

Supplementary table 4: GO term analysis with all 1,612 differentially expressed transcripts

GO.ID	Term	Annotated	Significant	Expected	weight01	corrBonf	fdr
GO:1901797	negative regulation of signal transducti...	23	4	0.23	7.6e-05	0.316768	0.316768
GO:0051865	protein autoubiquitination	51	4	0.51	0.0017	1	1
GO:0015031	protein transport	1573	32	15.83	0.0018	1	1
GO:0006892	post-Golgi vesicle-mediated transport	68	4	0.68	0.0022	1	1
GO:0009225	nucleotide-sugar metabolic process	28	3	0.28	0.0027	1	1
GO:0006826	iron ion transport	29	3	0.29	0.0030	1	1
GO:0010927	cellular component assembly involved in ...	278	9	2.8	0.0049	1	1
GO:0031324	negative regulation of cellular metaboli...	2193	30	22.07	0.0056	1	1
GO:0008333	endosome to lysosome transport	37	3	0.37	0.0061	1	1
GO:0042254	ribosome biogenesis	221	7	2.22	0.0064	1	1
GO:0007029	endoplasmic reticulum organization	40	3	0.4	0.0076	1	1
GO:1901016	regulation of potassium ion transmembran...	40	3	0.4	0.0076	1	1
GO:0010976	positive regulation of neuron projection...	260	10	2.62	0.0076	1	1
GO:0050821	protein stabilization	121	5	1.22	0.0076	1	1
GO:0042981	regulation of apoptotic process	1337	23	13.46	0.0077	1	1
GO:0051893	regulation of focal adhesion assembly	43	3	0.43	0.0092	1	1
GO:0006493	protein O-linked glycosylation	43	3	0.43	0.0092	1	1
GO:0042787	protein ubiquitination involved in ubiqu...	127	5	1.28	0.0093	1	1
GO:0017157	regulation of exocytosis	162	7	1.63	0.0094	1	1
GO:0034329	cell junction assembly	149	6	1.5	0.0099	1	1
GO:0007163	establishment or maintenance of cell pol...	154	5	1.55	0.0103	1	1
GO:0006914	autophagy	432	12	4.35	0.0110	1	1
GO:0017148	negative regulation of translation	152	5	1.53	0.0111	1	1
GO:1901137	carbohydrate derivative biosynthetic pro...	571	12	5.75	0.0119	1	1
GO:0000209	protein polyubiquitination	164	6	1.65	0.0132	1	1
GO:0007030	Golgi organization	93	4	0.94	0.0145	1	1
GO:0040011	locomotion	1457	19	14.66	0.0166	1	1
GO:0031338	regulation of vesicle fusion	20	2	0.2	0.0170	1	1
GO:0097576	vacuole fusion	20	2	0.2	0.0170	1	1
GO:0033539	fatty acid beta-oxidation using acyl-CoA...	20	2	0.2	0.0170	1	1
GO:0031398	positive regulation of protein ubiquitin...	100	4	1.01	0.0185	1	1

