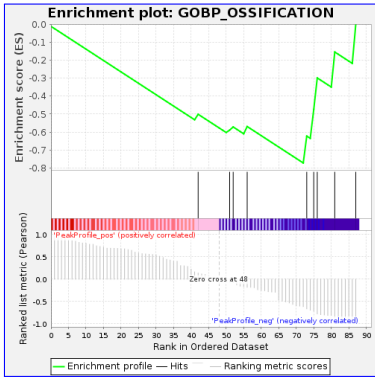
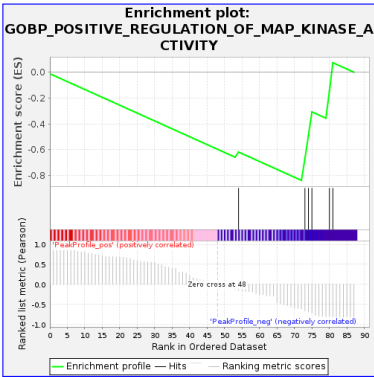
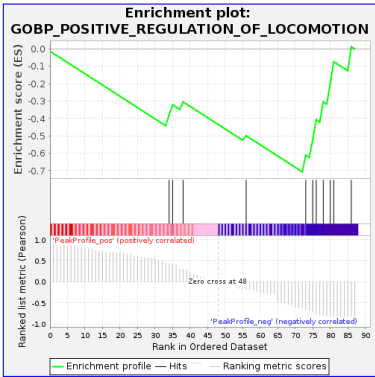
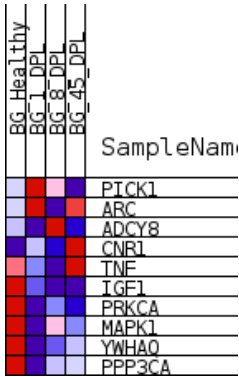
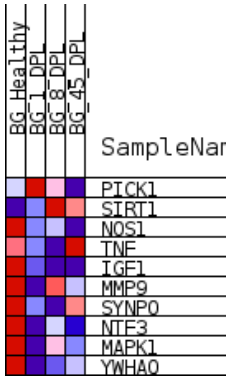
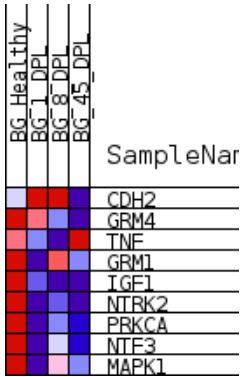
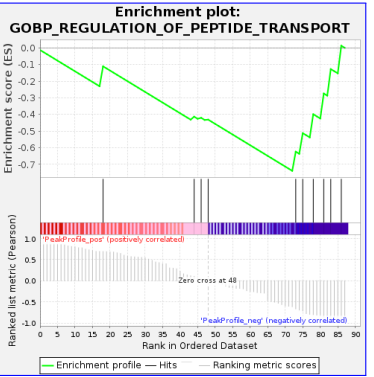
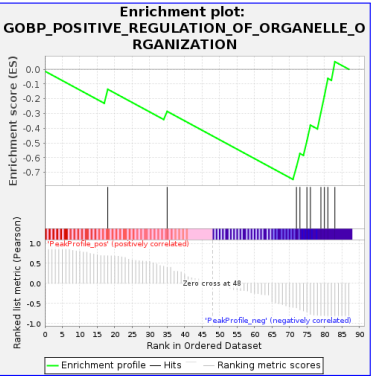
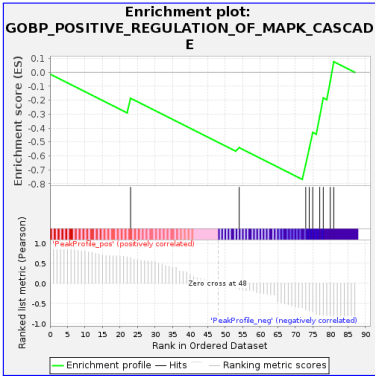


Figure S25: Enrichment plots (upper) and corresponding gene set Heatmaps (lower) of SC caudal 8 DPL peak deregulated pathways ($FDR \leq 0.1$). Up-regulated pathways are framed in red, down-regulated in blue.

