

Table S3. Enriched GO biological process terms in down-regulated genes

GO ID	Enrichment (p-value)	Number down-regulated	Total	Term	Ontology
GO:0007268	1.9E-23	92	296	synaptic transmission	BP
GO:0005887	2.0E-21	127	524	integral component of plasma membrane	CC
GO:0005886	9.9E-19	289	1763	plasma membrane	CC
GO:0045211	6.4E-18	55	152	postsynaptic membrane	CC
GO:0030054	3.1E-16	88	348	cell junction	CC
GO:0016021	1.0E-14	330	2216	integral component of membrane	CC
GO:0007218	4.4E-12	26	55	neuropeptide signaling pathway	BP
GO:0007186	5.5E-12	61	236	G-protein coupled receptor signaling pathway	BP
GO:0006811	2.8E-10	46	169	ion transport	BP
GO:0043204	3.7E-09	24	62	perikaryon	CC
GO:0051930	1.1E-08	14	24	regulation of sensory perception of pain	BP
GO:0042734	1.5E-08	23	61	presynaptic membrane	CC
GO:0070588	2.4E-08	27	83	calcium ion transmembrane transport	BP
GO:0005216	3.4E-08	26	78	ion channel activity	MF
GO:0005509	3.8E-08	73	377	calcium ion binding	MF
GO:0007187	5.3E-08	14	26	G-protein coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger	BP
GO:0007165	8.2E-08	114	692	signal transduction	BP
GO:0051965	8.3E-08	20	52	positive regulation of synapse assembly	BP
GO:0007156	8.8E-08	19	48	homophilic cell adhesion via plasma membrane adhesion molecules	BP
GO:0005576	1.4E-07	77	412	extracellular region	CC
GO:0030594	2.2E-07	13	25	neurotransmitter receptor activity	MF
GO:0031226	2.2E-07	10	15	intrinsic component of plasma membrane	CC
GO:0005230	2.3E-07	13	25	extracellular ligand-gated ion channel activity	MF

GO:0004930	2.4E-07	27	91	G-protein coupled receptor activity	MF
GO:0008146	2.4E-07	16	37	sulfotransferase activity	MF
GO:0008076	3.6E-07	24	75	voltage-gated potassium channel complex	CC
GO:0061337	3.9E-07	22	66	cardiac conduction	BP
GO:0007409	5.0E-07	24	78	axonogenesis	BP
GO:0071805	5.1E-07	21	62	potassium ion transmembrane transport	BP
GO:0007626	5.1E-07	22	67	locomotory behavior	BP
GO:0031290	8.6E-07	10	16	retinal ganglion cell axon guidance	BP
GO:0007200	1.0E-06	11	20	phospholipase C-activating G-protein coupled receptor signaling pathway	BP
GO:0006813	1.0E-06	27	96	potassium ion transport	BP
GO:0007193	1.7E-06	15	37	adenylate cyclase-inhibiting G-protein coupled receptor signaling pathway	BP
GO:0004890	2.6E-06	10	18	GABA-A receptor activity	MF
GO:0042755	3.5E-06	10	18	eating behavior	BP
GO:0016079	3.9E-06	7	9	synaptic vesicle exocytosis	BP
GO:0005516	6.2E-06	29	118	calmodulin binding	MF
GO:0043198	6.3E-06	14	36	dendritic shaft	CC
GO:0034707	6.7E-06	13	32	chloride channel complex	CC
GO:0007267	6.7E-06	24	87	cell-cell signaling	BP
GO:1902476	8.4E-06	17	52	chloride transmembrane transport	BP
GO:0060291	9.5E-06	14	37	long-term synaptic potentiation	BP
GO:0034220	1.0E-05	30	127	ion transmembrane transport	BP
GO:0010700	1.1E-05	5	5	negative regulation of norepinephrine secretion	BP
GO:0006821	1.5E-05	14	39	chloride transport	BP
GO:0008420	1.6E-05	20	69	CTD phosphatase activity	MF
GO:0043565	1.7E-05	40	196	sequence-specific DNA binding	MF
GO:0042472	2.0E-05	12	30	inner ear morphogenesis	BP
GO:0005251	2.7E-05	10	22	delayed rectifier potassium channel activity	MF
GO:0004970	2.9E-05	7	11	ionotropic glutamate receptor activity	MF
GO:0030165	3.1E-05	20	73	PDZ domain binding	MF