GO:1900271	regulation of long-term synaptic potenti...	21	2	0.21	0.0187	1	1
GO:0032400	melanosome localization	21	2	0.21	0.0187	1	1
GO:1902253	regulation of intrinsic apoptotic signal...	21	2	0.21	0.0187	1	1
GO:0043161	proteasome-mediated ubiquitin-dependent ...	317	9	3.19	0.0188	1	1
GO:0006887	exocytosis	294	12	2.96	0.0190	1	1
GO:0021766	hippocampus development	57	3	0.57	0.0197	1	1
GO:0006906	vesicle fusion	78	5	0.79	0.0202	1	1
GO:0048193	Golgi vesicle transport	184	9	1.85	0.0211	1	1
GO:0008283	cell proliferation	1768	18	17.79	0.0212	1	1
GO:0048522	positive regulation of cellular process	4420	66	44.49	0.0220	1	1
GO:0032232	negative regulation of actin filament bu...	23	2	0.23	0.0222	1	1
GO:1903531	negative regulation of secretion by cell	190	5	1.91	0.0238	1	1
GO:1904292	regulation of ERAD pathway	24	2	0.24	0.0241	1	1
GO:0006536	glutamate metabolic process	24	2	0.24	0.0241	1	1
GO:0030968	endoplasmic reticulum unfolded protein r...	62	3	0.62	0.0246	1	1
GO:0006888	ER to Golgi vesicle-mediated transport	63	3	0.63	0.0257	1	1
GO:0019318	hexose metabolic process	201	5	2.02	0.0257	1	1
GO:0090075	relaxation of muscle	25	2	0.25	0.0260	1	1
GO:0070207	protein homotrimerization	25	2	0.25	0.0260	1	1
GO:0045892	negative regulation of transcription, DN...	1080	13	10.87	0.0264	1	1
GO:0050885	neuromuscular process controlling balanc...	64	3	0.64	0.0267	1	1
GO:0034622	cellular macromolecular complex assembly	741	12	7.46	0.0294	1	1
GO:0090662	ATP hydrolysis coupled transmembrane tra...	31	2	0.31	0.0298	1	1
GO:0045932	negative regulation of muscle contractio...	27	2	0.27	0.0300	1	1
GO:0032008	positive regulation of TOR signaling	27	2	0.27	0.0300	1	1
GO:0010107	potassium ion import	27	2	0.27	0.0300	1	1
GO:1901068	guanosine-containing compound metabolic ...	27	2	0.27	0.0300	1	1
GO:0030970	retrograde protein transport, ER to cyto...	27	2	0.27	0.0300	1	1
GO:0010043	response to zinc ion	28	2	0.28	0.0321	1	1
GO:0007026	negative regulation of microtubule depol...	28	2	0.28	0.0321	1	1
GO:1901381	positive regulation of potassium ion tra...	28	2	0.28	0.0321	1	1
GO:0010506	regulation of autophagy	184	6	1.85	0.0335	1	1
GO:0006403	RNA localization	141	5	1.42	0.0337	1	1

GO:0009790	embryo development	1043	12	10.5	0.0339	1	1
GO:0006829	zinc II ion transport	29	2	0.29	0.0343	1	1
GO:0032007	negative regulation of TOR signaling	29	2	0.29	0.0343	1	1
GO:0061001	regulation of dendritic spine morphogene...	30	2	0.3	0.0365	1	1
GO:0001964	startle response	30	2	0.3	0.0365	1	1
GO:1902017	regulation of cilium assembly	30	2	0.3	0.0365	1	1
GO:0031098	stress-activated protein kinase signalin...	240	3	2.42	0.0368	1	1
GO:0034645	cellular macromolecule biosynthetic proc...	4013	52	40.39	0.0372	1	1
GO:0051650	establishment of vesicle localization	147	6	1.48	0.0378	1	1
GO:0009150	purine ribonucleotide metabolic process	387	7	3.89	0.0382	1	1
GO:0007346	regulation of mitotic cell cycle	423	7	4.26	0.0384	1	1
GO:0009205	purine ribonucleoside triphosphate metab...	180	5	1.81	0.0392	1	1
GO:0099518	vesicle cytoskeletal trafficking	38	2	0.38	0.0395	1	1
GO:2000785	regulation of autophagosome assembly	32	2	0.32	0.0410	1	1
GO:0051290	protein heterotetramerization	33	2	0.33	0.0434	1	1
GO:0032781	positive regulation of ATPase activity	33	2	0.33	0.0434	1	1
GO:0006998	nuclear envelope organization	33	2	0.33	0.0434	1	1
GO:0000910	cytokinesis	118	4	1.19	0.0438	1	1
GO:0031532	actin cytoskeleton reorganization	79	3	0.8	0.0455	1	1
GO:0021884	forebrain neuron development	34	2	0.34	0.0458	1	1
GO:0097306	cellular response to alcohol	80	3	0.81	0.0470	1	1
GO:0048813	dendrite morphogenesis	131	5	1.32	0.0474	1	1
GO:0070830	bicellular tight junction assembly	35	2	0.35	0.0483	1	1
GO:0032109	positive regulation of response to nutri...	48	3	0.48	0.0490	1	1
GO:0043547	positive regulation of GTPase activity	255	8	1.79	0.00045	1	1
GO:0009225	nucleotide-sugar metabolic process	28	3	0.2	0.00098	1	1
GO:0035058	nonmotile primary cilium assembly	32	3	0.22	0.00145	1	1
GO:0016568	chromatin modification	531	6	3.73	0.00252	1	1
GO:0015031	protein transport	1573	20	11.06	0.00256	1	1
GO:0043462	regulation of ATPase activity	49	3	0.34	0.00547	1	1
GO:0032870	cellular response to hormone stimulus	448	6	3.15	0.00614	1	1
GO:0090174	organelle membrane fusion	95	3	0.67	0.00619	1	1
GO:0007264	small GTPase mediated signal transductio...	459	12	3.23	0.00658	1	1