2.4.6 CTX-M 1 DPL Peak Pathways







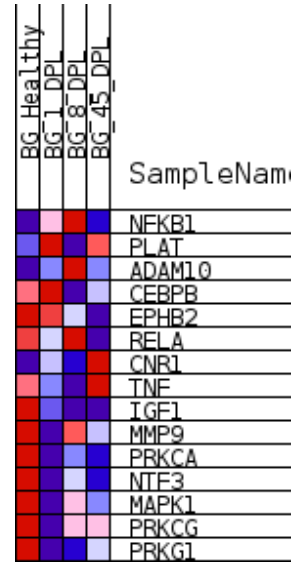
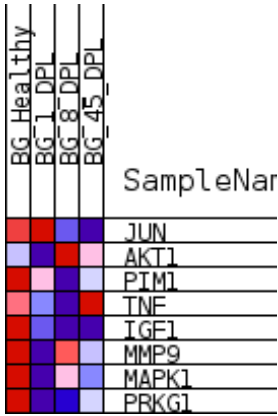
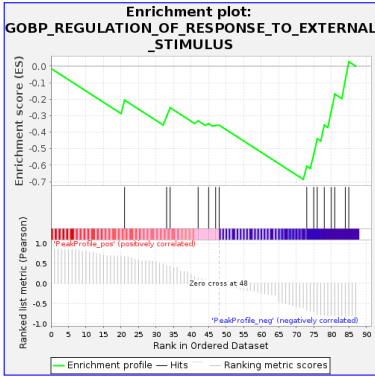
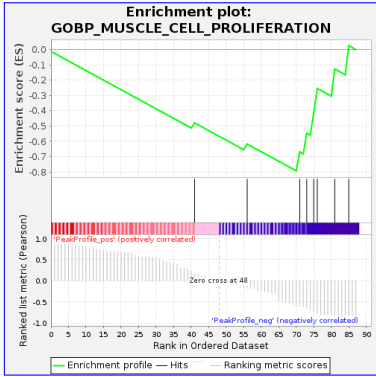
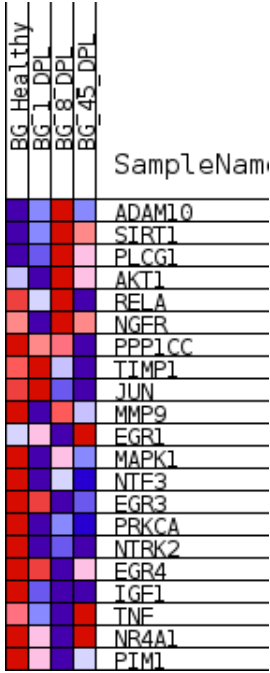
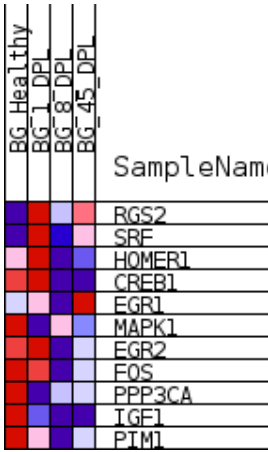
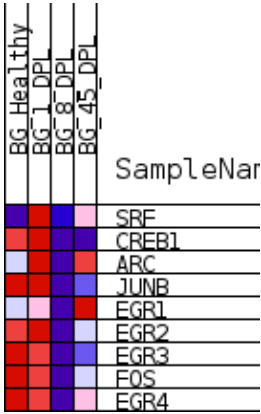
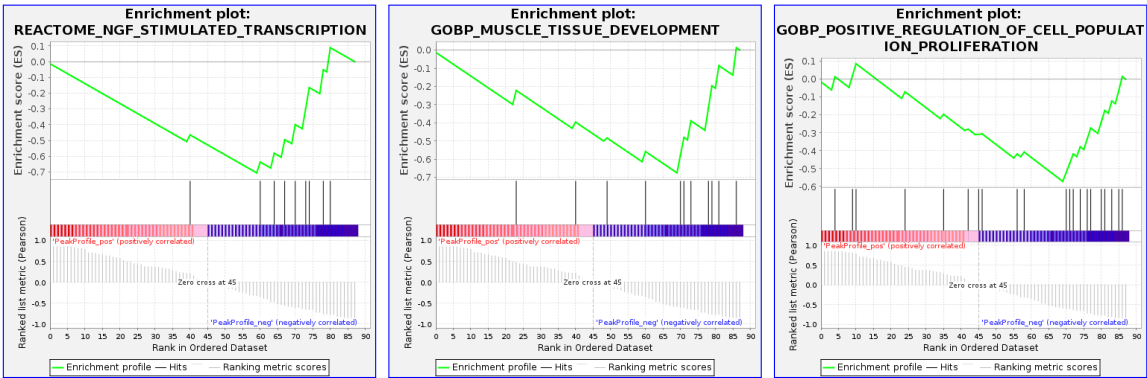