GO:0009607	3.6E-05	7	11	response to biotic stimulus	BP
GO:1901379	3.6E-05	7	11	regulation of potassium ion transmembrane transport	BP
GO:0005615	3.7E-05	75	457	extracellular space	CC
GO:0005267	5.2E-05	17	58	potassium channel activity	MF
GO:0000158	5.3E-05	18	63	NA	NA
GO:0004723	5.3E-05	18	63	calcium-dependent protein serine/threonine phosphatase activity	MF
GO:0005963	5.3E-05	18	63	magnesium-dependent protein serine/threonine phosphatase complex	CC
GO:0015071	5.3E-05	18	63	NA	NA
GO:0017018	5.3E-05	18	63	myosin phosphatase activity	MF
GO:0017020	5.3E-05	18	63	myosin phosphatase regulator activity	MF
GO:0017023	5.3E-05	18	63	myosin phosphatase complex	CC
GO:0030357	5.3E-05	18	63	NA	NA
GO:0016594	5.4E-05	7	12	glycine binding	MF
GO:0030425	6.2E-05	43	227	dendrite	CC
GO:0005234	6.2E-05	7	12	extracellular-glutamate-gated ion channel activity	MF
GO:0007204	6.5E-05	15	48	positive regulation of cytosolic calcium ion concentration	BP
GO:0006810	6.6E-05	58	338	transport	BP
GO:0001601	6.7E-05	5	6	peptide YY receptor activity	MF
GO:0004983	6.7E-05	5	6	neuropeptide Y receptor activity	MF
GO:0007215	7.3E-05	6	9	glutamate receptor signaling pathway	BP
GO:0005245	7.9E-05	12	34	voltage-gated calcium channel activity	MF
GO:0004724	8.2E-05	18	65	magnesium-dependent protein serine/threonine phosphatase activity	MF
GO:0043005	8.9E-05	33	161	neuron projection	CC
GO:0043025	9.3E-05	48	266	neuronal cell body	CC
GO:0003700	9.5E-05	78	498	transcription factor activity, sequence-specific DNA binding	MF
GO:0001662	1.0E-04	12	34	behavioral fear response	BP
GO:0043195	1.1E-04	15	50	terminal bouton	CC

GO:0046010	1.1E-04	4	4	positive regulation of circadian sleep/wake cycle, non-REM sleep	BP
GO:0042312	1.2E-04	4	4	regulation of vasodilation	BP
GO:0090331	1.2E-04	4	4	negative regulation of platelet aggregation	BP
GO:0007399	1.2E-04	38	198	nervous system development	BP
GO:0032281	1.2E-04	9	21	AMPA glutamate receptor complex	CC
GO:0005261	1.3E-04	15	51	cation channel activity	MF
GO:0008597	1.3E-04	18	67	calcium-dependent protein serine/threonine phosphatase regulator activity	MF
GO:0016934	1.9E-04	5	7	extracellular-glycine-gated chloride channel activity	MF
GO:0060012	1.9E-04	5	7	synaptic transmission, glycinergic	BP
GO:0055085	1.9E-04	56	338	transmembrane transport	BP
GO:0043083	2.0E-04	5	7	synaptic cleft	CC
GO:0043647	2.0E-04	11	32	inositol phosphate metabolic process	BP
GO:0032809	2.0E-04	7	14	neuronal cell body membrane	CC
GO:0014050	2.1E-04	5	7	negative regulation of glutamate secretion	BP
GO:0043113	2.1E-04	7	14	receptor clustering	BP
GO:0034332	2.1E-04	11	32	adherens junction organization	BP
GO:0017075	2.1E-04	8	18	syntaxin-1 binding	MF
GO:0090102	2.2E-04	7	14	cochlea development	BP
GO:0006816	2.2E-04	17	65	calcium ion transport	BP
GO:0007189	2.2E-04	8	18	adenylate cyclase-activating G-protein coupled receptor signaling pathway	BP