GO:0097576	vacuole fusion	20	2	0.14	0.00858	1	1
GO:0007007	inner mitochondrial membrane organizatio...	20	2	0.14	0.00858	1	1
GO:0035268	protein mannosylation	21	2	0.15	0.00945	1	1
GO:0030182	neuron differentiation	1240	13	8.72	0.01089	1	1
GO:0045732	positive regulation of protein catabolic...	177	5	1.24	0.01102	1	1
GO:1904292	regulation of ERAD pathway	24	2	0.17	0.01224	1	1
GO:0034198	cellular response to amino acid starvati...	25	2	0.18	0.01325	1	1
GO:0021697	cerebellar cortex formation	25	2	0.18	0.01325	1	1
GO:0048011	neurotrophin TRK receptor signaling path...	26	2	0.18	0.01429	1	1
GO:0009060	aerobic respiration	56	3	0.39	0.01629	1	1
GO:0051301	cell division	599	9	4.21	0.01640	1	1
GO:0051452	intracellular pH reduction	29	2	0.2	0.01760	1	1
GO:0007067	mitotic nuclear division	391	8	2.75	0.01851	1	1
GO:0071385	cellular response to glucocorticoid stim...	30	2	0.21	0.01878	1	1
GO:0007080	mitotic metaphase plate congression	31	2	0.22	0.01998	1	1
GO:2000785	regulation of autophagosome assembly	32	2	0.22	0.02121	1	1
GO:0033108	mitochondrial respiratory chain complex ...	33	2	0.23	0.02248	1	1
GO:0046579	positive regulation of Ras protein signa...	34	2	0.24	0.02378	1	1
GO:0031572	G2 DNA damage checkpoint	35	2	0.25	0.02510	1	1
GO:0030501	positive regulation of bone mineralizati...	35	2	0.25	0.02510	1	1
GO:0006468	protein phosphorylation	1645	14	11.57	0.02682	1	1
GO:0050953	sensory perception of light stimulus	132	2	0.93	0.02781	1	1
GO:0008333	endosome to lysosome transport	37	2	0.26	0.02784	1	1
GO:0042073	intraciliary transport	38	2	0.27	0.02926	1	1
GO:0019725	cellular homeostasis	710	11	4.99	0.03059	1	1
GO:0071300	cellular response to retinoic acid	39	2	0.27	0.03070	1	1
GO:0051898	negative regulation of protein kinase B ...	39	2	0.27	0.03070	1	1
GO:0006754	ATP biosynthetic process	40	2	0.28	0.03217	1	1
GO:0051262	protein tetramerization	133	4	0.94	0.03313	1	1
GO:1904356	regulation of telomere maintenance via t...	48	2	0.34	0.03450	1	1
GO:0051649	establishment of localization in cell	2135	22	15.01	0.03553	1	1
GO:0006821	chloride transport	93	3	0.65	0.03644	1	1
GO:0006493	protein O-linked glycosylation	43	2	0.3	0.03674	1	1