Figure S26: Enrichment plots (upper) and corresponding gene set Heatmaps (lower) of CTX-M 1 DPL peak deregulated pathways ($FDR \leq 0.1$). Up-regulated pathways are framed in red, down-regulated in blue.

2.4.7 CTX-M 8 DPL Peak Pathways



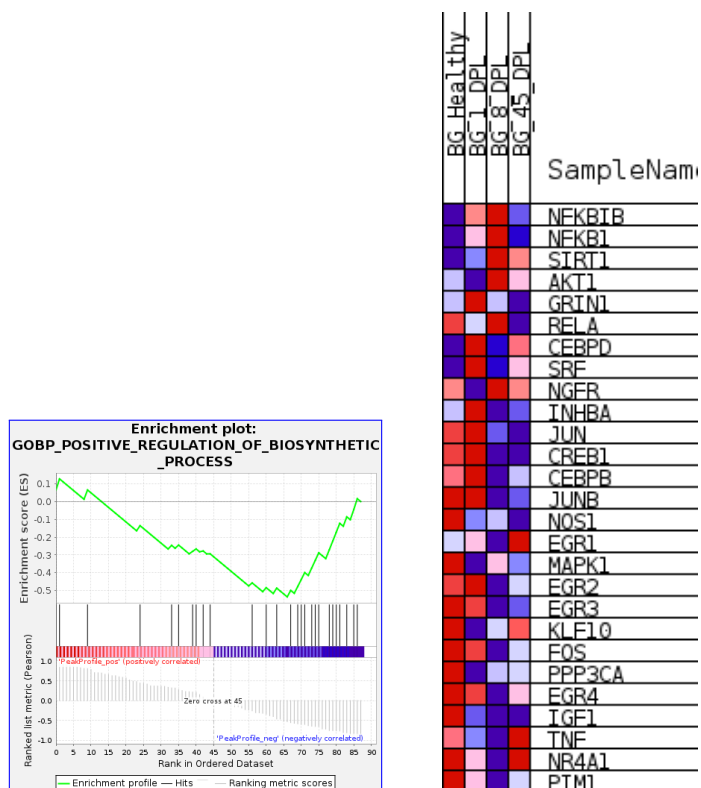
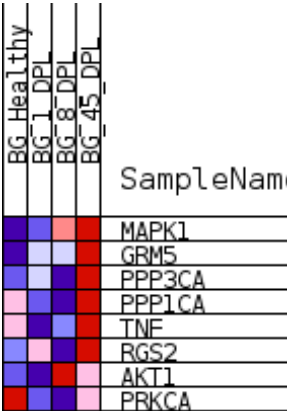
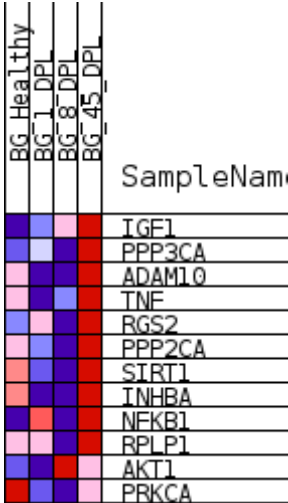
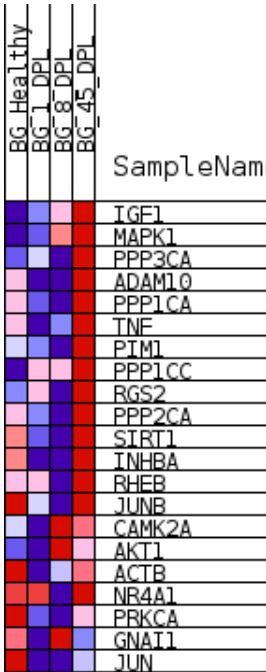
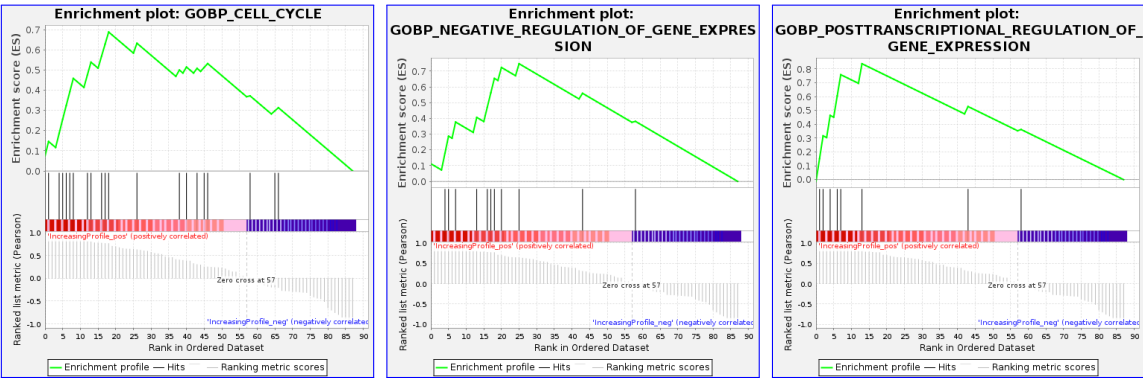


Figure S27: Enrichment plots (upper) and corresponding gene set Heatmaps (lower) of CTX-M 8 DPL peak deregulated pathways ($FDR \leq 0.1$). Up-regulated pathways are framed in red, down-regulated in blue.

2.4.8 BG 45 DPL Peak Pathways



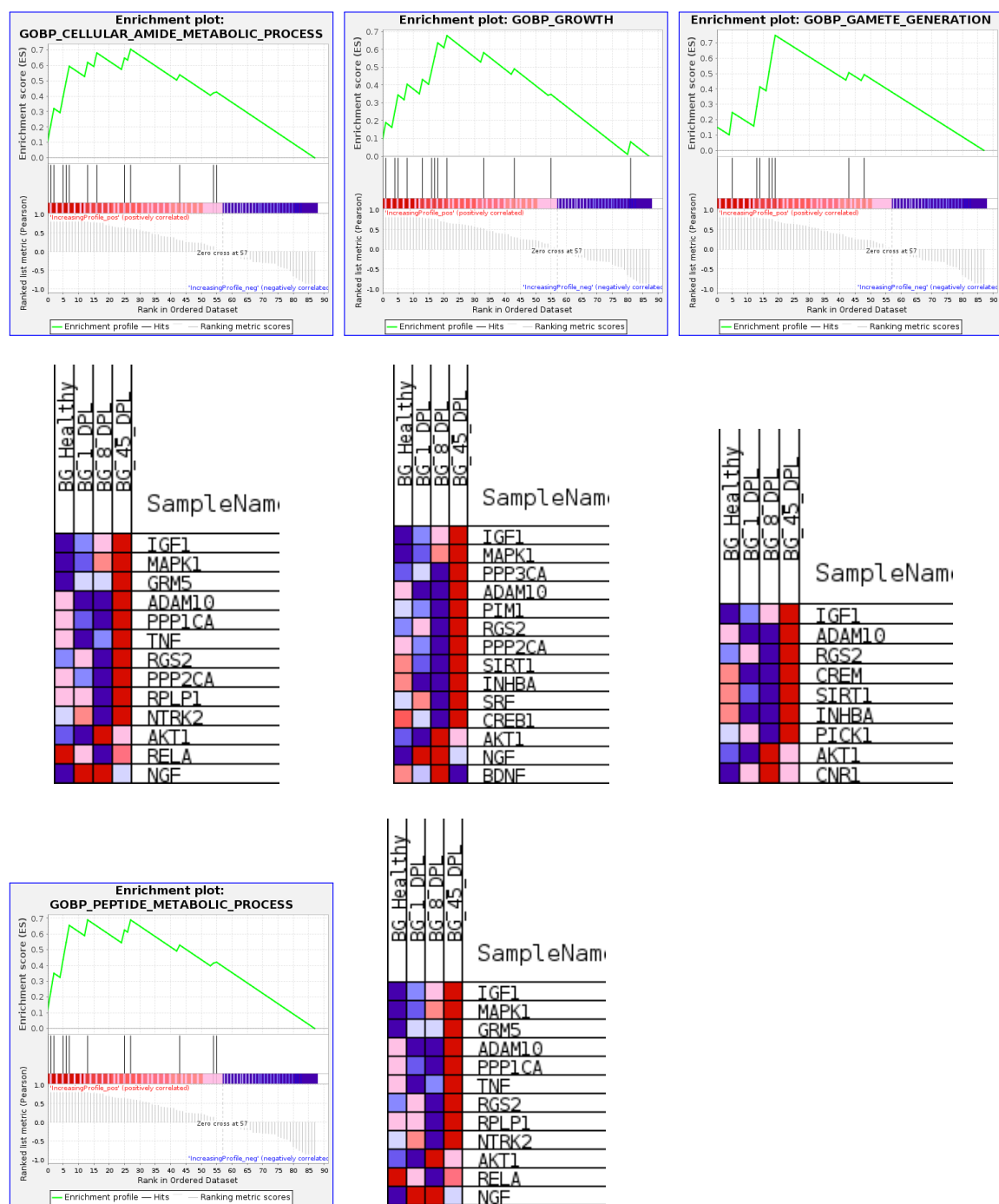


Figure S28: Enrichment plots (upper) and corresponding gene set Heatmaps (lower) of BG 45 DPL peak deregulated pathways ($FDR \leq 0.1$). Up-regulated pathways are framed in red, down-regulated in blue.