GO:0007420	brain development	521	7	3.66	0.03724	1	1
GO:0043271	negative regulation of ion transport	130	3	0.91	0.04133	1	1
GO:0006914	autophagy	432	8	3.04	0.04142	1	1
GO:0007265	Ras protein signal transduction	267	7	1.88	0.04295	1	1
GO:0008156	negative regulation of DNA replication	49	2	0.34	0.04657	1	1
GO:1901655	cellular response to ketone	50	2	0.35	0.04829	1	1
GO:0009225	nucleotide-sugar metabolic process	28	6	0.48	6.6e-06	0.0275088	0.0275088
GO:0015031	protein transport	1573	52	26.89	1.6e-05	0.066688	0.033344
GO:0097576	vacuole fusion	20	4	0.34	0.00033	1	0.40638
GO:0008333	endosome to lysosome transport	37	5	0.63	0.00039	1	0.40638
GO:1901797	negative regulation of signal transducti...	23	4	0.39	0.00057	1	0.47237333
GO:1904292	regulation of ERAD pathway	24	4	0.41	0.00068	1	0.47237333
GO:0006493	protein O-linked glycosylation	43	5	0.74	0.00080	1	0.47634286
GO:0006914	autophagy	432	20	7.39	0.00108	1	0.55573333
GO:0010976	positive regulation of neuron projection...	260	13	4.44	0.00120	1	0.55573333
GO:0043547	positive regulation of GTPase activity	255	12	4.36	0.00142	1	0.591856
GO:0017157	regulation of exocytosis	162	10	2.77	0.00187	1	0.61626857
GO:1901137	carbohydrate derivative biosynthetic pro...	571	20	9.76	0.00192	1	0.61626857
GO:2000785	regulation of autophagosome assembly	32	4	0.55	0.00207	1	0.61626857
GO:0035058	nonmotile primary cilium assembly	32	4	0.55	0.00207	1	0.61626857
GO:0016197	endosomal transport	199	13	3.4	0.00248	1	0.64372444
GO:0051262	protein tetramerization	133	8	2.27	0.00254	1	0.64372444
GO:0090174	organelle membrane fusion	95	9	1.62	0.00272	1	0.64372444
GO:0007264	small GTPase mediated signal transductio...	459	18	7.85	0.00278	1	0.64372444
GO:0031324	negative regulation of cellular metaboli...	2193	49	37.49	0.00323	1	0.70856
GO:0017148	negative regulation of translation	152	7	2.6	0.00358	1	0.746072
GO:0051301	cell division	599	20	10.24	0.00414	1	0.82169143
GO:0042981	regulation of apoptotic process	1337	33	22.86	0.00442	1	0.83738909
GO:0007029	endoplasmic reticulum organization	40	4	0.68	0.00472	1	0.85534609
GO:0035268	protein mannosylation	21	3	0.36	0.00524	1	0.91001333
GO:0032418	lysosome localization	51	3	0.87	0.00577	1	0.9619744
GO:0051893	regulation of focal adhesion assembly	43	4	0.74	0.00613	1	0.98268615
GO:0048522	positive regulation of cellular process	4420	100	75.56	0.00689	1	1