2.4.9 CB 8 DPL Pathways

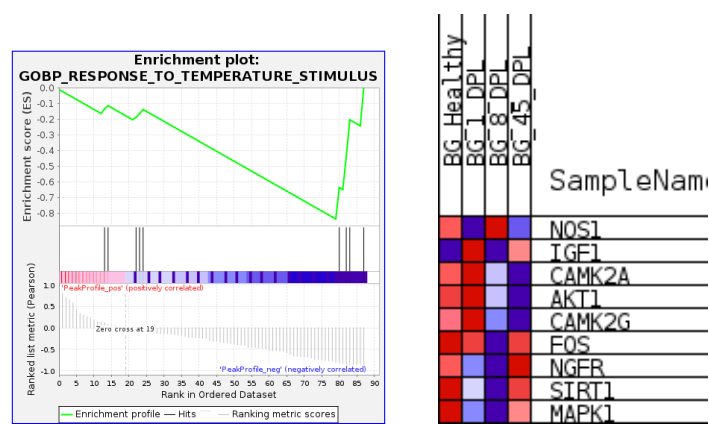
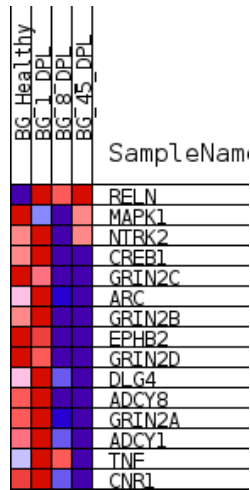
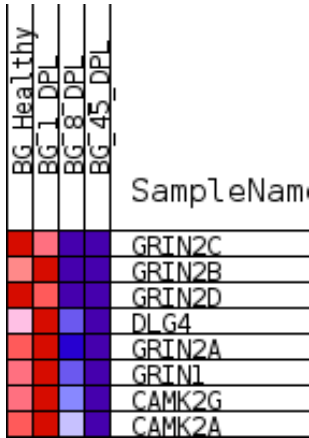
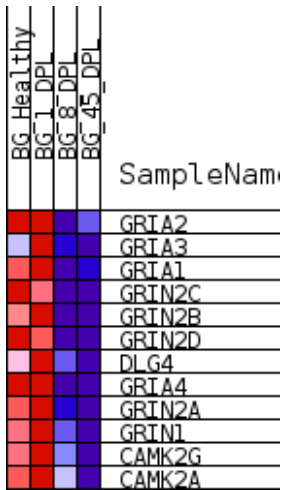
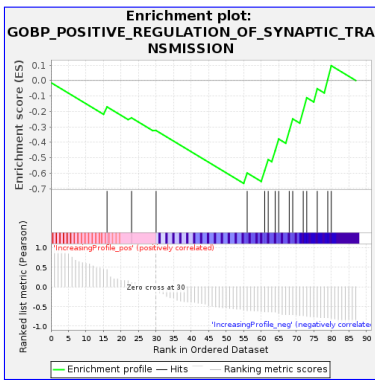
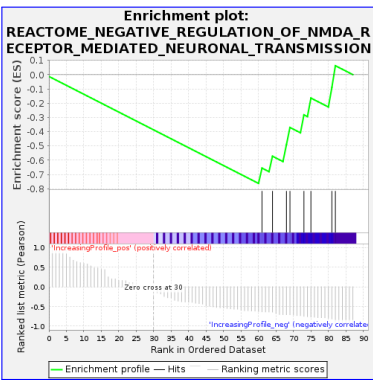
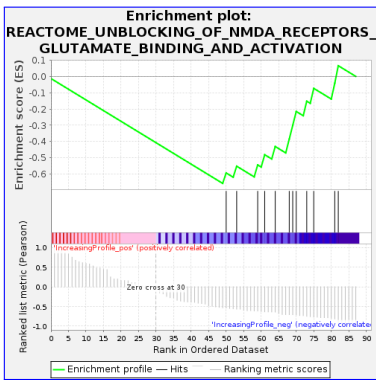


Figure S29: Enrichment plots (upper) and corresponding gene set Heatmaps (lower) of CB 8 DPL peak deregulated pathways ($FDR \leq 0.1$). Up-regulated pathways are framed in red, down-regulated in blue.

2.4.10 CB 45 DPL Peak Pathways



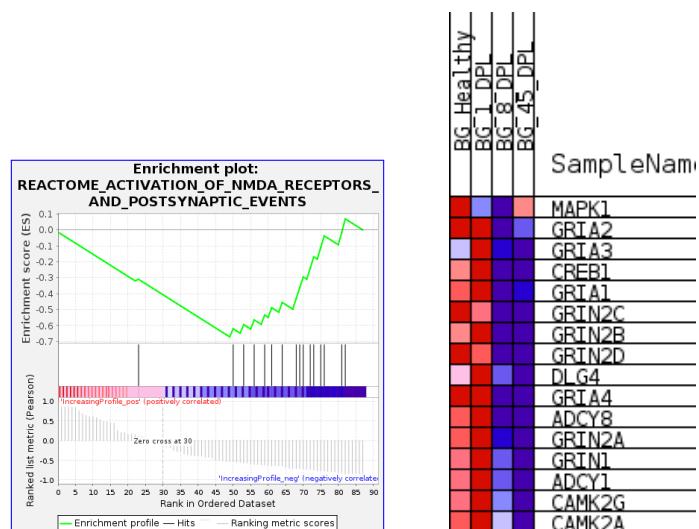


Figure S30: Enrichment plots (upper) and corresponding gene set Heatmaps (lower) of CB 45 DPL peak deregulated pathways ($FDR \leq 0.1$). Up-regulated pathways are framed in red, down-regulated in blue.

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