GO:0043161	proteasome-mediated ubiquitin-dependent ...	317	15	5.42	0.00760	1	1
GO:0034198	cellular response to amino acid starvati...	25	3	0.43	0.00862	1	1
GO:0007265	Ras protein signal transduction	267	9	4.56	0.00893	1	1
GO:0010639	negative regulation of organelle organiz...	304	12	5.2	0.00943	1	1
GO:0006892	post-Golgi vesicle-mediated transport	68	4	1.16	0.00960	1	1
GO:0031398	positive regulation of protein ubiquitin...	100	6	1.71	0.01021	1	1
GO:1901068	guanosine-containing compound metabolic ...	27	3	0.46	0.01069	1	1
GO:0032008	positive regulation of TOR signaling	27	3	0.46	0.01069	1	1
GO:0051865	protein autoubiquitination	51	4	0.87	0.01116	1	1
GO:1901381	positive regulation of potassium ion tra...	28	3	0.48	0.01183	1	1
GO:0001895	retina homeostasis	49	3	0.84	0.01196	1	1
GO:0097306	cellular response to alcohol	80	5	1.37	0.01200	1	1
GO:0016482	cytoplasmic transport	920	32	15.73	0.01255	1	1
GO:0006826	iron ion transport	29	3	0.5	0.01303	1	1
GO:0007067	mitotic nuclear division	391	13	6.68	0.01312	1	1
GO:0010605	negative regulation of macromolecule met...	2198	47	37.58	0.01382	1	1
GO:0034654	nucleobase-containing compound biosynthe...	3378	62	57.75	0.01424	1	1
GO:1902017	regulation of cilium assembly	30	3	0.51	0.01429	1	1
GO:0031098	stress-activated protein kinase signalin...	240	4	4.1	0.01458	1	1
GO:0034329	cell junction assembly	149	8	2.55	0.01688	1	1
GO:0006906	vesicle fusion	78	6	1.33	0.01701	1	1
GO:0051028	mRNA transport	88	5	1.5	0.01753	1	1
GO:0050821	protein stabilization	121	6	2.07	0.01784	1	1
GO:0006998	nuclear envelope organization	33	3	0.56	0.01850	1	1
GO:0032781	positive regulation of ATPase activity	33	3	0.56	0.01850	1	1
GO:0051290	protein heterotetramerization	33	3	0.56	0.01850	1	1
GO:0033108	mitochondrial respiratory chain complex ...	33	3	0.56	0.01850	1	1
GO:0008283	cell proliferation	1768	28	30.22	0.01857	1	1
GO:0010927	cellular component assembly involved in ...	278	16	4.75	0.02025	1	1
GO:0048813	dendrite morphogenesis	131	6	2.24	0.02143	1	1
GO:0030968	endoplasmic reticulum unfolded protein r...	62	4	1.06	0.02154	1	1
GO:0007030	Golgi organization	93	5	1.59	0.02172	1	1
GO:0042787	protein ubiquitination involved in ubiqu...	127	6	2.17	0.02206	1	1

GO:0006888	ER to Golgi vesicle-mediated transport	63	4	1.08	0.02270	1	1
GO:0030433	ER-associated ubiquitin-dependent protei...	63	4	1.08	0.02270	1	1
GO:0045921	positive regulation of exocytosis	86	5	1.47	0.02313	1	1
GO:0030099	myeloid cell differentiation	339	7	5.8	0.02353	1	1
GO:0051649	establishment of localization in cell	2135	66	36.5	0.02443	1	1
GO:0045732	positive regulation of protein catabolic...	177	7	3.03	0.02615	1	1
GO:0042254	ribosome biogenesis	221	7	3.78	0.02671	1	1
GO:0007160	cell-matrix adhesion	172	8	2.94	0.02849	1	1
GO:0071300	cellular response to retinoic acid	39	3	0.67	0.02876	1	1
GO:0042771	intrinsic apoptotic signaling pathway in...	39	3	0.67	0.02876	1	1
GO:0043462	regulation of ATPase activity	49	5	0.84	0.02948	1	1
GO:0043271	negative regulation of ion transport	130	4	2.22	0.02985	1	1
GO:1901016	regulation of potassium ion transmembran...	40	3	0.68	0.03071	1	1
GO:0045806	negative regulation of endocytosis	40	3	0.68	0.03071	1	1
GO:0031122	cytoplasmic microtubule organization	40	3	0.68	0.03071	1	1
GO:0006915	apoptotic process	1659	44	28.36	0.03239	1	1
GO:0009790	embryo development	1043	16	17.83	0.03326	1	1
GO:0006473	protein acetylation	170	4	2.91	0.03357	1	1
GO:0072503	cellular divalent inorganic cation homeo...	375	9	6.41	0.03374	1	1
GO:0002444	myeloid leukocyte mediated immunity	77	3	1.32	0.03383	1	1
GO:0019076	viral release from host cell	33	2	0.56	0.03385	1	1
GO:0042384	cilium assembly	193	11	3.3	0.03476	1	1
GO:0016236	macroautophagy	302	12	5.16	0.03624	1	1
GO:1901888	regulation of cell junction assembly	65	6	1.11	0.03662	1	1
GO:0006468	protein phosphorylation	1645	31	28.12	0.03664	1	1
GO:0031623	receptor internalization	80	4	1.37	0.03687	1	1
GO:0016239	positive regulation of macroautophagy	43	3	0.74	0.03696	1	1
GO:0090316	positive regulation of intracellular pro...	239	6	4.09	0.03706	1	1
GO:0007346	regulation of mitotic cell cycle	423	12	7.23	0.03729	1	1
GO:0006897	endocytosis	481	14	8.22	0.03951	1	1
GO:0019725	cellular homeostasis	710	19	12.14	0.04008	1	1
GO:0006487	protein N-linked glycosylation	69	5	1.18	0.04101	1	1
GO:0007163	establishment or maintenance of cell pol...	154	5	2.63	0.04143	1	1

GO:0010501	RNA secondary structure unwinding	45	3	0.77	0.04147	1	1
GO:0016568	chromatin modification	531	11	9.08	0.04153	1	1
GO:0000209	protein polyubiquitination	164	7	2.8	0.04239	1	1
GO:0045893	positive regulation of transcription, DN...	1382	21	23.63	0.04288	1	1
GO:0001649	osteoblast differentiation	201	5	3.44	0.04511	1	1
GO:0042987	amyloid precursor protein catabolic proc...	20	2	0.34	0.04521	1	1
GO:0033539	fatty acid beta-oxidation using acyl-CoA...	20	2	0.34	0.04521	1	1
GO:0007007	inner mitochondrial membrane organizatio...	20	2	0.34	0.04521	1	1
GO:0031338	regulation of vesicle fusion	20	2	0.34	0.04521	1	1
GO:0071108	protein K48-linked deubiquitination	20	2	0.34	0.04521	1	1
GO:0006623	protein targeting to vacuole	20	2	0.34	0.04521	1	1
GO:0040011	locomotion	1457	26	24.91	0.04535	1	1
GO:0051348	negative regulation of transferase activ...	280	5	4.79	0.04555	1	1
GO:0043408	regulation of MAPK cascade	621	7	10.62	0.04566	1	1
GO:0009150	purine ribonucleotide metabolic process	387	11	6.62	0.04873	1	1
GO:0034622	cellular macromolecular complex assembly	741	23	12.67	0.04906	1	1
GO:1900271	regulation of long-term synaptic potenti...	21	2	0.36	0.04942	1	1
GO:0032400	melanosome localization	21	2	0.36	0.04942	1	1
GO:1902253	regulation of intrinsic apoptotic signal...	21	2	0.36	0.04942	1	1

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NA	upreg
NA	upreg
NA	upreg
Eif2b2;Rapgef	downreg
Guk1;Dpm1;C	downreg
Hap1;Bbs7;Ce	downreg
Bag6;Kdm3b;#	downreg
Rab7;Ptprn;Gf	downreg
Hnrnpu;Pxx;O	downreg
Mstn;Hnrnpu;	downreg
Rab7;Ubqln1;l	downreg
Rab7;Itprkb;Dii	downreg

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